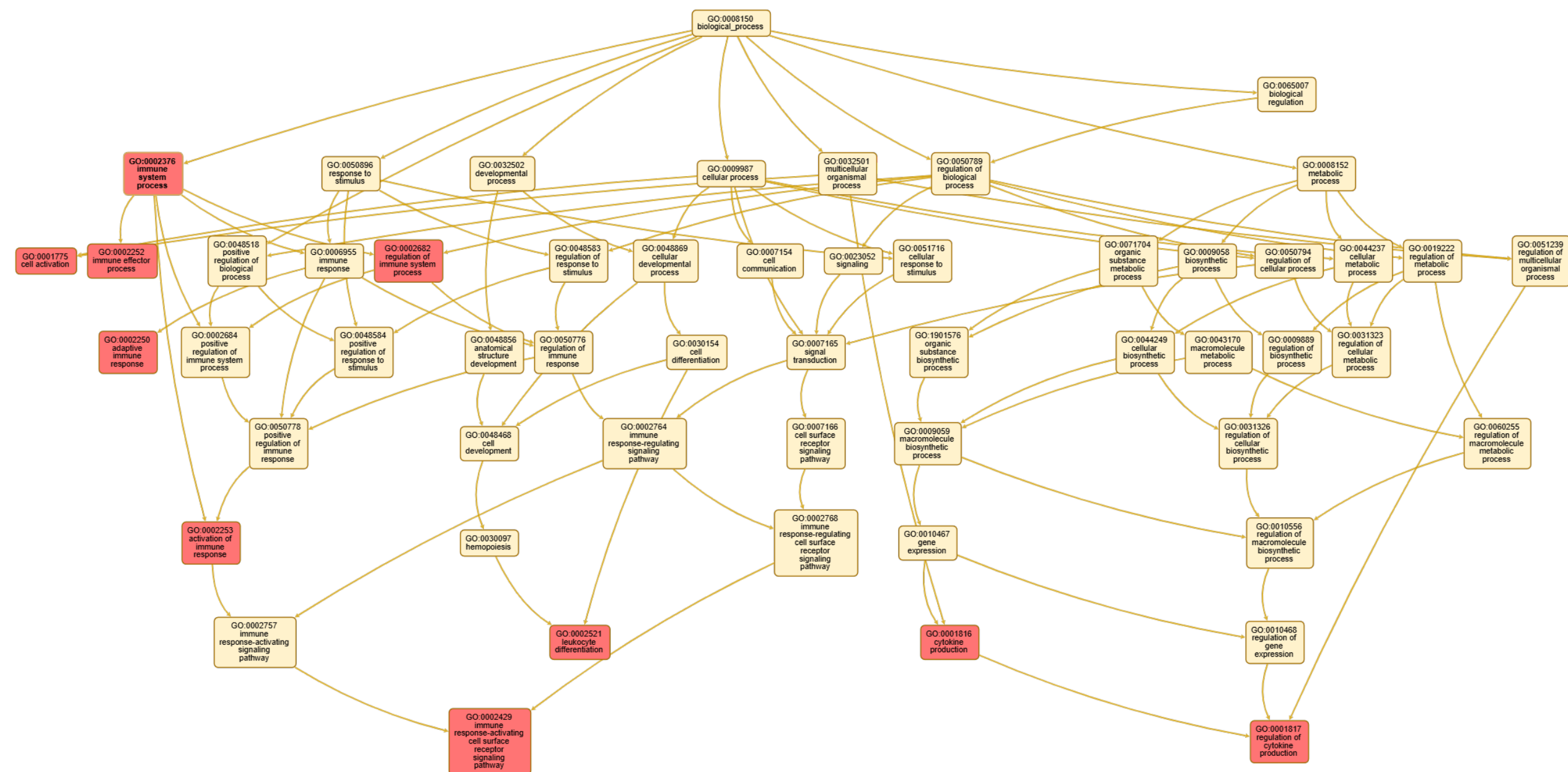


Supplemental Figure 1. Survival and Hematologic Profiles of Leukemic Vehicle- and AZA-treated Immunodeficient Mice. C1498 leukemia cells (80,000) were implanted in NSG immunodeficient mice via tail vein injection. Treatment with DMSO in diluent (Vehicle) (n=9) or 5mg/kg/mouse AZA (n=10) by intraperitoneal injection began on day 3 after implantation and continued thrice weekly until survival endpoints. **(A)** Mice were euthanized once they showed signs of terminal disease state and survival was recorded for each mouse and displayed as a Kaplan-Meier curve. Statistical significance was analyzed using the Log-rank (Mantel-Cox) test. The arrow (\uparrow) indicates the timepoint at which retroorbital blood was drawn to assess hematologic profiles. **(B)** Drawn blood was stained and smeared for complete blood counts. Manually counted WBCs for C1498-Vehicle mice are shown as percentages of total WBC counted. Blood from C1498-AZA mice showed an extremely low WBC count that could not accurately be displayed graphically.

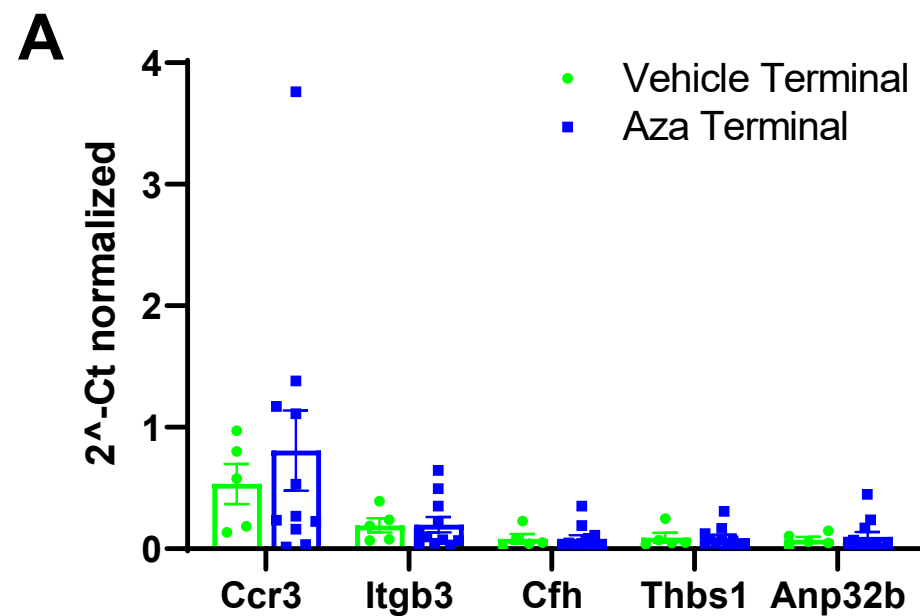


Enriched Gene Ontology Categories

GO Identification	GO Name
GO:0001775	Cell Activation
GO:0001816	Cytokine Production
GO:0001817	Regulation of Cytokine Production
GO:0002250	Adaptive Immune Response
GO:0002252	Immune Effector Process

GO Identification	GO Name
GO:0002253	Activation if Immune Response
GO:0002376	Immune System Process
GO:0002429	Immune Response-Activating Cell Surface Receptor Signaling Pathway
GO:0002521	Leukocyte Differentiation
GO:0002682	Regulation of Immune System Process

Supplemental Figure 2. Map and Listing of Gene Ontologies Enriched in the Mouse PanCancer Immune Profiling Panel. Genes to be probed for expression were analyzed for Network Topology using the WEB-based Gene Set Analysis Toolkit (WebGestalt). The mapping of enriched gene ontologies is shown in red with the linked ancestor ontologies in off-white. The top ten enriched ontologies are shown with their Gene Ontology (GO) identification number.



Supplemental Figure 3. Expression of Significant Genes in Blood of Terminally Ill Mice. C1498 cells (80,000) were implanted in C57Bl/6 mice via tail vein injection. Treatment with DMSO in diluent (Vehicle) (n=5) or 5mg/kg/mouse AZA (n=11) by intraperitoneal injection began on day 3 after implantation and continued thrice weekly until survival endpoints. Mice were euthanized once they showed signs of terminal disease including, but not limited to, labored breathing, a hunched posture, or decreased mobility. Whole blood was taken just prior to euthanasia and RNA isolated from the blood was analyzed for expression of the genes found to be significantly different between Vehicle and Aza-treated samples in the analysis of blood from week2 of treatment: *Ccr3*, *Cfh*, *Itgb3*, *Thbs1*, *Anp32b*. Expression was determined by qPCR and transformed Ct's (2^{-Ct}) normalized to *gapdh* are presented as a bar graph.

Supplemental Table 1. Statistically significant genes in PBMC of human AML or MDS patients of AZA-treated samples compared to PBMCs pre-treatment.

GeneID	padj	pvalue	lfcSE	stat	log2Fold Change	baseMean	Symbol	Description
5196	2.88e-16	2.09e-20	0.73	9.26	6.7220	914.99	PF4	platelet factor 4
81027	2.99e-16	4.35e-20	0.67	9.18	6.1426	954.86	TUBB1	tubulin beta 1 class VI
5473	3.79e-15	8.26e-19	0.79	8.86	7.0157	5007.51	PPBP	pro-platelet basic protein
10398	4.75e-15	1.38e-18	0.71	8.80	6.2499	225.77	MYL9	myosin light chain 9
4603	5.53e-15	2.01e-18	0.55	8.76	4.8364	403.83	MYBL1	MYB proto-oncogene like 1
4512	2.35e-14	1.02e-17	0.52	8.57	4.4742	880614.15	COX1	cytochrome c oxidase subunit I
64919	4.61e-14	2.34e-17	0.66	8.48	5.5624	301.09	BCL11B	BCL11 transcription factor B
9402	1.78e-13	1.04e-16	0.69	8.30	5.7090	491.35	GRAP2	GRB2 related adaptor protein 2
22806	1.61e-12	1.08e-15	0.56	8.02	4.5250	524.4	IKZF3	IKAROS family zinc finger 3
4514	1.61e-12	1.17e-15	0.66	8.01	5.2682	973257	COX3	cytochrome c oxidase subunit III
4579	2.73e-12	2.18e-15	0.67	7.93	5.3151	65989.37	TRNY	tRNA-Tyr
3575	4.61e-12	4.02e-15	0.81	7.85	6.3551	304.01	IL7R	interleukin 7 receptor
4511	9.34e-12	8.82e-15	0.67	7.76	5.1702	72358.19	TRNC	tRNA-Cys
57595	1.61e-11	1.64e-14	0.74	7.68	5.7026	151.43	PDZD4	PDZ domain containing 4
1053763							LOC105	
33	1.80e-11	1.96e-14	0.60	7.65	4.6184	1825.52	376333	uncharacterized LOC105376333
3934	6.47e-11	7.51e-14	0.95	7.48	7.1088	364.24	LCN2	lipocalin 2
6374	6.84e-10	8.44e-13	0.83	7.15	5.9436	88.61	CXCL5	C-X-C motif chemokine ligand 5
3932	9.55e-10	1.25e-12	0.72	7.10	5.1383	184.67	LCK	LCK proto-oncogene, Src family tyrosine kinase
83888	9.67e-10	1.35e-12	0.71	7.09	5.0282	242.84	FGFBP2	fibroblast growth factor binding protein 2
4513	9.67e-10	1.40e-12	0.65	7.08	4.5795	474435.28	COX2	cytochrome c oxidase subunit II
7049	2.13e-09	3.40e-12	0.56	6.96	3.8800	348.17	TGFBR3	transforming growth factor beta receptor 3
6352	2.13e-09	3.34e-12	0.72	6.96	5.0378	979.12	CCL5	C-C motif chemokine ligand 5
923	3.68e-09	6.15e-12	0.78	6.88	5.3526	96.99	CD6	CD6 molecule
800	3.79e-09	6.60e-12	0.91	6.87	6.2487	138.44	CALD1	caldesmon 1

7535	4.22e-09	7.65e-12	0.54	6.84	3.7253	633.74	ZAP70	zeta chain of T cell receptor associated protein kinase 70
9235	4.44e-09	8.38e-12	0.78	6.83	5.3229	271.94	IL32	interleukin 32
388228	1.55e-08	3.04e-11	0.75	6.64	4.9571	101.06	SBK1	SH3 domain binding kinase 1
5197	1.60e-08	3.24e-11	0.97	6.64	6.4052	65.81	PF4V1	platelet factor 4 variant 1
340205	1.83e-08	3.85e-11	0.93	6.61	6.1137	94.12	TREML1	triggering receptor expressed on myeloid cells like 1
9806	1.85e-08	4.04e-11	0.68	6.60	4.4550	432.84	SPOCK2	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 2
399844	1.85e-08	4.17e-11	0.60	6.60	3.9782	2082.94	LINC01002	long intergenic non-protein coding RNA 1002
4519	1.87e-08	4.34e-11	0.71	6.59	4.6491	612427.62	CYTB	cytochrome b
9047	2.77e-08	6.84e-11	0.66	6.52	4.2718	170.51	SH2D2A	SH2 domain containing 2A
4540	2.77e-08	6.81e-11	0.69	6.52	4.5075	641497.04	ND5	NADH dehydrogenase subunit 5
1667	3.17e-08	8.30e-11	1.06	6.50	6.8993	704.86	DEFA1	defensin alpha 1
728358	3.17e-08	8.30e-11	1.06	6.50	6.8993	704.86	DEFA1B	defensin alpha 1B
83699	3.22e-08	8.64e-11	0.73	6.49	4.7208	173.77	SH3BGRL2	SH3 domain binding glutamate rich protein like 2
5335	3.42e-08	9.45e-11	0.62	6.48	4.0306	203.92	PLCG1	phospholipase C gamma 1
1079843							LOC107984360	
60	3.68e-08	1.04e-10	1.01	6.46	6.4975	67.89		
4538	3.73e-08	1.08e-10	0.69	6.45	4.4463	939275.04	ND4	NADH dehydrogenase subunit 4
3820	4.08e-08	1.21e-10	0.76	6.44	4.8871	124.97	KLRB1	killer cell lectin like receptor B1
10417	5.66e-08	1.77e-10	0.59	6.38	3.7395	430.09	SPON2	spondin 2
915	5.66e-08	1.75e-10	0.93	6.38	5.9533	63.29	CD3D	CD3 delta subunit of T-cell receptor complex
10666	6.27e-08	2.00e-10	0.74	6.36	4.7147	503.28	CD226	CD226 molecule
919	1.05e-07	3.42e-10	0.72	6.28	4.5127	332.77	CD247	CD247 molecule
1019285							LOC101928512	
12	1.11e-07	3.71e-10	0.68	6.27	4.2679	127.67		uncharacterized LOC101928512
8784	1.16e-07	4.05e-10	0.86	6.25	5.3934	129.67	TNFRSF18	TNF receptor superfamily member 18
3001	1.16e-07	4.01e-10	0.82	6.25	5.1487	272.2	GZMA	granzyme A

30009	1.16e-07	4.12e-10	0.69	6.25	4.3091	289.63	TBX21	T-box transcription factor 21
171558	1.48e-07	5.36e-10	1.04	6.21	6.4553	74.34	PTCRA	pre T cell antigen receptor alpha
219670	1.95e-07	7.20e-10	1.12	6.16	6.9115	53.56	ENKUR	enkurin, TRPC channel interacting protein
116987	2.02e-07	7.64e-10	0.78	6.15	4.8038	82.03	AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1
84433	2.21e-07	8.51e-10	0.58	6.14	3.5854	494.22	CARD1 1	caspase recruitment domain family member 11
3702	2.43e-07	9.52e-10	0.80	6.12	4.9201	181.27	ITK	IL2 inducible T cell kinase
7504	2.63e-07	1.05e-09	1.01	6.10	6.1531	72.04	XK	X-linked Kx blood group antigen, Kell and VPS13A binding protein
2815	3.03e-07	1.23e-09	0.98	6.08	5.9768	82.38	GP9	glycoprotein IX platelet
9848	3.25e-07	1.34e-09	0.79	6.06	4.8097	87.75	MFAP3L	microfibril associated protein 3 like
84281	3.62e-07	1.53e-09	0.75	6.04	4.5399	256.17	C2orf88	chromosome 2 open reading frame 88
916	4.20e-07	1.80e-09	0.89	6.01	5.3772	118.84	CD3E	CD3 epsilon subunit of T-cell receptor complex
8631	4.37e-07	1.90e-09	0.67	6.01	4.0193	126.18	SKAP1	src kinase associated phosphoprotein 1
3493	4.44e-07	1.97e-09	0.85	6.00	5.0916	76.01	IGHA1	immunoglobulin heavy constant alpha 1
286	6.56e-07	2.95e-09	0.87	5.93	5.1352	90.7	ANK1	ankyrin 1
55287	7.24e-07	3.31e-09	1.08	5.92	6.4090	57.91	TMEM4 0	transmembrane protein 40
1132194 67	7.37e-07	3.42e-09	0.76	5.91	4.5044	76179.7	MIR121 36	microRNA 12136
321	7.39e-07	3.49e-09	0.93	5.91	5.4982	147.92	APBA2	amyloid beta precursor protein binding family A member 2
4574	7.85e-07	3.76e-09	0.77	5.89	4.5471	35610.06	TRNS1	tRNA-Ser
2781	8.06e-07	3.92e-09	0.83	5.89	4.8570	70.27	GNAZ	G protein subunit alpha z
53637	8.09e-07	3.99e-09	0.90	5.88	5.3183	170.03	S1PR5	sphingosine-1-phosphate receptor 5
3002	8.70e-07	4.36e-09	0.79	5.87	4.6264	378.29	GZMB	granzyme B
925	8.77e-07	4.57e-09	1.01	5.86	5.9427	145.77	CD8A	CD8a molecule
2017	8.77e-07	4.47e-09	0.84	5.87	4.9530	125.5	CTTN	cortactin
27087	8.77e-07	4.58e-09	0.73	5.86	4.3039	92.01	B3GAT1	beta-1,3-glucuronyltransferase 1
4563	9.39e-07	4.97e-09	0.84	5.85	4.9028	850.27	TRNG	tRNA-Gly

2039	9.40e-07	5.05e-09	0.83	5.85	4.8690	158.75	DMTN	dematin actin binding protein
940	1.01e-06	5.48e-09	1.31	5.83	7.6261	62.42	CD28	CD28 molecule
5551	1.20e-06	6.60e-09	0.64	5.80	3.7325	814.54	PRF1	perforin 1
9580	1.51e-06	8.45e-09	0.90	5.76	5.2089	57.92	SOX13	SRY-box transcription factor 13
3824	1.63e-06	9.33e-09	0.76	5.74	4.3793	701.43	KLRD1	killer cell lectin like receptor D1
4157	1.63e-06	9.32e-09	0.72	5.74	4.1180	107.67	MC1R	melanocortin 1 receptor
23531	2.10e-06	1.22e-08	0.75	5.70	4.2533	356.73	MMD	monocyte to macrophage differentiation associated
10578	2.17e-06	1.28e-08	0.77	5.69	4.3968	2002.81	GNLY	granulysin
3690	2.18e-06	1.30e-08	0.77	5.69	4.3970	947.38	ITGB3	integrin subunit beta 3
4646	2.19e-06	1.32e-08	0.78	5.68	4.4177	83.08	MYO6	myosin VI
4576	2.74e-06	1.67e-08	0.80	5.64	4.5201	2420	TRNT	tRNA-Thr
9651	3.05e-06	1.88e-08	0.68	5.62	3.8051	181.4	PLCH2	phospholipase C eta 2
29094	3.51e-06	2.19e-08	0.84	5.60	4.6699	138.21	LGALSL	galectin like
1132184							MIR103	
88	3.99e-06	2.52e-08	0.79	5.57	4.4242	1190.1	96B	microRNA 10396b
917	4.20e-06	2.68e-08	1.26	5.56	7.0159	43.66	CD3G	CD3 gamma subunit of T-cell receptor complex
1731	4.28e-06	2.77e-08	0.62	5.56	3.4521	165.85	SEPTIN1	septin 1
1001333							LOC100	
31	4.54e-06	2.97e-08	0.59	5.54	3.2556	1856.97	133331	replaced by ID 100288069
1079870							FAM27E	family with sequence similarity 27
01	5.10e-06	3.37e-08	0.75	5.52	4.1566	123.26	4	member E4
1053773							LOC105	
84	5.24e-06	3.51e-08	1.78	5.51	9.8185	36.96	377384	uncharacterized LOC105377384
22885	5.24e-06	3.54e-08	1.02	5.51	5.6055	48.88	ABLIM3	actin binding LIM protein family member 3
2812	5.95e-06	4.06e-08	0.99	5.49	5.4339	165.72	GP1BB	glycoprotein Ib platelet subunit beta
4818	7.21e-06	4.97e-08	0.70	5.45	3.8226	662.86	NKG7	natural killer cell granule protein 7
22981	7.48e-06	5.21e-08	0.98	5.44	5.3075	64.59	NINL	ninein like
28526	8.20e-06	5.78e-08	0.83	5.43	4.4807	165.56	TRDC	T cell receptor delta constant

116173	8.31e-06	5.91e-08	1.19	5.42	6.4650	50.94	CMTM5	CKLF like MARVEL transmembrane domain containing 5
4555	9.49e-06	6.82e-08	0.79	5.40	4.2726	353.74	TRND	tRNA-Asp
51176	9.82e-06	7.13e-08	1.02	5.39	5.4696	100.03	LEF1	lymphoid enhancer binding factor 1
3560	9.90e-06	7.26e-08	0.81	5.38	4.3773	842.89	IL2RB	interleukin 2 receptor subunit beta
1005067							SLFN12	
36	1.00e-05	7.41e-08	0.64	5.38	3.4365	213.79	L	schlafen family member 12 like
139105	1.24e-05	9.26e-08	1.42	5.34	7.5958	41.53	BEND2	BEN domain containing 2
1005077							C13orf4	
47	1.41e-05	1.06e-07	0.72	5.32	3.8251	387.43	6	chromosome 13 open reading frame 46
57121	1.57e-05	1.19e-07	0.90	5.29	4.7810	57.28	LPAR5	lysophosphatidic acid receptor 5
10225	1.69e-05	1.30e-07	0.73	5.28	3.8536	249.02	CD96	CD96 molecule
4318	1.83e-05	1.44e-07	1.00	5.26	5.2383	60.45	MMP9	matrix metalloproteinase 9
128611	1.83e-05	1.44e-07	0.70	5.26	3.6576	276.18	ZNF831	zinc finger protein 831
152789	1.94e-05	1.53e-07	1.01	5.25	5.3183	46.41	JAKMIP1	janus kinase and microtubule interacting protein 1
389813	2.04e-05	1.63e-07	0.79	5.24	4.1191	80.25	AJM1	apical junction component 1 homolog
1001320							LOC100	
62	2.17e-05	1.75e-07	0.59	5.22	3.0796	1831.83	132062	uncharacterized LOC100132062
4068	2.35e-05	1.91e-07	0.98	5.21	5.0978	53.69	SH2D1A	SH2 domain containing 1A
10316	2.41e-05	1.99e-07	0.71	5.20	3.7122	101.1	NMUR1	neuromedin U receptor 1
2791	2.41e-05	2.01e-07	0.86	5.20	4.4424	208.83	GNG11	G protein subunit gamma 11
342618	2.41e-05	2.01e-07	0.91	5.20	4.7030	103.18	SLFN14	schlafen family member 14
5159	2.99e-05	2.52e-07	0.76	5.16	3.9102	102.47	PDGFRB	platelet derived growth factor receptor beta
23762	3.02e-05	2.57e-07	0.76	5.15	3.8987	79.18	OSBP2	oxysterol binding protein 2
1079872						3084253.9	LOC107	
06	3.11e-05	2.68e-07	0.83	5.14	4.2491	2	987206	replaced by ID 6029
6029	3.11e-05	2.68e-07	0.83	5.14	4.2491	2	3084253.4	RNA component of signal recognition particle 7SL1
4541	3.16e-05	2.75e-07	0.84	5.14	4.3254	185894.86	ND6	NADH dehydrogenase subunit 6
2999	3.16e-05	2.78e-07	0.85	5.14	4.3693	128.86	GZMH	granzyme H
1901	4.07e-05	3.61e-07	0.92	5.09	4.6579	78.89	S1PR1	sphingosine-1-phosphate receptor 1

401124	4.53e-05	4.04e-07	0.89	5.07	4.4885	82.71	DTHD1	death domain containing 1	
1019278							THRB-		
54	5.07e-05	4.56e-07	1.89	5.04	9.5540	31.05	AS2	THRB antisense RNA 2	
1053781						4041673.7	LOC105		
79	5.99e-05	5.48e-07	0.84	5.01	4.2007	4	378179	uncharacterized LOC105378179	
378706	5.99e-05	5.48e-07	0.84	5.01	4.2008	4041641.8	1	RN7SL2	RNA component of signal recognition particle 7SL2
387882	8.09e-05	7.46e-07	1.01	4.95	5.0084	135.94	C12orf7	5	chromosome 12 open reading frame 75
1236	8.44e-05	7.85e-07	1.26	4.94	6.2013	33.87	CCR7		C-C motif chemokine receptor 7
4508	8.78e-05	8.22e-07	0.85	4.93	4.2116	605386.23	ATP6		ATP synthase F0 subunit 6
6775	9.32e-05	8.80e-07	0.67	4.92	3.2960	190.45	STAT4		signal transducer and activator of transcription 4
4753	9.57e-05	9.10e-07	1.74	4.91	8.5485	40.75	NELL2		neural EGFL like 2
2625	1.03e-04	9.87e-07	0.77	4.89	3.7669	137.39	GATA3		GATA binding protein 3
9214	1.24e-04	1.20e-06	0.82	4.86	3.9582	90.93	FCMR		Fc mu receptor
84886	1.27e-04	1.23e-06	0.75	4.85	3.6446	119.31	C1orf19	8	chromosome 1 open reading frame 198
347404	1.39e-04	1.37e-06	0.99	4.83	4.8007	48.83	LANCL3		LanC like family member 3
8654	1.45e-04	1.43e-06	0.70	4.82	3.3488	165.13	PDE5A		phosphodiesterase 5A
4568	1.49e-04	1.48e-06	0.94	4.81	4.5051	868.52	TRNL2		tRNA-Leu
2113	1.49e-04	1.50e-06	0.70	4.81	3.3880	955.33	ETS1		ETS proto-oncogene 1, transcription factor
1098642							RNA45S		
79	1.52e-04	1.53e-06	0.83	4.81	3.9706	538366.19	N2		RNA, 45S pre-ribosomal N2
114804	1.62e-04	1.64e-06	1.20	4.79	5.7492	36.05	RNF157		ring finger protein 157
1001319							FAM27E		family with sequence similarity 27 member E3
97	1.67e-04	1.71e-06	0.90	4.78	4.2977	114.65	3		
2811	1.67e-04	1.72e-06	0.74	4.78	3.5548	200.93	GP1BA		glycoprotein Ib platelet subunit alpha
1000085							RNA28S		
89	2.15e-04	2.23e-06	0.58	4.73	2.7227	1773.16	N5		RNA, 28S ribosomal N5
5727	2.75e-04	2.88e-06	0.87	4.68	4.0578	63.79	PTCH1		patched 1
914	3.16e-04	3.33e-06	0.98	4.65	4.5406	154.04	CD2		CD2 molecule

4509	3.46e-04	3.67e-06	0.81	4.63	3.7444	70464.84	ATP8	ATP synthase F0 subunit 8
1002332							PCED1	
09	3.64e-04	3.88e-06	0.94	4.62	4.3254	57.35	B-AS1	PCED1B antisense RNA 1
							CDC14	
8555	3.67e-04	3.95e-06	1.16	4.61	5.3280	32.12	B	cell division cycle 14B
1098642							RNA28S	
72	3.78e-04	4.09e-06	0.58	4.61	2.6636	1416.82	N4	RNA, 28S ribosomal N4
1098642							RNA28S	
82	4.00e-04	4.36e-06	0.58	4.59	2.6780	1379.87	N2	RNA, 28S ribosomal N2
1292	4.05e-04	4.43e-06	1.01	4.59	4.6293	484.55	COL6A2	collagen type VI alpha 2 chain
								megakaryocyte and platelet inhibitory receptor G6b
80739	4.31e-04	4.75e-06	0.91	4.58	4.1749	571.27	MPIG6B	
1053798							LOC105	
57	4.54e-04	5.04e-06	0.84	4.56	3.8449	58.53	379857	replaced by ID 642819
4638	4.54e-04	5.08e-06	0.91	4.56	4.1321	130.67	MYLK	myosin light chain kinase
6678	4.66e-04	5.24e-06	0.82	4.55	3.7413	360.13	SPARC	secreted protein acidic and cysteine rich
8436	5.11e-04	5.82e-06	0.90	4.53	4.0978	545.74	CAVIN2	caveolae associated protein 2
								RNA component of signal recognition particle 7SL3
378707	5.11e-04	5.86e-06	0.76	4.53	3.4260	338691.09	RN7SL3	
1053724							LIM2-	
46	5.11e-04	5.86e-06	1.06	4.53	4.7926	39.8	AS1	LIM2 and SIGLEC10 antisense RNA 1
1066322							RNA28S	
64	5.16e-04	5.95e-06	0.59	4.53	2.6802	1688.58	N1	RNA, 28S ribosomal N1
5730	5.73e-04	6.66e-06	0.85	4.50	3.8484	74.51	PTGDS	prostaglandin D2 synthase
							SHISAL	
348378	6.02e-04	7.04e-06	1.00	4.49	4.5061	49.36	2A	shisa like 2A
81606	6.29e-04	7.40e-06	0.74	4.48	3.3265	112.26	LBH	LBH regulator of WNT signaling pathway
79616	6.35e-04	7.52e-06	1.03	4.48	4.6155	38.45	CCNJL	cyclin J like
4535	6.37e-04	7.58e-06	0.86	4.48	3.8383	713934.18	ND1	NADH dehydrogenase subunit 1
							PRKAR	protein kinase cAMP-dependent type II regulatory subunit beta
5577	6.62e-04	7.93e-06	0.77	4.47	3.4346	474.72	2B	
4564	6.70e-04	8.08e-06	0.93	4.46	4.1357	1883.31	TRNH	tRNA-His
1079864							LOC107	
61	6.71e-04	8.13e-06	1.32	4.46	5.9042	26.15	986461	uncharacterized LOC107986461

4566	7.44e-04	9.07e-06	0.89	4.44	3.9404	1543.83	TRNK	tRNA-Lys
9886	7.46e-04	9.16e-06	0.78	4.44	3.4675	92.92	RHOBT B1	Rho related BTB domain containing 1
728262	8.18e-04	1.01e-05	0.59	4.41	2.6184	2010.11	FAM157 A	family with sequence similarity 157 member A
4550	8.18e-04	1.02e-05	0.90	4.41	3.9566	262.81	RNR2	l-rRNA
8530	8.88e-04	1.11e-05	0.71	4.39	3.1021	207.99	CST7	cystatin F
6095	9.03e-04	1.13e-05	0.75	4.39	3.3120	244.43	RORA	RAR related orphan receptor A
85379	9.15e-04	1.16e-05	1.22	4.39	5.3521	27.68	KIAA16 71	KIAA1671
54843	9.23e-04	1.17e-05	0.71	4.38	3.1244	141.13	SYTL2	synaptotagmin like 2
28951	9.79e-04	1.25e-05	0.70	4.37	3.0415	101.4	TRIB2	tribbles pseudokinase 2
3003	1.03e-03	1.33e-05	1.34	4.36	5.8517	76.63	GZMK	granzyme K
1005008 62	1.14e-03	1.47e-05	0.93	4.33	4.0309	11787.95	MIR364 8-1	microRNA 3648-1
1035047 31	1.15e-03	1.49e-05	0.93	4.33	4.0231	23318.02	MIR364 8-2	microRNA 3648-2
1002891 24	1.25e-03	1.64e-05	1.10	4.31	4.7453	54.17	FAM27E 2	family with sequence similarity 27 member E2
50852	1.28e-03	1.68e-05	1.82	4.30	7.8346	25.64	TRAT1	T cell receptor associated transmembrane adaptor 1
149628	1.30e-03	1.71e-05	0.74	4.30	3.1719	148.48	PYHIN1	pyrin and HIN domain family member 1
154075	1.30e-03	1.76e-05	0.84	4.29	3.6147	206.39	SAMD3	sterile alpha motif domain containing 3
23224	1.30e-03	1.75e-05	0.68	4.29	2.8986	1317.56	SYNE2	spectrin repeat containing nuclear envelope protein 2
9437	1.30e-03	1.74e-05	0.91	4.30	3.9240	76.34	NCR1	natural cytotoxicity triggering receptor 1
1132185 01	1.30e-03	1.76e-05	1.04	4.29	4.4554	268.18	MIR103 96A	microRNA 10396a
4536	1.36e-03	1.85e-05	0.89	4.28	3.8011	734832.3	ND2	NADH dehydrogenase subunit 2
343413	1.37e-03	1.87e-05	0.81	4.28	3.4488	73.61	FCRL6	Fc receptor like 6
6403	1.46e-03	2.00e-05	0.88	4.27	3.7668	135.52	SELP	selectin P
9254	1.69e-03	2.34e-05	0.88	4.23	3.7231	57.73	CACNA 2D2	calcium voltage-gated channel auxiliary subunit alpha2delta 2

8277	1.69e-03	2.34e-05	1.21	4.23	5.1177	51.12	TKTL1	transketolase like 1
6043	1.81e-03	2.53e-05	0.94	-4.21	-3.9531	122.45	SNORA 63	small nucleolar RNA, H/ACA box 63
9953	1.82e-03	2.55e-05	0.84	4.21	3.5489	94.43	HS3ST3 B1	heparan sulfate-glucosamine 3- sulfotransferase 3B1
2920	1.85e-03	2.60e-05	0.64	-4.21	-2.6869	371.47	CXCL2	C-X-C motif chemokine ligand 2
28639	1.86e-03	2.63e-05	0.95	4.20	4.0018	55.35	TRBC1	T cell receptor beta constant 1
8807	1.88e-03	2.67e-05	0.69	4.20	2.9035	136.42	IL18RA P	interleukin 18 receptor accessory protein
5583	1.88e-03	2.69e-05	0.60	4.20	2.5272	810.23	PRKCH	protein kinase C eta
1001287 31	1.91e-03	2.75e-05	0.59	4.19	2.4621	589.79	OST4	oligosaccharyltransferase complex subunit 4, non-catalytic
1001302 31	1.95e-03	2.81e-05	1.03	4.19	4.3111	108.49	LINC00 861	long intergenic non-protein coding RNA 861
666	2.02e-03	2.93e-05	0.94	4.18	3.9099	43.61	BOK	BCL2 family apoptosis regulator BOK
143872	2.09e-03	3.05e-05	1.18	4.17	4.9206	31.45	ARHGA P42	Rho GTPase activating protein 42
1793	2.14e-03	3.14e-05	0.87	-4.16	-3.5991	192.46	DOCK1	dedicator of cytokinesis 1
84131	2.33e-03	3.43e-05	0.61	4.14	2.5401	289.46	CEP78	centrosomal protein 78
259215	2.48e-03	3.68e-05	1.24	4.13	5.1340	28.73	LY6G6F	lymphocyte antigen 6 family member G6F
51348	2.48e-03	3.69e-05	0.95	4.13	3.8998	150	KLRF1	killer cell lectin like receptor F1
81563	2.59e-03	3.87e-05	0.72	4.12	2.9448	137.04	C1orf21	chromosome 1 open reading frame 21
1053778 06	2.68e-03	4.03e-05	0.85	4.11	3.4713	109.15	LOC105 377806	
4050	2.77e-03	4.18e-05	0.66	4.10	2.6877	138.21	LTB	lymphotoxin beta
81794	2.98e-03	4.53e-05	0.65	4.08	2.6647	253.96	ADAMT S10	ADAM metalloproteinase with thrombospondin type 1 motif 10
339541	3.11e-03	4.75e-05	1.00	-4.07	-4.0516	148.54	ARMH1	armadillo like helical domain containing 1
58486	3.25e-03	4.97e-05	0.72	-4.06	-2.9294	120.56	ZBED5	zinc finger BED-type containing 5
3693	3.59e-03	5.52e-05	0.83	4.03	3.3455	79.38	ITGB5	integrin subunit beta 5
8787	3.68e-03	5.69e-05	0.93	4.03	3.7281	42.63	RGS9	regulator of G protein signaling 9

10158	3.90e-03	6.09e-05	1.88	4.01	7.5241	20.9	PDZK11 P1	PDZK1 interacting protein 1
57732	3.90e-03	6.07e-05	0.68	4.01	2.7084	117.73	ZFYVE2 8	zinc finger FYVE-type containing 28
22914	3.90e-03	6.12e-05	0.94	4.01	3.7704	103.95	KLRK1	killer cell lectin like receptor K1
54796	3.98e-03	6.27e-05	1.01	4.00	4.0214	46.94	BNC2	basonuclin 2
1019295 31	4.34e-03	6.87e-05	1.33	3.98	5.2740	22.25	LINC01 871	long intergenic non-protein coding RNA 1871
79993	4.55e-03	7.23e-05	0.89	3.97	3.5273	135.06	ELOVL7	ELOVL fatty acid elongase 7
93010	4.56e-03	7.29e-05	0.98	3.97	3.9048	37.06	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N- acetylglucosaminyltransferase 7
864	4.57e-03	7.32e-05	0.60	3.97	2.3704	1024.65	RUNX3	RUNX family transcription factor 3
4900	4.76e-03	7.67e-05	0.68	3.95	2.6853	1430.52	NRGN	neurogranin
1099103 82	5.10e-03	8.25e-05	0.55	3.94	2.1542	1042.18	RNA28S N3	RNA, 28S ribosomal N3
1053798 07	5.44e-03	8.87e-05	1.17	3.92	4.5978	38.71	LOC105 379807	uncharacterized LOC105379807
92591	5.44e-03	8.88e-05	0.87	3.92	3.4114	171.51	ASB16	ankyrin repeat and SOCS box containing 16
124602	5.65e-03	9.27e-05	1.11	3.91	4.3402	44.07	KIF19	kinesin family member 19
9289	5.80e-03	9.56e-05	0.68	3.90	2.6365	465.08	ADGRG 1	adhesion G protein-coupled receptor G1
117157	5.92e-03	9.81e-05	0.99	3.90	3.8584	117.34	SH2D1B	SH2 domain containing 1B
54758	5.98e-03	9.95e-05	0.57	3.89	2.2291	299.45	KLHDC 4	kelch domain containing 4
760	6.08e-03	1.01e-04	0.82	3.89	3.1916	123.83	CA2	carbonic anhydrase 2
3823	6.16e-03	1.03e-04	0.92	3.88	3.5710	59.19	KLRC3	killer cell lectin like receptor C3
5874	6.32e-03	1.06e-04	0.87	3.88	3.3555	240.25	RAB27B	RAB27B, member RAS oncogene family
60509	6.62e-03	1.12e-04	0.61	3.86	2.3535	382.95	AGBL5	AGBL carboxypeptidase 5
4573	6.62e-03	1.12e-04	0.95	3.86	3.6809	306.24	TRNR	tRNA-Arg
2274	6.69e-03	1.14e-04	0.88	3.86	3.4101	48.27	FHL2	four and a half LIM domains 2
11098	6.80e-03	1.16e-04	0.91	3.85	3.5156	51.9	PRSS23	serine protease 23
4569	6.97e-03	1.20e-04	0.89	3.85	3.4226	682.49	TRNM	tRNA-Met

4537	7.23e-03	1.25e-04	0.92	3.84	3.5099	157586.17	ND3	NADH dehydrogenase subunit 3
4539	7.81e-03	1.35e-04	0.93	3.82	3.5386	139355.36	ND4L	NADH dehydrogenase subunit 4L
23043	8.03e-03	1.40e-04	0.56	3.81	2.1283	380.44	TNIK	TRAF2 and NCK interacting kinase
10125	8.03e-03	1.40e-04	0.71	3.81	2.6914	163.54	RASGR P1	RAS guanyl releasing protein 1
26030	8.07e-03	1.42e-04	0.53	3.81	2.0257	470.15	PLEKH G3	pleckstrin homology and RhoGEF domain containing G3
6932	8.10e-03	1.43e-04	0.82	3.80	3.1000	387.11	TCF7	transcription factor 7
9495	8.39e-03	1.49e-04	0.93	3.79	3.5344	48.48	AKAP5	A-kinase anchoring protein 5
1079870							LOC107	
26	8.62e-03	1.53e-04	0.93	3.79	3.5297	95.78	987026	uncharacterized LOC107987026
1098642							RNA45S	
71	8.86e-03	1.58e-04	0.90	3.78	3.4098	426294.63	N4	RNA, 45S pre-ribosomal N4
10123	9.12e-03	1.64e-04	0.58	3.77	2.1911	1100.53	ARL4C	ADP ribosylation factor like GTPase 4C
1005280							KLRC4-	
32	9.52e-03	1.71e-04	0.93	3.76	3.5015	120.66	KLRK1	KLRC4-KLRK1 readthrough
820	1.03e-02	1.87e-04	1.21	3.74	4.5029	32.12	CAMP	cathelicidin antimicrobial peptide
83988	1.03e-02	1.87e-04	0.79	3.74	2.9563	63.94	NCALD	neurocalcin delta
11278	1.07e-02	1.95e-04	0.75	3.73	2.8096	242.64	KLF12	KLF transcription factor 12
57211	1.08e-02	1.97e-04	1.88	-3.72	-7.0025	68.04	ADGRG 6	adhesion G protein-coupled receptor G6
387509	1.11e-02	2.04e-04	1.05	3.71	3.9001	32.45	GPR153	G protein-coupled receptor 153
4575	1.11e-02	2.04e-04	0.98	3.71	3.6310	1251.35	TRNS2	tRNA-Ser
55930	1.12e-02	2.07e-04	1.82	-3.71	-6.7664	65.57	MYO5C	myosin VC
1027246							LOC102	
46	1.13e-02	2.10e-04	0.71	3.71	2.6310	165.84	724646	uncharacterized LOC102724646
129049	1.13e-02	2.12e-04	1.47	3.70	5.4433	22.97	SGSM1	small G protein signaling modulator 1
440823	1.25e-02	2.34e-04	0.72	3.68	2.6367	193.92	MIAT	myocardial infarction associated transcript
9124	1.27e-02	2.39e-04	0.80	3.67	2.9344	198.16	PDLIM1	PDZ and LIM domain 1
3674	1.27e-02	2.39e-04	0.85	3.67	3.1086	365.67	ITGA2B	integrin subunit alpha 2b
84879	1.31e-02	2.49e-04	1.64	-3.66	-5.9959	37.54	MFSD2 A	MFSD2 lysolipid transporter A, lysophospholipid

23345	1.31e-02	2.49e-04	0.53	3.66	1.9435	2229.53	SYNE1	spectrin repeat containing nuclear envelope protein 1
1053766							LOC105	
26	1.32e-02	2.52e-04	1.92	-3.66	-7.0378	27.27	376626	uncharacterized LOC105376626
54438	1.33e-02	2.55e-04	0.56	3.66	2.0469	310.53	GFOD1	glucose-fructose oxidoreductase domain containing 1
2696	1.35e-02	2.59e-04	1.16	3.65	4.2418	26.77	GIPR	gastric inhibitory polypeptide receptor
55655	1.35e-02	2.61e-04	1.06	3.65	3.8808	45.33	NLRP2	NLR family pyrin domain containing 2
54855	1.41e-02	2.74e-04	1.11	3.64	4.0208	282.75	TENT5C	terminal nucleotidyltransferase 5C
161882	1.43e-02	2.79e-04	0.65	3.63	2.3771	129.01	ZFPM1	zinc finger protein, FOG family member 1
26051	1.52e-02	2.97e-04	0.60	3.62	2.1631	192.26	PPP1R1 6B	protein phosphatase 1 regulatory subunit 16B
1122682							LOC112	
84	1.52e-02	2.97e-04	0.73	3.62	2.6257	547.02	268284	
28638	1.55e-02	3.06e-04	0.90	3.61	3.2520	98.06	TRBC2	T cell receptor beta constant 2
3039	1.61e-02	3.18e-04	2.13	3.60	7.6657	3003.76	HBA1	hemoglobin subunit alpha 1
8542	1.62e-02	3.21e-04	0.76	3.60	2.7336	760.21	APOL1	apolipoprotein L1
122416	1.75e-02	3.49e-04	0.76	3.58	2.7136	105.46	ANKRD 9	ankyrin repeat domain 9
23336	1.75e-02	3.50e-04	1.06	3.57	3.7834	31.75	SYNM	synemin
3004	1.75e-02	3.49e-04	1.19	3.58	4.2615	31.8	GZMM	granzyme M
4571	1.80e-02	3.62e-04	0.89	3.57	3.1609	5876.29	TRNP	tRNA-Pro
284	1.84e-02	3.71e-04	1.34	-3.56	-4.7648	124.32	ANGPT 1	angiopoietin 1
1066338							SNORD	
00	1.85e-02	3.75e-04	0.80	-3.56	-2.8334	164.61	133	small nucleolar RNA, C/D box 133
59352	1.86e-02	3.78e-04	1.10	3.55	3.9145	51.9	LGR6	leucine rich repeat containing G protein-coupled receptor 6
7293	1.89e-02	3.85e-04	0.99	3.55	3.5203	57.36	TNFRS F4	TNF receptor superfamily member 4
9053	1.93e-02	3.96e-04	1.52	-3.54	-5.3839	75.24	MAP7	microtubule associated protein 7
3494	1.93e-02	3.96e-04	1.22	3.54	4.3330	30.15	IGHA2	immunoglobulin heavy constant alpha 2 (A2m marker)

3738	1.96e-02	4.03e-04	0.59	3.54	2.0960	401.84	KCNA3	potassium voltage-gated channel subfamily A member 3
494470	1.99e-02	4.12e-04	1.00	3.53	3.5138	62.46	RNF165	ring finger protein 165
139065	1.99e-02	4.13e-04	0.94	-3.53	-3.3180	76.99	SLITRK4	SLIT and NTRK like family member 4
202020	2.09e-02	4.35e-04	1.92	-3.52	-6.7558	22.42	TAPT1-AS1	TAPT1 antisense RNA 1 (head to head)
5521	2.10e-02	4.41e-04	0.94	3.51	3.3171	51.66	PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta
256691	2.10e-02	4.39e-04	1.45	-3.52	-5.0834	113.64	MAMDC2	MAM domain containing 2
23348	2.10e-02	4.41e-04	1.01	3.51	3.5339	53.89	DOCK9	dedicator of cytokinesis 9
1030211								
64	2.10e-02	4.43e-04	2.02	3.51	7.0951	15.17	CASC21	cancer susceptibility 21
84002	2.10e-02	4.45e-04	0.98	-3.51	-3.4341	150.14	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
6622	2.15e-02	4.57e-04	0.83	3.50	2.9029	160.64	SNCA	synuclein alpha
2322	2.17e-02	4.65e-04	0.82	-3.50	-2.8844	205.22	FLT3	fms related receptor tyrosine kinase 3
3040	2.17e-02	4.62e-04	2.22	3.50	7.7566	3930.13	HBA2	hemoglobin subunit alpha 2
6915	2.17e-02	4.65e-04	1.28	3.50	4.4765	34.89	TBXA2R	thromboxane A2 receptor
1000374								
17	2.35e-02	5.07e-04	0.75	3.48	2.6199	275.03	DDTL	D-dopachrome tautomerase like
5729	2.41e-02	5.22e-04	0.91	3.47	3.1667	65.68	PTGDR	prostaglandin D2 receptor
8809	2.53e-02	5.48e-04	0.98	3.46	3.3904	73.66	IL18R1	interleukin 18 receptor 1
10178	2.64e-02	5.75e-04	0.96	3.44	3.2996	49.23	TENM1	teneurin transmembrane protein 1
1053694								
02	2.65e-02	5.79e-04	1.94	-3.44	-6.6822	21.29	LOC105369402	uncharacterized LOC105369402
652966	2.68e-02	5.88e-04	0.93	-3.44	-3.2043	118.06	SNORD10	small nucleolar RNA, C/D box 10
10826	2.69e-02	5.92e-04	0.69	3.44	2.3688	210.39	FAXDC2	fatty acid hydroxylase domain containing 2
6080	2.84e-02	6.27e-04	0.74	-3.42	-2.5439	587.68	SNORA73A	small nucleolar RNA, H/ACA box 73A
54541	2.89e-02	6.40e-04	0.64	3.41	2.1916	140.83	DDIT4	DNA damage inducible transcript 4

8320	2.95e-02	6.55e-04	1.12	3.41	3.8075	35.91	EOMES	eomesodermin
8425	2.95e-02	6.57e-04	0.67	3.41	2.2964	323.27	LTBP4	latent transforming growth factor beta binding protein 4
8510	2.96e-02	6.64e-04	0.81	3.40	2.7449	81.45	MMP23 B	matrix metalloproteinase 23B
55607	2.96e-02	6.62e-04	1.01	3.40	3.4504	32.61	PPP1R9 A	protein phosphatase 1 regulatory subunit 9A
4684	3.15e-02	7.09e-04	0.87	3.39	2.9587	221.2	NCAM1	neural cell adhesion molecule 1
158038	3.16e-02	7.13e-04	1.10	3.38	3.7310	27.66	LINGO2	leucine rich repeat and Ig domain containing 2
54797	3.20e-02	7.24e-04	0.80	3.38	2.7041	293.08	MED18	mediator complex subunit 18
54910	3.20e-02	7.27e-04	0.72	3.38	2.4343	114.63	SEMA4 C	semaphorin 4C
1668	3.59e-02	8.19e-04	2.06	3.35	6.8952	845.14	DEFA3	defensin alpha 3
1005268							SEPT5- GP1BB	SEPT5-GP1BB readthrough
33	3.65e-02	8.36e-04	1.09	3.34	3.6273	233.04	TRNN	tRNA-Asn
4570	3.65e-02	8.37e-04	0.81	3.34	2.6991	4503.41	RGS18	regulator of G protein signaling 18
64407	3.70e-02	8.55e-04	0.62	3.33	2.0712	910.06	CHI3L1	chitinase 3 like 1
1116	3.70e-02	8.57e-04	1.17	3.33	3.9016	77.95	MYB	MYB proto-oncogene, transcription factor
4602	3.70e-02	8.54e-04	1.19	-3.33	-3.9641	309.63	BPI	bactericidal permeability increasing protein
671	3.79e-02	8.80e-04	0.90	3.33	3.0079	407.29	CTSW	cathepsin W
1521	3.79e-02	8.84e-04	0.74	3.33	2.4454	352.02	ATP binding cassette subfamily B member 1	
5243	3.95e-02	9.24e-04	0.88	3.31	2.9062	82.04	JRKL	JRK like
8690	3.99e-02	9.36e-04	0.90	-3.31	-2.9668	59.6	SCML4	Scm polycomb group protein like 4
256380	4.00e-02	9.40e-04	0.90	3.31	2.9675	105.59	RPS27	ribosomal protein S27
6232	4.03e-02	9.53e-04	0.59	3.30	1.9478	2438.21	AUTS2	activator of transcription and developmental regulator AUTS2
26053	4.03e-02	9.51e-04	0.71	3.30	2.3556	184.35	ARHGE F12	Rho guanine nucleotide exchange factor 12
23365	4.07e-02	9.67e-04	0.72	3.30	2.3616	246.27	FAM234 B	family with sequence similarity 234 member B
57613	4.09e-02	9.74e-04	1.97	-3.30	-6.4960	18.72		

652965	4.14e-02	9.89e-04	0.76	-3.29	-2.5110	441.42	SNORA 48	small nucleolar RNA, H/ACA box 48
1027243 64	4.34e-02	1.04e-03	0.60	3.28	1.9821	212.36	SEC22B 4P	SEC22 homolog B4, pseudogene megakaryocyte-associated tyrosine kinase
4145	4.40e-02	1.06e-03	0.79	3.28	2.5723	216.52	MATK	kinase
55759	4.43e-02	1.07e-03	0.91	-3.27	-2.9844	63.19	WDR12	WD repeat domain 12
60312	4.52e-02	1.09e-03	1.08	3.27	3.5314	46.95	AFAP1	actin filament associated protein 1
84628	4.63e-02	1.12e-03	0.69	3.26	2.2385	142.89	NTNG2	netrin G2
4549	4.67e-02	1.14e-03	1.11	3.25	3.6065	148.56	RNR1	s-rRNA
1008615 32	4.68e-02	1.14e-03	0.94	3.25	3.0486	269159.77	RNA45S N5	RNA, 45S pre-ribosomal N5
1053792 82	4.87e-02	1.20e-03	0.80	3.24	2.5973	156.8	LOC105 379282	
4092	4.87e-02	1.19e-03	0.73	3.24	2.3625	169.55	SMAD7	SMAD family member 7
79037	4.95e-02	1.22e-03	0.82	3.23	2.6512	75.01	PVRIG	PVR related immunoglobulin domain containing
144203	4.96e-02	1.23e-03	1.14	3.23	3.6825	26.84	OVOS2	alpha-2-macroglobulin like 1 pseudogene

Supplemental Table 2. “Panel Plus” user added genes to the Mouse PanCancer Immune Profiling panel with optimized probe target sequences.

Customer Identifier	Accession	Position	Target Sequence
abat	NM_001170 978.1	3561-3660	GAGCCACAGTGTTCATATACAGATACTTCCGCAGGTCCTTAGAGTTCAAAGGGTTTTAA TCCAGGACATAAGCAGAAATCGCTCTCTTTAGTGAAGGGAGC
Akt1	NM_001165 894.1	899-998	GCCATGAAGATCCTCAAGAAGGAGGTCATCGTCGCCAAGGATGAGGTTGCCACAC GCTTACTGAGAACCGTGTCTGCAGAACTCTAGGCATCCCTTC
Bad	NM_007522 .3	1147-1246	TTCGAGGCCTTAGGAAAAAAAAAGAGGATCGCTGTGTCCCTTTAACAGGGAGAAGAG CTGACGTACAGCTTGAGTCCCTTCGGTGCCTGCAATAGCCAC
bbc3	NM_133234 .1	1462-1561	CCCCAATCCCATCCATCTCATTGCATAGGTTTAGAGAGAGCACGTGTGACCACTGG CATTCAATTTGGGGGGTGGGAGATATTGGCGGAAGCCACCCAG
birc3	NM_007464 .3	426-525	CCCTGTCATCTCACCATGAACATGGTTCAAGACAGCGCCTTTCTAGCCAAGCTGATG AAGAGTGCTGACACCTTTGAGTTGAAGTATGACTTTTCCTGTG
blm	NM_001042 527.2	265-364	AAAGATGTGAACGTGTCTGAGGCCTTTTCATTCACTGAGTCTCCACTCCACAAACCAA AGCAGCAGGCAAAGATTGAAGGCTTCTTTAAACATTTCCCTG
casp9	NM_015733 .4	1676-1775	ATAACTGTCCTGCTAAGATAGGATTTTGAAGTGGGGCAGGCTGCTCTTTCCCTTTGG CGATGCAAACATGCTCCTAGCAGCTTTTCAGGTTGTAGGGCAAT
ctnnb1	NM_007614 .2	2976-3075	TTGGTCGAGGAGTAACAATACAAATGGATTTGGGGAGTGACTCACGCAGTGAAGAAT GCACACGAATGGATCACAAGATGGCGTTATCAAACCCTAGCCT
dbn1	NM_019813 .4	2571-2670	CGAAATTTAAACATGGCAATAAATGGCTCGTGGGCTCTGGCTCCCTGGGACCCTTC CCCTTCTCTTTACCCTCGCTGCTTGGTCAGAAGGAATTATCAG
ddx52	NM_030096 .2	501-600	AGGAAAAGGTCAACTTCTTTTCGGAACAAGCACAAGATACATGTCCAAGGAACTGATC TTCCTGACCCAATTGCTACATTTTCAGCAACTTGACCAGGAATA
mdm2	NM_010786 .4	1665-1764	GTCATGTTTCACGTGTGCAAAGAAGCTAAAAAAAAAGAAACAAGCCCTGCCAGTGTG CAGACAGCCAATCCAAATGATTGTGCTAACTTACTTCAACTAG
pdk4	NM_013743 .2	1356-1455	AGCGGATGACGCCTGACATTTTACGGGATCAAAGTGGGTCTGTGGCATTGCTGCTTC GTGAATGTGTGTGGACTCTAGTTTCCGCAAACAACGCAACAC
psmb5	NM_011186 .1	335-434	TGCAGCTTCTGGGAGCGGTTGTTGGCTCGGCAGTGTGCAATCTATGAGCTTCGCAAT AAGGAACGCATCTCGGTGCGCAGCAGCCTCCAACTGCTCGCTA
psmc4	NM_011874 .2	1147-1246	TGCACCTGGAAGACTATGTGGCCCGTCCAGATAAGATTTTCAGGAGCCGATATCAACT CCATCTGTCAGGAGAGTGGAAATGTTGGCTGTCCGTGAGAACCG
Ripk1	NM_009068 .3	3186-3285	GCTTTGGCCTTGTGGCCATTCTGGCACTCATTGGCACTTCATCCTCCTTTGTTGGG CTATCCTGTACTCAGTAGGATATTTGGGAACATTCCTGGCCTC

Ripk3	NM_019955		CACAGAACATGGAACCATGATGTAGCAGTCAAGATCGTGA ACTCGAAGAAGATATCC
	.1	271-370	TGGGAGGTGAAGGCTATGGTTAATCTTCGTAATGAGAACGTTT
rock1	NM_009071		AAGTTGGTTGAACTTGCTTTCCGCTGCGGGCAAGAAGGTATCGTCACAAGTAGCAGC
	.2	416-515	ATCATGTCTGACTGGGGACAGTTTTGAGACTCGGTTTGAAAAA
slc24a3	NM_053195		CAGGAGAGGGTCCGCTGATGGCAGGAAGGTTTGT TTTGTTTGGGAGTGAGTCCTAG
	.2	2271-2370	GTTACGGGGCTCAGGGAAATTGTTTAATTTGAGGGGGCGCTTTT
tnfsf9	NM_009404		GCTCTATGGCCTAGTCGCTTTGGTTTTGCTGCTTCTGATCGCCGCCTGTGTTCCCTATC
	.3	293-392	TTCACCCGCACCGAGCCTCGGCCAGCGCTCACAATCACCACC
ubb	NM_011664		TCCTCCGTCTGAGGGGTGGCTATTAATTATTCGGTCTGCATTCCCAGTGGGCAGTGA
	.4	1324-1423	TGGCATTACTCTGCACTCTAGCCACTTGCCCCAATTTAAGTTT