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Hemisphere	Regions of interest	Phonology	Semantic	Sentence
Left hemisphere	Planum temporale (PT)	x		
	Rolandic sulcus (RolS)	**x**		
	Superior temporal gyrus (T1)	x		
	Supramarginalis gyrus (SMG)	**x**		
	Precentral gyrus (Prec)	**x**		
	Dorsal part of the pars triangularis of the inferior frontal gyrus (F3td)	x		
	Anterior fusiform gyrus (Fusa)		x	
	Opercular part of the inferior frontal gyrus (PrF3op)		x	
	Angular gyrus (AG)		**x**	
	Pars orbitaris of the left inferior frontal gyrus (F3orb)		**x**	
	Posterior part of the middle frontal gyrus (F2p)			**x**
	Posterior ending of the superior temporal gyrus (STSp)			**x**
	Posterior part of the middle temporal gyrus (T2p)			x
	Temporal pole (Pole)		**x**	**x**
	Lateral/middle part of T2 (T2ml)		**x**	**x**
	Dorsal part of the pars opercularis (F3opd)		**x**	**x**
	Ventral part of the pars triangularis (F3tv)		x	x
	Posterior part of the left inferior temporal gyrus (T3p)	**x**	**x**	
	Anterior part of T1 (T1a)	**x**	**x**	**x**
Right hemisphere	Anterior part of the middle frontal gyrus (F2antR)	x		
	Precentral gyrus (PrecR)	**x**		
	Anterior part of tT1 overlapping the Heschl’s gyrus (T1a/HeschlR)	x		
	Superior temporal gyrus (T1R)	x		
	Middle part of the STS (T2pR)			x
	Upper part of the pars opercularis of F3 (F3opdR)		x	x

Note: Bold phenotypes represents FCs with significant heritability after false discovery rate correction at $p<0.05$.

Phenotype	P value	h^2	SE	FDR P value
F3opd_SMG	3.8858e-16	0.143085	0.018056	1.16574e-13
AG_F3tv	9.992e-15	0.133426	0.0179	1.4988e-12
T2ml_STSp	5.0371e-13	0.123611	0.017817	5.0371e-11
STSp_T1R	7.5961e-13	0.123237	0.017888	5.6970750000000005e-11
Pole_STSp	1.0457e-12	0.12179	0.017839	6.2742e-11
Pole_T2ml	2.1435e-12	0.118543	0.017727	1.07175e-10
PT_T1	4.9045e-12	0.118866	0.017877	2.1019285714285713e-10
F2p_STSp	1.3203e-11	0.115631	0.017798	4.951125e-10
T2ml_SMG	2.7522e-11	0.11216	0.017705	8.2566e-10
T2ml_AG	2.6209e-11	0.114751	0.017844	8.2566e-10
AG_F2antR	3.8704e-11	0.113222	0.017836	1.0555636363636364e-09
PrF3op_SMG	5.1329e-11	0.114377	0.017961	1.283225e-09
F3tv_STSp	9.2723e-11	0.111882	0.01789	2.1397615384615387e-09
RolS_PrecR	2.2724e-10	0.110825	0.017981	4.869428571428571e-09
PrF3op_F3tv	9.4977e-10	0.106623	0.017983	1.8995399999999997e-08
F3tv_SMG	1.9262e-09	0.103729	0.017911	3.611625e-08
F2p_SMG	2.8369e-09	0.099209	0.017622	5.0062941176470594e-08
STSp_F3orb	3.7081e-09	0.101059	0.017802	6.180166666666667e-08
SMG_F2antR	1.317e-08	0.096583	0.017754	2.0794736842105263e-07
T1_F3tv	1.4007e-07	0.091235	0.017907	2.10105e-06
Fusa_AG	1.794e-07	0.0866	0.01758	2.562857142857143e-06
F3opd_F3td	1.8925e-07	0.089293	0.01785	2.580681818181818e-06
T2p_T3p	3.8638e-07	0.084325	0.017579	5.0397391304347825e-06
Prec_F3opd	4.8207e-07	0.084597	0.017645	6.025875e-06
T2ml_F3tv	5.6358e-07	0.083375	0.017642	6.76296e-06
SMG_F3orb	6.2518e-07	0.084135	0.017708	7.213615384615385e-06
Prec_SMG	6.5433e-07	0.083548	0.017631	7.270333333333333e-06
F3tv_F3orb	1.0351e-06	0.083137	0.017748	1.1090357142857142e-05
SMG_F3td	1.7991e-06	0.081891	0.017835	1.7991e-05
T2ml_F3td	1.7851e-06	0.080841	0.01772	1.7991e-05
AG_T1a	2.5503e-06	0.078469	0.017596	2.4680322580645163e-05
F3opd_T2ml	2.6626e-06	0.078433	0.017624	2.4961875e-05
AG_SMG	2.877e-06	0.080434	0.017847	2.538529411764706e-05
F3tv_F2antR	2.8001e-06	0.078039	0.017578	2.538529411764706e-05
Pole_T1a	3.0043e-06	0.077865	0.017622	2.5751142857142858e-05
T1_PrF3op	4.7379e-06	0.076509	0.017603	3.94825e-05
AG_STSp	4.9848e-06	0.076665	0.017643	4.0417297297297304e-05
F3opd_STSp	5.2766e-06	0.077101	0.017715	4.165736842105263e-05
PrF3op_T3p	6.4761e-06	0.074129	0.017521	4.9816153846153846e-05
PrF3op_F2antR	7.0454e-06	0.074811	0.017603	5.2840500000000003e-05
T2ml_F3orb	9.0511e-06	0.07515	0.017779	6.622756097560976e-05
T1a_STSp	1.067e-05	0.072739	0.017536	7.621428571428571e-05
F3opdR_F2antR	1.1282e-05	0.073398	0.017628	7.871162790697674e-05
Pole_F3opd	1.5498e-05	0.073106	0.017736	0.00010566818181818181
AG_T3p	1.8595e-05	0.070762	0.01753	0.00012396666666666668
STSp_T2pR	2.3762e-05	0.070433	0.017629	0.0001549695652173913
F3opd_PrF3op	3.2513e-05	0.069213	0.017614	0.00020752978723404255

T1_T1a/HeschlR	3.6045e-05	0.06916	0.017661	0.00022528124999999998
Prec_AG	4.1421e-05	0.06933	0.017751	0.00025359795918367345
F3tv_T2pR	4.251e-05	0.067067	0.017501	0.0002541588235294118
T1a_T1a/HeschlR	4.3207e-05	0.068425	0.017662	0.0002541588235294118
PrF3op_AG	4.5151e-05	0.067181	0.01758	0.00026048653846153847
T1_T1a	5.0854e-05	0.067867	0.01767	0.0002878528301886792
Prec_F3tv_RolOp	5.5864e-05	0.066566	0.017584	0.00031035555555555556
Pole_AG	5.7086e-05	0.065955	0.017525	0.0003113781818181818
F3opd_AG	6.102e-05	0.064642	0.017401	0.00032689285714285714
F3tv_F3opdR	6.2863e-05	0.065788	0.017518	0.0003308578947368421
F3orb_F2antR	7.8212e-05	0.066301	0.017712	0.0003846491803278689
PT_T1a/HeschlR	7.7413e-05	0.066029	0.017663	0.0003846491803278689
SMG_T3p	7.7787e-05	0.066515	0.017725	0.0003846491803278689
T1a_SMG	7.5932e-05	0.065428	0.017581	0.0003846491803278689
Prec_T1	8.2673e-05	0.065155	0.017575	0.00040003064516129033
Prec_T2p	8.4773e-05	0.064923	0.017579	0.0004036809523809524
PrF3op_STSp	9.1453e-05	0.064689	0.017576	0.0004286859375
T2ml_PrF3op	0.00013238	0.064308	0.01774	0.0006109846153846153
Fusa_T2p	0.00013858	0.063197	0.017621	0.0006299090909090909
F3opd_T3p	0.00017382	0.062951	0.017724	0.0007782985074626865
T2ml_T1R	0.00019324	0.061051	0.017536	0.000852529411764706
F2p_F3tv	0.00020405	0.060978	0.017568	0.0008836714285714286
T2ml_F3opdR	0.00020619	0.062341	0.017732	0.0008836714285714286
F3opd_F2p	0.0002127	0.059706	0.017397	0.0008987323943661971
T2ml_T1a	0.00021766	0.062438	0.017782	0.0009069166666666668
Pole_T1R	0.0002334	0.061741	0.017731	0.0009591780821917809
SMG_T2pR	0.00024161	0.059208	0.017447	0.00097036
AG_F3orb	0.00024259	0.060372	0.017564	0.00097036
AG_T2p	0.00026321	0.059726	0.017516	0.0010389868421052631
STSp_F3opdR	0.00061509	0.055036	0.017452	0.0023964545454545454
F2p_T2ml	0.00069194	0.05667	0.017744	0.0026613076923076924
T2p_RolS	0.00070926	0.05567	0.017608	0.002693392405063291
T3p_F3orb	0.00072091	0.054682	0.017478	0.0027034125
T1a/HeschlR_T1R	0.00081139	0.055158	0.017635	0.0030051481481481483
F3tv_RolS	0.0010102	0.054803	0.017743	0.0036513253012048193
F3orb_T2pR	0.0010072	0.051674	0.017288	0.0036513253012048193
T2ml_T2pR	0.0010751	0.0531	0.017536	0.0038396428571428574
F3tv_T1R	0.0011414	0.052596	0.017508	0.004028470588235294
F3td_T3p	0.001177	0.053444	0.017665	0.004072758620689655
T2p_F3opdR	0.0011811	0.050276	0.017205	0.004072758620689655
F3opd_F3orb	0.0013438	0.051631	0.01748	0.004581136363636364
F2p_PrF3op	0.0014604	0.051168	0.017478	0.004922696629213482
F3tv_T2p	0.0015213	0.051726	0.017601	0.005015274725274725
T1_RolS	0.0015125	0.051945	0.01762	0.005015274725274725
Prec_F3opdR	0.0015897	0.051569	0.017608	0.005183804347826087
T1_AG	0.001621	0.050772	0.017481	0.005229032258064516
STSp_F3td	0.0017185	0.051715	0.017699	0.0053703125
F3tv_T1a/HeschlR	0.0016959	0.051083	0.017605	0.0053703125
STSp_F2antR	0.0017051	0.050964	0.017571	0.0053703125
F3tv_T3p	0.0021128	0.049782	0.017543	0.006534432989690722

Fusa_T3p	0.0023718	0.04862	0.017463	0.007260612244897958
Prec_Fusa	0.002608	0.049563	0.017718	0.007903030303030302
F3opdR_T2pR	0.0029553	0.046875	0.017387	0.0088659
F3tv_RolOp_F3td	0.0031344	0.047305	0.017509	0.009218823529411765
F3opdR_T1R	0.0031071	0.047125	0.017465	0.009218823529411765
SMG_F3opdR	0.0034507	0.046359	0.017414	0.010050582524271845
F3orb_F3opdR	0.0038804	0.043742	0.017142	0.011193461538461538
Fusa_STSp	0.0041801	0.046207	0.017613	0.011830471698113207
T1_T1R	0.0041501	0.045576	0.017464	0.011830471698113207
F3td_F2antR	0.0046048	0.043687	0.017254	0.012910654205607476
PrF3op_T1R	0.0046951	0.045926	0.017672	0.013041944444444443
F2antR_T2pR	0.0048831	0.045285	0.017595	0.013439724770642201
T1_F3orb	0.0049719	0.044522	0.017494	0.01355972727272727
Prec_RolS	0.0056496	0.044567	0.01762	0.01526918918918919
F2p_AG	0.0059333	0.044539	0.017677	0.015892767857142855
T1a_F3orb	0.0060002	0.044457	0.017681	0.015929734513274337
T1a_T1R	0.0065148	0.042695	0.017421	0.017144210526315793
PT_T1R	0.0068357	0.042334	0.017404	0.017832260869565218
T2pR_PrecR	0.0078292	0.041986	0.01751	0.020247931034482757
Pole_F2p	0.0081415	0.041209	0.017393	0.020875641025641024
F3opd_F2antR	0.0083959	0.041398	0.017466	0.02134550847457627
Prec_F3td	0.0091195	0.041614	0.017623	0.022990336134453778
SMG_T2p	0.0097762	0.040337	0.01747	0.0244405
PT_AG	0.0099548	0.040569	0.017526	0.024681322314049587
PrF3op_F3opdR	0.010361	0.040279	0.017516	0.025477868852459017
PrF3op_F3td	0.011451	0.039057	0.017414	0.027704032258064514
Fusa_T1a	0.011411	0.039653	0.017505	0.027704032258064514
T2pR_T1R	0.013512	0.037623	0.01734	0.0324288
T2p_F2antR	0.013944	0.0387	0.017595	0.0332
T2ml_T2p	0.014149	0.036146	0.01709	0.03342283464566929
T2ml_T1	0.014456	0.037889	0.017498	0.03388125
F2antR_T1a/HeschlR	0.014975	0.038576	0.017672	0.03482558139534884
F3opd_T1R	0.015998	0.03773	0.017587	0.03691846153846153
F3td_T1R	0.016956	0.03663	0.017451	0.03883053435114503
F3opd_T1	0.017388	0.037128	0.017578	0.03922105263157895
F3opd_T1a	0.017311	0.036128	0.017353	0.03922105263157895
F2p_T2p	0.017929	0.036495	0.017494	0.04013955223880597
Prec_F2antR	0.0185	0.035961	0.017444	0.04111111111111111
Fusa_SMG	0.019285	0.035685	0.017409	0.042407299270072994
AG_PrecR	0.019366	0.036554	0.01762	0.042407299270072994
SMG_T1R	0.019518	0.035105	0.017327	0.042430434782608696
F2antR_T1R	0.020186	0.035751	0.017503	0.04356690647482014
F2p_T2pR	0.021678	0.035227	0.017513	0.04645285714285714
T1_SMG	0.022995	0.034586	0.017456	0.04892553191489362
F2p_T1	0.023312	0.034744	0.017515	0.04925070422535211
STSp_SMG	0.025033	0.034228	0.01752	0.052516783216783214
F2p_T1a	0.025393	0.034026	0.017483	0.052902083333333336
F3tv_T1a	0.025701	0.033396	0.017344	0.053174482758620696
Prec_T3p	0.026262	0.033914	0.017513	0.053963013698630144
T2ml_F2antR	0.028099	0.032696	0.017332	0.057344897959183676

Pole_F3orb	0.029043	0.032337	0.017317	0.05887094594594595
F3opd_T2pR	0.032226	0.032059	0.017455	0.06488456375838926
Prec_F3orb	0.036763	0.030209	0.01723	0.07347417218543047
PrF3op_T2pR	0.036982	0.030994	0.017438	0.07347417218543047
RolS_F3opdR	0.037675	0.030696	0.017406	0.07435855263157895
PT_RolS	0.03822	0.030529	0.017403	0.07467290322580644
AG_T1R	0.038581	0.030888	0.017498	0.07467290322580644
T1a_RolS	0.038461	0.031088	0.017548	0.07467290322580644
PrF3op_T2p	0.040816	0.030008	0.017388	0.0784923076923077
Pole_PT	0.041623	0.028871	0.017104	0.0795343949044586
PT_F2antR	0.04302	0.029028	0.017209	0.08168354430379747
T1_PrecR	0.043377	0.02975	0.017435	0.0818433962264151
Pole_PrF3op	0.044381	0.029334	0.017387	0.083214375
RolS_F2antR	0.044847	0.029525	0.017457	0.08356583850931676
T1_T2p	0.047643	0.029116	0.017487	0.08822777777777778
Pole_T1	0.048333	0.028583	0.017357	0.08895644171779142
PrF3op_PrecR	0.05013	0.028004	0.017274	0.09170121951219513
F3opd_RolS	0.051655	0.027777	0.017282	0.09391818181818182
Pole_F3tv	0.052115	0.028232	0.017443	0.09418373493975904
T1_T2pR	0.054995	0.027845	0.017463	0.0987934131736527
Pole_T2p	0.058384	0.027374	0.017463	0.10425714285714285
F2p_F2antR	0.059932	0.02652	0.017274	0.10638816568047336
T1_F2antR	0.061803	0.026279	0.017294	0.10897894736842105
PT_T2ml	0.062118	0.027032	0.017531	0.10897894736842105
F3tv_PrecR	0.06389	0.026512	0.017453	0.1101551724137931
T2ml_T1a/HeschlR	0.063623	0.026239	0.017348	0.1101551724137931
AG_F3td	0.063505	0.026448	0.017406	0.1101551724137931
T2p_T1R	0.068555	0.025693	0.017387	0.11752285714285715
PT_T2pR	0.070362	0.025275	0.017332	0.11993522727272726
F3opd_F3tv	0.072431	0.025427	0.017446	0.12276440677966101
F2p_T1R	0.074494	0.02451	0.017234	0.12555168539325842
AG_RolS	0.076881	0.024695	0.017383	0.12885083798882682
STSp_T3p	0.079086	0.024867	0.017534	0.13108176795580112
T2ml_T3p	0.079059	0.024715	0.017479	0.13108176795580112
F2p_F3opdR	0.079731	0.024479	0.017426	0.13142472527472526
T1_STSp	0.08256	0.024289	0.017475	0.13534426229508195
T3p_T2pR	0.084009	0.023893	0.017395	0.13697119565217392
Fusa_PrF3op	0.087616	0.023487	0.017379	0.14208
STSp_T2p	0.088833	0.023142	0.017311	0.14322032085561498
T1_Fusa	0.089274	0.023686	0.017521	0.14322032085561498
T3p_RolS	0.092383	0.02283	0.017327	0.14551884816753927
AG_T2pR	0.092647	0.022977	0.017401	0.14551884816753927
Prec_PrF3op	0.091683	0.022546	0.017192	0.14551884816753927
Fusa_T1a/HeschlR	0.091747	0.023454	0.017538	0.14551884816753927
T3p_F3opdR	0.093837	0.022158	0.017159	0.14662031250000002
Prec_STSp	0.096469	0.022214	0.017256	0.14995181347150258
T2ml_RolS	0.098784	0.022648	0.017501	0.15275876288659793
T1a_F2antR	0.10306	0.021924	0.017386	0.15855384615384616
SMG_PrecR	0.10434	0.021373	0.017227	0.15970408163265307
Prec_T1a	0.10545	0.02149	0.017311	0.15977272727272726

PT_STSp	0.10512	0.022064	0.017525	0.15977272727272726
PT_T2p	0.10636	0.021461	0.01733	0.159915
T3p_T1R	0.10661	0.021009	0.017171	0.159915
T1_F3opdR	0.11208	0.020925	0.017331	0.16728358208955224
F3td_T2pR	0.1139	0.020993	0.017411	0.1674292682926829 3
PT_T1a	0.11293	0.021292	0.017501	0.16742926829268293
F3opdR_PrecR	0.11428	0.020773	0.017345	0.16742926829268293
T1a_F3opdR	0.11441	0.020961	0.017415	0.16742926829268293
Fusa_F3tv	0.1192	0.020265	0.017302	0.1711004784688995
F3orb_T1R	0.11885	0.020809	0.017515	0.1711004784688995
PT_F3opd	0.11843	0.020148	0.017232	0.1711004784688995
PrF3op_F3orb	0.11795	0.0207	0.017438	0.1711004784688995
F3orb_RolS	0.12439	0.020042	0.017392	0.17766824644549764
Fusa_F2antR	0.12496	0.019988	0.017388	0.17766824644549764
F3opd_F3opdR	0.12676	0.020131	0.017513	0.17853521126760563
F2p_T3p	0.12666	0.019672	0.017313	0.17853521126760563
Fusa_T1R	0.12763	0.019715	0.017365	0.17892056074766352
F3td_F3orb	0.12887	0.019991	0.017526	0.1798186046511628
RolS_T1R	0.13014	0.019467	0.017347	0.18075
F3td_F3opdR	0.13104	0.019771	0.017521	0.18116129032258063
F2p_F3orb	0.13208	0.019339	0.017359	0.18176146788990827
Fusa_RolS	0.13324	0.019122	0.017315	0.18252054794520547
F3orb_T1a/HeschlR	0.13475	0.01877	0.017207	0.18375
T1a_T2p	0.13873	0.018545	0.017234	0.1883212669683258
T1R_PrecR	0.14237	0.0183	0.01725	0.19239189189189188
Prec_T1a/HeschlR	0.14977	0.018223	0.017472	0.20148430493273542
Pole_SMG	0.15318	0.017792	0.017395	0.20333628318584074
SMG_T1a/HeschlR	0.15274	0.017593	0.017295	0.20333628318584074
Prec_T2ml	0.152	0.017788	0.017344	0.20333628318584074
Pole_T1a/HeschlR	0.15539	0.017813	0.017475	0.2053612334801762
RolS_T1a/HeschlR	0.15729	0.01766	0.017464	0.2069605263157895
T2p_F3orb	0.16806	0.016826	0.017432	0.2201659388646288
T2p_T2pR	0.17132	0.016129	0.017191	0.22236206896551725
T3p_F2antR	0.17166	0.016568	0.01742	0.22236206896551725
F3opd_T2p	0.17196	0.016526	0.017408	0.22236206896551725
Pole_RolS	0.17709	0.015945	0.017294	0.2280128755364807
F2antR_PrecR	0.19887	0.014783	0.017414	0.25496153846153846
STSp_T1a/HeschlR	0.2346	0.012696	0.017425	0.2994893617021277
STSp_RolS	0.2373	0.012498	0.017396	0.3015189873417722
Prec_PrecR	0.2382	0.012511	0.017438	0.3015189873417722
Fusa_F3orb	0.2413	0.012364	0.017457	0.3041596638655462
Pole_T2pR	0.25232	0.011454	0.017252	0.3167196652719665
T3p_PrecR	0.27593	0.010279	0.017287	0.3449125
Fusa_F3td	0.28163	0.010029	0.017322	0.35057676348547717
T2pR_T1a/HeschlR	0.2861	0.009608	0.017158	0.35466942148760333
T1a_T3p	0.28927	0.009551	0.017243	0.355672131147541
Pole_PrecR	0.28928	0.009771	0.017436	0.355672131147541
Pole_F3td	0.30359	0.00873	0.017136	0.3717428571428572
T2p_F3td	0.30575	0.008997	0.017488	0.3728658536585366
Fusa_F3opdR	0.30754	0.008559	0.017157	0.37353036437246956

Pole_Fusa	0.3287	0.007569	0.017168	0.3976209677419355
T1_T3p	0.33369	0.007289	0.01711	0.40203614457831327
Fusa_PrecR	0.34545	0.006847	0.017242	0.41453999999999996
Pole_F2antR	0.36017	0.006288	0.0174	0.4304820717131474
Prec_Pole	0.36367	0.005992	0.017216	0.4312292490118577
PrF3op_T1a	0.36224	0.005962	0.017083	0.4312292490118577
PT_SMG	0.36966	0.005787	0.017315	0.43660629921259836
T2p_T1a/HeschlR	0.39113	0.004832	0.017353	0.4601529411764706
PT_F3tv	0.42601	0.003137	0.017011	0.49923046875
Pole_F3opdR	0.5	1,00E-06	0.017279	0.5
STSp_PrecR	0.5	1,00E-06	0.017026	0.5
T1a_PrecR	0.5	1,00E-06	0.017425	0.5
F2p_T1a/HeschlR	0.5	1,00E-06	0.017331	0.5
Fusa_T2pR	0.44619	0.002307	0.017122	0.5
F3td_PrecR	0.5	1,00E-06	0.017424	0.5
T2ml_Fusa	0.5	1,00E-06	0.017395	0.5
PT_F2p	0.5	1,00E-06	0.017399	0.5
PT_F3opdR	0.5	1,00E-06	0.017343	0.5
PT_F3orb	0.5	1,00E-06	0.017166	0.5
F3td_RolS	0.5	1,00E-06	0.01708	0.5
Prec_T2pR	0.4498	0.002227	0.017419	0.5
PrF3op_RolS	0.5	1,00E-06	0.017272	0.5
F3orb_PrecR	0.5	1,00E-06	0.017381	0.5
AG_F3opdR	0.5	1,00E-06	0.017246	0.5
T1a_T2pR	0.46503	0.001511	0.017201	0.5
F2p_PrecR	0.5	1,00E-06	0.017261	0.5
PrF3op_T1a/HeschlR	0.5	1,00E-06	0.017359	0.5
F2p_RolS	0.5	1,00E-06	0.017335	0.5
F2p_Fusa	0.5	1,00E-06	0.017206	0.5
F3opdR_T1a/HeschlR	0.43467	0.002787	0.017075	0.5
T1a_F3td	0.5	1,00E-06	0.01708	0.5
Prec_T1R	0.49947	2.2e-05	0.016903	0.5
T2p_PrecR	0.5	1,00E-06	0.017217	0.5
T1a/HeschlR_PrecR	0.5	1,00E-06	0.016987	0.5
T2ml_PrecR	0.5	1,00E-06	0.017292	0.5
F3opd_T1a/HeschlR	0.5	1,00E-06	0.017285	0.5
PT_Fusa	0.5	1,00E-06	0.01736	0.5
SMG_RolS	0.5	1,00E-06	0.0173	0.5
Pole_T3p	0.5	1,00E-06	0.017169	0.5
AG_T1a/HeschlR	0.49923	3.3e-05	0.017235	0.5
F3opd_PrecR	0.5	1,00E-06	0.017067	0.5
PT_T3p	0.5	1,00E-06	0.017343	0.5
PT_F3td	0.5	1,00E-06	0.017642	0.5
RolS_T2pR	0.5	1,00E-06	0.017092	0.5
PT_PrecR	0.5	1,00E-06	0.017182	0.5
T1_F3td	0.5	1,00E-06	0.017244	0.5
F2p_F3td	0.5	1,00E-06	0.017338	0.5
Prec_F2p	0.5	1,00E-06	0.017259	0.5
T3p_T1a/HeschlR	0.5	1,00E-06	0.017368	0.5
F3opd_Fusa	0.5	1,00E-06	0.017196	0.5

PT_PrF3op	0.5	1,00E-06	0.017079	0.5
Prec_PT	0.5	1,00E-06	0.017299	0.5
F3td_T1a/HeschlR	0.5	1,00E-06	0.017407	0.5

CHR	SNP	BP	A1	A2	P value	Z-stat	N
2	rs2717046	58041936	C	T	7.509071256533833e-14	7.478648684332633	31894.0
2	rs2717066	58029645	C	A	9.79095283479027e-14	7.443692134154676	32006.0
2	rs11695135	57998040	A	C	1.402962952252713e-13	7.396048960718104	31964.0
2	2:58029698_GA_G	58029698	GA	G	2.2843870492019533e-13	7.331001736579746	31575.0
2	rs762523673	57944587	TA	T	2.300842238678481e-13	7.330039897642196	30496.0
2	rs2717079	58065936	T	A	3.5951928343580125e-13	7.269988057019218	31914.0
2	rs10204616	57980955	A	T	3.762865538931088e-13	7.263827956399022	32036.0
2	rs13025126	57956088	G	A	4.756659718561889e-13	7.23207596792804	31768.0
2	rs2125925	57971343	A	G	4.972377109334335e-13	7.226051919294318	32030.0
2	rs11679364	57975524	T	G	5.601130650623536e-13	7.209855442848077	32030.0
2	rs2947349	58059803	C	A	8.159166509241092e-13	7.158454490341638	31899.0
2	rs11125729	57975170	T	C	8.252758119625963e-13	7.156890471883142	32030.0
2	rs3886275	57973344	A	C	8.316935801960934e-13	7.155828022329335	32028.0
2	rs13002041	57972834	C	A	8.382083902838332e-13	7.1547577063762775	32024.0
2	rs7567497	57974429	A	T	8.724965022511116e-13	7.149255738822888	32032.0
2	rs2290867	57952870	A	C	9.22657307832851e-13	7.141577646704316	31821.0
2	rs12990792	57993568	G	A	9.901417374212297e-13	7.1318702752907575	32058.0
2	rs717817	57973452	C	T	9.946420124661571e-13	7.131246228859893	32027.0
2	rs70954867	58004577	A	AT	1.0071693047278785e-12	7.129523571404032	31910.0
2	rs7588492	57995852	A	G	1.050504443479496e-12	7.123722502441468	32040.0
2	rs13402331	57947440	T	C	1.1182120128750344e-12	7.1151129766265475	31800.0
2	rs10186791	57957572	G	A	1.2362338995419529e-12	7.1012612955872045	31848.0
2	rs10496078	57993643	G	A	1.3432180603233644e-12	7.089783666725836	31970.0
2	2:58008036_CT_C	58008036	CT	C	1.344804532198401e-12	7.089620303649722	30524.0
2	rs6709720	57967563	A	G	1.3571681570540057e-12	7.088353630702332	31972.0
2	rs13418015	57948635	A	G	1.44687051685477e-12	7.079488934648515	31798.0
2	rs1568452	58012833	C	T	1.4806833531893423e-12	7.076286735313048	32002.0
2	rs747713243	57944289	GTTGA	G	1.5320066842750308e-12	7.0715607847089315	30732.0
2	rs1402399	58045395	T	C	1.7031534764195436e-12	7.056853227586067	32019.0
2	rs10496079	57997136	G	C	1.7578655315805634e-12	7.0524563609521564	32094.0
2	rs754784696	57995420	CACTGCAACCTCTGCCT	C	1.8011464853968762e-12	7.04907222631785	31558.0
2	rs6756221	58008155	T	C	1.8756343501621482e-12	7.043430605233335	32065.0
2	2:58025739_TA_T	58025739	TA	T	1.98199304258768e-12	7.035744872113369	32067.0
2	rs2717067	58095252	G	C	2.1869505778929644e-12	7.022012440295446	31937.0
2	rs2953441	58041482	C	T	2.2064663280911888e-12	7.020771386097072	32012.0
2	rs1474215	58032029	C	G	2.263595032794922e-12	7.017199373613589	32115.0
2	rs2717018	58035491	C	T	2.3418209565171767e-12	7.012449084455942	32030.0
2	rs2683629	58037369	A	G	2.4374518328118458e-12	7.0068489382227	32020.0
2	rs2953439	58039357	T	C	2.441604914322157e-12	7.006610643753325	32018.0
2	rs4671319	57950346	G	A	2.450050110564384e-12	7.006127301054232	31806.0
2	rs12997222	57987201	C	G	2.550559138505833e-12	7.000497099624357	32032.0
2	rs2717052	58047263	C	A	2.6097337244071257e-12	6.997283236956407	32019.0
2	rs2717071	58030962	G	A	2.632890120618841e-12	6.996044995013306	32118.0
2	rs7598169	58040729	C	T	2.6615181469845307e-12	6.994528849317216	32007.0
2	rs2717075	58032530	G	C	2.8076048141908846e-12	6.987032870388254	32107.0
2	rs2717048	58025937	C	T	2.8488681332895767e-12	6.98498480513149	32133.0
2	rs2683630	58058069	C	G	2.8702760734587363e-12	6.983933675562249	32001.0
2	rs2125924	57943567	T	C	2.8976660739236828e-12	6.982599981614809	31789.0
2	rs2683628	58036044	A	G	2.901616570869728e-12	6.982408641977428	32034.0
2	rs2683619	58032759	C	T	3.08752837905613e-12	6.973681416423547	32077.0
2	rs2717055	58044220	G	A	3.1786612528173614e-12	6.969589932933111	32013.0
2	rs2683621	58046995	A	G	3.2977151430537547e-12	6.964414853888366	32009.0

2	rs2717054	58046683	G	A	3.3717263583317575e-12	6.961289267349797	32015.0
2	rs1402398	58042241	G	A	3.4665385475904886e-12	6.957382092382258	32015.0
2	rs2683614	58026312	G	A	3.4668157932338197e-12	6.9573708215549805	32136.0
2	rs2717053	58047101	G	C	3.474504213900687e-12	6.957058616863455	32011.0
2	rs7561842	57995586	C	T	3.4937292174916584e-12	6.956280899567088	32052.0
2	rs6545665	58023218	G	A	3.803358069783314e-12	6.9443021077191185	32137.0
2	rs10865304	58002818	G	T	3.9390187567150486e-12	6.939352238613156	32129.0
2	rs11676055	58017224	C	T	4.018724989299623e-12	6.936521363730384	32142.0
2	rs2683616	58035555	G	A	4.173080467304795e-12	6.931192391601898	32033.0
2	rs13026612	58014723	C	T	4.2019843160646536e-12	6.930216034061496	32153.0
2	rs13026830	58014831	C	T	4.399808385818316e-12	6.923705266978315	32186.0
2	rs954593	58027337	C	T	4.570473597500106e-12	6.918314931281322	32123.0
2	2:57944589_TA_T	57944589	TA	T	4.61693865900516e-12	6.916881530867037	31063.0
2	rs4296411	58008872	A	C	4.6872699531209335e-12	6.914738561494605	32129.0
2	rs2683620	58032553	A	T	4.75293794694769e-12	6.912765947786868	32094.0
2	rs10166481	58016412	G	A	4.799590883779733e-12	6.911380697018104	32145.0
2	rs6545664	58023134	C	T	4.8723988156808785e-12	6.9092449893533825	32126.0
2	rs12713358	58007475	A	T	4.947716119983998e-12	6.90706834328845	32123.0
2	rs6737913	58007759	G	A	5.122247456164546e-12	6.902146760628173	32129.0
2	rs12991325	58016879	C	T	5.2058935066123285e-12	6.899846023034012	32129.0
2	rs11898858	58006624	G	A	5.2430655488259674e-12	6.898835189190768	32129.0
2	rs6545663	58023009	A	T	5.4461797015394634e-12	6.893432945788772	32134.0
2	rs1568450	58011697	A	G	5.4533759225226845e-12	6.893245189793202	32140.0
2	rs6761347	58010040	T	A	5.513784004873107e-12	6.8916785957517455	32136.0
2	rs2683615	58027493	C	A	5.77640683131602e-12	6.885057819863727	32134.0
2	rs1589407	58019903	T	C	6.114830298944072e-12	6.876948267629175	32133.0
2	rs6730037	58005792	G	A	6.382510026711893e-12	6.870839661209673	32127.0
2	rs10195687	57956533	T	G	6.637012260509859e-12	6.865260294841688	30956.0
2	rs2090793	58021528	G	A	6.831652151435925e-12	6.861132997671249	32131.0
2	2:57958740_AT_A	57958740	AT	A	7.2726263925100866e-12	6.852193157094956	30959.0
2	rs4672223	58021882	C	A	7.382042436312638e-12	6.850057279921237	32135.0
2	rs13016665	57995348	C	A	7.585676138068826e-12	6.846163532231407	31377.0
2	rs13032423	57992112	G	A	7.590666038505336e-12	6.8460694097598696	32026.0
2	rs2717076	58061127	C	T	8.978237879762524e-12	6.8219988607527675	31983.0
2	rs34035400	57979248	T	TC	1.0663460561044457e-11	6.797250487503264	31344.0
2	rs4671320	57955644	C	G	1.0827401565139252e-11	6.795051271028208	30905.0
2	rs6720888	57945522	A	G	1.1898896428705287e-11	6.781433842511929	31719.0
2	rs10496076	57942987	T	C	1.2500983103621435e-11	6.774300234350301	31700.0
2	2:58006919_GA_G	58006919	GA	G	1.6801244888995532e-11	6.731422385463492	31353.0
2	rs10196378	57951208	T	G	1.7949525851836266e-11	6.7217983441656735	31734.0
2	rs2678870	58153375	T	A	2.205387733850836e-11	6.691735800270817	31457.0
2	rs1460255	57978858	T	C	2.443785238474017e-11	6.676702377103402	32004.0
2	rs2678869	58153374	A	C	2.536859778891077e-11	6.67121977566787	31449.0
2	rs2678900	58177683	T	G	3.3523663684299326e-11	6.6301981081747074	31911.0
2	rs200493119	58154132	C	CG	3.550819683793183e-11	6.621703825229244	31990.0
2	rs540927767	58154133	T	TG	3.550819683793183e-11	6.621703825229244	31990.0
2	rs2139054	58156583	A	C	3.7083772274730795e-11	6.615284549858058	32146.0
2	rs2678871	58153602	G	A	3.722021311095729e-11	6.614741275750567	31315.0
2	rs2717002	58142647	T	G	3.8680837122187476e-11	6.609044528366264	32151.0
2	rs2683618	58033361	A	G	4.195036041680869e-11	6.5970202077931965	32001.0
2	rs2717068	58094873	A	C	4.204053324410885e-11	6.596701733804897	32186.0
2	rs908731	58135010	C	G	4.568074311588503e-11	6.58437351047073	32134.0
2	rs2312141	58155358	A	T	4.671864965451051e-11	6.58103439066585	32146.0
2	rs908730	58135011	G	A	4.771220096525593e-11	6.577905275304311	31892.0

2	rs2717004	58143854	C	A	4.954565724890802e-11	6.572294757013515	32130.0
2	rs2717015	58155253	T	C	5.062431743716292e-11	6.569088128209432	32147.0
2	rs2717003	58143438	A	G	5.202366244763265e-11	6.565026348535002	32122.0
2	rs7557715	57973818	C	T	5.4037119689802747e-11	6.559365741753241	32002.0
2	rs2678873	58154601	G	A	5.4757340303383944e-11	6.5573909082168536	32144.0
2	rs2465804	58148180	G	A	5.5002343775255674e-11	6.556724900470686	32151.0
2	rs2678880	58158283	C	T	5.6194189905930995e-11	6.553525877227467	32155.0
2	rs2678881	58140977	G	A	5.983692333840129e-11	6.544144492310271	32162.0
2	rs2717007	58149116	G	A	6.225621735678367e-11	6.538217804341795	32152.0
2	rs2678893	58167143	A	G	6.498793297339463e-11	6.531790701488059	31518.0
2	rs2678915	58119574	C	T	6.677197742802412e-11	6.527734368726225	32084.0
2	rs2678905	58135872	A	G	6.730540209240214e-11	6.52654210664636	32127.0
2	rs1040224	58139865	G	C	7.00071125732075e-11	6.520641962172031	32148.0
2	rs2678901	58138651	A	G	7.006641984620112e-11	6.520514956828962	32144.0
2	rs2678886	58161221	A	G	7.212038918647845e-11	6.516180074849907	32157.0
2	rs1040225	58139593	A	G	7.248312883468831e-11	6.515427080276327	32144.0
2	rs11410659	58145483	A	AT	7.255176124644291e-11	6.515285024095081	32127.0
2	rs2717010	58151817	A	G	7.264672457106099e-11	6.515088684442151	32145.0
2	rs2678904	58137755	G	T	7.495260467269011e-11	6.510396686020832	32186.0
2	rs2678903	58137930	A	G	7.62883407826805e-11	6.507742891087599	32156.0
2	rs2717024	58161397	C	G	7.858665339407565e-11	6.503281278830475	32159.0
2	rs2678890	58164435	C	T	7.904095685540438e-11	6.50241448175816	32186.0
2	2:57971694_GAAAA_G	57971694	GAAAA	G	7.938673861258053e-11	6.5017579997209465	27885.0
2	rs2717011	58152075	T	C	8.177266487209052e-11	6.4973029991758775	32118.0
2	rs2459982	58150941	A	C	8.241143924385449e-11	6.49613184725004	32151.0
2	rs2717014	58154249	T	C	8.288372022848787e-11	6.495271643788983	32157.0
2	rs2717023	58161355	C	T	8.433023290534931e-11	6.492666503191044	32160.0
2	rs2717001	58137618	C	T	8.982133723183451e-11	6.483159693547808	32142.0
2	rs2678892	58167140	G	A	9.015062741680626e-11	6.4826077999802765	31772.0
2	rs2717022	58160639	G	C	9.23177405796327e-11	6.479024130374065	32155.0
2	rs10694743	58149555	G	GCTAA	9.313760211575412e-11	6.477689763362997	31917.0
2	rs2678887	58161752	C	A	9.377967288290532e-11	6.476652754281639	32164.0
2	rs2678888	58162191	A	G	9.540620104491484e-11	6.474056497863742	32161.0
2	rs2678879	58158152	A	G	9.623318398756093e-11	6.472753019968161	32148.0
2	rs2678883	58159670	A	G	9.727648543454776e-11	6.471124118938718	32165.0
2	rs2717019	58159473	T	G	9.989130451977444e-11	6.467115492663632	32164.0
2	rs2717033	58166769	T	C	1.003161196388558e-10	6.466473937085437	32092.0
2	2:57971686_AAAAG_A	57971686	AAAAG	A	1.0730299105885727e-10	6.456287051652602	28278.0
2	rs10192098	57971698	A	G	1.137357566425249e-10	6.447465891876822	28628.0
2	2:57944288_AGTTG_A	57944288	AGTTG	A	1.1380448180828348e-10	6.447374308120757	28211.0
2	rs1568253	58170004	T	C	1.2171348690034406e-10	6.437180098060972	32094.0
2	rs112345168	58007905	T	A	1.2360602349898663e-10	6.434836852733957	32035.0
2	rs59098844	58044533	G	C	1.2549593764805905e-10	6.432531590796591	31989.0
2	rs1568254	58170161	C	A	1.308890180370703e-10	6.426135177831644	32060.0
2	rs2678906	58134048	T	A	1.321051669433591e-10	6.424728405042805	32117.0
2	rs2678889	58164223	A	G	1.3370833475592232e-10	6.422893167492071	32172.0
2	rs2176546	58156772	G	C	1.4422191637712941e-10	6.411365551206032	31391.0
2	rs2683634	58113995	T	C	1.518528093372511e-10	6.403502056206875	32092.0
2	rs2678891	58166643	T	G	1.5421120136638274e-10	6.40114977658657	32170.0
2	rs2678882	58159362	T	A	1.571753160248631e-10	6.398242706218817	32165.0
2	rs970941	58166181	G	A	1.591276109496912e-10	6.396357102210738	32172.0
2	rs2717036	58168098	T	C	1.7041806053127746e-10	6.385876893364757	32101.0
2	rs11433420	58037203	T	TA	1.7240782506601732e-10	6.384100514460116	31750.0
2	2:58165967_TTC_T	58165967	TTC	T	1.754988159125896e-10	6.381380349092268	32153.0

2	rs2717031	58166468	T	C	1.8627206460450842e-10	6.372252343143579	32165.0
2	rs1518394	58171287	A	G	1.8703166620754984e-10	6.371628355310698	32082.0
2	rs2678908	58130327	C	T	1.9489515852226858e-10	6.365310424609946	32115.0
2	rs2717034	58167258	T	G	2.1658607047346155e-10	6.34909442448742	31924.0
2	rs2717032	58166760	T	C	2.1893019018983542e-10	6.347437980949673	32103.0
2	rs66490669	58040174	T	C	2.3238840117095002e-10	6.338250752756887	31988.0
2	rs2717056	58128804	C	T	2.4546089963083733e-10	6.3298114878031955	32093.0
2	rs2678894	58167260	G	C	3.1863273414313694e-10	6.289430492216134	31892.0
2	rs1356544	58123724	T	C	3.436154865625484e-10	6.2777011868663175	32043.0
2	rs2717020	58159852	T	C	3.6114780196782717e-10	6.2699570098353075	32039.0
2	rs1356545	58123798	T	C	3.6815460684928515e-10	6.266964260737129	32042.0
2	rs34738965	58160798	G	GT	3.6938255039266993e-10	6.266445513735445	31829.0
2	rs2717029	58165595	G	T	3.920585364773792e-10	6.257157057943985	32045.0
2	rs1518393	58171220	A	C	4.293770582666652e-10	6.24295624044365	30817.0
2	rs2717040	58169494	T	C	4.612037532345532e-10	6.231766777994716	32095.0
2	rs2717030	58165694	T	C	4.780809461575725e-10	6.226135397721006	32048.0
2	rs2678896	58169388	A	G	4.841172465276129e-10	6.224168281848755	32080.0
2	rs2717039	58169166	G	T	5.083219249677849e-10	6.21651372950103	31989.0
2	rs2678885	58160138	T	G	5.304242646916319e-10	6.20982859118433	32035.0
2	rs2717021	58160605	G	A	5.838425690807059e-10	6.1947320767967975	32039.0
2	rs2717041	58172107	C	T	5.862092206935854e-10	6.194094843803301	32045.0
2	rs2717035	58167440	C	T	6.0612276042444e-10	6.188830340474175	32120.0
2	rs2717025	58163146	G	T	6.232256912549632e-10	6.184441879343302	32029.0
2	rs2953440	58039936	C	T	6.278383726728433e-10	6.183278422119954	31140.0
2	rs2678874	58154915	T	A	6.280396846155336e-10	6.183227835313652	32037.0
2	rs1401100	58168856	G	T	6.347140145895304e-10	6.181559567319177	32093.0
2	rs68119977	58078939	T	G	6.428125546194884e-10	6.1795581471700025	31947.0
2	rs2717026	58163178	A	G	6.534427397782493e-10	6.176968089051997	32031.0
2	rs2312143	58155829	G	A	7.412868960084963e-10	6.157015300853003	32040.0
2	rs13011472	57961602	C	G	7.509231289987038e-10	6.154968724815363	31828.0
2	rs2717005	58145060	A	G	7.802993256855536e-10	6.1488841739851186	32050.0
2	rs62158166	114077218	G	C	8.696490048426408e-10	6.13166349248832	31803.0
2	rs2678895	58139906	A	T	8.841255681399849e-10	6.12903701618565	32087.0
2	rs2717038	58168831	A	G	9.725575113458217e-10	6.11384996027404	31996.0
2	rs2717000	58136220	C	G	9.726655354912617e-10	6.113832245361495	32110.0
2	rs867740	58135023	T	C	9.987139503655902e-10	6.1096155988314065	32116.0
2	rs12616641	114079248	C	A	1.0352198148425894e-09	6.103883150596727	31792.0
2	rs2717012	58152280	C	A	1.0523498503794608e-09	6.101260878601733	32028.0
2	rs2683632	58116640	T	C	1.0546480668889708e-09	6.100912237651203	32186.0
2	rs765106764	58130295	TA	T	1.0712386840286953e-09	6.0984171889841035	32057.0
2	rs951965	58144542	C	A	1.086093372448454e-09	6.09621497012119	32057.0
2	rs2678907	58133522	A	G	1.1326451901864956e-09	6.089499075599543	32077.0
2	rs2717063	58110969	C	A	1.1353003012507847e-09	6.089124188412862	31314.0
2	rs2678902	58138581	G	A	1.1584979761741794e-09	6.08588469498637	32096.0
2	rs6720288	58111064	A	G	1.170811156021617e-09	6.084190794909186	32107.0
2	rs62158168	114078381	C	G	1.2639686162508764e-09	6.071911153655794	31798.0
2	rs11682175	57987593	T	C	1.2785519848169445e-09	6.070069133558503	31916.0
2	rs34967704	58150658	G	GT	1.301437898222938e-09	6.067219312147462	29452.0
2	rs2678916	58119582	G	T	1.3377408163134379e-09	6.0627974634729505	32152.0
2	rs2717013	58152537	G	A	1.3676377612098019e-09	6.059242852320146	32033.0
2	rs1533725	58111922	T	G	1.4855149773372213e-09	6.045929011950247	32110.0
2	rs2717059	58119657	C	G	1.5171172228633376e-09	6.042534683447893	32162.0
2	rs2717060	58119122	A	G	1.53821636617549e-09	6.04030662097888	32162.0
2	rs2717057	58127907	C	T	1.5520242839244666e-09	6.0388645767326485	32132.0

2	rs35185782	58169712	T	TG	1.5611519081542134e-09	6.037918172190772	31929.0
2	rs2678911	58115072	G	C	1.5899735751718672e-09	6.034964784362972	32143.0
2	rs2678917	58120553	T	A	1.6042147323951215e-09	6.033524683179313	32161.0
2	rs62158169	114081827	C	T	1.7560111217112142e-09	6.018904790252428	31833.0
2	2:58167698_GA_G	58167698	GA	G	1.8173082916987509e-09	6.013347553692409	31935.0
2	rs2678913	58117095	T	C	1.9067708757113082e-09	6.0055562114454135	32173.0
2	rs2030237	58196110	A	G	1.950133348638669e-09	6.001907050700856	31821.0
2	rs11387884	58126250	C	CT	1.994684086599985e-09	5.998239317832078	32149.0
2	rs2678897	58169418	G	A	1.9993313462616354e-09	5.997861329942781	31730.0
2	rs2465805	58148349	C	T	2.0272168303128795e-09	5.995611067330472	32045.0
2	rs2678898	58171964	T	C	2.044298798455136e-09	5.994247458611572	31843.0
2	rs62158170	114082175	A	G	2.145329402490224e-09	5.986402614078817	31848.0
2	rs2717008	58149158	T	C	2.146458700537828e-09	5.9863169761032085	32045.0
2	rs2678918	58121391	C	T	2.1469921833258327e-09	5.986276535805888	32142.0
2	rs781157235	58115023	GCTAT	G	2.330216518509272e-09	5.972935776432117	32014.0
2	rs7606466	57942325	C	G	2.413965327697891e-09	5.9671749548492565	31695.0
2	rs2678914	58117926	C	G	2.647671675789205e-09	5.9520730330130815	32160.0
2	rs2678909	58150768	T	C	2.703116108355669e-09	5.948681153815977	32099.0
2	rs11688767	57988194	A	T	2.82050659497444e-09	5.9417178055990245	32019.0
2	rs2139053	58156539	T	C	2.838538928832563e-09	5.940673248909506	32117.0
2	rs62141276	48214217	G	A	3.260361758521317e-09	5.9179211596293415	31243.0
2	2:58114255_CAT_C	58114255	CAT	C	3.4487512714418724e-09	5.908672705049372	31713.0
2	rs7573056	58229428	A	C	3.4534302677763477e-09	5.908449316872248	31775.0
2	rs7600005	48212055	G	A	3.4616021564957447e-09	5.908059874141163	31250.0
2	rs199993536	114082628	T	TA	3.6096074540096334e-09	5.901157210496769	31456.0
2	rs6717480	58210522	C	A	3.786755864022748e-09	5.8932487985970345	31813.0
2	rs10172295	58201202	G	A	3.850876669734966e-09	5.890474768318746	31758.0
2	2:58225035_GA_G	58225035	GA	G	4.229429511596792e-09	5.874960982998737	32045.0
2	rs2459981	58127925	C	A	4.2365243948535626e-09	5.874683316100464	32095.0
2	rs4672228	58237405	T	C	4.644581577154848e-09	5.8594301628841015	31713.0
2	rs2678910	58112266	A	T	4.767318338502343e-09	5.85509694880216	32070.0
2	2:58047881_CAA_C	58047881	CAA	C	5.51218864711555e-09	5.83092218691396	30062.0
2	rs4672226	58203057	C	T	5.6737748794352885e-09	5.8260996397533376	31725.0
2	rs6722461	57970943	A	G	5.854459831672264e-09	5.820862844514839	31913.0
2	rs2678884	58160123	A	C	6.359046829817534e-09	5.807030731331679	32133.0
2	rs2717027	58164454	G	A	6.4087698251746e-09	5.805725989050696	32141.0
2	rs2678922	58127647	A	G	6.4483235335337515e-09	5.804695103377244	31764.0
2	rs2678923	58127648	A	C	6.4483235335337515e-09	5.804695103377244	31764.0
2	rs2043890	58350571	G	A	6.577663541719292e-09	5.801366547769947	31914.0
2	rs62158161	114065572	C	T	8.105166786222006e-09	5.7662565111120125	31596.0
2	rs6737318	114083120	A	G	8.266233075762942e-09	5.762937667077415	31861.0
2	rs17396357	48252311	C	T	8.635586990735586e-09	5.7555583821790846	31972.0
2	rs375442013	58364359	C	CAT	8.685063602642473e-09	5.754593285245908	31215.0
2	rs2717042	58177082	C	A	1.0210498276436132e-08	5.727194664998169	32055.0
2	rs7556815	114085785	G	A	1.2556660014912192e-08	5.691990828868012	31884.0
2	rs12615370	114068017	T	G	1.3019778500892385e-08	5.685805138745737	31853.0
2	rs62158163	114071717	T	C	1.4009022444895443e-08	5.673278472417987	31909.0
2	rs62158206	114084596	T	C	1.4023388158134007e-08	5.673102966709871	31879.0
2	rs11891807	48288816	T	G	1.4205839848827815e-08	5.670889026404753	32070.0
2	rs986512	58275666	G	A	1.4279965185570747e-08	5.669997441742872	31777.0
2	rs56163359	114071473	T	C	1.4560674025713104e-08	5.666661323095875	31907.0
2	rs6545677	58211509	A	G	1.4686161699637607e-08	5.665190109903842	32051.0
2	rs56093896	114103966	C	A	1.535550798847022e-08	5.657543304931606	32082.0
2	2:58002123_CA_C	58002123	CA	C	1.5875374188645882e-08	5.651824387789941	24995.0

2	rs6712131	48256981	G	C	1.6663787615773528e-08	5.643489311788851	32109.0
2	rs966721	58197305	T	A	1.7083062502817758e-08	5.639211481577844	31335.0
2	rs2678899	58176213	A	G	1.9200464167785536e-08	5.619055081979496	31990.0
2	rs1807282	114110036	A	T	2.0499543768891307e-08	5.607731736120582	32027.0
2	rs2863957	114089551	C	A	2.0674322918976568e-08	5.6062617511243795	32108.0
2	rs62158211	114106139	G	T	2.072762263554e-08	5.605815872338141	32076.0
2	rs1964463	114069021	A	G	2.102975056585652e-08	5.603309268224422	31760.0
2	rs62158213	114110568	G	A	2.1822585877712768e-08	5.596894142901268	31982.0
2	rs10188070	58299326	A	G	2.1986066378411718e-08	5.595599536817773	31849.0
2	rs60758951	48285113	T	C	2.2509981461125985e-08	5.591512708884102	32081.0
2	rs113257513	58283746	A	ACT	2.2656522335425278e-08	5.5903861294254025	31271.0
2	rs2717006	58146956	T	A	2.3555198766426994e-08	5.5836282062748674	31174.0
2	rs4618068	114109355	C	T	2.5349194254202704e-08	5.57085520189422	32036.0
2	rs848294	58381785	T	C	2.5663554533216797e-08	5.5687077279453865	31906.0
2	rs7601767	48277490	G	A	2.56914485633948e-08	5.568518411637247	32041.0
2	rs762952217	58284638	CTCTT	C	2.619078709026455e-08	5.565162737409644	31543.0
2	rs2312147	58222928	T	C	2.668416939665912e-08	5.561907522799853	32186.0
2	rs6727241	48257032	T	C	2.8070161024372345e-08	5.553066261065291	32103.0
2	rs56030357	48270092	T	C	2.821351458741609e-08	5.552176106725428	32078.0
2	2:114073498_GGAA_G	114073498	GGAA	G	2.8406660479239024e-08	5.550983681510545	31461.0
2	rs968653	58296890	A	G	2.90614720191729e-08	5.5469988094951335	31838.0
2	rs1823125	114090412	A	G	2.952169680898016e-08	5.5442498955059145	32186.0
2	rs62158160	114065390	C	T	3.039524367751013e-08	5.53914469618479	32186.0
2	rs12620940	58311684	T	C	3.0423191153335044e-08	5.538983725251036	32186.0
2	rs10172212	58379496	A	C	3.0698070522181826e-08	5.5374080849489165	31918.0
2	rs75534727	58433639	G	GA	3.1625279565639913e-08	5.532192361892594	32008.0
2	rs2717043	58179019	C	T	3.224668192509657e-08	5.528779242831654	31992.0
2	2:58300783_ATATATT_A	58300783	ATATATT	A	3.274511813306779e-08	5.52608733122048	31753.0
2	rs3771224	58460029	C	T	3.498155417567774e-08	5.514478562280622	32005.0
2	rs111789636	114065433	A	AC	3.601482088335681e-08	5.5093563267206775	31682.0
2	rs72816437	48274592	A	T	3.762596894116509e-08	5.501647010267156	32083.0
2	rs7563432	48281138	G	A	3.9308476891759804e-08	5.493930710268429	31948.0
2	rs2118899	58322226	A	C	4.0937073974179195e-08	5.486760853121716	32072.0
2	rs62135450	48274591	G	T	4.127857499780008e-08	5.485292534398298	32082.0
2	2:114068802_CTG_C	114068802	CTG	C	4.129171577574041e-08	5.485236269898231	31521.0
2	rs11686281	58478157	G	A	4.167054967596864e-08	5.483621648160112	31735.0
2	rs848286	58394543	T	C	4.190861254198733e-08	5.482614270732932	31944.0
2	rs760021402	57947592	A	AG	4.2054532479580835e-08	5.4819995408598805	30285.0
2	rs10205421	58297664	G	A	4.223263003054405e-08	5.481252049880153	31825.0
2	2:58295946_GAA_G	58295946	GAA	G	4.394208145194627e-08	5.474228884612881	30963.0
2	rs1100190	58399905	G	C	4.4103159897692726e-08	5.473580820945632	31956.0
2	2:58141384_CT_C	58141384	CT	C	4.67827261922551e-08	5.463124115639486	30136.0
2	rs12477242	58452792	C	G	4.776684140154312e-08	5.45942895954222	32088.0
2	rs10641725	58385305	T	TCTTA	4.970693734381633e-08	5.452355579274296	31724.0
3	rs35124509	89521693	T	C	8.951490491166745e-59	16.164670730505776	32186.0
3	rs67316928	89482234	T	C	2.2235205955887675e-58	16.108500103666593	31898.0
3	rs12636275	89523038	C	A	1.7184515800019518e-57	15.981540806482005	32183.0
3	rs7637670	89493167	G	A	4.092314447437357e-56	15.782710354814027	31881.0
3	rs987748	89494030	C	A	4.443269278981398e-56	15.777516905629911	31871.0
3	rs11921985	89467357	A	G	5.58817602232919e-56	15.763037034636396	31882.0
3	rs35968370	89466339	A	T	7.583394688902125e-56	15.743733733295667	31913.0
3	rs3792572	89456555	T	A	1.2885955707060912e-55	15.710157027986815	31862.0
3	rs6772953	89451721	G	C	4.2053007111931054e-55	15.63499163743103	31733.0
3	rs2117137	89525505	A	G	6.634070713893656e-55	15.60592546327857	32186.0

3	rs6771054	89489529	T	C	1.187567416322715e-54	15.568721771575609	31807.0
3	rs7632502	89469453	T	A	1.3548350705909942e-54	15.560290064350387	31884.0
3	rs7650184	89530057	C	A	1.4508910942888975e-54	15.555905297060995	32100.0
3	rs7633500	89497082	G	A	3.353540540788501e-54	15.502173269547448	31754.0
3	rs12637608	89551301	T	C	2.3682094318701987e-49	14.767651875512593	32107.0
3	rs11918555	89541934	C	T	2.9732507515879407e-49	14.752306906494406	32145.0
3	rs66757381	89561048	C	T	6.89975045802501e-49	14.695392527204035	32087.0
3	rs7632427	89534377	T	C	7.745241742373457e-49	14.687560423691096	32186.0
3	rs7652296	89587262	A	G	2.038268454556522e-48	14.621836584658427	32017.0
3	rs724972	89581408	A	T	2.1511326499406396e-48	14.61816728392228	32029.0
3	3:89598352_GGT_G	89598352	GGT	G	3.926244060484671e-48	14.577139870253431	31649.0
3	rs73145338	89594767	C	T	1.2489838155625544e-47	14.497908197764525	31947.0
3	3:89605220_AT_A	89605220	AT	A	1.3528406829227533e-47	14.492423510153527	31076.0
3	rs7621573	89595252	C	T	1.423214629664844e-47	14.488940346980755	31919.0
3	rs6551413	89640350	C	G	1.5924487000903963e-47	14.481220213742724	31866.0
3	rs1520596	89645542	T	C	1.7336831258291088e-47	14.475378677028447	31804.0
3	rs7635916	89633140	G	A	1.8185171058628946e-47	14.472093525538519	31929.0
3	rs2346843	89590826	C	T	1.91652838353516e-47	14.46848289724526	31379.0
3	rs73153219	89625902	C	T	2.0184888284954327e-47	14.464916810328946	31903.0
3	rs66499884	89659012	T	G	2.1104002592478637e-47	14.461852616159408	31820.0
3	rs6795325	89642054	T	C	2.153574542599331e-47	14.46045881801668	31873.0
3	rs10511145	89597679	C	A	2.1770159658898093e-47	14.45971366159283	31919.0
3	rs17027018	89604774	C	T	4.2359286376946544e-47	14.413823989224207	31904.0
3	rs60243237	89694053	C	T	1.4182183353612012e-46	14.330146149982513	31971.0
3	rs7637504	89702469	A	T	1.5850368649410514e-45	14.161530662606447	31992.0
3	rs6551415	89705161	G	T	1.961831348329957e-45	14.14653693495054	31983.0
3	rs7653735	89722185	T	A	2.160790038267325e-45	14.139740729766256	31893.0
3	rs11925143	89723684	G	A	2.160790038267325e-45	14.139740729766256	31893.0
3	3:89578046_AT_A	89578046	AT	A	2.2104143297724543e-45	14.13814272149066	31525.0
3	rs59381722	89701482	T	G	2.4554615106874172e-45	14.130741211099329	31957.0
3	rs7613412	89724217	A	T	1.0552795041617076e-44	14.027693656968848	31857.0
3	3:89474553_GT_G	89474553	GT	G	1.6916164367285679e-44	13.994183344909814	29984.0
3	rs138643396	89698092	C	CATA	3.995100932935117e-44	13.932949496821193	31553.0
3	rs6806912	89751353	T	C	4.635446937112305e-44	13.922329682644449	31703.0
3	rs55747880	89612941	C	A	1.6963013271361605e-40	13.323220141295652	30731.0
3	rs113141104	89519238	C	T	2.130285595219879e-34	12.230725065484496	32136.0
3	rs73154904	89784599	G	A	2.3967314601994482e-34	12.221148969219243	31956.0
3	3:89521831_TGAAAG_T	89521831	TGAAAG	T	4.358711945226208e-34	12.172437081506205	31726.0
3	3:89521838_TTTG_T	89521838	TTTG	T	4.358711945226208e-34	12.172437081506205	31726.0
3	rs2881488	89500488	C	G	4.5873648618979695e-34	12.168263763758773	32066.0
3	rs73139131	89524686	A	G	4.712229754332276e-34	12.166071174532108	32169.0
3	rs12152372	89500365	T	C	4.7277310452630885e-34	12.165803013136616	32067.0
3	rs73139119	89522285	C	T	4.8121989583688715e-34	12.16435695313519	32175.0
3	rs73139121	89522433	A	G	4.8121989583688715e-34	12.16435695313519	32175.0
3	rs73139125	89524056	A	G	4.86615850845712e-34	12.163446324992645	32168.0
3	rs752364173	89521820	TTG	T	5.086378933853708e-34	12.159831025145804	31522.0
3	3:89521060_CTAT_C	89521060	CTAT	C	5.2711575148126775e-34	12.156915572536152	32096.0
3	rs1912965	89518332	A	G	5.4441508530182e-34	12.154276659348998	32174.0
3	rs17026944	89521131	G	A	5.6822267158763476e-34	12.150778023459663	32174.0
3	rs73139105	89519651	T	C	5.975161131929003e-34	12.146667797797086	32173.0
3	rs73139281	89503890	C	T	6.294167261135255e-34	12.14241349126854	32072.0
3	rs73139127	89524436	T	A	6.5079036662616175e-34	12.139681278125027	32169.0
3	rs73139129	89524562	A	G	6.5079036662616175e-34	12.139681278125027	32169.0
3	rs73139110	89521509	C	A	6.656015008185531e-34	12.137839750925092	32175.0

3	rs1054750	89521725	T	C	6.656015008185531e-34	12.137839750925092	32175.0
3	rs73139115	89521900	G	T	6.656015008185531e-34	12.137839750925092	32175.0
3	rs73139117	89521965	T	G	6.656015008185531e-34	12.137839750925092	32175.0
3	rs73139118	89522263	A	T	6.656015008185531e-34	12.137839750925092	32175.0
3	rs17801380	89522483	G	T	6.656015008185531e-34	12.137839750925092	32175.0
3	rs568140553	89507219	C	CT	6.7105871920243474e-34	12.137171478228593	32166.0
3	rs112335559	89525297	A	T	6.839014297255552e-34	12.135619865381939	32174.0
3	rs1499780	89526072	G	C	6.8725714606096485e-34	12.135219208056874	32145.0
3	rs73139284	89503958	A	G	7.385252451907957e-34	12.12932850647392	32070.0
3	rs112297761	89521602	T	TC	7.40428213065958e-34	12.1291177549397	32186.0
3	rs6795074	89516652	T	C	7.405766000218071e-34	12.129101343872426	32173.0
3	rs60759140	89499848	G	C	7.763155003845734e-34	12.12524093822266	32070.0
3	3:89525668_TTA_T	89525668	TTA	T	8.06368640239917e-34	12.122128956075336	32167.0
3	rs1512183	89505054	A	T	8.173770519243504e-34	12.1210177944235	32069.0
3	rs144317613	89525080	T	TA	8.3388110064114e-34	12.119379460088535	32169.0
3	rs73139286	89504295	T	A	8.524771043880922e-34	12.117571616383467	32069.0
3	rs1912966	89518464	T	A	8.839216187399613e-34	12.114601996365206	32174.0
3	rs73141108	89517119	C	T	9.825239001958323e-34	12.10592758305944	32172.0
3	rs73139290	89505343	G	A	1.0297803921421346e-33	12.10207250311624	32085.0
3	rs73141113	89518499	T	C	1.065092544241515e-33	12.099304856697852	32156.0
3	rs73139296	89505734	C	T	1.1231023416837813e-33	12.09495027717014	32150.0
3	rs73139276	89500196	T	A	1.2492816448238664e-33	12.086202969599947	32056.0
3	rs73139288	89505327	T	G	1.2733488493443587e-33	12.084634669108985	32083.0
3	rs1157608	89506464	T	G	1.2767054732686833e-33	12.084418283067858	32167.0
3	rs73139302	89508186	A	G	1.2767054732686833e-33	12.084418283067858	32167.0
3	rs2346836	89498096	C	A	1.3199988484344871e-33	12.081676914851734	32054.0
3	rs59541469	89501671	C	T	1.3232551407927183e-33	12.081474349526589	32071.0
3	rs73141104	89508390	C	T	1.4430070062537633e-33	12.07434957981874	32169.0
3	rs7626735	89506958	C	A	1.760382248883153e-33	12.057984516973775	32167.0
3	rs1157607	89506364	C	T	1.8259277218740954e-33	12.05497279599488	32165.0
3	rs73139104	89519229	A	C	2.8204062080665332e-33	12.019095855578687	32089.0
3	rs73137387	89464194	T	C	2.842747603927414e-33	12.018443824953088	32144.0
3	3:89502123_TTAG_T	89502123	TTAG	T	2.9227864031127075e-33	12.016148969924753	32014.0
3	rs73137381	89458550	A	G	5.622845142782373e-33	11.96194615138918	32127.0
3	rs73137382	89461363	C	G	5.685328557449497e-33	11.961028585156445	32132.0
3	rs112087049	89509550	G	T	6.718465552659549e-33	11.947156671814835	31639.0
3	rs12639506	89480265	A	G	6.734043461223811e-33	11.946964148289151	32060.0
3	rs73137384	89463290	C	T	8.66546209322167e-33	11.925983443944228	32186.0
3	rs1520594	89839468	G	A	1.4517297871720451e-32	11.882938313093266	31872.0
3	rs1028013	89484268	T	C	1.851508682777583e-32	11.862593020508704	32034.0
3	rs73137393	89471701	T	C	1.8734580303555448e-32	11.861606424818172	32052.0
3	rs73139261	89492406	A	G	1.9480248430977406e-32	11.858338435873929	32061.0
3	rs7650466	89530358	C	T	1.979202719921633e-32	11.857008702969685	32155.0
3	rs12631313	89528461	A	T	2.1783627042218823e-32	11.848976041520336	32156.0
3	rs73139135	89527937	T	C	2.201000048843261e-32	11.848109592133696	32139.0
3	rs12636710	89528477	G	A	2.522427270223264e-32	11.83667964524282	32154.0
3	rs73139134	89527709	G	C	2.5283320052248286e-32	11.83648348937165	32110.0
3	rs73139147	89530347	G	A	2.6164438768368684e-32	11.833609247184715	32109.0
3	rs73139139	89528313	T	G	2.7083798421587544e-32	11.83071096440336	32155.0
3	rs3762717	89528948	T	C	2.774317311891175e-32	11.828691829388484	32156.0
3	rs73139144	89529177	G	A	2.774317311891175e-32	11.828691829388484	32156.0
3	rs73139148	89530956	G	A	3.2874115402937284e-32	11.814437652248008	32186.0
3	rs1512185	89473615	G	A	3.700964839236591e-32	11.804474358473456	32067.0
3	rs73139257	89482779	A	G	4.369686149111807e-32	11.790494337320304	32067.0

3	rs2117138	89531522	A	G	4.871407475534304e-32	11.781337173322179	32096.0
3	rs73137395	89478753	A	C	5.060927565432197e-32	11.778119988430715	32059.0
3	rs73139133	89527708	G	A	5.834765341784511e-32	11.766118834088745	32095.0
3	rs12634269	89532768	A	C	6.125068506026581e-32	11.762020560058415	32051.0
3	rs12629165	89533017	G	A	1.103532834613903e-31	11.71221888407099	32092.0
3	rs12634341	89533031	A	C	1.714240700584585e-31	11.674822052967135	32094.0
3	rs7616322	89493283	C	T	2.7285679952090175e-31	11.635229014656305	32042.0
3	rs6793538	89987871	G	A	4.679446434164816e-31	11.589114600238792	31188.0
3	rs2346840	89533267	T	G	5.410663614883453e-31	11.576670984323128	32123.0
3	rs6551412	89496502	G	A	5.959792887169778e-31	11.56837912162692	32039.0
3	rs569866494	89526980	G	GA	2.2488388462955567e-30	11.453867259517214	31755.0
3	3:89519266_GA_G	89519266	GA	G	4.773109150773868e-30	11.388467439247075	30599.0
3	rs566480002	89529769	T	TA	5.416492877368453e-30	11.37744249145664	31365.0
3	rs529961766	89520326	G	GA	1.0843304562121236e-29	11.31673710829741	30260.0
3	rs6800436	89516072	G	A	1.449181050169444e-29	11.29127556806742	30313.0
3	rs66708608	89486373	C	T	2.5664867205642913e-29	11.240935296282306	32013.0
3	rs56163827	89612938	C	A	1.3964222474385536e-28	11.090412574898878	30447.0
3	rs2048518	89533905	T	C	8.038473720589526e-28	10.9327390764573	32180.0
3	rs73144998	89534592	G	T	8.958658375650495e-28	10.922902205199994	32183.0
3	rs12638777	89537160	C	T	8.958658375650495e-28	10.922902205199994	32183.0
3	rs2048521	89534253	G	A	8.975192792453661e-28	10.922734771102254	32181.0
3	rs73145002	89537618	T	C	9.295561610160961e-28	10.919549603285034	32183.0
3	3:89557699_GTA_G	89557699	GTA	G	1.0925478181620514e-27	10.904865451302326	32125.0
3	rs150837250	89522314	A	AGTTATAATTAG	1.1042594287427312e-27	10.903895658106732	30757.0
3	rs4857499	89541330	C	A	1.1923476161134748e-27	10.896912525664392	32162.0
3	rs2048519	89533978	G	A	1.2037307074401732e-27	10.8960477120753	32181.0
3	rs4857498	89540977	G	A	1.2110706847543614e-27	10.89549435881797	32162.0
3	rs3762718	89535066	T	G	1.2641847900725812e-27	10.89158656337247	32185.0
3	rs2196083	89536546	T	C	1.2641847900725812e-27	10.89158656337247	32185.0
3	rs12634044	89537651	A	G	1.3123367016179446e-27	10.888182096847077	32185.0
3	rs972030	89538498	G	T	1.3396586199830622e-27	10.886305045473962	32179.0
3	rs373216501	89603917	A	ATATT	1.367574677841199e-27	10.884425988856693	27080.0
3	rs17026984	89544978	G	A	1.5218490013063815e-27	10.874682379825847	32132.0
3	rs7633599	89544591	C	A	1.568441373658271e-27	10.871931839205699	32152.0
3	rs7613315	89544773	G	C	1.6283616117014822e-27	10.86851126198152	32151.0
3	rs56371328	89539124	G	A	1.6312453876536898e-27	10.868349804691038	32181.0
3	rs73146961	89550459	T	C	1.6581293311754257e-27	10.866858099295339	32131.0
3	rs57902683	89539011	C	CA	1.7661352654864078e-27	10.86109759207028	32173.0
3	rs4857500	89541486	T	C	1.7751396886867855e-27	10.860633230852383	32168.0
3	rs1036285	89544061	T	C	1.795792777099463e-27	10.85957690751417	32161.0
3	3:89541782_TTA_T	89541782	TTA	T	1.8969587483156426e-27	10.854570790683413	32154.0
3	rs12633609	89545727	T	G	1.9447601976653147e-27	10.85229679794777	32134.0
3	rs1512188	89546183	A	G	1.9447601976653147e-27	10.85229679794777	32134.0
3	rs73146943	89546728	A	G	1.9447601976653147e-27	10.85229679794777	32134.0
3	rs73146907	89538747	G	A	2.116253886018867e-27	10.84457141472540 6	32185.0
3	3:89540269_AT_A	89540269	AT	A	2.1434407087129462e-27	10.843404043329228	32096.0
3	rs2117136	89542699	A	G	2.257819071764473e-27	10.838648452146403	32165.0
3	rs113675293	89539536	C	T	2.2813820776397823e-27	10.837698487511911	32182.0
3	rs73146926	89542293	A	G	2.344895402352717e-27	10.835185554090504	32169.0
3	rs138183278	89564090	C	CT	2.381668974199593e-27	10.833761268306048	32112.0
3	rs138490449	89561661	A	AT	2.441484682372452e-27	10.831490476025945	32123.0
3	rs55979407	89539275	A	G	2.4584038954619587e-27	10.830858174952263	32182.0
3	rs1512189	89546332	A	G	2.472261533654048e-27	10.83034349685822	32107.0
3	rs12632281	89547621	G	A	2.5413479514140863e-27	10.827819548596482	32134.0

3	rs73146947	89548135	T	G	2.5413479514140863e-27	10.827819548596482	32134.0
3	rs73146950	89548243	T	C	2.5413479514140863e-27	10.827819548596482	32134.0
3	rs1567657	89548519	G	A	2.5413479514140863e-27	10.827819548596482	32134.0
3	rs1567658	89548606	T	A	2.5413479514140863e-27	10.827819548596482	32134.0
3	rs1039991	89558311	C	G	2.5436700424053712e-27	10.827735901861944	32131.0
3	rs73146980	89558578	C	A	2.5436700424053712e-27	10.827735901861944	32131.0
3	rs73146983	89559082	A	G	2.5436700424053712e-27	10.827735901861944	32131.0
3	rs6774870	89564891	C	T	2.5436700424053712e-27	10.827735901861944	32131.0
3	rs73146959	89549970	A	C	2.576479687754328e-27	10.826562053908848	32133.0
3	rs112404167	89550630	C	T	2.576479687754328e-27	10.826562053908848	32133.0
3	rs12637511	89550844	T	C	2.576479687754328e-27	10.826562053908848	32133.0
3	rs73146972	89553348	A	G	2.576479687754328e-27	10.826562053908848	32133.0
3	rs17026990	89555257	A	C	2.6234700920161517e-27	10.824906418507693	32132.0
3	rs73146960	89550445	T	C	2.714492679559277e-27	10.821781397676618	32017.0
3	rs73146954	89549680	C	G	2.785313970805014e-27	10.819420996241135	32130.0
3	rs73146956	89549684	G	T	2.785313970805014e-27	10.819420996241135	32130.0
3	rs111618480	89552134	T	C	2.785313970805014e-27	10.819420996241135	32130.0
3	rs2048520	89534248	T	C	3.2622582074091816e-27	10.804924344952171	32186.0
3	rs73147002	89565128	T	G	3.3624115351557566e-27	10.802148764132427	32130.0
3	rs73146976	89557065	T	C	3.4152739040461376e-27	10.800716652592824	32133.0
3	rs369052772	89540272	T	A	3.4856607424536485e-27	10.798843527469863	32146.0
3	rs73146992	89562178	A	G	3.55820571596455e-27	10.796951818985901	32133.0
3	rs73146995	89562209	T	C	3.55820571596455e-27	10.796951818985901	32133.0
3	rs73146968	89552927	A	G	3.559918051182249e-27	10.796907631000972	32134.0
3	rs6784577	89564308	A	G	3.56034626322845e-27	10.796896583989813	32107.0
3	rs1028012	89549422	C	T	3.596139397862578e-27	10.795977819988911	32135.0
3	rs17745025	89549919	T	C	3.596139397862578e-27	10.795977819988911	32135.0
3	rs12634697	89550993	G	A	3.596139397862578e-27	10.795977819988911	32135.0
3	rs12638168	89551544	T	C	3.596139397862578e-27	10.795977819988911	32135.0
3	rs73146970	89553168	A	G	3.596139397862578e-27	10.795977819988911	32135.0
3	3:89544326_CGGTGGAAATCTCCTTATTAAATTGTGGGCAAGAGGCAACCCAT_C	89544326	CGGTGGAAATCTCCTTATTAAATTGTGGGCAAGAGGCAACCCAT	C	3.6140614841923615e-27	10.795521184434161	32153.0
3	rs1039990	89558086	G	A	3.663697144673911e-27	10.79426814613955	32132.0
3	rs73146988	89561044	T	C	3.743832503749657e-27	10.792280251745398	32129.0
3	rs12629999	89551518	A	G	3.866681469009881e-27	10.789313242686283	32099.0
3	rs73146986	89560884	A	G	3.9481125338653936e-27	10.787397626151623	32101.0
3	rs12629758	89556408	A	G	4.7695045012755785e-27	10.77000979539768	32135.0
3	rs73149107	89565849	C	A	4.8838291618050594e-27	10.76782870644882	32106.0
3	3:89550504_GCT_G	89550504	GCT	G	8.460289213847959e-27	10.717113072636256	31977.0
3	3:89571180_TAGAG_T	89571180	TAGAG	T	1.1696079257089568e-26	10.68710837082095	32053.0
3	rs56082199	89586973	A	G	1.3923595360475923e-26	10.670923254454554	32053.0
3	rs12637036	89584170	G	A	1.4480352542814996e-26	10.667279828292077	32058.0
3	rs7613900	89588889	A	T	1.4549802246022167e-26	10.666835124426909	32015.0
3	rs73145320	89586535	T	C	1.539755857096151e-26	10.661570203527463	32049.0
3	rs73145303	89568714	T	C	1.6013161469637508e-26	10.65792417451105	32044.0
3	rs73145310	89578097	T	C	1.647701821151799e-26	10.655267555634452	32063.0
3	rs73153218	89619808	G	A	1.7082761933463243e-26	10.651907816874218	31826.0
3	rs907548	89574852	C	T	1.7267190726967966e-26	10.650908317236627	32069.0
3	rs73145312	89578575	C	T	1.7289737472607043e-26	10.650786853356921	32062.0
3	rs73149115	89568284	C	T	1.7565920462418609e-26	10.649311611969566	32023.0
3	rs73145305	89570713	G	T	1.9837772710432688e-26	10.637982715592027	32068.0
3	rs73145304	89568989	C	T	2.0477447933856712e-26	10.635024698625793	32060.0
3	rs73149109	89567344	G	A	2.1085133089568557e-26	10.632298265254553	32023.0

3	rs1080592	89567568	T	C	2.1085133089568557e-26	10.632298265254553	32023.0
3	rs12633325	89566836	A	C	2.1453889243206907e-26	10.63068153462124	31972.0
3	rs73145316	89580407	C	T	2.27813383747485e-26	10.625081380462733	32066.0
3	rs73145307	89576040	G	A	2.388734992769955e-26	10.62065716033171	32069.0
3	rs73145309	89576389	C	T	2.388734992769955e-26	10.62065716033171	32069.0
3	rs113307255	89567826	T	C	2.4665604164515568e-26	10.617664114037382	32024.0
3	rs73145328	89587686	T	C	2.5448092563605392e-26	10.61474772156756	32036.0
3	rs73145332	89589327	A	C	2.821248872600302e-26	10.60511228947913	32000.0
3	rs73145351	89607237	C	T	3.1918197968532016e-26	10.593569951098264	31968.0
3	rs73145353	89607824	G	T	3.1918197968532016e-26	10.593569951098264	31968.0
3	rs73145357	89611766	T	C	3.193786747773497e-26	10.593512301943477	31953.0
3	rs73149113	89567867	C	T	3.3829301513281343e-26	10.588126962611044	32026.0
3	rs73145345	89598696	C	A	3.5897451691503644e-26	10.582569943952826	31967.0
3	rs73145336	89593317	A	G	4.4587697993596816e-26	10.56224325497722	31975.0
3	rs2069183	89645017	G	A	4.653348539712592e-26	10.55823377885366	31917.0
3	rs111835258	89601496	G	A	5.082531926373201e-26	10.549947808965586	31905.0
3	rs148078210	89565641	G	GGTAT	5.75811034797151e-26	10.53821551275048	31675.0
3	rs149898163	89568422	T	TTTCC	7.162306516475435e-26	10.517669723825133	31421.0
3	rs2346837	89542599	C	T	1.0317838392087264e-25	10.483212344190592	32016.0
3	rs73153241	89695319	C	G	1.327491623932497e-25	10.459360080939712	31963.0
3	rs764684400	89443128	AG	A	1.335026547193961e-25	10.458823740849986	30348.0
3	rs6551410	89442305	T	A	1.7743551880347218e-25	10.431831091972935	31084.0
3	rs73153266	89720111	A	G	2.159855083524976e-25	10.413136701393666	31978.0
3	rs7619303	89552554	G	A	2.2543435154844878e-25	10.40906094453326	31595.0
3	rs113288647	89720352	C	T	2.2823775966376477e-25	10.407884226107942	31896.0
3	rs4035593	89542601	T	TAA	2.3500044075822696e-25	10.40510355713966	32017.0
3	3:89532085_TA_T	89532085	TA	T	2.513042744421292e-25	10.398713040480953	24150.0
3	rs73146965	89552553	A	G	2.5882888048917957e-25	10.39590105942823	31579.0
3	rs7617395	89722541	G	T	3.174711903303252e-25	10.376415787949199	31896.0
3	rs537614374	89606871	T	TA	4.1124934029191508e-25	10.351669897068911	31637.0
3	rs73153262	89719269	G	T	4.553872931086922e-25	10.341906309116991	31979.0
3	rs73153258	89715585	G	A	4.575222065087582e-25	10.34145816031753	31976.0
3	rs1915304	89704393	C	T	4.736454700573093e-25	10.338139100563355	31977.0
3	rs73153252	89712192	C	T	5.477206684587232e-25	10.324202488290256	31974.0
3	3:89626776_AT_A	89626776	AT	A	6.106209203019268e-25	10.31376372026957	31592.0
3	3:89704472_GCT_G	89704472	GCT	G	6.113704232416414e-25	10.313645870272843	27881.0
3	rs73149103	89565651	G	A	7.737303881357452e-25	10.290994527806085	31555.0
3	rs1979837	89590902	T	C	2.4915751946711942e-24	10.177789234306914	30154.0
3	rs12633626	89744949	G	A	4.7877431650747086e-24	10.114022076773246	31874.0
3	rs73153279	89727968	T	C	5.8474022923107146e-24	10.094422852826892	31876.0
3	rs73153282	89728408	C	T	7.32060551870652e-24	10.072352115911162	31879.0
3	rs73153283	89732193	G	T	1.3213678949018154e-23	10.014116821815577	31853.0
3	3:89590098_GT_G	89590098	GT	G	1.5469355360374415e-23	9.998518748257672	31214.0
3	rs559264903	89578492	T	TA	1.6092464119171708e-23	9.994606779902801	31121.0
3	rs111215243	89687803	T	A	3.149503083359805e-23	9.927857359632752	31459.0
3	rs6787562	90010903	G	C	7.258310384788044e-23	9.844243642993883	31183.0
3	rs819293	89613664	G	A	9.255914712165478e-23	9.819764907263902	31784.0
3	rs6773817	89753400	G	A	1.844826967289189e-21	9.513426998689422	31935.0
3	rs144848844	89400269	A	C	2.50370527865417e-21	9.481617913008145	29257.0
3	rs6419884	89279467	C	T	4.17649897663145e-21	9.42808353144902	31866.0
3	rs73153293	89756242	C	T	6.1617812355941376e-21	9.387197656703117	31920.0
3	rs2279829	147106319	C	T	7.573075408782388e-21	9.365444630642157	31996.0
3	rs145565219	89936402	G	A	1.1944220691778567e-20	9.317207737267145	31737.0
3	rs6782527	89442369	C	T	3.271150066668919e-20	9.209674615429613	31621.0

3	3:89694510_GATA_G	89694510	GATA	G	3.433193121359274e-20	9.204483189261083	30795.0
3	rs7645408	89446132	G	A	4.045385175624901e-20	9.18684328542306	31543.0
3	rs28623022	89448936	T	A	4.454225705859832e-20	9.176477747067702	31456.0
3	rs9844971	89440509	T	C	5.262933536408853e-20	9.158488384862592	31675.0
3	rs6800041	89448196	T	C	7.608277643728348e-20	9.118625972109804	31475.0
3	rs754715969	147160015	T	TAA	1.0416242268842731e-19	9.084514591454818	27177.0
3	rs201982816	89448885	T	TTA	2.0911080496906448e-19	9.008386209361358	30354.0
3	rs562459635	89448888	T	TG	2.0911080496906448e-19	9.008386209361358	30354.0
3	rs9832305	89392778	T	C	2.3009071192842657e-19	8.997893093699291	31666.0
3	rs9825569	89431650	T	C	4.2265574396489144e-19	8.93087413563343	32151.0
3	rs62275019	89433648	T	G	4.903641336735189e-19	8.914422729666835	32140.0
3	3:89420088_TGTGCACCTAGAC_T	89420088	TGTGCACCTAGAC	T	5.78589359814372e-19	8.896070304268948	31929.0
3	rs57670516	89419645	T	C	6.132004368999415e-19	8.889616750436222	32109.0
3	rs9864984	89428776	C	T	6.155152593018303e-19	8.889198061030989	32186.0
3	rs9849029	89433059	A	G	6.628380410151539e-19	8.880963329487672	32120.0
3	rs9854073	89426589	C	A	8.892735216675079e-19	8.848218577310432	32137.0
3	rs1512908	89340134	G	A	9.474330731024583e-19	8.841144174158819	31919.0
3	rs73154916	89803713	C	T	9.656893114307028e-19	8.839011788737258	31982.0
3	rs62275018	89423863	A	G	9.801496775915032e-19	8.837350843530574	32149.0
3	rs7615949	89432683	C	G	1.061883570710988e-18	8.828395113155755	32129.0
3	3:89924704_TG_T	89924704	TG	T	1.1510019724651969e-18	8.819375157488546	31633.0
3	rs1879650	89856887	G	T	1.6387896280086018e-18	8.77972217451943	31965.0
3	rs112407114	89797398	G	C	1.8425355728276288e-18	8.766532122875683	31939.0
3	rs1284258	89823487	C	T	2.14719992770873e-18	8.749279105700076	32186.0
3	rs73154925	89859312	T	C	2.1808392770051567e-18	8.747524553325581	31799.0
3	rs73004625	147095294	T	C	2.423706873173051e-18	8.735597901822286	31731.0
3	rs67707172	89447021	C	A	2.4966766720480126e-18	8.732244551160692	30152.0
3	rs2175670	89343044	A	G	3.1296129582609436e-18	8.706659556826548	31912.0
3	rs9863107	89343789	T	G	3.2462072002572397e-18	8.702510804966371	31911.0
3	rs9852380	89341738	T	G	3.262505376219695e-18	8.70194262282431	31908.0
3	rs59127701	89291916	T	TA	3.2754841893712824e-18	8.701492160079262	31881.0
3	rs58858051	89291909	A	T	3.396892344367472e-18	8.69736173935998	31880.0
3	rs9852722	89341946	T	C	3.405206809340993e-18	8.697084229821387	31907.0
3	rs13064615	89799433	A	G	3.4107097332457774e-18	8.696900927946766	31816.0
3	rs9829401	89300610	A	C	3.7458987955561315e-18	8.686253080969497	32159.0
3	rs6776281	89290164	T	A	4.0302827024318935e-18	8.677932453670369	31882.0
3	rs73151349	89892899	T	G	4.048371503249283e-18	8.677422993081567	31617.0
3	3:89333590_CT_C	89333590	CT	C	4.083687417036498e-18	8.676434785195742	31781.0
3	rs6796339	89286159	C	T	4.1294159829279396e-18	8.675167671839697	31868.0
3	rs9821666	89339548	G	T	5.586271478024964e-18	8.640714170790641	31958.0
3	rs1567731	89316027	C	T	5.812381934196596e-18	8.636180168783785	32078.0
3	rs62278164	89292567	T	C	5.858693536768759e-18	8.635273033201042	31930.0
3	rs62278163	89291836	C	T	5.909990595892147e-18	8.634276469720103	31956.0
3	rs73146387	89291564	G	C	6.4079549890623786e-18	8.625023401740412	31958.0
3	rs6773815	89299059	C	T	7.708917550385314e-18	8.603844844148826	32186.0
3	rs9863058	89322805	C	T	8.228066782170996e-18	8.596365207498073	31978.0
3	rs2063590	89323932	G	C	8.363882389047915e-18	8.594485314629805	32011.0
3	rs9862195	89299752	C	T	8.653699637624356e-18	8.590572564227545	32181.0
3	rs62278168	89301573	A	G	9.182605808791333e-18	8.58375421517716	32155.0
3	rs62278170	89302617	G	T	9.231769796630686e-18	8.583140237628704	32176.0
3	rs4264747	89882102	A	G	9.264580242684526e-18	8.582732281836911	31760.0
3	rs9875278	89335463	C	T	9.271056543436971e-18	8.582651925874993	32015.0
3	rs7610812	89544397	G	T	9.705104529365587e-18	8.577388900075999	29707.0
3	rs62278166	89300779	A	G	9.92208086755152e-18	8.574844443757444	32169.0

3	rs62278161	89291713	C	G	1.0022267787003767e-17	8.573688041050904	31950.0
3	rs9847087	89297308	C	G	1.052743992685718e-17	8.5680255980217	32158.0
3	rs4857502	89324919	G	A	1.0531021273177992e-17	8.567986419948426	32013.0
3	rs9851954	89297904	G	A	1.071998319617582e-17	8.565937706431143	32172.0
3	rs17026816	89297593	A	G	1.1211909758681766e-17	8.56076699500289	32166.0
3	rs62274986	89327148	G	A	1.1308317746376124e-17	8.559779924041887	32018.0
3	rs2137487	89325520	C	G	1.1328164069722655e-17	8.559577758972743	32017.0
3	rs6786328	89298926	A	G	1.16381596454475e-17	8.556464557515906	32161.0
3	rs113895673	89917796	G	C	1.1979802133523987e-17	8.553126943534943	31531.0
3	rs4857497	89294149	T	G	1.2207436491401375e-17	8.550954857680994	32167.0
3	rs6786204	89298813	A	C	1.2781140153784774e-17	8.545653098354157	32162.0
3	rs9883541	89294657	T	C	1.2920815928464792e-17	8.544397880558034	32158.0
3	rs62278171	89305928	G	A	1.4548602030378493e-17	8.53068313668469	32124.0
3	rs13062221	89778009	T	C	1.5450578954548635e-17	8.523722318525921	31522.0
3	rs28620812	89305668	C	T	1.698189223331339e-17	8.512775324696976	32093.0
3	rs17738248	89296363	C	A	1.698764977855183e-17	8.51273603231002	32144.0
3	rs62278172	89306038	G	A	1.7096344562709778e-17	8.511996699837841	32099.0
3	rs993187	89314820	A	G	1.7623995448202314e-17	8.50847232418279	32082.0
3	rs17800551	89317315	G	T	1.8084899014844495e-17	8.50547795121253	32016.0
3	rs13316356	89309959	C	A	1.8744651902973194e-17	8.501320211293205	32107.0
3	rs17800347	89314429	T	G	1.8976319374674594e-17	8.499894431211366	32083.0
3	3:89318905_TC_T	89318905	TC	T	2.1277451210908605e-17	8.486597848149406	31900.0
3	rs62274981	89310605	G	T	2.2533247923934874e-17	8.479928444534966	32098.0
3	rs62274982	89310731	G	A	2.290802471486581e-17	8.478009002136924	32098.0
3	rs9866618	89319577	T	C	2.4572131401868222e-17	8.46984427676608	32001.0
3	rs993186	89314862	T	G	2.499367594878629e-17	8.467862659920447	32089.0
3	rs9848971	89279394	A	G	2.5313863138568422e-17	8.466379420716931	31860.0
3	rs373013392	89439750	CA	C	2.696684065970805e-17	8.45900503187241	29576.0
3	rs62274984	89318317	G	A	2.754619989965204e-17	8.45652552156826	32008.0
3	rs2137488	89308704	A	G	2.958124275774189e-17	8.448206261721108	32086.0
3	rs28834186	89305272	G	A	4.1665012565082885e-17	8.408115677146737	32023.0
3	rs9829367	89660010	A	T	4.665674966354006e-17	8.394830331937165	28964.0
3	rs6794975	89292824	G	A	5.622927218930671e-17	8.372874935503052	32018.0
3	rs1503729	147098210	A	G	6.965716865818574e-17	8.347611655838868	31870.0
3	rs1398534	89329307	A	G	8.401730566528879e-17	8.325438274921273	31802.0
3	rs1398531	89289709	G	T	9.920486473570192e-17	8.30573327027642	31635.0
3	3:89428011_CATCA_C	89428011	CATCA	C	1.0768396030530895e-16	8.29599069920798	30229.0
3	rs1512907	89355961	T	C	1.1795876848197795e-16	8.28515156268433	32009.0
3	rs73153260	89718078	G	A	1.217972640429066e-16	8.28133964122349	31471.0
3	rs34756405	89344320	G	GA	1.651896013077431e-16	8.244978729211276	31802.0
3	rs9310121	89378987	A	G	1.7942389623803234e-16	8.23508920121678	31893.0
3	rs9833400	89389507	A	G	1.7989317139833846e-16	8.23477649520648	31805.0
3	rs6768381	89358071	T	C	1.832139780118669e-16	8.23258635790944	32047.0
3	rs4449340	89323876	C	T	1.931290901172546e-16	8.22627267426393	32166.0
3	rs13088663	89360266	G	T	1.9700777459114611e-16	8.223889402414693	32038.0
3	rs9836060	89405548	A	G	1.97953915108408e-16	8.22331506217326	29812.0
3	rs58036688	89369748	C	CT	2.0390822675046563e-16	8.219761532057811	31994.0
3	rs772938042	89344535	ACCCT	A	2.0493209970897519e-16	8.219160809819899	31819.0
3	rs145483821	89344540	T	G	2.0493209970897519e-16	8.219160809819899	31819.0
3	rs9846844	89379639	G	A	2.1497145051334567e-16	8.21342252392949	31872.0
3	rs9310122	89379408	A	G	2.194829151720302e-16	8.210929399727403	31881.0
3	rs528144226	89394756	C	CT	2.229402377691001e-16	8.20905277181706	29234.0
3	rs9866959	89379935	T	C	2.4037845562896364e-16	8.200004288383518	31873.0
3	rs7619025	89368629	C	A	2.4502198462010956e-16	8.197703897151381	32116.0

3	rs34468928	89431649	A	C	2.4755876354110865e-16	8.196465269918455	30247.0
3	rs1512911	89348525	T	C	2.537334383798858e-16	8.193501906304915	31960.0
3	rs59969878	89369856	G	A	2.758078411351061e-16	8.183460006426648	32107.0
3	rs9310119	89378042	C	G	2.791650024531702e-16	8.182002611233706	31917.0
3	rs954964	89355632	A	G	2.802865119614386e-16	8.181519593910629	31959.0
3	rs35173319	89386361	G	T	2.8348226461549136e-16	8.180153608320891	31843.0
3	rs62274987	89334443	C	A	2.8573927711274628e-16	8.179197990698547	32173.0
3	rs9877514	89330825	C	T	2.9444267370133904e-16	8.17558135812544	32174.0
3	rs12495537	89347020	A	G	2.945043814387409e-16	8.175556093978344	31955.0
3	rs9873545	89377717	A	G	2.9920316990224404e-16	8.173647499802309	31932.0
3	rs907712	89326567	C	T	3.03186612567399e-16	8.172052469307966	32175.0
3	rs9289747	147100140	A	C	3.1209275528822503e-16	8.168559773669013	31914.0
3	rs9845870	89345921	T	C	3.1299833872270804e-16	8.168210152396485	31962.0
3	rs3852000	147116084	A	G	3.162629653508853e-16	8.166957991405937	31946.0
3	rs1040017	89329632	T	G	3.359417418417972e-16	8.15966978682056	32149.0
3	rs1398532	89367901	T	C	3.3616450787921624e-16	8.159589715652498	32186.0
3	rs9809011	89349617	A	G	3.4558186461469287e-16	8.156251707917361	31934.0
3	rs9817553	89384566	T	G	3.4848998068994305e-16	8.155239019239993	31827.0
3	rs35448293	89386010	A	G	3.5644911563780554e-16	8.152509440132665	31821.0
3	rs1398535	89326021	G	A	3.6600546633079487e-16	8.149310373353723	32174.0
3	rs13076853	89382776	A	C	3.7202290092231295e-16	8.147337958248695	31838.0
3	rs11923303	89380944	G	A	3.97422124159334e-16	8.139344969200003	31870.0
3	rs9866945	89349818	T	C	4.189703155278116e-16	8.132949176904534	31909.0
3	rs7644070	89370107	G	A	4.2047960137992436e-16	8.132513428276992	32113.0
3	rs9990016	89364033	G	A	4.2105476304644517e-16	8.132347777834422	32085.0
3	rs9833437	89283869	C	T	4.272137974683421e-16	8.130587783303412	31710.0
3	rs1512910	89332453	A	G	4.335791725058324e-16	8.128794909007764	32186.0
3	rs1016584	89343169	C	T	4.338585445549007e-16	8.128716816409355	31968.0
3	rs28675360	89386151	C	T	4.740638079629221e-16	8.117965423038127	31818.0
3	rs12636413	147191972	G	C	4.865408802094442e-16	8.11481114327969	31922.0
3	rs13100388	89383148	T	A	4.956322786734662e-16	8.11256258932043	31850.0
3	rs35511518	89383683	T	C	5.085838501549347e-16	8.109428526949532	31834.0
3	rs2089076	147180677	C	A	5.101070326088081e-16	8.10906512345137	31925.0
3	rs11128072	89317917	C	T	6.3884032510978625e-16	8.081673353162671	32063.0
3	rs67851870	17554860	A	G	6.57350173000865e-16	8.078190213181902	31950.0
3	rs62273364	147111779	T	C	6.724550735472953e-16	8.075418685477322	31938.0
3	rs17800641	89320454	A	G	6.843340594797125e-16	8.073281820694675	32063.0
3	rs112856289	89404980	T	A	6.848446444420301e-16	8.073190794781219	29824.0
3	rs994129	89318462	A	G	6.891700170909206e-16	8.0724223490608	32061.0
3	rs9879028	89273019	G	A	7.164296633585105e-16	8.067686078715036	31785.0
3	rs9289750	147169065	C	G	7.265112748616537e-16	8.065979287593262	31877.0
3	rs56318686	147171254	G	A	7.351453096910442e-16	8.06453601693495	31871.0
3	rs56224184	147171246	T	G	7.635790380704428e-16	8.059898371865003	31878.0
3	rs6551409	89302171	G	T	7.952287630892564e-16	8.054932200088661	32119.0
3	rs9310117	89275906	T	C	8.017158987083697e-16	8.053938383547427	31866.0
3	rs9853389	89312308	T	C	8.339574438911184e-16	8.049113702125544	32011.0
3	rs9838512	89284596	G	A	8.524184048897732e-16	8.046433256280805	31918.0
3	rs16859501	147200660	G	C	8.82173154810002e-16	8.042231103449511	31773.0
3	rs6771477	89293142	C	A	9.446929045130196e-16	8.033838810474531	32004.0
3	rs9836340	89405754	A	G	9.63206523303085e-16	8.031458505064485	29233.0
3	rs9868782	89384121	G	A	1.0247886729169184e-15	8.023853072235863	31706.0
3	3:89302973_GT_G	89302973	GT	G	1.0424410622937103e-15	8.021755940503175	32047.0
3	rs9842599	89407256	A	G	1.070115135273004e-15	8.018537616317486	29280.0
3	3:147180141_CT_C	147180141	CT	C	1.0895012780350197e-15	8.01633159742598	31217.0

3	rs9817310	89280754	C	T	1.0897083731700632e-15	8.016308240682188	31880.0
3	rs6771336	89293015	C	T	1.0923097951196077e-15	8.016015217231583	32000.0
3	rs6770978	89286172	G	A	1.1091590005535587e-15	8.014133812173496	31841.0
3	rs1567732	89315893	G	A	1.1184622415019417e-15	8.013107028642871	32060.0
3	rs4857496	89294023	A	T	1.145918117882314e-15	8.010125107476027	32109.0
3	rs9837346	89280847	T	C	1.1544399637944396e-15	8.009213869868061	31880.0
3	rs9809046	89273974	G	C	1.1557965041419524e-15	8.009069427187951	31835.0
3	rs9877953	89295480	A	T	1.1710152669556687e-15	8.007460302623857	32111.0
3	rs7631682	89394143	A	C	1.440783058665348e-15	7.981916655272943	29214.0
3	rs9833875	147134032	A	G	1.450201728718655e-15	7.981112534032029	31890.0
3	rs1512912	89307931	C	T	1.453104338529484e-15	7.980865759714201	32061.0
3	rs58262807	147109829	T	C	1.4719346338627097e-15	7.979276539973727	31940.0
3	rs150021232	89408982	T	C	1.6503407680220206e-15	7.965142056722393	29889.0
3	rs9860266	89394547	A	T	1.7672933374597318e-15	7.956671343700322	29206.0
3	rs9867299	89300497	G	A	1.7787347082262198e-15	7.955872523474218	31952.0
3	rs9818183	147174864	T	C	2.049509435997693e-15	7.9383121969436585	31922.0
3	rs1566797	147172921	T	G	2.0985157931753328e-15	7.935380133841058	31880.0
3	rs11720653	17439510	T	C	2.2004373846671023e-15	7.929492223330338	32186.0
3	rs6765994	147189001	A	G	2.303109023185991e-15	7.923826511492237	31918.0
3	rs28885734	89305269	A	T	2.3034253997348907e-15	7.923809440276942	31961.0
3	rs6802591	147194290	T	C	2.328795664892687e-15	7.922447960454446	31915.0
3	rs13321297	17528764	T	A	2.7982495804173758e-15	7.899588828893387	31990.0
3	rs9870741	17407930	T	G	2.820351945654182e-15	7.898608066182803	32113.0
3	rs9820816	147170593	T	C	2.8330456111279296e-15	7.898048217666086	31878.0
3	rs17801001	89414555	A	C	3.1065918857493598e-15	7.886548364947201	29381.0
3	rs137962487	147220939	T	TTC	3.6126883903627855e-15	7.86768325878388	31715.0
3	rs73145317	89583712	T	C	3.70079807346588e-15	7.864667260354607	31386.0
3	rs7428532	89281752	G	A	4.78593526501675e-15	7.83241321968594	31656.0
3	rs9852407	147148217	A	G	4.9562633891476926e-15	7.8280166437604946	31905.0
3	rs56778250	147139132	A	G	5.153512751591107e-15	7.8231073337130175	31908.0
3	rs4377462	147164159	T	C	5.215831066851714e-15	7.821594700014725	31935.0
3	rs2202286	147149477	A	T	5.310213780059834e-15	7.819337320963037	31917.0
3	rs9680882	147154084	A	G	5.375600861317765e-15	7.817796480680863	31922.0
3	rs62275016	89414583	A	G	5.384633121519347e-15	7.817585088019173	29386.0
3	3:147129057_AAC_A	147129057	AAC	A	5.677729225187083e-15	7.8109083480712425	31668.0
3	rs62275015	89408594	C	A	6.3607084979239944e-15	7.796580830294457	29297.0
3	rs9289749	147142513	A	G	6.881875997838025e-15	7.786632473971232	31895.0
3	rs872976	89326991	C	A	7.6798388622911446e-15	7.772753029236783	32100.0
3	rs576273791	89285743	A	AG	8.246924495012534e-15	7.763727106720131	30860.0
3	rs870899	89417171	C	T	9.568840028389665e-15	7.744858429243394	29488.0
3	rs870898	89417064	C	T	1.1842286210217828e-14	7.717726612310463	29491.0
3	rs17801031	89415802	C	A	1.2870349062480923e-14	7.707105411881276	29417.0
3	rs535492055	147147025	G	GA	1.3033953230812089e-14	7.705492597513938	31263.0
3	rs9289748	147137976	T	G	1.3227318874282768e-14	7.703611882766221	31902.0
3	rs55787722	90012103	C	T	1.4987543019569104e-14	7.687638615981567	31155.0
3	rs111211173	89660044	T	C	1.717167251768538e-14	7.670208697012378	26868.0
3	rs9862638	89373598	T	C	2.0129562018472328e-14	7.649797776205621	31860.0
3	rs1521800	90001588	G	T	2.157082583690568e-14	7.640900176030357	32186.0
3	rs9880313	89373637	A	G	2.4448913188963245e-14	7.624759836514331	31857.0
3	rs35317084	89354462	C	T	3.72354644931431e-14	7.5703030194439815	30628.0
3	rs112252173	89525767	A	T	3.7962811043889496e-14	7.5677896247569345	26047.0
3	rs11916858	147140680	T	G	6.068879942107278e-14	7.506587022094298	31932.0
3	rs68153678	147203820	A	G	9.462480284891812e-14	7.448196516358862	31730.0
3	rs12638746	89331055	G	A	1.0074834603733543e-13	7.439917307879063	31643.0

3	rs9310120	89378413	T	C	1.1062104678739018e-13	7.427557803255984	31754.0
3	rs9869999	17717340	G	T	1.2280475406069287e-13	7.413720326905844	31820.0
3	rs138801589	89561919	A	AGT	1.5513721632938339e-13	7.3826777408603155	22126.0
3	rs752023841	89618888	TA	T	1.6449582191582022e-13	7.37487783334365	22221.0
3	rs9858940	147207565	C	T	2.0531881707418883e-13	7.345286503310769	31610.0
3	rs112604674	89989681	C	T	2.1128943782207192e-13	7.341451679415924	31173.0
3	rs924761	147224071	G	C	2.153897950954789e-13	7.338879266459442	31395.0
3	rs7640489	147223564	A	G	2.1884763941897758e-13	7.336747061559472	31391.0
3	rs9858966	147207613	C	T	2.2890964728783343e-13	7.3307257678749025	31611.0
3	rs9883675	90310464	A	G	2.6314893301971564e-13	7.312023571601587	31657.0
3	rs7631038	147220482	A	G	3.0904221471336187e-13	7.290397341398351	31632.0
3	rs924763	147218975	T	C	3.161924299830873e-13	7.287315259977714	31633.0
3	rs13085441	17738547	T	C	3.1894025473255797e-13	7.286148991381482	31883.0
3	rs9847935	147212708	A	G	3.2558273554026603e-13	7.283369968645599	31643.0
3	rs12632762	147209965	A	C	3.3132928390496866e-13	7.281010339941561	31639.0
3	rs9289752	147212354	G	A	3.3338712775669663e-13	7.280175117567388	31642.0
3	rs4611784	147220252	G	C	3.597281601836409e-13	7.2699095967359675	31630.0
3	rs6788190	17786057	T	C	4.808135006133577e-13	7.230614473825928	31655.0
3	rs9844783	147220661	T	G	5.596292760886334e-13	7.20997310894746	31616.0
3	rs9682090	90315330	C	T	5.753782715324425e-13	7.206193021222365	31927.0
3	rs6797260	89302486	A	T	6.150411580820877e-13	7.197105632084337	31635.0
3	rs9713415	90307719	C	G	6.555171023066513e-13	7.188406797270695	31946.0
3	rs6551461	90286317	T	A	6.872856080532412e-13	7.181941043501119	32051.0
3	rs9310523	17626394	C	T	7.182387975948142e-13	7.175917459195283	31999.0
3	rs9865864	147224629	T	C	7.277636008166256e-13	7.1741151080564585	31502.0
3	rs9985472	17681459	A	G	7.877209025694796e-13	7.163275024742397	31984.0
3	rs7637642	90034785	C	G	8.056250635593625e-13	7.160194786552596	31876.0
3	rs28708984	90041154	T	G	8.375607221247537e-13	7.1548637453750885	31887.0
3	rs61039064	90044732	C	G	8.560640792937313e-13	7.151865532335742	31927.0
3	rs13075167	89303172	T	C	8.797288157993054e-13	7.148122359079532	31620.0
3	rs9855515	17679106	G	A	8.947197393795441e-13	7.1458019627795935	31987.0
3	3:17727954_CTAAT_C	17727954	CTAAT	C	9.236661468926549e-13	7.141427463626982	31734.0
3	rs6804837	17787399	G	A	9.995804976644642e-13	7.130564597352464	31733.0
3	rs4908969	17779407	T	C	1.256481209935759e-12	7.099016158026602	31843.0
3	rs6577617	17715644	G	T	1.260188911620979e-12	7.098608875569947	31751.0
3	rs13083917	17713516	T	A	1.3968217470519504e-12	7.0843661195827625	31932.0
3	rs9681644	17659105	C	T	1.398782844405605e-12	7.0841718079927185	31340.0
3	rs9631465	147107606	A	G	1.439950419803685e-12	7.080153337097938	31934.0
3	rs9681893	17757024	T	A	1.4689738684642383e-12	7.0773874708478015	31896.0
3	3:17796107_TG_T	17796107	TG	T	1.495777063840084e-12	7.074880402103785	31585.0
3	rs4431138	17749777	G	C	1.5043214900468253e-12	7.074090447549058	31898.0
3	rs12634674	17704685	T	G	1.507208674578149e-12	7.073824514545777	31935.0
3	rs6577619	17715678	C	T	1.5442490690737242e-12	7.070456438785641	31758.0
3	rs11717504	90179080	A	T	1.6076911427963519e-12	7.064867679630378	31740.0
3	rs4908963	17758260	T	C	1.6195377460790889e-12	7.063848104993688	31887.0
3	rs12631291	17758297	G	A	1.6195377460790889e-12	7.063848104993688	31887.0
3	rs34786175	17717997	C	T	1.6491084078515494e-12	7.061334699156908	31768.0
3	3:17758749_CA_C	17758749	CA	C	1.6788074629960413e-12	7.058854495169465	31235.0
3	rs6802945	90270589	A	G	1.708952710959944e-12	7.0563806639797235	31957.0
3	rs556500778	17720571	GA	G	1.760832064967557e-12	7.052221812364813	31454.0
3	rs9819028	147219323	G	A	1.8265461440229507e-12	7.047123182520893	31421.0
3	rs7617683	17728919	T	C	1.8653144782180828e-12	7.0441989657435835	31881.0
3	rs35423549	17739615	T	C	1.8681049163922254e-12	7.043990794629867	31850.0
3	rs6803312	17771005	T	C	1.890136975972773e-12	7.042357799922111	31846.0

3	rs113165984	89989689	T	C	1.8944097059398822e-12	7.042043272121112	30928.0
3	rs4908966	17773919	A	G	1.909539316601717e-12	7.0409351059565175	31838.0
3	rs7431897	17762335	G	T	1.935316599957125e-12	7.0390667417514905	31885.0
3	rs7652156	17780490	C	G	2.0115942432398438e-12	7.033677748388014	31843.0
3	rs11929111	17777546	A	G	2.022007160615868e-12	7.0329576768375714	31844.0
3	rs6577644	17766733	A	G	2.0998399577532326e-12	7.027687856842192	31848.0
3	rs6577643	17766697	C	G	2.1073021945322184e-12	7.0271927177473446	31847.0
3	rs9880456	17777123	A	G	2.1526638426927968e-12	7.024219359353872	31847.0
3	rs10689924	17696951	T	TTA	2.1639893063691348e-12	7.023486588274659	32018.0
3	rs4482690	17767046	T	A	2.20612838985696e-12	7.0207927846632945	31850.0
3	rs34990533	17718227	T	C	2.214816467403188e-12	7.020243665938968	31761.0
3	rs79003773	90348777	T	G	2.221167641618076e-12	7.0198435832888855	31446.0
3	rs12632570	17763501	A	C	2.304114648535416e-12	7.014719057717426	31845.0
3	rs57309958	17732035	T	G	2.3468230580647905e-12	7.012150647658568	31858.0
3	rs9681232	17760883	A	G	2.3506260322643044e-12	7.011924170709113	31888.0
3	rs11128839	17703391	C	T	2.351323276438534e-12	7.011882687001928	31932.0
3	rs4909012	17756467	C	A	2.361352221301839e-12	7.011287329322928	31896.0
3	rs4909010	17736023	G	A	2.3616550670433108e-12	7.011269389806065	31893.0
3	rs4908959	17736035	G	A	2.3616550670433108e-12	7.011269389806065	31893.0
3	rs12497320	17754558	G	A	2.373324845097752e-12	7.0105798262162775	31890.0
3	rs6810235	17753801	C	A	2.383427441572933e-12	7.009985547191025	31890.0
3	rs61081795	17709275	T	C	2.397738599300175e-12	7.009147917180012	31933.0
3	rs4513482	17708780	C	T	2.401854078446696e-12	7.008907946453973	31933.0
3	rs4243835	17706179	A	G	2.402835900039937e-12	7.008850756701626	31934.0
3	rs4243836	17706261	C	T	2.402835900039937e-12	7.008850756701626	31934.0
3	rs7632240	17711352	C	A	2.412482636786042e-12	7.008290063331605	31922.0
3	rs4566567	17749177	C	T	2.418114650889453e-12	7.007963731833024	31898.0
3	rs4568172	17749661	A	G	2.418114650889453e-12	7.007963731833024	31898.0
3	rs35642812	17741409	C	G	2.4621218442585295e-12	7.0054392308914375	31893.0
3	rs199634373	17741172	A	AC	2.484093018765783e-12	7.004195356346671	31850.0
3	rs7633601	17734215	T	C	2.4877172135095427e-12	7.003991213714072	31904.0
3	rs4589965	17709985	C	T	2.4987612866898425e-12	7.0033709201172725	31937.0
3	rs10510477	17721297	T	C	2.5279906791613894e-12	7.001742128081176	31891.0
3	rs6577622	17724339	T	C	2.545156197569473e-12	7.0007941757539545	31893.0
3	rs11128843	17736281	C	T	2.5840509709595368e-12	6.99866923681335	31853.0
3	rs12632939	17741107	C	A	2.5840509709595368e-12	6.99866923681335	31853.0
3	rs7630695	17726483	A	G	2.594998193360649e-12	6.998076812530364	31897.0
3	rs4908958	17728043	G	A	2.596245092785621e-12	6.99800949036788	31898.0
3	rs34297417	17728287	T	C	2.596245092785621e-12	6.99800949036788	31898.0
3	rs4128509	17731099	T	C	2.596245092785621e-12	6.99800949036788	31898.0
3	rs12487916	17733795	G	C	2.596245092785621e-12	6.99800949036788	31898.0
3	rs13071934	17757928	G	C	2.59792934643583e-12	6.997918605053169	31887.0
3	rs4908964	17758859	C	T	2.59792934643583e-12	6.997918605053169	31887.0
3	rs11128844	17736387	C	T	2.611567756004917e-12	6.997184773649369	31896.0
3	rs4243838	17759733	T	C	2.6168836895469927e-12	6.996899760807812	31894.0
3	rs6809062	17711772	G	A	2.639479772359708e-12	6.9956945783870985	31933.0
3	rs6797952	17735318	A	G	2.642502887043374e-12	6.995534105800493	31901.0
3	rs763203017	17688987	TAAGAA	T	2.6448942023750945e-12	6.99540729778978	32011.0
3	rs8179983	17764309	C	T	2.6468850677449966e-12	6.995301810806179	31892.0
3	rs34487714	17763899	T	C	2.6560323793145802e-12	6.994818133928543	31893.0
3	rs11128841	17721451	C	T	2.705528724414522e-12	6.992228953309332	31892.0
3	rs4602424	17722619	A	T	2.705528724414522e-12	6.992228953309332	31892.0
3	rs13085167	17717405	C	T	2.709320310619848e-12	6.9920325331452145	31897.0
3	rs35697509	17763957	G	T	2.7721460606280917e-12	6.988816552683426	31893.0

3	rs9816920	17739024	A	C	2.8477768888937683e-12	6.985038592487374	31898.0
3	rs11712168	17736700	G	C	2.851514577062112e-12	6.984854445981207	31858.0
3	rs4909009	17720104	C	A	2.8518566807052323e-12	6.984837603219857	31892.0
3	rs6577616	17715524	C	T	2.8743415464246065e-12	6.9837349298245455	31928.0
3	rs13097908	17719764	A	G	2.9077699423113257e-12	6.982111115868727	31896.0
3	rs13065637	17710414	T	C	2.9110733219957922e-12	6.9819516463721705	31930.0
3	rs11927637	17781315	A	G	2.923272014544493e-12	6.981364292428776	31840.0
3	rs11719266	17781576	A	G	2.9397957471945867e-12	6.980572513770193	31839.0
3	rs7622878	17738416	C	T	2.9534353141073288e-12	6.979922218694592	31893.0
3	rs6795189	17711724	T	A	2.9989462960844103e-12	6.9777734963060185	31931.0
3	3:17758810_CTTTA_C	17758810	CTTTA	C	3.18952794393819e-12	6.969109760175615	31795.0
3	3:89357752_AT_A	89357752	AT	A	3.2073589858498615e-12	6.968325314580415	24303.0
3	rs11386338	17676494	C	CA	3.3371221038424933e-12	6.962742185695863	32008.0
3	3:17761502_TAA_T	17761502	TAA	T	3.3504953358339763e-12	6.962178944164588	31835.0
3	rs62275606	90355890	A	G	3.363706721928822e-12	6.961624679466237	31668.0
3	rs555285785	17745398	T	G	3.5194864238576627e-12	6.955245483487438	31822.0
3	rs373576726	17745406	GT	G	3.5194864238576627e-12	6.955245483487438	31822.0
3	rs4484221	17702593	C	G	3.53888525397634e-12	6.954470561666048	31946.0
3	rs12488591	17795931	T	C	3.653202940045209e-12	6.949986838215603	31718.0
3	rs4908972	17796192	T	C	3.653202940045209e-12	6.949986838215603	31718.0
3	rs13064990	17696489	A	G	3.8332351814758496e-12	6.943197278877039	31691.0
3	3:90299284_CAT_C	90299284	CAT	C	4.055873215682047e-12	6.935220749547025	32003.0
3	rs4908939	17793850	G	A	4.0920831680837146e-12	6.9339641774377325	31711.0
3	rs6789697	17700708	G	A	4.175326011720528e-12	6.931116301074304	31999.0
3	rs9867064	17792574	C	T	4.359820472076567e-12	6.924997881050645	31714.0
3	rs4435674	17794200	C	T	4.396610975366511e-12	6.923808199165312	31715.0
3	rs4566568	17798924	A	G	4.435578236675783e-12	6.922558723937961	31715.0
3	rs73151380	90000532	A	T	4.6644706576945485e-12	6.915429774991282	31156.0
3	rs6809775	17802881	T	C	4.7202090346207644e-12	6.913745735241778	31712.0
3	rs7647914	17742786	A	G	4.733587530132952e-12	6.913344428287775	31849.0
3	rs9868785	90066423	G	A	4.778048524979328e-12	6.912018699552486	31909.0
3	rs4444738	17742738	A	G	4.8959920673787646e-12	6.908559624813582	31843.0
3	rs13061771	17743799	C	T	4.8959920673787646e-12	6.908559624813582	31843.0
3	rs11128848	17744210	A	G	4.8959920673787646e-12	6.908559624813582	31843.0
3	rs4908973	17800423	T	C	4.949623205302797e-12	6.90701365173695	31714.0
3	rs7609916	17804464	A	G	4.961002241989991e-12	6.906687751474344	31716.0
3	rs34485427	17694291	C	A	5.074732058971656e-12	6.903470159008832	32013.0
3	rs1464463	90056380	G	A	5.0889816608216386e-12	6.903072008537888	31940.0
3	rs13317478	17464862	T	C	5.242404381643454e-12	6.8988531071274055	32037.0
3	rs4908940	17797271	A	C	5.2715815546688474e-12	6.898064492419145	31717.0
3	rs12487248	17697696	C	T	5.2727117825146296e-12	6.8980340302193035	32005.0
3	rs62277724	90281205	G	A	5.49922756875775e-12	6.892054551300879	32050.0
3	rs4908992	17693974	A	G	5.631568925574133e-12	6.888671814473199	32014.0
3	rs13096559	17694643	G	T	5.631568925574133e-12	6.888671814473199	32014.0
3	rs6796448	17801811	C	T	5.68439905234404e-12	6.88734315305969	31713.0
3	rs7647928	17742839	A	G	5.9753278771336245e-12	6.880236492606926	31847.0
3	rs4396913	90047036	T	C	6.0232202310429865e-12	6.879099213694418	31937.0
3	rs283917	17328509	A	G	6.052223819418952e-12	6.8784147791061425	32045.0
3	rs73143703	90281792	C	T	6.159462747593839e-12	6.875911742275027	32090.0
3	rs55701200	17690427	C	T	6.251961412698973e-12	6.873786826666192	32015.0
3	rs7427588	17806424	A	G	6.3273081710072575e-12	6.872078580023108	31708.0
3	rs6768666	17692937	T	C	6.647816578809861e-12	6.865028100723753	31997.0
3	rs11426295	17757500	T	TG	6.961950781984316e-12	6.8584339476238885	31787.0
3	rs6551450	90129328	A	C	7.404977784896984e-12	6.849613500826952	32019.0

3	rs11128837	17697175	T	C	7.574146631497768e-12	6.846381240893978	32009.0
3	rs6792422	17701005	G	T	7.68104337592372e-12	6.844375071837683	32002.0
3	rs754076021	17698320	AAT	A	8.390732971745232e-12	6.831711734561948	31886.0
3	rs283926	17357820	G	A	8.560881359320345e-12	6.8288319026073205	32040.0
3	rs9824116	90319290	A	G	8.687141991052624e-12	6.826730910655702	31653.0
3	rs6768637	17692849	T	C	8.873230839460203e-12	6.823688287785388	32014.0
3	rs9864344	90121955	T	G	8.966119244884789e-12	6.822192842814637	32009.0
3	rs9847461	17607956	C	G	8.968948986827473e-12	6.822147524373449	31755.0
3	rs9851877	90258929	G	A	8.980205935606082e-12	6.821967382448863	32049.0
3	rs13071728	17690673	A	C	9.011572204724779e-12	6.8214666011474785	32017.0
3	rs9881089	17624602	C	A	9.129622352589657e-12	6.819597046393375	31980.0
3	rs5014632	17695082	A	G	9.409487295378278e-12	6.8152578028134805	32017.0
3	rs57107595	17706556	G	GA	9.893030981062307e-12	6.808050253900029	31277.0
3	rs9857910	17697786	A	T	9.916208953112847e-12	6.807713498964951	32007.0
3	rs137965771	90386418	C	A	9.99180997743898e-12	6.806620419600885	31241.0
3	rs11397577	90081678	A	AT	1.0051734312568243e-11	6.805759743267554	31643.0
3	rs4470554	17671037	T	C	1.0165761288485024e-11	6.8041357998555485	32020.0
3	rs9880971	17624579	C	A	1.0415935494109378e-11	6.800634527033478	31980.0
3	rs283939	17343995	T	C	1.103371952287868e-11	6.7923294824508265	32059.0
3	rs17273020	17415705	C	T	1.1072421490980412e-11	6.791824476437116	32133.0
3	rs9843225	17527551	T	C	1.1480787335145779e-11	6.786598823299585	31832.0
3	rs7372028	90294773	G	T	1.153899133211317e-11	6.785868882454113	31784.0
3	rs146780908	17704760	T	TTTAAAATGG	1.1695201280349536e-11	6.783927527970923	31638.0
3	rs9821955	17650745	A	G	1.1888215159119055e-11	6.7815635626716055	31993.0
3	rs6779834	17668766	G	A	1.1985521488861453e-11	6.780386006566283	32007.0
3	rs113450730	90135516	T	G	1.2460849968489966e-11	6.774765158393402	32031.0
3	rs2733481	17320397	G	A	1.2519235942139481e-11	6.774089267018537	32186.0
3	rs11435463	90122867	A	AT	1.2691133957532184e-11	6.772117110282802	31789.0
3	rs4908987	17688490	T	C	1.2732371032448164e-11	6.771647896190382	31998.0
3	rs9681617	17655388	T	C	1.2790707050047855e-11	6.770986658587939	31990.0
3	rs9877921	90108491	C	T	1.2928665012122016e-11	6.769434586777487	32045.0
3	3:90306556_GC_G	90306556	GC	G	1.3253358594725208e-11	6.765844768794855	32020.0
3	3:89312113_CTTTTTTTTT_C	89312113	CTTTTTTTTT	C	1.3331935447788465e-11	6.7649889710855815	30681.0
3	rs12714734	90107488	A	C	1.3574377814650967e-11	6.762379276954781	32019.0
3	rs9853571	17640071	T	C	1.379527753197024e-11	6.760040916864492	31990.0
3	rs924762	147223899	C	T	1.3976457574959524e-11	6.7581502278723695	31404.0
3	3:17663199_CT_C	17663199	CT	C	1.7034474248273265e-11	6.729416554789053	30598.0
3	rs7429932	90283951	A	G	1.7219558707937205e-11	6.7278438293478136	32047.0
3	rs71105145	90176889	T	TA	1.7441798633384762e-11	6.725977108037249	31684.0
3	rs9816940	90146579	C	T	1.8316989979939764e-11	6.718845574747562	32118.0
3	rs75980247	17740272	G	A	1.9228896373012745e-11	6.711761383019455	31398.0
3	rs141333755	90185094	C	CA	1.9241220694527848e-11	6.711667911487239	32066.0
3	rs5846968	17796108	G	T	1.9628853249251715e-11	6.70875751335181	29246.0
3	rs9875185	90394152	A	G	1.964250464264342e-11	6.7086560456620905	31262.0
3	rs60759458	90045885	G	C	1.985507106528537e-11	6.707084933923726	31846.0
3	rs283923	17325703	A	G	2.0031544315681183e-11	6.705793053980978	32136.0
3	rs9857243	90395814	A	G	2.051737918191796e-11	6.702293226047133	31222.0
3	rs9837548	90156142	C	T	2.0642054178261244e-11	6.701408183394675	32138.0
3	rs283907	17336419	T	C	2.1194869900242616e-11	6.697545879302278	32119.0
3	rs283909	17333068	A	G	2.175380812159352e-11	6.693739801336408	32112.0
3	rs73143764	90405465	G	C	2.3111244716020672e-11	6.684880949360141	30977.0
3	rs283919	17328070	G	C	2.322520095726821e-11	6.684160591538907	32088.0
3	rs283921	17325889	G	A	2.375832435869218e-11	6.680835842284638	32129.0
3	rs7433265	90275692	A	G	2.375850949566848e-11	6.6808347004387425	32038.0

3	rs6763681	17409517	G	A	2.3905586058517858e-11	6.6799303358274535	32034.0
3	rs2470349	17304712	G	A	2.4290084774249862e-11	6.677591566949777	31544.0
3	rs76900983	90363402	C	A	2.4611963086865608e-11	6.675661397826332	31268.0
3	rs2596678	17320600	T	C	2.4695300093957433e-11	6.675165687980456	32134.0
3	rs2596681	17320850	T	A	2.4849840762344805e-11	6.674250759206821	32059.0
3	rs283915	17329768	T	C	2.6021794248527122e-11	6.6674884444057385	32107.0
3	rs7433880	90174960	C	A	2.605949271846171e-11	6.667275902862492	32173.0
3	rs283916	17329413	A	G	2.610049512862385e-11	6.667045075343088	32106.0
3	rs2470347	17313703	T	A	2.6388068218399025e-11	6.665436057033777	32077.0
3	rs283908	17334741	T	C	2.6551819833526336e-11	6.664527492617422	32115.0
3	rs9815264	90276511	G	A	2.68407497294016e-11	6.66293768066142	32056.0
3	rs9815542	90276661	G	A	2.68407497294016e-11	6.66293768066142	32056.0
3	rs283922	17325841	T	C	2.7065534177050327e-11	6.661712367054516	32129.0
3	rs1840943	90460310	T	A	2.764769483309361e-11	6.658584697266695	31451.0
3	rs73153370	90056125	T	A	2.791038350528269e-11	6.657194447939745	31839.0
3	rs10049142	17387061	A	G	2.8134816986677296e-11	6.656016768164017	32083.0
3	rs2596679	17320788	T	C	2.822618555432561e-11	6.655539957522713	32139.0
3	3:17807171_CAAAAA_C	17807171	CAAAAA	C	2.867227950450393e-11	6.653233479894247	31500.0
3	rs10049143	17387080	A	C	2.8972933195137268e-11	6.651698714317143	32082.0
3	rs10433560	17803974	C	T	2.909320473836321e-11	6.6510891177300175	31248.0
3	rs9857806	90189355	G	A	2.94984436179467e-11	6.6490531676246025	32168.0
3	rs2733523	17322432	G	A	2.9840780533051234e-11	6.647354460573151	32142.0
3	rs149460172	90408448	T	G	3.009595324679452e-11	6.646100632197946	30985.0
3	rs6577618	17715648	A	T	3.0157270777768555e-11	6.645800890258384	31747.0
3	rs17043492	17402565	T	C	3.0273455487688325e-11	6.645234570341692	32125.0
3	rs2470577	17313311	A	G	3.048157134471134e-11	6.644225447197192	32078.0
3	rs7432427	90299370	A	T	3.064798511710054e-11	6.643423371457423	31947.0
3	rs4312680	17788430	G	A	3.096426462281933e-11	6.641910658054526	31726.0
3	rs17043494	17402806	T	C	3.127235029439718e-11	6.640451604868798	32122.0
3	rs6785870	17387479	T	C	3.174126815864995e-11	6.638257653565363	32100.0
3	rs2733479	17320931	G	T	3.177578420590788e-11	6.638097417150288	32135.0
3	3:17392222_AG_A	17392222	AG	A	3.1908026379740784e-11	6.6374850720345	32120.0
3	rs2733487	17315969	A	C	3.1911741920947105e-11	6.637467903180543	32132.0
3	rs79430269	90403309	G	A	3.216789963608309e-11	6.636288936156372	31514.0
3	3:90392328_CTAGA_C	90392328	CTAGA	C	3.235795806331464e-11	6.635420114098173	31487.0
3	rs12638179	90456907	C	G	3.2859504406008797e-11	6.633151135222247	30949.0
3	rs2733524	17322397	G	T	3.295500207709091e-11	6.6327229508169925	32123.0
3	rs283906	17337410	C	A	3.339928185933326e-11	6.63074675964393	32112.0
3	rs9857738	90431024	A	G	3.4547255327156096e-11	6.625757231106981	31036.0
3	rs9856356	90406018	A	G	3.457995381332456e-11	6.625617499876428	30958.0
3	rs283913	17330957	A	C	3.50936957897676e-11	6.623438927192893	32119.0
3	rs2733485	17318438	A	C	3.5339957281176577e-11	6.622405674092777	32134.0
3	rs283925	17325403	C	G	3.54324009761069e-11	6.622019620894389	32140.0
3	rs2733514	17323931	T	C	3.5716148917956886e-11	6.620840790147581	32138.0
3	rs2596674	17315986	C	T	3.5999348741899645e-11	6.6196733396057175	32137.0
3	rs283912	17331582	A	T	3.656929522077085e-11	6.61735081650173	32121.0
3	rs7426793	90251951	C	A	3.721093387522339e-11	6.6147781615916985	32043.0
3	rs2596675	17316259	C	G	3.746343295219191e-11	6.613777649308427	32133.0
3	rs283947	17354812	G	A	3.8045340154371094e-11	6.611496778225224	32170.0
3	rs9820410	90431093	G	A	3.838508051244863e-11	6.6101808480995174	31045.0
3	rs62277418	90431424	C	A	3.838508051244863e-11	6.6101808480995174	31045.0
3	rs75342952	17386077	C	T	3.902549846497424e-11	6.6077309908659885	32114.0
3	rs283949	17355801	G	C	3.9229054402710186e-11	6.606960541187829	32139.0
3	rs4908970	17788866	A	G	3.931509127736396e-11	6.606636071137466	31731.0

3	rs28808578	90335353	G	A	3.945564206458915e-11	6.606107504958096	31808.0
3	rs283935	17367357	A	T	3.966785890452737e-11	6.605312906710787	32128.0
3	rs71266497	17333904	C	CTTGA	3.9677685395959016e-11	6.605276214460268	32035.0
3	rs4908938	17787557	G	A	3.985713286256979e-11	6.604607714458687	31745.0
3	rs4488868	17771429	T	C	4.04672520493996e-11	6.60235664813253	31846.0
3	rs9682382	90342103	C	A	4.060840955115057e-11	6.601840571961873	31779.0
3	rs4908971	17789074	T	C	4.1498024314096404e-11	6.598627952584303	31741.0
3	rs35500376	17601086	A	AT	4.154041946158659e-11	6.598476540484098	30588.0
3	rs2060625	17339152	G	T	4.1887601881058506e-11	6.597242255058798	32123.0
3	rs283911	17331704	C	T	4.2026169927163466e-11	6.596752417643219	32123.0
3	rs9714360	90357513	G	T	4.2157690476030006e-11	6.59628895266878	31557.0
3	rs144184070	90358160	G	A	4.2270979048824655e-11	6.595890868049959	31568.0
3	rs9713426	90338187	C	T	4.3053807824005735e-11	6.593168284471479	31805.0
3	rs283938	17343457	T	C	4.325566879071583e-11	6.592474091867447	32149.0
3	rs2060627	17339381	C	G	4.340977450614585e-11	6.5919462581266695	32122.0
3	rs5023579	17788324	A	T	4.436607595809167e-11	6.588711217906033	29805.0
3	rs13318609	17395320	T	C	4.4848352145487115e-11	6.587105532012856	32138.0
3	rs6551451	90156286	C	T	4.505503036459839e-11	6.586422584398056	32133.0
3	rs12488093	17388506	T	C	4.5184375657491726e-11	6.585996733385879	32141.0
3	rs11374153	17779317	C	CA	4.543082592639431e-11	6.585188621885175	29799.0
3	rs9810980	90349804	T	C	4.5446273026969496e-11	6.585138113714327	31513.0
3	rs2733478	17321551	A	G	4.572838801086521e-11	6.584218610699789	32140.0
3	rs283948	17355617	C	G	4.6465835120943494e-11	6.581841001725683	32138.0
3	3:90308526_TA_T	90308526	TA	T	4.6534794366754424e-11	6.581620560489414	30577.0
3	rs2596640	17288440	A	G	4.70483132025095e-11	6.579988981954751	32055.0
3	rs2060624	17338719	C	T	4.759166941306228e-11	6.578281464810266	32123.0
3	rs7429720	90228124	T	G	4.806174431102522e-11	6.576819554712597	32107.0
3	rs283931	17361581	T	C	4.8327028800041327e-11	6.576000695476942	32146.0
3	rs2470580	17367746	T	C	4.8327028800041327e-11	6.576000695476942	32146.0
3	rs17043422	17383881	C	T	4.83594974441569e-11	6.575900776026603	32146.0
3	rs761041249	17714993	AGT	A	4.851317501382226e-11	6.575428735276426	31791.0
3	rs34502358	17377815	T	C	4.8738387278214067e-11	6.574739602508626	32125.0
3	rs28408438	17384023	T	C	4.8776022803848926e-11	6.574624744487263	32145.0
3	rs28454413	17383964	C	T	4.904708914257682e-11	6.573800042412517	32145.0
3	rs767685	17324733	A	G	4.925991707191575e-11	6.573155645883522	32144.0
3	rs4582042	17421879	C	T	4.9661859156779535e-11	6.571946047980727	32171.0
3	rs2596677	17318844	T	C	5.087620877587458e-11	6.568348938985747	32141.0
3	rs13095571	17532320	T	C	5.1200634302221194e-11	6.5674021516154735	31885.0
3	rs9877959	90263752	C	A	5.143973683473012e-11	6.5667081157068266	32014.0
3	rs2596638	17287018	C	T	5.2303853511152606e-11	6.564225914395305	32056.0
3	rs2596639	17287135	G	A	5.2303853511152606e-11	6.564225914395305	32056.0
3	rs2733488	17315496	T	C	5.233774575827299e-11	6.564129377441825	32116.0
3	rs12637691	90355883	C	G	5.294131827617789e-11	6.56242035795571	31644.0
3	rs6802891	17297337	T	C	5.337246668791118e-11	6.561211189167997	31976.0
3	rs147324072	17718175	C	T	5.4454217061053323e-11	6.5582189524137675	31769.0
3	rs2084572	17315758	A	G	5.478593708087261e-11	6.557313021771454	32135.0
3	rs2596636	17283809	T	A	5.484212164033272e-11	6.5571601127443095	32059.0
3	rs9798932	90461784	G	A	5.493645340118397e-11	6.556903728533144	31007.0
3	rs2167118	17283278	G	A	5.53307308631461e-11	6.555836763153791	32060.0
3	rs36172181	17719478	G	A	5.545280485236896e-11	6.5555079227327955	31901.0
3	rs187303	17357075	G	A	5.554132480207315e-11	6.555269912113168	32139.0
3	rs2470583	17280812	G	A	5.666161959575846e-11	6.5522893391934725	32058.0
3	rs56399694	90361837	G	A	5.669436518259791e-11	6.552203088428433	31769.0
3	rs13322641	17378509	G	A	5.7152567166866246e-11	6.551001284838223	32138.0

3	rs2596680	17320823	C	G	5.8082193903473704e-11	6.548591686069328	32103.0
3	rs9849053	90152502	G	A	5.884024527573764e-11	6.5466545722031615	32103.0
3	rs10470576	90154964	C	T	5.884024527573764e-11	6.5466545722031615	32103.0
3	rs2596673	17270823	A	G	5.987155673754076e-11	6.544058006998358	31975.0
3	rs4417835	147256611	A	G	5.997995691426401e-11	6.543787629794822	31617.0
3	rs4908965	17768038	T	C	6.082980817290828e-11	6.541684301833628	31848.0
3	rs2592099	17369313	G	T	6.101875790302335e-11	6.541220570144469	32145.0
3	rs4908967	17774944	C	A	6.107466262370033e-11	6.5410836346842265	31837.0
3	rs2733497	17280282	C	T	6.120828654130726e-11	6.540756826524771	32058.0
3	rs2733501	17274801	T	C	6.146268317453347e-11	6.540136565167125	32049.0
3	rs11927654	17723430	G	A	6.156634426825017e-11	6.539884541931246	31894.0
3	rs62275565	90351548	C	G	6.230160927966493e-11	6.5381087714862485	31809.0
3	rs1375817	17266023	T	C	6.259996445082675e-11	6.537394040679718	32050.0
3	rs186005608	90483873	C	A	6.273977526423265e-11	6.537060259741365	31385.0
3	rs9838264	90351314	A	T	6.303535103075735e-11	6.536356997602062	31797.0
3	3:17397140_AT_A	17397140	AT	A	6.334691587338075e-11	6.535619175911579	32087.0
3	rs283937	17341329	C	T	6.342638568806846e-11	6.5354315502904425	32107.0
3	rs7630286	17371566	C	T	6.345615120523385e-11	6.5353613340649455	32076.0
3	rs7630433	17371582	G	C	6.345615120523385e-11	6.5353613340649455	32076.0
3	rs12490933	17754925	A	G	6.35401544222618e-11	6.535163345857673	31887.0
3	rs2596671	17266560	T	C	6.385663563347623e-11	6.534419719561633	32051.0
3	rs2596647	17300133	A	C	6.397313349259684e-11	6.534146895410168	32043.0
3	rs11128852	17776334	T	C	6.397411748835413e-11	6.5341445930790805	31847.0
3	rs11128840	17704787	C	G	6.42823485775731e-11	6.5334251002074515	31935.0
3	rs6806610	17705696	G	A	6.42823485775731e-11	6.5334251002074515	31935.0
3	rs6780587	17709796	C	T	6.42823485775731e-11	6.5334251002074515	31935.0
3	rs145367119	90049321	C	T	6.444667617972763e-11	6.533042893912648	29845.0
3	3:17343781_GTA_G	17343781	GTA	G	6.445262348399996e-11	6.533029079075513	32154.0
3	3:17648762_CA_C	17648762	CA	C	6.506009982099186e-11	6.531624515366473	31927.0
3	rs747681042	17375416	AGGGAGAATG	A	6.517425288645024e-11	6.531362010991927	32109.0
3	rs1545424	17266007	T	A	6.540818060143423e-11	6.530825476999426	32051.0
3	rs34422952	17800933	A	AT	6.543131703920895e-11	6.530772513550287	29439.0
3	rs374899793	17741045	T	TAAATAAAG	6.628847728675223e-11	6.528823120055892	25168.0
3	rs34002492	17741698	C	G	6.692690333233655e-11	6.527387135401845	31893.0
3	rs2596665	17259109	A	G	6.717322939085549e-11	6.526836663472451	32067.0
3	rs283927	17358421	G	A	6.773880521008964e-11	6.525580188609568	32145.0
3	rs11708672	17703137	C	T	6.795517262722006e-11	6.525102221458359	31935.0
3	rs283928	17359316	C	T	6.809212171874403e-11	6.524800462174404	32145.0
3	rs2348003	17292100	T	C	6.836105891443882e-11	6.524209598255785	32037.0
3	rs2252237	17263417	C	T	6.900061119883254e-11	6.522813562096026	32057.0
3	3:17273959_GA_G	17273959	GA	G	6.967817147894517e-11	6.5213482989092775	31991.0
3	rs13069155	17767422	A	G	6.970333243392485e-11	6.5212941556126784	31852.0
3	rs2348002	17251689	T	C	6.97172551096506e-11	6.5212642039318975	32011.0
3	rs13072194	90189970	C	T	6.984375567166853e-11	6.520992332552599	32169.0
3	rs13353435	17430574	T	C	7.008882213371768e-11	6.520467010131734	32166.0
3	rs4435673	17749125	A	G	7.010174383523746e-11	6.520439361159028	31897.0
3	rs7636787	17433760	G	C	7.030233092570759e-11	6.520010796656934	32161.0
3	rs2733500	17276149	G	A	7.03363573274781e-11	6.519938216175518	32058.0
3	rs10433561	17803996	T	G	7.163266541177574e-11	6.517198377211733	31719.0
3	rs2596667	17263274	C	T	7.170806126390438e-11	6.517040518455827	32056.0
3	rs1449881	17286817	T	G	7.175543002799003e-11	6.51694142393168	32053.0
3	rs7645459	17808236	C	G	7.200158211431801e-11	6.516427506378317	31716.0
3	rs6551407	89270605	C	T	7.256822258213377e-11	6.5152509717672356	31912.0
3	rs62275605	90354891	C	T	7.301416131376979e-11	6.514331354495455	31794.0

3	rs773279507	17281259	TG	T	7.311848968747522e-11	6.5141170008672855	31978.0
3	rs7651998	17711127	G	A	7.440650764623108e-11	6.511494996084712	31930.0
3	rs8179891	17727378	T	G	7.464157496402109e-11	6.511021265731821	31897.0
3	rs12634893	17729692	T	C	7.464157496402109e-11	6.511021265731821	31897.0
3	rs10510478	17730282	A	G	7.464157496402109e-11	6.511021265731821	31897.0
3	rs4408889	17730418	T	C	7.464157496402109e-11	6.511021265731821	31897.0
3	rs56059241	17732173	C	A	7.464157496402109e-11	6.511021265731821	31897.0
3	rs4243837	17733234	G	A	7.464157496402109e-11	6.511021265731821	31897.0
3	rs6789467	17802134	G	C	7.468111055804245e-11	6.510941733137558	31719.0
3	rs4611850	17798649	T	G	7.489748884749038e-11	6.510507179285071	31721.0
3	rs9830414	90358707	T	C	7.515138454255336e-11	6.509998841715555	31683.0
3	rs11128842	17735345	G	C	7.51738787137695e-11	6.509953886002097	31895.0
3	rs35460334	17737277	C	T	7.51738787137695e-11	6.509953886002097	31895.0
3	rs2198957	90355214	G	A	7.529049329414704e-11	6.50972103666537	31686.0
3	rs752814983	17336486	AAT	A	7.539860739704535e-11	6.509505475438412	32037.0
3	rs2596669	17265041	C	T	7.602659528592089e-11	6.50825931961228	32057.0
3	rs4643736	17792256	G	T	7.613633591281728e-11	6.508042588060771	31722.0
3	rs2733491	17308965	G	A	7.616379547054446e-11	6.507988404765503	32053.0
3	rs11128849	17764670	T	C	7.623511906189814e-11	6.507847758004508	31891.0
3	rs11128850	17764748	A	G	7.623511906189814e-11	6.507847758004508	31891.0
3	rs1449879	17277391	A	G	7.62503276843369e-11	6.507817783962687	32056.0
3	rs9682018	90364375	G	A	7.62983129427688e-11	6.507723250119509	31672.0
3	rs4349529	17792118	A	G	7.636624539659218e-11	6.5075895184697545	31723.0
3	rs35811992	17793235	G	A	7.636624539659218e-11	6.5075895184697545	31723.0
3	rs728022	17305303	G	C	7.683342495234359e-11	6.506672968808999	32043.0
3	rs4615062	17434502	C	A	7.740844927700991e-11	6.505552293785633	32163.0
3	rs13076724	17758473	A	G	7.771245117376833e-11	6.504963104367636	31885.0
3	rs2733517	17323763	G	A	7.870091630794183e-11	6.5030628083722055	32120.0
3	rs283918	17328219	C	G	7.900447061208541e-11	6.502483916239567	31987.0
3	rs2596652	17368197	C	A	7.912997737849163e-11	6.502245204305607	32149.0
3	rs11412361	17399660	C	CT	7.915182470508473e-11	6.502203688863753	31711.0
3	rs11713917	17382262	G	A	8.03121277846429e-11	6.5000147670045125	32139.0
3	rs1449886	17261930	G	A	8.244600275284007e-11	6.4960687306719125	32058.0
3	rs283944	17346655	C	A	8.24940376997804e-11	6.495981056792062	32186.0
3	rs7627064	17737834	T	C	8.330082307442581e-11	6.494515916963308	31892.0
3	rs1597394	17260188	C	T	8.331295197656576e-11	6.494493996643692	32053.0
3	rs776423900	17313583	TGGAAA	T	8.427472186455086e-11	6.492765668527159	32058.0
3	rs283941	17344551	C	A	8.44660559354879e-11	6.4924241368056474	32174.0
3	rs283946	17347636	T	C	8.44660559354879e-11	6.4924241368056474	32174.0
3	rs283943	17346355	C	T	8.480711932367973e-11	6.491817209726034	32175.0
3	rs9856430	90348280	C	T	8.518411878966293e-11	6.4911491047493755	31719.0
3	rs2596637	17285288	T	G	8.674856680994849e-11	6.488407191614907	32048.0
3	rs12629181	90483648	C	A	8.825007479941249e-11	6.485820686411516	30867.0
3	rs283924	17325616	G	A	8.88344293380907e-11	6.484825689003768	31890.0
3	rs2596645	17296356	T	C	8.896919256950251e-11	6.4845971319511975	32039.0
3	3:17331124_CA_C	17331124	CA	C	8.941164694451039e-11	6.483849106770532	30840.0
3	rs2733502	17274422	C	T	8.994297850457061e-11	6.482955591527452	32047.0
3	rs13079096	17795076	T	A	9.151859788214483e-11	6.480335974153067	31725.0
3	rs2596646	17296401	T	C	9.192148444934949e-11	6.479673216366381	32043.0
3	rs2596672	17267023	G	A	9.270342514599837e-11	6.478394971747619	32048.0
3	rs2733498	17276455	T	C	9.301248372705238e-11	6.477892655668027	32057.0
3	rs13093375	17435598	A	G	9.325832140089187e-11	6.4774942570894405	32163.0
3	rs7609645	89248378	G	A	9.331898841143923e-11	6.477396099564541	31960.0
3	rs4908968	17778320	T	C	9.515356648305372e-11	6.474456899914402	31847.0

3	rs7642719	17435581	G	A	9.542979609188414e-11	6.474019154873448	32162.0
3	rs2060628	17275173	G	C	9.600518555400523e-11	6.473111290866616	32055.0
3	rs2733505	17271758	C	T	9.663644914134896e-11	6.472121366621279	31990.0
3	rs11719326	17781780	A	C	9.690580717820529e-11	6.471700892247704	31841.0
3	rs2733508	17270788	T	C	9.912309764921869e-11	6.468282440836528	31930.0
3	rs2596670	17265224	G	A	9.939397017671778e-11	6.467869964664018	32050.0
3	rs6442679	17397851	C	T	9.996693781066171e-11	6.467001076373732	32137.0
3	rs6551402	89246713	G	A	1.0053470959041452e-10	6.4661448568664746	31964.0
3	3:17316598_AT_A	17316598	AT	A	1.0056006879252172e-10	6.466106724686258	32096.0
3	rs6795664	89246622	A	G	1.0152840628779274e-10	6.4646576419887305	31965.0
3	rs7645756	17397336	T	C	1.0180186903077416e-10	6.464250860967742	32132.0
3	rs2122368	17261455	G	A	1.0188202521695844e-10	6.464131829555779	32053.0
3	rs2733509	17264355	A	G	1.0265171733544593e-10	6.462993479699921	32052.0
3	rs144807058	89392008	T	TAC	1.0331026410528122e-10	6.462026114672063	25352.0
3	rs9812199	17555377	C	T	1.0463108758760251e-10	6.460103943644234	32021.0
3	rs62245860	17292933	T	C	1.0476464230125769e-10	6.459910906109365	31923.0
3	rs113252352	90356125	A	G	1.0517756195819036e-10	6.45931559768286	31299.0
3	rs2733520	17246392	G	A	1.0520487906995922e-10	6.459276295074582	32186.0
3	rs2060629	17279526	T	C	1.0529732703920684e-10	6.459143359145933	32059.0
3	rs1375818	17270900	T	C	1.0596936753989195e-10	6.458180411327232	32047.0
3	rs2733507	17270795	T	C	1.0661876495361552e-10	6.457255563009628	31922.0
3	rs2733499	17276334	C	T	1.067254769967556e-10	6.4571041145702095	32056.0
3	rs9852861	17513896	C	T	1.0684453206375884e-10	6.456935323205072	32042.0
3	rs1597393	17259757	T	C	1.0805715752286675e-10	6.455226510544772	32061.0
3	rs2596664	17254290	T	G	1.0848452561403641e-10	6.454628734666112	32121.0
3	rs2596666	17263042	G	A	1.0853505987399673e-10	6.454558202740582	32053.0
3	rs34983821	17757940	G	GA	1.0855826369887157e-10	6.4545258273379575	31722.0
3	rs35417636	17262695	A	AT	1.1012747534210573e-10	6.45235191708529	31971.0
3	rs9682244	90484101	A	C	1.1064395731599012e-10	6.451643026819402	30788.0
3	rs2596663	17254001	A	T	1.111916765180496e-10	6.450894787722068	32122.0
3	rs2167119	17262139	A	G	1.1168324389627578e-10	6.450226319069508	32053.0
3	rs7653828	90180985	C	T	1.1269603112300756e-10	6.4488580783122496	32186.0
3	rs2733504	17271759	A	G	1.1314234559233491e-10	6.448258934231408	31982.0
3	rs781571315	17347602	CACTTCCAGG	C	1.164373196339529e-10	6.4439058659766175	32168.0
3	rs62245914	17385662	T	C	1.1872194360682964e-10	6.440957721437262	32049.0
3	rs7644389	17502918	T	C	1.1986157999087842e-10	6.439507769905656	32043.0
3	rs1463218	17301087	G	C	1.226519262977228e-10	6.4360137515635785	32027.0
3	rs7613953	17743150	G	T	1.2295797699565838e-10	6.4356352597700122	31842.0
3	rs2733494	17297521	C	T	1.240790536061838e-10	6.434256648638472	32011.0
3	rs9839588	17667278	T	C	1.27253730329169e-10	6.430417742637543	32035.0
3	3:89248669_CAT_C	89248669	CAT	C	1.2945724595270534e-10	6.427807837699769	31549.0
3	rs7627732	17784818	T	C	1.3108211667526236e-10	6.425910961172381	31752.0
3	rs9861749	17409919	G	A	1.3135187580066631e-10	6.425598270018632	32161.0
3	rs9881850	17554181	C	T	1.3257863577630085e-10	6.424184143278418	32021.0
3	3:147256440_TA_T	147256440	TA	T	1.3342407088300354e-10	6.423217006531988	29073.0
3	rs11128838	17697368	G	A	1.3497570394307724e-10	6.4214574951102925	32018.0
3	rs35204863	17241552	T	TC	1.3523174461236616e-10	6.421169053188461	31972.0
3	rs1449883	17253429	T	A	1.3615601098307074e-10	6.4201322458478085	32127.0
3	rs35997387	17739538	C	A	1.406713355274898e-10	6.415164009113338	31675.0
3	rs55740247	90362832	T	A	1.4145998331070252e-10	6.41431227294002	31143.0
3	rs1449884	17256687	G	C	1.4191907055150115e-10	6.413818595147129	32118.0
3	rs2470586	17297663	C	T	1.4494575445808801e-10	6.410602404683499	32029.0
3	3:17260971_GT_G	17260971	GT	G	1.4620861937288644e-10	6.409279833048678	30820.0
3	rs2247106	17308770	A	G	1.468312758378202e-10	6.408631841778978	32055.0

3	3:17303337_GTT_G	17303337	GTT	G	1.468748143975356e-10	6.408586632214668	31988.0
3	rs9883518	17485883	T	C	1.476303857076324e-10	6.407804140984278	32044.0
3	rs145581379	17606493	G	GAAAACAA	1.4778869924531e-10	6.407640682962817	31958.0
3	rs142250908	90206899	T	A	1.4967881172577231e-10	6.405702258994558	31755.0
3	rs6442680	17418533	T	C	1.500136184975251e-10	6.405361390122372	32168.0
3	rs2733510	17263805	C	T	1.5024294175920043e-10	6.4051283434001824	32007.0
3	rs2733493	17302355	T	C	1.5069918981977796e-10	6.404665719319255	32034.0
3	rs62276591	90380252	A	T	1.5101099861984427e-10	6.404350339691867	31242.0
3	rs9848610	17419843	A	G	1.513257430778287e-10	6.404032635505778	32173.0
3	rs17043541	17426846	T	C	1.5247067361737924e-10	6.402882360274936	32163.0
3	rs17043539	17426748	C	G	1.5391735805144452e-10	6.401440933740537	32164.0
3	rs7623979	17406857	A	G	1.580627671930674e-10	6.397382749866451	32100.0
3	rs11128836	17683892	T	C	1.5850750311088727e-10	6.396953565711813	32019.0
3	rs6788763	17519053	T	C	1.587737308000255e-10	6.396697210290648	32049.0
3	rs6807020	17692815	C	G	1.6004829262172697e-10	6.395475701923263	32012.0
3	rs62276586	90376687	C	G	1.6230832307968725e-10	6.393332931764972	31203.0
3	rs61236237	17691510	T	C	1.6356862835539613e-10	6.392150644464508	32015.0
3	rs7650617	17743260	A	G	1.6413822271668568e-10	6.391619227994566	31839.0
3	rs149819143	90035767	C	CA	1.650513879002891e-10	6.390771017645331	30076.0
3	rs9815204	17631880	C	T	1.6986029390829932e-10	6.38637848140959	32000.0
3	rs2733519	17249128	A	G	1.7100965893087818e-10	6.38534663102537	32124.0
3	rs9847477	17607991	C	G	1.725457884361337e-10	6.383978090192692	31856.0
3	rs9821024	90330554	C	A	1.7423155328598603e-10	6.382489872453733	31665.0
3	rs9812906	17525505	G	A	1.7593755022828534e-10	6.3809980485359885	32046.0
3	rs9799070	90400831	G	A	1.7690464886866338e-10	6.380158625491532	31335.0
3	rs6782889	17692938	G	T	1.788410330965863e-10	6.378491273461911	31995.0
3	3:17304858_CAA_C	17304858	CAA	C	1.8270051683886703e-10	6.375219981164969	30877.0
3	rs6784025	17701058	A	T	1.8399958589070883e-10	6.374134063902567	32001.0
3	3:17702996_CT_C	17702996	CT	C	1.844868085627637e-10	6.37372871540896	30547.0
3	3:17339063_TA_T	17339063	TA	T	1.903427508855578e-10	6.368937012808582	28235.0
3	rs6799259	17427142	T	C	1.904422463645999e-10	6.368856849831783	32161.0
3	rs12493567	17426616	A	G	1.9150382529228545e-10	6.368004079518408	32167.0
3	rs7648883	17407522	C	T	1.9353310644691061e-10	6.366386725531818	32144.0
3	rs9310524	17640706	C	T	1.9436869262610882e-10	6.3657255669560495	31990.0
3	rs2348001	17251577	T	G	1.958651085658917e-10	6.364548435356218	32127.0
3	rs2733518	17249603	T	C	1.960371879962197e-10	6.364413635506259	32124.0
3	rs9310526	17643034	T	G	1.9748197205436042e-10	6.3632863902980255	31991.0
3	rs2733516	17252724	T	G	1.9892821424943902e-10	6.362166047707905	32129.0
3	rs9860854	17645229	G	C	2.01962088656118e-10	6.359841462768397	31985.0
3	rs58595750	90290037	C	CT	2.0445910088858053e-10	6.357953678630509	27240.0
3	rs11720651	89261061	A	G	2.074457938519988e-10	6.355725047737504	31920.0
3	rs149092028	90049995	A	C	2.076781580452919e-10	6.355552977107049	29596.0
3	rs7617933	17252067	G	T	2.0968266647000828e-10	6.35407635735964	32119.0
3	rs7644020	17481548	C	T	2.1090248482686714e-10	6.3531845132929625	32049.0
3	rs10212255	17451108	A	G	2.1430247397254985e-10	6.350725026915907	32069.0
3	rs12494513	17427622	A	G	2.203491734283313e-10	6.346443671289508	32164.0
3	rs9798866	90490026	G	A	2.2217509490868184e-10	6.345173374506732	30936.0
3	rs112433497	90376972	C	A	2.2976437971891068e-10	6.340000524759537	31330.0
3	rs4377510	17686288	G	A	2.3053616870875642e-10	6.339483856097232	32014.0
3	rs35234876	17432517	G	C	2.359376362886403e-10	6.335914480107903	32167.0
3	rs9856545	90402558	C	A	2.427739329665769e-10	6.331509682025085	31330.0
3	rs73143751	90378437	C	T	2.4394195433035207e-10	6.330769234699491	31347.0
3	rs723813	17240402	C	G	2.497525591814647e-10	6.327136409554676	32119.0
3	rs9682919	90368237	A	G	2.533729421033016e-10	6.324914435285116	31249.0

3	rs62277419	90434757	C	T	2.5350674407508574e-10	6.324832911087443	31043.0
3	rs62275607	90356428	T	A	2.57607718273616e-10	6.322354398918903	31194.0
3	rs62275608	90356435	C	G	2.57607718273616e-10	6.322354398918903	31194.0
3	rs2198953	90375306	T	G	2.690145334006776e-10	6.3156579112057685	31241.0
3	rs4637311	17686445	C	T	2.711350014235499e-10	6.3144437016411175	32011.0
3	rs10687921	17770840	T	TGA	2.7446030763826254e-10	6.3125581348778255	29717.0
3	rs6793041	90205657	C	A	2.7729895963208907e-10	6.310966086976216	28858.0
3	rs62266068	90497467	A	T	2.8094615293357186e-10	6.3089437729291475	31046.0
3	rs9840464	90369496	C	T	2.820314450571651e-10	6.308346942799133	31183.0
3	rs62264901	90478305	C	T	2.8281191940284167e-10	6.30791912462621	31023.0
3	rs2733521	17243164	G	A	2.8775618798119094e-10	6.305235411469523	32121.0
3	rs113465892	17747914	TAC	T	2.891676184069592e-10	6.304477557141579	31319.0
3	rs9682654	90473594	G	T	2.971113808104428e-10	6.3002784648407175	30403.0
3	rs2198954	90372187	A	G	2.9730370065633415e-10	6.3001781690454735	31304.0
3	rs2733528	17236255	A	G	3.0117821958917317e-10	6.298170969163297	32121.0
3	rs7651278	17443745	C	T	3.065169848080715e-10	6.295446136743219	32168.0
3	rs9799179	90414184	C	A	3.075560857886289e-10	6.294921185749429	31057.0
3	rs2470581	17244668	C	G	3.2418850464484887e-10	6.286746302475202	32124.0
3	rs2347959	90039465	G	A	3.245224241893099e-10	6.286586408252963	31638.0
3	rs11425835	17471456	T	TA	3.276094392887528e-10	6.285115781495564	32035.0
3	rs62276658	90403891	G	T	3.327013874945474e-10	6.282719335615753	31317.0
3	rs2733526	17238792	T	C	3.44090281131076e-10	6.277486431471587	32122.0
3	rs76658459	90357875	C	A	3.446358001699724e-10	6.277240043421522	31249.0
3	rs2596657	17238673	G	A	3.4597345727539264e-10	6.276637487785997	32112.0
3	3:17279462_TA_T	17279462	TA	T	3.5200627563014284e-10	6.273947928023027	31835.0
3	rs9823767	17615737	A	G	3.631101345215965e-10	6.2691131818530845	31948.0
3	rs2596658	17245725	C	T	3.639473451150596e-10	6.268754524751627	32129.0
3	rs2733529	17235874	C	T	3.7459253199487286e-10	6.264263110704932	32108.0
3	rs201902007	90423228	G	GA	3.8994082240492825e-10	6.258001999684257	30734.0
3	rs759739186	17421533	GTGTA	G	4.0559207247942577e-10	6.2518603198392855	31603.0
3	rs10656408	17791796	C	CATATAT	4.057895634302807e-10	6.25178431025808	29811.0
3	rs10662235	17564583	G	GTAT	4.1862793810347685e-10	6.246919027517609	31844.0
3	rs2279832	147101640	T	C	4.2303786447138963e-10	6.245281376143963	31865.0
3	rs6772394	17488124	C	T	4.269819844730177e-10	6.243830760147801	32045.0
3	rs9854201	17471528	A	G	4.3115906002323777e-10	6.242308657171183	32063.0
3	rs2733527	17237409	A	T	4.435781149933546e-10	6.237866794871361	32118.0
3	rs5846952	17227194	T	TA	4.466940896612823e-10	6.236771372195902	30893.0
3	rs11915971	17779893	A	T	4.4952226867524217e-10	6.2357835619466675	31374.0
3	rs13320693	17464812	A	T	4.53919788554256e-10	6.234259605856604	31984.0
3	rs9310528	17661932	C	T	4.65980034532062e-10	6.230152941805053	31886.0
3	3:17398486_TAA_T	17398486	TAA	T	4.825367803379669e-10	6.224681002575593	31926.0
3	rs9681339	90473595	A	T	5.014400051011565e-10	6.218653263966407	30379.0
3	rs9839103	147228736	C	T	5.192440872668541e-10	6.213175472825212	30662.0
3	rs13320647	17589880	A	C	5.510672237216866e-10	6.2038259718734174	31997.0
3	rs13327810	17464911	C	A	5.550205194263967e-10	6.202701499846581	32061.0
3	rs9875973	17584573	T	C	5.610342300051409e-10	6.201005864453286	31970.0
3	rs11128078	90030538	C	T	5.639810392481288e-10	6.200181441631368	31639.0
3	rs9810675	17449619	C	T	5.813910681366148e-10	6.195394819039035	32071.0
3	rs11708391	17414753	A	C	6.051400128786527e-10	6.189086161939107	32140.0
3	rs34892692	17448866	G	A	6.343949519271295e-10	6.1816389275722035	32059.0
3	rs11717644	17461255	C	T	6.467329307355059e-10	6.1785981117027555	32070.0
3	rs2316653	90442925	A	G	6.468243081586934e-10	6.178575802654545	30932.0
3	rs9878954	17509481	T	A	6.584988755999898e-10	6.175750548408445	32053.0
3	3:17462769_ACT_A	17462769	ACT	A	7.197403675217658e-10	6.161686938799421	31959.0

3	rs6442683	17462945	G	A	7.208793010605877e-10	6.161436605115073	32064.0
3	3:17602111_TA_T	17602111	TA	T	7.385612456162229e-10	6.157598893192391	31738.0
3	3:17267802_CT_C	17267802	CT	C	7.56675543313846e-10	6.153759184047128	28760.0
3	rs6787756	17453223	T	C	7.615572085178094e-10	6.152739747768706	32063.0
3	rs1463221	17221017	T	C	7.641088184674238e-10	6.152209429857828	31285.0
3	rs9756494	17588575	A	G	7.642845150439375e-10	6.1521729772745966	31994.0
3	rs6442681	17454766	A	T	7.745374977985819e-10	6.150059776681527	32063.0
3	rs1875748	147102874	C	T	7.950917193115554e-10	6.145904382829273	31859.0
3	rs9799190	90461761	A	G	8.038964801731507e-10	6.144156312684956	30886.0
3	rs7632989	17462283	G	T	9.121844394591506e-10	6.1240636240694	32066.0
3	rs2733530	17233114	A	G	9.504347412558647e-10	6.1175189289598455	31312.0
3	rs9848766	17412485	G	C	9.632048006194992e-10	6.115391035002253	32156.0
3	rs9874826	17410188	A	T	9.65556376675017e-10	6.115002189874545	32157.0
3	rs112149405	89886780	T	C	9.66241531715435e-10	6.114889069708164	31537.0
3	rs201959300	17385963	T	C	9.7795541039246e-10	6.112967096120636	32110.0
3	rs283936	17367376	A	T	9.867431298342778e-10	6.111539918037486	32125.0
3	rs9820703	17414107	A	G	9.89838248815261e-10	6.111040202074029	32159.0
3	rs10663489	17526824	T	TTTA	9.93551795459552e-10	6.110442646064807	31959.0
3	rs9823064	17520222	A	G	1.0594379758376213e-09	6.100187979985567	32046.0
3	rs2198947	90487716	G	C	1.0601338807411276e-09	6.1000830214806445	30521.0
3	rs6763593	17379330	G	A	1.0899885989996202e-09	6.095642359874638	32134.0
3	rs9811041	89367555	G	A	1.1027216446578372e-09	6.093784386146092	31205.0
3	rs56328245	90456144	T	A	1.1094005526337707e-09	6.092818163683464	30722.0
3	rs9310517	17550666	G	A	1.111586516395955e-09	6.0925031568228745	32050.0
3	rs2733515	17323831	T	C	1.132352843794062e-09	6.089540405665464	32130.0
3	3:17776417_C_CA	17776417	C	CA	1.1494198590563922e-09	6.087144832585776	28297.0
3	rs62266110	93537923	G	A	1.1768907828427615e-09	6.0833608269175325	31789.0
3	rs9821318	17567220	C	T	1.1778794040157895e-09	6.083226259291004	32005.0
3	rs9757853	90436845	A	G	1.1825386208317286e-09	6.082593541818183	30957.0
3	rs2596656	17235490	G	A	1.2114388726085825e-09	6.078722382657428	32043.0
3	rs2100628	90439303	A	G	1.2388983816427347e-09	6.075126732870567	30808.0
3	rs9831141	90433267	C	T	1.2394911708167675e-09	6.075049970576347	31152.0
3	rs9757339	17569829	T	C	1.2469750894894139e-09	6.074083918519257	31980.0
3	rs2733489	17312588	A	G	1.2493539451106585e-09	6.073778030545197	32078.0
3	rs10510475	17422679	A	T	1.2956195165956787e-09	6.0679391752891245	32172.0
3	rs283942	17346033	A	G	1.3229206069877164e-09	6.06458832758192	32148.0
3	rs1449882	17311336	T	C	1.328104640842911e-09	6.0639596784468806	32064.0
3	rs35521582	17496173	T	C	1.3432634597981624e-09	6.0621350530453535	32029.0
3	rs283930	17360961	A	T	1.3520189599944006e-09	6.06109030044814	32140.0
3	rs283934	17367065	T	C	1.3520288961259135e-09	6.061089118566817	32140.0
3	rs1992737	17422005	A	G	1.355899505192296e-09	6.060629360817982	32175.0
3	rs9850127	17398386	T	C	1.368712803681188e-09	6.0591164499841605	32100.0
3	rs13318886	17399281	G	T	1.4141720161802712e-09	6.053858091339857	32131.0
3	rs17200839	17425832	C	T	1.4187071239722966e-09	6.053342575643916	32186.0
3	rs34958195	17434610	G	GT	1.4282187406436758e-09	6.052266566195757	31092.0
3	rs4312642	17434006	A	G	1.4579018234152366e-09	6.048952997151655	32164.0
3	rs1470667	17309934	C	A	1.472343250946373e-09	6.0473645845670685	32054.0
3	rs9817290	17408297	A	C	1.4861727235914304e-09	6.045857650499399	32129.0
3	rs9866664	90437988	A	G	1.5705946810903372e-09	6.0369447495101545	30947.0
3	rs35863421	17521749	A	AG	1.5730029574227416e-09	6.036697401490853	31873.0
3	rs2060623	17338680	T	C	1.5762581594218193e-09	6.036363653774417	32109.0
3	rs9713931	90390418	A	G	1.597602478388743e-09	6.034191774732009	31224.0
3	rs11389760	17440236	A	AC	1.5985863227505005e-09	6.034092347263081	32159.0
3	rs2348004	17295308	G	A	1.633961377025016e-09	6.030556395053347	32015.0

3	rs2733496	17281330	C	T	1.6602153843614626e-09	6.027980049290748	32024.0
3	rs2596641	17291294	A	G	1.6658060979982918e-09	6.027436554029865	32019.0
3	rs6762516	17375264	T	A	1.6707422185051005e-09	6.026958169828683	32136.0
3	rs9858006	90390344	A	T	1.7021074303941292e-09	6.023950214086997	31225.0
3	rs9861554	90349123	C	G	1.7040276100930848e-09	6.0237678257257805	31410.0
3	rs62245947	17497051	T	G	1.705263136152051e-09	6.023650575084336	32034.0
3	rs1521806	90090619	A	C	1.7153297908557355e-09	6.022698329326974	31854.0
3	rs7647905	17433383	T	C	1.7274894739377767e-09	6.02155533069468	32167.0
3	rs34096182	89465849	A	T	1.7416575977787074e-09	6.020233388473454	30026.0
3	rs36029966	17389500	C	CA	1.7523842740917609e-09	6.019239498488884	32072.0
3	rs11449656	17371025	T	TA	1.7847858927003157e-09	6.016272900552857	32100.0
3	rs1867772	17391339	T	A	1.7907626987786938e-09	6.015731419711689	32141.0
3	rs7614318	17440747	C	G	1.8019316936768264e-09	6.014724245504999	32165.0
3	rs283929	17359916	C	T	1.8462300987663765e-09	6.010788613645768	32142.0
3	rs9843640	17441862	C	G	1.941805314923773e-09	6.002601720292059	32166.0
3	rs2596643	17294388	A	G	1.9491244723370795e-09	6.001991050476347	32019.0
3	rs2733495	17296298	A	T	1.9742851995278287e-09	5.999908687719621	32011.0
3	3:17442866_CATATGT_C	17442866	CATATGT	C	2.1013376346676632e-09	5.989773279452883	32022.0
3	rs528162866	17747475	C	CT	2.1352085799300925e-09	5.987172071963976	29292.0
3	rs2348005	17295756	T	C	2.2611172495202192e-09	5.977842829186933	31999.0
3	rs9864494	17473346	A	G	2.279827717811538e-09	5.976499844293282	32057.0
3	rs1449888	17272276	T	C	2.283351798664924e-09	5.9762480976306485	32012.0
3	3:90272973_AAAAT_A	90272973	AAAAT	A	2.293738966218558e-09	5.975508274455246	31144.0
3	rs9877833	90138312	G	A	2.304407585880217e-09	5.974751794434964	31912.0
3	rs9835988	17517721	A	G	2.395120388063961e-09	5.968454075208341	32066.0
3	rs283940	17344285	A	T	2.414498597022578e-09	5.9671389003014275	32170.0
3	rs1449885	17261756	A	G	2.437753730424244e-09	5.9655741083863605	32022.0
3	3:17346381_TA_T	17346381	TA	T	2.458025378920036e-09	5.964221884959509	32158.0
3	rs5846961	17467525	G	GA	2.467846148299688e-09	5.963570689973358	32071.0
3	rs11419267	17487665	C	CT	2.4715838302346407e-09	5.96332351487291	32044.0
3	rs1449887	17272228	A	T	2.5233245633718826e-09	5.959938774090163	32013.0
3	rs283945	17346756	C	T	2.546924255988956e-09	5.958417333848318	32171.0
3	rs7615612	17516671	G	C	2.579184589222341e-09	5.956359617993027	31446.0
3	rs17200818	17410411	T	A	2.622271132217394e-09	5.953650109747441	32160.0
3	rs62273833	147255596	G	A	2.642474894101568e-09	5.952394489936948	31149.0
3	rs62276243	90121534	C	T	2.750462075101354e-09	5.9458379157627546	31841.0
3	rs3058046	147090583	G	GAA	2.774697214046381e-09	5.944400928654988	30090.0
3	rs9681592	90485493	A	G	2.851523816326651e-09	5.939925069182968	31188.0
3	rs4974357	90127762	T	C	3.071391871134277e-09	5.9277363035417485	31858.0
3	rs1446303	17482564	T	C	3.168542233341763e-09	5.922619072286135	32049.0
3	rs2028874	17426715	C	G	3.3590318363439358e-09	5.913014211822586	32171.0
3	rs17804073	90124806	T	A	3.439290490621876e-09	5.909125291642253	31877.0
3	rs2596648	17302558	A	G	3.602949024415061e-09	5.901461777527333	32005.0
3	rs2733492	17308296	C	A	3.655730159262074e-09	5.899062380332516	32043.0
3	rs9830240	17398284	G	T	3.781867856487939e-09	5.893462138105296	31939.0
3	rs2596650	17307841	C	T	3.784217801437365e-09	5.8933595401153624	32039.0
3	rs7613624	147237920	T	C	3.797031045207153e-09	5.892801205862018	30816.0
3	rs9851518	17455397	A	G	3.950817449624112e-09	5.886239473461068	32063.0
3	rs6801690	17406273	C	T	4.084444692510904e-09	5.8807366942570365	32142.0
3	rs2596649	17307395	G	A	4.0863896788412025e-09	5.880657900317372	32041.0
3	rs9870604	147234379	C	G	4.160197250889698e-09	5.8776945188184975	30792.0
3	rs2596655	17232635	G	A	4.251465012227832e-09	5.874100073796918	31239.0
3	rs75948196	90420549	T	C	4.3411943332016224e-09	5.870638693351692	30960.0
3	rs7652792	17439143	G	A	4.409280998516757e-09	5.86805834697288	32163.0

3	rs2596662	17253663	A	T	4.414620385550493e-09	5.867857637772263	32080.0
3	rs6792443	17458313	G	T	4.455959820786778e-09	5.866311623608463	32060.0
3	rs35742571	17459374	A	AT	4.696869794338952e-09	5.8575706671798	31877.0
3	rs73004648	147137674	A	G	4.759360259641056e-09	5.855374598792473	32043.0
3	3:17428891_AT_A	17428891	AT	A	4.913473099116154e-09	5.850076386163192	32165.0
3	rs75162052	147137597	T	C	5.116264616483677e-09	5.84334583702532	32041.0
3	rs57499472	147239337	T	C	5.15222874753324e-09	5.842179365820226	30828.0
3	rs9842092	147241494	A	G	5.233879866726416e-09	5.839560211412637	30829.0
3	rs5846955	17306752	A	AG	5.348886418802155e-09	5.835937752263532	31962.0
3	rs7625855	17470782	T	A	6.136832127763889e-09	5.81298565727831	32064.0
3	rs9310516	17470827	T	A	6.136832127763889e-09	5.81298565727831	32064.0
3	rs1374197	17394615	A	G	6.245441011947333e-09	5.810049402299937	31882.0
3	rs2168715	90452164	A	C	6.498409661178453e-09	5.803398501490575	30903.0
3	rs79769556	90423789	A	G	6.671965352986565e-09	5.7989795844944965	30918.0
3	rs71105148	90190366	C	CA	7.146937653828485e-09	5.7874348871536885	28351.0
3	rs2733525	17238881	C	T	7.193843407579309e-09	5.7863355751113	32071.0
3	rs10865749	17450271	A	T	7.2551279569350886e-09	5.784909729195174	32072.0
3	rs2121262	17470114	C	T	7.469262367275186e-09	5.7800180222270825	32064.0
3	rs9813532	17465704	G	A	7.54419878536488e-09	5.7783383277946445	32059.0
3	rs9882273	17464102	C	T	7.616666788650926e-09	5.7767293232286585	32061.0
3	rs9824952	17448437	T	A	7.940389199298085e-09	5.76971885911191	32059.0
3	rs12488687	17461342	A	T	8.005571972349632e-09	5.768340944530977	32059.0
3	rs201380658	17393317	AG	A	8.087976844122914e-09	5.766614497257367	30357.0
3	3:17474521_CCCCA_C	17474521	CCCCA	C	8.276724485687683e-09	5.762723673453406	32023.0
3	rs6442682	17461731	T	C	8.305424831044279e-09	5.762139616369718	32070.0
3	rs1120412	17452025	G	A	8.305779766114334e-09	5.762132405669299	32066.0
3	rs34633537	17852607	G	GA	8.460693380244274e-09	5.759013505305696	31957.0
3	rs2733522	17243002	T	C	8.472629166308509e-09	5.758775509080987	32071.0
3	rs7625175	17455081	C	T	8.911219892393935e-09	5.750248829042838	32066.0
3	rs34732565	90144346	T	A	9.08373065623957e-09	5.747006374034588	31900.0
3	rs9681820	90481415	A	T	9.819561357021818e-09	5.733816420058807	30981.0
3	rs2198951	90460470	G	C	9.890160353991436e-09	5.732601858673518	30910.0
3	rs1532769	147090343	C	T	1.0184218144155572e-08	5.727632011390803	31249.0
3	rs12632358	17740995	C	T	1.065505002779513e-08	5.719957821055236	29932.0
3	rs9830582	17458832	C	A	1.0659810173248368e-08	5.719881929857707	32078.0
3	rs1394041	147096847	C	A	1.0727280084204777e-08	5.7188097817204655	31806.0
3	3:17452696_AT_A	17452696	AT	A	1.3708605455888141e-08	5.676989286787379	30456.0
3	rs4974358	90141506	A	G	1.4208940691664729e-08	5.670851638774238	31972.0
3	rs34185023	147095042	G	A	1.4300303536887922e-08	5.6697535966276185	31821.0
3	rs142854083	17774212	A	TAAA TAAA TAAA TAAA TAAA	1.4438276666651231e-08	5.668108219232932	30741.0
3	rs9865185	89252480	A	C	1.4836749275724107e-08	5.663440661114489	31788.0
3	rs7632016	147100106	A	C	1.7641899785133312e-08	5.633665553340478	32022.0
3	rs6577596	17832829	C	T	2.2395682062269682e-08	5.592396374669118	31716.0
3	rs112272175	89269015	C	T	2.24688252982316e-08	5.591830390511554	31673.0
3	rs2060626	17339260	T	A	2.2635658772900946e-08	5.590546092122966	29018.0
3	rs2596682	17221849	C	A	2.291470943477489e-08	5.588418334076179	31272.0
3	rs2596676	17220717	G	A	2.2988711049416235e-08	5.58785829183338	31257.0
3	rs10804719	147117260	A	G	2.333680813045812e-08	5.5852471593706134	32018.0
3	rs283914	17330649	T	C	2.3381263670837704e-08	5.584916417063188	32064.0
3	rs73004638	147113586	A	T	2.436295750902088e-08	5.57776421283271	32011.0
3	rs2470578	17330092	G	A	2.5688301175816943e-08	5.5685397629165925	31801.0
3	rs73004642	147116846	A	C	2.6149752873805392e-08	5.565436145606383	32017.0
3	rs374871846	89979666	AC	A	2.7571019574792272e-08	5.556200476076803	27026.0

3	rs62274613	89157751	G	A	2.8025679008703726e-08	5.553343369121187	32010.0
3	rs62274656	89271959	C	T	2.8504831533809592e-08	5.550380614746951	31957.0
3	rs62274657	89272043	C	G	2.938196051321304e-08	5.5450801165635095	31955.0
3	rs2279830	147105790	T	C	2.996055757166998e-08	5.541667044712511	32186.0
3	rs12107172	147134039	A	G	3.0809350587529045e-08	5.536774103732859	32023.0
3	rs7373232	89268266	A	G	3.21498690295381e-08	5.529306779811202	31959.0
3	rs73004644	147124706	G	A	3.2359367948082e-08	5.528167144065436	32039.0
3	rs62274614	89159719	C	T	3.2631838258342037e-08	5.526695616038647	32004.0
3	rs57468276	89269988	A	T	3.4479578660735746e-08	5.517020215133528	31965.0
3	rs1463222	17221252	C	A	3.4899737659542324e-08	5.514890401152521	31266.0
3	rs9824191	17453982	T	C	3.5010773137913804e-08	5.5143317094901345	32062.0
3	rs62274654	89271419	C	G	3.828366102729661e-08	5.498591620260124	31960.0
3	rs1503738	147093600	A	G	4.30290559708264e-08	5.477946343696077	31457.0
3	rs9809894	89261561	A	T	4.322257883663679e-08	5.477152053945327	31992.0
3	rs9852594	89262358	C	A	4.403254876593951e-08	5.473864626328236	31991.0
3	rs9310112	89260495	A	C	4.51494112300714e-08	5.469426496832137	31998.0
3	rs9852981	89253461	T	C	4.8516767742428295e-08	5.456662350193096	32017.0
3	rs76407105	90329812	G	A	4.935801479370472e-08	5.4536077493821	31436.0
5	rs145120402	93174765	A	C	1.8342886641780968e-09	6.011840399143533	32127.0
5	5:94068140_AC_A	94068140	AC	A	6.7993445650989546e-09	5.7958069423521925	31981.0
5	rs11955446	94073541	T	C	9.945874699859212e-09	5.731649302485057	32092.0
5	rs369272402	93106457	G	A	1.0568052384284206e-08	5.72135066333192	32059.0
5	rs115877304	92797166	C	T	1.1105662817024772e-08	5.7129158126540815	32184.0
5	rs9791082	94075700	T	C	1.1245505958331708e-08	5.710786788866312	32100.0
5	rs7442779	92788278	A	G	1.2380968628457991e-08	5.694395640362044	32186.0
5	rs11955417	94073489	T	C	1.2896839546535178e-08	5.687426082530264	32095.0
5	rs11135411	94072196	A	T	1.3228063419128444e-08	5.683092553355047	32085.0
5	rs10684163	93998112	G	GTTA	1.3667150269273305e-08	5.6775075422171195	32054.0
5	rs200712407	93280729	T	TA	1.4138860793113416e-08	5.671698550493665	32117.0
5	rs17083079	92683607	G	A	1.4279443174335546e-08	5.670003704796567	32186.0
5	rs72773593	94068179	T	G	1.5587772116202267e-08	5.654965344305387	32134.0
5	5:92797041_TG_T	92797041	TG	T	1.5933130384938252e-08	5.651200290175116	32181.0
5	rs140083818	93150564	G	A	1.661870673012065e-08	5.6439554769913185	32154.0
5	rs880264	94069803	T	C	1.6626696663996366e-08	5.643872766489857	31943.0
5	rs35111621	94067705	A	G	1.6689572242714282e-08	5.643223232545884	32128.0
5	rs12523457	94069338	C	T	1.6896249002667543e-08	5.641104785849002	32119.0
5	rs141834426	93385558	G	C	1.7166811229392963e-08	5.638369229636546	32161.0
5	rs12109404	94072931	A	G	1.768156577594884e-08	5.633278416558889	31955.0
5	rs2003118	94069530	G	A	1.7728439717585573e-08	5.632822016473777	32126.0
5	rs61152231	94067762	A	G	1.784697721963519e-08	5.631673053977108	32137.0
5	rs74765438	94080778	G	GA	1.7902745712377323e-08	5.631135061101539	31943.0
5	rs57402656	94065844	G	GT	1.7918105660953198e-08	5.630987171095782	31991.0
5	rs199920547	93961802	C	CA	1.84174153676272e-08	5.626245525115798	31941.0
5	rs61238929	94079820	T	C	1.8422418248498005e-08	5.62619865022276	32015.0
5	rs67577452	94068397	A	G	1.893610225423365e-08	5.621450259368147	32137.0
5	rs67573880	94068468	A	G	1.893610225423365e-08	5.621450259368147	32137.0
5	rs114072973	93372299	C	A	1.97020529407094e-08	5.6145973099942195	32154.0
5	rs12515845	94069040	T	G	2.0298945456439636e-08	5.609433945501047	32125.0
5	rs114891177	93397741	C	T	2.033055720835697e-08	5.609164617797831	32138.0
5	rs1451735	93983612	C	A	2.469223853612216e-08	5.575427742024976	32186.0
5	rs115840240	93509229	G	A	2.5653435267643315e-08	5.568776456594041	31920.0
5	rs17083945	94049046	T	C	3.4196639092687804e-08	5.518468685653462	32186.0
5	rs1390644	94000772	G	T	3.783847730314352e-08	5.500654150151289	32171.0
5	rs7735473	94063520	T	G	3.8052210577467335e-08	5.499661006674137	32155.0

5	rs78371824	94042149	A	AT	3.80733840953267e-08	5.4995629154516585	32121.0
5	rs75522556	93970841	C	CCT	3.859468230726556e-08	5.497164418483997	32072.0
5	rs67674687	94060082	C	G	3.888293750538777e-08	5.495851608610331	32162.0
5	rs2201620	94004124	C	T	3.9184055835361716e-08	5.494490256559926	32141.0
5	rs66901899	94062810	A	C	3.920829823461168e-08	5.494381098641886	32164.0
5	rs72773517	93970216	C	T	3.975420029750141e-08	5.491940203508388	32121.0
5	5:92872910_GA_G	92872910	GA	G	4.000339006564027e-08	5.490836785587875	32068.0
5	rs1006626	94015064	C	T	4.049792993616618e-08	5.488666553165093	32153.0
5	rs66578784	94015540	T	C	4.049792993616618e-08	5.488666553165093	32153.0
5	rs67313609	94016254	T	G	4.049792993616618e-08	5.488666553165093	32153.0
5	rs143236930	94006853	T	TTATC	4.111161485642439e-08	5.4860089190386345	32149.0
5	rs6890092	94024807	G	A	4.280990766094194e-08	5.4788500024400815	32151.0
5	rs12653116	94024851	G	A	4.280990766094194e-08	5.4788500024400815	32151.0
5	5:94000377_CT_C	94000377	CT	C	4.32969448825642e-08	5.4768477448038695	32162.0
5	rs17083887	94003296	G	A	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs2220965	94003758	G	A	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs72773547	94004908	A	C	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs72773549	94005100	T	C	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs17083888	94007823	A	G	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs1124668	94013241	T	G	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs67831380	94015736	T	G	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs2270626	94024016	G	C	4.3445075404239205e-08	5.4762430952682495	32153.0
5	rs2032813	94001252	A	G	4.662003306897137e-08	5.463742244618361	32173.0
5	rs6556851	93993844	G	A	4.7241614353506325e-08	5.461391799312943	32170.0
5	rs66696350	93994219	C	T	4.7241614353506325e-08	5.461391799312943	32170.0
5	rs2132548	93996763	T	G	4.818322916965352e-08	5.457887676916075	32174.0
5	rs2044911	93998902	A	T	4.818322916965352e-08	5.457887676916075	32174.0
5	rs66483218	93988485	G	A	4.851861883658346e-08	5.456655572605651	32183.0
5	rs12651956	94036583	A	G	4.868001267879463e-08	5.456065607480955	32146.0
5	rs12655665	93992069	C	T	4.902116143185066e-08	5.4548247739043	32173.0
5	rs7735659	93996182	T	A	4.9940132871793876e-08	5.4515234569137485	32174.0
6	rs4262195	96929475	T	C	7.197157893193263e-09	5.786258158688043	32153.0
6	rs144345632	96886894	T	TA	7.265397365586511e-09	5.784671947576885	32114.0
6	rs11153023	96968525	C	T	8.185721475553405e-09	5.764588708368089	32165.0
6	rs9398072	96911304	T	C	8.697501927762305e-09	5.754351502537402	32166.0
6	rs11152952	96894303	A	G	8.705461725132107e-09	5.7541969521387655	32119.0
6	rs11152953	96894305	C	T	8.705461725132107e-09	5.7541969521387655	32119.0
6	rs12190520	96928620	A	C	9.019472416931042e-09	5.74820709855625	32155.0
6	rs12201449	96959382	C	T	9.198334390044896e-09	5.7448852491926745	32165.0
6	6:96893385_CAG_C	96893385	CAG	C	9.519722964580184e-09	5.739071136566513	32099.0
6	rs4078038	96904366	T	C	9.702708214008913e-09	5.7358454971722175	32172.0
6	rs2472895	96870387	A	T	1.0008580127052474e-08	5.730583402676022	32178.0
6	rs2499813	96875338	T	C	1.0008580127052474e-08	5.730583402676022	32178.0
6	rs4486027	96911886	T	C	1.0346439624473771e-08	5.7249496916168425	32164.0
6	rs4839837	96908706	G	A	1.0385649866645693e-08	5.724307488594034	32175.0
6	rs9400016	96940883	G	T	1.1079938990910542e-08	5.713310276925482	32173.0
6	rs2472884	96863965	C	T	1.1507933232072181e-08	5.706860040868146	32172.0
6	rs12194971	96911073	T	C	1.171060621960076e-08	5.703886510920026	32176.0
6	rs35487471	96879715	C	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs72931061	96880285	G	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs34209750	96882215	G	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs13207333	96882254	T	C	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs4486019	96883814	T	C	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs67996804	96884387	C	T	1.1961567516206782e-08	5.700273057167312	32185.0

6	rs34236778	96884556	C	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11757063	96884886	G	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11752584	96884952	C	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11757102	96885073	G	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs35035182	96885300	T	C	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs35410524	96885405	C	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12208884	96885572	G	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs13213297	96887569	C	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs13202091	96887771	T	C	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs140961595	96888323	A	G	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs148083617	96888353	A	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12210834	96890407	A	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12205655	96891733	T	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12529248	96895377	T	G	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12213426	96896035	T	C	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12190507	96898265	T	G	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12190508	96898269	T	C	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs34826652	96899085	A	G	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs28623445	96899116	G	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11152959	96900272	C	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11152960	96900398	A	G	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs12195315	96905711	T	G	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11152968	96908653	C	T	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11152969	96908712	A	C	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11152970	96909077	A	G	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs13201795	96910471	G	A	1.1961567516206782e-08	5.700273057167312	32185.0
6	rs11153071	97039741	G	A	1.2031878143044842e-08	5.699273900797943	31955.0
6	rs2472888	96865501	T	C	1.2138579228209842e-08	5.697768400114338	32178.0
6	rs139140529	96903530	T	TTCTAAG	1.2181069281380896e-08	5.69717246309208	32100.0
6	rs12205728	96891838	T	C	1.2354949615121169e-08	5.694754596811173	32183.0
6	rs12193732	96942609	G	A	1.2397830559683924e-08	5.6941634055785455	32175.0
6	rs10447413	96943434	G	C	1.2397830559683924e-08	5.6941634055785455	32175.0
6	rs112107820	96943946	C	T	1.2397830559683924e-08	5.6941634055785455	32175.0
6	rs11153018	96956137	G	A	1.2397830559683924e-08	5.6941634055785455	32175.0
6	rs12208682	96921307	G	C	1.2471364537930623e-08	5.693154216516754	32148.0
6	rs146759159	96944004	G	T	1.248943798966697e-08	5.6929070595212385	32171.0
6	rs6921291	97066242	C	T	1.2521483907412662e-08	5.692469680219324	32142.0
6	rs2472889	96866803	T	G	1.2927599343506168e-08	5.687019112494964	32186.0
6	rs12199452	96880703	G	A	1.3100215886116972e-08	5.68475260425986	32181.0
6	rs11152951	96894135	C	G	1.3282625382310893e-08	5.682388828096013	32164.0
6	rs12203657	96883285	G	A	1.3390986132219229e-08	5.6809995097169725	32186.0
6	rs147506219	96889290	C	A	1.3908048410642165e-08	5.6745170266471865	32186.0
6	rs142957763	96890032	G	A	1.3908048410642165e-08	5.6745170266471865	32186.0
6	rs2472887	96865437	A	G	1.390814693875232e-08	5.674515813842371	32186.0
6	rs11417499	96866499	C	CT	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2472890	96867646	C	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2142652	96868504	A	C	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2499809	96870110	C	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2472897	96870569	G	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2092095	96870864	T	G	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2092096	96870919	T	C	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2263192	96873037	C	G	1.390814693875232e-08	5.674515813842371	32186.0
6	rs1116113	96873586	G	C	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2472904	96874962	T	G	1.390814693875232e-08	5.674515813842371	32186.0

6	rs2472906	96875318	G	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2472908	96875998	A	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2472911	96877055	A	G	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2499814	96877245	C	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2499816	96878206	C	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2499817	96878321	C	T	1.390814693875232e-08	5.674515813842371	32186.0
6	rs2472882	96863474	C	T	1.3945242081251579e-08	5.674059793419876	32180.0
6	rs2472883	96863817	C	T	1.3945242081251579e-08	5.674059793419876	32180.0
6	rs2499807	96864053	T	G	1.3945242081251579e-08	5.674059793419876	32180.0
6	rs1303852	96864523	C	T	1.3945242081251579e-08	5.674059793419876	32180.0
6	rs2179126	96871350	A	G	1.4353955417355738e-08	5.6691119544594955	32185.0
6	rs2142653	96871520	C	A	1.4353955417355738e-08	5.6691119544594955	32185.0
6	rs12213375	96902134	A	G	1.4527125929726536e-08	5.6670567264151845	32183.0
6	rs75303492	96902999	G	A	1.4527125929726536e-08	5.6670567264151845	32183.0
6	rs12208449	96903253	C	T	1.4527125929726536e-08	5.6670567264151845	32183.0
6	rs12191653	96903898	T	C	1.4527125929726536e-08	5.6670567264151845	32183.0
6	rs12210146	96903962	C	T	1.4527125929726536e-08	5.6670567264151845	32183.0
6	rs4077932	96905144	C	T	1.4527125929726536e-08	5.6670567264151845	32183.0
6	rs11755945	96908038	G	C	1.4527125929726536e-08	5.6670567264151845	32183.0
6	rs2499804	96861216	T	C	1.4558212639347637e-08	5.666690303298651	32185.0
6	rs2472881	96862562	C	T	1.4558212639347637e-08	5.666690303298651	32185.0
6	rs2205755	96864704	A	G	1.4558212639347637e-08	5.666690303298651	32185.0
6	rs2472886	96864876	C	T	1.4558212639347637e-08	5.666690303298651	32185.0
6	rs2472893	96870048	G	C	1.4558418728947923e-08	5.666687876630551	32186.0
6	rs2273622	97058567	A	G	1.477671313042931e-08	5.664136053485628	32150.0
6	rs34242766	96872828	C	CA	1.5226315407558652e-08	5.658993688649467	32146.0
6	rs9373978	97056255	T	C	1.5834026921500586e-08	5.652272530960173	32110.0
6	rs13208422	96892119	C	T	1.725020750039938e-08	5.637534478157657	32184.0
6	rs2472880	96860130	G	A	1.7356835917286702e-08	5.636472875880543	32183.0
6	rs6568443	96944473	T	C	1.790265237875031e-08	5.631135960121127	32167.0
6	rs2499801	96854594	G	A	1.8047232473831608e-08	5.629748746361807	32086.0
6	rs760619	96857431	A	G	1.8514990807853505e-08	5.625333507415743	32088.0
6	rs12208011	96991105	G	A	1.855808724781166e-08	5.624932178739016	32183.0
6	rs10457159	96993139	G	A	1.855808724781166e-08	5.624932178739016	32183.0
6	rs3734238	96996228	A	T	1.855808724781166e-08	5.624932178739016	32183.0
6	rs3734239	96996244	A	G	1.855808724781166e-08	5.624932178739016	32183.0
6	rs34756237	96854540	T	TA	1.9584276538476583e-08	5.615634042668363	31913.0
6	rs6916232	96985959	A	T	1.98633142548538e-08	5.6131875166612994	32185.0
6	rs12204342	97054314	G	T	2.0153973680185632e-08	5.6106743237043295	32142.0
6	rs4265039	96878929	T	C	2.0804598821952385e-08	5.6051738887070055	32172.0
6	rs4346856	96880270	C	T	2.0804598821952385e-08	5.6051738887070055	32172.0
6	rs2064947	97052754	C	T	2.1775426464067423e-08	5.5972693493090775	32149.0
6	rs926276	96868735	C	T	2.19305046288764e-08	5.596038480336651	32168.0
6	rs12190397	97036465	G	A	2.236447747255332e-08	5.592638382776396	32090.0
6	rs12212614	97036466	T	G	2.236447747255332e-08	5.592638382776396	32090.0
6	rs12530462	97053514	C	T	2.2537978021701546e-08	5.5912969273839925	32148.0
6	rs4343922	96876903	C	T	2.2554593152867565e-08	5.591168990433197	32177.0
6	rs9486205	96877006	C	T	2.2554593152867565e-08	5.591168990433197	32177.0
6	rs13206547	97006942	T	C	2.2677282321877e-08	5.5902271027116175	32173.0
6	rs34051754	97007754	A	T	2.2677282321877e-08	5.5902271027116175	32173.0
6	rs4839826	96853616	C	T	2.3026096257317047e-08	5.587576026554098	31993.0
6	rs6568392	96861476	G	T	2.334158356131465e-08	5.585211601603699	32167.0
6	rs11153064	97021959	A	G	2.3427604148388207e-08	5.584572300224953	32171.0
6	rs3798294	97049587	G	A	2.3681224256591145e-08	5.582700582505454	32147.0

6	rs3798289	97023632	T	C	2.373266964839396e-08	5.582323289810205	32170.0
6	rs11153059	97014537	T	A	2.460685785323787e-08	5.576030658261048	32173.0
6	rs11153058	97012746	C	T	2.4852172545471726e-08	5.574303791896439	32172.0
6	rs12527021	97025496	C	T	2.4960861963575042e-08	5.5735439668401465	32168.0
6	rs13210597	96969694	C	A	2.5270349098967107e-08	5.5713978666438475	32163.0
6	6:96969558_GAACCCCCAGCGCCGCGGTAC_G	96969558	GAACCCCCAGCGCCGCGGTAC	G	2.546993140628335e-08	5.5700273751407945	31983.0
6	rs74221529	28680690	T	TA	2.5578582020377243e-08	5.569285668093932	26930.0
6	rs12214469	97019471	G	T	2.588914007725708e-08	5.567182371548926	32167.0
6	rs12204068	97036201	C	T	2.715992078432288e-08	5.558823479990467	32152.0
6	rs142257404	96984849	C	CAT	2.7337396308392496e-08	5.557686409026506	32184.0
6	rs6920913	96874297	A	G	2.773218233667587e-08	5.555182523792388	32133.0
6	rs35300731	96875349	C	CG	2.8015140473871862e-08	5.5534090831918	31950.0
6	rs9386648	97035656	T	C	2.8240681141498203e-08	5.55200791068886	32154.0
6	rs11153067	97039421	A	T	2.9214986240355743e-08	5.5460772061806205	32151.0
6	rs12207570	96987884	T	G	2.9302218257178866e-08	5.545555611034255	32186.0
6	rs2145535	97034715	G	A	3.0028283296374926e-08	5.541271727635776	32160.0
6	rs12208556	96903486	C	T	3.010749273870184e-08	5.540810475747254	32138.0
6	rs11756315	97008678	G	A	3.0828040605419376e-08	5.53666784150109	32171.0
6	rs200992455	97062117	ATAAT	A	3.2025135601595215e-08	5.529988733165904	32017.0
6	rs12197411	97039621	G	A	3.2446103467552235e-08	5.5276974123837705	32141.0
6	rs12525695	97039818	G	A	3.2638826886894314e-08	5.526658029593632	32154.0
6	rs9486719	97060124	G	A	3.3077140760372865e-08	5.524316140774461	32110.0
6	rs10872018	97026429	G	A	3.4254891477899416e-08	5.518169522648507	32167.0
6	rs12208124	97027942	C	T	3.44466263923172e-08	5.517188315395654	32165.0
6	rs13202675	97028427	C	T	3.44466263923172e-08	5.517188315395654	32165.0
6	rs3798296	97052286	G	A	3.5278327315430915e-08	5.512992498942244	32156.0
6	rs4839833	96882069	T	C	3.64093221337398e-08	5.507438172353678	32174.0
6	rs3798295	97052164	C	T	3.663348218542855e-08	5.506357216704617	32158.0
6	rs6923212	97061940	T	C	3.702689707644587e-08	5.504475488604517	32119.0
6	rs3906199	97049899	C	A	3.833782203423869e-08	5.49834228177656	32161.0
6	rs6924957	96853579	G	T	3.924372742845882e-08	5.4942216868363225	32009.0
6	rs1157316	96869710	G	A	4.113214715125233e-08	5.485920668072157	32172.0
6	rs13208321	96860354	A	G	4.195875327310651e-08	5.482402804707823	32137.0
6	6:96890391_AAC_A	96890391	AAC	A	4.649137291940286e-08	5.464232552773115	32089.0
6	rs11751075	97065751	G	A	4.776367978584963e-08	5.459440712187559	32118.0
6	rs11759769	97065212	G	A	4.843673574501173e-08	5.456955618924575	32121.0
10	rs4880259	134298687	T	C	4.508961432972106e-17	8.39884379292765	29501.0
10	rs11146399	134308479	C	T	5.503654932591339e-16	8.099828874727846	32033.0
10	rs11146400	134308575	C	T	5.579365481328456e-16	8.098166542010222	32035.0
10	rs4469802	134309194	G	A	7.732138798449122e-16	8.058365415682667	32022.0
10	rs4880400	134313795	T	C	1.0224780358603788e-15	8.024130209862609	32097.0
10	rs11146401	134313336	C	A	1.4602767365264618e-15	7.980258052331684	32120.0
10	rs35974361	134307547	C	G	1.5083154621191118e-15	7.976262038123653	32031.0
10	rs4454641	134307845	C	T	1.799713061243937e-15	7.954420903432577	32052.0
10	rs796953214	134309294	ATT	A	1.821553447497812e-15	7.952927234292401	31784.0
10	rs35263482	134313046	G	C	2.022029132986991e-15	7.9399867130618365	31992.0
10	rs35133675	134312857	C	T	2.406803752990105e-15	7.9183513913494785	32186.0
10	10:134312221_CACAA_C	134312221	CACAA	C	3.3161458194685373e-15	7.878394400038856	29589.0
10	rs7915907	134316231	G	A	5.788851709847463e-15	7.808465322329078	31962.0
10	rs67221163	134297909	C	G	6.552749215637474e-15	7.79282472369671	31711.0
10	rs71481917	134297801	C	T	7.883924929787514e-15	7.769431363381061	30916.0
10	rs57472801	134322756	A	G	9.539882660931271e-15	7.745243528791251	31745.0
10	rs7897053	134316342	C	T	1.7793118674599962e-14	7.665647546168928	31956.0

10	rs7917322	134306694	A	C	1.8653002955682653e-14	7.659588324802858	31090.0
10	rs4356146	134324520	G	A	2.093333047833664e-14	7.644761295339781	31724.0
10	rs11187838	96038686	G	A	4.2917313033974e-14	7.551833440068696	32147.0
10	rs2274224	96039597	G	C	5.049986986642375e-14	7.530620223036226	32186.0
10	rs7084359	134297562	A	C	5.877560539023701e-14	7.51078109325326	31837.0
10	rs57866767	96023077	T	C	6.855622855055232e-14	7.490606197873143	32139.0
10	rs3891783	96015793	C	G	6.894184578704718e-14	7.489870037653303	32139.0
10	rs10786156	96014622	C	G	7.468100049579422e-14	7.479367788191028	32139.0
10	rs7083220	134284485	G	A	8.010723377127049e-14	7.470143795428133	32155.0
10	rs9645539	134282867	G	T	9.598010224717971e-14	7.446319635920517	31875.0
10	rs11819412	134297803	G	C	9.847909623093286e-14	7.442926218060664	31133.0
10	rs10735665	134308936	G	A	1.043280898859151e-13	7.435303572358428	32018.0
10	rs11146402	134323354	C	G	1.1676556619761485e-13	7.42040178792245	31717.0
10	10:96026184_CA_C	96026184	CA	C	1.2073208668189555e-13	7.4159763034235775	31917.0
10	rs12762160	134330662	C	T	1.2559451019952514e-13	7.410742211508107	31313.0
10	rs11379033	134325396	C	CA	1.478293105137883e-13	7.389096989850744	31120.0
10	rs11596664	134280157	C	T	1.482216672420236e-13	7.38874450194884	31747.0
10	rs10747062	134285515	C	T	1.485203015482186e-13	7.3884768269320675	32132.0
10	rs10747061	134285403	G	A	2.1826563960480998e-13	7.337103612380594	32156.0
10	rs10781576	134285017	T	C	2.19278175959502e-13	7.336483900656723	32186.0
10	rs11146393	134299369	G	C	2.405872474501524e-13	7.324055423314602	31763.0
10	rs61861415	134328497	T	C	2.5388030908469136e-13	7.3168389114944015	31385.0
10	rs200898494	134299394	A	AG	3.1172050039237527e-13	7.289234747996606	31465.0
10	rs4880397	134309321	C	G	3.11869145734844e-13	7.289170511538463	32036.0
10	rs10870313	134310920	A	G	3.156833903200461e-13	7.287532405802485	31965.0
10	rs11814088	134298002	A	C	3.1840617023815953e-13	7.286374900040142	31820.0
10	rs10870314	134310923	T	G	3.765233955795692e-13	7.263742888352753	31955.0
10	rs7080018	134301505	G	A	5.410387895424326e-13	7.214571989497416	31929.0
10	rs4492738	134300136	T	C	5.933744352233561e-13	7.201995978071093	31939.0
10	rs4592360	134300069	A	G	5.963998680296833e-13	7.2013026833470475	31937.0
10	rs4309079	134300091	C	T	6.260333474957793e-13	7.194688911191922	31934.0
10	rs7903563	134300816	G	A	7.435485968066305e-13	7.1711785352399655	31943.0
10	rs4880396	134298833	T	C	7.460960526637285e-13	7.170710360150287	31766.0
10	rs4501914	134308062	C	T	7.574386324413606e-13	7.168644673091168	32186.0
10	rs11146395	134299444	T	C	7.825654384829695e-13	7.1641747216956935	31752.0
10	rs4293055	134323744	G	A	8.019254548016124e-13	7.1608257231068215	31495.0
10	rs543302184	96009182	T	TA	1.324066465091119e-12	7.091770832009837	30691.0
10	rs7080472	96012950	G	T	1.484423407411613e-12	7.075936955168742	31940.0
10	rs7096828	134301541	C	T	1.5309795102694828e-12	7.071653836089679	31966.0
10	rs7914305	134312761	C	T	1.652873068056089e-12	7.061017893580643	31964.0
10	rs61861416	134333189	T	A	2.0093864012123997e-12	7.033830894274732	30952.0
10	rs11596632	134279989	C	A	2.0632144190394627e-12	7.0301433586987425	31517.0
10	rs7918535	134300351	A	G	2.1668849492925253e-12	7.023299840532359	31951.0
10	rs7897891	134284005	T	C	2.9129910699348014e-12	6.981859149156841	31712.0
10	10:134303087_AG_A	134303087	AG	A	2.9544155561831077e-12	6.979875597084392	31783.0
10	rs12572574	134281065	C	T	3.132384377583428e-12	6.9716529838953205	31599.0
10	rs7917077	134305875	T	A	3.742350590645925e-12	6.946584784492347	31441.0
10	rs7914354	134334476	A	G	3.796200835261439e-12	6.944568039094263	30876.0
10	rs4593926	134281537	A	G	4.045781625797275e-12	6.935572911887697	31491.0
10	rs34102287	134331173	C	T	4.702499223453563e-12	6.914278684473759	30935.0
10	rs10870316	134321788	G	A	4.8995817747026744e-12	6.908455630628014	31837.0
10	rs10870317	134321883	G	C	5.3143179118716205e-12	6.896917082362893	31833.0
10	rs10747060	134285007	A	G	5.426028775359202e-12	6.893959998599807	31841.0
10	rs11591553	134323564	G	A	5.5975357092005364e-12	6.8895342248941205	31722.0

10	rs7090098	134320629	G	A	5.971001940904423e-12	6.880339658270646	31864.0
10	rs71503747	134304818	C	T	5.997122655095898e-12	6.879717837933923	30316.0
10	rs4497325	134302745	G	A	6.353751246874942e-12	6.871483790556253	32050.0
10	rs5025116	134320913	C	T	6.50461582493483e-12	6.868136083827987	31854.0
10	rs61861413	134326732	G	A	7.367172859675429e-12	6.850345715835326	31664.0
10	rs10735666	134322595	C	A	8.071625049381277e-12	6.8372704950253045	31637.0
10	rs11146397	134303122	T	C	8.307068403221574e-12	6.833148843921718	32143.0
10	rs10747063	134317884	C	T	1.0237974201001445e-11	6.803116565445973	31848.0
10	rs7086785	134316795	T	C	1.1307133896980027e-11	6.78879836458131	31909.0
10	rs10870315	134316622	A	G	1.1415220006620805e-11	6.787425462792664	31889.0
10	rs139032047	134304807	C	A	1.3152606812709075e-11	6.766949379012942	29973.0
10	rs71503746	134304802	G	A	1.3219783080215665e-11	6.766211963506348	29797.0
10	rs10781577	134325083	G	T	1.3418596867656795e-11	6.764050832741418	31588.0
10	rs11146398	134303274	T	C	1.3469926177200972e-11	6.763497970450421	32186.0
10	rs7894289	134305663	G	A	2.275826163692291e-11	6.687134553866423	30701.0
10	rs7093232	134303666	G	A	2.530307144250132e-11	6.671599266352523	32037.0
10	rs79361141	134304808	C	A	2.5735232153973962e-11	6.669113986323622	30417.0
10	rs10747064	134322499	C	T	3.580626510439153e-11	6.62046831942667	31669.0
10	rs11187844	96056629	C	A	7.449547612740312e-11	6.511315526300487	31901.0
10	rs7907962	134287486	A	G	7.866417789894608e-11	6.503133018285553	30475.0
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10	rs35364222	134296800	T	C	9.152344500176895e-11	6.480327983588389	31866.0
10	rs7904728	134295644	G	A	1.385228174250261e-10	6.417508291801415	32120.0
10	rs4344410	134294911	C	A	4.89945396730622e-10	6.222291581631027	32016.0
10	rs7923337	134295750	A	T	5.722881646151891e-10	6.197879803253204	32133.0
10	rs10747068	134335157	A	G	8.130444520354161e-10	6.142359772913839	28423.0
10	rs7095973	134324510	T	C	8.393782519584108e-10	6.137296144650871	31678.0
10	rs753724	96051417	G	T	8.474703943185124e-10	6.13577123017936	32180.0
10	rs11187840	96050351	A	G	8.991669143104533e-10	6.126352131568465	32163.0
10	rs12220091	96053689	C	T	1.0664123647871142e-09	6.099139106994366	32182.0
10	rs75017201	96055152	C	T	1.0664123647871142e-09	6.099139106994366	32182.0
10	rs3740365	96053239	T	A	1.0974119598630194e-09	6.094556606071854	32183.0
10	rs769015184	96049708	AC	A	1.3089632122842845e-09	6.066292902156383	32140.0
10	rs3781266	96052747	A	G	1.3681948132374006e-09	6.05917734265741	32182.0
10	rs11187842	96052511	C	T	2.1051480825203594e-09	5.989478615108893	32186.0
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10	rs4509684	134286579	C	T	2.3661538095337906e-09	5.97043945428576	30614.0
10	rs4486544	134294345	T	C	2.742066681100417e-09	5.946338585361418	31672.0
10	rs11146404	134326869	A	G	2.870438404284808e-09	5.938841139382259	31523.0
10	rs4412685	134294337	A	G	2.886947059474323e-09	5.937900754646733	31669.0
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10	rs12360525	134289214	A	T	3.133292905811434e-09	5.924457887070626	31503.0
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10	rs11187837	96035980	T	C	3.5910208638460205e-09	5.9020087628729465	32186.0
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10	rs4576738	134294398	G	A	6.393412599686308e-09	5.806127912051996	31548.0
10	rs2077218	96071561	G	A	7.2919590692838575e-09	5.784058440926818	31871.0
10	rs11187845	96060198	C	A	7.771044273502751e-09	5.773350746165256	32182.0
10	rs11146388	134288095	G	A	7.924842405929412e-09	5.770049130831633	31467.0
10	rs200197176	96055963	C	CA	7.951285316975931e-09	5.769487759590603	32010.0
10	rs10781575	134280542	C	T	8.547751317426325e-09	5.7572850348932265	30144.0
10	rs11187847	96063440	C	G	8.796288004349406e-09	5.7524430980208985	32165.0

10	rs12217792	96062386	T	C	8.922820878887288e-09	5.750028874857671	32173.0
10	rs11146389	134290675	T	G	9.792243886330027e-09	5.734288659530687	32186.0
10	rs4242719	134290895	T	C	9.959870496461384e-09	5.731410829458055	32180.0
10	rs372868680	134304572	G	A	1.0336874123084594e-08	5.725106718615635	26110.0
10	rs4880382	134290769	A	G	1.0380865178548989e-08	5.724385728018667	32184.0
10	rs35908501	134290607	C	T	1.0518954378181126e-08	5.7221416554067055	32180.0
10	rs10870311	134290526	C	A	1.1422431492958501e-08	5.708129777089063	32175.0
10	rs10870312	134290544	C	A	1.1453698624559652e-08	5.707664379311956	32176.0
10	rs10870310	134290153	G	A	1.2125665747339857e-08	5.6979499176098365	32154.0
10	rs10747058	134276427	G	T	1.2153216817882458e-08	5.697562874544871	31302.0
10	rs4880390	134296740	T	G	1.2898808534548391e-08	5.6874000034344565	31928.0
10	rs11816277	134296796	A	G	1.2952465406306794e-08	5.686690807100817	31938.0
10	rs7898918	134276762	G	A	1.3651981715908724e-08	5.6776975548434745	31568.0
10	rs4880258	134293640	G	A	1.3769274930651107e-08	5.6762335604193686	31927.0
10	rs56094089	134289658	T	C	1.4654100512552693e-08	5.665564829395205	31787.0
10	rs7096883	96069149	G	A	1.4776857383835465e-08	5.664134379326696	32171.0
10	rs4880385	134296241	C	T	1.4823078792702371e-08	5.663598764240249	32186.0
10	rs4880383	134295388	T	G	1.6702462516060403e-08	5.643090363620527	32150.0
10	rs4880381	134289543	A	T	1.9049440232855808e-08	5.620419441253746	31764.0
10	rs12771233	134291950	C	T	1.927591563531653e-08	5.618377347359412	31980.0
10	rs4880384	134295412	A	G	2.1428391460668057e-08	5.600054912798445	32163.0
10	rs12358548	134273093	T	A	2.7301359692661493e-08	5.557916711914437	32083.0
10	rs10787738	118777371	C	T	3.4236147452205936e-08	5.518265731247902	30800.0
11	rs11218557	122099839	T	C	1.2464323864899471e-08	5.693250592916878	31941.0
11	rs10892820	122120972	T	G	1.38594196355121e-08	5.675116630254277	31716.0
11	rs4127499	122176383	G	A	1.965344634739912e-08	5.615024440812554	32186.0
11	rs10892823	122128720	T	G	2.4543313926902302e-08	5.5764806933890165	31750.0
11	rs17337676	122132835	G	A	2.6847885743111573e-08	5.560840257902767	31754.0
11	rs10750202	122133372	A	G	3.9934397271703946e-08	5.491141618547697	31756.0
11	rs10892822	122124710	C	T	4.686732286065681e-08	5.462803525844152	31759.0
14	rs186347	59072226	G	T	2.088812305545398e-11	6.6996766444809115	31582.0
14	rs160459	59074136	A	C	3.009831399689939e-11	6.6460890809515245	32186.0
14	rs160458	59074878	T	C	7.369881980320526e-11	6.5129300836411925	31575.0
14	rs160460	59072964	A	G	1.8501390581295992e-10	6.373291369079907	31654.0
14	rs10782438	59072144	T	C	1.139520201158146e-09	6.088530116890116	31609.0
14	rs468213	59071100	C	G	2.1961397723828772e-09	5.982592306756784	31522.0
14	rs170239	59064739	C	T	2.4584735860110557e-09	5.964192110128144	31447.0
14	rs149142	59071725	T	C	2.880563469249779e-09	5.938263761505443	31601.0
14	rs221326	59069053	G	T	6.285716910176658e-09	5.808973146903211	31543.0
14	rs183400	59064730	C	T	4.6060415643556655e-08	5.465884514618648	31430.0
15	rs1440802	39635124	T	C	1.003264426053347e-31	11.720291283567304	32084.0
15	rs530653020	39633074	T	TA	4.089044471473289e-31	11.60066166457904	32111.0
15	rs5812099	39633877	A	AG	5.030460954055212e-31	11.582917079319868	32142.0
15	rs17694988	39636227	T	C	5.0592061130992065e-31	11.582428729203016	32107.0
15	rs71471500	39632013	C	G	7.394326587208771e-31	11.549857115153193	32137.0
15	rs7182018	39632269	A	G	7.395323097815078e-31	11.549845533223973	32138.0
15	rs1080066	39634222	A	G	1.6492128982617422e-30	11.480709647945735	32186.0
15	rs2033939	39633904	G	A	1.8508740402272843e-30	11.470731791569252	32152.0
15	rs11639391	39631771	C	T	3.915485110331933e-30	11.405714632088108	32132.0
15	rs4924345	39639898	A	C	3.761294813836875e-29	11.207145251213028	31998.0
15	rs4924346	39639992	G	A	3.8360538262484317e-29	11.205402673043961	31978.0
15	15:39640223_TTAAA_T	39640223	TTAAA	T	5.480639751552537e-28	10.967432850121407	31741.0
15	rs550614297	39640378	G	GA	8.798646845869065e-28	10.924538566330936	31531.0
15	rs28520337	39647894	T	C	5.317029944391902e-24	10.103748107662494	31643.0

15	rs574500639	39632734	T	TAC	2.762888912491769e-23	9.940910935884553	31822.0
15	rs34680120	39664000	C	A	2.1600033993622744e-18	8.748608127196812	32140.0
15	rs1837636	39661779	C	T	1.0057181932250956e-17	8.573287725237199	32186.0
15	rs4566132	39661138	G	A	2.3385374914593398e-17	8.475608598799981	32159.0
15	rs4923822	39662277	A	G	1.03855342042465e-15	8.022214778410742	32022.0
15	rs11629938	39626935	G	A	1.610559054323356e-14	7.678425397017933	32071.0
15	rs10520128	39627146	G	C	5.2713275909708294e-14	7.525017469153091	32066.0
15	rs12591944	39627982	A	C	5.4820024315590295e-14	7.519895540148804	31996.0
15	rs8025239	39623588	G	A	7.264782978334865e-14	7.482994668635992	32062.0
15	rs12595360	39625987	C	G	1.0022316550340508e-13	7.440607703164034	31944.0
15	15:39625576_ACT_A	39625576	ACT	A	1.2943951374925129e-13	7.406742428061791	31999.0
15	rs72722978	39628675	C	T	1.9539972300765807e-13	7.351906333476349	31910.0
15	rs4702	91426560	G	A	3.7705468908363357e-13	7.263552251032982	32186.0
15	rs773225188	39631994	AAGAG	A	6.594332253670534e-13	7.187593335651549	31403.0
15	rs8032326	39619456	C	A	5.0360107939395915e-12	6.904557636537796	32186.0
15	rs16968876	39636877	C	T	8.97969466977613e-12	6.821975559301237	31917.0
15	rs6224	91423543	G	T	4.886248673375258e-11	6.574361197508928	31804.0
15	rs11372849	91419432	T	TC	5.2979422210413684e-11	6.562313106986054	31414.0
15	rs16968890	39638991	G	C	1.0066687469709907e-10	6.465946225660579	31948.0
15	rs7183988	91428589	T	G	1.7658202163711128e-10	6.380438160280219	31955.0
15	rs17514846	91416550	C	A	2.830281105954788e-10	6.30780082301566	31337.0
15	rs2071382	91428197	T	C	3.276211975652744e-10	6.285110205864173	31970.0
15	rs7177338	91428636	G	A	3.312961310757099e-10	6.283377100366999	31950.0
15	rs1894401	91429042	G	A	3.503889036264062e-10	6.2746645453339776	31981.0
15	rs8039305	91422543	T	C	5.634662823476524e-10	6.200325150671808	31771.0
15	rs11539637	91428290	C	T	6.233674012213628e-10	6.184406010904782	31943.0
15	rs8033007	39619661	G	C	7.09354584270465e-10	6.163987693333132	32158.0
15	rs978740	39655920	C	T	7.122082397681491e-10	6.163352267873036	31831.0
15	rs56113415	39621418	G	A	5.450276098992282e-09	5.832806501939312	32117.0
15	rs11638016	39621773	T	C	5.732272021074552e-09	5.8243866704669145	32072.0
15	rs3910644	39648234	C	T	7.87810735134866e-09	5.7710457641289965	31154.0
17	rs62073094	44316219	C	T	2.13287849079083e-16	8.2143661529309	30258.0
17	rs28434724	44312278	A	G	3.417830122355649e-16	8.157587303086428	30400.0
17	17:44270659_G_A	44270659	G	A	5.3690367959712e-16	8.102841047469974	31162.0
17	rs9908639	44200192	A	G	7.269001835554949e-16	8.065913914756733	31520.0
17	rs146895044	44166992	A	AAAATATG	9.690427459411694e-16	8.030717476095408	31603.0
17	17:44266982_T_C	44266982	T	C	1.378355579070789e-15	7.987381037311898	31307.0
17	rs2696461	44285844	C	T	4.1734793872419705e-15	7.8496055100203215	30674.0
17	rs56807059	44189270	A	C	4.651963238220654e-15	7.835980972849088	31590.0
17	rs11655181	44332093	G	A	4.7281277156267305e-15	7.833940453520714	30363.0
17	rs2016034	44189598	A	G	5.448534290102809e-15	7.816099428898584	31452.0
17	rs8068300	44202690	T	C	5.635245115901575e-15	7.811854818021024	31563.0
17	17:44224272_G_A	44224272	G	A	5.841373000630384e-15	7.807326664453987	31551.0
17	rs2732634	44319047	A	G	6.12657229696107e-15	7.801314276785388	30344.0
17	17:44222424_G_C	44222424	G	C	6.883752693979011e-15	7.786598008032664	31556.0
17	rs62073102	44319735	C	G	7.761565907087313e-15	7.771412545015654	30253.0
17	rs8070420	44185479	G	T	8.077938286891876e-15	7.76635118980803	31610.0
17	rs60521849	44172812	G	A	8.438923542335159e-15	7.760809138525095	31613.0
17	rs2158258	44163809	A	C	9.194383518591518e-15	7.749929148398963	32174.0
17	rs11079732	44161581	T	C	1.1688228860338078e-14	7.719395950440285	32174.0
17	rs8065825	44175489	A	G	1.1700608596082432e-14	7.719261008151095	31614.0
17	rs8064986	44119367	A	G	1.1816714426070542e-14	7.718002219102359	32132.0
17	rs11652924	44182267	T	C	1.3278333333467694e-14	7.70312021510791	31588.0
17	rs11654640	44162230	G	A	1.3310946129784842e-14	7.7028068721159295	32186.0

17	rs6503455	44140748	C	T	1.3783520164396154e-14	7.6983492636561985	32079.0
17	rs9904766	44186952	T	C	1.3982135245140943e-14	7.696520523128266	31584.0
17	rs72836329	44161763	C	T	1.4045405462530557e-14	7.695943329908069	32133.0
17	rs7521	44105395	A	G	1.4350380161318967e-14	7.693196551425887	31932.0
17	rs7220988	44109474	G	A	1.4406409059492114e-14	7.692698174437496	32186.0
17	rs35173354	44212633	T	TA	1.448100275080826e-14	7.69203761505191	31107.0
17	rs143437112	44222045	T	TA	1.4776354172690798e-14	7.689454612264255	31219.0
17	rs113564729	44179095	G	A	1.888184334855864e-14	7.6580220776557075	31591.0
17	17:44329580_AT_A	44329580	AT	A	2.329237985971001e-14	7.6310087884511155	29428.0
17	rs113042517	44139453	G	A	2.3648050221099208e-14	7.62905512938946	32138.0
17	17:44291980_G_A	44291980	G	A	2.7589075071189735e-14	7.609156391840178	30969.0
17	rs11654745	44131096	G	A	2.8072808355485715e-14	7.606909340756143	32146.0
17	rs7213077	44119051	T	C	2.946716625002523e-14	7.600639175764982	32169.0
17	rs8078067	44125466	G	A	3.0864487649235227e-14	7.594641853734182	32145.0
17	17:44236005_C_T	44236005	C	T	3.1716502443640664e-14	7.5911147051925125	31436.0
17	rs2532231	44274474	C	T	3.1841021524474027e-14	7.590607044648504	31058.0
17	rs10514899	44119987	C	G	3.2417572680618755e-14	7.588281628652442	32155.0
17	17:44221843_A_G	44221843	A	G	3.701082879538306e-14	7.571089028173356	31509.0
17	rs62063662	44119840	T	C	4.162144509646456e-14	7.55582459292876	32145.0
17	rs4792827	44131305	T	C	4.525871664883928e-14	7.544913681717287	32186.0
17	rs16940845	44116843	C	A	5.54497518594104e-14	7.518402078825425	32186.0
17	17:44235827_C_A	44235827	C	A	6.414129976668959e-14	7.4993372625050405	31424.0
17	17:44262950_G_A	44262950	G	A	7.905298590330521e-14	7.471886826823125	31063.0
17	rs7206949	44247017	C	A	9.121445721906327e-14	7.453038779941987	31433.0
17	rs62071628	44356058	G	A	9.372049721569844e-14	7.449463594156009	29940.0
17	rs916896	44098797	C	T	9.501552202862083e-14	7.44765273390392	31873.0
17	rs2732610	44365490	C	T	1.4632985329522965e-13	7.39045260467646	28524.0
17	17:44286384_C_A	44286384	C	A	1.5677689447218874e-13	7.381278310002557	30912.0
17	rs28787973	44084349	T	A	1.6261729526153812e-13	7.376407892845621	31447.0
17	rs28753217	44084350	A	T	1.6261729526153812e-13	7.376407892845621	31447.0
17	17:44270181_G_A	44270181	G	A	1.772164883371061e-13	7.364947581948904	31009.0
17	rs7225002	44189067	A	G	2.0855535071878594e-13	7.343194343001845	32016.0
17	rs4988900	44342378	G	A	2.1510463799243e-13	7.3390566005727855	30044.0
17	rs41543317	44087500	A	G	2.72179029812221e-13	7.307489774832258	32186.0
17	rs11654982	44284600	G	A	2.8773910537242517e-13	7.300013383248197	30935.0
17	rs56087321	44084403	G	C	8.070230228141074e-13	7.15995711665839	31994.0
17	rs4510068	44184828	G	T	9.779838480860608e-13	7.1335702129148535	31147.0
17	17:44265839_C_T	44265839	C	T	1.1781176311389222e-12	7.107911847653782	31488.0
17	17:44289832_A_G	44289832	A	G	1.708862261797252e-12	7.056388022347883	31415.0
17	rs2532351	44336997	C	G	3.341428429409897e-12	6.962560574598143	29681.0
17	rs5820605	44102682	C	CT	4.549285068847872e-12	6.9189733248548215	31797.0
17	rs556046991	44212908	AT	A	2.5284615680573183e-11	6.671706325089718	30379.0
17	17:44776768_GAC_G	44776768	GAC	G	2.7670825585399068e-11	6.6584617624473985	27910.0
17	rs7225145	44363740	C	A	1.0468120415860143e-10	6.4600314778510475	27604.0
17	rs12946693	44084008	T	C	3.5501898495868213e-10	6.272621601170705	30782.0
17	rs141698966	44113227	T	TG	9.486148463518452e-10	6.1178244482294035	31241.0
17	17:43850935_CA_C	43850935	CA	C	1.7293561995738133e-09	6.02138055476673	31964.0
17	17:43975360_ATTACTGTATAAGCTGCTTATAT_A	43975360	ATTACTGTATAAGCTGCTTATAT	A	1.817261697786532e-09	6.013351708151768	31537.0
17	rs201474071	44113197	G	GA	2.063508245962949e-09	5.992727216507348	31754.0
17	rs552290972	43947883	T	G	2.345121521146673e-09	5.971895905764653	30687.0
17	17:44125277_CT_C	44125277	CT	C	2.4498426228045372e-09	5.964766404918502	31244.0
17	rs3874943	44572068	A	G	2.5195362927716274e-09	5.960184288844944	27960.0
17	rs55767267	43960325	T	C	2.9062622168003382e-09	5.936807127465631	31886.0

17	rs56127309	43960341	G	A	2.9062622168003382e-09	5.936807127465631	31886.0
17	rs56365901	43960323	A	G	3.363145642852868e-09	5.9128126890820525	31885.0
17	rs113758975	44207523	T	A	3.627707827590935e-09	5.9003320268691155	31745.0
17	17:44238616_TAAAAAAAA_T	44238616	TAAAAAAAA	T	3.763144394135963e-09	5.894281823598792	30703.0
17	rs62063672	44125288	A	G	3.781960260626573e-09	5.893458102592508	31311.0
17	rs11653367	44191483	A	G	4.224703479899445e-09	5.875146193674572	31486.0
17	rs55657917	43844560	T	G	4.772312670729565e-09	5.854922931424293	31909.0
17	rs111905143	44184808	C	G	4.9122925833058585e-09	5.850116352840077	32065.0
17	rs56194509	43844559	T	G	4.929924900067284e-09	5.8495203763914905	31910.0
17	rs112384186	44129398	G	GA	4.9344669353585786e-09	5.849367190484272	31969.0
17	rs1987152	44156180	A	G	4.938160365611556e-09	5.84924272596936	32017.0
17	rs1987151	44156181	T	A	4.938160365611556e-09	5.84924272596936	32017.0
17	rs146712066	43970012	C	CAG	4.9889700481133636e-09	5.847539629369838	31857.0
17	rs62055546	43964567	A	C	5.098216431587452e-09	5.8439342269399	31956.0
17	rs368385820	44106792	T	TA	5.12279839108671e-09	5.843133326832207	31170.0
17	rs78005814	44125175	A	C	5.264651549300895e-09	5.838583438455203	26395.0
17	rs113161176	43974354	G	A	5.365659004771693e-09	5.835415793866591	32108.0
17	rs10221243	44212310	G	A	5.5518526502616836e-09	5.8297257994907685	32040.0
17	rs7207582	44210933	A	G	5.732365591624566e-09	5.824383944090744	32042.0
17	17:44127285_CTT_C	44127285	CTT	C	5.859930651890654e-09	5.820706747588661	32093.0
17	rs112166495	44005361	G	A	5.903844898784417e-09	5.8194588700593135	31862.0
17	rs112572874	44072984	A	G	5.991871885911168e-09	5.816984434847938	32096.0
17	rs62061820	44185431	T	C	6.0742608604278374e-09	5.814700313852785	32040.0
17	rs8070942	44208674	G	T	6.3931664243754524e-09	5.806134362495151	32053.0
17	rs137941099	44003625	T	TAA	6.436529570610816e-09	5.8050018436902455	31798.0
17	rs9303525	44187257	A	G	6.510220896236532e-09	5.803094155298064	32055.0
17	rs6503457	44208312	G	T	6.589502368966091e-09	5.801065063555706	32050.0
17	rs200924217	44010463	A	AC	6.677133490488729e-09	5.798849719070576	32103.0
17	rs9910284	44200191	C	T	6.787093327748542e-09	5.7961095610645925	31742.0
17	rs2696578	44227623	T	C	6.866835012913628e-09	5.794149304538688	32033.0
17	rs112790197	44182845	T	TG	6.938460764720714e-09	5.792407341025692	32055.0
17	rs2532387	44313522	G	T	7.018141668292813e-09	5.790489904675497	31628.0
17	17:44212782_T_C	44212782	T	C	7.029339306356394e-09	5.790222143617128	32050.0
17	rs2668669	44284734	G	C	7.089644127740483e-09	5.7887872122919575	31844.0
17	rs2696441	44274985	C	A	7.237490140509601e-09	5.7853188864642275	31999.0
17	rs17689182	43783573	C	T	7.464685432067008e-09	5.7801211442091445	31999.0
17	rs2696459	44285142	G	C	7.580921467356801e-09	5.777521106106148	31613.0
17	rs62062271	44091988	T	C	7.826731463699745e-09	5.772148019227184	31960.0
17	rs62062324	44114362	A	T	7.827904281718493e-09	5.772122778376504	31749.0
17	rs62062325	44114364	C	A	7.827904281718493e-09	5.772122778376504	31749.0
17	rs62057121	43900760	G	A	7.885584212843481e-09	5.770885933083626	31758.0
17	rs4471723	44205690	C	T	7.950994239275908e-09	5.769493929153912	32064.0
17	rs2732666	44286198	G	A	7.976385425108773e-09	5.768956572248392	31885.0
17	rs79857651	44013475	G	A	8.00516699267329e-09	5.768349471769907	32036.0
17	rs113756354	44013483	A	G	8.00516699267329e-09	5.768349471769907	32036.0
17	rs113141256	43991468	T	TA	8.005737952935895e-09	5.768337449770316	32140.0
17	17:44183002_C_A	44183002	C	A	8.007451073610568e-09	5.7683013837230765	32081.0
17	rs16940904	44186063	C	T	8.139461127296319e-09	5.7655445204118765	31950.0
17	rs2696658	44245766	G	A	8.292381343594003e-09	5.762404809987661	32030.0
17	rs2532252	44257783	A	G	8.33967854983302e-09	5.761445110299026	31604.0
17	rs2004674	44075110	A	T	8.380549158328217e-09	5.760620064166237	32045.0
17	rs2532402	44304130	C	G	8.432364624567446e-09	5.7595796820975576	31640.0
17	rs62061813	44181118	G	A	8.781696169491658e-09	5.7527236756998015	32062.0
17	rs111952388	44181454	C	T	8.781696169491658e-09	5.7527236756998015	32062.0

17	rs62061814	44181508	T	G	8.781696169491658e-09	5.7527236756998015	32062.0
17	rs7220752	44138201	T	C	8.849983965520486e-09	5.751414492192211	32136.0
17	rs62062789	44025033	T	C	8.990046245816046e-09	5.748759732385103	32031.0
17	rs62062790	44025045	C	T	8.990046245816046e-09	5.748759732385103	32031.0
17	rs201722973	44161747	C	CCAACAA	9.019076026939812e-09	5.748214531246369	32176.0
17	rs2532315	44213934	G	A	9.071923182049246e-09	5.747226387073598	31708.0
17	rs62054372	43798775	G	C	9.080642081525762e-09	5.7470638977292285	31764.0
17	17:43798790_TTTC_T	43798790	TTTC	T	9.080642081525762e-09	5.7470638977292285	31764.0
17	rs62061848	44192946	C	T	9.09920515535972e-09	5.746718452517286	31889.0
17	rs62063298	44048323	G	T	9.100629644840502e-09	5.746691972121361	31939.0
17	rs62063299	44048336	T	C	9.100629644840502e-09	5.746691972121361	31939.0
17	rs62055545	43964561	C	T	9.115275716936577e-09	5.746419943967272	31871.0
17	rs9907738	44151546	T	G	9.152838703954849e-09	5.745724207134223	32138.0
17	17:44024749_CT_C	44024749	CT	C	9.199580751573985e-09	5.7448623226173545	25804.0
17	rs8080583	44162597	C	A	9.208616587039008e-09	5.744696200439411	32138.0
17	rs112439933	44005226	A	C	9.25017531913764e-09	5.743934185472909	32124.0
17	17:44263341_GA_G	44263341	GA	G	9.260577265792153e-09	5.743743977624972	31990.0
17	rs113313477	44005186	G	A	9.358106492034937e-09	5.741970613508898	32119.0
17	rs7221390	44116950	T	G	9.42750567347102e-09	5.740719642018024	32129.0
17	rs2066899	44155732	C	T	9.42750567347102e-09	5.740719642018024	32140.0
17	rs8077487	44115440	T	C	9.43488254132351e-09	5.740587195258987	32128.0
17	rs62061817	44182706	A	G	9.474748270521084e-09	5.739873169936041	32062.0
17	rs62062133	44114372	T	C	9.502340489183279e-09	5.7393806805580665	31771.0
17	rs7218319	44126365	C	T	9.528927600124829e-09	5.738907444500238	32134.0
17	rs2097760	44168677	A	G	9.587635626554305e-09	5.737867003672412	32137.0
17	17:44292021_C_CAAA	44292021	C	CAAA	9.631488714112438e-09	5.7370938591622345	31895.0
17	rs34579536	44108906	A	G	9.676088810140791e-09	5.736311046424043	32186.0
17	rs2696694	44343370	C	G	9.746831908265065e-09	5.735076541377636	30735.0
17	rs2696690	44344178	T	G	9.833930999654512e-09	5.733568523087111	31132.0
17	17:43996716_GC_G	43996716	GC	G	1.0003248259976625e-08	5.730673783696318	31925.0
17	rs4383188	44197603	T	C	1.0028645654448288e-08	5.730243688830643	32075.0
17	rs17573907	44099082	C	T	1.0057248730507933e-08	5.729760572748196	32174.0
17	rs62062286	44096486	C	T	1.0169719399655156e-08	5.727873765069468	32139.0
17	rs62056842	43991515	T	G	1.0174125328745758e-08	5.727800264704152	32128.0
17	17:44104278_TG_T	44104278	TG	T	1.0201686751161462e-08	5.727341181821134	32150.0
17	rs78556223	44026478	A	G	1.0261254101117566e-08	5.726353089473003	32014.0
17	rs2004673	44075099	T	C	1.0384436298507755e-08	5.724327329595718	32046.0
17	rs55703644	44274766	T	C	1.0397933653611111e-08	5.724106783894618	32042.0
17	rs111657460	44166362	G	GA	1.0456250366158628e-08	5.7231570806458585	32134.0
17	rs62061717	44012248	T	A	1.0469765016451486e-08	5.722937725776888	32009.0
17	rs7350980	44110271	G	A	1.0477569726427747e-08	5.72281117366795	32131.0
17	rs1029463	44150161	T	G	1.0509516905837769e-08	5.7222941086111065	31902.0
17	17:44161091_GCTCCCCTGGTAAGTCCTAAA_G	44161091	GCTCCCCTGGTAAGTCCTAAA	G	1.0578876443579533e-08	5.72117676316835	31621.0
17	rs4597358	44110670	C	G	1.0670238098857621e-08	5.71971579204759	32128.0
17	rs62062290	44099129	C	A	1.0761763244878894e-08	5.718264346205183	32182.0
17	rs62057063	43856730	C	T	1.0860218739791629e-08	5.716716329061586	32130.0
17	rs111324579	44082181	A	G	1.0897173786277804e-08	5.716138802390118	32155.0
17	rs2532343	44344097	G	C	1.0919684784044884e-08	5.715787936794063	31285.0
17	rs76924476	44199029	T	C	1.0960879223779716e-08	5.715147679782088	32053.0
17	rs113343439	44314217	A	G	1.109803958939614e-08	5.7130326190496525	32135.0
17	17:44617964_TA_T	44617964	TA	T	1.127573554916828e-08	5.710329945665555	24240.0
17	rs1029464	44149348	A	C	1.1311031160568889e-08	5.70979804621208	32085.0
17	rs62062277	44093753	T	G	1.1376948637395873e-08	5.7088089847934285	32117.0
17	rs55686102	44202608	C	T	1.1401643569912871e-08	5.708439882015022	32098.0

17	rs78765934	44261613	T	TCC	1.1454599412845998e-08	5.707650989770802	31949.0
17	rs17577159	44188477	T	G	1.1460606536654154e-08	5.707561724543995	32104.0
17	rs62061823	44188645	C	T	1.1460606536654154e-08	5.707561724543995	32104.0
17	rs35095455	44249911	T	TA	1.1463367602877696e-08	5.707520710641857	31998.0
17	rs2532246	44262418	G	A	1.1494596762329644e-08	5.707057488280466	31935.0
17	rs62063786	44061023	G	A	1.1525582796761422e-08	5.7065990793488535	32186.0
17	17:44058699_TAGG_T	44058699	TAGG	T	1.165265937673128e-08	5.704731544771029	31776.0
17	rs62063300	44048350	T	C	1.1661328529001888e-08	5.704604863856237	31949.0
17	rs4581739	44204739	T	C	1.1731491510169164e-08	5.703582938351105	32095.0
17	rs113638513	44204749	A	G	1.1731491510169164e-08	5.703582938351105	32095.0
17	17:44003580_GA_G	44003580	GA	G	1.173656053059945e-08	5.703509338157732	32113.0
17	rs17577369	44192923	A	G	1.174637227729239e-08	5.703366963154106	31867.0
17	rs111697872	43840726	C	CTT	1.1750282586896844e-08	5.7033102541508045	31913.0
17	rs62063280	44037299	G	C	1.1892244391697479e-08	5.701263783491683	32098.0
17	rs113201171	44082249	A	T	1.1999309197316695e-08	5.69973601782045	32168.0
17	rs17661027	44193097	C	A	1.20386153221461e-08	5.699178459477285	32088.0
17	rs2696605	44213921	A	C	1.213082158106812e-08	5.697877422455728	31737.0
17	rs77926909	43994252	T	C	1.2141386274598999e-08	5.697728967878548	32144.0
17	rs2696629	44327438	C	G	1.2173651456289728e-08	5.697276354859926	31479.0
17	rs75210307	43940012	T	C	1.2175116136244289e-08	5.6972558361318635	31670.0
17	rs74944644	43940020	T	C	1.2175116136244289e-08	5.6972558361318635	31670.0
17	rs2532247	44262403	C	T	1.2242418763008577e-08	5.6963155703547415	31931.0
17	rs1918793	44228169	C	T	1.228459207976397e-08	5.695728935359227	31985.0
17	rs12150087	44210988	C	G	1.2309389618270796e-08	5.6953849120653794	32098.0
17	rs1468241	44196153	A	G	1.2355984669810972e-08	5.694740303247832	32095.0
17	rs62055934	43848638	G	A	1.2375669197289433e-08	5.694468691456607	31958.0
17	rs77635460	44186593	T	C	1.2388195796965373e-08	5.6942960649313	32100.0
17	rs2696569	44266290	G	C	1.2420840781774168e-08	5.693846986729873	31550.0
17	rs78929339	44189910	A	G	1.2435347419987253e-08	5.693647795210402	32005.0
17	rs78590209	44098862	A	G	1.2442650981671116e-08	5.693547595001906	32186.0
17	rs55744103	44316280	T	C	1.245004682320814e-08	5.693446186990813	32135.0
17	rs62061816	44182336	C	A	1.245797572558895e-08	5.693337534912724	32101.0
17	rs111854640	44276431	T	TAGAA	1.2534611686377576e-08	5.692290819441827	31731.0
17	17:43972025_TC_T	43972025	TC	T	1.2553865033433435e-08	5.692028829174291	32150.0
17	rs111750615	44156132	T	TTTA	1.2591479197284734e-08	5.6915181182271075	32021.0
17	rs9709338	44094871	A	G	1.2608410416095024e-08	5.691288716131664	32018.0
17	17:44265192_AT_A	44265192	AT	A	1.2621525157595216e-08	5.691111229334996	31785.0
17	rs55857174	44137386	T	TAA	1.2685146846171165e-08	5.690252747941858	31940.0
17	rs17650842	44037491	A	G	1.2748271867040671e-08	5.6894050929992295	32121.0
17	rs113138968	44314261	C	T	1.2764146342859638e-08	5.689192569226142	32157.0
17	rs9899964	44314342	T	C	1.2764146342859638e-08	5.689192569226142	32157.0
17	rs974294	44150163	T	G	1.2817956641416064e-08	5.688474075282652	31961.0
17	rs77095128	44204304	T	G	1.2883096075054548e-08	5.687608221567945	32098.0
17	rs17660907	44191085	G	A	1.2918755151845635e-08	5.687136029855043	32108.0
17	rs79772780	44189855	G	A	1.292012507414096e-08	5.68711791483531	31916.0
17	rs55909047	44209957	A	G	1.2929078741216775e-08	5.686999562921853	32106.0
17	rs2732631	44289232	G	T	1.2972287866391269e-08	5.686429530498604	31747.0
17	rs62061810	44178884	G	A	1.2977974158376992e-08	5.686354652009177	32107.0
17	17:44251554_ATG_A	44251554	ATG	A	1.2978799791092566e-08	5.686343782524999	31316.0
17	rs56257094	44201667	G	A	1.2988895022601303e-08	5.686210932740496	32099.0
17	rs55672516	44201680	A	C	1.2988895022601303e-08	5.686210932740496	32099.0
17	rs55669501	44202564	G	A	1.2988895022601303e-08	5.686210932740496	32099.0
17	rs55885063	44202952	C	G	1.2988895022601303e-08	5.686210932740496	32099.0
17	rs56273589	44203131	C	G	1.2988895022601303e-08	5.686210932740496	32099.0

17	rs62063171	44203311	C	T	1.2988895022601303e-08	5.686210932740496	32099.0
17	rs62063172	44203366	T	C	1.2988895022601303e-08	5.686210932740496	32099.0
17	rs76380490	44203413	C	T	1.2988895022601303e-08	5.686210932740496	32099.0
17	rs113120855	44203520	C	T	1.2988895022601303e-08	5.686210932740496	32099.0
17	17:44238130_AT_A	44238130	AT	A	1.2992292422576544e-08	5.686166246682251	31893.0
17	rs34847058	44285460	G	GA	1.3000008675557232e-08	5.6860647968385445	31769.0
17	17:44048939_AG_A	44048939	AG	A	1.3000835683577132e-08	5.6860539271783255	31987.0
17	rs79301522	44207932	A	G	1.3066240341538411e-08	5.685196410957714	32095.0
17	rs62064668	44082981	G	A	1.30851847717582e-08	5.6849488106018375	32143.0
17	rs35014258	44192592	A	AT	1.3086664494636077e-08	5.684929485551902	32133.0
17	rs111327992	44126691	G	A	1.3097489958919875e-08	5.684788170490058	32157.0
17	rs2532289	44238571	C	G	1.326458476114663e-08	5.682621199805998	31987.0
17	rs2532256	44255017	T	C	1.3280432943912072e-08	5.682417051363528	32069.0
17	17:44285467_A_G	44285467	A	G	1.3302971166540527e-08	5.682127132413973	31784.0
17	rs111541901	43994358	C	T	1.3306355134979376e-08	5.6820836441664735	32160.0
17	rs1881195	44257473	T	C	1.3307577331118151e-08	5.6820679400511205	31889.0
17	rs62063174	44205122	C	G	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs17661348	44207066	A	G	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs62063202	44208945	C	T	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs62063203	44209313	T	C	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs111724389	44209364	G	A	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs112401617	44209474	A	T	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs111424940	44211502	G	A	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs62063207	44211902	A	G	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs62063208	44212032	C	A	1.3329501532715356e-08	5.681786471647012	32108.0
17	rs2532316	44213712	G	A	1.334589722172127e-08	5.681576273470894	32086.0
17	rs2942163	44282007	T	C	1.334589722172127e-08	5.681576273470894	32068.0
17	rs62062778	44022528	A	G	1.334702868792924e-08	5.681561776953956	32160.0
17	rs2696630	44327482	G	A	1.3350706603100502e-08	5.681514663192817	31412.0
17	rs2532274	44247164	A	G	1.3379693137836802e-08	5.681143788998659	31986.0
17	rs62061771	44169406	G	A	1.3403438095770652e-08	5.680840560412812	32144.0
17	rs111689007	43981103	C	A	1.3432726718631917e-08	5.680467256014563	32180.0
17	rs17577954	44209628	T	C	1.3454473026867577e-08	5.680190594980607	32105.0
17	rs75686108	44022376	C	T	1.3477586574570167e-08	5.679897015494713	32163.0
17	rs112003140	43980998	G	A	1.3497592621304009e-08	5.679643300948688	32177.0
17	rs78729125	43970108	C	A	1.3587309242380043e-08	5.6785099987296475	32170.0
17	rs77727624	43790770	A	G	1.3593835915044665e-08	5.67842783756996	31843.0
17	rs2532236	44271430	A	G	1.3618723038718737e-08	5.678114896757539	32075.0
17	rs2532423	44285952	T	C	1.3620839061405951e-08	5.678088314660332	32012.0
17	rs1528075	44220454	T	G	1.3733354060271753e-08	5.676680615381238	32090.0
17	rs62055489	43950441	C	A	1.3743927742705082e-08	5.676548902230616	31916.0
17	rs1816	44276618	A	G	1.377151504909594e-08	5.6762057184594354	31850.0
17	rs62056859	43994435	A	G	1.3778809492125065e-08	5.676115087844011	32162.0
17	rs62061847	44191682	G	A	1.3829879194351662e-08	5.675481869139421	32109.0
17	17:44282744_G_C	44282744	G	C	1.3830172112089745e-08	5.675478243776992	32064.0
17	rs112402370	44092744	A	G	1.3845314478917476e-08	5.6752909323857805	31806.0
17	rs17577313	44191835	A	G	1.3917340317897564e-08	5.6744026871640685	32103.0
17	rs62055876	43832940	A	G	1.3964181600160998e-08	5.673827419119629	32109.0
17	rs56119705	44209985	T	C	1.3977494546333131e-08	5.673664262001751	32106.0
17	rs2668657	44282892	T	C	1.399437548706368e-08	5.673457594183887	31571.0
17	rs12185233	43923654	G	C	1.4088921056165821e-08	5.6723045615076515	32186.0
17	rs740710	44214815	C	G	1.41123066038136e-08	5.672020522139162	32088.0
17	rs1918802	44215045	T	C	1.41123066038136e-08	5.672020522139162	32088.0
17	rs2696603	44215823	A	G	1.41123066038136e-08	5.672020522139162	32088.0

17	rs2532313	44217293	G	A	1.41123066038136e-08	5.672020522139162	32088.0
17	rs2532308	44220942	G	A	1.41123066038136e-08	5.672020522139162	32088.0
17	17:44221350_G_A	44221350	G	A	1.41123066038136e-08	5.672020522139162	32088.0
17	rs2696590	44221602	G	C	1.41123066038136e-08	5.672020522139162	32088.0
17	rs1406074	44222067	T	G	1.41123066038136e-08	5.672020522139162	32088.0
17	rs1918798	44222335	G	A	1.41123066038136e-08	5.672020522139162	32088.0
17	rs2696458	44284420	C	T	1.4118781666943559e-08	5.671941957262657	31913.0
17	rs9944484	43990662	G	A	1.417518781689061e-08	5.671259032654301	32174.0
17	rs12150320	44213204	C	T	1.4198814017473974e-08	5.670973767934006	32089.0
17	17:44279371_TCAAA_T	44279371	TCAAA	T	1.4222077426296612e-08	5.6706933337770975	32049.0
17	rs382104	44305026	G	A	1.4259155330449068e-08	5.670247289362929	32024.0
17	rs2696600	44216226	A	G	1.4298749085903576e-08	5.669772221705316	32089.0
17	rs62062279	44093964	T	C	1.4320354377379992e-08	5.669513528161421	32175.0
17	rs62062280	44093993	C	T	1.4320354377379992e-08	5.669513528161421	32175.0
17	rs112073200	44201791	G	C	1.4325811238024417e-08	5.669448249760468	32094.0
17	17:43841356_CTT_C	43841356	CTT	C	1.4338450687139852e-08	5.6692971414373945	31769.0
17	rs77084869	43982903	A	G	1.4355961733755425e-08	5.669088005413522	32179.0
17	rs74573628	43982961	T	C	1.4355961733755425e-08	5.669088005413522	32179.0
17	rs62056805	43983363	G	A	1.4355961733755425e-08	5.669088005413522	32179.0
17	rs62054833	43933673	T	C	1.4363458412531882e-08	5.668998547639752	32155.0
17	rs740711	44214814	G	A	1.4416347892423576e-08	5.668368703900398	32014.0
17	17:44155925_TACAA_T	44155925	TACAA	T	1.442316326742013e-08	5.668287705112364	32133.0
17	rs17770186	43964191	C	A	1.4424384265299169e-08	5.668273197828037	32183.0
17	rs62060915	44251548	G	A	1.4435886969544584e-08	5.668136586990582	32080.0
17	rs2696664	44251698	G	A	1.4435886969544584e-08	5.668136586990582	32080.0
17	rs2732643	44251907	C	T	1.4435886969544584e-08	5.668136586990582	32080.0
17	rs17573593	44082603	A	C	1.4444952955703834e-08	5.668028990110214	32177.0
17	rs62061853	44196125	T	C	1.4454942188110674e-08	5.667910511898155	32105.0
17	rs62063163	44201865	C	T	1.4461877474290664e-08	5.667828302065617	32095.0
17	rs62063164	44201887	C	T	1.4461877474290664e-08	5.667828302065617	32095.0
17	rs62063165	44202147	A	G	1.4461877474290664e-08	5.667828302065617	32095.0
17	rs62063166	44202231	A	G	1.4461877474290664e-08	5.667828302065617	32095.0
17	rs17577024	44186252	G	A	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17577052	44186301	T	C	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs62061822	44186894	A	C	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17577094	44187492	A	G	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs62061824	44188755	T	C	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs55794067	44188764	T	C	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17660847	44189373	C	T	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17660865	44189408	T	C	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17660936	44191159	C	T	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs4548919	44192395	G	T	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs4606752	44192618	A	G	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs62061849	44193882	C	T	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17661045	44194152	T	A	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17577447	44194381	T	A	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs62061850	44194519	T	C	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs62061852	44195424	A	C	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs727425	44195495	G	A	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs17661141	44196015	C	G	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs1468240	44196447	T	A	1.4501205034190557e-08	5.667362842215812	32110.0
17	rs112813897	44196799	G	A	1.4501205034190557e-08	5.667362842215812	32110.0
17	17:44243543_TA_T	44243543	TA	T	1.450703646504456e-08	5.667293928949545	32076.0
17	rs112102887	44179749	G	A	1.4521778749498228e-08	5.6671198310949435	32110.0

17	rs112893440	44179969	G	A	1.4521778749498228e-08	5.6671198310949435	32110.0
17	rs17576842	44179992	A	G	1.4521778749498228e-08	5.6671198310949435	32110.0
17	rs62061772	44169437	T	C	1.4582540474274828e-08	5.6664040776776154	32151.0
17	rs56240678	44176170	C	G	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs62061808	44177337	C	T	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs77604208	44177669	C	T	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs17660464	44177993	C	A	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs17576779	44178272	C	T	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs17660488	44178337	T	C	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs62061809	44178839	T	C	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs62061811	44180173	T	G	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs17576870	44180442	A	G	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs17660595	44180954	A	G	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs62061812	44180997	C	T	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs62061815	44181681	A	G	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs17576954	44181933	T	C	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs77924366	44182181	T	C	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs62061818	44182917	C	G	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs111676341	44183403	A	G	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs17576989	44183616	C	A	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs79923708	44183790	G	A	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs76761511	44185245	C	A	1.4582694747662427e-08	5.666402264076862	32111.0
17	rs62056775	43969952	T	C	1.4599932017891488e-08	5.6661997441695355	32176.0
17	rs62056776	43969995	C	T	1.4599932017891488e-08	5.6661997441695355	32176.0
17	rs17770343	43970154	T	C	1.4599932017891488e-08	5.6661997441695355	32176.0
17	rs34200189	44343125	C	T	1.4610593096461796e-08	5.666074603857435	31522.0
17	rs111880194	44194621	C	G	1.4642931968502232e-08	5.665695550326655	32107.0
17	rs62063301	44048941	G	C	1.4668150199158358e-08	5.665400523841102	32107.0
17	rs62063302	44048943	G	A	1.4668150199158358e-08	5.665400523841102	32107.0
17	rs55788678	43992233	C	T	1.4694861718536931e-08	5.665088564316528	32027.0
17	17:43989129_CA_C	43989129	CA	C	1.4757582417822114e-08	5.664358219202338	32178.0
17	rs199995459	43989149	A	AAC	1.4757582417822114e-08	5.664358219202338	32178.0
17	rs66619507	43989151	A	AC	1.4757582417822114e-08	5.664358219202338	32178.0
17	rs113906906	43989159	G	GC	1.4757582417822114e-08	5.664358219202338	32178.0
17	17:43989509_TA_T	43989509	TA	T	1.4757582417822114e-08	5.664358219202338	32178.0
17	17:43774255_TAGCC_T	43774255	TAGCC	T	1.4760548399984342e-08	5.664323756817423	32091.0
17	rs2696682	44310101	A	G	1.480239452093904e-08	5.663838253360081	32023.0
17	rs2532314	44217112	G	T	1.4802864189849892e-08	5.663832811777213	32090.0
17	rs1918799	44218242	C	T	1.4802864189849892e-08	5.663832811777213	32090.0
17	rs113089855	44256811	A	AACAAG	1.4844200020717588e-08	5.663354550642258	32062.0
17	rs2696703	44260967	G	A	1.4846240996840432e-08	5.663330969800586	32075.0
17	rs62055525	43958736	G	A	1.491132984132945e-08	5.662580599102138	32145.0
17	rs62062772	44020314	C	T	1.4922056133213005e-08	5.662457247483374	32177.0
17	rs62062773	44020545	A	G	1.4922056133213005e-08	5.662457247483374	32177.0
17	rs2732590	44266972	A	G	1.494679748327177e-08	5.662173051792737	32072.0
17	rs62062771	44020282	G	A	1.4961345195018435e-08	5.662006160305352	32173.0
17	rs761294768	44262203	CTTTTTT	C	1.4980235746671896e-08	5.661789682796763	32064.0
17	rs75839508	44022319	G	A	1.5007240173080026e-08	5.661480683828107	32167.0
17	17:44061608_GT_G	44061608	GT	G	1.5033921448897772e-08	5.661175912496357	32162.0
17	rs80120913	44177755	C	G	1.504139417959669e-08	5.6610906481590275	32110.0
17	rs2696697	44257788	T	C	1.5054228211434793e-08	5.6609443070020085	31675.0
17	rs430688	43685707	T	C	1.5055077120938775e-08	5.6609346315114415	31906.0
17	rs111878933	43856341	C	T	1.509470970387831e-08	5.660483505956402	32059.0
17	rs111735741	43856372	G	A	1.509470970387831e-08	5.660483505956402	32059.0

17	rs62063281	44038785	A	G	1.5103542661074415e-08	5.66038311990287	32186.0
17	rs1122381	44205839	A	G	1.515376313671144e-08	5.659813448622416	32105.0
17	rs55709241	44041101	T	C	1.5153976735995342e-08	5.6598110295974315	31917.0
17	rs56280951	44041107	G	A	1.5153976735995342e-08	5.6598110295974315	31917.0
17	rs111678697	44197032	T	C	1.5193008097457935e-08	5.659369552062273	32109.0
17	rs1966345	44197806	T	C	1.5193008097457935e-08	5.659369552062273	32109.0
17	rs62061854	44198080	C	T	1.5193008097457935e-08	5.659369552062273	32109.0
17	rs112560196	44200078	A	T	1.5193008097457935e-08	5.659369552062273	32109.0
17	rs75652502	44200510	C	A	1.5193008097457935e-08	5.659369552062273	32109.0
17	rs62061859	44201109	C	G	1.5193008097457935e-08	5.659369552062273	32109.0
17	rs55802590	44201344	G	C	1.5193008097457935e-08	5.659369552062273	32109.0
17	17:44325593_TAA_T	44325593	TAA	T	1.5240835097416602e-08	5.658830088017088	31817.0
17	rs62062777	44022068	G	A	1.5288378848105168e-08	5.658295446172117	32175.0
17	rs34256996	44197775	G	GCA	1.5305786867496383e-08	5.658100092283383	32050.0
17	rs3087534	44198806	T	C	1.5309130568436687e-08	5.658062593769796	32105.0
17	rs62062797	44027366	T	G	1.532742573560103e-08	5.657857560185351	32003.0
17	rs74863825	43963120	C	T	1.5380055840294728e-08	5.657269058414851	32177.0
17	rs62056761	43969686	T	A	1.5380055840294728e-08	5.657269058414851	32177.0
17	rs17770337	43969779	G	T	1.5380055840294728e-08	5.657269058414851	32177.0
17	rs62056773	43969833	A	G	1.5380055840294728e-08	5.657269058414851	32177.0
17	rs62056774	43969901	G	A	1.5380055840294728e-08	5.657269058414851	32177.0
17	rs62056777	43970303	G	A	1.5380055840294728e-08	5.657269058414851	32177.0
17	rs2696604	44214094	A	G	1.5414010192337196e-08	5.656890423202205	32086.0
17	rs62062798	44027383	A	G	1.5434602942729444e-08	5.6566611816965855	32000.0
17	17:43947176_AC_A	43947176	AC	A	1.5440476000529367e-08	5.656595856402808	31848.0
17	rs62064663	44080039	T	G	1.5445045449826602e-08	5.6565450476761425	32163.0
17	rs2732670	44283479	T	C	1.545799942736159e-08	5.656401088833977	31925.0
17	rs17577496	44194835	T	C	1.5460504365957716e-08	5.656373264722557	32109.0
17	rs55933304	43992305	G	A	1.5474452169318255e-08	5.6562184167035685	32115.0
17	17:44126473_AG_A	44126473	AG	A	1.5517626734911468e-08	5.6557399520549465	32128.0
17	rs78773690	44126478	T	C	1.5517626734911468e-08	5.6557399520549465	32128.0
17	rs111164082	44047037	T	A	1.553961406386533e-08	5.655496783070992	31773.0
17	rs62054832	43933579	C	A	1.555165986548028e-08	5.655363704118821	32137.0
17	rs28416808	44021218	C	T	1.5553357964488248e-08	5.655344952005117	32173.0
17	rs17576695	44172327	T	A	1.555609721710122e-08	5.655314706619028	32112.0
17	rs35631660	43832337	A	G	1.558845615664487e-08	5.6549578072032975	32159.0
17	rs529311580	43699113	A	G	1.5595430186242067e-08	5.654880982160933	31863.0
17	rs17661385	44207778	A	G	1.5599550144886507e-08	5.654835612886558	32105.0
17	rs112915466	43958744	A	G	1.5600429207557104e-08	5.654825934093138	32151.0
17	rs56343551	43959092	G	T	1.5647970816190766e-08	5.654303271475945	32176.0
17	rs55975673	43959113	A	G	1.5647970816190766e-08	5.654303271475945	32176.0
17	rs112638515	44016601	A	AG	1.5654695307121113e-08	5.654229468348861	32173.0
17	rs62055947	43852605	C	T	1.5661091714153657e-08	5.6541592946015165	32097.0
17	rs10514901	44194735	G	T	1.5667656209341226e-08	5.654087305729983	32110.0
17	rs62061851	44194891	C	T	1.5667656209341226e-08	5.654087305729983	32110.0
17	rs56227067	43939609	A	T	1.5671739693320283e-08	5.65404253939495	32153.0
17	rs79115768	44021061	C	T	1.5672401978272502e-08	5.654035279978718	32176.0
17	rs62062774	44021463	T	C	1.5672401978272502e-08	5.654035279978718	32176.0
17	17:43951599_CAGAT_C	43951599	CAGAT	C	1.5688968027099458e-08	5.653853793615996	32111.0
17	rs62056841	43990041	A	C	1.5700021600430884e-08	5.653732801685147	32163.0
17	rs2532417	44289220	C	T	1.5706270246174382e-08	5.65366444088261	32036.0
17	rs113271363	43996721	C	G	1.5715730800532446e-08	5.653560991738008	32177.0
17	rs2055794	43951717	G	A	1.5730846078731442e-08	5.653395834846817	32174.0
17	rs76618565	44068481	G	A	1.5740432005334742e-08	5.653291174196489	32181.0

17	rs2696599	44217226	A	G	1.574203945539724e-08	5.653273629865727	32087.0
17	rs62062776	44022043	A	C	1.5761119426375143e-08	5.6530655164923935	32171.0
17	rs2055795	43951995	C	T	1.5776833035174098e-08	5.652894305129718	32175.0
17	rs2055796	43952191	A	T	1.5776833035174098e-08	5.652894305129718	32175.0
17	rs62055494	43953016	C	T	1.5776833035174098e-08	5.652894305129718	32175.0
17	rs62055496	43953307	C	T	1.5776833035174098e-08	5.652894305129718	32175.0
17	rs62055497	43953529	A	G	1.5776833035174098e-08	5.652894305129718	32175.0
17	rs113952577	44010661	A	G	1.578255593575453e-08	5.652831991047036	32175.0
17	rs17564871	44011018	A	G	1.578255593575453e-08	5.652831991047036	32175.0
17	rs62060800	44145592	A	G	1.5795120116126962e-08	5.652695262299527	32175.0
17	rs62060801	44145860	A	G	1.5795120116126962e-08	5.652695262299527	32175.0
17	rs17659743	44146165	C	G	1.5795120116126962e-08	5.652695262299527	32175.0
17	rs62060802	44146336	A	C	1.5795120116126962e-08	5.652695262299527	32175.0
17	rs75975083	44146357	T	C	1.5795120116126962e-08	5.652695262299527	32175.0
17	rs77950913	44146451	T	C	1.5795120116126962e-08	5.652695262299527	32175.0
17	rs79782347	44146567	T	C	1.5795120116126962e-08	5.652695262299527	32175.0
17	rs147317628	44277476	C	CTTTAG	1.580396539591499e-08	5.652599067554778	31685.0
17	rs76159289	44098861	G	T	1.586188540758542e-08	5.651970461495058	32186.0
17	rs10445337	44067400	T	C	1.5949071794986193e-08	5.651028418588432	32186.0
17	rs79406732	43940497	C	T	1.5950138624160674e-08	5.651016922575581	32148.0
17	rs62061727	44017124	G	T	1.5971152568881555e-08	5.650790631135135	32186.0
17	rs2532239	44266227	T	C	1.597761953287015e-08	5.6507210489673625	32038.0
17	rs17649641	43997372	T	C	1.60194073006468e-08	5.6502720862161375	32170.0
17	rs146122400	44782224	A	AGT	1.6028996400598114e-08	5.6501692225445925	28928.0
17	rs55960528	43968994	T	C	1.6048756396278798e-08	5.649957442535808	32170.0
17	rs55877243	43969019	T	C	1.6048756396278798e-08	5.649957442535808	32170.0
17	17:44279557_TA_T	44279557	TA	T	1.60544064964506e-08	5.649896933501612	32024.0
17	rs76402917	44126477	G	A	1.6106252284915896e-08	5.649342661229283	32108.0
17	rs62061710	44007727	C	T	1.6142403389254844e-08	5.648957201942871	32181.0
17	rs62061711	44007764	T	C	1.6142403389254844e-08	5.648957201942871	32181.0
17	17:44027836_GC_G	44027836	GC	G	1.615888785845711e-08	5.648781715373413	32155.0
17	rs55719714	43939638	G	A	1.619925910331536e-08	5.6483526737219325	32152.0
17	rs56299858	43939659	G	A	1.619925910331536e-08	5.6483526737219325	32152.0
17	17:44177304_TA_T	44177304	TA	T	1.620729958474991e-08	5.64826734827466	31914.0
17	rs62055948	43852621	T	C	1.622487680616186e-08	5.648080962194964	32095.0
17	rs767058	43998767	T	C	1.6232986886003778e-08	5.647995030296722	32156.0
17	rs62055486	43949092	T	G	1.6235100728731368e-08	5.647972639523085	32173.0
17	rs796654785	44284962	A	AG	1.623647201431751e-08	5.6479581157630445	31910.0
17	rs62063849	44073062	T	G	1.625459507484153e-08	5.647766279993343	32152.0
17	rs111372048	44136577	A	C	1.627039029984253e-08	5.647599254115653	32174.0
17	rs17575822	44144345	A	G	1.627039029984253e-08	5.647599254115653	32174.0
17	rs17575850	44144387	C	A	1.627039029984253e-08	5.647599254115653	32174.0
17	rs17659731	44144634	G	A	1.627039029984253e-08	5.647599254115653	32174.0
17	rs75641221	44145373	T	C	1.627039029984253e-08	5.647599254115653	32174.0
17	rs55876817	43958139	A	C	1.6341080297847714e-08	5.646853670320683	32155.0
17	rs76475392	44243351	T	TCG	1.6379073763134556e-08	5.646454237654327	32075.0
17	rs72245049	44243354	A	AG	1.6379073763134556e-08	5.646454237654327	32075.0
17	rs2316773	43946536	C	T	1.6380514611336868e-08	5.646439107453866	32173.0
17	rs17577650	44205500	A	G	1.639441076516199e-08	5.646293251665482	32104.0
17	rs62063200	44206482	C	T	1.639441076516199e-08	5.646293251665482	32104.0
17	rs10514903	44206646	C	G	1.639441076516199e-08	5.646293251665482	32104.0
17	rs17661428	44208144	C	G	1.639441076516199e-08	5.646293251665482	32104.0
17	rs17577877	44208218	A	G	1.639441076516199e-08	5.646293251665482	32104.0
17	rs75676226	43947171	G	A	1.6403527380979158e-08	5.6461976277234776	31836.0

17	rs75229280	44196653	G	A	1.6404335422150246e-08	5.646189154691317	32105.0
17	rs17660251	44166646	C	T	1.6409184489090754e-08	5.646138316414134	32173.0
17	rs113246445	43851209	A	AT	1.6421197753907394e-08	5.646012430534867	32157.0
17	rs147319425	44003133	A	AAAG	1.6432988373213812e-08	5.645888964677875	32180.0
17	rs113909426	44196822	G	A	1.644345660958568e-08	5.645779418277972	32107.0
17	rs62062274	44093319	G	A	1.649636026160344e-08	5.64522683422776	32186.0
17	rs138939613	43841624	G	GATGGATGA	1.654430832282164e-08	5.644727496617726	32123.0
17	rs62062769	44019643	G	A	1.661043824904894e-08	5.644041111640657	32182.0
17	rs62062770	44019680	T	C	1.661043824904894e-08	5.644041111640657	32182.0
17	rs17426195	43832367	G	A	1.6611431584547413e-08	5.644030821718526	32160.0
17	rs2696456	44283761	A	T	1.664125875655792e-08	5.643722121303632	31990.0
17	rs62056837	43988884	T	C	1.6643483274856193e-08	5.6436991198831175	32174.0
17	rs62064422	43668017	G	A	1.6686919721310232e-08	5.643250586274861	31737.0
17	17:43914979_AC_A	43914979	AC	A	1.6687389276927867e-08	5.6432457437454255	32032.0
17	rs2732630	44289150	A	C	1.6721584235246092e-08	5.642893446214223	32034.0
17	rs55944735	43958172	A	G	1.6723995747974846e-08	5.642868627741804	32148.0
17	rs17649571	43994952	A	G	1.6734881206496987e-08	5.642756641523667	32177.0
17	rs112310745	44082432	G	A	1.674718719253342e-08	5.642630126520812	31927.0
17	rs62062783	44023520	T	G	1.6791184328379537e-08	5.642178539361438	32177.0
17	rs34232924	44023828	C	CGTG	1.6791184328379537e-08	5.642178539361438	32177.0
17	rs35163442	44023842	G	A	1.6791184328379537e-08	5.642178539361438	32177.0
17	rs3785884	44057595	G	A	1.6822866179420575e-08	5.64185406755858	32160.0
17	rs75257002	43843395	C	T	1.685757051576501e-08	5.641499321132812	32091.0
17	rs55721252	43958099	T	C	1.690250584143878e-08	5.641041046144041	32158.0
17	rs62055888	43838720	C	T	1.6916241320605208e-08	5.640901200316831	31975.0
17	rs138190012	44197417	T	TGAA	1.6920167753531742e-08	5.640861244165512	32028.0
17	rs2532305	44223060	G	A	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs1918797	44223243	G	A	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs1918796	44223387	T	C	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs1918795	44224686	A	T	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs1406071	44225485	T	C	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs1406070	44225802	C	T	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs2696585	44226030	G	A	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs2532304	44226126	A	C	1.6962463221676373e-08	5.640431407199746	32090.0
17	rs367820416	43982069	T	G	1.7030172111224256e-08	5.639745462887162	32186.0
17	rs62056803	43982159	A	G	1.7030172111224256e-08	5.639745462887162	32186.0
17	rs572543580	43914981	C	G	1.7044368887318875e-08	5.639601974300356	32033.0
17	rs9897621	44113392	T	A	1.705168145707174e-08	5.6395281105287145	30255.0
17	rs56042957	43992244	G	A	1.712810750627347e-08	5.638757971735994	32102.0
17	rs55810795	43992283	A	G	1.712810750627347e-08	5.638757971735994	32102.0
17	rs62055893	43842494	A	G	1.7151848427921437e-08	5.638519415734012	32139.0
17	rs62055477	43945687	C	A	1.7153597130754428e-08	5.6385018569178875	32180.0
17	rs78637438	43945855	G	A	1.7153597130754428e-08	5.6385018569178875	32180.0
17	rs2316771	43945931	T	C	1.7153597130754428e-08	5.6385018569178875	32180.0
17	rs62055478	43945938	C	T	1.7153597130754428e-08	5.6385018569178875	32180.0
17	rs12150170	44090646	A	G	1.7175138596374174e-08	5.638285700425402	32185.0
17	rs62062266	44090704	A	G	1.7175138596374174e-08	5.638285700425402	32185.0
17	rs17573858	44090796	T	C	1.7175138596374174e-08	5.638285700425402	32185.0
17	rs62062267	44090854	C	T	1.7175138596374174e-08	5.638285700425402	32185.0
17	rs62062268	44090858	C	T	1.7175138596374174e-08	5.638285700425402	32185.0
17	rs62062269	44091092	G	C	1.7175138596374174e-08	5.638285700425402	32185.0
17	17:44163547_ACG_A	44163547	ACG	A	1.7175621622093454e-08	5.63828085655253	32166.0
17	rs111362359	43954416	A	AC	1.7209466550353988e-08	5.6379417821939	32125.0
17	rs78834738	44022434	G	A	1.7231258534628826e-08	5.6377238024285194	32035.0

17	rs55900347	44176092	G	A	1.7247923419902477e-08	5.63755728831928	32109.0
17	rs1815	44276578	T	C	1.7289563660488493e-08	5.637141904552935	31827.0
17	rs62062781	44022632	G	A	1.732168042233269e-08	5.636822185701022	32160.0
17	17:44303564_C_T	44303564	C	T	1.733111974265017e-08	5.636728327756746	31022.0
17	rs2696601	44216158	T	C	1.7387372817817178e-08	5.636170014200799	32181.0
17	rs2696587	44222460	T	G	1.7399598834126198e-08	5.63604890267097	32091.0
17	rs1467963	43978934	T	G	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs62056800	43979468	T	A	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs62056801	43979504	G	A	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs113834264	43979622	G	A	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs2099151	43979822	A	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs2082068	43979971	C	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs1984937	43980530	A	C	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs62056802	43980762	A	G	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs113589236	43981795	G	A	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs113029914	43981831	A	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs112275277	43981958	C	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs62056804	43982286	C	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs75617973	43983159	T	C	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs62056806	43983801	A	G	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs62056807	43984253	G	C	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs1467966	43984399	C	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs79492906	43984864	C	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs62056811	43985247	C	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs74509629	43985597	C	T	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs79290980	43985662	T	C	1.7414036377790996e-08	5.635905990011746	32185.0
17	rs17649700	43997901	G	C	1.7422361653633985e-08	5.635823633045801	32174.0
17	rs62058962	43998151	C	T	1.7422361653633985e-08	5.635823633045801	32174.0
17	rs1467969	43998328	C	T	1.7422361653633985e-08	5.635823633045801	32174.0
17	rs1467970	43998574	T	G	1.7422361653633985e-08	5.635823633045801	32174.0
17	rs767057	43998822	A	G	1.7422361653633985e-08	5.635823633045801	32174.0
17	rs17649518	43994386	C	A	1.743179351684591e-08	5.635730375435699	32156.0
17	rs62055937	43848968	G	T	1.7474237499830987e-08	5.635311315761906	32091.0
17	rs112535292	44344300	G	T	1.7476816839613408e-08	5.6352858811884365	30814.0
17	rs146453014	44172493	A	AT	1.748154659903445e-08	5.635239251043206	32104.0
17	rs2532262	44252510	T	C	1.7485540230205692e-08	5.63519988783904	32000.0
17	rs2668668	44284641	T	G	1.7495497482224488e-08	5.635101782245767	31975.0
17	rs62061726	44016341	G	A	1.750170821264075e-08	5.635040617375357	32185.0
17	rs77561671	43976627	G	T	1.7508597887566464e-08	5.634972790740013	32185.0
17	rs62060768	44134984	G	A	1.7540127432221545e-08	5.634662722848171	32179.0
17	rs1122380	44206079	C	T	1.754635369997522e-08	5.634601556477394	32100.0
17	rs62055515	43956370	G	T	1.7559182941920917e-08	5.634475589431555	32169.0
17	rs62055516	43956390	T	C	1.7559182941920917e-08	5.634475589431555	32169.0
17	rs62055517	43956425	C	T	1.7559182941920917e-08	5.634475589431555	32169.0
17	rs62055518	43956505	A	C	1.7559182941920917e-08	5.634475589431555	32169.0
17	rs56364632	43956642	T	C	1.7559182941920917e-08	5.634475589431555	32169.0
17	rs55768605	43956734	C	A	1.7559182941920917e-08	5.634475589431555	32169.0
17	rs535791904	43958207	C	CAAAAAAAT	1.7568070113343078e-08	5.634388380957434	32171.0
17	rs55780786	44209875	T	C	1.757609704295297e-08	5.634309650720012	32106.0
17	rs3089	44209919	C	G	1.757609704295297e-08	5.634309650720012	32106.0
17	rs113260576	44193908	C	CCAACAA	1.765699868539633e-08	5.633518089782053	32182.0
17	rs17573266	44072881	C	G	1.766723790285813e-08	5.633418158024321	32182.0
17	rs62062782	44023087	G	A	1.770470713891394e-08	5.6330529481280625	32176.0
17	rs1476554	44159102	C	T	1.7717587672235054e-08	5.6329275758485675	32186.0

17	rs145503157	43859929	C	CACG	1.771908166179805e-08	5.632913039875293	32139.0
17	rs17564983	44011825	A	C	1.7720575774907004e-08	5.632898503890213	32174.0
17	17:44007773_CAAAA_C	44007773	CAAAA	C	1.7739636550946084e-08	5.632713169045707	32175.0
17	rs2732669	44284542	G	A	1.7746742763866594e-08	5.632644122240447	32013.0
17	rs111555239	44006453	C	CT	1.775796878438311e-08	5.632535100426687	32174.0
17	rs112791677	44001549	G	GC	1.7774321327612724e-08	5.632376411933286	32182.0
17	rs55895732	43968937	T	C	1.7780191869506874e-08	5.632319477550741	32184.0
17	rs41384744	44137070	A	G	1.77845023072101e-08	5.632277685175954	32177.0
17	rs1560310	43978534	G	A	1.7799565646333607e-08	5.632131713941879	32186.0
17	rs56371647	43855503	C	T	1.7825095593688503e-08	5.6318845898029695	32133.0
17	rs62063851	44074435	C	G	1.7839691302145328e-08	5.631743461006758	32165.0
17	rs55967721	43948977	G	A	1.784044332973342e-08	5.631736192540767	32095.0
17	rs77924424	44012915	T	C	1.7895676838661088e-08	5.6312031636569895	32180.0
17	rs76475191	44290849	T	A	1.7904856785074718e-08	5.631114727784213	32064.0
17	rs56338487	43960812	A	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055538	43960997	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055539	43961044	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055540	43961142	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs17770108	43961292	G	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055541	43962017	G	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs77129180	43963046	G	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs80254317	43963282	C	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs112425426	43963416	C	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055542	43963844	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs17770120	43963943	C	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs17770150	43964163	G	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs17691449	43964283	G	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055548	43964899	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs113327263	43965063	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055549	43965595	G	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055552	43965955	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055553	43966178	C	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055554	43966260	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055555	43966282	G	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs111941646	43966608	A	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055556	43966749	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
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17	rs62055558	43966955	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62055559	43967138	T	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs17691466	43968219	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs17691508	43968463	C	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs55943606	43968874	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs112297913	43969258	G	GC	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs17691610	43970662	G	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs76594404	43971457	G	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs80233201	43971481	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056778	43971604	C	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs11575895	43971785	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056779	43971937	C	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs11575896	43972142	G	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs111972148	43973121	G	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs76324150	43973233	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs113347741	43973408	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs78720789	43973413	A	G	1.7910895430667437e-08	5.631056577931129	32186.0

17	rs62056780	43973652	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056781	43973899	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs74496580	43974065	C	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056782	43974230	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs80346216	43974476	G	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs76632685	43974477	A	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056783	43974549	G	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056784	43974889	C	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056785	43975263	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056786	43975285	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056789	43975415	A	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056790	43975417	G	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056791	43976064	T	C	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056792	43976644	G	A	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056793	43977018	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056794	43977049	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs1864324	43977702	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs1864325	43977827	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056795	43978041	C	T	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62056796	43978120	A	G	1.7910895430667437e-08	5.631056577931129	32186.0
17	rs62059007	44005615	A	G	1.7917376615223474e-08	5.6309941877745135	32182.0
17	rs113139571	44099856	G	GC	1.7930534825883564e-08	5.630867589603918	32162.0
17	rs12150336	44125704	C	T	1.7937148986130492e-08	5.6308039873142635	32175.0
17	rs35134656	44103927	C	CT	1.7962367713696416e-08	5.63056169080707	32168.0
17	rs34043286	44117119	A	G	1.797044504782219e-08	5.6304841552320575	32186.0
17	rs113518470	43850932	C	T	1.7971581208575324e-08	5.63047325176488	32155.0
17	rs12150515	44090685	G	T	1.7975937144094745e-08	5.630431455079186	32184.0
17	rs754512	44055647	A	T	1.798408362717603e-08	5.63035331318761	32174.0
17	rs62060762	44133396	G	A	1.801847763417664e-08	5.630023780837887	32182.0
17	rs62060763	44133403	T	C	1.801847763417664e-08	5.630023780837887	32182.0
17	rs75944932	44072423	A	C	1.8041780737843905e-08	5.6298008584552655	32179.0
17	17:44012257_CG_C	44012257	CG	C	1.8045012574997114e-08	5.629769964101674	32158.0
17	17:44250669_TA_T	44250669	TA	T	1.8048118208213343e-08	5.629740281241128	32001.0
17	rs10445370	43935118	G	A	1.8095274032255358e-08	5.629290186119532	32180.0
17	rs56347602	43939255	T	C	1.811193112930293e-08	5.629131468855238	32180.0
17	rs62061730	44017342	A	G	1.811193112930293e-08	5.629131468855238	32178.0
17	rs1076222	44109769	C	G	1.814350636491146e-08	5.6288309926228415	32175.0
17	rs111459873	44113787	T	TG	1.815593479385414e-08	5.6287128604646375	32185.0
17	rs62060844	44153836	C	T	1.8160780955131198e-08	5.628666819002093	32165.0
17	rs74825921	44153909	A	G	1.8176092951851927e-08	5.628521424132329	32185.0
17	17:43849572_AT_A	43849572	AT	A	1.8213277140201245e-08	5.628168836668515	32143.0
17	rs62060796	44143029	G	T	1.8215963419373868e-08	5.62814339194367	32183.0
17	rs55894109	43957221	C	T	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs56249780	43957328	C	T	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs56387391	43959261	G	A	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs2019816	43959661	G	A	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs2006305	43959752	A	T	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs2019822	43959918	T	A	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs62055529	43960020	A	G	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs79580365	43960172	C	T	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs55937610	43960283	A	G	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs56194412	43960600	T	C	1.8217882428089383e-08	5.628125217118069	32185.0
17	rs79412431	43940021	G	A	1.8241438406225568e-08	5.627902271089016	31659.0
17	rs12150570	44126218	G	A	1.825284304586086e-08	5.6277944320676605	32178.0

17	17:44168295_CTTA_C	44168295	CTTA	C	1.8265344918702985e-08	5.6276762930681885	32032.0
17	rs369585371	44215416	A	AG	1.828388878168477e-08	5.627501203578409	32132.0
17	rs111321973	43953170	C	T	1.828440236913505e-08	5.627496356786163	32183.0
17	rs112950348	44033188	G	A	1.8291144515970435e-08	5.627432742516301	31709.0
17	rs41382552	44118999	A	G	1.82980818390558e-08	5.627367310460005	32177.0
17	rs77768866	44121917	C	T	1.82980818390558e-08	5.627367310460005	32177.0
17	rs112281640	44081218	C	CT	1.8314214660058785e-08	5.6272152405904325	32010.0
17	rs79765413	44022433	T	C	1.831640105485157e-08	5.627194641385243	32036.0
17	rs62055488	43950394	C	T	1.832218980611719e-08	5.6271401139629456	32183.0
17	rs62055490	43950533	A	G	1.832218980611719e-08	5.6271401139629456	32183.0
17	rs10491140	43950976	G	T	1.832218980611719e-08	5.6271401139629456	32183.0
17	rs62055491	43951120	T	C	1.832218980611719e-08	5.6271401139629456	32183.0
17	rs34416056	43951220	T	G	1.832218980611719e-08	5.6271401139629456	32183.0
17	rs62055492	43951345	C	A	1.832218980611719e-08	5.6271401139629456	32183.0
17	17:44045574_AC_A	44045574	AC	A	1.8343430581064684e-08	5.62694017866005	32179.0
17	rs62061712	44009876	C	A	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs7501759	44009921	A	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs2316782	44010040	A	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs2316783	44010118	G	C	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs4255816	44010364	C	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs62061713	44010405	A	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs62061714	44010452	C	A	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs78077519	44010984	G	A	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs17650258	44011073	G	A	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs62061715	44011526	A	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs17564948	44011749	A	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs62061716	44012096	A	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs17650335	44012343	G	A	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs17650417	44013103	G	T	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs62061720	44013189	C	T	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs12150111	44013938	A	G	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs12150460	44014137	G	T	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs12150195	44014263	T	C	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs55874169	44014384	G	A	1.8356186635108443e-08	5.626820216406343	32184.0
17	rs62063856	44076466	A	G	1.83700477573754e-08	5.626689953452677	32146.0
17	rs80348388	43952634	A	T	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs62055493	43952944	T	C	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs62055495	43953043	A	C	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs62055498	43953814	G	A	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs62055499	43953991	C	G	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs62055500	43954134	G	A	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs62055501	43954227	G	A	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs62055502	43954284	G	A	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs916793	43954686	G	A	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs4441322	43955030	A	G	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs113414067	43955093	T	C	1.8389535135268136e-08	5.62650697784233	32184.0
17	rs55905252	43955365	C	A	1.8389535135268136e-08	5.62650697784233	32184.0
17	17:43848646_AG_A	43848646	AG	A	1.839631529652097e-08	5.6264433600561485	31962.0
17	rs78681971	44106219	C	T	1.8409689081199895e-08	5.626317941472553	32181.0
17	rs74548327	43973080	A	G	1.841570069675768e-08	5.626261593706863	32184.0
17	rs62064664	44081462	T	C	1.841932152285706e-08	5.626227663783895	32180.0
17	rs62063673	44125484	T	G	1.8439378014487505e-08	5.626039836261129	32177.0
17	rs2158072	43950195	T	C	1.844222647739435e-08	5.626013176711074	32182.0
17	rs2040845	43767188	G	C	1.84429386605418e-08	5.626006511817354	31947.0

17	rs62062768	44019479	C	G	1.8472680175585146e-08	5.625728401767181	32182.0
17	rs62061719	44012989	C	T	1.847832275616277e-08	5.625675687610405	32183.0
17	rs17650381	44013024	T	C	1.847832275616277e-08	5.625675687610405	32183.0
17	rs62061721	44013346	T	C	1.847832275616277e-08	5.625675687610405	32183.0
17	rs56318865	44147411	G	A	1.851396839060105e-08	5.625343039523072	32185.0
17	rs56041778	44147511	G	C	1.851396839060105e-08	5.625343039523072	32185.0
17	rs55947022	44147574	G	A	1.851396839060105e-08	5.625343039523072	32185.0
17	rs55929190	44147599	G	C	1.851396839060105e-08	5.625343039523072	32185.0
17	rs56323408	44147721	C	T	1.851396839060105e-08	5.625343039523072	32185.0
17	rs12150125	43986432	G	A	1.855033259128316e-08	5.6250043259200275	32121.0
17	rs62060794	44142566	C	T	1.8568182475249623e-08	5.624838299380213	32183.0
17	rs10445336	43934948	A	G	1.8577635395850848e-08	5.624750437996989	32171.0
17	rs55836887	43668815	A	G	1.8614710239923808e-08	5.6244062595973165	31812.0
17	rs62062323	44113224	C	T	1.862013393913532e-08	5.6243559653685296	32184.0
17	rs9896485	44050828	G	C	1.8620330005472286e-08	5.624354147502191	31249.0
17	17:44221042_C_T	44221042	C	T	1.862170252651901e-08	5.624341422432661	32158.0
17	rs56040418	43958079	C	T	1.8629808959205825e-08	5.624266283742441	32172.0
17	rs17564153	43995098	G	A	1.8642891143266973e-08	5.624145091641967	32171.0
17	rs62063305	44050282	G	A	1.864544321857753e-08	5.624121459086771	32185.0
17	rs17651134	44050340	G	A	1.864544321857753e-08	5.624121459086771	32185.0
17	rs62063306	44050395	C	A	1.864544321857753e-08	5.624121459086771	32185.0
17	rs62063774	44050463	T	C	1.864544321857753e-08	5.624121459086771	32185.0
17	rs62063775	44050823	G	T	1.864544321857753e-08	5.624121459086771	32185.0
17	rs62063776	44050850	A	G	1.864544321857753e-08	5.624121459086771	32185.0
17	rs1800547	44051846	A	G	1.864544321857753e-08	5.624121459086771	32185.0
17	rs17651213	44051924	G	A	1.864544321857753e-08	5.624121459086771	32185.0
17	rs17572361	44052009	T	C	1.864544321857753e-08	5.624121459086771	32185.0
17	rs17651243	44052284	G	A	1.864544321857753e-08	5.624121459086771	32185.0
17	rs62063777	44053171	A	G	1.864544321857753e-08	5.624121459086771	32185.0
17	rs2217394	44053448	A	G	1.864544321857753e-08	5.624121459086771	32185.0
17	rs62063778	44053989	G	A	1.864544321857753e-08	5.624121459086771	32185.0
17	rs17651285	44054237	G	A	1.864544321857753e-08	5.624121459086771	32185.0
17	rs112578465	44125066	C	T	1.865722646795108e-08	5.624012385350765	32176.0
17	rs62063680	44131559	C	A	1.866010792830025e-08	5.623985722780873	32181.0
17	rs62060850	44157982	A	T	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs62060851	44157992	T	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs77138434	44159555	C	A	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs111913701	44159631	T	G	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs111519055	44159672	A	G	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs77925835	44159695	C	T	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs17659953	44159725	C	T	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs17576165	44159849	T	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs17576200	44159988	G	A	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs62060852	44160050	G	A	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs62060853	44160592	G	A	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs17660017	44160674	G	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs55987700	44161146	T	G	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs113788190	44161302	A	G	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs112364920	44161360	A	T	1.8664627460828654e-08	5.623943910943562	32184.0
17	17:44161478_CTCACACCTGTAATCCCAGCACTTTGGGAAGCTGAGGCGGGTGGA_C	44161478	CTCACACCTGTAATCCCAGCACTTTGGGAAGCTGAGGCGGGTGGA	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs113955100	44161522	A	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs62060855	44161860	C	T	1.8664627460828654e-08	5.623943910943562	32184.0

17	rs62060856	44161875	A	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs2316955	44161985	T	G	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs17660065	44162284	T	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs55864131	44163411	T	C	1.8664627460828654e-08	5.623943910943562	32184.0
17	17:44163551_AGT_A	44163551	AGT	A	1.8664627460828654e-08	5.623943910943562	32184.0
17	17:44179168_AACC_A	44179168	AACC	A	1.8664627460828654e-08	5.623943910943562	32184.0
17	rs62056840	43989689	T	C	1.8711195191868134e-08	5.623513667524141	32174.0
17	rs17770296	43969136	C	T	1.8721113715652386e-08	5.623422163716851	32179.0
17	rs62061858	44200033	T	C	1.872144223176493e-08	5.623419133781455	32083.0
17	rs55653657	43956778	A	G	1.875300611349402e-08	5.623128257595542	32166.0
17	rs12150527	43986462	A	G	1.876327560670554e-08	5.623033721817364	32168.0
17	17:44104410_TCTC_T	44104410	TCTC	T	1.8833003425946265e-08	5.62239316816773	32180.0
17	rs78938131	44157622	T	G	1.883472178328147e-08	5.622377411592308	32185.0
17	17:44157676_CT_C	44157676	CT	C	1.883472178328147e-08	5.622377411592308	32185.0
17	rs62055547	43964755	C	T	1.8837101301106704e-08	5.622355594772682	32184.0
17	rs17691556	43969168	T	A	1.8853303073623486e-08	5.622207118488356	32181.0
17	rs12150576	44015624	G	A	1.888117559214277e-08	5.621951978813066	32185.0
17	rs12150242	44015816	A	G	1.888117559214277e-08	5.621951978813066	32185.0
17	rs12150104	44015929	G	A	1.888117559214277e-08	5.621951978813066	32185.0
17	rs62061725	44016157	G	C	1.888117559214277e-08	5.621951978813066	32185.0
17	rs113537106	44016462	A	G	1.888117559214277e-08	5.621951978813066	32185.0
17	rs62061728	44017180	T	G	1.888117559214277e-08	5.621951978813066	32185.0
17	rs62061731	44017666	C	A	1.888117559214277e-08	5.621951978813066	32185.0
17	rs62061732	44017941	G	T	1.888117559214277e-08	5.621951978813066	32185.0
17	rs62062791	44025273	G	A	1.8881374353589016e-08	5.621950160702569	32182.0
17	rs62062792	44025347	T	C	1.8881374353589016e-08	5.621950160702569	32182.0
17	rs78026984	44025592	G	C	1.8881374353589016e-08	5.621950160702569	32182.0
17	rs113395365	44025650	T	C	1.8881374353589016e-08	5.621950160702569	32182.0
17	rs62063681	44131592	A	G	1.8882235676899308e-08	5.6219422822216085	32182.0
17	rs62063682	44131622	G	A	1.8882235676899308e-08	5.6219422822216085	32182.0
17	rs62063683	44131717	G	A	1.8882235676899308e-08	5.6219422822216085	32182.0
17	rs79180862	44131798	C	T	1.8882235676899308e-08	5.6219422822216085	32182.0
17	rs55711631	43958431	T	C	1.8884687346446983e-08	5.621919858833741	32180.0
17	rs55886302	43936011	A	G	1.8888862529085026e-08	5.621881678405983	32181.0
17	rs56136075	43936298	C	A	1.8888862529085026e-08	5.621881678405983	32181.0
17	rs76563578	43933879	C	G	1.890517429304776e-08	5.6217325921463015	32159.0
17	17:43934587_GT_G	43934587	GT	G	1.891857883326624e-08	5.621610170793235	32175.0
17	rs62056760	43968572	G	A	1.892355813878035e-08	5.621564717107423	32178.0
17	17:44133818_TA_T	44133818	TA	T	1.8937041906624586e-08	5.621441688552141	32167.0
17	rs74457229	43972581	C	T	1.8949138811566547e-08	5.6213313863698735	32186.0
17	rs757055	43946875	C	T	1.8960711069626185e-08	5.6212259319996285	32170.0
17	17:44290910_A_G	44290910	A	G	1.900000194852798e-08	5.620868352211257	31936.0
17	17:44293963_T_A	44293963	T	A	1.900266862499195e-08	5.620844109255179	32062.0
17	rs62061729	44017283	A	G	1.900720281730497e-08	5.620802896154489	32184.0
17	rs62062293	44100553	C	A	1.9018476214117096e-08	5.620700469066808	32182.0
17	rs7687	44103296	T	C	1.902434898094589e-08	5.620647134019864	32185.0
17	rs17652748	44103616	C	T	1.902434898094589e-08	5.620647134019864	32185.0
17	rs2158257	44104343	A	C	1.902434898094589e-08	5.620647134019864	32185.0
17	rs17574228	44104509	T	C	1.902434898094589e-08	5.620647134019864	32185.0
17	rs17574361	44108202	A	G	1.902434898094589e-08	5.620647134019864	32185.0
17	rs17652961	44108355	G	A	1.902434898094589e-08	5.620647134019864	32185.0
17	rs17574425	44109188	C	G	1.902434898094589e-08	5.620647134019864	32185.0
17	rs55881134	44109248	G	A	1.902434898094589e-08	5.620647134019864	32185.0
17	rs1467968	43986396	C	T	1.9047256403058693e-08	5.620439247035908	32172.0

17	rs4371195	43986420	A	G	1.9047256403058693e-08	5.620439247035908	32172.0
17	rs17585012	44227510	A	T	1.905648042870355e-08	5.6203556066936216	32113.0
17	rs147091683	44101775	A	AT	1.9065575058303763e-08	5.62027317814784	32170.0
17	rs78229689	44106806	G	A	1.906805006892691e-08	5.620250752668966	32183.0
17	rs733969	44089727	G	A	1.9071395178441992e-08	5.620220447923149	32185.0
17	rs62063684	44132269	T	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62063685	44132379	A	G	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62063687	44132592	A	G	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060760	44132887	C	T	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17575437	44133031	T	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17653889	44133070	A	T	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060761	44133162	A	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs111259120	44133534	C	T	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060764	44133633	A	G	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060765	44133648	A	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17575507	44134095	A	G	1.9078957245938833e-08	5.620151959008602	32184.0
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17	rs62060769	44135026	G	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs1107820	44135359	T	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17575556	44135827	G	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17653998	44135985	A	G	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060785	44136634	G	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17654016	44137925	T	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs2316951	44139083	G	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs2316952	44139190	G	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17575683	44139662	C	T	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs112411928	44139762	C	G	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs2316953	44140341	G	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs2838	44141347	A	G	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs12150127	44141732	G	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060792	44141955	T	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs76307183	44142121	G	A	1.9078957245938833e-08	5.620151959008602	32184.0
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17	rs62060795	44142663	C	T	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs17575773	44142879	C	T	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060797	44143344	G	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs12150344	44143484	G	A	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060798	44144152	T	C	1.9078957245938833e-08	5.620151959008602	32184.0
17	rs62060799	44144251	G	T	1.9078957245938833e-08	5.620151959008602	32184.0
17	17:44092729_TAAA_T	44092729	TAAA	T	1.9093956231335654e-08	5.620016192598079	31794.0
17	rs12150506	44090536	G	A	1.9108564560327418e-08	5.61988406179908	32185.0
17	rs17572467	44054388	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17572495	44054596	T	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62063779	44054671	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62063780	44056238	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs2163129	44056433	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs62063784	44059775	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0

17	rs56234850	44060248	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs63750417	44060775	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62063787	44061036	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62063788	44061696	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs62063790	44062915	G	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62063791	44062993	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs1529534	44063140	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17572795	44063393	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17572823	44063563	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17572851	44063766	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs62063794	44066088	T	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs112385572	44066172	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17651700	44066634	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs372810927	44066868	C	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs113134013	44066995	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs17651754	44067546	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs10445338	44067682	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs75743061	44068112	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs1052551	44068924	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs62063800	44069198	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
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17	rs78599197	44069970	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62063842	44070111	G	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62064674	44088772	C	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs76723223	44089108	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs733968	44089715	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs4283261	44089921	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062265	44090035	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs75666751	44090148	A	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs4306559	44090236	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs747152	44090339	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062270	44091195	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs75534191	44091724	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062272	44092108	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062273	44092243	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062275	44093496	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0

17	rs62062276	44093627	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062278	44093860	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062281	44094112	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062282	44094374	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17652502	44094471	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs2316948	44094667	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062283	44095055	C	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs111976319	44095335	C	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062284	44095570	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062285	44095661	T	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs55726761	44099669	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062292	44099809	A	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs77747656	44099827	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062294	44100666	A	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062295	44100906	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062296	44100916	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062297	44101004	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs7350928	44108100	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs36076725	44110532	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs35833914	44110541	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs77009866	44110888	A	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062321	44111109	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17574604	44111613	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17653162	44111827	C	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062322	44112385	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17653193	44112441	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17653211	44112638	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17653255	44112743	C	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs4608377	44113359	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12185225	44113491	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150438	44113963	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150162	44114218	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062134	44114432	A	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17574796	44115074	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs17574824	44115107	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12185243	44115351	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs11079729	44115569	C	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150542	44115730	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150090	44115886	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs41437445	44116238	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62062136	44116312	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs10514897	44117397	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs75546272	44130668	T	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62063686	44132458	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs111990897	44138377	GA	GAA	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs111990897	44138377	G	GA	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs150514510	44142231	T	TA	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs146149698	44142491	C	CCA	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs55831516	44148267	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060809	44148613	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060810	44148674	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs1117253	44149297	A	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150625	44149448	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150627	44149537	C	G	1.9111514359379523e-08	5.6198573930791484	32186.0

17	rs12150628	44149581	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150611	44149741	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs74850776	44150042	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs974295	44150152	A	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs974293	44150233	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs974292	44150464	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs974291	44150480	A	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150551	44150920	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs12150558	44151156	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060812	44151667	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060834	44151697	A	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs113989747	44151969	C	CA	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060835	44152390	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060836	44152447	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs112597362	44152736	G	GCT	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060837	44152760	T	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs368572568	44152812	T	CCCAAGTGAGGCACCTGGGT	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060838	44153144	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060839	44153227	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060841	44153386	A	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060842	44153607	T	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060843	44153626	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs76154201	44154033	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs75530705	44154048	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs112197756	44154105	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060845	44154393	A	G	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060846	44154461	A	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs74481389	44154607	T	C	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs62060847	44154946	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs56100031	44155157	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs55972730	44155707	C	T	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs2316954	44156167	G	A	1.9111514359379523e-08	5.6198573930791484	32186.0
17	rs56167560	43792411	A	G	1.9118823739493804e-08	5.619791327215463	32057.0
17	rs55849973	43792418	T	C	1.9118823739493804e-08	5.619791327215463	32057.0
17	rs113912415	44007785	A	G	1.912036643596991e-08	5.619777386680962	32172.0
17	rs62054841	43937104	G	A	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs62054842	43937162	C	T	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs62054843	43937184	T	C	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs62054844	43937333	T	G	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs55888391	43938107	A	G	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs76329216	43938499	G	A	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs62054846	43938634	A	G	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs55646970	43938796	A	G	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs55673092	43938882	G	A	1.91266726383752e-08	5.6197204122097055	32182.0
17	rs62056835	43988623	G	A	1.913861975881557e-08	5.619612523884325	32179.0
17	rs2106784	43949892	C	T	1.9141842706753038e-08	5.619583430292	32181.0
17	rs112454267	44005329	G	A	1.9156755765267813e-08	5.619448871812402	32179.0
17	rs62056856	43992939	T	C	1.915944401391537e-08	5.619424626933757	32182.0
17	rs739642	43946838	C	A	1.9175514009628392e-08	5.619279763099554	32182.0
17	rs56398500	43947488	A	G	1.9175514009628392e-08	5.619279763099554	32182.0
17	rs62055483	43948040	C	T	1.9175514009628392e-08	5.619279763099554	32182.0
17	rs78238042	43948159	G	A	1.9175514009628392e-08	5.619279763099554	32182.0

17	rs56327054	43943957	G	C	1.9177868465523206e-08	5.6192585486321125	32175.0
17	rs733966	44089563	C	T	1.919004889041742e-08	5.6191488391278455	32184.0
17	rs733967	44089690	T	C	1.919624295318227e-08	5.619093074923172	32185.0
17	rs113796169	44005254	T	A	1.9197320381597044e-08	5.619083376782888	32180.0
17	rs753235	43946223	G	A	1.9202506335282376e-08	5.6190367044092735	32133.0
17	rs111739681	43898459	C	T	1.9206211428960207e-08	5.6190033669250425	32173.0
17	rs35168513	44275172	A	ACT	1.9207761039635642e-08	5.618989425776863	31737.0
17	rs62063671	44124837	A	G	1.924822900987232e-08	5.618625739814208	32177.0
17	17:44296522_T_C	44296522	T	C	1.9255522118162867e-08	5.618560275556184	32071.0
17	rs10445371	44065410	G	A	1.9264236882173603e-08	5.618482081823107	32185.0
17	rs919464	44065901	C	T	1.9264236882173603e-08	5.618482081823107	32185.0
17	rs62060858	44164090	G	C	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs62060859	44164133	G	A	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs55692232	44164323	G	A	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs3912061	44165098	C	T	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs74348235	44165852	A	G	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs17660167	44166311	C	T	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs17660294	44167101	T	C	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs62061766	44167464	G	A	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs79923630	44167661	G	T	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs62061767	44167729	A	G	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs111364350	44168508	C	T	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs62061770	44169377	G	C	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs111970616	44169581	T	C	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs17660337	44169605	T	C	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs62061788	44169759	G	A	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs62061789	44169769	C	T	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs17660398	44170612	C	T	1.9283436506755184e-08	5.618309933175943	32183.0
17	rs62061792	44171554	G	A	1.929581803535456e-08	5.618199005529698	32030.0
17	rs56289364	43947928	A	G	1.9303331940816704e-08	5.618131721212616	32181.0
17	rs55673340	43948733	C	T	1.9303331940816704e-08	5.618131721212616	32181.0
17	rs77092481	43949008	C	T	1.9303331940816704e-08	5.618131721212616	32181.0
17	rs17577975	44210442	C	T	1.9307597866133944e-08	5.618093532703923	32077.0
17	rs17573607	44083081	G	A	1.931125510932152e-08	5.6180607996316265	32164.0
17	rs78136862	44085743	T	C	1.9312542078659842e-08	5.618049282425286	32184.0
17	rs62064670	44085852	T	A	1.9312542078659842e-08	5.618049282425286	32184.0
17	rs62064671	44086100	T	C	1.9312542078659842e-08	5.618049282425286	32184.0
17	rs3912060	44165435	C	T	1.9319655794434408e-08	5.6179856345724035	32178.0
17	rs17660132	44165803	T	C	1.9319655794434408e-08	5.6179856345724035	32178.0
17	rs62061764	44166197	A	G	1.9319655794434408e-08	5.6179856345724035	32178.0
17	rs12149995	44092801	G	A	1.9326433150640832e-08	5.6179250173592505	32182.0
17	rs112746008	44126650	C	T	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs74977736	44126977	G	C	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs12150447	44128125	A	C	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs12150064	44128407	C	A	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs17653836	44128876	T	A	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs17575423	44129253	T	C	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs62063676	44129800	G	A	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs62063677	44129885	C	T	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs62063678	44129949	C	G	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs79649865	44130587	T	G	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs111853996	44130878	A	G	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs112674766	44130924	A	T	1.9334975938915028e-08	5.617848639378409	32184.0
17	rs112074397	44131022	T	C	1.9334975938915028e-08	5.617848639378409	32184.0

17	rs78104015	44052733	A	G	1.9340401853207505e-08	5.617800145253169	32176.0
17	rs74829364	44084533	T	C	1.934691492127344e-08	5.617741952129459	32183.0
17	rs62064669	44084676	C	T	1.934691492127344e-08	5.617741952129459	32183.0
17	rs62063669	44122626	C	A	1.935166538924977e-08	5.617699519524156	32185.0
17	rs77105679	44122896	G	A	1.935166538924977e-08	5.617699519524156	32185.0
17	17:43954982_TTCTCTTCCTCA_T	43954982	TTCTCTTCCTCA	T	1.937781341552966e-08	5.617466138396959	31883.0
17	rs112116311	43989898	T	G	1.9393246795865605e-08	5.617328533033664	32177.0
17	rs78209533	43989909	A	G	1.9393246795865605e-08	5.617328533033664	32177.0
17	rs55760800	43996908	T	G	1.9393246795865605e-08	5.617328533033664	32177.0
17	rs56303672	43996960	A	G	1.9393246795865605e-08	5.617328533033664	32177.0
17	rs17564020	43991781	G	T	1.9406173869043003e-08	5.617213355925144	32181.0
17	rs17572613	44058004	A	G	1.9420471517372392e-08	5.6170860540482375	32185.0
17	rs75690239	43941710	C	T	1.9424558456633766e-08	5.61704968191712	32180.0
17	rs62062786	44024660	G	C	1.9425239695167358e-08	5.617043619888079	32181.0
17	rs62062787	44024865	T	C	1.9425239695167358e-08	5.617043619888079	32181.0
17	rs62062788	44024906	A	G	1.9425239695167358e-08	5.617043619888079	32181.0
17	rs113762994	43847095	C	T	1.943927842230604e-08	5.616918741633143	32143.0
17	rs370644144	43933956	G	GTGTTTGTTTGTT	1.9455442080906158e-08	5.61677506994172	32157.0
17	rs754513	44055638	T	A	1.9460150432686044e-08	5.616733241257862	32170.0
17	rs56101773	43957269	T	C	1.946813671332537e-08	5.616662314135753	32182.0
17	rs111447859	43987184	T	C	1.9488424016150845e-08	5.616482267102056	32168.0
17	rs10445335	43934896	T	A	1.951386362079759e-08	5.6162567510909644	32169.0
17	rs79252344	44120608	A	G	1.954070618216852e-08	5.616019107488698	32184.0
17	rs62056838	43989087	A	G	1.9561136227795475e-08	5.615838447741403	32180.0
17	rs62056839	43989221	T	C	1.9561136227795475e-08	5.615838447741403	32180.0
17	rs17564780	44005413	A	G	1.9583235189436923e-08	5.61564323616627	32180.0
17	rs62059008	44006085	A	G	1.9583235189436923e-08	5.61564323616627	32180.0
17	rs62059009	44006130	T	C	1.9583235189436923e-08	5.61564323616627	32180.0
17	rs62061705	44006252	T	C	1.9583235189436923e-08	5.61564323616627	32180.0
17	rs62063783	44059215	C	T	1.9583784543512533e-08	5.615638386162144	32182.0
17	rs17564829	44006601	T	C	1.962379061674828e-08	5.615285544836743	32181.0
17	rs62061709	44007493	C	T	1.962379061674828e-08	5.615285544836743	32181.0
17	rs17572248	44049867	A	G	1.965608748663744e-08	5.615001205443412	32184.0
17	rs62064672	44086521	G	A	1.9656914529265967e-08	5.6149939301757925	32185.0
17	rs17572893	44064208	G	A	1.965836193597276e-08	5.614981198450344	32182.0
17	rs62065457	43574611	G	A	1.966442839593437e-08	5.614927846359504	32021.0
17	rs393208	43704310	T	G	1.967587694323588e-08	5.614827204482522	32146.0
17	rs62060840	44153258	A	G	1.9677118744681155e-08	5.6148162914739	32179.0
17	rs9901937	44063723	A	C	1.96887125980155e-08	5.614714436405967	32182.0
17	rs41374248	44120442	A	G	1.969478824181389e-08	5.614661083520031	32185.0
17	rs41399444	44121469	C	T	1.969478824181389e-08	5.614661083520031	32185.0
17	rs62063668	44122484	C	T	1.969478824181389e-08	5.614661083520031	32185.0
17	rs62641967	44047216	T	G	1.970017500843308e-08	5.6146137933291	32177.0
17	rs62060786	44136763	C	T	1.971731176470958e-08	5.614463433943207	32180.0
17	rs62060787	44136803	G	T	1.971731176470958e-08	5.614463433943207	32180.0
17	rs55714296	44137189	A	T	1.971731176470958e-08	5.614463433943207	32180.0
17	rs113093579	43934116	T	G	1.9725470675126963e-08	5.6143918915339	32154.0
17	rs739643	43946707	T	C	1.9738061248380567e-08	5.614281545901298	32181.0
17	rs62062785	44024562	G	T	1.973861486093812e-08	5.614276695528217	32184.0
17	rs111306685	44025407	C	CT	1.973861486093812e-08	5.614276695528217	32184.0
17	rs111582708	44082955	A	AT	1.9748582490996094e-08	5.614189388587956	32166.0
17	rs112902492	43958213	A	AAT	1.9752598625061206e-08	5.614154223172274	32179.0
17	rs75945623	43937505	C	T	1.979682899040038e-08	5.613767399040232	32176.0
17	rs1467962	43978604	A	G	1.981113099816641e-08	5.613642497927036	32185.0

17	rs1560311	43978625	T	C	1.981113099816641e-08	5.613642497927036	32185.0
17	rs62063276	44036408	T	G	1.985235792437288e-08	5.613282947624162	32112.0
17	rs12150469	44092497	T	C	1.9857856559198564e-08	5.613235047460249	32184.0
17	rs17572169	44045974	C	T	1.9864679725845048e-08	5.613175626825616	32179.0
17	rs62063296	44046202	C	T	1.9864679725845048e-08	5.613175626825616	32179.0
17	rs74373419	44047609	C	T	1.9864679725845048e-08	5.613175626825616	32179.0
17	rs62063297	44047802	A	T	1.9864679725845048e-08	5.613175626825616	32179.0
17	rs62062801	44028011	T	G	1.987443109472128e-08	5.613090739862548	32167.0
17	rs75242405	44049329	C	T	1.988850919945701e-08	5.612968259392109	32182.0
17	rs76640332	44189858	G	A	1.9891995388303748e-08	5.6129379423145895	31996.0
17	rs62062799	44027521	G	T	1.9901480853701113e-08	5.6128554796039545	32169.0
17	rs111962225	43934016	G	C	1.991013323158656e-08	5.612780292683762	32154.0
17	rs112206871	44041817	A	G	1.9910691576158745e-08	5.612775441903873	32170.0
17	17:44104576_CCTT_C	44104576	CCTT	C	1.991250630205309e-08	5.612759676860153	32049.0
17	rs62063853	44074613	A	G	1.9914740033488536e-08	5.612740273710363	32043.0
17	rs55930267	43792091	C	T	1.9920884061901257e-08	5.612686914939994	31593.0
17	17:44294983_C_A	44294983	C	A	1.993233925669153e-08	5.6125874731707865	32087.0
17	rs430789	44295157	A	G	1.993233925669153e-08	5.6125874731707865	32087.0
17	rs55893711	44119320	C	T	1.993331743834289e-08	5.612578984213675	32184.0
17	rs10514898	44119636	A	C	1.993331743834289e-08	5.612578984213675	32184.0
17	rs62063670	44123248	T	C	1.993331743834289e-08	5.612578984213675	32184.0
17	rs74571696	44123685	G	A	1.993331743834289e-08	5.612578984213675	32184.0
17	rs79698033	44123717	C	T	1.993331743834289e-08	5.612578984213675	32184.0
17	rs62055469	43943655	A	C	1.993492455324273e-08	5.612565038061111	32172.0
17	rs62055470	43943657	A	G	1.993492455324273e-08	5.612565038061111	32172.0
17	rs62055471	43943755	T	C	1.993492455324273e-08	5.612565038061111	32172.0
17	rs78962882	44084844	G	C	1.9998542366428748e-08	5.612013853157038	32180.0
17	rs56249080	43939432	G	T	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62054857	43939936	G	A	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62054858	43940188	T	C	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62054859	43940685	G	A	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055460	43940825	G	C	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055461	43941350	C	T	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055462	43941476	A	C	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055463	43941491	A	G	2.002561736780426e-08	5.611779791507313	32181.0
17	rs77652965	43941608	C	G	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055464	43941858	T	G	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055465	43942046	T	A	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055466	43942656	G	A	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055467	43942820	T	C	2.002561736780426e-08	5.611779791507313	32181.0
17	rs56036719	43943974	C	T	2.002561736780426e-08	5.611779791507313	32181.0
17	rs55781174	43944158	C	T	2.002561736780426e-08	5.611779791507313	32181.0
17	rs12150223	43944204	T	C	2.002561736780426e-08	5.611779791507313	32181.0
17	rs62055476	43945495	A	G	2.002561736780426e-08	5.611779791507313	32181.0
17	rs1078830	43946112	T	C	2.002561736780426e-08	5.611779791507313	32181.0
17	rs2950705	44343121	A	G	2.002645965348912e-08	5.611772514930292	31534.0
17	rs80020809	44172391	C	T	2.0027652951007043e-08	5.611762206441108	32108.0
17	rs76090253	44002969	A	C	2.0051533547878417e-08	5.611556035410863	32182.0
17	rs55788597	44003397	T	A	2.0051533547878417e-08	5.611556035410863	32182.0
17	rs56197117	44003446	A	G	2.0051533547878417e-08	5.611556035410863	32182.0
17	rs56249311	44003599	C	T	2.0051533547878417e-08	5.611556035410863	32182.0
17	rs62059004	44003893	A	G	2.0051533547878417e-08	5.611556035410863	32182.0
17	rs76500077	44004076	T	C	2.0051533547878417e-08	5.611556035410863	32182.0
17	rs62063303	44049133	T	C	2.0080015992242932e-08	5.611310446231721	32181.0

17	rs62061821	44186055	G	A	2.0086773200486548e-08	5.611252232006368	32053.0
17	17:44155299_CT_C	44155299	CT	C	2.010064653789345e-08	5.611132770971892	32183.0
17	17:43914990_AAC_A	43914990	AAC	A	2.0103535063175102e-08	5.611107908422871	32137.0
17	rs62056850	43992581	C	T	2.0109454288619142e-08	5.611056970409697	32172.0
17	rs55979424	43900081	C	T	2.013392444311482e-08	5.61084654636672	32144.0
17	rs55691306	43978295	G	C	2.01396406982654e-08	5.610797426853619	32184.0
17	17:44201358_TG_T	44201358	TG	T	2.0173406078816967e-08	5.6105075583402835	32103.0
17	rs55662347	44070545	G	A	2.0197740191931856e-08	5.610298947133199	32185.0
17	rs55913645	44070956	T	A	2.0197740191931856e-08	5.610298947133199	32185.0
17	rs17573175	44071089	C	G	2.0197740191931856e-08	5.610298947133199	32185.0
17	rs62063845	44071294	T	C	2.0197740191931856e-08	5.610298947133199	32185.0
17	rs55886080	44072041	T	A	2.0197740191931856e-08	5.610298947133199	32185.0
17	rs77527347	44058017	G	T	2.0224158250830104e-08	5.610072746768979	32185.0
17	rs62054834	43934314	T	C	2.0243089568463703e-08	5.609910826790427	32157.0
17	rs2316774	43946642	T	C	2.026189625937031e-08	5.609750118247364	32176.0
17	rs55929431	44000202	G	A	2.026210926334569e-08	5.609748298897105	32177.0
17	rs79860128	43990072	A	G	2.028334967753644e-08	5.609566969393926	32183.0
17	rs17563965	43990919	A	G	2.028334967753644e-08	5.609566969393926	32183.0
17	rs17563986	43991272	A	G	2.028334967753644e-08	5.609566969393926	32183.0
17	rs55682376	43991888	G	A	2.028334967753644e-08	5.609566969393926	32183.0
17	rs62056851	43992806	A	G	2.028334967753644e-08	5.609566969393926	32183.0
17	rs75046472	43997499	A	T	2.028334967753644e-08	5.609566969393926	32183.0
17	rs17564223	43997520	C	T	2.028334967753644e-08	5.609566969393926	32183.0
17	rs767056	43998910	C	T	2.028334967753644e-08	5.609566969393926	32183.0
17	rs767059	43999100	G	C	2.028334967753644e-08	5.609566969393926	32183.0
17	rs62058964	43999406	A	G	2.028334967753644e-08	5.609566969393926	32183.0
17	rs62058965	43999529	G	C	2.028334967753644e-08	5.609566969393926	32183.0
17	rs1052590	44102638	A	G	2.028725915378252e-08	5.609533614268576	32175.0
17	rs62063854	44074619	G	A	2.0311656746170576e-08	5.609325598175318	32041.0
17	rs17689918	43910088	G	A	2.0318988751940103e-08	5.609263132229311	32176.0
17	rs2950013	43668455	T	G	2.032767662100854e-08	5.609189143156892	31782.0
17	rs17652449	44088937	G	C	2.033465803901513e-08	5.609129709090339	32184.0
17	rs10445369	43934776	A	G	2.0357042910289763e-08	5.608939276160251	32167.0
17	rs62062802	44028045	G	T	2.0360395590319967e-08	5.6089107716938535	32163.0
17	rs62063846	44071674	A	G	2.0360538269564084e-08	5.608909558736831	32184.0
17	rs55736025	44072017	C	A	2.0360538269564084e-08	5.608909558736831	32184.0
17	rs62063850	44073739	G	A	2.0360538269564084e-08	5.608909558736831	32184.0
17	rs17652121	44073973	T	C	2.0360538269564084e-08	5.608909558736831	32184.0
17	17:44127471_GTGGTTTCACCA_G	44127471	GTGGTTTCACCA	G	2.038116572968801e-08	5.608734285582871	32133.0
17	rs62056848	43992456	G	A	2.042491507366072e-08	5.6083631132386325	32182.0
17	rs62056849	43992463	G	C	2.042491507366072e-08	5.6083631132386325	32182.0
17	rs76627340	43937460	G	A	2.04477555551307e-08	5.6081696396352765	32179.0
17	rs79889833	43937633	A	G	2.04477555551307e-08	5.6081696396352765	32179.0
17	rs77625338	43937671	C	T	2.04477555551307e-08	5.6081696396352765	32179.0
17	rs77489223	43937736	C	T	2.04477555551307e-08	5.6081696396352765	32179.0
17	rs17574040	44102865	A	C	2.0474781140858214e-08	5.607940986317135	32177.0
17	rs112887308	44128754	G	GA	2.049200399932537e-08	5.607795423001585	32184.0
17	rs77426526	43962982	G	A	2.050378112164755e-08	5.607695954055176	32186.0
17	rs113894932	44080408	G	C	2.0532677512599388e-08	5.6074521314949335	32178.0
17	rs56189701	43987801	T	C	2.054807645063801e-08	5.6073223340511	32149.0
17	rs12150254	44090455	T	C	2.054822041934163e-08	5.60732112098644	32183.0
17	rs62062793	44026321	T	C	2.0554484015322007e-08	5.6072683525940885	32176.0
17	rs62062289	44097235	G	C	2.0556428270556028e-08	5.607251976164834	32178.0
17	rs1052587	44102604	T	C	2.0556428270556028e-08	5.607251976164834	32178.0

17	rs1052594	44102689	G	C	2.0556428270556028e-08	5.607251976164834	32178.0
17	rs2696591	44318663	G	A	2.056528771538364e-08	5.607177372241979	32064.0
17	rs62064665	44081527	T	C	2.0600690783049118e-08	5.6068795599886085	32180.0
17	rs9468	44101563	T	C	2.061122948970679e-08	5.606791003861852	32101.0
17	rs62057066	43858307	T	C	2.0617367472556333e-08	5.606739447010944	31951.0
17	rs62062800	44027753	A	G	2.0652135015803413e-08	5.606447693092217	32169.0
17	17:43994508_GAGA_G	43994508	GAGA	G	2.0762018034686628e-08	5.605528728155333	32152.0
17	rs17653906	44133142	G	A	2.0774020052264144e-08	5.605428640016315	32178.0
17	rs62055468	43943000	A	C	2.0802925515605065e-08	5.605187819594768	32178.0
17	rs62061793	44171565	C	A	2.085019095825281e-08	5.604794735473286	32029.0
17	rs62063291	44043378	T	C	2.0851797495909337e-08	5.604781389873217	32186.0
17	rs62056908	43783590	G	A	2.090715099540381e-08	5.604322173845836	31470.0
17	rs7502888	43986992	G	C	2.091828292479801e-08	5.6042299652444445	32177.0
17	rs111240522	44066874	G	A	2.093088659058055e-08	5.604125623359512	32186.0
17	rs79193046	43967562	T	C	2.0995340010145992e-08	5.603592984958767	32185.0
17	rs17576631	44170018	G	C	2.1007327134716083e-08	5.603494099320055	32113.0
17	rs112596352	44170238	G	A	2.1007327134716083e-08	5.603494099320055	32113.0
17	rs62061790	44170414	G	A	2.1007327134716083e-08	5.603494099320055	32113.0
17	rs62061791	44171024	T	C	2.1007327134716083e-08	5.603494099320055	32113.0
17	rs111295615	44184428	T	C	2.100909267676697e-08	5.603479539425275	32071.0
17	rs55825513	44176215	G	A	2.101262419733787e-08	5.603450419600186	32144.0
17	rs56294117	44042783	G	A	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs112415880	44042868	G	A	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs62063292	44043636	C	T	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs62063293	44043819	G	A	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs17650991	44044508	A	C	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs75145092	44044823	T	A	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs113857334	44044940	T	C	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs77513497	44045474	A	G	2.1033678242930907e-08	5.603276912993716	32178.0
17	rs11079723	43841729	T	C	2.109304985955393e-08	5.602788537467838	32149.0
17	rs56166491	44042221	A	G	2.1149179294952453e-08	5.602328056910987	32177.0
17	rs112542080	44216966	G	GC	2.1151697081037352e-08	5.602307429046258	32077.0
17	rs12150516	43944519	C	T	2.1154585491671302e-08	5.602283767642748	32180.0
17	rs62055475	43945106	T	C	2.1154585491671302e-08	5.602283767642748	32180.0
17	rs5026246	43572896	T	G	2.11574002124724e-08	5.602260712911808	32186.0
17	rs62064675	44088926	C	T	2.124982272241781e-08	5.6015053506988055	32186.0
17	rs62064666	44082514	T	C	2.1269099254153042e-08	5.6013482070846905	32149.0
17	rs62064662	44079721	A	G	2.129920190068361e-08	5.601103084561831	32181.0
17	rs62063304	44049900	A	G	2.1350188287842538e-08	5.600688674246862	32182.0
17	rs55711941	44040823	C	T	2.1355943887602283e-08	5.600641953887786	32177.0
17	rs1967981	43999785	C	G	2.137726032023736e-08	5.600469026822507	32182.0
17	rs1476127	43999793	G	A	2.137726032023736e-08	5.600469026822507	32182.0
17	rs8079501	44000234	A	T	2.137726032023736e-08	5.600469026822507	32182.0
17	rs56002706	44000505	C	T	2.137726032023736e-08	5.600469026822507	32182.0
17	rs8078495	44000610	G	A	2.137726032023736e-08	5.600469026822507	32182.0
17	rs17649866	44000914	T	C	2.137726032023736e-08	5.600469026822507	32182.0
17	rs62058968	44001228	G	A	2.137726032023736e-08	5.600469026822507	32182.0
17	rs17564493	44001379	C	T	2.137726032023736e-08	5.600469026822507	32182.0
17	rs17649918	44001621	A	G	2.137726032023736e-08	5.600469026822507	32182.0
17	rs17649954	44001661	A	G	2.137726032023736e-08	5.600469026822507	32182.0
17	rs55685451	44001957	T	G	2.137726032023736e-08	5.600469026822507	32182.0
17	rs17564591	44002062	A	C	2.137726032023736e-08	5.600469026822507	32182.0
17	rs62059003	44002431	C	T	2.137726032023736e-08	5.600469026822507	32182.0
17	rs17650063	44002555	A	G	2.137726032023736e-08	5.600469026822507	32182.0

17	rs17564703	44002595	C	T	2.137726032023736e-08	5.600469026822507	32182.0
17	rs17650651	44030311	T	G	2.13861670382034e-08	5.600396821693861	32148.0
17	rs16940799	44102933	T	C	2.1424379914569368e-08	5.6000873678437175	32176.0
17	rs62059005	44004472	A	G	2.1482651885109493e-08	5.599616502311225	32180.0
17	rs55823844	43978320	G	A	2.1506049322335973e-08	5.599427788550347	32186.0
17	rs62063294	44044157	G	A	2.1570200328179856e-08	5.598911394423793	32177.0
17	rs17650973	44044220	A	T	2.1570200328179856e-08	5.598911394423793	32177.0
17	rs62063295	44044431	C	T	2.1570200328179856e-08	5.598911394423793	32177.0
17	rs150246512	43956305	CTT	C	2.160162792718521e-08	5.5986589566214535	32161.0
17	rs62621252	43922942	T	C	2.1621822655600665e-08	5.598496933367898	32186.0
17	rs62061706	44006896	T	C	2.1645671698472042e-08	5.5983057804527965	32176.0
17	rs17649635	43995990	A	G	2.1689272191517988e-08	5.597956845264715	32180.0
17	rs56113217	43926948	A	G	2.1707648046854728e-08	5.597809987030146	32136.0
17	rs62054835	43934672	A	C	2.1710838798950122e-08	5.597784499114674	32167.0
17	rs55996632	43935888	C	T	2.17152458316056e-08	5.5977493014574655	32186.0
17	rs73984689	44184404	G	A	2.1722694190157173e-08	5.597689829396645	32063.0
17	rs74903707	44028707	G	A	2.1746728410265376e-08	5.597498060997684	32163.0
17	rs759528501	44275649	CTAT	C	2.178580151748716e-08	5.59718673640575	32000.0
17	rs56240566	44062689	A	C	2.1863618826398868e-08	5.59656831925668	32026.0
17	rs2266497	44294786	A	G	2.187869440075451e-08	5.596448760189417	32086.0
17	rs17573245	44072854	T	C	2.1879459930072432e-08	5.596442691179933	32183.0
17	rs17565025	44012463	T	C	2.190504370122556e-08	5.596239985081231	32163.0
17	rs16940671	43908151	C	T	2.191769321168216e-08	5.596139844993807	32122.0
17	rs56269136	43926992	C	T	2.200243741791044e-08	5.595470409292952	32141.0
17	rs79600142	43897722	T	C	2.2047745026196213e-08	5.595113528535139	32182.0
17	rs2469922	44298178	A	G	2.214916955414281e-08	5.594317197521585	32099.0
17	rs55707339	43842462	T	C	2.217040886929405e-08	5.594150886115777	32129.0
17	rs62063782	44058716	G	T	2.2250973642615435e-08	5.593521438082791	32176.0
17	rs2732594	44267170	G	T	2.225665583103918e-08	5.593477127020964	31842.0
17	rs17649553	43994648	C	T	2.226241730961857e-08	5.593432208846341	32152.0
17	17:43974343_TCGC_T	43974343	TCGC	T	2.234995315041119e-08	5.592751138388787	31964.0
17	rs62057103	43887480	T	C	2.2360508253951333e-08	5.5926691896621765	32058.0
17	rs140819255	43966910	A	AAGG	2.2376467460916907e-08	5.592545355319115	32150.0
17	rs2696607	44319167	G	A	2.2392516148421694e-08	5.592420913082024	32031.0
17	rs112137135	43900817	A	G	2.2398860446931987e-08	5.592371742984064	32174.0
17	rs2429444	44298279	C	T	2.2408419383122358e-08	5.592297684063107	32078.0
17	rs2696581	44227186	G	A	2.2415787192851507e-08	5.592240622062571	32154.0
17	rs2696580	44227196	T	C	2.2415787192851507e-08	5.592240622062571	32154.0
17	rs79348289	44172698	T	C	2.246224332649256e-08	5.591881248687842	32106.0
17	rs75412750	44172773	C	T	2.246224332649256e-08	5.591881248687842	32106.0
17	rs62061795	44173179	C	A	2.246224332649256e-08	5.591881248687842	32106.0
17	rs17576709	44173356	C	G	2.246224332649256e-08	5.591881248687842	32106.0
17	rs62061796	44173408	G	A	2.246224332649256e-08	5.591881248687842	32106.0
17	rs62061802	44174351	T	A	2.246224332649256e-08	5.591881248687842	32106.0
17	rs62061803	44174513	C	A	2.246224332649256e-08	5.591881248687842	32106.0
17	rs79346219	44184375	A	G	2.2462871758023704e-08	5.59187639224148	32079.0
17	rs5820609	44149210	G	GA	2.247740904625917e-08	5.5917640865518985	32112.0
17	rs17659881	44157597	A	G	2.2482361687240428e-08	5.591725841750847	32186.0
17	17:44172205_CA_C	44172205	CA	C	2.2506511298593898e-08	5.591539473059084	32165.0
17	rs17763634	43921754	T	C	2.254030042787556e-08	5.591279039291943	32175.0
17	rs9897399	43804317	A	G	2.2544162955445285e-08	5.591249292536657	32174.0
17	rs62056812	43987154	G	A	2.2554255885159875e-08	5.591171586493722	32141.0
17	rs62063789	44061898	T	C	2.2590800910157905e-08	5.590890506349883	32171.0
17	17:43965429_TC_T	43965429	TC	T	2.259498795112708e-08	5.590858330587542	32081.0

17	rs62056809	43984669	A	G	2.26084232170706e-08	5.590755124921866	32071.0
17	rs62062794	44026394	A	G	2.2648300874907278e-08	5.590449146980902	32173.0
17	rs112647192	43994623	G	A	2.2661212566787092e-08	5.590350188710159	32178.0
17	rs17572147	44044985	A	G	2.2719841432509105e-08	5.589901530546952	32172.0
17	rs17691328	43955487	C	T	2.2725561525377265e-08	5.589857817648454	32177.0
17	rs1724404	44323425	C	T	2.2728024777920486e-08	5.589838996784283	31820.0
17	17:43897026_TGGAG_T	43897026	TGGAG	T	2.276810923761204e-08	5.5895330031844255	32179.0
17	rs55822644	43792090	G	C	2.2813685885644554e-08	5.589185718397294	31606.0
17	rs62054840	43936812	G	A	2.2827009214957102e-08	5.589084324540231	32081.0
17	rs56301449	43960918	T	C	2.282812648724831e-08	5.589075824430315	32173.0
17	rs8712	44101871	A	G	2.2838663404886002e-08	5.5889956803384075	32091.0
17	rs574194744	43837868	T	TTTA TGTT ATG	2.289029924635972e-08	5.5886034548351615	32011.0
17	rs112480703	44189799	T	C	2.2890379266655776e-08	5.588602847668277	31855.0
17	rs17651549	44061278	C	T	2.2915118677303253e-08	5.588415232115014	32186.0
17	rs113277432	44033169	T	C	2.295873656098267e-08	5.588084926816107	31726.0
17	rs17661015	44192957	T	C	2.297864818525149e-08	5.587934344436785	31798.0
17	rs113651837	43895168	T	TG	2.302673054622678e-08	5.587571241393355	32097.0
17	rs17690176	43916773	A	C	2.309815100705541e-08	5.587033252441702	32177.0
17	rs2429445	44298209	T	C	2.311034475758325e-08	5.586941561967222	32098.0
17	rs200860866	43773525	T	TAAA A	2.312408037286556e-08	5.586838333718744	32116.0
17	rs80143279	43776742	T	C	2.3125131072791592e-08	5.586830439769359	32087.0
17	rs62062795	44027090	C	T	2.3128687635217146e-08	5.586803721761003	32171.0
17	rs878887	43912582	C	T	2.3134346907889454e-08	5.586761215756437	32181.0
17	rs878888	43912635	A	G	2.3134346907889454e-08	5.586761215756437	32181.0
17	rs4525537	43912723	T	C	2.3134346907889454e-08	5.586761215756437	32181.0
17	rs4640231	43912786	G	C	2.3134346907889454e-08	5.586761215756437	32181.0
17	rs4482334	43912830	T	C	2.3134346907889454e-08	5.586761215756437	32181.0
17	rs62055945	43851851	G	A	2.3137823991302453e-08	5.586735104875023	32168.0
17	rs56043078	43853235	T	G	2.3137823991302453e-08	5.586735104875023	32168.0
17	rs77965652	43853457	A	G	2.3137823991302453e-08	5.586735104875023	32168.0
17	rs55849949	43853526	A	G	2.3137823991302453e-08	5.586735104875023	32168.0
17	rs55991914	43854267	C	T	2.3137823991302453e-08	5.586735104875023	32168.0
17	rs62055955	43854340	A	G	2.3137823991302453e-08	5.586735104875023	32168.0
17	rs62056879	43781426	T	C	2.3143566343446548e-08	5.586691991475843	32145.0
17	17:44316878_CA_C	44316878	CA	C	2.3160558943850765e-08	5.586564472363511	32166.0
17	rs2696670	44317103	T	C	2.3160558943850765e-08	5.586564472363511	32166.0
17	rs62063675	44126575	C	T	2.3178859883039577e-08	5.586427236494498	32159.0
17	rs12150235	44015745	A	G	2.3211123442934252e-08	5.586185553070111	32182.0
17	rs55780945	44040120	C	T	2.322069747951333e-08	5.58611389755841	32168.0
17	rs17652066	44073145	G	C	2.322832702468717e-08	5.586056815843847	32171.0
17	rs2696582	44226561	T	G	2.3229301186047573e-08	5.586049528803357	32056.0
17	17:44264269_GT_G	44264269	GT	G	2.3266999489102326e-08	5.585767760962954	30519.0
17	rs2316784	44021699	G	T	2.329425428993004e-08	5.585564326683442	31990.0
17	rs4327091	44021717	G	A	2.329425428993004e-08	5.585564326683442	31990.0
17	rs10445334	43934826	T	G	2.3294742720806736e-08	5.5855606830633295	32166.0
17	rs17689882	43906828	G	A	2.3343065536021888e-08	5.585200568283975	32186.0
17	rs62056810	43984672	T	C	2.3389279808623214e-08	5.584856843204876	32077.0
17	rs77044307	44172408	C	G	2.339402061029441e-08	5.584821620120801	32105.0
17	rs16940672	43908152	C	T	2.33954920851012e-08	5.584810688804753	32122.0
17	rs62062779	44022577	A	C	2.3428869861497443e-08	5.5845629105173815	32118.0
17	rs79892630	43781505	C	T	2.3504715502436075e-08	5.584001145571412	32168.0
17	rs56303031	43853922	G	A	2.352763939962284e-08	5.583831701657067	32166.0
17	rs17564619	44002138	A	G	2.3550667496219512e-08	5.583661648804454	32181.0
17	rs62062784	44024552	C	G	2.3648205331295163e-08	5.582943157672171	32186.0

17	rs1078268	44075901	A	G	2.3649775099762645e-08	5.5829316178498045	32115.0
17	rs17650579	44030115	C	T	2.3662006267274658e-08	5.582841728452546	32151.0
17	rs62062803	44028183	T	C	2.3721100561467915e-08	5.5824080665057805	32148.0
17	rs62055950	43853133	T	C	2.3727564999845942e-08	5.582360691034778	32167.0
17	rs142222997	44057770	G	GCAGGAGAATTGTTAC	2.372806233586224e-08	5.582357046762584	32153.0
17	rs1078269	44075837	T	C	2.3731875584831315e-08	5.582329107317793	32114.0
17	rs2458207	44296251	T	C	2.3774940628084777e-08	5.582013874473717	32078.0
17	17:44303525_G_A	44303525	G	A	2.3774940628084777e-08	5.582013874473717	32144.0
17	17:44129997_AAAC_A	44129997	AAAC	A	2.3817749485558042e-08	5.5817010656830774	32168.0
17	rs2532385	44313950	C	A	2.3830232287878798e-08	5.581609955298768	32165.0
17	rs2696675	44314066	A	G	2.3830232287878798e-08	5.581609955298768	32165.0
17	rs74872829	43938394	A	G	2.3835893270730723e-08	5.581568651771797	32148.0
17	rs62054384	43804306	T	C	2.384072279783808e-08	5.581533422217611	32176.0
17	rs62054388	43805590	C	T	2.385055134869469e-08	5.5814617480830275	32173.0
17	rs62057107	43896032	C	T	2.38519676536656e-08	5.581451422124736	32172.0
17	rs62055946	43851971	C	A	2.391277977796735e-08	5.581008615132913	32167.0
17	rs62062813	44032956	G	A	2.3916538589328623e-08	5.580981281009078	32096.0
17	rs76761706	43776741	T	C	2.3939354463456367e-08	5.5808154530965375	32079.0
17	rs140713557	43953179	A	G	2.3976507177097885e-08	5.580545751672484	32178.0
17	rs62063852	44074581	A	G	2.3991752770560137e-08	5.5804351972119575	32128.0
17	rs62070943	44304203	T	C	2.404040105290708e-08	5.580082876244683	32148.0
17	17:44304298_T_A	44304298	T	A	2.404040105290708e-08	5.580082876244683	32148.0
17	rs681485	43707619	C	A	2.4123072421269024e-08	5.579485737115928	32186.0
17	rs76070179	44304490	T	C	2.4219465851401122e-08	5.5787919858737505	32148.0
17	17:44303606_AG_A	44303606	AG	A	2.42214956783502e-08	5.578777405874453	32146.0
17	17:43839150_AT_A	43839150	AT	A	2.4311312895873574e-08	5.578133444061779	32080.0
17	rs112947543	44025678	G	GCT	2.4313520056940785e-08	5.578117648480986	32007.0
17	rs62057061	43856639	C	G	2.435124190939233e-08	5.577847906411751	32186.0
17	rs17650597	44030195	A	T	2.4439226834316985e-08	5.577220315103852	32152.0
17	rs17650633	44030231	T	C	2.4439226834316985e-08	5.577220315103852	32152.0
17	rs2696684	44244397	G	A	2.454251257903789e-08	5.576486375966784	32035.0
17	rs55690782	44137311	G	A	2.4555539067902188e-08	5.576394023877961	32172.0
17	rs55649944	44119463	C	T	2.457577783777457e-08	5.576250634164416	32001.0
17	rs56406462	44119474	T	C	2.457577783777457e-08	5.576250634164416	32001.0
17	rs62055544	43964539	A	G	2.458873579733959e-08	5.576158888448607	31836.0
17	rs112836774	44084002	T	C	2.4595603655313872e-08	5.576110281256318	31863.0
17	17:44301546_T_C	44301546	T	C	2.463255062043791e-08	5.575849015336753	32123.0
17	rs9891103	44091886	C	T	2.4677992479175507e-08	5.57552819987605	32099.0
17	rs62057065	43858187	G	T	2.468281688747977e-08	5.575494173656655	32159.0
17	rs56146262	43931907	C	A	2.4692813245862743e-08	5.575423690567899	32143.0
17	rs2316765	43912454	T	C	2.4730162305002508e-08	5.575160591759628	32183.0
17	rs878886	43912490	C	G	2.4730162305002508e-08	5.575160591759628	32183.0
17	rs56127111	43913315	C	T	2.4730162305002508e-08	5.575160591759628	32183.0
17	17:44303668_G_T	44303668	G	T	2.473344269343896e-08	5.575137502072276	32138.0
17	rs2696444	44288672	G	A	2.4741559171207692e-08	5.575080385349303	32028.0
17	rs3029044	43907641	C	CAGGTGG	2.475244280072053e-08	5.575003824349705	32182.0
17	rs56406407	43792099	T	C	2.4791870414042102e-08	5.5747267437098165	31597.0
17	rs450237	43709225	T	C	2.481775657989016e-08	5.57454505912033	32012.0
17	rs199504614	43781720	T	TAAAAAAAAGAG	2.4830492936351112e-08	5.5744557352514414	32172.0
17	rs62055938	43849656	C	A	2.4836993545544104e-08	5.574410161677257	32164.0
17	rs62055939	43849787	A	T	2.4836993545544104e-08	5.574410161677257	32164.0
17	rs62055940	43849896	A	G	2.4836993545544104e-08	5.574410161677257	32164.0
17	rs76885724	43850519	C	T	2.4836993545544104e-08	5.574410161677257	32164.0

17	rs62055942	43850966	A	G	2.4836993545544104e-08	5.574410161677257	32164.0
17	rs62055943	43851018	T	C	2.4836993545544104e-08	5.574410161677257	32164.0
17	rs62055957	43854536	C	A	2.4836993545544104e-08	5.574410161677257	32164.0
17	rs16940677	43911898	C	T	2.4893662721145408e-08	5.5740133628557516	32180.0
17	rs78328427	43916932	G	A	2.489453153383575e-08	5.574007286235749	32180.0
17	rs55920545	43803773	A	AG	2.490913203201084e-08	5.5739051987113335	32169.0
17	rs4074462	43855228	G	T	2.4937574932236062e-08	5.573706490967775	32165.0
17	rs62063855	44075535	T	C	2.502746128510316e-08	5.573079969850911	32104.0
17	rs62062805	44030773	A	G	2.5059971511023737e-08	5.572853906412462	32130.0
17	rs76839282	44029178	G	C	2.5082980865804005e-08	5.572694080269824	32155.0
17	rs373685009	43790598	G	GAA	2.5097426962805417e-08	5.572593808387332	32091.0
17	rs79501144	43900697	C	T	2.5126869687052632e-08	5.572389616635845	32177.0
17	rs62057123	43901238	A	G	2.5126869687052632e-08	5.572389616635845	32177.0
17	rs62055901	43845041	G	A	2.518032094527859e-08	5.5720195131503285	32156.0
17	rs17689608	43896528	C	G	2.51884053682048e-08	5.571963601942153	32174.0
17	rs62057108	43896616	T	C	2.51884053682048e-08	5.571963601942153	32174.0
17	rs62057109	43896637	T	C	2.51884053682048e-08	5.571963601942153	32174.0
17	rs62057110	43896734	T	C	2.51884053682048e-08	5.571963601942153	32174.0
17	rs62057113	43897449	A	T	2.51884053682048e-08	5.571963601942153	32174.0
17	rs17762361	43781778	A	G	2.52341477860469e-08	5.571647578787278	32153.0
17	rs17650818	44036787	T	C	2.5308741236099104e-08	5.571133421503205	32140.0
17	rs12150260	44090538	T	G	2.537106751487499e-08	5.57070494582015	32096.0
17	rs56971664	43918613	T	C	2.5416159702107087e-08	5.570395586080085	32177.0
17	rs10514904	44207887	C	T	2.5450318931372344e-08	5.570161587441014	32069.0
17	rs2532392	44309856	G	A	2.545333775221642e-08	5.5701409224791645	32110.0
17	rs2469927	44310164	T	C	2.545333775221642e-08	5.5701409224791645	32110.0
17	rs3108507	44310234	T	C	2.545333775221642e-08	5.5701409224791645	32110.0
17	rs62056808	43984646	T	C	2.5454758495237828e-08	5.570131197782981	32075.0
17	rs62055879	43836578	G	A	2.546701563074139e-08	5.570047322059152	32151.0
17	rs2469934	43704419	T	C	2.549421513684253e-08	5.569861335356797	32166.0
17	rs373853	43704491	G	A	2.549421513684253e-08	5.569861335356797	32166.0
17	rs71363552	43834671	A	AC	2.550488938084501e-08	5.569788398867682	32101.0
17	rs62057062	43856710	G	A	2.5542729238989054e-08	5.569530079745685	32165.0
17	17:44028469_CA_C	44028469	CA	C	2.5553958215731657e-08	5.5694534950073376	32137.0
17	17:43918301_GCCAGGAGTTCGAGA_G	43918301	GCCAGGAGTTCGAGA	G	2.5564478629099384e-08	5.569381772495007	32144.0
17	rs2873268	43930955	G	A	2.5593922667447655e-08	5.569181191062268	32155.0
17	rs62071573	44342994	C	T	2.559722604042624e-08	5.5691587014887975	31379.0
17	rs55787105	43853109	G	A	2.561008638971493e-08	5.569071174231227	32161.0
17	rs76294809	43849327	G	A	2.5616518939105715e-08	5.5690274104419775	32163.0
17	rs2732593	44267164	C	T	2.5628226667605576e-08	5.568947784384376	31825.0
17	rs2696568	44266342	T	C	2.566427646851236e-08	5.568702825666077	31947.0
17	rs62055900	43845002	C	G	2.5693026633242585e-08	5.568507707266639	32152.0
17	rs17334923	43827244	C	T	2.5735178848569517e-08	5.5682220160543725	32163.0
17	17:44219831_T_A	44219831	T	A	2.5765983774991066e-08	5.568013519377291	32083.0
17	rs78917495	43858482	C	T	2.5820587215582816e-08	5.567644541173142	32155.0
17	rs56070245	43847868	T	C	2.5856000493129383e-08	5.567405643486248	32168.0
17	rs56387266	43847912	T	C	2.5856000493129383e-08	5.567405643486248	32168.0
17	rs150334020	44078680	T	TA	2.586474849754748e-08	5.567346678426727	32174.0
17	rs62055885	43838014	A	G	2.5918201297065425e-08	5.566986804988088	32148.0
17	rs113793114	44037079	G	A	2.593745994501312e-08	5.566857321727959	32141.0
17	rs76830096	43857129	A	C	2.5944877811156505e-08	5.566807473462673	32167.0
17	rs62063277	44036462	T	A	2.598643818123028e-08	5.5665284421954295	32141.0
17	rs56180212	43960911	A	G	2.600139412278229e-08	5.5664281357753085	32159.0
17	rs62057070	43859640	A	G	2.6033963780078528e-08	5.566209891380319	32182.0

17	rs62057071	43859691	C	G	2.6033963780078528e-08	5.566209891380319	32182.0
17	rs141412361	44102443	C	CCT	2.6062756301698208e-08	5.566017177544046	32161.0
17	rs62057069	43859065	T	C	2.6139658657488088e-08	5.565503466489539	32179.0
17	17:44107321_CT_C	44107321	CT	C	2.6149959486481147e-08	5.565434767917551	31867.0
17	rs62057064	43857033	C	T	2.6183076687161224e-08	5.565214079570914	32163.0
17	rs62062780	44022593	C	T	2.618344184388564e-08	5.565211647728252	32115.0
17	rs55787734	43799052	A	G	2.6210751445570054e-08	5.565029866553965	32013.0
17	rs17763596	43921210	G	T	2.62352533429196e-08	5.564866930688727	32183.0
17	rs62061707	44006954	T	C	2.6285424143734787e-08	5.56453375870656	32031.0
17	rs242561	44026548	T	C	2.631549835776017e-08	5.564334338933666	32165.0
17	rs62054382	43802525	C	T	2.6346524752505835e-08	5.564128836965827	32180.0
17	rs392116	43703555	A	G	2.636104051000369e-08	5.564032773106753	32165.0
17	rs385383	43704031	C	A	2.636104051000369e-08	5.564032773106753	32165.0
17	rs17660228	44166500	G	A	2.636729021058442e-08	5.563991429008754	32160.0
17	17:43721690_CAAAAAAAA_C	43721690	CAAAAAAAA	C	2.6396628050929803e-08	5.563797475274549	32173.0
17	rs57631148	44304740	A	T	2.6430604210742e-08	5.56357311864762	32149.0
17	rs445354	44305252	G	A	2.6430604210742e-08	5.56357311864762	32149.0
17	rs62064661	44078892	G	A	2.643687007575164e-08	5.563531773488172	32177.0
17	rs4309444	43895797	T	C	2.646471548422541e-08	5.563348151185262	32167.0
17	rs34303488	43848181	C	T	2.6478279774897752e-08	5.563258771435863	32167.0
17	rs62055899	43844977	T	A	2.6499054642428954e-08	5.5631219648328365	32152.0
17	17:44304910_G_C	44304910	G	C	2.6583055225480688e-08	5.562569863564368	32139.0
17	rs62055894	43843943	G	A	2.6601407164700777e-08	5.562449469176508	32163.0
17	rs62055903	43846668	C	A	2.660446702829371e-08	5.5624294033664885	32166.0
17	rs111374028	43846820	G	A	2.660446702829371e-08	5.5624294033664885	32166.0
17	rs113934115	43847039	C	T	2.660446702829371e-08	5.5624294033664885	32166.0
17	rs10445362	43914554	C	A	2.66054870594836e-08	5.562422714758152	32184.0
17	rs10445363	43914558	G	A	2.66054870594836e-08	5.562422714758152	32184.0
17	rs62054802	43914598	G	C	2.66054870594836e-08	5.562422714758152	32184.0
17	rs62054803	43914728	G	T	2.66054870594836e-08	5.562422714758152	32184.0
17	rs62054805	43915054	A	G	2.66054870594836e-08	5.562422714758152	32184.0
17	rs62054806	43915312	C	T	2.66054870594836e-08	5.562422714758152	32184.0
17	rs10445364	43916356	G	A	2.66054870594836e-08	5.562422714758152	32184.0
17	rs10445333	43916509	A	G	2.66054870594836e-08	5.562422714758152	32184.0
17	rs17763533	43918190	T	C	2.66054870594836e-08	5.562422714758152	32184.0
17	rs112583797	43918418	A	G	2.66054870594836e-08	5.562422714758152	32184.0
17	rs74922289	43918524	A	G	2.66054870594836e-08	5.562422714758152	32184.0
17	rs56150806	43919301	T	C	2.66054870594836e-08	5.562422714758152	32184.0
17	rs17690314	43919884	T	G	2.66054870594836e-08	5.562422714758152	32184.0
17	rs56233672	43920300	T	C	2.66054870594836e-08	5.562422714758152	32184.0
17	rs56354807	43920378	C	T	2.66054870594836e-08	5.562422714758152	32184.0
17	rs55718212	43920411	T	C	2.66054870594836e-08	5.562422714758152	32184.0
17	rs17690326	43920974	T	C	2.66054870594836e-08	5.562422714758152	32184.0
17	rs62054814	43921572	T	A	2.66054870594836e-08	5.562422714758152	32184.0
17	rs78074121	43896690	T	C	2.66708488476045e-08	5.561994638627192	32170.0
17	rs55962674	43799033	C	T	2.6696237436012492e-08	5.5618286347598564	32166.0
17	rs55653963	43799509	A	C	2.6696237436012492e-08	5.5618286347598564	32166.0
17	rs62054378	43799667	C	A	2.6696237436012492e-08	5.5618286347598564	32166.0
17	rs77819001	43799804	C	A	2.6696237436012492e-08	5.5618286347598564	32166.0
17	rs76667867	43799810	G	C	2.6696237436012492e-08	5.5618286347598564	32166.0
17	rs2532294	44233433	G	C	2.6718017935680107e-08	5.561686344505663	32038.0
17	rs2532293	44233589	T	C	2.6718017935680107e-08	5.561686344505663	32038.0
17	rs17662235	44233776	T	C	2.6718017935680107e-08	5.561686344505663	32038.0
17	rs17585214	44233811	C	T	2.6718017935680107e-08	5.561686344505663	32038.0

17	rs1528074	44234060	A	G	2.6718017935680107e-08	5.561686344505663	32038.0
17	rs1406068	44234526	C	T	2.6718017935680107e-08	5.561686344505663	32038.0
17	rs79772576	44106220	A	G	2.6763962929126413e-08	5.5613865583460536	32186.0
17	rs4479288	43793828	G	A	2.6765362063046315e-08	5.561377436984622	32153.0
17	17:44106515_AAAG_A	44106515	AAAG	A	2.67688135665658e-08	5.561354937606549	32166.0
17	rs12185235	43923703	C	T	2.6773851678981403e-08	5.561322100625653	32176.0
17	rs112493812	44314179	G	A	2.680372623749612e-08	5.561127509873339	32152.0
17	rs62056880	43782304	T	C	2.6812694974362482e-08	5.56106913223524	32174.0
17	rs8073146	43893751	A	G	2.6818488846764685e-08	5.561031429909475	32046.0
17	rs113263403	44016011	A	AT	2.6818488846764685e-08	5.561031429909475	32173.0
17	rs1526126	43812218	C	T	2.681951692003017e-08	5.5610247407788655	32170.0
17	rs1526128	43779624	C	T	2.68303607716788e-08	5.560954200703983	32067.0
17	rs1526129	43779657	T	C	2.6843266813114168e-08	5.560870281977056	32178.0
17	rs75916678	43849366	T	C	2.6911357863414442e-08	5.560428181899663	32139.0
17	rs62056878	43780561	C	T	2.6970594733975595e-08	5.560044452075112	32149.0
17	17:43898362_AAGG_A	43898362	AAGG	A	2.6970594733975595e-08	5.560044452075112	32126.0
17	rs144416125	44296523	G	A	2.697943017417813e-08	5.5599872871818805	32081.0
17	rs436667	43709415	C	T	2.701630643279994e-08	5.559748895446765	32186.0
17	rs56268325	43847741	T	C	2.702459156395899e-08	5.559695378498542	32167.0
17	rs192252295	43702296	T	C	2.7073128366718446e-08	5.559382179514583	32116.0
17	rs62054383	43802907	T	C	2.7080864437636863e-08	5.559332310432877	32176.0
17	rs62055928	43847374	G	A	2.7107296623152422e-08	5.559162024716722	32165.0
17	rs62054809	43918239	C	T	2.71114525506186e-08	5.559135265385506	32176.0
17	rs113399561	44205350	A	ATT	2.711183039317192e-08	5.5591328327170455	31828.0
17	rs2696586	44225234	T	C	2.7114097556874947e-08	5.559118236699367	32064.0
17	rs611351	43692935	A	G	2.7114947791168254e-08	5.559112763189669	32158.0
17	17:44296230_T_A	44296230	T	A	2.718589254668265e-08	5.558656631501583	32062.0
17	rs62057073	43861117	C	T	2.7222950526661038e-08	5.558418830239973	32186.0
17	rs2532416	44289291	A	C	2.7238224081290686e-08	5.5583209111554215	31953.0
17	rs2532271	44248042	G	A	2.7241545530461914e-08	5.558299624327044	32037.0
17	rs60814418	43850645	C	T	2.727820271026079e-08	5.558064859341171	32137.0
17	rs17689104	43782492	A	G	2.7297785649227886e-08	5.557939568995677	32175.0
17	rs56367860	44034673	T	G	2.7366148514128024e-08	5.557502870549703	32126.0
17	rs77017444	44028796	T	C	2.742397808762933e-08	5.5571342839068665	32149.0
17	rs17762882	43898887	T	C	2.742646190220844e-08	5.557118469788735	32171.0
17	rs17689653	43898963	A	T	2.742646190220844e-08	5.557118469788735	32171.0
17	rs62061708	44006956	A	G	2.7432767960248893e-08	5.557078326195367	32037.0
17	17:44293205_A_G	44293205	A	G	2.7467572365122473e-08	5.556856926578536	31186.0
17	rs12185268	43923683	A	G	2.7476758758618253e-08	5.55679853501457	32186.0
17	rs17689471	43892973	T	C	2.7525132621144225e-08	5.5564913679226215	32173.0
17	rs62054387	43805525	A	C	2.7525803736099644e-08	5.556487110123924	32182.0
17	rs55757142	43894485	G	GA	2.7547863578619313e-08	5.556347210460618	32096.0
17	rs62056934	43790005	A	G	2.7548823095162643e-08	5.556341127841767	32115.0
17	rs56023973	43917776	G	T	2.755947592873085e-08	5.556273610633731	32182.0
17	rs17763515	43917818	G	A	2.755947592873085e-08	5.556273610633731	32182.0
17	rs10514879	43802971	C	T	2.7592035258077573e-08	5.556067407854644	32178.0
17	rs56082319	43844798	G	A	2.7607607893446665e-08	5.5559688676349115	32163.0
17	rs1918792	44228529	G	A	2.762222708768328e-08	5.555876409651645	32039.0
17	rs1918791	44228609	C	G	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2696576	44228770	A	G	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2696575	44228824	A	G	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2532300	44229986	T	C	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2696573	44230647	C	T	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2532299	44231117	T	C	2.762222708768328e-08	5.555876409651645	32039.0

17	rs2532298	44231295	G	A	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2532297	44231326	G	A	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2696572	44231617	A	T	2.762222708768328e-08	5.555876409651645	32039.0
17	rs2109092	44232959	G	A	2.762222708768328e-08	5.555876409651645	32039.0
17	17:43777957_AATC_A	43777957	AATC	A	2.7666708336910344e-08	5.555595383113613	32072.0
17	17:43797157_TA_T	43797157	TA	T	2.76892645768165e-08	5.5554530433141265	32182.0
17	rs62063859	44078616	G	A	2.7736942509953992e-08	5.555152544465806	32181.0
17	rs62064660	44078832	G	A	2.7736942509953992e-08	5.555152544465806	32181.0
17	rs111520035	44039410	A	G	2.774814979779533e-08	5.555081981252034	32154.0
17	rs11079724	43841912	C	T	2.7779573168309848e-08	5.554884281111722	32154.0
17	rs17651093	44049550	G	A	2.7831473765036232e-08	5.554558223188331	32181.0
17	rs111985258	43795859	A	G	2.784882739917257e-08	5.554449333118957	32183.0
17	rs55943044	43872228	G	A	2.786842356637587e-08	5.554326450792828	32171.0
17	rs4617909	43806451	C	T	2.788463456233309e-08	5.554224859322027	32179.0
17	rs2532291	44238424	G	A	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs17662403	44238938	T	C	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs17585426	44238966	T	C	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs2532288	44239958	C	T	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs1918789	44240107	T	C	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs2141299	44240986	C	A	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs2696567	44241304	C	G	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs2532286	44241664	T	C	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs4792844	44242969	T	C	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs4792843	44243179	A	G	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs17585608	44243979	C	T	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs17585644	44244581	T	C	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs2696657	44244926	T	G	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs2696659	44245876	A	G	2.7914070927013094e-08	5.554040533205699	32039.0
17	rs1880752	43806264	C	T	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs2902662	43806925	G	A	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs2864087	43807063	C	T	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs79226879	43807485	T	C	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs17563599	43807955	A	C	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs17649138	43808067	G	A	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054389	43808321	G	A	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054390	43808443	A	C	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs55947210	43808763	A	G	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054392	43808945	C	T	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs4390635	43809016	C	T	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054393	43809264	T	G	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs75986348	43809328	A	G	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs17649162	43810371	G	C	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054394	43810608	T	A	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs113790915	43810782	G	C	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054395	43811060	T	G	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054396	43811510	T	C	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs17563718	43811673	C	T	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62054397	43811792	C	T	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs4569335	43811950	A	C	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs1526125	43812177	C	T	2.7948792458349235e-08	5.553823354455409	32180.0
17	rs62055895	43844044	A	G	2.7988623494998248e-08	5.553574538587728	32164.0
17	rs62055896	43844201	C	T	2.7988623494998248e-08	5.553574538587728	32164.0
17	rs55725840	43844486	T	A	2.7988623494998248e-08	5.553574538587728	32164.0
17	rs56109643	43844859	A	G	2.7988623494998248e-08	5.553574538587728	32164.0

17	rs112320018	44030263	A	AC	2.802294804667896e-08	5.5533603960016205	32146.0
17	rs2316772	43946423	A	C	2.8049304493849017e-08	5.553196137168629	32125.0
17	rs4277389	43895653	A	G	2.813704101660211e-08	5.552650422004256	32168.0
17	rs2696660	44246211	A	G	2.8147230750427633e-08	5.552587149604854	32038.0
17	rs2532278	44246405	C	A	2.8147230750427633e-08	5.552587149604854	32038.0
17	17:44246624_C_A	44246624	C	A	2.8147230750427633e-08	5.552587149604854	32038.0
17	rs2532275	44246997	G	A	2.8147230750427633e-08	5.552587149604854	32038.0
17	rs2532273	44247314	C	T	2.8147230750427633e-08	5.552587149604854	32038.0
17	rs2532272	44247673	G	A	2.8147230750427633e-08	5.552587149604854	32038.0
17	rs2316764	43895602	T	G	2.8155757632764207e-08	5.552534219637443	32166.0
17	rs111355814	43977748	G	GGCTGGCCCATA	2.826890429788565e-08	5.551833339108727	31660.0
17	rs79065019	44124535	T	C	2.829992034462458e-08	5.5516416873125145	32186.0
17	rs35282504	43832618	G	A	2.8334125833916365e-08	5.551430563752907	32170.0
17	rs76669427	43836051	T	A	2.8367680598491984e-08	5.551223696755415	32169.0
17	rs62057067	43858326	C	T	2.837577904524846e-08	5.551173804945358	32168.0
17	rs62057158	43907143	G	A	2.8379532752253477e-08	5.551150684303316	32182.0
17	rs62057068	43858629	A	G	2.842421944773628e-08	5.5508756680609945	32173.0
17	rs77692262	43917086	A	G	2.8435896790239756e-08	5.550803871090021	32183.0
17	rs1881193	44248769	T	C	2.8523229733062368e-08	5.550267818504508	32036.0
17	rs17688944	43779419	T	A	2.8553724155116826e-08	5.550081017748939	32180.0
17	rs17571739	44032915	T	C	2.8617796758346897e-08	5.549689155760318	32094.0
17	17:43811990_CTTAG_C	43811990	CTTAG	C	2.8620984162194948e-08	5.5496696841335	32171.0
17	rs56288604	43931380	A	G	2.8633139331440204e-08	5.549595448362006	32157.0
17	rs78506181	43897480	A	G	2.863473382720533e-08	5.549585712500298	32182.0
17	rs62055875	43832864	T	C	2.8641910135092776e-08	5.5495419010570775	32169.0
17	rs2316769	43930798	A	G	2.8674824105146826e-08	5.549341097237346	32167.0
17	rs62054442	43829353	A	G	2.867771831618432e-08	5.549323450733422	32164.0
17	rs2532344	44343930	A	G	2.8698185560563112e-08	5.549198707709687	30783.0
17	rs62060864	44235893	C	T	2.8740463228104864e-08	5.548941308382294	32037.0
17	rs1528072	44236725	C	A	2.8740463228104864e-08	5.548941308382294	32037.0
17	rs2532292	44237068	A	T	2.8740463228104864e-08	5.548941308382294	32037.0
17	rs2696571	44237372	G	C	2.8740463228104864e-08	5.548941308382294	32037.0
17	rs2696570	44237790	G	A	2.8740463228104864e-08	5.548941308382294	32037.0
17	rs76527351	44212527	A	G	2.8802540815049885e-08	5.548564026085875	32130.0
17	rs17689116	43782558	T	C	2.8855912127436797e-08	5.548240287197462	32170.0
17	rs2903705	43573231	C	G	2.8857016691709816e-08	5.548233593286502	32136.0
17	17:44270809_A_G	44270809	A	G	2.8864247590265453e-08	5.548189778534773	32030.0
17	rs62065452	43573061	T	C	2.8881830094765843e-08	5.548083283899564	31991.0
17	rs56302057	44034486	A	G	2.890334525218248e-08	5.547953055313376	32129.0
17	rs112954158	43671066	G	GA	2.8906764993926668e-08	5.547932364703136	31900.0
17	rs58879558	44095467	T	C	2.8956395831721048e-08	5.547632348167942	32165.0
17	rs62061798	44173812	G	A	2.8966876284587245e-08	5.547569058033651	32113.0
17	rs62057152	43904110	G	C	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs17689824	43904397	C	T	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs62057153	43904528	T	C	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs62057154	43904610	C	T	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs62057155	43904673	C	T	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs62057156	43904948	G	C	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs78872653	43905134	G	A	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs62057157	43905313	G	C	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs17763086	43905481	T	G	2.9020142110379302e-08	5.547247735439372	32184.0
17	rs62055871	43831112	G	A	2.9047922733010406e-08	5.547080377637774	32177.0
17	rs56201245	44034340	C	T	2.9052976554661964e-08	5.547049948778516	32130.0
17	rs56369036	43841571	T	A	2.9058435649910683e-08	5.547017085552438	32161.0

17	17:43775212_CCTT_C	43775212	CCTT	C	2.9064603614845525e-08	5.546979962205985	32115.0
17	rs2668653	44288156	T	C	2.9097386121135187e-08	5.546782781174061	31923.0
17	rs2458210	44298102	G	A	2.9146120817988486e-08	5.546490048538688	32090.0
17	rs117646503	43893260	T	C	2.9180820748682804e-08	5.546281907246488	32182.0
17	rs17762769	43893403	G	A	2.9180820748682804e-08	5.546281907246488	32182.0
17	rs28364025	43894102	T	C	2.9180820748682804e-08	5.546281907246488	32182.0
17	rs28364023	43894159	C	T	2.9180820748682804e-08	5.546281907246488	32182.0
17	rs55779147	43894510	G	A	2.9180820748682804e-08	5.546281907246488	32182.0
17	rs17688922	43779351	G	A	2.9185592615749843e-08	5.5462533028447165	32155.0
17	rs112460810	43900215	T	TAA	2.9338288559312564e-08	5.545340372403554	32180.0
17	17:44094133_CA_C	44094133	CA	C	2.9348496079512536e-08	5.545279508719148	32061.0
17	rs750783539	44137009	AAAAAAGAG	A	2.937873074165259e-08	5.545099351000823	32164.0
17	17:43796396_TG_T	43796396	TG	T	2.9405517968571584e-08	5.544939885562178	32177.0
17	rs62056875	43778003	T	A	2.9443388031965017e-08	5.544714683859642	32181.0
17	rs17762165	43778602	C	T	2.9443388031965017e-08	5.544714683859642	32181.0
17	rs62063282	44039043	G	A	2.9500795814255632e-08	5.544373832652044	32134.0
17	17:44102741_TCA_T	44102741	TCA	T	2.9531903242561263e-08	5.544189405097115	32130.0
17	rs4792845	44242788	C	T	2.953858063963084e-08	5.544149841182759	32033.0
17	rs78440279	43816052	C	T	2.954844534789572e-08	5.544091408164735	32173.0
17	rs17688682	43775929	C	G	2.9549678663409538e-08	5.544084104024076	32180.0
17	rs12150454	43776061	C	T	2.957805884768067e-08	5.5439161079665435	32178.0
17	rs4401083	43806015	G	A	2.9599464461553525e-08	5.543789501200519	32178.0
17	rs62055878	43835854	C	A	2.9608937170911635e-08	5.5437335017684655	32173.0
17	rs62057143	43901528	T	C	2.9619030933488715e-08	5.543673850006902	32186.0
17	rs62057146	43903106	A	G	2.9630673845602518e-08	5.543605067626999	32181.0
17	17:43777835_TATCCTGCTTCCC_T	43777835	TATCCTGCTTCCC	T	2.966831213164293e-08	5.543382892647902	32117.0
17	rs739644	43895008	C	G	2.9678632164847268e-08	5.543322022309524	32183.0
17	rs12150390	43896228	T	C	2.9678632164847268e-08	5.543322022309524	32183.0
17	rs62057112	43897202	T	A	2.9678632164847268e-08	5.543322022309524	32183.0
17	rs78587102	43897246	A	G	2.9678632164847268e-08	5.543322022309524	32183.0
17	rs79959255	44077708	G	T	2.970878679982161e-08	5.543144279737182	32177.0
17	rs62054380	43800987	C	A	2.9758938773474378e-08	5.542849052729998	32177.0
17	rs17563501	43801695	C	T	2.9758938773474378e-08	5.542849052729998	32177.0
17	rs62063271	44036047	G	A	2.9783683345720328e-08	5.542703567940234	32130.0
17	rs62054811	43918651	C	G	2.9791245330351006e-08	5.542659130927782	32181.0
17	rs17650901	44039691	A	G	2.9824208534493324e-08	5.542465554710308	32157.0
17	rs62056881	43782455	G	T	2.988868315964689e-08	5.542087527195354	32170.0
17	rs62057144	43901558	A	G	2.9914053545363036e-08	5.541938992461254	32186.0
17	rs2696671	44316888	A	G	2.9937154771922944e-08	5.541803849132683	32186.0
17	rs41280118	43903089	C	T	3.004017785172413e-08	5.541202388074288	32184.0
17	rs62057148	43903485	G	C	3.004017785172413e-08	5.541202388074288	32184.0
17	rs62057149	43903546	A	G	3.004017785172413e-08	5.541202388074288	32184.0
17	rs62057150	43903548	C	T	3.004017785172413e-08	5.541202388074288	32184.0
17	rs17690679	43924803	A	G	3.0080731249699966e-08	5.540966181243062	32183.0
17	rs1876831	43907745	C	T	3.030663213519985e-08	5.539656029052926	32183.0
17	rs16940665	43907896	T	C	3.030663213519985e-08	5.539656029052926	32183.0
17	rs55763795	43908773	G	C	3.030663213519985e-08	5.539656029052926	32183.0
17	rs55865707	43908826	T	G	3.030663213519985e-08	5.539656029052926	32183.0
17	rs62062806	44031420	G	A	3.0310530619863484e-08	5.539633502363817	32153.0
17	rs55978005	44031540	G	T	3.0310530619863484e-08	5.539633502363817	32153.0
17	rs17571857	44035706	A	G	3.034310743012957e-08	5.539445372961671	32131.0
17	rs56280222	43803788	T	C	3.040403043909232e-08	5.539094071019646	32184.0
17	rs62054820	43926755	A	G	3.043533033969961e-08	5.538913851057498	32173.0
17	rs112570965	43801092	T	C	3.050300775687821e-08	5.538524788941274	32179.0

17	rs17649019	43801593	G	A	3.050300775687821e-08	5.538524788941274	32179.0
17	rs62054763	43910262	C	G	3.052146188077649e-08	5.5384188456800425	32182.0
17	rs16940674	43910507	C	T	3.052146188077649e-08	5.5384188456800425	32182.0
17	rs1876830	43911352	C	T	3.052146188077649e-08	5.5384188456800425	32182.0
17	rs1876829	43911443	T	C	3.052146188077649e-08	5.5384188456800425	32182.0
17	rs1876828	43911525	C	T	3.052146188077649e-08	5.5384188456800425	32182.0
17	rs1876827	43911832	T	C	3.052146188077649e-08	5.5384188456800425	32182.0
17	rs28364021	43912282	C	T	3.052146188077649e-08	5.5384188456800425	32182.0
17	rs17763199	43910183	G	A	3.0536742532620314e-08	5.5383311680243095	32175.0
17	rs4335809	43902216	C	T	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs4341787	43902505	C	T	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs4523962	43902522	G	A	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs3885074	43902738	C	A	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs3885075	43902799	A	G	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs41280116	43902842	C	T	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs34283254	43902861	C	A	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs1396862	43902997	G	A	3.055564147739159e-08	5.5382227881065464	32185.0
17	rs80190331	44035233	A	T	3.0602300802622316e-08	5.537955488763862	32135.0
17	rs62054435	43825339	C	G	3.066661136535968e-08	5.5375877173152395	32178.0
17	17:43855501_AC_A	43855501	AC	A	3.067311366456745e-08	5.537550574414557	32096.0
17	rs62054440	43827391	G	C	3.068729549323072e-08	5.537469590445952	32166.0
17	rs12150451	43827431	A	G	3.068729549323072e-08	5.537469590445952	32166.0
17	rs62073112	44324572	A	G	3.069700255167919e-08	5.537414180151142	31843.0
17	rs12150048	43827471	G	C	3.0739706633931027e-08	5.5371706163824275	32165.0
17	rs56026128	43931244	G	C	3.0760011461312155e-08	5.537054922431726	32141.0
17	rs62055933	43848461	G	A	3.076022526622324e-08	5.537053704596691	32122.0
17	rs62055883	43837446	C	G	3.0785036520777606e-08	5.536912435170517	32154.0
17	rs62054815	43923266	G	A	3.0796165172341164e-08	5.536849107134931	32186.0
17	rs17762308	43780948	T	C	3.080772602152142e-08	5.536783343168619	32158.0
17	rs16940681	43912159	G	C	3.0820576397410083e-08	5.5367102718116685	32170.0
17	rs2907480	44327712	C	T	3.083761123624525e-08	5.536613451804422	31636.0
17	rs4340365	43930980	C	T	3.0898003771258036e-08	5.536270619519828	32147.0
17	rs55638417	43900434	A	G	3.093141415698994e-08	5.5360812368822145	32175.0
17	rs55746658	44034575	T	C	3.095001467656803e-08	5.535975888117147	32131.0
17	rs62063275	44036287	A	G	3.098864842187824e-08	5.5357572722282775	32136.0
17	rs1034927	44334419	C	T	3.112007583139072e-08	5.535015541607523	32186.0
17	rs17662115	44227531	T	C	3.115956714970728e-08	5.534793260027852	31968.0
17	rs17426174	43830938	G	C	3.1185235748722455e-08	5.5346489277712525	32177.0
17	rs62054839	43936804	A	G	3.11929295304855e-08	5.534605688767506	32077.0
17	rs62055550	43965680	G	A	3.124868367697357e-08	5.534292659626446	32170.0
17	rs62055551	43965687	C	G	3.124868367697357e-08	5.534292659626446	32170.0
17	rs368673667	43708418	C	G	3.126410378125077e-08	5.534206179794	32156.0
17	rs16940668	43907966	G	A	3.1270838841138594e-08	5.534168420862933	32180.0
17	17:43814370_AC_A	43814370	AC	A	3.1281270126084984e-08	5.5341099552641975	32168.0
17	rs12150608	43775402	T	C	3.1318350493474866e-08	5.53390227904208	32178.0
17	rs17690987	43931626	T	C	3.136342677908584e-08	5.533650141036731	32157.0
17	rs62054426	43820741	A	T	3.136800328595502e-08	5.533624561620443	32179.0
17	rs62054427	43821062	A	G	3.136800328595502e-08	5.533624561620443	32179.0
17	rs74464991	43821685	C	A	3.136800328595502e-08	5.533624561620443	32179.0
17	rs2004260	43822398	T	C	3.136800328595502e-08	5.533624561620443	32179.0
17	rs75643244	43823326	A	G	3.136800328595502e-08	5.533624561620443	32179.0
17	rs62054431	43823880	C	T	3.136800328595502e-08	5.533624561620443	32179.0
17	rs62054432	43823889	C	A	3.136800328595502e-08	5.533624561620443	32179.0
17	rs111497072	43824201	G	A	3.136800328595502e-08	5.533624561620443	32179.0

17	rs62054433	43824348	T	C	3.136800328595502e-08	5.533624561620443	32179.0
17	rs62054434	43824382	T	G	3.136800328595502e-08	5.533624561620443	32179.0
17	rs12150683	43824848	A	G	3.136800328595502e-08	5.533624561620443	32179.0
17	rs12150332	43824908	C	T	3.136800328595502e-08	5.533624561620443	32179.0
17	rs75715199	43825478	G	A	3.136800328595502e-08	5.533624561620443	32179.0
17	rs62054438	43825711	A	C	3.136800328595502e-08	5.533624561620443	32179.0
17	rs62054439	43825725	G	T	3.136800328595502e-08	5.533624561620443	32179.0
17	rs17334797	43825912	A	G	3.136800328595502e-08	5.533624561620443	32179.0
17	rs12150363	43826351	A	G	3.136800328595502e-08	5.533624561620443	32179.0
17	rs12150672	43826637	G	A	3.136800328595502e-08	5.533624561620443	32179.0
17	rs17334894	43827209	G	A	3.136800328595502e-08	5.533624561620443	32179.0
17	rs12150604	43828221	T	A	3.136800328595502e-08	5.533624561620443	32179.0
17	rs17334944	43828617	G	A	3.136800328595502e-08	5.533624561620443	32179.0
17	rs17426064	43828698	C	T	3.136800328595502e-08	5.533624561620443	32179.0
17	rs17426106	43828935	G	C	3.136800328595502e-08	5.533624561620443	32179.0
17	17:43928629_GCACA_G	43928629	GCACA	G	3.140409342597686e-08	5.533422970180063	32084.0
17	rs12150547	43775546	A	G	3.145387941932075e-08	5.5331452453247865	32181.0
17	rs4566212	43895751	G	A	3.148525367313643e-08	5.5329704469901655	32176.0
17	rs55645418	43832115	A	G	3.1530784388935636e-08	5.532717077733919	32178.0
17	rs7350923	43834970	C	T	3.158504562753334e-08	5.532415588010599	32176.0
17	rs11079717	43835351	T	C	3.158504562753334e-08	5.532415588010599	32176.0
17	rs757501	43756685	A	G	3.160984986014779e-08	5.532277936469312	32178.0
17	rs62057118	43899727	A	G	3.164214588107248e-08	5.532098866066528	32162.0
17	rs1912151	43902944	C	T	3.166655409573922e-08	5.531963648453353	32185.0
17	rs413917	43723189	G	A	3.1694943579553196e-08	5.531806502376847	32186.0
17	rs17761985	43776787	C	T	3.1699347282376545e-08	5.5317821385205805	32181.0
17	rs56380663	43804619	C	T	3.17041920479587e-08	5.531755338240398	32186.0
17	rs62054429	43823125	G	A	3.172732478973945e-08	5.531627427259713	32178.0
17	rs28439278	43838071	C	T	3.1733606530115284e-08	5.531592708407307	32159.0
17	rs17688767	43777542	A	G	3.1756980893607535e-08	5.531463578049686	32182.0
17	rs62056874	43777578	C	T	3.1756980893607535e-08	5.531463578049686	32182.0
17	rs17688773	43777710	T	C	3.1756980893607535e-08	5.531463578049686	32182.0
17	rs12150091	43776242	A	G	3.1787326549620783e-08	5.5312960726607	32180.0
17	rs12150464	43776371	C	T	3.1787326549620783e-08	5.5312960726607	32180.0
17	rs12150435	43776391	G	C	3.1787326549620783e-08	5.5312960726607	32180.0
17	rs11079725	43923934	T	C	3.182189999875133e-08	5.5311054191659235	32186.0
17	rs12373139	43924130	G	A	3.182189999875133e-08	5.5311054191659235	32186.0
17	rs112916880	44036129	C	T	3.184489570237336e-08	5.53097872179116	32135.0
17	rs36047693	43833824	G	C	3.1848545555517685e-08	5.5309586206829655	32177.0
17	rs34195569	43833921	G	A	3.1848545555517685e-08	5.5309586206829655	32177.0
17	rs34211253	43834074	C	G	3.1848545555517685e-08	5.5309586206829655	32177.0
17	rs34008514	43834314	A	G	3.1848545555517685e-08	5.5309586206829655	32177.0
17	rs12943085	43834482	G	A	3.1848545555517685e-08	5.5309586206829655	32177.0
17	rs188710438	43573649	C	T	3.1865804956464104e-08	5.530863596956962	32111.0
17	rs77849344	43840864	G	A	3.190245622421044e-08	5.530661974432441	32156.0
17	rs17762073	43777745	C	A	3.1929722289630223e-08	5.530512126614388	32181.0
17	rs2668716	44343371	G	A	3.1967111652889e-08	5.530306845250906	31286.0
17	rs17650771	44035367	A	G	3.1981768434872526e-08	5.5302264376659584	32133.0
17	rs12373123	43924073	T	C	3.1998542980034895e-08	5.530134455819222	32186.0
17	rs41457044	43911424	C	T	3.200298801233503e-08	5.530110089687952	32181.0
17	rs62054824	43929992	C	T	3.2013325051264305e-08	5.530053438304592	32163.0
17	rs62054424	43819384	G	A	3.205737746719399e-08	5.529812211053032	32179.0
17	rs17563923	43819450	G	A	3.205737746719399e-08	5.529812211053032	32179.0
17	rs62054425	43819480	C	T	3.205737746719399e-08	5.529812211053032	32179.0

17	rs17690661	43924521	G	A	3.205982656449533e-08	5.529798809443776	32183.0
17	rs55943825	43924776	C	T	3.205982656449533e-08	5.529798809443776	32183.0
17	rs62056870	43773784	C	A	3.208053989774584e-08	5.529685504528321	32182.0
17	rs62054381	43801185	A	G	3.210148928028927e-08	5.529570980551921	32178.0
17	rs12948216	43836673	C	T	3.2149344196696114e-08	5.529309643841941	32167.0
17	rs62055692	43754909	A	G	3.21583875823211e-08	5.529260300119018	32177.0
17	rs62054831	43932381	C	T	3.2207555709221176e-08	5.5289922577673245	32147.0
17	rs2696626	44327070	G	A	3.221270026443182e-08	5.528964234926182	31104.0
17	rs968027	43781250	C	T	3.226553441521052e-08	5.5286766936748775	32128.0
17	rs17563433	43800351	A	C	3.2320361043739246e-08	5.528378791195427	32178.0
17	rs77370070	43800404	T	G	3.2320361043739246e-08	5.528378791195427	32178.0
17	rs17687740	43756376	G	C	3.235617647888565e-08	5.528184451324166	32174.0
17	rs62063264	44033401	C	T	3.2405753402895314e-08	5.527915783640228	32024.0
17	rs62055869	43830685	G	A	3.2407891041817087e-08	5.527904208297964	32178.0
17	rs17688410	43772251	C	T	3.241036637528847e-08	5.5278908052607365	32183.0
17	rs4479290	44021744	T	C	3.2434229084855484e-08	5.5277616482060665	32041.0
17	rs62057122	43901001	C	T	3.244076056065516e-08	5.527726312623166	32168.0
17	rs56205560	43804389	T	A	3.247591751529355e-08	5.527536230360159	32184.0
17	rs2532230	44275619	A	G	3.2489674936846025e-08	5.527461902772695	31899.0
17	rs55989971	43798160	G	A	3.251675538544118e-08	5.527315683667462	32178.0
17	rs55938136	43798360	A	G	3.251675538544118e-08	5.527315683667462	32178.0
17	17:43908476_GT_G	43908476	GT	G	3.2520367782570045e-08	5.527296187696557	32180.0
17	rs201825478	43774408	A	AAGAAAGAAAGAG	3.253764499177018e-08	5.527202972292327	32177.0
17	rs9906974	43822772	T	C	3.261567362456833e-08	5.526782583068363	31556.0
17	rs112556326	43575946	G	T	3.2631188067848216e-08	5.526699113309064	32108.0
17	rs1724397	43665809	C	T	3.2657363834575606e-08	5.526558371446995	32025.0
17	rs1724398	43665838	A	G	3.2657363834575606e-08	5.526558371446995	32025.0
17	rs56046792	43797246	C	T	3.270126285686974e-08	5.526322580653758	32177.0
17	rs56323722	43798015	A	C	3.270126285686974e-08	5.526322580653758	32177.0
17	17:44327642_AC_A	44327642	AC	A	3.271920207256715e-08	5.526226313752642	32105.0
17	rs62055868	43830640	C	T	3.275761075372185e-08	5.526020373960684	32177.0
17	rs75403953	43798546	A	G	3.2784682422357345e-08	5.525875361680325	32179.0
17	rs16940676	43911036	G	A	3.281109271106217e-08	5.525734004041506	32182.0
17	rs62056873	43776945	T	C	3.2830458310880055e-08	5.525630422304684	32181.0
17	rs17573447	44079567	C	T	3.285770300749895e-08	5.525484797555556	32166.0
17	17:44184819_CAAAGGT_C	44184819	CAAAGGT	C	3.286363365760183e-08	5.525453113352868	31707.0
17	rs80072429	43818611	G	A	3.2907461710856224e-08	5.525219135966747	32182.0
17	rs77114624	43818657	T	C	3.2907461710856224e-08	5.525219135966747	32182.0
17	rs76311426	43818690	G	T	3.2907461710856224e-08	5.525219135966747	32182.0
17	rs17563861	43818906	A	G	3.2907461710856224e-08	5.525219135966747	32182.0
17	rs17563889	43818946	A	T	3.2907461710856224e-08	5.525219135966747	32182.0
17	rs62054825	43930033	G	A	3.2910088645755264e-08	5.525205121599192	32164.0
17	rs56385754	43927255	G	T	3.2914543483234385e-08	5.525181358081311	32170.0
17	rs62063263	44033394	G	C	3.291968441453706e-08	5.525153938598417	32020.0
17	rs113927637	43807911	A	G	3.293236874253001e-08	5.5250863036944455	32174.0
17	rs62066460	43574935	C	T	3.2948831223202825e-08	5.5249985607356775	32109.0
17	rs62054804	43914809	C	T	3.2956607975052136e-08	5.524957126411263	32183.0
17	rs377660109	44263022	C	CAT	3.2959925078014505e-08	5.5249394558613965	32010.0
17	rs1052553	44073889	A	G	3.2962670514064715e-08	5.5249248319448725	32164.0
17	rs2907478	44331297	G	T	3.306544203108806e-08	5.524378254500624	32123.0
17	rs79322350	43790401	A	G	3.325161480797955e-08	5.523392301160449	32172.0
17	rs4479289	43793951	G	A	3.3306233598385544e-08	5.523104061036136	32175.0
17	rs4609898	43794182	G	A	3.3306233598385544e-08	5.523104061036136	32175.0
17	rs4605208	43794209	G	C	3.3306233598385544e-08	5.523104061036136	32175.0

17	rs75310534	43794286	C	T	3.3306233598385544e-08	5.523104061036136	32175.0
17	rs113856644	43932277	G	A	3.338236114446653e-08	5.5227030765720215	32160.0
17	rs17563683	43811072	A	G	3.339104911279691e-08	5.5226573710858835	32179.0
17	rs79882507	43837782	A	G	3.3464928294926025e-08	5.522269174454172	32158.0
17	rs4564621	43895501	G	C	3.3480373817520515e-08	5.522188121348282	32177.0
17	rs2316763	43895530	C	T	3.348873821734327e-08	5.522144242822124	32175.0
17	rs4566211	43895696	G	A	3.348873821734327e-08	5.522144242822124	32175.0
17	rs56226437	44042361	T	C	3.3512797273595925e-08	5.5220180914605415	32064.0
17	rs55907036	44042366	G	A	3.3512797273595925e-08	5.5220180914605415	32064.0
17	rs76007856	43795238	G	A	3.354909220221227e-08	5.521827948598748	32176.0
17	rs111415173	43795573	C	T	3.354909220221227e-08	5.521827948598748	32176.0
17	rs113991678	43795634	C	T	3.354909220221227e-08	5.521827948598748	32176.0
17	rs112995313	43795768	T	C	3.354909220221227e-08	5.521827948598748	32176.0
17	rs1880750	43796541	T	A	3.354909220221227e-08	5.521827948598748	32176.0
17	rs113155081	43752078	A	AC	3.3603956552632214e-08	5.521540902185014	32142.0
17	rs189777036	43574229	T	C	3.3608853181987685e-08	5.521515305466088	32110.0
17	rs62063857	44076665	A	G	3.362751341341905e-08	5.521417793820744	32186.0
17	rs12150141	43775145	G	A	3.363521371588008e-08	5.521377570112356	32180.0
17	rs62057117	43899657	C	G	3.3677946758356666e-08	5.521154509726183	32165.0
17	rs418891	43693538	G	T	3.369080041555169e-08	5.52108746917642	32171.0
17	rs55973918	43792252	C	A	3.3701437528500406e-08	5.521032008168292	32175.0
17	rs1568949	43792975	G	A	3.3701437528500406e-08	5.521032008168292	32175.0
17	rs1105571	43793200	A	T	3.3701437528500406e-08	5.521032008168292	32175.0
17	rs1105570	43793342	A	G	3.3701437528500406e-08	5.521032008168292	32175.0
17	rs1105569	43793388	C	T	3.3701437528500406e-08	5.521032008168292	32175.0
17	rs7502937	43793665	A	G	3.3701437528500406e-08	5.521032008168292	32175.0
17	rs78917479	43899611	C	T	3.373699636252597e-08	5.5208467305881275	32169.0
17	rs62057116	43899655	T	C	3.373699636252597e-08	5.5208467305881275	32169.0
17	rs62057101	43885291	G	A	3.375853667036053e-08	5.52073458796366	32174.0
17	rs2942164	43721283	G	C	3.3783137183402664e-08	5.520606598240686	32186.0
17	rs62056866	43771493	G	A	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs62056867	43771627	A	G	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs56200760	43772018	G	T	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs17688391	43772109	C	A	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs55927630	43772407	C	T	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs17688434	43772540	G	A	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs17688452	43773085	G	A	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs10491144	43773124	A	C	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs10491143	43773248	A	T	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs62056869	43773447	T	C	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs17688511	43773607	T	G	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs17688534	43773877	A	T	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs17688558	43773943	A	G	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs56162163	43774497	A	T	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs56391096	43774845	C	T	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs17761838	43774959	T	C	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs62056872	43775015	T	C	3.3796499102382603e-08	5.520537117722296	32183.0
17	rs12150621	43838482	G	T	3.382734503984589e-08	5.520376823919091	32158.0
17	rs81632	43710127	T	A	3.3871374600418596e-08	5.520148265634709	32184.0
17	17:43827156_GA_G	43827156	GA	G	3.387583939455478e-08	5.520125104899122	32170.0
17	rs566127718	43575452	A	G	3.390922612006399e-08	5.519952007926791	32106.0
17	rs200133133	43576046	T	TG	3.395465554493667e-08	5.5197167396412015	32104.0
17	rs17769490	43925605	G	A	3.3957717700750335e-08	5.5197008924435	32178.0
17	rs77063768	43925729	A	G	3.3957717700750335e-08	5.5197008924435	32178.0

17	rs62054818	43926056	A	C	3.3957717700750335e-08	5.5197008924435	32178.0
17	rs62064421	43667934	C	G	3.4014534385989547e-08	5.519407107238791	31979.0
17	rs55942528	43932028	A	G	3.403530393327792e-08	5.519299831771972	32135.0
17	rs62056946	43798401	G	A	3.404829120970183e-08	5.519232784278897	32176.0
17	rs78052495	43768347	C	T	3.405183403679462e-08	5.519214498555403	32024.0
17	rs62057114	43899401	C	T	3.405277885168598e-08	5.519209622359312	32168.0
17	rs62057115	43899417	G	C	3.405277885168598e-08	5.519209622359312	32168.0
17	rs149079649	44203806	C	CA	3.4081253445104184e-08	5.5190627263297936	32131.0
17	rs62061856	44200015	T	C	3.4094139656052484e-08	5.518996287480888	32092.0
17	rs76493835	43807642	T	G	3.410703064076069e-08	5.518929848385509	32178.0
17	rs62061807	44177097	C	T	3.4140166990875507e-08	5.51875917801984	32147.0
17	rs56254732	43932049	C	T	3.41418246361071e-08	5.51875064445886	32133.0
17	rs113316734	44084157	T	C	3.4170253677776526e-08	5.5186043542097405	32173.0
17	rs62055718	43766418	C	T	3.4261501372117504e-08	5.518135607820934	31989.0
17	rs62056877	43778828	T	G	3.4265541236767136e-08	5.5181148827298845	32125.0
17	rs56317731	44032073	A	G	3.434584110884289e-08	5.517703423751748	32149.0
17	rs80184151	43879308	A	G	3.435751477737279e-08	5.517643685217931	32186.0
17	rs111411180	44156401	T	TA	3.4360016783490094e-08	5.517630884077618	32130.0
17	rs78471340	43768346	G	A	3.437121842756125e-08	5.51757358362311	32030.0
17	rs1608955	43815713	C	T	3.4372410302365666e-08	5.5175674878192895	32179.0
17	rs1608956	43815820	T	A	3.4372410302365666e-08	5.5175674878192895	32179.0
17	rs62054819	43926149	A	G	3.447350920302588e-08	5.517051165704892	32166.0
17	rs62073097	44316389	G	A	3.448570367878971e-08	5.51698898659477	32114.0
17	rs62053958	43751223	A	T	3.452518535700596e-08	5.51678781740648	32179.0
17	rs62055660	43751308	T	C	3.452518535700596e-08	5.51678781740648	32179.0
17	rs113486004	43751427	T	C	3.452518535700596e-08	5.51678781740648	32179.0
17	rs62056910	43784222	T	C	3.4601162349024815e-08	5.516401322382399	32164.0
17	rs62056909	43783803	A	G	3.4633928426983526e-08	5.516234895299768	32023.0
17	rs3865315	44165169	C	T	3.4781933242383125e-08	5.515485039811344	32065.0
17	rs56080482	44032597	G	A	3.480111074447326e-08	5.515388104980955	32146.0
17	rs62056906	43782708	T	C	3.482041931728536e-08	5.5152905599679185	32161.0
17	rs62056864	43770995	G	A	3.483840986387038e-08	5.515199720696769	32184.0
17	rs62056865	43771193	T	C	3.483840986387038e-08	5.515199720696769	32184.0
17	rs2668639	44324539	T	C	3.488070536548372e-08	5.5149863380461515	31828.0
17	rs28768976	43688317	A	G	3.490042015133093e-08	5.514886961829708	32137.0
17	rs62055956	43854449	C	T	3.493164746751046e-08	5.514729665832344	32126.0
17	rs17571718	44032768	T	C	3.494436409502258e-08	5.51466564962393	32139.0
17	rs17687849	43759719	A	G	3.4991758298159716e-08	5.514427263444762	32184.0
17	rs77310586	43765381	G	C	3.4991758298159716e-08	5.514427263444762	32184.0
17	rs17688126	43765080	A	G	3.5014932832370335e-08	5.514310812776519	32184.0
17	rs62053959	43751246	C	T	3.5021487521131554e-08	5.514277889413644	32178.0
17	rs62060790	44137676	A	T	3.503581491383578e-08	5.5142059455582055	32155.0
17	rs62060791	44137678	G	A	3.503581491383578e-08	5.5142059455582055	32155.0
17	rs113728380	43760199	C	T	3.5068497983300534e-08	5.514041936875175	32181.0
17	rs739645	43894990	T	G	3.509865604902733e-08	5.513890730513327	32181.0
17	rs241036	43731719	A	C	3.516404509446507e-08	5.5135633155887005	32186.0
17	rs140510364	44107606	A	AT	3.523736878826704e-08	5.5131968720476285	31987.0
17	rs10451283	43814020	T	C	3.526559127360855e-08	5.513056024032913	32174.0
17	rs7210219	44018519	T	C	3.530093111026578e-08	5.512879810021799	30978.0
17	rs17688875	43778406	A	G	3.532124580270651e-08	5.5127785928854385	32153.0
17	rs56319902	43871982	C	T	3.535100423181964e-08	5.512630424600003	32186.0
17	rs112169475	43760192	A	G	3.5387776916655774e-08	5.512447499099965	32182.0
17	rs56329743	43931245	G	A	3.5439690083240964e-08	5.51218957097041	32153.0
17	rs62055717	43766415	A	G	3.5458731311301466e-08	5.512095057368865	31991.0

17	rs12150455	43827508	A	G	3.5469177530096854e-08	5.512043227117552	32178.0
17	rs76728632	43818160	A	C	3.5517638218624244e-08	5.511802976699446	32181.0
17	rs62054823	43929029	A	G	3.554743556415087e-08	5.511655410124129	32126.0
17	rs62057119	43899736	G	A	3.5555073535069737e-08	5.511617603615784	32164.0
17	rs17762954	43899786	C	T	3.5555073535069737e-08	5.511617603615784	32164.0
17	rs647483	43729432	C	T	3.557701083873297e-08	5.511509061906429	32184.0
17	rs78555354	44032879	A	G	3.5588477737216466e-08	5.511452351650585	32135.0
17	rs75500942	43816106	C	A	3.561895041544179e-08	5.511301733217561	32180.0
17	rs62054418	43816306	G	A	3.561895041544179e-08	5.511301733217561	32180.0
17	rs17762535	43787130	T	C	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056922	43787563	C	G	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs56397077	43788419	C	A	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056925	43788649	T	C	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056926	43788666	C	G	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056935	43790446	A	G	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs75076131	43790649	C	A	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056936	43790911	A	T	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056937	43791181	A	C	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056939	43791332	T	C	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs62056940	43791344	T	A	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs78803763	43791405	C	A	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs77387379	43791429	G	A	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs75990322	43791468	T	C	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs113661667	43791610	T	C	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs74579538	43791652	G	A	3.565624324437751e-08	5.5111175745458745	32174.0
17	rs650927	43709867	T	G	3.5678612575392644e-08	5.511007200394684	32185.0
17	rs671740	43709893	A	G	3.5678612575392644e-08	5.511007200394684	32185.0
17	rs16940633	43710371	G	A	3.5678612575392644e-08	5.511007200394684	32185.0
17	rs17686610	43710384	A	C	3.5678612575392644e-08	5.511007200394684	32185.0
17	rs2942170	43711312	C	T	3.5678612575392644e-08	5.511007200394684	32185.0
17	rs2040844	43767219	A	C	3.5684547079835254e-08	5.510977929787433	32185.0
17	rs62055884	43837567	C	T	3.5700871953977704e-08	5.5108974353708335	32163.0
17	17:44254993_GT_G	44254993	GT	G	3.5773308938814616e-08	5.5105406943972515	31691.0
17	rs62056920	43787226	G	A	3.5780498566236814e-08	5.510505324819525	32173.0
17	rs62056921	43787306	T	C	3.5780498566236814e-08	5.510505324819525	32173.0
17	rs12150658	43826305	G	A	3.5793269842244536e-08	5.510442513155876	32179.0
17	rs17688032	43763202	G	A	3.581138046817069e-08	5.510353478769785	32186.0
17	17:43819597_AC_A	43819597	AC	A	3.591687302740046e-08	5.5098357289458235	32172.0
17	rs62053956	43750315	A	G	3.5921228482972986e-08	5.509814384403341	32182.0
17	rs55821155	44032470	C	G	3.5928447234313165e-08	5.509779013391217	32147.0
17	rs138325961	43971238	T	TTAGATACATCA	3.593404896875489e-08	5.509751570316446	32100.0
17	rs1724413	43670073	G	T	3.60517583535248e-08	5.509175865898538	31694.0
17	rs113072604	43741627	A	AT	3.611150518105404e-08	5.508884347493561	32172.0
17	rs62056927	43788767	G	A	3.6140413404223836e-08	5.508743465559549	32173.0
17	rs62056929	43789144	G	A	3.6140413404223836e-08	5.508743465559549	32173.0
17	17:43809559_GT_G	43809559	GT	G	3.6186262468029605e-08	5.508520247758817	32058.0
17	rs1526127	43812398	C	G	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054398	43812599	A	G	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054399	43812624	G	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054400	43812649	T	C	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054411	43812684	A	G	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054412	43813002	G	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs17563787	43813252	C	G	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054413	43813370	G	C	3.6200680356514286e-08	5.508450110443748	32182.0

17	rs62054414	43813415	G	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs76421814	43814427	T	C	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs56006248	43815141	A	G	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs56298110	43815336	A	G	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054417	43815859	A	C	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054419	43816605	A	C	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054420	43816655	C	G	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs62054421	43816657	G	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs17563800	43817459	C	T	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs56295996	43817557	C	T	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs56384960	43817608	G	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs56178230	43817832	G	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs80157557	43817898	G	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	rs17563827	43818222	C	A	3.6200680356514286e-08	5.508450110443748	32182.0
17	17:43926093_GATGA_G	43926093	GATGA	G	3.6203062984104864e-08	5.508438522513081	31484.0
17	rs885639	43928614	T	G	3.6209584645258666e-08	5.5084068081381785	32159.0
17	rs56167344	43797087	A	T	3.621686016360773e-08	5.508371434346075	32142.0
17	rs17688056	43763241	C	T	3.625752906811529e-08	5.508173827739405	32183.0
17	rs34739559	43949342	G	A	3.629409390450489e-08	5.507996345873084	31935.0
17	rs111920741	44333412	G	A	3.6301008842286265e-08	5.507962800992825	31907.0
17	rs62056863	43770595	A	G	3.632163559271736e-08	5.507862775885974	32185.0
17	rs77301847	43810902	A	G	3.6341770317166585e-08	5.507765189877524	31746.0
17	rs113520245	44033132	C	T	3.6386105209390584e-08	5.507550498787291	31688.0
17	rs1706722	43684094	T	C	3.643541432590775e-08	5.5073120178830655	31744.0
17	rs56108117	43757776	T	C	3.643806449323019e-08	5.5072992093559	32182.0
17	rs56378021	43757777	C	T	3.643806449323019e-08	5.5072992093559	32182.0
17	17:43913360_TGAGGGCAGGAGG_T	43913360	TGAGGGCAGGAGG	T	3.652474054644246e-08	5.506880792431387	32128.0
17	rs62055693	43756910	T	C	3.6525752536457107e-08	5.506875912876061	32185.0
17	17:43769819_AAAATT_A	43769819	AAAATT	A	3.659121067296127e-08	5.506560568794176	32129.0
17	rs757502	43756506	C	T	3.660958996470194e-08	5.506472125066298	32170.0
17	rs17652036	44073027	G	A	3.6609843535396464e-08	5.506470905149759	32140.0
17	rs62054428	43822511	G	A	3.6682562446931016e-08	5.506121395638491	32176.0
17	rs76171147	43823229	T	C	3.670835892459555e-08	5.505997571260946	32186.0
17	rs383241	43705356	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs376120	43705518	A	G	3.671191845388397e-08	5.505980491969278	32186.0
17	rs594591	43707620	G	T	3.671191845388397e-08	5.505980491969278	32186.0
17	rs2942169	43711539	G	C	3.671191845388397e-08	5.505980491969278	32186.0
17	rs241045	43712337	C	T	3.671191845388397e-08	5.505980491969278	32186.0
17	rs241044	43712464	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs241042	43712657	T	C	3.671191845388397e-08	5.505980491969278	32186.0
17	rs241041	43713925	A	G	3.671191845388397e-08	5.505980491969278	32186.0
17	rs241039	43714673	A	T	3.671191845388397e-08	5.505980491969278	32186.0
17	rs2942168	43714850	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs2942167	43715018	T	C	3.671191845388397e-08	5.505980491969278	32186.0
17	rs2942165	43715619	G	C	3.671191845388397e-08	5.505980491969278	32186.0
17	rs117368197	43715924	A	G	3.671191845388397e-08	5.505980491969278	32186.0
17	rs413778	43716885	A	G	3.671191845388397e-08	5.505980491969278	32186.0
17	rs389217	43717131	C	T	3.671191845388397e-08	5.505980491969278	32186.0
17	rs3108317	43719870	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs1706746	43721457	C	T	3.671191845388397e-08	5.505980491969278	32186.0
17	rs3418	43723462	C	T	3.671191845388397e-08	5.505980491969278	32186.0
17	rs393675	43723605	T	C	3.671191845388397e-08	5.505980491969278	32186.0
17	rs449501	43724555	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs448830	43725212	G	A	3.671191845388397e-08	5.505980491969278	32186.0

17	rs434428	43725684	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs434598	43725762	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs434971	43725992	G	A	3.671191845388397e-08	5.505980491969278	32186.0
17	rs385691	43726125	A	C	3.671191845388397e-08	5.505980491969278	32186.0
17	rs455028	43726574	T	C	3.671191845388397e-08	5.505980491969278	32186.0
17	rs241035	43731896	C	T	3.671191845388397e-08	5.505980491969278	32186.0
17	rs62055700	43758742	T	C	3.6743714956888776e-08	5.50582799757174	32184.0
17	rs62053957	43750939	T	C	3.67951551414605e-08	5.505581563880859	32183.0
17	rs62055751	43767538	A	G	3.685049374559409e-08	5.5053168268806525	32185.0
17	rs75691066	44045585	C	A	3.6852663045387044e-08	5.505306456918514	32142.0
17	rs424243	43727887	A	T	3.6873469153714466e-08	5.505207026976764	32184.0
17	rs62053953	43749454	G	A	3.690910877234945e-08	5.505036835795454	32186.0
17	rs62056876	43778752	C	T	3.691958991414744e-08	5.504986815140759	32152.0
17	rs34579278	43833981	A	G	3.696359136511305e-08	5.504776970871898	32172.0
17	rs453997	43727061	C	T	3.6976264090753444e-08	5.5047165791877655	32185.0
17	rs422112	43728137	G	A	3.6976264090753444e-08	5.5047165791877655	32185.0
17	rs413844	43729384	G	A	3.6976264090753444e-08	5.5047165791877655	32185.0
17	rs241038	43730598	G	A	3.6976264090753444e-08	5.5047165791877655	32185.0
17	rs241037	43730636	G	T	3.6976264090753444e-08	5.5047165791877655	32185.0
17	rs241032	43734145	T	C	3.6994064293298334e-08	5.504631786479503	32178.0
17	rs674692	43695967	A	G	3.701494860621404e-08	5.504532352792246	32143.0
17	rs675726	43696254	A	G	3.701494860621404e-08	5.504532352792246	32143.0
17	rs143345034	43696920	C	T	3.701494860621404e-08	5.504532352792246	32143.0
17	17:44130328_TC_T	44130328	TC	T	3.704251306492258e-08	5.504401197084408	32098.0
17	rs2732625	44332429	C	T	3.7063167523765334e-08	5.504302982181274	32126.0
17	rs413519	43685826	A	G	3.7130983089119044e-08	5.5039808823220415	32070.0
17	rs143143028	44170129	C	CAA	3.7255885438319916e-08	5.5033891307420095	31881.0
17	rs17689378	43881790	C	T	3.732559695772039e-08	5.503059693555584	32186.0
17	rs62055932	43848412	A	G	3.7389870292894336e-08	5.502756483975331	32143.0
17	rs77555455	44035516	G	A	3.739103519525221e-08	5.502750993211269	32128.0
17	rs2950009	43666244	A	G	3.742133513926251e-08	5.502608232754802	32030.0
17	rs2950010	43666251	C	G	3.743649413013168e-08	5.502536852099861	32119.0
17	rs12150610	43775479	T	C	3.744232611291778e-08	5.502509397926059	32178.0
17	rs2873269	43931122	C	T	3.7539786899742076e-08	5.502051212058276	32157.0
17	rs757500	43756833	C	A	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs55651627	43758011	G	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs112155389	43758078	G	A	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17687838	43759048	T	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs76333921	43759426	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs76453925	43759431	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17761100	43760389	A	G	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17761124	43760516	A	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055704	43760577	G	A	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055705	43760599	A	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055706	43760685	T	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs75115093	43761381	A	G	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055707	43761482	T	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs2049515	43761856	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055709	43762429	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055711	43762554	A	G	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17688002	43762594	A	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs2040846	43762846	A	G	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs4486953	43763007	T	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17688068	43763935	A	G	3.7586593861779556e-08	5.501831571534178	32186.0

17	rs62055712	43764565	A	G	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055713	43764685	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17688090	43764987	G	A	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17761387	43765450	G	A	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055716	43765778	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17688205	43766352	G	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17688249	43766754	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055753	43767631	G	A	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17688296	43767815	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62055754	43768230	C	G	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs55972157	43768703	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs17761581	43769088	T	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs56283089	43769321	A	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs56312737	43769516	C	A	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs74765707	43770416	T	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62056861	43770443	T	C	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs62056862	43770525	C	T	3.7586593861779556e-08	5.501831571534178	32186.0
17	rs56290582	43788371	C	T	3.7591668047084514e-08	5.501807776982367	32172.0
17	rs241034	43733048	A	T	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241033	43733983	G	A	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241031	43734304	T	C	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241030	43734503	A	G	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241029	43734643	T	C	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241028	43735276	C	T	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241027	43735478	A	G	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241026	43735555	G	A	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241024	43736763	C	T	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241023	43737040	G	A	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241021	43738627	T	G	3.765091648253655e-08	5.501530171542176	32185.0
17	rs241020	43738676	C	A	3.765091648253655e-08	5.501530171542176	32185.0
17	17:43746187_TC_T	43746187	TC	T	3.7681553138283726e-08	5.501386791223204	32180.0
17	rs55980621	43768496	C	T	3.769094457454167e-08	5.501342861704282	32184.0
17	rs55669046	43768501	C	T	3.769094457454167e-08	5.501342861704282	32184.0
17	rs1706748	43722509	C	G	3.772461605432588e-08	5.501185446710036	32182.0
17	rs113871181	43852733	G	A	3.777544001042181e-08	5.500948101331852	32105.0
17	17:43734255_TA_T	43734255	TA	T	3.7782762090692286e-08	5.500913933100693	32184.0
17	rs62055697	43758148	C	T	3.779335541677192e-08	5.500864511079586	32185.0
17	rs17761046	43758382	T	C	3.779335541677192e-08	5.500864511079586	32185.0
17	rs56168907	43837091	T	C	3.780159668190928e-08	5.500826071635549	32162.0
17	rs62056912	43784948	G	T	3.783287717461231e-08	5.500680245058068	32167.0
17	rs62054822	43927708	A	G	3.790522027956596e-08	5.500343436040021	32170.0
17	rs4609899	43807113	C	T	3.7935271938506986e-08	5.500203707251651	32165.0
17	rs4471726	43807134	T	C	3.794380613714663e-08	5.5001640460432375	32166.0
17	17:43893146_CCCAGTTCAGTGTGT_C	43893146	CCCAGTTCAGTGTGT	C	3.796324486816303e-08	5.500073740194902	32117.0
17	rs3108318	43719829	G	T	3.800872753996719e-08	5.499862617989188	32095.0
17	rs62064424	43668239	T	C	3.81007759663926e-08	5.499436094727134	31951.0
17	rs62055719	43766497	T	C	3.8127285228853264e-08	5.499313444526871	32181.0
17	rs77220413	43764378	G	A	3.814246034497955e-08	5.4992432711489965	32186.0
17	rs62073155	44333121	G	A	3.81560569934822e-08	5.4991804199771614	32146.0
17	rs62054817	43925966	G	A	3.8157905448128256e-08	5.499171877082409	32174.0
17	rs56110538	43768727	G	A	3.816741317204504e-08	5.499127942130751	32184.0
17	rs62056928	43788782	C	T	3.8168205587118066e-08	5.499124280879916	32171.0
17	rs113448888	44108482	A	AGCCCTCT	3.8181150648238686e-08	5.499064480343653	32114.0
17	rs112245406	43756171	A	AAAAC	3.8223846968633615e-08	5.498867381244335	32116.0

17	rs112695020	44037106	C	CA	3.823522291139548e-08	5.498814902480753	32073.0
17	rs17425752	43906726	A	C	3.826129425875895e-08	5.498694688919536	32145.0
17	rs56220242	43792326	C	T	3.832939999970981e-08	5.498381031463467	32167.0
17	rs56160448	43792358	A	G	3.832939999970981e-08	5.498381031463467	32167.0
17	rs1880749	43792586	A	C	3.832939999970981e-08	5.498381031463467	32167.0
17	rs370739771	44255146	C	CT	3.834677667024303e-08	5.498301090649825	30569.0
17	rs190796367	44333293	A	G	3.835062445724713e-08	5.498283393780254	32148.0
17	rs55747440	43837115	A	G	3.8399218703425435e-08	5.4980600455786215	32163.0
17	rs241022	43737730	T	C	3.842367137684136e-08	5.497947760184788	32184.0
17	rs111273167	43740967	C	T	3.844840534351232e-08	5.497834253582108	32186.0
17	rs62053940	43741028	A	G	3.844840534351232e-08	5.497834253582108	32186.0
17	rs17760577	43741452	C	T	3.844840534351232e-08	5.497834253582108	32186.0
17	rs17760631	43743045	T	C	3.844840534351232e-08	5.497834253582108	32186.0
17	rs4528616	43683597	T	G	3.846849653923763e-08	5.497742105219738	32092.0
17	rs62056915	43785627	A	T	3.8553098626559806e-08	5.4973545887057735	32166.0
17	rs56100013	43768467	C	T	3.856256939395242e-08	5.4973112595665565	32184.0
17	rs2532372	43671235	C	T	3.8580450010123496e-08	5.497229483159062	31987.0
17	rs62053954	43749949	G	A	3.8580583478084046e-08	5.497228872885958	32184.0
17	rs62053955	43749980	T	C	3.8580583478084046e-08	5.497228872885958	32184.0
17	rs17687625	43750238	A	G	3.8580583478084046e-08	5.497228872885958	32184.0
17	rs1724412	43670018	G	A	3.87528662132884e-08	5.496442823870502	31783.0
17	rs444071	43707951	C	T	3.8766005491175384e-08	5.4963830143810215	32185.0
17	rs396593	43707955	C	A	3.8766005491175384e-08	5.4963830143810215	32185.0
17	rs17762912	43899161	A	C	3.8766944177995385e-08	5.496378742266991	32172.0
17	rs2532384	44317210	C	A	3.879551772597827e-08	5.496248747452748	32144.0
17	rs366858	43726588	C	T	3.879954382647845e-08	5.496230438248186	32185.0
17	rs62057111	43897130	A	G	3.88376778606795e-08	5.496057110184426	32179.0
17	rs370670279	43669049	A	AC	3.883875259033097e-08	5.496052227679467	32124.0
17	rs184745911	43698899	A	G	3.890678846924988e-08	5.4957434065365325	32098.0
17	rs78487840	43757161	C	T	3.9030924295999643e-08	5.49518128956491	32186.0
17	rs62062796	44027316	G	A	3.9054690350353065e-08	5.495073868895997	32155.0
17	rs2693349	43666511	A	T	3.9099830822971936e-08	5.494870011991601	32027.0
17	rs75788861	43822769	C	T	3.913108062409524e-08	5.494729019781338	31566.0
17	rs2158474	43761939	G	C	3.926148379578634e-08	5.494141845481507	32184.0
17	rs62055708	43761974	C	A	3.926148379578634e-08	5.494141845481507	32184.0
17	rs76927677	43761985	A	T	3.926148379578634e-08	5.494141845481507	32184.0
17	rs17761207	43762255	T	C	3.926148379578634e-08	5.494141845481507	32184.0
17	17:44288114_TA_T	44288114	TA	T	3.9287696984024674e-08	5.494024042082318	31785.0
17	rs55711776	43669250	A	G	3.933364532677643e-08	5.493817731672099	31998.0
17	rs56400821	43760080	C	A	3.935160393948267e-08	5.493737160097438	32178.0
17	rs56357543	43894547	C	T	3.936058625753368e-08	5.493696874174197	32172.0
17	rs56099546	43894609	A	G	3.936058625753368e-08	5.493696874174197	32172.0
17	17:43742454_AC_A	43742454	AC	A	3.937392734410112e-08	5.493637055514959	32183.0
17	rs62053951	43749168	G	C	3.951837561155437e-08	5.492990635015013	32185.0
17	rs62053952	43749261	T	C	3.951837561155437e-08	5.492990635015013	32185.0
17	rs17687534	43749579	T	C	3.951837561155437e-08	5.492990635015013	32185.0
17	rs17687571	43750010	G	A	3.951837561155437e-08	5.492990635015013	32185.0
17	rs17760817	43750137	G	C	3.951837561155437e-08	5.492990635015013	32185.0
17	rs62055661	43752039	C	T	3.951837561155437e-08	5.492990635015013	32185.0
17	rs62055662	43752566	C	T	3.951837561155437e-08	5.492990635015013	32185.0
17	rs62055663	43753454	A	G	3.951837561155437e-08	5.492990635015013	32185.0
17	rs62055664	43753642	A	G	3.951837561155437e-08	5.492990635015013	32185.0
17	rs76717812	43754010	T	C	3.951837561155437e-08	5.492990635015013	32185.0
17	rs17687667	43754099	G	A	3.951837561155437e-08	5.492990635015013	32185.0

17	rs79073784	43754209	G	C	3.951837561155437e-08	5.492990635015013	32185.0
17	rs62055714	43764796	G	T	3.956773477604288e-08	5.492770272931184	32185.0
17	rs62055715	43764847	G	A	3.956773477604288e-08	5.492770272931184	32185.0
17	rs35879086	43830382	G	A	3.9633732303241736e-08	5.49247604564554	32167.0
17	rs111957446	44179723	T	C	3.97476323012416e-08	5.491969377374328	32123.0
17	rs17760733	43746276	G	T	3.9996438449544734e-08	5.490867477019694	32183.0
17	rs79675109	43746418	T	A	3.9996438449544734e-08	5.490867477019694	32183.0
17	rs17687504	43746721	A	G	3.9996438449544734e-08	5.490867477019694	32183.0
17	rs62053945	43746839	T	C	3.9996438449544734e-08	5.490867477019694	32183.0
17	rs62053946	43747677	C	T	3.9996438449544734e-08	5.490867477019694	32183.0
17	rs62053947	43747683	G	A	3.9996438449544734e-08	5.490867477019694	32183.0
17	rs62053949	43748101	A	G	3.9996438449544734e-08	5.490867477019694	32183.0
17	rs62053950	43748412	A	G	3.9996438449544734e-08	5.490867477019694	32183.0
17	17:44029510_TGATG_T	44029510	TGATG	T	4.002548430873058e-08	5.4907392736844205	32081.0
17	rs17571781	44033802	T	C	4.003849248186777e-08	5.490681887132295	32125.0
17	17:43950444_CA_C	43950444	CA	C	4.0118431297076336e-08	5.490329627353512	31808.0
17	rs56323832	43768633	G	A	4.013396612499538e-08	5.490261250302444	32182.0
17	rs74514268	43836191	G	A	4.0208670951907525e-08	5.4899327926152415	32170.0
17	rs62054762	43909022	G	T	4.0247465547154884e-08	5.489762456238568	32003.0
17	rs8072451	43893716	C	T	4.042731559810085e-08	5.488974858383769	32065.0
17	rs62066125	43702701	C	G	4.044827941667506e-08	5.488883274990339	32163.0
17	rs2696462	44286089	G	A	4.055101600489803e-08	5.488435120166723	31729.0
17	rs56013908	43836920	T	C	4.05515765769718e-08	5.488432677875389	32156.0
17	rs62053948	43748046	C	T	4.0677757903938884e-08	5.487883764449598	32180.0
17	rs62054760	43908989	C	T	4.068338112855907e-08	5.487859340769485	32004.0
17	rs368303226	43798784	A	AGAG	4.089847669958917e-08	5.486927552503543	32154.0
17	rs2188888	43953695	T	C	4.104457204460076e-08	5.486297377263427	32034.0
17	rs62055665	43754505	A	C	4.1044713857461073e-08	5.486296766617754	32184.0
17	rs62055690	43754576	C	G	4.1044713857461073e-08	5.486296766617754	32184.0
17	rs62055691	43754850	T	C	4.1044713857461073e-08	5.486296766617754	32184.0
17	rs439558	43717803	T	C	4.1169410925656896e-08	5.485760611682926	32186.0
17	rs62056911	43784624	T	C	4.118406369397058e-08	5.485697713184396	32169.0
17	rs62054761	43909008	C	T	4.127579494575778e-08	5.485304439894855	32004.0
17	rs191247549	44326105	G	C	4.129105538327725e-08	5.48523909706774	32126.0
17	rs17689218	43785808	T	C	4.142292413622057e-08	5.484675428952448	32168.0
17	rs62056916	43785938	C	T	4.142292413622057e-08	5.484675428952448	32168.0
17	rs62056917	43786013	G	T	4.142292413622057e-08	5.484675428952448	32168.0
17	rs62064409	43666431	T	C	4.146172010652132e-08	5.484509928228432	32031.0
17	17:44035222_GAA_G	44035222	GAA	G	4.149582119602732e-08	5.484364579467988	32046.0
17	rs112972619	43776425	C	T	4.155979891084071e-08	5.484092200043572	31852.0
17	17:44078816_TA_T	44078816	TA	T	4.167537509517772e-08	5.4836011737573305	31993.0
17	rs62055689	43754569	G	A	4.168286100130112e-08	5.483569415374904	32183.0
17	rs112637166	43751101	A	G	4.181826603659983e-08	5.482995922588413	32171.0
17	17:44195611_CA_C	44195611	CA	C	4.1849040813125735e-08	5.4828658306155990	31957.0
17	rs55840731	43769277	C	G	4.18507752632684e-08	5.48285850146226	32176.0
17	rs643024	43690468	C	T	4.197816036238208e-08	5.482321022044027	32103.0
17	rs3919455	43953707	C	T	4.212032256983217e-08	5.481723057240609	32033.0
17	rs2214258	43953719	G	C	4.212032256983217e-08	5.481723057240609	32033.0
17	rs62056919	43786698	C	T	4.217271725820815e-08	5.481503167308666	32163.0
17	rs74398257	43756340	T	C	4.251293393354541e-08	5.480081758105996	32180.0
17	rs147268270	44101849	T	TC	4.254420934036169e-08	5.479951644968195	31742.0
17	rs62064423	43668187	A	G	4.256007590205618e-08	5.479885671748519	31990.0
17	rs28439143	43987723	G	A	4.261315342896555e-08	5.479665148389719	32186.0
17	17:43920219_AAAG_A	43920219	AAAG	A	4.264376492817247e-08	5.479538086606801	32131.0

17	rs62056930	43789640	A	C	4.266865262942536e-08	5.479434848244572	32153.0
17	rs17650872	44039516	G	T	4.268147018764252e-08	5.4793817016367665	32145.0
17	rs62064418	43667836	C	A	4.268928043358622e-08	5.479349324890362	31759.0
17	17:44260931_GGAGAGA_G	44260931	GGAGAGA	G	4.27413353404337e-08	5.479133682048863	31787.0
17	17:44260939_GA_G	44260939	GA	G	4.27413353404337e-08	5.479133682048863	31787.0
17	rs62056918	43786676	T	G	4.2761702315941496e-08	5.479049379042454	32164.0
17	rs62064419	43667915	T	C	4.2946619323637904e-08	5.478285746781464	32006.0
17	rs55801356	43837237	A	G	4.317447103219554e-08	5.477349183733881	32158.0
17	rs1568951	43792895	T	G	4.3175514161612873e-08	5.47734490707798	32174.0
17	rs1568950	43792896	T	C	4.3175514161612873e-08	5.47734490707798	32174.0
17	rs150592114	44333331	A	G	4.327965310880003e-08	5.476918458263115	30979.0
17	17:43798584_CA_C	43798584	CA	C	4.340710172944503e-08	5.476397908128688	32148.0
17	rs2696594	44220790	A	G	4.346466346195538e-08	5.476163289038521	31802.0
17	rs62064415	43667537	C	T	4.364397191563788e-08	5.475434361689466	31662.0
17	rs2902661	43807099	G	A	4.412045088701528e-08	5.473511390894092	32148.0
17	rs17687462	43744990	C	T	4.4309897692307736e-08	5.4727524113866615	32177.0
17	rs56328224	43572419	C	T	4.431387206882576e-08	5.472736522583146	32026.0
17	rs62053939	43740856	C	T	4.446807164251538e-08	5.4721211261583775	32186.0
17	17:43733707_GC_G	43733707	GC	G	4.453883873954013e-08	5.471839393432158	32175.0
17	rs62055752	43767628	G	A	4.457018952365929e-08	5.471714720703196	32173.0
17	17:43760759_AT_A	43760759	AT	A	4.4732976041531197e-08	5.4710687309534665	32130.0
17	17:44204299_AC_A	44204299	AC	A	4.484620571542011e-08	5.4706207414131125	31744.0
17	rs17652337	44083323	C	T	4.485486780954675e-08	5.470586515285016	31978.0
17	rs62073156	44333568	T	C	4.4857033589093564e-08	5.470577958742771	32136.0
17	rs55946323	44031946	A	G	4.488241177755955e-08	5.47047772465789	32144.0
17	rs138070769	43781726	A	AAAGAG	4.510149429803841e-08	5.4696147104339765	32125.0
17	rs78568882	43784935	C	G	4.514724219225904e-08	5.4694350124412825	32157.0
17	rs62066086	43688387	A	G	4.525915774430455e-08	5.468996150583633	32097.0
17	rs62066087	43688579	A	G	4.525915774430455e-08	5.468996150583633	32097.0
17	17:43762168_CT_C	43762168	CT	C	4.5378854669623086e-08	5.468527937918856	32179.0
17	rs62055698	43758238	C	T	4.5459347250077873e-08	5.468213751802933	32181.0
17	rs61667602	43785349	T	C	4.5714113343674044e-08	5.467222868059473	32159.0
17	rs2532309	44220785	G	A	4.5750847771906457e-08	5.46708043547786	31795.0
17	rs62055889	43838919	G	A	4.599119910644416e-08	5.466151233765216	32150.0
17	rs56155809	44119500	C	CTT	4.602037804174151e-08	5.466038748182516	31824.0
17	17:43814930_GCGTA_G	43814930	GCGTA	G	4.610611659230668e-08	5.465708623372866	32135.0
17	rs62063266	44033488	C	T	4.611994464945056e-08	5.465655436029004	32125.0
17	rs62055701	43758787	G	A	4.638377046783034e-08	5.464643623725539	32019.0
17	rs62055702	43758790	C	T	4.638377046783034e-08	5.464643623725539	32019.0
17	rs7502718	43793651	G	A	4.707730273118991e-08	5.462010198384951	32169.0
17	rs62055886	43838678	G	A	4.726923999486996e-08	5.461288032935883	32114.0
17	rs62055887	43838710	T	C	4.726923999486996e-08	5.461288032935883	32114.0
17	rs34039488	27320232	G	A	4.7422230508020914e-08	5.460714437942859	31978.0
17	rs112904481	43766494	A	AC	4.744020356224431e-08	5.460647170802476	32167.0
17	rs2942166	43715427	T	C	4.7649999746248186e-08	5.459863795780676	32185.0
17	17:43683792_ATGG_A	43683792	ATGG	A	4.786400132129488e-08	5.45906815502009	32167.0
17	rs111370985	43852742	T	C	4.7930481536743276e-08	5.458821688800632	32089.0
17	rs11079721	43840107	C	A	4.794451496122485e-08	5.458769704177463	32117.0
17	rs532036186	43959596	CT	C	4.80154039030534e-08	5.45850733242473	31650.0
17	rs62064420	43667922	G	C	4.804501261146834e-08	5.458397856827787	32061.0
17	rs568589031	44311099	G	A	4.806619628244283e-08	5.458319572191846	31729.0
17	rs2532389	44311107	G	C	4.806619628244283e-08	5.458319572191846	31729.0
17	rs62073222	44374710	A	G	4.8359899613955495e-08	5.4572376190285725	23951.0
17	rs375647	43693341	A	G	4.843906169489807e-08	5.456947089103856	32128.0

17	rs2141300	44258914	A	G	4.8449737439503776e-08	5.456907943659128	31742.0
17	rs117365970	43893259	G	A	4.8755638029570635e-08	5.45578981578513	32110.0
17	rs62064417	43667792	C	T	4.8940456012793466e-08	5.455117559806073	31503.0
17	rs62063265	44033468	G	A	4.897315200719213e-08	5.4549988877965445	32123.0
17	rs62063262	44033002	T	C	4.9018692344638335e-08	5.454833724413245	32128.0
17	rs62057147	43903298	G	A	4.9356982113501856e-08	5.453611468056416	32143.0
17	rs34097347	43949448	C	A	4.944897372052344e-08	5.453280502415764	31939.0
17	rs389978	43717415	A	G	4.952289240128637e-08	5.4530149913641885	32182.0
17	rs113343751	44333532	C	G	4.957507520864914e-08	5.4528277853545495	32143.0
17	rs111891516	44198962	T	TA	4.961569905761597e-08	5.4526821793281295	32052.0
17	rs200422537	44331803	A	ATTTT	4.9667806688046064e-08	5.452495581640127	31892.0
17	rs2316956	44162056	T	A	4.970901815494881e-08	5.452348137502433	31923.0
17	rs62063269	44034833	G	A	4.9720994564540985e-08	5.452305311176965	32104.0
17	rs2732677	44342123	G	C	4.97636192699658e-08	5.452152970989569	30487.0
17	rs2532261	44253203	A	C	4.984314392428153e-08	5.451869088630539	31629.0
18	rs7234875	73114340	T	C	5.719962038078088e-14	7.51433802050141	32186.0
18	rs7231353	73109128	A	C	2.4874962193190062e-12	7.004003653460147	31869.0
18	rs7407699	73110452	G	C	3.7131410785140635e-12	6.947690644649823	32029.0
18	rs6566091	73107145	A	G	1.2580119089949947e-11	6.773387748219499	32011.0
18	rs10460110	73105287	T	C	1.6529841541532062e-11	6.733791136562622	32019.0
18	rs4274504	73102466	T	C	1.722861821551898e-11	6.727767273229808	32037.0
18	rs11151123	73107776	C	T	3.1837315227321664e-11	6.637812189163254	32044.0
22	rs2542028	47196524	A	G	3.0626057109556033e-12	6.9748209684906515	31938.0
22	rs801593	47195050	G	C	8.481045943624013e-12	6.8301760991401625	32186.0
22	rs801592	47196383	T	G	9.846628833208065e-12	6.808726764044822	32182.0
22	rs809031	47191699	A	G	1.0080353444030328e-11	6.805350466848145	32111.0
22	rs801597	47190735	T	G	1.1371712070918635e-11	6.787976559775465	32104.0
22	rs710119	47199148	A	G	2.0987560288025753e-11	6.698982583455219	32029.0
22	rs710122	47198055	G	A	2.3010809873499833e-11	6.6855187223354395	32099.0
22	rs910868	47198932	C	G	6.802133167180513e-11	6.5249563697014015	31887.0
22	rs910867	47198930	T	A	7.45428869124417e-11	6.5112199734893705	31892.0
22	rs801652	47202691	C	T	9.809235692532744e-11	6.469862160141076	31944.0
22	rs801656	47201690	A	G	1.1916106927980164e-10	6.4403974202827134	31548.0
22	rs4823877	47200353	T	C	1.2204880708498223e-10	6.436762336726692	31496.0
22	rs4823878	47200354	T	C	1.5181624236894216e-10	6.4035388087640355	31482.0
22	rs910865	47198133	G	C	2.631400757667044e-10	6.319071170837108	31919.0
22	rs17822045	47208009	C	T	2.6328342883298037e-10	6.318986995635189	31913.0
22	rs62233790	47206644	A	G	3.460402905686263e-10	6.2766074420229065	31910.0
22	rs710118	47199389	G	C	3.8948464124822953e-10	6.258184596646344	31748.0
22	22:47168498_CATATACAT_C	47168498	CATATACAT	C	1.5683446648449386e-09	6.037176177246598	30616.0
22	rs139577	47208945	G	A	4.892453819870287e-09	5.850789401327728	31282.0
22	rs145865429	47206351	A	AT	1.9613525990791032e-08	5.615376009043104	29117.0

Note: Bold rows represents FCs extracted from non british replication dataset significantly associated with the lead SNP identified in the discovery sample at the p=0.05 threshold.

CHR	SNP	BP	A1	A2	P value	Z-stat	N
10	**rs11187838**	**96038686**	**G**	**A**	**0.029236832632864824**	**2.180278380453736**	**4734.0**
10	rs11146399	134308479	C	T	0.28794094063036857	1.0626494769648172	4682.0
3	rs67851870	17554860	A	G	0.3508043494236116	0.9330302511281164	4710.0
3	**rs35124509**	**89521693**	**T**	**C**	**0.003255078387998134**	**2.9425627224280984**	**4754.0**
3	rs62266110	93537923	G	A	0.9361934712998444	0.08005505195419887	4652.0
3	rs2279829	147106319	C	T	0.6847156850862024	0.40603663165285736	4682.0
6	rs4262195	96929475	T	C	0.7098970843773096	0.3719943119238445	4749.0
15	**rs1440802**	**39635124**	**T**	**C**	**0.009584804947221632**	**2.590458959618914**	**4692.0**
15	rs4702	91426560	G	A	0.4220213678843896	0.8029193209635919	4754.0
2	rs62141276	48214217	G	A	0.27258732810218	1.0971236842802248	4563.0
2	rs2717046	58041936	C	T	0.9522042271394622	0.059938988788391635	4680.0
2	rs62158166	114077218	G	C	0.3888361442755477	0.8617299430041099	4642.0
18	rs7234875	73114340	T	C	0.8250427443389228	0.2210638154437743	4754.0
5	rs145120402	93174765	A	C	0.10257126040076994	1.632513958457583	4744.0
5	5:94068140_AC_A	94068140	AC	A	0.30022036800097285	1.0359609344902436	4694.0
14	rs186347	59072226	G	T	0.9203976014436072	0.0999328939702151	4629.0
22	rs2542028	47196524	A	G	0.6040247767444131	0.5186214087336436	4729.0
11	rs11218557	122099839	T	C	0.7774024921231244	0.2827056404346454	4651.0
17	rs34039488	27320232	G	A	0.4619048505517788	0.7357138640842442	4706.0
17	17:44270659_G_A	44270659	G	A	0.4504527168736029	0.7546604931459203	4551.0

Genomic Locus	Lead SNP	chr	Functional category	Non effect allele	Effect allele	MAF	mvGWAS P value	Nearest gene	pheno_label	univariate P value	Beta	univariate Z value
5	rs35124509	3	exonic	C	T	0.4018	8,9515E-59	EPHA3	Pole_STSp	1,4963E-15	-6,4371E-02	-7,98
									Pole_T2ml	5,9579E-15	6,2982E-02	7,80
									AG_F3orb	4,0019E-13	5,8557E-02	7,26
									T1a_STSp	1,8916E-11	-5,4194E-02	-6,71
									STSp_F3orb	2,0435E-11	-5,4103E-02	-6,70
									SMG_T3p	1,0825E-09	4,9217E-02	6,10
									AG_STSp	2,0124E-09	4,8411E-02	6,00
									F2p_AG	6,6439E-09	4,6821E-02	5,80
									T2ml_SMG	2,7656E-08	-4,4853E-02	-5,56
11	rs11187838	10	intronic	A	G	0.4354	4,2917E-14	PLCE1	RolS_PrecR	1,8523E-07	-4,1372E-02	-5,21
									T1a_T1a/HeschlR	9,6142E-06	-3,5124E-02	-4,43
15	rs1440802	15	NcRNA intronic	C	T	0.09091	1,0033E-31	RP11-624L4.1	Prec_F3opd	2,7889E-19	-1,2300E-01	-8,98
									RolS_PrecR	8,4664E-17	-1,1409E-01	-8,32

Note: Bold phenotypes represents pair of FCs with significant genetic correlation after false discovery rate correction at p<0.05.

Phenotype 1	Phenotype 2	P value	rG	SE	FDR
T1a_STSp	**Pole_STSp**	**2.29E-05**	**54.8%**	**0.132**	**0.000847**
SMG_T3p	**AG_STSp**	**9.78E-05**	**65.6%**	**0.192**	**0.00181**
STSp_F3orb	**Pole_STSp**	**0.000221**	**40.4%**	**0.111**	**0.00272**
AG_F3orb	**T2ml_SMG**	**0.00101**	**-46.9%**	**0.158**	**0.00939**
AG_F3orb	**SMG_T3p**	**0.00376**	**53.6%**	**0.211**	**0.0139**
Pole_T2ml	**STSp_F3orb**	**0.00325**	**-31.4%**	**0.113**	**0.0139**
AG_F3orb	**T1a_STSp**	**0.00284**	**-52.5%**	**0.196**	**0.0139**
Pole_T2ml	**AG_STSp**	**0.00285**	**36.2%**	**0.132**	**0.0139**
Pole_T2ml	**T2ml_SMG**	**0.00252**	**-30.5%**	**0.109**	**0.0139**
Pole_T2ml	**Pole_STSp**	**0.00353**	**-28.7%**	**0.099**	**0.0139**
AG_F3orb	**Pole_STSp**	**0.00634**	**-36.5%**	**0.15**	**0.018**
Pole_T2ml	**SMG_T3p**	**0.00681**	**35.1%**	**0.146**	**0.018**
F2p_AG	**AG_STSp**	**0.00639**	**54.5%**	**0.25**	**0.018**
SMG_T3p	**STSp_F3orb**	**0.00553**	**-39.6%**	**0.16**	**0.018**
F2p_AG	**T1a_STSp**	**0.0107**	**-51.2%**	**0.225**	**0.0258**
AG_F3orb	**STSp_F3orb**	**0.0112**	**-38.2%**	**0.142**	**0.0258**
T1a_STSp	**STSp_F3orb**	**0.0121**	**32.9%**	**0.153**	**0.0263**
AG_F3orb	**F2p_AG**	**0.0139**	**53.5%**	**0.243**	**0.0285**
Pole_STSp	**T2ml_SMG**	**0.0168**	**22.9%**	**0.109**	**0.0316**
T1a_STSp	**SMG_T3p**	**0.0171**	**-38.3%**	**0.187**	**0.0316**
F2p_AG	**T2ml_SMG**	**0.024**	**-34.9%**	**0.18**	**0.0404**
SMG_T3p	**T2ml_SMG**	**0.0233**	**-29.0%**	**0.144**	**0.0404**
STSp_F3orb	T2ml_SMG	0.0398	20.7%	0.12	0.064
AG_STSp	T2ml_SMG	0.0484	-22.3%	0.137	0.0746
T1a_STSp	T2ml_SMG	0.056	21.9%	0.137	0.0828
SMG_T3p	Pole_STSp	0.0605	-21.8%	0.142	0.0861
AG_STSp	Pole_STSp	0.0706	-19.3%	0.127	0.0968
AG_STSp	STSp_F3orb	0.0866	-19.6%	0.139	0.114
F2p_AG	SMG_T3p	0.0902	31.1%	0.232	0.115
Prec_F3opd	RolS_PrecR	0.098	16.9%	0.131	0.121
Pole_T2ml	T1a_STSp	0.108	-16.6%	0.135	0.129
AG_F3orb	AG_STSp	0.191	16.0%	0.184	0.221
F2p_AG	Pole_STSp	0.208	14.0%	0.176	0.233
Pole_T2ml	F2p_AG	0.215	-13.7%	0.176	0.234
T1a_STSp	AG_STSp	0.222	-12.8%	0.164	0.234
F2p_AG	STSp_F3orb	0.388	5.4%	0.189	0.399
Pole_T2ml	AG_F3orb	0.456	1.6%	0.148	0.456

Note: Bold phenotypes represents tracts significantly associated with the lead SNP after Bonferroni correction (p=6.94e-4 (0.05/(3*9+5*9))

CHR	SNP	Pheno	Metric	Beta	P	Z
15	rs1440802	Corpus callosum	L3	-3,4428E-02	1,2803E-02	-2,4892
			ISOVF	-3,3499E-02	1,5433E-02	-2,4221
			FA	3,2574E-02	1,8515E-02	2,3551
			MD	-3,2090E-02	2,0335E-02	-2,3201
			L2	-3,1503E-02	2,2745E-02	-2,2777
			L1	-2,4891E-02	7,1920E-02	-1,7996
			ICVF	2,0728E-02	1,3398E-01	1,4986
			MO	-7,1922E-03	6,0309E-01	-0,5200
			OD	-7,1261E-03	6,0642E-01	-0,5152
		Frontal Aslant Tract Left	**MO**	**-6,4280E-02**	**3,3396E-06**	**-4,6487**
			OD	5,6007E-02	5,1196E-05	4,0501
			L1	-5,4971E-02	7,0339E-05	-3,9751
			ISOVF	-3,4517E-02	1,2573E-02	-2,4956
			MD	-3,0007E-02	3,0042E-02	-2,1695
			L3	-1,9929E-02	1,4963E-01	-1,4408
			ICVF	9,3029E-03	5,0123E-01	0,6726
			FA	-8,9362E-03	5,1825E-01	-0,6460
			L2	-3,8335E-03	7,8167E-01	-0,2771
		Arcuate Anterior Segment Left	**OD**	**-2,3504E-01**	**2,4732E-65**	**-17,0702**
			MO	2,0941E-01	3,8548E-52	15,1943
			FA	1,4842E-01	5,9537E-27	10,7496
			L2	-1,4630E-01	3,1250E-26	-10,5956
			L1	1,0825E-01	4,7482E-15	7,8334
			L3	-4,8700E-02	4,2921E-04	-3,5214
			ISOVF	-4,6469E-02	7,7922E-04	-3,3601
			MD	-3,2275E-02	1,9622E-02	-2,3335
			ICVF	1,8871E-02	1,7246E-01	1,3644
		Inferior Fronto Occipital fasciculus Left	**MO**	**4,1907E-02**	**2,4978E-07**	**5,1579**
			OD	-3,2217E-02	7,3529E-05	-3,9646
			L1	2,0604E-02	1,1242E-02	2,5351
			FA	1,1022E-02	1,7507E-01	1,3561
			MD	8,8824E-03	2,7448E-01	1,0928
			ISOVF	4,8581E-03	5,5004E-01	0,5977
			L2	-4,7179E-03	5,6162E-01	-0,5804
			L3	4,6885E-03	5,6406E-01	0,5768
			ICVF	-3,7015E-03	6,4883E-01	-0,4554
		Uncinate Left	**MO**	**4,2154E-02**	**2,1220E-07**	**5,1883**
			OD	-2,3885E-02	3,2932E-03	-2,9390
			L1	2,2805E-02	5,0163E-03	2,8060
			FA	1,2425E-02	1,2634E-01	1,5287
			MD	9,7547E-03	2,3009E-01	1,2001
			ICVF	-8,3742E-03	3,0287E-01	-1,0303
			L3	7,2253E-03	3,7404E-01	0,8889
			L2	-5,9861E-03	4,6144E-01	-0,7365
			ISOVF	-1,5708E-04	9,8458E-01	-0,0193

3	rs35124509	Arcuate Anterior Segment Left	MO	-2,3605E-02	3,6791E-03	-2,9044
			L2	2,2630E-02	5,3612E-03	2,7845
			FA	-1,6705E-02	3,9844E-02	-2,0554
			ISOVF	1,2345E-02	1,2880E-01	1,5189
			MD	1,0160E-02	2,1131E-01	1,2500
			ICVF	-1,0146E-02	2,1193E-01	-1,2483
			L3	7,1300E-03	3,8037E-01	0,8772
			OD	5,8026E-03	4,7529E-01	0,7139
			L1	-7,7840E-04	9,2371E-01	-0,0958
		Arcuate Long Segment Left	**OD**	**-3,6813E-02**	**5,8822E-06**	**-4,5306**
			L1	2,0134E-02	1,3239E-02	2,4773
			MO	1,4725E-02	7,0039E-02	1,8117
			MD	1,2833E-02	1,1437E-01	1,5788
			ISOVF	1,2218E-02	1,3278E-01	1,5032
			L3	7,4946E-03	3,5649E-01	0,9221
			ICVF	-6,6475E-03	4,1345E-01	-0,8178
			FA	3,6834E-03	6,5043E-01	0,4532
			L2	1,7721E-03	8,2741E-01	0,2180
		Arcuate Posterior Segment Left	**L3**	**4,1222E-02**	**3,9039E-07**	**5,0736**
			ICVF	-3,8005E-02	2,9062E-06	-4,6773
			MD	3,6748E-02	6,1105E-06	4,5225
			FA	-3,6428E-02	7,3549E-06	-4,4832
			L2	3,0797E-02	1,5079E-04	3,7898
			L1	2,1984E-02	6,8311E-03	2,7050
			MO	1,6926E-02	3,7298E-02	2,0825
			ISOVF	1,4388E-02	7,6693E-02	1,7702
			OD	4,6444E-03	5,6773E-01	0,5714

rs ID	chr	position	Data base	tissue	gene	tested Allele	P value	signed stats	FDR p value
rs73145317	3	89583712	GTEx/v8	Pancreas	EPHA3	C	3.35696E-11	0.45158	3.49803E-07
rs73139276	3	89500196	GTEx/v8	Pancreas	EPHA3	A	9.15352E-11	0.390181	3.49803E-07
rs73139288	3	89505327	GTEx/v8	Pancreas	EPHA3	G	9.30731E-11	0.388198	3.49803E-07
rs73139129	3	89524562	GTEx/v8	Pancreas	EPHA3	G	9.30731E-11	0.388198	3.49803E-07
rs972030	3	89538498	GTEx/v8	Pancreas	EPHA3	T	1.06317E-10	0.383465	3.49803E-07
rs4857500	3	89541486	GTEx/v8	Pancreas	EPHA3	C	1.06317E-10	0.383465	3.49803E-07
rs1512189	3	89546332	GTEx/v8	Pancreas	EPHA3	G	1.07905E-10	0.384892	3.49803E-07
rs12629999	3	89551518	GTEx/v8	Pancreas	EPHA3	G	1.07905E-10	0.384892	3.49803E-07
rs73146986	3	89560884	GTEx/v8	Pancreas	EPHA3	G	1.07905E-10	0.384892	3.49803E-07
rs6784577	3	89564308	GTEx/v8	Pancreas	EPHA3	G	1.07905E-10	0.384892	3.49803E-07
rs73145303	3	89568714	GTEx/v8	Pancreas	EPHA3	C	1.07905E-10	0.384892	3.49803E-07
rs73139133	3	89527708	GTEx/v8	Pancreas	EPHA3	A	1.35747E-10	0.384023	3.49803E-07
rs144317613	3	89525080	GTEx/v8	Pancreas	EPHA3	TA	1.49946E-10	0.383137	3.49803E-07
rs73149103	3	89565651	GTEx/v8	Pancreas	EPHA3	A	1.5191E-10	0.38131	3.49803E-07
rs73139261	3	89492406	GTEx/v8	Pancreas	EPHA3	G	1.57576E-10	0.386012	3.49803E-07
rs12637036	3	89584170	GTEx/v8	Pancreas	EPHA3	A	1.7134E-10	0.385057	3.49803E-07
rs56082199	3	89586973	GTEx/v8	Pancreas	EPHA3	G	1.7134E-10	0.385057	3.49803E-07
rs73145336	3	89593317	GTEx/v8	Pancreas	EPHA3	G	1.7134E-10	0.385057	3.49803E-07
rs1036285	3	89544061	GTEx/v8	Pancreas	EPHA3	C	1.81497E-10	0.361236	3.49803E-07
rs17026984	3	89544978	GTEx/v8	Pancreas	EPHA3	A	1.81497E-10	0.361236	3.49803E-07
rs111618480	3	89552134	GTEx/v8	Pancreas	EPHA3	C	1.81497E-10	0.361236	3.49803E-07
rs2048518	3	89533905	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs2048520	3	89534248	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs2048521	3	89534253	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs73144998	3	89534592	GTEx/v8	Pancreas	EPHA3	T	1.83068E-10	0.364599	3.49803E-07
rs73145002	3	89537618	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs56371328	3	89539124	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs4857498	3	89540977	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs4857499	3	89541330	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs2346837	3	89542599	GTEx/v8	Pancreas	EPHA3	T	1.83068E-10	0.364599	3.49803E-07
rs12633609	3	89545727	GTEx/v8	Pancreas	EPHA3	G	1.83068E-10	0.364599	3.49803E-07
rs1512188	3	89546183	GTEx/v8	Pancreas	EPHA3	G	1.83068E-10	0.364599	3.49803E-07
rs73146943	3	89546728	GTEx/v8	Pancreas	EPHA3	G	1.83068E-10	0.364599	3.49803E-07
rs12632281	3	89547621	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs73146947	3	89548135	GTEx/v8	Pancreas	EPHA3	G	1.83068E-10	0.364599	3.49803E-07
rs73146950	3	89548243	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs1567657	3	89548519	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs1567658	3	89548606	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs73146959	3	89549970	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs73146960	3	89550445	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs112404167	3	89550630	GTEx/v8	Pancreas	EPHA3	T	1.83068E-10	0.364599	3.49803E-07
rs12637511	3	89550844	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs73146972	3	89553348	GTEx/v8	Pancreas	EPHA3	G	1.83068E-10	0.364599	3.49803E-07
rs17026990	3	89555257	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs73146976	3	89557065	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07
rs1039991	3	89558311	GTEx/v8	Pancreas	EPHA3	G	1.83068E-10	0.364599	3.49803E-07
rs73146980	3	89558578	GTEx/v8	Pancreas	EPHA3	A	1.83068E-10	0.364599	3.49803E-07
rs73146983	3	89559082	GTEx/v8	Pancreas	EPHA3	G	1.83068E-10	0.364599	3.49803E-07
rs138490449	3	89561661	GTEx/v8	Pancreas	EPHA3	AT	1.83068E-10	0.364599	3.49803E-07
rs138183278	3	89564090	GTEx/v8	Pancreas	EPHA3	CT	1.83068E-10	0.364599	3.49803E-07
rs6774870	3	89564891	GTEx/v8	Pancreas	EPHA3	T	1.83068E-10	0.364599	3.49803E-07
rs113307255	3	89567826	GTEx/v8	Pancreas	EPHA3	C	1.83068E-10	0.364599	3.49803E-07

rs2346836	3	89498096	GTEx/v8	Pancreas	EPHA3	A	2.29119E-10	0.368817	3.49803E-07
rs60759140	3	89499848	GTEx/v8	Pancreas	EPHA3	C	2.29119E-10	0.368817	3.49803E-07
rs12152372	3	89500365	GTEx/v8	Pancreas	EPHA3	C	2.29119E-10	0.368817	3.49803E-07
rs2881488	3	89500488	GTEx/v8	Pancreas	EPHA3	G	2.29119E-10	0.368817	3.49803E-07
rs59541469	3	89501671	GTEx/v8	Pancreas	EPHA3	T	2.29119E-10	0.368817	3.49803E-07
3:89502123_TTAG_T	3	89502123	GTEx/v8	Pancreas	EPHA3	T	2.29119E-10	0.368817	3.49803E-07
rs73139290	3	89505343	GTEx/v8	Pancreas	EPHA3	A	2.29119E-10	0.368817	3.49803E-07
rs73139296	3	89505734	GTEx/v8	Pancreas	EPHA3	T	2.29119E-10	0.368817	3.49803E-07
rs1157608	3	89506464	GTEx/v8	Pancreas	EPHA3	G	2.29119E-10	0.368817	3.49803E-07
rs73139302	3	89508186	GTEx/v8	Pancreas	EPHA3	G	2.29119E-10	0.368817	3.49803E-07
rs73141104	3	89508390	GTEx/v8	Pancreas	EPHA3	T	2.29119E-10	0.368817	3.49803E-07
rs1912965	3	89518332	GTEx/v8	Pancreas	EPHA3	G	2.29119E-10	0.368817	3.49803E-07
rs113141104	3	89519238	GTEx/v8	Pancreas	EPHA3	T	2.29119E-10	0.368817	3.49803E-07
rs73139105	3	89519651	GTEx/v8	Pancreas	EPHA3	C	2.29119E-10	0.368817	3.49803E-07
rs112297761	3	89521602	GTEx/v8	Pancreas	EPHA3	TC	2.29119E-10	0.368817	3.49803E-07
rs73139119	3	89522285	GTEx/v8	Pancreas	EPHA3	T	2.29119E-10	0.368817	3.49803E-07
rs73139121	3	89522433	GTEx/v8	Pancreas	EPHA3	G	2.29119E-10	0.368817	3.49803E-07
rs73139131	3	89524686	GTEx/v8	Pancreas	EPHA3	G	2.29119E-10	0.368817	3.49803E-07
rs1512183	3	89505054	GTEx/v8	Pancreas	EPHA3	T	2.32543E-10	0.364957	3.49803E-07
rs17026944	3	89521131	GTEx/v8	Pancreas	EPHA3	A	2.32543E-10	0.364957	3.49803E-07
rs73139125	3	89524056	GTEx/v8	Pancreas	EPHA3	G	2.32543E-10	0.364957	3.49803E-07
rs2048519	3	89533978	GTEx/v8	Pancreas	EPHA3	A	2.81579E-10	0.37063	3.49803E-07
rs3762718	3	89535066	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs2196083	3	89536546	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs12634044	3	89537651	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs73146907	3	89538747	GTEx/v8	Pancreas	EPHA3	A	2.81579E-10	0.37063	3.49803E-07
rs57902683	3	89539011	GTEx/v8	Pancreas	EPHA3	CA	2.81579E-10	0.37063	3.49803E-07
rs55979407	3	89539275	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs113675293	3	89539536	GTEx/v8	Pancreas	EPHA3	T	2.81579E-10	0.37063	3.49803E-07
rs73146926	3	89542293	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs4035593	3	89542601	GTEx/v8	Pancreas	EPHA3	TAA	2.81579E-10	0.37063	3.49803E-07
rs2117136	3	89542699	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs7633599	3	89544591	GTEx/v8	Pancreas	EPHA3	A	2.81579E-10	0.37063	3.49803E-07
rs7613315	3	89544773	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs1028012	3	89549422	GTEx/v8	Pancreas	EPHA3	T	2.81579E-10	0.37063	3.49803E-07
rs17745025	3	89549919	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs73146961	3	89550459	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs12634697	3	89550993	GTEx/v8	Pancreas	EPHA3	A	2.81579E-10	0.37063	3.49803E-07
rs12638168	3	89551544	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs73146970	3	89553168	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs12629758	3	89556408	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs1039990	3	89558086	GTEx/v8	Pancreas	EPHA3	A	2.81579E-10	0.37063	3.49803E-07
rs73146988	3	89561044	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs73146992	3	89562178	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs73146995	3	89562209	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs73147002	3	89565128	GTEx/v8	Pancreas	EPHA3	G	2.81579E-10	0.37063	3.49803E-07
rs148078210	3	89565641	GTEx/v8	Pancreas	EPHA3	GGTAT	2.81579E-10	0.37063	3.49803E-07
rs12633325	3	89566836	GTEx/v8	Pancreas	EPHA3	C	2.81579E-10	0.37063	3.49803E-07
rs73149113	3	89567867	GTEx/v8	Pancreas	EPHA3	T	2.81579E-10	0.37063	3.49803E-07
rs73137381	3	89458550	GTEx/v8	Pancreas	EPHA3	G	3.0069E-10	0.379833	3.49803E-07
rs73137382	3	89461363	GTEx/v8	Pancreas	EPHA3	G	3.0069E-10	0.379833	3.49803E-07
rs73137393	3	89471701	GTEx/v8	Pancreas	EPHA3	C	3.0069E-10	0.379833	3.49803E-07
rs73137387	3	89464194	GTEx/v8	Pancreas	EPHA3	C	3.01355E-10	0.378092	3.49803E-07
rs12639506	3	89480265	GTEx/v8	Pancreas	EPHA3	G	3.01355E-10	0.378092	3.49803E-07

rs12631313	3	89528461	GTEx/v8	Pancreas	EPHA3	T	3.17901E-10	0.363797	3.49803E-07
rs7650466	3	89530358	GTEx/v8	Pancreas	EPHA3	T	3.17901E-10	0.363797	3.49803E-07
rs2117138	3	89531522	GTEx/v8	Pancreas	EPHA3	G	3.17901E-10	0.363797	3.49803E-07
rs12634269	3	89532768	GTEx/v8	Pancreas	EPHA3	C	3.23497E-10	0.359939	3.49803E-07
rs73146965	3	89552553	GTEx/v8	Pancreas	EPHA3	G	3.46782E-10	0.359264	3.49803E-07
rs73145304	3	89568989	GTEx/v8	Pancreas	EPHA3	T	3.558E-10	0.35898	3.49803E-07
rs73145310	3	89578097	GTEx/v8	Pancreas	EPHA3	C	3.558E-10	0.35898	3.49803E-07
rs73145312	3	89578575	GTEx/v8	Pancreas	EPHA3	T	3.558E-10	0.35898	3.49803E-07
rs73145320	3	89586535	GTEx/v8	Pancreas	EPHA3	C	3.558E-10	0.35898	3.49803E-07
rs1157607	3	89506364	GTEx/v8	Pancreas	EPHA3	T	4.14668E-10	0.372333	3.49803E-07
rs7626735	3	89506958	GTEx/v8	Pancreas	EPHA3	A	4.14668E-10	0.372333	3.49803E-07
rs568140553	3	89507219	GTEx/v8	Pancreas	EPHA3	CT	4.14668E-10	0.372333	3.49803E-07
rs6795074	3	89516652	GTEx/v8	Pancreas	EPHA3	C	4.14668E-10	0.372333	3.49803E-07
rs73141108	3	89517119	GTEx/v8	Pancreas	EPHA3	T	4.14668E-10	0.372333	3.49803E-07
rs1912966	3	89518464	GTEx/v8	Pancreas	EPHA3	A	4.14668E-10	0.372333	3.49803E-07
rs73139104	3	89519229	GTEx/v8	Pancreas	EPHA3	C	4.14668E-10	0.372333	3.49803E-07
3:89519266_GA_G	3	89519266	GTEx/v8	Pancreas	EPHA3	G	4.14668E-10	0.372333	3.49803E-07
3:89521060_CTAT_C	3	89521060	GTEx/v8	Pancreas	EPHA3	C	4.14668E-10	0.372333	3.49803E-07
rs73139110	3	89521509	GTEx/v8	Pancreas	EPHA3	A	4.14668E-10	0.372333	3.49803E-07
rs1054750	3	89521725	GTEx/v8	Pancreas	EPHA3	C	4.14668E-10	0.372333	3.49803E-07
rs73139115	3	89521900	GTEx/v8	Pancreas	EPHA3	T	4.14668E-10	0.372333	3.49803E-07
rs73139117	3	89521965	GTEx/v8	Pancreas	EPHA3	G	4.14668E-10	0.372333	3.49803E-07
rs73139118	3	89522263	GTEx/v8	Pancreas	EPHA3	T	4.14668E-10	0.372333	3.49803E-07
rs150837250	3	89522314	GTEx/v8	Pancreas	EPHA3	AGTTATAATTAG	4.14668E-10	0.372333	3.49803E-07
rs17801380	3	89522483	GTEx/v8	Pancreas	EPHA3	T	4.14668E-10	0.372333	3.49803E-07
rs73139127	3	89524436	GTEx/v8	Pancreas	EPHA3	A	4.14668E-10	0.372333	3.49803E-07
rs1499780	3	89526072	GTEx/v8	Pancreas	EPHA3	C	4.14668E-10	0.372333	3.49803E-07
rs73145305	3	89570713	GTEx/v8	Pancreas	EPHA3	T	4.85418E-10	0.370693	3.49803E-07
3:89571180_TAGAG_T	3	89571180	GTEx/v8	Pancreas	EPHA3	T	4.85418E-10	0.370693	3.49803E-07
rs907548	3	89574852	GTEx/v8	Pancreas	EPHA3	T	4.85418E-10	0.370693	3.49803E-07
rs73145307	3	89576040	GTEx/v8	Pancreas	EPHA3	A	4.85418E-10	0.370693	3.49803E-07
rs73145309	3	89576389	GTEx/v8	Pancreas	EPHA3	T	4.85418E-10	0.370693	3.49803E-07
rs73145316	3	89580407	GTEx/v8	Pancreas	EPHA3	T	4.85418E-10	0.370693	3.49803E-07
rs73145332	3	89589327	GTEx/v8	Pancreas	EPHA3	C	4.85418E-10	0.370693	3.49803E-07
rs112087049	3	89509550	GTEx/v8	Pancreas	EPHA3	T	4.96309E-10	0.397999	3.49803E-07
rs73139281	3	89503890	GTEx/v8	Pancreas	EPHA3	T	5.01652E-10	0.365232	3.49803E-07
rs73139284	3	89503958	GTEx/v8	Pancreas	EPHA3	G	5.01652E-10	0.365232	3.49803E-07
rs73139286	3	89504295	GTEx/v8	Pancreas	EPHA3	A	5.01652E-10	0.365232	3.49803E-07
rs73149107	3	89565849	GTEx/v8	Pancreas	EPHA3	A	5.51674E-10	0.364495	3.49803E-07
rs73153260	3	89718078	GTEx/v8	Pancreas	EPHA3	A	5.52434E-10	0.429495	3.49803E-07
rs73139134	3	89527709	GTEx/v8	Pancreas	EPHA3	C	5.82105E-10	0.366907	3.49803E-07
rs73139135	3	89527937	GTEx/v8	Pancreas	EPHA3	C	5.82105E-10	0.366907	3.49803E-07
rs73139139	3	89528313	GTEx/v8	Pancreas	EPHA3	G	5.82105E-10	0.366907	3.49803E-07
rs12636710	3	89528477	GTEx/v8	Pancreas	EPHA3	A	5.82105E-10	0.366907	3.49803E-07
rs3762717	3	89528948	GTEx/v8	Pancreas	EPHA3	C	5.82105E-10	0.366907	3.49803E-07
rs73139147	3	89530347	GTEx/v8	Pancreas	EPHA3	A	5.82105E-10	0.366907	3.49803E-07
rs73139148	3	89530956	GTEx/v8	Pancreas	EPHA3	A	5.82105E-10	0.366907	3.49803E-07
rs12629165	3	89533017	GTEx/v8	Pancreas	EPHA3	A	5.82105E-10	0.366907	3.49803E-07
rs752364173	3	89521820	GTEx/v8	Pancreas	EPHA3	T	6.57419E-10	0.352038	3.49803E-07
3:89521831_TGAAAG_T	3	89521831	GTEx/v8	Pancreas	EPHA3	T	6.57419E-10	0.352038	3.49803E-07
3:89521838_TTTG_T	3	89521838	GTEx/v8	Pancreas	EPHA3	T	6.57419E-10	0.352038	3.49803E-07

3:89544326_CGGTGGAAATCTCCTTATTAAATTGTGGGCAAGAGGCAACCCAT_C	3	89544326	GTEx/v8	Pancreas	EPHA3	C	7.02079E-10	0.363859	3.49803E-07
rs7619303	3	89552554	GTEx/v8	Pancreas	EPHA3	A	7.96E-10	0.346987	3.49803E-07
rs73149109	3	89567344	GTEx/v8	Pancreas	EPHA3	A	8.72692E-10	0.347768	3.49803E-07
rs1080592	3	89567568	GTEx/v8	Pancreas	EPHA3	C	8.72692E-10	0.347768	3.49803E-07
rs12633626	3	89744949	GTEx/v8	Pancreas	EPHA3	A	9.26126E-10	0.377684	3.49803E-07
3:89694510_GATA_G	3	89694510	GTEx/v8	Artery Tibial	EPHA3	G	1.01112E-09	-0.175842	7.80657E-07
3:89626776_AT_A	3	89626776	GTEx/v8	Pancreas	EPHA3	A	1.1209E-09	0.36937	3.49803E-07
rs73139144	3	89529177	GTEx/v8	Pancreas	EPHA3	A	1.27678E-09	0.360298	3.49803E-07
rs12634341	3	89533031	GTEx/v8	Pancreas	EPHA3	C	1.33245E-09	0.355856	3.49803E-07
rs2346840	3	89533267	GTEx/v8	Pancreas	EPHA3	G	1.33245E-09	0.355856	3.49803E-07
rs73153266	3	89720111	GTEx/v8	Pancreas	EPHA3	G	1.69953E-09	0.360744	3.49803E-07
rs66708608	3	89486373	GTEx/v8	Pancreas	EPHA3	T	1.80707E-09	0.343463	3.49803E-07
rs73145345	3	89598696	GTEx/v8	Pancreas	EPHA3	A	2.0732E-09	0.365608	3.49803E-07
rs111835258	3	89601496	GTEx/v8	Pancreas	EPHA3	A	2.0732E-09	0.365608	3.49803E-07
rs73145351	3	89607237	GTEx/v8	Pancreas	EPHA3	T	2.0732E-09	0.365608	3.49803E-07
rs73145353	3	89607824	GTEx/v8	Pancreas	EPHA3	T	2.0732E-09	0.365608	3.49803E-07
rs73145357	3	89611766	GTEx/v8	Pancreas	EPHA3	C	2.0732E-09	0.365608	3.49803E-07
rs819293	3	89613664	GTEx/v8	Pancreas	EPHA3	A	2.07428E-09	0.356596	3.49803E-07
rs73153262	3	89719269	GTEx/v8	Pancreas	EPHA3	T	2.21545E-09	0.362082	3.49803E-07
rs113288647	3	89720352	GTEx/v8	Pancreas	EPHA3	T	2.21545E-09	0.362082	3.49803E-07
rs2069183	3	89645017	GTEx/v8	Pancreas	EPHA3	A	2.26183E-09	0.357285	3.49803E-07
rs73153241	3	89695319	GTEx/v8	Pancreas	EPHA3	G	2.4658E-09	0.355974	3.49803E-07
rs73153252	3	89712192	GTEx/v8	Pancreas	EPHA3	T	3.18359E-09	0.354961	3.49803E-07
rs7617395	3	89722541	GTEx/v8	Pancreas	EPHA3	T	3.18359E-09	0.354961	3.49803E-07
rs73153218	3	89619808	GTEx/v8	Pancreas	EPHA3	A	3.88508E-09	0.357171	3.49803E-07
rs73153258	3	89715585	GTEx/v8	Pancreas	EPHA3	A	4.43857E-09	0.356589	3.49803E-07
rs73137384	3	89463290	GTEx/v8	Pancreas	EPHA3	T	5.37938E-09	0.332038	3.49803E-07
rs6773817	3	89753400	GTEx/v8	Artery Tibial	EPHA3	A	5.93098E-09	-0.168368	7.80657E-07
rs73137395	3	89478753	GTEx/v8	Pancreas	EPHA3	C	6.16802E-09	0.343206	3.49803E-07
rs73139257	3	89482779	GTEx/v8	Pancreas	EPHA3	G	6.16802E-09	0.343206	3.49803E-07
rs13064615	3	89799433	GTEx/v8	Artery Tibial	EPHA3	G	7.12193E-09	-0.168807	7.80657E-07
rs112149405	3	89886780	GTEx/v8	Pancreas	EPHA3	C	8.46419E-09	0.408213	3.49803E-07
rs73153282	3	89728408	GTEx/v8	Pancreas	EPHA3	T	9.61374E-09	0.344833	3.49803E-07
rs73151380	3	90000532	GTEx/v8	Pancreas	EPHA3	T	9.80386E-09	0.393419	3.49803E-07
rs73153279	3	89727968	GTEx/v8	Pancreas	EPHA3	C	1.0246E-08	0.342672	3.49803E-07
rs73153283	3	89732193	GTEx/v8	Pancreas	EPHA3	T	1.0246E-08	0.342672	3.49803E-07
rs1284258	3	89823487	GTEx/v8	Artery Tibial	EPHA3	T	1.04495E-08	-0.16652	7.80657E-07
rs112604674	3	89989681	GTEx/v8	Pancreas	EPHA3	T	1.15883E-08	0.392034	3.49803E-07
rs1512185	3	89473615	GTEx/v8	Pancreas	EPHA3	A	1.17088E-08	0.324867	3.49803E-07
rs73153293	3	89756242	GTEx/v8	Pancreas	EPHA3	T	1.51089E-08	0.368874	3.49803E-07
rs6551412	3	89496502	GTEx/v8	Pancreas	EPHA3	A	2.13147E-08	0.340301	3.49803E-07
rs4264747	3	89882102	GTEx/v8	Artery Tibial	EPHA3	G	2.39483E-08	-0.162136	7.80657E-07
rs1879650	3	89856887	GTEx/v8	Artery Tibial	EPHA3	T	2.83016E-08	-0.161113	7.80657E-07
rs7616322	3	89493283	GTEx/v8	Pancreas	EPHA3	T	3.30748E-08	0.319057	3.49803E-07
rs13062221	3	89778009	GTEx/v8	Artery Tibial	EPHA3	C	3.38194E-08	-0.160623	7.80657E-07
rs112407114	3	89797398	GTEx/v8	Pancreas	EPHA3	C	4.05413E-08	0.351939	3.49803E-07
rs2196083	3	89536546	GTEx/v8	Brain Cerebellum	EPHA3	C	5.10725E-08	-0.379543	0.000131411
rs2048519	3	89533978	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs3762718	3	89535066	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs12634044	3	89537651	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411

rs73146907	3	89538747	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs57902683	3	89539011	GTEx/v8	Brain Cerebellum	EPHA3	CA	5.20018E-08	-0.380424	0.000131411
rs55979407	3	89539275	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs113675293	3	89539536	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
rs4857500	3	89541486	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs73146926	3	89542293	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs4035593	3	89542601	GTEx/v8	Brain Cerebellum	EPHA3	TAA	5.20018E-08	-0.380424	0.000131411
rs2117136	3	89542699	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
3:89544326_CGGTGGAAATCTCCTTATTAAATTGTGGGCAAGAGGCAACCCAT_C	3	89544326	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs7633599	3	89544591	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs7613315	3	89544773	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs1028012	3	89549422	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
rs17745025	3	89549919	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs73146961	3	89550459	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs12634697	3	89550993	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs12638168	3	89551544	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs73146970	3	89553168	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs12629758	3	89556408	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs1039990	3	89558086	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs73146988	3	89561044	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs73146992	3	89562178	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs73146995	3	89562209	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs73147002	3	89565128	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs148078210	3	89565641	GTEx/v8	Brain Cerebellum	EPHA3	GGTAT	5.20018E-08	-0.380424	0.000131411
rs73149103	3	89565651	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs73149107	3	89565849	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs12633325	3	89566836	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs73149113	3	89567867	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
rs73145305	3	89570713	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
3:89571180_TAGAG_T	3	89571180	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
rs907548	3	89574852	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
rs73145307	3	89576040	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs73145309	3	89576389	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
rs73145316	3	89580407	GTEx/v8	Brain Cerebellum	EPHA3	T	5.20018E-08	-0.380424	0.000131411
rs12637036	3	89584170	GTEx/v8	Brain Cerebellum	EPHA3	A	5.20018E-08	-0.380424	0.000131411
rs73145332	3	89589327	GTEx/v8	Brain Cerebellum	EPHA3	C	5.20018E-08	-0.380424	0.000131411
rs73145336	3	89593317	GTEx/v8	Brain Cerebellum	EPHA3	G	5.20018E-08	-0.380424	0.000131411
rs2346840	3	89533267	GTEx/v8	Brain Cerebellum	EPHA3	G	5.26884E-08	-0.389826	0.000131411
rs73139276	3	89500196	GTEx/v8	Brain Cerebellum	EPHA3	A	5.55208E-08	-0.397101	0.000131411
rs73139288	3	89505327	GTEx/v8	Brain Cerebellum	EPHA3	G	5.55208E-08	-0.397101	0.000131411
rs1157607	3	89506364	GTEx/v8	Brain Cerebellum	EPHA3	T	5.55208E-08	-0.397101	0.000131411

rs7626735	3	89506958	GTEx/v8	Brain Cerebellum	EPHA3	A	5.55208E-08	-0.397101	0.000131411
rs568140553	3	89507219	GTEx/v8	Brain Cerebellum	EPHA3	CT	5.55208E-08	-0.397101	0.000131411
rs6795074	3	89516652	GTEx/v8	Brain Cerebellum	EPHA3	C	5.55208E-08	-0.397101	0.000131411
rs73141108	3	89517119	GTEx/v8	Brain Cerebellum	EPHA3	T	5.55208E-08	-0.397101	0.000131411
rs1912966	3	89518464	GTEx/v8	Brain Cerebellum	EPHA3	A	5.55208E-08	-0.397101	0.000131411
rs73139104	3	89519229	GTEx/v8	Brain Cerebellum	EPHA3	C	5.55208E-08	-0.397101	0.000131411
3:89519266_GA_G	3	89519266	GTEx/v8	Brain Cerebellum	EPHA3	G	5.55208E-08	-0.397101	0.000131411
3:89521060_CTAT_C	3	89521060	GTEx/v8	Brain Cerebellum	EPHA3	C	5.55208E-08	-0.397101	0.000131411
rs73139110	3	89521509	GTEx/v8	Brain Cerebellum	EPHA3	A	5.55208E-08	-0.397101	0.000131411
rs1054750	3	89521725	GTEx/v8	Brain Cerebellum	EPHA3	C	5.55208E-08	-0.397101	0.000131411
rs73139115	3	89521900	GTEx/v8	Brain Cerebellum	EPHA3	T	5.55208E-08	-0.397101	0.000131411
rs73139117	3	89521965	GTEx/v8	Brain Cerebellum	EPHA3	G	5.55208E-08	-0.397101	0.000131411
rs73139118	3	89522263	GTEx/v8	Brain Cerebellum	EPHA3	T	5.55208E-08	-0.397101	0.000131411
rs150837250	3	89522314	GTEx/v8	Brain Cerebellum	EPHA3	AGTTATAATTAG	5.55208E-08	-0.397101	0.000131411
rs17801380	3	89522483	GTEx/v8	Brain Cerebellum	EPHA3	T	5.55208E-08	-0.397101	0.000131411
rs73139127	3	89524436	GTEx/v8	Brain Cerebellum	EPHA3	A	5.55208E-08	-0.397101	0.000131411
rs73139129	3	89524562	GTEx/v8	Brain Cerebellum	EPHA3	G	5.55208E-08	-0.397101	0.000131411
rs1499780	3	89526072	GTEx/v8	Brain Cerebellum	EPHA3	C	5.55208E-08	-0.397101	0.000131411
rs73137381	3	89458550	GTEx/v8	Brain Cerebellum	EPHA3	G	7.06753E-08	-0.399375	0.000131411
rs73137382	3	89461363	GTEx/v8	Brain Cerebellum	EPHA3	G	7.06753E-08	-0.399375	0.000131411
rs73137387	3	89464194	GTEx/v8	Brain Cerebellum	EPHA3	C	7.06753E-08	-0.399375	0.000131411
rs73137393	3	89471701	GTEx/v8	Brain Cerebellum	EPHA3	C	7.06753E-08	-0.399375	0.000131411
rs12639506	3	89480265	GTEx/v8	Brain Cerebellum	EPHA3	G	7.06753E-08	-0.399375	0.000131411
rs112087049	3	89509550	GTEx/v8	Brain Cerebellum	EPHA3	T	7.14504E-08	-0.411656	0.000131411
rs144317613	3	89525080	GTEx/v8	Brain Cerebellum	EPHA3	TA	7.4538E-08	-0.396948	0.000131411
rs1512189	3	89546332	GTEx/v8	Brain Cerebellum	EPHA3	G	7.98666E-08	-0.377125	0.000131411
rs6784577	3	89564308	GTEx/v8	Brain Cerebellum	EPHA3	G	7.98666E-08	-0.377125	0.000131411
rs56082199	3	89586973	GTEx/v8	Brain Cerebellum	EPHA3	G	7.98666E-08	-0.377125	0.000131411
rs12629165	3	89533017	GTEx/v8	Brain Cerebellum	EPHA3	A	8.19033E-08	-0.386321	0.000131411
rs12634341	3	89533031	GTEx/v8	Brain Cerebellum	EPHA3	C	8.19033E-08	-0.386321	0.000131411
rs73153218	3	89619808	GTEx/v8	Artery Tibial	EPHA3	A	8.97526E-08	0.177382	7.80657E-07
rs148078210	3	89565641	GTEx/v8	Artery Tibial	EPHA3	GGTAT	1.02345E-07	0.171217	7.80657E-07
rs73154925	3	89859312	GTEx/v8	Pancreas	EPHA3	C	1.30179E-07	0.328276	3.49803E-07
rs972030	3	89538498	GTEx/v8	Brain Cerebellum	EPHA3	T	1.33265E-07	-0.369879	0.000131411
rs11128078	3	90030538	GTEx/v8	Artery Tibial	EPHA3	T	1.43479E-07	-0.157932	7.80657E-07
rs12634341	3	89533031	GTEx/v8	Artery Tibial	EPHA3	C	1.51111E-07	0.169578	7.80657E-07
rs73139133	3	89527708	GTEx/v8	Brain Cerebellum	EPHA3	A	1.51833E-07	-0.378354	0.000131411
rs73139134	3	89527709	GTEx/v8	Brain Cerebellum	EPHA3	C	1.51833E-07	-0.378354	0.000131411
rs73139135	3	89527937	GTEx/v8	Brain Cerebellum	EPHA3	C	1.51833E-07	-0.378354	0.000131411
rs73139139	3	89528313	GTEx/v8	Brain Cerebellum	EPHA3	G	1.51833E-07	-0.378354	0.000131411
rs12636710	3	89528477	GTEx/v8	Brain Cerebellum	EPHA3	A	1.51833E-07	-0.378354	0.000131411
rs3762717	3	89528948	GTEx/v8	Brain Cerebellum	EPHA3	C	1.51833E-07	-0.378354	0.000131411
rs73139144	3	89529177	GTEx/v8	Brain Cerebellum	EPHA3	A	1.51833E-07	-0.378354	0.000131411
rs73139147	3	89530347	GTEx/v8	Brain Cerebellum	EPHA3	A	1.51833E-07	-0.378354	0.000131411

rs73139148	3	89530956	GTEx/v8	Brain Cerebellum	EPHA3	A	1.51833E-07	-0.378354	0.000131411
rs6551412	3	89496502	GTEx/v8	Brain Cerebellum	EPHA3	A	1.56124E-07	-0.387105	0.000131411
rs819293	3	89613664	GTEx/v8	Artery Tibial	EPHA3	A	1.56358E-07	0.170458	7.80657E-07
rs2347959	3	90039465	GTEx/v8	Artery Tibial	EPHA3	A	1.56916E-07	-0.156664	7.80657E-07
rs113165984	3	89989689	GTEx/v8	Pancreas	EPHA3	C	1.6939E-07	0.400186	3.49803E-07
rs73146986	3	89560884	GTEx/v8	Brain Cerebellum	EPHA3	G	1.86176E-07	-0.371667	0.000131411
rs12629165	3	89533017	GTEx/v8	Artery Tibial	EPHA3	A	2.12155E-07	0.17036	7.80657E-07
rs73146907	3	89538747	GTEx/v8	Artery Tibial	EPHA3	A	2.33274E-07	0.166443	7.80657E-07
rs57902683	3	89539011	GTEx/v8	Artery Tibial	EPHA3	CA	2.33274E-07	0.166443	7.80657E-07
rs55979407	3	89539275	GTEx/v8	Artery Tibial	EPHA3	G	2.33274E-07	0.166443	7.80657E-07
rs113675293	3	89539536	GTEx/v8	Artery Tibial	EPHA3	T	2.33274E-07	0.166443	7.80657E-07
rs73146926	3	89542293	GTEx/v8	Artery Tibial	EPHA3	G	2.33274E-07	0.166443	7.80657E-07
rs4035593	3	89542601	GTEx/v8	Artery Tibial	EPHA3	TAA	2.33274E-07	0.166443	7.80657E-07
3:89544326_CGGTGGAAATCTCCTTATTAAATTGTGGGCAAGAGGCAACCCAT_C	3	89544326	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs7633599	3	89544591	GTEx/v8	Artery Tibial	EPHA3	A	2.33274E-07	0.166443	7.80657E-07
rs7613315	3	89544773	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs1028012	3	89549422	GTEx/v8	Artery Tibial	EPHA3	T	2.33274E-07	0.166443	7.80657E-07
rs17745025	3	89549919	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs73146961	3	89550459	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs12634697	3	89550993	GTEx/v8	Artery Tibial	EPHA3	A	2.33274E-07	0.166443	7.80657E-07
rs12638168	3	89551544	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs73146970	3	89553168	GTEx/v8	Artery Tibial	EPHA3	G	2.33274E-07	0.166443	7.80657E-07
rs12629758	3	89556408	GTEx/v8	Artery Tibial	EPHA3	G	2.33274E-07	0.166443	7.80657E-07
rs1039990	3	89558086	GTEx/v8	Artery Tibial	EPHA3	A	2.33274E-07	0.166443	7.80657E-07
rs73146988	3	89561044	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs73146992	3	89562178	GTEx/v8	Artery Tibial	EPHA3	G	2.33274E-07	0.166443	7.80657E-07
rs73146995	3	89562209	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs73147002	3	89565128	GTEx/v8	Artery Tibial	EPHA3	G	2.33274E-07	0.166443	7.80657E-07
rs73149107	3	89565849	GTEx/v8	Artery Tibial	EPHA3	A	2.33274E-07	0.166443	7.80657E-07
rs12633325	3	89566836	GTEx/v8	Artery Tibial	EPHA3	C	2.33274E-07	0.166443	7.80657E-07
rs73149113	3	89567867	GTEx/v8	Artery Tibial	EPHA3	T	2.33274E-07	0.166443	7.80657E-07
rs73153218	3	89619808	GTEx/v8	Brain Cerebellum	EPHA3	A	2.3627E-07	-0.37069	0.000131411
rs73139261	3	89492406	GTEx/v8	Brain Cerebellum	EPHA3	G	2.49711E-07	-0.388801	0.000131411
rs7632427	3	89534377	GTEx/v8	Brain Cerebellum	EPHA3	C	2.51175E-07	-0.326002	0.000131411
rs12629999	3	89551518	GTEx/v8	Brain Cerebellum	EPHA3	G	2.55552E-07	-0.36834	0.000131411
rs73145303	3	89568714	GTEx/v8	Brain Cerebellum	EPHA3	C	2.55552E-07	-0.36834	0.000131411
rs1521806	3	90090619	GTEx/v8	Artery Tibial	EPHA3	C	2.55872E-07	-0.151229	7.80657E-07
rs2346840	3	89533267	GTEx/v8	Artery Tibial	EPHA3	G	2.57258E-07	0.166189	7.80657E-07
rs73146986	3	89560884	GTEx/v8	Artery Tibial	EPHA3	G	2.62731E-07	0.172075	7.80657E-07
rs2117136	3	89542699	GTEx/v8	Artery Tibial	EPHA3	G	2.64986E-07	0.165797	7.80657E-07
rs73145305	3	89570713	GTEx/v8	Artery Tibial	EPHA3	T	2.73133E-07	0.167896	7.80657E-07
3:89571180_TAGAG_T	3	89571180	GTEx/v8	Artery Tibial	EPHA3	T	2.73133E-07	0.167896	7.80657E-07
rs907548	3	89574852	GTEx/v8	Artery Tibial	EPHA3	T	2.73133E-07	0.167896	7.80657E-07
rs73145307	3	89576040	GTEx/v8	Artery Tibial	EPHA3	A	2.73133E-07	0.167896	7.80657E-07
rs73145309	3	89576389	GTEx/v8	Artery Tibial	EPHA3	T	2.73133E-07	0.167896	7.80657E-07
rs73145316	3	89580407	GTEx/v8	Artery Tibial	EPHA3	T	2.73133E-07	0.167896	7.80657E-07
rs73145332	3	89589327	GTEx/v8	Artery Tibial	EPHA3	C	2.73133E-07	0.167896	7.80657E-07
rs972030	3	89538498	GTEx/v8	Artery Tibial	EPHA3	T	2.77633E-07	0.169134	7.80657E-07
rs4857500	3	89541486	GTEx/v8	Artery Tibial	EPHA3	C	2.77633E-07	0.169134	7.80657E-07

rs9854073	3	89426589	GTEx/v8	Brain Cerebellum	EPHA3	A	2.78818E-07	-0.344028	0.000131411
rs9849029	3	89433059	GTEx/v8	Brain Cerebellum	EPHA3	G	2.78818E-07	-0.344028	0.000131411
rs73154916	3	89803713	GTEx/v8	Pancreas	EPHA3	T	2.84441E-07	0.320594	3.49803E-07
rs73139133	3	89527708	GTEx/v8	Artery Tibial	EPHA3	A	3.03609E-07	0.170551	7.80657E-07
rs3762718	3	89535066	GTEx/v8	Artery Tibial	EPHA3	G	3.11902E-07	0.163772	7.80657E-07
rs9868782	3	89384121	GTEx/v8	Artery Tibial	EPHA3	A	3.16316E-07	0.159098	7.80657E-07
rs2048519	3	89533978	GTEx/v8	Artery Tibial	EPHA3	A	3.1845E-07	0.164341	7.80657E-07
rs2196083	3	89536546	GTEx/v8	Artery Tibial	EPHA3	C	3.1845E-07	0.164341	7.80657E-07
rs12634044	3	89537651	GTEx/v8	Artery Tibial	EPHA3	G	3.1845E-07	0.164341	7.80657E-07
rs73145353	3	89607824	GTEx/v8	Brain Cerebellum	EPHA3	T	3.24758E-07	-0.368663	0.000131411
3:89626776_AT_A	3	89626776	GTEx/v8	Brain Cerebellum	EPHA3	A	3.24758E-07	-0.368663	0.000131411
rs7632502	3	89469453	GTEx/v8	Brain Cerebellum	EPHA3	A	3.25559E-07	-0.324027	0.000131411
rs1512189	3	89546332	GTEx/v8	Artery Tibial	EPHA3	G	3.55683E-07	0.169577	7.80657E-07
rs6784577	3	89564308	GTEx/v8	Artery Tibial	EPHA3	G	3.55683E-07	0.169577	7.80657E-07
rs73149103	3	89565651	GTEx/v8	Artery Tibial	EPHA3	A	3.55683E-07	0.169577	7.80657E-07
rs12637036	3	89584170	GTEx/v8	Artery Tibial	EPHA3	A	3.55683E-07	0.169577	7.80657E-07
rs56082199	3	89586973	GTEx/v8	Artery Tibial	EPHA3	G	3.55683E-07	0.169577	7.80657E-07
rs73145336	3	89593317	GTEx/v8	Artery Tibial	EPHA3	G	3.55683E-07	0.169577	7.80657E-07
rs73139134	3	89527709	GTEx/v8	Artery Tibial	EPHA3	C	3.83286E-07	0.167029	7.80657E-07
rs73139135	3	89527937	GTEx/v8	Artery Tibial	EPHA3	C	3.83286E-07	0.167029	7.80657E-07
rs73139139	3	89528313	GTEx/v8	Artery Tibial	EPHA3	G	3.83286E-07	0.167029	7.80657E-07
rs12636710	3	89528477	GTEx/v8	Artery Tibial	EPHA3	A	3.83286E-07	0.167029	7.80657E-07
rs3762717	3	89528948	GTEx/v8	Artery Tibial	EPHA3	C	3.83286E-07	0.167029	7.80657E-07
rs73139144	3	89529177	GTEx/v8	Artery Tibial	EPHA3	A	3.83286E-07	0.167029	7.80657E-07
rs73139147	3	89530347	GTEx/v8	Artery Tibial	EPHA3	A	3.83286E-07	0.167029	7.80657E-07
rs73139148	3	89530956	GTEx/v8	Artery Tibial	EPHA3	A	3.83286E-07	0.167029	7.80657E-07
rs34732565	3	90144346	GTEx/v8	Artery Tibial	EPHA3	A	3.86359E-07	-0.150768	7.80657E-07
rs73145345	3	89598696	GTEx/v8	Artery Tibial	EPHA3	A	4.57662E-07	0.168804	7.80657E-07
rs111835258	3	89601496	GTEx/v8	Artery Tibial	EPHA3	A	4.57662E-07	0.168804	7.80657E-07
rs73145351	3	89607237	GTEx/v8	Artery Tibial	EPHA3	T	4.57662E-07	0.168804	7.80657E-07
rs73145353	3	89607824	GTEx/v8	Artery Tibial	EPHA3	T	4.57662E-07	0.168804	7.80657E-07
rs73145357	3	89611766	GTEx/v8	Artery Tibial	EPHA3	C	4.57662E-07	0.168804	7.80657E-07
rs73139288	3	89505327	GTEx/v8	Artery Tibial	EPHA3	G	4.65482E-07	0.166579	7.80657E-07
rs73146960	3	89550445	GTEx/v8	Brain Cerebellum	EPHA3	C	4.77005E-07	-0.346034	0.000131411
rs73145345	3	89598696	GTEx/v8	Brain Cerebellum	EPHA3	A	4.99521E-07	-0.364614	0.000131411
rs111835258	3	89601496	GTEx/v8	Brain Cerebellum	EPHA3	A	4.99521E-07	-0.364614	0.000131411
rs73145351	3	89607237	GTEx/v8	Brain Cerebellum	EPHA3	T	4.99521E-07	-0.364614	0.000131411
rs73145357	3	89611766	GTEx/v8	Brain Cerebellum	EPHA3	C	4.99521E-07	-0.364614	0.000131411
rs7633500	3	89497082	GTEx/v8	Brain Cerebellum	EPHA3	A	5.31007E-07	-0.33354	0.000131411
rs3792572	3	89456555	GTEx/v8	Brain Cerebellum	EPHA3	A	5.45397E-07	-0.318779	0.000131411
rs35968370	3	89466339	GTEx/v8	Brain Cerebellum	EPHA3	T	5.45397E-07	-0.318779	0.000131411
rs11921985	3	89467357	GTEx/v8	Brain Cerebellum	EPHA3	G	5.45397E-07	-0.318779	0.000131411
rs6782527	3	89442369	GTEx/v8	Pancreas	EPHA3	T	5.49846E-07	0.301598	3.49803E-07
rs12629999	3	89551518	GTEx/v8	Artery Tibial	EPHA3	G	5.60355E-07	0.167557	7.80657E-07
rs73145303	3	89568714	GTEx/v8	Artery Tibial	EPHA3	C	5.60355E-07	0.167557	7.80657E-07
rs35317084	3	89354462	GTEx/v8	Artery Tibial	EPHA3	T	5.74001E-07	-0.150164	7.80657E-07
rs9854073	3	89426589	GTEx/v8	Artery Tibial	EPHA3	A	6.43643E-07	0.155106	7.80657E-07
rs9849029	3	89433059	GTEx/v8	Artery Tibial	EPHA3	G	6.43643E-07	0.155106	7.80657E-07
rs73139129	3	89524562	GTEx/v8	Artery Tibial	EPHA3	G	6.47764E-07	0.164125	7.80657E-07
3:89626776_AT_A	3	89626776	GTEx/v8	Artery Tibial	EPHA3	A	7.076E-07	0.165047	7.80657E-07

rs73137387	3	89464194	GTEx/v8	Artery Tibial	EPHA3	C	7.18472E-07	0.163632	7.80657E-07
rs73153293	3	89756242	GTEx/v8	Artery Tibial	EPHA3	T	7.34654E-07	0.172034	7.80657E-07
rs1157607	3	89506364	GTEx/v8	Artery Tibial	EPHA3	T	7.37407E-07	0.163625	7.80657E-07
rs7626735	3	89506958	GTEx/v8	Artery Tibial	EPHA3	A	7.41145E-07	0.163105	7.80657E-07
rs6551412	3	89496502	GTEx/v8	Artery Tibial	EPHA3	A	7.48723E-07	0.162863	7.80657E-07
rs6772953	3	89451721	GTEx/v8	Brain Cerebellum	EPHA3	C	7.62522E-07	-0.312523	0.000131411
rs112087049	3	89509550	GTEx/v8	Artery Tibial	EPHA3	T	7.66988E-07	0.168789	7.80657E-07
rs73137395	3	89478753	GTEx/v8	Brain Cerebellum	EPHA3	C	7.73151E-07	-0.359363	0.000131411
rs73139257	3	89482779	GTEx/v8	Brain Cerebellum	EPHA3	G	7.73151E-07	-0.359363	0.000131411
rs73139276	3	89500196	GTEx/v8	Artery Tibial	EPHA3	A	7.79111E-07	0.164089	7.80657E-07
rs62276243	3	90121534	GTEx/v8	Artery Tibial	EPHA3	T	9.02879E-07	-0.145657	7.80657E-07
rs4974357	3	90127762	GTEx/v8	Artery Tibial	EPHA3	C	9.02879E-07	-0.145657	7.80657E-07
rs7645408	3	89446132	GTEx/v8	Brain Cerebellum	EPHA3	A	9.04261E-07	-0.328249	0.000131411
rs28623022	3	89448936	GTEx/v8	Brain Cerebellum	EPHA3	A	9.04261E-07	-0.328249	0.000131411
rs73137381	3	89458550	GTEx/v8	Artery Tibial	EPHA3	G	9.14616E-07	0.164052	7.80657E-07
rs73137382	3	89461363	GTEx/v8	Artery Tibial	EPHA3	G	9.14616E-07	0.164052	7.80657E-07
rs57670516	3	89419645	GTEx/v8	Brain Cerebellum	EPHA3	C	9.44625E-07	-0.331888	0.000131411
3:89420088_TGTGCACCTAGAC_T	3	89420088	GTEx/v8	Brain Cerebellum	EPHA3	T	9.44625E-07	-0.331888	0.000131411
rs12639506	3	89480265	GTEx/v8	Artery Tibial	EPHA3	G	9.92726E-07	0.1612	7.80657E-07
rs57670516	3	89419645	GTEx/v8	Artery Tibial	EPHA3	C	1.00519E-06	0.152977	7.80657E-07
3:89420088_TGTGCACCTAGAC_T	3	89420088	GTEx/v8	Artery Tibial	EPHA3	T	1.00519E-06	0.152977	7.80657E-07
rs6795074	3	89516652	GTEx/v8	Artery Tibial	EPHA3	C	1.01653E-06	0.161217	7.80657E-07
rs73141108	3	89517119	GTEx/v8	Artery Tibial	EPHA3	T	1.01653E-06	0.161217	7.80657E-07
rs1912966	3	89518464	GTEx/v8	Artery Tibial	EPHA3	A	1.01653E-06	0.161217	7.80657E-07
rs73139104	3	89519229	GTEx/v8	Artery Tibial	EPHA3	C	1.01653E-06	0.161217	7.80657E-07
3:89519266_GA_G	3	89519266	GTEx/v8	Artery Tibial	EPHA3	G	1.01653E-06	0.161217	7.80657E-07
3:89521060_CTAT_C	3	89521060	GTEx/v8	Artery Tibial	EPHA3	C	1.01653E-06	0.161217	7.80657E-07
rs73139110	3	89521509	GTEx/v8	Artery Tibial	EPHA3	A	1.01653E-06	0.161217	7.80657E-07
rs1054750	3	89521725	GTEx/v8	Artery Tibial	EPHA3	C	1.01653E-06	0.161217	7.80657E-07
rs73139115	3	89521900	GTEx/v8	Artery Tibial	EPHA3	T	1.01653E-06	0.161217	7.80657E-07
rs73139117	3	89521965	GTEx/v8	Artery Tibial	EPHA3	G	1.01653E-06	0.161217	7.80657E-07
rs73139118	3	89522263	GTEx/v8	Artery Tibial	EPHA3	T	1.01653E-06	0.161217	7.80657E-07
rs150837250	3	89522314	GTEx/v8	Artery Tibial	EPHA3	AGTTATAATTAG	1.01653E-06	0.161217	7.80657E-07
rs17801380	3	89522483	GTEx/v8	Artery Tibial	EPHA3	T	1.01653E-06	0.161217	7.80657E-07
rs73139127	3	89524436	GTEx/v8	Artery Tibial	EPHA3	A	1.01653E-06	0.161217	7.80657E-07
rs568140553	3	89507219	GTEx/v8	Artery Tibial	EPHA3	CT	1.01848E-06	0.160739	7.80657E-07
rs73139261	3	89492406	GTEx/v8	Artery Tibial	EPHA3	G	1.0393E-06	0.164521	7.80657E-07
rs1499780	3	89526072	GTEx/v8	Artery Tibial	EPHA3	C	1.05303E-06	0.161305	7.80657E-07
rs2048518	3	89533905	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs2048520	3	89534248	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs2048521	3	89534253	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs73144998	3	89534592	GTEx/v8	Brain Cerebellum	EPHA3	T	1.06295E-06	-0.335412	0.000131411
rs73145002	3	89537618	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs56371328	3	89539124	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs4857498	3	89540977	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs4857499	3	89541330	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs1036285	3	89544061	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411

rs17026984	3	89544978	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs12633609	3	89545727	GTEx/v8	Brain Cerebellum	EPHA3	G	1.06295E-06	-0.335412	0.000131411
rs1512188	3	89546183	GTEx/v8	Brain Cerebellum	EPHA3	G	1.06295E-06	-0.335412	0.000131411
rs73146943	3	89546728	GTEx/v8	Brain Cerebellum	EPHA3	G	1.06295E-06	-0.335412	0.000131411
rs12632281	3	89547621	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs73146947	3	89548135	GTEx/v8	Brain Cerebellum	EPHA3	G	1.06295E-06	-0.335412	0.000131411
rs73146950	3	89548243	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs1567657	3	89548519	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs1567658	3	89548606	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs73146959	3	89549970	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs112404167	3	89550630	GTEx/v8	Brain Cerebellum	EPHA3	T	1.06295E-06	-0.335412	0.000131411
rs12637511	3	89550844	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs111618480	3	89552134	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs73146972	3	89553348	GTEx/v8	Brain Cerebellum	EPHA3	G	1.06295E-06	-0.335412	0.000131411
rs17026990	3	89555257	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs73146976	3	89557065	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs1039991	3	89558311	GTEx/v8	Brain Cerebellum	EPHA3	G	1.06295E-06	-0.335412	0.000131411
rs73146980	3	89558578	GTEx/v8	Brain Cerebellum	EPHA3	A	1.06295E-06	-0.335412	0.000131411
rs73146983	3	89559082	GTEx/v8	Brain Cerebellum	EPHA3	G	1.06295E-06	-0.335412	0.000131411
rs138490449	3	89561661	GTEx/v8	Brain Cerebellum	EPHA3	AT	1.06295E-06	-0.335412	0.000131411
rs138183278	3	89564090	GTEx/v8	Brain Cerebellum	EPHA3	CT	1.06295E-06	-0.335412	0.000131411
rs6774870	3	89564891	GTEx/v8	Brain Cerebellum	EPHA3	T	1.06295E-06	-0.335412	0.000131411
rs113307255	3	89567826	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs73145304	3	89568989	GTEx/v8	Brain Cerebellum	EPHA3	T	1.06295E-06	-0.335412	0.000131411
rs73145310	3	89578097	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs73145312	3	89578575	GTEx/v8	Brain Cerebellum	EPHA3	T	1.06295E-06	-0.335412	0.000131411
rs73145320	3	89586535	GTEx/v8	Brain Cerebellum	EPHA3	C	1.06295E-06	-0.335412	0.000131411
rs67316928	3	89482234	GTEx/v8	Brain Cerebellum	EPHA3	C	1.0649E-06	-0.313684	0.000131411
rs17804073	3	90124806	GTEx/v8	Artery Tibial	EPHA3	A	1.07195E-06	-0.145091	7.80657E-07
rs12636275	3	89523038	GTEx/v8	Brain Cerebellum	EPHA3	A	1.08168E-06	-0.311412	0.000131411
rs73137393	3	89471701	GTEx/v8	Artery Tibial	EPHA3	C	1.13522E-06	0.162812	7.80657E-07
rs7650184	3	89530057	GTEx/v8	Brain Cerebellum	EPHA3	A	1.16781E-06	-0.311417	0.000131411
rs17738248	3	89296363	GTEx/v8	Artery Tibial	EPHA3	A	1.18583E-06	0.1608	7.80657E-07
rs9868782	3	89384121	GTEx/v8	Brain Cerebellum	EPHA3	A	1.19018E-06	-0.33257	0.000131411
rs1521800	3	90001588	GTEx/v8	Artery Tibial	EPHA3	T	1.24942E-06	-0.143263	7.80657E-07
rs73145338	3	89594767	GTEx/v8	Brain Cerebellum	EPHA3	T	1.25465E-06	-0.306581	0.000131411
rs7621573	3	89595252	GTEx/v8	Brain Cerebellum	EPHA3	T	1.25465E-06	-0.306581	0.000131411
rs10511145	3	89597679	GTEx/v8	Brain Cerebellum	EPHA3	A	1.25465E-06	-0.306581	0.000131411
3:89598352_GGT_G	3	89598352	GTEx/v8	Brain Cerebellum	EPHA3	G	1.25465E-06	-0.306581	0.000131411
rs17027018	3	89604774	GTEx/v8	Brain Cerebellum	EPHA3	T	1.25465E-06	-0.306581	0.000131411
rs73153219	3	89625902	GTEx/v8	Brain Cerebellum	EPHA3	T	1.25465E-06	-0.306581	0.000131411
rs7635916	3	89633140	GTEx/v8	Brain Cerebellum	EPHA3	A	1.25465E-06	-0.306581	0.000131411
rs6551413	3	89640350	GTEx/v8	Brain Cerebellum	EPHA3	G	1.25465E-06	-0.306581	0.000131411

rs6795325	3	89642054	GTEx/v8	Brain Cerebellum	EPHA3	C	1.25465E-06	-0.306581	0.000131411
rs66499884	3	89659012	GTEx/v8	Brain Cerebellum	EPHA3	G	1.25465E-06	-0.306581	0.000131411
rs2063590	3	89323932	GTEx/v8	Artery Tibial	EPHA3	C	1.27188E-06	0.162629	7.80657E-07
rs73151349	3	89892899	GTEx/v8	Pancreas	EPHA3	G	1.33186E-06	0.312228	3.49803E-07
rs4396913	3	90047036	GTEx/v8	Artery Tibial	EPHA3	C	1.37457E-06	0.15249	7.80657E-07
rs1464463	3	90056380	GTEx/v8	Artery Tibial	EPHA3	A	1.37457E-06	0.15249	7.80657E-07
rs2346836	3	89498096	GTEx/v8	Brain Cerebellum	EPHA3	A	1.39977E-06	-0.345515	0.000131411
rs60759140	3	89499848	GTEx/v8	Brain Cerebellum	EPHA3	C	1.39977E-06	-0.345515	0.000131411
rs12152372	3	89500365	GTEx/v8	Brain Cerebellum	EPHA3	C	1.39977E-06	-0.345515	0.000131411
rs2881488	3	89500488	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs59541469	3	89501671	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
3:89502123_TTAG_T	3	89502123	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
rs73139281	3	89503890	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
rs73139284	3	89503958	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs73139286	3	89504295	GTEx/v8	Brain Cerebellum	EPHA3	A	1.39977E-06	-0.345515	0.000131411
rs1512183	3	89505054	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
rs73139290	3	89505343	GTEx/v8	Brain Cerebellum	EPHA3	A	1.39977E-06	-0.345515	0.000131411
rs73139296	3	89505734	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
rs1157608	3	89506464	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs73139302	3	89508186	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs73141104	3	89508390	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
rs1912965	3	89518332	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs113141104	3	89519238	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
rs73139105	3	89519651	GTEx/v8	Brain Cerebellum	EPHA3	C	1.39977E-06	-0.345515	0.000131411
rs17026944	3	89521131	GTEx/v8	Brain Cerebellum	EPHA3	A	1.39977E-06	-0.345515	0.000131411
rs112297761	3	89521602	GTEx/v8	Brain Cerebellum	EPHA3	TC	1.39977E-06	-0.345515	0.000131411
rs73139119	3	89522285	GTEx/v8	Brain Cerebellum	EPHA3	T	1.39977E-06	-0.345515	0.000131411
rs73139121	3	89522433	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs73139125	3	89524056	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs73139131	3	89524686	GTEx/v8	Brain Cerebellum	EPHA3	G	1.39977E-06	-0.345515	0.000131411
rs9877921	3	90108491	GTEx/v8	Artery Tibial	EPHA3	T	1.40136E-06	0.152782	7.80657E-07
rs62276239	3	90077991	GTEx/v8	Artery Tibial	EPHA3	T	1.40499E-06	0.158179	7.80657E-07
rs55889178	3	90078249	GTEx/v8	Artery Tibial	EPHA3	A	1.40499E-06	0.158179	7.80657E-07
rs1520596	3	89645542	GTEx/v8	Brain Cerebellum	EPHA3	C	1.45459E-06	-0.299389	0.000131411
rs73146965	3	89552553	GTEx/v8	Brain Cerebellum	EPHA3	G	1.4669E-06	-0.331695	0.000131411
rs35124509	3	89521693	GTEx/v8	Brain Cerebellum	EPHA3	C	1.48256E-06	-0.305957	0.000131411
rs62274981	3	89310605	GTEx/v8	Brain Cerebellum	EPHA3	T	1.48407E-06	-0.326947	0.000131411
rs17800347	3	89314429	GTEx/v8	Brain Cerebellum	EPHA3	G	1.48407E-06	-0.326947	0.000131411
rs993186	3	89314862	GTEx/v8	Brain Cerebellum	EPHA3	G	1.48407E-06	-0.326947	0.000131411
rs1567731	3	89316027	GTEx/v8	Brain Cerebellum	EPHA3	T	1.48407E-06	-0.326947	0.000131411
rs17800551	3	89317315	GTEx/v8	Brain Cerebellum	EPHA3	T	1.48407E-06	-0.326947	0.000131411
rs62274984	3	89318317	GTEx/v8	Brain Cerebellum	EPHA3	A	1.48407E-06	-0.326947	0.000131411
rs12633626	3	89744949	GTEx/v8	Brain Cerebellum	EPHA3	A	1.526E-06	-0.348666	0.000131411
rs60243237	3	89694053	GTEx/v8	Brain Cerebellum	EPHA3	T	1.52877E-06	-0.305415	0.000131411

rs987748	3	89494030	GTEx/v8	Brain Cerebellum	EPHA3	A	1.53426E-06	-0.31043	0.000131411
rs6800041	3	89448196	GTEx/v8	Brain Cerebellum	EPHA3	C	1.53723E-06	-0.323538	0.000131411
rs12714734	3	90107488	GTEx/v8	Artery Tibial	EPHA3	C	1.57366E-06	0.151478	7.80657E-07
rs9816940	3	90146579	GTEx/v8	Artery Tibial	EPHA3	T	1.58919E-06	0.153017	7.80657E-07
rs9837548	3	90156142	GTEx/v8	Artery Tibial	EPHA3	T	1.58919E-06	0.153017	7.80657E-07
rs7637670	3	89493167	GTEx/v8	Brain Cerebellum	EPHA3	A	1.60292E-06	-0.309849	0.000131411
rs11918555	3	89541934	GTEx/v8	Brain Cerebellum	EPHA3	T	1.62669E-06	-0.301267	0.000131411
rs12637608	3	89551301	GTEx/v8	Brain Cerebellum	EPHA3	C	1.62669E-06	-0.301267	0.000131411
rs66757381	3	89561048	GTEx/v8	Brain Cerebellum	EPHA3	T	1.62669E-06	-0.301267	0.000131411
rs724972	3	89581408	GTEx/v8	Brain Cerebellum	EPHA3	T	1.62669E-06	-0.301267	0.000131411
rs7652296	3	89587262	GTEx/v8	Brain Cerebellum	EPHA3	G	1.62669E-06	-0.301267	0.000131411
rs993187	3	89314820	GTEx/v8	Artery Tibial	EPHA3	G	1.68692E-06	0.158464	7.80657E-07
rs11925143	3	89723684	GTEx/v8	Brain Cerebellum	EPHA3	A	1.70688E-06	-0.30234	0.000131411
rs7632427	3	89534377	eQTLGen	eQTLGen trans eQTLs	RBBP9	C	1.8006E-06	-4.7745	0.0140155531990103
rs7633500	3	89497082	GTEx/v8	Pancreas	EPHA3	A	1.89641E-06	0.259798	3.49803E-07
rs6806912	3	89751353	GTEx/v8	Brain Cerebellum	EPHA3	C	1.9144E-06	-0.305863	0.000131411
rs7653735	3	89722185	GTEx/v8	Brain Cerebellum	EPHA3	A	1.95581E-06	-0.303396	0.000131411
rs9863058	3	89322805	GTEx/v8	Brain Cerebellum	EPHA3	T	1.9655E-06	-0.322799	0.000131411
rs4857502	3	89324919	GTEx/v8	Brain Cerebellum	EPHA3	A	1.9655E-06	-0.322799	0.000131411
rs2137487	3	89325520	GTEx/v8	Brain Cerebellum	EPHA3	G	1.9655E-06	-0.322799	0.000131411
rs9875278	3	89335463	GTEx/v8	Brain Cerebellum	EPHA3	T	1.9655E-06	-0.322799	0.000131411
rs9821666	3	89339548	GTEx/v8	Brain Cerebellum	EPHA3	T	1.9655E-06	-0.322799	0.000131411
rs1512908	3	89340134	GTEx/v8	Brain Cerebellum	EPHA3	A	1.9655E-06	-0.322799	0.000131411
rs9852380	3	89341738	GTEx/v8	Brain Cerebellum	EPHA3	G	1.9655E-06	-0.322799	0.000131411
rs9852722	3	89341946	GTEx/v8	Brain Cerebellum	EPHA3	C	1.9655E-06	-0.322799	0.000131411
rs73137384	3	89463290	GTEx/v8	Brain Cerebellum	EPHA3	T	1.97372E-06	-0.344073	0.000131411
rs9832305	3	89392778	GTEx/v8	Brain Cerebellum	EPHA3	C	2.03152E-06	-0.317078	0.000131411
rs7615949	3	89432683	GTEx/v8	Brain Cerebellum	EPHA3	G	2.05275E-06	-0.317964	0.000131411
rs113450730	3	90135516	GTEx/v8	Artery Tibial	EPHA3	G	2.23345E-06	0.156885	7.80657E-07
rs2117138	3	89531522	GTEx/v8	Brain Cerebellum	EPHA3	G	2.25084E-06	-0.332679	0.000131411
rs12634269	3	89532768	GTEx/v8	Brain Cerebellum	EPHA3	C	2.25084E-06	-0.332679	0.000131411
rs819293	3	89613664	GTEx/v8	Brain Cerebellum	EPHA3	A	2.2568E-06	-0.340532	0.000131411
rs12633626	3	89744949	GTEx/v8	Artery Tibial	EPHA3	A	2.299E-06	0.157899	7.80657E-07
rs2346837	3	89542599	GTEx/v8	Brain Cerebellum	EPHA3	T	2.39154E-06	-0.326146	0.000131411
rs11923303	3	89380944	GTEx/v8	Brain Cerebellum	EPHA3	A	2.42101E-06	-0.296307	0.000131411
rs9864984	3	89428776	GTEx/v8	Brain Cerebellum	EPHA3	T	2.5615E-06	-0.315584	0.000131411
rs9825569	3	89431650	GTEx/v8	Brain Cerebellum	EPHA3	C	2.5615E-06	-0.315584	0.000131411
rs62275019	3	89433648	GTEx/v8	Brain Cerebellum	EPHA3	G	2.5615E-06	-0.315584	0.000131411
rs7619303	3	89552554	GTEx/v8	Brain Cerebellum	EPHA3	A	2.58965E-06	-0.320493	0.000131411
rs73149109	3	89567344	GTEx/v8	Brain Cerebellum	EPHA3	A	2.58965E-06	-0.320493	0.000131411
rs1080592	3	89567568	GTEx/v8	Brain Cerebellum	EPHA3	C	2.58965E-06	-0.320493	0.000131411
rs62278163	3	89291836	GTEx/v8	Brain Cerebellum	EPHA3	T	2.68546E-06	-0.32343	0.000131411
rs6786328	3	89298926	GTEx/v8	Brain Cerebellum	EPHA3	G	2.68546E-06	-0.32343	0.000131411
rs62278168	3	89301573	GTEx/v8	Brain Cerebellum	EPHA3	G	2.68546E-06	-0.32343	0.000131411

rs28620812	3	89305668	GTEx/v8	Brain Cerebellum	EPHA3	T	2.68546E-06	-0.32343	0.000131411
rs62278172	3	89306038	GTEx/v8	Brain Cerebellum	EPHA3	A	2.68546E-06	-0.32343	0.000131411
rs9310120	3	89378413	GTEx/v8	Brain Cerebellum	EPHA3	C	2.72467E-06	-0.291525	0.000131411
rs35511518	3	89383683	GTEx/v8	Brain Cerebellum	EPHA3	C	2.88981E-06	-0.293769	0.000131411
rs55931912	3	90038054	GTEx/v8	Artery Tibial	EPHA3	A	2.94174E-06	0.160673	7.80657E-07
rs6782527	3	89442369	GTEx/v8	Brain Cerebellum	EPHA3	T	2.94697E-06	-0.323056	0.000131411
rs1512185	3	89473615	GTEx/v8	Brain Cerebellum	EPHA3	A	2.95573E-06	-0.333755	0.000131411
rs2069183	3	89645017	GTEx/v8	Brain Cerebellum	EPHA3	A	2.97291E-06	-0.333067	0.000131411
rs2137488	3	89308704	GTEx/v8	Brain Cerebellum	EPHA3	G	3.01033E-06	-0.321737	0.000131411
rs62274982	3	89310731	GTEx/v8	Brain Cerebellum	EPHA3	A	3.01033E-06	-0.321737	0.000131411
rs9866618	3	89319577	GTEx/v8	Brain Cerebellum	EPHA3	C	3.01033E-06	-0.321737	0.000131411
rs138643396	3	89698092	GTEx/v8	Brain Cerebellum	EPHA3	CATA	3.03531E-06	-0.29645	0.000131411
rs59381722	3	89701482	GTEx/v8	Brain Cerebellum	EPHA3	G	3.03531E-06	-0.29645	0.000131411
rs7637504	3	89702469	GTEx/v8	Brain Cerebellum	EPHA3	T	3.03531E-06	-0.29645	0.000131411
rs6551415	3	89705161	GTEx/v8	Brain Cerebellum	EPHA3	T	3.03531E-06	-0.29645	0.000131411
rs9875278	3	89335463	GTEx/v8	Artery Tibial	EPHA3	T	3.09831E-06	0.148813	7.80657E-07
rs35448293	3	89386010	GTEx/v8	Brain Cerebellum	EPHA3	G	3.10479E-06	-0.294378	0.000131411
rs144317613	3	89525080	GTEx/v8	Artery Tibial	EPHA3	TA	3.16115E-06	0.154826	7.80657E-07
rs35173319	3	89386361	GTEx/v8	Brain Cerebellum	EPHA3	T	3.26506E-06	-0.293781	0.000131411
rs12631313	3	89528461	GTEx/v8	Brain Cerebellum	EPHA3	T	3.26615E-06	-0.327927	0.000131411
rs7650466	3	89530358	GTEx/v8	Brain Cerebellum	EPHA3	T	3.26615E-06	-0.327927	0.000131411
rs112407114	3	89797398	GTEx/v8	Artery Tibial	EPHA3	C	3.30588E-06	0.157525	7.80657E-07
rs12638746	3	89331055	GTEx/v8	Artery Tibial	EPHA3	A	3.30854E-06	-0.141292	7.80657E-07
rs9848971	3	89279394	GTEx/v8	Brain Cerebellum	EPHA3	G	3.5827E-06	-0.323238	0.000131411
rs4857502	3	89324919	GTEx/v8	Artery Tibial	EPHA3	A	3.61635E-06	0.14766	7.80657E-07
rs1567731	3	89316027	GTEx/v8	Artery Tibial	EPHA3	T	3.66393E-06	0.147438	7.80657E-07
rs28620812	3	89305668	GTEx/v8	Artery Tibial	EPHA3	T	3.66811E-06	0.147499	7.80657E-07
rs62278172	3	89306038	GTEx/v8	Artery Tibial	EPHA3	A	3.66811E-06	0.147499	7.80657E-07
rs9817553	3	89384566	GTEx/v8	Brain Cerebellum	EPHA3	G	3.69048E-06	-0.289832	0.000131411
rs6776967	3	90025022	GTEx/v8	Artery Tibial	EPHA3	T	3.79842E-06	0.151056	7.80657E-07
rs9310119	3	89378042	GTEx/v8	Brain Cerebellum	EPHA3	G	3.8657E-06	-0.290574	0.000131411
rs28675360	3	89386151	GTEx/v8	Brain Cerebellum	EPHA3	T	3.88293E-06	-0.291267	0.000131411
rs9863058	3	89322805	GTEx/v8	Artery Tibial	EPHA3	T	3.93751E-06	0.146765	7.80657E-07
rs62274986	3	89327148	GTEx/v8	Brain Cerebellum	EPHA3	A	3.93801E-06	-0.317653	0.000131411
rs73153370	3	90056125	GTEx/v8	Artery Tibial	EPHA3	A	3.94503E-06	0.151255	7.80657E-07
rs57670516	3	89419645	GTEx/v8	Pancreas	EPHA3	C	4.16777E-06	0.26691	3.49803E-07
3:89420088_TGTGCACCTAGAC_T	3	89420088	GTEx/v8	Pancreas	EPHA3	T	4.16777E-06	0.26691	3.49803E-07
rs9854073	3	89426589	GTEx/v8	Pancreas	EPHA3	A	4.16777E-06	0.26691	3.49803E-07
rs9849029	3	89433059	GTEx/v8	Pancreas	EPHA3	G	4.16777E-06	0.26691	3.49803E-07
rs2137487	3	89325520	GTEx/v8	Artery Tibial	EPHA3	G	4.23081E-06	0.146733	7.80657E-07
rs9821666	3	89339548	GTEx/v8	Artery Tibial	EPHA3	T	4.23081E-06	0.146733	7.80657E-07
rs1512908	3	89340134	GTEx/v8	Artery Tibial	EPHA3	A	4.23081E-06	0.146733	7.80657E-07
rs9852380	3	89341738	GTEx/v8	Artery Tibial	EPHA3	G	4.23081E-06	0.146733	7.80657E-07
rs9852722	3	89341946	GTEx/v8	Artery Tibial	EPHA3	C	4.23081E-06	0.146733	7.80657E-07
rs1398534	3	89329307	GTEx/v8	Brain Cerebellum	EPHA3	G	4.2324E-06	-0.313436	0.000131411
rs17800551	3	89317315	GTEx/v8	Artery Tibial	EPHA3	T	4.30899E-06	0.146349	7.80657E-07
rs62274984	3	89318317	GTEx/v8	Artery Tibial	EPHA3	A	4.30899E-06	0.146349	7.80657E-07

rs752364173	3	89521820	GTEx/v8	Brain Cerebellum	EPHA3	T	4.47555E-06	-0.325467	0.000131411
3:89521831_TGAAAG_T	3	89521831	GTEx/v8	Brain Cerebellum	EPHA3	T	4.47555E-06	-0.325467	0.000131411
3:89521838_TTTG_T	3	89521838	GTEx/v8	Brain Cerebellum	EPHA3	T	4.47555E-06	-0.325467	0.000131411
rs6797260	3	89302486	GTEx/v8	Artery Tibial	EPHA3	T	4.47908E-06	-0.139789	7.80657E-07
rs9866618	3	89319577	GTEx/v8	Artery Tibial	EPHA3	C	4.49777E-06	0.146776	7.80657E-07
rs6771054	3	89489529	GTEx/v8	Brain Cerebellum	EPHA3	C	4.69366E-06	-0.293501	0.000131411
rs7644070	3	89370107	GTEx/v8	Brain Cerebellum	EPHA3	A	4.75765E-06	-0.288734	0.000131411
rs113895673	3	89917796	GTEx/v8	Pancreas	EPHA3	C	4.8159E-06	0.292706	3.49803E-07
rs62274986	3	89327148	GTEx/v8	Artery Tibial	EPHA3	A	4.83202E-06	0.147343	7.80657E-07
rs6782527	3	89442369	GTEx/v8	Artery Tibial	EPHA3	T	4.95543E-06	0.1499	7.80657E-07
rs55787722	3	90012103	GTEx/v8	Artery Tibial	EPHA3	T	5.00725E-06	0.14935	7.80657E-07
rs62274981	3	89310605	GTEx/v8	Artery Tibial	EPHA3	T	5.03773E-06	0.145415	7.80657E-07
rs17800347	3	89314429	GTEx/v8	Artery Tibial	EPHA3	G	5.03773E-06	0.145415	7.80657E-07
rs993186	3	89314862	GTEx/v8	Artery Tibial	EPHA3	G	5.03773E-06	0.145415	7.80657E-07
rs13100388	3	89383148	GTEx/v8	Brain Cerebellum	EPHA3	A	5.04914E-06	-0.284963	0.000131411
rs6419884	3	89279467	GTEx/v8	Brain Cerebellum	EPHA3	T	5.19678E-06	0.292251	0.000131411
rs9833400	3	89389507	GTEx/v8	Brain Cerebellum	EPHA3	G	5.2433E-06	-0.286472	0.000131411
rs7619303	3	89552554	GTEx/v8	Artery Tibial	EPHA3	A	5.32619E-06	0.145109	7.80657E-07
rs1036285	3	89544061	GTEx/v8	Artery Tibial	EPHA3	C	5.391E-06	0.145676	7.80657E-07
rs17026984	3	89544978	GTEx/v8	Artery Tibial	EPHA3	A	5.391E-06	0.145676	7.80657E-07
rs111618480	3	89552134	GTEx/v8	Artery Tibial	EPHA3	C	5.391E-06	0.145676	7.80657E-07
rs62278164	3	89292567	GTEx/v8	Brain Cerebellum	EPHA3	C	5.41224E-06	-0.317954	0.000131411
rs9883541	3	89294657	GTEx/v8	Brain Cerebellum	EPHA3	C	5.41224E-06	-0.317954	0.000131411
rs62274982	3	89310731	GTEx/v8	Artery Tibial	EPHA3	A	5.71992E-06	0.146085	7.80657E-07
rs2137488	3	89308704	GTEx/v8	Artery Tibial	EPHA3	G	5.78921E-06	0.145371	7.80657E-07
rs12634269	3	89532768	GTEx/v8	Artery Tibial	EPHA3	C	5.8533E-06	0.146048	7.80657E-07
rs62278163	3	89291836	GTEx/v8	Artery Tibial	EPHA3	T	5.90756E-06	0.14456	7.80657E-07
rs6786328	3	89298926	GTEx/v8	Artery Tibial	EPHA3	G	5.90756E-06	0.14456	7.80657E-07
rs62278168	3	89301573	GTEx/v8	Artery Tibial	EPHA3	G	5.90756E-06	0.14456	7.80657E-07
rs112407114	3	89797398	GTEx/v8	Brain Cerebellum	EPHA3	C	6.08314E-06	-0.333729	0.000131411
rs62275018	3	89423863	GTEx/v8	Brain Cerebellum	EPHA3	G	6.32511E-06	-0.305486	0.000131411
rs9310121	3	89378987	GTEx/v8	Brain Cerebellum	EPHA3	G	6.34498E-06	-0.28251	0.000131411
rs9310122	3	89379408	GTEx/v8	Brain Cerebellum	EPHA3	G	6.34498E-06	-0.28251	0.000131411
rs9846844	3	89379639	GTEx/v8	Brain Cerebellum	EPHA3	A	6.34498E-06	-0.28251	0.000131411
rs73153293	3	89756242	GTEx/v8	Brain Cerebellum	EPHA3	T	6.37713E-06	-0.339017	0.000131411
rs145565219	3	89936402	GTEx/v8	Artery Tibial	EPHA3	A	6.39268E-06	0.153684	7.80657E-07
rs7613412	3	89724217	GTEx/v8	Brain Cerebellum	EPHA3	T	6.6714E-06	-0.290591	0.000131411
rs62278164	3	89292567	GTEx/v8	Artery Tibial	EPHA3	C	6.71388E-06	0.145209	7.80657E-07
rs9883541	3	89294657	GTEx/v8	Artery Tibial	EPHA3	C	6.71388E-06	0.145209	7.80657E-07
rs73145304	3	89568989	GTEx/v8	Artery Tibial	EPHA3	T	7.14309E-06	0.145168	7.80657E-07
rs73145310	3	89578097	GTEx/v8	Artery Tibial	EPHA3	C	7.14309E-06	0.145168	7.80657E-07
rs73145312	3	89578575	GTEx/v8	Artery Tibial	EPHA3	T	7.14309E-06	0.145168	7.80657E-07
rs73145320	3	89586535	GTEx/v8	Artery Tibial	EPHA3	C	7.14309E-06	0.145168	7.80657E-07
rs13075167	3	89303172	GTEx/v8	Artery Tibial	EPHA3	C	7.14359E-06	-0.136941	7.80657E-07
rs113895673	3	89917796	GTEx/v8	Artery Tibial	EPHA3	C	7.21958E-06	0.152514	7.80657E-07
rs9862638	3	89373598	GTEx/v8	Artery Tibial	EPHA3	C	7.31028E-06	0.125044	7.80657E-07
rs1398532	3	89367901	GTEx/v8	Brain Cerebellum	EPHA3	C	7.58961E-06	-0.281373	0.000131411
rs59969878	3	89369856	GTEx/v8	Brain Cerebellum	EPHA3	A	7.58961E-06	-0.281373	0.000131411
rs993187	3	89314820	GTEx/v8	Pancreas	EPHA3	G	7.78447E-06	0.274968	3.49803E-07

rs9866959	3	89379935	GTEx/v8	Brain Cerebellum	EPHA3	C	7.983E-06	-0.279055	0.000131411
rs7616322	3	89493283	GTEx/v8	Brain Cerebellum	EPHA3	T	8.01438E-06	-0.320833	0.000131411
rs7645408	3	89446132	GTEx/v8	Pancreas	EPHA3	A	8.33515E-06	0.250421	3.49803E-07
rs28623022	3	89448936	GTEx/v8	Pancreas	EPHA3	A	8.33515E-06	0.250421	3.49803E-07
rs113895673	3	89917796	GTEx/v8	Brain Cerebellum	EPHA3	C	8.55292E-06	-0.324874	0.000131411
3:89924704_TG_T	3	89924704	GTEx/v8	Brain Cerebellum	EPHA3	T	8.55292E-06	-0.324874	0.000131411
rs145565219	3	89936402	GTEx/v8	Brain Cerebellum	EPHA3	A	8.55292E-06	-0.324874	0.000131411
rs9848971	3	89279394	GTEx/v8	Artery Tibial	EPHA3	G	8.76038E-06	0.142057	7.80657E-07
rs62275018	3	89423863	GTEx/v8	Pancreas	EPHA3	G	9.33406E-06	0.250575	3.49803E-07
rs7615949	3	89432683	GTEx/v8	Pancreas	EPHA3	G	9.33406E-06	0.250575	3.49803E-07
rs9873545	3	89377717	GTEx/v8	Brain Cerebellum	EPHA3	G	9.40869E-06	-0.278237	0.000131411
rs2063590	3	89323932	GTEx/v8	Pancreas	EPHA3	C	9.50719E-06	0.270994	3.49803E-07
rs1512185	3	89473615	GTEx/v8	Artery Tibial	EPHA3	A	9.59551E-06	0.141066	7.80657E-07
rs1398534	3	89329307	GTEx/v8	Artery Tibial	EPHA3	G	9.64593E-06	0.141256	7.80657E-07
rs73153279	3	89727968	GTEx/v8	Brain Cerebellum	EPHA3	C	9.69777E-06	-0.314789	0.000131411
rs73153282	3	89728408	GTEx/v8	Brain Cerebellum	EPHA3	T	9.69777E-06	-0.314789	0.000131411
rs6551410	3	89442305	GTEx/v8	Brain Cerebellum	EPHA3	A	1.01844E-05	-0.28014	0.000131411
rs9990016	3	89364033	GTEx/v8	Brain Cerebellum	EPHA3	A	1.08374E-05	-0.28036	0.000131411
rs73149109	3	89567344	GTEx/v8	Artery Tibial	EPHA3	A	1.08887E-05	0.140148	7.80657E-07
rs1080592	3	89567568	GTEx/v8	Artery Tibial	EPHA3	C	1.08887E-05	0.140148	7.80657E-07
rs73137395	3	89478753	GTEx/v8	Artery Tibial	EPHA3	C	1.09323E-05	0.143333	7.80657E-07
rs73139257	3	89482779	GTEx/v8	Artery Tibial	EPHA3	G	1.09323E-05	0.143333	7.80657E-07
3:89924704_TG_T	3	89924704	GTEx/v8	Artery Tibial	EPHA3	T	1.09412E-05	0.149669	7.80657E-07
rs17738248	3	89296363	GTEx/v8	Pancreas	EPHA3	A	1.09578E-05	0.272841	3.49803E-07
rs73137384	3	89463290	GTEx/v8	Artery Tibial	EPHA3	T	1.17861E-05	0.140098	7.80657E-07
rs2069183	3	89645017	GTEx/v8	Artery Tibial	EPHA3	A	1.20408E-05	0.144339	7.80657E-07
rs954964	3	89355632	GTEx/v8	Brain Cerebellum	EPHA3	G	1.22093E-05	-0.273862	0.000131411
rs13088663	3	89360266	GTEx/v8	Brain Cerebellum	EPHA3	T	1.22093E-05	-0.273862	0.000131411
rs9839323	3	89190113	GTEx/v8	Lung	CGGBP1	A	1.23179E-05	0.183962	1.81917E-48
rs993187	3	89314820	GTEx/v8	Brain Cerebellum	EPHA3	G	1.23204E-05	-0.303884	0.000131411
rs7615949	3	89432683	GTEx/v8	Artery Tibial	EPHA3	G	1.24482E-05	0.135002	7.80657E-07
rs13323078	3	89168325	GTEx/v8	Lung	CGGBP1	A	1.27567E-05	0.182688	1.81917E-48
rs145565219	3	89936402	GTEx/v8	Pancreas	EPHA3	A	1.31568E-05	0.28696	3.49803E-07
rs9873545	3	89377717	GTEx/v8	Artery Tibial	EPHA3	G	1.32482E-05	0.122036	7.80657E-07
rs73151349	3	89892899	GTEx/v8	Artery Tibial	EPHA3	G	1.33999E-05	0.148574	7.80657E-07
rs9867299	3	89300497	GTEx/v8	Artery Tibial	EPHA3	A	1.35373E-05	0.122174	7.80657E-07
rs1512183	3	89505054	GTEx/v8	Artery Tibial	EPHA3	T	1.38036E-05	0.140822	7.80657E-07
rs73153283	3	89732193	GTEx/v8	Brain Cerebellum	EPHA3	T	1.40234E-05	-0.309356	0.000131411
rs752364173	3	89521820	GTEx/v8	Artery Tibial	EPHA3	T	1.40686E-05	0.138789	7.80657E-07
3:89521831_TGAAAG_T	3	89521831	GTEx/v8	Artery Tibial	EPHA3	T	1.40686E-05	0.138789	7.80657E-07
3:89521838_TTTG_T	3	89521838	GTEx/v8	Artery Tibial	EPHA3	T	1.40686E-05	0.138789	7.80657E-07
rs66708608	3	89486373	GTEx/v8	Brain Cerebellum	EPHA3	T	1.46451E-05	-0.319235	0.000131411
rs7616322	3	89493283	GTEx/v8	Artery Tibial	EPHA3	T	1.47881E-05	0.138523	7.80657E-07
rs12637608	3	89551301	GTEx/v8	Artery Tibial	EPHA3	C	1.48728E-05	0.125146	7.80657E-07
rs56371328	3	89539124	GTEx/v8	Artery Tibial	EPHA3	A	1.50588E-05	0.139235	7.80657E-07
rs4857498	3	89540977	GTEx/v8	Artery Tibial	EPHA3	A	1.50588E-05	0.139235	7.80657E-07
rs4857499	3	89541330	GTEx/v8	Artery Tibial	EPHA3	A	1.50588E-05	0.139235	7.80657E-07
rs12633609	3	89545727	GTEx/v8	Artery Tibial	EPHA3	G	1.50588E-05	0.139235	7.80657E-07
rs1512188	3	89546183	GTEx/v8	Artery Tibial	EPHA3	G	1.50588E-05	0.139235	7.80657E-07

rs73146943	3	89546728	GTEx/v8	Artery Tibial	EPHA3	G	1.50588E-05	0.139235	7.80657E-07
rs12632281	3	89547621	GTEx/v8	Artery Tibial	EPHA3	A	1.50588E-05	0.139235	7.80657E-07
rs73146947	3	89548135	GTEx/v8	Artery Tibial	EPHA3	G	1.50588E-05	0.139235	7.80657E-07
rs73146950	3	89548243	GTEx/v8	Artery Tibial	EPHA3	C	1.50588E-05	0.139235	7.80657E-07
rs1567657	3	89548519	GTEx/v8	Artery Tibial	EPHA3	A	1.50588E-05	0.139235	7.80657E-07
rs1567658	3	89548606	GTEx/v8	Artery Tibial	EPHA3	A	1.50588E-05	0.139235	7.80657E-07
rs73146959	3	89549970	GTEx/v8	Artery Tibial	EPHA3	C	1.50588E-05	0.139235	7.80657E-07
rs73146960	3	89550445	GTEx/v8	Artery Tibial	EPHA3	C	1.50588E-05	0.139235	7.80657E-07
rs112404167	3	89550630	GTEx/v8	Artery Tibial	EPHA3	T	1.50588E-05	0.139235	7.80657E-07
rs12637511	3	89550844	GTEx/v8	Artery Tibial	EPHA3	C	1.50588E-05	0.139235	7.80657E-07
rs73146972	3	89553348	GTEx/v8	Artery Tibial	EPHA3	G	1.50588E-05	0.139235	7.80657E-07
rs17026990	3	89555257	GTEx/v8	Artery Tibial	EPHA3	C	1.50588E-05	0.139235	7.80657E-07
rs73146976	3	89557065	GTEx/v8	Artery Tibial	EPHA3	C	1.50588E-05	0.139235	7.80657E-07
rs1039991	3	89558311	GTEx/v8	Artery Tibial	EPHA3	G	1.50588E-05	0.139235	7.80657E-07
rs73146980	3	89558578	GTEx/v8	Artery Tibial	EPHA3	A	1.50588E-05	0.139235	7.80657E-07
rs73146983	3	89559082	GTEx/v8	Artery Tibial	EPHA3	G	1.50588E-05	0.139235	7.80657E-07
rs138490449	3	89561661	GTEx/v8	Artery Tibial	EPHA3	AT	1.50588E-05	0.139235	7.80657E-07
rs138183278	3	89564090	GTEx/v8	Artery Tibial	EPHA3	CT	1.50588E-05	0.139235	7.80657E-07
rs6774870	3	89564891	GTEx/v8	Artery Tibial	EPHA3	T	1.50588E-05	0.139235	7.80657E-07
rs113307255	3	89567826	GTEx/v8	Artery Tibial	EPHA3	C	1.50588E-05	0.139235	7.80657E-07
rs73153282	3	89728408	GTEx/v8	Artery Tibial	EPHA3	T	1.51422E-05	0.141824	7.80657E-07
rs73153241	3	89695319	GTEx/v8	Brain Cerebellum	EPHA3	G	1.52792E-05	-0.306774	0.000131411
rs73145317	3	89583712	GTEx/v8	Brain Cerebellum	EPHA3	C	1.53352E-05	-0.364409	0.000131411
rs10511145	3	89597679	GTEx/v8	Artery Tibial	EPHA3	A	1.56217E-05	0.125943	7.80657E-07
3:89598352_GGT_G	3	89598352	GTEx/v8	Artery Tibial	EPHA3	G	1.56217E-05	0.125943	7.80657E-07
rs17027018	3	89604774	GTEx/v8	Artery Tibial	EPHA3	T	1.56217E-05	0.125943	7.80657E-07
rs2346837	3	89542599	GTEx/v8	Artery Tibial	EPHA3	T	1.58851E-05	0.139109	7.80657E-07
rs35173319	3	89386361	GTEx/v8	Artery Tibial	EPHA3	T	1.60562E-05	0.122651	7.80657E-07
rs73151349	3	89892899	GTEx/v8	Brain Cerebellum	EPHA3	G	1.61632E-05	-0.318556	0.000131411
rs73145338	3	89594767	GTEx/v8	Artery Tibial	EPHA3	T	1.61827E-05	0.125766	7.80657E-07
rs7621573	3	89595252	GTEx/v8	Artery Tibial	EPHA3	T	1.61827E-05	0.125766	7.80657E-07
rs1398531	3	89289709	GTEx/v8	Artery Tibial	EPHA3	T	1.65645E-05	0.136374	7.80657E-07
rs11923303	3	89380944	GTEx/v8	Artery Tibial	EPHA3	A	1.6566E-05	0.122508	7.80657E-07
rs2063590	3	89323932	GTEx/v8	Brain Cerebellum	EPHA3	C	1.67149E-05	-0.303021	0.000131411
rs9310119	3	89378042	GTEx/v8	Artery Tibial	EPHA3	G	1.73911E-05	0.121808	7.80657E-07
rs59127701	3	89291916	GTEx/v8	Brain Cerebellum	EPHA3	TA	1.87081E-05	-0.316913	0.000131411
rs6795325	3	89642054	GTEx/v8	Artery Tibial	EPHA3	C	1.91183E-05	0.124312	7.80657E-07
rs17026944	3	89521131	GTEx/v8	Artery Tibial	EPHA3	A	1.91548E-05	0.137791	7.80657E-07
rs73139125	3	89524056	GTEx/v8	Artery Tibial	EPHA3	G	1.91548E-05	0.137791	7.80657E-07
rs66708608	3	89486373	GTEx/v8	Artery Tibial	EPHA3	T	1.93534E-05	0.138853	7.80657E-07
rs73153262	3	89719269	GTEx/v8	Brain Cerebellum	EPHA3	T	1.93534E-05	-0.304517	0.000131411
rs73146965	3	89552553	GTEx/v8	Artery Tibial	EPHA3	G	1.95703E-05	0.137552	7.80657E-07
rs2117138	3	89531522	GTEx/v8	Artery Tibial	EPHA3	G	1.98743E-05	0.138908	7.80657E-07
rs1398532	3	89367901	GTEx/v8	Artery Tibial	EPHA3	C	1.98916E-05	0.120029	7.80657E-07
rs59969878	3	89369856	GTEx/v8	Artery Tibial	EPHA3	A	1.98916E-05	0.120029	7.80657E-07
rs9833400	3	89389507	GTEx/v8	Artery Tibial	EPHA3	G	2.02599E-05	0.120321	7.80657E-07
rs2048518	3	89533905	GTEx/v8	Artery Tibial	EPHA3	C	2.06431E-05	0.136366	7.80657E-07
rs2048520	3	89534248	GTEx/v8	Artery Tibial	EPHA3	C	2.06431E-05	0.136366	7.80657E-07
rs2048521	3	89534253	GTEx/v8	Artery Tibial	EPHA3	A	2.06431E-05	0.136366	7.80657E-07
rs73144998	3	89534592	GTEx/v8	Artery Tibial	EPHA3	T	2.06431E-05	0.136366	7.80657E-07
rs73145002	3	89537618	GTEx/v8	Artery Tibial	EPHA3	C	2.06431E-05	0.136366	7.80657E-07
rs13316356	3	89309959	GTEx/v8	Brain Cerebellum	EPHA3	A	2.07124E-05	-0.291246	0.000131411

rs73145317	3	89583712	GTEx/v8	Artery Tibial	EPHA3	C	2.08052E-05	0.161437	7.80657E-07
rs9864984	3	89428776	GTEx/v8	Artery Tibial	EPHA3	T	2.08171E-05	0.130228	7.80657E-07
rs62275019	3	89433648	GTEx/v8	Artery Tibial	EPHA3	G	2.08171E-05	0.130228	7.80657E-07
rs66499884	3	89659012	GTEx/v8	Artery Tibial	EPHA3	G	2.09777E-05	0.123858	7.80657E-07
rs7644070	3	89370107	GTEx/v8	Artery Tibial	EPHA3	A	2.11239E-05	0.12014	7.80657E-07
rs73153219	3	89625902	GTEx/v8	Artery Tibial	EPHA3	T	2.13843E-05	0.123247	7.80657E-07
rs7635916	3	89633140	GTEx/v8	Artery Tibial	EPHA3	A	2.13843E-05	0.123247	7.80657E-07
rs6551413	3	89640350	GTEx/v8	Artery Tibial	EPHA3	G	2.13843E-05	0.123247	7.80657E-07
rs73153283	3	89732193	GTEx/v8	Artery Tibial	EPHA3	T	2.13896E-05	0.139189	7.80657E-07
rs7619025	3	89368629	GTEx/v8	Brain Cerebellum	EPHA3	A	2.14141E-05	-0.269323	0.000131411
rs7645408	3	89446132	GTEx/v8	Artery Tibial	EPHA3	A	2.14353E-05	0.130754	7.80657E-07
rs28623022	3	89448936	GTEx/v8	Artery Tibial	EPHA3	A	2.14353E-05	0.130754	7.80657E-07
rs17738248	3	89296363	GTEx/v8	Brain Cerebellum	EPHA3	A	2.15453E-05	-0.299737	0.000131411
rs9832305	3	89392778	GTEx/v8	Artery Tibial	EPHA3	C	2.16588E-05	0.131238	7.80657E-07
rs7632427	3	89534377	GTEx/v8	Artery Tibial	EPHA3	C	2.25104E-05	0.123488	7.80657E-07
rs11918555	3	89541934	GTEx/v8	Artery Tibial	EPHA3	T	2.3178E-05	0.12223	7.80657E-07
rs9825569	3	89431650	GTEx/v8	Artery Tibial	EPHA3	C	2.42845E-05	0.12901	7.80657E-07
rs113450730	3	90135516	GTEx/v8	Pancreas	EPHA3	G	2.43056E-05	0.265272	3.49803E-07
rs62275018	3	89423863	GTEx/v8	Artery Tibial	EPHA3	G	2.50397E-05	0.130801	7.80657E-07
rs13076853	3	89382776	GTEx/v8	Brain Cerebellum	EPHA3	C	2.50427E-05	-0.266047	0.000131411
3:89924704_TG_T	3	89924704	GTEx/v8	Pancreas	EPHA3	T	2.51441E-05	0.272398	3.49803E-07
rs9868785	3	90066423	GTEx/v8	Artery Tibial	EPHA3	A	2.55363E-05	0.130904	7.80657E-07
rs28675360	3	89386151	GTEx/v8	Artery Tibial	EPHA3	T	2.58705E-05	0.117655	7.80657E-07
rs2175670	3	89343044	GTEx/v8	Brain Cerebellum	EPHA3	G	2.59143E-05	-0.28772	0.000131411
rs9825569	3	89431650	GTEx/v8	Pancreas	EPHA3	C	2.60809E-05	0.232839	3.49803E-07
rs66757381	3	89561048	GTEx/v8	Artery Tibial	EPHA3	T	2.63229E-05	0.121893	7.80657E-07
rs724972	3	89581408	GTEx/v8	Artery Tibial	EPHA3	T	2.63229E-05	0.121893	7.80657E-07
rs7652296	3	89587262	GTEx/v8	Artery Tibial	EPHA3	G	2.63229E-05	0.121893	7.80657E-07
rs9990016	3	89364033	GTEx/v8	Artery Tibial	EPHA3	A	2.63903E-05	0.119686	7.80657E-07
rs73153279	3	89727968	GTEx/v8	Artery Tibial	EPHA3	C	2.64971E-05	0.13768	7.80657E-07
rs6776281	3	89290164	GTEx/v8	Brain Cerebellum	EPHA3	A	2.65931E-05	-0.292638	0.000131411
rs13100388	3	89383148	GTEx/v8	Artery Tibial	EPHA3	A	2.66441E-05	0.117524	7.80657E-07
rs12631313	3	89528461	GTEx/v8	Artery Tibial	EPHA3	T	2.69776E-05	0.136535	7.80657E-07
rs7650466	3	89530358	GTEx/v8	Artery Tibial	EPHA3	T	2.69776E-05	0.136535	7.80657E-07
rs9866959	3	89379935	GTEx/v8	Artery Tibial	EPHA3	C	2.77804E-05	0.116908	7.80657E-07
rs9864984	3	89428776	GTEx/v8	Pancreas	EPHA3	T	2.79974E-05	0.233258	3.49803E-07
rs62275019	3	89433648	GTEx/v8	Pancreas	EPHA3	G	2.79974E-05	0.233258	3.49803E-07
rs73153260	3	89718078	GTEx/v8	Artery Tibial	EPHA3	A	2.82023E-05	0.15922	7.80657E-07
rs35448293	3	89386010	GTEx/v8	Artery Tibial	EPHA3	G	2.82312E-05	0.117986	7.80657E-07
rs1520596	3	89645542	GTEx/v8	Artery Tibial	EPHA3	C	2.8462E-05	0.121829	7.80657E-07
rs9817553	3	89384566	GTEx/v8	Artery Tibial	EPHA3	G	2.90737E-05	0.117745	7.80657E-07
rs35511518	3	89383683	GTEx/v8	Artery Tibial	EPHA3	C	2.90995E-05	0.116405	7.80657E-07
rs60759140	3	89499848	GTEx/v8	Artery Tibial	EPHA3	C	2.91486E-05	0.136034	7.80657E-07
rs73153266	3	89720111	GTEx/v8	Brain Cerebellum	EPHA3	G	2.92949E-05	-0.298481	0.000131411
rs113288647	3	89720352	GTEx/v8	Brain Cerebellum	EPHA3	T	2.92949E-05	-0.298481	0.000131411
rs73154925	3	89859312	GTEx/v8	Artery Tibial	EPHA3	C	2.94586E-05	0.138919	7.80657E-07
rs2346836	3	89498096	GTEx/v8	Artery Tibial	EPHA3	A	2.9937E-05	0.136087	7.80657E-07
rs59541469	3	89501671	GTEx/v8	Artery Tibial	EPHA3	T	2.9937E-05	0.136087	7.80657E-07
3:89502123_TTAG_T	3	89502123	GTEx/v8	Artery Tibial	EPHA3	T	2.9937E-05	0.136087	7.80657E-07
rs6551450	3	90129328	GTEx/v8	Artery Tibial	EPHA3	C	3.03179E-05	0.12845	7.80657E-07
rs9851954	3	89297904	GTEx/v8	Artery Tibial	EPHA3	A	3.07249E-05	0.131839	7.80657E-07
rs73153260	3	89718078	GTEx/v8	Brain Cerebellum	EPHA3	A	3.12578E-05	-0.356663	0.000131411

rs73153252	3	89712192	GTEx/v8	Brain Cerebellum	EPHA3	T	3.13471E-05	-0.294404	0.000131411
rs7617395	3	89722541	GTEx/v8	Brain Cerebellum	EPHA3	T	3.13471E-05	-0.294404	0.000131411
rs1567731	3	89316027	GTEx/v8	Pancreas	EPHA3	T	3.15741E-05	0.246698	3.49803E-07
rs73141104	3	89508390	GTEx/v8	Artery Tibial	EPHA3	T	3.18627E-05	0.136308	7.80657E-07
rs9868782	3	89384121	GTEx/v8	Pancreas	EPHA3	A	3.19825E-05	0.23913	3.49803E-07
rs9310121	3	89378987	GTEx/v8	Artery Tibial	EPHA3	G	3.20658E-05	0.117263	7.80657E-07
rs6776281	3	89290164	GTEx/v8	Artery Tibial	EPHA3	A	3.20719E-05	0.13161	7.80657E-07
rs73153241	3	89695319	GTEx/v8	Artery Tibial	EPHA3	G	3.42799E-05	0.137103	7.80657E-07
rs73153258	3	89715585	GTEx/v8	Brain Cerebellum	EPHA3	A	3.43172E-05	-0.298648	0.000131411
rs9310122	3	89379408	GTEx/v8	Artery Tibial	EPHA3	G	3.45233E-05	0.117072	7.80657E-07
rs60243237	3	89694053	GTEx/v8	Artery Tibial	EPHA3	T	3.53066E-05	0.120952	7.80657E-07
rs6796339	3	89286159	GTEx/v8	Brain Cerebellum	EPHA3	T	3.56632E-05	-0.28695	0.000131411
rs62278161	3	89291713	GTEx/v8	Brain Cerebellum	EPHA3	G	3.56632E-05	-0.28695	0.000131411
rs58858051	3	89291909	GTEx/v8	Brain Cerebellum	EPHA3	T	3.56632E-05	-0.28695	0.000131411
rs6794975	3	89292824	GTEx/v8	Brain Cerebellum	EPHA3	A	3.56632E-05	-0.28695	0.000131411
rs4857497	3	89294149	GTEx/v8	Brain Cerebellum	EPHA3	G	3.56632E-05	-0.28695	0.000131411
rs9847087	3	89297308	GTEx/v8	Brain Cerebellum	EPHA3	G	3.56632E-05	-0.28695	0.000131411
rs17026816	3	89297593	GTEx/v8	Brain Cerebellum	EPHA3	G	3.56632E-05	-0.28695	0.000131411
rs9851954	3	89297904	GTEx/v8	Brain Cerebellum	EPHA3	A	3.56632E-05	-0.28695	0.000131411
rs6786204	3	89298813	GTEx/v8	Brain Cerebellum	EPHA3	C	3.56632E-05	-0.28695	0.000131411
rs6773815	3	89299059	GTEx/v8	Brain Cerebellum	EPHA3	T	3.56632E-05	-0.28695	0.000131411
rs9862195	3	89299752	GTEx/v8	Brain Cerebellum	EPHA3	T	3.56632E-05	-0.28695	0.000131411
rs62278166	3	89300779	GTEx/v8	Brain Cerebellum	EPHA3	G	3.56632E-05	-0.28695	0.000131411
rs62278170	3	89302617	GTEx/v8	Brain Cerebellum	EPHA3	T	3.56632E-05	-0.28695	0.000131411
rs28834186	3	89305272	GTEx/v8	Brain Cerebellum	EPHA3	A	3.56632E-05	-0.28695	0.000131411
rs62278171	3	89305928	GTEx/v8	Brain Cerebellum	EPHA3	A	3.56632E-05	-0.28695	0.000131411
rs9863058	3	89322805	GTEx/v8	Pancreas	EPHA3	T	3.69984E-05	0.241311	3.49803E-07
rs6800041	3	89448196	GTEx/v8	Pancreas	EPHA3	C	3.74788E-05	0.228794	3.49803E-07
rs9310120	3	89378413	GTEx/v8	Artery Tibial	EPHA3	C	3.90585E-05	0.11677	7.80657E-07
rs12714734	3	90107488	GTEx/v8	Brain Cerebellum	EPHA3	C	3.96629E-05	-0.310278	0.000131411
rs9877921	3	90108491	GTEx/v8	Brain Cerebellum	EPHA3	T	3.96629E-05	-0.310278	0.000131411
rs9816940	3	90146579	GTEx/v8	Brain Cerebellum	EPHA3	T	3.96629E-05	-0.310278	0.000131411
rs9837548	3	90156142	GTEx/v8	Brain Cerebellum	EPHA3	T	3.96629E-05	-0.310278	0.000131411
rs6551451	3	90156286	GTEx/v8	Artery Tibial	EPHA3	T	4.00647E-05	0.126988	7.80657E-07
rs12152372	3	89500365	GTEx/v8	Artery Tibial	EPHA3	C	4.02235E-05	0.132899	7.80657E-07
rs2881488	3	89500488	GTEx/v8	Artery Tibial	EPHA3	G	4.13729E-05	0.132921	7.80657E-07
rs9846844	3	89379639	GTEx/v8	Artery Tibial	EPHA3	A	4.16688E-05	0.115754	7.80657E-07
rs73154916	3	89803713	GTEx/v8	Artery Tibial	EPHA3	T	4.24218E-05	0.136449	7.80657E-07
rs73139302	3	89508186	GTEx/v8	Artery Tibial	EPHA3	G	4.3432E-05	0.133646	7.80657E-07
rs62278170	3	89302617	GTEx/v8	Artery Tibial	EPHA3	T	4.39208E-05	0.129245	7.80657E-07
rs28834186	3	89305272	GTEx/v8	Artery Tibial	EPHA3	A	4.39208E-05	0.129245	7.80657E-07
rs62278171	3	89305928	GTEx/v8	Artery Tibial	EPHA3	A	4.39208E-05	0.129245	7.80657E-07
rs73139290	3	89505343	GTEx/v8	Artery Tibial	EPHA3	A	4.46616E-05	0.133674	7.80657E-07
rs73139296	3	89505734	GTEx/v8	Artery Tibial	EPHA3	T	4.46616E-05	0.133674	7.80657E-07
rs1157608	3	89506464	GTEx/v8	Artery Tibial	EPHA3	G	4.46616E-05	0.133674	7.80657E-07
rs10470576	3	90154964	GTEx/v8	Artery Tibial	EPHA3	T	4.6124E-05	0.126504	7.80657E-07
rs62278161	3	89291713	GTEx/v8	Artery Tibial	EPHA3	G	4.63024E-05	0.129185	7.80657E-07
rs58858051	3	89291909	GTEx/v8	Artery Tibial	EPHA3	T	4.63024E-05	0.129185	7.80657E-07

rs4857497	3	89294149	GTEx/v8	Artery Tibial	EPHA3	G	4.63024E-05	0.129185	7.80657E-07
rs9847087	3	89297308	GTEx/v8	Artery Tibial	EPHA3	G	4.63024E-05	0.129185	7.80657E-07
rs17026816	3	89297593	GTEx/v8	Artery Tibial	EPHA3	G	4.63024E-05	0.129185	7.80657E-07
rs6786204	3	89298813	GTEx/v8	Artery Tibial	EPHA3	C	4.63024E-05	0.129185	7.80657E-07
rs6773815	3	89299059	GTEx/v8	Artery Tibial	EPHA3	T	4.63024E-05	0.129185	7.80657E-07
rs9862195	3	89299752	GTEx/v8	Artery Tibial	EPHA3	T	4.63024E-05	0.129185	7.80657E-07
rs6419884	3	89279467	GTEx/v8	Artery Tibial	EPHA3	T	4.90317E-05	-0.120956	7.80657E-07
rs9811041	3	89367555	GTEx/v8	Artery Tibial	EPHA3	A	4.97505E-05	0.115675	7.80657E-07
rs9864344	3	90121955	GTEx/v8	Artery Tibial	EPHA3	G	5.13438E-05	0.124283	7.80657E-07
rs9880313	3	89373637	GTEx/v8	Artery Tibial	EPHA3	G	5.25287E-05	0.111212	7.80657E-07
rs6796339	3	89286159	GTEx/v8	Artery Tibial	EPHA3	T	5.25489E-05	0.128922	7.80657E-07
rs2175670	3	89343044	GTEx/v8	Artery Tibial	EPHA3	G	5.32925E-05	0.128139	7.80657E-07
rs62278164	3	89292567	GTEx/v8	Pancreas	EPHA3	C	5.51258E-05	0.241565	3.49803E-07
rs9883541	3	89294657	GTEx/v8	Pancreas	EPHA3	C	5.51258E-05	0.241565	3.49803E-07
rs6800041	3	89448196	GTEx/v8	Artery Tibial	EPHA3	C	5.5413E-05	0.123822	7.80657E-07
rs2137488	3	89308704	GTEx/v8	Pancreas	EPHA3	G	5.58479E-05	0.239656	3.49803E-07
rs9829401	3	89300610	GTEx/v8	Artery Tibial	EPHA3	C	5.604E-05	0.126952	7.80657E-07
rs6768381	3	89358071	GTEx/v8	Brain Cerebellum	EPHA3	C	5.66641E-05	-0.254543	0.000131411
rs13316356	3	89309959	GTEx/v8	Artery Tibial	EPHA3	A	5.8345E-05	0.127116	7.80657E-07
rs62274982	3	89310731	GTEx/v8	Pancreas	EPHA3	A	5.89355E-05	0.238939	3.49803E-07
rs9866618	3	89319577	GTEx/v8	Pancreas	EPHA3	C	5.89355E-05	0.238939	3.49803E-07
rs62274614	3	89159719	GTEx/v8	Lung	CGGBP1	T	5.98457E-05	0.159774	1.81917E-48
rs73153266	3	89720111	GTEx/v8	Artery Tibial	EPHA3	G	5.98562E-05	0.131977	7.80657E-07
rs1912965	3	89518332	GTEx/v8	Artery Tibial	EPHA3	G	6.09446E-05	0.13059	7.80657E-07
rs113141104	3	89519238	GTEx/v8	Artery Tibial	EPHA3	T	6.09446E-05	0.13059	7.80657E-07
rs73139105	3	89519651	GTEx/v8	Artery Tibial	EPHA3	C	6.09446E-05	0.13059	7.80657E-07
rs112297761	3	89521602	GTEx/v8	Artery Tibial	EPHA3	TC	6.09446E-05	0.13059	7.80657E-07
rs73139119	3	89522285	GTEx/v8	Artery Tibial	EPHA3	T	6.09446E-05	0.13059	7.80657E-07
rs73139121	3	89522433	GTEx/v8	Artery Tibial	EPHA3	G	6.09446E-05	0.13059	7.80657E-07
rs73139131	3	89524686	GTEx/v8	Artery Tibial	EPHA3	G	6.09446E-05	0.13059	7.80657E-07
rs11397577	3	90081678	GTEx/v8	Artery Tibial	EPHA3	AT	6.18786E-05	0.12282	7.80657E-07
rs35124509	3	89521693	GTEx/v8	Artery Tibial	EPHA3	C	6.27184E-05	0.115674	7.80657E-07
rs9829401	3	89300610	GTEx/v8	Brain Cerebellum	EPHA3	C	6.43403E-05	-0.278778	0.000131411
rs73153258	3	89715585	GTEx/v8	Artery Tibial	EPHA3	A	6.46822E-05	0.132007	7.80657E-07
rs113288647	3	89720352	GTEx/v8	Artery Tibial	EPHA3	T	6.46822E-05	0.132007	7.80657E-07
rs62278166	3	89300779	GTEx/v8	Artery Tibial	EPHA3	G	6.53018E-05	0.126675	7.80657E-07
rs9848971	3	89279394	GTEx/v8	Pancreas	EPHA3	G	6.80201E-05	0.237246	3.49803E-07
rs62274986	3	89327148	GTEx/v8	Pancreas	EPHA3	A	6.81299E-05	0.236006	3.49803E-07
rs138643396	3	89698092	GTEx/v8	Artery Tibial	EPHA3	CATA	6.83504E-05	0.115926	7.80657E-07
rs9849053	3	90152502	GTEx/v8	Artery Tibial	EPHA3	A	6.87755E-05	0.123791	7.80657E-07
rs6768381	3	89358071	GTEx/v8	Artery Tibial	EPHA3	C	6.90531E-05	0.112763	7.80657E-07
rs73139281	3	89503890	GTEx/v8	Artery Tibial	EPHA3	T	6.91831E-05	0.129367	7.80657E-07
rs73139284	3	89503958	GTEx/v8	Artery Tibial	EPHA3	G	6.91831E-05	0.129367	7.80657E-07
rs7632502	3	89469453	GTEx/v8	Pancreas	EPHA3	A	6.92594E-05	0.197124	3.49803E-07
rs112604674	3	89989681	GTEx/v8	Brain Cerebellum	EPHA3	T	6.99043E-05	-0.338171	0.000131411
rs62278163	3	89291836	GTEx/v8	Pancreas	EPHA3	T	7.08915E-05	0.237296	3.49803E-07
rs6786328	3	89298926	GTEx/v8	Pancreas	EPHA3	G	7.08915E-05	0.237296	3.49803E-07
rs62278168	3	89301573	GTEx/v8	Pancreas	EPHA3	G	7.08915E-05	0.237296	3.49803E-07
rs7637504	3	89702469	GTEx/v8	Artery Tibial	EPHA3	T	7.31685E-05	0.11595	7.80657E-07
rs6551415	3	89705161	GTEx/v8	Artery Tibial	EPHA3	T	7.31685E-05	0.11595	7.80657E-07
rs73139286	3	89504295	GTEx/v8	Artery Tibial	EPHA3	A	7.60748E-05	0.129484	7.80657E-07
rs62274981	3	89310605	GTEx/v8	Pancreas	EPHA3	T	7.6395E-05	0.234437	3.49803E-07
rs17800347	3	89314429	GTEx/v8	Pancreas	EPHA3	G	7.6395E-05	0.234437	3.49803E-07

rs993186	3	89314862	GTEx/v8	Pancreas	EPHA3	G	7.6395E-05	0.234437	3.49803E-07
rs17800551	3	89317315	GTEx/v8	Pancreas	EPHA3	T	7.6395E-05	0.234437	3.49803E-07
rs62274984	3	89318317	GTEx/v8	Pancreas	EPHA3	A	7.6395E-05	0.234437	3.49803E-07
rs7617395	3	89722541	GTEx/v8	Artery Tibial	EPHA3	T	8.13187E-05	0.130073	7.80657E-07
rs7650184	3	89530057	GTEx/v8	Artery Tibial	EPHA3	A	8.18324E-05	0.114079	7.80657E-07
rs73154916	3	89803713	GTEx/v8	Brain Cerebellum	EPHA3	T	8.21604E-05	-0.287448	0.000131411
rs73154925	3	89859312	GTEx/v8	Brain Cerebellum	EPHA3	C	8.21604E-05	-0.287448	0.000131411
rs9832305	3	89392778	GTEx/v8	Pancreas	EPHA3	C	8.51643E-05	0.219124	3.49803E-07
rs4857502	3	89324919	GTEx/v8	Pancreas	EPHA3	A	8.79202E-05	0.231574	3.49803E-07
rs2137487	3	89325520	GTEx/v8	Pancreas	EPHA3	G	8.79202E-05	0.231574	3.49803E-07
rs9875278	3	89335463	GTEx/v8	Pancreas	EPHA3	T	8.79202E-05	0.231574	3.49803E-07
rs9821666	3	89339548	GTEx/v8	Pancreas	EPHA3	T	8.79202E-05	0.231574	3.49803E-07
rs1512908	3	89340134	GTEx/v8	Pancreas	EPHA3	A	8.79202E-05	0.231574	3.49803E-07
rs9852380	3	89341738	GTEx/v8	Pancreas	EPHA3	G	8.79202E-05	0.231574	3.49803E-07
rs9852722	3	89341946	GTEx/v8	Pancreas	EPHA3	C	8.79202E-05	0.231574	3.49803E-07
rs59381722	3	89701482	GTEx/v8	Artery Tibial	EPHA3	G	9.00303E-05	0.113931	7.80657E-07
rs9877833	3	90138312	GTEx/v8	Artery Tibial	EPHA3	A	9.26656E-05	0.124891	7.80657E-07
rs6794975	3	89292824	GTEx/v8	Artery Tibial	EPHA3	A	9.30529E-05	0.123722	7.80657E-07
rs73153262	3	89719269	GTEx/v8	Artery Tibial	EPHA3	T	9.40759E-05	0.128978	7.80657E-07
rs3792572	3	89456555	GTEx/v8	Pancreas	EPHA3	A	9.54529E-05	0.195036	3.49803E-07
rs6806912	3	89751353	GTEx/v8	Artery Tibial	EPHA3	C	9.74849E-05	0.114539	7.80657E-07
rs9862638	3	89373598	GTEx/v8	Brain Cerebellum	EPHA3	C	9.82701E-05	-0.238562	0.000131411
rs7637642	3	90034785	GTEx/v8	Artery Tibial	EPHA3	G	9.98799E-05	0.119569	7.80657E-07
rs6796339	3	89286159	GTEx/v8	Pancreas	EPHA3	T	9.99846E-05	0.227202	3.49803E-07
rs62278161	3	89291713	GTEx/v8	Pancreas	EPHA3	G	9.99846E-05	0.227202	3.49803E-07
rs58858051	3	89291909	GTEx/v8	Pancreas	EPHA3	T	9.99846E-05	0.227202	3.49803E-07
rs4857497	3	89294149	GTEx/v8	Pancreas	EPHA3	G	9.99846E-05	0.227202	3.49803E-07
rs9847087	3	89297308	GTEx/v8	Pancreas	EPHA3	G	9.99846E-05	0.227202	3.49803E-07
rs17026816	3	89297593	GTEx/v8	Pancreas	EPHA3	G	9.99846E-05	0.227202	3.49803E-07
rs6786204	3	89298813	GTEx/v8	Pancreas	EPHA3	C	9.99846E-05	0.227202	3.49803E-07
rs6773815	3	89299059	GTEx/v8	Pancreas	EPHA3	T	9.99846E-05	0.227202	3.49803E-07
rs9862195	3	89299752	GTEx/v8	Pancreas	EPHA3	T	9.99846E-05	0.227202	3.49803E-07
rs7619025	3	89368629	GTEx/v8	Artery Tibial	EPHA3	A	0.000102538	0.110193	7.80657E-07
rs28620812	3	89305668	GTEx/v8	Pancreas	EPHA3	T	0.000103808	0.232001	3.49803E-07
rs62278172	3	89306038	GTEx/v8	Pancreas	EPHA3	A	0.000103808	0.232001	3.49803E-07
rs954964	3	89355632	GTEx/v8	Artery Tibial	EPHA3	G	0.000104111	0.108869	7.80657E-07
rs1398534	3	89329307	GTEx/v8	Pancreas	EPHA3	G	0.000104464	0.229195	3.49803E-07
rs6794975	3	89292824	GTEx/v8	Pancreas	EPHA3	A	0.000105087	0.223728	3.49803E-07
rs4396913	3	90047036	GTEx/v8	Pancreas	EPHA3	C	0.000105226	0.237452	3.49803E-07
rs1464463	3	90056380	GTEx/v8	Pancreas	EPHA3	A	0.000105226	0.237452	3.49803E-07
rs73153252	3	89712192	GTEx/v8	Artery Tibial	EPHA3	T	0.000109319	0.128448	7.80657E-07
rs73151380	3	90000532	GTEx/v8	Artery Tibial	EPHA3	T	0.000111011	0.144157	7.80657E-07
rs13323078	3	89168325	GTEx/v8	Testis	CGGBP1	A	0.000111676	0.139843	4.33153E-08
rs28708984	3	90041154	GTEx/v8	Artery Tibial	EPHA3	G	0.000115862	0.118686	7.80657E-07
rs61039064	3	90044732	GTEx/v8	Artery Tibial	EPHA3	G	0.000115862	0.118686	7.80657E-07
rs35968370	3	89466339	GTEx/v8	Pancreas	EPHA3	T	0.000118817	0.193052	3.49803E-07
rs11921985	3	89467357	GTEx/v8	Pancreas	EPHA3	G	0.000118817	0.193052	3.49803E-07
rs4974358	3	90141506	GTEx/v8	Artery Tibial	EPHA3	G	0.000123858	0.123031	7.80657E-07
rs7653735	3	89722185	GTEx/v8	Artery Tibial	EPHA3	A	0.000124606	0.112649	7.80657E-07
rs11925143	3	89723684	GTEx/v8	Artery Tibial	EPHA3	A	0.000124606	0.112649	7.80657E-07
rs112604674	3	89989681	GTEx/v8	Artery Tibial	EPHA3	T	0.000126338	0.143135	7.80657E-07
rs112149405	3	89886780	GTEx/v8	Artery Tibial	EPHA3	C	0.000132367	0.150956	7.80657E-07
rs9811041	3	89367555	GTEx/v8	Brain Cerebellum	EPHA3	A	0.00013287	-0.24166	0.000131411

rs55787722	3	90012103	GTEx/v8	Brain Cerebellum	EPHA3	T	0.000144208	-0.27232	0.000131411
rs9839323	3	89190113	GTEx/v8	Testis	CGGBP1	A	0.000146528	0.137448	4.33153E-08
rs6776281	3	89290164	GTEx/v8	Pancreas	EPHA3	A	0.000148275	0.221329	3.49803E-07
rs9851954	3	89297904	GTEx/v8	Pancreas	EPHA3	A	0.000148275	0.221329	3.49803E-07
rs9880313	3	89373637	GTEx/v8	Brain Cerebellum	EPHA3	G	0.000150532	-0.230663	0.000131411
rs67316928	3	89482234	GTEx/v8	Pancreas	EPHA3	C	0.000150556	0.194504	3.49803E-07
rs1398531	3	89289709	GTEx/v8	Brain Cerebellum	EPHA3	T	0.000151381	-0.264304	0.000131411
rs13088663	3	89360266	GTEx/v8	Artery Tibial	EPHA3	T	0.000156515	0.105987	7.80657E-07
rs55787722	3	90012103	GTEx/v8	Pancreas	EPHA3	T	0.000158209	0.240878	3.49803E-07
rs12636275	3	89523038	GTEx/v8	Artery Tibial	EPHA3	A	0.000159547	0.109133	7.80657E-07
rs6772953	3	89451721	GTEx/v8	Pancreas	EPHA3	C	0.000161016	0.188937	3.49803E-07
rs62274614	3	89159719	GTEx/v8	Testis	CGGBP1	T	0.000161492	0.13353	4.33153E-08
rs12714734	3	90107488	GTEx/v8	Pancreas	EPHA3	C	0.000165118	0.230208	3.49803E-07
rs9877921	3	90108491	GTEx/v8	Pancreas	EPHA3	T	0.000165118	0.230208	3.49803E-07
rs1512907	3	89355961	GTEx/v8	Brain Cerebellum	EPHA3	C	0.000169535	-0.238335	0.000131411
rs59127701	3	89291916	GTEx/v8	Pancreas	EPHA3	TA	0.000172713	0.239554	3.49803E-07
rs4396913	3	90047036	GTEx/v8	Brain Cerebellum	EPHA3	C	0.000182088	-0.281997	0.000131411
rs1464463	3	90056380	GTEx/v8	Brain Cerebellum	EPHA3	A	0.000182088	-0.281997	0.000131411
rs9866945	3	89349818	GTEx/v8	Brain Cerebellum	EPHA3	C	0.000185539	-0.238202	0.000131411
rs7613412	3	89724217	GTEx/v8	Artery Tibial	EPHA3	T	0.000188152	0.109455	7.80657E-07
rs13076853	3	89382776	GTEx/v8	Artery Tibial	EPHA3	C	0.000197313	0.105664	7.80657E-07
rs872976	3	89326991	GTEx/v8	Artery Tibial	EPHA3	A	0.000215792	-0.103644	7.80657E-07
rs1520594	3	89839468	GTEx/v8	Brain Cerebellum	EPHA3	A	0.000215974	-0.235442	0.000131411
rs9310117	3	89275906	GTEx/v8	Brain Cerebellum	EPHA3	C	0.000216519	0.238833	0.000131411
rs6771336	3	89293015	GTEx/v8	Brain Cerebellum	EPHA3	T	0.000216519	-0.238833	0.000131411
rs62274987	3	89334443	GTEx/v8	Brain Cerebellum	EPHA3	A	0.000221208	-0.23515	0.000131411
rs67316928	3	89482234	GTEx/v8	Artery Tibial	EPHA3	C	0.000251611	0.106047	7.80657E-07
rs59127701	3	89291916	GTEx/v8	Artery Tibial	EPHA3	TA	0.000338775	0.122222	7.80657E-07
rs60759458	3	90045885	GTEx/v8	Artery Tibial	EPHA3	C	0.000353926	0.110068	7.80657E-07
rs1512907	3	89355961	GTEx/v8	Artery Tibial	EPHA3	C	0.000359544	0.101588	7.80657E-07
rs13075167	3	89303172	PsychENCODE	PsychENCODE eQTLs	EPHA3	C	0.000383092	-0.0451166	0.0265128367062786
rs6551410	3	89442305	GTEx/v8	Artery Tibial	EPHA3	A	0.000422515	0.101978	7.80657E-07
rs13064615	3	89799433	PsychENCODE	PsychENCODE eQTLs	EPHA3	G	0.00044599	-0.0417326	0.0300805785656357
rs7619303	3	89552554	GTEx/v8	Thyroid	EPHA3	A	0.000457637	0.10083	0.000440998
rs62274987	3	89334443	GTEx/v8	Artery Tibial	EPHA3	A	0.000463358	0.100651	7.80657E-07
rs55787722	3	90012103	GTEx/v8	Thyroid	EPHA3	T	0.000580418	0.101037	0.000440998
rs4264747	3	89882102	PsychENCODE	PsychENCODE eQTLs	EPHA3	G	0.000646709	-0.0412393	0.0407642701527111
rs6797260	3	89302486	CMC	CMC SVA cis	EPHA3	A		1.0	0.049
rs13075167	3	89303172	CMC	CMC SVA cis	EPHA3	T		1.0	0.049
rs12638746	3	89331055	CMC	CMC SVA cis	EPHA3	G		1.0	0.049
rs2274224	10	96039597	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	2.3506E-168	27.6564	0.0
rs11187838	10	96038686	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	2.7379E-167	27.5675	0.0
rs10786156	10	96014622	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	9.0949E-166	27.4404	0.0
rs57866767	10	96023077	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	5.1534E-165	27.3771	0.0
rs7080472	10	96012950	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	1.1918E-164	27.3464	0.0
rs3891783	10	96015793	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	2.3181E-163	27.2379	0.0
rs2274224	10	96039597	eQTLGen	eQTLGen cis eQTLs	HELLS	C	1.5774E-32	2,5062E+06	0.0

rs11187838	10	96038686	eQTLGen	eQTLGen cis eQTLs	HELLS	A	1.1038E-31	1,9080E+06	0.0
rs7080472	10	96012950	eQTLGen	eQTLGen cis eQTLs	HELLS	T	2.1997E-31	1,6943E+06	0.0
rs10786156	10	96014622	eQTLGen	eQTLGen cis eQTLs	HELLS	G	2.4504E-31	1,6600E+06	0.0
rs2077218	10	96071561	eQTLGen	eQTLGen cis eQTLs	HELLS	G	2.6229E-31	1,6395E+06	0.0
rs3891783	10	96015793	eQTLGen	eQTLGen cis eQTLs	HELLS	G	3.7006E-31	1,5318E+06	0.0
rs57866767	10	96023077	eQTLGen	eQTLGen cis eQTLs	HELLS	C	4.9097E-31	1,4437E+06	0.0
rs11187844	10	96056629	eQTLGen	eQTLGen cis eQTLs	HELLS	A	2.6845E-27	2,3119E+06	0.0
rs2077218	10	96071561	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	3.3973E-27	-10.8011	0.0
rs79193572	10	96119713	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	2.1704E-26	1,6059E+06	0.0
rs74825688	10	96119687	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	2.2801E-26	10.625	0.0
rs113544984	10	96127448	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	2.8489E-26	1,5138E+06	0.0
rs11187906	10	96124838	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	3.4829E-26	1,4448E+06	0.0
rs10509672	10	96115957	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	3.8096E-26	1,4145E+06	0.0
rs7101207	10	96122857	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	4.1845E-26	1,3816E+06	0.0
rs79746649	10	96120218	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	4.2565E-26	1,3761E+06	0.0
rs11187907	10	96125361	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	5.3345E-26	1,2987E+06	0.0
rs11187890	10	96102758	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	5.7346E-26	1,2739E+06	0.0
rs11187897	10	96106603	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	6.6543E-26	1,2231E+06	0.0
rs11187895	10	96106240	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	8.3501E-26	1,1449E+06	0.0
rs12217792	10	96062386	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	2.4075E-25	10.403	0.0
rs112252876	10	96123355	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	2.4689E-25	7,6948E+05	0.0
rs11187883	10	96096866	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	4.22E-25	5,8211E+05	0.0
rs11187882	10	96095861	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	5.1026E-25	5,1600E+05	0.0
rs7096883	10	96069149	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	6.5107E-25	4,2980E+05	0.0
rs11187877	10	96092121	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	9.7611E-25	2,8772E+05	0.0
rs11187870	10	96087866	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	1.0962E-24	2,4681E+05	0.0
rs7100626	10	96069674	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	1.1616E-24	2,2636E+05	0.0
rs11187852	10	96070132	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	1.3016E-24	1,8618E+05	0.0
rs752140	10	96071396	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	1.3016E-24	10.241	0.0
rs75409190	10	96072425	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	1.4196E-24	1,5514E+05	0.0
rs11187864	10	96082506	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	1.4343E-24	1,5222E+05	0.0
rs11187856	10	96076869	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	1.4917E-24	1,3797E+05	0.0
rs11187866	10	96085991	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	1.9264E-24	4,7392E+04	0.0
rs11187863	10	96081457	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	2.1134E-24	1,4154E+04	0.0
rs11187840	10	96050351	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	2.3184E-24	10.185	0.0
rs75017201	10	96055152	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	3.1871E-24	10.1538	0.0
rs11187847	10	96063440	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	3.77E-24	10.1376	0.0
rs11187845	10	96060198	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	4.2536000000000004E-24	10.1258	0.0
rs3781266	10	96052747	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	1.5677E-23	2,9492E+06	0.0
rs3740365	10	96053239	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	2.2898E-23	2,8115E+06	0.0
rs753724	10	96051417	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	2.4225E-23	2,7914E+06	0.0
rs12220091	10	96053689	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	2.4371E-23	2,7889E+06	0.0
rs11187842	10	96052511	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	3.5754E-23	2,6490E+06	0.0

rs7078844	10	96081140	eQTLGen	eQTLGen cis eQTLs	HELLS	T	4.4823E-23	2,5672E+06	0.0
rs3740359	10	96100119	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	6.3939E-22	9.623	0.0
rs3740360	10	96025491	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	1.301E-17	1,2917E+06	0.0
rs17109875	10	96026575	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	2.3589E-17	1,0404E+06	0.0
rs11187837	10	96035980	eQTLGen	eQTLGen cis eQTLs	TBC1D12	C	3.1089E-17	9,2245E+05	0.0
rs3891783	10	96015793	eQTLcatalogue	BLUEPRINTge T-cell	NOC3L	C	8.90201E-17	0.0946773	4.451E-13
rs2274224	10	96039597	eQTLcatalogue	BLUEPRINTge T-cell	NOC3L	G	9.14876E-17	0.0946486	4.57438E-13
rs10786156	10	96014622	eQTLcatalogue	BLUEPRINTge T-cell	NOC3L	C	9.30907E-17	0.0946158	4.65454E-13
rs11187838	10	96038686	eQTLcatalogue	BLUEPRINTge T-cell	NOC3L	G	9.34357E-17	0.094607	4.67178E-13
rs7080472	10	96012950	BIOSQTL	BIOS eQTL geneLevel	NOC3L	T	1.2781E-16	8.2757861	0.0
rs11187838	10	96038686	BIOSQTL	BIOS eQTL geneLevel	NOC3L	A	2.42798E-16	8.1989633	0.0
rs57866767	10	96023077	BIOSQTL	BIOS eQTL geneLevel	NOC3L	C	3.3781E-16	8.1590575	0.0
rs10786156	10	96014622	BIOSQTL	BIOS eQTL geneLevel	NOC3L	G	3.4918E-16	8.1550176	0.0
rs3891783	10	96015793	BIOSQTL	BIOS eQTL geneLevel	NOC3L	G	3.4918E-16	8.1550176	0.0
rs7080472	10	96012950	eQTLcatalogue	BLUEPRINTge T-cell	NOC3L	G	5.68476E-16	0.0922238	2.84238E-12
rs3891783	10	96015793	PsychENCODE	PsychENCODE eQTLs	NOC3L	G	1.55666E-15	0.084497	6.05693225367462E-13
rs7080472	10	96012950	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	2.15698E-15	0.0843385	8.29043545618019E-13
rs7096883	10	96069149	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	2.57371E-15	0.354412	1.28686E-11
rs57866767	10	96023077	PsychENCODE	PsychENCODE eQTLs	NOC3L	C	2.91938E-15	0.0836983	1.10909695717759E-12
rs11187847	10	96063440	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	3.28649E-15	0.347624	1.64325E-11
rs11187842	10	96052511	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	3.77209E-15	0.34516	1.88605E-11
rs3781266	10	96052747	eQTLcatalogue	GEUVADISge LCL	PLCE1	A	3.77209E-15	0.34516	1.88605E-11
rs3740365	10	96053239	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	3.77209E-15	0.34516	1.88605E-11
rs12220091	10	96053689	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	3.77209E-15	0.34516	1.88605E-11
rs11187845	10	96060198	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	4.8482E-15	0.34562	2.4241E-11
rs11187826	10	95988042	eQTLGen	eQTLGen cis eQTLs	HELLS	G	6.9055E-15	2,1778E+06	0.0
rs7100626	10	96069674	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	1.44145E-14	0.356819	7.20725E-11
rs11187852	10	96070132	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	1.44145E-14	0.356819	7.20725E-11
rs11187877	10	96092121	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	1.44145E-14	0.356819	7.20725E-11
rs3740360	10	96025491	eQTLGen	eQTLGen cis eQTLs	HELLS	C	1.6881E-14	1,7625E+06	0.0
rs11187863	10	96081457	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	1.87895E-14	0.336752	9.39475E-11
rs11187866	10	96085991	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	1.87895E-14	0.336752	9.39475E-11
rs11187883	10	96096866	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	1.87895E-14	0.336752	9.39475E-11
rs17109875	10	96026575	eQTLGen	eQTLGen cis eQTLs	HELLS	C	1.9726E-14	1,6898E+06	0.0
rs752140	10	96071396	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	2.1749E-14	0.337652	1.08745E-10
rs769015184	10	96049708	eQTLcatalogue	GEUVADISge LCL	PLCE1	AC	2.76489E-14	0.339981	1.38245E-10
rs11187840	10	96050351	eQTLcatalogue	GEUVADISge LCL	PLCE1	A	2.76489E-14	0.339981	1.38245E-10
rs75017201	10	96055152	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	2.76489E-14	0.339981	1.38245E-10
rs34309017	10	96061619	eQTLcatalogue	GEUVADISge LCL	PLCE1	ACTT	3.52825E-14	0.340472	1.76413E-10
rs12217792	10	96062386	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	3.52825E-14	0.340472	1.76413E-10
rs11187906	10	96124838	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	4.8199E-14	0.36095	2.40995E-10
rs113544984	10	96127448	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	4.8199E-14	0.36095	2.40995E-10
rs75409190	10	96072425	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	5.25935E-14	0.351622	2.62967E-10

rs771106747	10	96072873	eQTLcatalogue	GEUVADISge LCL	PLCE1	CTA	5.25935E-14	0.351622	2.62967E-10
rs749295068	10	96073508	eQTLcatalogue	GEUVADISge LCL	PLCE1	AGAT	5.25935E-14	0.351622	2.62967E-10
rs11187856	10	96076869	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	5.25935E-14	0.351622	2.62967E-10
rs11187864	10	96082506	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	5.25935E-14	0.351622	2.62967E-10
rs11187870	10	96087866	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	5.25935E-14	0.351622	2.62967E-10
rs145707916	10	96092992	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	5.25935E-14	0.351622	2.62967E-10
rs750148755	10	96095271	eQTLcatalogue	GEUVADISge LCL	PLCE1	CATTTT	5.25935E-14	0.351622	2.62967E-10
rs11187882	10	96095861	eQTLcatalogue	GEUVADISge LCL	PLCE1	A	5.25935E-14	0.351622	2.62967E-10
rs10509672	10	96115957	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	5.63913E-14	7.5163545	0.0
rs7078844	10	96081140	eQTLGen	eQTLGen cis eQTLs	TBC1D12	T	6.266E-14	-7.5022	0.0
rs74825688	10	96119687	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	6.33328E-14	7.501064	0.0
rs79193572	10	96119713	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	6.33328E-14	7.501064	0.0
rs79746649	10	96120218	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	6.33328E-14	7.501064	0.0
rs11187890	10	96102758	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	6.3606E-14	0.358744	3.1803E-10
rs11187890	10	96102758	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	6.43065E-14	7.4990833	0.0
rs11187895	10	96106240	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	6.46015E-14	7.4985075	0.0
rs11187897	10	96106603	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	6.46015E-14	7.4985075	0.0
rs7101207	10	96122857	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	6.98985E-14	0.352103	3.49493E-10
rs112252876	10	96123355	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	6.98985E-14	0.352103	3.49493E-10
rs11187838	10	96038686	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	7.16731E-14	0.0800871	2.4E-11
rs113544984	10	96127448	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	9.62128E-14	7.4461691	0.0
rs11187907	10	96125361	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	1.24034E-13	7.41242	0.0
rs79746649	10	96120218	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	1.30501E-13	0.346373	6.52505E-10
rs2274224	10	96039597	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	1.4491E-13	-0.223116	3.86001E-30
rs200197176	10	96055963	eQTLcatalogue	GEUVADISge LCL	PLCE1	C	1.62082E-13	0.325176	8.1041E-10
rs7080472	10	96012950	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	1.67957E-13	-0.226956	3.86001E-30
rs11187826	10	95988042	eQTLcatalogue	GEUVADISge LCL	PLCE1	A	1.90711E-13	0.294603	9.53555E-10
rs11187826	10	95988042	eQTLGen	eQTLGen cis eQTLs	TBC1D12	G	2.0948E-13	5,5791E+05	0.0
rs7101207	10	96122857	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	2.40687E-13	7.3240743	0.0
rs112252876	10	96123355	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	2.40687E-13	7.3240743	0.0
rs2077218	10	96071561	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	2.68338E-13	-7.30937	0.0
rs3740360	10	96025491	eQTLcatalogue	GEUVADISge LCL	PLCE1	A	2.69319E-13	0.304952	1.34659E-09
rs17109875	10	96026575	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	2.69319E-13	0.304952	1.34659E-09
rs11187837	10	96035980	eQTLcatalogue	GEUVADISge LCL	PLCE1	T	2.69319E-13	0.304952	1.34659E-09
rs113544984	10	96127448	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	2.9121E-13	-7.2983	0.0
rs10786156	10	96014622	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	3.41914E-13	-0.220278	3.86001E-30
rs3891783	10	96015793	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	3.41914E-13	-0.220278	3.86001E-30
rs57866767	10	96023077	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	3.41914E-13	-0.220278	3.86001E-30
rs11187895	10	96106240	eQTLcatalogue	GEUVADISge LCL	PLCE1	G	4.57228E-13	0.341015	2.28614E-09
rs11187897	10	96106603	eQTLcatalogue	GEUVADISge LCL	PLCE1	A	4.57228E-13	0.341015	2.28614E-09

rs778275808	10	96114212	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	TCTC	4.57228E-13	0.341015	2.28614E-09
rs10509672	10	96115957	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	G	4.57228E-13	0.341015	2.28614E-09
rs79193572	10	96119713	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	A	4.57228E-13	0.341015	2.28614E-09
rs11187837	10	96035980	eQTLGen	eQTLGen cis eQTLs	HELLS	C	6.3849E-13	7,8530E+03	0.0
rs3740359	10	96100119	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	1.0708E-12	-0.356669	3.86001E-30
rs11187907	10	96125361	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	1.0715E-12	-7.121	0.0
rs11187890	10	96102758	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	T	1.08793E-12	0.300083	5.43965E-09
rs778275808	10	96114212	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	TCTC	1.08984E-12	0.300056	5.4492E-09
rs11187895	10	96106240	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.09049E-12	0.300052	5.45245E-09
rs11187897	10	96106603	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	A	1.09049E-12	0.300052	5.45245E-09
rs10509672	10	96115957	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.09049E-12	0.300052	5.45245E-09
rs74825688	10	96119687	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.09049E-12	0.300052	5.45245E-09
rs79193572	10	96119713	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	A	1.09049E-12	0.300052	5.45245E-09
rs11187863	10	96081457	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	1.47096E-12	7.0772858	0.0
rs11187864	10	96082506	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	1.47096E-12	7.0772858	0.0
rs11187866	10	96085991	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	1.47096E-12	7.0772858	0.0
rs11187870	10	96087866	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	1.47096E-12	7.0772858	0.0
rs11187877	10	96092121	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	1.47096E-12	7.0772858	0.0
rs11187895	10	96106240	eQTLGen	eQTLGen cis eQTLs	PDLIM1	C	1.6108E-12	-7.0644	0.0
rs7100626	10	96069674	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	1.61777E-12	7.0640675	0.0
rs11187852	10	96070132	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	1.61777E-12	7.0640675	0.0
rs752140	10	96071396	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	1.61777E-12	7.0640675	0.0
rs75409190	10	96072425	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	1.62477E-12	7.0635281	0.0
rs11187856	10	96076869	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	1.62477E-12	7.0635281	0.0
rs11187882	10	96095861	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	1.63181E-12	7.0629935	0.0
rs11187883	10	96096866	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	1.63181E-12	7.0629935	0.0
rs11187906	10	96124838	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	1.665E-12	-7.06	0.0
rs7080472	10	96012950	GTEx/v8	Adrenal Gland	NOC3L	T	1.68803E-12	0.425729	2.32596E-10
rs79193572	10	96119713	eQTLGen	eQTLGen cis eQTLs	PDLIM1	G	1.8573E-12	-7.0447	0.0
rs11187838	10	96038686	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	1.92734E-12	-0.211574	3.86001E-30
rs11187897	10	96106603	eQTLGen	eQTLGen cis eQTLs	PDLIM1	G	2.0772E-12	-7.029	0.0
rs74825688	10	96119687	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	G	2.11766E-12	0.329638	1.05883E-08
rs10509672	10	96115957	eQTLGen	eQTLGen cis eQTLs	PDLIM1	C	2.2603E-12	-7.0174	0.0
rs74825688	10	96119687	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	2.2831E-12	-7.0159	0.0
rs11187870	10	96087866	eQTLGen	eQTLGen cis eQTLs	PDLIM1	C	2.5706E-12	-6.9993	0.0
rs11187890	10	96102758	eQTLGen	eQTLGen cis eQTLs	PDLIM1	C	2.6602E-12	-6.9945	0.0
rs11187864	10	96082506	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	2.83248E-12	0.986452	1.20882E-07
rs11187870	10	96087866	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	2.83248E-12	0.986452	1.20882E-07

rs11187877	10	96092121	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	2.83248E-12	0.986452	1.20882E-07
rs145707916	10	96092992	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	GA	2.83248E-12	0.986452	1.20882E-07
rs750148755	10	96095271	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	2.83248E-12	0.986452	1.20882E-07
rs11187882	10	96095861	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	2.83248E-12	0.986452	1.20882E-07
rs11187890	10	96102758	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	2.83248E-12	0.986452	1.20882E-07
rs11187895	10	96106240	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	2.83248E-12	0.986452	1.20882E-07
rs11187897	10	96106603	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	2.83248E-12	0.986452	1.20882E-07
rs778275808	10	96114212	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	2.83248E-12	0.986452	1.20882E-07
rs10509672	10	96115957	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	2.83248E-12	0.986452	1.20882E-07
rs79193572	10	96119713	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	2.83248E-12	0.986452	1.20882E-07
rs79746649	10	96120218	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	2.83248E-12	0.986452	1.20882E-07
rs3891783	10	96015793	GTEx/v8	Adrenal Gland	NOC3L	G	3.25993E-12	0.407875	2.32596E-10
rs57866767	10	96023077	GTEx/v8	Adrenal Gland	NOC3L	C	3.25993E-12	0.407875	2.32596E-10
rs10786156	10	96014622	GTEx/v8	Adrenal Gland	NOC3L	G	3.32979E-12	0.40716	2.32596E-10
rs2274224	10	96039597	GTEx/v8	Adrenal Gland	NOC3L	C	3.32979E-12	0.40716	2.32596E-10
rs112252876	10	96123355	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	3.4221E-12	-6.959	0.0
rs11187864	10	96082506	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	3.6788E-12	-6.9489	0.0
rs11187883	10	96096866	eQTLGen	eQTLGen cis eQTLs	HELLS	C	4.6392E-12	2,6533E+06	0.0
rs11187844	10	96056629	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	C	4.66285E-12	0.245293	2.33142E-08
rs3740359	10	96100119	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	4.9781E-12	-6.9062	0.0
rs11187840	10	96050351	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	5.02742E-12	6.9048625	0.0
rs753724	10	96051417	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	5.02742E-12	6.9048625	0.0
rs3740365	10	96053239	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	5.02742E-12	6.9048625	0.0
rs12220091	10	96053689	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	5.02742E-12	6.9048625	0.0
rs75017201	10	96055152	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	5.02742E-12	6.9048625	0.0
rs11187863	10	96081457	eQTLGen	eQTLGen cis eQTLs	HELLS	G	5.4474E-12	2,5696E+06	0.0
rs11187907	10	96125361	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	5.7302E-12	2,5433E+06	0.0
rs11187840	10	96050351	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	5.80787E-12	0.9539	1.20882E-07
rs75017201	10	96055152	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	5.80787E-12	0.9539	1.20882E-07
rs11187877	10	96092121	eQTLGen	eQTLGen cis eQTLs	HELLS	A	5.935E-12	2,5251E+06	0.0
rs79746649	10	96120218	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	5.9769E-12	-6.8802	0.0
rs7101207	10	96122857	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	6.0614E-12	2,5141E+06	0.0
rs7101207	10	96122857	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	6.1643E-12	-6.8757	0.0
rs11187906	10	96124838	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	6.2602E-12	2,4970E+06	0.0
rs11187882	10	96095861	eQTLGen	eQTLGen cis eQTLs	HELLS	C	6.3397E-12	2,4907E+06	0.0
rs113544984	10	96127448	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	6.5108E-12	2,4769E+06	0.0
rs10509672	10	96115957	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	6.70783E-12	0.133806	3.35392E-08

rs74825688	10	96119687	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	6.70783E-12	0.133806	3.35392E-08
rs79193572	10	96119713	eQTLcatalogue	TwinsUK ge LCL	PLCE1	A	6.70783E-12	0.133806	3.35392E-08
rs79746649	10	96120218	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	6.70783E-12	0.133806	3.35392E-08
rs2274224	10	96039597	GTEx/v8	Lung	NOC3L	C	6.8562E-12	0.169146	6.99161E-23
rs3891783	10	96015793	GTEx/v8	Lung	NOC3L	G	7.03959E-12	0.169026	6.99161E-23
rs57866767	10	96023077	GTEx/v8	Lung	NOC3L	C	7.03959E-12	0.169026	6.99161E-23
rs3781266	10	96052747	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	7.04201E-12	6.8569227	0.0
rs11187842	10	96052511	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	7.48896E-12	6.8481774	0.0
rs10786156	10	96014622	GTEx/v8	Lung	NOC3L	G	7.60516E-12	0.168552	6.99161E-23
rs11187845	10	96060198	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	7.6979E-12	-0.362676	3.86001E-30
rs11187847	10	96063440	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	7.6979E-12	-0.362676	3.86001E-30
rs11187838	10	96038686	GTEx/v8	Adrenal Gland	NOC3L	A	8.06874E-12	0.400858	2.32596E-10
rs11187845	10	96060198	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	8.41476E-12	0.271954	4.20738E-08
rs12217792	10	96062386	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	T	8.41476E-12	0.271954	4.20738E-08
rs11187847	10	96063440	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	8.41476E-12	0.271954	4.20738E-08
rs7096883	10	96069149	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	8.41476E-12	0.271954	4.20738E-08
rs11187866	10	96085991	eQTLGen	eQTLGen cis eQTLs	HELLS	G	8.6951E-12	2,3260E+06	0.0
rs3740359	10	96100119	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	8.87869E-12	6.8237607	0.0
rs11187856	10	96076869	eQTLGen	eQTLGen cis eQTLs	HELLS	A	9.335E-12	2,2880E+06	0.0
10:96112261_AAAAAAAC_A	10	96112261	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	AAAAAAAC	1.01771E-11	0.313995	5.08855E-08
rs112252876	10	96123355	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	1.0741E-11	2,2146E+06	0.0
rs11187852	10	96070132	eQTLGen	eQTLGen cis eQTLs	HELLS	A	1.0892E-11	2,2077E+06	0.0
rs11187847	10	96063440	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	1.13699E-11	6.7880264	0.0
rs7096883	10	96069149	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	1.13699E-11	6.7880264	0.0
rs75409190	10	96072425	eQTLGen	eQTLGen cis eQTLs	HELLS	T	1.137E-11	2,1847E+06	0.0
rs11187856	10	96076869	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.17547E-11	0.273524	5.87735E-08
rs7100626	10	96069674	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.18126E-11	0.273463	5.9063E-08
rs11187852	10	96070132	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.18329E-11	0.273449	5.91645E-08
rs752140	10	96071396	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.18329E-11	0.273449	5.91645E-08
rs75409190	10	96072425	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.18329E-11	0.273449	5.91645E-08
rs771106747	10	96072873	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	CTA	1.18329E-11	0.273449	5.91645E-08
rs749295068	10	96073508	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	AGAT	1.18329E-11	0.273449	5.91645E-08
rs11187863	10	96081457	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	T	1.18329E-11	0.273449	5.91645E-08
rs11187864	10	96082506	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.18329E-11	0.273449	5.91645E-08
rs11187866	10	96085991	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.18329E-11	0.273449	5.91645E-08
rs11187870	10	96087866	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.18329E-11	0.273449	5.91645E-08

rs11187877	10	96092121	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.18329E-11	0.273449	5.91645E-08
rs11187882	10	96095861	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	A	1.18329E-11	0.273449	5.91645E-08
rs34309017	10	96061619	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.21124E-11	0.952596	1.20882E-07
rs12217792	10	96062386	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	1.21124E-11	0.952596	1.20882E-07
rs7096883	10	96069149	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.21124E-11	0.952596	1.20882E-07
rs11187877	10	96092121	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	1.2458E-11	-6.7748	0.0
rs12217792	10	96062386	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	1.25097E-11	6.7742715	0.0
rs7100626	10	96069674	eQTLGen	eQTLGen cis eQTLs	HELLS	A	1.2807E-11	2,1218E+06	0.0
rs11187906	10	96124838	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	T	1.28242E-11	0.291148	6.4121E-08
rs11187907	10	96125361	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.28242E-11	0.291148	6.4121E-08
rs113544984	10	96127448	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.28242E-11	0.291148	6.4121E-08
rs7101207	10	96122857	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.29283E-11	0.291223	6.46415E-08
rs7100626	10	96069674	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.346E-11	0.959887	1.20882E-07
rs11187852	10	96070132	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.346E-11	0.959887	1.20882E-07
rs75409190	10	96072425	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	1.346E-11	0.959887	1.20882E-07
rs771106747	10	96072873	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	1.346E-11	0.959887	1.20882E-07
rs749295068	10	96073508	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.346E-11	0.959887	1.20882E-07
rs11187856	10	96076869	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.346E-11	0.959887	1.20882E-07
rs752140	10	96071396	eQTLGen	eQTLGen cis eQTLs	HELLS	T	1.4723E-11	2,0484E+06	0.0
rs74825688	10	96119687	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.50065E-11	0.937552	1.20882E-07
rs11187845	10	96060198	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	1.5135E-11	6.7467696	0.0
rs11187856	10	96076869	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	1.9462E-11	-6.71	0.0
rs3740359	10	96100119	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	1.9489E-11	1,8990E+06	0.0
rs7100626	10	96069674	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.02485E-11	0.128196	1.01243E-07
rs11187852	10	96070132	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	2.02485E-11	0.128196	1.01243E-07
rs752140	10	96071396	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.02485E-11	0.128196	1.01243E-07
rs75409190	10	96072425	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.02485E-11	0.128196	1.01243E-07
rs11187856	10	96076869	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	2.02485E-11	0.128196	1.01243E-07
rs11187863	10	96081457	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	2.02485E-11	0.128196	1.01243E-07
rs11187864	10	96082506	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.02485E-11	0.128196	1.01243E-07
rs11187866	10	96085991	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.02485E-11	0.128196	1.01243E-07
rs11187870	10	96087866	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	2.02485E-11	0.128196	1.01243E-07
rs11187877	10	96092121	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	2.02485E-11	0.128196	1.01243E-07
rs11187882	10	96095861	eQTLcatalogue	TwinsUK ge LCL	PLCE1	A	2.02485E-11	0.128196	1.01243E-07
rs11187883	10	96096866	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	2.02485E-11	0.128196	1.01243E-07

rs7101207	10	96122857	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	2.19128E-11	0.133521	1.09564E-07
rs112252876	10	96123355	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.19128E-11	0.133521	1.09564E-07
rs11187906	10	96124838	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	2.19128E-11	0.133521	1.09564E-07
rs11187907	10	96125361	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.19128E-11	0.133521	1.09564E-07
rs113544984	10	96127448	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.19128E-11	0.133521	1.09564E-07
rs75409190	10	96072425	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	2.2135E-11	-6.6911	0.0
rs11187890	10	96102758	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	2.49173E-11	0.128949	1.24586E-07
rs11187895	10	96106240	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	2.49173E-11	0.128949	1.24586E-07
rs11187897	10	96106603	eQTLcatalogue	TwinsUK ge LCL	PLCE1	A	2.49173E-11	0.128949	1.24586E-07
rs11187882	10	96095861	eQTLGen	eQTLGen cis eQTLs	PDLIM1	C	2.496E-11	-6.6734	0.0
rs7100626	10	96069674	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	2.5234E-11	-6.6719	0.0
rs11187863	10	96081457	eQTLGen	eQTLGen cis eQTLs	PDLIM1	G	3.0736E-11	-6.6429	0.0
rs11187907	10	96125361	eQTLGen	eQTLGen cis eQTLs	HELLS	T	3.4491E-11	1,5930E+06	0.0
rs113544984	10	96127448	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	3.47759E-11	0.940054	1.20882E-07
rs11187883	10	96096866	eQTLGen	eQTLGen cis eQTLs	PDLIM1	C	3.7055E-11	-6.6153	0.0
rs7101207	10	96122857	eQTLGen	eQTLGen cis eQTLs	HELLS	A	4.0021E-11	1,5126E+06	0.0
rs7080472	10	96012950	GTEx/v8	Lung	NOC3L	T	4.03452E-11	0.165385	6.99161E-23
rs11187852	10	96070132	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	4.3687E-11	-6.5909	0.0
rs2077218	10	96071561	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	5.1754E-11	-6.5657	0.0
rs74825688	10	96119687	eQTLGen	eQTLGen cis eQTLs	HELLS	A	5.352E-11	1,3548E+06	0.0
rs7101207	10	96122857	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	5.68167E-11	0.931326	1.20882E-07
rs112252876	10	96123355	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	5.68167E-11	0.931326	1.20882E-07
rs11187838	10	96038686	GTEx/v8	Lung	NOC3L	A	5.94459E-11	0.161642	6.99161E-23
rs752140	10	96071396	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	5.9975E-11	-6.5437	0.0
rs112252876	10	96123355	eQTLGen	eQTLGen cis eQTLs	HELLS	T	6.0216E-11	1,2909E+06	0.0
rs11187906	10	96124838	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	6.20974E-11	6.5386326	0.0
rs11187906	10	96124838	eQTLGen	eQTLGen cis eQTLs	HELLS	A	6.7279E-11	1,2299E+06	0.0
rs10509672	10	96115957	eQTLGen	eQTLGen cis eQTLs	HELLS	C	6.8274E-11	1,2219E+06	0.0
rs753724	10	96051417	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	6.9572E-11	-0.339785	3.86001E-30
rs11187842	10	96052511	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	6.9572E-11	-0.339785	3.86001E-30
rs3781266	10	96052747	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	6.9572E-11	-0.339785	3.86001E-30
rs3740365	10	96053239	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	6.9572E-11	-0.339785	3.86001E-30
rs12220091	10	96053689	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	6.9572E-11	-0.339785	3.86001E-30
rs11187866	10	96085991	eQTLGen	eQTLGen cis eQTLs	PDLIM1	G	7.5051E-11	-6.5102	0.0
rs3740359	10	96100119	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	C	7.60307E-11	0.257729	3.80154E-07
rs79746649	10	96120218	eQTLGen	eQTLGen cis eQTLs	HELLS	T	7.9576E-11	1,1379E+06	0.0
rs11187895	10	96106240	eQTLGen	eQTLGen cis eQTLs	HELLS	C	8.2265E-11	1,1193E+06	0.0
rs79193572	10	96119713	eQTLGen	eQTLGen cis eQTLs	HELLS	G	8.493E-11	1,1021E+06	0.0
rs11187897	10	96106603	eQTLGen	eQTLGen cis eQTLs	HELLS	G	8.5609E-11	1,0973E+06	0.0

rs753724	10	96051417	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	9.1525E-11	0.86599	1.20882E-07
rs11187842	10	96052511	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	9.1525E-11	0.86599	1.20882E-07
rs3781266	10	96052747	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	9.1525E-11	0.86599	1.20882E-07
rs3740365	10	96053239	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	9.1525E-11	0.86599	1.20882E-07
rs12220091	10	96053689	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	9.1525E-11	0.86599	1.20882E-07
rs11187890	10	96102758	eQTLGen	eQTLGen cis eQTLs	HELLS	C	9.4938E-11	1,0407E+06	0.0
rs3740359	10	96100119	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	1.0089E-10	0.121466	5.0445E-07
rs11187907	10	96125361	eQTLcatalogue	GEUVADIS ge LCL	PLCE1	C	1.20612E-10	0.293466	6.0306E-07
rs11187907	10	96125361	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	1.25898E-10	0.900331	1.20882E-07
rs3740359	10	96100119	eQTLGen	eQTLGen cis eQTLs	HELLS	T	1.3681E-10	8,3839E+05	0.0
rs79746649	10	96120218	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	1.425E-10	8,1611E+05	0.0
rs12220091	10	96053689	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.65134E-10	0.240279	8.2567E-07
rs769015184	10	96049708	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	AC	1.65229E-10	0.240282	8.26145E-07
rs753724	10	96051417	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.65229E-10	0.240282	8.26145E-07
rs11187842	10	96052511	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.65229E-10	0.240282	8.26145E-07
rs3781266	10	96052747	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	A	1.65229E-10	0.240282	8.26145E-07
rs3740365	10	96053239	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	T	1.65229E-10	0.240282	8.26145E-07
rs75017201	10	96055152	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	1.65229E-10	0.240282	8.26145E-07
rs11187845	10	96060198	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	A	1.82938E-10	0.86298	1.20882E-07
rs11187847	10	96063440	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	1.82938E-10	0.86298	1.20882E-07
rs74825688	10	96119687	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	1.8829E-10	6,5978E+05	0.0
rs7080472	10	96012950	GTEx/v8	Skin Sun Exposed Lower leg	NOC3L	T	2.07651E-10	0.149208	4.18218E-20
rs113544984	10	96127448	eQTLGen	eQTLGen cis eQTLs	HELLS	A	2.0897E-10	6,0207E+05	0.0
rs10509672	10	96115957	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	2.1531E-10	5,8491E+05	0.0
rs11187864	10	96082506	eQTLGen	eQTLGen cis eQTLs	HELLS	T	2.8671E-10	6.306	0.0
rs79193572	10	96119713	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	2.8782E-10	4,2128E+05	0.0
rs3740360	10	96025491	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	3.29122E-10	6.2844446	0.0
rs752140	10	96071396	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	3.39376E-10	-0.338477	3.86001E-30
rs11187837	10	96035980	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	4.05749E-10	6.2518755	0.0
rs11187895	10	96106240	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	4.1574E-10	2,1236E+05	0.0
rs2274224	10	96039597	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	4.18698E-10	0.135701	2.09349E-06
rs3891783	10	96015793	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	4.20614E-10	0.135685	2.10307E-06
rs10786156	10	96014622	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	C	4.21663E-10	0.135662	2.10832E-06

rs11187838	10	96038686	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	4.23274E-10	0.135644	2.11637E-06
rs17109875	10	96026575	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	C	5.44194E-10	6.2059539	0.0
rs11187863	10	96081457	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	5.69704E-10	-0.333231	3.86001E-30
rs11187866	10	96085991	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	5.69704E-10	-0.333231	3.86001E-30
rs11187883	10	96096866	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	5.69704E-10	-0.333231	3.86001E-30
rs34309017	10	96061619	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	6.42319E-10	-0.337731	3.86001E-30
rs12217792	10	96062386	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	6.42319E-10	-0.337731	3.86001E-30
rs11187890	10	96102758	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	7.6705E-10	6.1517	1.316E-05
rs75409190	10	96072425	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	8.07901E-10	-0.344158	3.86001E-30
rs771106747	10	96072873	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	8.07901E-10	-0.344158	3.86001E-30
rs749295068	10	96073508	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	8.07901E-10	-0.344158	3.86001E-30
rs11187856	10	96076869	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	8.07901E-10	-0.344158	3.86001E-30
rs11187863	10	96081457	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	1.09697E-09	0.828697	1.20882E-07
rs11187866	10	96085991	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	1.09697E-09	0.828697	1.20882E-07
rs11187883	10	96096866	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	1.09697E-09	0.828697	1.20882E-07
rs7096883	10	96069149	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	1.15214E-09	-0.331235	3.86001E-30
rs7096883	10	96069149	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	1.16776E-09	0.112521	5.8388E-06
rs7080472	10	96012950	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	G	1.24509E-09	0.131762	6.22545E-06
rs11187870	10	96087866	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	1.34499E-09	-0.342164	3.86001E-30
rs11187897	10	96106603	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	1.3646E-09	6.0596	1.3094E-05
rs3891783	10	96015793	GTEx/v8	Skin Sun Exposed Lower leg	NOC3L	G	1.41912E-09	0.141003	4.18218E-20
rs57866767	10	96023077	GTEx/v8	Skin Sun Exposed Lower leg	NOC3L	C	1.41912E-09	0.141003	4.18218E-20
rs7100626	10	96069674	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	1.47359E-09	-0.337229	3.86001E-30
rs11187852	10	96070132	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	1.47359E-09	-0.337229	3.86001E-30
rs11187882	10	96095861	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	1.4751E-09	-0.337177	3.86001E-30
rs74825688	10	96119687	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	1.4816E-09	-0.33994	3.86001E-30
rs10786156	10	96014622	GTEx/v8	Nerve Tibial	NOC3L	G	1.48976E-09	0.168244	1.32457E-19
rs752140	10	96071396	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	1.5184E-09	6.0425	1.3080E-05
rs79193572	10	96119713	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	1.55958E-09	-0.341493	3.86001E-30
rs10786156	10	96014622	GTEx/v8	Skin Sun Exposed Lower leg	NOC3L	G	1.65539E-09	0.140345	4.18218E-20
rs2274224	10	96039597	GTEx/v8	Nerve Tibial	NOC3L	C	1.95095E-09	0.166488	1.32457E-19
rs12217792	10	96062386	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	2.09527E-09	0.108906	1.04764E-05

rs11187847	10	96063440	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.09527E-09	0.108906	1.04764E-05
rs3891783	10	96015793	GTEx/v8	Nerve Tibial	NOC3L	G	2.42323E-09	0.166243	1.32457E-19
rs57866767	10	96023077	GTEx/v8	Nerve Tibial	NOC3L	C	2.42323E-09	0.166243	1.32457E-19
rs7100626	10	96069674	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	2.5503E-09	2,8063E+06	2.603E-05
rs11187852	10	96070132	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	2.6071E-09	2,7931E+06	2.602E-05
rs11187864	10	96082506	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	2.65113E-09	-0.330345	3.86001E-30
rs11187877	10	96092121	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	2.65113E-09	-0.330345	3.86001E-30
rs145707916	10	96092992	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	GA	2.65113E-09	-0.330345	3.86001E-30
rs750148755	10	96095271	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	2.65113E-09	-0.330345	3.86001E-30
rs778275808	10	96114212	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	2.75585E-09	-0.334894	3.86001E-30
rs10509672	10	96115957	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	2.75585E-09	-0.334894	3.86001E-30
rs79746649	10	96120218	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	2.75585E-09	-0.334894	3.86001E-30
rs2274224	10	96039597	GTEx/v8	Skin Sun Exposed Lower leg	NOC3L	C	2.84729E-09	0.13795	4.18218E-20
rs11187890	10	96102758	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	2.86262E-09	-0.331106	3.86001E-30
rs11187895	10	96106240	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	2.86262E-09	-0.331106	3.86001E-30
rs11187897	10	96106603	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	2.86262E-09	-0.331106	3.86001E-30
rs11187863	10	96081457	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	2.8642E-09	2,7373E+06	2.6E-05
rs11187866	10	96085991	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	2.8993E-09	2,7292E+06	2.6E-05
rs7101207	10	96122857	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	3.28002E-09	-0.335045	3.86001E-30
rs112252876	10	96123355	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	3.28002E-09	-0.335045	3.86001E-30
rs113544984	10	96127448	eQTLcatalogue	GENCORDge LCL	PLCE1	C	3.28253E-09	0.293762	1.64127E-05
rs11187826	10	95988042	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	G	3.39212E-09	5.9115847	6.013E-06
rs752140	10	96071396	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	3.75953E-09	0.803891	1.20882E-07
rs112252876	10	96123355	eQTLcatalogue	GENCORDge LCL	PLCE1	C	3.84298E-09	0.287768	1.92149E-05
rs7101207	10	96122857	eQTLcatalogue	GENCORDge LCL	PLCE1	G	3.89754E-09	0.28761	1.94877E-05
rs11187907	10	96125361	eQTLcatalogue	GENCORDge LCL	PLCE1	C	4.00496E-09	0.287654	2.00248E-05
rs11187906	10	96124838	eQTLcatalogue	GENCORDge LCL	PLCE1	T	4.02821E-09	0.287628	2.0141E-05
rs11187883	10	96096866	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	4.379E-09	2,4812E+06	3.237E-05
rs11187840	10	96050351	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	4.40204E-09	-0.315138	3.86001E-30
rs75017201	10	96055152	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	4.40204E-09	-0.315138	3.86001E-30
rs113544984	10	96127448	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	A	4.55401E-09	-0.335199	3.86001E-30
rs11187838	10	96038686	GTEx/v8	Skin Sun Exposed Lower leg	NOC3L	A	4.67744E-09	0.136601	4.18218E-20
rs75409190	10	96072425	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	5.0293E-09	2,3976E+06	3.233E-05
rs11187844	10	96056629	eQTLGen	eQTLGen cis eQTLs	TBC1D12	A	5.8637E-09	2,3041E+06	4.520E-05
rs11187856	10	96076869	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	6.4366E-09	2,2467E+06	4.517E-05

rs11187877	10	96092121	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	7.0975E-09	2,1872E+06	4.514E-05
rs7096883	10	96069149	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	8.6744E-09	2,0634E+06	5.795E-05
rs3740360	10	96025491	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	9.05253E-09	0.798488	1.20882E-07
rs17109875	10	96026575	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	9.05253E-09	0.798488	1.20882E-07
rs11187837	10	96035980	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	C	9.05253E-09	0.798488	1.20882E-07
rs11187847	10	96063440	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	9.8903E-09	1,9823E+06	5.787E-05
rs12217792	10	96062386	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	1.0186E-08	1,9644E+06	5.786E-05
rs11187844	10	96056629	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	1.04815E-08	0.235889	5.24075E-05
rs11187882	10	96095861	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	1.0753E-08	1,9308E+06	5.782E-05
rs11187870	10	96087866	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	1.1675E-08	1,8789E+06	6.421E-05
rs12217792	10	96062386	eQTLGen	eQTLGen cis eQTLs	HELLS	C	1.1758E-08	1,8749E+06	6.420E-05
rs7096883	10	96069149	eQTLGen	eQTLGen cis eQTLs	HELLS	A	1.1953E-08	1,8651E+06	6.418E-05
rs3740359	10	96100119	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	1.21116E-08	0.272238	6.0558E-05
rs7080472	10	96012950	GTEx/v8	Nerve Tibial	NOC3L	T	1.27639E-08	0.159332	1.32457E-19
rs11187842	10	96052511	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	1.39637E-08	0.264935	6.98185E-05
rs3781266	10	96052747	eQTLcatalogue	GENCORD ge LCL	PLCE1	A	1.40013E-08	0.264926	7.00065E-05
rs3740365	10	96053239	eQTLcatalogue	GENCORD ge LCL	PLCE1	T	1.41153E-08	0.2649	7.05765E-05
rs12220091	10	96053689	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	1.41728E-08	0.264887	7.0864E-05
rs75017201	10	96055152	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	1.45863E-08	0.264791	7.29315E-05
rs11187838	10	96038686	GTEx/v8	Nerve Tibial	NOC3L	A	1.48555E-08	0.158012	1.32457E-19
rs11187845	10	96060198	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	1.512E-08	1,7182E+06	7.684E-05
rs3740365	10	96053239	eQTLGen	eQTLGen cis eQTLs	HELLS	A	1.6441E-08	1,6653E+06	8.958E-05
rs753724	10	96051417	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	1.69177E-08	0.264207	8.45885E-05
rs11187840	10	96050351	eQTLGen	eQTLGen cis eQTLs	HELLS	G	1.7486E-08	1,6269E+06	9.593E-05
rs753724	10	96051417	eQTLGen	eQTLGen cis eQTLs	HELLS	T	1.7567E-08	1,6240E+06	9.591E-05
rs75017201	10	96055152	eQTLGen	eQTLGen cis eQTLs	HELLS	T	1.977E-08	1,5491E+06	1.085E-4
rs752140	10	96071396	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	1.9801E-08	0.0969569	3.523E-06
rs752140	10	96071396	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	1.98151E-08	0.269571	9.90755E-05
rs11187847	10	96063440	eQTLGen	eQTLGen cis eQTLs	HELLS	G	2.0093E-08	1,5389E+06	1.085E-4
rs11187856	10	96076869	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.01876E-08	0.269417	0.000100938
rs11187845	10	96060198	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	2.02127E-08	0.0997346	0.000101063
rs749295068	10	96073508	eQTLcatalogue	GENCORD ge LCL	PLCE1	AGAT	2.02287E-08	0.269401	0.000101144
rs11187863	10	96081457	eQTLcatalogue	GENCORD ge LCL	PLCE1	T	2.02492E-08	0.269347	0.000101246
rs11187864	10	96082506	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	2.02492E-08	0.269347	0.000101246
rs11187866	10	96085991	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	2.02492E-08	0.269347	0.000101246
rs11187870	10	96087866	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.02492E-08	0.269347	0.000101246
rs11187877	10	96092121	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.02492E-08	0.269347	0.000101246
rs145707916	10	96092992	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.02492E-08	0.269347	0.000101246
rs12217792	10	96062386	eQTLGen	eQTLGen cis eQTLs	PDLIM1	C	2.0256E-08	-5.6096	0.0001085152559683
rs75409190	10	96072425	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	2.02982E-08	0.269356	0.000101491
rs7100626	10	96069674	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	2.03023E-08	0.269338	0.000101511
rs11187852	10	96070132	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.03023E-08	0.269338	0.000101511

rs771106747	10	96072873	eQTLcatalogue	GENCORD ge LCL	PLCE1	CTA	2.03044E-08	0.269369	0.000101522
rs750148755	10	96095271	eQTLcatalogue	GENCORD ge LCL	PLCE1	CATTTT	2.04426E-08	0.269275	0.000102213
rs79746649	10	96120218	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	2.04781E-08	0.268979	0.00010239
rs11187842	10	96052511	eQTLGen	eQTLGen cis eQTLs	HELLS	T	2.0539E-08	1,5246E+06	0.0001085014041358
rs11187882	10	96095861	eQTLcatalogue	GENCORD ge LCL	PLCE1	A	2.05663E-08	0.269242	0.000102831
rs11187890	10	96102758	eQTLcatalogue	GENCORD ge LCL	PLCE1	T	2.06772E-08	0.269218	0.000103386
rs11187895	10	96106240	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.12925E-08	0.268952	0.000106463
rs11187883	10	96096866	eQTLcatalogue	GENCORD ge LCL	PLCE1	T	2.12993E-08	0.268805	0.000106496
rs11187897	10	96106603	eQTLcatalogue	GENCORD ge LCL	PLCE1	A	2.13815E-08	0.268908	0.000106907
rs10509672	10	96115957	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.16348E-08	0.268776	0.000108174
rs778275808	10	96114212	eQTLcatalogue	GENCORD ge LCL	PLCE1	TCTC	2.17765E-08	0.268773	0.000108882
rs11187840	10	96050351	eQTLcatalogue	GENCORD ge LCL	PLCE1	A	2.20621E-08	0.262863	0.000110311
rs79193572	10	96119713	eQTLcatalogue	GENCORD ge LCL	PLCE1	A	2.21705E-08	0.268385	0.000110852
rs7096883	10	96069149	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	2.3343E-08	-5.5851	0.0001147666411629
rs769015184	10	96049708	eQTLcatalogue	GENCORD ge LCL	PLCE1	AC	2.47513E-08	0.262186	0.000123756
rs74825688	10	96119687	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	2.62812E-08	0.26629	0.000131406
rs3781266	10	96052747	eQTLGen	eQTLGen cis eQTLs	HELLS	G	2.6457E-08	1,3643E+06	0.0001146204788588
rs17109875	10	96026575	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	T	2.74731E-08	0.184435	0.000137365
rs11187837	10	96035980	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	T	2.74823E-08	0.184411	0.000137411
rs3740360	10	96025491	eQTLcatalogue	BLUEPRINT ge monocyte	NOC3L	A	2.76868E-08	0.184361	0.000138434
rs12220091	10	96053689	eQTLGen	eQTLGen cis eQTLs	HELLS	T	2.8731E-08	1,3121E+06	0.0001272669424117
rs11187907	10	96125361	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	T	2.91468E-08	-0.309692	3.86001E-30
rs10786156	10	96014622	GTEx/v8	Skin Not Sun Exposed Suprapubic	NOC3L	G	3.68785E-08	0.151155	2.01564E-23
rs3891783	10	96015793	GTEx/v8	Skin Not Sun Exposed Suprapubic	NOC3L	G	3.68785E-08	0.151155	2.01564E-23
rs57866767	10	96023077	GTEx/v8	Skin Not Sun Exposed Suprapubic	NOC3L	C	3.68785E-08	0.151155	2.01564E-23
rs7096883	10	96069149	eQTLcatalogue	GENCORD ge LCL	PLCE1	G	3.69827E-08	0.262001	0.000184913
rs11187840	10	96050351	eQTLcatalogue	TwinsUK ge LCL	PLCE1	A	3.7527E-08	0.0963516	0.000187635
rs753724	10	96051417	eQTLcatalogue	TwinsUK ge LCL	PLCE1	G	3.7527E-08	0.0963516	0.000187635
rs11187842	10	96052511	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	3.7527E-08	0.0963516	0.000187635
rs3781266	10	96052747	eQTLcatalogue	TwinsUK ge LCL	PLCE1	A	3.7527E-08	0.0963516	0.000187635
rs3740365	10	96053239	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	3.7527E-08	0.0963516	0.000187635
rs12220091	10	96053689	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	3.7527E-08	0.0963516	0.000187635
rs75017201	10	96055152	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	3.7527E-08	0.0963516	0.000187635
rs200197176	10	96055963	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	3.77732E-08	0.25545	0.000188866
rs11187845	10	96060198	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	3.87215E-08	0.097552	6.591E-06
10:96112261_AAAAAAAC_A	10	96112261	eQTLcatalogue	GENCORD ge LCL	PLCE1	AAAAAAAC	3.88536E-08	0.25946	0.000194268
rs75409190	10	96072425	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	3.92785E-08	0.102328	6.68E-06
rs12217792	10	96062386	eQTLcatalogue	GENCORD ge LCL	PLCE1	T	4.12977E-08	0.261741	0.000206488

rs752140	10	96071396	GTEx/v8	Muscle Skeletal	NOC3L	T	4.2379E-08	0.260214	7.35621E-14
rs11187863	10	96081457	GTEx/v8	Muscle Skeletal	NOC3L	G	4.2379E-08	0.260214	7.35621E-14
rs11187866	10	96085991	GTEx/v8	Muscle Skeletal	NOC3L	G	4.2379E-08	0.260214	7.35621E-14
rs11187883	10	96096866	GTEx/v8	Muscle Skeletal	NOC3L	C	4.2379E-08	0.260214	7.35621E-14
rs34309017	10	96061619	eQTLcatalogue	GENCORD ge LCL	PLCE1	ACTT	4.27059E-08	0.261633	0.00021353
rs7080472	10	96012950	GTEx/v8	Skin Not Sun Exposed Suprapubic	NOC3L	T	4.38581E-08	0.151839	2.01564E-23
rs11187845	10	96060198	eQTLGen	eQTLGen cis eQTLs	HELLS	A	4.4649E-08	1,0279E+06	0.0001774510425248
rs11187845	10	96060198	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	4.51948E-08	0.261443	0.000225974
rs11187882	10	96095861	PsychENCODE	PsychENCODE eQTLs	NOC3L	C	4.61283E-08	0.101642	7.755E-06
rs11187856	10	96076869	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	4.68244E-08	0.101697	7.864E-06
rs11187847	10	96063440	PsychENCODE	PsychENCODE eQTLs	NOC3L	G	4.94659E-08	0.0960576	8.276E-06
rs11187847	10	96063440	eQTLGen	eQTLGen cis eQTLs	PDLIM1	G	5.6354E-08	-5.43	0.0002400657021921
rs11187864	10	96082506	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	6.74076E-08	0.100225	1.104E-05
rs113544984	10	96127448	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	6.75766E-08	0.102717	1.106E-05
rs2274224	10	96039597	GTEx/v8	Heart Left Ventricle	NOC3L	C	7.19999E-08	0.19175	3.09268E-10
rs10786156	10	96014622	GTEx/v8	Heart Left Ventricle	NOC3L	G	7.68073E-08	0.190819	3.09268E-10
rs2274224	10	96039597	GTEx/v8	Skin Not Sun Exposed Suprapubic	NOC3L	C	7.79403E-08	0.147484	2.01564E-23
rs11187906	10	96124838	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	7.89484E-08	0.102219	1.279E-05
rs7080472	10	96012950	GTEx/v8	Esophagus Muscularis	NOC3L	T	8.19561E-08	0.153403	2.723E-20
rs11187864	10	96082506	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	8.2214E-08	6,2944E+05	0.0003272704386682
rs7078844	10	96081140	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	9.9519E-08	-5.3274	0.0003455425017277
rs12220091	10	96053689	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	1.00415E-07	0.093271	1.6E-05
rs3781266	10	96052747	PsychENCODE	PsychENCODE eQTLs	NOC3L	G	1.0346E-07	0.0931764	1.645E-05
rs7100626	10	96069674	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	1.13755E-07	0.097166	1.796E-05
rs75017201	10	96055152	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	1.16476E-07	0.0941142	1.836E-05
rs7096883	10	96069149	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	1.25814E-07	0.0938882	1.972E-05
rs79193572	10	96119713	PsychENCODE	PsychENCODE eQTLs	NOC3L	G	1.30794E-07	0.0996592	2.045E-05
rs3891783	10	96015793	GTEx/v8	Heart Left Ventricle	NOC3L	G	1.31784E-07	0.188086	3.09268E-10
rs57866767	10	96023077	GTEx/v8	Heart Left Ventricle	NOC3L	C	1.31784E-07	0.188086	3.09268E-10
rs10509672	10	96115957	PsychENCODE	PsychENCODE eQTLs	NOC3L	C	1.32438E-07	0.099585	2.06849591120053E-05
rs11187845	10	96060198	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	1.3348E-07	-5.274	0.0004511560874741
rs11187907	10	96125361	GTEx/v8	Muscle Skeletal	NOC3L	T	1.34121E-07	0.270996	7.35621E-14
rs11187840	10	96050351	PsychENCODE	PsychENCODE eQTLs	NOC3L	G	1.38003E-07	0.0935981	2.14874417863028E-05
rs11187838	10	96038686	GTEx/v8	Skin Not Sun Exposed Suprapubic	NOC3L	A	1.42965E-07	0.146108	2.01564E-23
rs11187838	10	96038686	GTEx/v8	Heart Left Ventricle	NOC3L	A	1.43393E-07	0.187213	3.09268E-10
rs11187890	10	96102758	GTEx/v8	Muscle Skeletal	NOC3L	C	1.52809E-07	0.267003	7.35621E-14
rs11187897	10	96106603	PsychENCODE	PsychENCODE eQTLs	NOC3L	G	1.5365E-07	0.0982801	2.37379907205247E-05
rs74825688	10	96119687	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	1.58469E-07	0.0973335	2.4430127491122E-05
rs11187895	10	96106240	GTEx/v8	Muscle Skeletal	NOC3L	C	1.60775E-07	0.268698	7.35621E-14
rs11187897	10	96106603	GTEx/v8	Muscle Skeletal	NOC3L	G	1.60775E-07	0.268698	7.35621E-14

rs11187826	10	95988042	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	G	1.96608E-07	-0.25953	3.86001E-30
rs11187838	10	96038686	GTEx/v8	Pancreas	NOC3L	A	2.08079E-07	0.254395	9.42454E-11
rs7096883	10	96069149	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	2.1392E-07	-0.384583	0.000644523
rs11187826	10	95988042	eQTLcatalogue	GENCORDge T-cell	PLCE1	A	2.19202E-07	0.384369	0.00109601
rs2274224	10	96039597	GTEx/v8	Esophagus Muscularis	NOC3L	C	2.22318E-07	0.14706	2.7232299999999997E-20
rs11187840	10	96050351	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	2.3916E-07	5.166	0.0007907845579078
rs3740359	10	96100119	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	2.42044E-07	0.403517	0.00121022
rs10786156	10	96014622	GTEx/v8	Pancreas	NOC3L	G	2.53785E-07	0.25422	9.42454E-11
rs74825688	10	96119687	GTEx/v8	Muscle Skeletal	NOC3L	A	2.59297E-07	0.26993	7.35621E-14
rs3891783	10	96015793	GTEx/v8	Pancreas	NOC3L	G	2.63886E-07	0.253623	9.42454E-11
rs57866767	10	96023077	GTEx/v8	Pancreas	NOC3L	C	2.63886E-07	0.253623	9.42454E-11
rs75017201	10	96055152	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	2.7328E-07	5.1411	0.0009131569139023
rs79193572	10	96119713	GTEx/v8	Muscle Skeletal	NOC3L	G	2.73463E-07	0.271213	7.35621E-14
rs11187842	10	96052511	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	2.7357E-07	5.1409	0.0009131569139023
rs752140	10	96071396	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	2.74207E-07	-0.370555	0.000644523
rs11187838	10	96038686	GTEx/v8	Colon Transverse	NOC3L	A	2.82625E-07	0.148369	4.35915E-08
rs3740365	10	96053239	eQTLGen	eQTLGen cis eQTLs	NOC3L	A	2.8395E-07	5.134	0.0009374805984975
rs113544984	10	96127448	GTEx/v8	Muscle Skeletal	NOC3L	A	2.88143E-07	0.271515	7.35621E-14
rs11187838	10	96038686	eQTLcatalogue	TwinsUK ge skin	NOC3L	G	2.89308E-07	0.0989956	0.00144654
rs79746649	10	96120218	GTEx/v8	Muscle Skeletal	NOC3L	T	2.93423E-07	0.267286	7.35621E-14
rs3740360	10	96025491	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	3.03193E-07	-0.26005	3.86001E-30
rs17109875	10	96026575	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	3.03193E-07	-0.26005	3.86001E-30
rs11187837	10	96035980	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	3.03193E-07	-0.26005	3.86001E-30
rs7101207	10	96122857	GTEx/v8	Muscle Skeletal	NOC3L	A	3.07502E-07	0.26767	7.35621E-14
rs112252876	10	96123355	GTEx/v8	Muscle Skeletal	NOC3L	T	3.07502E-07	0.26767	7.35621E-14
rs3781266	10	96052747	eQTLGen	eQTLGen cis eQTLs	NOC3L	G	3.0781E-07	5.1188	0.0009988212668279
rs778275808	10	96114212	GTEx/v8	Muscle Skeletal	NOC3L	T	3.11067E-07	0.268918	7.35621E-14
rs10509672	10	96115957	GTEx/v8	Muscle Skeletal	NOC3L	C	3.11067E-07	0.268918	7.35621E-14
rs753724	10	96051417	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	3.13234E-07	-0.372223	0.000644523
rs11187842	10	96052511	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	3.13234E-07	-0.372223	0.000644523
rs3781266	10	96052747	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	3.13234E-07	-0.372223	0.000644523
rs3740365	10	96053239	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	3.13234E-07	-0.372223	0.000644523
rs12220091	10	96053689	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	3.13234E-07	-0.372223	0.000644523
rs11187890	10	96102758	PsychENCODE	PsychENCODE eQTLs	NOC3L	C	3.24704E-07	0.09449	4.7507000772688E-05
rs12220091	10	96053689	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	3.249E-07	5.1085	0.0010662699150703
rs753724	10	96051417	eQTLGen	eQTLGen cis eQTLs	NOC3L	T	3.294E-07	5.1058	0.0010722697409198
rs11187870	10	96087866	eQTLGen	eQTLGen cis eQTLs	HELLS	C	3.3185E-07	5.1046	0.001078267335936
rs112252876	10	96123355	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	3.46649E-07	0.0955999	5.04639294195705E-05

rs7080472	10	96012950	eQTLcatalogue	TwinsUK ge skin	NOC3L	G	3.47022E-07	0.0981732	0.00173511
rs7100626	10	96069674	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	3.47683E-07	-0.384603	0.000644523
rs11187852	10	96070132	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	3.47683E-07	-0.384603	0.000644523
rs10786156	10	96014622	eQTLcatalogue	TwinsUK ge skin	NOC3L	C	3.48198E-07	0.0985294	0.00174099
rs3891783	10	96015793	eQTLcatalogue	TwinsUK ge skin	NOC3L	C	3.48198E-07	0.0985294	0.00174099
rs57866767	10	96023077	eQTLcatalogue	TwinsUK ge skin	NOC3L	T	3.48198E-07	0.0985294	0.00174099
rs2274224	10	96039597	GTEx/v8	Pancreas	NOC3L	C	3.48768E-07	0.251721	9.42454E-11
rs79746649	10	96120218	PsychENCODE	PsychENCODE eQTLs	NOC3L	T	3.54686E-07	0.094936	5.1543436990261E-05
rs75409190	10	96072425	GTEx/v8	Muscle Skeletal	NOC3L	T	3.61127E-07	0.257218	7.35621E-14
rs771106747	10	96072873	GTEx/v8	Muscle Skeletal	NOC3L	C	3.61127E-07	0.257218	7.35621E-14
rs749295068	10	96073508	GTEx/v8	Muscle Skeletal	NOC3L	A	3.61127E-07	0.257218	7.35621E-14
rs11187856	10	96076869	GTEx/v8	Muscle Skeletal	NOC3L	A	3.61127E-07	0.257218	7.35621E-14
rs11187882	10	96095861	GTEx/v8	Muscle Skeletal	NOC3L	C	3.61127E-07	0.257218	7.35621E-14
rs10786156	10	96014622	GTEx/v8	Esophagus Muscularis	NOC3L	G	3.66095E-07	0.145079	2.7232299999999997E-20
rs7101207	10	96122857	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	3.79043E-07	0.0952988	5.47969109279773E-05
rs11187863	10	96081457	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	3.88596E-07	-0.364458	0.000644523
rs11187866	10	96085991	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	3.88596E-07	-0.364458	0.000644523
rs11187883	10	96096866	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	3.88596E-07	-0.364458	0.000644523
rs11187826	10	95988042	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	G	3.8943E-07	0.687209	1.20882E-07
rs7100626	10	96069674	GTEx/v8	Muscle Skeletal	NOC3L	A	3.96229E-07	0.253129	7.35621E-14
rs11187852	10	96070132	GTEx/v8	Muscle Skeletal	NOC3L	A	3.96229E-07	0.253129	7.35621E-14
rs11187877	10	96092121	GTEx/v8	Muscle Skeletal	NOC3L	A	3.96229E-07	0.253129	7.35621E-14
rs11187844	10	96056629	eQTLcatalogue	TwinsUK ge LCL	PLCE1	C	3.97134E-07	0.0760026	0.00198567
rs11187864	10	96082506	GTEx/v8	Muscle Skeletal	NOC3L	T	4.12789E-07	0.254895	7.35621E-14
rs145707916	10	96092992	GTEx/v8	Muscle Skeletal	NOC3L	GA	4.12789E-07	0.254895	7.35621E-14
rs750148755	10	96095271	GTEx/v8	Muscle Skeletal	NOC3L	C	4.12789E-07	0.254895	7.35621E-14
rs11187844	10	96056629	PsychENCODE	PsychENCODE eQTLs	NOC3L	A	4.17472E-07	0.0796474	5.99069241685944E-05
rs3740360	10	96025491	eQTLcatalogue	GENCORD ge LCL	PLCE1	A	4.30425E-07	0.214894	0.00215212
rs17109875	10	96026575	eQTLcatalogue	GENCORD ge LCL	PLCE1	T	4.30538E-07	0.214855	0.00215269
rs11187837	10	96035980	eQTLcatalogue	GENCORD ge LCL	PLCE1	T	4.31649E-07	0.214915	0.00215825
rs10786156	10	96014622	GTEx/v8	Colon Transverse	NOC3L	G	4.43133E-07	0.147768	4.35915E-08
rs3891783	10	96015793	GTEx/v8	Colon Transverse	NOC3L	G	4.43133E-07	0.147768	4.35915E-08
rs57866767	10	96023077	GTEx/v8	Colon Transverse	NOC3L	C	4.43133E-07	0.147768	4.35915E-08
rs11187840	10	96050351	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	4.88307E-07	-0.372062	0.000644523
rs75017201	10	96055152	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	4.88307E-07	-0.372062	0.000644523
rs7101207	10	96122857	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	4.96061E-07	-0.391535	0.000644523
rs112252876	10	96123355	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	4.96061E-07	-0.391535	0.000644523
rs11187890	10	96102758	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	4.97744E-07	-0.382886	0.000644523

rs3891783	10	96015793	GTEx/v8	Esophagus Muscularis	NOC3L	G	4.98044E-07	0.143689	2.7232299999999997E-20
rs57866767	10	96023077	GTEx/v8	Esophagus Muscularis	NOC3L	C	4.98044E-07	0.143689	2.7232299999999997E-20
rs11187877	10	96092121	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	5.00681E-07	-0.377836	0.000644523
rs11187838	10	96038686	GTEx/v8	Skin Sun Exposed Lower leg	PLCE1	A	5.53023E-07	0.1259	0.000666445
rs7080472	10	96012950	GTEx/v8	Heart Left Ventricle	NOC3L	T	5.53501E-07	0.180376	3.09268E-10
rs2274224	10	96039597	GTEx/v8	Colon Transverse	NOC3L	C	5.7305E-07	0.145736	4.35915E-08
rs10786156	10	96014622	GTEx/v8	Skin Sun Exposed Lower leg	PLCE1	G	5.83892E-07	0.125559	0.000666445
rs11187870	10	96087866	GTEx/v8	Muscle Skeletal	NOC3L	C	5.88352E-07	0.253513	7.35621E-14
rs7080472	10	96012950	GTEx/v8	Artery Aorta	NOC3L	T	5.98593E-07	0.163228	1.86975E-08
rs11187845	10	96060198	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	6.06255E-07	-0.367463	0.000644523
rs11187847	10	96063440	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	6.06255E-07	-0.367463	0.000644523
rs10786156	10	96014622	GTEx/v8	Artery Aorta	NOC3L	G	6.18786E-07	0.162455	1.86975E-08
rs7080472	10	96012950	GTEx/v8	Colon Transverse	NOC3L	T	6.21534E-07	0.145514	4.35915E-08
rs3891783	10	96015793	GTEx/v8	Skin Sun Exposed Lower leg	PLCE1	G	6.68793E-07	0.125003	0.000666445
rs57866767	10	96023077	GTEx/v8	Skin Sun Exposed Lower leg	PLCE1	C	6.68793E-07	0.125003	0.000666445
rs7078844	10	96081140	GTEx/v8	Nerve Tibial	HELLS	C	7.10111E-07	-0.252012	5.533110000000001E-26
rs7080472	10	96012950	GTEx/v8	Pancreas	NOC3L	T	7.15314E-07	0.239439	9.42454E-11
rs3891783	10	96015793	GTEx/v8	Artery Tibial	PLCE1	G	7.18774E-07	0.123127	1.21915E-07
rs57866767	10	96023077	GTEx/v8	Artery Tibial	PLCE1	C	7.18774E-07	0.123127	1.21915E-07
10:96112261_AAAAAAAC_A	10	96112261	eQTLcatalogue	GENCORDge T-cell	PLCE1	AAAAAAAC	7.20664E-07	0.382443	0.00360332
rs7080472	10	96012950	GTEx/v8	Artery Tibial	PLCE1	T	8.33992E-07	0.123308	1.21915E-07
rs79746649	10	96120218	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	8.5631E-07	-0.38324	0.000644523
rs11187838	10	96038686	GTEx/v8	Esophagus Muscularis	NOC3L	A	8.82021E-07	0.140769	2.7232299999999997E-20
rs79746649	10	96120218	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	9.21774E-07	0.38583	0.00460887
rs752140	10	96071396	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	9.39565E-07	0.386047	0.00469783
rs11187890	10	96102758	eQTLcatalogue	GENCORDge T-cell	PLCE1	T	9.44539E-07	0.385938	0.00472269
rs11187882	10	96095861	eQTLcatalogue	GENCORDge T-cell	PLCE1	A	9.46492E-07	0.385876	0.00473246
rs11187856	10	96076869	eQTLcatalogue	GENCORDge T-cell	PLCE1	G	9.48129E-07	0.385897	0.00474064
rs749295068	10	96073508	eQTLcatalogue	GENCORDge T-cell	PLCE1	AGAT	9.48173E-07	0.385896	0.00474087
rs771106747	10	96072873	eQTLcatalogue	GENCORDge T-cell	PLCE1	CTA	9.50361E-07	0.385857	0.00475181
rs11187863	10	96081457	eQTLcatalogue	GENCORDge T-cell	PLCE1	T	9.50792E-07	0.385788	0.00475396
rs11187864	10	96082506	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	9.50792E-07	0.385788	0.00475396
rs11187866	10	96085991	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	9.50792E-07	0.385788	0.00475396
rs11187870	10	96087866	eQTLcatalogue	GENCORDge T-cell	PLCE1	G	9.50792E-07	0.385788	0.00475396
rs11187877	10	96092121	eQTLcatalogue	GENCORDge T-cell	PLCE1	G	9.50792E-07	0.385788	0.00475396
rs145707916	10	96092992	eQTLcatalogue	GENCORDge T-cell	PLCE1	G	9.50792E-07	0.385788	0.00475396
rs7100626	10	96069674	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	9.51672E-07	0.385791	0.00475836
rs11187852	10	96070132	eQTLcatalogue	GENCORDge T-cell	PLCE1	G	9.51672E-07	0.385791	0.00475836
rs75409190	10	96072425	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	9.51792E-07	0.385813	0.00475896
rs750148755	10	96095271	eQTLcatalogue	GENCORDge T-cell	PLCE1	CATTTT	9.54195E-07	0.385738	0.00477098

rs3740359	10	96100119	DICE	T CD4 TH1	PLCE1	T	9.6971259049E-07	0.898080559827	0.049
rs34309017	10	96061619	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	9.70292E-07	-0.366366	0.000644523
rs12217792	10	96062386	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	9.70292E-07	-0.366366	0.000644523
rs11187847	10	96063440	eQTLcatalogue	GENCORD ge LCL	PLCE1	C	9.70592E-07	0.233046	0.00485296
rs11187895	10	96106240	eQTLcatalogue	GENCORD ge T-cell	PLCE1	G	9.72079E-07	0.38546	0.00486039
rs11187897	10	96106603	eQTLcatalogue	GENCORD ge T-cell	PLCE1	A	9.73083E-07	0.385427	0.00486541
rs11187883	10	96096866	eQTLcatalogue	GENCORD ge T-cell	PLCE1	T	9.73666E-07	0.385218	0.00486833
rs10509672	10	96115957	eQTLcatalogue	GENCORD ge T-cell	PLCE1	G	9.83222E-07	0.385218	0.00491611
rs778275808	10	96114212	eQTLcatalogue	GENCORD ge T-cell	PLCE1	TCTC	9.90757E-07	0.385175	0.00495378
rs79193572	10	96119713	eQTLcatalogue	GENCORD ge T-cell	PLCE1	A	1.00326E-06	0.384625	0.0050163
rs753724	10	96051417	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	1.0311E-06	-4.8856	0.0031823745410036
rs2274224	10	96039597	GTEx/v8	Artery Aorta	NOC3L	C	1.05756E-06	0.158624	1.86975E-08
rs7080472	10	96012950	GTEx/v8	Colon Sigmoid	NOC3L	T	1.10378E-06	0.193204	1.73346E-11
rs74825688	10	96119687	eQTLcatalogue	GENCORD ge T-cell	PLCE1	G	1.1056E-06	0.382039	0.005528
rs10786156	10	96014622	GTEx/v8	Artery Tibial	PLCE1	G	1.11843E-06	0.12099	1.21915E-07
rs11187842	10	96052511	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	1.1205E-06	-4.869	0.003400403645037
rs3740365	10	96053239	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	1.1515E-06	-4.8636	0.0034784203447854
rs74825688	10	96119687	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	1.16396E-06	-0.375083	0.000644523
rs11187845	10	96060198	eQTLcatalogue	GENCORD ge T-cell	PLCE1	C	1.18769E-06	0.380044	0.00593845
rs34309017	10	96061619	eQTLcatalogue	GENCORD ge T-cell	PLCE1	ACTT	1.19242E-06	0.37961	0.0059621
rs12217792	10	96062386	eQTLcatalogue	GENCORD ge T-cell	PLCE1	T	1.19698E-06	0.379327	0.0059849
rs11187847	10	96063440	eQTLcatalogue	GENCORD ge T-cell	PLCE1	C	1.20172E-06	0.379013	0.0060086
rs2274224	10	96039597	GTEx/v8	Skin Sun Exposed Lower leg	PLCE1	C	1.20492E-06	0.12172	0.000666445
rs7096883	10	96069149	eQTLcatalogue	GENCORD ge T-cell	PLCE1	G	1.21204E-06	0.378282	0.0060602
rs2274224	10	96039597	GTEx/v8	Artery Tibial	PLCE1	C	1.26595E-06	0.120273	1.21915E-07
rs3891783	10	96015793	GTEx/v8	Artery Aorta	NOC3L	G	1.312E-06	0.158283	1.86975E-08
rs57866767	10	96023077	GTEx/v8	Artery Aorta	NOC3L	C	1.312E-06	0.158283	1.86975E-08
rs3740359	10	96100119	GTEx/v8	Muscle Skeletal	NOC3L	T	1.31362E-06	0.221014	7.35621E-14
rs75017201	10	96055152	eQTLcatalogue	GENCORD ge T-cell	PLCE1	C	1.33148E-06	0.367203	0.0066574
rs12220091	10	96053689	eQTLcatalogue	GENCORD ge T-cell	PLCE1	C	1.33264E-06	0.367032	0.0066632
rs3740365	10	96053239	eQTLcatalogue	GENCORD ge T-cell	PLCE1	T	1.33285E-06	0.367006	0.00666425
rs753724	10	96051417	eQTLcatalogue	GENCORD ge T-cell	PLCE1	G	1.3329E-06	0.367893	0.0066645
rs3781266	10	96052747	eQTLcatalogue	GENCORD ge T-cell	PLCE1	A	1.33329E-06	0.366955	0.00666645
rs11187842	10	96052511	eQTLcatalogue	GENCORD ge T-cell	PLCE1	C	1.33345E-06	0.366938	0.00666725
rs11187840	10	96050351	eQTLcatalogue	GENCORD ge T-cell	PLCE1	A	1.36086E-06	0.368475	0.0068043
rs11187840	10	96050351	eQTLGen	eQTLGen cis eQTLs	PDLIM1	G	1.3708E-06	-4.8291	0.0041417591801878
rs769015184	10	96049708	eQTLcatalogue	GENCORD ge T-cell	PLCE1	AC	1.38142E-06	0.36852	0.0069071
rs11187844	10	96056629	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	A	1.42697E-06	4.8213458	0.0011833705299216
rs75409190	10	96072425	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	1.56355E-06	-0.365914	0.000644523
rs771106747	10	96072873	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	1.56355E-06	-0.365914	0.000644523

rs11187856	10	96076869	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	1.56355E-06	-0.365914	0.000644523
rs75017201	10	96055152	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	1.5803E-06	-4.8007	0.0046780776024852
rs2077218	10	96071561	GTEx/v8	Nerve Tibial	HELLS	A	1.61786E-06	-0.253004	5.533110000000001E-26
rs11187838	10	96038686	BIOSQTL	BIOS eQTL geneLevel	PLCE1	A	1.65622E-06	4.7915542	0.0013530961111398
rs3740359	10	96100119	GTEx/v8	Cells EBV-transformed lymphocytes	PLCE1	T	1.67783E-06	0.600178	1.20882E-07
rs7080472	10	96012950	GTEx/v8	Thyroid	TBC1D12	T	1.69106E-06	-0.142239	1.4449E-10
rs3781266	10	96052747	eQTLGen	eQTLGen cis eQTLs	PDLIM1	G	1.7971E-06	-4.7749	0.0053287912890078
rs7078844	10	96081140	BIOSQTL	BIOS eQTL geneLevel	TBC1D12	T	1.81863E-06	-4.77257	0.0014319563201813
rs12220091	10	96053689	eQTLGen	eQTLGen cis eQTLs	PDLIM1	T	1.9017E-06	-4.7636	0.0055572444822764
rs7080472	10	96012950	GTEx/v8	Skin Sun Exposed Lower leg	PLCE1	T	1.96357E-06	0.12091	0.000666445
rs11187863	10	96081457	DICE	T CD4 TH1	PLCE1	G	2.1750695116E-06	0.887821580882	0.049
rs11187866	10	96085991	DICE	T CD4 TH1	PLCE1	G	2.1750695116E-06	0.887821580882	0.049
rs11187877	10	96092121	DICE	T CD4 TH1	PLCE1	A	2.1750695116E-06	0.887821580882	0.049
rs11187883	10	96096866	DICE	T CD4 TH1	PLCE1	C	2.1750695116E-06	0.887821580882	0.049
rs11187890	10	96102758	DICE	T CD4 TH1	PLCE1	C	2.1750695116E-06	0.887821580882	0.049
rs11187864	10	96082506	DICE	T CD4 TH1	PLCE1	T	2.18983857164E-06	0.900338651896	0.049
rs11187870	10	96087866	DICE	T CD4 TH1	PLCE1	C	2.18983857164E-06	0.900338651896	0.049
rs145707916	10	96092992	DICE	T CD4 TH1	PLCE1	GA	2.18983857164E-06	0.900338651896	0.049
rs750148755	10	96095271	DICE	T CD4 TH1	PLCE1	C	2.18983857164E-06	0.900338651896	0.049
rs11187882	10	96095861	DICE	T CD4 TH1	PLCE1	C	2.18983857164E-06	0.900338651896	0.049
rs11187895	10	96106240	DICE	T CD4 TH1	PLCE1	C	2.18983857164E-06	0.900338651896	0.049
rs11187897	10	96106603	DICE	T CD4 TH1	PLCE1	G	2.18983857164E-06	0.900338651896	0.049
rs11187863	10	96081457	GTEx/v8	Thyroid	NOC3L	G	2.19445E-06	-0.172139	0.00220997
rs11187866	10	96085991	GTEx/v8	Thyroid	NOC3L	G	2.19445E-06	-0.172139	0.00220997
rs11187883	10	96096866	GTEx/v8	Thyroid	NOC3L	C	2.19445E-06	-0.172139	0.00220997
rs11187864	10	96082506	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	2.20876E-06	-0.359052	0.000644523
rs145707916	10	96092992	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	GA	2.20876E-06	-0.359052	0.000644523
rs750148755	10	96095271	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	2.20876E-06	-0.359052	0.000644523
rs11187895	10	96106240	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	2.23083E-06	-0.36371	0.000644523
rs11187897	10	96106603	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	2.23083E-06	-0.36371	0.000644523
rs749295068	10	96073508	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	2.24181E-06	-0.362577	0.000644523
rs11187838	10	96038686	GTEx/v8	Brain Nucleus accumbens basal ganglia	NOC3L	A	2.24908E-06	0.20893	0.000164102
rs752140	10	96071396	GTEx/v8	Thyroid	NOC3L	T	2.28464E-06	-0.172467	0.00220997
rs11187837	10	96035980	eQTLcatalogue	GENCORDge T-cell	PLCE1	T	2.31571E-06	0.335699	0.0115785
rs17109875	10	96026575	eQTLcatalogue	GENCORDge T-cell	PLCE1	T	2.32943E-06	0.335494	0.0116471
rs3740360	10	96025491	eQTLcatalogue	GENCORDge T-cell	PLCE1	A	2.33243E-06	0.335539	0.0116621
10:96112261_AAAAAAAC_A	10	96112261	DICE	T CD4 TH1	PLCE1	A	2.33720404313E-06	0.948074989332	0.049
rs11187845	10	96060198	GTEx/v8	Muscle Skeletal	NOC3L	A	2.44081E-06	0.230282	7.35621E-14

rs11187847	10	96063440	GTEx/v8	Muscle Skeletal	NOC3L	G	2.44081E-06	0.230282	7.35621E-14
rs7080472	10	96012950	GTEx/v8	Brain Cerebellar Hemisphere	NOC3L	T	2.48212E-06	0.273389	1.25929E-05
rs10786156	10	96014622	BIOSQTL	BIOS eQTL geneLevel	PLCE1	G	2.48935E-06	4.7090961	0.0019017998266455
rs3891783	10	96015793	BIOSQTL	BIOS eQTL geneLevel	PLCE1	G	2.48935E-06	4.7090961	0.0019017998266455
rs57866767	10	96023077	BIOSQTL	BIOS eQTL geneLevel	PLCE1	C	2.48935E-06	4.7090961	0.0019017998266455
rs11187838	10	96038686	GTEx/v8	Artery Aorta	NOC3L	A	2.9258E-06	0.151503	1.86975E-08
rs34309017	10	96061619	GTEx/v8	Muscle Skeletal	NOC3L	A	3.04275E-06	0.230309	7.35621E-14
rs12217792	10	96062386	GTEx/v8	Muscle Skeletal	NOC3L	C	3.04275E-06	0.230309	7.35621E-14
rs11187882	10	96095861	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	3.14149E-06	-0.35578	0.000644523
rs7096883	10	96069149	GTEx/v8	Muscle Skeletal	NOC3L	A	3.18816E-06	0.227145	7.35621E-14
rs7101207	10	96122857	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	G	3.24912E-06	0.109848	0.0162456
rs11187906	10	96124838	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	T	3.28105E-06	0.10976	0.0164052
rs11187907	10	96125361	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	C	3.28105E-06	0.10976	0.0164052
rs113544984	10	96127448	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	C	3.28105E-06	0.10976	0.0164052
rs7080472	10	96012950	eQTLcatalogue	Quach 2016 ge monocyte Pam3CSK4	NOC3L	G	3.41441E-06	-0.105905	0.017072
rs10786156	10	96014622	GTEx/v8	Brain Nucleus accumbens basal ganglia	NOC3L	G	3.46741E-06	0.204556	0.000164102
rs3891783	10	96015793	GTEx/v8	Brain Nucleus accumbens basal ganglia	NOC3L	G	3.46741E-06	0.204556	0.000164102
rs57866767	10	96023077	GTEx/v8	Brain Nucleus accumbens basal ganglia	NOC3L	C	3.46741E-06	0.204556	0.000164102
rs2274224	10	96039597	GTEx/v8	Brain Nucleus accumbens basal ganglia	NOC3L	C	3.46741E-06	0.204556	0.000164102
rs778275808	10	96114212	DICE	T CD4 TH1	PLCE1	T	3.54266627324E-06	0.944577708395	0.049
rs10509672	10	96115957	DICE	T CD4 TH1	PLCE1	C	3.54266627324E-06	0.944577708395	0.049
rs74825688	10	96119687	DICE	T CD4 TH1	PLCE1	A	3.54266627324E-06	0.944577708395	0.049
rs79193572	10	96119713	DICE	T CD4 TH1	PLCE1	G	3.54266627324E-06	0.944577708395	0.049
rs11187906	10	96124838	DICE	T CD4 TH1	PLCE1	A	3.54266627324E-06	0.944577708395	0.049
rs11187907	10	96125361	DICE	T CD4 TH1	PLCE1	T	3.54266627324E-06	0.944577708395	0.049
rs113544984	10	96127448	DICE	T CD4 TH1	PLCE1	A	3.54266627324E-06	0.944577708395	0.049
rs79746649	10	96120218	DICE	T CD4 TH1	PLCE1	T	3.56488559879E-06	0.92935546315	0.049
rs7101207	10	96122857	DICE	T CD4 TH1	PLCE1	A	3.56488559879E-06	0.92935546315	0.049
rs112252876	10	96123355	DICE	T CD4 TH1	PLCE1	T	3.56488559879E-06	0.92935546315	0.049
rs11187826	10	95988042	eQTLcatalogue	TwinsUK ge LCL	PLCE1	A	3.67082E-06	0.0676536	0.0183541
rs778275808	10	96114212	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	3.89634E-06	-0.362682	0.000644523
rs10509672	10	96115957	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	3.89634E-06	-0.362682	0.000644523
rs79193572	10	96119713	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	3.89634E-06	-0.362682	0.000644523
rs7080472	10	96012950	BIOSQTL	BIOS eQTL geneLevel	PLCE1	T	3.98429E-06	4.6122133	0.0028727838883029

rs3740360	10	96025491	eQTLcatalogue	TwinsUK ge LCL	PLCE1	A	4.12006E-06	0.0676965	0.0206003
rs17109875	10	96026575	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	4.12006E-06	0.0676965	0.0206003
rs11187837	10	96035980	eQTLcatalogue	TwinsUK ge LCL	PLCE1	T	4.23178E-06	0.0679173	0.0211589
rs11187907	10	96125361	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	4.23293E-06	-0.353893	0.000644523
rs11187838	10	96038686	GTEx/v8	Brain Cerebellar Hemisphere	NOC3L	A	4.63289E-06	0.260394	1.25929E-05
rs2274224	10	96039597	GTEx/v8	Brain Cerebellar Hemisphere	NOC3L	C	4.63289E-06	0.260394	1.25929E-05
rs11187870	10	96087866	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	4.63963E-06	-0.352852	0.000644523
rs2274224	10	96039597	GTEx/v8	Thyroid	TBC1D12	C	4.82673E-06	-0.135379	1.4449E-10
rs10786156	10	96014622	GTEx/v8	Thyroid	TBC1D12	G	5.24533E-06	-0.134688	1.4449E-10
rs3891783	10	96015793	GTEx/v8	Thyroid	TBC1D12	G	5.26247E-06	-0.134964	1.4449E-10
rs57866767	10	96023077	GTEx/v8	Thyroid	TBC1D12	C	5.26247E-06	-0.134964	1.4449E-10
rs7080472	10	96012950	GTEx/v8	Brain Nucleus accumbens basal ganglia	NOC3L	T	5.39627E-06	0.203249	0.000164102
rs11187906	10	96124838	BIOSQTL	BIOS eQTL geneLevel	HELLS	A	5.58289E-06	4.5416722	0.0039545499652674
rs11187906	10	96124838	BIOSQTL	BIOS eQTL geneLevel	RP11-119K6.6	A	5.58289E-06	4.5416722	0.0039545499652674
rs3740359	10	96100119	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	T	5.74462E-06	-0.311868	0.000644523
rs11187838	10	96038686	GTEx/v8	Artery Tibial	PLCE1-AS1	A	5.76321E-06	0.138868	2.47435E-06
rs200197176	10	96055963	eQTLcatalogue	GENCORD ge T-cell	PLCE1	C	5.83724E-06	0.342589	0.0291862
rs11187826	10	95988042	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	G	5.84747E-06	-0.330764	0.000644523
rs752140	10	96071396	GTEx/v8	Whole Blood	TBC1D12	T	5.9535E-06	0.239486	0.00686763
rs7080472	10	96012950	GTEx/v8	Artery Tibial	PLCE1-AS1	T	6.16553E-06	0.139554	2.47435E-06
rs7078844	10	96081140	eQTLcatalogue	BrainSeq ge brain	NOC3L	T	6.27308E-06	0.0839191	0.0313654
rs2274224	10	96039597	GTEx/v8	Adipose Subcutaneous	NOC3L	C	6.31202E-06	0.114183	3.06299E-11
rs10786156	10	96014622	GTEx/v8	Brain Cerebellar Hemisphere	NOC3L	G	6.40412E-06	0.257037	1.25929E-05
rs3891783	10	96015793	GTEx/v8	Brain Cerebellar Hemisphere	NOC3L	G	6.40412E-06	0.257037	1.25929E-05
rs57866767	10	96023077	GTEx/v8	Brain Cerebellar Hemisphere	NOC3L	C	6.40412E-06	0.257037	1.25929E-05
rs10786156	10	96014622	GTEx/v8	Spleen	NOC3L	G	6.95933E-06	0.238458	1.49159E-15
rs3891783	10	96015793	GTEx/v8	Spleen	NOC3L	G	6.95933E-06	0.238458	1.49159E-15
rs57866767	10	96023077	GTEx/v8	Spleen	NOC3L	C	6.95933E-06	0.238458	1.49159E-15
rs2274224	10	96039597	GTEx/v8	Spleen	NOC3L	C	6.95933E-06	0.238458	1.49159E-15
rs11187890	10	96102758	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	T	7.12973E-06	0.104697	0.0356487
rs11187895	10	96106240	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	G	7.13783E-06	0.104684	0.0356892
rs11187897	10	96106603	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	A	7.13783E-06	0.104684	0.0356892
rs10509672	10	96115957	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	G	7.13783E-06	0.104684	0.0356892
rs74825688	10	96119687	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	G	7.13783E-06	0.104684	0.0356892
rs79193572	10	96119713	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	A	7.13783E-06	0.104684	0.0356892
rs778275808	10	96114212	eQTLcatalogue	BLUEPRINT ge T-cell	NOC3L	TCTC	7.15045E-06	0.104677	0.0357522
rs11187838	10	96038686	GTEx/v8	Spleen	NOC3L	A	7.73019E-06	0.237346	1.49159E-15
rs749295068	10	96073508	GTEx/v8	Whole Blood	TBC1D12	A	7.96594E-06	0.249853	0.00686763
rs10786156	10	96014622	GTEx/v8	Colon Sigmoid	NOC3L	G	8.39325E-06	0.178254	1.73346E-11

rs3891783	10	96015793	GTEx/v8	Colon Sigmoid	NOC3L	G	8.39325E-06	0.178254	1.73346E-11
rs57866767	10	96023077	GTEx/v8	Colon Sigmoid	NOC3L	C	8.39325E-06	0.178254	1.73346E-11
rs7080472	10	96012950	GTEx/v8	Adipose Subcutaneous	NOC3L	T	9.22157E-06	0.113545	3.06299E-11
rs113544984	10	96127448	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	A	9.24866E-06	-0.349983	0.000644523
rs7078844	10	96081140	GTEx/v8	Thyroid	PLCE1-AS1	C	9.37332E-06	-0.158645	0.00721889
rs11187844	10	96056629	eQTLcatalogue	GENCORDge T-cell	PLCE1	C	9.51488E-06	0.299103	0.0475744
rs2274224	10	96039597	eQTLcatalogue	Fairfax 2014 LPS2	NOC3L	G	9.7278E-06	-0.128461	0.048639
rs11187890	10	96102758	GTEx/v8	Thyroid	NOC3L	C	1.02717E-05	-0.167326	0.00220997
rs10786156	10	96014622	GTEx/v8	Prostate	NOC3L	G	1.05232E-05	0.195047	7.10224E-08
rs3891783	10	96015793	GTEx/v8	Prostate	NOC3L	G	1.05232E-05	0.195047	7.10224E-08
rs57866767	10	96023077	GTEx/v8	Prostate	NOC3L	C	1.05232E-05	0.195047	7.10224E-08
rs3740360	10	96025491	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	1.0598E-05	7,8427E+05	0.0299060977059313
rs7078844	10	96081140	GTEx/v8	Thyroid	PLCE1	C	1.07686E-05	-0.152078	1.91428E-05
rs7096883	10	96069149	GTEx/v8	Whole Blood	TBC1D12	A	1.08788E-05	0.237684	0.00686763
rs11187838	10	96038686	GTEx/v8	Colon Sigmoid	NOC3L	A	1.09622E-05	0.174007	1.73346E-11
rs7100626	10	96069674	GTEx/v8	Whole Blood	TBC1D12	A	1.12809E-05	0.242268	0.00686763
rs11187852	10	96070132	GTEx/v8	Whole Blood	TBC1D12	A	1.12809E-05	0.242268	0.00686763
rs11187838	10	96038686	GTEx/v8	Skin Not Sun Exposed Suprapubic	RP11-76P2.4	A	1.15234E-05	0.222711	5.98468E-07
rs2274224	10	96039597	GTEx/v8	Colon Sigmoid	NOC3L	C	1.17053E-05	0.173093	1.73346E-11
rs7080472	10	96012950	GTEx/v8	Heart Atrial Appendage	NOC3L	T	1.20317E-05	0.164229	2.17353E-13
rs17109875	10	96026575	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	1.2032E-05	6,8346E+05	0.0338453327007472
rs10786156	10	96014622	GTEx/v8	Skin Not Sun Exposed Suprapubic	RP11-76P2.4	G	1.21338E-05	0.219968	5.98468E-07
rs3891783	10	96015793	GTEx/v8	Skin Not Sun Exposed Suprapubic	RP11-76P2.4	G	1.21338E-05	0.219968	5.98468E-07
rs57866767	10	96023077	GTEx/v8	Skin Not Sun Exposed Suprapubic	RP11-76P2.4	C	1.21338E-05	0.219968	5.98468E-07
rs10786156	10	96014622	GTEx/v8	Spleen	RP11-76P2.4	G	1.21461E-05	0.37517	9.37816E-08
rs3891783	10	96015793	GTEx/v8	Spleen	RP11-76P2.4	G	1.21461E-05	0.37517	9.37816E-08
rs57866767	10	96023077	GTEx/v8	Spleen	RP11-76P2.4	C	1.21461E-05	0.37517	9.37816E-08
rs2274224	10	96039597	GTEx/v8	Spleen	RP11-76P2.4	C	1.21461E-05	0.37517	9.37816E-08
rs11187838	10	96038686	GTEx/v8	Brain Hippocampus	NOC3L	A	1.21767E-05	0.237097	0.000170124
rs2274224	10	96039597	GTEx/v8	Brain Hippocampus	NOC3L	C	1.21767E-05	0.237097	0.000170124
rs7101207	10	96122857	BIOSQTL	BIOS eQTL geneLevel	HELLS	A	1.23339E-05	4.3716277	0.0083205004812319
rs7101207	10	96122857	BIOSQTL	BIOS eQTL geneLevel	RP11-119K6.6	A	1.23339E-05	4.3716277	0.0083205004812319
rs112252876	10	96123355	BIOSQTL	BIOS eQTL geneLevel	HELLS	T	1.23339E-05	4.3716277	0.0083205004812319
rs112252876	10	96123355	BIOSQTL	BIOS eQTL geneLevel	RP11-119K6.6	T	1.23339E-05	4.3716277	0.0083205004812319
rs2274224	10	96039597	GTEx/v8	Prostate	NOC3L	C	1.26886E-05	0.192241	7.10224E-08
rs7080472	10	96012950	GTEx/v8	Skin Not Sun Exposed Suprapubic	PLCE1	T	1.28165E-05	0.13641	9.09957E-06
rs11187863	10	96081457	GTEx/v8	Whole Blood	TBC1D12	G	1.29458E-05	0.229961	0.00686763
rs11187866	10	96085991	GTEx/v8	Whole Blood	TBC1D12	G	1.29458E-05	0.229961	0.00686763
rs11187883	10	96096866	GTEx/v8	Whole Blood	TBC1D12	C	1.29458E-05	0.229961	0.00686763

rs7096883	10	96069149	DICE	T CD4 TH1	PLCE1	A	1.33719940329E-05	0.827716391619	0.049
rs7100626	10	96069674	DICE	T CD4 TH1	PLCE1	A	1.33719940329E-05	0.827716391619	0.049
rs11187852	10	96070132	DICE	T CD4 TH1	PLCE1	A	1.33719940329E-05	0.827716391619	0.049
rs752140	10	96071396	DICE	T CD4 TH1	PLCE1	T	1.33719940329E-05	0.827716391619	0.049
rs11187864	10	96082506	DICE	T CD4 TH1 17	PLCE1	T	1.35358306881E-05	0.825812915876	0.049
rs11187870	10	96087866	DICE	T CD4 TH1 17	PLCE1	C	1.35358306881E-05	0.825812915876	0.049
rs145707916	10	96092992	DICE	T CD4 TH1 17	PLCE1	GA	1.35358306881E-05	0.825812915876	0.049
rs750148755	10	96095271	DICE	T CD4 TH1 17	PLCE1	C	1.35358306881E-05	0.825812915876	0.049
rs11187882	10	96095861	DICE	T CD4 TH1 17	PLCE1	C	1.35358306881E-05	0.825812915876	0.049
rs11187895	10	96106240	DICE	T CD4 TH1 17	PLCE1	C	1.35358306881E-05	0.825812915876	0.049
rs11187897	10	96106603	DICE	T CD4 TH1 17	PLCE1	G	1.35358306881E-05	0.825812915876	0.049
rs7080472	10	96012950	GTEx/v8	Skin Sun Exposed Lower leg	RP11-76P2.4	T	1.35417E-05	0.210063	1.123E-06
rs3740360	10	96025491	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	1.36375E-05	-0.307083	0.000644523
rs17109875	10	96026575	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	1.36375E-05	-0.307083	0.000644523
rs11187837	10	96035980	GTEx/v8	Adipose Visceral Omentum	PLCE1-AS1	C	1.36375E-05	-0.307083	0.000644523
rs3891783	10	96015793	GTEx/v8	Artery Tibial	PLCE1-AS1	G	1.3673E-05	0.133394	2.47435E-06
rs57866767	10	96023077	GTEx/v8	Artery Tibial	PLCE1-AS1	C	1.3673E-05	0.133394	2.47435E-06
rs11187845	10	96060198	DICE	T CD4 TH1	PLCE1	A	1.38155069706E-05	0.838348523246	0.049
rs34309017	10	96061619	DICE	T CD4 TH1	PLCE1	A	1.38155069706E-05	0.838348523246	0.049
rs12217792	10	96062386	DICE	T CD4 TH1	PLCE1	C	1.38155069706E-05	0.838348523246	0.049
rs11187847	10	96063440	DICE	T CD4 TH1	PLCE1	G	1.38155069706E-05	0.838348523246	0.049
rs75409190	10	96072425	DICE	T CD4 TH1	PLCE1	T	1.38155069706E-05	0.838348523246	0.049
rs771106747	10	96072873	DICE	T CD4 TH1	PLCE1	C	1.38155069706E-05	0.838348523246	0.049
rs749295068	10	96073508	DICE	T CD4 TH1	PLCE1	A	1.38155069706E-05	0.838348523246	0.049
rs11187856	10	96076869	DICE	T CD4 TH1	PLCE1	A	1.38155069706E-05	0.838348523246	0.049
rs11187837	10	96035980	eQTLGen	eQTLGen cis eQTLs	NOC3L	C	1.4029E-05	5,6111E+05	0.0391420118343195
rs11187838	10	96038686	GTEx/v8	Thyroid	TBC1D12	A	1.41454E-05	-0.12905	1.4449E-10
rs10786156	10	96014622	GTEx/v8	Brain Hippocampus	NOC3L	G	1.45003E-05	0.237209	0.000170124
rs3891783	10	96015793	GTEx/v8	Brain Hippocampus	NOC3L	G	1.45003E-05	0.237209	0.000170124
rs57866767	10	96023077	GTEx/v8	Brain Hippocampus	NOC3L	C	1.45003E-05	0.237209	0.000170124
rs34309017	10	96061619	GTEx/v8	Whole Blood	TBC1D12	A	1.51594E-05	0.2357	0.00686763
rs12217792	10	96062386	GTEx/v8	Whole Blood	TBC1D12	C	1.51594E-05	0.2357	0.00686763
rs11187838	10	96038686	GTEx/v8	Heart Atrial Appendage	NOC3L	A	1.52536E-05	0.162842	2.17353E-13
rs75409190	10	96072425	GTEx/v8	Whole Blood	TBC1D12	T	1.57792E-05	0.240261	0.00686763
rs771106747	10	96072873	GTEx/v8	Whole Blood	TBC1D12	C	1.57792E-05	0.240261	0.00686763
rs11187856	10	96076869	GTEx/v8	Whole Blood	TBC1D12	A	1.57792E-05	0.240261	0.00686763
rs2274224	10	96039597	GTEx/v8	Skin Sun Exposed Lower leg	RP11-76P2.4	C	1.60059E-05	0.205582	1.123E-06
rs10786156	10	96014622	GTEx/v8	Artery Tibial	PLCE1-AS1	G	1.67528E-05	0.132008	2.47435E-06
rs10786156	10	96014622	GTEx/v8	Heart Atrial Appendage	NOC3L	G	1.7044E-05	0.160855	2.17353E-13
rs3891783	10	96015793	GTEx/v8	Heart Atrial Appendage	NOC3L	G	1.7044E-05	0.160855	2.17353E-13

rs57866767	10	96023077	GTEx/v8	Heart Atrial Appendage	NOC3L	C	1.7044E-05	0.160855	2.17353E-13
rs778275808	10	96114212	DICE	T CD4 TH1 17	PLCE1	T	1.74378734524E-05	0.871571813104	0.049
rs10509672	10	96115957	DICE	T CD4 TH1 17	PLCE1	C	1.74378734524E-05	0.871571813104	0.049
rs74825688	10	96119687	DICE	T CD4 TH1 17	PLCE1	A	1.74378734524E-05	0.871571813104	0.049
rs79193572	10	96119713	DICE	T CD4 TH1 17	PLCE1	G	1.74378734524E-05	0.871571813104	0.049
rs11187906	10	96124838	DICE	T CD4 TH1 17	PLCE1	A	1.74378734524E-05	0.871571813104	0.049
rs11187907	10	96125361	DICE	T CD4 TH1 17	PLCE1	T	1.74378734524E-05	0.871571813104	0.049
rs113544984	10	96127448	DICE	T CD4 TH1 17	PLCE1	A	1.74378734524E-05	0.871571813104	0.049
rs11187838	10	96038686	GTEx/v8	Adipose Subcutaneous	NOC3L	A	1.74632E-05	0.109597	3.06299E-11
rs11187877	10	96092121	GTEx/v8	Thyroid	NOC3L	A	1.74843E-05	-0.162551	0.00220997
rs7080472	10	96012950	GTEx/v8	Spleen	NOC3L	T	1.75545E-05	0.224477	1.49159E-15
rs11187882	10	96095861	GTEx/v8	Whole Blood	TBC1D12	C	1.77453E-05	0.239411	0.00686763
rs11187844	10	96056629	eQTLGen	eQTLGen cis eQTLs	PDLIM1	A	1.7948E-05	-4.2889	0.0491932634554234
rs7100626	10	96069674	GTEx/v8	Thyroid	NOC3L	A	1.81872E-05	-0.162883	0.00220997
rs11187852	10	96070132	GTEx/v8	Thyroid	NOC3L	A	1.81872E-05	-0.162883	0.00220997
rs753724	10	96051417	GTEx/v8	Muscle Skeletal	NOC3L	T	1.82552E-05	0.20526	7.35621E-14
rs11187842	10	96052511	GTEx/v8	Muscle Skeletal	NOC3L	T	1.82552E-05	0.20526	7.35621E-14
rs3781266	10	96052747	GTEx/v8	Muscle Skeletal	NOC3L	G	1.82552E-05	0.20526	7.35621E-14
rs3740365	10	96053239	GTEx/v8	Muscle Skeletal	NOC3L	A	1.82552E-05	0.20526	7.35621E-14
rs12220091	10	96053689	GTEx/v8	Muscle Skeletal	NOC3L	T	1.82552E-05	0.20526	7.35621E-14
rs3891783	10	96015793	GTEx/v8	Skin Sun Exposed Lower leg	RP11-76P2.4	G	1.96428E-05	0.204197	1.123E-06
rs57866767	10	96023077	GTEx/v8	Skin Sun Exposed Lower leg	RP11-76P2.4	C	1.96428E-05	0.204197	1.123E-06
rs7080472	10	96012950	GTEx/v8	Prostate	NOC3L	T	1.9685E-05	0.188107	7.10224E-08
rs11187838	10	96038686	GTEx/v8	Artery Tibial	PLCE1	A	2.06124E-05	0.106027	1.21915E-07
rs2274224	10	96039597	GTEx/v8	Skin Not Sun Exposed Suprapubic	RP11-76P2.4	C	2.0648E-05	0.214	5.98468E-07
rs11187845	10	96060198	GTEx/v8	Whole Blood	TBC1D12	A	2.10554E-05	0.225987	0.00686763
rs11187847	10	96063440	GTEx/v8	Whole Blood	TBC1D12	G	2.10554E-05	0.225987	0.00686763
rs10786156	10	96014622	GTEx/v8	Adipose Subcutaneous	NOC3L	G	2.14308E-05	0.107454	3.06299E-11
rs11187895	10	96106240	GTEx/v8	Thyroid	NOC3L	C	2.14366E-05	-0.162118	0.00220997
rs11187897	10	96106603	GTEx/v8	Thyroid	NOC3L	G	2.14366E-05	-0.162118	0.00220997
rs3891783	10	96015793	GTEx/v8	Adipose Subcutaneous	NOC3L	G	2.14918E-05	0.107701	3.06299E-11
rs57866767	10	96023077	GTEx/v8	Adipose Subcutaneous	NOC3L	C	2.14918E-05	0.107701	3.06299E-11
rs10786156	10	96014622	GTEx/v8	Skin Sun Exposed Lower leg	RP11-76P2.4	G	2.15253E-05	0.203092	1.123E-06
rs2274224	10	96039597	GTEx/v8	Artery Tibial	PLCE1-AS1	C	2.18917E-05	0.13008	2.47435E-06
rs7096883	10	96069149	GTEx/v8	Thyroid	NOC3L	A	2.23774E-05	-0.157473	0.00220997
rs11187840	10	96050351	GTEx/v8	Muscle Skeletal	NOC3L	G	2.264E-05	0.204891	7.35621E-14
rs75017201	10	96055152	GTEx/v8	Muscle Skeletal	NOC3L	T	2.264E-05	0.204891	7.35621E-14
rs7080472	10	96012950	GTEx/v8	Nerve Tibial	PLCE1	T	2.35053E-05	0.140728	1.91043E-25
rs7080472	10	96012950	GTEx/v8	Colon Transverse	RP11-76P2.4	T	2.41297E-05	0.26705	2.2326E-06
rs7080472	10	96012950	GTEx/v8	Skin Not Sun Exposed Suprapubic	RP11-76P2.4	T	2.42629E-05	0.214514	5.98468E-07

rs11187877	10	96092121	GTEx/v8	Whole Blood	TBC1D12	A	2.46351E-05	0.232016	0.00686763
rs11187838	10	96038686	GTEx/v8	Muscle Skeletal	NOC3L	A	2.53713E-05	0.114667	7.35621E-14
rs11187907	10	96125361	BIOSQTL	BIOS eQTL geneLevel	HELLS	T	2.59241E-05	4.2066091	0.0160794899241402
rs11187907	10	96125361	BIOSQTL	BIOS eQTL geneLevel	RP11-119K6.6	T	2.59241E-05	4.2066091	0.0160794899241402
rs113544984	10	96127448	BIOSQTL	BIOS eQTL geneLevel	HELLS	A	2.67387E-05	4.1997961	0.0165349572331722
rs113544984	10	96127448	BIOSQTL	BIOS eQTL geneLevel	RP11-119K6.6	A	2.67387E-05	4.1997961	0.0165349572331722
rs10786156	10	96014622	GTEx/v8	Brain Cerebellar Hemisphere	PLCE1	G	2.68601E-05	0.243306	0.0391634
rs3891783	10	96015793	GTEx/v8	Brain Cerebellar Hemisphere	PLCE1	G	2.68601E-05	0.243306	0.0391634
rs57866767	10	96023077	GTEx/v8	Brain Cerebellar Hemisphere	PLCE1	C	2.68601E-05	0.243306	0.0391634
rs11187838	10	96038686	GTEx/v8	Skin Not Sun Exposed Suprapubic	PLCE1	A	2.70779E-05	0.131307	9.09957E-06
rs10786156	10	96014622	GTEx/v8	Skin Not Sun Exposed Suprapubic	PLCE1	G	2.85818E-05	0.129644	9.09957E-06
rs3891783	10	96015793	GTEx/v8	Skin Not Sun Exposed Suprapubic	PLCE1	G	2.85818E-05	0.129644	9.09957E-06
rs57866767	10	96023077	GTEx/v8	Skin Not Sun Exposed Suprapubic	PLCE1	C	2.85818E-05	0.129644	9.09957E-06
rs7080472	10	96012950	GTEx/v8	Muscle Skeletal	NOC3L	T	2.88251E-05	0.114279	7.35621E-14
rs11187864	10	96082506	GTEx/v8	Whole Blood	TBC1D12	T	2.9558E-05	0.230494	0.00686763
rs145707916	10	96092992	GTEx/v8	Whole Blood	TBC1D12	GA	2.9558E-05	0.230494	0.00686763
rs750148755	10	96095271	GTEx/v8	Whole Blood	TBC1D12	C	2.9558E-05	0.230494	0.00686763
rs11187838	10	96038686	GTEx/v8	Brain Cerebellar Hemisphere	PLCE1	A	3.05367E-05	0.241508	0.0391634
rs2274224	10	96039597	GTEx/v8	Brain Cerebellar Hemisphere	PLCE1	C	3.05367E-05	0.241508	0.0391634
rs2274224	10	96039597	GTEx/v8	Heart Atrial Appendage	NOC3L	C	3.21677E-05	0.156215	2.17353E-13
rs2274224	10	96039597	GTEx/v8	Muscle Skeletal	NOC3L	C	3.2592E-05	0.112813	7.35621E-14
rs11187870	10	96087866	GTEx/v8	Thyroid	NOC3L	C	3.43653E-05	-0.158631	0.00220997
rs11187864	10	96082506	GTEx/v8	Thyroid	NOC3L	T	3.55691E-05	-0.157449	0.00220997
rs145707916	10	96092992	GTEx/v8	Thyroid	NOC3L	GA	3.55691E-05	-0.157449	0.00220997
rs750148755	10	96095271	GTEx/v8	Thyroid	NOC3L	C	3.55691E-05	-0.157449	0.00220997
rs11187882	10	96095861	GTEx/v8	Thyroid	NOC3L	C	3.55691E-05	-0.157449	0.00220997
rs2077218	10	96071561	BIOSQTL	BIOS eQTL geneLevel	NOC3L	G	3.60874E-05	-4.13111	0.0217668071075289
rs3891783	10	96015793	GTEx/v8	Muscle Skeletal	NOC3L	G	3.63252E-05	0.112317	7.35621E-14
rs57866767	10	96023077	GTEx/v8	Muscle Skeletal	NOC3L	C	3.63252E-05	0.112317	7.35621E-14
rs75409190	10	96072425	GTEx/v8	Thyroid	NOC3L	T	3.71677E-05	-0.157685	0.00220997
rs771106747	10	96072873	GTEx/v8	Thyroid	NOC3L	C	3.71677E-05	-0.157685	0.00220997
rs749295068	10	96073508	GTEx/v8	Thyroid	NOC3L	A	3.71677E-05	-0.157685	0.00220997
rs11187856	10	96076869	GTEx/v8	Thyroid	NOC3L	A	3.71677E-05	-0.157685	0.00220997
rs3740359	10	96100119	GTEx/v8	Whole Blood	TBC1D12	T	3.72385E-05	0.207278	0.00686763
rs10786156	10	96014622	GTEx/v8	Muscle Skeletal	NOC3L	G	3.72999E-05	0.112118	7.35621E-14
rs7080472	10	96012950	GTEx/v8	Brain Hippocampus	NOC3L	T	3.88052E-05	0.225972	0.000170124
10:96112261_AAAAAAAC_A	10	96112261	DICE	T CD4 TH1 17	PLCE1	A	4.05134739452E-05	0.825353456446	0.049
rs10786156	10	96014622	GTEx/v8	Nerve Tibial	PLCE1	G	4.08489E-05	0.136054	1.91043E-25
rs769015184	10	96049708	DICE	T CD4 TH1	PLCE1	A	4.16589029341E-05	0.760076218492	0.049

rs11187840	10	96050351	DICE	T CD4 TH1	PLCE1	G	4.16589029341E-05	0.760076218492	0.049
rs753724	10	96051417	DICE	T CD4 TH1	PLCE1	T	4.16589029341E-05	0.760076218492	0.049
rs11187842	10	96052511	DICE	T CD4 TH1	PLCE1	T	4.16589029341E-05	0.760076218492	0.049
rs3781266	10	96052747	DICE	T CD4 TH1	PLCE1	G	4.16589029341E-05	0.760076218492	0.049
rs3740365	10	96053239	DICE	T CD4 TH1	PLCE1	A	4.16589029341E-05	0.760076218492	0.049
rs12220091	10	96053689	DICE	T CD4 TH1	PLCE1	T	4.16589029341E-05	0.760076218492	0.049
rs2274224	10	96039597	GTEx/v8	Skin Not Sun Exposed Suprapubic	PLCE1	C	4.22949E-05	0.1268	9.09957E-06
rs7080472	10	96012950	GTEx/v8	Spleen	RP11-76P2.4	T	4.24579E-05	0.346219	9.37816E-08
rs7080472	10	96012950	GTEx/v8	Brain Cerebellar Hemisphere	PLCE1	T	4.31362E-05	0.242741	0.0391634
rs7078844	10	96081140	GTEx/v8	Brain Cerebellum	HELLS	C	4.34404E-05	-0.28832	1.07902E-06
rs11187907	10	96125361	BIOSQTL	BIOS eQTL geneLevel	NOC3L	T	4.38874E-05	4.0861408	0.0259650235592606
rs113544984	10	96127448	BIOSQTL	BIOS eQTL geneLevel	NOC3L	A	4.38874E-05	4.0861408	0.0259650235592606
rs3740360	10	96025491	DICE	T CD4 TH1	PLCE1	C	4.42723585059E-05	0.755815010248	0.049
rs17109875	10	96026575	DICE	T CD4 TH1	PLCE1	C	4.42723585059E-05	0.755815010248	0.049
rs11187837	10	96035980	DICE	T CD4 TH1	PLCE1	C	4.42723585059E-05	0.755815010248	0.049
rs34309017	10	96061619	GTEx/v8	Thyroid	NOC3L	A	4.48906E-05	-0.152426	0.00220997
rs12217792	10	96062386	GTEx/v8	Thyroid	NOC3L	C	4.48906E-05	-0.152426	0.00220997
rs11187826	10	95988042	PsychENCODE	PsychENCODE eQTLs	NOC3L	G	4.65866E-05	0.0668799	0.0043080936142294
rs75017201	10	96055152	DICE	T CD4 TH1	PLCE1	T	4.7192585625E-05	0.749469540464	0.049
rs11187840	10	96050351	GTEx/v8	Whole Blood	TBC1D12	G	4.78334E-05	0.218164	0.00686763
rs75017201	10	96055152	GTEx/v8	Whole Blood	TBC1D12	T	4.78334E-05	0.218164	0.00686763
rs11187863	10	96081457	DICE	T CD4 TH1 17	PLCE1	G	4.90263652512E-05	0.764200029398	0.049
rs11187866	10	96085991	DICE	T CD4 TH1 17	PLCE1	G	4.90263652512E-05	0.764200029398	0.049
rs11187877	10	96092121	DICE	T CD4 TH1 17	PLCE1	A	4.90263652512E-05	0.764200029398	0.049
rs11187883	10	96096866	DICE	T CD4 TH1 17	PLCE1	C	4.90263652512E-05	0.764200029398	0.049
rs11187890	10	96102758	DICE	T CD4 TH1 17	PLCE1	C	4.90263652512E-05	0.764200029398	0.049
rs3891783	10	96015793	GTEx/v8	Nerve Tibial	PLCE1	G	5.14442E-05	0.134396	1.91043E-25
rs57866767	10	96023077	GTEx/v8	Nerve Tibial	PLCE1	C	5.14442E-05	0.134396	1.91043E-25
rs778275808	10	96114212	DICE	T CD4 naive TREG	PLCE1	T	5.26981619237E-05	0.803940206822	0.049
rs10509672	10	96115957	DICE	T CD4 naive TREG	PLCE1	C	5.26981619237E-05	0.803940206822	0.049
rs74825688	10	96119687	DICE	T CD4 naive TREG	PLCE1	A	5.26981619237E-05	0.803940206822	0.049
rs79193572	10	96119713	DICE	T CD4 naive TREG	PLCE1	G	5.26981619237E-05	0.803940206822	0.049
rs11187906	10	96124838	DICE	T CD4 naive TREG	PLCE1	A	5.26981619237E-05	0.803940206822	0.049
rs11187907	10	96125361	DICE	T CD4 naive TREG	PLCE1	T	5.26981619237E-05	0.803940206822	0.049
rs113544984	10	96127448	DICE	T CD4 naive TREG	PLCE1	A	5.26981619237E-05	0.803940206822	0.049
rs3891783	10	96015793	GTEx/v8	Nerve Tibial	RP11-76P2.4	G	5.28035E-05	0.188273	5.10248E-05
rs57866767	10	96023077	GTEx/v8	Nerve Tibial	RP11-76P2.4	C	5.28035E-05	0.188273	5.10248E-05
rs7101207	10	96122857	BIOSQTL	BIOS eQTL geneLevel	NOC3L	A	5.52101E-05	4.0325847	0.0318882681564246
rs778275808	10	96114212	GTEx/v8	Colon Transverse	CYP2C19	T	5.57377E-05	0.212138	0.023149
rs10509672	10	96115957	GTEx/v8	Colon Transverse	CYP2C19	C	5.57377E-05	0.212138	0.023149
rs74825688	10	96119687	GTEx/v8	Colon Transverse	CYP2C19	A	5.57377E-05	0.212138	0.023149
rs79193572	10	96119713	GTEx/v8	Colon Transverse	CYP2C19	G	5.57377E-05	0.212138	0.023149

rs113544984	10	96127448	GTEx/v8	Colon Transverse	CYP2C19	A	5.57377E-05	0.212138	0.023149
rs79746649	10	96120218	GTEx/v8	Colon Transverse	CYP2C19	T	5.59505E-05	0.209954	0.023149
rs7101207	10	96122857	GTEx/v8	Colon Transverse	CYP2C19	A	5.59505E-05	0.209954	0.023149
rs112252876	10	96123355	GTEx/v8	Colon Transverse	CYP2C19	T	5.59505E-05	0.209954	0.023149
rs3740359	10	96100119	GTEx/v8	Thyroid	NOC3L	T	5.65973E-05	-0.141322	0.00220997
rs11187845	10	96060198	DICE	T CD4 TH1 17	PLCE1	A	5.72412574339E-05	0.773056370538	0.049
rs34309017	10	96061619	DICE	T CD4 TH1 17	PLCE1	A	5.72412574339E-05	0.773056370538	0.049
rs12217792	10	96062386	DICE	T CD4 TH1 17	PLCE1	C	5.72412574339E-05	0.773056370538	0.049
rs11187847	10	96063440	DICE	T CD4 TH1 17	PLCE1	G	5.72412574339E-05	0.773056370538	0.049
rs75409190	10	96072425	DICE	T CD4 TH1 17	PLCE1	T	5.72412574339E-05	0.773056370538	0.049
rs771106747	10	96072873	DICE	T CD4 TH1 17	PLCE1	C	5.72412574339E-05	0.773056370538	0.049
rs749295068	10	96073508	DICE	T CD4 TH1 17	PLCE1	A	5.72412574339E-05	0.773056370538	0.049
rs11187856	10	96076869	DICE	T CD4 TH1 17	PLCE1	A	5.72412574339E-05	0.773056370538	0.049
rs7078844	10	96081140	GTEx/v8	Brain Cerebellar Hemisphere	HELLS	C	5.74834E-05	-0.278659	8.15147E-08
rs112252876	10	96123355	BIOSQTL	BIOS eQTL geneLevel	NOC3L	T	5.86444E-05	4.0183398	0.0336986057285402
rs3740360	10	96025491	GTEx/v8	Thyroid	NOC3L	C	5.9122E-05	-0.136651	0.00220997
rs17109875	10	96026575	GTEx/v8	Thyroid	NOC3L	C	5.9122E-05	-0.136651	0.00220997
rs7101207	10	96122857	GTEx/v8	Adipose Visceral Omentum	NOC3L	A	5.96319E-05	0.160985	0.000238073
rs112252876	10	96123355	GTEx/v8	Adipose Visceral Omentum	NOC3L	T	5.96319E-05	0.160985	0.000238073
rs753724	10	96051417	GTEx/v8	Whole Blood	TBC1D12	T	6.22965E-05	0.209754	0.00686763
rs11187842	10	96052511	GTEx/v8	Whole Blood	TBC1D12	T	6.22965E-05	0.209754	0.00686763
rs3781266	10	96052747	GTEx/v8	Whole Blood	TBC1D12	G	6.22965E-05	0.209754	0.00686763
rs3740365	10	96053239	GTEx/v8	Whole Blood	TBC1D12	A	6.22965E-05	0.209754	0.00686763
rs12220091	10	96053689	GTEx/v8	Whole Blood	TBC1D12	T	6.22965E-05	0.209754	0.00686763
rs11187845	10	96060198	GTEx/v8	Thyroid	NOC3L	A	6.31024E-05	-0.147662	0.00220997
rs11187847	10	96063440	GTEx/v8	Thyroid	NOC3L	G	6.31024E-05	-0.147662	0.00220997
rs11187838	10	96038686	GTEx/v8	Spleen	RP11-76P2.4	A	6.34948E-05	0.344413	9.37816E-08
rs7080472	10	96012950	GTEx/v8	Artery Tibial	NOC3L	T	6.38049E-05	0.099248	1.31505E-07
rs11187890	10	96102758	GTEx/v8	Whole Blood	TBC1D12	C	6.51491E-05	0.222292	0.00686763
rs79746649	10	96120218	DICE	T CD4 TH1 17	PLCE1	T	6.7940652152E-05	0.800331492037	0.049
rs7101207	10	96122857	DICE	T CD4 TH1 17	PLCE1	A	6.7940652152E-05	0.800331492037	0.049
rs112252876	10	96123355	DICE	T CD4 TH1 17	PLCE1	T	6.7940652152E-05	0.800331492037	0.049
rs2274224	10	96039597	GTEx/v8	Artery Tibial	RP11-76P2.4	C	6.81555E-05	0.188221	5.41051E-05
rs113544984	10	96127448	GTEx/v8	Adipose Visceral Omentum	NOC3L	A	6.84112E-05	0.161311	0.000238073
rs11187870	10	96087866	GTEx/v8	Whole Blood	TBC1D12	C	6.8925E-05	0.222498	0.00686763
rs11187907	10	96125361	GTEx/v8	Colon Transverse	CYP2C19	T	7.07444E-05	0.203081	0.023149
rs79746649	10	96120218	GTEx/v8	Colon Transverse	CYP2C9	T	7.09602E-05	0.229437	0.0239192
rs7101207	10	96122857	GTEx/v8	Colon Transverse	CYP2C9	A	7.09602E-05	0.229437	0.0239192
rs112252876	10	96123355	GTEx/v8	Colon Transverse	CYP2C9	T	7.09602E-05	0.229437	0.0239192
rs11187870	10	96087866	GTEx/v8	Colon Transverse	CYP2C19	C	7.10595E-05	0.207839	0.023149
rs2274224	10	96039597	GTEx/v8	Colon Transverse	RP11-76P2.4	C	7.1415E-05	0.251217	2.2326E-06
rs2077218	10	96071561	GTEx/v8	Thyroid	PLCE1	A	7.35307E-05	-0.140544	1.91428E-05
rs10786156	10	96014622	GTEx/v8	Colon Transverse	RP11-76P2.4	G	7.37059E-05	0.251868	2.2326E-06
rs3891783	10	96015793	GTEx/v8	Colon Transverse	RP11-76P2.4	G	7.37059E-05	0.251868	2.2326E-06

rs57866767	10	96023077	GTEx/v8	Colon Transverse	RP11-76P2.4	C	7.37059E-05	0.251868	2.2326E-06
rs11187838	10	96038686	GTEx/v8	Nerve Tibial	PLCE1	A	7.57587E-05	0.131345	1.91043E-25
rs11187838	10	96038686	GTEx/v8	Skin Sun Exposed Lower leg	RP11-76P2.4	A	7.65039E-05	0.189406	1.123E-06
rs11187895	10	96106240	GTEx/v8	Whole Blood	TBC1D12	C	7.77315E-05	0.220691	0.00686763
rs11187897	10	96106603	GTEx/v8	Whole Blood	TBC1D12	G	7.77315E-05	0.220691	0.00686763
rs3891783	10	96015793	GTEx/v8	Artery Tibial	RP11-76P2.4	G	7.82492E-05	0.18693	5.41051E-05
rs57866767	10	96023077	GTEx/v8	Artery Tibial	RP11-76P2.4	C	7.82492E-05	0.18693	5.41051E-05
rs2274224	10	96039597	GTEx/v8	Nerve Tibial	PLCE1	C	7.91228E-05	0.130521	1.91043E-25
rs11187838	10	96038686	GTEx/v8	Whole Blood	NOC3L	A	7.92195E-05	0.0850059	0.000592991
rs79746649	10	96120218	GTEx/v8	Whole Blood	TBC1D12	T	8.02709E-05	0.220546	0.00686763
rs11187838	10	96038686	GTEx/v8	Colon Transverse	RP11-76P2.4	A	8.22798E-05	0.247262	2.2326E-06
rs7080472	10	96012950	GTEx/v8	Nerve Tibial	RP11-76P2.4	T	8.43931E-05	0.183804	5.10248E-05
rs10786156	10	96014622	GTEx/v8	Artery Tibial	RP11-76P2.4	G	8.49316E-05	0.18596	5.41051E-05
rs11187895	10	96106240	BIOSQTL	BIOS eQTL geneLevel	NOC3L	C	8.53708E-05	3.9289554	0.0465583340594232
rs11187897	10	96106603	BIOSQTL	BIOS eQTL geneLevel	NOC3L	G	8.53708E-05	3.9289554	0.0465583340594232
rs10509672	10	96115957	BIOSQTL	BIOS eQTL geneLevel	NOC3L	C	8.53708E-05	3.9289785	0.0465583340594232
rs74825688	10	96119687	BIOSQTL	BIOS eQTL geneLevel	NOC3L	A	8.53708E-05	3.9289785	0.0465583340594232
rs79193572	10	96119713	BIOSQTL	BIOS eQTL geneLevel	NOC3L	G	8.53708E-05	3.9289785	0.0465583340594232
rs79746649	10	96120218	BIOSQTL	BIOS eQTL geneLevel	NOC3L	T	8.53708E-05	3.9289785	0.0465583340594232
rs7078844	10	96081140	GTEx/v8	Cells Cultured fibroblasts	PLCE1-AS1	C	8.71297E-05	-0.147185	3.86001E-30
rs2274224	10	96039597	GTEx/v8	Whole Blood	NOC3L	C	8.78308E-05	0.084549	0.000592991
rs11187890	10	96102758	BIOSQTL	BIOS eQTL geneLevel	NOC3L	C	9.03293E-05	3.9152898	0.0491618170763485
rs2077218	10	96071561	GTEx/v8	Thyroid	PLCE1-AS1	A	9.06102E-05	-0.143826	0.00721889
rs10786156	10	96014622	GTEx/v8	Whole Blood	NOC3L	G	9.22693E-05	0.0845518	0.000592991
rs778275808	10	96114212	GTEx/v8	Whole Blood	TBC1D12	T	9.58649E-05	0.218869	0.00686763
rs10509672	10	96115957	GTEx/v8	Whole Blood	TBC1D12	C	9.58649E-05	0.218869	0.00686763
rs11187895	10	96106240	GTEx/v8	Colon Transverse	CYP2C19	C	9.87863E-05	0.202956	0.023149
rs11187897	10	96106603	GTEx/v8	Colon Transverse	CYP2C19	G	9.87863E-05	0.202956	0.023149
rs11187890	10	96102758	GTEx/v8	Colon Transverse	CYP2C19	C	9.91947E-05	0.200806	0.023149
rs11187840	10	96050351	GTEx/v8	Thyroid	NOC3L	G	9.98719E-05	-0.143413	0.00220997
rs75017201	10	96055152	GTEx/v8	Thyroid	NOC3L	T	9.98719E-05	-0.143413	0.00220997
rs74825688	10	96119687	GTEx/v8	Whole Blood	TBC1D12	A	0.000101837	0.217022	0.00686763
rs10786156	10	96014622	GTEx/v8	Nerve Tibial	RP11-76P2.4	G	0.00010197	0.180963	5.10248E-05
rs3740360	10	96025491	GTEx/v8	Whole Blood	TBC1D12	C	0.000102034	0.192773	0.00686763
rs17109875	10	96026575	GTEx/v8	Whole Blood	TBC1D12	C	0.000102034	0.192773	0.00686763
rs11187837	10	96035980	GTEx/v8	Whole Blood	TBC1D12	C	0.000102034	0.192773	0.00686763
rs7080472	10	96012950	GTEx/v8	Artery Tibial	RP11-76P2.4	T	0.000105243	0.184919	5.41051E-05
rs79193572	10	96119713	GTEx/v8	Whole Blood	TBC1D12	G	0.000110383	0.218162	0.00686763
rs11187907	10	96125361	GTEx/v8	Colon Transverse	CYP2C9	T	0.000117747	0.218194	0.0239192
rs11187837	10	96035980	GTEx/v8	Thyroid	NOC3L	C	0.000120608	-0.13038	0.00220997
rs11187838	10	96038686	GTEx/v8	Artery Tibial	RP11-76P2.4	A	0.000121227	0.181833	5.41051E-05
rs3891783	10	96015793	GTEx/v8	Whole Blood	NOC3L	G	0.000124756	0.0828281	0.000592991
rs57866767	10	96023077	GTEx/v8	Whole Blood	NOC3L	C	0.000124756	0.0828281	0.000592991
rs778275808	10	96114212	GTEx/v8	Colon Transverse	CYP2C9	T	0.000130747	0.223355	0.0239192
rs10509672	10	96115957	GTEx/v8	Colon Transverse	CYP2C9	C	0.000130747	0.223355	0.0239192
rs74825688	10	96119687	GTEx/v8	Colon Transverse	CYP2C9	A	0.000130747	0.223355	0.0239192

rs79193572	10	96119713	GTEx/v8	Colon Transverse	CYP2C9	G	0.000130747	0.223355	0.0239192
rs113544984	10	96127448	GTEx/v8	Colon Transverse	CYP2C9	A	0.000130747	0.223355	0.0239192
rs11187838	10	96038686	GTEx/v8	Colon Transverse	CYP2C9	A	0.000131607	0.121358	0.0239192
rs7080472	10	96012950	GTEx/v8	Whole Blood	NOC3L	T	0.000132449	0.0827353	0.000592991
rs11187864	10	96082506	GTEx/v8	Colon Transverse	CYP2C19	T	0.000136789	0.197872	0.023149
rs145707916	10	96092992	GTEx/v8	Colon Transverse	CYP2C19	GA	0.000136789	0.197872	0.023149
rs750148755	10	96095271	GTEx/v8	Colon Transverse	CYP2C19	C	0.000136789	0.197872	0.023149
rs11187882	10	96095861	GTEx/v8	Colon Transverse	CYP2C19	C	0.000136789	0.197872	0.023149
rs11187877	10	96092121	GTEx/v8	Colon Transverse	CYP2C19	A	0.00013711	0.195787	0.023149
rs7078844	10	96081140	GTEx/v8	Skin Not Sun Exposed Suprapubic	NOC3L	C	0.000137394	0.132453	2.01564E-23
rs753724	10	96051417	GTEx/v8	Thyroid	NOC3L	T	0.000138111	-0.138724	0.00220997
rs11187842	10	96052511	GTEx/v8	Thyroid	NOC3L	T	0.000138111	-0.138724	0.00220997
rs3781266	10	96052747	GTEx/v8	Thyroid	NOC3L	G	0.000138111	-0.138724	0.00220997
rs3740365	10	96053239	GTEx/v8	Thyroid	NOC3L	A	0.000138111	-0.138724	0.00220997
rs12220091	10	96053689	GTEx/v8	Thyroid	NOC3L	T	0.000138111	-0.138724	0.00220997
rs11187838	10	96038686	GTEx/v8	Colon Transverse	MTND4P20	A	0.000139292	0.116351	0.0452717
rs11187863	10	96081457	GTEx/v8	Colon Transverse	CYP2C9	G	0.000141772	0.203738	0.0239192
rs11187866	10	96085991	GTEx/v8	Colon Transverse	CYP2C9	G	0.000141772	0.203738	0.0239192
rs11187883	10	96096866	GTEx/v8	Colon Transverse	CYP2C9	C	0.000141772	0.203738	0.0239192
rs11187845	10	96060198	GTEx/v8	Thyroid	PLCE1	A	0.000142332	-0.183373	1.91428E-05
rs11187847	10	96063440	GTEx/v8	Thyroid	PLCE1	G	0.000142332	-0.183373	1.91428E-05
rs2274224	10	96039597	GTEx/v8	Nerve Tibial	RP11-76P2.4	C	0.000156152	0.175538	5.10248E-05
rs2274224	10	96039597	GTEx/v8	Colon Transverse	CYP2C9	C	0.000157209	0.1209	0.0239192
rs752140	10	96071396	GTEx/v8	Colon Transverse	CYP2C9	T	0.00016468	0.202017	0.0239192
rs11187838	10	96038686	GTEx/v8	Nerve Tibial	RP11-76P2.4	A	0.000182236	0.174418	5.10248E-05
rs2274224	10	96039597	GTEx/v8	Muscle Skeletal	CYP2C8	C	0.00020384	0.15337	5.87392E-21
rs753724	10	96051417	GTEx/v8	Thyroid	PLCE1	T	0.000252113	-0.173953	1.91428E-05
rs11187842	10	96052511	GTEx/v8	Thyroid	PLCE1	T	0.000252113	-0.173953	1.91428E-05
rs3781266	10	96052747	GTEx/v8	Thyroid	PLCE1	G	0.000252113	-0.173953	1.91428E-05
rs3740365	10	96053239	GTEx/v8	Thyroid	PLCE1	A	0.000252113	-0.173953	1.91428E-05
rs12220091	10	96053689	GTEx/v8	Thyroid	PLCE1	T	0.000252113	-0.173953	1.91428E-05
rs79746649	10	96120218	GTEx/v8	Thyroid	NOC3L	T	0.000260305	-0.141234	0.00220997
rs10786156	10	96014622	GTEx/v8	Muscle Skeletal	CYP2C8	G	0.000285424	0.150035	5.87392E-21
rs3891783	10	96015793	GTEx/v8	Muscle Skeletal	CYP2C8	G	0.000318235	0.148928	5.87392E-21
rs57866767	10	96023077	GTEx/v8	Muscle Skeletal	CYP2C8	C	0.000318235	0.148928	5.87392E-21
rs11187826	10	95988042	CMC	CMC SVA cis	NOC3L	G		1.0	0.049
rs7080472	10	96012950	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs10786156	10	96014622	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs3891783	10	96015793	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs57866767	10	96023077	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs3740360	10	96025491	CMC	CMC SVA cis	NOC3L	C		1.0	0.049
rs17109875	10	96026575	CMC	CMC SVA cis	NOC3L	C		1.0	0.049
rs11187837	10	96035980	CMC	CMC SVA cis	NOC3L	C		1.0	0.049
rs11187838	10	96038686	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs2274224	10	96039597	CMC	CMC SVA cis	NOC3L	C		1.0	0.009

rs769015184	10	96049708	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs11187840	10	96050351	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs753724	10	96051417	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs11187842	10	96052511	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs3781266	10	96052747	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs3740365	10	96053239	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs12220091	10	96053689	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs75017201	10	96055152	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs200197176	10	96055963	CMC	CMC SVA cis	NOC3L	CA		1.0	0.009
rs11187844	10	96056629	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs11187845	10	96060198	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs34309017	10	96061619	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs12217792	10	96062386	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs11187847	10	96063440	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs7096883	10	96069149	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs7100626	10	96069674	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs11187852	10	96070132	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs752140	10	96071396	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs75409190	10	96072425	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs771106747	10	96072873	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs749295068	10	96073508	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs11187856	10	96076869	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs7078844	10	96081140	CMC	CMC SVA cis	HELLS	T		1.0	0.049
rs11187863	10	96081457	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs11187864	10	96082506	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs11187866	10	96085991	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs11187870	10	96087866	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs11187877	10	96092121	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs145707916	10	96092992	CMC	CMC SVA cis	NOC3L	GA		1.0	0.009
rs750148755	10	96095271	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs11187882	10	96095861	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs11187883	10	96096866	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs3740359	10	96100119	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs11187890	10	96102758	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs11187895	10	96106240	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs11187897	10	96106603	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
10:96112261_AAAAAAAC_A	10	96112261	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs778275808	10	96114212	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs10509672	10	96115957	CMC	CMC SVA cis	NOC3L	C		1.0	0.009
rs74825688	10	96119687	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs79193572	10	96119713	CMC	CMC SVA cis	NOC3L	G		1.0	0.009
rs79746649	10	96120218	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs7101207	10	96122857	CMC	CMC SVA cis	NOC3L	A		1.0	0.009

rs112252876	10	96123355	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs11187906	10	96124838	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs11187907	10	96125361	CMC	CMC SVA cis	NOC3L	T		1.0	0.009
rs113544984	10	96127448	CMC	CMC SVA cis	NOC3L	A		1.0	0.009
rs7080472	10	96012950	CMC	CMC NoSVA cis	PLCE1	T		1.0	0.049
rs7080472	10	96012950	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs10786156	10	96014622	CMC	CMC NoSVA cis	PLCE1	G		1.0	0.049
rs10786156	10	96014622	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.009
rs3891783	10	96015793	CMC	CMC NoSVA cis	PLCE1	G		1.0	0.049
rs3891783	10	96015793	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.009
rs57866767	10	96023077	CMC	CMC NoSVA cis	PLCE1	C		1.0	0.049
rs57866767	10	96023077	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.009
rs11187838	10	96038686	CMC	CMC NoSVA cis	PLCE1	A		1.0	0.049
rs11187838	10	96038686	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.009
rs2274224	10	96039597	CMC	CMC NoSVA cis	PLCE1	C		1.0	0.049
rs2274224	10	96039597	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.009
rs769015184	10	96049708	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs11187840	10	96050351	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.049
rs753724	10	96051417	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs11187842	10	96052511	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs3781266	10	96052747	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.049
rs3740365	10	96053239	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs12220091	10	96053689	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs75017201	10	96055152	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs200197176	10	96055963	CMC	CMC NoSVA cis	NOC3L	CA		1.0	0.009
rs11187845	10	96060198	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs34309017	10	96061619	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs12217792	10	96062386	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs11187847	10	96063440	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.049
rs7096883	10	96069149	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs7100626	10	96069674	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs11187852	10	96070132	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs752140	10	96071396	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs75409190	10	96072425	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs771106747	10	96072873	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs749295068	10	96073508	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs11187856	10	96076869	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs11187863	10	96081457	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.049
rs11187864	10	96082506	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs11187866	10	96085991	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.049
rs11187870	10	96087866	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs11187877	10	96092121	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs145707916	10	96092992	CMC	CMC NoSVA cis	NOC3L	GA		1.0	0.049

rs750148755	10	96095271	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs11187882	10	96095861	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs11187883	10	96096866	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs3740359	10	96100119	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs11187890	10	96102758	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs11187895	10	96106240	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs11187897	10	96106603	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.049
10:96112261_AAAAAAAC_A	10	96112261	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs778275808	10	96114212	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs10509672	10	96115957	CMC	CMC NoSVA cis	NOC3L	C		1.0	0.049
rs74825688	10	96119687	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs79193572	10	96119713	CMC	CMC NoSVA cis	NOC3L	G		1.0	0.049
rs79746649	10	96120218	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs7101207	10	96122857	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs112252876	10	96123355	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs11187906	10	96124838	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs11187907	10	96125361	CMC	CMC NoSVA cis	NOC3L	T		1.0	0.049
rs113544984	10	96127448	CMC	CMC NoSVA cis	NOC3L	A		1.0	0.049
rs16968876	15	39636877	eQTLGen	eQTLGen cis eQTLs	THBS1	C	3.7769E-210	-30.9371	0.0
rs16968890	15	39638991	eQTLGen	eQTLGen cis eQTLs	THBS1	G	1.0259E-208	-30.8304	0.0
rs3910645	15	39648251	eQTLGen	eQTLGen cis eQTLs	THBS1	G	2.2440999999999998E-203	-30.4294	0.0
rs3910644	15	39648234	eQTLGen	eQTLGen cis eQTLs	THBS1	C	1.0002E-196	-29.9225	0.0
rs11638679	15	39640148	eQTLGen	eQTLGen cis eQTLs	THBS1	T	1.1882E-85	-19.6133	0.0
rs34680120	15	39664000	eQTLGen	eQTLGen cis eQTLs	THBS1	A	3.1042E-38	-12.9284	0.0
rs4566132	15	39661138	eQTLGen	eQTLGen cis eQTLs	THBS1	G	6.7617E-38	-12.8684	0.0
rs1837636	15	39661779	eQTLGen	eQTLGen cis eQTLs	THBS1	C	3.4541999999999998E-37	-12.7419	0.0
rs72722976	15	39624864	eQTLGen	eQTLGen cis eQTLs	THBS1	G	3.3560000000000004E-36	1,3649E+06	0.0
rs12592015	15	39628131	eQTLGen	eQTLGen cis eQTLs	THBS1	A	9.8428E-36	1,0526E+06	0.0
rs3910644	15	39648234	BIOSQTL	BIOS eQTL geneLevel	THBS1	C	1.35871E-34	-12.2671	0.0
rs3910644	15	39648234	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	C	1.35871E-34	-12.2671	0.0
rs3910645	15	39648251	BIOSQTL	BIOS eQTL geneLevel	THBS1	G	1.7692400000000001E-34	-12.2457	0.0
rs3910645	15	39648251	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	G	1.7692400000000001E-34	-12.2457	0.0
rs1440802	15	39635124	eQTLGen	eQTLGen cis eQTLs	THBS1	C	2.7421E-34	-12.2101	0.0
rs28520337	15	39647894	eQTLGen	eQTLGen cis eQTLs	THBS1	C	6.0685000000000004E-34	-12.1453	0.0
rs71471500	15	39632013	eQTLGen	eQTLGen cis eQTLs	THBS1	G	2.7098000000000002E-33	-12.0223	0.0
rs11639391	15	39631771	eQTLGen	eQTLGen cis eQTLs	THBS1	T	7.3753E-33	-11.9392	0.0
rs7182018	15	39632269	eQTLGen	eQTLGen cis eQTLs	THBS1	G	1.5586E-32	-11.8769	0.0
rs17694988	15	39636227	eQTLGen	eQTLGen cis eQTLs	THBS1	C	1.9747E-32	-11.857	0.0
rs4924346	15	39639992	eQTLGen	eQTLGen cis eQTLs	THBS1	A	4.3746E-32	-11.7902	0.0
rs4924345	15	39639898	eQTLGen	eQTLGen cis eQTLs	THBS1	C	7.2122E-31	-11.5519	0.0
rs1080066	15	39634222	eQTLGen	eQTLGen cis eQTLs	THBS1	G	7.6265000000000005E-31	-11.547	0.0
rs2033939	15	39633904	eQTLGen	eQTLGen cis eQTLs	THBS1	A	9.0583E-31	-11.5322	0.0

rs4923822	15	39662277	eQTLGen	eQTLGen cis eQTLs	THBS1	A	1.8796000000000002E-30	-11.4694	0.0
rs978740	15	39655920	eQTLGen	eQTLGen cis eQTLs	THBS1	C	6.1505E-28	-10.9568	0.0
rs16968890	15	39638991	BIOSQTL	BIOS eQTL geneLevel	THBS1	G	9.96844E-28	-10.913	0.0
rs16968890	15	39638991	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	G	9.96844E-28	-10.913	0.0
rs16968876	15	39636877	BIOSQTL	BIOS eQTL geneLevel	THBS1	C	1.23112E-27	-10.8939	0.0
rs16968876	15	39636877	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	C	1.23112E-27	-10.8939	0.0
rs3910644	15	39648234	eQTLcatalogue	Fairfax 2014 naive	THBS1	C	3.20905E-14	0.848997	1.60452E-10
rs3910645	15	39648251	eQTLcatalogue	Fairfax 2014 naive	THBS1	G	2.42235E-13	0.823476	1.21117E-09
rs16968890	15	39638991	eQTLcatalogue	Fairfax 2014 naive	THBS1	G	4.96976E-13	0.793931	2.48488E-09
rs16968876	15	39636877	eQTLcatalogue	Fairfax 2014 naive	THBS1	C	5.2124E-13	0.796074	2.6062E-09
rs773225188	15	39631994	eQTLcatalogue	Fairfax 2014 naive	THBS1	AAGAG	7.77307E-13	0.78881	3.88653E-09
rs56003663	15	39617295	eQTLGen	eQTLGen cis eQTLs	THBS1	C	9.5054E-12	-6.8136	0.0
rs4923822	15	39662277	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	A	1.42704E-09	-6.05233	6.12782645995465E-06
rs4923822	15	39662277	BIOSQTL	BIOS eQTL geneLevel	THBS1	A	1.98781E-09	-5.99861	6.08309507877608E-06
rs4566132	15	39661138	BIOSQTL	BIOS eQTL geneLevel	THBS1	G	2.82253E-09	-5.94143	6.03937673632081E-06
rs4566132	15	39661138	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	G	2.82253E-09	-5.94143	6.03937673632081E-06
rs1837636	15	39661779	BIOSQTL	BIOS eQTL geneLevel	THBS1	C	2.82253E-09	-5.94143	6.03937673632081E-06
rs1837636	15	39661779	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	C	2.82253E-09	-5.94143	6.03937673632081E-06
rs34680120	15	39664000	BIOSQTL	BIOS eQTL geneLevel	THBS1	A	2.82253E-09	-5.94143	6.03937673632081E-06
rs34680120	15	39664000	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	A	2.82253E-09	-5.94143	6.03937673632081E-06
rs11638679	15	39640148	eQTLGen	eQTLGen cis eQTLs	C15orf54	T	8.0695E-09	-5.7669	5.79822187862389E-05
rs11638016	15	39621773	eQTLGen	eQTLGen cis eQTLs	THBS1	C	1.8572E-08	-5.6248	9.58466453674121E-05
rs56113415	15	39621418	eQTLGen	eQTLGen cis eQTLs	THBS1	A	3.7254E-08	-5.5033	0.0001523035918263
rs11638679	15	39640148	BIOSQTL	BIOS eQTL geneLevel	THBS1	T	6.41607E-08	-5.40673	5.63443768311922E-05
rs11638679	15	39640148	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	T	6.41607E-08	-5.40673	5.63443768311922E-05
rs3910645	15	39648251	eQTLcatalogue	BLUEPRINT ge monocyte	THBS1	G	7.11506E-08	0.845224	0.000355753
rs3910644	15	39648234	eQTLcatalogue	BLUEPRINT ge monocyte	THBS1	C	7.90024E-08	0.84269	0.000395012
rs2033939	15	39633904	BIOSQTL	BIOS eQTL geneLevel	THBS1	A	1.39884E-07	-5.26522	8.847600088476E-05
rs8032326	15	39619456	eQTLGen	eQTLGen cis eQTLs	THBS1	A	1.8283E-07	-5.2159	0.0006118881118881
rs8033007	15	39619661	eQTLGen	eQTLGen cis eQTLs	THBS1	C	3.8506E-07	-5.0762	0.0012003464917708
rs1080066	15	39634222	BIOSQTL	BIOS eQTL geneLevel	THBS1	G	5.84104E-07	-4.99636	0.0005052116570942
rs28520337	15	39647894	BIOSQTL	BIOS eQTL geneLevel	THBS1	C	6.5653E-07	-4.97369	0.0005301664722722
rs28520337	15	39647894	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	C	6.5653E-07	-4.97369	0.0005301664722722
rs16968890	15	39638991	eQTLcatalogue	BLUEPRINT ge monocyte	THBS1	G	7.00785E-07	0.796662	0.00350393
rs12591944	15	39627982	eQTLGen	eQTLGen cis eQTLs	THBS1	C	1.2149E-06	-4.853	0.0036831175177131
rs1440802	15	39635124	BIOSQTL	BIOS eQTL geneLevel	THBS1	C	1.53212E-06	-4.80687	0.0012847743874009
rs72722978	15	39628675	eQTLGen	eQTLGen cis eQTLs	THBS1	T	1.7935E-06	-4.7753	0.0053233558435237
rs8025239	15	39623588	eQTLGen	eQTLGen cis eQTLs	THBS1	A	2.0892E-06	-4.7445	0.0060943006440636

rs16968890	15	39638991	eQTLcatalogue	Fairfax 2014 LPS24	THBS1	G	2.28413E-06	0.227449	0.0114206
rs4924345	15	39639898	BIOSQTL	BIOS eQTL geneLevel	THBS1	C	2.33078E-06	-4.72221	0.0017824310520939
rs4924345	15	39639898	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	C	2.33078E-06	-4.72221	0.0017824310520939
rs16968876	15	39636877	eQTLcatalogue	Fairfax 2014 LPS24	THBS1	C	2.85595E-06	0.225868	0.0142798
rs16968876	15	39636877	eQTLcatalogue	BLUEPRINT ge monocyte	THBS1	C	2.8667E-06	0.752794	0.0143335
rs773225188	15	39631994	eQTLcatalogue	Fairfax 2014 LPS24	THBS1	AAGAG	3.7226E-06	0.222135	0.018613
rs3910644	15	39648234	GTEx/v8	Whole Blood	THBS1	T	4.45129E-06	0.127755	3.8153199999999997E-20
rs1837636	15	39661779	PsychENCODE	PsychENCODE eQTLs	RP11-37C7.1	T	5.27257E-06	-0.222586	0.0006116329885143
rs3910644	15	39648234	eQTLcatalogue	Fairfax 2014 IFN24	THBS1	C	5.33505E-06	0.461593	0.0266752
rs10520128	15	39627146	eQTLGen	eQTLGen cis eQTLs	THBS1	C	7.0029E-06	-4.4934	0.0199808623886131
rs11629938	15	39626935	eQTLGen	eQTLGen cis eQTLs	THBS1	A	8.6916E-06	-4.4473	0.0246107963018193
rs34680120	15	39664000	PsychENCODE	PsychENCODE eQTLs	RP11-37C7.1	A	9.31429E-06	0.216218	0.0010235897899314
rs16968890	15	39638991	eQTLcatalogue	Fairfax 2014 IFN24	THBS1	G	9.51089E-06	0.431862	0.0475544
rs3910644	15	39648234	eQTLcatalogue	BLUEPRINT ge monocyte	RP11-624L4.1	C	9.5575E-06	0.327274	0.0477875
rs4924346	15	39639992	BIOSQTL	BIOS eQTL geneLevel	THBS1	A	2.08303E-05	-4.25569	0.0133721749753324
rs4924346	15	39639992	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	A	2.08303E-05	-4.25569	0.0133721749753324
rs16968876	15	39636877	GTEx/v8	Whole Blood	THBS1	T	2.227E-05	0.119692	3.8153199999999997E-20
rs17694988	15	39636227	BIOSQTL	BIOS eQTL geneLevel	THBS1	C	2.25922E-05	-4.23748	0.014281031980147
rs17694988	15	39636227	BIOSQTL	BIOS eQTL geneLevel	CTD-2033D15.1	C	2.25922E-05	-4.23748	0.014281031980147
rs12592015	15	39628131	DICE	T CD4 naive	PAK6	A	2.38152860034E-05	1.15860040249	0.049
rs773225188	15	39631994	GTEx/v8	Whole Blood	THBS1	A	2.69055E-05	0.11834	3.8153199999999997E-20
rs16968890	15	39638991	GTEx/v8	Whole Blood	THBS1	C	3.04173E-05	0.118313	3.8153199999999997E-20
rs3910645	15	39648251	GTEx/v8	Whole Blood	THBS1	C	3.82701E-05	0.115051	3.8153199999999997E-20
rs4923822	15	39662277	PsychENCODE	PsychENCODE eQTLs	RP11-37C7.1	G	4.82356E-05	-0.204656	0.0044418712164
rs8032326	15	39619456	PsychENCODE	PsychENCODE eQTLs	RP11-37C7.1	A	0.000314673	0.162609	0.0224872458661352
rs2033939	15	39633904	PsychENCODE	PsychENCODE eQTLs	RP11-37C7.1	A	0.000399035	0.157412	0.0274319167847911

Center of mass of the language processing regions of interests retained in both left and right hemispheres. Each ROIs is characterized by their abbreviated anatomical label and their center of mass stereotactic coordinates (x, y, z, in mm)

Hemisphere	ROIs	x	y	z
Left hemisphere	Prec	-46.763359	2.010178	25.857506
	RolS	-45.287982	-9.405896	44.176871
	F3orb	-35.821290	35.303807	-10.772339
	T3p	-45.903226	-56.483871	-7.359447
	F3td	-42.150235	25.107981	14.544601
	T2p	-39.306773	-65.254980	2.051793
	SMG	-40.684932	-50.252055	40.865753
	T1a	-54.076294	-11.858311	-5.858311
	F3tv	-45.202073	14.242228	4.231865
	STSp	-47.122995	-56.926916	24.071301
	PrF3op	-39.616883	2.909091	39.344156
	Fusa	-35.273273	-37.173173	-12.890891
	T1	-50.465171	-38.564345	14.323495
	T2ml	-54.990991	-39.625225	-2.846847
	F2p	-34.726790	10.944297	48.801061
	F3opd	-43.908772	21.976608	25.702924
	PT	-59.899083	-28.119266	8.678899
	Pole	-45.000000	5.196759	-26.796296
	AG	-43.936872	-70.852224	22.203730
Right hemisphere	T1R	51.842553	-38.519149	3.404255
	F3opdR	49.679389	14.931298	27.480916
	F2antR	46.641026	39.807692	5.064103
	T2pR	54.768421	-42.115789	-7.736842
	T1a/HeschlR	56.540260	-13.387013	0.815584
	PrecR	52.686275	-1.490196	24.156863