SUPPLEMENTARY INFORMATION

Resolving sub-clonal heterogeneity within cell-line growths by single cell sequencing genomic DNA

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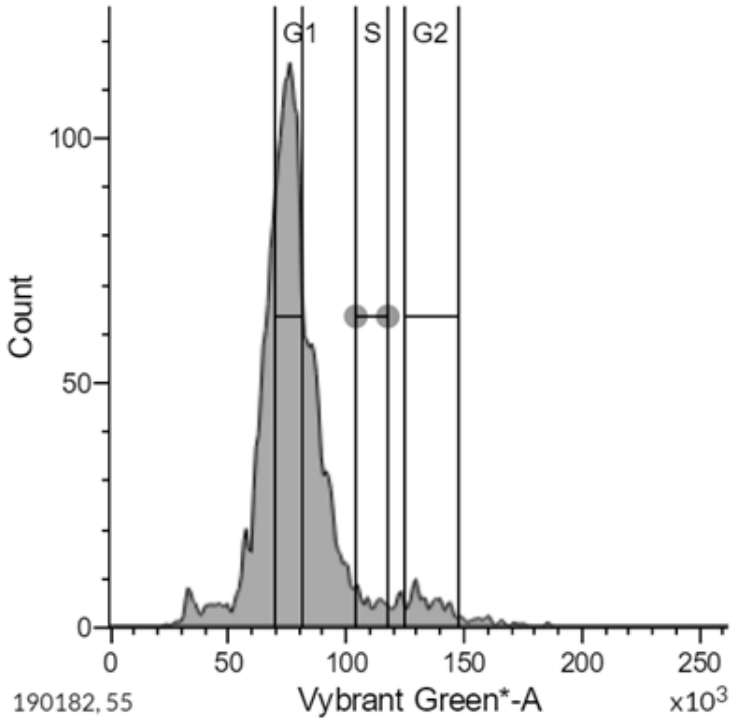
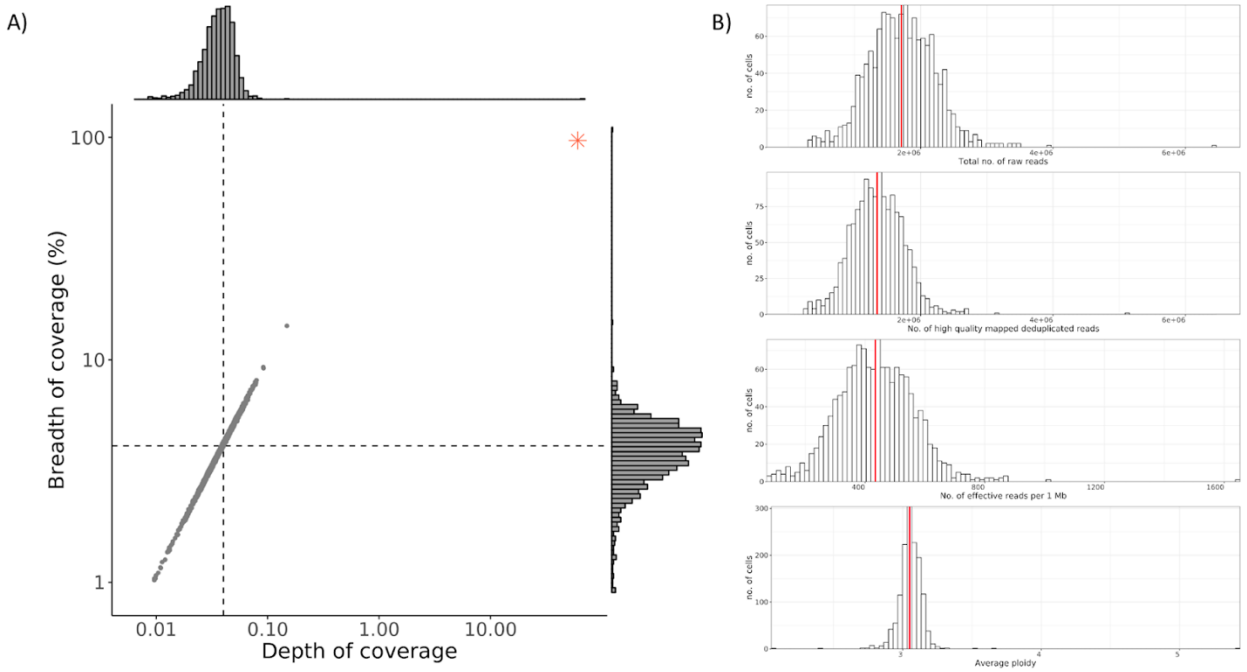
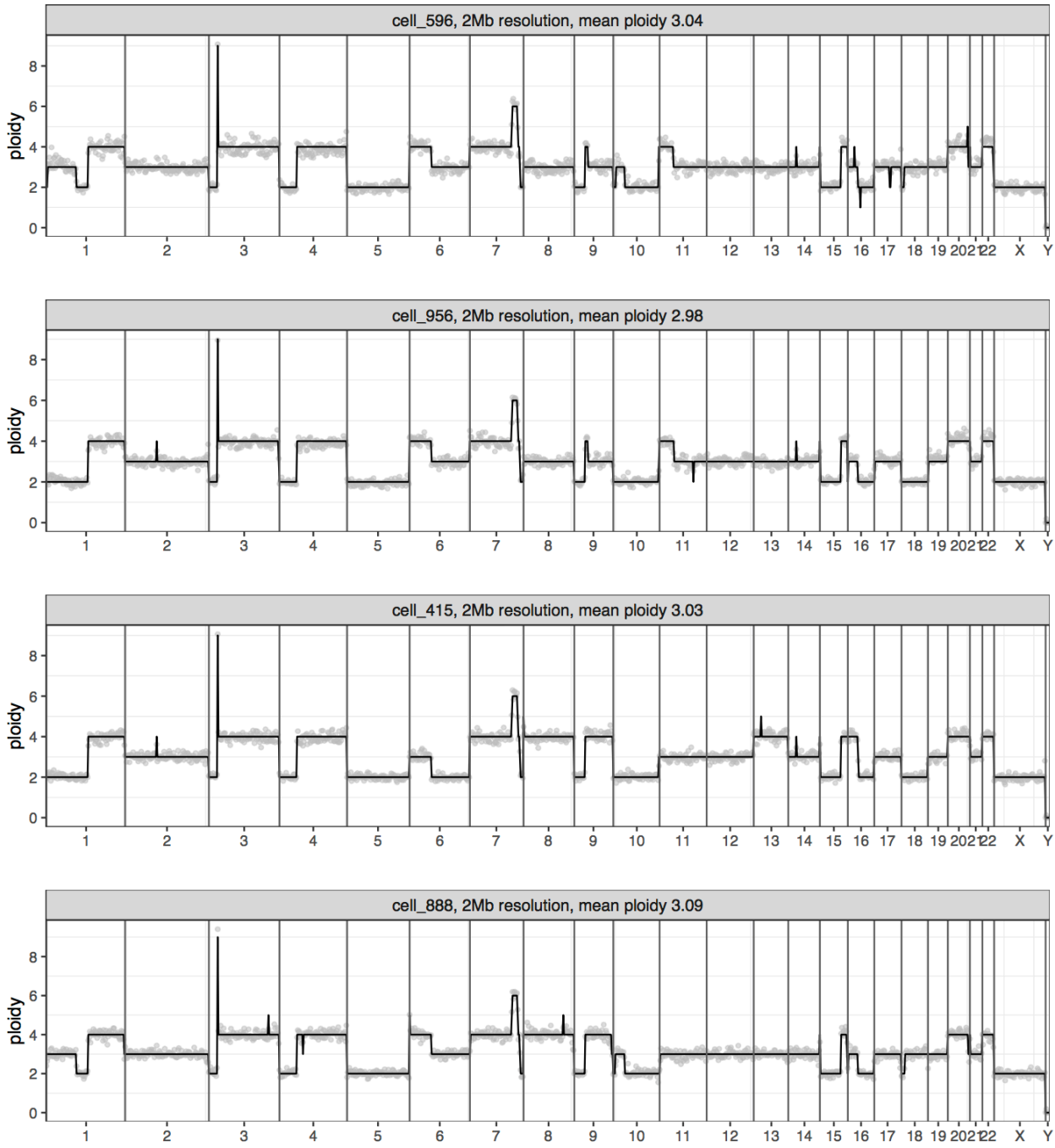


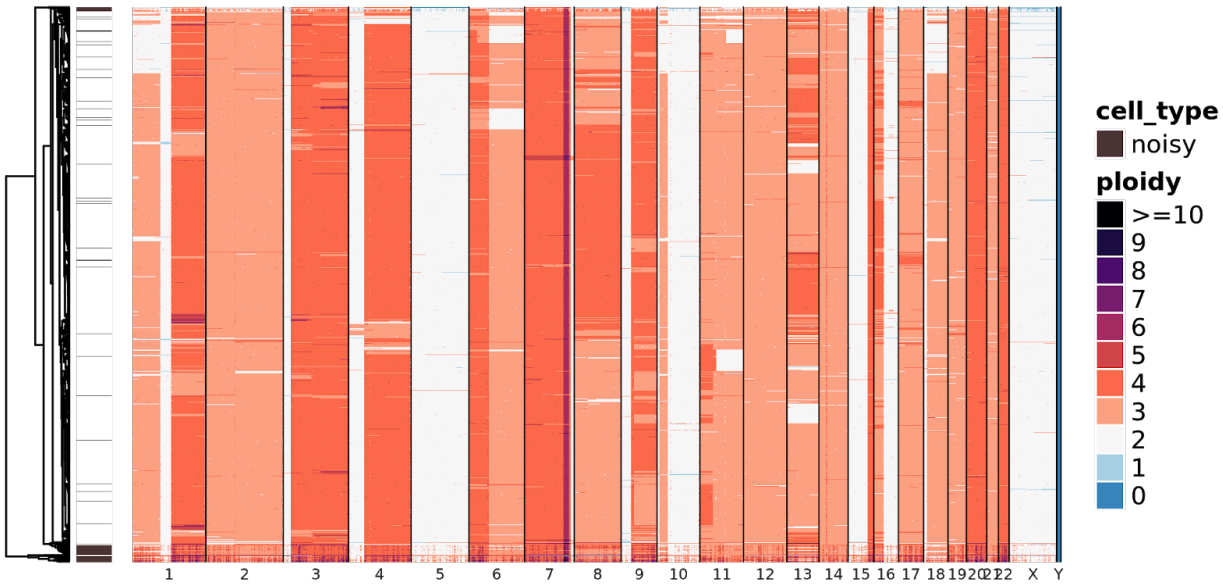
Supplementary Figure 1 | Distribution of DNA content in COLO829 nuclei by flow cytometry. Cells in the G1 phase were selected for scCNV library preparation.



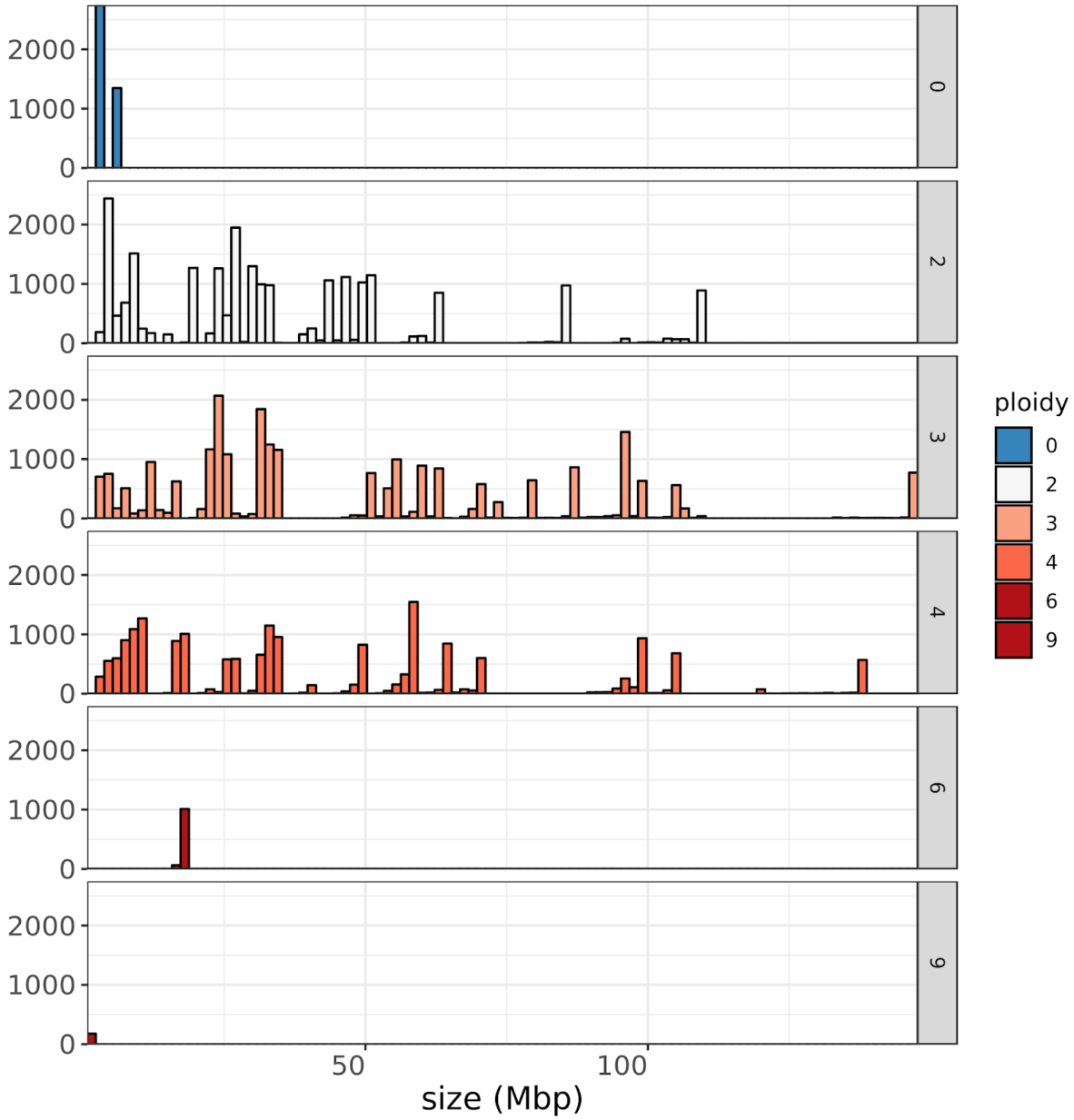
Supplementary Figure 2 | Sequencing depth . A) Depth of coverage versus breadth of coverage. A scatter plot depicted the effective depth of coverage (x-axis) versus the percent of the genome with at least 1x coverage (y-axis) for each cell. The dashed lines represent the median single cell values (0.04 depth of coverage, 4.11 breadth of coverage). The red asterix plots the values for aggregated data as a pseudo bulk experiment (60.68x depth of coverage, 95.97% breadth of coverage). **B)** Histogram of summary data quality metrics. Histogram depicting the distribution of per cell summary metrics with the median indicated by the red line: Total number of raw reads (median value 1,709,262); Number of high quality mapped deduplicated reads (median value 1,343,083); Number of effective reads per 1 Mb (median value 434) and Average ploidy (median value 3.048).



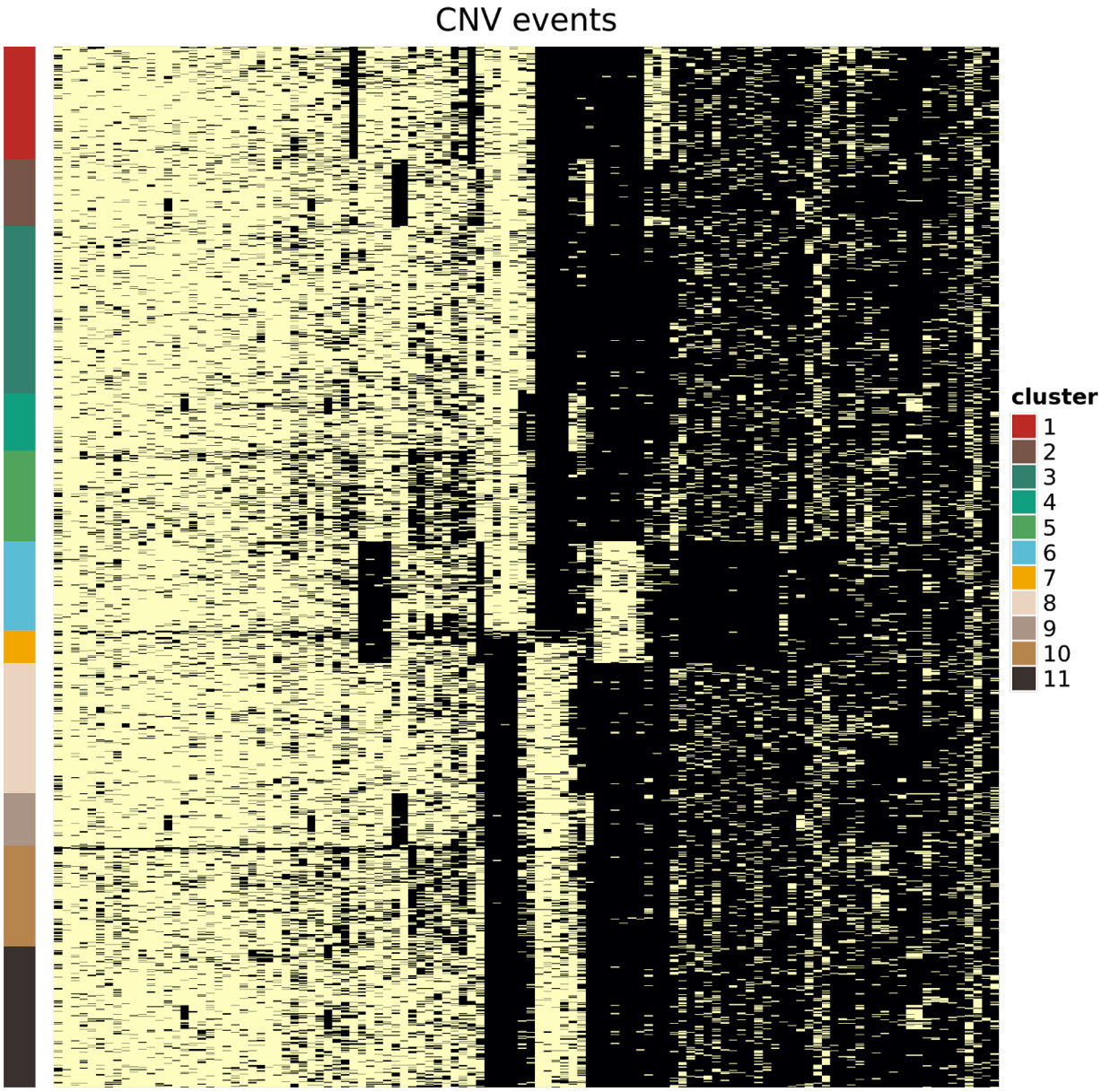
Supplementary Figure 3 | Four representative single cell ploidy plots. Copy number profiles plotted at a resolution of 2 Mb bins. Solid black line indicates ploidy call and gray dots indicate raw read counts for each bin.



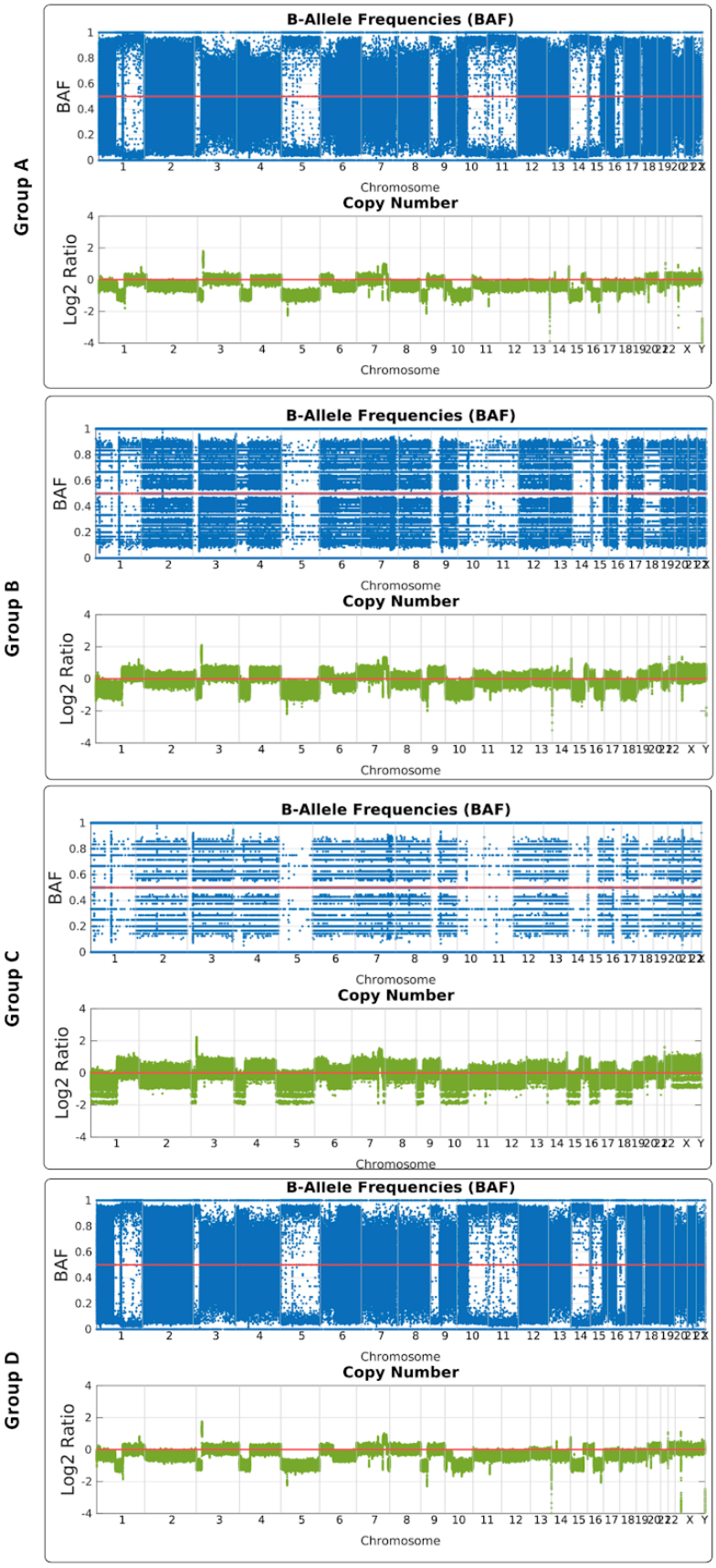
Supplementary Figure 4 | Heatmap of raw data. Heatmap showing hierarchical clustering of 1,475 single cell CNV profiles at 2 Mb resolution. Each row depicts the whole genome of a single cell and colors represent the called ploidy as specified by the legend on the right. Color-bar on the right marks single cells labeled by the pipeline as noisy in brown.



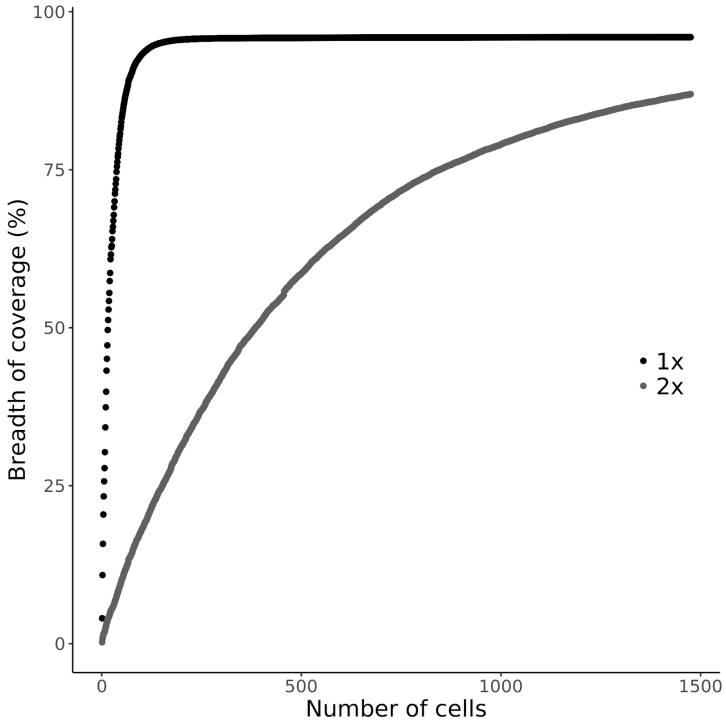
Supplementary Figure 5 | Size distribution of CNV events by ploidy. Histogram of the 114 CNV events that passed the following filtering criteria: event quality > 15; event size > 2 Mb and event frequency > 0.05.



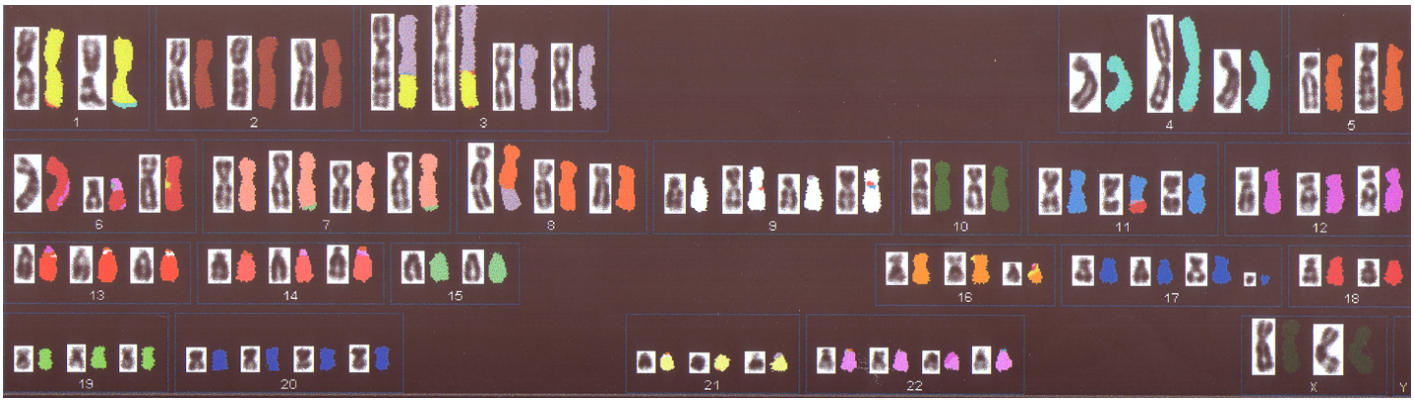
Supplementary Figure 6 | CNV events within each cluster. Heatmap with one row for each cell and one column for each of the 122 polymorphic CNV events that passed filtering, ordered by their frequency in the population. The cells are ordered by membership in DAPC clusters. The presence or absence of a mutation is depicted in yellow and black, respectively.



Supplementary Figure 7 | Log2(Fold Change) and LOH for each group. The upper graphs show the Log2(Fold Change) using the program tCoNuT, which was used previously for bulk sequencing and produces allele fraction plots. It is important to note that that tCoNuT, like other bulk copy number tools cannot determine copy number natively without assumptions for deconvoluting potential mixtures. Single cell copy numbers as used elsewhere do not require this assumption and absolute ploidy can be better inferred. The lower graphs provide the allele fractions of known heterozygous SNPs determined previously from sequencing on the lymphoblastic germline pair. For example in *Group A* at chr5 when copy number is 1, we see allele fractions partitioning into 0 and 1 allele fractions indicating homozygosity. The relative noise is dependent on number of reads over a SNP, and thus greater spread is shown. SNPs across a region or segment could be averaged together to get a regional LOH, value, though individual SNPs are shown in these examples. In the figure above we observe loss of heterozygosity (LOH) for chromosomes 5, 10, 11 and 14. We also see some chromosomes with partial LOH. Within the main figure 4, chromosome 1, 10, and 18 are shown, whereas this figure shows all chromosomes.



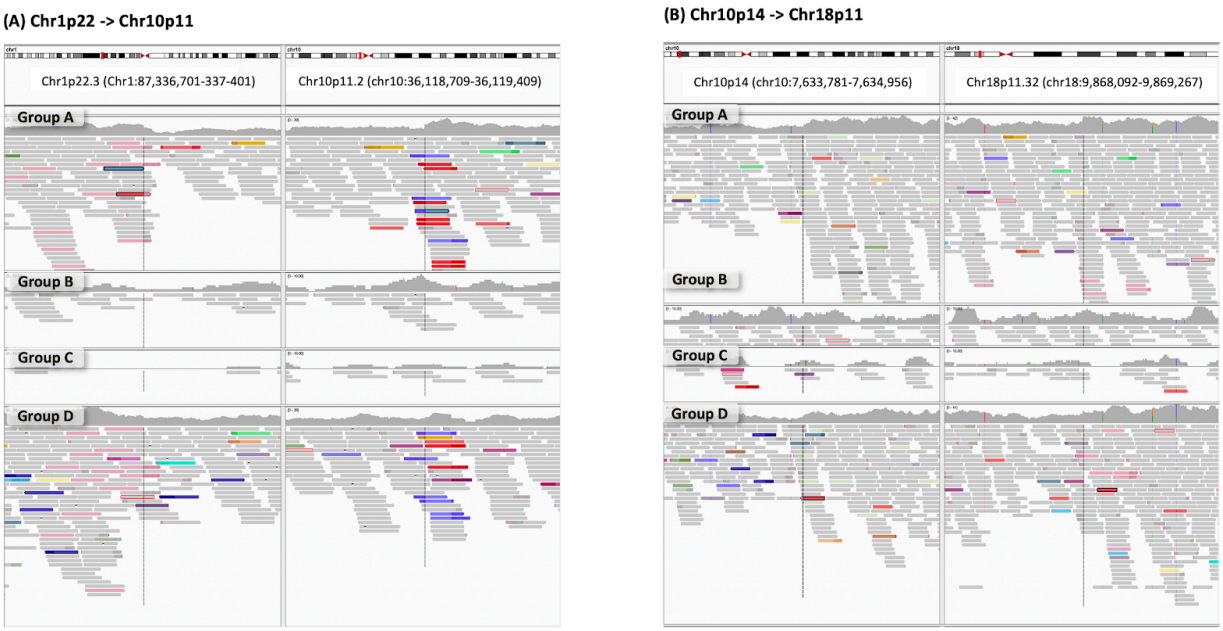
Supplementary Figure 8 | Cumulative breadth of coverage. A cumulative plot of genome coverage at two different depths 1x and 2x (black and gray, respectively). Number of cells needed to achieve 75% coverage across the genome is 37 at 1x depth and 845 at 2x depth.



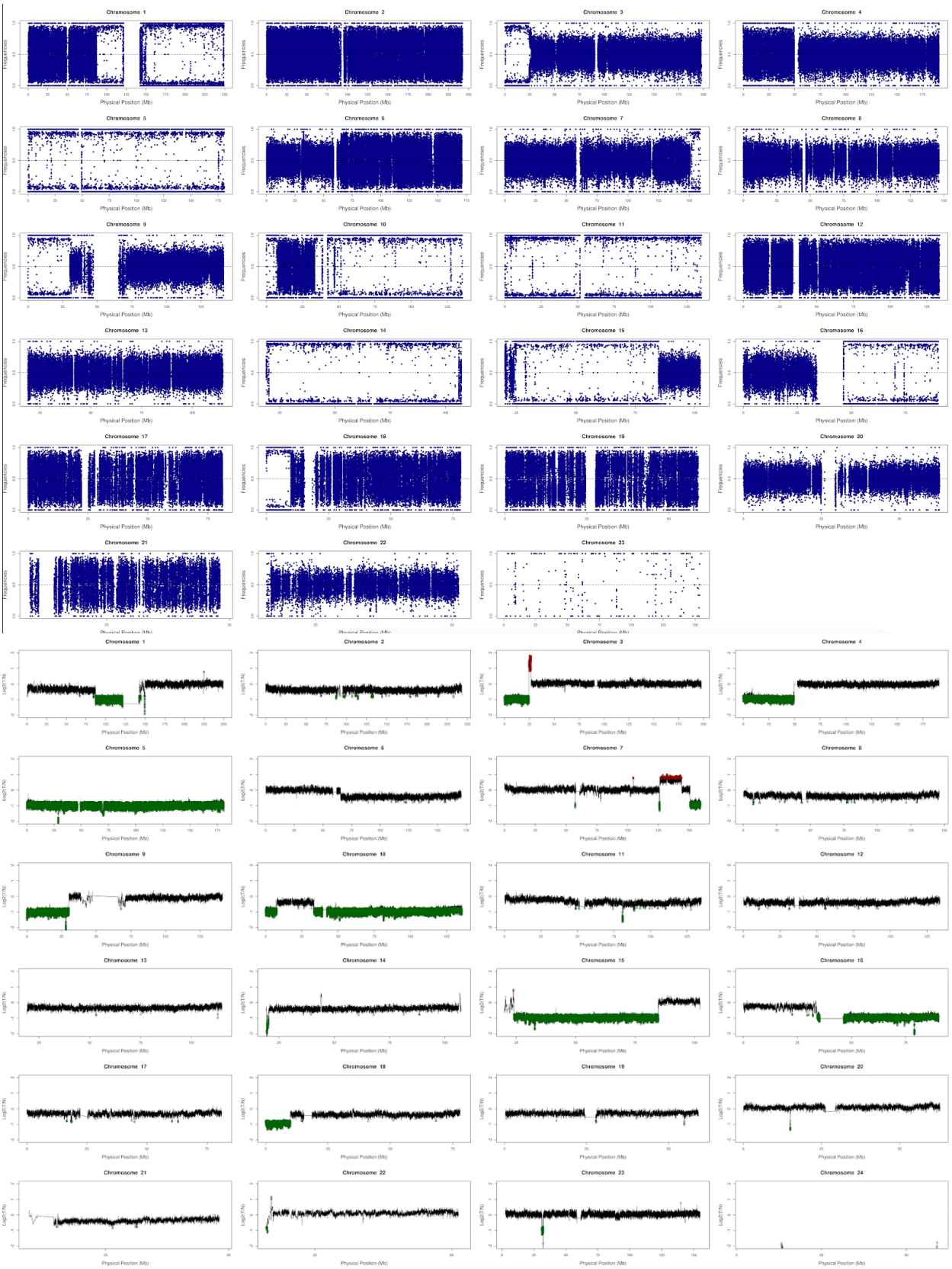
Supplementary Figure 9 | Spectral Karyotype (SKY) of COLO829 cell-line. SKY multicolour-FISH Karyotype from 10 metaphases, performed without knowledge of the single cell sequencing and from a separate sample of the cell line, as described[10] but without any confirmation. The karyotype can be regarded as pseudo-tetraploid with losses. It shows clear signs of endoreduplication, several abnormal chromosomes being present in two copies. There is evidence of Dutrillaux's monosomic pattern of karyotype evolution with endoreduplication - e.g. 2 copies each of chromosomes 1, 3 and an unbalanced 1;3 translocation; 2 each of 7, 15 and a probable 7;15 translocation. Consensus karyotype: 69 chromosomes (mode 68) 2 x 1, 2 x 3, 3 x 2, der(?)t(1;3)(q?;p22-24?) x 2, 4 x 2, iso(4), 5 x 2, 6 x 2, del(6) x 2, 7 x 2, der(7)t(7;15?*) x 2, 8 x 3, 9 x 2, del(9) x 2, 10 x 2, 11 x 3**, 12 x 3, 13 x 3, 14 x 3, 15 x 2, 16 x 2, del(16), 17 x 3, 18 x 2, 19 x 3, 20 x 4, 21 x 3, 22 x 4, X x 2.

* the fragment is identified by SKY as chromosome 15 but the fragment is very small so this identification is unreliable.

** In 6/10 metaphases there are 3 elevens. In four of these there is an additional unbalanced 1;18 translocation, der(?)t(1p?;18q?), while in the other 4 metaphases one eleven is replaced by a der(?)t(11;18). A possible explanation is that the consensus should include the 1;18 translocation and three elevens, but in some metaphases one eleven and the 1;18 have combined to yield the single der(?)t(11;18).



Supplementary Figure 10 | IGV Traces of anomalous reads spanning translocations. In left is a split view of Chr1p22 and Chr10p11, showing on the left reads in pink whose parter maps to chr10p11 shown in blue (red reads map 2.7Mb upstream). In the right is a split view of chr10p14 and Chr18p11 where on the partner of light green reads on chromosome 10p11(left) map to Chr18p11.32 (pink reads). Read coloring is formally defined within the IGV manual, and are set to indicate instances where the insert distances between paired reads is beyond 1000bp. Reads mapping within the same chromosome are red, reads mapping to chromosome 18 are in pink, reads mapping to chromosome 10 are blue, reads mapping to chromosome 1 are light green.



Supplementary Figure 11 | Exemplary Loss of Heterozygosity (LOH) broken out by chromosome for Group A (upper) and copy number estimate shown by chromosome.

Supplementary Table 1 | Aggregate summary metrics. Summary metrics describing sequencing data quality by group.

Groups	Number of cells	Number of reads	Number of effective reads	Average ploidy	Median reads per Mb
A	653	1,106,320,742	866,039,383	3.03	428
B	117	195,118,990	152,584,425	2.95	416
C	43	78,145,878	60,875,291	3.01	450
D	560	975,448,264	763,375,990	3.11	435

Supplementary Table 2 | Per cell summary metrics. Per cell metrics describing sequencing and CNV estimation data quality.

barcode	total_num_reads	num_unmapped_reads	num_duplicate_reads	num_lowmapq_reads	num_mapped_dedup_reads	effective_reads_per_1Mbp	effective_depth_of_coverage	breadth_of_coverage_percent	mean_ploidy	raw_mapd	normalized_mapd	is_noisy
AAACCTGAGGCTACGA-1	1474382	14559	162572	129544	1167707	377	0.034061409	3.583452633	3.024427318	0.097366283	0.095937271	0
AAACCTGGTCCTTGGG-1	2008984	34666	217429	183078	1573811	508	0.045954133	4.790426567	3.115261147	0.085370623	0.085370623	0
AAACCTGTCACACGGC-1	1317000	74665	138878	112449	991008	320	0.028780153	3.0426807	3.087988182	0.105997248	0.10452012	0
AAACCTGTCGATACAC-1	2317026	39831	253774	206942	1816479	587	0.052921028	5.471836533	3.141717404	0.084710744	0.081279279	0
AAACGGGAGCAGATCG-1	1339444	63506	140596	118291	1017051	329	0.029609209	3.125955133	3.007868648	0.101492014	0.100216564	0
AAACGGGCAAAGTAAC-1	1477800	26950	159618	138195	1153037	372	0.033729644	3.5298458	2.995454545	0.100199795	0.101997012	0
AAACGGGCAACCTCAA-1	1595138	22541	172915	143540	1256142	406	0.036628118	3.840771333	3.093311835	0.094287391	0.094494211	0
AAACGGGGTCTTCGTC-1	1421664	29372	155391	126737	1110164	359	0.032357084	3.406371133	3.097976261	0.099142644	0.100191291	0
AAACGGGTCACGCTCT-1	1947700	69453	203082	170985	1504180	486	0.043601468	4.5173273	3.110392748	0.095612311	0.095115229	0
AAACGGGTCAGCGGCT-1	1874782	77070	194127	167465	1436120	464	0.041812765	4.379685167	3.104920385	0.088254406	0.088273856	0
AAAGATGAGAATTGTG-1	1360902	18396	149620	110941	1081945	350	0.031547124	3.319917867	3.019837493	0.102167465	0.098182972	0
AAAGATGAGCCACCTG-1	1401994	37826	151902	114344	1097922	355	0.031966123	3.362255867	3.295852273	0.126780578	0.124095547	1
AAAGCAAGTGACACGA-1	1627784	21922	177338	141815	1286709	416	0.037520406	3.930806	2.99614311	0.093248267	0.091966727	0
AAAGCAATCGCGGACT-1	2535646	66346	270589	221324	1977387	639	0.057652785	5.9424639	2.924726828	0.081466752	0.080154264	0
AAAGCAATCTCACCTG-1	1362442	41465	145952	118863	1056162	341	0.030766899	3.2326992	3.016306123	0.097433428	0.097433428	0
AAAGTAGTCTCAGCGG-1	1588694	72155	164063	139314	1213162	392	0.0354518	3.717024933	3.071467129	0.096109253	0.094734635	0
AAAGTAGTCTTGCGAA-1	1743832	21599	190415	151535	1380283	446	0.040302052	4.212429	3.109763721	0.093638707	0.092047768	0
AAATGCCAGTGGAGAA-1	1887248	24398	206852	159160	1496838	484	0.043653634	4.5483168	3.217591145	0.091792681	0.087716553	0
AAATGCCGTCGCGCTA-1	1270338	34801	127771	116846	990920	320	0.0288885	3.060221167	3.096571218	0.102880182	0.105037849	0
AACACGTAGGACAGAA-1	1715456	26131	187931	141367	1360027	439	0.039683552	4.1453637	3.039962489	0.090117962	0.088450146	0
AACCATGAGGAATCGC-1	1755616	29575	184714	160968	1380359	446	0.040288294	4.222308	2.9406127	0.090392407	0.092221475	0
AACCATGAGGCTATCT-1	2232400	56542	240451	200646	1734761	560	0.05028511	5.1617407	3.022067702	0.090892961	0.090312027	1
AACCATGCATTCATCT-1	2499372	69982	268612	222164	1938614	626	0.056290364	5.774783533	3.144110356	0.083626078	0.084799031	0
AACCATGTCGACGAAG-1	1875222	33941	202787	159999	1478495	478	0.043146902	4.502720333	3.072046662	0.087085148	0.088366009	0
AACCGCGGTAACAGCG-1	1166466	48495	120434	102263	895274	289	0.026036977	2.760984133	3.05008627	0.111992158	0.108989662	0
AACCGCGGTTTACTTC-1	1988752	62880	205591	184180	1536101	496	0.044735569	4.655430567	3.047010005	0.088926653	0.088679451	0
AACCGCGTCCTACGAA-1	563392	7733	53940	48652	453067	146	0.0131859	1.413549933	3.029506986	0.154139539	0.147379952	0
AACGTTGGTGGTAACG-1	1827248	62088	191353	157117	1416690	458	0.041250358	4.3122855	3.039901684	0.09630223	0.093155669	0
AACTCAGAGTGGGTAC-1	2821904	73049	301236	250316	2197303	710	0.063968984	6.547577067	2.900968998	0.078979288	0.078016643	0
AACTCAGAGTGGTAGC-1	2247774	30306	243754	206857	1766857	571	0.051485642	5.318281967	3.037099937	0.082656861	0.08161954	0
AACTCAGCATGCAGTT-1	1867088	14187	208911	153233	1490757	482	0.043465605	4.5154008	3.11380768	0.088638568	0.087189797	0
AACTCAGTCGAGTATC-1	3006250	21408	332188	260471	2392183	773	0.069816244	7.090951033	2.924756626	0.076415497	0.075939943	0
AACTCAGTCTAACACG-1	1403818	90210	145694	121478	1046436	338	0.030443965	3.2138271	3.095987898	0.1051481	0.102782668	0
AACTCCCTCAGTTCTT-1	2126942	49183	229009	191197	1657553	535	0.048225871	5.007724567	3.134622898	0.088129786	0.087240166	0
AACTCCCTCCAGGATA-1	1534614	15986	170798	126146	1221684	395	0.035560949	3.7311491	3.026584373	0.095971137	0.095608002	0
AACTCCCTCGATAGGG-1	1475146	15241	162822	121556	1175527	380	0.034315791	3.600711433	2.985248265	0.097488988	0.096216596	0
AACTCCCTCTAATGGC-1	2693360	65471	290321	232267	2105301	680	0.061300555	6.2800128	3.167214862	0.079541131	0.079541131	0
AACTCTTAGTAGCC-1	2286696	49254	244128	204061	1789253	578	0.052149528	5.4014467	3.011585535	0.088088396	0.088574925	0
AACTCTTGTCTTACCC-1	1792512	54661	191208	159484	1387159	448	0.040445744	4.219485567	3.046055576	0.091453925	0.089293918	0
AACTCTTTCCTGCGTT-1	1948040	19303	214334	176285	1538118	497	0.044688642	4.625854433	3.105571181	0.086000033	0.086000033	1
AACTGGTAGAAACCAT-1	6448042	48827	710064	589019	5100132	1648	0.148897051	14.4383907	3.081798283	0.050573647	0.050573647	0
AACTGGTAGCTGAACG-1	1725966	92510	179330	150747	1303379	421	0.037917929	3.983259233	3.143699347	0.093700469	0.093335474	0
AACTGGTAGGGCCATA-1	1855552	20621	201050	158042	1475839	477	0.043092167	4.488310433	3.035765023	0.089645377	0.089243381	0
AACTGGTGTCGTGAAG-1	1255874	27883	123899	104209	999883	323	0.029186444	3.076570033	3.086339776	0.102153256	0.102153256	0
AACTGGTGTTCAGTAC-1	2249426	50915	244846	197894	1755771	567	0.050985723	5.247257533	3.006791654	0.080135328	0.080135328	0
AACTGGTTCGTACGCG-1	980516	138696	90446	80860	670514	217	0.019437477	2.075725667	3.054446165	0.120807581	0.124841242	0
AACTTTCCACGTAGGA-1	1367584	18896	151288	112795	1084605	350	0.031604757	3.325611067	3.057852531	0.101656719	0.099247645	0
AACTTTCTCTGCTGAA-1	1688648	22641	186709	151057	1328241	429	0.038749421	4.0454271	3.091688631	0.090553483	0.088523146	0
AAGACCTCACAAGCGA-1	774862	40377	79832	71791	582862	188	0.017061097	1.828308833	3.010372811	0.139719946	0.13524537	0
AAGACCTCACCAGTGC-1	1547280	122948	155960	131134	1137238	367	0.032934267	3.4613962	3.072078406	0.098307929	0.097219793	0
AAGACCTCACTCCCTA-1	2081424	27512	225963	175333	1652616	534	0.048210729	4.991967	3.308575897	0.121725674	0.119637301	1
AAGACCTCACTTGAGT-1	1968878	19080	216679	166042	1567077	506	0.045742909	4.751080033	3.08331972	0.086776176	0.085854819	0
AAGACCTCATAGCACT-1	2356728	60362	251951	210185	1834230	593	0.053478813	5.5286958	3.072519355	0.084303431	0.083832883	0
AAGACCTGTGGACGTA-1	1273004	15331	139501	106601	1011571	327	0.029516765	3.1151629	3.140806659	0.105485391	0.102580799	0
AAGACCTTCACGGTAT-1	2233960	17432	248183	181187	1787158	577	0.05212545	5.3641339	3.068237517	0.085376316	0.080627504	0
AAGACCTTCCGAGATT-1	1166124	26337	127734	96854	915199	296	0.02671377	2.816703467	3.018662254	0.109037378	0.105013852	0
AAGCCGCCATCTCACC-1	2708982	74197	285899	237985	2110901	682	0.061513954	6.314070333	3.043628071	0.080022708	0.079190761	0
AAGGAGCCAAGAATCA-1	1116436	41741	116288	100776	857631	277	0.025076927	2.661535433	3.018511549	0.111501177	0.113028341	0
AAGGCAGAGAGCCCAA-1	2335452	14835	255573	210527	1854517	599	0.054147331	5.599737033	3.072701689	0.080106992	0.081562932	0
AAGGCAGGTAAAGTCA-1	3459226	194178	350672	310763	2603613	841	0.075704884	7.6920089	3.047464443	0.068770368	0.067686204	0
AAGGTTCAGCGTGTGA-1	1431840	19756	150647	121448	1139989	368	0.033251916	3.492838367	2.909760066	0.102286839	0.095630929	0
AAGGTTCCAGATTGTC-1	2080386	47393	225218	179731	1628044	526	0.047436772	4.9170601	3.014072401	0.086751793	0.085054525	0
AAGGTTCGTCGAATT-1	1763662	42806	187132	148263	1385461	448	0.040337872	4.2054647	2.978691214	0.093311446	0.092194392	0
AAGGTTCGTGTAATGA-1	874982	20862	91887	73200	689033	223	0.020055948	2.133062767	3.084092571	0.123041112	0.122001727	0
AAGGTTCGTTGAGCAG-1	1748494	58248	181067	153257	1355922	438	0.039574736	4.143653467	3.034990164	0.091991493	0.090799195	0
AAGGTTCGTTTGCCTC-1	2575348	38730	278037	214739	2043842	660	0.05953717	6.102514167	3.552102078	0.132374251	0.132374251	1
AAGGTTCTCCGCGACA-1	2134632	69346	223136	187515	1654635	534	0.048231319	5.024670833	2.952552774	0.086350371	0.086350371	0
AAGTCTGAGGCCGTT-1	1663256	18066	181469	140776	1322945	427	0.038595661	4.025418733	3.108119625	0.093715987	0.093597908	0
AAGTCTGAGTGCGATG-1	1709082	23876	188048	133689	1363469	440	0.039843722	4.152287333	2.98986505	0.090676158	0.090578468	0
AAGTCTGTCACCGCGA-1	1405766	16157	149493	131967	1108149	358	0.032291929	3.415382333	3.002989951	0.100584012	0.100109823	0
AATCCAGGTTGAACAA-1	1472704	24058	162103	129085	1157458	374	0.033768803	3.5431151	3.048945735	0.093381783	0.093381783	0
AATCCAGTCGACTGCG-1	1501682	101547	153596	132549	1113990	360	0.032409317	3.4175184	2.981799841	0.101928189	0.100844939	0
AATCGGTAGAAGGGTA-1	1738968	20720	187638	144910	1385700	448	0.040410101	4.222183	3.084431219	0.097108865	0.093875085	0
AATCGGTCAGATGAAT-1	2083510	18324	232455	169505	1663226	537	0.048516826	5.0141978	3.15247242	0.089356775	0.083903648	0
AATCGGTCATGAATGA-1	1141724	21695	124020	96014	899995	291	0.026150378	2.770480167	3.058156794	0.106586341	0.110073637	0
AATCGGTGTGCGCTTG-1	1377036	36062	145279	120108	1075587	347	0.031342054	3.299241667	3.121105178	0.101415096	0.100277759	0
ACACCAAGTGCAACCC-1	1564696	61763	164251	138949	1199733	388	0.034921638	3.6709974	3.035879663	0.094193068	0.094981267	0
ACACCCTAGCGTAATA-1	1308692	19257	142891	105386	1041158	336	0.030332771	3.193255233	3.100212341	0.105521785	0.103687227	0
ACACCCTCAACGCCGT-1	2677530	23668	284999	243202	2125661	687	0.061982831	6.390309767	3.07863356	0.072123215	0.072123215	0
ACACCGGAGTGTGAAT-1	2298220	21337	260232	191802	1824849	589	0.053210932	5.493141067	3.03444356	0.082292507	0.077533505	0
ACACCGGTCTGTGGCG-1	1500758	61695	156073	133208	1149782	371	0.03348087	3.534954067	3.080574814	0.102033577	0.099738367	0
ACACTGAAGACAGGCT-1	2166830	41758	237185	190773	1697114	548	0.049312887	5.095376333	3.000113666	0.087629544	0.086901296	0
ACACTGAAGCTCTCGG-1	1732842	34867	184174	165484	1348317	436	0.03936718	4.120503	3.046892093	0.098925254	0.094127327	0
ACACTGACACAGACCC-1	1749536	61962	185899	157247	1344428	434	0.039159413	4.103213933	3.03137695	0.091223368	0.089724053	0
ACACTGACAGAGGCTA-1	2149830	49924	231901	195011	1672994	540	0.048825964	5.073285233	3.092605744	0.084236344	0.08413419	0
ACACTGACAGTTCCGG-1	2435104	54813	263137	222177	1894977	612	0.055279632	5.718920433	2.980186273	0.077411177	0.076989279	0
ACAGCCGAGTCTCGTA-1	1325632	12262	144257	111403	1057710	342	0.030840806	3.249797767	3.035836287	0.104421375	0.101959922	0
ACAGCCGGTGATTGTC-1	2070006	33065	224963	172111	1639867	530	0.047820785	4.9551575	3.059110151	0.098641944	0.093297281	1

ACAGCCGGTTTGGCGC-1	1300972	20708	138945	120580	1020739	330	0.029695062	3.144617367	3.056738848	0.105839368	0.105839368	0
ACAGCTAAGACTCGGA-1	2329338	36147	255300	186817	1851074	598	0.05592884	5.563354867	3.730724366	0.142051914	0.142003883	1
ACAGCTACAAGCTACT-1	2054712	25559	227526	190268	1611359	521	0.046946572	4.8795573	3.072039558	0.084071237	0.085329516	1
ACAGCTACAGAACAGC-1	1390540	25218	147780	142095	1075447	347	0.031320565	3.270889167	3.046268073	0.123598583	0.106551431	0
ACAGCTATCCGAAGCC-1	2047718	67040	219115	181967	1579596	510	0.045983917	4.788213533	3.038096524	0.086802322	0.086345479	0
ACATACGAGCCGAACA-1	1933334	82909	202149	172557	1475719	477	0.042939418	4.4796397	3.039761022	0.089031637	0.087489465	0
ACATACGAGGTAACGC-1	2155174	38268	230722	193333	1692851	547	0.049287004	5.131931267	3.046721736	0.085187709	0.085468485	0
ACATACGAGTTAGGGC-1	1843254	56872	195811	159734	1430837	462	0.041699229	4.3516068	3.108740278	0.089285868	0.087070242	0
ACATACGCACTCCGAG-1	1852398	56273	197785	154926	1443414	466	0.042020874	4.3845015	3.037744025	0.092099546	0.087989202	0
ACATACGGTATAAGTG-1	1216200	16186	131761	97258	970995	314	0.028311585	2.986117567	3.141729879	0.108040973	0.106239597	0
ACATACGGTCTCTCGT-1	1947230	17401	207461	180122	1542246	498	0.045008917	4.6810789	2.964606422	0.090716768	0.085540393	0
ACATCAGAGTGTACGG-1	1548242	30265	165430	138008	1214539	392	0.035438602	3.729571833	3.141483965	0.094647312	0.093557268	0
ACATCAGAGTTAGGGC-1	2162160	68138	230836	186021	1677165	542	0.048843643	5.0707868	3.044915965	0.085819087	0.083514394	0
ACATGGTTCGAGCACC-1	2342724	42177	250391	208241	1841915	595	0.053685334	5.5509165	3.094818583	0.079690932	0.080236603	0
ACCAGTAAGATTCACC-1	1976604	34859	211875	189856	1540014	497	0.04495541	4.6606386	2.915582109	0.09155485	0.08523766	0
ACCAGTAGTGTTACGT-1	1900212	14933	209610	164185	1511484	488	0.044075688	4.5936624	3.03761348	0.082385431	0.083474961	0
ACCAGTATCGTTCGAA-1	1747368	17087	189798	157215	1383268	447	0.040387415	4.213793267	3.130242669	0.089748891	0.088434455	0
ACCCACTAGTTATCGC-1	1888022	33922	201901	173865	1478334	478	0.043060069	4.489605733	3.047354849	0.090463628	0.087961445	0
ACCCACTGTAGGGTGT-1	2538200	14179	276220	219811	2027990	655	0.0591447	6.07621214	3.098019858	0.079529912	0.078203858	0
ACCGTAACACGTAGGA-1	1380940	13625	148441	116163	1102711	356	0.032154616	3.387403767	3.012291852	0.100655279	0.099934378	0
ACCGTAACATCTCGTC-1	1371276	27029	145865	119787	1078595	348	0.031406954	3.312304133	3.047964476	0.104143741	0.101846825	0
ACCTTTAAGTGGGCTA-1	1984054	31521	215983	173725	1562825	505	0.045653576	4.752964833	3.073153056	0.087346541	0.087971547	0
ACGAGCCGTGCGCTTG-1	480602	16054	50702	39264	374582	121	0.010972491	1.1839196	3.006909039	0.165813839	0.166136113	0
ACGAGGACACCGGCAT-1	2202826	39079	235824	198605	1729318	559	0.050400606	5.1903268	2.949807498	0.082234569	0.081124728	0
ACGAGGACAGTAGGGT-1	1970072	20694	211295	168772	1569311	507	0.045824131	4.755401733	2.900216673	0.086821051	0.088564303	0
ACGAGGACATCTCGAA-1	1589852	13520	175320	138171	1262841	408	0.036813441	3.8619104	2.963469995	0.097026897	0.090469689	0
ACGATACAGAAGATTC-1	2405454	45256	258237	206864	1895097	612	0.055211206	5.684149267	3.034979292	0.084124204	0.08313122	0
ACGATACCAGCCAAAG-1	1565708	43644	170207	130158	1221699	395	0.035579155	3.730359167	3.096921274	0.096255677	0.097437977	0
ACGATACCAGTCCCTT-1	2182200	51047	233881	196106	1701166	550	0.049620587	5.136295233	3.120036095	0.083921356	0.083654971	0
ACGATACTCGAGGTGA-1	2134112	23342	233072	180790	1696908	548	0.049549346	5.133871267	3.095033425	0.085013719	0.08237047	0
ACGATGTCAACATGGG-1	1533672	18629	167922	128048	1219073	394	0.035624279	3.727744667	3.072894475	0.093725177	0.095030389	0
ACGATGTGTCATACCA-1	1729378	53666	184144	143803	1347765	435	0.039166738	4.0891198	3.036356662	0.098969759	0.096214583	0
ACGATGTTCTTCACAT-1	3345290	27813	369751	280877	2666849	861	0.077807053	7.906098167	3.078657514	0.07609091	0.07609091	0
ACGCAGCGTTACGGCC-1	1792344	57475	185968	168114	1380787	446	0.040184418	4.200522933	2.971514243	0.090680299	0.088751421	0
ACGCAGCTCCGCTCTA-1	2087834	29942	224002	185826	1648064	532	0.048021425	4.992167267	3.108778436	0.085242302	0.086010237	0
ACGCCAGCAAGAGAGA-1	1496968	26486	159756	127188	1183538	382	0.034569834	3.6316096	3.066274643	0.099224777	0.096272719	0
ACGCCAGCAAGGGTGT-1	2271446	17733	244522	201180	1808011	584	0.052738271	5.446306333	2.874476928	0.084700755	0.08500079	0
ACGCCAGCACAGCTGC-1	1625818	24915	175227	146652	1279024	413	0.037190945	3.894130367	2.405532311	0.093930142	0.095435505	0
ACGCCAGTCCACCCAT-1	2425936	23263	261979	213298	1927396	623	0.056289291	5.790497933	3.031712879	0.081790805	0.079392069	0
ACGCCAGTCTCGGAAT-1	2524986	35640	270869	220915	1997562	645	0.058245061	5.999015767	3.10649454	0.082614331	0.079362381	0
ACGCCGAAGACAAGCC-1	2059208	82015	213546	184685	1578962	510	0.045918662	4.777867533	3.052397528	0.085790207	0.087685137	0
ACGCCGAAGCAGCCTC-1	1879398	33050	194090	171141	1481117	478	0.043161277	4.507858033	3.03377188	0.085986667	0.086625096	0
ACGCCGACATGACCGC-1	1274780	29596	133322	115760	996102	322	0.028963708	3.064372933	3.031834421	0.104529933	0.103030621	0
ACGGAGAAGCCCTAAT-1	1510314	12939	167795	118186	1211394	391	0.035365851	3.697122133	3.044725235	0.102422677	0.102156751	1
ACGGAGAAGCGAACA-1	1870200	59658	200760	165518	1444264	467	0.04211348	4.395974267	3.060841769	0.092934158	0.090285877	0
ACGGAGAGTTGCAGCC-1	1687642	66288	176812	155015	1289527	417	0.037574239	3.9443703	3.092616925	0.097058217	0.096416639	0
ACGGAGATCGGATCCG-1	1698712	36263	180595	153861	1327993	429	0.038666782	4.045069267	3.090801242	0.093251565	0.092367631	0
ACGGCCAAGAAGGTTT-1	2095810	58802	225630	170473	1640905	530	0.047833024	4.944299767	3.131815501	0.106846154	0.106290561	1
ACGGCCAAGAATGTGT-1	2317226	15830	251569	195441	1854386	599	0.054170794	5.567949033	3.16001307	0.081579968	0.080154444	0
ACGGCCACAACGAAAT-1	1818180	29968	197937	153539	1436736	464	0.041907997	4.348304167	2.989077325	0.08821607	0.088891438	0
ACGGCCACACACACGC-1	1745414	33669	187703	154960	1369082	442	0.03983508	4.169640667	3.132814775	0.089239635	0.090296218	0
ACGGGCTAGTCTAGCT-1	2027816	67519	211866	174659	1573772	508	0.045693949	4.739875233	3.120302301	0.089259435	0.087321671	0
ACGGGCTATCGGTCG-1	1082650	153573	97437	91438	740202	239	0.021415896	2.282546467	3.077201602	0.121474159	0.121474159	0
ACGGGCTATGCAGTT-1	1555772	19283	166411	132949	1237129	400	0.036089276	3.771228433	3.118545609	0.094622538	0.092835435	0
ACGGGCTGTCGTCTTC-1	2180516	59532	224953	194276	1701755	550	0.049553681	5.1406903	3.046652366	0.084406043	0.082046355	0
ACGGGTCCACGATGGA-1	1712888	19805	185174	139869	1368040	442	0.039957114	4.171670333	3.225529406	0.089381461	0.089452451	0
ACGGGTCTCGTCCCTA-1	1148600	9419	123872	104283	911026	294	0.026611324	2.817042633	3.047678216	0.10857965	0.109505651	0
ACGTCAAAGATGTGGC-1	2449318	41004	265303	216361	1926650	622	0.05619078	5.790395767	3.033245011	0.080239317	0.079049282	0
ACGTCAAGGAGCGAG-1	2217700	51849	231815	191802	1742234	563	0.050832196	5.277068233	3.017137011	0.084226197	0.083394547	0
ACGTCAACATTTGTGG-1	1383764	24743	151157	118318	1089546	352	0.031795891	3.3498854	3.00124984	0.105654742	0.10112401	0
ACTATCTAGAAGGCCT-1	2340500	45750	244962	206087	1843701	596	0.053762996	5.561933233	3.079507183	0.081917808	0.079889741	0
ACTATCTAGTACAGTA-1	1373640	10603	151092	109642	1102303	356	0.032171528	3.3730243	2.936983713	0.101853901	0.102282196	0
ACTATCTCATGGCTAT-1	2381058	24025	260827	207782	1888424	610	0.055100183	5.672152967	2.989273054	0.081251062	0.079224372	0
ACTATCTTCGGAGAAC-1	2561748	31205	277288	226690	2026565	655	0.059167535	6.0588698	3.388715224	0.093515303	0.094152367	1
ACTATCTTCTCGAACA-1	2087154	61595	221458	182462	1621639	524	0.047239503	4.9084405	3.082060499	0.084946899	0.085283738	0
ACTATCTTCTGGTAGT-1	1379718	5169	151366	122603	1100580	356	0.032233351	3.374320867	3.073016392	0.098855663	0.099042487	0
ACTGAACAGCTAAACA-1	1813600	50069	196045	157746	1409740	455	0.041107915	4.306804667	3.073844427	0.088706972	0.089138143	0
ACTGAACAGTGCGATG-1	1410344	18306	154109	116718	1121211	362	0.032742614	3.438070667	3.046910406	0.104102781	0.103905052	0
ACTGAACCACGCGATC-1	2013756	61007	212582	178930	1561237	504	0.04551106	4.726455133	3.058686063	0.092290925	0.09067528	0
ACTGAGTCACGTTTAG-1	1102454	16367	120770	93160	872157	282	0.025507936	2.700768867	3.170097016	0.108813419	0.110268539	0
ACTGAGTTCTTCTAAC-1	2190698	22791	242101	192580	1733226	560	0.050609432	5.2344077	3.032377218	0.081053923	0.080287096	0
ACTGATGCACGACTAT-1	2184730	22637	242816	187936	1731341	559	0.050534506	5.223113867	3.080569091	0.088297215	0.083819471	0
ACTGATGCATACCAGT-1	2430222	13424	269744	211919	1935135	625	0.056503135	5.818503667	3.096903218	0.080059274	0.078694419	0
ACTGATGGTACGTCAT-1	2376510	23895	257856	208841	1885918	609	0.054981658	5.666858133	3.147523979	0.085689203	0.08075692	0
ACTGATGTCGTTCGTC-1	1803874	31510	189485	160372	1422507	460	0.041483939	4.335570633	3.093830581	0.087089762	0.087962696	0
ACTGATGTCTTATGGG-1	1536906	16390	167930	127867	1224719	396	0.035839708	3.7464362	3.043617225	0.09557357	0.093558139	0
ACTGCTCAGATAGCAT-1	1975236	15691	218189	171038	1570318	507	0.045775088	4.755239333	3.206565667	0.085855248	0.085988091	0
ACTGCTCAGCGCCTTG-1	1238026	14333	133668	107576	982449	317	0.028676488	3.029836333	3.047631899	0.108652568	0.10527842	0
ACTGCTCAATCGTCA-1	1772796	65297	186642	159768	1361089	440	0.039581459	4.154666133	3.106394919	0.090209465	0.089435262	0
ACTGCTCGTGGAAAGA-1	1125862	20746	118026	100092	886998	287	0.025923185	2.744586533	2.949218639	0.110110618	0.110110618	0
ACTTACTCACATAAAG-1	1145880	15642	127372	93137	909729	294	0.026486209	2.7934199	3.125732302	0.110359012	0.10959121	0
ACTTACTTCCGAGATT-1	1161312	30222	126547	96522	908021	293	0.026498883	2.796564633	3.047326184	0.111954611	0.109939767	0
ACTTACTTCTCATGTT-1	830544	5440	92263	66095	666746	215	0.019556487	2.063727167	3.029907551	0.126517812	0.130726055	0
ACTTGTTAGGGTTTCT-1	2007414	67129	208535	180126	1551624	501	0.045093868	4.668288967	3.086407739	0.093588969	0.089122439	0
ACTTGTTAGTTGTAGA-1	1407786	12403	153720	119717	1121946	362	0.032773897	3.447640233	3.156688115	0.099948837	0.098970935	0
ACTTGTTGTCTAGGTT-1	2230772	26787	243670	185047	1775268	573	0.051795108	5.359951533	5.411388583	0.079391008	0.079391008	0
ACTTGTTTCTCAGATG-1	1354672	15772	151326	109253	1078321	348	0.031508377	3.308018633	3.046968233	0.102145154	0.099140309	0
ACTTGTTTCTGTGGCG-1	1437846	110970	144459	124653	1057764	342	0.030723092	3.238338333	3.17890827	0.102472444	0.100926321	0
ACTTTCACAAACGAGC-1	2284376	30787	245830	212764	1794995	580	0.052342236	5.398161667	3.106089773	0.083718647	0.082206056	0
ACTTTCACACATTCAG-1	1881816	25671	207654	163702	1484789	480	0.043340149	4.527164267	3.164901363	0.088559292	0.088963935	0
ACTTTCACAGCGGTCT-1	1699466	77603	176749	150333	1294781	418	0.037617491	3.9313497	3.166321023	0.092560531	0.094528253	0
ACTTTCAGTAGCAGTG-1	2130118	25382	235611	175558	1693567	547	0.049247292	5.1126856	2.854217732	0.079162952	0.078942267	0
AGAATAGAGAAAGCTT-1	561428	4795	58768	49587	448278	145	0.01307636	1.401687	3.135153942	0.167327965	0.1532965	0
AGAATAGAGTCAAGGC-1	1274676	41008	133170	110554	989944	320	0.028964719	3.063083833	3.027646365	0.107340015	0.105737256	0

AGAATAGCAAGCAAGC-1	2156808	44481	227759	190487	1694081	547	0.049406282	5.112295633	2.967717643	0.085479864	0.083294191	0
AGAATAGGTGAAGCCA-1	1572888	52876	163326	143226	1213460	392	0.035362654	3.7213061	3.033423077	0.097017399	0.097017399	0
AGACGTTTCCTCAGTC-1	1918948	26735	210538	162272	1519403	491	0.044235042	4.604272233	3.037907958	0.088403319	0.088556612	0
AGAGCGAAGTCCATAC-1	2044638	35223	218603	168348	1622464	524	0.047287512	4.890652167	3.112902653	0.086209627	0.08564284	0
AGAGCGACAGTGTGGA-1	1460510	22996	149562	128787	1159165	374	0.033863924	3.559892733	2.922134379	0.096894229	0.095514297	0
AGAGCGAGTTTGTCAG-1	2044704	49614	214486	181666	1598938	517	0.046655888	4.850100467	2.958417389	0.086154332	0.08403797	0
AGAGCGATCCCACGGA-1	1990708	49217	203124	171154	1567213	506	0.045640518	4.761051433	3.069606854	0.085818954	0.085188129	0
AGAGCGATCGTGCCTT-1	528298	7433	45153	45646	430066	139	0.012560575	1.347902567	2.942494531	0.160100003	0.160100003	0
AGAGCTTAGACGTCGA-1	1901952	23668	199568	176547	1502169	485	0.043834308	4.575904767	3.019696001	0.080964695	0.081844519	0
AGAGCTTCATTCTTCA-1	1950338	65432	202472	175183	1507251	487	0.043876453	4.571817367	3.016754856	0.088704655	0.088931732	0
AGAGTGGAGGCATGGT-1	1550684	17525	165018	134619	1233522	398	0.035976035	3.7670154	3.109204667	0.096247216	0.096247216	0
AGAGTGGCACTACATG-1	848824	14877	91631	68597	673719	218	0.019592001	2.075590933	2.926195227	0.12482493	0.127679228	0
AGAGTGGCATGAAAGT-1	1634482	33198	173472	148342	1279470	413	0.037343874	3.904139367	3.066837151	0.093745959	0.095522393	0
AGAGTGGGTACAAGGC-1	1574718	62628	164436	135532	1212122	392	0.035291039	3.704511433	3.144035231	0.093973977	0.095234517	0
AGAGTGGGTTCTTCGC-1	2160054	42859	225552	197871	1693772	547	0.049381983	5.14037O5	3.09598579	0.085432457	0.083441706	0
AGATCTGCACCAGTGC-1	1302742	111607	130852	112584	947699	306	0.027392843	2.904960333	3.003018637	0.110801733	0.10833319	0
AGATCTGTCTTCTTGA-1	1027810	17927	111568	89262	809053	261	0.0236172	2.506383433	3.151715517	0.110572552	0.111794884	0
AGATTGCAGCAAAGTT-1	1725934	45722	184586	150101	1345525	435	0.039155553	4.076863833	3.144242657	0.095546842	0.09340975O	0
AGATTGCCAGAATTCC-1	1775544	73194	183743	160486	1358121	439	0.03940685	4.109750467	3.141270382	0.091239103	0.092254147	0
AGATTGCCATGATGCT-1	2359312	52078	251012	214016	1842206	595	0.053201518	5.4074756	3.018030178	0.0875062	0.08479324	0
AGATTGCGTCACCGCA-1	1361118	25537	148711	122783	1064087	344	0.030926321	3.2684244	3.000106522	0.103068232	0.103068232	0
AGATTGCTCGCGAGAA-1	1617266	19635	172416	137220	1287995	416	0.037576083	3.931550167	3.050215921	0.09602684	0.092561879	0
AGCAGCCAGGGTCGAT-1	2197878	29517	233974	198460	1735927	561	0.050672239	5.250421533	3.283035353	0.081620525	0.081620525	0
AGCAGCCAGTGTGATA-1	1620070	16473	177381	135473	1290743	417	0.037708206	3.941775667	3.110052196	0.093259462	0.090649856	0
AGCAGCCGTTGACGGA-1	1443074	28203	155875	128520	1130476	365	0.032949853	3.478139333	3.14314121	0.101264371	0.098761295	0
AGCAGGCTCTCATGTT-1	1247746	13976	136865	99636	997269	322	0.02910808	3.055169933	3.098491249	0.104614137	0.101126923	0
AGCATACCAGGTACGA-1	1474976	23637	159689	130397	1161253	375	0.033815691	3.560159367	3.020477743	0.097256597	0.096098827	0
AGCATACCATCATGGT-1	1791440	16376	195968	152142	1426954	461	0.041667075	4.327912133	2.832952156	0.090749601	0.090749601	0
AGCCTAAAGTAAGTAC-1	2358660	59689	252197	209593	1837181	593	0.053447476	5.528049633	3.063391937	0.083021023	0.083341018	0
AGCCTAACACGTCATA-1	1577272	22571	171513	138100	1245088	402	0.036342669	3.811247	2.990751264	0.098630928	0.096221741	0
AGCCTAAGTCTCTCGT-1	2205756	33923	236537	196392	1738904	562	0.050758799	5.262497333	3.013732248	0.081779361	0.082401627	0
AGCCTAAGTGTCGCTG-1	1209060	25888	129084	110236	943852	305	0.027478375	2.903478767	3.040305344	0.103093333	0.104352378	0
AGCCTAATCCTCATCG-1	1593474	58089	167157	149951	1218277	394	0.035471316	3.736384133	3.063203525	0.100146994	0.098470001	0
AGCGGTCAGCGTAGTG-1	1023310	17482	106164	80445	819219	265	0.02388401	2.519530667	3.039068215	0.114023001	0.111648753	0
AGCGGTCCACAAGCGA-1	1365968	44907	141731	126755	1052575	340	0.030660726	3.246291167	3.108231502	0.097617216	0.099952199	0
AGCGGTCCAGGCCGTT-1	1148618	11633	121041	105371	910573	294	0.026533706	2.8174782	2.988449654	0.106565146	0.107953076	0
AGCGGTCGTAACTGTC-1	1374064	26408	138507	117266	1091883	353	0.031798974	3.347293433	3.063481127	0.109992841	0.106060754	1
AGCGGTCGTCATCTGA-1	919006	18041	93317	82387	725261	234	0.021152135	2.257329233	2.922124949	0.124304729	0.123691695	0
AGCGGTCTCATCGCCT-1	1720890	29976	181616	158431	1350867	436	0.039301563	4.121036333	2.861561308	0.094711954	0.092806781	0
AGCGTATAGGCTATCT-1	2271176	38756	238477	205649	1788294	578	0.05174908	5.2981225	3.129033404	0.084654327	0.085006466	0
AGCGTATCAGTGTGGA-1	1763302	21936	185483	160013	1395870	451	0.040754746	4.247786033	3.099565993	0.092988907	0.088487988	0
AGCGTCGCACTCACCT-1	329072	21274	24516	27433	255849	83	0.007439767	0.808143467	3.091444192	0.202630239	0.191800209	0
AGCTCCTAGACTTCCA-1	1971326	52313	208430	181948	1528635	494	0.044484478	4.6452097	3.045161703	0.088704676	0.085352278	0
AGCTCCTAGGATGCGT-1	2353654	20983	253451	211655	1867565	603	0.054495186	5.618355233	2.999019629	0.080396012	0.080759701	0
AGCTCCTGAGTACCTA-1	1787978	24588	194188	155884	1413318	457	0.041262715	4.305795233	3.067225936	0.085437463	0.086391948	0
AGCTCCTGTAGTAGTA-1	654126	9848	62407	52142	529729	171	0.01547593	1.6500158	3.065543045	0.138996835	0.138320039	0
AGCTCCTTCGAGTTGT-1	2480190	25318	273164	219795	1961913	634	0.057235343	5.895325367	3.110919332	0.077788927	0.077247803	0
AGCTCTCAGCCGGTAA-1	1532874	15948	168798	128963	1219165	394	0.035608948	3.726568233	2.993757014	0.09378936	0.094398821	0
AGCTCTCAGTTAGCGG-1	1500694	45535	158641	139343	1157175	374	0.033725253	3.550303967	3.056084258	0.102155779	0.098523681	0
AGCTCTCGTACAACGG-1	1331684	33482	141517	117259	1039426	336	0.030322955	3.204334967	3.117052772	0.10090187	0.101664733	0
AGCTCTCGTACTCCGG-1	1850330	51131	194030	166326	1438843	465	0.041962515	4.3804916	3.036522023	0.089909879	0.089106476	0
AGCTCTCTCGATTACC-1	2812576	58022	295117	254261	2205176	712	0.063958728	6.489611833	3.075038361	0.081157984	0.079902206	0
AGCTCTCTGAGTTGT-1	3359056	31623	367746	277568	2682119	866	0.078285805	7.913010467	4.325234842	0.125119579	0.125119579	1
AGCTTGAAGCCCGTT-1	1720304	23476	186376	147660	1362792	440	0.039825946	4.1376289	3.016888605	0.095196976	0.089450383	0
AGCTTGAAGTCGCGTC-1	1053408	52122	98986	88481	813819	263	0.023684823	2.5099128	4.699638435	0.152915307	0.152915307	1
AGCTTGACACATCGAT-1	1968272	23166	216453	172744	1555909	503	0.045311812	4.6991641	2.914184009	0.09464809	0.092702729	1
AGCTTGAGTCAACTGT-1	2299630	43004	250500	200548	1805578	583	0.052700057	5.4480065	3.108053195	0.0833082	0.082573039	0
AGGCCACAGATCTGAA-1	1749286	27152	185499	151857	1384778	447	0.040337724	4.213841667	3.07027338	0.087132657	0.086964727	0
AGGCCACAGTTGCGT-1	2204010	30928	237658	197792	1737632	561	0.050733872	5.249468267	3.048412873	0.083782048	0.080772231	0
AGGCCACGTGGCGTC-1	1423172	37314	150379	125953	1109526	358	0.032314932	3.406177833	3.000369321	0.096717111	0.098356915	0
AGGCCACTCAAGAGGC-1	1892180	38572	202662	163886	1487060	480	0.043325615	4.517488	2.966464216	0.090024812	0.08962511	0
AGGCCACTCCACCGGA-1	1603934	32574	170544	144874	1255942	406	0.036584129	3.844998967	3.140054411	0.090084149	0.091609034	0
AGGCCACTCTAGCTAG-1	409572	3201	43476	33921	328974	106	0.009612159	1.038991633	3.038397625	0.181373079	0.175496421	0
AGGCCGTAGCACAGGT-1	1583174	15312	173080	133501	1261281	407	0.036874958	3.866255933	3.143004247	0.094611003	0.093961567	0
AGGCCGTCATAGTGAA-1	1649578	19734	178405	136028	1315411	425	0.038364494	4.0086198	3.023141341	0.09412431	0.094374613	0
AGGCCGTGTCTAGGTT-1	417406	4283	44720	32526	335877	108	0.009827153	1.0562403	3.034644328	0.182642423	0.182642423	0
AGGCCGTGTCTCTATT-1	750368	22606	79750	59082	588930	190	0.017158877	1.8215811	3.034321417	0.128367768	0.132775678	0
AGGCCGTGTGTGTATC-1	1148566	27913	119625	100513	900515	291	0.026291303	2.780606433	2.999424769	0.114266837	0.110833141	0
AGGCCGTTCGTTAGGT-1	1801584	17503	193153	150139	1440789	465	0.042106187	4.387917567	3.024531947	0.091926877	0.091042759	0
AGGCCGTTCTGCACAA-1	1537946	13667	167960	129639	1226680	396	0.035798326	3.746041633	2.999239981	0.09784165	0.096891759	0
AGGGAGTTCGCTATGA-1	876860	12731	93741	73801	696587	225	0.020275435	2.152470567	3.099620069	0.118109483	0.119282838	0
AGGGATGAGGCATTGG-1	1663006	31429	180490	138202	1312885	424	0.038318826	4.014689167	3.035017576	0.095834927	0.092147237	0
AGGGATGCAAATCGCT-1	1401128	40333	150137	129017	1081641	349	0.031482126	3.324889367	3.169809847	0.099356491	0.101128004	0
AGGGATGGTATAAGTG-1	1149906	19981	124271	90984	914670	295	0.026666984	2.814235133	2.972223011	0.107295848	0.10589313	0
AGGGATGTCGTACGCG-1	893812	133266	82388	68572	609586	197	0.01774024	1.9008593	3.03236115	0.134096269	0.129364559	0
AGGGATGTCTGGCCTT-1	1978200	52721	209735	175412	1540332	498	0.044828087	4.663919133	2.966789563	0.089551548	0.087588747	0
AGGGTGAGTCCTACCT-1	1846048	21366	196755	167070	1460857	472	0.042498688	4.433703067	3.065491792	0.089080199	0.090014913	0
AGGGTGAGTGACTGAG-1	1702810	28855	181835	143145	1348975	436	0.039390755	4.113775267	3.015918228	0.090255251	0.089502727	0
AGGTCATAGCCATGCC-1	861790	4740	92524	76985	687541	222	0.020067168	2.141876333	3.130373643	0.128597655	0.124515747	0
AGGTCATAGGCATTTC-1	2690112	90212	283915	239171	2076814	671	0.059996559	6.084890167	3.151966077	0.086005509	0.085088698	1
AGGTCATAGTGATTGA-1	1689778	22184	183484	141027	1343083	434	0.039168435	4.0873525	3.010681591	0.093728168	0.092958044	0
AGGTCATCAACATAAG-1	1174394	15627	129094	91346	938327	303	0.027418795	2.881191933	3.046460931	0.111822744	0.109433147	0
AGGTCATTCGACAATC-1	2533004	37228	275819	226325	1993632	644	0.057993473	5.945801967	3.047537513	0.07929588	0.078320134	0
AGGTCATTCGCGGCAT-1	2614406	47636	277343	223643	2065784	667	0.060215849	6.1721901	3.080780954	0.078036424	0.077922745	0
AGGTCCGCAGTGTGGA-1	1863294	24403	202809	158068	1478014	477	0.043176622	4.501095	2.995651618	0.091251477	0.089331377	0
AGGTCCGGTTGCCTCT-1	3346364	40672	357020	280321	2668351	862	0.077779102	7.9095452	2.842413903	0.098164342	0.098164342	1
AGGTCCGTCTCGACGG-1	1075000	94614	103951	94696	781739	253	0.022783577	2.428875767	3.061461004	0.116626259	0.114173925	0
AGTAGTCCAATCGCGC-1	1347544	39366	138889	123782	1045507	338	0.030438488	3.2221532	3.070319713	0.105434103	0.10816717	0
AGTCTTTAGTCTAGCT-1	1757466	24188	191071	160807	1381400	446	0.040149387	4.175805133	2.918222689	0.091972992	0.091972992	0
AGTCTTTGTTCCACAA-1	1696910	14501	188090	144795	1349524	436	0.039333171	4.114171967	3.109465249	0.092673814	0.091358931	0
AGTCTTTTCGTCTAC-1	2442606	40672	265703	221502	1914729	619	0.055856444	5.7734663	3.106367861	0.081495182	0.080163436	0
AGTGAGGAGGCATGGT-1	1666548	18462	178529	148797	1320760	427	0.038545755	4.034064233	2.973534448	0.091553745	0.091891211	0
AGTGAGGCATTCCGAA-1	1648850	23461	178964	137282	1309143	423	0.038175487	3.987958	2.938579791	0.090520298	0.093213992	0
AGTGAGGTCTGTATGG-1	1237886	21509	133156	99947	983274	318	0.028707147	3.022858633	2.985521756	0.107002386	0.104174017	0

AGTGGGAAGCTGAAAT-1	1490226	36794	157588	132316	1163528	376	0.033895017	3.557828	3.108770235	0.098696662	0.097026677	0
AGTGGGATCTCACCAGC-1	1978564	42869	208403	180238	1547054	500	0.045106961	4.709262133	3.047462059	0.087613557	0.089622417	0
AGTGGGATCTGACGCG-1	592084	177657	44217	38054	332156	107	0.009612948	1.042086633	3.121591014	0.161938344	0.169504918	0
AGTGGGATCTGGGACC-1	1927970	53434	200149	174713	1499674	484	0.043682922	4.5523684	3.140047447	0.090020696	0.088305152	0
AGTGTCACATGTAGCT-1	1892756	57650	197711	172374	1465021	473	0.042408426	4.405439567	3.118092166	0.093100892	0.091984156	0
AGTGTCAGTACGTCAT-1	2299514	22851	245912	203154	1827597	590	0.053315924	5.4916656	3.174907131	0.08045447	0.080076041	0
AGTGTCATCGAGCGTC-1	459060	45085	36731	36910	340334	110	0.009920517	1.069982567	3.075239806	0.169163897	0.167422671	0
AGTTGGTCAAACGAGC-1	2297322	47934	242853	201074	1805461	583	0.052653154	5.448442233	3.065757591	0.081712516	0.081095118	0
AGTTGGTCACTTCAGA-1	1380784	19083	148848	123652	1089201	352	0.031800664	3.348369933	3.119108321	0.100975167	0.09953487	0
AGTTGGTGTGTTCGAT-1	2197724	28037	238073	185774	1745840	564	0.050898742	5.2592854	3.114321037	0.086512712	0.083922449	0
ATAACGCCAACTGGAG-1	1633966	27716	178350	133748	1294152	418	0.037747828	3.9454821	2.992149814	0.093127091	0.093264072	0
ATAACGCCACTTTCCG-1	1491974	125952	147673	126689	1091660	353	0.031778458	3.356884067	3.080169376	0.09975734	0.09975734	0
ATAACGCGTGCCATTA-1	1066366	13213	111443	87408	854302	276	0.024879644	2.628302433	3.011752509	0.110566824	0.109181002	0
ATAACGCGTGCTCGAC-1	1482980	60366	150134	136338	1136142	367	0.033069285	3.479349867	3.098668788	0.096776066	0.097489479	0
ATAACGCTCCACTTCG-1	1359418	87900	137189	116187	1018142	329	0.029627614	3.135118967	3.033646028	0.103041904	0.104082418	0
ATAAGAGAGGCCTTG-1	962836	18972	96333	81371	766160	247	0.022368929	2.3683318	2.923421025	0.116149964	0.1138576	0
ATAAGAGAGTAGCCGA-1	1766028	24052	184462	162312	1395202	451	0.040708318	4.254402967	3.021925244	0.091070329	0.08999183	0
ATAAGAGCACGCTCAC-1	1923086	40385	192026	172885	1517790	490	0.044271089	4.6048537	3.047690745	0.089157223	0.087402921	0
ATAAGAGTCCGTGCTT-1	2169648	76523	223539	186154	1683432	544	0.049035212	5.074431067	3.177838879	0.083238835	0.084094245	0
ATAGACCGTACCGCTG-1	1066608	32690	109798	93470	830650	268	0.024171501	2.5663864	3.046567775	0.114307193	0.109126515	0
ATAGACCGTCCGAATT-1	1419948	40923	145886	123415	1109724	358	0.032328595	3.3939711	3.038751651	0.093175952	0.094536517	0
ATCACGAGTACCTAGT-1	1363550	10720	151820	114518	1086492	351	0.031754131	3.327121167	3.093358329	0.102322145	0.100989869	0
ATCATCTCATTACGCA-1	1111666	57838	114091	95954	843783	273	0.024518383	2.6064685	3.041226719	0.115094106	0.114188872	0
ATCATCTGTGCGAAAC-1	2060480	64865	216164	190571	1588880	513	0.046243751	4.809747367	2.706719126	0.086284701	0.0867528	0
ATCATGGAGTCCAGGA-1	1407318	16771	152163	124295	1114089	360	0.032485614	3.419469933	3.094611289	0.098210797	0.09773197	0
ATCCGAACAGCCAAG-1	1578844	38222	172314	134998	1233310	398	0.035927912	3.769150133	3.080589255	0.096002777	0.094600629	0
ATCCGAACAGTAATCC-1	2136110	72536	226911	199460	1637203	529	0.047484221	4.8896513	3.091830502	0.09093289	0.088214773	0
ATCCGAACATTCCGAA-1	1630784	15642	179768	141355	1294019	418	0.037714044	3.945072	3.031704198	0.09351833	0.092960022	0
ATCGAGTGTCGGAAGT-1	2006760	37408	211820	176055	1581477	511	0.046189328	4.7856537	3.024615079	0.08520628	0.085615149	0
ATCGAGTTCTGTGAAC-1	2395576	46901	260437	216339	1871899	605	0.054497131	5.6056252	3.097042278	0.08097007	0.079564362	0
ATCTACTAGGGATGGG-1	2243542	25124	240907	194336	1783175	576	0.052102973	5.372276467	3.062564372	0.081146123	0.077335945	0
ATCTACTAGTCACGCC-1	1218714	77336	123496	105423	912459	295	0.026521964	2.813396533	3.037725533	0.113991438	0.111485821	0
ATCTACTAGTTTGCGT-1	2018732	24268	218536	174761	1601167	517	0.046717501	4.852593867	3.083351685	0.084552506	0.085514678	0
ATCTACTCAGTGCTGC-1	1869846	61539	197307	169369	1441631	466	0.041918418	4.3723061	3.09101308	0.092589504	0.092595723	0
ATCTGCCATTCGTTT-1	1907868	52012	206181	157952	1491723	482	0.04346324	4.524551767	3.087888905	0.091098702	0.090487793	0
ATCTGCCGTCATGCCG-1	1474172	58169	155039	125925	1135039	367	0.032977291	3.472968533	2.919518031	0.100677608	0.096420616	0
ATCTGCCTCCGCATT-1	2262360	27429	245848	205020	1784063	576	0.05181607	5.352986367	3.021787313	0.082319085	0.08157567	0
ATGAGGGAGGAGGTAGA-1	1567174	14967	165020	136004	1251183	404	0.036573547	3.8403556	3.070503168	0.098352273	0.095818013	0
ATGAGGGAGTTTGCGT-1	1008106	17222	107020	90035	793829	256	0.023240011	2.469176367	3.032866383	0.116876157	0.116876157	0
ATGAGGGTCCGACCAG-1	1942688	56312	203040	174595	1508741	487	0.043975265	4.5877036	3.049438059	0.088278537	0.087012533	0
ATGCGATCATTACAGC-1	1909072	52262	201697	169549	1485564	480	0.043211991	4.500713433	3.075562975	0.0891428	0.087521738	0
ATGCGATGTCAAGTTC-1	2058878	104904	211876	184501	1557597	503	0.045104044	4.6538191	3.179768897	0.090574869	0.088390852	0
ATGCGATGTGATCCTA-1	2085366	33770	224296	184043	1643257	531	0.04794138	4.963607333	3.071358547	0.087753191	0.087266572	0
ATGCGATGTTTAGGAA-1	1470398	18040	158690	124689	1168979	378	0.034072363	3.5788921	3.121255826	0.095290695	0.094863344	0
ATGGGAGAGTCCCACG-1	1766016	34326	189818	158677	1383195	447	0.040208424	4.2134936	3.035173595	0.094134316	0.090766932	0
ATGGGAGGTACCGTGC-1	1385244	60296	139029	121939	1063980	344	0.030932442	3.262052533	3.137004396	0.102294989	0.101197135	0
ATGGGAGTCGGAGAGT-1	1975858	34805	209927	169141	1561985	505	0.045619693	4.735090867	2.959424902	0.088808111	0.086337311	0
ATGGGAGTCTTAAGGC-1	1826300	67326	192514	156042	1410418	456	0.041097733	4.296669133	3.115217947	0.089298604	0.089962246	0
ATGGGAGTCTTCTAAC-1	2084424	22514	225818	184041	1652051	534	0.048239738	5.0031236	3.106227575	0.083307849	0.081645377	0
ATGTGTGGCAAAGTAAC-1	2569986	39138	275783	228889	2026176	655	0.05914677	6.091579033	3.188429787	0.075207603	0.076189977	0
ATGTGTGGTCTGTCT-1	1995796	74139	203644	177756	1540257	498	0.044687175	4.617085167	3.158436945	0.090986539	0.089578389	0
ATTACTCAGTAATCCC-1	1337548	26864	141917	116809	1051958	340	0.030764596	3.250707433	3.011244655	0.105755499	0.106521129	0
ATTACTCACACACGC-1	1548624	45305	163553	137239	1202527	388	0.035001052	3.676174233	3.047204051	0.098126055	0.099315894	0
ATTACTCCATCCCAAA-1	1987428	16436	219320	154340	1597332	516	0.046582195	4.822011433	3.771541333	0.141879491	0.140008827	1
ATTACTCGTAAAGTCA-1	1744250	52039	180308	156162	1355741	438	0.039433127	4.127583	2.955779366	0.094309345	0.093588856	0
ATTACTCGTAGCGTCC-1	1670256	59486	165415	144106	1301249	420	0.037846569	3.949823767	3.001519412	0.100548567	0.09522938	0
ATTATCCAGCGATGAC-1	2217690	39668	241927	193510	1742585	563	0.050813994	5.2627629	3.063954025	0.084168073	0.081576849	0
ATTATCCAGGAGTACC-1	2707544	35067	289054	243790	2139633	691	0.062329197	6.382326533	3.136278382	0.078477025	0.076157035	0
ATTATCCTCCGATACA-1	2139058	21981	229721	196304	1691052	546	0.049317571	5.108521867	2.777008261	0.086556331	0.085288966	0
ATTCTACAGAGCCCAA-1	2060292	22490	219590	182448	1635764	528	0.0477225	4.954347167	2.944145706	0.093042607	0.093128964	1
ATTCTACAGCTAAGAT-1	2064014	14793	228841	169328	1651052	533	0.048195085	4.985337667	2.963087677	0.085101675	0.084175553	0
ATTCTACAGCTATGCT-1	2596256	36588	281287	229536	2048845	662	0.059551579	6.0883123	2.989998153	0.081210287	0.081210287	0
ATTCTACCAGCGCTTG-1	1452584	56756	152366	126294	1117168	361	0.03255095	3.4311143	3.105762673	0.104128246	0.100776669	0
ATTCTACGTGGAAAGA-1	1591534	24363	169634	141647	1255890	406	0.036730197	3.857382267	3.144478617	0.093540158	0.094047604	0
ATTCTACTCTCCCTAG-1	1510114	16220	164234	126805	1202855	389	0.035136408	3.6800159	3.137884749	0.098618769	0.09447671	0
ATTGGACTCGTAGCGC-1	1502062	34205	155188	141608	1171061	378	0.034091309	3.5875044	3.118677292	0.102657624	0.098518056	0
ATTGGTGAGGGATACC-1	2898504	36297	307873	264693	2289641	740	0.066589811	6.730545967	3.134991334	0.080125052	0.076933884	0
ATTGGTGCACTAAGGG-1	1321824	25484	140623	109817	1045900	338	0.030539829	3.217182233	3.104599301	0.103206742	0.101168889	0
ATTGGTGTCGCCAACG-1	1482642	49269	154248	132413	1146712	370	0.033319327	3.504995833	3.10595829	0.095741267	0.096858061	0
ATTTCTGAGTAGGTGC-1	1845118	93176	189058	165375	1397509	451	0.040489794	4.219122133	2.985819783	0.09149749	0.090020103	0
ATTTCTGCACACACGC-1	1595764	45601	169772	140549	1239842	401	0.036164772	3.794070933	3.047636296	0.098452769	0.096132399	0
ATTTCTGCACTAACTG-1	1008686	21032	110333	83713	793608	256	0.02312485	2.451968367	3.018147209	0.117774508	0.114419546	0
ATTTCTGTCACACGGC-1	1453340	97174	150025	124396	1081745	349	0.031395006	3.310948267	3.014474946	0.100164721	0.098925344	0
CAACCAAAGTACGCGA-1	1597864	21992	172280	146078	1257514	406	0.036706816	3.863218233	3.036903409	0.094499379	0.094278815	0
CAACCAACAGGACCAA-1	2383248	31888	263675	204989	1882696	608	0.054895062	5.644899967	3.420929191	0.113811415	0.113811415	1
CAACCAAGTTCGATAC-1	2184686	56982	238559	189257	1699888	549	0.049453485	5.122475567	3.084998757	0.084065414	0.082895283	0
CAACCTCAGACTTCCA-1	2057964	63195	219232	188474	1587063	513	0.046241875	4.8158543	2.985362665	0.087438411	0.086138597	0
CAACCTCCAAGAACTA-1	1797418	41635	193005	164085	1398693	452	0.040783497	4.2561898	3.238520118	0.089537275	0.090395684	0
CAACCTCTCAACTGCA-1	1758068	75293	185033	154587	1343155	434	0.039096418	4.095538067	3.049996094	0.091796676	0.093617344	0
CAACCTCTCTGAAGCT-1	1979090	84286	207340	176098	1511366	488	0.043935039	4.5664448	3.149577445	0.089649852	0.088202545	0
CAACTAGGTCGTCTTC-1	1909782	48781	201426	171116	1488459	481	0.043383801	4.525891533	3.108283196	0.085867864	0.085867864	0
CAACTAGGTTAGGAA-1	1891012	20874	206809	154091	1509238	488	0.044026727	4.576249533	3.190401091	0.105697113	0.105438172	1
CAACTAGTCGACCATA-1	1807742	21965	195938	154350	1435489	464	0.041938014	4.371614367	3.012053755	0.09330378	0.090452159	0
CAAGAAAAGCAAAGCC-1	1752374	64436	183082	159416	1345440	435	0.039222606	4.114444833	3.005206669	0.092162654	0.094093578	0
CAAGAAACATAGGACG-1	1418324	45284	144868	130069	1098103	355	0.031899746	3.362620567	2.854314465	0.101363577	0.101363577	0
CAAGAAAGTTTGTCTT-1	2477684	54833	267058	218578	1937215	626	0.056480331	5.823839	3.046951826	0.081697062	0.081875163	0
CAAGAAATCGAACAAA-1	1458782	30671	156567	127737	1143807	369	0.033305719	3.495096533	3.197160995	0.09447116	0.091437441	0
CAAGATCAGAATCGTA-1	1818014	34506	194101	158414	1430993	462	0.041712241	4.3520173	3.219108588	0.111694782	0.111551102	1
CAAGATCAGGTGTTAA-1	1190032	19321	130293	94865	945553	305	0.027586259	2.907830533	3.017025357	0.103580542	0.103429902	0
CAAGATCCAATCCATG-1	1473704	10809	161272	121793	1179830	381	0.034425745	3.611339467	3.066071505	0.105198217	0.101471305	1
CAAGATCCATTACGCA-1	1066406	53836	107686	93919	810965	262	0.023568025	2.509716	2.916521085	0.120624669	0.115225017	0
CAAGATCGTGCTTAGT-1	930938	14282	100135	79489	737032	238	0.021535447	2.284486133	3.12105009	0.12361219	0.120276877	0
CAAGATCGTGTTCGAT-1	1884784	23427	205586	158409	1497362	484	0.043685095	4.5423082	3.116891604	0.092643431	0.090361415	0
CAAGATCGTTGAACAA-1	1925126	41205	209169	150760	1523992	492	0.044413612	4.6114049	3.780541555	0.137842668	0.136743016	1

CAAGATCTCACACGTA-1	991914	12484	107692	81580	790158	255	0.023013542	2.435500633	3.037202994	0.121628821	0.116786107	0
CAAGGCCAAACCCTA-1	1982342	34460	210586	177131	1560165	504	0.045499442	4.738578333	3.207876622	0.084360017	0.084360017	0
CAAGGCCGTCACCTGG-1	1642794	16366	174084	150650	1301694	420	0.037984392	3.980356533	3.045971052	0.09541856	0.094411553	0
CAAGTTGTCGCGGCAT-1	2345074	44713	249073	205616	1845672	596	0.053863238	5.560302867	3.143348322	0.082821352	0.083367702	0
CACAAACCAAGAATCA-1	1729018	67888	182399	160697	1318034	426	0.038366752	4.009094767	3.032866651	0.09653591	0.091907152	0
CACAAACCAGGCCTTG-1	1351118	17069	145960	120904	1067185	345	0.031105434	3.278082667	2.986091577	0.096941961	0.097064539	0
CACAAACCATCAAGAA-1	1165236	17462	128755	96458	922561	298	0.026889665	2.838878167	3.047493928	0.11209445	0.109224276	0
CACAAACTCGAGAGGT-1	2443022	24979	267409	206032	1944602	628	0.056820198	5.843351667	3.049721166	0.082299467	0.079579961	0
CACACAAGTACGTTTG-1	928390	20228	101387	77988	728787	235	0.021232293	2.263496533	3.01765625	0.117243272	0.116471876	0
CACACAAGTTGCACTA-1	1933074	34106	212271	170927	1515770	490	0.044184454	4.600446	3.133785782	0.084475217	0.084982044	0
CACACCTGTACGTGCC-1	2062168	35032	220476	187637	1619023	523	0.047089689	4.889799167	3.141059062	0.0865587	0.086558862	0
CACACTCAGACGTCGA-1	2053630	22949	217545	186061	1627075	526	0.047478526	4.942961233	3.141051047	0.082146815	0.083602286	0
CACACTCAGCGTAGTG-1	1192988	6904	129618	95532	960934	310	0.028099984	2.955771133	3.122481149	0.106505245	0.103953171	0
CACACTCGTTAAAGGT-1	2103860	23152	230295	182487	1667926	539	0.048760026	5.048418333	3.009809841	0.08461972	0.08477514	0
CACACTCTCTACAGTG-1	1359016	9662	152476	103334	1093544	353	0.031936724	3.341532667	3.001150617	0.098627228	0.096331187	0
CACACTCTCTTCTTGA-1	2613982	33908	289054	199878	2091142	676	0.06108842	6.2823981	2.712066405	0.114845132	0.114845132	1
CACAGGCCATAGTGTC-1	2029164	38403	212992	170413	1607356	519	0.046819279	4.855185333	2.998415799	0.092037576	0.086417265	0
CACAGGCGTAGTCTGT-1	2309698	28174	250334	204225	1826965	590	0.053342574	5.4959476	3.164826655	0.078036549	0.078651936	0
CACAGGCTCCGTCTAC-1	2688526	49236	285156	249771	2104363	680	0.061367495	6.295448267	2.876395234	0.071789887	0.07251362	0
CACAGTAAGTCGTACT-1	2200514	39005	237214	193563	1730732	559	0.050397763	5.219707967	3.081170377	0.086395515	0.085912878	0
CACATAGAGGTATCGG-1	1183238	10630	126100	108176	938332	303	0.027391	2.893459	2.914334212	0.114091348	0.110658795	0
CACATAGAGTCGTCCG-1	1515588	57818	155019	134938	1167813	377	0.033978205	3.580842433	3.169035695	0.096275507	0.095912789	0
CACATAGCACAACTTG-1	1050146	17569	113673	88780	830124	268	0.024182653	2.565279033	3.093081386	0.110535305	0.112199818	0
CACATAGGTACAATAG-1	1199238	12084	131995	93874	961285	311	0.028054842	2.950229667	3.188603531	0.109001291	0.108953086	0
CACATAGGTTGGTGAG-1	2356402	20803	252947	197040	1885612	609	0.05507309	5.6918504	3.06920639	0.080163426	0.080163426	0
CACATAGTCTCAGTTT-1	1270040	47238	135468	104184	983150	318	0.028613145	3.015816267	3.049484492	0.106395602	0.103756911	0
CACATTIAGCAGCGTA-1	1491390	19800	161357	131303	1178930	381	0.034392231	3.6129607	2.948396352	0.098328031	0.098052822	0
CACATTIAGGAATCGC-1	1788962	34177	185234	172467	1397084	451	0.040719766	4.253678067	3.046801074	0.094168534	0.092212784	0
CACATTTCATGGAGAC-1	1666454	92810	172264	143753	1257627	406	0.036591425	3.8443176	3.035002735	0.096454132	0.094607793	0
CACATTTGTCGCTTCT-1	1757246	135783	174807	147486	1299170	420	0.03781055	3.9602074	3.001122191	0.095752837	0.095752837	0
CACATTTGTTTCCTGC-1	2148104	51278	231960	185871	1678995	542	0.048864179	5.043830467	3.042189087	0.08653235	0.08637982	0
CACCACTCATCTAAGC-1	1668586	59918	176146	144962	1287560	416	0.037440282	3.926901567	3.048625072	0.097970564	0.093402462	0
CACCACTGTCATGTTG-1	1316502	9603	145111	104483	1057305	342	0.030818023	3.234075733	3.200086642	0.105972239	0.103616163	0
CACCAGGAGACAGTTA-1	1559160	19763	171614	129296	1238487	400	0.03612783	3.785085533	3.129568602	0.095698047	0.096346331	0
CACCAGGAGGAGTAGA-1	1392524	17119	150017	121675	1103713	357	0.032289982	3.404810733	3.049786902	0.098582256	0.09949105	0
CACCAGGCAATCTCTT-1	1906360	104015	196994	170916	1434435	463	0.041766678	4.3389478	3.070338194	0.091310537	0.087684687	0
CACCAGGCACGGCTGT-1	1937944	30805	208909	176708	1521522	491	0.044396381	4.6231115	3.067488367	0.090932528	0.088326177	0
CACCAGGCATTACTTC-1	1964936	116751	198865	179890	1469430	475	0.042561497	4.423673	3.049172291	0.091000425	0.089485077	0
CACCTTGAGGCTCTCG-1	1682028	30158	179114	152624	1320132	426	0.038484609	4.046814633	3.077061301	0.096785777	0.091425229	0
CACCTTGCAGACACAG-1	1506556	13544	165383	126112	1201517	388	0.035047324	3.675612133	2.999730075	0.097557947	0.096757213	0
CACCTTGCAGACAGTG-1	1167746	7345	129372	96153	934876	302	0.027236624	2.875836167	2.769659649	0.112960963	0.108018225	0
CACCTTGTCCGACGTG-1	1201956	10831	130159	101537	959429	310	0.027912864	2.948543467	3.114056773	0.109595445	0.10604133	0
CACTCCAAGCAGACTG-1	1537726	14797	169410	132680	1220839	394	0.035390546	3.7114328	3.002130863	0.099970291	0.097099322	0
CACTCCAAGTGTCCAT-1	3946044	36235	431076	350045	3128688	1011	0.091421551	9.2212151	3.141047874	0.062160242	0.063227203	0
CAGAATCAGGGATGGG-1	2840352	24671	308520	243478	2263683	731	0.066114011	6.7573483	3.108206436	0.081856135	0.081856135	1
CAGAATCTCGAAAGGC-1	1891002	60973	196657	170970	1462402	472	0.042655192	4.458532267	3.02222317	0.087376953	0.087376953	0
CAGAATCTCGGAATGG-1	1225462	11899	130654	104135	978774	316	0.028550801	3.011946667	3.04646852	0.112917241	0.111593102	0
CAGAATCTCTACGGGC-1	2253986	71928	235339	199186	1747533	565	0.050911135	5.281735667	3.146310803	0.07902844	0.079290348	0
CAGAGAGAGTCGTACT-1	2352722	50537	245415	206056	1850714	598	0.053917879	5.5658189	3.001221634	0.08711482	0.084943367	0
CAGAGAGAGTGAAGAG-1	1478856	20427	156862	124942	1176625	380	0.034324704	3.608175967	3.10594051	0.101274798	0.100235971	0
CAGAGAGCACGAGCTC-1	1774744	52820	186143	162178	1373603	444	0.040001568	4.185607533	3.13860261	0.090185855	0.090544604	0
CAGAGAGTCCGAAGCC-1	1705046	63664	176436	154110	1310836	423	0.038233998	4.019616833	3.100105105	0.09371606	0.092919834	0
CAGAGAGTCCGAGATT-1	1155904	42167	121931	94700	897106	290	0.026197245	2.763708733	3.234893514	0.109084548	0.109084548	0
CAGATCAAGAAGGGTA-1	1734182	17335	186685	147320	1382842	447	0.040384936	4.216310267	2.981912861	0.09170747	0.091885929	0
CAGATCACATGCCGCA-1	1223384	68330	125705	102848	926501	299	0.026925257	2.851030033	3.038350931	0.116217107	0.114460693	1
CAGATCAGTTCTGTCC-1	2148434	83796	226658	188404	1649576	533	0.047881561	4.9450431	3.033485854	0.08925158	0.09032128	0
CAGCAGCGTTCAAGGG-1	1627262	23578	173280	140863	1289541	417	0.037623303	3.9476944	3.110804976	0.098387713	0.096416835	0
CAGCAGCTCCCGGACA-1	1666458	67209	172420	150578	1276251	412	0.037159283	3.8980215	3.257905883	0.124362349	0.123446837	1
CAGCAGCTCGCAACGC-1	1471326	29835	153922	127792	1159777	375	0.033759072	3.5558087	2.99610812	0.1005587	0.098032183	0
CAGCATAAGCGTTGCC-1	1967240	32020	211599	175080	1548541	500	0.045222155	4.707643133	3.020674515	0.089996748	0.088435738	0
CAGCATACAAACGGGT-1	2404860	50224	257668	217096	1879872	607	0.054887542	5.659009167	3.021835643	0.080833971	0.079576122	0
CAGCATACACGGAATG-1	1409624	14844	153066	117269	1124445	363	0.032796582	3.444442667	3.09794953	0.104063051	0.101565969	0
CAGCATAGTCCGCAGT-1	2033658	30808	217829	183230	1601791	517	0.046681942	4.846023567	3.122813748	0.089004641	0.087618766	0
CAGCCGAAGCGTCAAG-1	1362142	12211	142308	121258	1086365	351	0.031720829	3.341885167	3.045185301	0.103428574	0.103428574	0
CAGCCGACAAACCGAG-1	1934040	42893	208502	169865	1512780	489	0.044060794	4.592530967	3.354003441	0.114962202	0.114627548	1
CAGCGACAGCGCCTCA-1	1779958	31732	188649	162297	1397280	451	0.040733308	4.2494217	3.096851647	0.089900021	0.089784253	0
CAGCGACCAAGTCGGA-1	1834776	26808	197830	162518	1447620	468	0.042207866	4.410499733	3.038100854	0.092498097	0.091444546	0
CAGCTAATCCACTTCG-1	1364382	34342	146702	127806	1055532	341	0.030690493	3.2488078	3.144119569	0.097905374	0.098244086	0
CAGCTAATCGAAAGGC-1	2131100	53270	225661	195028	1657141	535	0.048249805	5.022174367	3.036382367	0.086622451	0.085172597	0
CAGCTGGAGCCACCTG-1	1344510	9808	144109	119732	1070861	346	0.031148232	3.2741524	2.991271555	0.103786316	0.101445495	0
CAGCTGGGTCCTTGGG-1	1598564	17058	172500	141194	1267812	410	0.037042855	3.8858174	3.022776503	0.0903093	0.092059113	0
CAGCTGGTCACGGTAT-1	2317042	32578	249417	191528	1843519	596	0.053706398	5.5315445	3.001349566	0.083494453	0.080823439	0
CAGGTGCCGAGCATGTT-1	1211912	13658	131366	94811	972077	314	0.028363309	2.9803552	3.144247505	0.104912773	0.105203312	0
CAGGTGCTCGAGGTGA-1	1542410	19206	161765	132391	1229048	397	0.035856848	3.763961	3.13177353	0.098896097	0.096888131	0
CAGTAACAGACCACGA-1	3172984	34101	344305	283953	2510625	811	0.07325867	7.483114167	3.086413789	0.067127382	0.067339226	0
CAGTAACAGCACCGCT-1	1872596	97273	192526	164935	1417862	458	0.041293209	4.325315767	3.109573569	0.091550959	0.091788048	0
CAGTAACCACACCTAA-1	1163364	10172	129244	95135	928813	300	0.027140454	2.860819867	3.009871598	0.107057769	0.106233733	0
CAGTAACCATACGTTG-1	960866	8542	105429	74022	772873	250	0.022603045	2.391350833	3.144620148	0.123669736	0.119851878	0
CAGTCCTAGTCAAGGC-1	1663460	54138	176876	145983	1286463	416	0.037426059	3.921003433	3.120669082	0.0943415	0.09327306	0
CAGTCCTGTCTTCACC-1	2654606	53363	285662	236403	2079178	672	0.060637447	6.2349062	3.022116443	0.075799411	0.075529548	0
CATATGGTCTAGACAC-1	2190552	49579	227484	210433	1703056	550	0.049611835	5.1519616	3.099322414	0.082441828	0.082654153	0
CATATTCCAGTAGAAT-1	944598	5651	102968	78281	757698	245	0.022194856	2.344679733	3.035925592	0.12605078	0.121101664	0
CATATTCGTCGCGCTA-1	1456806	45022	145073	133927	1132784	366	0.033009108	3.4713631	3.062532403	0.099785576	0.099723478	0
CATATTCGTGACCTGC-1	2194712	48274	231466	194156	1720816	556	0.05014238	5.1916818	3.142900116	0.081806639	0.083317721	0
CATATTCTCTTGCTTA-1	1745252	19774	186370	152115	1386993	448	0.04049298	4.230865933	3.119178345	0.094213673	0.09163831	0
CATCAAGTCCTACGAA-1	1292354	14362	142175	112046	1023771	331	0.029808468	3.144663133	3.103958076	0.098270695	0.100233643	0
CATCAAGTCTAGCCTC-1	1936188	42093	203728	176775	1513592	489	0.044182151	4.612622067	3.067859223	0.090567345	0.088854853	0
CATCAAGTCTCCATGC-1	861250	19557	93483	67811	680399	220	0.019937511	2.120938	3.072394624	0.119737478	0.120953151	0
CATCAGAGTTAGTGAA-1	1848376	16636	202758	158478	1470504	475	0.042867983	4.4630392	3.022221907	0.087816962	0.087834853	0
CATCCACCATTACAGC-1	2145348	64069	229629	180207	1671443	540	0.048604205	5.0351886	2.897610897	0.086157784	0.084686221	0
CATCCACTCCTGCGTT-1	1880724	46527	201187	161541	1471469	475	0.042860826	4.4599898	3.15650086	0.088925049	0.0895555	0
CATCCACTCCTTGAAG-1	1150670	9958	128273	97456	914983	296	0.02677273	2.824968	3.037549548	0.107877789	0.107370924	0
CATCGAACAATGGGAC-1	2130288	106028	222168	182676	1619416	523	0.04709756	4.904087	3.060867218	0.088242545	0.084986262	0
CATCGAACACGACGCT-1	1490770	89436	151836	126513	1122985	363	0.032646802	3.4358403	3.105751747	0.12825662	0.129381225	1

CATCGAACATTTCGTT-1	1699224	27548	184226	144439	1343011	434	0.039102581	4.086608867	3.104212246	0.095348887	0.091467305	0
CATCGAAGTGCTCGAC-1	1639564	43619	172083	152945	1270917	411	0.036959962	3.8742628	3.095286114	0.094336494	0.094012531	0
CATCGAAGTTTGGCGC-1	1335302	48508	137663	119909	1029222	332	0.029960412	3.1659727	3.045423551	0.106472668	0.105051972	0
CATCGGGCACCCAAAT-1	2032452	27036	223609	166025	1615782	522	0.047116435	4.8229961	3.097529434	0.089316046	0.085285175	0
CATCGGGTCTCAGTTT-1	1473728	69926	156649	119774	1127379	364	0.032778375	3.441406367	3.044830182	0.101884961	0.100650497	0
CATGACACAACTCGCG-1	777788	71451	75117	65515	565705	183	0.01640252	1.762613333	3.046929691	0.137557003	0.132870605	0
CATGACAGTTTACTCT-1	2172104	95810	225968	191806	1658520	536	0.048025304	4.939264933	3.189062078	0.097212671	0.095394562	1
CATGACATCTCCGGAG-1	1568590	20516	166384	138106	1243584	402	0.03631234	3.811180633	3.099857205	0.099159135	0.097825721	0
CATGCCTGTCCGCAAC-1	2225014	34727	236967	202839	1750481	565	0.050945972	5.2705876	3.026614943	0.084344354	0.084453862	0
CATGCCTGTTACGGCC-1	1722280	35215	182601	164982	1339482	433	0.038976587	4.074889233	3.060549664	0.096649873	0.093045758	0
CATGCCTTCATGTGAC-1	2072428	46502	219769	185529	1620628	524	0.047210641	4.9043615	3.130275138	0.083843643	0.084605473	0
CATGGCGAGATATGGT-1	1958860	19573	211885	158726	1568676	507	0.045845386	4.7574801	3.045589552	0.089383324	0.086786014	0
CATGGCGCAGTCGGAA-1	797928	12642	84291	66710	634285	205	0.018594529	1.9882921	3.108719114	0.131005622	0.129136956	0
CATGGCGCATTTGCGA-1	555382	6119	57978	50679	440606	142	0.012879764	1.389392667	2.910910847	0.155277681	0.153079916	0
CATGGCGTCGAGCACC-1	832524	22845	71074	75381	663224	214	0.019352581	2.070670133	3.134123828	0.124376726	0.127485053	0
CATTATCAGCGTGAAC-1	2578918	49940	272708	225105	2031165	656	0.059238997	6.088024067	3.047621754	0.079983391	0.079364727	0
CATTATCCAACAGCCC-1	1041272	39354	107291	94142	800485	259	0.023389264	2.490006533	3.135348385	0.120549121	0.120193261	0
CATTATCCATAGGTCT-1	4119828	157262	412876	362343	3187347	1030	0.091834417	9.090414267	3.177268076	0.085530783	0.085530783	1
CATTATCGTAGAAGG-1	1289738	8519	134863	111724	1034632	334	0.030267281	3.1898554	3.061892721	0.103716114	0.103745886	0
CATTCGCAGCAAATCA-1	2069318	94509	214843	179313	1580653	511	0.046019035	4.7839259	3.009198488	0.08562156	0.08617256	0
CATTCGCCACGCACGT-1	1499436	27556	158099	136232	1177549	380	0.034345838	3.5979809	3.004603417	0.104500002	0.099901386	0
CCAATCCGTCAAGCCC-1	1518854	83271	154447	131380	1149756	371	0.033475339	3.527414267	2.930275177	0.100931798	0.099227766	0
CCAATCCTCCGACGTG-1	1038500	16441	111213	86067	824779	266	0.023961547	2.5396019	2.987573053	0.121559224	0.11735385	1
CCACCTAAGCTCCTTC-1	2333238	54287	247855	213557	1817539	587	0.052915871	5.4486446	3.109640711	0.084620198	0.081204889	0
CCACCTAAGTGGTAGC-1	2819020	23751	314679	248923	2231667	721	0.065052307	6.648738	3.021405077	0.079658054	0.078581152	0
CCACCTAAGTTAGGTA-1	1533368	11662	168247	123262	1230197	397	0.03587655	3.761328533	3.04702682	0.102283183	0.100528589	1
CCACCTAGTTCGAGCC-1	1443238	84463	146910	129206	1082659	350	0.031516396	3.3330021	2.907310733	0.104482803	0.104008508	0
CCACGGAAGACTGTAA-1	1362894	15869	145102	108168	1093755	353	0.031715842	3.3277473	3.081269399	0.106512975	0.102926828	0
CCACGGACAAAGTGGC-1	2764182	33997	303195	222935	2204055	712	0.064280665	6.584963233	4.319796485	0.147060799	0.147060799	1
CCACGGACAGAAGACC-1	2244778	60109	234007	200669	1749993	565	0.050920427	5.2669944	3.11915335	0.082582582	0.083585775	0
CCACTACAGACAAAGG-1	1303838	10658	142717	111096	1039367	336	0.030349435	3.203572967	3.079971586	0.102440786	0.10300518	0
CCACTACAGAGACTAT-1	1957250	22063	213289	166056	1555842	503	0.045391394	4.7124118	3.027965271	0.089037625	0.087139292	1
CCACTACTCTACGGCG-1	1005072	64878	101137	87973	751084	243	0.021789337	2.323451367	3.056400133	0.116816241	0.118947753	0
CCACTACTCTCGGAAT-1	2590632	36409	280649	223299	2050275	662	0.05977173	6.143101433	3.118657072	0.080655487	0.077971244	0
CCAGCGATCTACAGTG-1	1080628	14437	117828	85861	862502	279	0.025019448	2.639526633	2.983874518	0.1131981	0.112845636	0
CCATGTCTCGAGTACT-1	2195948	60394	232538	189247	1713769	554	0.049952154	5.1725539	3.030984075	0.091623391	0.088923945	0
CCATGTCTCGCTGAAT-1	1423912	19745	152685	125435	1126047	364	0.032807593	3.432056633	3.130147884	0.10012276	0.100492304	0
CCATTCGAGTGCTGCC-1	2016674	54727	212415	177452	1572080	508	0.045870466	4.762353567	3.02468706	0.091874845	0.088054897	0
CCATTCGCACATAAAG-1	1134864	12700	125307	91455	905402	292	0.026394447	2.785054533	3.106716476	0.111821729	0.111062171	0
CCCAATCGTCGACCAC-1	2185784	51776	222876	200972	1710160	552	0.049845776	5.167617067	2.955684555	0.084922902	0.084186368	0
CCCAGTTAGCACGCCT-1	2071046	60665	216533	190897	1602951	518	0.046680255	4.856996933	3.174450159	0.089537421	0.086243707	0
CCCATACAGCCACGTC-1	1188740	30847	126489	102521	928883	300	0.027002391	2.856022367	2.916234532	0.111025193	0.107253706	0
CCCATACCAACGAAAT-1	1926286	33499	206859	168495	1517433	490	0.044252309	4.596507033	2.917374627	0.089063067	0.087354741	0
CCCATACCACAAGCTT-1	1789668	116127	182162	151371	1340008	433	0.038954023	4.079265767	3.043598375	0.094062886	0.092869364	0
CCCATACCATCTTTCA-1	1726126	78372	175896	155637	1316221	425	0.038309048	4.018839167	2.989254109	0.09121458	0.09198234	0
CCCTCCTAGCAATCTC-1	2956678	50191	315387	251316	2339784	756	0.068251678	6.977899467	2.769408519	0.101589542	0.101589542	1
CCCTCCTCAGAATTCC-1	1609118	78850	162984	143542	1223742	395	0.035537397	3.718200133	3.017356845	0.102890529	0.098055735	0
CCCTCCTGTATTCGCA-1	1118800	39483	114055	103616	861646	278	0.025080974	2.654751067	3.034976604	0.117007329	0.113952885	0
CCCGGGATCACAATGT-1	1278264	13265	137914	105949	1021136	330	0.02978967	3.124733633	3.036200381	0.100532822	0.102965265	0
CCGGTAGAGCCAGTTT-1	1334556	58485	132447	109832	1033792	334	0.030072848	3.1621244	2.989823094	0.109399071	0.107345104	0
CCGGTAGAGCCTATGT-1	416750	5912	42314	32470	336054	109	0.009772588	1.048926633	3.00515398	0.177187606	0.172792232	0
CCGGTAGGTTCAGTAC-1	2180036	58397	225555	187195	1708889	552	0.049744978	5.1313449	3.002486431	0.087660932	0.086101791	0
CCGGTAGTCGAGTTGT-1	2292410	35433	239561	196162	1821254	588	0.053260601	5.503595867	3.003019174	0.082671635	0.081534192	0
CCGGTAGTCGCGATGC-1	1351426	44332	137523	113547	1056024	341	0.030735482	3.237693267	3.109921951	0.103296274	0.101006173	0
CCGTACTAGGCTCATT-1	1942124	36088	199129	166966	1539941	497	0.044926167	4.666113567	3.205143868	0.086423123	0.086425008	0
CCGTACTTCGGAGAGT-1	1747252	19932	185489	155321	1386510	448	0.040537741	4.227180567	2.896149474	0.09232074	0.091112967	0
CCGTGGAAGTAGATGT-1	1260710	26687	128976	101156	1003891	324	0.029157273	3.071701167	3.109937085	0.107421282	0.10655571	0
CCGTGGACACCAAAGG-1	946662	9488	97137	81474	758563	245	0.022118144	2.355058067	3.13896721	0.116664631	0.114339434	0
CCGTGGACACTGGCCA-1	1445510	46353	144686	126682	1127789	364	0.032824053	3.464837833	2.988734515	0.101564215	0.09994302	0
CCGTGGAGTCAACCGC-1	640124	15586	60323	57542	506673	164	0.014741518	1.580894833	3.042224621	0.145569656	0.147044507	0
CCGTTCAAGTCGCCGT-1	2035446	23552	209026	181368	1621500	524	0.047267563	4.917614	3.142883532	0.087005164	0.085787862	0
CCTAAAGGTACCGTGC-1	1243776	46411	128052	110346	958967	310	0.027888401	2.9471118	3.107868137	0.10849734	0.106254396	0
CCTAAAGTCAAGCCGC-1	1537612	16542	162673	142891	1215506	393	0.035457668	3.734648633	3.037934047	0.097823625	0.096879615	0
CCTACACAGGGATCTG-1	484660	3565	53439	41539	386117	125	0.011300511	1.215420433	3.029604493	0.164619597	0.165390755	0
CCTACACAACCGCTG-1	975884	18856	103875	86228	766925	248	0.022305086	2.3680561	2.987677294	0.123047018	0.119256821	0
CCTACACGTGGAAGGG-1	1835666	14078	194920	156800	1469868	475	0.042932256	4.477480433	3.0814264	0.089731758	0.088296032	0
CCTACACTCGCGATGC-1	1559590	39518	162674	146887	1210511	391	0.035201655	3.693471067	3.130901912	0.098758539	0.096346185	0
CCTACACTCGTTATTC-1	2175604	42149	231522	188271	1713662	554	0.049824044	5.146113633	3.22477641	0.084354647	0.084077862	0
CCTACACTCTCAGATG-1	963422	11643	105567	78705	767507	248	0.0223925	2.379014467	2.984660616	0.11636765	0.115234527	0
CCTACCATCGGAGAGT-1	1835762	16302	197301	161268	1460891	472	0.042682893	4.4362076	2.952258825	0.088619568	0.087058738	0
CCTAGCTCAATCCGTA-1	1056978	11035	113506	90980	841457	272	0.024568881	2.6031397	3.025838014	0.113415215	0.111208005	0
CCTAGCTTCATGTCAG-1	1898290	17077	204875	163866	1512472	489	0.044214768	4.597760067	3.046934716	0.087189949	0.086869516	0
CCTAGCTTCTACATGG-1	1041660	7911	113352	86255	834142	269	0.024321711	2.5681664	3.054034669	0.110805327	0.112811552	0
CCTATTAAGCCAACAG-1	1267868	15635	136738	109598	1005897	325	0.029329422	3.094562467	3.046630358	0.103215933	0.102076079	0
CCTATTACAACAGCCC-1	1252004	60568	127948	115999	947489	306	0.027562091	2.9239806	3.021051286	0.106883923	0.106883923	0
CCTATTACACGAGTTT-1	1175852	61566	121358	96311	896617	290	0.026114357	2.762864233	3.08807591	0.108026642	0.110122632	0
CCTATTAGTATTCGTG-1	958152	9371	101614	80355	766812	248	0.022349945	2.371164967	3.04552782	0.118831577	0.116626095	0
CCTATTAGTGACCCAC-1	2067548	28843	219818	182638	1636249	529	0.04774126	4.954334967	3.019546821	0.088762312	0.088748546	0
CCTATTATCGAACCCG-1	1295192	42853	131573	120488	1000278	323	0.029089953	3.083704033	2.991798739	0.10645367	0.103417402	0
CCTCTGACATGGGCCT-1	1626814	77879	168080	152149	1228706	397	0.035779979	3.753770633	2.941390406	0.102659578	0.09603784	0
CCTTACGAGTGACTCT-1	1754386	75780	179257	170786	1328563	429	0.038483818	3.9767946	2.934507832	0.104435114	0.098624255	0
CCTTACGCAAGGTATA-1	1468810	11290	159381	120769	1177370	380	0.034396962	3.6057068	3.01705716	0.099685019	0.096888761	0
CCTTACGCATACGTTG-1	1006224	10050	108505	80568	807101	261	0.023543257	2.486580033	2.897869047	0.116461993	0.114317207	0
CCTTACGTCATCAGCA-1	1504350	42862	156605	127678	1177205	380	0.034321714	3.610882133	3.170590826	0.095350166	0.094845554	0
CCTTCCCCAACCCTGG-1	1575962	12697	169033	138471	1255761	406	0.036654866	3.841571133	3.033778649	0.096032997	0.094423511	0
CCTTCCCCAACGTCTA-1	1817908	43010	192616	164028	1418254	458	0.04134362	4.3208427	3.059488374	0.090809598	0.089121934	0
CCTTCCCGTTCAGGTT-1	1694660	24383	182617	138091	1349569	436	0.039354856	4.112665633	3.071710685	0.092256499	0.090459843	0
CCTTCCCTCGCGGACT-1	2050046	46035	214846	184208	1604957	518	0.046728603	4.845035	2.985304145	0.089090817	0.085770045	0
CCTTCGAAGGTGTTAA-1	1401088	16519	153925	113399	1117245	361	0.032599099	3.415647233	3.127166316	0.112885397	0.109581471	1
CCTTCGAAGTCGTCCG-1	1693476	45337	175468	152401	1320270	426	0.038408118	4.035253067	3.206790737	0.088881931	0.091309034	0
CCTTCGATCAGCAGCC-1	1722542	51913	181552	156484	1332593	430	0.038817053	4.0649955	2.754725962	0.089872244	0.090579615	0
CCTTCGATCAGTACCA-1	2142354	59744	227802	183099	1671709	540	0.048629465	5.0442593	3.082047237	0.084993575	0.083795302	0
CGAACATAGGCTAGTG-1	1480506	13051	161909	116417	1189129	384	0.03471488	3.632922867	2.983017139	0.099890169	0.09806791	0
CGAACATGTGACTGAG-1	1382770	15416	149996	134251	1083107	350	0.031641299	3.317707267	2.058132845	0.104618959	0.104174908	0

CGAACATTCAGTACCA-1	2148394	48823	228924	188575	1682072	543	0.048941104	5.080563433	3.009293535	0.080530416	0.080787058	0
CGAACATTCTGGGATT-1	1519344	41931	162564	126803	1188046	384	0.0346916	3.635237333	3.143560173	0.097641207	0.095362412	0
CGAATGTAGTACGACG-1	1426342	32493	148871	127547	1117431	361	0.032433703	3.4169298	2.977258841	0.101805633	0.101805633	0
CGAATGTCAGACAGTG-1	1338032	12233	146804	104602	1074393	347	0.031369086	3.295534567	3.140815167	0.106761605	0.103310249	0
CGAATGTCAGCCCATG-1	1143972	10785	124248	96891	912048	295	0.026593352	2.814320367	3.116965376	0.109629412	0.107721666	0
CGAATGTGTGTCAACT-1	2357762	88055	245848	218626	1805233	583	0.052561526	5.426710667	3.076750382	0.086988275	0.082486644	0
CGACCTTAGGGTAACC-1	1258438	20218	133529	112249	992442	321	0.028918691	3.051503733	3.143517598	0.108110338	0.105988674	0
CGACCTTAGTGTTTGC-1	2188530	74852	227238	195990	1690450	546	0.04922356	5.1166358	3.045921811	0.083718198	0.084270308	0
CGACCTTCAGTCGGAA-1	1778448	13729	195386	155289	1414044	457	0.041206559	4.304715	2.959141053	0.089443342	0.088539087	0
CGACTTCGTGGTGCAA-1	1744136	17817	185550	154936	1385833	448	0.040444265	4.228205233	3.052149331	0.089513632	0.088980994	0
CGAGAAGCAAACTCAC-1	2477078	40756	262920	229109	1944293	628	0.056719544	5.852171933	3.143746226	0.077793572	0.078285362	0
CGAGAAGTCCGAGATT-1	1016972	34507	108194	82513	791758	256	0.023128642	2.4440609	3.118636725	0.124355243	0.127883459	1
CGAGCACAGGCGATAC-1	2158970	51247	229803	179207	1698713	549	0.049497493	5.122792333	3.01069173	0.086084918	0.085664782	0
CGAGCACCACGATGGA-1	1678868	17816	179208	135181	1346663	435	0.03930458	4.1065903	3.308262396	0.120854351	0.121043797	1
CGAGCACGAGATATCC-1	1889582	75681	196412	161726	1455763	470	0.042251788	4.371760367	2.914028371	0.094835681	0.092273852	0
CGAGCACGTCGAGTAG-1	343464	9168	31598	26752	275946	89	0.008033105	0.8666299	2.968632407	0.189519313	0.191629913	0
CGAGCACTCAAGTTGC-1	1805596	38366	189155	167254	1410821	456	0.041085969	4.302524667	3.108889015	0.084895407	0.084895407	0
CGAGCACTCGGAAGAC-1	1926266	72299	193499	165750	1494718	483	0.043576107	4.544577533	3.043908121	0.087129844	0.089049136	0
CGAGCACTCTGATCAG-1	1820306	21160	193213	161955	1443978	466	0.042170325	4.401477767	2.883137912	0.089079906	0.089377631	0
CGAGCCAAGCTGGTCC-1	1951710	61554	201483	171413	1517260	490	0.044033118	4.5694158	2.991084495	0.095186119	0.094264226	0
CGAGCCAAGGCATTTC-1	2237266	65543	230560	195846	1745317	564	0.050321366	5.130891067	3.03029808	0.08997202	0.089707251	1
CGAGCCACAAGAACTA-1	1589222	41654	165668	145203	1236697	399	0.036052537	3.7864152	3.021389956	0.092931724	0.093825847	0
CGAGCCACAGACGAGT-1	2070508	37207	220476	183209	1629616	526	0.047577055	4.931601733	3.191411967	0.083701966	0.083345154	0
CGAGCCACAGGACCAA-1	1804880	20873	189680	164570	1429757	462	0.041699948	4.358821633	2.986801165	0.088339018	0.08767696	0
CGAGCCACATAGTGAA-1	1358980	14795	145889	113244	1085052	351	0.031617177	3.327787633	3.060361173	0.103306732	0.101395228	0
CGATCGGGTACCGTGC-1	1496770	64643	153610	128283	1150234	372	0.033419882	3.516942167	3.074631953	0.09932335	0.098132113	0
CGATGGCTCATCGCGG-1	2162090	41153	225029	179754	1716154	554	0.050008102	5.191420967	4.479600759	0.117620208	0.117620208	1
CGATGGCTCGACAATC-1	2559804	49842	267733	212367	2029862	656	0.05906969	6.0417001	3.518475332	0.128309497	0.125134692	1
CGATGTAAGATCGGGT-1	2377726	29888	252704	204255	1890879	611	0.055216544	5.696744833	3.045996859	0.077632274	0.079135459	0
CGATGTACAAGTACAA-1	1296938	16032	140285	106126	1034495	334	0.030060611	3.162617933	2.997529023	0.108042332	0.103919237	0
CGATGTAGTCGCCAAC-1	367326	3105	35119	31141	297961	96	0.008709902	0.943983233	3.049572577	0.180590162	0.18201443	0
CGATGTATCTCCAGCT-1	561236	11227	59593	50085	440331	142	0.012860527	1.382100167	2.915619275	0.155885834	0.15310397	0
CGATTGAAGCTAGCCC-1	1698570	83075	172577	150416	1292502	418	0.037606604	3.953399167	3.141614166	0.094070955	0.094066148	0
CGATTGACACCTCCAT-1	1961760	20872	211484	172691	1556713	503	0.045503996	4.7313784	2.918223668	0.087403403	0.088695461	0
CGATTGAGTAAGAAGG-1	1363116	12149	146058	113640	1091269	353	0.031916699	3.360823	3.003032584	0.095656472	0.095656472	0
CGATTGAGTACTCCGG-1	1845060	24862	195973	168821	1455404	470	0.042477243	4.441960733	3.048004602	0.086656822	0.085607148	0
CGATTGAGTATTCGCA-1	1750174	56348	183494	151761	1358571	439	0.039559769	4.1530741	3.04420019	0.093576335	0.09260972	0
CGATTGAGTCAACTCA-1	1480450	43704	157932	136270	1142544	369	0.033225904	3.4861054	3.03279783	0.105482754	0.098161774	0
CGATTGAGTGCATCTA-1	1754316	29993	186564	151898	1385861	448	0.04039558	4.220101733	3.034126178	0.092569803	0.090407596	0
CGATTGAGTTGGCGTC-1	1516144	83879	150376	128771	1153118	372	0.033579	3.529186233	3.037356159	0.118217191	0.118217191	1
CGATTGATCGTGCTAA-1	1771556	13391	193330	145494	1419341	458	0.041400225	4.305628633	3.253779398	0.120424673	0.1180887	1
CGCCAAGAGGCTCAGA-1	1693462	13969	184756	146293	1348444	436	0.03937136	4.124616633	3.073836276	0.09362089	0.091428262	0
CGCCAAGCATAGGTCT-1	2155770	72872	214828	193507	1674563	541	0.048089467	4.870143233	2.981287962	0.093425868	0.093165367	1
CGCGGTAGTCGGAAGT-1	2052592	42452	214872	177329	1617939	523	0.04725868	4.9047119	3.109414632	0.085024731	0.083492845	0
CGCGTTTCAAAGCTT-1	2137846	36807	223571	194298	1683170	544	0.049007556	5.1064282	3.139177622	0.080896741	0.080896741	0
CGCGTTTGTTGAACTC-1	1216418	16242	126888	105461	967827	313	0.028258384	2.9822901	2.94057901	0.120874878	0.120874878	1
CGCGTTTTCTGGATCA-1	2059390	67399	212019	181103	1598869	516	0.046534442	4.8442183	3.108150537	0.084128606	0.085803001	0
CGCTATCAGGGATTTA-1	1965940	30304	209092	166645	1559899	504	0.045550926	4.734718067	3.180456095	0.099664876	0.098100239	1
CGCTATCGTGATTGTC-1	2033294	41042	213930	169523	1608799	520	0.046852392	4.854877167	2.999396174	0.08684798	0.084919248	0
CGCTATCTCCGGCTAG-1	1670860	18484	179356	148689	1324331	428	0.038681771	4.048924167	3.169886913	0.094033051	0.092995347	0
CGCTATCTCGACTTCC-1	2075530	65721	215389	186045	1608375	520	0.046779397	4.850945267	3.153732478	0.087208548	0.087311307	0
CGCTTCACAAGCACGA-1	1475008	15596	156589	133370	1169453	378	0.034099746	3.5946963	3.045859438	0.09753253	0.095879095	0
CGCTTCACACGAAGGT-1	2160344	21364	232354	187257	1719369	555	0.050203306	5.1996286	2.926952803	0.082835828	0.081670113	0
CGCTTCAGTTCTAGTG-1	1125858	10442	123382	86312	905722	293	0.026464776	2.786333567	3.039223483	0.112076048	0.10882621	0
CGGACACAGACGCTTT-1	2279682	90829	237807	201293	1749753	565	0.05092207	5.282295633	3.181534002	0.084169152	0.08215828	0
CGGACACGTAGTAGTA-1	1179800	13142	130791	94287	941580	304	0.027461848	2.898907	2.984392973	0.104294226	0.106273974	0
CGGACACGTCTAGGTT-1	1425554	23793	154782	116280	1130699	365	0.03299077	3.464803133	3.107460969	0.097939358	0.098166887	0
CGGACACTCGAGTTGT-1	2539928	39105	276136	222285	2002402	647	0.058415071	6.0041277	2.996910489	0.076561324	0.077960211	0
CGGACGTCACTTGCTC-1	318906	2638	34223	27581	254464	82	0.007429967	0.806293267	3.066369922	0.200467593	0.20363059	0
CGGACGTTCCTGATTT-1	2189420	72218	235230	176236	1705736	551	0.04955984	5.117037433	3.055690124	0.093311264	0.093171871	1
CGGAGCTAGGCTACGA-1	1415898	9461	162235	127161	1117041	361	0.032548156	3.440116033	3.071341831	0.101466785	0.098245839	0
CGGAGCTGTCCGAAGA-1	1349038	21643	151981	118411	1057003	341	0.030842733	3.255923333	3.104127467	0.101141302	0.100333567	0
CGGAGCTTCTAGACAC-1	2244246	62228	249449	197465	1735104	560	0.050526125	5.2387393	3.108122505	0.081918221	0.079921158	0
CGGAGTCAGAAACCTA-1	1116420	24811	121079	103571	866959	280	0.025275752	2.6820006	3.065763034	0.115097845	0.111812554	0
CGGAGTCAGCATGGCA-1	2001692	53690	218702	172657	1556643	503	0.045329141	4.724172233	3.083985138	0.084180152	0.084710122	0
CGGAGTCAGCCAACAG-1	1462388	23969	161942	126379	1150098	372	0.033492163	3.523158067	3.06412551	0.095297027	0.095686603	0
CGGAGTCCAGAGGGAT-1	2891232	44068	312975	254950	2279239	736	0.066509804	6.800387833	3.184105443	0.074475843	0.074475843	0
CGGAGTCCAGCTTGAT-1	3160210	32843	348492	266420	2512455	812	0.073218564	7.462112733	3.037301452	0.067936598	0.066710324	0
CGGAGTCGTATCAGTC-1	1544512	25173	174847	132727	1211765	391	0.03530745	3.7008477	3.089177631	0.093254624	0.092795813	0
CGGAGTCGTCTTCACC-1	1830202	34642	192569	169211	1433780	463	0.041811763	4.370971733	3.110430755	0.088543555	0.088543555	0
CGGCTAGAGACGCACA-1	1764988	23547	186281	162522	1392638	450	0.040598309	4.249622967	3.010355776	0.088675467	0.08776305	0
CGGCTAGAGTAGCCGA-1	1733798	6645	186940	161369	1378844	445	0.040242073	4.217474667	3.073471446	0.093730481	0.091590753	0
CGGCTAGAGTAGTATG-1	1272664	12240	138067	97388	1024969	331	0.02992082	3.145150067	2.997776625	0.105874965	0.105795625	0
CGGCTAGGTGTCAACT-1	2996998	67147	318703	266036	2345112	758	0.068394622	7.007945833	2.93081618	0.072745607	0.073044926	0
CGGCTAGGTTCTTCGC-1	1976848	33868	211107	178245	1553628	502	0.045324104	4.7249509	2.978735951	0.0914803	0.091413088	0
CGGCTAGTCATGTGAC-1	2053004	56203	215644	178289	1602868	518	0.046691605	4.856228767	3.06913499 6	0.084791659	0.083939045	0
CGGGTCAGTCATTACG-1	1552808	31640	163699	136234	1221235	394	0.035482946	3.724395533	3.005420381	0.097765404	0.096501275	0
CGGTTAACACCACATA-1	1270688	10741	141264	104608	1014075	328	0.029588975	3.1140416	3.13241539	0.105146632	0.103621209	0
CGGTTAACATGGAGAC-1	1498302	104708	151215	128010	1114369	360	0.032419558	3.4171267	2.997954705	0.098773103	0.09959121	0
CGTAGCGAGGACAGAA-1	1180076	15168	121516	98800	944592	305	0.027531339	2.905745867	3.033501218	0.105040508	0.106026699	0
CGTAGCGAGTACGATA-1	1236012	12302	131506	102018	990186	320	0.028847102	3.027583	3.139678051	0.09882375	0.09882375	0
CGTAGCGCAACGGGAT-1	1587150	17055	160982	133511	1275602	412	0.037296799	3.8849361	3.003189487	0.100662729	0.097948111	0
CGTAGGCAGGCGTTGA-1	1084734	16901	104742	95325	867766	280	0.025317433	2.689115967	3.04192229	0.115174428	0.109683775	0
CGTAGGCACTTGTTT-1	1328928	34264	121929	110305	1062430	343	0.030967144	3.246652733	3.009145844	0.103872194	0.102256919	0
CGTAGGCCATGAGGGT-1	1709230	30056	159809	148095	1371270	443	0.040037392	4.1726686	3.041909064	0.092343454	0.091042365	0
CGTAGGCGTTGAACAA-1	1527450	27372	153095	128221	1218762	394	0.035540104	3.723282767	3.560688425	0.137336532	0.137336532	1
CGTCACTAGGCGCTCT-1	1903772	53819	189760	164639	1495554	483	0.043463025	4.534249733	3.074450025	0.091774458	0.090285576	0
CGTCACTAGTCCCACG-1	1526544	20560	158092	137905	1209987	391	0.035189623	3.7037983	3.059660786	0.096177632	0.095894489	0
CGTCACTCATTCCGAA-1	1515310	15582	161060	128295	1210373	391	0.035277863	3.7071591	3.047565947	0.095296598	0.092106725	0
CGTCACTTCGTTACCC-1	2000396	22121	212880	176879	1588516	513	0.046236181	4.810863767	3.1446212	0.082039367	0.081452631	0
CGTCACTTCTTAGCTT-1	1458070	84081	147266	121206	1105517	357	0.032158885	3.3604032	3.015565612	0.140675295	0.140675295	1
CGTCAGGAGCAGGCTA-1	1527678	32382	154354	135539	1205403	389	0.03518498	3.698296533	2.940615435	0.096113874	0.092637486	0
CGTCAGGAGGACAGCT-1	1527512	42237	153792	140363	1191120	385	0.034703085	3.657480367	2.998110702	0.095648262	0.09530804 9	0
CGTCAGGCACGAGCTC-1	1277054	45275	130755	114934	986090	319	0.028722727	3.038112133	3.046093095	0.104993677	0.103600498	0

CGTCATGTAGATGTA-1	856004	11200	86610	68326	689868	223	0.020070448	2.129878933	2.998870859	0.11940271	0.121479744	0
CGTCCATTCTCCACAC-1	2261368	58891	236159	191907	1774411	573	0.051684896	5.3540041	3.011403602	0.085501897	0.081899965	0
CGTCTACCAACGACTT-1	1810266	37553	186456	160975	1425282	460	0.041445643	4.328347767	3.098777186	0.091330796	0.091093904	0
CGTCTACCAAGACGAC-1	1287782	20438	133208	108240	1025896	331	0.029991754	3.1611919	2.641412132	0.13897844	0.137894809	1
CGTCTACCACAGCTGC-1	1566836	50419	153256	137943	1225218	396	0.035689298	3.7490021	3.265588931	0.0959431	0.0959431	0
CGTCTACGTGGAGCTA-1	1612578	48519	163870	141223	1258966	407	0.036718456	3.857782	3.099096219	0.09586259	0.094173526	0
CGTCTACTCTAAGGC-1	1624182	57473	166136	142202	1258371	406	0.036640768	3.842845833	3.249960938	0.095563647	0.095563647	0
CGTGAGCTCGAATGTC-1	1474586	28227	147809	128549	1170001	378	0.034089169	3.5751218	3.02306425	0.099664807	0.099664807	0
CGTGTAAAGTTATCGC-1	1296870	32280	116722	106930	1040938	336	0.030340915	3.188387233	4.040878962	0.150169026	0.150169026	1
CGTGTAAGTAGGTTTC-1	1200112	49514	104926	107762	937910	303	0.027271992	2.882236067	3.153406428	0.106159608	0.106159608	0
CGTGTAAGTTTCCGAA-1	1069042	18652	103870	90994	855526	276	0.024903713	2.633148633	3.001398929	0.112026035	0.11223839	0
CGTGTCTCAACCGCTG-1	561062	14089	50039	49135	447799	145	0.013013182	1.398346867	3.007562041	0.151918899	0.146535128	0
CGTGTCTCACAGCTAT-1	1019540	18698	94079	88603	818160	264	0.023803447	2.520560033	3.089156233	0.114906707	0.111612645	0
CGTGTCTATCCATCC-1	1065860	58156	92685	94804	820215	265	0.023782541	2.526501767	3.107425869	0.113917663	0.114738243	0
CGTGTCTTCCAACAAC-1	1304530	21459	122330	112239	1048502	339	0.030528301	3.212134233	2.888343654	0.103957743	0.102364398	0
CGTGTCTTCCGAGTCG-1	758556	22010	67223	69933	599390	194	0.017359875	1.862627067	3.125389712	0.130734206	0.125173532	0
CGTGTCTTCGTTGAA-1	1085152	11904	101242	93296	878710	284	0.025598769	2.711610467	3.099141329	0.113507578	0.111478881	0
CGTGTCTTCTGGGACC-1	1249184	32063	114553	112388	990180	320	0.028818333	3.051273033	2.971897704	0.113199887	0.112806338	1
CGTTAGAAGGGTAACC-1	1962970	34043	201856	179821	1547250	500	0.04502531	4.668406767	3.110819067	0.089901162	0.088631057	0
CGTTAGAAGTGGCACA-1	1747090	32014	183794	161003	1370279	443	0.0399684	4.187541567	3.047082892	0.088000853	0.085504199	0
CGTTAGAGTCATTCAA-1	1819246	20179	191152	158861	1449054	468	0.042312736	4.419032333	3.140867082	0.089852713	0.087021225	0
CGTTAGATCAGCCTGG-1	1890494	22916	198496	167954	1501128	485	0.043797465	4.569540367	3.108940929	0.087506704	0.088208283	0
CGTTCTGAGCTGCGAA-1	1713214	22873	179651	147780	1362910	440	0.039729403	4.155219667	3.038428754	0.093552412	0.090640457	0
CGTTCTGAGGCTAGCA-1	1593886	57906	161829	139414	1234737	399	0.035925359	3.7787763	3.060055261	0.096239458	0.095846518	0
CGTTCTGGTTGAACAA-1	1553610	15878	165343	135072	1237317	400	0.036092728	3.7966688	3.109311396	0.09686683	0.094260737	0
CGTTCTGTCTCTAGTT-1	1345264	23410	143652	108747	1069455	345	0.031158203	3.276483967	3.14158695	0.106424549	0.099919684	0
CGTTGGGAGGCGCTCT-1	1660516	89504	159156	143097	1268759	410	0.036880549	3.866992733	3.143487185	0.095359577	0.095326369	0
CGTTGGGAGTCCCACG-1	1886736	12994	198184	170367	1505191	486	0.043781336	4.577657933	3.025501325	0.089755476	0.086078881	0
CTAACTTAGGGATGGG-1	2390956	16866	253506	215612	1904972	615	0.055700603	5.7358368	3.156351468	0.077399607	0.076847069	0
CTAACTTGTTGACGGA-1	1475372	36077	157947	128908	1152440	372	0.033596678	3.536945633	3.144316721	0.101394701	0.098694754	0
CTAACTTTCTTGGCCT-1	2119528	91541	218779	190476	1618732	523	0.047067813	4.898149867	3.08417695	0.092322576	0.090279252	0
CTAAGACGTGATTGTC-1	2081728	32821	224345	175754	1648808	533	0.048068205	4.977690467	3.109839362	0.086901226	0.086963097	0
CTAATGGCAACCTGAT-1	1718314	17066	186825	142959	1371464	443	0.04003356	4.170205033	3.042408574	0.091785458	0.092584103	0
CTACACCAGTTACCCA-1	1958588	60403	206718	167964	1523503	492	0.044354111	4.629236667	3.016740651	0.088999901	0.085584082	0
CTACACCGTACCGTGC-1	1555884	42826	162026	136786	1214246	392	0.035303895	3.707090933	3.119404151	0.097042807	0.096598519	0
CTACATTCACGAGATG-1	1003378	9074	109793	83999	800512	259	0.023417138	2.4778293	3.167192048	0.118303211	0.116576924	0
CTACATTTCAAAGTGA-1	1559394	18679	168518	138887	1233310	398	0.035985596	3.7766569	3.044849165	0.09820599	0.096442306	0
CTACATTTCACGTTAG-1	1528406	9107	168006	126221	1225072	396	0.0357958	3.746199633	3.088261197	0.096814348	0.09699749	0
CTACCCACAGTAGGGT-1	2157756	16509	234716	185599	1720932	556	0.050253513	5.1932489	3.052444621	0.085181507	0.083930582	0
CTACCCAGTAGAACAT-1	2353070	36677	254140	209280	1852973	599	0.054068063	5.583048233	3.107911932	0.079946022	0.07912283	0
CTACCCAGTATATGAG-1	1089474	9226	119248	86667	874333	282	0.025510375	2.687337233	3.073386936	0.110560528	0.110309541	0
CTACGTCGTAGTGGCA-1	1545156	55036	148526	137100	1204494	389	0.03509039	3.695667833	3.009249853	0.095477954	0.096567373	0
CTAGAGTTCGACAATC-1	2030534	43385	213719	176129	1597301	516	0.046504562	4.818978933	3.095566873	0.090475805	0.087801758	0
CTAGCCTAGGGATACC-1	3113612	45134	329328	274740	2464410	796	0.071582578	7.21001918	3.064339202	0.076610104	0.075563579	0
CTAGCCTTCCAACGAT-1	2121236	32899	230296	186094	1671947	540	0.04879306	5.057247533	2.921123859	0.084012584	0.081305627	0
CTAGCCTTCTCCGGAG-1	1832240	19858	196106	159233	1457043	471	0.042484065	4.438456967	3.054795007	0.095222995	0.091999596	0
CTAGCCTTCTTGGATG-1	940192	12741	102392	78371	746688	241	0.02176956	2.317985367	2.969414204	0.124466028	0.120055896	0
CTAGCCTTCTTGTCCG-1	1383720	25384	146577	130856	1080903	349	0.031498144	3.3335749	3.145155676	0.098591508	0.101380616	0
CTAGTGACAGTTTGCA-1	1906118	55236	199053	179562	1472267	476	0.042893913	4.493857567	3.01199838	0.086045215	0.086229583	0
CTAGTGAGTAGGGTGT-1	1960660	29613	206076	170498	1554473	502	0.045458609	4.7179248	3.10617319	0.090680571	0.088180024	0
CTAGTGATCTAAGGC-1	2560254	62047	268051	211049	2019107	652	0.058867817	6.0466642	2.697471764	0.116611617	0.116611617	1
CTCACACCTAGGTCT-1	327056	2826	34877	28125	261228	84	0.007624999	0.826155533	3.06905389	0.195228871	0.199457096	0
CTCACAGTCTCTCTG-1	1495918	20166	160517	128269	1186966	383	0.034656715	3.646884433	3.036616897	0.094412411	0.094875573	0
CTCACACTCAAGAGGC-1	2071306	54424	219228	182541	1615113	522	0.04706732	4.891227633	3.034239034	0.083363121	0.084712562	0
CTCAGAACATGGAGAC-1	1688592	65014	176089	153020	1294469	418	0.03767659	3.956617167	3.096021597	0.091829391	0.093110915	0
CTCAGAATCATGACCA-1	2000786	51382	212940	176225	1560239	504	0.04536542	4.7227471	3.011010478	0.086531912	0.086037822	0
CTCATTAGTGTTCCGG-1	2253188	20534	241162	208554	1782938	576	0.052034523	5.4071209	3.2069284	0.083426564	0.081867434	0
CTCATTATCATTGGAC-1	1463202	35485	145228	131485	1151004	372	0.033488103	3.5243579	3.019333348	0.104325116	0.103806784	1
CTCATTATCTGATCAG-1	1501058	11591	160293	133403	1195771	386	0.0349011	3.653897233	2.758148853	0.093801825	0.093801825	0
CTCCTAGAGGAGTACC-1	2763282	28714	299137	250751	2184680	706	0.063662812	6.5240663	3.035823885	0.078652034	0.076497298	0
CTCCTAGCAAACCGAG-1	1563740	15633	166675	136542	1244890	402	0.036289342	3.811587767	3.06562662	0.097550723	0.095756039	0
CTCGAAAAGCAGGTCA-1	2285172	54679	236644	201940	1791909	579	0.052162523	5.3902435	3.064757859	0.085205805	0.085943593	0
CTCGAAACAAGCTACT-1	1975938	47327	211690	179274	1537647	497	0.044849458	4.675464833	3.035554482	0.085418231	0.085903952	0
CTCGAAACATTTGTGG-1	1583110	20931	171427	141419	1249333	404	0.03638018	3.817449667	3.175836429	0.095546106	0.096686208	0
CTCGAAATCTACAAGC-1	2286928	55356	244776	201887	1784909	577	0.051973004	5.382899333	3.104763055	0.078236923	0.079604333	0
CTCGAGGAGCGATATA-1	1127428	11930	120783	92320	902395	292	0.026336249	2.7811031	3.168086677	0.110343678	0.107689797	0
CTCGAGGAGTGACATA-1	1450604	15001	155857	123205	1156541	374	0.033745701	3.546709667	3.089834096	0.101246607	0.097694343	0
CTCGAGGCAACTAGTC-1	1256054	17485	137605	103090	997874	322	0.029113872	3.065941367	3.007549019	0.103258312	0.099868202	0
CTCGAGGCAAGAATCA-1	1917166	73487	197937	170916	1474826	476	0.042934146	4.477838733	3.036442165	0.088850377	0.088620471	0
CTCGAGGCAAGTGTTC-1	2530396	83816	263584	222531	1960465	633	0.056914471	5.841298967	3.110339046	0.080418918	0.079721384	0
CTCGAGGGTCATGTTG-1	1208110	12446	128280	94304	973080	314	0.028419392	2.9924117	3.052217393	0.108598181	0.107906959	0
CTCGGAGAGAGCAATT-1	1380234	42952	146410	113540	1077332	348	0.031410026	3.3020091	3.079942893	0.101833668	0.102480522	0
CTCGGAGAGCTAACAA-1	1148382	16213	123609	97643	910917	294	0.026510858	2.8047236	2.976884072	0.107621346	0.105815703	0
CTCGGAGTCCACTAAG-1	1127786	10427	124394	91174	901791	291	0.026230658	2.763890367	3.028395938	0.108325242	0.109467182	0
CTCGGGAAGTGTTAGA-1	1086558	14814	114747	91561	865436	280	0.025334325	2.682456533	3.099958105	0.119023147	0.11721102	0
CTCGGGACAAGGGTGT-1	1852084	29013	183354	167900	1471817	475	0.042941982	4.454483367	2.970665739	0.094505531	0.090080585	0
CTCGGGATCATATCTC-1	2347498	43649	241693	215304	1846852	597	0.053714975	5.537878133	3.079866439	0.081804424	0.081587434	0
CTCGTACAGAGCTTCT-1	1707842	61590	168877	151166	1326209	428	0.038592984	4.0413505	3.106658429	0.093188539	0.093408881	0
CTCGTACAGCTGCGAA-1	1506866	13044	159950	132667	1201205	388	0.035013864	3.672032133	3.017811488	0.096144591	0.092721417	0
CTCGTACCACGTACAT-1	1392466	11753	149129	120273	1111311	359	0.032390161	3.4060444	3.011575882	0.100579748	0.098989968	0
CTCGTACCACGTTTAG-1	1017728	7727	108943	86717	814341	263	0.023805404	2.528387833	3.020280922	0.11094554	0.109822986	0
CTCGTACCATGCCATA-1	1401664	13665	147200	116738	1124061	363	0.03280752	3.451266767	2.98432918	0.102711589	0.101284571	0
CTCGTACGTTGCCTCT-1	1926940	41840	200068	170757	1514275	489	0.044026277	4.5806802	3.119848538	0.08879369	0.089327653	0
CTCGTCAAGCGGCTTC-1	1937546	45395	197517	180330	1514304	489	0.044134374	4.6051607	3.014394623	0.084633441	0.084402212	0
CTCGTCACAACGACGA-1	1169706	7971	126257	105027	930451	301	0.027140094	2.8762414	2.997755921	0.109017193	0.108069849	0
CTCGTCACAAGGTGAC-1	2379404	27065	261445	219291	1871603	605	0.054468836	5.641332567	3.059064685	0.083036265	0.082664522	0
CTCGTCAGTGTCCCTT-1	2062898	49037	214362	183490	1616009	522	0.047117519	4.887136767	3.046675192	0.086456425	0.086336405	0
CTCGTCATCACTGCGG-1	1832716	17204	193852	164337	1457323	471	0.042481094	4.437792867	3.007473024	0.086396807	0.086858796	0
CTCTAATGTATCGCCG-1	900322	38672	89970	80783	690897	223	0.020044247	2.138781	3.032719372	0.124292118	0.123826826	0
CTCTAATTCATATCTC-1	2380144	30615	247426	215230	1886873	610	0.054812533	5.6182659	3.166246368	0.084554504	0.084554504	0
CTCTACGAGAAAGTGG-1	1638324	13021	174957	142413	1307933	423	0.038199491	4.002699933	3.084457924	0.093192981	0.093673781	0
CTCTACGGTGATTGGG-1	2120548	22138	224005	186674	1687731	545	0.0492855	5.125126633	3.089007765	0.082912574	0.082912574	0
CTGAAGTAGTGATTGA-1	443610	2809	47634	37859	355308	115	0.010414924	1.123269433	3.084361132	0.171023474	0.170009204	0
CTGAAGTCAGACTTGT-1	596420	4356	64716	51746	475602	154	0.013910614	1.4905837	3.1104633	0.160810591	0.158074567	0

CTGAAGTGTAACGGCA-1	1902978	72754	199621	165034	1465569	473	0.042662696	4.457422533	3.081537379	0.088519466	0.089200565	0
CTGAAGTGTCAACCGC-1	1320288	38113	138178	120671	1023326	331	0.029790664	3.146162267	2.984300666	0.106719634	0.105070744	0
CTGAAGTGTCCACAG-1	1428234	13240	156141	122560	1136293	367	0.033062068	3.473943067	3.17162239	0.101202051	0.099015825	0
CTGAAGTTCGTAGCGC-1	1367116	24192	141288	126217	1075419	347	0.031325224	3.317167833	3.088183083	0.102826412	0.102826412	0
CTGATAGAGCAGCGTA-1	1181584	14862	124325	103446	938951	303	0.027436522	2.9010493	3.134874869	0.106246545	0.104990891	0
CTGATAGCAGCTCATA-1	1553248	14719	167225	135488	1235816	399	0.036078473	3.7733072	2.995929241	0.092266373	0.092674369	0
CTGATAGTCAGAAACA-1	1537562	38305	161344	145742	1192171	385	0.034774663	3.652282733	3.058908771	0.101834517	0.095929179	0
CTGATCCGTTCGTCAA-1	1696836	15592	181047	153512	1346685	435	0.039304368	4.1021824	3.02087521	0.095379332	0.092068477	0
CTGCCTAGTGGTCAGA-1	1938248	12978	206739	181199	1537332	497	0.044861043	4.680603867	3.11474676	0.089646995	0.088526282	0
CTGCCTAGTTCCACAA-1	1323522	10719	145921	113899	1052983	340	0.030751861	3.241486	2.771150322	0.101382131	0.101653732	0
CTGCCTATCGTAGCGC-1	1402058	17933	145451	131879	1106795	358	0.032211239	3.391182033	3.045507493	0.104149384	0.101045308	0
CTGCGGAAGAGTGACC-1	2253888	39985	228552	206359	1778992	575	0.051873029	5.364512233	3.195462491	0.082609261	0.08120857	0
CTGCGGAAGATGTCTC-1	2097292	43793	213585	188166	1651748	534	0.04812277	4.988983433	3.143177814	0.082486877	0.083263919	0
CTGCGGAAGTTGTCGT-1	1437632	35351	140076	127987	1134218	366	0.033089927	3.482450233	2.971983325	0.102500698	0.100634521	0
CTGCGGAGTCTCCACT-1	2302124	43820	242140	213695	1802469	582	0.052483142	5.415455567	3.144684962	0.085789383	0.084892361	0
CTGCGGATCAGAAACA-1	1794346	50036	187028	164039	1393243	450	0.040634764	4.257108267	2.913233999	0.090116101	0.090116101	0
CTGCGGATCCAAAGAA-1	1294600	23917	137384	112916	1020383	330	0.029718838	3.1313968	3.083663612	0.109444621	0.104363896	0
CTGCGGATCCCAGAAT-1	2037080	31364	217101	176835	1611780	521	0.047007967	4.860889233	3.050676612	0.084439999	0.084115103	0
CTGCTGTAGTAGGCCA-1	2904584	46632	307361	257150	2293441	741	0.06690233	6.878235	3.04479817	0.070958185	0.070842514	0
CTGCTGTAGTCTCGGC-1	1587634	46644	166037	143424	1231529	398	0.035867426	3.781468433	3.016763269	0.095915563	0.096778388	0
CTGCTGTCAACATAAG-1	999008	8249	108803	78317	803639	260	0.023518168	2.480268167	3.01775837	0.115024183	0.113822096	0
CTGGTCTAGCGATATA-1	1369272	12013	147479	111928	1097852	355	0.03203925	3.360740733	2.985688107	0.104414385	0.103164377	0
CTGGTCTAGGTCGGAT-1	2144268	25502	228582	180198	1709986	552	0.049937113	5.168721	2.936170364	0.085501076	0.083118416	0
CTGGTCTTCCTGATTT-1	2043226	73879	214536	164843	1589968	514	0.046226042	4.782915867	3.22314678	0.118126368	0.120136739	1
CTGGTCTTCTCCTAG-1	1760714	10573	189650	145661	1414830	457	0.041297216	4.306031767	2.827139368	0.090564736	0.088004571	0
CTGTGCTCAATGGGAC-1	1792334	85480	181386	157408	1368060	442	0.039808665	4.174099333	3.045392853	0.092743723	0.093281284	0
CTGTGCTCAGACACGA-1	1560768	12728	167697	138184	1242159	401	0.03619035	3.810207633	3.000028408	0.096595105	0.09340183	0
CTGTGCTCATGGCTCG-1	1031146	31848	103607	95599	800092	258	0.02321614	2.4718329	3.014880213	0.115128148	0.113494355	0
CTGTGCTGTGGGCCTT-1	1782228	35880	185357	163305	1397686	451	0.040753745	4.260388433	3.005888955	0.092581503	0.089405956	0
CTGTTAAGAGTCTGG-1	2009608	17905	213162	177429	1601112	517	0.046778974	4.8758432	3.088770973	0.082092232	0.08255897	0
CTGTTAAGCTGCCCA-1	1733476	40875	181142	158901	1352558	437	0.039452659	4.1385167	3.141778428	0.093901957	0.093999334	0
CTGTTAAGGCTATCT-1	2211484	53041	233677	191273	1733493	560	0.050345876	5.187961733	3.109609866	0.091706718	0.087791857	0
CTGTTTACACGCCTGA-1	1466792	16859	157859	129248	1162826	376	0.033941439	3.567886333	3.018909473	0.099649224	0.097774395	0
CTGTTTAGTCTCTTTA-1	1054114	14082	112038	92653	835341	270	0.024443221	2.586924333	2.917447086	0.110020654	0.110018126	0
CTGTTTATCACCAGCG-1	600228	27944	61771	54027	456486	147	0.01319896	1.413432567	2.944189613	0.147719573	0.143954214	0
CTTAACTAGCATCTTG-1	797650	8617	86789	67259	634985	205	0.018538829	1.971474667	2.983313688	0.125362199	0.125749205	0
CTTAACTGTGGAAAGA-1	1335630	21708	141310	117150	1055462	341	0.030852233	3.258244967	3.072816361	0.100825335	0.101093223	0
CTTAACTTCCTTGCAC-1	2206996	52103	237378	194151	1723364	557	0.050213775	5.2020779	2.9041598	0.089730691	0.086152171	0
CTTACCGAGGGCTTCC-1	2357294	65991	245239	214025	1832039	592	0.053331553	5.514133267	2.895529067	0.083993979	0.083993979	0
CTTACCGGTAAGTAAC-1	2149550	18786	229482	194908	1706374	551	0.049816621	5.164468867	3.119499893	0.081608867	0.081173409	0
CTTACCGGTCACCTGG-1	1495446	16363	158509	131671	1188903	384	0.034709698	3.647437767	3.163036683	0.096466298	0.094218776	0
CTTACCGGTGCTATTG-1	1344662	12942	145731	106768	1079221	349	0.031485573	3.3107972	3.100494374	0.100402233	0.098392658	0
CTTACCGTCACACGTA-1	1179048	9844	127635	97632	943937	305	0.027515661	2.897565533	3.085791989	0.108736155	0.109693089	0
CTTACCGTCCGCGACA-1	1663906	45922	172190	152250	1293544	418	0.03765714	3.9596711	3.097094068	0.09157913	0.093586337	0
CTTAGGACACAGGCAC-1	2162164	39880	227760	191897	1702627	550	0.049644444	5.156974133	3.046675523	0.082369825	0.084887742	0
CTTAGGATCTGGGCTG-1	1481830	34948	153830	130188	1162864	376	0.033888596	3.569604567	3.119705053	0.099946647	0.10084129	0
CTTCTCTAGCTGCCCA-1	2289280	53969	241452	209231	1784628	576	0.052005103	5.3963407	3.107273787	0.079286156	0.079918073	0
CTTCTCTAGGTCGGAT-1	2191864	22693	235133	188443	1745595	564	0.050982455	5.2703951	3.105562619	0.086059049	0.082589925	0
CTTCTCTCAATGTAGA-1	976130	8538	105744	82690	779158	252	0.022754777	2.415797333	3.001966771	0.118342639	0.115189679	0
CTTCTCTCAGCTATGT-1	1263638	15403	138880	100588	1008767	326	0.02944899	3.0968291	3.109206751	0.108412539	0.105914628	0
CTTCTCTCATCGCATA-1	1557172	17041	166138	131029	1242964	402	0.036271866	3.783456533	2.967222546	0.09790768	0.095658259	0
CTTCTCTTCCTATGAG-1	1250368	9979	136683	100188	1003518	324	0.029300541	3.075587533	3.0032322	0.106112775	0.10521838	0
CTTGGCTAGACAGAGA-1	1600858	15526	172364	135920	1277048	413	0.037331676	3.913358767	3.060517606	0.09430851	0.0937657	0
CTTGGCTAGCGCCTTG-1	1253604	6889	142183	107036	997496	322	0.029108119	3.0783841	3.071516348	0.102039166	0.100918306	0
CTTGGCTAGTCTCGTA-1	1046986	11947	110730	96485	827824	267	0.024145741	2.5531081	3.00358703	0.113264749	0.111579134	0
CTTGGCTGTTCTAGTG-1	1180350	12674	129704	93240	944732	305	0.027542008	2.896158567	3.095774068	0.108621867	0.106120356	0
CTTTGCGGTCAAAGCG-1	1068926	35869	110974	96164	825919	267	0.023993883	2.557689433	3.114620182	0.112343159	0.113216065	0
CTTTGCGTCCTCAGTC-1	1471636	29145	152586	124223	1165682	377	0.033927155	3.551343533	3.018356376	0.100917226	0.095813637	0
GAAACTCGTGCGAACA-1	1571848	82219	162120	137717	1189792	384	0.034709358	3.6423319	3.094240726	0.097142868	0.098054525	0
GAAACTCGTTCGTCAA-1	2135930	27021	230601	190929	1687379	545	0.049259709	5.110496567	2.979772072	0.084960479	0.083211653	0
GAAACTCTCACGCTCT-1	2130534	106771	218451	192550	1612762	521	0.046673393	4.811697433	3.000518599	0.08935311	0.087046346	0
GAAACTCTCACGTAGT-1	1542580	15913	170467	129785	1226415	396	0.03581356	3.741242833	3.042750401	0.094557746	0.093273384	0
GAAACTCTCTGGTGAT-1	2495682	28178	275288	218563	1973653	638	0.05765117	5.926617433	2.976117579	0.081069753	0.077453221	0
GAAATGAAGGCTCTTA-1	1624258	36501	176006	140795	1270956	411	0.037095872	3.8867127	3.072867677	0.097114455	0.094399575	0
GAAATGACACCCTCTA-1	3053208	50683	331744	263350	2407431	778	0.070268292	7.194647133	3.071199204	0.071206171	0.070016325	0
GAACATCGTACTTGCA-1	1716378	80359	177834	155279	1302906	421	0.03790936	3.972400433	3.050301511	0.09048902	0.0917392	0
GAACATCTATGCGCG-1	913584	74014	89652	81012	668906	216	0.019455263	2.085101733	3.001604977	0.126304485	0.125028462	0
GAACCTACAAAGGTTA-1	1874472	15467	206866	163088	1489051	481	0.043479318	4.5191123	3.029858487	0.090336444	0.08918915	0
GAACCTACAATCGCGC-1	1155310	23774	119606	115712	896218	290	0.026104245	2.764222367	3.111349462	0.111685547	0.108421981	0
GAACCTAGTCACATGT-1	1320126	16512	148517	101515	1053582	340	0.03074443	3.228522067	3.032847182	0.100351012	0.099074915	0
GAACCTAGTCGAGTAG-1	1478760	18729	156095	123110	1180826	381	0.034519334	3.624958133	3.023052013	0.096022323	0.096465549	0
GAACCTAGTTCGAGCC-1	1327568	54281	138490	117847	1016950	329	0.029541528	3.1145524	3.011322792	0.10361213	0.101656405	0
GAACGGACACTTGCAA-1	1806992	20850	198891	154785	1432466	463	0.041755683	4.350981333	3.072373375	0.087650834	0.087327631	0
GAACGGACAGGTCTGC-1	2242342	43803	243718	180991	1773830	573	0.051648559	5.335640633	3.324063411	0.125915174	0.12395808	1
GAACGGAGTACGTTTG-1	1641982	30817	178954	142092	1290119	417	0.037602925	3.932228267	3.083304916	0.093672218	0.093226763	0
GAACGGATCTTCACGC-1	2074354	30954	224088	186351	1632961	527	0.047557803	4.9460844	3.14422544	0.086541769	0.086801784	0
GAAGCAGAGGGAGTAA-1	1747690	20773	193324	145277	1388316	448	0.040430343	4.2181149	3.164989454	0.091741223	0.091516455	0
GAAGCAGCACACGCAC-1	2517470	37601	273868	222433	1983568	641	0.05782491	5.955686333	3.025062336	0.079392679	0.07923693	0
GAATAAGAGGCTACGA-1	1310700	15219	142569	114065	1038847	336	0.03031693	3.202001333	3.008851569	0.107183957	0.103695582	0
GAATAAGCAAATACGA-1	1444902	28523	156080	126632	1133667	366	0.033020363	3.477850333	3.142372111	0.098606309	0.096146788	0
GAATAAGCAGAGATCG-1	1405216	90974	142076	122745	1049421	339	0.030502127	3.223729967	2.790193697	0.106124835	0.102260099	0
GAATGAACAACCTGCG-1	1353282	114117	135817	113857	989491	320	0.028754164	3.044604833	3.032668134	0.107976624	0.106225734	0
GAATGAATCTTCACAT-1	1419246	14180	155458	128195	1121413	362	0.032700565	3.424381333	3.031093308	0.101512537	0.099594309	0
GACACGCCAAATGATG-1	1339860	17337	148031	106291	1068201	345	0.031238517	3.272402133	3.138061583	0.102200963	0.102213792	0
GACAGAGAGCCTAACT-1	2165482	63675	231520	191947	1678340	542	0.048705597	5.0075142	3.142702879	0.08445602	0.08445602	0
GACAGAGCACAGACCC-1	1853144	35133	196862	171059	1450090	468	0.042228588	4.427032433	3.111223199	0.08924619	0.089764452	0
GACAGAGCAGTAATCC-1	2410034	63379	256031	208503	1882121	608	0.054553541	5.603322767	3.101909878	0.086467359	0.086467359	0
GACAGAGCATCGGGCT-1	1206666	97913	108314	100954	899485	291	0.026140103	2.7692769	3.000127856	0.108934316	0.11134635	0
GACAGAGTCAGCCGA-1	1977856	26529	213053	179911	1558363	503	0.045458385	4.7368325	3.035723163	0.085453581	0.0858874	0
GACAGAGTCCTACGAA-1	1480510	16990	165520	122338	1175662	380	0.034257549	3.598007567	3.097890475	0.096885677	0.094605732	0
GACAGAGTCCTGCGTT-1	2125662	50676	234646	180134	1660206	536	0.048283671	4.997184467	3.019277759	0.088629931	0.088218794	0
GACCAATAGACTTTCG-1	1551048	75972	162503	139935	1172638	379	0.03414249	3.5937185	3.020096611	0.098492683	0.096527375	0
GACCAATAGGACAGAA-1	1526494	16098	168112	125003	1217281	393	0.035524867	3.725419	3.077322005	0.098513191	0.09294981	0
GACCAATTCCGGCTAG-1	2078448	47228	227554	184269	1619397	523	0.047290496	4.918062067	3.012175025	0.086372042	0.084574453	0

GACCTGGGTAGCCCTG-1	1507576	30056	160550	130904	1186066	383	0.03461075	3.6470282	3.064097919	0.095999814	0.097439951	0
GACGCGTAGTAACCCT-1	1314248	56235	124120	116042	1017851	329	0.029634674	3.1338713	3.066245721	0.102695246	0.102695246	0
GACGCGTCAGGTCAAG-1	1014420	31407	91650	87949	803414	260	0.023429188	2.491088867	3.093265831	0.119603439	0.115098895	0
GACGGCTGTGTAATGA-1	1000748	18661	109270	79280	793537	256	0.023098136	2.444537467	2.966153212	0.117263836	0.114776129	0
GACGGCTGTTGAGCAG-1	1885472	49625	202240	166556	1467051	474	0.042808146	4.4797851	3.084720841	0.090263068	0.089157872	0
GACGTGCGTGCGTCAC-1	1450280	16227	143118	132494	1158441	374	0.033737767	3.545438667	3.047979941	0.097451603	0.097451603	0
GACTAACCACCCGTGA-1	1395092	23880	152241	122273	1096698	354	0.031977537	3.371270333	2.984218302	0.099639901	0.099127411	0
GACTAACCAGACACAG-1	1446066	22168	160403	123529	1139966	368	0.033261087	3.490100967	2.878661326	0.100443411	0.099138281	0
GACTACACACAATCAC-1	2660244	39481	289705	248051	2083007	673	0.060716634	6.2424244	3.18591201	0.076658997	0.076522248	0
GACTGCGCAGTAGGGT-1	2170000	36102	235259	185900	1712739	553	0.050026979	5.181878	3.050870452	0.083284338	0.083284338	0
GACTGCGGTGTCTGTA-1	1635618	16369	178566	139524	1301159	420	0.037953245	3.9728971	3.051660464	0.093585147	0.091834371	0
GACTGCGTCATATCTC-1	2264826	25519	242691	199311	1797305	581	0.052105801	5.362400933	3.070489777	0.083592645	0.083280216	0
GACTGCGTCGTAGCGC-1	670938	9237	60215	60752	540734	175	0.01573814	1.691431467	2.993369303	0.143123183	0.140546077	0
GAGCAGAAGAATCGTA-1	2216978	48046	239225	188015	1741692	563	0.050811488	5.266044067	3.084447507	0.085787459	0.0840052	0
GAGCAGAAGTTATCGC-1	2176558	36693	235012	197154	1707699	552	0.049729883	5.155134933	3.055013675	0.087779692	0.086653753	0
GAGCAGATCCGCCTAT-1	1711856	22022	188377	151855	1349602	436	0.039351329	4.091451767	3.068046202	0.093719704	0.09199494	0
GAGGTGAAGCCGAACA-1	2121278	69618	223005	190890	1637765	529	0.04768697	4.964064667	3.031619992	0.084417538	0.08385759	0
GAGGTGACACTAACTG-1	1059550	30858	113973	87748	826971	267	0.024081367	2.558490233	2.96361519	0.110460944	0.112755599	0
GAGGTGACAGCTATGT-1	1249364	17608	137760	97935	996061	322	0.029071743	3.054865433	3.034710039	0.103394281	0.100634976	0
GAGGTGACAGTGAATA-1	2726140	35698	297126	226754	2166562	700	0.063187278	6.491346267	3.044153686	0.072366932	0.071952718	0
GAGGTGATCACACGGC-1	1401554	48905	148657	117683	1086309	351	0.031545617	3.324517333	3.125536328	0.117556725	0.118438842	1
GAGTCCGAGGGTTCGA-1	2131810	33054	228821	194589	1675346	541	0.04887616	5.0922854	3.027165844	0.083107021	0.081583331	0
GAGTCCGCATACGGTT-1	1850328	24091	202755	148461	1475021	476	0.043016021	4.4760191	3.093631709	0.087752162	0.085159131	0
GAGTCCGGTACTGCTA-1	1311384	16339	140964	117972	1036109	335	0.030239065	3.181647967	3.037336855	0.106884186	0.103576913	0
GAGTCCGGTCCTAGTA-1	1067466	15559	117361	84528	850018	275	0.024753602	2.6171019	3.098224558	0.114169704	0.114045212	0
GAGTCCGTCAGACACT-1	2342610	41049	255765	207407	1838389	594	0.053505592	5.522209033	3.031324154	0.081281604	0.080735943	0
GATCAGTCAAGCACGA-1	1438234	25436	155044	129042	1128712	365	0.032928964	3.475754633	2.957936824	0.096280823	0.09809861	0
GATCAGTTCCACCCAT-1	2476684	27238	273097	211762	1964587	635	0.057389122	5.915584967	3.036962036	0.076831969	0.077662481	0
GATCAGTTCCGCTCTA-1	2021266	55838	215003	186603	1563822	505	0.045595863	4.748382033	3.126734249	0.089424265	0.085164429	0
GATCGATGTCCTACCT-1	692496	9082	75107	56286	552021	178	0.01611553	1.727162233	3.106981598	0.148158038	0.145026898	0
GATCGCGAGTCCATAC-1	1973362	22739	213469	165444	1571710	508	0.045862498	4.7475962	3.0168857	0.089034164	0.087312138	0
GATCGTAAGTAGGCCA-1	1791346	59937	183888	158114	1389407	449	0.040489652	4.2361245	3.012865231	0.088322654	0.087281407	0
GATCGTACAACCGGAA-1	1640214	24329	175127	142220	1298538	419	0.037899615	3.9782238	3.067719802	0.098139582	0.094615624	0
GATCGTACATACCAGT-1	2118092	33293	228755	188282	1667762	539	0.048694703	5.0415323	3.138066963	0.081609779	0.082855695	0
GATCGTACATGATGCT-1	2710516	64379	290815	238436	2116886	684	0.061344933	6.2422825	3.163201523	0.085760418	0.084237103	1
GATCTAGCAAGTGTTC-1	2368390	31654	257348	211351	1868037	603	0.054285403	5.588488167	3.108596192	0.085412275	0.082878267	0
GATCTAGTCACGCTCT-1	1557342	50925	165106	139675	1201636	388	0.034868083	3.621311033	3.005199861	0.106458133	0.10034133	0
GATGAAAAGTAATCCC-1	2292618	29727	246614	202032	1814245	586	0.052832474	5.453982867	3.12287395	0.083950471	0.083883712	0
GATGAAACAAGTGCAG-1	1735164	31412	188885	154798	1360069	439	0.039705169	4.1515519	2.87047707	0.090783918	0.088652508	1
GATGAAACATGCAGTT-1	1756572	28915	194158	144272	1389227	449	0.040497631	4.221143733	2.971020568	0.093727602	0.092974895	0
GATGAAAGTAACGGCA-1	1916592	84951	201128	169503	1461010	472	0.042573285	4.4446107	3.016580826	0.087529974	0.086045265	0
GATGAAAGTTCAGTAC-1	2110778	33609	230028	191638	1655503	535	0.048093077	4.952792467	2.903130017	0.086869133	0.086923523	0
GATGAGGCAATGGCTT-1	2266998	108079	238016	196308	1724595	557	0.050182023	5.187408	3.003829811	0.091524376	0.091145284	1
GATGCTAGTAGGCTGA-1	1521416	19389	165432	142624	1193971	386	0.034869701	3.676908867	3.068785737	0.095548724	0.095519433	0
GATGCTAGTCTCTCGT-1	2148888	41912	229747	186792	1690437	546	0.04933529	5.113525	2.992848926	0.086053893	0.085153952	0
GATGCTAGTTCCCTAC-1	2744570	28944	302181	233627	2179818	704	0.06346832	6.4779754	3.079342977	0.080868573	0.078277904	0
GATGCTAGTTGGAACG-1	1665998	87995	173298	144934	1259771	407	0.036658219	3.8463398	2.960847267	0.090797073	0.092004266	0
GATGCTATCACTATGG-1	1110078	16949	123829	88599	880701	284	0.025714216	2.7090558	3.108377008	0.115354161	0.112007878	0
GATGCTATCATCAGCA-1	1808598	39890	193938	160610	1414160	457	0.041136882	4.2957505	3.092979639	0.090124196	0.088761988	0
GATTCAGAGATGTGGC-1	2881214	31849	317688	251040	2280637	737	0.066539417	6.8103709	3.097838364	0.074389532	0.073366297	0
GATTCAGGTTCAGTGT-1	2196964	35687	239077	188028	1734172	560	0.050545926	5.216228833	3.142120551	0.087716322	0.086008679	0
GATTCAGTCGACAACT-1	2363820	66860	255198	214580	1827182	590	0.053148991	5.466758933	3.092181906	0.085699998	0.083781515	0
GCAAACTAGCCACGTC-1	1280606	22599	138617	111399	1007991	326	0.029314657	3.090762933	3.044396787	0.105751905	0.106634817	0
GCAAACTCAAGCCAAG-1	1970636	32455	213362	173018	1551801	501	0.045278175	4.7175169	3.142023056	0.084096916	0.083661195	0
GCAAACTCACATTGGT-1	2304558	30833	253175	192942	1827608	590	0.053358368	5.503516067	3.081819796	0.080413701	0.079181238	0
GCAAACTTCCTACGAA-1	1493416	19440	165142	127175	1181659	382	0.034400279	3.610446133	3.182539344	0.100484936	0.097690555	0
GCAATCAAGGCAACAC-1	2040878	38276	220581	183989	1598032	516	0.04654745	4.8263927	2.973894327	0.086502293	0.083612672	0
GCAATCAGTTAGTGAA-1	2844122	27445	313809	238324	2264544	732	0.066151562	6.7817772	3.122862603	0.072597467	0.070689066	0
GCAATCAGTTGCCTCT-1	2284926	51110	247231	197286	1789299	578	0.052132401	5.3734342	3.004440592	0.085478066	0.084612502	0
GCAATCATCCCTGAGG-1	1955304	29829	212996	167315	1545164	499	0.045125148	4.702526067	2.996079323	0.086022886	0.084392016	0
GCAATCATCCGTTCAC-1	3329206	24212	362848	305603	2636543	852	0.077159929	7.851600267	3.009597215	0.063775236	0.063232964	0
GCACATAGTGAGCGAT-1	2628698	42475	283979	237963	2064281	667	0.060225533	6.192304033	2.985358576	0.079038119	0.078528773	0
GCACTCTAGACTTTCG-1	1519538	90881	155091	131986	1141580	369	0.033226163	3.5074068	3.1464047	0.095345632	0.09710856	0
GCACTCTAGCATCTTG-1	1195050	21377	128951	98457	946265	306	0.027651376	2.9226492	3.128532167	0.107455851	0.105965383	0
GCACTCTAGTCCAGGA-1	1568648	20518	170669	136877	1240584	401	0.036212069	3.808155433	3.033669316	0.096348778	0.096319297	0
GCACTCTCAAGCATGG-1	1192130	15695	130380	100735	945320	305	0.027650322	2.9171426	3.081614974	0.107415174	0.107108926	0
GCACTCTTCCACCTTG-1	1427692	28006	154927	119921	1124838	363	0.032830372	3.4552007	3.077858051	0.097327179	0.09730119	0
GCAGCCACAGACACGA-1	1704214	28208	184453	146714	1344839	434	0.039198108	4.0858639	2.154069664	0.083564732	0.081002764	1
GCAGCCACATTGCATG-1	1239600	14768	136645	102956	985231	318	0.02867376	3.021949333	2.982728009	0.107036511	0.10653768	0
GCAGCCAGTCGTCTTC-1	2385760	22432	254762	222033	1886533	609	0.054962719	5.682672333	3.089569942	0.093613077	0.093613077	1
GCAGCCATCGCTCTAC-1	2487958	25187	269366	214977	1978428	639	0.057625639	5.922392267	3.0587458	0.080318827	0.078455008	0
GCAGTTAAGGCCCTTG-1	1509446	20626	164916	129629	1194275	386	0.034862012	3.656346067	3.106214232	0.094801539	0.096856946	0
GCAGTTAGTAGCAGTG-1	1449734	17626	158807	117095	1156206	373	0.033794401	3.545397167	3.108552842	0.100839918	0.10051095	0
GCAGTTAGTGGAAGGG-1	1980468	42189	211206	173171	1553902	502	0.045370147	4.722401833	2.993713417	0.084592204	0.085698546	0
GCAGTTATCGCCCAGA-1	1966408	19823	211963	174201	1560421	504	0.045549685	4.743428867	2.987555139	0.088305559	0.088914554	0
GCATACAAGATCCTGT-1	2392730	38323	263406	207929	1883072	608	0.054957698	5.675742867	3.01899458	0.081698688	0.081159666	0
GCATACAAGGACAGAA-1	1489600	19846	163454	123558	1182742	382	0.034509225	3.623158433	2.947626016	0.0973647	0.095312642	0
GCATACACACGTGCGT-1	1984236	40353	212795	178758	1552330	501	0.045267937	4.714747567	3.111939026	0.085088597	0.085727211	0
GCATACATCAGATGTC-1	1673148	14625	183577	140737	1334209	431	0.038897689	4.0566664	3.00917555	0.094238436	0.092993825	0
GCATACATCCGCTCTA-1	1703458	39949	183826	146943	1332740	431	0.03890419	4.0640419	3.031236236	0.089878028	0.091156646	0
GCATGATCACGATAGG-1	1351994	19141	145826	113885	1073142	347	0.031370797	3.3006619	3.019103893	0.100141611	0.098599609	0
GCATGATCACTCACCT-1	2106780	64803	221376	192370	1628231	526	0.047385202	4.933765667	3.168762522	0.085287861	0.085287861	0
GCATGATCATGACCGC-1	1244540	15452	130972	115272	982844	317	0.028584445	3.022511833	3.082922568	0.107686824	0.104312839	0
GCATGATGTCGCTCAG-1	1842078	42872	195426	167368	1436412	464	0.041909257	4.3852703	3.048477487	0.088146414	0.089335217	0
GCATGATGTTCGCGTG-1	1396812	41917	147413	116344	1091138	352	0.031751923	3.3469385	2.987036787	0.105147542	0.100789056	0
GCATGATTCCGTTAAG-1	1254200	21583	136786	104439	991392	320	0.028959035	3.058290833	3.038747523	0.102176359	0.101292125	0
GCATGCGAGTAACCCT-1	2227086	91553	231739	191040	1712754	553	0.049878367	5.179085	3.0184376	0.085546861	0.08398285	0
GCATGTATCCACAGCG-1	1077684	47690	112482	92792	824720	266	0.023897812	2.545190933	3.07210323	0.11729829	0.111778321	0
GCCAAATAGTAAGTAC-1	1949582	33242	208713	181667	1525960	493	0.04436075	4.5977005	3.062986644	0.087507252	0.084651737	0
GCCAAATCATCGGCGT-1	1585204	35825	166744	142314	1240321	401	0.036100626	3.791823667	3.102674481	0.092157279	0.092157279	1
GCCAAATCATTTGTGG-1	1337694	25725	138141	115251	1058577	342	0.030846839	3.248924433	3.037419291	0.102947705	0.100829551	0
GCCAAATTCCGCGGAT-1	2700238	43842	292444	232946	2131006	688	0.062189074	6.372317367	3.172082351	0.076799486	0.073196974	0
GCCAAATTCTACAGTG-1	1237550	16284	137427	98354	985485	318	0.02874898	3.0219803	3.035727728	0.10841836	0.103366789	0
GCCTCTAGTACGGTGA-1	1531882	21114	166086	128778	1215904	393	0.03546554	3.7245339	3.049646599	0.096928501	0.097903428	0

GCCTCTATCACGTAGT-1	1419696	14326	156326	122346	1126698	364	0.032922555	3.4554272	3.048362123	0.102377502	0.101427486	0
GCGACCACAACTCATG-1	1136444	18209	123847	93056	901332	291	0.026248254	2.769514733	3.039311481	0.103652108	0.104602808	0
GCGACCAGTCCTACCT-1	1891298	71540	199578	169206	1450974	469	0.042196593	4.400750267	2.884008041	0.091970732	0.089665349	0
GCGAGAAAGCTTCAGT-1	1119460	7521	121890	94084	895965	289	0.026171881	2.760192933	3.089326166	0.114496316	0.112441357	0
GCGCAGTAGCGATGAC-1	2212136	31338	244800	192987	1743011	563	0.050791746	5.266660233	2.999587986	0.084795099	0.082467346	0
GCGCAGTGTACTCGTA-1	1001110	14102	105180	84161	797667	258	0.023252843	2.470162667	3.018899953	0.114932278	0.117597535	0
GCGCAGTGTGACACGA-1	1393070	14829	149232	126156	1102853	356	0.032173614	3.3965511	3.106374213	0.099100041	0.100014594	0
GCGCAGTGTGACCAAG-1	1699622	34643	179720	144847	1340412	433	0.039222512	4.097738267	3.117900209	0.09530551	0.093869249	0
GCGCCAAAGCGAGAAA-1	1154256	21181	130667	95651	906757	293	0.026420885	2.798021633	3.033798036	0.112476028	0.108814456	0
GCGCCAAGTTGCCAAT-1	2001368	19288	214930	169184	1597966	516	0.046684363	4.8431654	3.043044288	0.087918427	0.084132242	0
GCGCCAATCCTCATCG-1	1388218	60090	142934	121297	1063897	344	0.030949828	3.2647979	3.171219353	0.099593979	0.099396853	0
GCGCGATAGGACTGGT-1	2082546	30088	221435	183834	1647189	532	0.048114145	4.980123167	3.106563432	0.082741137	0.084254232	0
GCGCGATAGGATATAC-1	1783566	21381	192003	150078	1420104	459	0.041428227	4.311192767	3.116289972	0.093549216	0.090382229	0
GCGCGATGTCATCTAG-1	786220	11571	84865	67995	621789	201	0.018169034	1.932812467	2.992012723	0.14570691	0.143186783	1
GCGGGTTAGGAGTTTA-1	3468752	87806	357613	307766	2715567	877	0.079353661	8.056599667	2.977217169	0.065007975	0.065007975	0
GCGGGTTAGTGTATCC-1	2134686	57681	219032	188563	1669410	539	0.048313446	4.965499167	3.041017151	0.083847749	0.085234433	0
GCGGGTTTCTATGCCC-1	1786222	32765	187875	171146	1394436	450	0.040545356	4.2169994	3.036351366	0.100398457	0.093364927	0
GCTCCTAAGATCCCGC-1	2217126	12386	239320	203833	1761587	569	0.051396997	5.329333533	3.113858678	0.080990471	0.080220724	0
GCTCCTAAGCCGAAA-1	1569384	24000	170193	135645	1239546	400	0.03614803	3.7945494	2.892923352	0.096614095	0.093717989	0
GCTCCTATCCCAGAAT-1	1973500	30021	213755	180520	1549204	500	0.045136819	4.6742327	2.980773875	0.084712928	0.084712928	0
GCTCTGTAGCATGGCA-1	1889490	29841	203833	168684	1487132	480	0.04331561	4.527392933	3.04766235	0.089311733	0.087208433	0
GCTCTGTAGTTAGCGG-1	1473400	43378	155035	134302	1140685	368	0.033261167	3.502342533	2.972685241	0.10085759	0.10131738	0
GCTCTGTCAAACTCAC-1	2338690	22205	254668	210923	1850894	598	0.053951013	5.582111967	2.970937171	0.080174493	0.07920302	0
GCTCTGTTCACTCATT-1	2039068	26192	224314	172988	1615574	522	0.047124909	4.882893467	2.990539034	0.085816903	0.086585158	0
GCTGCAGAGGAGTTGC-1	2145342	24600	230800	191143	1698799	549	0.049404521	5.125430267	3.0742614	0.087614577	0.086601345	0
GCTGCAGGTAACGTGG-1	1601104	28418	170676	136656	1265354	409	0.03697472	3.8746192	3.040706141	0.090306945	0.090306945	0
GCTGCAGGTCGCGAAA-1	1184218	29060	122966	107769	924423	299	0.026970945	2.858519567	3.113698027	0.106361241	0.104903508	0
GCTGCAGGTTGAACAA-1	1378032	26260	148603	120869	1082300	350	0.031538656	3.3124057	2.92472049	0.101450336	0.100685233	0
GCTGCGACACCTCCAT-1	2180056	24785	237846	190074	1727351	558	0.050421845	5.208405	3.081480534	0.083748554	0.082533339	0
GCTGCGATCACTACAG-1	1196642	16891	130169	98628	950954	307	0.027671594	2.926947267	3.110108226	0.110095855	0.104244951	0
GCTGCTTCACGATCTA-1	2009778	46929	218270	178555	1566024	506	0.045646137	4.7583443	3.111742438	0.089364508	0.087736537	0
GCTGCTTGTCATCTAG-1	1271376	13723	139301	108471	1009881	326	0.02952753	3.1090056	3.091755565	0.103493786	0.103493786	0
GCTGCTTTCAGTACAC-1	2594706	28978	282947	241106	2041675	660	0.059459654	6.117805267	3.113147371	0.076547431	0.075181457	0
GCTGGGTAGGCATATA-1	1019942	13332	109971	78207	818432	264	0.023928221	2.526921433	3.080781902	0.113967818	0.115128256	0
GCTGGGTCAACTCCGG-1	2003818	61327	208539	179873	1554079	502	0.045299218	4.7369394	2.988943367	0.083961261	0.083162585	0
GCTGGGTGTGTAGTTC-1	2150790	78467	221476	187721	1663126	537	0.048009844	4.917046367	2.971244894	0.088401051	0.089070305	0
GCTGGGTGTGTCGCTG-1	1083488	33420	111155	94914	843999	273	0.02462948	2.615526967	3.077092965	0.112552134	0.112552134	0
GCTGGGTTCTATGGTG-1	1179430	18997	127464	93994	938975	303	0.027392034	2.8785921	3.024250472	0.10586632	0.10647569	0
GCTTCCAAGGGTTTCT-1	2114276	63489	226483	188756	1635548	528	0.047591927	4.928545767	3.104959188	0.083995841	0.085598993	0
GCTTCCATCCTACGAA-1	1383004	16058	152214	118858	1095874	354	0.031944853	3.360852333	2.949855818	0.101092708	0.098330771	0
GCTTCCATCTGGCCTT-1	2235898	66248	236536	202863	1730251	559	0.050402382	5.228590933	3.108784619	0.082721347	0.081934021	0
GCTTCCATCTTCCGAC-1	1562214	37524	166789	147342	1210559	391	0.035232653	3.692380167	3.0966491	0.101968317	0.096086885	0
GCTTGAACAGTGCTTA-1	1907858	27898	207981	166443	1505536	486	0.043967841	4.575037067	3.019939903	0.08666868	0.085951881	0
GCTTGAAGTGAGCGAT-1	2641892	44237	285824	239980	2071851	669	0.060461778	6.195382633	2.991228694	0.095440983	0.095296133	1
GGAAAGCAGCCAGAAC-1	2147390	48220	227431	193417	1678322	542	0.048820358	5.043704733	2.992315614	0.08826692	0.087228323	0
GGAAAGCCATGACTCA-1	1805330	87916	187988	154409	1375017	444	0.039960363	4.177748967	3.095924658	0.090422541	0.088148011	0
GGAAAGCTCCACCTTG-1	1024530	20904	108410	90219	804997	260	0.023486247	2.487053367	3.019974863	0.117876784	0.114799225	0
GGAAAGCTCGTGTACA-1	1224228	29047	114052	107820	973309	314	0.028435231	3.0005882	3.144325211	0.106542738	0.106503394	0
GGAACTTAGGGTCTCC-1	2034862	13750	218315	193345	1609452	520	0.047032897	4.883649933	3.034424949	0.086651973	0.085101635	0
GGAACTTCACAAGCTT-1	384970	6873	41438	30273	306386	99	0.008935834	0.965921567	3.250678026	0.224546104	0.224546104	1
GGAACTTGTCGGGAAT-1	2125044	30224	230842	192963	1671015	540	0.048787707	5.050710967	2.963545699	0.08397347	0.082723821	0
GGAACTTGTTTCCATT-1	2006678	30783	219528	177324	1579043	510	0.046050611	4.7822081	3.024420042	0.086849674	0.086205717	0
GGAACTTTCCGATACA-1	1884300	49928	202080	166954	1465338	473	0.042715764	4.4421336	2.949379497	0.088699314	0.088212985	0
GGAATAATCTAAGACC-1	1922192	16715	205603	169403	1530471	494	0.044509785	4.618114667	3.121633912	0.1085547	0.1085547	1
GGACAAGAGGGATTTA-1	1730070	33024	187609	149545	1359892	439	0.03966722	4.146693567	3.0381591	0.092199968	0.089806455	0
GGACAAGGTGTAAAGT-1	584380	6228	63939	49791	464422	150	0.013594107	1.453776067	3.045282858	0.14658493	0.149554478	0
GGACAAGGTTCAGTAC-1	1868202	40044	200839	168189	1459130	471	0.042351675	4.369242867	2.932403731	0.093069566	0.092551832	0
GGACAAGTCGACGAAG-1	1799638	34909	192998	151754	1419977	459	0.041449417	4.3244544	2.934117831	0.09306896	0.090186927	0
GGACAAGTCGCGCACA-1	1676210	52543	175573	148622	1299472	420	0.037823346	3.970268967	3.106661363	0.093188151	0.091578687	0
GGACAGAAGGTATCGG-1	1786330	43952	191537	158790	1392051	450	0.04063412	4.2553263	2.890626665	0.092998267	0.092998267	0
GGACAGACAAACCCTA-1	2020568	50815	217363	180771	1571619	508	0.045860992	4.771284633	3.064808303	0.083490179	0.082223704	0
GGACAGACAGCCAGTC-1	1672180	24472	182937	141415	1323356	427	0.038509462	4.027986867	3.039098567	0.094487666	0.091095923	0
GGACATTAGTCAAGCG-1	1105060	110959	109411	93064	791626	256	0.022994249	2.446703267	2.772892524	0.115093295	0.11677698	0
GGACGTCAGAACTTCC-1	2248020	19705	242742	204418	1781155	575	0.05185345	5.3748853	3.017651655	0.081179634	0.080278905	0
GGACGTCCACACGTGC-1	1778986	34586	193117	157425	1393858	450	0.040520955	4.2343649	3.057730831	0.090386625	0.089840611	0
GGAGCAAAGGTGCTTT-1	2379744	56090	255102	210141	1858411	600	0.054038866	5.555326967	3.000241494	0.084029062	0.08230655	0
GGAGCAACACGAGCTC-1	2606732	27342	282881	222454	2074055	670	0.060514957	6.244203067	3.493896287	0.097029229	0.097029229	1
GGATGTTAGCCAGGAT-1	2517512	38568	272946	207528	1998470	646	0.058273923	5.982906333	3.008021599	0.075374659	0.076221388	0
GGATGTTAGTGTACCT-1	2090596	63638	220121	186411	1620426	523	0.047151012	4.8946039	3.023555578	0.086974661	0.086974661	0
GGATTACAGCCACCTG-1	1378584	37754	148784	116319	1075727	347	0.031337621	3.302494733	3.001143295	0.099802176	0.10032042	0
GGATTACGTACTGTTG-1	1255810	23756	136323	101847	993884	321	0.028969399	3.0563242	3.073144399	0.10839763	0.10659828	0
GGATTACTCCAACAAC-1	2254992	26544	243061	203461	1781926	576	0.05191863	5.3652253	3.067935922	0.086126394	0.085369169	0
GGATTACTCTCGGTTC-1	387132	2855	41428	33730	309119	100	0.009041154	0.975458633	3.024146598	0.191868686	0.187923039	0
GGCAATTGTACAACGG-1	1403666	58903	146902	118508	1079353	349	0.031476651	3.319677767	2.991177724	0.098373906	0.098373906	0
GGCAATTGTGCAACCC-1	1687972	30092	181641	152512	1323727	428	0.03847926	4.025946	3.016164674	0.094471381	0.093736223	0
GGCAATTTCTTGGATG-1	1460768	28610	159964	121103	1151091	372	0.033585528	3.3322566	3.109663263	0.105848369	0.100069599	0
GGCCGATTCTGACGCG-1	784478	126886	70759	60443	526390	170	0.015264412	1.640160667	3.151735694	0.135468921	0.137234815	0
GGCGACTGTTACTGAC-1	1920364	31606	208282	171279	1509197	488	0.043994761	4.571335667	3.014604036	0.088309739	0.084742618	0
GGCGACTGTTCCGTCT-1	2109792	43688	222805	191908	1651391	533	0.047836834	4.920229467	2.981569733	0.08965188	0.090865277	0
GGCGACTGTTGGAACG-1	1468714	93733	147908	131536	1095537	354	0.031853542	3.355657167	3.1061781	0.104906329	0.100966602	0
GGCGACTTCCTTATTG-1	1070734	19102	116899	83166	851567	275	0.024846022	2.621863	3.110307273	0.117908791	0.112281924	0
GGCTCGACAACTACTG-1	1156426	18761	127850	89158	920657	297	0.026797514	2.821837833	3.13171896	0.131819228	0.133369181	1
GGCTCGACAATGGCTT-1	2281420	94077	241632	198034	1747677	565	0.05086476	5.263622633	2.826766227	0.083810565	0.084136408	0
GGCTCGACATACTGCA-1	1705694	59064	180713	152049	1313868	424	0.038208023	4.000563467	3.131593713	0.094236485	0.094116841	0
GGCTCGACATCATGGT-1	1755774	18913	190235	139595	1407031	455	0.04113467	4.277713067	3.213947277	0.12173873	0.12173873	1
GGCTGGTCAACCTGCG-1	1140684	62288	116943	100005	861448	278	0.025031366	2.661605433	3.059652836	0.10871609	0.108700018	0
GGCTGGTTCCTACGAA-1	1276010	18884	139108	107622	1010396	326	0.029384382	3.104276467	2.975456986	0.100221739	0.101691167	0
GGCTGGTTCTGTGGCG-1	1433216	95065	145589	124125	1068437	345	0.031060575	3.280702133	3.058879939	0.100027742	0.099960763	0
GGGAATGCATGATTGTC-1	1897772	31866	204762	164907	1496237	483	0.043589667	4.5239738	3.112996959	0.085446017	0.086981508	0
GGGAATGCATCATGGT-1	1890202	21823	204921	152512	1510946	488	0.044145652	4.5846845	3.097117243	0.087561752	0.087069945	0
GGGAATGGTGGTACAG-1	1391714	27533	148012	119988	1096181	354	0.031970575	3.370131367	3.014215181	0.097950606	0.09816503	0
GGGACCTCATCCATCC-1	1929474	37118	204642	174871	1512843	489	0.043898288	4.561367867	3.12774254	0.085555745	0.083796839	0
GGGACCTGTCCGGGTT-1	1934026	50292	207266	171814	1504654	486	0.043806415	4.5520625	3.04489451	0.089193446	0.088621007	0
GGGACCTTCATCGACA-1	1810676	59627	190027	162308	1398714	452	0.040749255	4.270926733	2.986481687	0.093322513	0.092294866	0

GGGAGATAGGCTAGCA-1	1464372	81476	148641	124443	1109812	359	0.032276755	3.396830567	3.011594038	0.103625357	0.101485172	0
GGGAGATCACAGACCC-1	1445274	16720	153282	137037	1138235	368	0.033112131	3.487409533	3.094999645	0.097551081	0.098875391	0
GGGAGATCAGGCTTG-1	1322744	61694	134038	109678	1017334	329	0.029634641	3.1273177	3.082320364	0.104040786	0.102598551	0
GGGAGATCATGCAGTT-1	1610696	32403	172213	131210	1274870	412	0.037112186	3.884437167	3.056647465	0.099132984	0.094966948	0
GGGCACTGTGCAACCC-1	1673214	15677	179753	158546	1319238	426	0.038371518	4.0164547	3.144706843	0.093349688	0.09247291	0
GGGCACTGTTCAAGGG-1	1698298	43519	181239	149795	1323745	428	0.038650285	4.055688	3.167953737	0.09228736	0.089680329	0
GGGCATCACGCTGAC-1	2290296	40688	245640	205613	1798355	581	0.052392253	5.420374567	2.986430419	0.082881467	0.079505152	0
GGGCATCGTCTCTATT-1	827990	29393	87000	65324	646273	209	0.018833598	1.9986004	3.031525806	0.127816069	0.125584586	0
GGGCATCTCGAACCG-1	1123326	56474	115030	99332	852490	275	0.024788732	2.640591633	2.976532489	0.110860214	0.110860214	0
GGGTCTGCATCGGTCG-1	1079282	189727	93001	85205	711349	230	0.02057078	2.1924806	3.005723105	0.122371709	0.119515638	0
GGGTCTGTCCACGATA-1	1569498	23022	169627	136331	1240518	401	0.036185353	3.796488767	3.130163983	0.091140917	0.09221101	0
GGGTTGCGTGTCGCTG-1	1373334	39325	144117	121052	1068840	345	0.031163606	3.288426133	3.04180665	0.100745967	0.101794964	0
GGTATTGAGGGTTCGA-1	2073240	38561	217346	185050	1632283	527	0.04768345	4.960465867	2.938348963	0.086203725	0.083793186	0
GGTATTGAGGTTCCTA-1	1882342	39405	199714	170079	1473144	476	0.04297718	4.484453533	3.151106375	0.089310983	0.088926564	0
GGTGAAGGTATTCGTG-1	1246628	34043	131859	101387	979339	316	0.028520823	3.0128921	3.044196698	0.108376062	0.10543602	0
GGTGCGTCACTAACTG-1	738116	18923	73369	64911	580913	188	0.016917567	1.8065352	2.915717441	0.135975037	0.134444291	0
GGTGCGTGTGTTTCAG-1	1834224	44300	190541	159274	1440109	465	0.042074139	4.405351667	3.03859213	0.090032357	0.089373655	0
GGTGTTAGTCAGTGGA-1	1852090	28677	197814	167148	1458451	471	0.042593949	4.453754367	2.955483903	0.087557538	0.087974715	0
GTAACGTAGGCAGTCA-1	2001772	72998	210064	171982	1546728	500	0.044934947	4.654238867	3.037518202	0.088666133	0.089078704	0
GTAACGTAGTCGTAT-1	1844214	14606	204022	149438	1476148	477	0.043127049	4.472399033	3.068077852	0.095639637	0.094890625	1
GTAACGTTCCCACAAA-1	1116246	10907	122530	92843	889966	287	0.025963503	2.729980533	3.003813406	0.102803297	0.104546331	0
GTAACTGAGCCGTCGT-1	1257814	30327	120442	113606	993439	321	0.028961561	3.066166533	3.025107752	0.108256055	0.105861299	0
GTAACTGCATAGGGCA-1	1642580	59903	170003	151810	1260864	407	0.036683539	3.843016233	2.901381245	0.095753029	0.09533948	0
GTAACTGGTAGATGCG-1	1634170	97216	167123	139436	1230395	397	0.035725585	3.743003933	3.124192013	0.095018641	0.096035094	0
GTAACTGGTTGAACTC-1	2035178	34486	221429	183040	1596223	516	0.046497263	4.831227333	3.080909252	0.087264088	0.085633263	0
GTAACTGTCGAATGTC-1	1770892	18470	194034	154829	1403559	453	0.04091448	4.2600948	3.144631621	0.091701272	0.090223346	0
GTACGTACACTGGCCA-1	1606312	40276	168200	146002	1251834	404	0.036486075	3.842740067	2.968607732	0.097376631	0.09504945	0
GTACGTAGTGCGCTTG-1	1263726	43782	132324	109365	978255	316	0.028513093	3.016493	3.091430114	0.103142521	0.102085807	0
GTACTCCGTCAGTTTG-1	1334892	36216	142369	114123	1042184	337	0.030393146	3.194262633	2.956359014	0.104837605	0.102125765	0
GTACTCCGTTGGTATC-1	2846454	21926	308439	252168	2263921	731	0.065921134	6.727206767	3.011988686	0.075101852	0.075586041	0
GTACTTAGAGTAATC-1	2239942	24738	240418	204154	1770632	572	0.051473221	5.326178367	2.985659187	0.089545725	0.087273998	0
GTACTTTCAGGCCGTT-1	1991260	43421	215430	169752	1562657	505	0.045575805	4.7349636	3.089619358	0.084394794	0.084875202	0
GTACTTTTCAGTACAC-1	2374966	20315	259198	218719	1876734	606	0.054634413	5.645589533	3.143260063	0.080331976	0.080864509	0
GTAGGCCACGTGGCT-1	2141392	62480	223524	190381	1665007	538	0.048486815	5.035866067	3.060673647	0.088463094	0.088252045	0
GTAGGCCGTGTAATGA-1	1065974	20763	111345	85220	848646	274	0.024685543	2.614044367	3.001604692	0.109364782	0.110188677	0
GTAGGCTCCTTGCAC-1	2451642	27215	259484	221394	1943549	628	0.056639835	5.840827867	3.074964127	0.078540254	0.07719403	0
GTAGGCTCGTGCTAA-1	389230	2101	38896	32986	315247	102	0.009232303	1.000579067	3.077161765	0.188946594	0.188946594	0
GTAGGCTCTCGAGCG-1	1020332	90127	95815	88987	745403	241	0.021690516	2.3167042	2.968234359	0.118037919	0.115256473	0
GTAGTCAGTCATTACG-1	1645666	40285	174907	144186	1286288	416	0.037559748	3.928586733	3.002614546	0.093161192	0.095377007	0
GTAGTCATCGAACCCG-1	1257550	118777	123058	104485	911230	294	0.026486752	2.8071866	3.039002635	0.105174573	0.103161903	0
GTATCTTAGGGAGTAA-1	1635648	14206	176172	137134	1308136	423	0.03822822	3.9960803	2.958546647	0.091547556	0.092472624	0
GTATCTTAGGGATTTA-1	1875084	24057	201154	160999	1488874	481	0.043457073	4.5264354	3.073600455	0.090817347	0.090647063	0
GTATCTTCATTTGTGG-1	1351348	31057	146734	115280	1058277	342	0.030847717	3.253622933	2.987731629	0.105623456	0.103280723	0
GTATCTTGTCGCTTCT-1	1770066	88836	174652	154685	1351893	437	0.039283815	4.1061602	3.193944388	0.097796014	0.096691525	0
GTATCTTGTCTCGGTG-1	774170	20818	83043	60777	609532	197	0.017853147	1.902446067	3.033195374	0.131273389	0.127993029	0
GTATTCTCATAGGTCT-1	2330920	67938	241992	203999	1816991	587	0.052491338	5.367131367	2.960373672	0.087367284	0.08780864	0
GTATTCTCATGCAGTT-1	1598848	25942	173238	132186	1267482	409	0.036961082	3.8502267	2.985837565	0.098873686	0.097289455	0
GTCAAGTAGGACCAGT-1	1476490	32005	145279	133466	1165740	377	0.034050153	3.573816867	2.949946729	0.096644917	0.095370895	0
GTCACAAAGTGAACAT-1	2453136	24743	269655	213325	1945413	628	0.056755193	5.8373346	3.096696052	0.077679055	0.076751249	0
GTCACAAGTCAGTGGA-1	2014432	21212	221349	180384	1591487	514	0.046483077	4.835501367	3.22683554	0.085288719	0.085502515	0
GTCACGGGTATTGAAG-1	1433324	26861	152281	122714	1131468	365	0.032958049	3.464893667	3.094852758	0.095394308	0.09775826	0
GTCACGGTCCACAGAT-1	1775292	22176	192278	144423	1416415	458	0.041329321	4.301526767	3.031854372	0.092895443	0.089721	0
GTCATTAGCAAAGCC-1	1511770	18383	158710	143595	1191082	385	0.03458358	3.6389753	3.115326974	0.09546827	0.094547089	0
GTCATTTGTCGCTTCT-1	1483466	35535	154085	131660	1162186	375	0.033861231	3.5679104	3.072048075	0.103044878	0.103044878	0
GTCATTTTCCCTTATA-1	899814	14154	98075	73006	714579	231	0.020837688	2.211096267	2.9220865	0.12011275	0.120782399	0
GTCCTCAGTTTCCTGC-1	3228202	30552	352233	282062	2563355	828	0.074799936	7.619784767	2.970329803	0.07108829	0.070112591	0
GTCCTCATCTAAGACC-1	1913362	23407	203198	174860	1511897	488	0.044006035	4.565550367	3.142264467	0.090899084	0.089991499	0
GTCGGGTCACAGCTGC-1	885556	25783	82545	79272	697956	225	0.020338418	2.1634484	3.060128649	0.124289448	0.124156093	0
GTCTCGTCAGGTTAAA-1	696708	32079	72905	54023	537701	174	0.015603735	1.662614067	3.037659073	0.139063466	0.138186057	0
GTCTCGTCATTCCGAA-1	1540622	18202	165333	134074	1223013	395	0.03564067	3.7383638	3.138160044	0.091928443	0.093000884	0
GTCTCGTGTACGTGCC-1	1861646	14481	188363	165302	1493500	482	0.043445378	4.522677467	3.132970561	0.089542069	0.088852261	0
GTCTCGTTCACACGGC-1	1198602	24020	129472	103753	941357	304	0.027268499	2.8834418	3.034634618	0.10723361	0.10700517	0
GTCTCGTTCATTGCTT-1	2116490	48303	226083	178114	1663990	538	0.048463044	5.0273037	3.078546007	0.086222639	0.084601785	0
GTCTTCGAGGTGCTAG-1	905402	8112	98515	77063	721712	233	0.021129132	2.238332867	3.04192025	0.122883327	0.122402448	0
GTCTTCGAGTGTTGAA-1	1694516	22335	182912	144561	1344708	434	0.039234418	4.103284367	3.037509058	0.094878938	0.092133989	0
GTCTTCGTCTGGTAGT-1	1632334	19253	176747	139880	1296454	419	0.037934373	3.9564849	3.104458318	0.094023561	0.094758434	0
GTGAAGGGTCCTCGGA-1	1633264	28194	173116	146827	1285127	415	0.037477955	3.924708267	3.022338393	0.090832477	0.091343888	0
GTGAAGGGTCTCGTCT-1	2115862	107611	214629	182046	1611576	521	0.046828531	4.8593122	3.112649541	0.08871914	0.088659693	0
GTGCAGCAGCTGAAAT-1	1792186	39896	194953	152301	1405036	454	0.040969284	4.273322033	2.976950178	0.091532119	0.088308962	0
GTGCAGCCAAAGTTAG-1	1039452	30172	110392	89865	809023	261	0.023610648	2.507332733	2.998707616	0.114358081	0.112205642	0
GTGCAGCGTCCTACCT-1	1299694	58541	118854	111451	1010848	327	0.029395232	3.098637767	3.094415357	0.103374494	0.103597224	0
GTGCATACACTCTTAT-1	1093226	21456	120444	89034	862292	279	0.025094953	2.653809033	2.975702435	0.11274585	0.108489259	0
GTGCGGTCAATCGTCA-1	1711268	52186	177364	151508	1330210	430	0.03874931	4.0702481	2.939159096	0.093034038	0.094529476	0
GTGCGGTCAGATCGAG-1	980174	38188	101130	84929	755927	244	0.0220431	2.3396341	3.136760633	0.128055952	0.124571636	0
GTGCGGTGTACTCACA-1	1841358	25615	196108	167314	1452321	469	0.0423378	4.427631033	3.128866126	0.086874439	0.086366293	0
GTGCTTCGTGATACCT-1	2252352	69269	230266	199143	1753674	566	0.051013328	5.282086033	3.224049617	0.101951109	0.100893579	1
GTGGGTCCACAGAGCA-1	1481810	74488	150214	130563	1126545	364	0.032759416	3.452152367	3.016680988	0.099946927	0.098410379	0
GTGGGTCGTACCACTA-1	1341734	12203	142424	114857	1072250	346	0.03121292	3.2835632	3.063260392	0.100444938	0.101593609	0
GTGGGTCGTTGGAACG-1	1683602	94124	168932	144731	1275815	412	0.037139408	3.908941167	3.097200721	0.092640204	0.092640204	0
GTGGGTCTCCGCTTGT-1	1747864	54716	181506	151849	1359793	439	0.039680098	4.145982733	3.073307616	0.091852387	0.093497703	0
GTGGGTCTCCTAGACA-1	1730908	51546	181447	145675	1352240	437	0.039379205	4.118041333	3.044293862	0.09322998	0.092465077	0
GTGTGCGAGAAGGTTT-1	1837266	71453	191840	152393	1421580	459	0.041434519	4.317740167	3.005703773	0.093993735	0.091291511	0
GTGTGCGAGCGCGATA-1	1549748	26625	160136	136678	1226309	396	0.035800036	3.750629867	3.056336527	0.100554073	0.098854116	0
GTGTGCGAGGCTCTCG-1	1552632	61860	160532	138087	1192153	385	0.034708134	3.645746167	3.119507934	0.093540976	0.093540976	0
GTGTGCGGTCGCTTCT-1	607086	20047	46048	55563	485428	157	0.014076292	1.516978167	3.024836518	0.141466861	0.142390868	0
GTTAAGCAGTGTTTGC-1	1961858	41027	210453	177675	1532703	495	0.044622561	4.6521443	3.048411154	0.085016591	0.084837747	0
GTTAAGCCAGATATCC-1	1880652	53068	198457	171915	1457212	471	0.042061461	4.352649667	3.09974995	0.090632679	0.091308253	0
GTTAAGCTCCACTTAT-1	1114700	13744	123878	92192	884886	286	0.025766818	2.715397	3.112393794	0.111342831	0.110824099	0
GTTAAGCTCTGTCGAA-1	1699638	25331	184573	151630	1338104	432	0.039040787	4.083055567	3.080596018	0.096071151	0.09373875	0
GTTACAGAGTACACCT-1	2109174	43594	227138	192571	1645871	532	0.047926819	4.9692936	3.036850743	0.086193198	0.084861352	0
GTTACAGTGAGGTGAG-1	2256030	32381	243186	196696	1783767	576	0.052117528	5.403341767	3.081913397	0.081668922	0.082023423	0
GTTCATTGTCAAGTTC-1	1998780	50666	213268	181905	1552941	502	0.044866572	4.620334567	3.113578563	0.09389273	0.09389273	1
GTTCATTTCGAGTATC-1	3383148	24227	369239	295786	2693896	870	0.078524122	7.930237867	3.032839894	0.072799619	0.072260333	0
GTTCATTTCGTAGGGA-1	1758616	17675	188914	151523	1400504	452	0.040978257	4.2880114	3.024010457	0.093978705	0.092574819	0

GTTCATTTCTCTTCCT-1	2500448	86148	264900	224229	1925171	622	0.056041184	5.783205433	3.054840062	0.079472687	0.079929142	0
GTTCGGGTCAACAGTC-1	1619528	15864	177436	135603	1290625	417	0.037657843	3.933121167	3.114955674	0.090089994	0.088387205	0
GTTCTCGCAACCACG-1	1844272	82054	191909	161299	1409010	455	0.041003255	4.291125533	3.035637164	0.087873578	0.086646599	0
GTTCTCGCACGCACCA-1	2383140	63509	249735	213140	1856756	600	0.05410296	5.606783233	3.044880357	0.080431506	0.077218934	0
GTTCTCGCAGTGCTCG-1	1445760	43722	151910	129037	1121091	362	0.032537244	3.4317832	3.038235607	0.102041796	0.102041796	0
GTTCTCGGTCATGTTG-1	1426946	21829	154751	113578	1136788	367	0.033140846	3.475283267	3.140984305	0.100905367	0.100045999	0
GTTCTCGTCATGACCA-1	1926700	34403	204839	176308	1511150	488	0.044017541	4.585549333	3.066047787	0.08643448	0.087836924	0
GTTTCTAAGGTGATTA-1	1474894	14792	160824	126010	1173268	379	0.03424198	3.591324633	3.137968256	0.102475823	0.101351876	0
GTTTCTAAGTGGGATC-1	2129706	31555	228021	196455	1673675	541	0.048740485	5.046120867	3.139892582	0.086724879	0.085393309	0
GTTTCTAGTCCGGTGT-1	2294738	38806	248070	208924	1798938	581	0.052448355	5.407919867	3.030339625	0.082791774	0.080337898	0
GTTTCTATCAGATTCG-1	1549146	105927	156771	131347	1155101	373	0.033524796	3.5201264	3.133513245	0.100205931	0.10195152	0
TAAACCGAGGCTAGAC-1	1606784	59255	172177	138724	1236628	399	0.03594455	3.772815167	2.786122119	0.100407888	0.095219047	0
TAAACCGAGGTAGCCA-1	1883616	49185	201627	168819	1463985	473	0.042638881	4.459989833	3.038975707	0.088064812	0.089010031	0
TAAACCGTCCAAGGGA-1	2052240	21689	222509	180116	1627926	526	0.047570188	4.944835367	2.973779552	0.085991536	0.082768288	0
TAAGAGACAGCGTCAC-1	2021510	30838	207135	185908	1597629	516	0.046612458	4.8464496	3.114361211	0.087556081	0.085752913	0
TAAGAGACATCTCGTC-1	1438314	27253	154199	123417	1133445	366	0.033001567	3.471796067	3.038906609	0.102228963	0.098373614	0
TAAGAGAGTGTGTTCA-1	1709262	48093	177023	152680	1331466	430	0.03885601	4.071347267	3.046895533	0.096601904	0.093608064	0
TAAGAGATCCAGGTTA-1	1870170	18035	202464	158301	1491370	482	0.043481416	4.532251567	3.013277543	0.092614958	0.088445214	0
TAAGCGTTCATTGGAC-1	2005238	54013	213631	176753	1560841	504	0.045468	4.7339861	3.055968055	0.084665875	0.083192005	0
TAAGTGCAGGGATTCG-1	1838360	112233	183584	161008	1381535	446	0.040140794	4.197646933	3.026109067	0.091156818	0.089988679	0
TAAGTGCAGGTAAGTT-1	1846748	54539	194761	153129	1444319	467	0.042002948	4.360207933	3.067755798	0.089554369	0.091194077	0
TAAGTGCTCGGGTCAC-1	2548824	33163	271000	227126	2017535	652	0.058840149	6.065913733	3.097083102	0.08068748	0.08098319	0
TACACGACAAGCAAGC-1	2457252	51836	265080	215911	1924425	622	0.056110923	5.791251167	3.153943406	0.07861523	0.0795881	0
TACACGACACTAGGCC-1	1840308	87270	191647	170053	1391338	449	0.040438959	4.237664967	3.072875241	0.089145616	0.089145616	0
TACACGATCCGACCAG-1	1994292	59666	212915	177214	1544497	499	0.045021029	4.688506733	3.046838258	0.081193008	0.082048943	0
TACACGATCCGTTCAC-1	2617154	29936	283810	235621	2067787	668	0.060311595	6.189951833	2.953940264	0.075792921	0.075739094	0
TACAGTGAGTCCCGAC-1	1573904	59124	165585	137046	1212149	392	0.035265247	3.698016633	2.903111926	0.095695339	0.093762183	0
TACAGTGGTCAATTCG-1	1377138	127317	133646	118511	997664	322	0.028914494	3.0519058	3.119232818	0.102008863	0.101485807	0
TACAGTGGTCTAACGT-1	1992352	36011	210619	173128	1572594	508	0.045860036	4.769692033	3.036585886	0.084667341	0.08483458	0
TACCTATAGTAGGTGC-1	1772926	43195	185705	156623	1387403	448	0.040257508	4.212792533	3.141638492	0.093183879	0.090590427	0
TACCTATGTAAACAGT-1	1884048	16806	205766	172576	1488900	481	0.043443777	4.5236024	3.086331804	0.093790943	0.092250193	0
TACCTATGTCAGTTTG-1	1471908	29892	159045	125828	1157143	374	0.033721213	3.546665267	3.021670111	0.095727009	0.095727009	0
TACCTATGTTGAACAA-1	1627134	21265	177394	140625	1287850	416	0.037556918	3.933166733	3.011619731	0.097503679	0.09541239	0
TACCTTAAGACTGGCA-1	1965718	20795	212826	180607	1551490	501	0.045212203	4.710638433	2.91538877	0.086503626	0.086790213	0
TACCTTAAGGAGCGAG-1	1813566	45494	188916	169000	1410156	456	0.04113946	4.285842167	3.034252024	0.090067254	0.088637981	0
TACCTTAAGTGAATTG-1	1447110	19203	157720	119833	1150354	372	0.033577584	3.525355633	3.130051501	0.102142266	0.10000367	0
TACCTTACATTCCGAA-1	1798922	17481	198853	154623	1427965	461	0.041605488	4.3375444	2.957831197	0.093500743	0.08766323	0
TACCTTATCACTCATT-1	1841270	18579	202226	155135	1465330	473	0.042781928	4.432972867	2.957391953	0.088339479	0.08474174	0
TACGGATAGCTGAACG-1	1543264	89785	156329	134002	1163148	376	0.033824508	3.561573533	2.972797523	0.102887576	0.100850955	0
TACGGATAGTGTTAGA-1	1138328	12417	121299	99383	905229	292	0.026508456	2.806755833	2.960549677	0.109238983	0.110520069	0
TACGGATCAACACCGC-1	1280980	23555	132893	119139	1005393	325	0.02924133	3.092972833	2.979622856	0.104494799	0.104209962	0
TACGGATCAGAGGCAT-1	2658116	37968	284234	235997	2099917	678	0.06131188	6.292786933	3.037294613	0.076025963	0.075843835	0
TACGGATCATCCGTTC-1	2062042	34193	214906	180673	1632270	527	0.047324493	4.8944453	3.076870047	0.10770914	0.103634728	1
TACGGATGTGATGTTC-1	2629786	57253	279746	229188	2063599	667	0.05976055	6.059645633	3.129416864	0.078813164	0.080277963	0
TACGGATTAAGCCGCC-1	1825626	16398	192748	168876	1447604	468	0.042191896	4.408129233	3.106567684	0.090289182	0.092089561	0
TACGGATTCACACGGC-1	1225208	76669	124422	106882	917235	296	0.026598068	2.8251283	2.98828752	0.112535635	0.10789928	0
TACGGGCAGGTAAGTT-1	1748176	40338	184325	150730	1372783	443	0.039992115	4.161671633	3.14508556	0.091692189	0.090903422	0
TACGGGCGTATCTCTT-1	1818566	91090	186033	156396	1385047	447	0.040334224	4.194349767	3.059606506	0.093338711	0.09235289	0
TACGGTAAGAACAATC-1	2395126	40184	253628	216884	1884430	609	0.054874113	5.6413592	3.076477227	0.085404633	0.084261454	0
TACGGTAAGTTTCCTT-1	2008894	34502	214339	184723	1575330	509	0.045894132	4.765208333	2.91291624	0.090336247	0.089275258	0
TACGGTAGTGCTTTCC-1	2188622	90951	223078	199169	1675424	541	0.048630725	5.019006167	3.115155648	0.087836053	0.085980937	0
TACGGTATCTCGTGGG-1	2254158	32351	238433	200306	1783068	576	0.052069543	5.391689933	3.046808964	0.080859965	0.081305074	0
TACTCATAGAACAATC-1	1908910	21588	203637	174814	1508871	487	0.043997999	4.566169267	3.111281581	0.08930226	0.089589834	0
TACTCATAGAAGGTGA-1	2744076	18788	297741	219775	2207772	713	0.064471205	6.616008167	2.725081905	0.110486014	0.111082072	1
TACTCATAGGCATGGT-1	1899894	12973	207588	164357	1514976	489	0.044270956	4.593671667	3.061652351	0.09136594	0.086192342	0
TACTCATCAACGGCTC-1	1529160	40457	161249	147802	1179652	381	0.034354423	3.613087533	3.018038235	0.09930974	0.097187797	0
TACTCGCAGAAGGTGA-1	1807448	15870	198431	158835	1434312	463	0.04188882	4.381434533	3.055011261	0.092710832	0.090939921	0
TACTCGCAGGACGAAA-1	1696788	11323	187001	142709	1355755	438	0.039641256	4.1196104	3.253370192	0.130680165	0.130680165	1
TACTCGCCATGATGCT-1	2694362	67691	286408	237647	2102616	679	0.060945835	6.1905062	2.927095619	0.082892106	0.082452461	0
TACTCGCTCCACGATA-1	1660108	9588	184221	138339	1327960	429	0.038806552	4.053344067	2.973555234	0.096613646	0.091560813	0
TACTTGTAGTGGGTAC-1	2342126	50090	242355	206085	1843596	596	0.053615955	5.5212529	3.072042957	0.084584144	0.082268447	0
TACTTGTCAGACACAG-1	1152354	19407	124664	100750	907533	293	0.026414836	2.7858613	3.098120389	0.110917178	0.109883986	0
TACTTGTGTAGGTTTC-1	2237696	60061	225643	193912	1758080	568	0.0510299	5.245183733	3.0954151	0.093755519	0.092766627	1
TACTTGTGTTCGGTGC-1	1586448	103650	159654	138337	1184807	383	0.034314209	3.6003808	3.020198577	0.102745888	0.101117904	0
TACTTGTTCACCGGTG-1	1472560	24510	160367	122798	1164885	376	0.033907372	3.5579543	3.18585045	0.096535558	0.095476795	0
TAGACCAAGCGGCTTC-1	2639720	51525	286484	223094	2078617	671	0.060585722	6.2218663	3.964392388	0.132129298	0.132129298	1
TAGACCAAGTCGATAA-1	1448302	12233	159938	118882	1157249	374	0.03375581	3.535116533	3.123943522	0.101020814	0.098925996	0
TAGACCACATCCACGG-1	1388392	40812	149503	120884	1077193	348	0.031385537	3.308094767	3.035295538	0.100293418	0.09941708	0
TAGACCACATGATGCT-1	2362116	63280	254571	209409	1834856	593	0.053045659	5.3957752	3.142151778	0.08738112	0.086219694	0
TAGACCATCATCAGCA-1	1735454	35589	186189	151578	1362098	440	0.039643078	4.1472061	3.017394084	0.094260041	0.091597755	0
TAGAGCTAGCTTTCAG-1	1671676	23320	178206	154165	1315985	425	0.038448005	4.016525633	3.133997557	0.092198778	0.090791697	0
TAGAGCTAGGCTAGGT-1	1522574	17114	164059	126546	1214855	392	0.0354429	3.709278967	3.075013676	0.091171922	0.091415476	0
TAGAGCTCACGTCGGT-1	1873838	53519	190033	167370	1462916	473	0.042637764	4.452796133	3.025882336	0.09663332	0.09663332	1
TAGAGCTCATTGGTCA-1	1798664	52476	186267	160402	1399519	452	0.040591388	4.227031267	3.04577002	0.091616179	0.090952221	0
TAGAGCTTCTCAGATG-1	1066822	16807	115506	85641	848868	274	0.024754702	2.615024067	3.084252986	0.118236248	0.111015305	0
TAGCCGGAGTCGTGTT-1	1719226	35853	165496	144869	1373008	444	0.039965106	4.166606	3.086648676	0.093591441	0.092444112	0
TAGCCGGCAACCTCAA-1	1699768	14337	185035	151693	1348703	436	0.039355208	4.099660567	2.997223603	0.094315456	0.09076989	0
TAGCCGGCACCACACG-1	1613736	87616	166716	138992	1220412	394	0.035466549	3.7289898	3.14193695	0.097713836	0.097675164	0
TAGCCGGCACGCTGAC-1	2149056	31516	233674	198499	1685367	544	0.049138322	5.098764367	3.077626447	0.080284416	0.080484712	0
TAGCCGGGTTCCACAA-1	1720700	14396	190206	144618	1371480	443	0.039981265	4.171733933	3.121113534	0.092645728	0.092968793	0
TAGCCGGTCAGCGGCT-1	1652736	16042	180987	153479	1302228	421	0.03794329	3.977796667	3.038023057	0.093708298	0.092433383	0
TAGGCATAGCTAACA-1	1880108	43011	201242	168380	1467475	474	0.042739127	4.472179133	3.08244354	0.091694569	0.090843795	0
TAGGCATAGTAGGTGC-1	1831152	92209	187097	160619	1391227	449	0.040388379	4.221929433	2.938904674	0.092317314	0.093281819	0
TAGGCATAGTGAACAT-1	2297936	34347	247848	205435	1810306	585	0.052880005	5.464162867	3.01296395	0.081594676	0.081895536	0
TAGGCATCAATCGTCA-1	1677626	46443	176817	150514	1303852	421	0.037974718	3.980201733	3.142045172	0.090782586	0.09034173	0
TAGGCATGTCGGCATC-1	2017848	37585	213233	186154	1580876	511	0.046125569	4.8110013	3.015569619	0.08840677	0.088232286	0
TAGGCATGTTCAGTGC-1	2361030	67512	248871	209321	1835326	593	0.053313917	5.4729078	3.049120938	0.083683044	0.0838148	0
TAGTGGTCAAGTGTTC-1	2377520	66659	247470	209144	1854247	599	0.053917522	5.554775167	3.076293465	0.082902497	0.081753669	0
TAGTGGTCACACACGC-1	1573220	23809	169762	143012	1236637	399	0.036001704	3.7807721	3.010343921	0.097535314	0.092951225	0
TAGTGGTGTGTGACAG-1	1471092	26684	157461	125412	1161535	375	0.033869839	3.560299633	3.002350635	0.100299748	0.098285711	0
TAGTTGGAGAATGGGA-1	2231870	17582	242619	184770	1786899	577	0.052227332	5.388131367	3.448329553	0.12445789	0.12445789	1
TAGTTGGCATGAGAAT-1	2274300	27607	247737	194937	1804019	583	0.052701432	5.4342	2.961995823	0.087861884	0.083238694	0
TAGTTGGCATGGCACC-1	2029112	37042	217042	184565	1590463	514	0.046349106	4.8279328	3.038451156	0.085264114	0.086804847	0
TAGTTGGTCCTGATTT-1	2128642	77062	224142	176803	1650635	533	0.048034296	4.967066	2.841439765	0.08779661	0.08779661	0

TAGTTGGTCGAACCCG-1	978608	58920	97952	87306	734430	237	0.021372209	2.285116233	3.120054812	0.123919155	0.123904924	0
TATCAGGAGTCGGTAT-1	1895928	20292	204965	156337	1514334	489	0.044208812	4.579943567	3.068984375	0.088408242	0.085964452	0
TATCAGGGTGACCTGC-1	2035436	24126	229256	178225	1603829	518	0.046758622	4.853525367	3.12536936	0.102896559	0.100725232	1
TATCAGGGTTCGAGCC-1	1194712	78532	117765	107548	890867	288	0.02588351	2.742308967	3.020123125	0.111574242	0.108808232	0
TATCAGGGTTCGTCAA-1	2132816	24665	229122	188592	1690437	546	0.049316887	5.120336267	2.989728655	0.087162189	0.08686263	0
TATCAGGTCTGGTAGT-1	1484660	20849	159410	129624	1174777	379	0.034359066	3.600746067	3.061210141	0.0978681	0.098157159	0
TATCAGGTCTTCTTGA-1	1070870	12394	115449	94067	848960	274	0.0247734	2.628853433	3.114960898	0.112447556	0.112189801	0
TATCTCAAGACTGGGT-1	1943192	18108	211125	166154	1547805	500	0.045228185	4.700175433	3.026383837	0.088079902	0.088749325	0
TATCTCAGTAGTGGCA-1	1987226	47552	210026	176405	1553243	502	0.045205922	4.706531667	3.03515428	0.086128461	0.085422059	0
TATCTCAGTCCGAAGA-1	1332600	16196	144456	119894	1052054	340	0.03068444	3.2394976	3.208025283	0.102858496	0.100544042	0
TATCTCAGTGACCCGT-1	2399688	35833	255230	220159	1888466	610	0.055107937	5.696481633	3.106650944	0.079152825	0.079616981	0
TATGCCCAGGGCTTGA-1	1193432	8955	128593	108072	947812	306	0.027686248	2.9351697	3.145415936	0.104360195	0.103989722	0
TATGCCCTCTAGAACC-1	2119420	57842	221612	193340	1646626	532	0.047852412	4.951597333	3.033173504	0.087337155	0.08773609	0
TATTACCAGCCAGGAT-1	2357222	31599	254160	201168	1870295	604	0.054578677	5.602899433	3.215561034	0.07885708	0.07885708	0
TATTACCGTGCTATTG-1	1068362	14236	116007	81020	857099	277	0.025011776	2.639855933	3.036052349	0.113729029	0.114407409	0
TCAACGAAGAGCAATT-1	1514202	40925	163230	126395	1183652	382	0.03452396	3.6203681	3.006697443	0.09608982	0.098813516	0
TCAACGAAGCTGCACC-1	2731640	55908	295631	239785	2140316	691	0.062323655	6.381016233	3.261517586	0.101217011	0.101217011	1
TCAACGAAGGCTGCTC-1	2375976	35402	259367	212945	1868262	604	0.054500182	5.639611933	3.142790149	0.078940415	0.077403796	0
TCAACGATCTTTCGCG-1	1006886	87701	99167	86887	733131	237	0.021293752	2.2659808	3.000205948	0.124325758	0.122997971	0
TCACAAGCATTTCCAT-1	2428758	33245	268139	218792	1908582	617	0.055739015	5.735632467	3.100528048	0.079620771	0.079616424	0
TCACGAAGTCAAACTC-1	1883808	59643	200888	170401	1452876	469	0.042276497	4.414824933	3.03380994	0.088892474	0.090075376	0
TCACGAAGTGTCTAAC-1	2385080	20024	267184	204313	1893559	612	0.05527542	5.6887297	3.027020308	0.080188933	0.079646573	0
TCAGATGAGAGCCCAA-1	1782712	12819	193261	160107	1416525	458	0.041356747	4.325691467	3.110492292	0.090396302	0.089239886	0
TCAGATGTCCGATACA-1	2234366	32645	242764	200009	1758948	568	0.051348646	5.3113818	3.060627371	0.083400134	0.082244677	0
TCAGCAAGTAGATGCG-1	1717858	69067	180703	149643	1318445	426	0.038298375	4.013314867	3.17336828	0.09204946	0.09200351	0
TCAGCAAGTGTTTCAG-1	2142000	33022	234487	188049	1686442	545	0.049281704	5.1203846	3.008899274	0.080966075	0.082010651	0
TCAGCAAGTTGGTGAG-1	1805496	23764	196511	154542	1430679	462	0.041852428	4.365999	3.049341498	0.084281508	0.08582369	0
TCAGCTCAGTTGTCGT-1	2409122	39697	259176	217743	1892506	611	0.055219606	5.701687033	3.022730663	0.078378422	0.078378422	0
TCAGGATTCAGCAGCC-1	1890788	73172	198775	163177	1455664	470	0.042325748	4.4177091	3.23887997	0.112427382	0.111311027	1
TCAGGATTCGGGTCAC-1	2536316	35436	267269	229468	2004143	647	0.058426383	6.009323133	2.941340703	0.077788918	0.077788918	0
TCAGGTACATAGACAA-1	1369112	11427	151520	116338	1089827	352	0.03180681	3.335566733	3.095461292	0.104877998	0.101074052	0
TCAGGTACATGTAGCT-1	1784354	87745	185048	153143	1358418	439	0.039373614	4.099629967	3.119308615	0.091695668	0.092316008	0
TCAGGTATCAAGTGCT-1	2482604	74659	261254	221828	1924863	622	0.056058553	5.784886067	3.167909918	0.079709086	0.079301662	0
TCATTACAGCCAGTTT-1	1449460	59268	154061	119913	1116218	361	0.032456195	3.400645067	3.072161068	0.099878446	0.100094104	0
TCATTACCACGACCC-1	1703842	60908	177942	154422	1310570	423	0.038107208	3.9986053	3.01047801	0.093693184	0.094433549	0
TCATTACCATTCAGTG-1	1093652	11949	121086	85014	875603	283	0.025496159	2.674225433	2.993075825	0.115836704	0.110648578	0
TCATTACTCTCCACAC-1	2153296	53154	229852	189234	1681056	543	0.048962721	5.075311633	3.059659616	0.082729944	0.083647912	0
TCATTTGAGTAGCCGA-1	1970502	13022	212363	182168	1562949	505	0.045572831	4.751489233	3.107867371	0.089203524	0.089203524	0
TCATTTGAGTCTCGTA-1	1454064	13237	158614	119732	1162481	376	0.033913925	3.557729567	3.079127496	0.104366262	0.099789953	0
TCCACACCAAGCAAGC-1	1987106	41680	213393	181299	1550734	501	0.045166804	4.695992267	2.93807359	0.086718991	0.08713187	0
TCCACACGTGCTCGAC-1	1279132	49309	133570	120258	975995	315	0.028389809	3.0005559	3.06282187	0.109443716	0.103326904	0
TCCACACTCGCAACGC-1	1622502	27952	174283	146153	1274114	412	0.037075865	3.886508867	3.168780058	0.089282531	0.091521986	0
TCCCGATAGAATCGTA-1	1714450	11802	186425	147506	1368717	442	0.039944936	4.179425267	3.309900273	0.088813272	0.088697814	0
TCCCGATAGTGCGATG-1	1560746	16818	170267	129241	1244420	402	0.036354768	3.811432933	3.140919811	0.092670414	0.093716336	0
TCCCGATGTTAAGTAG-1	1467288	14425	161276	117597	1173990	379	0.034368288	3.601870367	3.107809781	0.10321635	0.097594892	0
TCGAGGCAGATCCTGT-1	2022518	26861	214784	175609	1605264	519	0.046851795	4.868547367	3.020345967	0.08244857	0.082337718	0
TCGAGGCCACCGAACC-1	1251800	57789	119127	110570	964314	312	0.028023378	2.963238567	2.847185729	0.107184538	0.106051786	0
TCGAGGCCAGTGAAAT-1	1564870	31340	161170	130508	1241852	401	0.036270595	3.787356767	2.995887346	0.094687357	0.092600434	0
TCGAGGCGTAAGAAGG-1	831570	14085	84042	69121	664322	215	0.019427947	2.073578667	2.511854971	0.120572043	0.121557928	1
TCGCGAGAGAGTTGGC-1	1757016	40278	170395	156789	1389554	449	0.040552641	4.247035667	2.960811473	0.092739676	0.091218985	0
TCGCGAGGTGATCCTA-1	1704922	29476	169892	151277	1354277	437	0.039528013	4.1386832	3.033847268	0.093346152	0.093369258	0
TCGCGAGGTTCAAGAA-1	918630	13371	91959	78718	734582	237	0.021331565	2.2744739	3.031315685	0.117110944	0.116227317	0
TCGCGAGTCCGCTTGT-1	1499842	21251	157210	130860	1190521	385	0.034740065	3.646671833	3.048385379	0.095924028	0.096760376	0
TCGCGAGTCTACGCG-1	869502	33313	83893	76510	675786	218	0.019629586	2.0963251	2.958857029	0.123615223	0.125576355	0
TCGCGTTAGACTGGGT-1	1524144	18854	150819	126856	1227615	397	0.03574705	3.74515	3.123850865	0.092588765	0.094887985	0
TCGCGTTAGGACGAAA-1	1245744	13566	120686	108300	1003192	324	0.029176966	3.078576567	3.110922484	0.102602023	0.104752288	0
TCGCGTTCAACAACTC-1	1240408	21638	118648	111291	988831	319	0.028765721	3.0411341	3.041434659	0.103263449	0.106729534	0
TCGCGTTGTCGCGAAA-1	1112142	9546	123767	98794	880035	284	0.025655342	2.7211949	3.114356942	0.114966438	0.110097885	0
TCGCGTTGTCTACGC-1	779442	11718	73885	71662	622177	201	0.018085483	1.938495933	2.96523937	0.127377853	0.128619531	0
TCGCGTTTCCGTATTT-1	809016	33189	78846	59682	637299	206	0.018570187	1.966083267	3.564289214	0.168044553	0.170914663	1
TCGGGACAGTCAAGGC-1	1443188	68931	141784	125941	1106532	357	0.032192986	3.3986331	3.106600283	0.100921843	0.100921843	0
TCGGGACGTTTCCATT-1	1709586	32267	177054	148644	1351621	437	0.039403376	4.115725867	3.094161771	0.090570369	0.090576515	0
TCGGGACTCGTAAGGG-1	815546	15420	81958	68581	649587	210	0.019017113	2.020077967	3.038223118	0.129631172	0.124338115	0
TCGGTAAGTATACACC-1	1902158	33803	196881	169280	1502194	485	0.043679214	4.553322867	3.015438063	0.091583938	0.090325061	0
TCGGTAATCAGAAACA-1	1452842	30640	148145	121939	1152118	372	0.03362408	3.535642933	3.662500089	0.100260321	0.100260321	0
TCGTACCCAATCCATG-1	703032	15761	65858	59422	561991	182	0.016336549	1.751279967	3.024922428	0.134192991	0.13902432	0
TCGTACCCACGTTTAG-1	467408	10349	43615	39923	373521	121	0.010898856	1.1791157	3.022875399	0.165467634	0.158921586	0
TCGTACCGTGTGACAG-1	713804	12504	67684	61364	572252	185	0.01671725	1.787778	3.106399898	0.135132332	0.134120751	0
TCGTAGACAATCCGTA-1	757554	7956	74918	67610	607070	196	0.017674093	1.8922723	3.091573895	0.132244439	0.130803199	0
TCGTAGAGTGACTGAG-1	1249064	18577	124440	102268	1003779	324	0.02925285	3.0885475	3.00949837	0.101652038	0.103444751	0
TCTATTGCAACGAAAT-1	1550156	27309	166373	136574	1219300	394	0.035554697	3.725597367	3.170744178	0.092663719	0.094544823	0
TCTATTGCAGAGATCG-1	1491700	63832	152949	131109	1143810	369	0.033250082	3.506239733	3.08438432	0.100770089	0.099524503	0
TCTATTGCATGCGTGC-1	1463972	46563	152919	133660	1130830	365	0.032846115	3.448698733	3.09257181	0.099286243	0.097966923	0
TCTATTGGTATTCGCA-1	1485748	41330	154350	130428	1159640	375	0.03373445	3.5473501	3.050445947	0.09892392	0.099207901	0
TCTATTGGTTGGCGTC-1	1309892	56782	129539	118581	1004990	325	0.029286836	3.1010971	3.02418341	0.102263945	0.101759004	0
TCTATTGTCAGCCGA-1	1435714	8394	154295	127456	1145569	370	0.033464417	3.518868467	3.081762257	0.095578972	0.097135823	0
TCTATTGTCATCGACA-1	1691866	32828	180721	151629	1326688	429	0.038648951	4.040234567	2.977955172	0.097095003	0.093814055	0
TCTCATAAGCAGCCCT-1	1914610	45999	201821	172317	1494473	483	0.04365011	4.560044267	3.102080389	0.090590517	0.090590517	0
TCTCATAAGGGATCTG-1	1826846	32333	193085	155081	1446347	467	0.042219191	4.401677933	3.057160925	0.091793597	0.091866872	0
TCTCATAGTGCACACC-1	1922910	44922	202785	170730	1504473	486	0.043782983	4.5588568	3.094669764	0.090290402	0.08894826	0
TCTCATATCTAAGACC-1	1919434	36747	201858	179158	1501671	485	0.04354388	4.488891867	2.964530795	0.095792709	0.090121616	0
TCTCATATCTGTTGTT-1	1915492	21120	210213	158209	1525950	493	0.044457448	4.609705933	2.967072547	0.091889034	0.091232638	0
TCTCTAAAGTAAGTAC-1	3199414	26317	349989	267759	2555349	825	0.07459488	7.625192267	3.142392339	0.065123412	0.064612121	0
TCTCTAAGTAGGTTTC-1	2811158	35105	299375	259192	2217486	716	0.064631517	6.631572033	3.058591613	0.074405561	0.073218337	0
TCTGAGAAGATCTGCT-1	1614660	46963	170188	147851	1249658	404	0.036439563	3.806809933	3.045866803	0.101752925	0.097130137	0
TCTGGAACACGTGGCT-1	2179820	90735	225571	191672	1671842	540	0.048656105	5.0534868	3.045488129	0.088527348	0.086383276	0
TCTGGAATCAGCGGCT-1	2129686	79186	222249	189823	1638428	529	0.047715771	4.969048533	3.110234878	0.088620685	0.087910695	0
TCTTCGGAGAGGGCTT-1	2299512	70552	243777	203395	1781788	576	0.051949805	5.374983233	3.019576077	0.087564576	0.084500925	0
TCTTCGGAGCCAGGAT-1	2313476	33011	252534	193239	1834692	593	0.053450381	5.507792533	3.000838247	0.083395649	0.081630146	0
TCTTCGGAGCTATGCT-1	2461126	54716	265431	219865	1921114	621	0.055784619	5.716179633	3.167027907	0.079664064	0.079664064	0
TCTTCGGGTCGGATGA-1	2103426	14088	229373	174624	1685341	544	0.04918171	5.1139456	3.048181902	0.084325521	0.084325521	0
TCTTTCCCACAGCTAT-1	1908746	21087	211015	162260	1514384	489	0.044236023	4.601227967	3.108020198	0.088522896	0.08551334	0
TCTTTCCCACTAGGCC-1	1827330	75098	192428	160970	1398834	452	0.04064839	4.237020033	3.012111439	0.088941913	0.089117618	0
TCTTTCCGTGGTGAGT-1	2129564	28226	231447	187834	1682057	543	0.049141497	5.082704567	2.974179204	0.086624963	0.085923215	0

TGAAAGAAGCATGAGC-1	2855072	53304	309220	240430	2252118	728	0.06547785	6.639474967	1.844582972	0.123332143	0.123332143	1
TGAAAGAAGGTACTCT-1	2405202	78936	253646	214812	1857808	600	0.053822853	5.519801067	3.147028739	0.083862208	0.083807081	0
TGAAAGACACCGTCGA-1	1794500	29796	189658	159050	1419996	459	0.041365309	4.3137469	3.530497381	0.129582722	0.128212542	1
TGACAACAGCGAACTG-1	1445430	37622	155968	124444	1127396	364	0.0328747	3.4672824	3.037330341	0.097228975	0.09649809	0
TGACAACAGCTCCTTC-1	2416094	54856	260468	226412	1874358	605	0.054573947	5.614417167	3.071969024	0.083393345	0.079977711	0
TGACGGCAGTTACGGG-1	1633552	54441	175684	139920	1263507	408	0.036806702	3.857627367	3.060383334	0.094447921	0.094447921	0
TGACGGCCAAGCACGA-1	1558486	14215	170157	141599	1232515	398	0.035936443	3.7842658	3.109346365	0.09632907	0.097112701	1
TGACGGCGTCCGATGC-1	1356338	51445	137956	116926	1050011	339	0.030513016	3.218863867	3.033563385	0.100819747	0.101379759	0
TGACGGCGTGTCAACT-1	2170004	62230	225873	200723	1681178	543	0.048974778	5.073674667	3.038201896	0.085646725	0.085174194	0
TGACTAGGTAGGGTGT-1	2310132	32885	246646	197514	1833087	592	0.05351069	5.5239914	3.073518022	0.0800951	0.081072366	0
TGACTAGTCCTCGCTA-1	1821144	25080	198781	158841	1438442	465	0.041785297	4.328979867	2.986659658	0.0928327	0.093590972	0
TGACTAGTCGGGCTTG-1	1650928	55814	175416	143120	1276578	412	0.037234729	3.906748567	3.037652239	0.095529789	0.095529789	0
TGACTAGTCTCATGTT-1	1780014	20443	198948	130902	1429721	462	0.041704168	4.330304567	3.442600699	0.124649058	0.124840574	1
TGACTTTAGATTCACC-1	2301090	33712	250247	210277	1806854	584	0.05266166	5.4429393	3.035469758	0.078268887	0.079929734	0
TGACTTTAGCAACGGT-1	2163340	50546	234468	194196	1684130	544	0.049124199	5.0935564	3.114092434	0.081999572	0.081999572	0
TGACTTTAGGTGTGCA-1	1787378	15000	195578	163894	1412906	456	0.041235461	4.2998279	2.948745996	0.088117964	0.088117964	0
TGACTTTAGTACAGTA-1	1181854	8987	131323	96081	945463	305	0.027611339	2.910682933	3.073652661	0.108493702	0.107849118	0
TGAGAGGAGTGTCCAT-1	2246190	30857	239147	200185	1776001	574	0.051879822	5.3431709	3.071426034	0.082182112	0.079518386	0
TGAGAGGGTCCCACAG-1	1274998	30185	135619	105503	1003691	324	0.029205907	3.081825967	3.042186901	0.102022481	0.099510792	0
TGAGAGGGTCGCGTAC-1	2287218	47869	232259	206250	1800840	582	0.052507691	5.420204133	3.049986857	0.080797919	0.080797919	0
TGAGAGGTCTACGGCG-1	1028696	109705	97781	84543	736667	238	0.021444762	2.286978967	3.098434004	0.121248648	0.11877367	0
TGAGCATCATAGGTCT-1	513730	4927	54398	42745	411660	133	0.01202147	1.2935369	3.096401539	0.165979854	0.165362042	0
TGAGCATCATCGGGCT-1	1674960	73389	173226	147939	1280406	414	0.037205671	3.8943667	3.106671874	0.09599866	0.096358153	0
TGAGCATTCTGTATGG-1	1263814	18346	137911	101915	1005642	325	0.029381168	3.091855867	2.927811399	0.102974575	0.105867354	0
TGAGCGAGGCATGGT-1	2230514	18235	245149	182230	1784900	577	0.052152634	5.3759433	3.127876002	0.081809335	0.081618828	0
TGAGCCGGTGCTGTAT-1	1483950	18989	162847	124426	1177688	380	0.034299336	3.604278533	3.058877011	0.098434442	0.097729371	0
TGAGCCGGTTCCCTAC-1	2850160	32697	311529	246758	2259176	730	0.06574085	6.701109767	3.142385235	0.080585868	0.076401185	0
TGAGGGACACCAATGT-1	1587742	19326	173797	131538	1263081	408	0.036805808	3.849797733	3.148286002	0.092765422	0.093065131	0
TGATTTCTCACGATAC-1	2264160	37396	247189	190991	1788584	578	0.052051663	5.3831451	3.044897524	0.088143788	0.083797329	0
TGATTTCTCCGACCAG-1	2242330	63221	240928	194338	1743843	563	0.050864673	5.269453367	3.077897534	0.080692727	0.081399508	0
TGCACTTAGTACGCGA-1	1570974	11805	168678	152865	1237626	400	0.036107073	3.799542033	3.071863434	0.09129586	0.093694244	0
TGCACTTCAGCCCGA-1	2126416	17097	230974	196023	1682322	543	0.049042675	5.087482	3.101381408	0.089714739	0.089540122	0
TGCCAAAAGACAGGCT-1	2205220	33594	240866	195316	1735444	561	0.050362034	5.1986704	3.104849996	0.084475637	0.085388156	0
TGCCAAACAAGTGTTC-1	2318874	48619	250360	209154	1810741	585	0.05258351	5.408093033	3.048254496	0.082998839	0.08339146	0
TGCCAAACACTACATG-1	1159192	15428	128451	92876	922437	298	0.026889479	2.8334616	3.09073673	0.113927365	0.113192954	0
TGCCCATAGGATGCGT-1	2322016	26031	249902	210296	1835787	593	0.053553383	5.5353585	2.989264654	0.082938338	0.082355028	0
TGCCCATAGGCCATAG-1	1179806	11927	132453	95052	940374	304	0.027405508	2.877125467	3.090991087	0.110113703	0.107881722	0
TGCCCATGTACCAGCC-1	1480952	34141	157916	138183	1150712	372	0.033434594	3.527727133	3.175128761	0.09815268	0.099764682	0
TGCCCATTCCAACAAC-1	2280048	42613	249404	199731	1788300	578	0.052184137	5.3928318	3.139472263	0.082650292	0.082580424	0
TGCCCTAAGCCAAACG-1	1356656	74585	140587	114172	1027312	332	0.029860053	3.147235967	3.114372772	0.098688163	0.098688163	0
TGCCCTACAAATTCCG-1	777146	95937	74855	63385	542969	175	0.015791569	1.6980025	3.173872294	0.161906754	0.158341636	1
TGCCCTAGTCGTAATC-1	1975040	51457	209701	171162	1542720	498	0.044757802	4.642507733	3.070620666	0.092433183	0.088201743	0
TGCCCTAGTGTAGTTC-1	1911972	53415	197436	186818	1474303	476	0.042523953	4.372696133	3.12513853	0.098267159	0.093047783	0
TGCCCTAGTTCTAGAC-1	1332094	35052	145172	116857	1035013	334	0.030070314	3.175142967	2.938426025	0.110306522	0.104334152	0
TGCGCAGAGAGGTACC-1	2591744	33170	276489	235836	2046249	661	0.059659311	6.130635167	2.971792668	0.082219126	0.080051685	0
TGCGCAGAGTACTTGC-1	2644076	52139	288877	217996	2085064	674	0.060636132	6.220085633	4.213582425	0.137010351	0.137010351	1
TGCGGGTCAGACAGTG-1	2046096	22868	217821	161263	1644144	531	0.047909237	4.982054333	3.073867551	0.082229454	0.083707994	0
TGCGGGTCATACGTCA-1	1722598	26392	181826	156019	1358361	439	0.039451685	4.109787033	3.09634138S	0.093814912	0.092925259	0
TGCGGGTCATCTGTAG-1	1201460	16588	127037	98139	959696	310	0.027976549	2.950293333	2.883502936	0.110425252	0.105812401	0
TGCGGGTTCTATGGTG-1	1058004	18855	112879	86075	840195	271	0.024440142	2.583938733	3.142219035	0.116078293	0.113178676	0
TGCGTGGAGTAGTGCG-1	1740654	61939	177294	157398	1344023	434	0.039124318	4.112230867	3.003047221	0.091864	0.092656977	0
TGCTACCGTACGTCAT-1	2338412	32231	251948	207502	1846731	597	0.053848683	5.557345533	3.019380368	0.08522223	0.081802217	0
TGCTACCTCCTGAAAC-1	2328798	57185	251701	197415	1822497	589	0.053076687	5.472549767	3.78013005	0.133720725	0.133720725	1
TGCTGCTTCGGAGAGT-1	1893980	30603	204229	168862	1490286	481	0.043508521	4.5235827	3.110624907	0.090581256	0.087734681	0
TGGACGCAGACGCTTT-1	2202638	52602	236071	198834	1715131	554	0.049821263	5.1413468	3.108028046	0.089715809	0.087198547	0
TGGACGCCATCGGCGT-1	1888278	24496	208867	176236	1478679	478	0.043051265	4.489986367	3.10999936	0.088229532	0.086696381	0
TGGACGCGTTACTGAC-1	2579716	48930	276725	215949	2038112	658	0.059413806	6.102296433	3.923585536	0.132668797	0.132668797	1
TGGACGCTCGAACCCG-1	1099690	94206	108603	92807	804074	260	0.023385061	2.491230233	3.097826319	0.118451133	0.114550716	0
TGGCCAGGTCCTAGTA-1	1081622	10923	119159	92642	858898	277	0.025005342	2.6334069	3.313451173	0.100811049	0.103749212	0
TGGCCAGTCAAGCCAT-1	2429658	18020	268174	215629	1927835	623	0.056254529	5.797977733	3.037953455	0.078442906	0.077700931	0
TGGCGCAGTCGACCAC-1	2510174	34666	269607	225037	1980864	640	0.0577571	5.954932467	3.012374972	0.077358669	0.079038133	0
TGGCGCAGTGTCCGAC-1	2057088	51484	217459	192990	1595155	515	0.046428273	4.8419747	3.074563148	0.085518767	0.086336798	0
TGGCGCATCCAACCGG-1	1653480	79616	170058	143265	1260541	407	0.036719662	3.854260367	3.037506483	0.094652758	0.095303736	0
TGGCGCATCCGGTTCT-1	2697504	82272	283406	233043	2098783	678	0.061026998	6.2583796	3.107118495	0.079939894	0.080148024	0
TGGCTGGAGTAAGTAC-1	2488488	69708	265930	216674	1936176	625	0.056346496	5.814364333	3.074736206	0.082311399	0.078424091	0
TGGCTGGCAACGCGCT-1	1279616	48076	131238	113366	986936	319	0.028682965	3.025945233	2.999573806	0.104871499	0.103700837	0
TGGCTGGGTCGAGTAG-1	1106740	17546	111502	88090	889602	287	0.026013373	2.7488078	3.058615082	0.120210438	0.120811857	1
TGGGAAGAGGAATGGA-1	1715148	19481	180949	150992	1363726	441	0.039728546	4.1606326	3.072323984	0.092723306	0.091157984	0
TGGGAAGCAAGGTGAC-1	2099758	49322	218925	192744	1638767	529	0.047776744	4.958985833	2.918677416	0.085996629	0.085231535	0
TGGGAAGGTGGTAACG-1	1753774	60578	180999	151271	1360926	440	0.0396101	4.1445208	3.016784578	0.088769045	0.089751218	0
TGGGAAGTCACTTTAC-1	2087938	60473	221803	173378	1632284	527	0.047544771	4.9363335	3.052657005	0.086052078	0.084871897	0
TGGGCGTAGGCTCAGA-1	1803992	18247	197036	161316	1427393	461	0.041678408	4.360065833	3.051034179	0.088222086	0.088273144	0
TGGGCGTGTTTCCTGC-1	2065052	30114	220357	196594	1617987	523	0.047237485	4.904689333	3.067431535	0.086477404	0.084336553	0
TGGGCGTTCACTGTTT-1	1628738	45453	173929	136418	1272938	411	0.037030956	3.8643664	3.064156197	0.093996453	0.095283801	0
TGGTTAGAGGGATGGG-1	2136016	27446	227248	191032	1690290	546	0.049415262	5.109077333	2.762450992	0.077885845	0.080686337	0
TGGTTAGAGTTAGCGG-1	1509668	56410	157554	133924	1161780	375	0.033887053	3.571696733	3.020323962	0.101588912	0.098339965	0
TGGTTAGTCTTATGGG-1	1720824	21747	186238	143678	1369161	442	0.040019666	4.182032267	3.048977127	0.093677668	0.091973687	0
TGGTTCCAGACAAAGG-1	1279028	21754	138799	110897	1007578	325	0.029427004	3.1106308	3.164177196	0.105412974	0.102548187	0
TGGTTCCAGAGTAAGG-1	958374	17717	103707	80834	756116	244	0.022100321	2.35485	3.062393454	0.120235971	0.119427301	0
TGGTTCCAGGTGCACA-1	2036712	23394	219339	187701	1606278	519	0.046816131	4.867484833	3.022094816	0.085064895	0.085325529	0
TGGTTCCTCACACCTC-1	1978410	30220	210729	189525	1547936	500	0.045095221	4.6917585	3.023925552	0.087341338	0.08666308	0
TGTATTCCAACATAAG-1	1119632	13749	121920	86867	897096	290	0.026196871	2.756805967	3.043910787	0.111815906	0.108764804	0
TGTATTCCAATCGCGC-1	1437018	40625	149085	130389	1116919	361	0.032512509	3.4302753	3.036806636	0.10028618	0.101031764	0
TGTCCCACAGTCGGAA-1	1277180	12412	137860	117169	1009739	326	0.029450601	3.1107462	3.054171904	0.106362034	0.103478361	0
TGTCCCAGTAGATAGT-1	1775788	13563	195489	145980	1420756	459	0.041532861	4.319871567	3.038462631	0.08922246	0.089671268	0
TGTGGTACATTATCGG-1	2011992	46673	213888	185191	1566240	506	0.045669386	4.764361367	2.873889043	0.090011291	0.090011291	0
TGTGGTACATTGAAGA-1	1353890	15942	147028	116939	1073981	347	0.03132305	3.2990804	3.040106534	0.098954405	0.099557534	0
TGTGGTAGTTGGGCC-1	1778828	89157	182485	158408	1348778	436	0.039210661	4.090710833	3.531602236	0.092120743	0.090091769	0
TGTGGTATCAAGCCGC-1	2098862	24944	221309	191189	1661420	537	0.048396289	5.032009967	3.141153237	0.086389544	0.085456139	0
TGTGTTTGTAAACCTC-1	1961044	35769	206872	183266	1535137	496	0.044711685	4.668730267	2.91513636	0.088265971	0.087412959	1
TGTTCCGCATAGAGCG-1	1049952	32599	108495	98293	810565	262	0.023596366	2.5237046	3.03280784	0.118320551	0.115384736	0
TTAACTCCAGCTCATA-1	1529170	13449	168292	129522	1217907	393	0.035558147	3.7234074	3.06188379	0.099634408	0.095964961	0
TTAACTCCATGCCTAT-1	2028180	22758	224155	177117	1604150	518	0.046836777	4.8517156	2.882402245	0.08920444	0.086001427	0
TTAACTCTCAGTACAC-1	2105048	34679	229456	185738	1655175	535	0.048248106	5.0062402	3.14321135	0.086020146	0.081571967	0

TTAACTCTCGATAGTC-1	1474440	17808	160921	120129	1175582	380	0.034241005	3.577867233	3.147446914	0.100643886	0.095227836	0
TTAGGACAGGCTGCA-1	1595386	32558	164107	147049	1251672	404	0.036456041	3.8217652	3.094770337	0.093285795	0.093285795	0
TTAGGACAGTTACCA-1	1550908	27499	166178	136792	1220439	394	0.03558407	3.7387442	2.949396581	0.093831592	0.093504739	0
TTAGGACTCTGAAGTC-1	1979764	52024	210974	170108	1546658	500	0.044987534	4.677815067	3.243281833	0.087948562	0.087308485	0
TTAGGCAAGGTAAGTT-1	1838286	41598	193838	158775	1444075	466	0.041963435	4.3667543	3.143374572	0.094744524	0.091035258	0
TTAGGCACACCAATGT-1	1659096	18028	182100	132665	1326303	428	0.038691834	4.0332062	2.989678345	0.095402005	0.092476229	0
TTAGGCAGTAACGACG-1	1420648	83201	143746	126740	1066961	345	0.031034127	3.280928533	2.704059093	0.096312458	0.099365881	0
TTAGTTCAGAGCCACA-1	2118102	24440	227912	192425	1673325	541	0.048824728	5.066397933	3.039220143	0.086366542	0.084610171	0
TTATGCTAGTGCCATT-1	2088700	24895	224114	181109	1658582	536	0.048367567	5.005697033	3.068885146	0.086917604	0.083263099	0
TTATGCTCAGAGACGT-1	1789210	22113	188081	172028	1406988	455	0.041107791	4.2985327	3.123509854	0.090509279	0.090509279	0
TTCCCAGAGGAGCGTT-1	3410494	50339	371398	297977	2690780	869	0.078588861	7.989324733	3.025966737	0.064819593	0.063545584	0
TTCCCAGCACGATCTA-1	2170762	31556	238421	187736	1713049	553	0.049962953	5.174475	3.080588214	0.082286245	0.083176806	0
TTCCCAGCAGATTGTC-1	2269404	32642	252997	181872	1801893	582	0.052483089	5.405535033	3.61962767	0.128563063	0.128563063	1
TTCCCAGGTTCTCTCG-1	1518232	59726	160765	133601	1164140	376	0.033947829	3.568523767	3.110572039	0.096483052	0.096893851	0
TTCCCAGTCCGCCTTA-1	1558652	26935	167826	136977	1226914	396	0.035807866	3.757928467	3.019722212	0.100214809	0.095940773	0
TTCGAAGGTACTCGCG-1	1097584	78473	109463	93208	816440	264	0.023725873	2.529146867	3.142569026	0.115683945	0.113221435	0
TTCGGTCAGCGATGAC-1	2026556	32170	219239	180082	1595065	515	0.046512354	4.828305467	2.922493945	0.084211565	0.084915579	0
TTCGGTCAGTGAATTG-1	1058934	20657	114151	87909	836217	270	0.024396762	2.5830278	3.032521942	0.112638425	0.112835725	0
TTCGGTCCACTTGAGT-1	1611112	16542	178030	132313	1284227	415	0.037518591	3.914983	3.012017899	0.09532526	0.094131156	0
TTCGGTCCATAGCACT-1	2238462	72314	236292	199512	1730344	559	0.050349712	5.222405633	3.144026198	0.084785477	0.083641909	0
TTCTACAAGAGGTAGA-1	1694298	8195	183875	153921	1348307	436	0.039395826	4.124490433	2.99416189	0.090071562	0.088822567	0
TTCTACAAGCAGAGAA-1	1574894	10153	173968	135173	1255600	406	0.03661971	3.831094067	3.135648122	0.099439762	0.096059036	0
TTCTACAAGTGACTCT-1	2012298	55001	214907	181782	1560608	504	0.045334068	4.6965471	2.984026194	0.092837694	0.090940493	0
TTCTACAGTCGCTTCT-1	888010	46345	60770	84420	696475	225	0.020109962	2.154067733	3.029495509	0.123385744	0.125334078	0
TTCTACAGTCTAACGT-1	1707524	26049	182750	157019	1341706	433	0.039116385	4.080855133	3.027665681	0.096551442	0.093348527	0
TTCTACATCTTAGCTT-1	1910458	67259	201417	166940	1474842	476	0.042920241	4.477946733	3.107831993	0.093060523	0.09022728	0
TTCTCAAAGGCACATG-1	1193874	13237	131242	97648	951747	307	0.027800827	2.9285391	3.006988289	0.105918162	0.10452414	0
TTCTCAACATACGGAG-1	1597084	22752	174803	132223	1267306	409	0.036932853	3.868071333	3.001512935	0.100648237	0.099907754	1
TTCTCAAGTAGGGTGT-1	2393238	30384	256764	204592	1901498	614	0.055474223	5.708763667	3.135010515	0.08464697	0.083351221	0
TTCTCAAGTGGCCACT-1	1674236	43591	179674	142926	1308045	423	0.038256929	4.012296967	3.000099454	0.090301191	0.089594098	0
TTCTCCTAGACAGACC-1	2387694	39929	253713	214503	1879549	607	0.054630064	5.605624233	3.007757335	0.084625881	0.082675197	0
TTCTCCTAGCAGCCCT-1	1833014	42327	195156	165598	1429933	462	0.041720331	4.361396533	3.113643628	0.090803904	0.088958474	0
TTCTCCTCATTCGTTT-1	2042690	52324	219670	173413	1597283	516	0.046449137	4.8151224	3.036506358	0.088653452	0.087666527	0
TTCTCCTTCATCGCGG-1	1724246	41249	182606	152687	1347704	435	0.039307074	4.1129284	2.936999595	0.093491467	0.092637133	0
TTCTTAGAGTACTTGC-1	1816392	45713	192679	159270	1418730	458	0.041290324	4.312421867	3.046341481	0.094283308	0.091475731	0
TTGAACGAGAATTGTG-1	1261492	19055	139620	107277	995540	322	0.029050556	3.062350367	2.991368961	0.103737354	0.104663631	0
TTGAACGAGCACGCCT-1	1932494	58414	203161	178296	1492623	482	0.043510522	4.547870567	2.984749362	0.089137176	0.087115229	0
TTGAACGAGTGTCCAT-1	2427774	19803	263911	221176	1922884	621	0.05613529	5.782304967	3.110133191	0.082190797	0.083340915	0
TTGACTTAGGGCTTCC-1	2166276	55418	230056	199682	1681120	543	0.04895468	5.067576667	3.099070108	0.087104504	0.084332644	0
TTGACTTAGTCCGTAT-1	2157434	17831	241457	177881	1720265	556	0.050215204	5.185823533	3.115134851	0.091242507	0.083895761	0
TTGCCGTAGAGTAATC-1	2024858	43498	216751	186412	1578197	510	0.04585224	4.744569633	3.022962789	0.087024323	0.087380481	0
TTGCCGTAGTCGTGTT-1	1775716	24061	188529	151571	1411555	456	0.04116602	4.278098033	3.108176253	0.089027017	0.089741527	0
TTGCCGTGTAACGCGA-1	1195024	21708	124798	109967	938551	303	0.027275758	2.887878967	3.046110677	0.105504833	0.10744099	0
TTGCCGTGTGCACTTA-1	1392326	20664	151122	119506	1101034	356	0.032064819	3.377338067	3.011639302	0.105595861	0.100182464	0
TTGCGTCAGGATGTAT-1	1799076	18768	191061	152468	1436779	464	0.041846457	4.347007633	3.120615188	0.090280685	0.088327953	0
TTGCGTCTCATTTGCT-1	1728188	56945	174456	153017	1343770	434	0.039125135	4.0976749	2.886227587	0.092236296	0.090847506	0
TTGGAACGTAAGGTGC-1	2068648	76586	213524	181729	1596809	516	0.046451737	4.8303182	3.097526321	0.087404416	0.085682804	0
TTGGCAATCATGGTGT-1	2502470	31371	274371	205370	1991358	643	0.058012858	5.947461133	3.014485238	0.081714822	0.080489835	0
TTGTAGGAGAGTACAT-1	1853772	16296	198373	158421	1480682	478	0.043220294	4.495245933	3.121473683	0.090192633	0.086523665	0
TTGTAGGTCTTCTTGA-1	846372	8967	90600	73754	673051	217	0.019675513	2.095048733	2.967917628	0.123608574	0.127052684	0
TTTACTGAGAAACGCC-1	1748232	57762	182000	157647	1350823	436	0.039343693	4.117528833	3.042934852	0.092619265	0.091344543	0
TTTACTGAGACAGACC-1	2507462	41263	269344	227167	1969688	636	0.057368802	5.902468533	3.143568471	0.080711903	0.081412665	0
TTTACTGAGCCCAATT-1	791808	23315	85173	59406	623914	202	0.018290932	1.942565367	3.034131898	0.1329755	0.12963281	0
TTTACTGCACCACATA-1	1627156	12186	181064	123935	1309971	423	0.038184502	3.972668633	4.341722325	0.142063155	0.142288013	1
TTTACTGGTAACAATG-1	1265020	14039	138758	102365	1009858	326	0.029491219	3.0987657	3.090294544	0.105374723	0.103842487	0
TTTACTGTCCACGATA-1	1610830	14013	177652	133902	1285263	415	0.037522447	3.9263845	3.047494584	0.097954365	0.096434892	0
TTTATGCAGTAGTATG-1	1110412	10943	120717	89115	889637	287	0.026015486	2.744050233	3.046512123	0.111317607	0.110367296	0
TTTATGCTCTGAAGGG-1	1640902	26590	172497	144502	1297313	419	0.037880672	3.9750998	2.951717721	0.094170306	0.095011192	0
TTTCCTCAGCTCCTTC-1	2516606	47918	272596	232277	1963815	634	0.057211154	5.9116326	3.107555909	0.08033103	0.080579297	0
TTTCCTCCAACAGCCC-1	1528114	78079	158612	136226	1155197	373	0.033614186	3.543141167	2.939779998	0.098787269	0.098787269	0
TTTCCTCCATTCAGCA-1	1630466	39279	175684	142551	1272952	411	0.037002093	3.8811907	3.081360001	0.101998451	0.098920324	1
TTTCCTCGTCAAGTCT-1	2199828	81390	230726	200244	1687468	545	0.048730802	4.9934283	2.895542324	0.093373999	0.093373999	1
TTTGCGCAGTGCCATT-1	2064206	28000	217583	182083	1636540	529	0.047712934	4.935847433	3.14365775	0.087003648	0.086134641	0
TTTGCGCCAACTCATG-1	986010	13517	106183	81906	784404	253	0.022856781	2.428664367	2.908530435	0.118646476	0.118646476	0
TTTGCGCTCGATAAGA-1	1067886	8933	115441	87614	855898	276	0.024961824	2.634196033	3.123445744	0.115750924	0.111189326	0
TTTGCGCTCTCATCCG-1	1469370	67617	152246	129953	1119554	362	0.032602735	3.431065867	3.005660712	0.099645637	0.099645637	0
TTTGGTTCAAGACGAC-1	1678288	58039	178003	149809	1292437	417	0.037571985	3.946982167	3.077345398	0.093458163	0.091135887	0
TTTGGTTGTGATGTTC-1	2501734	57366	264979	225337	1954052	631	0.056596783	5.740793067	3.098451375	0.084508055	0.08226134 5	0
TTTGGTTTCAGATTCG-1	1517258	145646	149613	127044	1094955	354	0.031717703	3.341627867	3.133985188	0.104922885	0.101959238	0
TTTGTCAGTGTGTTCA-1	2632962	41823	284940	228845	2077354	671	0.060549859	6.2191403	3.061144741	0.079651328	0.07953071	0
TTTGTCATCACTGCGG-1	1759810	30953	190198	159556	1379103	445	0.040243654	4.208228967	2.885560867	0.093087254	0.091058968	0

Supplementary Table 3 | DAPC classification of single cells. Assignment of each barcode to DAPC defined cluster and group.

cell_id	barcode	cluster	group
0	AAACCTGAGGCTACGA-1	4	A
1	AAACCTGGTCCTTGGG-1	4	A
2	AAACCTGTCACACGGC-1	9	D
3	AAACCTGTCGATACAC-1	11	D
4	AAACGGGAGCAGATCG-1	2	A
5	AAACGGGCAAAGTAAC-1	1	A
6	AAACGGGCAACCTCAA-1	4	A
7	AAACGGGGTCTTCGTC-1	8	D
8	AAACGGGTCACGCTCT-1	10	D
9	AAACGGGTCAGCGGCT-1	11	D
10	AAAGATGAGAATTGTG-1	3	A
12	AAAGCAAGTGACACGA-1	1	A
13	AAAGCAATCGCGGACT-1	5	A
14	AAAGCAATCTCACCTG-1	8	D
15	AAAGTAGTCTCAGCGG-1	11	D
16	AAAGTAGTCTTGCGAA-1	10	D
17	AAATGCCAGTGGAGAA-1	11	D
18	AAATGCCGTCGCGCTA-1	8	D
19	AACACGTAGGACAGAA-1	1	A
20	AACCATGAGGAATCGC-1	3	A
22	AACCATGCATTCATCT-1	10	D
23	AACCATGTCGACGAAG-1	8	D
24	AACCGCGGTAACAGCG-1	2	A
25	AACCGCGGTTTACTTC-1	3	A
26	AACCGCGTCCTACGAA-1	2	A
27	AACGTTGGTGGTAACG-1	5	A
28	AACTCAGAGTGGGTAC-1	7	C
29	AACTCAGAGTGGTAGC-1	4	A
30	AACTCAGCATGCAGTT-1	10	D
31	AACTCAGTCGAGTATC-1	5	A
32	AACTCAGTCTAACACG-1	8	D
33	AACTCCCTCAGTTCTT-1	10	D
34	AACTCCCTCCACGATA-1	11	D
35	AACTCCCTCGATAGGG-1	2	A
36	AACTCCCTCTAATGGC-1	10	D
37	AACTCTTAGAGTAGCC-1	5	A
38	AACTCTTGTCTTACCC-1	3	A
40	AACTGGTAGAAACCAT-1	5	A
41	AACTGGTAGCTGAACG-1	11	D

42	AACTGGTAGGGCCATA-1	1	A
43	AACTGGTGTCGTGAAG-1	9	D
44	AACTGGTGTTCAGTAC-1	5	A
45	AACTGGTTCGTACGCG-1	11	D
46	AACTTTCCACGTAGGA-1	8	D
47	AACTTTCTCTGCTGAA-1	11	D
48	AAGACCTCACAAGCGA-1	2	A
49	AAGACCTCACCAGTGC-1	8	D
51	AAGACCTCACTTGAGT-1	3	A
52	AAGACCTCATAGCACT-1	8	D
53	AAGACCTGTGGACGTA-1	11	D
54	AAGACCTTCACGGTAT-1	5	A
55	AAGACCTTCCGAGATT-1	6	B
56	AAGCCGCCATCTCACC-1	5	A
57	AAGGAGCCAAGAATCA-1	6	B
58	AAGGCAGAGAGCCCAA-1	3	A
59	AAGGCAGGTAAAGTCA-1	5	A
60	AAGGTTCAGCGTGTGA-1	6	B
61	AAGGTTCCAGATTGTC-1	5	A
62	AAGGTTCGTCCGAATT-1	2	A
63	AAGGTTCGTGTAATGA-1	9	D
64	AAGGTTCGTTGAGCAG-1	8	D
66	AAGGTTCTCCGCGACA-1	1	A
67	AAGTCTGAGGCCCGTT-1	8	D
68	AAGTCTGAGTGCGATG-1	1	A
69	AAGTCTGTCACCGCGA-1	1	A
70	AATCCAGGTTGAACAA-1	3	A
71	AATCCAGTCGACTGCG-1	5	A
72	AATCGGTAGAAGGGTA-1	4	A
73	AATCGGTCAGATGAAT-1	11	D
74	AATCGGTCATGAATGA-1	4	A
75	AATCGGTGTGCGCTTG-1	4	A
76	ACACCAAGTGCAACCC-1	1	A
77	ACACCCTAGCGTAATA-1	9	D
78	ACACCCTCAACGCCGT-1	8	D
79	ACACCGGAGTGTGAAT-1	3	A
80	ACACCGGTCTGTGGCG-1	7	C
81	ACACTGAAGACAGGCT-1	5	A
82	ACACTGAAGCTCTCGG-1	10	D
83	ACACTGACACAGACCC-1	10	D
84	ACACTGACAGAGGCTA-1	4	A
85	ACACTGACAGTTCCGG-1	5	A

86	ACAGCCGAGTCTCGTA-1	1	A
88	ACAGCCGGTTTGGCGC-1	4	A
91	ACAGCTACAGAACAGC-1	8	D
92	ACAGCTATCCGAAGCC-1	3	A
93	ACATACGAGCCGAACA-1	8	D
94	ACATACGAGGTAACGC-1	11	D
95	ACATACGAGTTAGGGC-1	8	D
96	ACATACGCACTCCGAG-1	1	A
97	ACATACGGTATAAGTG-1	9	D
98	ACATACGGTCTCTCGT-1	6	B
99	ACATCAGAGTGTACGG-1	11	D
100	ACATCAGAGTTAGGGC-1	3	A
101	ACATGGTTCGAGCACC-1	10	D
102	ACCAGTAAGATTCACC-1	6	B
103	ACCAGTAGTGTTACGT-1	1	A
104	ACCAGTATCGTTCGAA-1	8	D
105	ACCCACTAGTTATCGC-1	3	A
106	ACCCACTGTAGGGTGT-1	10	D
107	ACCGTAACACGTAGGA-1	1	A
108	ACCGTAACATCTCGTC-1	3	A
109	ACCTTTAAGTGGGCTA-1	3	A
110	ACGAGCCGTGCGCTTG-1	2	A
111	ACGAGGACACCGGCAT-1	1	A
112	ACGAGGACAGTAGGGT-1	5	A
113	ACGAGGACATCTCGAA-1	4	A
114	ACGATACAGAAGATTC-1	5	A
115	ACGATACCAGCCAAAG-1	8	D
116	ACGATACCAGTCCCTT-1	10	D
117	ACGATACTCGAGGTGA-1	8	D
118	ACGATGTCAACATGGG-1	1	A
119	ACGATGTGTCATACCA-1	1	A
120	ACGATGTTCTTCACAT-1	5	A
121	ACGCAGCGTTACGGCC-1	3	A
122	ACGCAGCTCCGCTCTA-1	11	D
123	ACGCCAGCAAGAGAGA-1	11	D
124	ACGCCAGCAAGGGTGT-1	6	B
125	ACGCCAGCACAGCTGC-1	5	A
126	ACGCCAGTCCACCCAT-1	5	A
127	ACGCCAGTCTCGGAAT-1	10	D
128	ACGCCGAAGACAAGCC-1	7	C
129	ACGCCGAAGCAGCCTC-1	3	A
130	ACGCCGACATGACCGC-1	1	A

132	ACGGAGAAGCCGAACA-1	8	D
133	ACGGAGAGTTGCAGCC-1	4	A
134	ACGGAGATCGGATCCG-1	11	D
136	ACGGCCAAGAATGTGT-1	10	D
137	ACGGCCACAACGAAAT-1	1	A
138	ACGGCCACACACACGC-1	10	D
139	ACGGGCTAGTCTAGCT-1	10	D
140	ACGGGCTCATCGGTCG-1	8	D
141	ACGGGCTCATGCAGTT-1	11	D
142	ACGGGCTGTCGTCTTC-1	7	C
143	ACGGGTCCACGATGGA-1	11	D
144	ACGGGTCTCGTCCCTA-1	2	A
145	ACGTCAAAGATGTGGC-1	5	A
146	ACGTCAAAGGAGCGAG-1	5	A
147	ACGTCAACATTTGTGG-1	1	A
148	ACTATCTAGAAGGCCT-1	11	D
149	ACTATCTAGTACAGTA-1	3	A
150	ACTATCTCATGGCTAT-1	5	A
152	ACTATCTTCTCGAACA-1	5	A
153	ACTATCTTCTGGTAGT-1	11	D
154	ACTGAACAGCTAAACA-1	11	D
155	ACTGAACAGTGCGATG-1	11	D
156	ACTGAACCACGCGATC-1	5	A
157	ACTGAGTCACGTTTAG-1	11	D
158	ACTGAGTTCTTCTAAC-1	6	B
159	ACTGATGCACGACTAT-1	10	D
160	ACTGATGCATACCAGT-1	10	D
161	ACTGATGGTACGTCAT-1	10	D
162	ACTGATGTCGTTCGTC-1	4	A
163	ACTGATGTCTTATGGG-1	2	A
164	ACTGCTCAGATAGCAT-1	11	D
165	ACTGCTCAGCGCCTTG-1	3	A
166	ACTGCTCCAATCGTCA-1	8	D
167	ACTGCTCGTGGAAAGA-1	3	A
168	ACTTACTCACATAAAG-1	11	D
169	ACTTACTTCCGAGATT-1	3	A
170	ACTTACTTCTCATGTT-1	4	A
171	ACTTGTTAGGGTTTCT-1	11	D
172	ACTTGTTAGTTGTAGA-1	11	D
173	ACTTGTTGTCTAGGTT-1	10	D
174	ACTTGTTTCTCAGATG-1	3	A
175	ACTTGTTTCTGTGGCG-1	11	D

176	ACTTTCACAAACGAGC-1	1	A
177	ACTTTCACACATTCAG-1	11	D
178	ACTTTCACAGCGGTCT-1	10	D
179	ACTTTCAGTAGCAGTG-1	3	A
180	AGAATAGAGAAAGCTT-1	9	D
181	AGAATAGAGTCAAGGC-1	3	A
182	AGAATAGCAAGCAAGC-1	1	A
183	AGAATAGGTGAAGCCA-1	3	A
184	AGACGTTTCCTCAGTC-1	5	A
185	AGAGCGAAGTCCATAC-1	3	A
186	AGAGCGACAGTGTGGA-1	6	B
187	AGAGCGAGTTTGTCAG-1	3	A
188	AGAGCGATCCCACGGA-1	3	A
189	AGAGCGATCGTGCCTT-1	4	A
190	AGAGCTTAGACGTCGA-1	6	B
191	AGAGCTTCATTCTTCA-1	3	A
192	AGAGTGGAGGCATGGT-1	8	D
193	AGAGTGGCACTACATG-1	6	B
194	AGAGTGGCATGAAAGT-1	8	D
195	AGAGTGGGTACAAGGC-1	11	D
196	AGAGTGGGTTCTTCGC-1	11	D
197	AGATCTGCACCAGTGC-1	1	A
198	AGATCTGTCTTCTTGA-1	11	D
199	AGATTGCAGCAAAGTT-1	4	A
200	AGATTGCCAGAATTCC-1	11	D
201	AGATTGCCATGATGCT-1	10	D
202	AGATTGCGTCACCGCA-1	2	A
203	AGATTGCTCGCGAGAA-1	3	A
204	AGCAGCCAGGGTCGAT-1	7	C
205	AGCAGCCAGTGTGATA-1	11	D
206	AGCAGCCGTTGACGGA-1	11	D
207	AGCAGCCTCTCATGTT-1	8	D
208	AGCATACCAGGTACGA-1	3	A
209	AGCATACCATCATGGT-1	3	A
210	AGCCTAAAGTAAGTAC-1	10	D
211	AGCCTAACACGTCATA-1	3	A
212	AGCCTAAGTCTCTCGT-1	3	A
213	AGCCTAAGTGTCGCTG-1	1	A
214	AGCCTAATCCTCATCG-1	4	A
215	AGCGGTCAGCGTAGTG-1	8	D
216	AGCGGTCCACAAGCGA-1	11	D
217	AGCGGTCCAGGCCGTT-1	3	A

219	AGCGGTCGTCATCTGA-1	6	B
220	AGCGGTCTCATCGCCT-1	7	C
221	AGCGTATAGGCTATCT-1	5	A
222	AGCGTATCAGTGTGGA-1	8	D
223	AGCGTCGCACTCACCT-1	9	D
224	AGCTCCTAGACTTCCA-1	3	A
225	AGCTCCTAGGATGCGT-1	5	A
226	AGCTCCTCAGTACCTA-1	3	A
227	AGCTCCTGTAGTAGTA-1	2	A
228	AGCTCCTTCGAGTTGT-1	8	D
229	AGCTCTCAGCCGGTAA-1	8	D
230	AGCTCTCAGTTAGCGG-1	4	A
231	AGCTCTCGTACAACGG-1	9	D
232	AGCTCTCGTACTCCGG-1	1	A
233	AGCTCTCGTGATTACC-1	10	D
235	AGCTTGAAGGCCCGTT-1	10	D
238	AGCTTGAGTCAACTGT-1	11	D
239	AGGCCACAGATCTGAA-1	11	D
240	AGGCCACAGTTTGCGT-1	3	A
241	AGGCCACGTTGGCGTC-1	1	A
242	AGGCCACTCAAGAGGC-1	1	A
243	AGGCCACTCCACCGGA-1	11	D
244	AGGCCACTCTAGCTAG-1	2	A
245	AGGCCGTAGCACAGGT-1	9	D
246	AGGCCGTCATAGTGAA-1	3	A
247	AGGCCGTGTCTAGGTT-1	2	A
248	AGGCCGTGTCTCTATT-1	2	A
249	AGGCCGTGTGTGTATC-1	1	A
250	AGGCCGTTCGTTAGGT-1	5	A
251	AGGCCGTTCTGCACAA-1	1	A
252	AGGGAGTTCGCTATGA-1	9	D
253	AGGGATGAGGCATTGG-1	3	A
254	AGGGATGCAAATCGCT-1	11	D
255	AGGGATGGTATAAGTG-1	4	A
256	AGGGATGTCGTACGCG-1	3	A
257	AGGGATGTCTGGCCTT-1	4	A
258	AGGGTGAGTCCTACCT-1	3	A
259	AGGGTGAGTGACTGAG-1	5	A
260	AGGTCATAGCCATGCC-1	2	A
262	AGGTCATAGTGATTGA-1	1	A
263	AGGTCATCAACATAAG-1	1	A
264	AGGTCATTCGACAATC-1	3	A

265	AGGTCATTCGCGGCAT-1	8	D
266	AGGTCCGCAGTGTGGA-1	2	A
268	AGGTCCGTCTCGAGCG-1	2	A
269	AGTAGTCCAATCGCGC-1	11	D
270	AGTCTTTAGTCTAGCT-1	6	B
271	AGTCTTTGTTCCACAA-1	11	D
272	AGTCTTTTCCGTCTAC-1	3	A
273	AGTGAGGAGGCATGGT-1	6	B
274	AGTGAGGCATTCCGAA-1	4	A
275	AGTGAGGTCTGTATGG-1	2	A
276	AGTGGGAAGCTGAAAT-1	9	D
277	AGTGGGAGTCACCAGC-1	5	A
278	AGTGGGATCTGACGCG-1	9	D
279	AGTGGGATCTGGGACC-1	11	D
280	AGTGTCACATGTAGCT-1	11	D
281	AGTGTCAGTACGTCAT-1	10	D
282	AGTGTCATCGAGCGTC-1	9	D
283	AGTTGGTCAAACGAGC-1	4	A
284	AGTTGGTCACTTCAGA-1	4	A
285	AGTTGGTGTGTTCGAT-1	10	D
286	ATAACGCCAACTGGAG-1	6	B
287	ATAACGCCACTTTCCG-1	11	D
288	ATAACGCGTGCCATTA-1	2	A
289	ATAACGCGTGCTCGAC-1	8	D
290	ATAACGCTCCACTTCG-1	1	A
291	ATAAGAGAGCGCCTTG-1	1	A
292	ATAAGAGAGTAGCCGA-1	5	A
293	ATAAGAGCAGCGTCAC-1	1	A
294	ATAAGAGTCCGTGCTT-1	11	D
295	ATAGACCGTACCGCTG-1	2	A
296	ATAGACCGTCCGAATT-1	1	A
297	ATCACGAGTACCTAGT-1	8	D
298	ATCATCTCATTACGCA-1	3	A
299	ATCATCTGTGCGAAAC-1	7	C
300	ATCATGGAGTCCAGGA-1	8	D
301	ATCCGAACAGCCAAAG-1	7	C
302	ATCCGAACAGTAATCC-1	4	A
303	ATCCGAACATTCCGAA-1	3	A
304	ATCGAGTGTCGGAAGT-1	1	A
305	ATCGAGTTCTGTGAAC-1	10	D
306	ATCTACTAGGGATGGG-1	10	D
307	ATCTACTAGTCACGCC-1	3	A

308	ATCTACTAGTTTGCGT-1	3	A
309	ATCTACTCAGTGCTGC-1	4	A
310	ATCTGCCCATTCGTTT-1	10	D
311	ATCTGCCGTCATGCCG-1	6	B
312	ATCTGCCTCCCGCATT-1	3	A
313	ATGAGGGAGAGGTAGA-1	10	D
314	ATGAGGGAGTTTGCGT-1	2	A
315	ATGAGGGTCCGACCAG-1	3	A
316	ATGCGATCATTACAGC-1	3	A
317	ATGCGATGTCAAGTTC-1	10	D
318	ATGCGATGTGATCCTA-1	8	D
319	ATGCGATGTTTAGGAA-1	8	D
320	ATGGGAGAGTCCCACG-1	3	A
321	ATGGGAGGTACCGTGC-1	11	D
322	ATGGGAGTCGGAGAGT-1	3	A
323	ATGGGAGTCTTAAGGC-1	11	D
324	ATGGGAGTCTTCTAAC-1	8	D
325	ATGTGTGCAAAGTAAC-1	11	D
326	ATGTGTGGTCTCGTCT-1	11	D
327	ATTACTCAGTAATCCC-1	3	A
328	ATTACTCCACACACGC-1	2	A
330	ATTACTCGTAAAGTCA-1	1	A
331	ATTACTCGTAGCGTCC-1	11	D
332	ATTATCCAGCGATGAC-1	3	A
333	ATTATCCAGGAGTACC-1	10	D
334	ATTATCCTCCGATACA-1	6	B
336	ATTCTACAGCTAAGAT-1	6	B
337	ATTCTACAGCTATGCT-1	5	A
338	ATTCTACCAGCGCTTG-1	9	D
339	ATTCTACGTGGAAAGA-1	11	D
340	ATTCTACTCTCCCTAG-1	11	D
341	ATTGGACTCGTAGCGC-1	8	D
342	ATTGGTGAGGGATACC-1	10	D
343	ATTGGTGCACTAAGGG-1	11	D
344	ATTGGTGTCGCCAACG-1	11	D
345	ATTTCTGAGTAGGTGC-1	7	C
346	ATTTCTGCACACACGC-1	3	A
347	ATTTCTGCACTAACTG-1	2	A
348	ATTTCTGTCACACGGC-1	6	B
349	CAACCAAAGTACGCGA-1	1	A
351	CAACCAAGTTCGATAC-1	11	D
352	CAACCTCAGACTTCCA-1	5	A

353	CAACCTCCAAGAACTA-1	4	A
354	CAACCTCTCAACTGCA-1	3	A
355	CAACCTCTCTGAAGCT-1	4	A
356	CAACTAGGTCGTCTTC-1	11	D
358	CAACTAGTCGACCATA-1	1	A
359	CAAGAAAAGCAAAGCC-1	6	B
360	CAAGAAACATAGGACG-1	6	B
361	CAAGAAAGTTTGTCTT-1	3	A
362	CAAGAAATCGAACAAA-1	3	A
364	CAAGATCAGGTGTTAA-1	6	B
366	CAAGATCCATTACGCA-1	6	B
367	CAAGATCGTGCTTAGT-1	4	A
368	CAAGATCGTGTTCGAT-1	10	D
370	CAAGATCTCACACGTA-1	8	D
371	CAAGGCCCAAACCCTA-1	11	D
372	CAAGGCCGTCACCTGG-1	3	A
373	CAAGTTGTCGCGGCAT-1	5	A
374	CACAAACCAAGAATCA-1	8	D
375	CACAAACCAGGCCTTG-1	6	B
376	CACAAACCATCAAGAA-1	2	A
377	CACAAACTCGAGAGGT-1	5	A
378	CACACAAGTACGTTTG-1	1	A
379	CACACAAGTTGCACTA-1	11	D
380	CACACCTGTACGTGCC-1	10	D
381	CACACTCAGACGTCGA-1	11	D
382	CACACTCAGCGTAGTG-1	11	D
383	CACACTCGTTAAAGGT-1	5	A
384	CACACTCTCTACAGTG-1	1	A
386	CACAGGCCATAGTGTC-1	5	A
387	CACAGGCGTAGTCTGT-1	11	D
388	CACAGGCTCCGTCTAC-1	7	C
389	CACAGTAAGTCGTACT-1	5	A
390	CACATAGAGGTATCGG-1	6	B
391	CACATAGAGTCGTCCG-1	11	D
392	CACATAGCACAACTTG-1	9	D
393	CACATAGGTACAATAG-1	4	A
394	CACATAGGTTGGTGAG-1	5	A
395	CACATAGTCTCAGTTT-1	3	A
396	CACATTTAGCAGCGTA-1	3	A
397	CACATTTAGGAATCGC-1	3	A
398	CACATTTCATGGAGAC-1	1	A
399	CACATTTGTCGCTTCT-1	10	D

400	CACATTTGTTTCCTGC-1	1	A
401	CACCACTCATCTAAGC-1	3	A
402	CACCACTGTCATGTTG-1	11	D
403	CACCAGGAGACAGTTA-1	11	D
404	CACCAGGAGGAGTAGA-1	2	A
405	CACCAGGCAATCTCTT-1	11	D
406	CACCAGGCACGGCTGT-1	11	D
407	CACCAGGCATTACTTC-1	3	A
408	CACCTTGAGGCTCTCG-1	11	D
409	CACCTTGCAGACACAG-1	3	A
410	CACCTTGCAGACAGTG-1	7	C
411	CACCTTGTCCGACGTG-1	8	D
412	CACTCCAAGCAGACTG-1	3	A
413	CACTCCAAGTGTCCAT-1	10	D
415	CAGAATCTCGAAAGGC-1	7	C
416	CAGAATCTCGGAATGG-1	2	A
417	CAGAATCTCTACGGGC-1	11	D
418	CAGAGAGAGTCGTACT-1	1	A
419	CAGAGAGAGTGAAGAG-1	8	D
420	CAGAGAGCACGAGCTC-1	8	D
421	CAGAGAGTCCGAAGCC-1	8	D
422	CAGAGAGTCCGAGATT-1	11	D
423	CAGATCAAGAAGGGTA-1	6	B
425	CAGATCAGTTCTGTCC-1	5	A
426	CAGCAGCGTTCAAGGG-1	8	D
428	CAGCAGCTCGCAACGC-1	1	A
429	CAGCATAAGCGTTGCC-1	10	D
430	CAGCATACAAACGGGT-1	5	A
431	CAGCATACACGGAATG-1	9	D
432	CAGCATAGTCCGCAGT-1	10	D
433	CAGCCGAAGCGTCAAG-1	2	A
435	CAGCGACAGCGCCTCA-1	8	D
436	CAGCGACCAAGTCGGA-1	8	D
437	CAGCTAATCCACTTCG-1	11	D
438	CAGCTAATCGAAAGGC-1	1	A
439	CAGCTGGAGCCACCTG-1	2	A
440	CAGCTGGGTCCTTGGG-1	3	A
441	CAGCTGGTCACGGTAT-1	5	A
442	CAGGTGCCAGCATGTT-1	11	D
443	CAGGTGCTCGAGGTGA-1	8	D
444	CAGTAACAGACCACGA-1	5	A
445	CAGTAACAGCACCGCT-1	8	D

446	CAGTAACCACACCTAA-1	2	A
447	CAGTAACCATACGTTG-1	11	D
448	CAGTCCTAGTCAAGGC-1	3	A
449	CAGTCCTGTCTTCACC-1	5	A
450	CATATGGTCTAGACAC-1	4	A
451	CATATTCCAGTAGAAT-1	1	A
452	CATATTCGTCGCGCTA-1	3	A
453	CATATTCGTGACCTGC-1	11	D
454	CATATTCTCTTGCTTA-1	4	A
455	CATCAAGTCCTACGAA-1	8	D
456	CATCAAGTCTAGCCTC-1	3	A
457	CATCAAGTCTCCATGC-1	11	D
458	CATCAGAGTTAGTGAA-1	5	A
459	CATCCACCATTACAGC-1	10	D
460	CATCCACTCCTGCGTT-1	10	D
461	CATCCACTCCTTGAAG-1	3	A
462	CATCGAACAATGGGAC-1	4	A
464	CATCGAACATTTCGTT-1	10	D
465	CATCGAAGTGCTCGAC-1	8	D
466	CATCGAAGTTTGGCGC-1	4	A
467	CATCGGGCACCCAAAT-1	10	D
468	CATCGGGTCTCAGTTT-1	3	A
469	CATGACACAACTCGCG-1	2	A
471	CATGACATCTCCGGAG-1	8	D
472	CATGCCTGTCCGCAAC-1	7	C
473	CATGCCTGTTACGGCC-1	3	A
474	CATGCCTTCATGTGAC-1	11	D
475	CATGGCGAGATATGGT-1	4	A
476	CATGGCGCAGTCGGAA-1	9	D
477	CATGGCGCATTTGCGA-1	6	B
478	CATGGCGTCGAGCACC-1	11	D
479	CATTATCAGCGTGAAC-1	3	A
480	CATTATCCAACAGCCC-1	10	D
482	CATTATCGTAAGAAGG-1	9	D
483	CATTCGCAGCAAATCA-1	1	A
484	CATTCGCCACGCACGT-1	7	C
485	CCAATCCGTCAAGCCC-1	6	B
487	CCACCTAAGCTCCTTC-1	10	D
488	CCACCTAAGTGGTAGC-1	5	A
490	CCACCTAGTTCGAGCC-1	6	B
491	CCACGGAAGACTGTAA-1	3	A
493	CCACGGACAGAAGACC-1	11	D

494	CCACTACAGACAAAGG-1	10	D
496	CCACTACTCTACGGCG-1	2	A
497	CCACTACTCTCGGAAT-1	10	D
498	CCAGCGATCTACAGTG-1	2	A
499	CCATGTCTCGAGTACT-1	5	A
500	CCATGTCTCGCTGAAT-1	11	D
501	CCATTCGAGTGCTGCC-1	1	A
502	CCATTCGCACATAAAG-1	8	D
503	CCCAATCGTCGACCAC-1	6	B
504	CCCAGTTAGCACGCCT-1	11	D
505	CCCATACAGCCACGTC-1	6	B
506	CCCATACCAACGAAAT-1	6	B
507	CCCATACCACAAGCTT-1	3	A
508	CCCATACCATCTTTCA-1	3	A
510	CCCTCCTCAGAATTCC-1	3	A
511	CCCTCCTGTATTCGCA-1	8	D
512	CCGGGATCACCAATGT-1	1	A
513	CCGGTAGAGCCAGTTT-1	6	B
514	CCGGTAGAGCCTATGT-1	9	D
515	CCGGTAGGTTCAGTAC-1	5	A
516	CCGGTAGTCGAGTTGT-1	5	A
517	CCGGTAGTCGCGATGC-1	8	D
518	CCGTACTAGGCTCATT-1	11	D
519	CCGTACTTCGGAGAGT-1	6	B
520	CCGTGGAAGTAGATGT-1	8	D
521	CCGTGGACACCAAAGG-1	9	D
522	CCGTGGACACTGGCCA-1	3	A
523	CCGTGGAGTCAACCGC-1	2	A
524	CCGTTCAAGTCGCCGT-1	11	D
525	CCTAAAGGTACCGTGC-1	9	D
526	CCTAAAGTCAAGCCGC-1	1	A
527	CCTACACAGGGATCTG-1	2	A
528	CCTACACCAACCGCTG-1	2	A
529	CCTACACGTGGAAGGG-1	8	D
530	CCTACACTCGCGATGC-1	9	D
531	CCTACACTCGTTATTC-1	11	D
532	CCTACACTCTCAGATG-1	2	A
533	CCTACCATCGGAGAGT-1	6	B
534	CCTAGCTCAATCCGTA-1	1	A
535	CCTAGCTTCATGTCAG-1	3	A
536	CCTAGCTTCTACATGG-1	4	A
537	CCTATTAAGCCAACAG-1	2	A

538	CCTATTACAACAGCCC-1	2	A
539	CCTATTACACGAGTTT-1	8	D
540	CCTATTAGTATTCGTG-1	3	A
541	CCTATTAGTGACCCAC-1	7	C
542	CCTATTATCGAACCCG-1	4	A
543	CCTCTGACATGGGCCT-1	5	A
544	CCTTACGAGTGACTCT-1	7	C
545	CCTTACGCAAGGTATA-1	3	A
546	CCTTACGCATACGTTG-1	1	A
547	CCTTACGTCATCAGCA-1	11	D
548	CCTTCCCCAACCCTGG-1	1	A
549	CCTTCCCCAACGTCTA-1	4	A
550	CCTTCCCGTTCAGGTT-1	8	D
551	CCTTCCCTCGCGGACT-1	10	D
553	CCTTCGAAGTCGTCCG-1	11	D
554	CCTTCGATCAGCAGCC-1	7	C
555	CCTTCGATCAGTACCA-1	10	D
556	CGAACATAGGCTAGTG-1	8	D
557	CGAACATGTGACTGAG-1	10	D
558	CGAACATTCAGTACCA-1	7	C
559	CGAACATTCTGGGATT-1	11	D
560	CGAATGTAGTACGACG-1	3	A
561	CGAATGTCAGACAGTG-1	11	D
562	CGAATGTCAGCCCATG-1	4	A
563	CGAATGTGTGTCAACT-1	5	A
564	CGACCTTAGGGTAACC-1	8	D
565	CGACCTTAGTGTTTGC-1	3	A
566	CGACCTTCAGTCGGAA-1	3	A
567	CGACTTCGTGGTGCAA-1	3	A
568	CGAGAAGCAAACTCAC-1	10	D
570	CGAGCACAGGCGATAC-1	3	A
572	CGAGCACCAGATATCC-1	7	C
573	CGAGCACGTCGAGTAG-1	9	D
574	CGAGCACTCAAGTTGC-1	8	D
575	CGAGCACTCGGAAGAC-1	3	A
576	CGAGCACTCTGATCAG-1	6	B
577	CGAGCCAAGCTGGTCC-1	5	A
579	CGAGCCACAAGAACTA-1	3	A
580	CGAGCCACAGACGAGT-1	11	D
581	CGAGCCACAGGACCAA-1	6	B
582	CGAGCCACATAGTGAA-1	8	D
583	CGATCGGGTACCGTGC-1	1	A

586	CGATGTAAGATCGGGT-1	5	A
587	CGATGTACAAGTACAA-1	1	A
588	CGATGTAGTCGCCAAC-1	2	A
589	CGATGTATCTCCAGCT-1	6	B
590	CGATTGAAGCTAGCCC-1	11	D
591	CGATTGACACCTCCAT-1	6	B
592	CGATTGAGTAAGAAGG-1	2	A
593	CGATTGAGTACTCCGG-1	3	A
594	CGATTGAGTATTCGCA-1	2	A
595	CGATTGAGTCAACTCA-1	1	A
596	CGATTGAGTGCATCTA-1	1	A
599	CGCCAAGAGGCTCAGA-1	8	D
601	CGCGGTAGTCGGAAGT-1	8	D
602	CGCGTTTCACAAGCTT-1	11	D
604	CGCGTTTTCTGGATCA-1	8	D
606	CGCTATCGTGATTGTC-1	1	A
607	CGCTATCTCCGGCTAG-1	11	D
608	CGCTATCTCGACTTCC-1	8	D
609	CGCTTCACAAGCACGA-1	3	A
610	CGCTTCACACGAAGGT-1	6	B
611	CGCTTCAGTTCTAGTG-1	1	A
612	CGGACACAGACGCTTT-1	10	D
613	CGGACACGTAGTAGTA-1	6	B
614	CGGACACGTCTAGGTT-1	11	D
615	CGGACACTCGAGTTGT-1	6	B
616	CGGACGTCACTTGCTC-1	2	A
618	CGGAGCTAGGCTACGA-1	11	D
619	CGGAGCTGTCCGAAGA-1	11	D
620	CGGAGCTTCTAGACAC-1	10	D
621	CGGAGTCAGAAACCTA-1	8	D
622	CGGAGTCAGCATGGCA-1	9	D
623	CGGAGTCAGCCAACAG-1	1	A
624	CGGAGTCCAGAGGCAT-1	5	A
625	CGGAGTCCAGCTTGAT-1	5	A
626	CGGAGTCGTATCAGTC-1	8	D
627	CGGAGTCGTCTTCACC-1	11	D
628	CGGCTAGAGACGCACA-1	8	D
629	CGGCTAGAGTAGCCGA-1	11	D
630	CGGCTAGAGTAGTATG-1	3	A
631	CGGCTAGGTGTCAACT-1	6	B
632	CGGCTAGGTTCTTCGC-1	10	D
633	CGGCTAGTCATGTGAC-1	8	D

634	CGGGTCAGTCATTACG-1	3	A
635	CGGTTAACACCACATA-1	11	D
636	CGGTTAACATGGAGAC-1	9	D
637	CGTAGCGAGGACAGAA-1	2	A
638	CGTAGCGAGTACGATA-1	6	B
639	CGTAGCGCAACGGGAT-1	3	A
640	CGTAGGCAGGCGTTGA-1	3	A
641	CGTAGGCCACTTGTTT-1	3	A
642	CGTAGGCCATGAGGGT-1	3	A
644	CGTCACTAGGCGCTCT-1	5	A
645	CGTCACTAGTCCCACG-1	8	D
646	CGTCACTCATTCCGAA-1	3	A
647	CGTCACTTCGTTACCC-1	11	D
649	CGTCAGGAGCAGGCTA-1	6	B
650	CGTCAGGAGGACAGCT-1	1	A
651	CGTCAGGCACGAGCTC-1	11	D
652	CGTCCATGTAGATGTA-1	3	A
653	CGTCCATTCTCCACAC-1	3	A
654	CGTCTACCAACGACTT-1	9	D
656	CGTCTACCACAGCTGC-1	10	D
657	CGTCTACGTGGAGCTA-1	8	D
658	CGTCTACTCTTAAGGC-1	11	D
659	CGTGAGCTCGAATGTC-1	10	D
661	CGTGTAAGTAGGTTTC-1	11	D
662	CGTGTAAGTTTCCGAA-1	1	A
663	CGTGTCTCAACCGCTG-1	6	B
664	CGTGTCTCACAGCTAT-1	11	D
665	CGTGTCTCATCCATCC-1	8	D
666	CGTGTCTTCCAACAAC-1	6	B
667	CGTGTCTTCCGAGTCG-1	9	D
668	CGTGTCTTCGTTGCAA-1	8	D
670	CGTTAGAAGGGTAACC-1	8	D
671	CGTTAGAAGTGGCACA-1	3	A
672	CGTTAGAGTCATCCAA-1	11	D
673	CGTTAGATCAGCCTGG-1	3	A
674	CGTTCTGAGCTGCGAA-1	1	A
675	CGTTCTGAGGCTAGCA-1	4	A
676	CGTTCTGGTTGAACAA-1	10	D
677	CGTTCTGTCTCTAGTT-1	11	D
678	CGTTGGGAGGCGCTCT-1	11	D
679	CGTTGGGAGTCCCACG-1	5	A
680	CTAACTTAGGGATGGG-1	10	D

681	CTAACTTGTTGACGGA-1	11	D
682	CTAACTTTCTTGGCCT-1	3	A
683	CTAAGACGTGATTGTC-1	11	D
684	CTAATGGCAACCTGAT-1	4	A
685	CTACACCAGTTACCCA-1	1	A
686	CTACACCGTACCGTGC-1	8	D
687	CTACATTCACGAGATG-1	8	D
688	CTACATTTCAAAGTGA-1	3	A
689	CTACATTTCACGTTAG-1	8	D
690	CTACCCACAGTAGGGT-1	10	D
691	CTACCCAGTAGAACAT-1	8	D
692	CTACCCAGTATATGAG-1	11	D
693	CTACGTCGTAGTGGCA-1	3	A
694	CTAGAGTTCGACAATC-1	9	D
695	CTAGCCTAGGGATACC-1	10	D
696	CTAGCCTTCCAACGAT-1	6	B
697	CTAGCCTTCTCCGGAG-1	5	A
698	CTAGCCTTCTTGGATG-1	3	A
699	CTAGCCTTCTTGTCCG-1	11	D
700	CTAGTGACAGTTTGCA-1	7	C
701	CTAGTGAGTAGGGTGT-1	8	D
703	CTCACACCATAGGTCT-1	2	A
704	CTCACACGTCTCTCTG-1	3	A
705	CTCACACTCAAGAGGC-1	3	A
706	CTCAGAACATGGAGAC-1	9	D
707	CTCAGAATCATGACCA-1	3	A
708	CTCATTAGTGTTCCGG-1	10	D
710	CTCATTATCTGATCAG-1	5	A
711	CTCCTAGAGGAGTACC-1	5	A
712	CTCCTAGCAAACCGAG-1	9	D
713	CTCGAAAAGCAGGTCA-1	5	A
714	CTCGAAACAAGCTACT-1	4	A
715	CTCGAAACATTTGTGG-1	7	C
716	CTCGAAATCTACAAGC-1	10	D
717	CTCGAGGAGCGATATA-1	11	D
718	CTCGAGGAGTGACATA-1	7	C
719	CTCGAGGCAACTAGTC-1	3	A
720	CTCGAGGCAAGAATCA-1	1	A
721	CTCGAGGCAAGTGTTC-1	10	D
722	CTCGAGGGTCATGTTG-1	6	B
723	CTCGGAGAGAGCAATT-1	3	A
724	CTCGGAGAGCTAACAA-1	2	A

725	CTCGGAGTCCACTAAG-1	8	D
726	CTCGGGAAGTGTTAGA-1	8	D
727	CTCGGGACAAGGGTGT-1	7	C
728	CTCGGGATCATATCTC-1	5	A
729	CTCGTACAGAGCTTCT-1	8	D
730	CTCGTACAGCTGCGAA-1	6	B
731	CTCGTACCACGTACAT-1	3	A
732	CTCGTACCACGTTTAG-1	3	A
733	CTCGTACCATGCCATA-1	2	A
734	CTCGTACGTTGCCTCT-1	11	D
735	CTCGTCAAGCGGCTTC-1	3	A
736	CTCGTCACAACGACGA-1	6	B
737	CTCGTCACAAGGTGAC-1	4	A
738	CTCGTCAGTGTCCCTT-1	5	A
739	CTCGTCATCACTGCGG-1	6	B
740	CTCTAATGTATCGCCG-1	3	A
741	CTCTAATTCATATCTC-1	10	D
742	CTCTACGAGAAAGTGG-1	11	D
743	CTCTACGGTGATTGGG-1	10	D
744	CTGAAGTAGTGATTGA-1	9	D
745	CTGAAGTCAGACTTGT-1	9	D
746	CTGAAGTGTAACGGCA-1	11	D
747	CTGAAGTGTCAACCGC-1	2	A
748	CTGAAGTGTCCCACAG-1	11	D
749	CTGAAGTTCGTAGCGC-1	8	D
750	CTGATAGAGCAGCGTA-1	6	B
751	CTGATAGCAGCTCATA-1	3	A
752	CTGATAGTCAGAAACA-1	8	D
753	CTGATCCGTTCGTCAA-1	3	A
754	CTGCCTAGTGGTCAGA-1	11	D
755	CTGCCTAGTTCCACAA-1	7	C
756	CTGCCTATCGTAGCGC-1	3	A
757	CTGCGGAAGAGTGACC-1	11	D
758	CTGCGGAAGATGTCTC-1	10	D
759	CTGCGGAAGTTGTCGT-1	6	B
760	CTGCGGAGTCTCCACT-1	11	D
761	CTGCGGATCAGAAACA-1	6	B
762	CTGCGGATCCAAAGAA-1	4	A
763	CTGCGGATCCCAGAAT-1	8	D
764	CTGCTGTAGTAGGCCA-1	3	A
765	CTGCTGTAGTCTCGGC-1	1	A
766	CTGCTGTCAACATAAG-1	3	A

767	CTGGTCTAGCGATATA-1	1	A
768	CTGGTCTAGGTCGGAT-1	6	B
770	CTGGTCTTCTCCCTAG-1	3	A
771	CTGTGCTCAATGGGAC-1	3	A
772	CTGTGCTCAGACACGA-1	1	A
773	CTGTGCTCATGGCTCG-1	2	A
774	CTGTGCTGTGGGCCTT-1	3	A
775	CTGTTTAAGAGTCTGG-1	8	D
776	CTGTTTAAGCTGCCCA-1	11	D
777	CTGTTTAAGGCTATCT-1	10	D
778	CTGTTTACACGCCTGA-1	6	B
779	CTGTTTAGTCTCTTTA-1	5	A
780	CTGTTTATCACCAGCG-1	2	A
781	CTTAACTAGCATCTTG-1	1	A
782	CTTAACTGTGGAAAGA-1	3	A
783	CTTAACTTCCTTGCAC-1	5	A
784	CTTACCGAGGGCTTCC-1	6	B
785	CTTACCGGTAAGTAAC-1	5	A
786	CTTACCGGTCACCTGG-1	8	D
787	CTTACCGGTGCTATTG-1	8	D
788	CTTACCGTCACACGTA-1	8	D
789	CTTACCGTCCGCGACA-1	4	A
790	CTTAGGACACACGCAC-1	5	A
791	CTTAGGATCTGGGCTG-1	11	D
792	CTTCTCTAGCTGCCCA-1	10	D
793	CTTCTCTAGGTCGGAT-1	11	D
794	CTTCTCTCAATGTAGA-1	9	D
795	CTTCTCTCAGCTATGT-1	11	D
796	CTTCTCTCATCGCATA-1	2	A
797	CTTCTCTTCCTATGAG-1	1	A
798	CTTGGCTAGACAGAGA-1	5	A
799	CTTGGCTAGCGCCTTG-1	8	D
800	CTTGGCTAGTCTCGTA-1	2	A
801	CTTGGCTGTTCTAGTG-1	9	D
802	CTTTGCGGTCAAAGCG-1	8	D
803	CTTTGCGTCCTCAGTC-1	4	A
804	GAAACTCGTGCGAACA-1	11	D
805	GAAACTCGTTCGTCAA-1	5	A
806	GAAACTCTCACGCTCT-1	5	A
807	GAAACTCTCACGTAGT-1	1	A
808	GAAACTCTCTGGTGAT-1	7	C
809	GAAATGAAGGCTCTTA-1	9	D

810	GAAATGACACCCTCTA-1	5	A
811	GAACATCGTACTTGCA-1	11	D
812	GAACATCTCATGCGCG-1	2	A
813	GAACCTACAAAGGTTA-1	7	C
814	GAACCTACAATCGCGC-1	1	A
815	GAACCTAGTCACATGT-1	10	D
816	GAACCTAGTCGAGTAG-1	4	A
817	GAACCTAGTTCGAGCC-1	1	A
818	GAACGGACACTTGCAA-1	11	D
820	GAACGGAGTACGTTTG-1	6	B
821	GAACGGATCTTCACGC-1	11	D
822	GAAGCAGAGGGAGTAA-1	10	D
823	GAAGCAGCACACGCAC-1	5	A
824	GAATAAGAGGCTACGA-1	1	A
825	GAATAAGCAAATACGA-1	8	D
826	GAATAAGCAGAGATCG-1	6	B
827	GAATGAACAACCTGCG-1	3	A
828	GAATGAATCTTCACAT-1	3	A
829	GACACGCCAAATGATG-1	11	D
830	GACAGAGAGCCTAACT-1	10	D
831	GACAGAGCACAGACCC-1	11	D
832	GACAGAGCAGTAATCC-1	10	D
833	GACAGAGCATCGGGCT-1	1	A
834	GACAGAGTCAGCCCGA-1	1	A
835	GACAGAGTCCTACGAA-1	8	D
836	GACAGAGTCCTGCGTT-1	7	C
837	GACCAATAGACTTTCG-1	3	A
838	GACCAATAGGACAGAA-1	11	D
839	GACCAATTCCGGCTAG-1	3	A
840	GACCTGGGTAGCCCTG-1	8	D
841	GACGCGTAGTAACCCT-1	9	D
842	GACGCGTCAGGTCAAG-1	9	D
843	GACGGCTGTGTAATGA-1	2	A
844	GACGGCTGTTGAGCAG-1	3	A
845	GACGTGCGTGCGTCAC-1	2	A
846	GACTAACCACCCGTGA-1	3	A
847	GACTAACCAGACACAG-1	6	B
848	GACTACACACAATCAC-1	10	D
849	GACTGCGCAGTAGGGT-1	5	A
850	GACTGCGGTGTCTGTA-1	3	A
851	GACTGCGTCATATCTC-1	10	D
852	GACTGCGTCGTAGCGC-1	2	A

853	GAGCAGAAGAATCGTA-1	3	A
854	GAGCAGAAGTTATCGC-1	3	A
855	GAGCAGATCCGCCTAT-1	8	D
856	GAGGTGAAGCCGAACA-1	5	A
857	GAGGTGACACTAACTG-1	3	A
858	GAGGTGACAGCTATGT-1	1	A
859	GAGGTGACAGTGAATA-1	5	A
861	GAGTCCGAGGGTTCGA-1	3	A
862	GAGTCCGCATACGGTT-1	8	D
863	GAGTCCGGTACTGCTA-1	1	A
864	GAGTCCGGTCCTAGTA-1	8	D
865	GAGTCCGTCAGACACT-1	1	A
866	GATCAGTCAAGCACGA-1	3	A
867	GATCAGTTCCACCCAT-1	1	A
868	GATCAGTTCCGCTCTA-1	6	B
869	GATCGATGTCCTACCT-1	9	D
870	GATCGCGAGTCCATAC-1	8	D
871	GATCGTAAGTAGGCCA-1	8	D
872	GATCGTACAACCGGAA-1	7	C
873	GATCGTACATACCAGT-1	9	D
875	GATCTAGCAAGTGTTC-1	10	D
876	GATCTAGTCACGCTCT-1	1	A
877	GATGAAAAGTAATCCC-1	10	D
879	GATGAAACATGCAGTT-1	5	A
880	GATGAAAGTAACGGCA-1	6	B
881	GATGAAAGTTCAGTAC-1	5	A
883	GATGCTAGTAGGCTGA-1	3	A
884	GATGCTAGTCTCTCGT-1	1	A
885	GATGCTAGTTCCCTAC-1	10	D
886	GATGCTAGTTGGAACG-1	6	B
887	GATGCTATCACTATGG-1	9	D
888	GATGCTATCATCAGCA-1	8	D
889	GATTCAGAGATGTGGC-1	10	D
890	GATTCAGGTTCAGTGT-1	10	D
891	GATTCAGTCGACAACT-1	4	A
892	GCAAACTAGCCACGTC-1	2	A
893	GCAAACTCAAGCCAAG-1	11	D
894	GCAAACTCACATTGGT-1	8	D
895	GCAAACTTCCTACGAA-1	9	D
896	GCAATCAAGGCAACAC-1	6	B
897	GCAATCAGTTAGTGAA-1	10	D
898	GCAATCAGTTGCCTCT-1	5	A

899	GCAATCATCCCTGAGG-1	5	A
900	GCAATCATCCGTTCAC-1	6	B
901	GCACATAGTGAGCGAT-1	5	A
902	GCACTCTAGACTTTCG-1	11	D
903	GCACTCTAGCATCTTG-1	11	D
904	GCACTCTAGTCCAGGA-1	1	A
905	GCACTCTCAAGCATGG-1	4	A
906	GCACTCTTCCACCTTG-1	8	D
908	GCAGCCACATTGCATG-1	6	B
910	GCAGCCATCGCTCTAC-1	5	A
911	GCAGTTAAGGCCCTTG-1	11	D
912	GCAGTTAGTAGCAGTG-1	8	D
913	GCAGTTAGTGGAAGGG-1	7	C
914	GCAGTTATCGCCCAGA-1	3	A
915	GCATACAAGATCCTGT-1	10	D
916	GCATACAAGGACAGAA-1	6	B
917	GCATACACACGTGCGT-1	8	D
918	GCATACATCAGATGTC-1	1	A
919	GCATACATCCGCTCTA-1	8	D
920	GCATGATCACGATAGG-1	3	A
921	GCATGATCACTCACCT-1	10	D
922	GCATGATCATGACCGC-1	8	D
923	GCATGATGTCGCTCAG-1	3	A
924	GCATGATGTTCGCGTG-1	1	A
925	GCATGATTCCGTTAAG-1	1	A
926	GCATGCGAGTAACCCT-1	1	A
927	GCATGTATCCACAGCG-1	9	D
928	GCCAAATAGTAAGTAC-1	3	A
930	GCCAAATCATTTGTGG-1	1	A
931	GCCAAATTCCGCGGAT-1	10	D
932	GCCAAATTCTACAGTG-1	3	A
933	GCCTCTAGTACGGTGA-1	8	D
934	GCCTCTATCACGTAGT-1	3	A
935	GCGACCACAACTCATG-1	2	A
936	GCGACCAGTCCTACCT-1	6	B
937	GCGAGAAAGCTTCAGT-1	2	A
938	GCGCAGTAGCGATGAC-1	1	A
939	GCGCAGTGTACTCGTA-1	1	A
940	GCGCAGTGTGACACGA-1	8	D
941	GCGCAGTGTGACCAAG-1	11	D
942	GCGCCAAAGCGAGAAA-1	2	A
943	GCGCCAAGTTGCCAAT-1	1	A

944	GCGCCAATCCTCATCG-1	11	D
945	GCGCGATAGGACTGGT-1	3	A
946	GCGCGATAGGATATAC-1	8	D
948	GCGGGTTAGGAGTTTA-1	10	D
949	GCGGGTTAGTGTATCC-1	5	A
950	GCGGGTTTCTATGCCC-1	3	A
951	GCTCCTAAGATCCCGC-1	7	C
952	GCTCCTAAGCCCGAAA-1	1	A
953	GCTCCTATCCCAGAAT-1	2	A
954	GCTCTGTAGCATGGCA-1	3	A
955	GCTCTGTAGTTAGCGG-1	6	B
956	GCTCTGTCAAACTCAC-1	6	B
957	GCTCTGTTCACTCATT-1	6	B
958	GCTGCAGAGGAGTTGC-1	10	D
959	GCTGCAGGTAACGTGG-1	6	B
960	GCTGCAGGTCGCGAAA-1	8	D
961	GCTGCAGGTTGAACAA-1	6	B
962	GCTGCGACACCTCCAT-1	10	D
963	GCTGCGATCACTACAG-1	9	D
964	GCTGCTTCACGATCTA-1	8	D
965	GCTGCTTGTCATCTAG-1	8	D
966	GCTGCTTTCAGTACAC-1	10	D
967	GCTGGGTAGGCATATA-1	8	D
968	GCTGGGTCAACTCCGG-1	3	A
969	GCTGGGTGTGTAGTTC-1	5	A
970	GCTGGGTGTGTCGCTG-1	4	A
971	GCTGGGTTCTATGGTG-1	1	A
972	GCTTCCAAGGGTTTCT-1	8	D
973	GCTTCCATCCTACGAA-1	3	A
974	GCTTCCATCTGGCCTT-1	8	D
975	GCTTCCATCTTCCGAC-1	8	D
976	GCTTGAACAGTGCTTA-1	1	A
978	GGAAAGCAGCCAGAAC-1	5	A
979	GGAAAGCCATGACTCA-1	8	D
980	GGAAAGCTCCACCTTG-1	2	A
981	GGAAAGCTCGTGTACA-1	11	D
982	GGAACTTAGGGTCTCC-1	10	D
984	GGAACTTGTCGGGAAT-1	6	B
985	GGAACTTGTTTCCATT-1	5	A
986	GGAACTTTCCGATACA-1	3	A
988	GGACAAGAGGGATTTA-1	1	A
989	GGACAAGGTGTAAAGT-1	2	A

990	GGACAAGGTTCAGTAC-1	6	B
991	GGACAAGTCGACGAAG-1	1	A
992	GGACAAGTCGCGCACA-1	3	A
993	GGACAGAAGGTATCGG-1	3	A
994	GGACAGACAAACCCTA-1	10	D
995	GGACAGACAGCCAGTC-1	1	A
996	GGACATTAGTCAAGCG-1	6	B
997	GGACGTCAGAACTTCC-1	1	A
998	GGACGTCCACACGTGC-1	10	D
999	GGAGCAAAGGTGCTTT-1	5	A
1001	GGATGTTAGCCAGGAT-1	5	A
1002	GGATGTTAGTGTACCT-1	3	A
1003	GGATTACAGCCACCTG-1	1	A
1004	GGATTACGTACTGTTG-1	8	D
1005	GGATTACTCCAACAAC-1	8	D
1006	GGATTACTCTCGGTTC-1	2	A
1007	GGCAATTGTACAACGG-1	2	A
1008	GGCAATTGTGCAACCC-1	1	A
1009	GGCAATTTCTTGGATG-1	10	D
1010	GGCCGATTCTGACGCG-1	2	A
1011	GGCGACTGTTACTGAC-1	1	A
1012	GGCGACTGTTCCGTCT-1	6	B
1013	GGCGACTGTTGGAACG-1	8	D
1014	GGCGACTTCCTTATTG-1	9	D
1016	GGCTCGACAATGGCTT-1	5	A
1017	GGCTCGACATACTGCA-1	10	D
1019	GGCTGGTCAACCTGCG-1	7	C
1020	GGCTGGTTCCTACGAA-1	1	A
1021	GGCTGGTTCTGTGGCG-1	4	A
1022	GGGAATGCAGATTGTC-1	8	D
1023	GGGAATGCATCATGGT-1	8	D
1024	GGGAATGGTGGTACAG-1	6	B
1025	GGGACCTCATCCATCC-1	11	D
1026	GGGACCTGTCCGGGTT-1	3	A
1027	GGGACCTTCATCGACA-1	6	B
1028	GGGAGATAGGCTAGCA-1	3	A
1029	GGGAGATCACAGACCC-1	8	D
1030	GGGAGATCAGCGCTTG-1	11	D
1031	GGGAGATCATGCAGTT-1	3	A
1032	GGGCACTGTGCAACCC-1	10	D
1033	GGGCACTGTTCAAGGG-1	9	D
1034	GGGCATCCACGCTGAC-1	1	A

1035	GGGCATCGTCTCTATT-1	2	A
1036	GGGCATCTCGAACCCG-1	3	A
1037	GGGTCTGCATCGGTCG-1	1	A
1038	GGGTCTGTCCACGATA-1	11	D
1039	GGGTTGCGTGTCGCTG-1	3	A
1040	GGTATTGAGGGTTCGA-1	6	B
1041	GGTATTGAGGTTCCTA-1	8	D
1042	GGTGAAGGTATTCGTG-1	2	A
1043	GGTGCGTCACTAACTG-1	6	B
1044	GGTGCGTGTGTTTCAG-1	1	A
1045	GGTGTTAGTCAGTGGA-1	6	B
1046	GTAACGTAGGCAGTCA-1	5	A
1048	GTAACGTTCCCACAAA-1	8	D
1049	GTAACTGAGCCGTCGT-1	2	A
1050	GTAACTGCATAGGGCA-1	6	B
1051	GTAACTGGTAGATGCG-1	11	D
1052	GTAACTGGTTGAACTC-1	8	D
1053	GTAACTGTCGAATGTC-1	11	D
1054	GTACGTACACTGGCCA-1	3	A
1055	GTACGTAGTGCGCTTG-1	2	A
1056	GTACTCCGTCAGTTTG-1	3	A
1057	GTACTCCGTTGGTATC-1	6	B
1058	GTACTTTAGAGTAATC-1	6	B
1059	GTACTTTCAGGCCGTT-1	10	D
1060	GTACTTTTCAGTACAC-1	11	D
1061	GTAGGCCCACGTGGCT-1	5	A
1062	GTAGGCCGTGTAATGA-1	3	A
1063	GTAGGCCTCCTTGCAC-1	10	D
1064	GTAGGCCTCGTGCTAA-1	2	A
1065	GTAGGCCTCTCGAGCG-1	6	B
1066	GTAGTCAGTCATTACG-1	1	A
1067	GTAGTCATCGAACCCG-1	2	A
1068	GTATCTTAGGGAGTAA-1	3	A
1069	GTATCTTAGGGATTTA-1	10	D
1070	GTATCTTCATTTGTGG-1	6	B
1071	GTATCTTGTCGCTTCT-1	11	D
1072	GTATCTTGTCTCGGTG-1	2	A
1073	GTATTCTCATAGGTCT-1	10	D
1074	GTATTCTCATGCAGTT-1	4	A
1075	GTCAAGTAGGACCAGT-1	6	B
1076	GTCACAAAGTGAACAT-1	8	D
1077	GTCACAAGTCAGTGGA-1	11	D

1078	GTCACGGGTATTGAAG-1	8	D
1079	GTCACGGTCCACAGAT-1	1	A
1080	GTCATTTAGCAAAGCC-1	8	D
1081	GTCATTTGTCGCTTCT-1	11	D
1082	GTCATTTTCCCTTATA-1	2	A
1083	GTCCTCAGTTTCCTGC-1	5	A
1084	GTCCTCATCTAAGACC-1	11	D
1085	GTCGGGTCACAGCTGC-1	9	D
1086	GTCTCGTCAGGTTAAA-1	2	A
1087	GTCTCGTCATTCCGAA-1	8	D
1088	GTCTCGTGTACGTGCC-1	8	D
1089	GTCTCGTTCACACGGC-1	2	A
1090	GTCTCGTTCATTGCTT-1	8	D
1091	GTCTTCGAGGTGCTAG-1	1	A
1092	GTCTTCGAGTGTTGAA-1	11	D
1093	GTCTTCGTCTGGTAGT-1	8	D
1094	GTGAAGGGTCCTCGGA-1	3	A
1095	GTGAAGGGTCTCGTCT-1	10	D
1096	GTGCAGCAGCTGAAAT-1	3	A
1097	GTGCAGCCAAAGTTAG-1	9	D
1098	GTGCAGCGTCCTACCT-1	11	D
1099	GTGCATACACTCTTAT-1	2	A
1100	GTGCGGTCAATCGTCA-1	4	A
1101	GTGCGGTCAGATCGAG-1	9	D
1102	GTGCGGTGTACTCACA-1	3	A
1104	GTGGGTCCACAGAGCA-1	3	A
1105	GTGGGTCGTACCACTA-1	2	A
1106	GTGGGTCGTTGGAACG-1	3	A
1107	GTGGGTCTCCGCTTGT-1	11	D
1108	GTGGGTCTCCTAGACA-1	8	D
1109	GTGTGCGAGAAGGTTT-1	1	A
1110	GTGTGCGAGCGCGATA-1	4	A
1111	GTGTGCGAGGCTCTCG-1	11	D
1112	GTGTGCGGTCGCTTCT-1	4	A
1113	GTTAAGCAGTGTTTGC-1	3	A
1114	GTTAAGCCAGATATCC-1	8	D
1115	GTTAAGCTCCACTTAT-1	9	D
1116	GTTAAGCTCTGTCGAA-1	11	D
1117	GTTACAGAGTACACCT-1	1	A
1118	GTTACAGTCAGGTGAG-1	4	A
1120	GTTCATTTCGAGTATC-1	5	A
1121	GTTCATTTCGTAGGGA-1	1	A

1122	GTTCATTTCTCTTCCT-1	5	A
1123	GTTCGGGTCAACAGTC-1	11	D
1124	GTTCTCGCAACCCACG-1	5	A
1125	GTTCTCGCACGCACCA-1	3	A
1126	GTTCTCGCAGTGCTCG-1	1	A
1127	GTTCTCGGTCATGTTG-1	11	D
1128	GTTCTCGTCATGACCA-1	8	D
1129	GTTTCTAAGGTGATTA-1	11	D
1130	GTTTCTAAGTGGGATC-1	8	D
1131	GTTTCTAGTCCGGTGT-1	6	B
1132	GTTTCTATCAGATTCG-1	9	D
1133	TAAACCGAGGCTAGAC-1	6	B
1134	TAAACCGAGGTAGCCA-1	5	A
1135	TAAACCGTCCAAGGGA-1	6	B
1136	TAAGAGACAGCGTCAC-1	10	D
1137	TAAGAGACATCTCGTC-1	9	D
1138	TAAGAGAGTGTGTTCA-1	3	A
1139	TAAGAGATCCAGGTTA-1	3	A
1140	TAAGCGTTCATTGGAC-1	8	D
1141	TAAGTGCAGGGATTCG-1	8	D
1142	TAAGTGCAGGTAAGTT-1	8	D
1143	TAAGTGCTCGGGTCAC-1	10	D
1144	TACACGACAAGCAAGC-1	10	D
1145	TACACGACACTAGGCC-1	3	A
1146	TACACGATCCGACCAG-1	3	A
1147	TACACGATCCGTTCAC-1	5	A
1148	TACAGTGAGTCCCGAC-1	3	A
1149	TACAGTGGTCAATTCG-1	9	D
1150	TACAGTGGTCTAACGT-1	1	A
1151	TACCTATAGTAGGTGC-1	10	D
1152	TACCTATGTAAACAGT-1	4	A
1153	TACCTATGTCAGTTTG-1	3	A
1154	TACCTATGTTGAACAA-1	3	A
1155	TACCTTAAGACTGGCA-1	6	B
1156	TACCTTAAGGAGCGAG-1	1	A
1157	TACCTTAAGTGAATTG-1	1	A
1158	TACCTTACATTCCGAA-1	1	A
1159	TACCTTATCACTCATT-1	1	A
1160	TACGGATAGCTGAACG-1	5	A
1161	TACGGATAGTGTTAGA-1	1	A
1162	TACGGATCAACACCGC-1	6	B
1163	TACGGATCAGAGGCAT-1	5	A

1165	TACGGATGTGATGTTC-1	10	D
1166	TACGGATTCAAGCCGC-1	8	D
1167	TACGGATTCACACGGC-1	6	B
1168	TACGGGCAGGTAAGTT-1	11	D
1169	TACGGGCGTATCTCTT-1	5	A
1170	TACGGTAAGAACAATC-1	10	D
1171	TACGGTAAGTTTCCTT-1	3	A
1172	TACGGTAGTGCTTTCC-1	3	A
1173	TACGGTATCTCGTGGG-1	5	A
1174	TACTCATAGAACAATC-1	10	D
1176	TACTCATAGGCATGGT-1	4	A
1177	TACTCATCAACGGCTC-1	6	B
1178	TACTCGCAGAAGGTGA-1	3	A
1180	TACTCGCCATGATGCT-1	5	A
1181	TACTCGCTCCACGATA-1	6	B
1182	TACTTGTAGTGGGTAC-1	10	D
1183	TACTTGTCAGACACAG-1	8	D
1185	TACTTGTGTTCGGTGC-1	10	D
1186	TACTTGTTCACCGGTG-1	10	D
1188	TAGACCAAGTCGATAA-1	9	D
1189	TAGACCACATCCACGG-1	1	A
1190	TAGACCACATGATGCT-1	10	D
1191	TAGACCATCATCAGCA-1	7	C
1192	TAGAGCTAGCTTTCAG-1	8	D
1193	TAGAGCTAGGCTAGGT-1	8	D
1195	TAGAGCTCATTGGTCA-1	3	A
1196	TAGAGCTTCTCAGATG-1	3	A
1197	TAGCCGGAGTCGTGTT-1	8	D
1198	TAGCCGGCAACCTCAA-1	8	D
1199	TAGCCGGCACCACACG-1	11	D
1200	TAGCCGGCACGCTGAC-1	10	D
1201	TAGCCGGGTTCCACAA-1	11	D
1202	TAGCCGGTCAGCGGCT-1	8	D
1203	TAGGCATAGCTAAACA-1	4	A
1204	TAGGCATAGTAGGTGC-1	6	B
1205	TAGGCATAGTGAACAT-1	8	D
1206	TAGGCATCAATCGTCA-1	9	D
1207	TAGGCATGTCGGCATC-1	3	A
1208	TAGGCATGTTCAGTAC-1	3	A
1209	TAGTGGTCAAGTGTTC-1	10	D
1210	TAGTGGTCACACACGC-1	6	B
1211	TAGTGGTGTGTGACAG-1	1	A

1213	TAGTTGGCATGAGAAT-1	5	A
1214	TAGTTGGCATGGCACC-1	1	A
1215	TAGTTGGTCCTGATTT-1	5	A
1216	TAGTTGGTCGAACCCG-1	9	D
1217	TATCAGGAGTCCGTAT-1	11	D
1219	TATCAGGGTTCGAGCC-1	7	C
1220	TATCAGGGTTCGTCAA-1	5	A
1221	TATCAGGTCTGGTAGT-1	3	A
1222	TATCAGGTCTTCTTGA-1	11	D
1223	TATCTCAAGACTGGGT-1	5	A
1224	TATCTCAGTAGTGGCA-1	3	A
1225	TATCTCAGTCCGAAGA-1	9	D
1226	TATCTCAGTGACCCGT-1	8	D
1227	TATGCCCAGGGCTTGA-1	11	D
1228	TATGCCCTCTAGAACC-1	3	A
1229	TATTACCAGCCAGGAT-1	4	A
1230	TATTACCGTGCTATTG-1	4	A
1231	TCAACGAAGAGCAATT-1	3	A
1233	TCAACGAAGGCTGCTC-1	11	D
1234	TCAACGATCTTTCGCG-1	6	B
1235	TCACAAGCATTTCCAT-1	8	D
1236	TCACGAAGTCAAACTC-1	3	A
1237	TCACGAAGTGTCTAAC-1	4	A
1238	TCAGATGAGAGCCCAA-1	8	D
1239	TCAGATGTCCGATACA-1	5	A
1240	TCAGCAAGTAGATGCG-1	11	D
1241	TCAGCAAGTGTTTCAG-1	3	A
1242	TCAGCAAGTTGGTGAG-1	3	A
1243	TCAGCTCAGTTGTCGT-1	5	A
1245	TCAGGATTCGGGTCAC-1	6	B
1246	TCAGGTACATAGACAA-1	3	A
1247	TCAGGTACATGTAGCT-1	10	D
1248	TCAGGTATCAAGTGCT-1	8	D
1249	TCATTACAGCCAGTTT-1	1	A
1250	TCATTACCACAGACCC-1	3	A
1251	TCATTACCATTCAGTG-1	1	A
1252	TCATTACTCTCCACAC-1	8	D
1253	TCATTTGAGTAGCCGA-1	8	D
1254	TCATTTGAGTCTCGTA-1	9	D
1255	TCCACACCAAGCAAGC-1	6	B
1256	TCCACACGTGCTCGAC-1	4	A
1257	TCCACACTCGCAACGC-1	6	B

1258	TCCCGATAGAATCGTA-1	11	D
1259	TCCCGATAGTGCGATG-1	9	D
1260	TCCCGATGTTAAGTAG-1	11	D
1261	TCGAGGCAGATCCTGT-1	3	A
1262	TCGAGGCCACCGAACC-1	6	B
1263	TCGAGGCCAGTGAAAT-1	3	A
1265	TCGCGAGAGAGTTGGC-1	1	A
1266	TCGCGAGGTGATCCTA-1	1	A
1267	TCGCGAGGTTCAAGAA-1	1	A
1268	TCGCGAGTCCGCTTGT-1	3	A
1269	TCGCGAGTCTACGGCG-1	2	A
1270	TCGCGTTAGACTGGGT-1	3	A
1271	TCGCGTTAGGACGAAA-1	7	C
1272	TCGCGTTCAACAACTC-1	3	A
1273	TCGCGTTGTCGCGAAA-1	8	D
1274	TCGCGTTGTCTAGCGC-1	2	A
1276	TCGGGACAGTCAAGGC-1	8	D
1277	TCGGGACGTTTCCATT-1	11	D
1278	TCGGGACTCGTAAGGG-1	2	A
1279	TCGGTAAGTATACACC-1	6	B
1280	TCGGTAATCAGAAACA-1	7	C
1281	TCGTACCCAATCCATG-1	9	D
1282	TCGTACCCACGTTTAG-1	2	A
1283	TCGTACCGTGTGACAG-1	11	D
1284	TCGTAGACAATCCGTA-1	4	A
1285	TCGTAGAGTGACTGAG-1	1	A
1286	TCTATTGCAACGAAAT-1	11	D
1287	TCTATTGCAGAGATCG-1	9	D
1288	TCTATTGCATGCGTGC-1	8	D
1289	TCTATTGGTATTCGCA-1	1	A
1290	TCTATTGGTTGGCGTC-1	2	A
1291	TCTATTGTCAGCCCGA-1	11	D
1292	TCTATTGTCATCGACA-1	1	A
1293	TCTCATAAGCAGCCCT-1	10	D
1294	TCTCATAAGGGATCTG-1	8	D
1295	TCTCATAGTGCACACC-1	10	D
1296	TCTCATATCTAAGACC-1	5	A
1297	TCTCATATCTGTTGTT-1	1	A
1298	TCTCTAAAGTAAGTAC-1	11	D
1299	TCTCTAAGTAGGTTTC-1	4	A
1300	TCTGAGAAGATCTGCT-1	6	B
1301	TCTGGAACACGTGGCT-1	3	A

1302	TCTGGAATCAGCGGCT-1	11	D
1303	TCTTCGGAGAGGGCTT-1	3	A
1304	TCTTCGGAGCCAGGAT-1	1	A
1305	TCTTCGGAGCTATGCT-1	10	D
1306	TCTTCGGGTCGGATGA-1	3	A
1307	TCTTTCCCACAGCTAT-1	11	D
1308	TCTTTCCCACTAGGCC-1	5	A
1309	TCTTTCCGTGGTGAGT-1	4	A
1311	TGAAAGAAGGTACTCT-1	10	D
1313	TGACAACAGCGAACTG-1	1	A
1314	TGACAACAGCTCCTTC-1	10	D
1315	TGACGGCAGTTACGGG-1	8	D
1317	TGACGGCGTCCGATGC-1	1	A
1318	TGACGGCGTGTCAACT-1	8	D
1319	TGACTAGGTAGGGTGT-1	11	D
1320	TGACTAGTCCTCGCTA-1	5	A
1321	TGACTAGTCGGGCTTG-1	1	A
1323	TGACTTTAGATTCACC-1	1	A
1324	TGACTTTAGCAACGGT-1	4	A
1325	TGACTTTAGGTGTGCA-1	6	B
1326	TGACTTTAGTACAGTA-1	8	D
1327	TGAGAGGAGTGTCCAT-1	10	D
1328	TGAGAGGGTCCCACAG-1	2	A
1329	TGAGAGGGTCGCGTAC-1	3	A
1330	TGAGAGGTCTACGGCG-1	8	D
1331	TGAGCATCATAGGTCT-1	9	D
1332	TGAGCATCATCGGGCT-1	10	D
1333	TGAGCATTCTGTATGG-1	3	A
1334	TGAGCCGAGGCATGGT-1	10	D
1335	TGAGCCGGTGCTGTAT-1	4	A
1336	TGAGCCGGTTCCCTAC-1	10	D
1337	TGAGGGACACCAATGT-1	4	A
1338	TGATTTCTCACGATAC-1	5	A
1339	TGATTTCTCCGACCAG-1	1	A
1340	TGCACCTAGTACGCGA-1	6	B
1341	TGCACCTTCAGCCCGA-1	7	C
1342	TGCCAAAAGACAGGCT-1	10	D
1343	TGCCAAACAAGTGTTC-1	3	A
1344	TGCCAAACACTACATG-1	2	A
1345	TGCCCATAGGATGCGT-1	1	A
1346	TGCCCATAGGCCATAG-1	11	D
1347	TGCCCATGTACCAGCC-1	11	D

1348	TGCCCATTCCAACAAC-1	11	D
1349	TGCCCTAAGCCAAACG-1	7	C
1351	TGCCCTAGTCGTAATC-1	3	A
1352	TGCCCTAGTGTAGTTC-1	4	A
1353	TGCCCTAGTTCTAGAC-1	6	B
1354	TGCGCAGAGAGGTACC-1	6	B
1356	TGCGGGTCAGACAGTG-1	10	D
1357	TGCGGGTCATACGTCA-1	8	D
1358	TGCGGGTCATCTGTAG-1	6	B
1359	TGCGGGTTCTATGGTG-1	9	D
1360	TGCGTGGAGTAGTGCG-1	3	A
1361	TGCTACCGTACGTCAT-1	7	C
1363	TGCTGCTTCGGAGAGT-1	8	D
1364	TGGACGCAGACGCTTT-1	8	D
1365	TGGACGCCATCGGCGT-1	10	D
1367	TGGACGCTCGAACCCG-1	8	D
1368	TGGCCAGGTCCTAGTA-1	7	C
1369	TGGCCAGTCAAGCCAT-1	5	A
1370	TGGCGCAGTCGACCAC-1	5	A
1371	TGGCGCAGTGTCCGAC-1	11	D
1372	TGGCGCATCCAACCGG-1	5	A
1373	TGGCGCATCCGGTTCT-1	10	D
1374	TGGCTGGAGTAAGTAC-1	10	D
1375	TGGCTGGCAACGCGCT-1	4	A
1377	TGGGAAGAGGAATGGA-1	11	D
1378	TGGGAAGCAAGGTGAC-1	6	B
1379	TGGGAAGGTGGTAACG-1	7	C
1380	TGGGAAGTCACTTTAC-1	3	A
1381	TGGGCGTAGGCTCAGA-1	3	A
1382	TGGGCGTGTTTCCTGC-1	3	A
1383	TGGGCGTTCACTGTTT-1	9	D
1384	TGGTTAGAGGGATGGG-1	3	A
1385	TGGTTAGAGTTAGCGG-1	3	A
1386	TGGTTAGTCTTATGGG-1	3	A
1387	TGGTTCCAGACAAAGG-1	11	D
1388	TGGTTCCAGAGTAAGG-1	9	D
1389	TGGTTCCAGGTGCACA-1	6	B
1390	TGGTTCCTCACACCTC-1	5	A
1391	TGTATTCCAACATAAG-1	1	A
1392	TGTATTCCAATCGCGC-1	1	A
1393	TGTCCCACAGTCGGAA-1	3	A
1394	TGTCCCAGTAGATAGT-1	1	A

1395	TGTGGTACATTATCGG-1	6	B
1396	TGTGGTACATTGAAGA-1	3	A
1397	TGTGGTAGTTTGGGCC-1	7	C
1398	TGTGGTATCAAGCCGC-1	11	D
1400	TGTTCCGCATAGAGCG-1	2	A
1401	TTAACTCCAGCTCATA-1	9	D
1402	TTAACTCCATGGCTAT-1	7	C
1403	TTAACTCTCAGTACAC-1	11	D
1404	TTAACTCTCGATAGTC-1	9	D
1405	TTAGGACAGAGCTGCA-1	1	A
1406	TTAGGACAGTTACCCA-1	3	A
1407	TTAGGACTCTGAAGTC-1	11	D
1408	TTAGGCAAGGTAAGTT-1	11	D
1409	TTAGGCACACCAATGT-1	5	A
1410	TTAGGCAGTAACGACG-1	7	C
1411	TTAGTTCAGAGCCACA-1	1	A
1412	TTATGCTAGTGCCATT-1	5	A
1413	TTATGCTCAGAGACGT-1	4	A
1414	TTCCCAGAGGAGCGTT-1	5	A
1415	TTCCCAGCACGATCTA-1	8	D
1417	TTCCCAGGTTCTCTCG-1	3	A
1418	TTCCCAGTCCGCCTTA-1	9	D
1419	TTCGAAGGTACTCGCG-1	9	D
1420	TTCGGTCAGCGATGAC-1	5	A
1421	TTCGGTCAGTGAATTG-1	1	A
1422	TTCGGTCCACTTGAGT-1	3	A
1423	TTCGGTCCATAGCACT-1	11	D
1424	TTCTACAAGAGGTAGA-1	8	D
1425	TTCTACAAGCAGAGAA-1	11	D
1426	TTCTACAAGTGACTCT-1	3	A
1427	TTCTACAGTCGCTTCT-1	4	A
1428	TTCTACAGTCTAACGT-1	1	A
1429	TTCTACATCTTAGCTT-1	8	D
1430	TTCTCAAAGGCACATG-1	4	A
1432	TTCTCAAGTAGGGTGT-1	10	D
1433	TTCTCAAGTGGCCACT-1	1	A
1434	TTCTCCTAGACAGACC-1	1	A
1435	TTCTCCTAGCAGCCCT-1	11	D
1436	TTCTCCTCATTCGTTT-1	1	A
1437	TTCTCCTTCATCGCGG-1	6	B
1438	TTCTTAGAGTACTTGC-1	3	A
1439	TTGAACGAGAATTGTG-1	4	A

1440	TTGAACGAGCACGCCT-1	3	A
1441	TTGAACGAGTGTCCAT-1	10	D
1442	TTGACTTAGGGCTTCC-1	8	D
1443	TTGACTTAGTCCGTAT-1	10	D
1444	TTGCCGTAGAGTAATC-1	3	A
1445	TTGCCGTAGTCGTGTT-1	8	D
1446	TTGCCGTGTAAGCGCA-1	3	A
1447	TTGCCGTGTGCACTTA-1	3	A
1448	TTGCGTCAGGATGTAT-1	4	A
1449	TTGCGTCTCATTTGCT-1	5	A
1450	TTGGAACGTAAGGTGC-1	8	D
1451	TTGGCAATCATGGTGT-1	5	A
1452	TTGTAGGAGAGTACAT-1	8	D
1453	TTGTAGGTCTTCTTGA-1	2	A
1454	TTTACTGAGAAACGCC-1	6	B
1455	TTTACTGAGACAGACC-1	10	D
1456	TTTACTGAGCCCAATT-1	2	A
1458	TTTACTGGTAACAATG-1	4	A
1459	TTTACTGTCCACGATA-1	3	A
1460	TTTATGCAGTAGTATG-1	2	A
1461	TTTATGCTCTGAAGGG-1	1	A
1462	TTTCCTCAGCTCCTTC-1	10	D
1463	TTTCCTCCAACAGCCC-1	1	A
1466	TTTGCGCAGTGCCATT-1	11	D
1467	TTTGCGCCAACTCATG-1	6	B
1468	TTTGCGCTCGATAAGA-1	9	D
1469	TTTGCGCTCTCATCCG-1	1	A
1470	TTTGGTTCAAGACGAC-1	11	D
1471	TTTGGTTGTGATGTTC-1	10	D
1472	TTTGGTTTCAGATTCG-1	11	D
1473	TTTGTCAGTGTGTTCA-1	10	D
1474	TTTGTCATCACTGCGG-1	6	B

Supplementary Table 4 | CNV events by cluster. Frequency of each of the 114 CNV events that passed filters across the 11 clusters and 4 groups. The start and end headers are the median values of the edges shared across all single cells for that event.

chrom	start	end	ploidy	event	Group A	Group B	Group C	Group D	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11
1	17200001	120520000	2	13	0	0.726	0.698	0.002	0	0	0	0	0	0.726	0.698	0.006	0	0	0
1	87340001	120520000	2	16	0.832	0.017	0.023	0.812	0.839	0.92	0.805	0.813	0.817	0.017	0.023	0.878	0.826	0.692	0.833
1	800001	12920000	2	14	0.021	0.88	0.907	0.03	0.007	0.034	0.018	0.04	0.025	0.88	0.907	0.035	0.029	0.015	0.038
1	13780001	16840000	2	15	0.011	0.487	0.605	0.014	0	0	0.009	0.027	0.025	0.487	0.605	0.023	0.014	0.008	0.011
1	149860001	249220000	3	54	0.115	0.12	0.047	0.109	0.161	0.08	0.086	0.12	0.133	0.12	0.047	0.087	0.101	0.12	0.124
1	17200001	87320000	3	51	0.646	0	0	0.698	0.705	0.761	0.629	0.627	0.533	0	0	0.738	0.87	0.504	0.737
1	800001	12920000	3	53	0.806	0.017	0	0.798	0.812	0.807	0.846	0.693	0.792	0.017	0	0.837	0.797	0.737	0.806
1	13780001	16840000	3	58	0.577	0.017	0	0.571	0.57	0.216	0.588	0.573	0.833	0.017	0	0.483	0.246	0.812	0.602
1	149860001	249160000	4	83	0.547	0.564	0.535	0.521	0.537	0.716	0.593	0.56	0.342	0.564	0.535	0.651	0.594	0.301	0.532
2	95400001	243000000	3	69	0.637	0.675	0.605	0.621	0.591	0.784	0.67	0.693	0.492	0.675	0.605	0.669	0.696	0.511	0.629
2	20001	87060000	3	71	0.559	0.556	0.442	0.571	0.604	0.795	0.624	0.52	0.233	0.556	0.442	0.674	0.797	0.165	0.683
2	33160001	87060000	3	72	0.123	0.068	0.116	0.15	0.134	0.023	0.072	0.133	0.267	0.068	0.116	0.081	0.029	0.429	0.059
2	20001	33120000	3	73	0.124	0.12	0.209	0.125	0.121	0.023	0.081	0.133	0.275	0.12	0.209	0.058	0.043	0.368	0.043
3	60001	24560000	2	28	0.945	0.906	0.837	0.898	0.987	0.989	0.914	0.96	0.908	0.906	0.837	0.919	0.928	0.85	0.903
3	93520001	197860000	4	92	0.593	0.65	0.372	0.564	0.685	0.739	0.633	0.507	0.35	0.65	0.372	0.605	0.696	0.353	0.629
3	26660001	90500000	4	93	0.701	0.59	0.558	0.668	0.698	0.818	0.742	0.693	0.55	0.59	0.558	0.779	0.768	0.496	0.651
3	24560001	26660000	9	114	0.118	0.145	0.116	0.139	0.134	0.273	0.072	0.173	0.033	0.145	0.116	0.105	0.333	0.045	0.167
4	80001	49080000	2	29	0.801	0.769	0.791	0.786	0.866	0.898	0.814	0.787	0.633	0.769	0.791	0.849	0.928	0.624	0.79
4	52680001	190900000	4	94	0.478	0.504	0.442	0.455	0.523	0.705	0.493	0.533	0.192	0.504	0.442	0.465	0.609	0.203	0.57
4	70300001	190900000	4	96	0.044	0.051	0.093	0.068	0.034	0.023	0.05	0.027	0.075	0.051	0.093	0.076	0.087	0.053	0.065
4	52680001	69360000	4	95	0.184	0.205	0.279	0.198	0.174	0.102	0.163	0.16	0.308	0.205	0.279	0.198	0.13	0.323	0.134
5	70740001	180700000	2	30	0.677	0.786	0.651	0.711	0.752	0.852	0.719	0.6	0.425	0.786	0.651	0.82	0.855	0.564	0.661
5	20001	46400000	2	31	0.841	0.897	0.767	0.846	0.893	0.875	0.833	0.907	0.725	0.897	0.767	0.884	0.942	0.654	0.914
5	49440001	68820000	2	32	0.93	0.983	0.907	0.93	0.946	0.955	0.946	0.96	0.842	0.983	0.907	0.953	0.957	0.85	0.957
6	65300001	170920000	2	33	0.046	0.248	0.14	0.021	0	0.102	0.063	0.027	0.042	0.248	0.14	0.023	0.029	0.03	0.011
6	65300001	170920000	3	74	0.625	0.521	0.488	0.641	0.725	0.659	0.615	0.693	0.45	0.521	0.488	0.808	0.623	0.414	0.656
6	220001	58780000	3	75	0.083	0.085	0.093	0.055	0.04	0.125	0.081	0.04	0.133	0.085	0.093	0.07	0.058	0.068	0.032
6	200001	58760000	4	100	0.686	0.41	0.442	0.67	0.772	0.716	0.719	0.707	0.483	0.41	0.442	0.669	0.768	0.466	0.78
6	61880001	65320000	4	97	0.064	0.026	0.023	0.054	0.054	0.034	0.086	0.013	0.092	0.026	0.023	0.052	0.043	0.053	0.059
6	61880001	65300000	4	98	0.121	0.034	0.093	0.082	0.141	0.102	0.14	0.147	0.058	0.034	0.093	0.093	0.116	0.083	0.059
6	61880001	65280000	4	99	0.038	0.077	0.07	0.064	0.04	0.034	0.041	0.013	0.05	0.077	0.07	0.07	0.043	0.075	0.059
7	150740001	159120000	2	34	0.908	0.889	0.791	0.918	0.933	0.92	0.9	0.933	0.867	0.889	0.791	0.913	0.913	0.925	0.919
7	80001	58040000	4	101	0.807	0.778	0.698	0.814	0.826	0.898	0.819	0.813	0.692	0.778	0.698	0.89	0.841	0.692	0.823
7	76820001	125740000	4	102	0.752	0.709	0.698	0.746	0.772	0.841	0.724	0.773	0.7	0.709	0.698	0.744	0.783	0.707	0.763
7	63260001	74140000	4	103	0.939	0.923	0.884	0.912	0.966	0.966	0.946	0.907	0.892	0.923	0.884	0.936	0.971	0.872	0.898
7	143800001	150740000	4	104	0.299	0.35	0.209	0.304	0.322	0.284	0.262	0.453	0.25	0.35	0.209	0.25	0.362	0.278	0.349
7	144100001	150740000	4	105	0.349	0.265	0.349	0.316	0.356	0.239	0.357	0.307	0.433	0.265	0.349	0.366	0.232	0.361	0.269
7	144160001	150720000	4	106	0.074	0.06	0.07	0.066	0.074	0.08	0.109	0.013	0.042	0.06	0.07	0.047	0.101	0.068	0.07

7	126140001	143860000	6	113	0.801	0.726	0.674	0.777	0.799	0.886	0.824	0.84	0.675	0.726	0.674	0.802	0.913	0.692	0.763
8	46880001	146300000	3	76	0.717	0.752	0.07	0.005	0.752	0.875	0.715	0.747	0.542	0.752	0.07	0	0.014	0.015	0
8	12400001	43780000	3	79	0.838	0.863	0.023	0	0.893	0.943	0.814	0.867	0.717	0.863	0.023	0	0	0	0
8	160001	7000000	3	77	0.873	0.855	0.07	0	0.866	0.864	0.905	0.893	0.817	0.855	0.07	0	0	0	0
8	8080001	11880000	3	78	0.975	0.991	0.07	0.002	0.98	0.989	0.986	0.987	0.933	0.991	0.07	0.006	0	0	0
8	46880001	146300000	4	107	0.002	0.009	0.442	0.679	0	0	0.005	0	0	0.009	0.442	0.744	0.783	0.526	0.688
8	12400001	43780000	4	110	0	0	0.535	0.859	0	0	0	0	0	0	0.535	0.855	0.928	0.782	0.892
8	160001	7000000	4	108	0	0	0.512	0.862	0	0	0	0	0	0	0.512	0.866	0.899	0.827	0.871
8	8080001	11880000	4	109	0	0	0.651	0.946	0	0	0	0	0	0	0.651	0.936	0.957	0.932	0.962
9	200001	30340000	2	35	0.879	0.94	0.86	0.888	0.899	0.92	0.896	0.88	0.792	0.94	0.86	0.901	0.957	0.827	0.892
9	71040001	1.41E+08	3	80	0.286	0.145	0.279	0.075	0.765	0.33	0.036	0.067	0.258	0.145	0.279	0.064	0.13	0.083	0.059
9	30340001	38760000	3	81	0.06	0.051	0.302	0.062	0.02	0.114	0.045	0.08	0.083	0.051	0.302	0.052	0.116	0.068	0.048
9	71040001	141020000	4	111	0.467	0.564	0.442	0.702	0	0.455	0.765	0.733	0.342	0.564	0.442	0.756	0.696	0.602	0.726
9	30340001	38760000	4	112	0.815	0.838	0.558	0.838	0.852	0.739	0.869	0.787	0.742	0.838	0.558	0.814	0.797	0.835	0.876
10	49400001	135420000	2	4	0.772	0.778	0.721	0.741	0.772	0.864	0.778	0.8	0.675	0.778	0.721	0.733	0.899	0.586	0.801
10	120001	39140000	2	5	0.003	0.923	0.837	0	0.007	0	0	0	0.008	0.923	0.837	0	0	0	0
10	120001	7720000	2	6	0.058	0	0	0.07	0.054	0.023	0.077	0.027	0.075	0	0	0.087	0.058	0.03	0.086
10	120001	7640000	2	7	0.219	0	0	0.243	0.195	0.159	0.186	0.373	0.258	0	0	0.192	0.145	0.346	0.253
10	120001	7580000	2	8	0.147	0	0	0.161	0.134	0.125	0.172	0.107	0.158	0	0	0.174	0.13	0.128	0.183
10	33360001	39140000	2	9	0.115	0	0	0.114	0.081	0.08	0.172	0.067	0.108	0	0	0.14	0.087	0.075	0.129
10	33380001	39140000	2	10	0.21	0	0	0.207	0.295	0.182	0.149	0.227	0.225	0	0	0.14	0.217	0.308	0.194
10	33420001	39140000	2	11	0.06	0	0	0.057	0.047	0.057	0.054	0.053	0.092	0	0	0.087	0.058	0.023	0.054
10	42380001	46160000	2	12	0.939	0.949	0.814	0.932	0.919	0.875	0.955	0.96	0.967	0.949	0.814	0.942	0.942	0.932	0.919
10	7360001	33500000	3	43	0.172	0	0	0.173	0.107	0.216	0.19	0.173	0.183	0	0	0.186	0.232	0.09	0.199
10	7620001	33400000	3	44	0.32	0	0	0.305	0.315	0.341	0.249	0.44	0.367	0	0	0.25	0.304	0.459	0.247
10	7680001	33300000	3	45	0.32	0	0	0.314	0.396	0.205	0.385	0.24	0.242	0	0	0.366	0.261	0.18	0.382
11	54800001	134940000	3	46	0.438	0.444	0.442	0.541	0.309	0.705	0.525	0.56	0.167	0.444	0.442	0.529	0.638	0.338	0.661
11	81120001	134940000	3	52	0.253	0.077	0.116	0.193	0.497	0.125	0.095	0.2	0.367	0.077	0.116	0.256	0.203	0.263	0.081
11	200001	51580000	3	47	0.476	0.744	0.651	0.8	0	0.602	0.756	0.8	0.258	0.744	0.651	0.82	0.826	0.774	0.79
11	54800001	80780000	3	48	0.084	0.051	0.047	0.075	0.181	0.034	0.041	0.027	0.117	0.051	0.047	0.128	0.014	0.098	0.032
11	54800001	80400000	3	49	0.057	0.043	0.047	0.077	0.081	0.057	0.018	0.133	0.05	0.043	0.047	0.11	0.072	0.083	0.043
11	40840001	51580000	3	50	0.15	0.06	0	0.002	0.523	0.068	0	0	0.117	0.06	0	0.006	0	0	0
11	200001	40840000	4	82	0.24	0.043	0.023	0.002	0.785	0.193	0	0	0.192	0.043	0.023	0	0.014	0	0
12	37860001	133840000	3	55	0.689	0.709	0.465	0.738	0.732	0.795	0.724	0.667	0.508	0.709	0.465	0.837	0.928	0.556	0.704
12	200001	34840000	3	56	0.864	0.906	0.721	0.884	0.832	0.92	0.864	0.92	0.825	0.906	0.721	0.884	0.942	0.805	0.919
13	19280001	115080000	2	17	0.075	0.017	0.023	0.059	0.067	0.091	0.068	0.027	0.117	0.017	0.023	0.058	0.116	0.045	0.048
13	19280001	115100000	3	57	0.51	0.436	0.395	0.371	0.732	0.625	0.552	0.093	0.333	0.436	0.395	0.738	0.42	0.293	0.07
13	19420001	115100000	4	84	0.133	0.274	0.279	0.282	0.007	0.148	0.077	0.56	0.117	0.274	0.279	0.017	0.261	0.211	0.586
14	20200001	107280000	3	59	0.135	0.111	0.07	0.1	0.027	0.864	0	0.093	0.008	0.111	0.07	0	0.797	0.008	0
14	44260001	107280000	3	61	0.639	0.65	0.698	0.621	0.711	0.011	0.792	0.813	0.617	0.65	0.698	0.797	0.029	0.549	0.731
14	20200001	43820000	3	60	0.757	0.744	0.837	0.8	0.852	0	0.928	0.827	0.833	0.744	0.837	0.919	0.029	0.865	0.93
15	30940001	82580000	2	18	0.87	0.761	0.814	0.855	0.879	0.989	0.842	0.88	0.817	0.761	0.814	0.89	0.928	0.759	0.866

15	23980001	28540000	2	19	0.905	0.94	0.814	0.911	0.933	0.864	0.896	0.907	0.917	0.94	0.814	0.93	0.812	0.91	0.93
15	84920001	102400000	4	85	0.874	0.88	0.86	0.905	0.906	0.875	0.878	0.853	0.842	0.88	0.86	0.907	0.913	0.902	0.903
16	46440001	90160000	2	20	0.851	0.795	0.674	0.77	0.872	0.943	0.86	0.92	0.7	0.795	0.674	0.762	0.855	0.639	0.839
16	80001	16280000	3	62	0.711	0.803	0.326	0.268	0.819	0.727	0.828	0.013	0.783	0.803	0.326	0.529	0.261	0.241	0.048
16	18800001	32660000	3	63	0.159	0.137	0.116	0.043	0.101	0.011	0.154	0	0.45	0.137	0.116	0.064	0	0.098	0
16	80001	16280000	4	86	0.11	0.043	0.465	0.582	0	0.102	0.014	0.733	0.042	0.043	0.465	0.314	0.536	0.556	0.866
17	25280001	81100000	3	64	0.787	0.795	0.721	0.734	0.846	0.909	0.824	0.44	0.775	0.795	0.721	0.872	0.841	0.684	0.602
17	40001	22240000	3	65	0.868	0.897	0.791	0.82	0.913	0.943	0.946	0.573	0.8	0.897	0.791	0.93	0.841	0.789	0.731
17	25280001	81080000	4	87	0.046	0.017	0.07	0.075	0	0.011	0	0.333	0.033	0.017	0.07	0	0.058	0.045	0.172
17	20001	22240000	4	88	0.043	0.017	0.07	0.091	0.007	0.011	0	0.32	0.017	0.017	0.07	0.006	0.072	0.068	0.194
18	18540001	7.80E+07	2	21	0.006	0.803	0.791	0.004	0	0.023	0.005	0	0.008	0.803	0.791	0.006	0	0.008	0
18	140001	15200000	2	22	0.002	0.923	0.93	0.002	0.007	0	0	0	0	0.923	0.93	0	0	0.008	0
18	140001	10060000	2	23	0.086	0	0	0.109	0.081	0.102	0.086	0.147	0.042	0	0	0.157	0.116	0.105	0.065
18	140001	9940000	2	24	0.067	0	0	0.061	0.101	0.034	0.05	0.08	0.075	0	0	0.058	0.043	0.068	0.065
18	140001	9880000	2	25	0.179	0	0	0.205	0.154	0.114	0.163	0.253	0.242	0	0	0.163	0.13	0.293	0.21
18	140001	9840000	2	26	0.107	0	0	0.096	0.128	0.068	0.113	0.053	0.133	0	0	0.11	0.159	0.053	0.091
18	140001	9760000	2	27	0.089	0	0	0.075	0.081	0.068	0.081	0.12	0.108	0	0	0.099	0.087	0.075	0.048
18	18540001	78000000	3	66	0.812	0.051	0.047	0.773	0.859	0.784	0.842	0.88	0.675	0.051	0.047	0.756	0.899	0.639	0.839
19	27740001	59100000	3	67	0.848	0.863	0.814	0.848	0.872	0.909	0.891	0.813	0.717	0.863	0.814	0.826	0.87	0.805	0.892
19	260001	24600000	3	68	0.868	0.846	0.767	0.846	0.893	0.92	0.896	0.8	0.792	0.846	0.767	0.895	0.884	0.782	0.833
20	29420001	62900000	4	89	0.827	0.838	0.744	0.9	0.859	0.864	0.814	0.88	0.75	0.838	0.744	0.936	0.928	0.835	0.903
20	60001	26320000	4	90	0.862	0.88	0.814	0.88	0.852	0.886	0.896	0.84	0.808	0.88	0.814	0.907	0.942	0.797	0.892
21	15220001	48060000	3	70	0.865	0.769	0.791	0.852	0.852	0.875	0.878	0.947	0.8	0.769	0.791	0.843	0.913	0.827	0.855
22	16860001	51180000	4	91	0.842	0.829	0.698	0.82	0.846	0.909	0.896	0.853	0.683	0.829	0.698	0.849	0.826	0.699	0.876
X	92380001	155240000	2	36	0.655	0.726	0.488	0.632	0.812	0.841	0.756	0.68	0.125	0.726	0.488	0.634	0.797	0.398	0.737
X	300001	58560000	2	42	0.069	0.034	0.047	0.066	0.047	0.318	0.014	0.08	0.008	0.034	0.047	0.023	0.304	0.03	0.043
X	114420001	155240000	2	37	0.167	0.137	0.14	0.175	0.06	0.045	0.095	0.12	0.55	0.137	0.14	0.174	0.058	0.323	0.113
X	300001	31300000	2	38	0.783	0.821	0.651	0.789	0.812	0.5	0.878	0.827	0.75	0.821	0.651	0.895	0.522	0.722	0.839
X	61720001	88460000	2	39	0.934	0.957	0.767	0.927	0.953	0.966	0.941	0.893	0.9	0.957	0.767	0.948	0.942	0.887	0.93
X	32300001	58560000	2	40	0.848	0.923	0.698	0.834	0.913	0.602	0.932	0.827	0.808	0.923	0.698	0.919	0.638	0.805	0.849
X	92380001	114200000	2	41	0.103	0.068	0.116	0.123	0.04	0.045	0.032	0.08	0.367	0.068	0.116	0.128	0.043	0.248	0.059
Y	13460001	19560000	0	1	0.982	0.974	1	0.98	0.973	1	0.982	1	0.967	0.974	1	1	0.986	0.94	0.989
Y	20800001	24520000	0	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Y	6620001	10080000	0	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Supplementary file 1 | R script to perform Clustering of single cell CNV data, generating a CNV mutation matrix with polymorphic events.

```
library(GenomicRanges)
library(dplyr)

# path to outs folder
PATH_2_OUTS <- "YOUR_PATH"

# read the per cell summary
per_cell_summary <- read.table(file.path(PATH_2_OUTS,"per_cell_summary_metrics.csv"), sep=",",header =
TRUE)

# define inputs and cutoffs
cells <- per_cell_summary$cell_id[per_cell_summary$is_noisy==0]
cells <- paste0("cell_",cells)
NCELLS <- length(cells)
EVENT_QUAL = 15
EVENT_SIZE = 2e6
EVENT_FREQ = .05
CUTOFF_N <- round(NCELLS*EVENT_FREQ)

#' read bed file and subset to keep events only from
#'terminal nodes that are not flagged as noisy
get_bed <- function(path_2_outs){
  df <- read.table(file.path(path_2_outs,"node_cnv_calls.bed"),header=FALSE,sep="\t")
  names(df) <- c("chrom", "start", "end", "node", "ploidy", "qual")
  nnodes <- max(df$node)
  ncells <- nnodes/2
  df$node <- ifelse(df$node>ncells,paste0("inode_",df$node),paste0("cell_",df$node))
  return(df)
}

bed <- get_bed(PATH_2_OUTS)
bed <- subset(bed,node %in% cells)
bed.gr <- makeGRangesFromDataFrame(bed, keep.extra.columns=TRUE,
                                   ignore.strand=TRUE,
                                   seqinfo=NULL,
                                   seqnames.field="chrom",
                                   start.field="start",
                                   end.field="end",
                                   starts.in.df.are.0based=TRUE)

# apply a quality and size cut off and
# order the events going from largest to smallest
bed.gr <- bed.gr[bed.gr$qual>EVENT_QUAL]
bed.gr <- bed.gr[width(bed.gr) > EVENT_SIZE]
bed.gr <- bed.gr[order(-width(bed.gr),start(bed.gr))]

#split bed file by ploidy and chromosome
bed.gr <- split(bed.gr,bed.gr$ploidy)
```

```
split.bed.gr <- lapply(bed.gr, function(x) split(x,seqnames(x)))

# find pairwise 90% reciprocal overalps with the same ploidy
events.byploidy <- list()
for (i in seq_along(split.bed.gr)){
  gr <- split.bed.gr[[i]]
  hits <- lapply(gr, function(x) findOverlaps(x,drop.self=FALSE,drop.redundant=TRUE,type="any",select="all"))
  xhits <- lapply(seq_along(gr), function(x) gr[[x]][queryHits(hits[[x]])])
  yhits <- lapply(seq_along(gr), function(x) gr[[x]][subjectHits(hits[[x]])])
  pmax <- lapply(seq_along(gr), function(x) pmax(width(yhits[[x]]),width(xhits[[x]])))
  overlaps <- lapply(seq_along(gr), function(x) pintersect(xhits[[x]],yhits[[x]]))
  frac <- lapply(seq_along(gr), function(x) width(overlaps[[x]])/pmax[[x]])
  merge <- lapply(frac, function(x) x>=0.9)

  final <- list()
  for(j in seq_along(gr)){
    tokeep <- yhits[[j]][merge[[j]]]
    tokeep$qhit <- queryHits(hits[[j]])[merge[[j]]]
    tokeep$subhit <- subjectHits(hits[[j]])[merge[[j]]]
    #the same subject hit is being grouped multiple times and supporting different queries
    tokeep <- tokeep[!duplicated(tokeep$subhit)]
    qcount <- table(tokeep$qhit)
    tokeep <- tokeep[tokeep$qhit %in% names(qcount[qcount>CUTOFF_N])]
    final[[j]] <- tokeep
  }
  final <- do.call("c",final)
  events.byploidy[[i]] <- final
}

# generate unique labels for shared events
label.qhit <- sapply(events.byploidy, function(x) paste0(x$qhit))
label.chr <- sapply(events.byploidy, function(x) as.vector(seqnames(x)))
label <- sapply(seq_along(label.qhit), function(i) paste0(label.chr[[i]],label.qhit[[i]]))
label <- sapply(seq_along(label),function(i) paste0("ploidy",i-1,"_chr",label[[i]]))
label <- unlist(label)
tokeep <- sapply(label,function(x) grepl("ploidy\\d+_chr[XY]*\\d+",x))
label <- label[tokeep]
label <- factor(label,labels = 1:length(unique(label)))

# make a single GenomicRanges object
events.05.gr <- do.call("c",events.byploidy)
events.05.gr$event <- label
events.05.gr$qhit <- NULL
events.05.gr$subhit <- NULL
rm(events.byploidy)
```

Supplementary file 2 | Python script to split BAM files by barcode assignment, generating a BAM file for each sub-clone.

```
import pysam
import pandas as pd
import sys
import os
import argparse

def parse_args():
  parser = argparse.ArgumentParser()
parser.add_argument('--bam', help='Input BAM file')
parser.add_argument('--out-root', help='Root directory to write output BAMs to')
parser.add_argument('--csv', help='CSV file with two columns: barcode and cluster.')
return parser.parse_args()

if __name__ == '__main__':
  args = parse_args()
df = pd.read_csv(args.csv)
assert 'barcode' in df.columns and 'cluster' in df.columns, 'Missing column identifiers'
assert os.path.exists(args.bam), 'Cannot find input BAM'
fh = pysam.Samfile(args.bam)
cluster_map = dict(zip(df.barcode, df.cluster))
os.makedirs(args.out_root)
out_handles = {}
for c in set(df.cluster):
  o = pysam.Samfile(os.path.join(args.out_root, 'cluster' + str(c) + '.bam'), 'wb', template=fh)
out_handles[c] = o
for rec in fh:
  if rec.has_tag('CB') and rec.get_tag('CB') in cluster_map:
  cluster = cluster_map[rec.get_tag('CB')]
out_handles[cluster].write(rec)
for h in out_handles.values():
  h.close()
```