SeqID	ProbeID	GeneName	Description
2271329	A_55_P2031466	Lrrc32	Mus musculus leucine rich repeat containing 3
2271288	A_55_P1985422	LOC100044227	Q811B0_MOUSE (Q811B0) Erythroid differen
2292890	A_55_P2034481	Erdr1	Mus musculus erythroid differentiation regulat
2290610	A_51_P349213	Fcrl1	Mus musculus Fc receptor-like 1 (Fcrl1), transc
2298425	A_51_P501844	Cyp26b1	Mus musculus cytochrome P450, family 26, su
2264815	A_55_P2062133	Etv3	Mus musculus ets variant gene 3 (Etv3), trans
2295558	A_30_P01027087	A_30_P01027087	lincRNA:chr3:79069438-79073704 reverse st
2285809	A_55_P2016166	Wfdc2	Mus musculus WAP four-disulfide core domain
2306135	A_30_P01021230	A_30_P01021230	lincRNA:chr3:37659958-37665945 forward st
2264323	A_52_P512427	2510049J12Rik	Mus musculus RIKEN cDNA 2510049J12 gen
2310774	A_55_P2107775	Apol9a	Mus musculus apolipoprotein L 9a (Apol9a), t
2286413	A_66_P128761	E430029J22Rik	Mus musculus pyrin domain containing 3 (Pyd
2276525	A_55_P1953341	Wfdc2	Mus musculus WAP four-disulfide core domain
2261113	A_55_P1967286	Gm1409	immunoglobulin kappa variable 5-39 [Source:
2286414	A_30_P01025525	A_30_P01025525	lincRNA:chr3:37659958-37665945 forward st
2275136	A_55_P2144686	Dmbt1	Mus musculus deleted in malignant brain tum
2259608	A_55_P2023637	Prg4	Mus musculus proteoglycan 4 (megakaryocyte
2282501	A_55_P2110136	Arhgap29	Mus musculus Rho GTPase activating protein
2263575	A_55_P2043367	Apol9a	Mus musculus apolipoprotein L 9a (Apol9a), t
2306577	A_66_P110633	Apol9b	Mus musculus apolipoprotein L 9b (Apol9b), t
2304380	A_30_P01024788	A_30_P01024788	lincRNA:chr3:79069438-79073704 reverse st
2307570	A_55_P2181222	E430029J22Rik	Mus musculus pyrin domain containing 3 (Pyd
2283521	A_52_P481279	Gm1060	Mus musculus coiled-coil domain containing 1
2300377	A_55_P1958018	LOC100047337	Q6EE68_PRODO (Q6EE68) Ribosomal prote
2292666	A_55_P1960894	Cabp1	Mus musculus calcium binding protein 1 (Cab
2286467	A_55_P2056192	NAP111293-1	Unknown
2296377	A_55_P2137828	Gprc5b	Mus musculus G protein-coupled receptor, fa
2295324	A_55_P2163098	Akr1c18	Mus musculus aldo-keto reductase family 1, m
2273936	A_55_P2022971	Tspan9	Mus musculus tetraspanin 9 (Tspan9), mRNA
2273566	A_30_P01025989	A_30_P01025989	lincRNA:chr3:84609788-84618062 reverse st
2310092	A_52_P880457	Ampd1	Mus musculus adenosine monophosphate de
2293698	A_55_P1973451	Stra6	Mus musculus stimulated by retinoic acid gen
2304572	A_30_P01030239	A_30_P01030239	lincRNA:chr13:28506971-28511732 reverse s
2264160	A_51_P466685	Fbxl22	Mus musculus F-box and leucine-rich repeat p
2289880	A_30_P01028589	A_30_P01028589	lincRNA:chr7:134835448-134842613 forward
2288947	A_55_P2050426	Ankrd50	Mus musculus ankyrin repeat domain 50 (Ank
2294793	A_55_P1962603	Cplx2	Mus musculus complexin 2 (Cplx2), mRNA [N
2259768	A_55_P2024634	Gm13546	predicted gene 13546 [Source:MGI Symbol;A
2286112	A_52_P588483	Fbln1	Mus musculus fibulin 1 (Fbln1), mRNA [NM_01
2295753	A_66_P105075	Mmp11	Mus musculus matrix metallopeptidase 11 (M
2259463	A_51_P268069	Six1	Mus musculus sine oculis-related homeobox 1
2287192	A_52_P382802	1700102P08Rik	Mus musculus RIKEN cDNA 1700102P08 gen
2267405	A_52_P257502	Igfbp4	Mus musculus insulin-like growth factor bindin
2285998	A_55_P2148400	Gm2264	Unknown
2296525	A_30_P01022835	A_30_P01022835	lincRNA:chr3:106858397-106896812 reverse
2290988	A_55_P2058297	Sgip1	Mus musculus SH3-domain GRB2-like (endop

2263864	A_52_P646783	Fbxl22	Mus musculus F-box and leucine-rich repeat p
2286408	A_30_P01024831	A_30_P01024831	lincRNA:chr8:19678750-20038750 forward st
2284827	A_51_P218682	4930588N13Rik	Mus musculus RIKEN cDNA 4930588N13 ger
2309983	A_55_P2183914	Gm7120	Mus musculus predicted gene 7120 (Gm7120
2276254	A_51_P114826	Cdh13	Mus musculus cadherin 13 (Cdh13), mRNA [N
2297654	A_55_P1962602	Gm2690	Mus musculus 2 days neonate sympathetic ga
2266301	A_55_P1989185	ENSMUST0000010	PREDICTED: Mus musculus predicted gene 6
2295189	A_52_P227267	Atp1a2	Mus musculus ATPase, Na+/K+ transporting,
2287554	A_51_P398766	Gbp1	Mus musculus guanylate binding protein 1 (G
2289922	A_55_P2070441	Sp6	Mus musculus trans-acting transcription factor
2264259	A_55_P2001233	E430029J22Rik	Mus musculus pyrin domain containing 3 (Pyd
2272018	A_55_P1966383	Gm2936	Unknown
2292116	A_55_P1964433	Zmynd12	Mus musculus zinc finger, MYND domain cont
2297550	A_55_P2044582	Iglon5	Mus musculus IgLON family member 5 (Iglon5
2292336	A_55_P2072995	ENSMUST0000010	immunoglobulin kappa variable 11-125 [Sourc
2268697	A_66_P121480	Sardh	Mus musculus sarcosine dehydrogenase (Sar
2290219	A_55_P2024669	Myo6	Mus musculus myosin VI (Myo6), mRNA [NM_
2283443	A_51_P290576	Plk2	Mus musculus polo-like kinase 2 (Drosophila)
2261730	A_55_P2176280	Prkar1b	Mus musculus protein kinase, cAMP depende
2267880	A_55_P2040775	Gm6837	Mus musculus 921-L mRNA for presynaptic pr
2298126	A_55_P2074736	Prkar1b	Mus musculus protein kinase, cAMP depende
2301495	A_52_P52946	4922501L14Rik	Mus musculus RIKEN cDNA 4922501L14 ger
2311237	A_51_P211854	Selp	Mus musculus selectin, platelet (Selp), mRNA
2289499	A_51_P258848	4933427G17Rik	Mus musculus RIKEN cDNA 4933427G17 ger
2303022	A_30_P01020912	A_30_P01020912	lincRNA:chr10:3231337-3231802 forward stra
2297898	A_52_P344152	Pik3ip1	phosphoinositide-3-kinase interacting protein
2312005	A_55_P1991770	Pdlim4	Mus musculus PDZ and LIM domain 4 (Pdlim4
2257498	A_51_P131408	Tnfrsf12a	Mus musculus tumor necrosis factor receptor s
2260729	A_55_P2148402	Cplx2	Mus musculus complexin 2 (Cplx2), mRNA [NM
2302158	A_66_P121965	1110032F04Rik	Mus musculus RIKEN cDNA 1110032F04 ger
2263644	A_52_P325443	Arhgap29	Mus musculus Rho GTPase activating protein
2278358	A_51_P214470	2610019F03Rik	Mus musculus RIKEN cDNA 2610019F03 ger
2281640	A_30_P01020388	A_30_P01020388	lincRNA:chrX:47890565-47915775 forward st
2303536	A_55_P2028576	Gm7057	Unknown
2303879	A_55_P1989698	Mmp11	Mus musculus matrix metallopeptidase 11 (Mn
2281996	A_55_P2026982	2610019F03Rik	Mus musculus RIKEN cDNA 2610019F03 ger
2265778	A_51_P258409	Hey1	Mus musculus hairy/enhancer-of-split related
2270098	A_55_P2064351	Vipr1	Mus musculus vasoactive intestinal peptide re
2310090	A_52_P900300	Gm6213	Mus musculus predicted gene 6213 (Gm6213
2272724	A_51_P293938	Rasl11b	Mus musculus RAS-like, family 11, member B
2289457	A_55_P2180445	Gm2742	Unknown
2298235	A_55_P2056533	Ntrk3	Mus musculus neurotrophic tyrosine kinase, re
2270946	A_66_P122621	ENSMUST0000006	Mus musculus 16 days neonate thymus cDNA
2303029	A_55_P2120866	LOC100044171	PREDICTED: Mus musculus hypothetical LOC
2300864	A_30_P01018048	A_30_P01018048	lincRNA:chr3:37659958-37665945 forward st
2302642	A_52_P202142	Sv2a	Mus musculus synaptic vesicle glycoprotein 2
2300019	A_52_P316933	Sh3bgrl2	Mus musculus SH3 domain binding glutamic a
2271862	A_55_P1968085	A_55_P1968085	Unknown
2257317	A_51_P391955	Dapl1	Mus musculus death associated protein-like 1
2271589	A_51_P349413	ENSMUST0000010	ADP-ribosylation factor-like 5C [Source:MGI S
2285704	A_55_P1997651	Espn	Mus musculus espin (Espn), transcript variant
2282251	A_55_P2384671	AK033123	predicted gene, 17641 [Source:MGI Symbol;A
2300919	A_55_P1960043	Sec31b	Mus musculus Sec31 homolog B (S. cerevisia
2299369	A_55_P1992571	Gm2952	predicted gene, 17684 [Source:MGI Symbol;A
2296596	A_55_P2103249	Cxcr1	Mus musculus chemokine (C-X-C motif) recept
2300416	A_55_P2391881	Gm12108	predicted gene 12108 [Source:MGI Symbol;A

2259114	A_55_P2172086	Gm10640	Mus musculus adult male testis cDNA, RIKEN
2280536	A_55_P2115044	LOC100047266	BY110436 RIKEN full-length enriched, 15 day
2269038	A_55_P2416464	4921511I17Rik	Mus musculus adult male testis cDNA, RIKEN
2295625	A_30_P01030370	A_30_P01030370	lincRNA:chr18:35967988-35968812 forward
2295422	A_55_P2043627	Fam89a	Mus musculus family with sequence similarity
2304442	A_66_P138298	Gm4371	Mus musculus predicted gene 4371 (Gm4371
2275740	A_51_P104418	Dusp10	Mus musculus dual specificity phosphatase 1
2256887	A_30_P01027107	A_30_P01027107	lincRNA:chr11:99048975-99062425 reverse
2297016	A_30_P01020593	A_30_P01020593	lincRNA:chr12:81217572-81233910 forward
2296384	A_55_P1979003	LOC100044493	Unknown
2272958	A_55_P2041728	Gm590	Mus musculus predicted gene 590 (Gm590),
2291699	A_30_P01017850	A_30_P01017850	lincRNA:chr5:54053328-54053870 forward s
2270383	A_52_P173442	Wscd2	Mus musculus WSC domain containing 2 (Ws
2266643	A_55_P2145356	Thada	Mus musculus mRNA for mKIAA1767 protein.
2295557	A_55_P2151521	ENSMUST0000010	microfibrillar-associated protein 3 [Source:MG
2292718	A_55_P1959639	LOC100045061	Unknown
2307321	A_55_P2054743	Sh3bgrl2	Mus musculus SH3 domain binding glutamic
2303379	A_55_P2056973	Treml2	Mus musculus triggering receptor expressed
2303803	A_55_P1999691	Usp27x	ubiquitin specific peptidase 27, X chromosom
2261528	A_55_P2007233	ENSMUST0000006	PREDICTED: Mus musculus Riken cDNA A53
2274870	A_55_P2167521	Gm15503	Mus musculus 16 days neonate thymus cDNA
2306017	A_30_P01025698	A_30_P01025698	lincRNA:chr10:122410471-122422759 revers
2260520	A_55_P1964332	LOC100048239	Unknown
2285616	A_55_P2120650	LOC100047155	Unknown
2297554	A_55_P2003309	Gm2073	Unknown
2298365	A_52_P565575	Arhgap20	Mus musculus Rho GTPase activating protein
2259438	A_55_P1981929	Scg5	Mus musculus secretogranin V (Scg5), mRNA
2302035	A_55_P1953508	Mobkl2c	Mus musculus MOB kinase activator 3C (Mob
2257397	A_52_P104091	Slc25a27	Mus musculus solute carrier family 25, membe
2300886	A_66_P107483	Treml2	Mus musculus triggering receptor expressed
2281872	A_51_P305532	Eif2s3x	Mus musculus eukaryotic translation initiation
2260440	A_55_P2170225	Sh3bgrl2	Mus musculus SH3 domain binding glutamic
2303472	A_66_P111090	Sctr	Mus musculus secretin receptor (Sctr), mRNA
2297274	A_55_P2007234	ENSMUST0000006	PREDICTED: Mus musculus Riken cDNA A53
2289855	A_51_P182728	Stx1a	Mus musculus syntaxin 1A (brain) (Stx1a), mR
2301960	A_30_P01027042	A_30_P01027042	lincRNA:chr11:120041124-120052299 revers
2288869	A_52_P509965	Ager	Mus musculus advanced glycosylation end pr
2270548	A_52_P108850	St8sia1	Mus musculus ST8 alpha-N-acetyl-neuraminid
2281384	A_51_P412225	Tbc1d16	Mus musculus TBC1 domain family, member
2291057	A_55_P2045129	Gm4361	Mus musculus adult male thymus cDNA, RIKE
2265157	A_52_P590535	Fbln2	Mus musculus fibulin 2 (Fbln2), transcript varia
2270323	A_30_P01030905	A_30_P01030905	lincRNA:chr15:85300937-85301522 forward
2291523	A_55_P2022519	Tmem108	Mus musculus transmembrane protein 108 (T
2268971	A_55_P1985890	Tiparp	Mus musculus TCDD-inducible poly(ADP-ribos
2280739	A_52_P64687	Camk2n1	Mus musculus calcium/calmodulin-dependent
2261093	A_51_P518051	Dusp4	Mus musculus dual specificity phosphatase 4
2292111	A_30_P01022122	A_30_P01022122	lincRNA:chr8:19678750-20038750 reverse s
2301761	A_52_P283524	Rcan3	Mus musculus regulator of calcineurin 3 (Rca
2306669	A_30_P01022858	A_30_P01022858	lincRNA:chr4:131737612-131738100 reverse
2264610	A_55_P2286493	4933405E24Rik	Mus musculus RIKEN cDNA 4933405E24 ge
2291561	A_55_P2159850	Gm4191	603275854F1 NCI_CGAP_Mam3 Mus muscu
2264814	A_52_P478394	Dleu7	Mus musculus deleted in lymphocytic leukemi
2309359	A_66_P108003	Espn	Mus musculus espin (Espn), transcript variant
2268077	A_55_P1994309	Ptgir	Mus musculus prostaglandin I receptor (IP) (P
2265319	A_55_P2091601	Col11a2	Mus musculus collagen, type XI, alpha 2 (Col
2261343	A_55_P2024046	Slc16a5	Mus musculus solute carrier family 16 (monoc

2312367	A_55_P2007205	ENSMUST0000006	predicted pseudogene 10749 [Source:MGI S
2299634	A_55_P2025755	Syce1l	Mus musculus synaptonemal complex central
2296586	A_55_P2113738	Gm4102	AV573893 Abe mouse ES cell Mus musculus
2284432	A_55_P2156905	Sox5	Mus musculus SRY-box containing gene 5 (S
2258300	A_55_P2096121	Gm2528	Unknown
2261843	A_51_P443819	2610034M16Rik	Mus musculus RIKEN cDNA 2610034M16 ge
2292229	A_55_P2004168	LOC100046325	Unknown
2306039	A_55_P2017789	Il4ra	Mus musculus interleukin 4 receptor, alpha (Il
2299042	A_55_P2084890	C2cd2l	Mus musculus C2 calcium-dependent domain
2259334	A_55_P1993858	Rmrp	Mus musculus RNA component of mitochondr
2283668	A_55_P2092156	Gm2911	Unknown
2282383	A_55_P2040774	Gm6837	Unknown
2281140	A_55_P2135526	Gzmc	Mus musculus granzyme C (Gzmc), mRNA [N
2281039	A_30_P01025873	A_30_P01025873	lincRNA:chr10:44707451-44707693 reverse s
2311127	A_55_P2075449	Ttll3	Mus musculus tubulin tyrosine ligase-like famil
2310150	A_55_P1993483	Gm7462	Unknown
2289783	A_55_P2004881	D18Ertd653e	Mus musculus DNA segment, Chr 18, ERATO
2266365	A_55_P2159149	Nsg2	neuron specific gene family member 2 [Sourc
2307063	A_55_P2005720	Gm4253	Unknown
2263518	A_55_P2021476	XM_001474821	Q6TXJ2_RAT (Q6TXJ2) LRRGT00007, partia
2269832	A_55_P2044917	Gpr83	Mus musculus G protein-coupled receptor 83
2305092	A_66_P121583	Gm7120	Mus musculus predicted gene 7120 (Gm7120
2270938	A_30_P01028003	A_30_P01028003	lincRNA:chrX:6950444-6952293 reverse stra
2262314	A_55_P2097072	Gm7219	Unknown
2296484	A_30_P01024498	A_30_P01024498	lincRNA:chr13:28506971-28511732 reverse s
2274282	A_30_P01030979	A_30_P01030979	lincRNA:chr10:120336296-120354471 revers
2260042	A_51_P434758	Fam83e	Mus musculus family with sequence similarity
2288082	A_30_P01027441	A_30_P01027441	lincRNA:chr13:28506971-28511732 reverse s
2279738	A_51_P471791	St8sia6	Mus musculus ST8 alpha-N-acetyl-neuraminid
2276748	A_30_P01021556	A_30_P01021556	lincRNA:chr8:19678750-20038750 forward st
2291650	A_55_P2097219	Gbp1	Mus musculus guanylate binding protein 1 (G
2275270	A_55_P1986680	Gm2334	Unknown
2289249	A_52_P629895	Adh1	Mus musculus alcohol dehydrogenase 1 (clas
2300284	A_30_P01021222	A_30_P01021222	lincRNA:chr17:8718223-8949898 forward stra
2309177	A_55_P2179604	Vash1	Mus musculus vasohibin 1 (Vash1), mRNA [N
2266013	A_30_P01021493	A_30_P01021493	lincRNA:chr3:93564825-93576725 forward st
2294141	A_55_P1954276	Emid1	Mus musculus EMI domain containing 1 (Emi
2280892	A_51_P382369	Zfp608	Mus musculus zinc finger protein 608 (Zfp608
2292220	A_55_P2000354	Rgs11	Mus musculus regulator of G-protein signaling
2275135	A_51_P419389	Bmpr2	Mus musculus bone morphogenic protein rece
2257193	A_55_P2024366	Raver2	Mus musculus ribonucleoprotein, PTB-binding
2278795	A_30_P01031078	A_30_P01031078	lincRNA:chr4:45079022-45096897 reverse st
2292045	A_55_P2007630	Sez6l2	Mus musculus seizure related 6 homolog like
2289113	A_51_P480013	Car11	Mus musculus carbonic anhydrase 11 (Car11
2286929	A_30_P01020222	A_30_P01020222	lincRNA:chr4:62367014-62386800 forward st
2310472	A_55_P2074045	Gm3655	Q8VKJ6_MYCTU (Q8VKJ6) PE_PGRS family
2258681	A_65_P16059	Tgfbr3	Mus musculus transforming growth factor, bet
2275961	A_52_P546459	Ube2d1	Mus musculus ubiquitin-conjugating enzyme E
2265884	A_30_P01032768	A_30_P01032768	lincRNA:chr11:99048975-99062425 reverse s
2267983	A_55_P2105452	Foxp1	Mus musculus forkhead box P1 (Foxp1), trans
2262856	A_30_P01030720	A_30_P01030720	lincRNA:chr10:62267317-62269871 reverse s
2304915	A_30_P01032149	A_30_P01032149	lincRNA:chr14:73729977-73751877 reverse s
2261471	A_55_P2161400	Sctr	Mus musculus secretin receptor (Sctr), mRNA
2267790	A_51_P363749	Irf6	Mus musculus interferon regulatory factor 6 (I
2309282	A_51_P418809	Airn	Mus musculus antisense Igf2r RNA (Airn), tran
2288204	A_55_P1964004	Gm3521	BY456555 RIKEN full-length enriched, adult

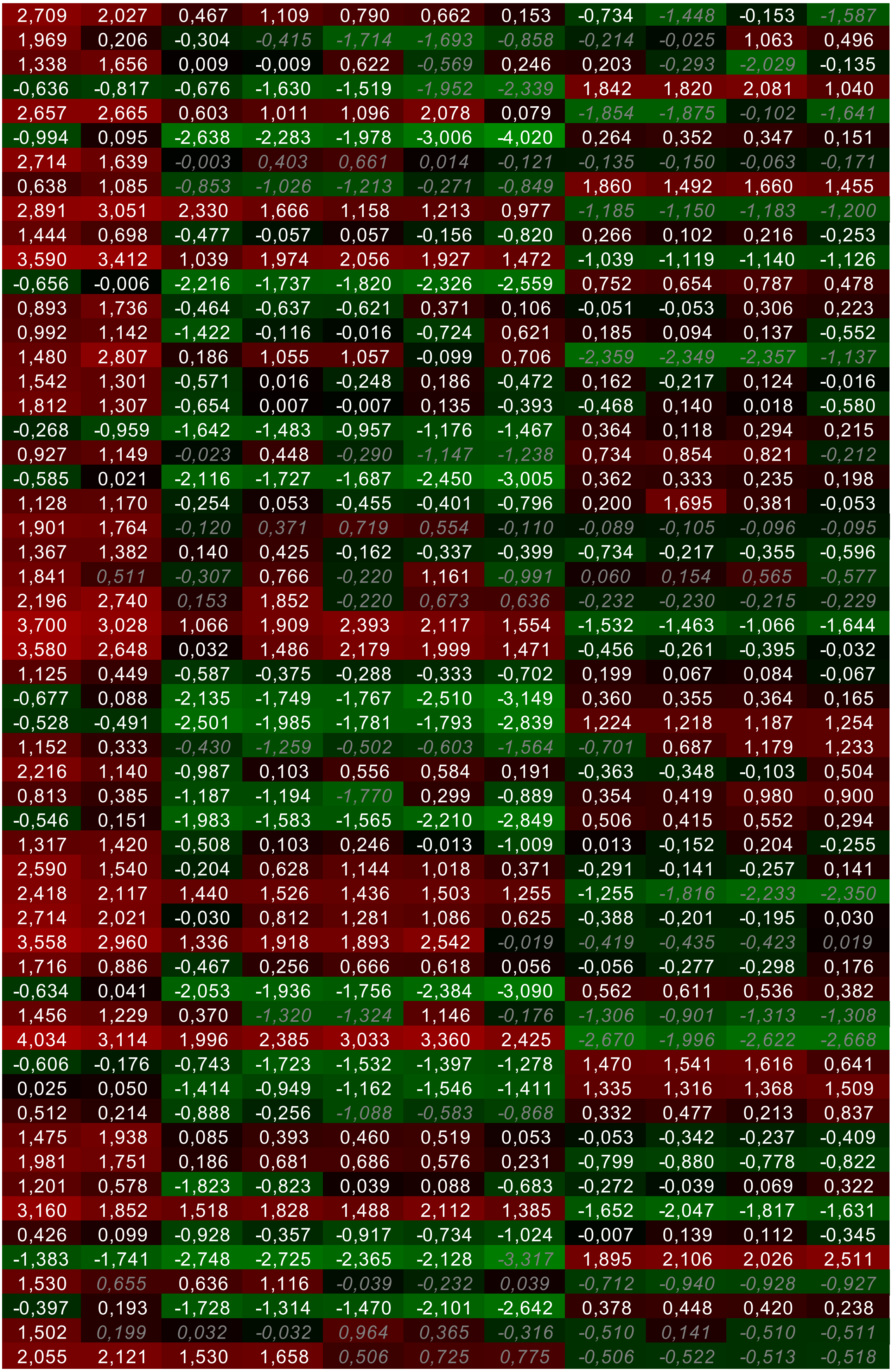
ANOVA p-value	Adjusted ANOVA p-value	Tukey p-value	Fold change	Log2 ratio	Median	wt_non-stim_1	wt_non-stim_2	wt_non-stim_3
1,26E-19	4,38E-16	2,26E-14	-1619,127	-10,661	10,425	4,432	4,248	4,223
4,28E-04	1,39E-03	3,50E-03	-38,479	-5,266	13,324	0,193	-0,022	1,055
4,09E-04	1,34E-03	3,46E-03	-26,373	-4,721	13,815	0,315	-0,030	1,024
1,48E-17	8,83E-15	2,34E-14	-12,915	-3,691	3,846	1,876	1,563	1,550
1,93E-12	5,27E-11	1,73E-10	-9,292	-3,216	2,221	3,218	3,987	3,684
3,93E-16	7,93E-14	4,35E-14	-7,803	-2,964	9,485	1,584	1,704	1,810
7,70E-07	4,13E-06	7,00E-06	-6,648	-2,733	2,511	2,254	2,209	2,529
3,97E-12	9,31E-11	7,09E-08	-6,021	-2,590	3,594	3,414	3,092	3,213
1,62E-08	1,24E-07	1,72E-05	-5,812	-2,539	5,013	0,072	-0,265	-0,566
4,68E-06	2,16E-05	2,25E-03	-5,724	-2,517	4,800	-0,144	*-1,212*	-0,286
1,84E-11	3,36E-10	4,44E-09	-5,307	-2,408	6,844	1,812	2,027	1,884
8,36E-17	2,89E-14	9,71E-09	-5,077	-2,344	6,113	3,829	3,835	3,883
9,68E-14	4,65E-12	5,84E-09	-5,049	-2,336	4,732	2,696	2,732	2,887
1,59E-07	9,82E-07	1,85E-02	-4,928	-2,301	8,962	4,887	5,658	4,321
1,39E-07	8,68E-07	2,51E-05	-4,510	-2,173	3,768	*0,072*	*-0,483*	
1,72E-04	6,02E-04	5,47E-04	-4,478	-2,163	2,008	*2,029*	2,470	*0,058*
2,20E-12	5,81E-11	5,26E-07	-4,463	-2,158	3,934	3,659	3,580	4,095
2,50E-04	8,48E-04	1,96E-03	-4,365	-2,126	3,462	1,313	*-0,075*	1,023
1,19E-11	2,32E-10	3,11E-09	-4,353	-2,122	9,361	2,081	2,086	2,083
1,19E-11	2,32E-10	3,75E-09	-4,296	-2,103	9,841	2,002	2,060	2,088
1,10E-05	4,74E-05	3,14E-04	-4,272	-2,095	2,907	1,495	2,006	2,407
2,63E-16	6,03E-14	2,67E-06	-4,243	-2,085	9,146	4,039	3,987	4,053
1,74E-14	1,27E-12	1,35E-08	-4,228	-2,080	8,074	2,634	2,887	2,792
1,45E-07	9,02E-07	3,53E-04	-3,992	-1,997	2,679	2,779	2,217	2,694
1,00E-03	3,06E-03	9,18E-04	-3,972	-1,990	3,412	0,945	*0,036*	1,155
1,46E-10	1,98E-09	1,63E-09	-3,945	-1,980	7,163	0,475	0,705	0,782
1,58E-06	7,97E-06	3,32E-02	-3,942	-1,979	3,321	1,848	3,695	3,095
3,71E-17	1,73E-14	1,89E-09	-3,910	-1,967	8,436	-1,877	-2,071	-2,055
7,50E-08	4,96E-07	1,81E-06	-3,834	-1,939	4,084	0,228	0,487	0,607
8,36E-06	3,68E-05	3,49E-03	-3,832	-1,938	4,015	0,340	0,343	-0,219
1,26E-13	5,75E-12	2,60E-06	-3,821	-1,934	4,243	3,759	3,667	3,630
2,14E-06	1,05E-05	3,19E-06	-3,750	-1,907	6,794	0,818	0,680	0,557
2,57E-06	1,25E-05	1,50E-04	-3,696	-1,886	3,097	2,156	2,245	2,131
2,43E-07	1,45E-06	8,32E-05	-3,638	-1,863	2,880	2,528	2,192	1,948
1,96E-02	4,66E-02	1,92E-02	-3,613	-1,853	2,982	4,146	1,849	*0,024*
4,24E-03	1,15E-02	2,74E-02	-3,543	-1,825	8,481	0,113	0,106	-0,022
7,27E-06	3,24E-05	2,54E-03	-3,543	-1,825	10,029	-1,074	-0,353	-1,383
3,78E-07	2,16E-06	4,85E-06	-3,489	-1,803	4,748	0,311	0,390	0,774
1,41E-06	7,18E-06	8,01E-04	-3,485	-1,801	4,788	-0,539	-0,171	-0,258
8,84E-10	9,45E-09	1,91E-07	-3,392	-1,762	5,941	1,881	1,358	1,877
2,94E-10	3,63E-09	9,36E-04	-3,313	-1,728	5,290	*-1,369*	-1,225	-1,270
3,91E-05	1,53E-04	1,13E-03	-3,310	-1,727	2,032	*1,808*	1,980	2,248
1,98E-09	1,92E-08	2,08E-05	-3,294	-1,720	6,800	2,729	2,581	2,278
1,44E-05	6,06E-05	3,24E-03	-3,272	-1,710	9,924	-0,956	-0,182	-1,445
5,77E-06	2,62E-05	4,27E-03	-3,245	-1,698	2,346	1,780	*1,025*	2,005
1,75E-03	5,10E-03	2,89E-02	-3,227	-1,690	3,277	1,515	1,412	1,119

1,12E-09	**1,16E-08**	**2,12E-05**	**-3,215**	-1,685	4,386	2,639	2,319	2,347
2,46E-03	**6,99E-03**	**1,80E-03**	**-3,198**	-1,677	3,530	0,821	0,819	*0,099*
1,86E-05	**7,68E-05**	**8,25E-04**	**-3,191**	-1,674	4,025	1,682	1,888	1,748
1,52E-06	**7,70E-06**	**3,93E-03**	**-3,149**	-1,655	5,676	0,025	0,155	0,232
1,16E-08	**9,24E-08**	**3,33E-03**	**-3,130**	-1,646	3,827	2,447	2,435	2,661
1,80E-06	**8,97E-06**	**2,86E-03**	**-3,125**	-1,644	8,996	-1,415	-0,701	-1,711
2,78E-05	**1,11E-04**	**4,10E-04**	**-3,084**	-1,625	2,227	2,668	*0,588*	*1,389*
5,41E-08	**3,68E-07**	**4,33E-05**	**-3,065**	-1,616	3,016	1,533	*0,196*	0,764
6,44E-13	**2,15E-11**	**2,84E-05**	**-3,021**	-1,595	3,290	2,587	2,808	2,435
8,60E-05	**3,17E-04**	**8,20E-04**	**-3,017**	-1,593	6,715	1,437	1,130	1,494
7,51E-16	**1,24E-13**	**6,62E-08**	**-2,971**	-1,571	9,641	3,474	3,498	3,579
1,53E-07	**9,48E-07**	**2,01E-03**	**-2,949**	-1,560	8,837	-1,217	-0,421	-1,451
4,71E-05	**1,82E-04**	**4,09E-04**	**-2,944**	-1,558	4,599	0,976	1,737	1,094
3,55E-05	**1,40E-04**	**2,04E-03**	**-2,940**	-1,556	4,840	1,659	1,691	1,440
1,85E-07	**1,13E-06**	**9,67E-03**	**-2,934**	-1,553	4,147	2,259	2,794	2,207
2,01E-09	**1,94E-08**	**2,55E-05**	**-2,928**	-1,550	6,039	1,145	1,349	1,207
2,68E-03	**7,56E-03**	**6,66E-03**	**-2,906**	-1,539	4,888	1,321	1,532	1,824
3,32E-06	**1,58E-05**	**1,16E-04**	**-2,902**	-1,537	6,898	0,217	0,070	0,207
1,38E-03	**4,10E-03**	**3,36E-03**	**-2,890**	-1,531	3,292	1,572	2,781	1,242
2,43E-07	**1,45E-06**	**3,59E-04**	**-2,890**	-1,531	12,796	-0,988	-0,510	-1,448
5,19E-06	**2,38E-05**	**1,68E-04**	**-2,888**	-1,530	7,097	1,176	0,993	0,986
5,00E-08	**3,43E-07**	**1,62E-06**	**-2,888**	-1,530	2,004	1,991	*1,679*	1,957
2,88E-08	**2,08E-07**	**9,11E-07**	**-2,886**	-1,529	4,472	1,493	1,330	1,345
1,43E-03	**4,23E-03**	**4,72E-02**	**-2,860**	-1,516	3,008	1,462	0,982	1,296
1,35E-04	**4,80E-04**	**1,03E-02**	**-2,850**	-1,511	2,103	*1,182*	1,902	2,146
6,96E-14	**3,67E-12**	**1,74E-05**	**-2,823**	-1,497	6,044	3,405	3,507	3,360
2,08E-09	**2,00E-08**	**2,81E-04**	**-2,795**	-1,483	8,519	2,968	3,089	2,930
1,03E-06	**5,40E-06**	**7,58E-07**	**-2,766**	-1,468	9,298	1,154	1,093	1,018
5,21E-07	**2,89E-06**	**8,41E-04**	**-2,749**	-1,459	12,123	-1,073	-0,508	-1,528
1,70E-12	**4,76E-11**	**1,11E-07**	**-2,747**	-1,458	10,810	-0,604	-0,594	-0,504
7,42E-03	**1,92E-02**	**9,17E-03**	**-2,732**	-1,450	3,334	1,213	*0,289*	0,848
6,54E-06	**2,94E-05**	**1,68E-03**	**-2,732**	-1,450	5,541	1,800	1,622	1,641
3,51E-03	**9,70E-03**	**2,02E-02**	**-2,730**	-1,449	4,947	0,262	-0,087	0,087
4,82E-07	**2,70E-06**	**8,60E-04**	**-2,709**	-1,438	10,977	-0,928	-0,339	-1,384
2,47E-08	**1,81E-07**	**2,08E-06**	**-2,700**	-1,433	7,365	1,622	1,331	1,780
1,39E-08	**1,08E-07**	**1,22E-04**	**-2,691**	-1,428	9,089	1,922	2,056	2,136
1,36E-10	**1,86E-09**	**9,28E-03**	**-2,685**	-1,425	5,423	3,104	3,056	2,865
5,17E-09	**4,48E-08**	**2,39E-04**	**-2,680**	-1,422	10,036	2,238	2,135	2,234
1,11E-08	**8,88E-08**	**3,91E-04**	**-2,678**	-1,421	2,311	3,464	3,021	3,313
1,13E-06	**5,87E-06**	**2,75E-04**	**-2,676**	-1,420	7,832	1,676	1,529	1,785
2,29E-07	**1,37E-06**	**7,85E-04**	**-2,674**	-1,419	9,061	-1,056	-0,388	-1,423
3,09E-04	**1,03E-03**	**1,31E-02**	**-2,648**	-1,405	3,147	1,085	1,644	1,105
3,55E-15	**3,84E-13**	**2,60E-03**	**-2,646**	-1,404	4,713	3,851	3,829	3,492
1,75E-08	**1,33E-07**	**1,19E-04**	**-2,635**	-1,398	6,496	0,013	0,001	0,310
2,96E-12	**7,36E-11**	**6,39E-08**	**-2,603**	-1,380	5,990	-0,179	-0,124	-0,031
5,25E-03	**1,40E-02**	**4,87E-03**	**-2,603**	-1,380	4,244	2,637	0,013	0,703
1,25E-13	**5,71E-12**	**3,23E-09**	**-2,588**	-1,372	6,752	1,765	1,695	1,865
4,51E-11	**7,21E-10**	**1,29E-06**	**-2,565**	-1,359	6,841	1,940	1,881	1,934
6,26E-04	**1,98E-03**	**3,11E-03**	**-2,558**	-1,355	12,639	0,614	0,807	0,672
7,22E-13	**2,36E-11**	**4,10E-03**	**-2,539**	-1,344	7,258	2,460	2,874	2,862
2,21E-05	**9,01E-05**	**1,57E-05**	**-2,537**	-1,343	8,023	0,425	0,450	0,437
7,63E-13	**2,48E-11**	**2,95E-04**	**-2,535**	-1,342	6,822	-0,986	-1,383	-1,750
2,11E-05	**8,63E-05**	**3,01E-02**	**-2,530**	-1,339	2,800	1,507	1,277	1,378
5,90E-07	**3,23E-06**	**4,96E-04**	**-2,516**	-1,331	11,861	-0,781	-0,304	-1,112
9,24E-05	**3,39E-04**	**1,03E-02**	**-2,509**	-1,327	2,280	*1,311*	1,359	1,694
6,05E-08	**4,08E-07**	**2,50E-02**	**-2,502**	-1,323	2,344	2,212	*0,770*	2,098

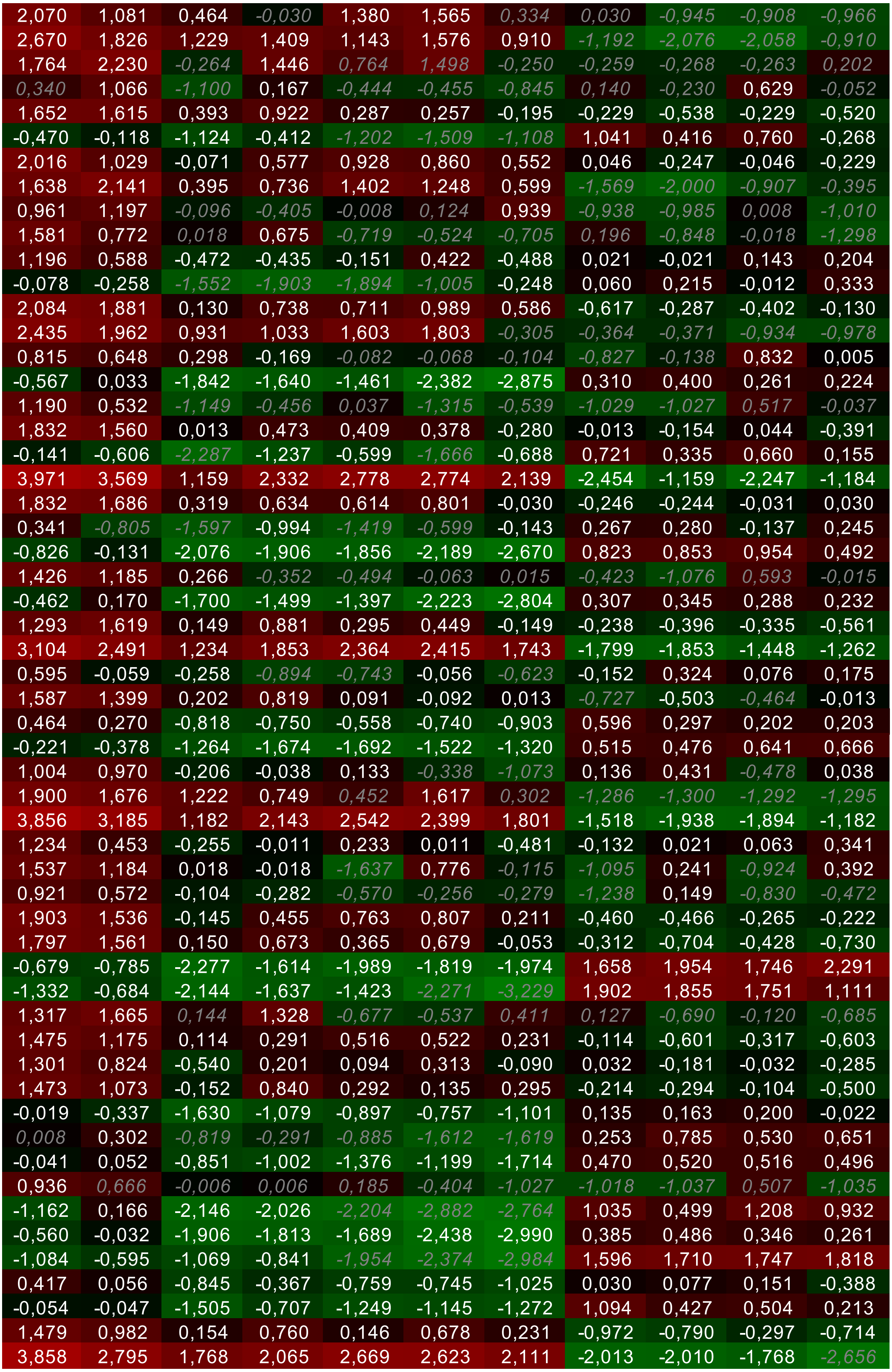
1,71E-07	1,05E-06	1,98E-02	-2,495	-1,319	2,981	1,565	1,783	1,994
2,42E-12	6,26E-11	6,64E-04	-2,491	-1,317	4,078	2,278	2,778	2,546
7,70E-05	2,86E-04	5,09E-03	-2,490	-1,316	2,294	1,905	3,259	2,080
1,20E-02	2,98E-02	1,30E-02	-2,486	-1,314	3,236	*0,185*	0,859	0,993
4,08E-08	2,85E-07	4,19E-05	-2,481	-1,311	8,078	1,598	1,172	1,544
6,45E-04	2,04E-03	1,13E-02	-2,474	-1,307	4,564	0,251	0,251	0,184
2,81E-08	2,04E-07	1,52E-04	-2,471	-1,305	7,445	1,990	1,881	1,646
2,10E-10	2,71E-09	4,20E-03	-2,467	-1,303	3,774	2,237	2,039	1,898
5,12E-05	1,96E-04	8,75E-03	-2,461	-1,299	3,021	1,359	1,517	1,292
1,52E-03	4,48E-03	2,86E-02	-2,455	-1,296	3,082	0,950	0,598	0,680
2,09E-04	7,20E-04	1,11E-03	-2,454	-1,295	5,591	0,796	0,875	0,860
4,76E-05	1,83E-04	4,05E-02	-2,454	-1,295	4,163	*-1,217*	*-0,838*	0,012
4,77E-13	1,68E-11	2,27E-07	-2,450	-1,293	8,661	2,008	2,004	1,968
5,60E-07	3,08E-06	2,61E-02	-2,432	-1,282	3,212	2,315	1,886	2,704
1,70E-03	4,98E-03	8,74E-03	-2,427	-1,279	3,752	1,198	1,354	1,291
3,62E-07	2,08E-06	4,73E-04	-2,422	-1,276	13,561	-0,858	-0,505	-1,329
8,40E-03	2,15E-02	1,51E-02	-2,412	-1,270	3,330	*0,642*	0,732	1,543
1,74E-11	3,21E-10	9,81E-09	-2,408	-1,268	8,602	1,716	1,646	1,595
6,78E-05	2,54E-04	2,98E-03	-2,402	-1,264	5,009	0,217	0,028	0,144
7,75E-11	1,15E-09	1,95E-02	-2,398	-1,262	6,307	3,594	3,528	3,676
3,00E-11	5,09E-10	3,58E-07	-2,385	-1,254	8,004	2,010	2,092	1,868
1,48E-03	4,37E-03	6,69E-03	-2,382	-1,252	4,473	0,120	0,401	0,258
8,44E-08	5,53E-07	1,17E-02	-2,378	-1,250	8,036	-1,374	-0,826	-1,867
1,62E-03	4,75E-03	7,26E-03	-2,375	-1,248	3,243	1,127	*0,607*	1,211
1,00E-06	5,25E-06	6,07E-04	-2,359	-1,238	13,481	-0,803	-0,297	-1,240
1,31E-09	1,33E-08	2,71E-05	-2,355	-1,236	8,030	1,662	1,356	1,531
5,07E-14	2,86E-12	9,74E-04	-2,331	-1,221	6,225	3,073	2,927	3,129
6,58E-03	1,72E-02	5,32E-03	-2,326	-1,218	4,164	0,740	-0,006	0,604
2,85E-04	9,57E-04	4,81E-02	-2,325	-1,217	4,332	1,309	1,184	1,172
2,94E-09	2,72E-08	1,64E-08	-2,320	-1,214	6,650	0,350	0,589	0,469
5,26E-14	2,94E-12	3,39E-10	-2,315	-1,211	10,697	-0,311	-0,422	-0,208
1,12E-05	4,82E-05	1,35E-04	-2,313	-1,210	4,142	0,712	1,019	1,221
2,59E-10	3,24E-09	1,39E-03	-2,313	-1,210	3,174	2,015	1,959	2,153
3,74E-13	1,37E-11	1,96E-04	-2,312	-1,209	5,873	3,304	3,352	3,406
7,21E-07	3,89E-06	1,84E-05	-2,309	-1,207	7,747	1,187	1,196	1,217
1,24E-03	3,73E-03	1,20E-02	-2,301	-1,202	3,883	1,597	1,134	0,933
6,71E-03	1,75E-02	1,81E-02	-2,297	-1,200	3,677	1,315	1,020	0,793
7,76E-09	6,45E-08	4,30E-04	-2,294	-1,198	7,973	1,653	1,627	1,676
4,54E-09	4,00E-08	1,56E-05	-2,291	-1,196	6,939	1,490	1,672	1,490
1,49E-12	4,30E-11	4,99E-05	-2,282	-1,190	6,474	-0,886	-0,644	-0,995
6,78E-09	5,71E-08	1,04E-02	-2,277	-1,187	5,932	-1,532	-0,956	-0,327
3,87E-05	1,51E-04	3,65E-03	-2,274	-1,185	2,508	*1,310*	1,466	1,329
2,50E-11	4,36E-10	3,49E-06	-2,272	-1,184	5,678	1,541	1,288	1,501
1,36E-07	8,50E-07	5,97E-06	-2,270	-1,183	8,569	1,176	1,278	1,327
4,53E-07	2,55E-06	3,75E-04	-2,267	-1,181	5,559	1,661	1,255	1,577
1,08E-06	5,63E-06	3,59E-06	-2,266	-1,180	11,910	0,552	0,340	0,101
7,74E-04	2,41E-03	2,28E-03	-2,264	-1,179	3,450	0,549	*-0,098*	0,295
3,44E-10	4,15E-09	3,58E-08	-2,255	-1,173	9,314	-0,025	-0,056	-0,005
3,17E-03	8,84E-03	1,15E-02	-2,255	-1,173	2,895	1,404	1,451	1,167
4,96E-08	3,40E-07	9,20E-04	-2,244	-1,166	5,838	-1,038	-0,719	-1,214
2,03E-07	1,23E-06	9,51E-04	-2,236	-1,161	13,117	-1,041	-0,744	-1,570
6,38E-07	3,47E-06	4,05E-02	-2,231	-1,158	5,298	-0,796	-0,868	-0,261
1,72E-05	7,14E-05	1,12E-05	-2,224	-1,153	8,012	0,523	0,394	0,374
1,62E-08	1,24E-07	7,51E-06	-2,221	-1,151	8,638	-0,098	-0,200	-0,134
3,57E-07	2,05E-06	1,05E-02	-2,211	-1,145	4,749	1,377	1,335	1,463
3,72E-14	2,24E-12	2,89E-03	-2,207	-1,142	6,017	3,157	3,253	3,267

8,16E-10	8,82E-09	3,13E-06	-2,205	-1,141	7,580	1,621	1,916	1,896
7,30E-04	2,29E-03	1,14E-02	-2,201	-1,138	3,889	0,844	1,182	1,087
1,65E-10	2,20E-09	2,21E-04	-2,193	-1,133	6,178	1,723	1,862	1,776
4,57E-07	2,57E-06	9,33E-04	-2,190	-1,131	13,821	-0,936	-0,543	-1,376
3,02E-06	1,45E-05	1,43E-03	-2,187	-1,129	14,182	-0,778	-0,344	-1,147
2,48E-06	1,21E-05	2,79E-03	-2,187	-1,129	1,970	*1,643*	*1,620*	1,985
1,27E-06	6,53E-06	8,28E-03	-2,184	-1,127	7,976	-0,932	-0,761	-1,785
9,77E-07	5,14E-06	1,60E-06	-2,181	-1,125	11,679	0,293	0,110	0,221
5,58E-04	1,78E-03	8,12E-03	-2,175	-1,121	3,620	1,315	1,245	1,081
1,91E-03	5,54E-03	6,28E-03	-2,166	-1,115	10,265	0,644	0,704	0,710
4,40E-06	2,04E-05	5,25E-04	-2,164	-1,114	14,013	-0,462	-0,028	-0,713
1,19E-06	6,16E-06	7,20E-04	-2,160	-1,111	13,810	-0,699	-0,345	-1,094
7,89E-06	3,49E-05	1,39E-02	-2,151	-1,105	8,294	0,514	0,383	0,563
5,71E-04	1,82E-03	1,04E-02	-2,147	-1,102	4,346	1,108	0,576	1,669
1,49E-06	7,56E-06	2,91E-03	-2,135	-1,094	6,039	1,133	0,886	1,156
3,71E-06	1,75E-05	1,02E-02	-2,132	-1,092	7,953	-0,632	-0,217	-1,098
6,78E-05	2,54E-04	4,64E-03	-2,129	-1,090	5,044	1,347	0,972	1,548
4,99E-08	3,42E-07	2,86E-02	-2,127	-1,089	3,368	1,920	1,666	1,867
6,58E-08	4,40E-07	3,69E-03	-2,126	-1,088	7,861	-1,161	-0,609	-1,374
1,24E-05	5,28E-05	4,26E-03	-2,124	-1,087	13,431	-0,538	-0,328	-0,894
8,47E-06	3,73E-05	1,15E-04	-2,124	-1,087	6,700	0,271	-0,185	0,061
1,78E-06	8,88E-06	8,71E-03	-2,124	-1,087	6,953	-0,045	-0,047	0,332
1,14E-04	4,11E-04	1,69E-02	-2,121	-1,085	4,579	0,296	-0,646	0,038
3,42E-03	9,47E-03	2,98E-02	-2,116	-1,081	4,099	0,305	0,121	-0,233
2,53E-06	1,23E-05	3,35E-03	-2,114	-1,080	2,676	1,683	2,154	2,320
3,66E-08	2,58E-07	5,54E-03	-2,101	-1,071	2,475	1,827	1,644	1,931
6,67E-05	2,50E-04	2,46E-03	-2,099	-1,070	5,328	0,022	-0,058	-0,222
1,11E-04	4,00E-04	3,55E-02	-2,085	-1,060	2,852	1,538	1,663	1,100
1,27E-11	2,45E-10	5,92E-05	-2,083	-1,059	8,404	1,970	1,911	2,172
2,41E-04	8,20E-04	5,87E-04	-2,081	-1,057	4,299	0,230	0,783	0,421
1,54E-10	2,07E-09	1,01E-02	-2,076	-1,054	3,788	2,658	2,723	2,851
9,46E-04	2,90E-03	7,98E-03	-2,069	-1,049	4,605	-0,527	0,005	1,407
9,81E-11	1,41E-09	2,13E-04	-2,069	-1,049	7,215	1,910	1,786	1,815
9,91E-07	5,21E-06	1,26E-03	-2,066	-1,047	5,088	1,182	1,265	1,265
1,03E-05	4,46E-05	1,12E-03	-2,065	-1,046	14,018	-0,440	-0,054	-0,704
3,52E-05	1,39E-04	7,74E-05	-2,061	-1,043	5,108	0,265	0,133	0,061
2,02E-04	6,97E-04	4,05E-02	-2,056	-1,040	4,401	1,366	0,829	1,156
4,11E-09	3,67E-08	1,44E-06	-2,052	-1,037	6,910	1,220	1,191	1,183
2,52E-06	1,22E-05	2,73E-03	-2,051	-1,036	5,799	0,899	1,202	1,346
4,32E-05	1,67E-04	1,71E-03	-2,049	-1,035	7,398	-0,143	0,333	-0,013
6,82E-09	5,74E-08	1,31E-03	-2,046	-1,033	6,199	1,641	1,685	1,570
2,68E-08	1,95E-07	8,55E-05	-2,043	-1,031	5,206	1,264	1,292	0,904
4,01E-10	4,74E-09	1,01E-03	-2,043	-1,031	6,840	1,810	1,767	1,707
6,29E-08	4,22E-07	2,52E-04	-2,038	-1,027	6,071	1,129	1,236	1,268
6,49E-09	5,49E-08	2,52E-02	-2,034	-1,024	3,588	1,568	1,264	1,589
8,43E-03	2,16E-02	1,52E-02	-2,031	-1,022	5,135	0,665	0,062	0,379
2,93E-08	2,11E-07	2,46E-06	-2,029	-1,021	8,675	0,925	1,098	1,052
3,65E-03	1,01E-02	3,06E-03	-2,028	-1,020	5,374	0,576	0,507	0,660
1,30E-10	1,79E-09	1,44E-03	-2,022	-1,016	4,533	2,113	1,656	1,565
9,89E-06	4,30E-05	3,04E-04	-2,022	-1,016	8,692	0,901	0,704	0,738
2,56E-04	8,67E-04	4,99E-02	-2,011	-1,008	4,785	3,421	0,725	1,109
8,05E-12	1,68E-10	8,40E-04	-2,008	-1,006	4,057	3,012	2,427	3,040
2,65E-07	1,56E-06	2,57E-02	-2,006	-1,004	2,796	1,657	1,290	2,094
4,79E-08	3,30E-07	3,20E-07	-2,006	-1,004	8,962	0,914	0,899	0,955
1,86E-04	6,47E-04	5,77E-04	-2,006	-1,004	4,939	0,964	0,619	0,642
2,41E-13	9,67E-12	1,57E-04	-2,000	-1,000	4,059	2,267	1,841	2,285

wt_non-stim_4	wt_non-stim_21	CD4creGARPfl-fl_non-stim_22	CD4creGARPfl-fl_non-stim_23	CD4creGARPfl-fl_non-stim_8	CD4creGARPfl-fl_non-stim_9	CD4creGARPfl-fl_non-stim_10	wt_stim_11	wt_stim_12	wt_stim_13	wt_stim_14
4,092	4,351	-6,339	-6,465	-6,413	-6,052	*-7,275*	4,042	3,853	4,000	3,538
0,844	0,308	-4,485	-5,691	0,022	-4,958	-6,331	0,064	-0,054	0,931	0,553
0,832	0,409	-3,932	-5,281	0,030	-4,312	-5,653	0,081	-0,155	0,926	0,518
1,784	1,972	*-1,923*	*-1,935*	*-1,907*	*-1,892*	*-1,550*	1,874	2,156	1,935	2,452
4,028	2,627	*0,242*	*0,552*	*0,467*	*0,397*	*0,611*	*-0,253*	*-0,267*	*-0,260*	*-0,248*
1,794	1,430	-1,335	-0,987	-1,259	-0,897	-1,426	1,137	1,210	1,141	1,156
1,225	2,752	*-0,022*	1,007	*-0,526*	*-0,522*	*-0,479*	*0,644*	*-0,034*	*0,022*	*0,184*
3,011	3,948	1,204	0,624	0,597	1,257	0,167	*-1,022*	*-0,565*	*-0,603*	*-1,225*
-0,591	0,139	*-2,946*	-1,366	*-2,840*	*-2,591*	*-2,804*	1,511	1,483	1,509	1,756
-1,535	0,174	*-1,819*	-0,968	*-2,807*	*-2,803*	*-2,822*	-0,117	0,318	0,641	0,228
1,718	1,894	-0,576	0,103	-0,351	-0,524	-0,529	0,077	0,066	-0,066	0,259
3,789	3,532	0,765	1,485	1,691	1,654	1,357	-1,443	-1,490	-1,256	-0,765
2,584	3,298	0,577	0,451	0,397	0,288	0,204	-0,779	-0,884	*-0,899*	*-1,323*
4,228	4,674	1,924	3,557	3,253	2,373	0,157	-1,263	-0,157	-0,762	-0,815
0,722	0,415	*-1,614*	*-1,438*	*-1,950*	*-1,929*	*-1,937*	0,951	1,348	1,198	1,481
2,577	2,158	*-0,075*	*0,132*	*-0,033*	*0,019*	*-0,005*	*-0,036*	*-0,063*	*-0,036*	*-0,076*
3,623	4,016	1,500	1,536	1,179	1,918	0,398	*-1,188*	*-1,890*	*-0,398*	*-0,692*
1,003	*0,075*	*-0,758*	*-1,178*	*-1,122*	*-0,580*	*-1,487*	*0,127*	0,518	*0,438*	0,277
1,882	2,041	-0,220	0,366	0,083	-0,040	-0,333	0,018	-0,018	-0,123	0,299
1,909	2,117	-0,341	0,339	-0,028	-0,043	-0,322	0,028	0,060	-0,168	0,273
1,816	2,740	*-0,727*	1,052	*-0,088*	*0,576*	*-1,002*	*0,583*	*0,098*	*-0,292*	*-0,114*
4,158	3,919	1,090	1,955	2,197	2,176	1,665	-1,142	-1,266	-1,090	-1,120
2,868	3,293	0,992	1,189	0,788	0,672	0,321	-0,896	-0,849	-0,777	-0,973
2,504	1,651	*-0,489*	*0,507*	1,474	1,365	*0,472*	*-0,744*	*-0,734*	*-0,718*	*-0,734*
1,410	0,775	*-1,045*	*-1,256*	*-0,993*	*0,305*	*-1,149*	*-0,203*	*0,280*	*-1,122*	*-1,181*
0,941	0,568	-1,077	-1,592	-0,932	-1,274	-1,279	0,822	0,977	0,720	0,917
3,595	1,086	*-0,228*	1,115	1,014	2,195	1,521	*-0,858*	*-0,012*	*0,012*	*-1,517*
-1,860	-1,345	-3,845	-3,525	-4,185	-3,625	-4,058	1,760	1,734	1,871	2,043
0,458	0,514	*-2,118*	*-1,236*	*-1,773*	*-1,452*	*-0,953*	0,673	0,516	0,889	1,105
0,548	*-0,357*	*-1,040*	*-1,598*	*-2,029*	*-2,054*	-0,109	1,561	1,544	1,508	1,247
3,839	3,536	0,953	1,829	2,189	1,732	1,087	*-2,348*	*-2,363*	*-2,352*	*-2,368*
0,711	0,527	-1,226	-0,502	-1,676	-0,815	-1,615	0,678	0,258	0,720	-0,130
1,983	1,307	*-0,244*	0,409	*0,244*	*0,529*	*-0,908*	*-0,966*	*-0,933*	*-0,863*	*-0,941*
2,273	2,430	1,087	1,015	*0,410*	*0,183*	*-0,856*	*-0,858*	*-0,204*	*-0,624*	*-0,858*
0,778	*-0,024*	*-1,097*	*-1,091*	*-1,076*	*0,086*	*-1,067*	*-0,507*	*-0,353*	*-0,571*	*-0,930*
0,035	0,022	-1,789	-5,049	-1,402	-0,364	*-4,872*	0,737	0,838	0,699	0,961
-0,567	0,380	-2,393	-1,879	-1,534	-2,852	-3,588	0,290	0,352	0,350	0,100
0,758	0,566	-1,237	*-1,531*	-0,964	-0,849	*-1,626*	0,613	1,102	0,386	0,383
-0,366	0,461	-1,186	-1,203	*-2,191*	*-2,058*	*-2,284*	0,427	0,849	1,301	0,919
1,768	1,539	-0,146	0,285	0,250	0,006	-0,639	-0,155	0,172	0,489	-0,006
-0,896	*-1,720*	*-3,071*	*-2,692*	*-2,998*	*-1,330*	*-3,154*	0,896	1,309	0,970	1,205
1,911	*0,496*	*0,185*	*0,526*	*-0,057*	*1,201*	*-0,073*	*0,027*	*-0,050*	*-0,054*	*0,378*
2,888	2,388	0,015	0,722	1,522	1,040	0,861	-0,491	-0,182	-0,360	-0,015
-0,496	0,513	-2,205	-1,799	-1,495	-2,793	-3,385	0,230	0,346	0,384	0,032
2,243	1,982	*0,218*	*-0,536*	*1,059*	*0,284*	1,557	*-0,538*	*-0,530*	*-0,173*	*-0,537*
1,519	*0,191*	*-0,278*	*-0,442*	0,779	*0,502*	*-0,974*	*-0,103*	*-0,932*	*0,136*	*-1,097*



2,709	2,027	0,467	1,109	0,790	0,662	0,153	-0,734	*-1,448*	-0,153	*-1,587*
1,969	0,206	-0,304	*-0,415*	*-1,714*	*-1,693*	*-0,858*	*-0,214*	*-0,025*	1,063	0,496
1,338	1,656	0,009	-0,009	0,622	*-0,569*	0,246	0,203	*-0,293*	*-2,029*	-0,135
-0,636	-0,817	-0,676	-1,630	-1,519	*-1,952*	*-2,339*	1,842	1,820	2,081	1,040
2,657	2,665	0,603	1,011	1,096	2,078	0,079	*-1,854*	*-1,875*	*-0,102*	*-1,641*
-0,994	0,095	-2,638	-2,283	-1,978	-3,006	-4,020	0,264	0,352	0,347	0,151
2,714	1,639	*-0,003*	*0,403*	*0,661*	*0,014*	*-0,121*	*-0,135*	*-0,150*	*-0,063*	*-0,171*
0,638	1,085	*-0,853*	*-1,026*	*-1,213*	*-0,271*	*-0,849*	1,860	1,492	1,660	1,455
2,891	3,051	2,330	1,666	1,158	1,213	0,977	*-1,185*	*-1,150*	*-1,183*	*-1,200*
1,444	0,698	-0,477	-0,057	0,057	-0,156	-0,820	0,266	0,102	0,216	-0,253
3,590	3,412	1,039	1,974	2,056	1,927	1,472	-1,039	-1,119	-1,140	-1,126
-0,656	-0,006	-2,216	-1,737	-1,820	-2,326	-2,559	0,752	0,654	0,787	0,478
0,893	1,736	-0,464	-0,637	-0,621	0,371	0,106	-0,051	-0,053	0,306	0,223
0,992	1,142	-1,422	-0,116	-0,016	-0,724	0,621	0,185	0,094	0,137	-0,552
1,480	2,807	0,186	1,055	1,057	-0,099	0,706	*-2,359*	*-2,349*	*-2,357*	*-1,137*
1,542	1,301	-0,571	0,016	-0,248	0,186	-0,472	0,162	-0,217	0,124	-0,016
1,812	1,307	-0,654	0,007	-0,007	0,135	-0,393	-0,468	0,140	0,018	-0,580
-0,268	-0,959	-1,642	-1,483	-0,957	-1,176	-1,467	0,364	0,118	0,294	0,215
0,927	1,149	*-0,023*	0,448	*-0,290*	*-1,147*	*-1,238*	0,734	0,854	0,821	*-0,212*
-0,585	0,021	-2,116	-1,727	-1,687	-2,450	-3,005	0,362	0,333	0,235	0,198
1,128	1,170	-0,254	0,053	-0,455	-0,401	-0,796	0,200	1,695	0,381	-0,053
1,901	1,764	*-0,120*	*0,371*	*0,719*	*0,554*	*-0,110*	*-0,089*	*-0,105*	*-0,096*	*-0,095*
1,367	1,382	0,140	0,425	-0,162	-0,337	-0,399	-0,734	-0,217	-0,355	-0,596
1,841	*0,511*	*-0,307*	0,766	*-0,220*	1,161	*-0,991*	*0,060*	*0,154*	*0,565*	*-0,577*
2,196	2,740	*0,153*	1,852	*-0,220*	*0,673*	*0,636*	*-0,232*	*-0,230*	*-0,215*	*-0,229*
3,700	3,028	1,066	1,909	2,393	2,117	1,554	-1,532	-1,463	-1,066	-1,644
3,580	2,648	0,032	1,486	2,179	1,999	1,471	-0,456	-0,261	-0,395	-0,032
1,125	0,449	-0,587	-0,375	-0,288	-0,333	-0,702	0,199	0,067	0,084	-0,067
-0,677	0,088	-2,135	-1,749	-1,767	-2,510	-3,149	0,360	0,355	0,364	0,165
-0,528	-0,491	-2,501	-1,985	-1,781	-1,793	-2,839	1,224	1,218	1,187	1,254
1,152	0,333	*-0,430*	*-1,259*	*-0,502*	*-0,603*	*-1,564*	*-0,701*	0,687	1,179	1,233
2,216	1,140	-0,987	0,103	0,556	0,584	0,191	-0,363	-0,348	-0,103	0,504
0,813	0,385	-1,187	-1,194	*-1,770*	0,299	-0,889	0,354	0,419	0,980	0,900
-0,546	0,151	-1,983	-1,583	-1,565	-2,210	-2,849	0,506	0,415	0,552	0,294
1,317	1,420	-0,508	0,103	0,246	-0,013	-1,009	0,013	-0,152	0,204	-0,255
2,590	1,540	-0,204	0,628	1,144	1,018	0,371	-0,291	-0,141	-0,257	0,141
2,418	2,117	1,440	1,526	1,436	1,503	1,255	-1,255	*-1,816*	*-2,233*	*-2,350*
2,714	2,021	-0,030	0,812	1,281	1,086	0,625	-0,388	-0,201	-0,195	0,030
3,558	2,960	1,336	1,918	1,893	2,542	*-0,019*	*-0,419*	*-0,435*	*-0,423*	*0,019*
1,716	0,886	-0,467	0,256	0,666	0,618	0,056	-0,056	-0,277	-0,298	0,176
-0,634	0,041	-2,053	-1,936	-1,756	-2,384	-3,090	0,562	0,611	0,536	0,382
1,456	1,229	0,370	*-1,320*	*-1,324*	1,146	*-0,176*	*-1,306*	*-0,901*	*-1,313*	*-1,308*
4,034	3,114	1,996	2,385	3,033	3,360	2,425	*-2,670*	*-1,996*	*-2,622*	*-2,668*
-0,606	-0,176	-0,743	-1,723	-1,532	-1,397	-1,278	1,470	1,541	1,616	0,641
0,025	0,050	-1,414	-0,949	-1,162	-1,546	-1,411	1,335	1,316	1,368	1,509
0,512	0,214	-0,888	-0,256	*-1,088*	*-0,583*	*-0,868*	0,332	0,477	0,213	0,837
1,475	1,938	0,085	0,393	0,460	0,519	0,053	-0,053	-0,342	-0,237	-0,409
1,981	1,751	0,186	0,681	0,686	0,576	0,231	-0,799	-0,880	-0,778	-0,822
1,201	0,578	-1,823	-0,823	0,039	0,088	-0,683	-0,272	-0,039	0,069	0,322
3,160	1,852	1,518	1,828	1,488	2,112	1,385	-1,652	-2,047	-1,817	-1,631
0,426	0,099	-0,928	-0,357	-0,917	-0,734	-1,024	-0,007	0,139	0,112	-0,345
-1,383	-1,741	-2,748	-2,725	-2,365	-2,128	*-3,317*	1,895	2,106	2,026	2,511
1,530	*0,655*	0,636	1,116	*-0,039*	*-0,232*	*0,039*	*-0,712*	*-0,940*	*-0,928*	*-0,927*
-0,397	0,193	-1,728	-1,314	-1,470	-2,101	-2,642	0,378	0,448	0,420	0,238
1,502	*0,199*	*0,032*	*-0,032*	*0,964*	*0,365*	*-0,316*	*-0,510*	*0,141*	*-0,510*	*-0,511*
2,055	2,121	1,530	1,658	*0,506*	*0,725*	*0,775*	*-0,506*	*-0,522*	*-0,513*	*-0,518*



2,070	1,081	0,464	*-0,030*	1,380	1,565	*0,334*	*0,030*	*-0,945*	*-0,908*	*-0,966*
2,670	1,826	1,229	1,409	1,143	1,576	0,910	*-1,192*	*-2,076*	*-2,058*	*-0,910*
1,764	2,230	*-0,264*	1,446	*0,764*	*1,498*	*-0,250*	*-0,259*	*-0,268*	*-0,263*	*0,202*
0,340	1,066	*-1,100*	0,167	*-0,444*	*-0,455*	*-0,845*	*0,140*	*-0,230*	0,629	*-0,052*
1,652	1,615	0,393	0,922	0,287	0,257	-0,195	-0,229	-0,538	-0,229	-0,520
-0,470	-0,118	-1,124	-0,412	*-1,202*	*-1,509*	*-1,108*	1,041	0,416	0,760	-0,268
2,016	1,029	-0,071	0,577	0,928	0,860	0,552	0,046	-0,247	-0,046	-0,229
1,638	2,141	0,395	0,736	1,402	1,248	0,599	*-1,569*	*-2,000*	*-0,907*	*-0,395*
0,961	1,197	*-0,096*	*-0,405*	*-0,008*	*0,124*	0,939	*-0,938*	*-0,985*	*0,008*	*-1,010*
1,581	0,772	*0,018*	0,675	*-0,719*	*-0,524*	*-0,705*	*0,196*	*-0,848*	*-0,018*	*-1,298*
1,196	0,588	-0,472	-0,435	-0,151	0,422	-0,488	0,021	-0,021	0,143	0,204
-0,078	-0,258	*-1,552*	*-1,903*	*-1,894*	*-1,005*	-0,248	0,060	0,215	-0,012	0,333
2,084	1,881	0,130	0,738	0,711	0,989	0,586	-0,617	-0,287	-0,402	-0,130
2,435	1,962	0,931	1,033	1,603	1,803	*-0,305*	*-0,364*	*-0,371*	*-0,934*	*-0,978*
0,815	0,648	0,298	-0,169	*-0,082*	*-0,068*	*-0,104*	*-0,827*	*-0,138*	0,832	0,005
-0,567	0,033	-1,842	-1,640	-1,461	-2,382	-2,875	0,310	0,400	0,261	0,224
1,190	0,532	*-1,149*	*-0,456*	*0,037*	*-1,315*	*-0,539*	*-1,029*	*-1,027*	*0,517*	*-0,037*
1,832	1,560	0,013	0,473	0,409	0,378	-0,280	-0,013	-0,154	0,044	-0,391
-0,141	-0,606	*-2,287*	-1,237	-0,599	*-1,666*	-0,688	0,721	0,335	0,660	0,155
3,971	3,569	1,159	2,332	2,778	2,774	2,139	-2,454	-1,159	-2,247	-1,184
1,832	1,686	0,319	0,634	0,614	0,801	-0,030	-0,246	-0,244	-0,031	0,030
0,341	*-0,805*	*-1,597*	-0,994	*-1,419*	*-0,599*	-0,143	0,267	0,280	-0,137	0,245
-0,826	-0,131	-2,076	-1,906	-1,856	-2,189	-2,670	0,823	0,853	0,954	0,492
1,426	1,185	0,266	*-0,352*	*-0,494*	*-0,063*	*0,015*	*-0,423*	*-1,076*	*0,593*	*-0,015*
-0,462	0,170	-1,700	-1,499	-1,397	-2,223	-2,804	0,307	0,345	0,288	0,232
1,293	1,619	0,149	0,881	0,295	0,449	-0,149	-0,238	-0,396	-0,335	-0,561
3,104	2,491	1,234	1,853	2,364	2,415	1,743	-1,799	-1,853	-1,448	-1,262
0,595	-0,059	-0,258	*-0,894*	*-0,743*	-0,056	*-0,623*	-0,152	0,324	0,076	0,175
1,587	1,399	0,202	0,819	0,091	-0,092	0,013	*-0,727*	-0,503	*-0,464*	-0,013
0,464	0,270	-0,818	-0,750	-0,558	-0,740	-0,903	0,596	0,297	0,202	0,203
-0,221	-0,378	-1,264	-1,674	-1,692	-1,522	-1,320	0,515	0,476	0,641	0,666
1,004	0,970	-0,206	-0,038	0,133	*-0,338*	*-1,073*	0,136	0,431	*-0,478*	0,038
1,900	1,676	1,222	0,749	*0,452*	1,617	*0,302*	*-1,286*	*-1,300*	*-1,292*	*-1,295*
3,856	3,185	1,182	2,143	2,542	2,399	1,801	-1,518	-1,938	-1,894	-1,182
1,234	0,453	-0,255	-0,011	0,233	0,011	-0,481	-0,132	0,021	0,063	0,341
1,537	1,184	0,018	-0,018	*-1,637*	0,776	*-0,115*	*-1,095*	0,241	*-0,924*	0,392
0,921	0,572	-0,104	-0,282	*-0,570*	*-0,256*	*-0,279*	*-1,238*	0,149	*-0,830*	*-0,472*
1,903	1,536	-0,145	0,455	0,763	0,807	0,211	-0,460	-0,466	-0,265	-0,222
1,797	1,561	0,150	0,673	0,365	0,679	-0,053	-0,312	-0,704	-0,428	-0,730
-0,679	-0,785	-2,277	-1,614	-1,989	-1,819	-1,974	1,658	1,954	1,746	2,291
-1,332	-0,684	-2,144	-1,637	-1,423	*-2,271*	*-3,229*	1,902	1,855	1,751	1,111
1,317	1,665	*0,144*	1,328	*-0,677*	*-0,537*	*0,411*	*0,127*	*-0,690*	*-0,120*	*-0,685*
1,475	1,175	0,114	0,291	0,516	0,522	0,231	-0,114	-0,601	-0,317	-0,603
1,301	0,824	-0,540	0,201	0,094	0,313	-0,090	0,032	-0,181	-0,032	-0,285
1,473	1,073	-0,152	0,840	0,292	0,135	0,295	-0,214	-0,294	-0,104	-0,500
-0,019	-0,337	-1,630	-1,079	-0,897	-0,757	-1,101	0,135	0,163	0,200	-0,022
0,008	0,302	*-0,819*	*-0,291*	*-0,885*	*-1,612*	*-1,619*	0,253	0,785	0,530	0,651
-0,041	0,052	-0,851	-1,002	-1,376	-1,199	-1,714	0,470	0,520	0,516	0,496
0,936	*0,666*	*-0,006*	*0,006*	*0,185*	*-0,404*	*-1,027*	*-1,018*	*-1,037*	*0,507*	*-1,035*
-1,162	0,166	-2,146	-2,026	*-2,204*	*-2,882*	*-2,764*	1,035	0,499	1,208	0,932
-0,560	-0,032	-1,906	-1,813	-1,689	-2,438	-2,990	0,385	0,486	0,346	0,261
-1,084	-0,595	-1,069	-0,841	*-1,954*	*-2,374*	*-2,984*	1,596	1,710	1,747	1,818
0,417	0,056	-0,845	-0,367	-0,759	-0,745	-1,025	0,030	0,077	0,151	-0,388
-0,054	-0,047	-1,505	-0,707	-1,249	-1,145	-1,272	1,094	0,427	0,504	0,213
1,479	0,982	0,154	0,760	0,146	0,678	0,231	-0,972	-0,790	-0,297	-0,714
3,858	2,795	1,768	2,065	2,669	2,623	2,111	-2,013	-2,010	-1,768	*-2,656*

2,000	1,544	0,392	0,970	0,763	0,755	-0,048	-0,168	-0,306	-0,111	-0,142
0,901	0,964	-0,175	0,535	*-1,006*	0,418	*-0,623*	*-1,066*	-0,026	0,071	*-1,242*
1,540	1,999	0,865	1,286	0,643	0,451	0,253	-0,494	-0,487	-0,565	-0,253
-0,602	-0,003	-1,732	-1,582	-1,507	-2,325	-2,786	0,282	0,334	0,231	0,226
-0,430	0,104	-1,560	-1,347	-1,217	-2,115	-2,705	0,169	0,268	0,206	0,175
2,104	2,503	*0,134*	*0,855*	*1,628*	*1,435*	*-0,159*	*-0,162*	*-0,157*	*0,185*	*-0,157*
-0,340	-0,091	-1,734	-1,888	-1,421	-2,126	-2,707	0,497	0,622	0,437	0,195
0,350	0,011	-0,991	-0,587	-0,590	-0,905	-1,317	0,119	-0,019	0,097	-0,300
1,064	0,310	0,426	-0,050	0,268	*-0,041*	*-0,949*	*-0,309*	*-0,389*	*-0,328*	*-0,564*
0,329	-0,241	-0,639	-1,108	-0,053	-0,137	-0,470	0,386	0,185	0,053	0,214
-0,238	0,322	-1,352	-1,010	-0,984	-1,633	-2,189	0,265	0,300	0,184	0,157
-0,450	0,134	-1,561	-1,371	-1,239	-2,082	-2,576	0,270	0,285	0,231	0,228
0,651	0,574	-0,641	-0,126	-0,172	-0,542	-0,825	-1,309	-1,362	-1,436	-1,784
0,445	1,329	0,146	0,904	-0,126	*-0,659*	0,005	*-0,722*	-0,356	-0,005	0,087
1,295	1,559	0,355	0,791	0,049	0,062	-0,049	-0,554	-0,435	-0,597	-0,860
-0,138	0,000	-1,309	-1,453	-0,976	-1,299	-1,576	0,541	0,352	0,539	0,207
1,218	0,983	-0,053	0,852	0,596	0,128	-0,630	-0,388	-0,217	-0,153	-0,552
1,972	1,904	-0,025	0,816	1,519	1,319	0,571	*-1,498*	*-1,500*	*-1,485*	*-0,007*
-0,691	-0,069	-1,512	-1,780	-1,654	-2,136	-2,472	0,855	0,478	0,785	0,594
-0,226	0,313	-1,415	-0,921	-0,842	-1,562	-2,013	0,289	0,255	0,233	0,133
0,127	0,018	-1,026	-0,978	-0,937	-1,124	-2,344	0,491	0,650	0,694	0,075
-0,335	-0,257	-0,499	-1,174	-0,616	-1,583	-1,134	1,575	1,416	1,692	1,010
-1,223	-0,015	-1,100	-1,032	*-0,778*	*-1,235*	*-2,123*	0,638	0,512	0,168	0,655
-0,143	-0,014	*-1,420*	0,014	*-1,095*	*-0,615*	*-1,893*	0,295	0,405	-0,110	0,017
2,092	1,629	*-0,111*	1,012	1,460	*1,025*	*-0,533*	*-0,789*	*-0,774*	*-0,766*	*-0,009*
1,876	1,750	*0,371*	2,055	*0,756*	*1,055*	*0,364*	*-0,432*	*-0,419*	*-0,385*	*-0,426*
0,647	-0,638	-0,622	-1,300	-0,753	*-1,724*	-1,128	-0,066	-0,022	0,044	0,279
1,133	1,521	*0,164*	0,841	*0,461*	*0,919*	*-0,931*	*-0,526*	*-0,908*	*-0,915*	*-0,164*
2,233	2,018	0,315	1,006	1,058	0,960	0,614	-0,656	-0,986	-0,673	-0,315
0,839	0,193	-0,405	-0,364	*-0,810*	*-1,367*	*-0,636*	0,111	0,571	0,147	0,495
2,675	3,138	2,408	2,262	1,171	1,670	0,453	*-0,453*	*-1,885*	*-1,887*	*-1,899*
-0,618	0,323	-0,846	*-2,340*	*-1,000*	*-1,189*	*-1,044*	0,574	0,147	0,797	-0,156
1,848	1,610	0,228	0,766	0,963	1,318	0,240	-0,971	-0,472	-0,522	-0,228
1,214	1,082	0,590	0,049	0,031	0,168	0,182	-0,031	-0,432	*-1,260*	-0,690
-0,183	0,344	-1,230	-0,916	-0,900	-1,656	-2,209	0,237	0,264	0,256	0,237
0,284	0,003	-1,009	-0,398	-0,187	-0,910	-0,933	0,255	0,285	0,105	-0,003
1,015	1,318	-0,415	0,972	0,115	0,431	-0,024	*-0,800*	0,154	*-0,767*	0,024
1,224	1,143	-0,007	0,385	0,154	0,440	-0,232	0,007	-0,074	0,164	-0,367
1,554	0,893	0,216	0,437	0,166	0,079	-0,079	-1,288	-0,157	-0,343	-0,483
0,212	0,260	-0,844	-0,219	-0,823	-0,604	-0,874	0,366	0,199	0,577	0,261
1,423	1,618	0,397	0,584	0,892	0,969	0,246	-0,622	-0,383	-0,579	-0,648
0,882	1,228	0,667	-0,001	0,068	0,197	0,232	-0,221	-0,486	-0,045	0,001
2,013	1,071	0,735	1,012	0,944	0,642	0,479	-1,498	-0,626	-0,713	-0,743
1,011	0,991	0,007	0,101	0,358	0,232	0,031	-0,186	-0,152	-0,886	-0,286
1,842	0,943	0,369	0,544	0,999	0,860	0,515	*-1,651*	*-1,077*	*-0,853*	*-1,636*
0,521	-0,170	-0,895	-0,281	0,053	-0,643	*-1,424*	-0,052	0,017	0,188	0,415
1,229	0,650	-0,312	-0,013	0,294	0,306	0,032	-0,140	0,013	-0,146	0,020
0,574	0,501	-0,170	0,468	-0,530	-0,446	-0,937	0,005	0,062	-0,012	0,108
1,770	1,875	0,390	0,755	1,130	0,885	0,611	*-1,140*	-0,789	-0,504	-0,438
0,803	0,525	-0,874	-0,278	0,210	-0,186	-0,698	0,215	0,359	0,186	0,405
0,871	1,364	-0,241	0,578	0,008	0,244	0,101	-1,195	-0,454	-0,732	0,172
2,724	2,438	0,818	1,718	1,728	1,961	1,050	*-1,859*	*-1,710*	*-1,278*	*-1,866*
1,950	1,684	*0,065*	1,078	*0,634*	1,791	*0,680*	*-0,822*	*-1,006*	*-0,309*	*-0,235*
1,131	0,892	-0,497	0,098	-0,089	-0,045	-0,620	0,236	0,045	0,233	-0,099
0,529	1,085	-0,471	0,137	-0,161	-0,362	-1,188	0,089	0,435	0,435	0,006
2,173	2,040	0,999	1,173	1,215	1,182	0,779	*-0,779*	*-1,876*	*-1,935*	*-1,960*

wt_stim_15	CD4creGARPfl-fl_stim_24	CD4creGARPfl-fl_stim_25	CD4creGARPfl-fl_stim_18	CD4creGARPfl-fl_stim_19	CD4creGARPfl-fl_stim_20	Refseq	GeneID
3,707	-3,751	-3,538	-3,994	-4,058	-4,571	NM_001113379	434215
0,905	-4,340	-5,221	0,526	-4,469	-5,653		
0,906	-3,899	-4,805	0,453	-4,118	-5,167	NM_133362	170942
2,155	*-1,889*	*-1,677*	*-1,870*	*-1,859*	*-1,862*	NM_178165	229499
-0,242	*-0,260*	*-0,247*	*-0,278*	*-0,285*	*-0,252*	NM_175475	232174
0,897	-1,520	-1,685	-1,513	-1,760	-1,632	NM_001083318	27049
0,902	*-0,535*	*-0,510*	*-0,523*	*-0,524*	*-0,505*		
-0,167	*-1,164*	*-1,755*	*-1,745*	*-1,739*	*-1,736*	NM_026323	67701
1,030	0,179	-0,210	1,474	0,342	-0,072		
0,385	0,475	0,741	0,117	0,854	0,660	NM_001101431	70291
0,535	-1,172	-1,344	-2,213	-1,429	-1,497	NM_173786	223672
-2,086	*-4,279*	*-4,279*	*-4,269*	*-4,262*	*-4,259*	NM_001162938	100033459
-0,204	*-2,658*	*-2,595*	*-1,815*	*-2,385*	*-2,608*	NM_026323	67701
-3,004	-0,382	-2,445	-4,390	-1,631	-2,904	XM_357633	
0,918	0,000	*-0,161*	*-1,117*	0,400	*-0,632*		
-0,007	*-0,090*	*0,005*	*0,018*	*-0,088*	*1,056*	NM_007769	12945
-0,612	*-1,889*	*-1,819*	*-1,829*	*-1,891*	*-1,838*	NM_021400	96875
0,780	*-1,474*	*-1,462*	0,606	*-1,456*	*-1,442*	NM_172525	214137
0,779	-0,920	-0,910	-1,260	-1,251	-1,219	NM_173786	223672
0,697	-0,876	-1,020	-1,429	-1,477	-1,390	NM_001168660	71898
-0,994	*-1,019*	*0,088*	*-1,007*	*-1,017*	*-1,016*		
-1,843	*-6,770*	*-5,372*	*-7,106*	*-6,505*	*-6,224*	NM_001162938	100033459
-0,321	-2,845	-2,317	-2,153	-2,197	-2,250	NM_001033460	381738
-0,727	*-0,746*	*-0,737*	*-0,735*	*-0,162*	*0,162*		
-0,036	*-0,268*	*0,246*	*0,342*	*-0,057*	*0,506*	NM_013879	29867
0,423	-0,989	-0,423	-0,552	-0,437	-0,683		
-0,688	*-1,500*	*-1,506*	*-1,506*	*-1,486*	*-1,501*	NM_022420	64297
1,885	1,547	1,861	1,345	1,578	1,434	NM_134066	105349
0,940	*-0,846*	*-0,228*	*-1,466*	-0,360	*-1,177*	NM_175414	109246
1,231	-0,014	0,014	*-1,015*	*-1,197*	0,228		
-2,303	*-0,953*	*-2,359*	*-2,338*	*-2,413*	*-2,381*	NM_001033303	229665
0,610	-0,142	-0,334	-0,611	0,130	-0,735	NM_001162476	20897
-0,613	0,932	*-0,251*	*0,483*	*-0,921*	*-0,764*		
-0,832	*-0,385*	*-0,825*	*-0,183*	*0,317*	*-0,836*	NM_175206	74165
0,610	*-0,462*	*0,082*	1,787	0,836	*0,463*		
0,765	-0,960	-3,231	-0,355	0,371	-3,419	NM_001167883	99696
1,588	1,297	0,037	0,883	-0,037	0,264	NM_009946	12890
0,243	*-1,675*	-0,243	-0,755	-1,092	*-0,982*		
2,159	-0,452	0,179	0,743	0,515	0,171	NM_010180	14114
-0,190	-1,032	-1,163	-0,760	-0,751	-1,136	NM_008606	17385
1,417	1,567	1,169	0,933	1,073	0,912	NM_009189	20471
-0,044	*-0,067*	*-0,036*	*-0,054*	*-0,059*	*-0,027*	NM_053216	112418
-1,233	-0,923	-0,852	-0,750	-0,765	-0,290	NM_010517	16010
1,578	1,326	0,058	0,915	-0,032	0,232		
-0,529	*-0,516*	*0,173*	*-0,527*	*-0,506*	*-0,520*		
-0,982	*-0,192*	*0,103*	*0,195*	*-1,158*	*-0,988*	NM_144906	73094

-1,195	-1,263	-1,134	-0,779	-0,405	-0,639	NM_175206	74165
0,025	0,196	0,416	-0,416	-0,743	-0,691		
-0,281	-0,299	-0,546	0,048	-0,667	-0,327	NM_029464	75860
0,506	0,709	-0,097	-0,025	0,376	-0,029	NM_001177666	633640
-0,079	-1,649	-1,809	-1,789	-1,893	-1,879	NM_019707	12554
1,664	1,239	-0,022	0,984	0,022	0,212		
0,062	-0,181	-0,004	-0,017	0,003	-0,068	XM_889664	625123
1,648	-1,209	-0,196	-1,210	-0,283	-1,205	NM_178405	98660
-1,030	-1,175	-1,000	-1,005	-1,153	-0,977	NM_010259	14468
-0,921	-1,064	-0,938	0,503	-0,617	-1,268	NM_031183	83395
-1,533	-2,464	-1,876	-2,399	-2,112	-2,425	NM_001162938	100033459
1,881	0,869	0,216	0,921	0,006	0,147		
-0,672	-0,611	-0,436	-1,504	-0,457	0,051	NM_001014900	332934
0,016	-1,998	-0,674	-1,049	-2,358	-0,442	NM_001164518	210094
-2,354	-0,706	-2,353	-2,344	0,099	-2,340		
0,338	-2,884	-1,942	-1,830	-1,269	-1,790	NM_138665	192166
-0,523	-0,334	-0,418	2,400	-0,815	-0,516	NM_001039546	17920
0,087	0,428	0,218	-0,070	-0,088	-0,269	NM_152804	20620
-1,186	-0,241	-0,238	-1,197	-1,256	0,023		19085
1,088	0,379	0,051	0,456	0,008	-0,008		12890
0,219	-0,422	-0,783	-0,989	-0,855	-1,114	NM_008923	19085
-0,086	0,882	0,086	-0,121	-0,128	-0,104	NM_175176	209601
-0,703	0,441	-0,288	-0,140	0,220	0,338	NM_011347	20344
-0,974	-0,978	-0,524	-0,946	-0,060	-0,938	NM_028955	74466
1,455	-0,240	-0,237	-0,153	-0,243	-0,243		
-1,172	-1,914	-2,035	-2,360	-2,816	-2,004		216505
-0,467	-0,827	-0,749	-0,919	-0,680	-0,654	NM_019417	30794
-0,507	0,105	0,227	-0,313	-0,128	-0,337	NM_013749	27279
1,225	0,598	0,093	0,493	-0,013	0,013	NM_009946	12890
1,092	0,491	0,763	0,906	0,818	0,596	NM_001167996	68725
-0,569	-0,941	0,065	-0,065	0,297	-1,564	NM_172525	214137
-0,905	-1,531	-1,988	-0,488	-0,705	-0,728	NM_173744	72148
-0,266	-0,980	-0,729	-0,972	0,556	-0,948		
1,347	0,548	0,227	0,456	-0,001	0,001		
0,045	-1,428	-1,005	-0,654	-0,749	-1,201	NM_008606	17385
-0,320	-1,325	-1,406	-0,594	-0,826	-0,681	NM_173744	72148
-3,138	-1,511	-1,465	-3,212	-1,922	-1,766	NM_010423	15213
-0,718	-2,145	-1,591	-0,745	-0,815	-1,115	NM_011703	22354
-0,377	-0,413	-0,325	-0,412	-0,043	-0,452	NR_044988	621335
-0,695	-0,965	-0,385	-0,527	-0,061	-0,582	NM_026878	68939
1,539	0,667	0,217	1,003	-0,041	0,194		
-1,311	0,176	-1,190	0,390	-1,336	0,215	NM_008746	18213
-2,599	-2,672	-2,613	-2,635	-2,180	-2,637		791369
1,204	0,303	-0,016	-0,001	0,236	-0,150	XR_106831	100044171
0,989	0,223	-0,025	0,086	0,401	-0,033		
-0,070	-0,707	0,303	-0,307	-0,527	-0,013	NM_022030	64051
-0,455	-1,121	-1,311	-1,110	-1,323	-1,032	NM_172507	212531
-0,360	-0,186	-0,905	-1,031	-1,265	-0,695		
0,096	-1,666	-1,384	-0,232	-0,390	-0,690	NM_029723	76747
-1,385	-1,690	-2,201	-1,813	-2,672	-1,868		217151
0,604	0,278	0,007	-0,149	-0,284	-0,354	NM_207687	56226
1,456	1,180	1,301	1,523	1,466	0,986		
-0,933	0,529	-0,930	-0,774	0,274	-0,943	NM_001033343	240667
1,146	0,471	0,173	0,405	0,024	-0,024	XM_001474842	
-0,506	-0,505	0,205	-0,503	-0,231	-0,500	NM_178241	227288
-0,509	-0,535	-0,516	-0,521	-0,550	-0,528	XR_105427	

-0,878	*-0,962*	*-0,886*	*-0,902*	*-0,951*	*-0,907*		100038516
-0,999	*-2,108*	*-2,035*	*-2,043*	*-2,098*	*-2,062*		
-0,202	*-0,256*	*-0,222*	*-0,238*	*1,296*	*-0,237*		70858
-1,031	*0,052*	*-0,417*	*-1,377*	*-0,610*	*0,334*		
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0,725	-0,027	0,027	*-1,337*	0,186	0,085	NR_028311	100043335
-0,381	-0,700	-0,721	-0,300	-0,405	-0,341	NM_022019	63953
-2,004	*-1,986*	*-2,001*	*-1,997*	*-1,987*	*-1,995*		
-0,298	*0,392*	*0,088*	*-0,928*	*-0,994*	*-0,932*		
0,189	*-1,287*	*-1,289*	*0,145*	*-1,272*	*-0,627*		
-0,609	-1,078	-0,481	-0,515	-0,151	0,183	NM_001195437	235634
0,186	0,661	0,486	0,609	0,373	0,383		
-0,877	-1,360	-1,337	-1,313	-1,205	-1,394	NM_177292	320916
-1,360	*-1,340*	*-1,341*	*-1,363*	*0,305*	*-1,349*		240174
-0,945	0,314	*-0,005*	0,366	*-0,118*	*-0,744*		216760
1,002	0,291	0,034	0,392	-0,001	0,001		
-1,229	*-0,306*	*0,311*	2,169	*-0,448*	*0,224*	NM_172507	212531
-0,034	-0,677	-0,644	-0,618	-0,578	-0,588	NM_001033405	328833
0,649	-0,031	-0,096	0,091	0,868	-0,028		54651
-3,313	*-3,400*	-2,329	*-2,622*	-1,760	*-3,477*	XR_035179	330578
-0,074	-1,293	-0,995	-0,513	-0,814	-1,028		
0,522	-0,087	0,087	-0,132	0,247	-0,150		
1,998	0,850	0,306	0,980	0,131	0,328		
-0,386	0,631	*0,350*	*-0,903*	*-0,086*	*-0,871*		
0,989	0,354	0,095	0,424	0,013	-0,013		
0,260	-1,045	-0,858	-0,924	-0,957	-1,335	NM_175535	244867
-1,234	-1,914	-2,275	-2,057	-1,940	*-2,479*	NM_009162	20394
0,420	*-0,639*	*-0,434*	0,325	0,006	0,289	NM_175308	100465
-1,701	-0,204	0,361	*-2,216*	-0,194	*-0,775*	NM_028711	74011
0,671	-0,310	-0,549	-0,480	-0,202	-0,290	NM_001033405	328833
0,590	0,208	0,217	0,381	0,362	0,288	NM_012010	26905
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-1,284	*-1,308*	*-1,295*	*-1,312*	*-1,334*	*-0,302*	NM_001012322	319229
-1,285	-1,854	-1,207	-1,721	-1,757	*-2,268*	XR_035179	330578
-0,451	-0,379	-0,570	-0,454	-0,424	-0,463	NM_016801	20907
-0,445	-0,060	*0,119*	*-1,001*	*-1,325*	*-0,816*		
0,537	0,104	*-0,138*	*0,188*	*-1,731*	0,237	NM_007425	11596
0,145	-2,216	-1,809	-0,772	-1,372	-1,015	NM_011374	20449
0,053	-0,501	-0,500	-0,169	-0,996	-0,575	NM_172443	207592
1,340	0,644	0,857	1,295	1,449	0,856		74750
2,397	0,762	0,568	0,876	1,142	0,327	NM_007992	14115
-0,685	*0,120*	*-0,685*	*-0,526*	*-0,681*	*-0,697*		
-0,854	-1,313	-1,113	-1,069	-0,774	-0,934	NM_178638	81907
0,351	-0,267	-0,563	-0,428	-0,601	-0,214	NM_178892	99929
-0,180	0,104	-0,436	-0,307	-1,004	-1,052	NM_025451	66259
0,019	0,071	0,033	-0,077	0,038	-0,042	NM_176933	319520
-0,598	*-0,617*	*-0,228*	*-0,008*	0,237	*0,185*		
0,365	0,043	0,053	-0,011	0,046	0,005	NM_022980	53902
0,847	*-0,673*	*-0,638*	*-0,178*	*-0,511*	*0,460*		
2,168	0,443	0,712	1,196	0,393	-0,166	NR_045506	71056
1,193	0,389	0,219	0,584	0,069	0,032		
0,261	0,555	0,822	0,636	1,370	1,011	NM_173419	239133
0,495	0,195	-0,030	-0,083	-0,195	-0,376	NM_207687	56226
0,499	0,182	0,047	0,181	0,266	0,062	NM_008967	19222
-0,146	-0,383	*-0,912*	-0,730	*-2,071*	*-1,108*	NM_009926	12815
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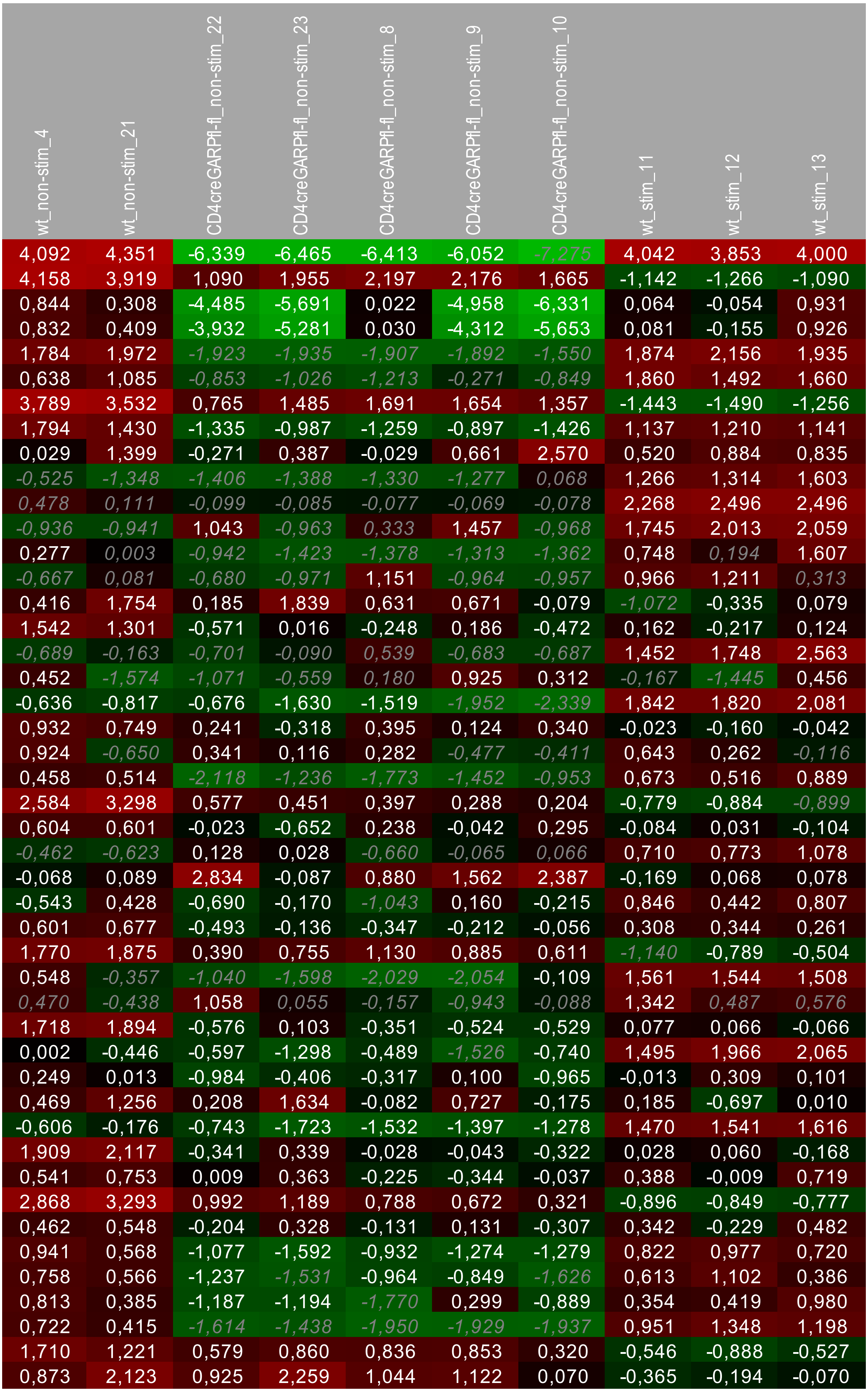
-0,883	*-0,800*	0,026	*-0,221*	*-0,749*	0,248	NM_029139	668110
-1,299	-1,373	-1,192	-1,018	-1,210	-1,456		
1,054	0,279	0,066	0,368	0,013	0,003	NM_011444	20678
0,975	0,266	0,024	0,359	0,018	-0,018		
-0,152	*-0,142*	*-0,151*	*-0,151*	*-0,134*	*-0,156*	NM_027001	69239
1,565	0,457	0,099	0,697	0,091	0,202		
-0,082	0,201	0,031	-0,075	0,287	-0,011	NM_001008700	16190
-0,659	*-0,186*	*0,041*	*0,206*	*-1,188*	*0,193*	NM_027909	71764
0,716	-0,466	-0,766	0,227	-0,323	-0,492	NR_001460	19782
0,948	0,381	0,049	0,351	0,028	-0,052		
1,000	0,316	0,031	0,349	0,022	-0,022		
-0,101	1,303	1,259	0,101	0,379	1,048	NM_010371	14940
0,044	-0,392	-0,333	-0,181	-0,235	-0,225		
0,082	-0,066	-0,577	-0,334	-1,203	-0,950	NM_001142732	101100
1,582	0,475	0,069	0,539	0,000	0,045		
-0,466	0,424	-0,092	-0,878	0,053	-0,291	NM_172631	52662
0,007	*-1,484*	*-1,484*	*-1,506*	*-1,480*	*-1,489*		18197
1,743	0,425	0,482	0,840	0,410	0,069		
0,994	0,563	0,103	0,407	-0,047	0,047		
0,132	-0,162	-0,018	-0,243	0,231	-0,278	NM_010287	14608
0,357	0,490	0,227	0,045	0,456	-0,078	NM_001039244	633640
0,425	0,151	0,063	0,015	-0,093	*-0,575*		
0,217	-0,414	0,869	0,129	-0,055	1,115		
-0,783	*0,074*	*-0,762*	*-0,709*	*0,009*	*-0,754*		
-0,364	*-0,432*	*-0,386*	*-0,404*	*-0,429*	*-0,403*		
0,787	0,426	0,027	0,625	0,279	0,472	NM_001033170	73813
-0,906	*-0,920*	*-0,898*	*-0,916*	*-0,675*	*0,831*		
-1,041	-2,350	-2,105	-1,479	-1,386	-1,398	NM_145838	241230
0,015	*-1,063*	-0,015	-0,034	*-0,954*	-0,343		
-1,890	*-1,886*	*-1,880*	*-1,897*	*-1,878*	*-1,869*	NM_010259	14468
1,315	0,217	-0,078	0,166	0,068	-0,005		
-0,956	-1,479	-1,644	-1,405	-1,296	-1,112	NM_007409	11522
-0,471	-1,023	-0,229	-0,079	-0,819	-0,101		
0,996	0,383	-0,026	0,330	0,026	0,076	NM_177354	238328
0,093	-0,184	0,115	-0,117	-0,156	-0,257		
-1,645	-0,185	-0,061	*-0,903*	-0,319	-0,169	NM_080595	140703
-0,289	-0,290	-0,284	-0,296	-0,530	-0,629	NM_175751	269023
-1,034	0,149	-0,308	-0,890	-0,961	-0,576	NM_001081069	50782
1,197	-0,306	0,013	0,063	-0,338	-0,160	NM_007561	12168
-1,060	-1,610	-0,856	-0,784	-0,246	-0,510	NM_183024	242570
-0,414	-0,468	-0,768	-0,550	-0,178	-0,710		
-0,982	-0,479	-0,638	-1,124	-0,899	-0,792	NM_144926	233878
-0,007	-0,651	-1,475	-0,981	-0,477	-0,590	NM_009800	12348
-1,638	*-1,633*	*-0,578*	*-1,068*	*-1,270*	*-0,369*		
0,911	-0,317	-0,277	0,348	-0,610	-0,017		
-0,088	-0,224	-0,378	-0,173	-0,418	-0,241	NM_011578	21814
-0,416	-0,005	0,388	-0,407	-0,434	-0,225	NM_145420	216080
-0,390	*-1,220*	*-1,453*	*-2,029*	*-2,030*	*-2,575*		
-0,485	-0,849	-0,850	-1,020	-0,288	-0,857	NM_001197321	108655
-0,008	*-2,509*	*-1,274*	*-1,087*	-1,007	-0,290		
-2,070	*-0,818*	*-1,557*	*-1,899*	*-1,252*	*-2,088*		
-1,004	*-0,450*	*-0,752*	*-0,624*	*-0,994*	*-0,065*	NM_001012322	319229
0,144	-0,354	-0,208	-0,368	-0,275	-0,669	NM_016851	54139
-0,467	-0,404	-0,006	-0,751	-0,504	-0,756	NR_027784	104103
-1,665	*-1,930*	*-1,665*	*-1,656*	*-1,911*	*-1,673*		

SeqID	ProbeID	GeneName	Description
2271329	A_55_P2031466	Lrrc32	Mus musculus leucine rich repeat containing
2307570	A_55_P2181222	E430029J22Rik	Mus musculus pyrin domain containing 3 (Pyd
2271288	A_55_P1985422	LOC100044227	Q811B0_MOUSE (Q811B0) Erythroid differen
2292890	A_55_P2034481	Erdr1	Mus musculus erythroid differentiation regulat
2290610	A_51_P349213	Fcrl1	Mus musculus Fc receptor-like 1 (Fcrl1), trans
2295189	A_52_P227267	Atp1a2	Mus musculus ATPase, Na+/K+ transporting,
2286413	A_66_P128761	E430029J22Rik	Mus musculus pyrin domain containing 3 (Pyd
2264815	A_55_P2062133	Etv3	Mus musculus ets variant gene 3 (Etv3), trans
2293489	A_51_P205779	Cd5l	Mus musculus CD5 antigen-like (Cd5l), mRNA
2280606	A_30_P0103165	A_30_P01031657	lincRNA:chr3:84609788-84618062 reverse st
2305426	A_52_P203316	Kcnf1	Mus musculus potassium voltage-gated chan
2290624	A_66_P103957	Bbs7	Mus musculus Bardet-Biedl syndrome 7 (hum
2307607	A_55_P2116536	Kcnf1	Mus musculus potassium voltage-gated chan
2311579	A_30_P0102377	A_30_P01023778	lincRNA:chr3:48896525-48994125 forward st
2261466	A_30_P0102202	A_30_P01022023	lincRNA:chr5:111602486-111603075 forward
2268697	A_66_P121480	Sardh	Mus musculus sarcosine dehydrogenase (Sar
2290566	A_30_P0102826	A_30_P01028268	lincRNA:chr3:37568488-37568964 forward st
2305499	A_30_P0102856	A_30_P01028564	lincRNA:chr10:98718526-98719169 reverse
2309983	A_55_P2183914	Gm7120	Mus musculus predicted gene 7120 (Gm7120
2310432	A_55_P2015715	Rab4a	Mus musculus RAB4A, member RAS oncoge
2278852	A_51_P335702	Tmem114	Mus musculus transmembrane protein 114 (T
2273936	A_55_P2022971	Tspan9	Mus musculus tetraspanin 9 (Tspan9), mRNA
2276525	A_55_P1953341	Wfdc2	Mus musculus WAP four-disulfide core domai
2306301	A_55_P2148641	Rab4a	Mus musculus RAB4A, member RAS oncoge
2288123	A_55_P2038422	Adamts17	Mus musculus a disintegrin-like and metallope
2296517	A_55_P1985693	Fhdc1	Mus musculus FH2 domain containing 1 (Fhd
2283507	A_55_P2269289	Dgkg	Mus musculus diacylglycerol kinase, gamma (
2284098	A_55_P2152956	Plekhm3	Mus musculus pleckstrin homology domain co
2265884	A_30_P0103276	A_30_P01032768	lincRNA:chr11:99048975-99062425 reverse
2273566	A_30_P0102598	A_30_P01025989	lincRNA:chr3:84609788-84618062 reverse st
2291814	A_55_P2065651	Trav17	Mus musculus 16 days neonate thymus cDNA
2310774	A_55_P2107775	Apol9a	Mus musculus apolipoprotein L 9a (Apol9a), t
2305960	A_55_P2014100	Gm7120	Mus musculus predicted gene 7120 (Gm7120
2295472	A_30_P0103357	A_30_P01033579	lincRNA:chr1:138473514-138476054 reverse
2301160	A_30_P0103273	A_30_P01032731	lincRNA:chr16:64796849-64843249 reverse
2303029	A_55_P2120866	LOC100044171	PREDICTED: Mus musculus hypothetical LO
2306577	A_66_P110633	Apol9b	Mus musculus apolipoprotein L 9b (Apol9b), t
2305000	A_52_P124734	Cybrd1	Mus musculus cytochrome b reductase 1 (Cyb
2283521	A_52_P481279	Gm1060	Mus musculus coiled-coil domain containing 1
2264156	A_55_P2344244	4930556H04Rik	Mus musculus adult male testis cDNA, RIKEN
2286467	A_55_P2056192	NAP111293-1	Unknown
2259768	A_55_P2024634	Gm13546	predicted gene 13546 [Source:MGI Symbol;A
2281640	A_30_P0102038	A_30_P01020388	lincRNA:chrX:47890565-47915775 forward st
2286414	A_30_P0102552	A_30_P01025525	lincRNA:chr3:37659958-37665945 forward st
2290597	A_55_P2082786	Trib2	Mus musculus tribbles homolog 2 (Drosophila
2279988	A_30_P0101903	A_30_P01019033	lincRNA:chr5:111602486-111603075 forward

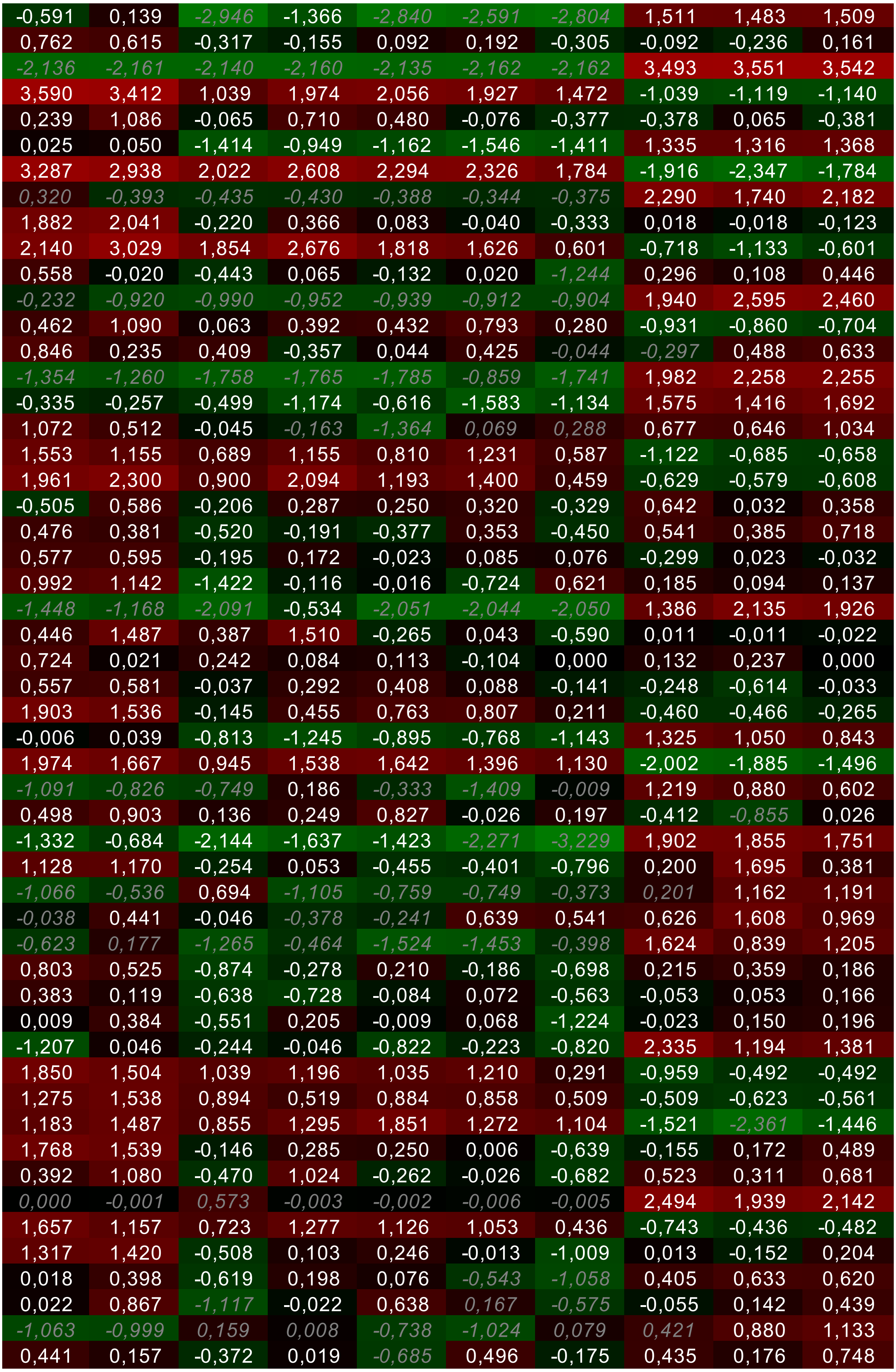
2306135	A_30_P0102123	A_30_P01021230	lincRNA:chr3:37659958-37665945 forward st
2282750	A_66_P114705	Adamts6	Mus musculus a disintegrin-like and metallope
2269394	A_51_P424471	Cnih3	Mus musculus cornichon homolog 3 (Drosoph
2264259	A_55_P2001233	E430029J22Rik	Mus musculus pyrin domain containing 3 (Pyd
2280238	A_30_P0102690	A_30_P01026900	lincRNA:chr12:12916233-12919835 forward s
2300864	A_30_P0101804	A_30_P01018048	lincRNA:chr3:37659958-37665945 forward st
2296830	A_55_P2036627	E430029J22Rik	Mus musculus pyrin domain containing 3 (Pyd
2290163	A_55_P1967538	Hunk	Mus musculus hormonally upregulated Neu-as
2263575	A_55_P2043367	Apol9a	Mus musculus apolipoprotein L 9a (Apol9a), t
2265173	A_30_P0101803	A_30_P01018036	lincRNA:chr14:73746324-73749119 reverse s
2261431	A_30_P0101918	A_30_P01019182	lincRNA:chr1:138473514-138476054 reverse
2311496	A_52_P385594	Tal2	Mus musculus T-cell acute lymphocytic leukem
2297589	A_55_P1954393	Susd4	Mus musculus sushi domain containing 4 (Sus
2295316	A_30_P0102390	A_30_P01023909	lincRNA:chr15:92174226-92201201 forward s
2307188	A_51_P399845	Fgf2	Mus musculus fibroblast growth factor 2 (Fgf2
2305092	A_66_P121583	Gm7120	Mus musculus predicted gene 7120 (Gm7120
2299510	A_55_P2032815	Rnase13	Mus musculus ribonuclease, RNase A family,
2304970	A_30_P0103291	A_30_P01032917	lincRNA:chr12:15735906-15798506 reverse s
2310555	A_30_P0102844	A_30_P01028440	lincRNA:chr10:96096995-96097589 forward s
2296265	A_55_P2009225	Cd34	Mus musculus CD34 antigen (Cd34), transcrip
2284245	A_55_P1989738	4930426L09Rik	Mus musculus RIKEN cDNA 4930426L09 ger
2280302	A_51_P263290	Galnt9	Mus musculus UDP-N-acetyl-alpha-D-galactos
2297550	A_55_P2044582	Iglon5	Mus musculus IgLON family member 5 (Iglon5
2298259	A_55_P2012439	Tnfrsf19	Mus musculus tumor necrosis factor receptor s
2293972	A_30_P0101868	A_30_P01018688	lincRNA:chr5:111538420-111540142 forward
2266129	A_55_P2012824	Gm9426	Unknown
2298772	A_30_P0102188	A_30_P01021888	lincRNA:chr3:19179899-19216399 reverse st
2270548	A_52_P108850	St8sia1	Mus musculus ST8 alpha-N-acetyl-neuraminid
2275787	A_65_P08768	Fbln1	fibulin 1 [Source:MGI Symbol;Acc:MGI:95487]
2282633	A_55_P2017207	A430078G23Rik	Mus musculus RIKEN cDNA A430078G23 ger
2282004	A_30_P0101908	A_30_P01019082	lincRNA:chr1:33893475-33903900 forward st
2294545	A_30_P0102937	A_30_P01029370	lincRNA:chr11:95627874-95640824 forward s
2265157	A_52_P590535	Fbln2	Mus musculus fibulin 2 (Fbln2), transcript varia
2298126	A_55_P2074736	Prkar1b	Mus musculus protein kinase, cAMP depende
2277509	A_30_P0102232	A_30_P01022326	lincRNA:chr4:114631940-114632618 reverse
2260687	A_30_P0103064	A_30_P01030644	lincRNA:chrX:135880775-135891525 reverse
2258834	A_30_P0103194	A_30_P01031947	lincRNA:chr3:84609788-84618062 reverse st
2267983	A_55_P2105452	Foxp1	Mus musculus forkhead box P1 (Foxp1), trans
2292501	A_30_P0102555	A_30_P01025555	lincRNA:chr1:138473514-138476054 reverse
2279076	A_55_P2016792	Inpp4b	Mus musculus inositol polyphosphate-4-phosp
2262540	A_55_P2170034	Rgl1	Mus musculus ral guanine nucleotide dissocia
2300201	A_30_P0102902	A_30_P01029025	lincRNA:chr2:164739589-164745000 forward
2303699	A_51_P112223	Gsta4	Mus musculus glutathione S-transferase, alph
2299879	A_66_P135471	Gm4759	Mus musculus predicted gene 4759 (Gm4759
2295753	A_66_P105075	Mmp11	Mus musculus matrix metallopeptidase 11 (Mn
2264648	A_30_P0101906	A_30_P01019065	lincRNA:chr17:12965849-12968519 forward s
2262051	A_55_P2316041	BC050972	cDNA sequence BC050972 [Source:MGI Sym
2266603	A_30_P0101793	A_30_P01017933	lincRNA:chr12:15735906-15798506 reverse s
2303879	A_55_P1989698	Mmp11	Mus musculus matrix metallopeptidase 11 (Mn
2297691	A_55_P2162122	Gm8721	predicted gene 8721 [Source:MGI Symbol;Ac
2268867	A_55_P2184023	Dnahc7a	Mus musculus adult male hypothalamus cDNA
2297276	A_52_P491554	Zfp759	Mus musculus zinc finger protein 759 (Zfp759
2259461	A_55_P1993168	Ppargc1b	Mus musculus peroxisome proliferative activat

ANOVA p-value	Adjusted ANOVA p-value	Tukey p-value	Fold change	Log2 ratio	Median	wt_non-stim_1	wt_non-stim_2	wt_non-stim_3
1,26E-19	4,38E-16	2,28E-14	-230,241	-7,847	10,425	4,432	4,248	4,223
2,63E-16	6,03E-14	1,56E-11	-41,184	-5,364	9,146	4,039	3,987	4,053
4,28E-04	1,39E-03	7,87E-03	-32,492	-5,022	13,324	0,193	-0,022	1,055
4,09E-04	1,34E-03	7,27E-03	-24,847	-4,635	13,815	0,315	-0,030	1,024
1,48E-17	8,83E-15	2,29E-14	-16,201	-4,018	3,846	1,876	1,563	1,550
5,41E-08	3,68E-07	3,85E-07	-7,220	-2,852	3,016	1,533	*0,196*	0,764
8,36E-17	2,89E-14	6,59E-10	-7,091	-2,826	6,113	3,829	3,835	3,883
3,93E-16	7,93E-14	7,23E-14	-6,835	-2,773	9,485	1,584	1,704	1,810
5,21E-04	1,67E-03	6,11E-04	-6,285	-2,652	5,157	-0,770	-0,133	*-2,379*
5,27E-05	2,02E-04	2,98E-04	-5,633	-2,494	3,430	*0,151*	*0,160*	0,786
5,59E-06	2,55E-05	1,21E-04	-5,483	-2,455	2,039	*0,459*	*-0,084*	*-0,077*
7,46E-04	2,33E-03	7,80E-03	-5,267	-2,397	2,873	*-0,917*	*-0,389*	*-0,333*
6,81E-05	2,55E-04	9,80E-04	-5,260	-2,395	3,499	*0,397*	*-0,536*	*-0,003*
6,46E-03	1,69E-02	1,11E-02	-4,231	-2,081	2,988	*-0,967*	*0,070*	*0,407*
7,06E-08	4,69E-07	8,37E-05	-4,179	-2,063	4,519	0,808	0,669	0,589
2,01E-09	1,94E-08	7,18E-07	-3,874	-1,954	6,039	1,145	1,349	1,207
2,89E-04	9,71E-04	6,79E-03	-3,837	-1,940	2,488	*-0,468*	*-0,175*	*0,942*
8,84E-03	2,26E-02	1,78E-02	-3,660	-1,872	3,431	*0,192*	0,525	*0,167*
1,52E-06	7,70E-06	9,25E-03	-3,593	-1,845	5,676	0,025	0,155	0,232
1,95E-13	8,11E-12	1,11E-10	-3,399	-1,765	10,496	1,004	0,972	0,982
1,97E-02	4,67E-02	2,06E-02	-3,387	-1,760	3,538	*-1,486*	0,922	1,263
7,50E-08	4,96E-07	1,78E-05	-3,329	-1,735	4,084	0,228	0,487	0,607
9,68E-14	4,65E-12	2,34E-06	-3,272	-1,710	4,732	2,696	2,732	2,887
1,80E-10	2,37E-09	1,41E-08	-3,178	-1,668	7,905	0,885	0,667	0,788
1,16E-04	4,17E-04	5,07E-05	-3,057	-1,612	3,548	0,691	*-0,028*	0,652
1,11E-05	4,78E-05	1,12E-02	-3,029	-1,599	6,625	0,647	0,599	0,189
3,32E-03	9,22E-03	4,00E-03	-2,998	-1,584	4,698	0,331	-0,063	0,063
2,63E-11	4,56E-10	4,11E-10	-2,942	-1,557	6,368	0,420	0,520	0,615
1,30E-10	1,79E-09	3,30E-04	-2,878	-1,525	4,533	2,113	1,656	1,565
8,36E-06	3,68E-05	5,85E-04	-2,872	-1,522	4,015	0,340	0,343	-0,219
6,80E-03	1,78E-02	8,42E-03	-2,854	-1,513	2,762	*-0,147*	*-0,242*	*0,367*
1,84E-11	3,36E-10	2,17E-07	-2,840	-1,506	6,844	1,812	2,027	1,884
4,11E-05	1,60E-04	2,40E-03	-2,825	-1,498	4,882	-0,009	0,013	0,787
1,25E-06	6,44E-06	7,82E-06	-2,815	-1,493	5,508	0,467	0,336	0,351
1,43E-04	5,06E-04	3,81E-02	-2,778	-1,474	4,585	1,001	0,860	0,673
1,75E-08	1,33E-07	1,46E-04	-2,774	-1,472	6,496	0,013	0,001	0,310
1,19E-11	2,32E-10	1,03E-06	-2,734	-1,451	9,841	2,002	2,060	2,088
6,61E-05	2,48E-04	2,65E-04	-2,676	-1,420	4,578	0,557	0,019	0,434
1,74E-14	1,27E-12	6,71E-07	-2,641	-1,401	8,074	2,634	2,887	2,792
7,39E-07	3,97E-06	1,83E-05	-2,606	-1,382	5,567	0,408	0,661	0,486
1,46E-10	1,98E-09	1,76E-07	-2,594	-1,375	7,163	0,475	0,705	0,782
3,78E-07	2,16E-06	4,73E-05	-2,583	-1,369	4,748	0,311	0,390	0,774
3,51E-03	9,70E-03	4,43E-02	-2,579	-1,367	4,947	0,262	-0,087	0,087
1,39E-07	8,68E-07	2,73E-04	-2,565	-1,359	3,768	*0,072*	*-0,483*	
1,32E-08	1,04E-07	1,13E-02	-2,535	-1,342	5,900	1,398	1,452	1,347
5,11E-07	2,84E-06	9,53E-03	-2,519	-1,333	5,119	0,994	0,964	0,961

1,62E-08	1,24E-07	1,64E-02	-2,512	-1,329	5,013	0,072	-0,265	-0,566
5,33E-05	2,04E-04	2,23E-03	-2,464	-1,301	6,937	0,598	0,860	0,971
2,11E-18	2,27E-15	1,54E-07	-2,420	-1,275	4,010	*-2,135*	*-2,153*	*-2,157*
7,51E-16	1,24E-13	6,66E-05	-2,415	-1,272	9,641	3,474	3,498	3,579
2,73E-05	1,10E-04	5,82E-03	-2,392	-1,258	4,832	0,611	0,870	0,624
2,96E-12	7,36E-11	1,47E-07	-2,377	-1,249	5,990	-0,179	-0,124	-0,031
3,73E-16	7,64E-14	1,29E-05	-2,372	-1,246	7,821	2,841	3,189	2,974
3,86E-06	1,81E-05	8,89E-03	-2,362	-1,240	2,417	*-0,374*	*-0,393*	*-0,387*
1,19E-11	2,32E-10	1,91E-06	-2,357	-1,237	9,361	2,081	2,086	2,083
7,72E-09	6,42E-08	4,96E-02	-2,341	-1,227	5,322	2,054	2,381	1,921
4,26E-03	1,16E-02	1,55E-02	-2,336	-1,224	4,462	0,299	0,114	0,446
9,53E-08	6,17E-07	2,72E-02	-2,304	-1,204	3,064	*-0,918*	*-0,931*	*-0,913*
2,03E-09	1,96E-08	1,42E-04	-2,301	-1,202	7,896	1,018	0,963	1,113
7,89E-03	2,04E-02	3,99E-02	-2,289	-1,195	3,763	1,440	*-0,151*	0,366
3,36E-12	8,13E-11	3,93E-04	-2,283	-1,191	3,816	*-1,069*	*-1,408*	*-1,702*
1,78E-06	8,88E-06	5,72E-03	-2,282	-1,190	6,953	-0,045	-0,047	0,332
3,17E-03	8,83E-03	6,75E-03	-2,277	-1,187	3,296	*-0,183*	1,178	*0,045*
1,52E-09	1,52E-08	5,56E-03	-2,277	-1,187	6,275	1,079	1,215	1,440
1,55E-10	2,08E-09	2,94E-03	-2,250	-1,170	7,292	2,143	2,320	1,996
6,18E-03	1,63E-02	3,60E-02	-2,249	-1,169	4,304	0,282	0,863	0,467
6,10E-04	1,94E-03	1,52E-03	-2,247	-1,168	5,491	0,131	0,611	0,352
5,33E-08	3,63E-07	6,68E-05	-2,238	-1,162	6,730	0,632	1,016	0,559
3,55E-05	1,40E-04	2,02E-02	-2,208	-1,143	4,840	1,659	1,691	1,440
3,74E-07	2,14E-06	3,06E-02	-2,207	-1,142	4,073	0,022	*-1,756*	*-0,750*
5,38E-04	1,72E-03	3,67E-02	-2,181	-1,125	4,827	0,285	0,591	0,599
2,48E-03	7,04E-03	8,32E-03	-2,178	-1,123	4,541	-0,011	-0,068	-0,050
1,45E-06	7,37E-06	5,28E-04	-2,155	-1,108	4,421	0,102	0,817	0,339
7,76E-09	6,45E-08	8,14E-04	-2,154	-1,107	7,973	1,653	1,627	1,676
7,26E-08	4,81E-07	4,57E-04	-2,149	-1,104	5,917	0,006	-0,146	0,241
1,96E-11	3,54E-10	3,85E-03	-2,148	-1,103	5,806	1,898	1,968	1,865
2,13E-03	6,11E-03	3,70E-02	-2,142	-1,099	3,449	*-0,045*	*0,149*	*-0,665*
3,66E-07	2,10E-06	2,18E-03	-2,136	-1,095	4,320	0,898	0,484	0,450
6,78E-09	5,71E-08	2,03E-02	-2,132	-1,092	5,932	-1,532	-0,956	-0,327
5,19E-06	2,38E-05	4,86E-04	-2,105	-1,074	7,097	1,176	0,993	0,986
3,89E-03	1,06E-02	2,76E-02	-2,104	-1,073	3,045	*-1,035*	*0,220*	*-0,089*
3,24E-03	9,00E-03	1,65E-03	-2,101	-1,071	3,412	*-0,852*	*-0,078*	0,405
6,24E-04	1,98E-03	1,16E-02	-2,098	-1,069	3,560	*0,114*	*-0,114*	0,444
9,89E-06	4,30E-05	1,96E-03	-2,092	-1,065	8,692	0,901	0,704	0,738
4,21E-06	1,96E-05	2,85E-05	-2,092	-1,065	6,137	0,520	0,123	0,109
1,25E-03	3,75E-03	3,14E-03	-2,086	-1,061	5,411	-0,093	0,271	0,914
9,55E-07	5,03E-06	4,08E-04	-2,082	-1,058	5,040	-0,620	-0,838	-0,893
5,35E-11	8,35E-10	6,38E-03	-2,053	-1,038	4,807	1,905	1,735	1,546
4,04E-13	1,46E-11	1,47E-05	-2,043	-1,031	6,881	1,619	1,474	1,692
2,82E-11	4,85E-10	1,76E-02	-2,038	-1,027	5,744	1,665	1,170	1,323
8,84E-10	9,45E-09	1,32E-04	-2,036	-1,026	5,941	1,881	1,358	1,877
1,91E-03	5,54E-03	1,01E-02	-2,029	-1,021	4,386	0,573	0,026	0,556
2,79E-06	1,34E-05	1,65E-03	-2,027	-1,019	1,774	*0,000*	*-0,001*	*-0,003*
1,52E-10	2,05E-09	2,79E-03	-2,027	-1,019	6,835	1,318	1,471	1,368
2,47E-08	1,81E-07	1,35E-03	-2,025	-1,018	7,365	1,622	1,331	1,780
7,02E-03	1,83E-02	2,63E-02	-2,022	-1,016	4,381	0,062	-0,018	0,834
8,55E-04	2,64E-03	8,74E-03	-2,021	-1,015	3,690	0,489	0,045	0,891
1,15E-06	5,97E-06	1,09E-02	-2,017	-1,012	3,052	*-1,055*	*-1,066*	*-1,053*
6,65E-03	1,74E-02	7,60E-03	-2,010	-1,007	4,264	0,274	0,454	-0,040



wt_non-stim_4	wt_non-stim_21	CD4creGARPfl-fl_non-stim_22	CD4creGARPfl-fl_non-stim_23	CD4creGARPfl-fl_non-stim_8	CD4creGARPfl-fl_non-stim_9	CD4creGARPfl-fl_non-stim_10	wt_stim_11	wt_stim_12	wt_stim_13
4,092	4,351	-6,339	-6,465	-6,413	-6,052	*-7,275*	4,042	3,853	4,000
4,158	3,919	1,090	1,955	2,197	2,176	1,665	-1,142	-1,266	-1,090
0,844	0,308	-4,485	-5,691	0,022	-4,958	-6,331	0,064	-0,054	0,931
0,832	0,409	-3,932	-5,281	0,030	-4,312	-5,653	0,081	-0,155	0,926
1,784	1,972	*-1,923*	*-1,935*	*-1,907*	*-1,892*	*-1,550*	1,874	2,156	1,935
0,638	1,085	*-0,853*	*-1,026*	*-1,213*	*-0,271*	*-0,849*	1,860	1,492	1,660
3,789	3,532	0,765	1,485	1,691	1,654	1,357	-1,443	-1,490	-1,256
1,794	1,430	-1,335	-0,987	-1,259	-0,897	-1,426	1,137	1,210	1,141
0,029	1,399	-0,271	0,387	-0,029	0,661	2,570	0,520	0,884	0,835
-0,525	*-1,348*	*-1,406*	*-1,388*	*-1,330*	*-1,277*	*0,068*	1,266	1,314	1,603
0,478	*0,111*	*-0,099*	*-0,085*	*-0,077*	*-0,069*	*-0,078*	2,268	2,496	2,496
-0,936	*-0,941*	1,043	*-0,963*	*0,333*	1,457	*-0,968*	1,745	2,013	2,059
0,277	*0,003*	*-0,942*	*-1,423*	*-1,378*	*-1,313*	*-1,362*	0,748	*0,194*	1,607
-0,667	*0,081*	*-0,680*	*-0,971*	1,151	*-0,964*	*-0,957*	0,966	1,211	*0,313*
0,416	1,754	0,185	1,839	0,631	0,671	-0,079	*-1,072*	-0,335	0,079
1,542	1,301	-0,571	0,016	-0,248	0,186	-0,472	0,162	-0,217	0,124
-0,689	*-0,163*	*-0,701*	*-0,090*	*0,539*	*-0,683*	*-0,687*	1,452	1,748	2,563
0,452	*-1,574*	*-1,071*	*-0,559*	*0,180*	0,925	0,312	*-0,167*	*-1,445*	0,456
-0,636	-0,817	-0,676	-1,630	-1,519	*-1,952*	*-2,339*	1,842	1,820	2,081
0,932	0,749	0,241	-0,318	0,395	0,124	0,340	-0,023	-0,160	-0,042
0,924	*-0,650*	0,341	0,116	0,282	*-0,477*	*-0,411*	0,643	0,262	*-0,116*
0,458	0,514	*-2,118*	*-1,236*	*-1,773*	*-1,452*	*-0,953*	0,673	0,516	0,889
2,584	3,298	0,577	0,451	0,397	0,288	0,204	-0,779	-0,884	*-0,899*
0,604	0,601	-0,023	-0,652	0,238	-0,042	0,295	-0,084	0,031	-0,104
-0,462	*-0,623*	0,128	0,028	*-0,660*	*-0,065*	*0,066*	0,710	0,773	1,078
-0,068	0,089	2,834	-0,087	0,880	1,562	2,387	-0,169	0,068	0,078
-0,543	0,428	-0,690	-0,170	*-1,043*	0,160	-0,215	0,846	0,442	0,807
0,601	0,677	-0,493	-0,136	-0,347	-0,212	-0,056	0,308	0,344	0,261
1,770	1,875	0,390	0,755	1,130	0,885	0,611	*-1,140*	-0,789	-0,504
0,548	*-0,357*	*-1,040*	*-1,598*	*-2,029*	*-2,054*	-0,109	1,561	1,544	1,508
0,470	*-0,438*	1,058	*0,055*	*-0,157*	*-0,943*	*-0,088*	1,342	*0,487*	*0,576*
1,718	1,894	-0,576	0,103	-0,351	-0,524	-0,529	0,077	0,066	-0,066
0,002	-0,446	-0,597	-1,298	-0,489	*-1,526*	-0,740	1,495	1,966	2,065
0,249	0,013	-0,984	-0,406	-0,317	0,100	-0,965	-0,013	0,309	0,101
0,469	1,256	0,208	1,634	-0,082	0,727	-0,175	0,185	-0,697	0,010
-0,606	-0,176	-0,743	-1,723	-1,532	-1,397	-1,278	1,470	1,541	1,616
1,909	2,117	-0,341	0,339	-0,028	-0,043	-0,322	0,028	0,060	-0,168
0,541	0,753	0,009	0,363	-0,225	-0,344	-0,037	0,388	-0,009	0,719
2,868	3,293	0,992	1,189	0,788	0,672	0,321	-0,896	-0,849	-0,777
0,462	0,548	-0,204	0,328	-0,131	0,131	-0,307	0,342	-0,229	0,482
0,941	0,568	-1,077	-1,592	-0,932	-1,274	-1,279	0,822	0,977	0,720
0,758	0,566	-1,237	*-1,531*	-0,964	-0,849	*-1,626*	0,613	1,102	0,386
0,813	0,385	-1,187	-1,194	*-1,770*	0,299	-0,889	0,354	0,419	0,980
0,722	0,415	*-1,614*	*-1,438*	*-1,950*	*-1,929*	*-1,937*	0,951	1,348	1,198
1,710	1,221	0,579	0,860	0,836	0,853	0,320	-0,546	-0,888	-0,527
0,873	2,123	0,925	2,259	1,044	1,122	0,070	-0,365	-0,194	-0,070



-0,591	0,139	*-2,946*	-1,366	*-2,840*	*-2,591*	*-2,804*	1,511	1,483	1,509
0,762	0,615	-0,317	-0,155	0,092	0,192	-0,305	-0,092	-0,236	0,161
-2,136	*-2,161*	*-2,140*	*-2,160*	*-2,135*	*-2,162*	*-2,162*	3,493	3,551	3,542
3,590	3,412	1,039	1,974	2,056	1,927	1,472	-1,039	-1,119	-1,140
0,239	1,086	-0,065	0,710	0,480	-0,076	-0,377	-0,378	0,065	-0,381
0,025	0,050	-1,414	-0,949	-1,162	-1,546	-1,411	1,335	1,316	1,368
3,287	2,938	2,022	2,608	2,294	2,326	1,784	-1,916	-2,347	-1,784
0,320	*-0,393*	*-0,435*	*-0,430*	*-0,388*	*-0,344*	*-0,375*	2,290	1,740	2,182
1,882	2,041	-0,220	0,366	0,083	-0,040	-0,333	0,018	-0,018	-0,123
2,140	3,029	1,854	2,676	1,818	1,626	0,601	-0,718	-1,133	-0,601
0,558	-0,020	-0,443	0,065	-0,132	0,020	*-1,244*	0,296	0,108	0,446
-0,232	*-0,920*	*-0,990*	*-0,952*	*-0,939*	*-0,912*	*-0,904*	1,940	2,595	2,460
0,462	1,090	0,063	0,392	0,432	0,793	0,280	-0,931	-0,860	-0,704
0,846	0,235	0,409	-0,357	0,044	0,425	*-0,044*	*-0,297*	0,488	0,633
-1,354	*-1,260*	*-1,758*	*-1,765*	*-1,785*	*-0,859*	*-1,741*	1,982	2,258	2,255
-0,335	-0,257	-0,499	-1,174	-0,616	-1,583	-1,134	1,575	1,416	1,692
1,072	0,512	-0,045	*-0,163*	*-1,364*	*0,069*	*0,288*	0,677	0,646	1,034
1,553	1,155	0,689	1,155	0,810	1,231	0,587	-1,122	-0,685	-0,658
1,961	2,300	0,900	2,094	1,193	1,400	0,459	-0,629	-0,579	-0,608
-0,505	0,586	-0,206	0,287	0,250	0,320	-0,329	0,642	0,032	0,358
0,476	0,381	-0,520	-0,191	-0,377	0,353	-0,450	0,541	0,385	0,718
0,577	0,595	-0,195	0,172	-0,023	0,085	0,076	-0,299	0,023	-0,032
0,992	1,142	-1,422	-0,116	-0,016	-0,724	0,621	0,185	0,094	0,137
-1,448	*-1,168*	*-2,091*	-0,534	*-2,051*	*-2,044*	*-2,050*	1,386	2,135	1,926
0,446	1,487	0,387	1,510	-0,265	0,043	-0,590	0,011	-0,011	-0,022
0,724	0,021	0,242	0,084	0,113	-0,104	0,000	0,132	0,237	0,000
0,557	0,581	-0,037	0,292	0,408	0,088	-0,141	-0,248	-0,614	-0,033
1,903	1,536	-0,145	0,455	0,763	0,807	0,211	-0,460	-0,466	-0,265
-0,006	0,039	-0,813	-1,245	-0,895	-0,768	-1,143	1,325	1,050	0,843
1,974	1,667	0,945	1,538	1,642	1,396	1,130	-2,002	-1,885	-1,496
-1,091	*-0,826*	*-0,749*	0,186	*-0,333*	*-1,409*	*-0,009*	1,219	0,880	0,602
0,498	0,903	0,136	0,249	0,827	-0,026	0,197	-0,412	*-0,855*	0,026
-1,332	-0,684	-2,144	-1,637	-1,423	*-2,271*	*-3,229*	1,902	1,855	1,751
1,128	1,170	-0,254	0,053	-0,455	-0,401	-0,796	0,200	1,695	0,381
-1,066	*-0,536*	0,694	*-1,105*	*-0,759*	*-0,749*	*-0,373*	*0,201*	1,162	1,191
-0,038	0,441	-0,046	*-0,378*	*-0,241*	0,639	0,541	0,626	1,608	0,969
-0,623	*0,177*	*-1,265*	*-0,464*	*-1,524*	*-1,453*	*-0,398*	1,624	0,839	1,205
0,803	0,525	-0,874	-0,278	0,210	-0,186	-0,698	0,215	0,359	0,186
0,383	0,119	-0,638	-0,728	-0,084	0,072	-0,563	-0,053	0,053	0,166
0,009	0,384	-0,551	0,205	-0,009	0,068	-1,224	-0,023	0,150	0,196
-1,207	0,046	-0,244	-0,046	-0,822	-0,223	-0,820	2,335	1,194	1,381
1,850	1,504	1,039	1,196	1,035	1,210	0,291	-0,959	-0,492	-0,492
1,275	1,538	0,894	0,519	0,884	0,858	0,509	-0,509	-0,623	-0,561
1,183	1,487	0,855	1,295	1,851	1,272	1,104	-1,521	*-2,361*	-1,446
1,768	1,539	-0,146	0,285	0,250	0,006	-0,639	-0,155	0,172	0,489
0,392	1,080	-0,470	1,024	-0,262	-0,026	-0,682	0,523	0,311	0,681
0,000	*-0,001*	*0,573*	*-0,003*	*-0,002*	*-0,006*	*-0,005*	2,494	1,939	2,142
1,657	1,157	0,723	1,277	1,126	1,053	0,436	-0,743	-0,436	-0,482
1,317	1,420	-0,508	0,103	0,246	-0,013	-1,009	0,013	-0,152	0,204
0,018	0,398	-0,619	0,198	0,076	*-0,543*	*-1,058*	0,405	0,633	0,620
0,022	0,867	*-1,117*	-0,022	0,638	*0,167*	*-0,575*	-0,055	0,142	0,439
-1,063	*-0,999*	*0,159*	*0,008*	*-0,738*	*-1,024*	*0,079*	*0,421*	0,880	1,133
0,441	0,157	-0,372	0,019	*-0,685*	0,496	-0,175	0,435	0,176	0,748

wt_stim_14	wt_stim_15	CD4creGARPfl-fl_stim_24	CD4creGARPfl-fl_stim_25	CD4creGARPfl-fl_stim_18	CD4creGARPfl-fl_stim_19	CD4creGARPfl-fl_stim_20	Refseq
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0,553	0,905	-4,340	-5,221	0,526	-4,469	-5,653	
0,518	0,906	-3,899	-4,805	0,453	-4,118	-5,167	NM_133362
2,452	2,155	*-1,889*	*-1,677*	*-1,870*	*-1,859*	*-1,862*	NM_178165
1,455	1,648	*-1,209*	*-0,196*	*-1,210*	*-0,283*	*-1,205*	NM_178405
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1,156	0,897	-1,520	-1,685	-1,513	-1,760	-1,632	NM_001083318
1,311	1,600	-1,436	*-1,558*	*-3,171*	*-2,815*	*-1,767*	NM_009690
1,228	1,598	*-0,040*	*-1,209*	*-1,200*	*0,040*	*-1,180*	
2,195	2,374	*0,069*	*-0,096*	*-0,081*	2,201	*-0,088*	NM_201531
2,173	1,642	*0,513*	*-0,935*	*-0,384*	1,652	*-0,923*	NM_027810
1,092	2,063	*0,139*	*0,367*	*-1,353*	*-1,370*	*-1,303*	NM_201531
1,140	1,696	*0,463*	*-0,941*	*-0,970*	*-0,070*	*-0,983*	
-0,757	*-0,148*	*-2,351*	*-2,391*	*-2,398*	*-2,479*	*-2,417*	
-0,016	0,338	*-2,884*	-1,942	-1,830	-1,269	-1,790	NM_138665
2,030	2,458	*0,090*	*-0,686*	1,466	1,361	*-0,671*	
0,285	0,925	*-1,603*	*-1,587*	*-1,578*	*-1,485*	*-1,593*	
1,040	0,506	0,709	-0,097	-0,025	0,376	-0,029	NM_001177666
-0,057	0,023	-1,807	-1,638	-1,853	-1,650	-1,899	NM_009003
0,180	1,008	*-1,584*	*-0,898*	*-1,499*	*-1,572*	*-0,164*	NM_029070
1,105	0,940	*-0,846*	*-0,228*	*-1,466*	-0,360	*-1,177*	NM_175414
-1,323	-0,204	*-2,658*	*-2,595*	*-1,815*	*-2,385*	*-2,608*	NM_026323
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1,455	*0,679*	*-1,580*	*-0,269*	*-1,559*	*-0,672*	*-0,838*	NM_001033877
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0,311	1,974	-0,316	*-0,778*	0,417	*-0,984*	*-0,927*	NM_138650
0,401	0,056	-1,143	-1,252	-1,520	-1,249	-0,958	NM_001039493
-0,438	*-0,390*	*-1,220*	*-1,453*	*-2,029*	*-2,030*	*-2,575*	
1,247	1,231	-0,014	0,014	*-1,015*	*-1,197*	0,228	
1,446	1,611	*-0,171*	*-0,055*	*-0,940*	*0,450*	*-0,300*	
0,259	0,535	-1,172	-1,344	-2,213	-1,429	-1,497	NM_173786
0,972	0,438	0,384	-0,002	-0,899	0,256	-0,149	NM_001177666
0,036	0,109	-1,393	*-1,855*	-1,237	-0,844	-1,498	
-0,010	*-0,522*	-0,437	*-1,484*	*-1,980*	-0,603	*-2,130*	
0,641	1,204	0,303	-0,016	-0,001	0,236	-0,150	XR_106831
0,273	0,697	-0,876	-1,020	-1,429	-1,477	-1,390	NM_001168660
0,779	-0,254	*-1,352*	-0,415	*-1,224*	-0,579	*-1,032*	NM_028593
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0,465	-0,448	-1,004	-1,477	-1,039	-0,882	-1,124	
0,917	0,423	-0,989	-0,423	-0,552	-0,437	-0,683	
0,383	0,243	*-1,675*	-0,243	-0,755	-1,092	*-0,982*	
0,900	-0,266	-0,980	-0,729	*-0,972*	0,556	*-0,948*	
1,481	0,918	0,000	*-0,161*	*-1,117*	0,400	*-0,632*	
-0,320	*-2,376*	-1,658	-1,857	-1,888	-2,131	*-2,509*	NM_144551
-0,691	-0,732	-1,121	*-1,698*	*-1,858*	*-1,436*	*-2,143*	

1,756	1,030	0,179	-0,210	1,474	0,342	-0,072	
0,166	0,966	-1,139	-1,488	-0,123	-1,264	-0,504	NM_001081020
4,331	3,826	2,135	2,189	2,591	2,705	2,276	NM_028408
-1,126	-1,533	-2,464	-1,876	-2,399	-2,112	-2,425	NM_001162938
0,086	0,139	-0,553	*-1,193*	*-1,206*	-0,636	*-1,799*	
1,509	0,989	0,223	-0,025	0,086	0,401	-0,033	
-1,869	-1,968	-3,252	-3,162	-3,150	-4,143	-3,091	NM_001162938
1,201	2,806	1,826	*1,052*	*-0,320*	*0,942*	*0,610*	NM_015755
0,299	0,779	-0,920	-0,910	-1,260	-1,251	-1,219	NM_173786
-1,250	-0,882	-1,326	-1,231	*-2,108*	*-2,175*	*-3,232*	
0,207	*-0,331*	*-1,268*	*-1,178*	*-1,017*	-0,048	-0,391	
3,161	*1,298*	1,346	1,256	*0,795*	2,337	*0,232*	NM_009317
-1,003	-0,063	-2,492	-2,236	-1,619	-1,455	-2,062	NM_144796
1,006	*-0,582*	*-0,540*	*-0,781*	*-0,707*	*-0,411*	*-0,948*	
2,089	2,848	1,064	0,859	1,398	1,647	0,893	NM_008006
1,010	0,357	0,490	0,227	0,045	0,456	-0,078	NM_001039244
0,667	*-0,052*	*-0,445*	*-0,520*	*-0,497*	*-0,580*	*-1,309*	NM_001011687
-0,587	-1,470	-2,285	-1,871	-0,957	-1,825	*-2,505*	
-0,459	-1,516	-1,949	-2,340	-1,777	-1,523	-1,745	
-0,392	*-0,341*	*-1,420*	-0,032	*-0,470*	*-1,155*	*-1,137*	NM_133654
1,065	-0,207	-0,651	-0,824	-0,222	-0,131	-0,627	NR_024323
0,279	-0,740	-1,421	-1,086	-1,195	-1,196	-0,819	NM_198306
-0,552	0,016	*-1,998*	-0,674	*-1,049*	*-2,358*	-0,442	NM_001164518
1,547	0,940	0,197	-0,022	0,406	0,691	1,000	NM_013869
0,071	*-0,831*	-0,824	*-1,136*	*-2,151*	-0,708	*-1,537*	
0,180	-0,199	-0,992	0,159	*-1,071*	-0,620	*-1,017*	
0,033	0,158	*-1,141*	*-1,145*	*-1,297*	*-1,019*	-0,543	
-0,222	0,145	-2,216	-1,809	-0,772	-1,372	-1,015	NM_011374
0,864	1,189	-0,300	0,745	-0,253	0,470	-0,053	
-2,269	-0,945	*-2,597*	*-3,054*	*-3,907*	*-2,988*	*-2,033*	NM_001033378
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-0,385	*-0,597*	*-1,507*	*-0,721*	*-1,848*	*-1,848*	*-1,200*	
1,111	2,397	0,762	0,568	0,876	1,142	0,327	NM_007992
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0,637	1,416	*0,143*	*0,089*	*-1,045*	*0,177*	*-0,558*	
0,481	*0,631*	*0,038*	*-0,440*	*-1,426*	*-0,211*	*-1,422*	
0,782	*0,631*	0,540	*-0,230*	*-1,451*	*-1,151*	0,492	
0,405	-0,485	-0,849	-0,850	-1,020	-0,288	-0,857	NM_001197321
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0,216	0,714	-1,276	-0,865	-0,754	-0,360	-1,123	NM_001024617
1,633	1,484	0,100	-0,507	0,477	0,425	0,466	NM_016846
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-0,887	-0,552	-1,286	-1,592	-1,611	-1,316	-2,028	NM_010357
-1,955	-0,855	*-2,734*	*-2,911*	*-2,145*	*-2,070*	*-2,548*	NR_003967
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2,266	*2,177*	*-0,005*	*1,698*	*1,627*	*1,158*	*-0,006*	
-0,499	-1,409	-1,518	-1,225	-1,708	-1,920	-1,421	
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0,639	*-0,325*	-0,544	-0,396	-0,332	-0,479	-0,165	
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1,004	*1,208*	*-0,150*	*0,385*	*0,523*	*-0,008*	*-0,070*	NM_172392
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2260536	A_55_P2096395	Cdc42bpa
2302604	A_51_P137111	Chek2
2278881	A_52_P30989	Cdkn3

2302014	A_51_P155142	Cdca8
2286831	A_51_P427917	Il31ra
2290025	A_55_P1975874	Bcl2l15
2264647	A_55_P1959421	ENSMUST0000010
2302700	A_55_P2092869	Anxa9
2267713	A_52_P112190	LOC100047053
2303584	A_52_P451073	Tnfrsf21
2289563	A_55_P1977451	ENSMUST0000010
2295190	A_55_P2096402	Cdc42bpa
2258389	A_55_P2087429	LOC100047162
2259508	A_55_P2170681	Cdca8
2300047	A_51_P312035	Cd300e
2303607	A_55_P2001267	XM_001472404
2311760	A_55_P2105878	Ccr10
2262726	A_51_P473170	Tnfsf4
2312288	A_51_P130095	Fcgr2b
2307080	A_51_P125135	Cdca5
2277727	A_52_P661044	Ccr3
2266724	A_55_P1996946	Cdc20
2265415	A_52_P186262	ENSMUST0000010
2270408	A_52_P546162	ENSMUST0000010
2291622	A_55_P1965050	Cks2
2258591	A_55_P1965338	Anxa8
2306096	A_51_P375146	Cd36
2262852	A_55_P2027737	Il1rl1
2285899	A_55_P2058028	ENSMUST0000010
2287578	A_55_P1986282	Cdkn1a
2266536	A_55_P2058023	ENSMUST0000010
2307552	A_51_P117581	Cables1
2279139	A_55_P2065510	ENSMUST0000010
2281798	A_55_P2066578	Ifi204
2310147	A_51_P284608	Cd74
2264800	A_51_P227004	Cks1b
2272946	A_55_P2092826	Anxa1
2295994	A_51_P241457	Lilrb4
2306283	A_55_P2137496	LOC100047815
2286855	A_55_P2061495	Cks1b
2279835	A_51_P271503	Il1r1

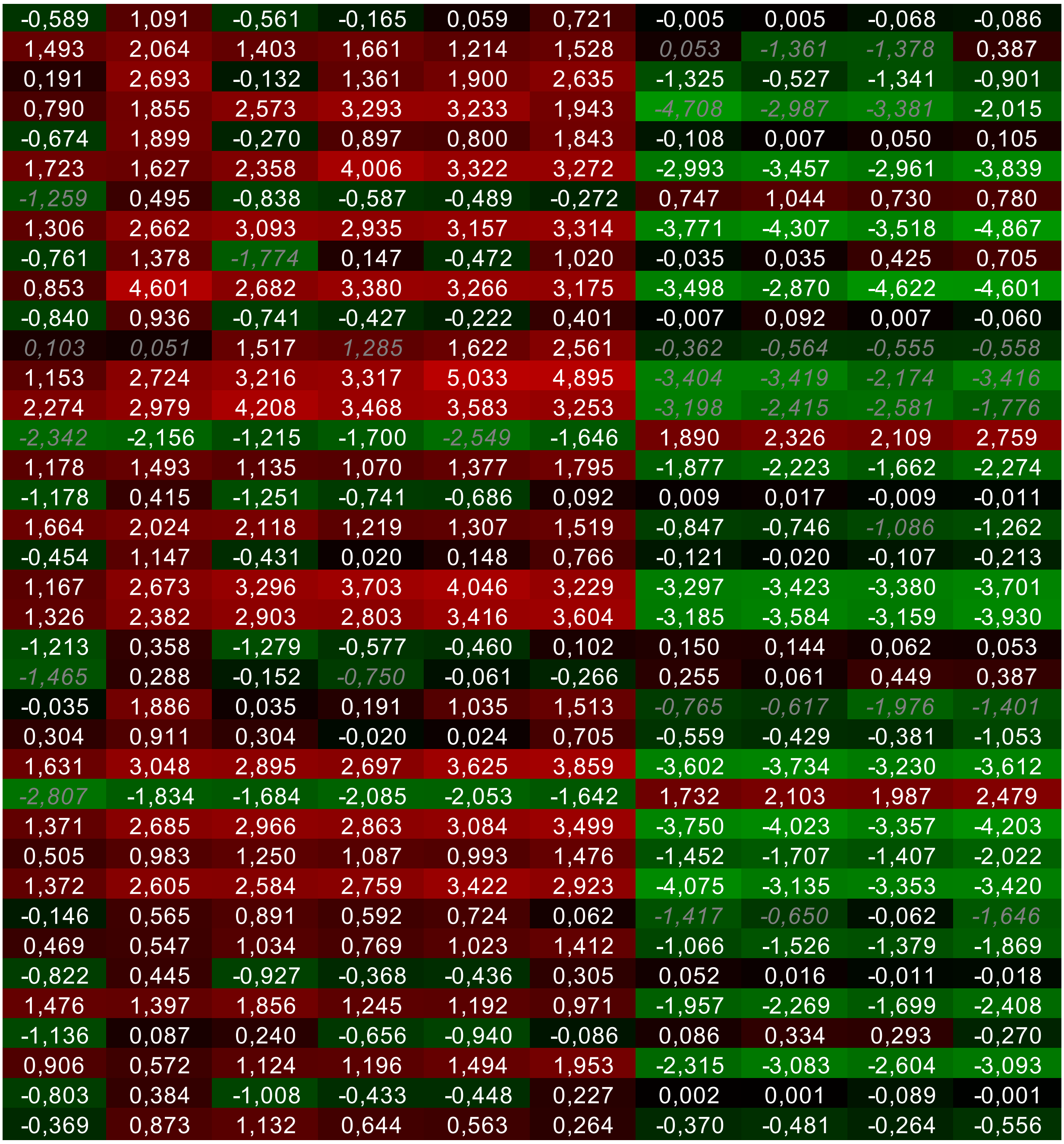
Description	ANOVA p-value
Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA [NM_011527]	**2,68E-07**
Mus musculus tumor necrosis factor, alpha-induced protein 2 (Tnfaip2), mRNA [NM_00	**1,78E-07**
Mus musculus tumor necrosis factor, alpha-induced protein 2 (Tnfaip2), mRNA [NM_00	**1,85E-07**
Mus musculus CD248 antigen, endosialin (Cd248), mRNA [NM_054042]	**1,69E-08**
Mus musculus leucine rich repeat containing 36 (Lrrc36), transcript variant 1, mRNA [N	**2,39E-05**
Mus musculus CD59a antigen (Cd59a), transcript variant 2, mRNA [NM_007652]	**5,22E-07**
Mus musculus CD24a antigen (Cd24a), mRNA [NM_009846]	**8,58E-09**
Mus musculus B-cell CLL/lymphoma 11A (zinc finger protein) (Bcl11a), transcript varian	**4,65E-09**
Mus musculus immunoglobulin heavy chain complex, mRNA (cDNA clone MGC:30346	**1,89E-14**
Mus musculus cytokine receptor-like factor 1 (Crlf1), mRNA [NM_018827]	**3,84E-04**
Mus musculus CD59b antigen (Cd59b), mRNA [NM_181858]	**3,26E-04**
Mus musculus cell division cycle 6 homolog (S. cerevisiae) (Cdc6), transcript variant 1,	**3,08E-06**
Mus musculus B-cell CLL/lymphoma 11A (zinc finger protein) (Bcl11a), transcript varian	**2,63E-07**
immunoglobulin kappa variable 6-13 [Source:MGI Symbol;Acc:MGI:1330829] [ENSMU	**1,04E-09**
Mus musculus cyclin-dependent kinase-like 1 (CDC2-related kinase) (Cdkl1), mRNA [N	**1,57E-02**
immunoglobulin kappa chain variable 19-93 [Source:MGI Symbol;Acc:MGI:107617] [E	**3,95E-09**
immunoglobulin heavy variable V1-23 [Source:MGI Symbol;Acc:MGI:3815050] [ENSM	**6,33E-10**
Mus musculus interleukin 1 receptor-like 1 (Il1rl1), transcript variant 2, mRNA [NM_0107	**6,08E-03**
Mus musculus BCL2-associated athanogene 2 (Bag2), mRNA [NM_145392]	**1,29E-06**
Mus musculus cyclin A2 (Ccna2), mRNA [NM_009828]	**1,06E-04**
Mus musculus cyclin B1 (Ccnb1), mRNA [NM_172301]	**3,92E-05**
Mus musculus mitogen-activated protein kinase kinase kinase 6 (Map3k6), mRNA [NM	**3,57E-04**
Mus musculus cyclin M1 (Cnnm1), mRNA [NM_031396]	**8,74E-06**
Mus musculus RAB38, member of RAS oncogene family (Rab38), mRNA [NM_028238	**1,15E-05**
Mus musculus cyclin E1 (Ccne1), mRNA [NM_007633]	**1,20E-05**
Mus musculus antigen identified by monoclonal antibody Ki 67 (Mki67), mRNA [NM_00	**4,09E-04**
PREDICTED: Mus musculus immunoglobulin heavy chain (J558 family) (Igh-VJ558), m	**4,37E-17**
immunoglobulin heavy variable V1-67 [Source:MGI Symbol;Acc:MGI:3645228] [ENSM	**1,13E-12**
immunoglobulin heavy variable V14-3 [Source:MGI Symbol;Acc:MGI:4439764] [ENSM	**1,50E-11**
Mus musculus cell division cycle 25 homolog C (S. pombe) (Cdc25c), mRNA [NM_0098	**2,94E-05**
Mus musculus cyclin B2 (Ccnb2), mRNA [NM_007630]	**1,15E-05**
Mus musculus immunoglobulin heavy chain complex, mRNA (cDNA clone MGC:11814	**9,82E-10**
Mus musculus CDC42 binding protein kinase alpha (Cdc42bpa), mRNA [NM_0010332	**7,75E-04**
Mus musculus interferon-induced protein 44 (Ifi44), mRNA [NM_133871]	**1,68E-07**
Mus musculus cyclin F (Ccnf), mRNA [NM_007634]	**2,23E-06**
Mus musculus cyclin E1 (Ccne1), mRNA [NM_007633]	**3,32E-06**
Mus musculus cyclin B1 (Ccnb1), mRNA [NM_172301]	**2,33E-05**
Mus musculus kit oncogene (Kit), transcript variant 1, mRNA [NM_001122733]	**5,64E-09**
immunoglobulin heavy variable V9-3 [Source:MGI Symbol;Acc:MGI:3642720] [ENSMU	**2,79E-08**
immunoglobulin kappa variable 4-86 [Source:MGI Symbol;Acc:MGI:2685305] [ENSMU	**5,59E-10**
immunoglobulin heavy variable 1-85 [Source:MGI Symbol;Acc:MGI:3645723] [ENSMU	**3,78E-11**
Mus musculus CD19 antigen (Cd19), mRNA [NM_009844]	**3,47E-04**
immunoglobulin kappa variable 6-20 [Source:MGI Symbol;Acc:MGI:1330836] [ENSMU	**2,95E-08**
Mus musculus CDC42 binding protein kinase alpha (Cdc42bpa), mRNA [NM_0010332	**4,05E-03**
Mus musculus CHK2 checkpoint homolog (S. pombe) (Chek2), mRNA [NM_016681]	**7,48E-05**
Mus musculus cyclin-dependent kinase inhibitor 3 (Cdkn3), mRNA [NM_028222]	**9,93E-05**

Mus musculus cell division cycle associated 8 (Cdca8), mRNA [NM_026560]	**4,03E-05**
Mus musculus interleukin 31 receptor A (Il31ra), mRNA [NM_139299]	**9,23E-04**
Mus musculus BCLl2-like 15 (Bcl2l15), transcript variant 1, mRNA [NM_001142959]	**9,86E-05**
immunoglobulin kappa chain variable 6-29 [Source:MGI Symbol;Acc:MGI:4439616] [E	**5,81E-09**
Mus musculus annexin A9 (Anxa9), transcript variant 1, mRNA [NM_001085383]	**3,20E-04**
immunoglobulin kappa variable 6-32 [Source:MGI Symbol;Acc:MGI:3641634] [ENSMU	**7,97E-11**
Mus musculus tumor necrosis factor receptor superfamily, member 21 (Tnfrsf21), mRN	**9,26E-06**
immunoglobulin kappa variable 4-80 [Source:MGI Symbol;Acc:MGI:4439653] [ENSMU	**7,78E-13**
Mus musculus CDC42 binding protein kinase alpha (Cdc42bpa), mRNA [NM_0010332	**5,94E-03**
immunoglobulin kappa variable 6-15 [Source:MGI Symbol;Acc:MGI:1330831] [ENSMU	**1,17E-10**
Mus musculus cell division cycle associated 8 (Cdca8), mRNA [NM_026560]	**1,23E-05**
Mus musculus CD300e antigen (Cd300e), mRNA [NM_172050]	**2,48E-03**
Mus musculus isolate 311 immunoglobulin heavy chain variable region mRNA, partial	**1,16E-09**
Mus musculus chemokine (C-C motif) receptor 10 (Ccr10), mRNA [NM_007721]	**5,02E-13**
Mus musculus tumor necrosis factor (ligand) superfamily, member 4 (Tnfsf4), mRNA [N	**1,49E-11**
Mus musculus Fc receptor, IgG, low affinity IIb (Fcgr2b), transcript variant 1, mRNA [N	**2,71E-07**
Mus musculus cell division cycle associated 5 (Cdca5), mRNA [NM_026410]	**2,26E-06**
Mus musculus chemokine (C-C motif) receptor 3 (Ccr3), mRNA [NM_009914]	**4,74E-06**
Mus musculus cell division cycle 20 homolog (S. cerevisiae) (Cdc20), mRNA [NM_0232	**8,23E-05**
immunoglobulin kappa chain variable 6-25 [Source:MGI Symbol;Acc:MGI:4439867] [E	**2,00E-13**
immunoglobulin kappa variable 4-58 [Source:MGI Symbol;Acc:MGI:2685923] [ENSMU	**2,53E-13**
Mus musculus CDC28 protein kinase regulatory subunit 2 (Cks2), mRNA [NM_025415]	**1,70E-06**
Mus musculus annexin A8 (Anxa8), mRNA [NM_013473]	**3,39E-04**
Mus musculus CD36 antigen (Cd36), transcript variant 2, mRNA [NM_007643]	**5,05E-05**
Mus musculus interleukin 1 receptor-like 1 (Il1rl1), transcript variant 1, mRNA [NM_001	**4,12E-04**
immunoglobulin kappa variable 4-63 [Source:MGI Symbol;Acc:MGI:3645235] [ENSMU	**5,78E-12**
Mus musculus cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a), transcript variant	**4,30E-11**
immunoglobulin kappa variable 4-57-1 [Source:MGI Symbol;Acc:MGI:2686264] [ENSM	**1,55E-12**
Mus musculus CDK5 and Abl enzyme substrate 1 (Cables1), transcript variant 2, mRN	**1,45E-09**
immunoglobulin heavy variable V1-20 [Source:MGI Symbol;Acc:MGI:3644607] [ENSM	**4,55E-11**
Mus musculus interferon activated gene 204, mRNA (cDNA clone MGC:18551 IMAGE	**4,84E-04**
Mus musculus CD74 antigen (invariant polypeptide of major histocompatibility complex	**7,57E-07**
Mus musculus CDC28 protein kinase 1b (Cks1b), mRNA [NM_016904]	**6,50E-06**
Mus musculus annexin A1 (Anxa1), mRNA [NM_010730]	**4,73E-08**
Mus musculus leukocyte immunoglobulin-like receptor, subfamily B, member 4 (Lilrb4),	**9,57E-07**
Mus musculus CD79A antigen (immunoglobulin-associated alpha), mRNA (cDNA clone	**1,06E-08**
Mus musculus CDC28 protein kinase 1b (Cks1b), mRNA [NM_016904]	**6,32E-06**
Mus musculus interleukin 1 receptor, type I (Il1r1), transcript variant 1, mRNA [NM_008	**2,03E-05**

Adjusted ANOVA p-value	Tukey p-value	Fold change	Log2 ratio	Median	wt_non-stim_1	wt_non-stim_2	wt_non-stim_3	wt_non-stim_4
1,58E-06	1,13E-05	19,932	4,317	6,904	-0,406	-0,273	0,377	0,203
1,09E-06	7,87E-06	19,576	4,291	7,822	-0,367	-0,383	-0,221	0,343
1,13E-06	1,10E-05	15,584	3,962	7,023	-0,652	-0,460	-0,079	0,214
1,29E-07	3,18E-05	12,978	3,698	4,184	1,173	1,159	0,780	0,597
9,68E-05	1,83E-04	12,711	3,668	3,620	*-0,050*	*-0,705*	*-0,261*	0,229
2,89E-06	1,52E-04	11,786	3,559	4,159	0,113	0,063	-0,113	0,416
7,06E-08	5,41E-06	11,592	3,535	8,841	0,657	0,454	0,691	0,649
4,09E-08	3,71E-05	9,389	3,231	7,075	0,257	0,501	0,535	1,049
1,36E-12	7,06E-06	8,497	3,087	10,262	3,018	1,568	2,828	2,732
1,26E-03	2,01E-04	8,421	3,074	6,711	-0,946	-1,138	-0,646	-1,289
1,09E-03	1,20E-03	7,923	2,986	2,134	*0,004*	*-0,002*	*0,017*	*-0,041*
1,47E-05	1,48E-05	6,788	2,763	7,696	-2,994	-2,808	-2,895	-2,794
1,55E-06	2,39E-03	6,212	2,635	5,739	0,271	0,266	-0,036	0,318
1,09E-08	7,14E-03	5,352	2,420	6,521	2,057	0,600	0,891	2,141
3,80E-02	3,94E-02	5,348	2,419	2,138	*-0,248*	*1,103*	*-0,266*	*-0,249*
3,54E-08	3,33E-02	4,857	2,280	9,436	1,654	1,455	2,844	1,827
7,07E-09	1,64E-02	4,827	2,271	5,936	1,318	2,745	2,574	0,959
1,60E-02	1,32E-02	4,656	2,219	4,575	-0,444	*-1,375*	*-1,526*	*-2,263*
6,63E-06	1,55E-05	4,579	2,195	9,061	-2,537	-2,325	-2,336	-2,193
3,85E-04	3,43E-04	4,380	2,131	11,879	-2,097	-1,652	-1,966	-2,189
1,53E-04	1,04E-04	4,356	2,123	10,940	-1,999	-1,615	-1,900	-2,117
1,18E-03	1,09E-03	4,272	2,095	4,772	*-1,601*	-0,721	-0,853	-0,718
3,84E-05	5,44E-05	4,249	2,087	5,115	*-3,224*	*-2,341*	*-3,237*	*-2,184*
4,93E-05	5,97E-04	4,187	2,066	6,362	-0,076	-0,285	0,275	0,321
5,13E-05	1,46E-04	4,155	2,055	12,326	-2,463	-2,166	-2,369	-2,242
1,34E-03	2,02E-04	4,056	2,020	12,761	-1,437	-1,177	-1,433	-1,673
1,94E-14	1,37E-06	4,053	2,019	14,047	2,644	1,617	2,475	2,367
3,41E-11	5,07E-04	3,840	1,941	9,697	1,345	1,539	2,148	1,650
2,83E-10	3,08E-03	3,558	1,831	11,483	1,607	1,342	2,012	1,514
1,17E-04	1,50E-04	3,543	1,825	7,105	-1,830	-1,678	-2,401	-2,067
4,93E-05	9,62E-05	3,465	1,793	11,146	-0,421	-0,084	-0,239	-0,326
1,04E-08	3,13E-02	3,425	1,776	7,989	1,482	1,615	1,944	1,574
2,42E-03	1,47E-03	3,385	1,759	3,974	*-0,942*	*-2,188*	*-1,052*	*-1,431*
1,03E-06	2,29E-03	3,340	1,740	3,951	0,262	-0,208	0,239	1,469
1,09E-05	2,52E-04	3,317	1,730	9,819	-2,287	-2,450	-2,532	-2,478
1,58E-05	5,54E-04	3,276	1,712	7,250	-3,121	-2,421	-2,664	-2,958
9,46E-05	1,32E-04	3,251	1,701	8,579	-1,749	-1,434	-1,812	-1,868
4,85E-08	3,32E-05	3,240	1,696	7,847	-0,029	0,068	0,163	0,029
2,02E-07	4,63E-02	3,184	1,671	8,565	1,359	1,864	1,294	0,694
6,34E-09	4,23E-02	3,180	1,669	8,696	2,370	1,584	2,512	0,951
6,22E-10	1,28E-02	3,173	1,666	10,629	1,808	1,686	2,282	1,798
1,15E-03	2,18E-02	3,147	1,654	8,944	-0,401	-1,145	-1,150	-1,302
2,13E-07	4,70E-02	3,091	1,628	6,601	1,137	0,832	1,381	0,930
1,10E-02	2,36E-03	3,078	1,622	5,332	-0,233	-0,935	-0,645	-0,948
2,78E-04	5,40E-04	3,046	1,607	6,216	-1,764	-1,720	-1,736	-2,388
3,62E-04	6,98E-04	3,036	1,602	8,032	-0,126	-0,059	-0,301	-0,338

1,57E-04	**1,65E-04**	**3,031**	1,600	12,619	-1,579	-1,235	-1,541	-1,606
2,84E-03	**3,41E-02**	**2,992**	1,581	3,200	*-1,353*	0,672	*-0,053*	*-0,321*
3,60E-04	**2,41E-02**	**2,986**	1,578	6,002	0,380	0,322	0,435	0,132
4,98E-08	**1,84E-02**	**2,977**	1,574	6,555	1,105	0,779	1,369	0,998
1,07E-03	**1,58E-04**	**2,971**	1,571	5,598	-0,706	-0,442	-0,777	-0,549
1,18E-09	**3,33E-02**	**2,924**	1,548	8,699	1,668	1,145	2,032	1,818
4,05E-05	**2,40E-03**	**2,916**	1,544	4,859	*-2,978*	*-1,555*	*-2,034*	*-2,396*
2,52E-11	**7,06E-03**	**2,807**	1,489	10,602	2,233	1,163	2,355	1,604
1,57E-02	**2,43E-02**	**2,738**	1,453	4,859	*-2,027*	-1,032	*-3,061*	*-1,306*
1,63E-09	**4,97E-03**	**2,706**	1,436	9,445	1,843	1,167	1,892	1,830
5,25E-05	**1,45E-04**	**2,668**	1,416	10,229	-1,735	-1,390	-1,637	-1,997
7,06E-03	**4,75E-02**	**2,667**	1,415	2,386	*0,388*	*-0,557*	*-0,559*	1,572
1,20E-08	**7,17E-03**	**2,663**	1,413	5,257	1,937	1,419	2,663	1,904
1,75E-11	**2,71E-03**	**2,661**	1,412	5,111	2,524	1,982	2,057	1,776
2,81E-10	**1,50E-02**	**2,617**	1,388	5,732	*-2,449*	*-3,097*	*-3,087*	*-3,786*
1,59E-06	**1,98E-02**	**2,617**	1,388	5,301	-0,075	0,010	-0,055	-0,010
1,11E-05	**4,90E-04**	**2,530**	1,339	12,369	-2,025	-1,757	-2,036	-2,208
2,19E-05	**4,60E-02**	**2,526**	1,337	5,021	0,182	0,276	0,123	0,151
3,04E-04	**1,27E-04**	**2,521**	1,334	12,441	-1,269	-1,040	-1,186	-1,356
8,28E-12	**1,99E-04**	**2,497**	1,320	9,090	1,975	1,343	2,008	2,194
1,00E-11	**2,74E-03**	**2,474**	1,307	10,069	2,247	1,337	2,467	1,597
8,51E-06	**1,68E-04**	**2,367**	1,243	9,031	-1,654	-1,842	-1,994	-1,702
1,12E-03	**1,63E-02**	**2,312**	1,209	3,914	*-2,151*	*-0,634*	*-1,360*	-0,204
1,94E-04	**8,81E-03**	**2,307**	1,206	3,908	*-0,171*	*-0,819*	*-1,091*	-0,054
1,35E-03	**6,00E-03**	**2,286**	1,193	9,511	-0,978	-0,860	-0,947	-0,889
1,26E-10	**2,60E-02**	**2,247**	1,168	11,099	2,184	1,467	2,889	1,880
6,91E-10	**1,46E-02**	**2,215**	1,147	6,361	*-4,350*	*-2,982*	-1,668	*-3,607*
4,43E-11	**1,52E-02**	**2,181**	1,125	11,259	2,071	1,148	2,661	1,842
1,46E-08	**6,01E-05**	**2,172**	1,119	7,342	0,032	-0,032	-0,176	-0,429
7,26E-10	**4,92E-02**	**2,169**	1,117	9,689	1,768	1,642	2,070	1,462
1,56E-03	**1,90E-02**	**2,169**	1,117	4,098	*-0,202*	*-1,672*	*-0,525*	*-2,217*
4,06E-06	**8,71E-03**	**2,169**	1,117	13,958	0,214	-0,165	-0,093	-0,237
2,93E-05	**3,05E-04**	**2,139**	1,097	12,494	-1,524	-1,345	-1,465	-1,570
3,26E-07	**3,72E-02**	**2,130**	1,091	9,126	0,154	-0,088	0,270	0,088
5,04E-06	**4,02E-02**	**2,126**	1,088	6,723	-0,851	-1,387	-1,173	-2,056
8,52E-08	**4,84E-02**	**2,094**	1,066	9,802	0,552	0,047	0,130	0,074
2,85E-05	**3,95E-04**	**2,091**	1,064	12,167	-1,553	-1,425	-1,498	-1,711
8,33E-05	**4,50E-03**	**2,075**	1,053	5,696	-0,282	-0,409	-0,562	-0,442

wt_non-stim_21	CD4creGARPfl-fl_non-stim_22	CD4creGARPfl-fl_non-stim_23	CD4creGARPfl-fl_non-stim_8	CD4creGARPfl-fl_non-stim_9	CD4creGARPfl-fl_non-stim_10	wt_stim_11	wt_stim_12	wt_stim_13	wt_stim_14
1,034	5,869	1,919	4,273	4,520	5,300	-1,539	-1,775	-0,780	-1,234
0,904	5,478	1,834	4,070	3,937	4,968	-1,483	-1,926	-1,076	-1,234
0,638	5,421	1,686	3,882	3,811	4,758	-1,608	-2,355	-1,137	-1,565
1,661	5,917	2,399	4,857	4,597	5,558	*-0,597*	*-1,047*	*-2,317*	*-0,711*
0,557	5,249	1,291	3,502	3,619	4,794	*-1,500*	*-0,010*	*-0,976*	*-0,016*
0,920	5,375	1,588	3,672	3,323	4,620	*-2,143*	*-2,152*	*-2,147*	*-1,664*
1,448	5,430	2,168	3,539	4,192	4,816	-0,917	-0,983	-0,833	-0,736
1,678	4,606	1,969	3,766	3,490	4,401	-2,078	-2,313	-1,745	-2,350
2,669	4,774	5,291	5,818	6,266	5,838	-5,493	-5,571	-5,472	-5,730
-1,099	3,304	-0,520	1,185	1,975	2,720	-0,047	0,012	0,117	0,292
0,010	4,466	*-0,020*	1,900	2,990	3,656	*-0,099*	*-0,074*	*0,002*	*-0,038*
-1,871	1,423	-1,449	-0,353	-0,045	0,983	0,074	0,107	0,198	-0,019
1,752	3,543	1,491	2,906	2,590	3,309	-2,071	-1,849	*-2,134*	*-3,884*
0,328	3,645	3,311	2,523	3,432	2,245	*-2,852*	*-4,082*	*-3,357*	*-4,414*
0,351	2,825	*-0,255*	*0,801*	2,171	2,922	*-0,238*	*0,146*	*-0,239*	*0,745*
0,890	2,156	3,934	3,344	5,025	4,313	-4,688	-4,925	-4,834	-4,275
1,893	2,544	4,165	4,680	4,288	2,705	*-4,167*	*-3,386*	*-4,169*	-2,157
0,623	1,601	-0,138	0,191	1,879	0,843	-0,432	-0,117	0,117	-0,803
-1,942	1,098	-1,400	-0,130	-0,376	0,499	-0,019	0,019	0,089	0,053
-0,904	1,431	-1,027	-0,419	0,166	0,746	0,004	0,011	-0,054	0,007
-0,875	1,352	-0,953	0,070	0,223	0,965	-0,166	-0,070	-0,218	-0,290
-0,407	1,851	0,190	1,375	1,267	1,663	-0,050	-0,714	-0,433	-0,418
-1,846	1,534	-1,101	-0,282	-0,254	1,065	0,259	-0,243	0,466	0,314
0,872	2,564	0,517	2,341	1,812	2,552	-0,667	-0,911	-0,095	-0,816
-1,715	1,035	-1,663	-0,339	-0,187	0,720	0,081	0,030	-0,014	0,072
-0,004	1,904	0,004	0,235	0,588	1,216	-0,428	-0,289	-0,363	-0,368
2,430	4,036	4,285	4,449	4,594	4,503	-5,922	-5,647	-5,419	-5,287
1,314	2,704	3,481	3,532	3,860	3,470	-3,898	-3,622	-3,411	-4,278
1,198	2,619	3,058	3,345	3,777	3,843	-3,923	-3,943	-3,733	-4,048
-0,696	1,274	-0,706	-0,413	-0,005	0,538	-0,028	-0,113	0,005	0,029
0,788	2,750	0,940	1,214	1,553	2,257	-0,374	-0,270	-0,418	-0,598
1,237	2,012	3,292	3,435	3,968	3,350	-2,939	-3,497	-3,325	-4,284
-1,259	1,062	*-1,002*	0,501	0,290	0,987	-0,040	0,241	*-0,280*	*-0,534*
0,531	2,002	1,971	2,096	2,009	1,795	*-0,901*	*-0,576*	*-2,062*	*-2,062*
-1,402	0,752	-1,363	-1,014	-0,720	0,082	0,023	0,042	-0,023	-0,036
-2,009	0,888	-2,031	-0,952	-0,965	0,029	0,288	0,398	0,312	0,442
-0,957	1,338	-0,836	-0,105	-0,047	0,799	-0,014	0,268	0,138	0,003
0,961	1,925	1,478	1,765	1,419	1,837	-0,913	-1,227	-1,049	-1,256
0,354	2,964	1,850	3,756	2,859	3,030	-3,395	-3,356	-3,499	-3,169
1,124	2,582	2,986	3,304	3,903	3,253	-3,112	-3,819	-3,368	-5,135
1,395	2,375	3,464	3,472	4,076	3,420	-3,737	-3,716	-3,232	-3,893
0,198	0,011	0,674	0,297	0,509	1,431	-0,883	-1,777	-1,334	-2,100
0,749	1,851	2,559	3,108	3,381	2,017	*-4,704*	*-3,734*	-2,423	-2,222
-0,381	1,798	-0,561	0,978	0,937	1,529	0,036	0,168	0,298	-0,360
-1,041	1,383	-1,029	-0,370	-0,129	0,799	0,415	0,525	0,129	0,454
0,972	2,863	0,865	0,997	1,476	2,224	-0,290	-0,180	-0,378	-0,460



-0,589	1,091	-0,561	-0,165	0,059	0,721	-0,005	0,005	-0,068	-0,086
1,493	2,064	1,403	1,661	1,214	1,528	*0,053*	*-1,361*	*-1,378*	0,387
0,191	2,693	-0,132	1,361	1,900	2,635	-1,325	-0,527	-1,341	-0,901
0,790	1,855	2,573	3,293	3,233	1,943	*-4,708*	*-2,987*	*-3,381*	-2,015
-0,674	1,899	-0,270	0,897	0,800	1,843	-0,108	0,007	0,050	0,105
1,723	1,627	2,358	4,006	3,322	3,272	-2,993	-3,457	-2,961	-3,839
-1,259	0,495	-0,838	-0,587	-0,489	-0,272	0,747	1,044	0,730	0,780
1,306	2,662	3,093	2,935	3,157	3,314	-3,771	-4,307	-3,518	-4,867
-0,761	1,378	*-1,774*	0,147	-0,472	1,020	-0,035	0,035	0,425	0,705
0,853	4,601	2,682	3,380	3,266	3,175	-3,498	-2,870	-4,622	-4,601
-0,840	0,936	-0,741	-0,427	-0,222	0,401	-0,007	0,092	0,007	-0,060
0,103	*0,051*	1,517	*1,285*	1,622	2,561	*-0,362*	*-0,564*	*-0,555*	*-0,558*
1,153	2,724	3,216	3,317	5,033	4,895	*-3,404*	*-3,419*	*-2,174*	*-3,416*
2,274	2,979	4,208	3,468	3,583	3,253	*-3,198*	*-2,415*	*-2,581*	*-1,776*
-2,342	-2,156	-1,215	-1,700	*-2,549*	-1,646	1,890	2,326	2,109	2,759
1,178	1,493	1,135	1,070	1,377	1,795	-1,877	-2,223	-1,662	-2,274
-1,178	0,415	-1,251	-0,741	-0,686	0,092	0,009	0,017	-0,009	-0,011
1,664	2,024	2,118	1,219	1,307	1,519	-0,847	-0,746	*-1,086*	-1,262
-0,454	1,147	-0,431	0,020	0,148	0,766	-0,121	-0,020	-0,107	-0,213
1,167	2,673	3,296	3,703	4,046	3,229	-3,297	-3,423	-3,380	-3,701
1,326	2,382	2,903	2,803	3,416	3,604	-3,185	-3,584	-3,159	-3,930
-1,213	0,358	-1,279	-0,577	-0,460	0,102	0,150	0,144	0,062	0,053
-1,465	0,288	-0,152	*-0,750*	-0,061	-0,266	0,255	0,061	0,449	0,387
-0,035	1,886	0,035	0,191	1,035	1,513	*-0,765*	*-0,617*	*-1,976*	*-1,401*
0,304	0,911	0,304	-0,020	0,024	0,705	-0,559	-0,429	-0,381	-1,053
1,631	3,048	2,895	2,697	3,625	3,859	-3,602	-3,734	-3,230	-3,612
-2,807	-1,834	-1,684	-2,085	-2,053	-1,642	1,732	2,103	1,987	2,479
1,371	2,685	2,966	2,863	3,084	3,499	-3,750	-4,023	-3,357	-4,203
0,505	0,983	1,250	1,087	0,993	1,476	-1,452	-1,707	-1,407	-2,022
1,372	2,605	2,584	2,759	3,422	2,923	-4,075	-3,135	-3,353	-3,420
-0,146	0,565	0,891	0,592	0,724	0,062	*-1,417*	*-0,650*	-0,062	*-1,646*
0,469	0,547	1,034	0,769	1,023	1,412	-1,066	-1,526	-1,379	-1,869
-0,822	0,445	-0,927	-0,368	-0,436	0,305	0,052	0,016	-0,011	-0,018
1,476	1,397	1,856	1,245	1,192	0,971	-1,957	-2,269	-1,699	-2,408
-1,136	0,087	0,240	-0,656	-0,940	-0,086	0,086	0,334	0,293	-0,270
0,906	0,572	1,124	1,196	1,494	1,953	-2,315	-3,083	-2,604	-3,093
-0,803	0,384	-1,008	-0,433	-0,448	0,227	0,002	0,001	-0,089	-0,001
-0,369	0,873	1,132	0,644	0,563	0,264	-0,370	-0,481	-0,264	-0,556

wt_stim_15	CD4creGARPfl-fl_stim_24	CD4creGARPfl-fl_stim_25	CD4creGARPfl-fl_stim_18	CD4creGARPfl-fl_stim_19	CD4creGARPfl-fl_stim_20	Refseq	GeneID
-0,053	0,178	-1,172	0,053	-0,175	-0,476	NM_011527	21349
-1,224	1,003	0,093	-0,093	-0,947	0,518	NM_009396	21928
-1,901	1,034	0,079	-0,252	-0,931	0,570	NM_009396	21928
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-1,110	0,941	*0,010*	1,990	*-1,011*	*-0,045*	NM_001170788	270091
-1,219	0,597	-0,063	*-0,146*	*-2,134*	*-1,125*	NM_007652	12509
-0,886	-0,490	-0,954	-0,748	-1,037	-0,454	NM_009846	12484
-1,139	-1,061	-1,366	-0,504	-1,245	-0,257	NM_016707	14025
-7,360	-1,568	-1,831	-2,058	-2,949	-2,655		16061
0,645	-0,255	-0,311	0,190	-0,012	0,050	NM_018827	12931
0,173	*-0,089*	*-0,060*	*0,028*	*-0,037*	*-0,016*	NM_181858	333883
0,235	-0,293	0,019	0,106	0,325	0,138	NM_011799	23834
-1,622	-0,971	*-2,158*	-0,398	-1,188	0,036	NM_001242934	14025
-3,461	-0,328	-1,277	*-2,753*	-2,004	-1,512		
-0,243	*-0,246*	*-0,146*	*0,921*	*-0,258*	*0,396*	NM_183294	71091
-3,809	-4,393	-1,253	-3,103	-0,890	-0,955		
-4,171	-1,337	-1,927	-1,862	*-2,527*	-0,959		
-1,079	1,425	1,576	-0,272	0,451	0,579	NM_010743	17082
-0,258	0,301	0,511	0,074	0,366	0,160	NM_145392	213539
0,690	-0,046	-0,004	0,180	0,324	0,130	NM_009828	12428
0,521	0,369	0,274	0,222	0,443	0,432	NM_172301	268697
-2,939	0,505	0,520	0,263	0,483	0,050	NM_016693	53608
1,303	-0,015	0,140	0,375	0,086	0,015	NM_031396	83674
-0,017	0,204	-0,458	0,017	-0,231	-0,065	NM_028238	72433
0,489	-0,176	0,014	0,437	0,370	0,421	NM_007633	12447
0,458	-0,104	0,024	0,023	0,068	0,190	NM_001081117	17345
-5,894	-1,650	-1,980	-1,617	-2,899	-2,458	XM_001472091	
-5,212	-1,314	-2,296	-3,040	-1,944	-1,653		
-5,808	-1,198	-2,637	-3,200	-2,271	-1,435		
0,151	0,291	0,325	0,231	0,416	0,233	NM_009860	12532
0,135	0,035	-0,015	-0,308	0,059	0,015	NM_007630	12442
-5,994	-1,237	-2,117	-3,417	-1,662	-1,510		16061
1,090	0,020	-0,020	0,510	0,712	0,260	NM_001033285	226751
-2,059	0,208	*-1,101*	*-0,894*	*-0,622*	*-0,497*	NM_133871	99899
0,592	0,247	0,215	0,350	0,356	0,439	NM_007634	12449
-0,175	0,108	0,524	-0,029	0,714	0,464	NM_007633	12447
0,029	0,538	0,543	-0,003	0,626	0,433	NM_172301	268697
-1,262	0,195	-0,103	-0,876	-0,869	-0,701	NM_001122733	16590
-6,528	-0,354	-2,295	-2,828	-1,515	-1,254		
-4,127	-2,044	-1,977	-3,782	-0,951	-1,221		
-5,938	-1,395	-2,121	-2,865	-1,665	-1,516		
-0,380	0,495	0,165	-0,011	0,613	1,809	NM_009844	12478
-3,321	-0,749	-2,246	*-3,728*	-0,934	-2,147		
0,714	0,360	-0,036	-0,060	0,114	-0,788	NM_001033285	226751
-0,247	0,447	0,467	-0,168	0,447	0,370	NM_016681	50883
0,041	0,326	-0,041	-0,233	0,188	0,270	NM_028222	72391

0,560	0,168	0,260	0,286	0,414	0,481	NM_026560	52276
-1,360	*-0,626*	*-0,675*	*-0,139*	*0,206*	*-1,344*	NM_139299	218624
-0,373	0,416	-0,595	-1,074	-0,786	-0,507	NM_001142959	229672
-2,439	-0,779	-2,078	*-2,746*	-1,239	-1,612		
-0,103	0,258	0,133	-0,011	0,204	-0,007	NM_001085383	71790
-4,742	-1,145	-1,943	-1,712	-1,312	-1,210		
-1,022	0,846	1,063	0,272	0,990	0,623	NM_178589	94185
-5,181	-1,501	-1,994	-2,609	-1,827	-1,163		
0,539	0,466	0,461	-0,522	0,476	-0,227	NM_001033285	226751
-5,720	-0,853	-1,889	-2,309	-1,432	-1,618		
0,069	0,159	0,317	0,073	0,475	0,393	NM_026560	52276
-0,551	*-0,229*	*-0,463*	*0,232*	*-0,051*	*0,668*	NM_172050	217306
-3,402	-1,166	*-2,458*	*-3,416*	-1,153	-1,260		
-3,220	*-2,363*	*-3,282*	*-3,236*	*-2,027*	*-3,296*	NM_007721	12777
1,215	2,091	2,267	1,547	2,126	1,933	NM_009452	22164
-2,545	1,102	0,279	-0,636	-0,466	1,180	NM_001077189	14130
0,645	0,074	0,178	0,343	0,516	0,513	NM_026410	67849
-2,623	-0,123	-0,630	*-1,255*	*-1,795*	-0,843	NM_009914	12771
0,212	0,332	0,338	0,024	0,229	0,238	NM_023223	107995
-4,463	-1,286	-1,621	-2,185	-1,167	-1,456		
-3,513	-1,664	-2,216	-2,311	-1,527	-1,326		
0,036	-0,036	0,189	-0,107	0,242	0,247	NM_025415	66197
0,301	0,067	0,363	*-0,152*	0,423	0,431	NM_013473	11752
-1,934	0,721	0,638	0,644	0,198	0,622	NM_007643	12491
-0,616	0,994	0,865	0,020	0,130	0,455	NM_001025602	17082
-5,271	-1,467	-2,356	-2,439	-1,499	-1,475		
1,642	2,663	2,222	2,028	1,873	2,193	NM_001111099	12575
-5,120	-1,572	-2,330	-2,549	-1,987	-1,148		
-1,495	0,146	0,129	-0,614	-0,367	0,152	NM_022021	63955
-5,724	-1,372	-2,095	-3,140	-1,894	-1,869		
-2,218	1,571	0,634	0,125	0,491	1,314		15951
-0,818	0,446	0,064	-0,149	-0,064	1,060	NM_001042605	16149
0,283	0,011	0,140	0,153	0,311	0,383	NM_016904	54124
-2,686	0,378	-0,287	-1,088	-0,881	-0,806	NM_010730	16952
-0,519	3,099	2,177	0,986	1,404	1,954	NM_013532	14728
-1,984	-1,010	-1,520	-1,550	-1,440	-0,047		12518
0,214	0,009	0,207	0,166	0,313	0,294	NM_016904	54124
-1,746	1,275	1,776	0,575	0,701	0,692	NM_008362	16177

SeqID	ProbeID	GeneName
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2272460	A_55_P1960148	AK007826
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2309975	A_51_P407657	ENSMUST0000010
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2276337	A_55_P1998011	Klra23
2266123	A_55_P2038987	Gas7
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2309508	A_66_P124806	Tlr4
2286312	A_55_P2097279	Lilrb3
2282902	A_55_P2186972	ENSMUST0000010
2291515	A_52_P42245	Klrb1a
2274816	A_55_P2011950	LOC435333
2269728	A_52_P15405	Blk
2287696	A_55_P2119377	Klri2
2264476	A_55_P2103948	ENSMUST0000010
2302088	A_55_P2068595	LOC100047095
2261784	A_52_P614207	LOC100047222
2281798	A_55_P2066578	Ifi204
2260279	A_55_P2025586	ENSMUST0000010
2276840	A_52_P408757	Fcgr3
2263287	A_51_P322640	Ccl24
2306096	A_51_P375146	Cd36
2266536	A_55_P2058023	ENSMUST0000010
2264295	A_55_P2187067	ENSMUST0000010
2262142	A_52_P63973	ENSMUST0000010
2287115	A_55_P2027731	Il1rl1
2291370	A_55_P2004526	Klra8
2258950	A_66_P112234	LOC676175
2285560	A_55_P2058040	ENSMUST0000010
2297182	A_66_P133367	ENSMUST0000010
2276960	A_51_P245989	Ccr2
2301307	A_55_P1997756	Il6
2265415	A_52_P186262	ENSMUST0000010
2308625	A_55_P2051270	Tctex1d1
2289471	A_55_P1979364	ENSMUST0000010
2311225	A_55_P2186978	ENSMUST0000010
2286864	A_55_P2062802	ENSMUST0000010
2306362	A_55_P2130497	ENSMUST0000010
2279875	A_55_P2003915	ENSMUST0000010
2281868	A_51_P513776	LOC640979
2260889	A_55_P1957459	Lilrb4
2257552	A_55_P1962400	Il1rn
2300373	A_55_P2276221	Gm5222
2290157	A_51_P288295	LOC677484
2257556	A_55_P2155560	LOC630565
2295024	A_55_P2060897	ENSMUST0000010
2308773	A_51_P405638	LOC100045791
2289484	A_52_P374653	ENSMUST0000010
2265453	A_51_P500882	Ncr1
2273411	A_66_P116173	Il23r

2295994	A_51_P241457	Lilrb4
2299041	A_52_P630429	ENSMUST0000010
2302866	A_55_P1974577	Nfam1
2278427	A_66_P109731	ENSMUST0000010
2270408	A_52_P546162	ENSMUST0000010
2259200	A_52_P30641	ENSMUST0000010
2309991	A_55_P2140348	Igh-VJ558
2275786	A_55_P2008437	Cdkn2a
2288305	A_55_P2079079	Cd19
2289185	A_55_P2117342	ENSMUST0000010
2286378	A_52_P578436	ENSMUST0000010
2285307	A_55_P1988183	Cdkn2b
2301163	A_55_P2003911	ENSMUST0000010
2295039	A_55_P2026258	ENSMUST0000010
2271312	A_52_P15966	ENSMUST0000010
2273241	A_55_P2199202	Il22
2298904	A_51_P150710	Igj
2307634	A_55_P2167347	ENSMUST0000010
2297923	A_55_P2180839	Il13
2291437	A_66_P140474	LOC100047316
2311645	A_55_P2094104	LOC100047070
2305911	A_55_P1987406	ENSMUST0000010
2287230	A_66_P113466	ENSMUST0000010
2270417	A_55_P2057283	ENSMUST0000010
2295017	A_51_P461665	Cxcl9
2258981	A_66_P127412	ENSMUST0000010
2260024	A_55_P2029319	Cd70
2285366	A_55_P1978994	ENSMUST0000010
2283726	A_52_P232813	Cxcl3
2267745	A_55_P2004541	Klra7
2279870	A_55_P2098697	Tnfaip2
2303775	A_55_P2036693	Cd40
2261055	A_55_P2030299	LOC544904
2272642	A_55_P2004527	Klra8
2302806	A_55_P2134277	Igh-2
2264069	A_55_P2145224	ENSMUST0000010
2272896	A_55_P1974014	LOC100046496
2307552	A_51_P117581	Cables1
2301716	A_55_P2087622	Il4i1
2261533	A_51_P114462	Ccl17
2278204	A_55_P1985985	Il3
2270460	A_51_P185660	Ccl9
2261676	A_51_P520966	Icosl
2270800	A_51_P242930	Lat2
2282732	A_55_P1971174	Cd1d2
2271993	A_51_P390937	LOC675735
2279139	A_55_P2065510	ENSMUST0000010
2298039	A_51_P470079	Il1r2
2268109	A_55_P2214531	Il9r
2303110	A_52_P68893	Ifng
2260776	A_66_P134171	ENSMUST0000010
2301510	A_51_P500090	Klra7
2305866	A_51_P333274	Gzmb
2309745	A_52_P638459	Ccl5
2310147	A_51_P284608	Cd74
2293209	A_51_P327796	Itgb5

2276850	A_51_P104768	Gm16697
2264647	A_55_P1959421	ENSMUST0000010
2297153	A_55_P2016462	Cxcl10
2272049	A_51_P109570	Klrb1b
2291885	A_55_P1977038	Cxcl9
2271948	A_55_P1964325	Klrb1b
2290350	A_51_P205334	Tnfrsf8
2261417	A_55_P1999033	LOC100046275
2277497	A_51_P405476	Fcer1g
2311424	A_55_P2067620	ENSMUST0000010
2288611	A_51_P196925	Cx3cl1
2262297	A_66_P120987	Cd79a
2260255	A_52_P99888	Cxcl16
2275538	A_51_P346668	Irf5
2286550	A_55_P1975560	Ifi204
2305609	A_51_P342652	Cd79b
2278627	A_55_P2032718	Klra9
2282597	A_55_P2132532	ENSMUST0000010
2294364	A_55_P2009375	Cdk18
2296320	A_55_P2004652	Klrc1
2288151	A_55_P2081164	Cd300lf
2294087	A_55_P2117614	Tnfrsf13c
2275179	A_51_P150302	Crtam
2279835	A_51_P271503	Il1r1
2264890	A_55_P2129047	Tlr7
2306283	A_55_P2137496	LOC100047815
2296282	A_55_P1970755	Hdac9
2306440	A_55_P2106121	Il21
2260286	A_55_P2014427	Il17re
2301794	A_55_P1992592	Il5ra
2309812	A_51_P234956	Xcl1
2305468	A_55_P2132533	ENSMUST0000010
2284569	A_52_P517098	Il18rap
2298628	A_55_P2157829	ENSMUST0000010
2299483	A_55_P2100475	Gas2l3
2302450	A_55_P2063755	Naip6
2289283	A_51_P378298	Faim3
2307398	A_55_P1984168	Casp4
2262852	A_55_P2027737	Il1rl1
2308900	A_51_P237865	Il4

Description	ANOVA p-value
Mus musculus chemokine (C-C motif) ligand 6 (Ccl6), mRNA [NM_009139]	**3,92E-04**
Mus musculus complement factor B (Cfb), transcript variant 1, mRNA [NM_00819	**3,12E-04**
PREDICTED: Mus musculus immunoglobulin heavy chain (J558 family) (Igh-VJ55	**1,11E-16**
PREDICTED: Mus musculus immunoglobulin heavy chain (J558 family) (Igh-VJ55	**4,37E-17**
Mus musculus immunoglobulin heavy chain complex, mRNA (cDNA clone MGC:3	**1,89E-14**
immunoglobulin kappa chain variable 19-93 [Source:MGI Symbol;Acc:MGI:10761	**3,95E-09**
immunoglobulin heavy variable V12-3 [Source:MGI Symbol;Acc:MGI:3646760] [E	**6,44E-04**
Mus musculus granzyme A (Gzma), mRNA [NM_010370]	**6,70E-04**
Mus musculus killer cell lectin-like receptor subfamily A, member 23 (Klra23), mRN	**1,05E-03**
Mus musculus growth arrest specific 7 (Gas7), transcript variant 2, mRNA [NM_00	**2,27E-06**
immunoglobulin kappa variable 10-94 [Source:MGI Symbol;Acc:MGI:3646140] [E	**7,44E-08**
Mus musculus killer cell lectin-like receptor subfamily B member 1C (Klrb1c), trans	**2,72E-12**
immunoglobulin kappa variable 3-9 [Source:MGI Symbol;Acc:MGI:1330856] [EN	**9,43E-07**
immunoglobulin kappa variable 3-12 [Source:MGI Symbol;Acc:MGI:1330815] [EN	**3,96E-08**
immunoglobulin kappa variable 6-15 [Source:MGI Symbol;Acc:MGI:1330831] [EN	**1,17E-10**
Mus musculus CD1d2 antigen (Cd1d2), mRNA [NM_007640]	**7,44E-10**
Mus musculus C-type lectin domain family 4, member e (Clec4e), mRNA [NM_019	**1,80E-02**
M.musculus mRNA for C2-Fcgamma fusion protein [X96776]	**2,56E-10**
Mus musculus killer cell lectin-like receptor family E member 1 (Klre1), mRNA [NM_	**1,50E-08**
Mus musculus killer cell lectin-like receptor subfamily K, member 1 (Klrk1), transcri	**1,47E-08**
Mus musculus killer cell lectin-like receptor, subfamily A, member 5 (Klra5), mRNA	**3,56E-03**
M.musculus immunoglobulin VDJ region (A8H). [X80960]	**1,42E-08**
Mus musculus killer cell lectin-like receptor subfamily A, member 23 (Klra23), mRN	**8,35E-03**
immunoglobulin heavy variable V1-54 [Source:MGI Symbol;Acc:MGI:3647133] [E	**4,61E-07**
immunoglobulin kappa variable 3-4 [Source:MGI Symbol;Acc:MGI:1330855] [EN	**4,63E-08**
Mus musculus interleukin 1 beta (Il1b), mRNA [NM_008361]	**2,60E-03**
Mus musculus Fc receptor, IgG, low affinity IIb (Fcgr2b), transcript variant 1, mRN	**2,71E-07**
immunoglobulin kappa chain variable 4-91 [Source:MGI Symbol;Acc:MGI:364227	**1,82E-09**
Mus musculus paired-Ig-like receptor A7 (Pira7), mRNA [NM_011094]	**1,46E-04**
immunoglobulin kappa variable 4-80 [Source:MGI Symbol;Acc:MGI:4439653] [EN	**7,78E-13**
Mus musculus transforming growth factor, beta induced (Tgfbi), mRNA [NM_0093	**4,72E-04**
Mus musculus interleukin 5 (Il5), mRNA [NM_010558]	**1,71E-08**
Mus musculus killer cell lectin-like receptor, subfamily A, member 4 (Klra4), transc	**1,00E-03**
Mus musculus granzyme C (Gzmc), mRNA [NM_010371]	**7,89E-06**
immunoglobulin kappa variable 1-135 [Source:MGI Symbol;Acc:MGI:3819952] [E	**1,99E-08**
immunoglobulin kappa variable 1-133 [Source:MGI Symbol;Acc:MGI:3648380] [E	**1,33E-11**
Mus musculus immunoresponsive gene 1 (Irg1), mRNA [NM_008392]	**1,27E-09**
Mus musculus integrin alpha X (Itgax), mRNA [NM_021334]	**8,42E-05**
Mus musculus chemokine (C-C motif) ligand 19 (Ccl19), mRNA [NM_011888]	**5,22E-03**
immunoglobulin heavy variable V1-23 [Source:MGI Symbol;Acc:MGI:3815050] [E	**6,33E-10**
immunoglobulin kappa variable 3-4 [Source:MGI Symbol;Acc:MGI:1330855] [EN	**2,24E-05**
Mus musculus interleukin 9 (Il9), mRNA [NM_008373]	**4,74E-12**
Mus musculus G1 to S phase transition 2 (Gspt2), mRNA [NM_008179]	**7,38E-03**
immunoglobulin kappa variable 1-132 [Source:MGI Symbol;Acc:MGI:3648800] [E	**8,05E-12**
Mus musculus leucine-rich repeat kinase 1 (Lrrk1), mRNA [NM_146191]	**1,38E-04**
immunoglobulin heavy variable V8-5 [Source:MGI Symbol;Acc:MGI:3645478] [EN	**8,29E-08**

immunoglobulin kappa chain variable 1-122 [Source:MGI Symbol;Acc:MGI:44397	**2,24E-11**
Mus musculus complement component 1, r subcomponent A (C1ra), mRNA [NM_	**2,64E-05**
Mus musculus lymphotoxin B receptor (Ltbr), mRNA [NM_010736]	**7,13E-05**
immunoglobulin kappa variable 3-10 [Source:MGI Symbol;Acc:MGI:1330821] [EN	**1,95E-06**
immunoglobulin kappa variable 1-110 [Source:MGI Symbol;Acc:MGI:4439558] [E	**1,46E-10**
immunoglobulin kappa variable 6-32 [Source:MGI Symbol;Acc:MGI:3641634] [EN	**7,97E-11**
Mus musculus cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (Cdkn2b	**5,27E-03**
PREDICTED: Mus musculus similar to immunoglobulin mu-chain-like (LOC100505	**4,84E-11**
immunoglobulin kappa chain variable 8-30 [Source:MGI Symbol;Acc:MGI:364225	**3,68E-11**
immunoglobulin kappa variable 1-131 [Source:MGI Symbol;Acc:MGI:3645551] [E	**1,90E-11**
Mus musculus Fc receptor-like A (Fcrla), transcript variant 2, mRNA [NM_145141]	**3,68E-08**
immunoglobulin kappa variable 4-63 [Source:MGI Symbol;Acc:MGI:3645235] [EN	**5,78E-12**
immunoglobulin heavy variable V1-42 [Source:MGI Symbol;Acc:MGI:3704123] [E	**4,88E-09**
Mus musculus toll-like receptor 4 (Tlr4), mRNA [NM_021297]	**3,71E-03**
Mus musculus leukocyte immunoglobulin-like receptor, subfamily B (with TM and	**5,65E-04**
Mus musculus immunoglobulin kappa light chain, variable region mRNA, clone B	**2,07E-10**
Mus musculus killer cell lectin-like receptor subfamily B member 1A (Klrb1a), trans	**1,21E-10**
immunoglobulin heavy variable 1-85 [Source:MGI Symbol;Acc:MGI:3645723] [EN	**3,78E-11**
Mus musculus B lymphoid kinase (Blk), mRNA [NM_007549]	**8,13E-07**
Mus musculus killer cell lectin-like receptor family I member 2 (Klri2), mRNA [NM_1	**3,38E-05**
immunoglobulin kappa variable 4-53 [Source:MGI Symbol;Acc:MGI:2686266] [EN	**1,21E-11**
Mus musculus predicted gene, 18756 (Gm18756), transcript variant 2, non-codin	**1,39E-02**
immunoglobulin kappa variable 3-7 [Source:MGI Symbol;Acc:MGI:1330852] [EN	**1,02E-06**
Mus musculus interferon activated gene 204, mRNA (cDNA clone MGC:18551 IM	**4,84E-04**
immunoglobulin heavy variable V3-8 [Source:MGI Symbol;Acc:MGI:3645298] [EN	**5,42E-09**
Mus musculus Fc receptor, IgG, low affinity III (Fcgr3), mRNA [NM_010188]	**2,89E-04**
Mus musculus chemokine (C-C motif) ligand 24 (Ccl24), mRNA [NM_019577]	**6,50E-14**
Mus musculus CD36 antigen (Cd36), transcript variant 2, mRNA [NM_007643]	**5,05E-05**
immunoglobulin kappa variable 4-57-1 [Source:MGI Symbol;Acc:MGI:2686264] [	**1,55E-12**
immunoglobulin kappa variable 1-117 [Source:MGI Symbol;Acc:MGI:4439721] [E	**2,38E-11**
immunoglobulin kappa chain variable 1-35 [Source:MGI Symbol;Acc:MGI:443961	**3,20E-10**
Mus musculus interleukin 1 receptor-like 1 (Il1rl1), transcript variant 1, mRNA [NM_	**4,30E-03**
Mus musculus killer cell lectin-like receptor, subfamily A, member 8 (Klra8), transc	**1,08E-03**
Mus musculus isolate C5-12 anti-GBM immunoglobulin kappa chain variable regi	**3,80E-07**
immunoglobulin kappa variable 4-73 [Source:MGI Symbol;Acc:MGI:3645825] [EN	**4,44E-12**
immunoglobulin kappa chain variable 8-27 [Source:MGI Symbol;Acc:MGI:443986	**4,21E-08**
Mus musculus chemokine (C-C motif) receptor 2 (Ccr2), mRNA [NM_009915]	**1,01E-11**
Mus musculus interleukin 6 (Il6), mRNA [NM_031168]	**2,48E-05**
immunoglobulin kappa chain variable 6-25 [Source:MGI Symbol;Acc:MGI:443986	**2,00E-13**
Mus musculus Tctex1 domain containing 1 (Tctex1d1), transcript variant 1, mRNA	**1,52E-03**
immunoglobulin heavy variable 1-83 [Source:MGI Symbol;Acc:MGI:3648939] [EN	**4,72E-09**
immunoglobulin kappa variable 4-78 [Source:MGI Symbol;Acc:MGI:3819775] [EN	**5,90E-13**
Mus musculus partial mRNA for immunoglobulin kappa light chain variable region	**2,57E-10**
immunoglobulin heavy variable V1-67 [Source:MGI Symbol;Acc:MGI:3645228] [E	**1,13E-12**
immunoglobulin kappa variable 6-13 [Source:MGI Symbol;Acc:MGI:1330829] [EN	**1,04E-09**
Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE-DB;Acc:IGH	**2,08E-12**
Mus musculus leukocyte immunoglobulin-like receptor, subfamily B, member 4 (Li	**3,42E-06**
Mus musculus interleukin 1 receptor antagonist (Il1rn), transcript variant 2, mRNA	**1,73E-09**
immunoglobulin kappa variable 17-121 [Source:MGI Symbol;Acc:MGI:3647671] [	**7,90E-10**
immunoglobulin heavy variable V1-7 [Source:MGI Symbol;Acc:MGI:3704122] [EN	**3,01E-12**
immunoglobulin heavy variable V1-5 [Source:MGI Symbol;Acc:MGI:3704121] [EN	**2,05E-10**
immunoglobulin kappa constant [Source:MGI Symbol;Acc:MGI:96495] [ENSMUS	**1,24E-12**
immunoglobulin heavy variable V9-3 [Source:MGI Symbol;Acc:MGI:3642720] [EN	**2,79E-08**
immunoglobulin kappa variable 3-10 [Source:MGI Symbol;Acc:MGI:1330821] [EN	**1,89E-05**
Mus musculus natural cytotoxicity triggering receptor 1 (Ncr1), mRNA [NM_01074	**3,16E-05**
Mus musculus interleukin 23 receptor (Il23r), mRNA [NM_144548]	**1,01E-05**

Mus musculus leukocyte immunoglobulin-like receptor, subfamily B, member 4 (Li	**9,57E-07**
immunoglobulin kappa variable 2-116 [Source:MGI Symbol;Acc:MGI:3647785] [E	**2,86E-11**
Mus musculus Nfat activating molecule with ITAM motif 1 (Nfam1), mRNA [NM_02	**2,47E-09**
immunoglobulin kappa chain variable 9-124 [Source:MGI Symbol;Acc:MGI:36468	**1,38E-07**
immunoglobulin kappa variable 4-58 [Source:MGI Symbol;Acc:MGI:2685923] [EN	**2,53E-13**
immunoglobulin kappa variable 4-86 [Source:MGI Symbol;Acc:MGI:2685305] [EN	**5,59E-10**
Mus musculus immunoglobulin heavy chain complex, mRNA (cDNA clone MGC:11	**9,82E-10**
Mus musculus cyclin-dependent kinase inhibitor 2A (Cdkn2a), transcript variant 1	**7,68E-07**
Mus musculus CD19 antigen (Cd19), mRNA [NM_009844]	**3,47E-04**
immunoglobulin kappa variable 2-116 [Source:MGI Symbol;Acc:MGI:3647785] [E	**1,28E-11**
immunoglobulin kappa chain variable 4-71 [Source:MGI Symbol;Acc:MGI:443965	**8,21E-13**
Mus musculus cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (Cdkn2b	**4,35E-06**
immunoglobulin kappa variable 6-17 [Source:MGI Symbol;Acc:MGI:1330833] [EN	**7,25E-11**
immunoglobulin kappa variable 12-46 [Source:MGI Symbol;Acc:MGI:4439773] [E	**6,58E-08**
immunoglobulin heavy variable 1-84 [Source:MGI Symbol;Acc:MGI:3644235] [EN	**7,02E-10**
Mus musculus interleukin 22 (Il22), mRNA [NM_016971]	**5,61E-07**
Mus musculus immunoglobulin joining chain (Igj), mRNA [NM_152839]	**5,03E-14**
immunoglobulin kappa variable 14-126 [Source:MGI Symbol;Acc:MGI:3643131] [	**4,32E-07**
Mus musculus interleukin 13 (Il13), mRNA [NM_008355]	**3,08E-14**
immunoglobulin kappa chain variable 4-70 [Source:MGI Symbol;Acc:MGI:268634	**6,13E-13**
immunoglobulin kappa variable 8-28 [Source:MGI Symbol;Acc:MGI:3642251] [EN	**3,50E-10**
immunoglobulin lambda variable 1 [Source:MGI Symbol;Acc:MGI:96530] [ENSMU	**1,02E-11**
immunoglobulin kappa chain variable 4-90 [Source:MGI Symbol;Acc:MGI:443983	**3,12E-10**
immunoglobulin lambda constant 2 [Source:MGI Symbol;Acc:MGI:99547] [ENSM	**3,54E-11**
Mus musculus chemokine (C-X-C motif) ligand 9 (Cxcl9), mRNA [NM_008599]	**9,38E-12**
immunoglobulin heavy variable V11-2 [Source:MGI Symbol;Acc:MGI:4947968] [E	**8,84E-07**
Mus musculus CD70 antigen (Cd70), mRNA [NM_011617]	**4,43E-09**
immunoglobulin heavy variable V9-2 [Source:MGI Symbol;Acc:MGI:3643816] [EN	**1,38E-07**
Mus musculus chemokine (C-X-C motif) ligand 3 (Cxcl3), mRNA [NM_203320]	**1,25E-07**
Mus musculus killer cell lectin-like receptor, subfamily A, member 7 (Klra7), transcr	**7,44E-03**
Mus musculus tumor necrosis factor, alpha-induced protein 2 (Tnfaip2), mRNA [N	**1,85E-07**
Mus musculus CD40 antigen (Cd40), transcript variant 1, mRNA [NM_011611]	**7,96E-08**
immunoglobulin heavy variable V14-3 [Source:MGI Symbol;Acc:MGI:4439764] [E	**1,50E-11**
Mus musculus killer cell lectin-like receptor, subfamily A, member 8 (Klra8), transcr	**1,03E-03**
immunoglobulin heavy variable V1-18 [Source:MGI Symbol;Acc:MGI:4439780] [E	**9,41E-10**
immunoglobulin lambda constant 3 [Source:MGI Symbol;Acc:MGI:99886] [ENSM	**3,06E-11**
immunoglobulin kappa variable 2-109 [Source:MGI Symbol;Acc:MGI:3642626] [E	**2,07E-10**
Mus musculus CDK5 and Abl enzyme substrate 1 (Cables1), transcript variant 2,	**1,45E-09**
Mus musculus interleukin 4 induced 1 (Il4i1), mRNA [NM_010215]	**2,05E-10**
Mus musculus chemokine (C-C motif) ligand 17 (Ccl17), mRNA [NM_011332]	**3,43E-11**
Mus musculus interleukin 3 (Il3), mRNA [NM_010556]	**6,10E-10**
Mus musculus chemokine (C-C motif) ligand 9 (Ccl9), mRNA [NM_011338]	**3,27E-03**
Mus musculus icos ligand (Icosl), mRNA [NM_015790]	**3,57E-13**
Mus musculus linker for activation of T cells family, member 2 (Lat2), transcript va	**1,04E-03**
Mus musculus CD1d2 antigen (Cd1d2), mRNA [NM_007640]	**1,20E-10**
immunoglobulin kappa variable 14-111 [Source:MGI Symbol;Acc:MGI:4439863] [	**3,41E-10**
immunoglobulin heavy variable V1-20 [Source:MGI Symbol;Acc:MGI:3644607] [E	**4,55E-11**
Mus musculus interleukin 1 receptor, type II (Il1r2), mRNA [NM_010555]	**8,06E-08**
Mus musculus interleukin 9 receptor (Il9r), transcript variant 1, mRNA [NM_00113	**2,32E-06**
Mus musculus interferon gamma (Ifng), mRNA [NM_008337]	**2,69E-04**
immunoglobulin kappa chain variable 8-24 [Source:MGI Symbol;Acc:MGI:494795	**1,56E-10**
Mus musculus killer cell lectin-like receptor, subfamily A, member 7 (Klra7), transcr	**1,20E-02**
Mus musculus granzyme B (Gzmb), mRNA [NM_013542]	**4,84E-09**
Mus musculus chemokine (C-C motif) ligand 5 (Ccl5), mRNA [NM_013653]	**8,56E-13**
Mus musculus CD74 antigen (invariant polypeptide of major histocompatibility cor	**7,57E-07**
Mus musculus integrin beta 5 (Itgb5), transcript variant 2, mRNA [NM_010580]	**2,23E-08**

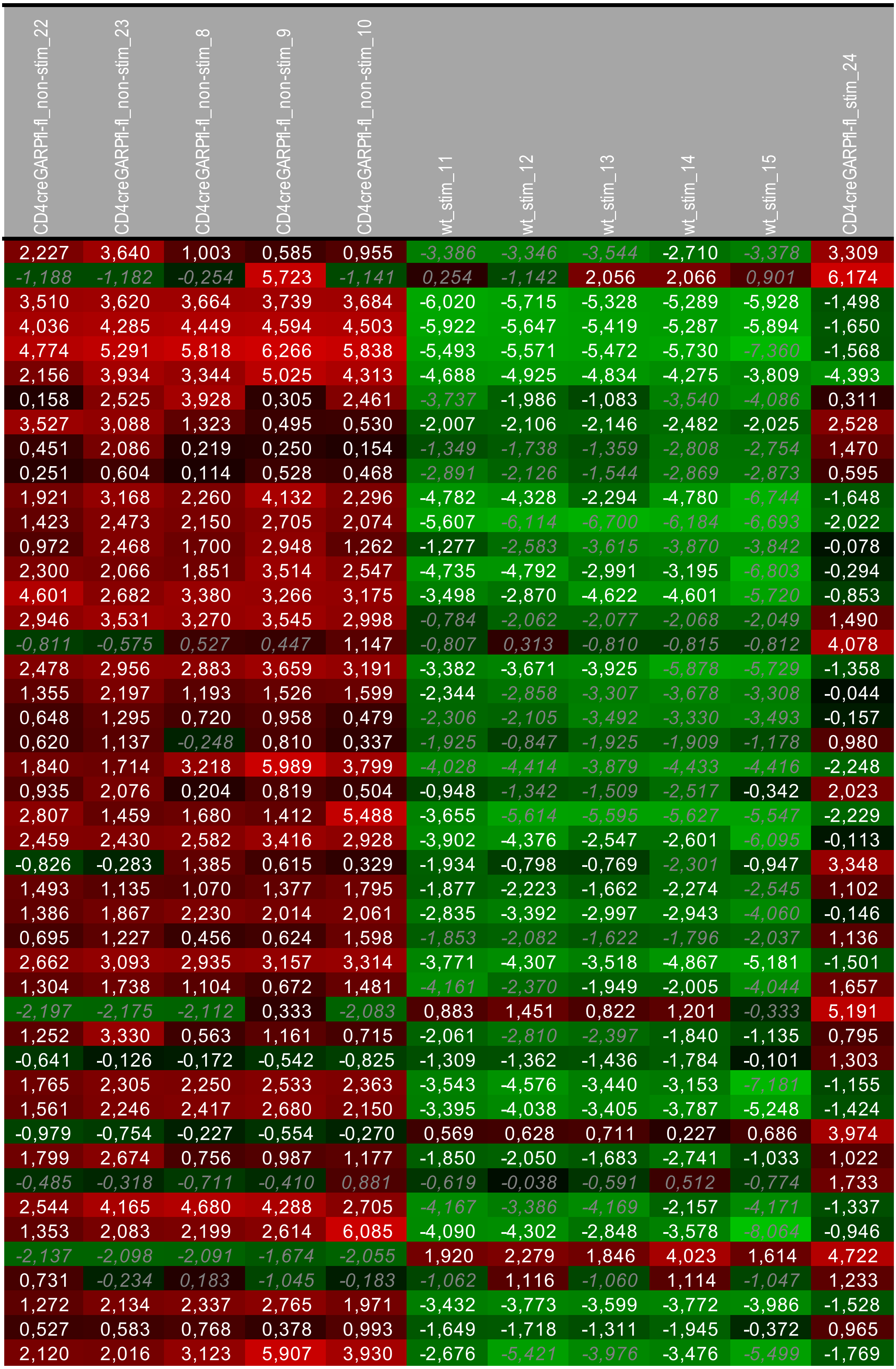
Immunoglobulin heavy chain V gene segment [Source:IMGT/GENE-DB;Acc:IGH	**3,11E-07**
immunoglobulin kappa chain variable 6-29 [Source:MGI Symbol;Acc:MGI:443961	**5,81E-09**
Mus musculus chemokine (C-X-C motif) ligand 10 (Cxcl10), mRNA [NM_021274]	**2,83E-06**
Mus musculus killer cell lectin-like receptor subfamily B member 1B (Klrb1b), mRN	**2,55E-04**
Mus musculus chemokine (C-X-C motif) ligand 9 (Cxcl9), mRNA [NM_008599]	**4,55E-11**
Mus musculus killer cell lectin-like receptor subfamily B member 1B (Klrb1b), mRN	**8,94E-06**
Mus musculus tumor necrosis factor receptor superfamily, member 8 (Tnfrsf8), mR	**1,11E-09**
immunoglobulin heavy variable V8-12 [Source:MGI Symbol;Acc:MGI:3642873] [E	**1,11E-07**
Mus musculus Fc receptor, IgE, high affinity I, gamma polypeptide (Fcer1g), mRN	**2,78E-04**
immunoglobulin kappa chain variable 2-137 [Source:MGI Symbol;Acc:MGI:44398	**6,92E-08**
Mus musculus chemokine (C-X3-C motif) ligand 1 (Cx3cl1), mRNA [NM_009142]	**4,44E-05**
Mus musculus CD79A antigen (immunoglobulin-associated alpha) (Cd79a), mRN	**1,50E-07**
Mus musculus chemokine (C-X-C motif) ligand 16 (Cxcl16), mRNA [NM_023158]	**7,75E-04**
Mus musculus interferon regulatory factor 5 (Irf5), transcript variant 2, mRNA [NM_	**5,45E-05**
Mus musculus interferon activated gene 204 (Ifi204), mRNA [NM_008329]	**1,13E-10**
Mus musculus CD79B antigen (Cd79b), mRNA [NM_008339]	**6,00E-09**
Mus musculus killer cell lectin-like receptor subfamily A, member 9 (Klra9), mRNA	**5,09E-03**
immunoglobulin kappa chain variable 15-103 [Source:MGI Symbol;Acc:MGI:9651	**2,42E-09**
Mus musculus cyclin-dependent kinase 18 (Cdk18), mRNA [NM_008795]	**1,60E-03**
Mus musculus killer cell lectin-like receptor subfamily C, member 1 (Klrc1), transcri	**3,44E-04**
Mus musculus CD300 antigen like family member F (Cd300lf), transcript variant 1,	**5,45E-03**
Mus musculus tumor necrosis factor receptor superfamily, member 13c (Tnfrsf13c	**1,50E-04**
Mus musculus cytotoxic and regulatory T cell molecule (Crtam), mRNA [NM_0194	**4,03E-09**
Mus musculus interleukin 1 receptor, type I (Il1r1), transcript variant 1, mRNA [NM	**2,03E-05**
Mus musculus toll-like receptor 7 (Tlr7), mRNA [NM_133211]	**3,01E-10**
Mus musculus CD79A antigen (immunoglobulin-associated alpha), mRNA (cDNA	**1,06E-08**
Mus musculus histone deacetylase 9 (Hdac9), mRNA [NM_024124]	**1,57E-06**
Mus musculus interleukin 21 (Il21), mRNA [NM_021782]	**7,52E-07**
Mus musculus interleukin 17 receptor E (Il17re), transcript variant 3, mRNA [NM_	**1,59E-08**
Mus musculus interleukin 5 receptor, alpha (Il5ra), mRNA [NM_008370]	**1,42E-02**
Mus musculus chemokine (C motif) ligand 1 (Xcl1), mRNA [NM_008510]	**1,30E-03**
immunoglobulin kappa chain variable 15-103 [Source:MGI Symbol;Acc:MGI:9651	**1,40E-09**
Mus musculus interleukin 18 receptor accessory protein (Il18rap), mRNA [NM_01	**1,47E-07**
chemokine (C-C motif) ligand 1 [Source:MGI Symbol;Acc:MGI:98258] [ENSMUST	**8,64E-13**
Mus musculus growth arrest-specific 2 like 3 (Gas2l3), transcript variant 2, mRNA	**8,20E-07**
Mus musculus NLR family, apoptosis inhibitory protein 6 (Naip6), mRNA [NM_010	**5,25E-10**
Mus musculus Fas apoptotic inhibitory molecule 3 (Faim3), mRNA [NM_026976]	**1,75E-09**
Mus musculus caspase 4, apoptosis-related cysteine peptidase (Casp4), mRNA [	**1,62E-08**
Mus musculus interleukin 1 receptor-like 1 (Il1rl1), transcript variant 1, mRNA [NM_	**4,12E-04**
Mus musculus interleukin 4 (Il4), mRNA [NM_021283]	**7,07E-12**

Adjusted ANOVA p-value	Tukey p-value	Fold change	Log2 ratio	Median	wt_non-stim_1	wt_non-stim_2	wt_non-stim_3	wt_non-stim_4	wt_non-stim_21
1,28E-03	**1,05E-03**	**20,620**	4,366	6,389	-0,298	-0,600	-1,745	-0,461	3,048
1,04E-03	**7,90E-03**	**14,291**	3,837	3,183	*-1,075*	*-1,129*	*-1,137*	*-0,984*	*-1,134*
3,47E-14	**4,90E-10**	**13,929**	3,800	14,844	2,474	1,498	2,306	2,205	2,251
1,94E-14	**7,47E-10**	**12,702**	3,667	14,047	2,644	1,617	2,475	2,367	2,430
1,36E-12	**5,05E-07**	**11,424**	3,514	10,262	3,018	1,568	2,828	2,732	2,669
3,54E-08	**1,09E-02**	**10,808**	3,434	9,436	1,654	1,455	2,844	1,827	0,890
2,04E-03	**3,80E-02**	**10,418**	3,381	5,908	-0,295	-0,562	4,328	0,321	0,860
2,11E-03	**3,08E-03**	**9,448**	3,240	10,766	-1,262	-0,978	-1,422	-1,262	2,422
3,19E-03	**1,30E-03**	**9,057**	3,179	4,685	*-1,067*	*-1,043*	-0,546	-0,735	2,239
1,11E-05	**1,66E-05**	**8,877**	3,150	4,763	-0,555	-0,693	-0,083	-0,588	0,710
4,93E-07	**2,29E-03**	**8,766**	3,132	8,507	0,612	0,255	1,575	0,578	1,555
6,87E-11	**8,66E-06**	**8,682**	3,118	9,508	2,156	2,317	2,076	1,725	1,877
4,97E-06	**1,09E-02**	**8,282**	3,050	5,732	2,059	0,078	1,207	1,550	1,056
2,77E-07	**2,07E-03**	**8,140**	3,025	8,850	1,003	0,747	1,895	1,048	0,294
1,63E-09	**2,23E-04**	**7,912**	2,984	9,445	1,843	1,167	1,892	1,830	0,853
8,13E-09	**8,66E-06**	**7,121**	2,832	4,036	*-0,812*	*-2,069*	-0,196	*-2,017*	*-1,611*
4,30E-02	**1,66E-02**	**6,845**	2,775	2,606	*-0,808*	*-0,167*	*0,072*	*0,083*	*-0,072*
3,21E-09	**6,70E-05**	**6,543**	2,710	7,959	1,815	1,930	1,780	0,808	1,914
1,16E-07	**1,11E-04**	**6,476**	2,695	6,158	0,378	0,525	0,516	0,044	1,862
1,14E-07	**4,38E-05**	**6,426**	2,684	5,445	0,596	0,478	0,513	0,157	0,548
9,82E-03	**5,80E-03**	**6,382**	2,674	3,763	*-1,934*	*-0,723*	*-1,757*	*-0,574*	2,070
1,11E-07	**6,47E-03**	**6,084**	2,605	6,333	1,808	1,056	1,605	2,385	0,645
2,14E-02	**9,87E-03**	**6,017**	2,589	4,873	-0,285	*-1,547*	-0,354	-0,353	2,737
2,59E-06	**2,18E-02**	**5,959**	2,575	7,436	1,451	0,518	1,657	0,112	-0,112
3,19E-07	**1,92E-03**	**5,784**	2,532	8,962	1,404	1,058	2,934	1,317	0,113
7,35E-03	**1,71E-03**	**5,720**	2,516	4,825	0,351	-0,047	-1,759	0,299	-1,104
1,59E-06	**1,97E-05**	**5,665**	2,502	5,301	-0,075	0,010	-0,055	-0,010	1,178
1,78E-08	**5,65E-05**	**5,626**	2,492	7,865	0,146	1,239	1,601	0,932	0,417
5,18E-04	**1,23E-03**	**5,594**	2,484	5,454	-0,225	0,118	-0,880	-0,951	1,899
2,52E-11	**7,96E-06**	**5,579**	2,480	10,602	2,233	1,163	2,355	1,604	1,306
1,52E-03	**9,59E-03**	**5,487**	2,456	6,004	-0,087	-0,021	-0,437	-0,220	2,963
1,31E-07	**2,36E-04**	**5,374**	2,426	4,255	*-1,795*	*-2,075*	*-2,089*	*-2,002*	*-2,090*
3,07E-03	**1,70E-02**	**5,329**	2,414	5,892	0,115	-0,719	-0,167	-0,115	2,994
3,49E-05	**1,40E-05**	**5,315**	2,410	8,294	0,514	0,383	0,563	0,651	0,574
1,50E-07	**3,15E-04**	**5,234**	2,388	9,184	1,829	1,149	1,662	1,217	0,541
2,54E-10	**1,44E-05**	**5,144**	2,363	11,313	1,917	1,446	2,011	1,612	0,864
1,30E-08	**6,49E-06**	**5,067**	2,341	4,981	-1,758	-1,099	-1,830	-1,410	-1,158
3,11E-04	**4,40E-03**	**5,032**	2,331	6,721	-0,015	0,015	-0,305	-0,442	2,274
1,39E-02	**7,73E-03**	**5,007**	2,324	2,644	*0,597*	*0,599*	*-0,878*	*-0,295*	*0,038*
7,07E-09	**1,07E-02**	**4,942**	2,305	5,936	1,318	2,745	2,574	0,959	1,893
9,12E-05	**2,59E-02**	**4,908**	2,295	9,978	0,984	0,505	2,970	1,242	-0,505
1,08E-10	**4,26E-04**	**4,901**	2,293	4,211	*-2,074*	*-2,084*	*-2,062*	*-2,119*	*-1,614*
1,91E-02	**3,87E-02**	**4,857**	2,280	3,058	*-0,372*	*-1,085*	*-1,070*	*-1,078*	*0,424*
1,68E-10	**1,88E-05**	**4,740**	2,245	9,109	1,882	1,388	2,035	1,635	0,707
4,90E-04	**8,68E-04**	**4,727**	2,241	6,279	-0,544	-1,644	-1,292	-1,040	0,703
5,44E-07	**1,95E-02**	**4,617**	2,207	7,457	2,817	1,020	1,779	2,278	0,789

3,98E-10	4,48E-05	4,528	2,179	11,475	1,939	1,551	2,232	1,663	0,846
1,06E-04	4,19E-05	4,528	2,179	3,475	*-0,409*	*-0,427*	*-0,655*	*-1,267*	*-0,313*
2,66E-04	1,33E-04	4,525	2,178	5,196	-0,961	-1,473	-1,020	-1,147	0,193
9,66E-06	3,77E-02	4,491	2,167	8,680	2,238	0,674	4,082	1,600	0,077
1,98E-09	2,59E-04	4,426	2,146	10,154	1,522	1,333	2,139	1,621	0,851
1,18E-09	3,88E-04	4,423	2,145	8,699	1,668	1,145	2,032	1,818	1,723
1,40E-02	2,42E-02	4,377	2,130	4,247	0,022	*-2,247*	1,329	*-1,084*	*-1,119*
7,66E-10	9,31E-04	4,377	2,130	9,478	1,483	1,406	1,769	1,471	1,403
6,07E-10	2,02E-04	4,368	2,127	10,696	1,407	1,030	1,798	1,835	1,047
3,46E-10	2,96E-05	4,362	2,125	5,329	1,522	0,824	1,520	1,627	0,526
2,59E-07	2,05E-04	4,347	2,120	7,533	0,378	-0,006	0,286	0,006	0,799
1,26E-10	3,27E-04	4,323	2,112	11,099	2,184	1,467	2,889	1,880	1,631
4,26E-08	3,31E-02	4,323	2,112	5,609	1,128	2,675	1,410	2,929	1,565
1,02E-02	3,57E-03	4,272	2,095	4,178	*-1,311*	*-1,541*	0,022	-0,229	-0,022
1,80E-03	1,19E-03	4,257	2,090	6,813	-0,386	-0,799	-1,164	-1,205	1,409
2,68E-09	9,75E-04	4,243	2,085	9,394	2,157	1,225	3,120	1,991	1,638
1,68E-09	6,00E-04	4,211	2,074	8,802	1,396	1,839	1,510	1,057	1,616
6,22E-10	7,41E-04	4,205	2,072	10,629	1,808	1,686	2,282	1,798	1,395
4,34E-06	5,17E-04	4,179	2,063	7,014	0,624	0,017	0,203	-0,162	0,595
1,33E-04	4,14E-03	4,170	2,060	5,552	0,113	-0,291	0,962	-0,113	1,451
2,35E-10	9,98E-04	4,158	2,056	9,993	2,344	1,346	2,875	1,922	1,496
3,41E-02	4,50E-02	4,150	2,053	2,031	*-0,003*	*-0,015*	*-0,008*	*0,009*	*-0,020*
5,35E-06	2,19E-02	4,144	2,051	10,743	0,899	0,296	2,736	0,819	-0,296
1,56E-03	1,97E-03	4,144	2,051	4,098	*-0,202*	*-1,672*	*-0,525*	*-2,217*	-0,146
4,68E-08	8,17E-03	4,138	2,049	8,832	1,763	1,807	1,716	1,636	0,887
9,69E-04	4,93E-03	4,132	2,047	5,107	-0,180	-0,022	0,022	0,102	1,647
3,47E-12	2,66E-04	4,130	2,046	5,991	*-4,097*	*-2,805*	*-3,409*	*-2,489*	*-3,626*
1,94E-04	4,57E-04	4,112	2,040	3,908	*-0,171*	*-0,819*	*-1,091*	-0,054	-0,035
4,43E-11	6,05E-05	4,101	2,036	11,259	2,071	1,148	2,661	1,842	1,371
4,19E-10	6,55E-05	4,095	2,034	11,345	1,837	1,545	2,258	1,730	0,921
3,90E-09	7,49E-05	4,093	2,033	9,210	1,808	1,238	1,703	1,325	0,638
1,17E-02	6,50E-03	4,073	2,026	3,721	*-1,819*	0,301	*-1,850*	*-1,831*	0,140
3,28E-03	1,71E-02	4,061	2,022	6,411	-0,143	-0,451	0,143	-0,292	2,288
2,17E-06	2,95E-02	4,033	2,012	7,026	1,865	0,016	1,806	1,932	-0,016
1,02E-10	2,26E-04	4,031	2,011	11,829	2,192	1,362	2,767	1,908	1,399
2,93E-07	1,53E-03	4,017	2,006	8,341	2,202	1,739	1,893	1,447	0,644
2,03E-10	4,01E-06	3,997	1,999	5,974	0,792	0,800	0,824	0,911	1,092
1,00E-04	9,94E-03	3,975	1,991	4,394	*-2,390*	*-1,936*	*-1,567*	*-2,416*	-0,102
8,28E-12	1,17E-05	3,910	1,967	9,090	1,975	1,343	2,008	2,194	1,167
4,48E-03	4,72E-03	3,910	1,967	2,745	*0,304*	*-0,831*	*-0,840*	*-0,868*	*0,599*
4,14E-08	1,28E-03	3,893	1,961	9,069	2,016	1,506	2,266	2,084	1,216
2,00E-11	6,29E-05	3,891	1,960	11,519	2,107	1,315	2,746	1,867	1,439
3,22E-09	6,72E-04	3,883	1,957	9,358	1,482	1,689	1,729	1,469	0,958
3,41E-11	1,48E-04	3,872	1,953	9,697	1,345	1,539	2,148	1,650	1,314
1,09E-08	2,67E-03	3,861	1,949	6,521	2,057	0,600	0,891	2,141	0,328
5,56E-11	1,68E-04	3,792	1,923	11,027	1,781	1,666	2,225	1,882	1,384
1,62E-05	3,53E-05	3,789	1,922	9,050	-0,697	-0,384	-0,666	-1,017	-0,446
1,71E-08	6,01E-04	3,776	1,917	3,889	*-1,779*	*-1,809*	*-1,810*	*-0,816*	*-1,813*
8,57E-09	5,57E-04	3,774	1,916	8,917	2,401	1,132	1,814	1,153	0,813
7,45E-11	1,90E-04	3,753	1,908	11,234	1,779	1,619	2,246	1,711	1,363
2,66E-09	1,58E-03	3,753	1,908	7,887	1,858	1,712	2,138	1,919	1,555
3,68E-11	3,08E-06	3,704	1,889	16,491	1,060	0,946	1,197	0,953	0,700
2,02E-07	7,43E-03	3,681	1,880	8,565	1,359	1,864	1,294	0,694	0,354
7,79E-05	4,92E-02	3,668	1,875	8,648	2,205	0,703	4,076	1,632	0,130
1,25E-04	1,56E-02	3,650	1,868	4,678	-0,364	0,048	0,337	-0,330	2,421
4,38E-05	1,67E-05	3,650	1,868	6,478	-0,219	-0,120	0,119	-0,612	-0,809

5,04E-06	**2,59E-04**	**3,650**	1,868	6,723	-0,851	-1,387	-1,173	-2,056	-1,136
4,90E-10	**2,03E-04**	**3,615**	1,854	9,672	1,595	1,618	1,846	1,541	0,949
2,33E-08	**6,76E-05**	**3,610**	1,852	6,554	0,534	0,263	0,299	0,393	1,836
8,62E-07	**3,78E-02**	**3,603**	1,849	9,450	1,944	1,463	2,055	2,032	0,742
1,00E-11	**1,32E-04**	**3,600**	1,848	10,069	2,247	1,337	2,467	1,597	1,326
6,34E-09	**8,10E-03**	**3,585**	1,842	8,696	2,370	1,584	2,512	0,951	1,124
1,04E-08	**7,44E-03**	**3,565**	1,834	7,989	1,482	1,615	1,944	1,574	1,237
4,12E-06	**3,69E-05**	**3,563**	1,833	6,066	-0,733	-0,519	-0,886	-0,752	-0,453
1,15E-03	**1,33E-03**	**3,555**	1,830	8,944	-0,401	-1,145	-1,150	-1,302	0,198
2,46E-10	**6,11E-05**	**3,548**	1,827	10,323	1,644	1,472	1,769	1,521	0,911
2,63E-11	**1,02E-04**	**3,533**	1,821	12,686	2,199	1,363	2,673	1,814	1,466
2,02E-05	**2,22E-04**	**3,519**	1,815	5,613	-0,092	-0,438	-0,739	-0,838	-0,309
1,09E-09	**4,27E-04**	**3,509**	1,811	11,980	1,739	1,009	1,858	1,843	1,017
4,40E-07	**1,41E-02**	**3,506**	1,810	9,559	1,598	1,095	2,143	1,557	0,645
7,74E-09	**2,05E-03**	**3,504**	1,809	4,786	1,647	0,344	2,137	2,425	1,384
3,08E-06	**2,09E-05**	**3,497**	1,806	4,668	*-0,892*	*-1,037*	-0,348	-0,150	*-1,229*
2,84E-12	**4,62E-06**	**3,473**	1,796	14,290	1,638	1,428	1,966	1,554	1,156
2,44E-06	**2,90E-03**	**3,458**	1,790	12,375	0,695	0,054	0,116	0,061	0,341
1,96E-12	**9,84E-04**	**3,427**	1,777	6,878	*-3,864*	*-3,542*	*-3,336*	*-3,750*	-2,602
2,06E-11	**3,21E-04**	**3,378**	1,756	11,264	2,354	1,427	2,813	2,107	1,628
4,21E-09	**1,37E-03**	**3,371**	1,753	11,045	1,759	0,830	1,960	2,027	1,082
2,04E-10	**2,88E-04**	**3,366**	1,751	13,483	1,607	1,469	2,014	1,624	0,966
3,82E-09	**2,20E-03**	**3,343**	1,741	9,204	2,151	1,024	2,564	1,688	1,433
5,88E-10	**2,63E-04**	**3,324**	1,733	15,135	1,311	0,965	1,613	1,336	0,814
1,91E-10	**1,46E-03**	**3,315**	1,729	5,630	*-2,339*	*-3,742*	*-3,742*	*-2,207*	*-3,119*
4,68E-06	**1,93E-03**	**3,260**	1,705	8,654	0,961	-0,015	0,015	0,289	0,539
3,91E-08	**4,82E-06**	**3,256**	1,703	7,538	-1,048	-1,498	-1,010	-1,187	-0,977
8,62E-07	**2,59E-02**	**3,245**	1,698	8,999	1,975	1,978	1,697	0,804	0,522
7,88E-07	**4,62E-05**	**3,242**	1,697	2,307	*-0,103*	*-0,208*	*-0,194*	*-0,216*	*-0,211*
1,93E-02	**2,02E-02**	**3,229**	1,691	6,882	-0,386	-0,722	-0,580	-0,285	2,331
1,13E-06	**2,14E-02**	**3,220**	1,687	7,023	-0,652	-0,460	-0,079	0,214	0,638
5,24E-07	**1,99E-04**	**3,207**	1,681	6,139	-1,200	-1,741	-1,066	-1,507	-0,401
2,83E-10	**5,86E-04**	**3,187**	1,672	11,483	1,607	1,342	2,012	1,514	1,198
3,15E-03	**2,96E-02**	**3,167**	1,663	6,699	0,029	-0,327	0,047	-0,345	2,549
9,99E-09	**1,26E-02**	**3,154**	1,657	8,471	1,784	1,448	2,046	1,384	1,451
5,18E-10	**1,55E-04**	**3,147**	1,654	14,881	1,204	0,839	1,488	1,304	0,785
2,68E-09	**1,52E-03**	**3,123**	1,643	9,552	1,453	1,649	1,854	1,516	0,973
1,46E-08	**2,97E-06**	**3,082**	1,624	7,342	0,032	-0,032	-0,176	-0,429	0,505
2,66E-09	**4,56E-05**	**3,069**	1,618	10,181	-1,469	-1,621	-1,781	-1,672	-0,671
5,73E-10	**2,96E-04**	**3,067**	1,617	7,732	-1,859	-3,313	-2,411	-2,869	-1,418
6,84E-09	**2,72E-02**	**3,067**	1,617	7,686	-2,886	-3,371	*-3,946*	-3,509	*-4,923*
9,08E-03	**4,60E-02**	**3,029**	1,599	7,157	-2,761	-1,652	-1,971	-2,304	1,493
1,32E-11	**1,22E-05**	**2,998**	1,584	8,505	1,465	1,115	1,384	1,155	1,054
3,17E-03	**2,85E-03**	**2,983**	1,577	6,826	-0,771	-0,968	-0,573	-0,944	0,428
1,67E-09	**2,82E-04**	**2,965**	1,568	7,926	1,222	0,878	1,002	0,992	0,522
4,12E-09	**7,56E-04**	**2,910**	1,541	12,411	1,128	1,062	1,315	1,153	0,467
7,26E-10	**1,92E-03**	**2,880**	1,526	9,689	1,768	1,642	2,070	1,462	1,372
5,30E-07	**1,09E-04**	**2,834**	1,503	10,524	-0,960	-0,595	-1,368	-1,790	-1,231
1,13E-05	**2,10E-02**	**2,797**	1,484	4,715	0,710	0,279	0,600	0,353	0,947
9,09E-04	**1,44E-03**	**2,759**	1,464	14,060	-0,152	0,003	0,064	-0,160	-0,575
2,10E-09	**6,62E-04**	**2,747**	1,458	9,865	1,637	0,985	1,374	1,757	0,716
2,99E-02	**2,05E-02**	**2,742**	1,455	5,843	-0,378	-1,076	-0,247	0,018	2,531
4,23E-08	**3,22E-03**	**2,736**	1,452	10,847	-2,300	-2,208	-2,281	-2,266	-1,127
2,71E-11	**3,17E-04**	**2,726**	1,447	14,643	1,359	1,583	1,464	1,108	1,778
4,06E-06	**3,83E-05**	**2,721**	1,444	13,958	0,214	-0,165	-0,093	-0,237	0,469
1,65E-07	**1,03E-05**	**2,709**	1,438	7,084	0,202	-0,038	-0,043	-0,146	0,290

1,81E-06	**2,28E-02**	**2,676**	1,420	9,957	0,365	0,000	0,467	0,140	0,000
4,98E-08	**3,58E-02**	**2,595**	1,376	6,555	1,105	0,779	1,369	0,998	0,790
1,36E-05	**6,75E-06**	**2,595**	1,376	9,845	-0,244	-0,058	-0,868	-0,994	-0,760
8,62E-04	**1,93E-03**	**2,583**	1,369	5,544	0,059	-0,499	0,131	-0,615	0,674
7,26E-10	**5,03E-04**	**2,578**	1,366	5,063	*-1,601*	*-2,488*	*-3,275*	*-1,778*	*-2,199*
3,92E-05	**4,64E-04**	**2,521**	1,334	7,760	0,114	-0,061	0,061	-0,661	0,466
1,15E-08	**2,99E-04**	**2,519**	1,333	5,734	-1,430	-1,186	-0,629	-1,810	-0,916
7,08E-07	**3,04E-02**	**2,509**	1,327	7,801	2,501	1,177	1,754	2,367	0,882
9,35E-04	**6,25E-03**	**2,485**	1,313	10,520	0,081	-0,296	-0,117	-0,506	1,807
4,61E-07	**2,22E-02**	**2,473**	1,306	8,076	1,508	1,715	1,583	1,236	0,967
1,72E-04	**1,07E-04**	**2,454**	1,295	6,555	-0,048	-0,659	0,039	-0,670	-0,085
9,31E-07	**2,44E-03**	**2,417**	1,273	6,318	0,467	0,023	0,270	-0,023	0,746
2,42E-03	**5,30E-04**	**2,403**	1,265	5,490	0,141	0,120	-0,010	0,182	-0,045
2,08E-04	**4,82E-05**	**2,383**	1,253	9,589	0,186	-0,270	-0,074	-0,123	0,345
1,58E-09	**7,36E-05**	**2,373**	1,247	8,409	0,559	0,429	0,336	0,815	0,745
5,12E-08	**5,16E-04**	**2,331**	1,221	12,774	0,543	0,107	0,273	0,064	0,979
1,36E-02	**4,28E-02**	**2,328**	1,219	5,456	-0,026	-0,218	-0,117	0,005	2,500
2,29E-08	**1,02E-02**	**2,326**	1,218	11,385	1,038	1,446	2,797	2,387	1,082
4,70E-03	**3,14E-02**	**2,326**	1,218	4,264	0,159	-0,166	0,024	-0,440	0,184
1,14E-03	**5,55E-03**	**2,315**	1,211	5,194	0,001	0,608	0,175	0,308	0,272
1,45E-02	**2,67E-02**	**2,291**	1,196	8,070	-0,355	-1,256	-0,761	-1,387	0,467
5,29E-04	**4,66E-03**	**2,278**	1,188	7,700	0,033	-0,274	-0,030	-0,324	0,643
3,60E-08	**4,81E-06**	**2,269**	1,182	10,455	-0,567	-0,446	-0,601	-0,581	-0,026
8,33E-05	**7,00E-05**	**2,269**	1,182	5,696	-0,282	-0,409	-0,562	-0,442	-0,369
3,70E-09	**2,32E-04**	**2,242**	1,165	7,658	1,131	1,013	1,210	1,036	1,106
8,52E-08	**1,32E-03**	**2,242**	1,165	9,802	0,552	0,047	0,130	0,074	0,906
7,93E-06	**7,93E-04**	**2,227**	1,155	6,039	-0,244	0,100	0,362	0,131	-0,355
4,04E-06	**2,80E-02**	**2,224**	1,153	7,990	-1,735	-0,199	-2,632	-1,907	-1,868
1,22E-07	**1,59E-04**	**2,198**	1,136	8,469	0,210	0,232	0,315	0,061	-0,061
3,47E-02	**1,53E-02**	**2,175**	1,121	7,028	0,000	-0,910	0,000	-0,650	0,354
3,87E-03	**2,38E-03**	**2,164**	1,114	11,820	-0,021	0,231	0,021	-0,311	-0,506
1,41E-08	**1,49E-02**	**2,152**	1,106	10,912	1,049	1,630	2,858	2,575	1,149
9,14E-07	**7,58E-03**	**2,133**	1,093	7,557	0,115	0,218	0,277	0,074	0,377
2,74E-11	**1,32E-03**	**2,120**	1,084	6,581	-2,028	-2,599	-2,205	-1,691	-2,094
4,37E-06	**4,10E-02**	**2,071**	1,050	3,271	*-1,439*	*-1,443*	*-1,445*	*-1,453*	*-1,445*
5,99E-09	**1,63E-03**	**2,066**	1,047	5,853	0,747	1,188	0,965	0,429	1,207
1,72E-08	**3,33E-02**	**2,058**	1,041	11,196	1,385	0,486	0,795	0,489	1,942
1,24E-07	**6,64E-07**	**2,042**	1,030	11,463	-0,175	-0,123	-0,141	-0,411	-0,263
1,35E-03	**4,38E-03**	**2,020**	1,014	9,511	-0,978	-0,860	-0,947	-0,889	0,304
1,50E-10	**1,98E-03**	**2,017**	1,012	11,424	-1,285	-1,032	-1,039	-1,471	-1,897



CD4creGARPfl-fl_non-stim_22	CD4creGARPfl-fl_non-stim_23	CD4creGARPfl-fl_non-stim_8	CD4creGARPfl-fl_non-stim_9	CD4creGARPfl-fl_non-stim_10	wt_stim_11	wt_stim_12	wt_stim_13	wt_stim_14	wt_stim_15	CD4creGARPfl-fl_stim_24
2,227	3,640	1,003	0,585	0,955	*-3,386*	*-3,346*	*-3,544*	-2,710	*-3,378*	3,309
-1,188	*-1,182*	*-0,254*	5,723	*-1,141*	*0,254*	*-1,142*	2,056	2,066	*0,901*	6,174
3,510	3,620	3,664	3,739	3,684	-6,020	-5,715	-5,328	-5,289	-5,928	-1,498
4,036	4,285	4,449	4,594	4,503	-5,922	-5,647	-5,419	-5,287	-5,894	-1,650
4,774	5,291	5,818	6,266	5,838	-5,493	-5,571	-5,472	-5,730	*-7,360*	-1,568
2,156	3,934	3,344	5,025	4,313	-4,688	-4,925	-4,834	-4,275	-3,809	-4,393
0,158	2,525	3,928	0,305	2,461	*-3,737*	-1,986	-1,083	*-3,540*	*-4,086*	0,311
3,527	3,088	1,323	0,495	0,530	-2,007	-2,106	-2,146	-2,482	-2,025	2,528
0,451	2,086	0,219	0,250	0,154	*-1,349*	*-1,738*	*-1,359*	*-2,808*	*-2,754*	1,470
0,251	0,604	0,114	0,528	0,468	*-2,891*	*-2,126*	*-1,544*	*-2,869*	*-2,873*	0,595
1,921	3,168	2,260	4,132	2,296	-4,782	-4,328	-2,294	-4,780	*-6,744*	-1,648
1,423	2,473	2,150	2,705	2,074	-5,607	*-6,114*	*-6,700*	*-6,184*	*-6,693*	-2,022
0,972	2,468	1,700	2,948	1,262	-1,277	*-2,583*	*-3,615*	*-3,870*	*-3,842*	-0,078
2,300	2,066	1,851	3,514	2,547	-4,735	-4,792	-2,991	-3,195	*-6,803*	-0,294
4,601	2,682	3,380	3,266	3,175	-3,498	-2,870	-4,622	-4,601	*-5,720*	-0,853
2,946	3,531	3,270	3,545	2,998	*-0,784*	*-2,062*	*-2,077*	*-2,068*	*-2,049*	1,490
-0,811	*-0,575*	*0,527*	*0,447*	1,147	*-0,807*	*0,313*	*-0,810*	*-0,815*	*-0,812*	4,078
2,478	2,956	2,883	3,659	3,191	-3,382	-3,671	-3,925	*-5,878*	*-5,729*	-1,358
1,355	2,197	1,193	1,526	1,599	-2,344	*-2,858*	*-3,307*	*-3,678*	*-3,308*	-0,044
0,648	1,295	0,720	0,958	0,479	*-2,306*	*-2,105*	*-3,492*	*-3,330*	*-3,493*	-0,157
0,620	1,137	*-0,248*	0,810	0,337	*-1,925*	*-0,847*	*-1,925*	*-1,909*	*-1,178*	0,980
1,840	1,714	3,218	5,989	3,799	*-4,028*	*-4,414*	*-3,879*	*-4,433*	*-4,416*	-2,248
0,935	2,076	0,204	0,819	0,504	-0,948	*-1,342*	*-1,509*	*-2,517*	-0,342	2,023
2,807	1,459	1,680	1,412	5,488	-3,655	*-5,614*	*-5,595*	*-5,627*	*-5,547*	-2,229
2,459	2,430	2,582	3,416	2,928	-3,902	-4,376	-2,547	-2,601	*-6,095*	-0,113
-0,826	-0,283	1,385	0,615	0,329	-1,934	-0,798	-0,769	*-2,301*	-0,947	3,348
1,493	1,135	1,070	1,377	1,795	-1,877	-2,223	-1,662	-2,274	*-2,545*	1,102
1,386	1,867	2,230	2,014	2,061	-2,835	-3,392	-2,997	-2,943	*-4,060*	-0,146
0,695	1,227	0,456	0,624	1,598	*-1,853*	*-2,082*	*-1,622*	*-1,796*	*-2,037*	1,136
2,662	3,093	2,935	3,157	3,314	-3,771	-4,307	-3,518	-4,867	-5,181	-1,501
1,304	1,738	1,104	0,672	1,481	*-4,161*	*-2,370*	-1,949	-2,005	*-4,044*	1,657
-2,197	*-2,175*	*-2,112*	0,333	*-2,083*	0,883	1,451	0,822	1,201	*-0,333*	5,191
1,252	3,330	0,563	1,161	0,715	-2,061	*-2,810*	*-2,397*	-1,840	-1,135	0,795
-0,641	-0,126	-0,172	-0,542	-0,825	-1,309	-1,362	-1,436	-1,784	-0,101	1,303
1,765	2,305	2,250	2,533	2,363	-3,543	-4,576	-3,440	-3,153	*-7,181*	-1,155
1,561	2,246	2,417	2,680	2,150	-3,395	-4,038	-3,405	-3,787	-5,248	-1,424
-0,979	-0,754	-0,227	-0,554	-0,270	0,569	0,628	0,711	0,227	0,686	3,974
1,799	2,674	0,756	0,987	1,177	-1,850	-2,050	-1,683	-2,741	-1,033	1,022
-0,485	*-0,318*	*-0,711*	*-0,410*	*0,881*	*-0,619*	*-0,038*	*-0,591*	*0,512*	*-0,774*	1,733
2,544	4,165	4,680	4,288	2,705	*-4,167*	*-3,386*	*-4,169*	-2,157	*-4,171*	-1,337
1,353	2,083	2,199	2,614	6,085	-4,090	-4,302	-2,848	-3,578	*-8,064*	-0,946
-2,137	*-2,098*	*-2,091*	*-1,674*	*-2,055*	1,920	2,279	1,846	4,023	1,614	4,722
0,731	*-0,234*	*0,183*	*-1,045*	*-0,183*	*-1,062*	1,116	*-1,060*	1,114	*-1,047*	1,233
1,272	2,134	2,337	2,765	1,971	-3,432	-3,773	-3,599	-3,772	-3,986	-1,528
0,527	0,583	0,768	0,378	0,993	-1,649	-1,718	-1,311	-1,945	-0,372	0,965
2,120	2,016	3,123	5,907	3,930	-2,676	*-5,421*	*-3,976*	-3,476	*-5,499*	-1,769

1,557	2,254	2,498	2,687	2,153	-3,347	-3,854	-3,289	-3,668	-5,075	-1,489
0,205	-0,031	*0,031*	*0,267*	0,277	*-0,111*	0,285	*-1,034*	*-1,519*	*-1,459*	1,076
-0,392	0,126	0,249	-0,006	0,346	-1,486	-1,483	-0,796	-1,616	0,006	1,056
1,430	3,001	3,692	3,008	2,420	-1,788	-2,911	-1,813	-3,516	*-4,527*	-0,404
1,408	2,106	2,542	2,443	1,975	-3,676	-3,924	-2,813	-3,758	-5,208	-1,613
1,627	2,358	4,006	3,322	3,272	-2,993	-3,457	-2,961	-3,839	*-4,742*	-1,145
-0,844	-0,022	*-0,806*	*-2,222*	0,086	0,493	0,064	-0,163	*-1,702*	*-0,808*	2,890
2,617	2,824	3,312	3,883	3,440	-4,075	-3,549	-3,530	-4,100	*-6,338*	-1,403
1,382	2,147	2,239	2,566	1,817	-3,121	-3,704	-2,859	-3,895	-4,734	-1,577
1,336	2,093	1,852	2,150	1,914	*-3,100*	*-3,461*	*-3,477*	*-2,592*	*-3,433*	-1,076
0,777	1,313	1,014	1,418	2,101	-2,955	-3,418	-2,739	-3,683	-2,019	-0,465
3,048	2,895	2,697	3,625	3,859	-3,602	-3,734	-3,230	-3,612	-5,271	-1,467
1,649	1,890	3,317	1,968	3,094	*-2,427*	*-3,653*	*-3,637*	*-3,653*	*-3,645*	-1,296
0,094	0,132	0,114	*-0,526*	0,125	0,088	*-1,847*	*-1,121*	*-1,913*	*-1,717*	0,377
0,148	1,196	0,033	0,413	1,329	-1,508	-1,158	-1,295	-2,189	-1,334	1,401
2,831	2,429	2,383	3,078	3,715	-3,904	-3,732	-2,823	-4,273	*-5,750*	-1,225
0,859	2,068	1,691	2,152	1,615	-4,153	-4,214	-4,079	-4,561	-3,335	-1,380
2,375	3,464	3,472	4,076	3,420	-3,737	-3,716	-3,232	-3,893	-5,938	-1,395
0,909	2,036	1,126	0,889	1,498	-2,264	-2,431	-1,970	-2,018	*-4,348*	-0,201
1,090	2,121	0,619	0,754	0,536	-1,190	*-2,331*	*-2,095*	*-2,404*	*-3,362*	0,927
2,887	2,698	2,499	3,359	3,824	-3,730	-3,684	-3,092	-4,016	-4,970	-1,599
-0,030	*0,194*	*-0,004*	*0,186*	*0,006*	*-0,024*	*-0,016*	*0,772*	*0,000*	*0,063*	*0,000*
1,496	1,996	2,282	2,879	5,159	-3,885	-3,947	-2,949	-3,746	-5,877	-1,244
0,565	0,891	0,592	0,724	0,062	*-1,417*	*-0,650*	-0,062	*-1,646*	*-2,218*	1,571
2,363	2,374	2,441	2,512	2,047	-4,276	-3,434	-3,612	-4,795	*-6,997*	-0,887
0,917	1,378	0,729	-0,033	1,370	-1,214	*-2,237*	*-1,543*	*-1,910*	*-1,891*	1,800
-3,488	*-3,858*	*-2,544*	*-4,074*	*-2,526*	3,605	3,276	3,559	2,489	3,995	6,321
1,886	0,035	0,191	1,035	1,513	*-0,765*	*-0,617*	*-1,976*	*-1,401*	*-1,934*	0,721
2,685	2,966	2,863	3,084	3,499	-3,750	-4,023	-3,357	-4,203	-5,120	-1,572
1,543	2,242	2,491	2,675	2,141	-3,332	-3,657	-3,079	-3,875	-5,082	-1,623
1,786	2,306	2,308	2,592	2,360	-3,016	-3,841	-3,001	-2,830	*-5,091*	-0,842
0,133	*-0,470*	*-1,720*	*0,006*	0,746	*-0,554*	*-1,099*	*-0,006*	*-1,851*	*-1,847*	1,199
0,749	2,412	0,390	0,729	0,415	-1,666	-1,841	-1,201	-1,962	-1,301	0,356
4,475	3,432	2,668	2,751	2,991	-2,526	-2,834	-2,633	-2,363	*-5,004*	0,493
2,855	2,776	2,642	3,173	3,715	-3,842	-3,698	-3,243	-3,939	-5,261	-1,516
1,308	2,345	2,285	3,258	1,742	-3,093	-3,031	-3,944	-3,042	*-6,571*	-1,080
1,545	2,034	1,229	1,440	1,156	*-2,880*	*-3,255*	*-2,604*	*-3,135*	*-4,074*	-0,924
-0,542	0,328	*-2,064*	*-2,397*	*-2,410*	0,457	0,730	1,111	0,102	-0,171	5,317
2,673	3,296	3,703	4,046	3,229	-3,297	-3,423	-3,380	-3,701	-4,463	-1,286
-0,680	*0,064*	*-0,859*	*-0,791*	1,368	*-0,839*	*-0,222*	*0,706*	*-0,064*	*-0,804*	2,103
2,265	2,880	2,749	3,306	3,095	-3,509	-3,385	-3,057	-4,717	*-7,228*	-1,216
2,750	2,839	2,739	3,194	3,640	-3,851	-3,832	-3,363	-3,899	-4,867	-1,580
1,289	2,142	1,612	2,631	2,425	-3,426	-2,781	-2,973	-3,200	-4,694	-0,958
2,704	3,481	3,532	3,860	3,470	-3,898	-3,622	-3,411	-4,278	*-5,212*	-1,314
3,645	3,311	2,523	3,432	2,245	*-2,852*	*-4,082*	*-3,357*	*-4,414*	*-3,461*	-0,328
2,340	3,442	3,464	4,049	3,474	-3,758	-3,745	-3,393	-3,835	-5,304	-1,384
0,658	0,838	-0,065	-0,291	0,443	-0,004	0,190	0,004	-0,532	-0,627	2,948
-1,600	*-1,225*	*-1,363*	*-1,777*	*-0,189*	0,939	1,498	1,511	0,189	0,568	2,862
1,797	2,607	2,227	4,108	2,704	-3,021	-2,936	-3,240	-2,975	*-4,751*	-0,813
2,788	3,354	3,498	3,806	3,704	-3,818	-3,857	-3,610	-4,134	-5,766	-1,363
2,170	2,636	2,377	2,993	2,543	-4,011	-3,100	-3,828	-2,725	*-6,077*	-1,555
1,265	1,358	1,352	1,468	1,582	-3,223	-3,516	-3,205	-3,540	-4,170	-1,384
2,964	1,850	3,756	2,859	3,030	-3,395	-3,356	-3,499	-3,169	*-6,528*	-0,354
1,368	2,952	3,696	3,065	2,322	-1,864	-2,484	-1,755	-3,627	*-6,802*	-0,409
2,798	3,538	1,875	1,733	1,722	*-2,743*	*-2,752*	*-1,712*	*-1,916*	*-1,820*	1,490
0,324	1,525	0,710	0,448	-0,119	-0,325	-0,599	-0,242	-0,567	-1,145	1,574

0,087	0,240	-0,656	-0,940	-0,086	0,086	0,334	0,293	-0,270	-0,519	3,099
1,334	2,147	1,849	2,850	2,379	-3,082	-2,762	-2,882	-3,547	-4,026	-1,017
0,910	1,734	1,151	1,331	1,502	-2,884	*-3,705*	-2,388	*-3,347*	*-2,964*	-0,520
1,399	2,349	1,811	3,500	2,239	-2,825	-3,393	-4,869	-2,737	*-6,485*	-1,543
2,382	2,903	2,803	3,416	3,604	-3,185	-3,584	-3,159	-3,930	-3,513	-1,664
2,582	2,986	3,304	3,903	3,253	-3,112	-3,819	-3,368	-5,135	-4,127	-2,044
2,012	3,292	3,435	3,968	3,350	-2,939	-3,497	-3,325	-4,284	*-5,994*	-1,237
0,156	-0,032	-0,259	0,032	0,794	0,614	-0,224	-0,157	-0,620	0,808	2,596
0,011	0,674	0,297	0,509	1,431	-0,883	-1,777	-1,334	-2,100	-0,380	0,495
1,451	2,226	2,075	2,753	2,417	-3,014	-3,093	-3,035	-3,555	-4,316	-1,093
2,738	2,715	2,669	3,174	3,426	-3,571	-3,654	-3,211	-4,011	-4,838	-1,538
-0,418	-0,215	-0,292	0,026	0,647	0,479	-0,026	0,409	-0,201	0,325	2,882
1,795	2,218	2,734	2,893	2,125	-3,197	-3,532	-3,154	-3,739	-5,315	-1,721
1,519	3,461	2,429	3,336	2,804	-3,245	-3,202	-2,755	-4,546	*-6,493*	-1,435
2,814	1,748	2,586	2,000	2,621	*-2,920*	*-2,461*	*-2,885*	*-2,900*	*-2,911*	-1,091
-0,368	-0,053	0,366	-0,237	0,241	-0,060	0,391	0,053	0,566	*-0,889*	2,971
1,842	2,157	2,347	2,706	2,821	-3,823	-3,960	-3,585	-4,023	-4,522	-1,946
-0,054	0,419	0,936	1,403	2,066	-2,838	-3,532	-3,473	-3,775	-2,661	-0,681
-5,101	-3,176	*-3,264*	-2,940	*-3,379*	3,009	2,937	2,706	2,602	3,326	4,926
2,752	2,946	2,712	3,384	3,853	-3,543	-3,424	-3,112	-3,730	-4,439	-1,595
1,984	2,242	3,071	3,061	2,746	-3,183	-3,508	-2,913	-3,661	-5,462	-1,755
2,146	2,058	2,402	3,033	3,053	-3,520	-3,697	-2,982	-3,878	-4,456	-1,167
1,793	2,904	2,666	2,911	2,943	-3,565	-3,379	-2,999	-3,900	*-5,738*	-1,824
1,284	1,406	1,616	2,479	2,025	-3,044	-3,730	-3,229	-3,668	-3,765	-1,056
-1,714	-1,818	*-1,903*	*-3,626*	-1,787	2,600	2,187	2,761	1,714	2,207	4,932
0,433	0,683	0,871	1,431	2,292	-2,466	-3,543	-3,194	-3,156	-2,137	-0,152
-0,106	0,211	-0,465	-0,750	0,087	-0,007	0,091	0,007	-0,159	0,149	2,060
2,994	1,731	3,814	2,975	3,269	-3,006	-3,154	-3,070	-3,158	*-6,984*	-0,522
-0,282	*-0,262*	*0,383*	*-0,101*	*-0,203*	*1,380*	*1,549*	*0,946*	*0,047*	*-0,047*	3,530
0,600	1,864	0,285	0,709	0,702	-0,915	-1,744	-1,009	-1,687	-0,743	1,354
5,421	1,686	3,882	3,811	4,758	-1,608	-2,355	-1,137	-1,565	-1,901	1,034
-1,124	-0,457	-0,562	-0,633	0,631	0,897	0,393	0,736	-0,393	0,583	2,475
2,619	3,058	3,345	3,777	3,843	-3,923	-3,943	-3,733	-4,048	-5,808	-1,198
1,142	2,889	0,494	0,997	0,572	-1,077	-1,953	-1,375	-1,693	-1,804	0,713
3,156	2,749	2,602	3,741	2,998	-3,758	-3,443	-2,958	-4,066	*-6,615*	-1,384
1,173	1,336	1,472	2,239	1,913	-3,032	-3,662	-3,199	-3,785	-3,715	-1,035
1,272	2,112	1,741	2,846	2,446	-2,841	-2,483	-2,775	-3,436	-4,019	-0,973
0,983	1,250	1,087	0,993	1,476	-1,452	-1,707	-1,407	-2,022	-1,495	0,146
-0,822	-0,219	-0,725	-0,784	-0,357	0,937	0,535	0,623	0,219	0,898	2,346
-1,576	-1,528	-1,832	-1,226	-0,772	1,403	0,878	1,105	0,772	1,627	3,076
-5,025	-3,773	*-5,787*	*-4,588*	-1,903	2,021	2,121	2,224	1,903	2,107	6,071
0,908	1,908	-0,218	-0,776	0,001	-0,063	-0,001	-0,373	0,092	-0,141	5,190
0,919	1,597	1,683	1,737	1,385	-2,634	-3,161	-2,499	-3,359	-3,059	-0,919
-0,117	0,731	0,310	0,074	0,401	-1,215	-1,147	-0,710	-1,085	0,106	0,715
1,219	1,769	1,628	1,885	1,459	-1,621	-2,355	-1,951	-2,350	-3,013	-0,544
0,889	1,397	1,572	2,096	1,779	-3,130	-3,664	-3,646	-3,571	-3,656	-1,040
2,605	2,584	2,759	3,422	2,923	-4,075	-3,135	-3,353	-3,420	*-5,724*	-1,372
-0,400	-0,044	-0,710	-1,055	0,099	0,169	0,331	0,044	-0,480	0,311	1,916
0,988	1,376	1,353	0,977	1,047	*-2,828*	*-1,185*	*-2,867*	*-2,050*	-0,316	-0,279
-0,179	-0,303	-0,003	0,209	-0,246	0,030	0,338	-0,120	-0,225	-0,133	3,864
1,468	1,854	1,955	2,974	1,820	-3,023	-2,900	-2,972	-3,311	-4,388	-1,565
0,527	2,196	-0,018	0,484	0,429	-1,040	*-2,291*	-0,864	*-2,182*	-0,623	1,584
-0,585	-1,081	-1,872	-2,409	-2,482	0,922	1,024	0,819	0,585	0,623	3,190
2,383	2,113	1,798	1,949	1,845	-4,238	-4,214	-4,485	-4,789	-4,373	-1,108
0,547	1,034	0,769	1,023	1,412	-1,066	-1,526	-1,379	-1,869	-0,818	0,446
0,453	1,150	0,439	0,692	1,012	-1,399	-1,425	-1,133	-1,563	-0,964	0,038

2,919	1,778	1,936	2,082	5,102	-4,426	-4,426	-4,350	-4,017	*-7,254*	-1,864
1,855	2,573	3,293	3,233	1,943	*-4,708*	*-2,987*	*-3,381*	-2,015	*-2,439*	-0,779
0,058	0,436	0,239	0,173	0,522	-0,514	-0,766	-0,546	-1,122	-1,033	1,073
1,171	1,372	0,541	0,764	0,587	-1,428	-1,395	-1,102	*-3,287*	*-1,609*	1,760
-1,580	*-2,478*	-0,967	*-1,549*	*-1,863*	1,673	1,867	1,953	0,967	1,360	4,190
0,953	1,457	0,661	1,053	0,497	-1,364	-1,551	-1,287	-2,031	-1,716	1,281
-1,329	-0,579	-1,202	-0,805	-0,348	0,797	0,768	0,452	0,348	0,424	2,076
2,294	2,094	3,703	5,503	4,133	-2,424	*-5,374*	-2,744	-2,779	*-5,659*	-1,806
1,265	2,101	0,944	1,232	1,277	-0,814	-1,189	-0,919	-1,318	-0,849	1,613
1,313	2,272	1,353	2,113	2,417	-3,710	-2,944	-3,182	-2,435	*-6,155*	-0,967
0,157	0,636	0,450	0,721	0,496	-0,350	-0,859	-0,694	-1,491	-0,653	1,177
0,463	1,049	1,244	1,339	1,953	-2,589	-2,024	-1,576	-1,998	-1,373	-0,543
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0,158	0,741	-0,015	0,015	0,260	-0,530	-0,650	-0,521	-0,707	-1,064	0,746
0,486	1,056	0,848	0,766	0,433	-2,339	-2,176	-2,061	-2,368	-2,443	-0,336
0,772	1,413	0,991	1,248	1,659	-2,157	-2,497	-2,310	-2,832	-1,416	-0,745
0,754	2,091	0,450	0,796	0,833	-0,845	-1,000	-0,723	-1,334	-0,839	0,912
1,680	1,754	1,659	1,723	1,501	-3,171	-3,541	-2,956	-2,317	-5,049	-1,953
0,569	0,875	0,318	0,486	0,813	*-2,005*	*-1,242*	-0,137	*-1,332*	*-0,550*	0,552
-0,001	0,575	0,349	1,070	0,389	-1,241	-0,681	-1,107	-1,281	*-3,401*	0,639
0,014	0,821	0,287	0,351	1,446	-0,604	-1,136	-0,922	-1,764	0,034	0,274
0,342	0,720	0,644	0,918	1,444	-0,896	-1,464	-1,158	-1,253	-0,224	-0,062
-0,847	-0,197	-0,669	-0,655	-0,346	0,201	0,189	0,026	0,067	0,388	1,636
0,873	1,132	0,644	0,563	0,264	-0,370	-0,481	-0,264	-0,556	*-1,746*	1,275
0,588	0,988	0,539	0,545	0,021	-1,654	-2,069	-1,551	-1,969	-2,005	-0,804
0,572	1,124	1,196	1,494	1,953	-2,315	-3,083	-2,604	-3,093	-1,984	-1,010
0,390	0,750	1,236	0,801	1,084	-1,239	-1,896	-0,872	-1,256	-0,619	-0,084
-0,551	-1,846	-2,218	-2,538	-0,757	0,587	0,825	0,543	0,199	0,230	2,760
0,789	2,035	1,085	0,883	0,594	-1,815	-1,609	-1,702	-1,684	-1,973	-0,146
-0,272	0,517	-0,074	0,587	1,206	-0,629	-1,525	-0,496	-1,587	0,363	0,723
-0,679	0,193	0,327	0,652	0,367	-0,861	-1,095	-1,200	-0,594	-1,004	0,943
1,712	1,974	1,724	1,854	1,656	-2,807	-3,330	-2,815	-1,997	-4,469	-1,710
1,272	0,939	0,589	0,522	0,144	-1,954	-2,057	-1,679	-2,467	-2,727	-0,074
-1,956	-2,031	-2,193	-2,511	-2,101	1,804	2,023	1,691	1,978	1,691	4,390
0,068	*-0,999*	*-1,430*	*-0,178*	*-1,015*	*0,178*	0,793	1,079	*-0,068*	*0,129*	2,009
1,521	1,683	1,239	0,980	1,115	*-2,230*	*-2,714*	-1,703	*-3,261*	*-2,442*	-1,111
1,598	2,169	1,495	1,876	2,413	-2,151	-2,648	-2,519	-3,026	-1,660	-1,197
0,378	0,896	0,711	0,685	0,908	-0,748	-0,633	-0,646	-0,718	-0,774	0,806
0,911	0,304	-0,020	0,024	0,705	-0,559	-0,429	-0,381	-1,053	-0,616	0,994
-2,637	-1,553	-1,387	-1,245	-1,697	1,363	1,199	1,297	1,032	1,061	2,211

CD4creGARPfl-fl_stim_25	CD4creGARPfl-fl_stim_18	CD4creGARPfl-fl_stim_19	CD4creGARPfl-fl_stim_20	Refseq	GeneID
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4,380	4,737	3,797	5,578	NM_008198	14962
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2,955	-0,067	0,067	1,134	NM_010370	14938
1,592	1,441	-0,133	0,133	NM_024470	79410
0,281	*-1,217*	0,503	0,083	NM_001109657	14457
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-1,889	-2,309	-1,432	-1,618		
1,358	0,196	0,769	0,681	NM_007640	12480
3,172	*0,291*	*-0,575*	1,965	NM_019948	56619
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-0,413	*-1,959*	-0,948	-0,646	NM_033078	27007
0,765	0,248	0,457	0,903	NM_008463	16636
-1,809	*-2,652*	-1,242	-0,645		
1,840	-0,204	0,778	1,246	NM_024470	79410
-3,020	*-3,840*	-3,413	0,400		
-1,370	-1,600	-1,751	-0,898		
2,114	0,365	0,047	1,569	NM_008361	16176
0,279	-0,636	-0,466	1,180	NM_001077189	14130
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0,949	-0,817	-0,118	0,631	NM_011094	18730
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0,021	1,107	*-2,757*	0,086	NM_009369	21810
3,818	2,893	2,957	3,309	NM_010558	16191
1,625	-0,926	-0,316	0,353	NM_010649	16635
1,259	0,101	0,379	1,048	NM_010371	14940
-1,228	-2,146	-1,059	-0,541		
-1,688	-2,233	-1,365	-0,864		
2,970	2,395	1,795	3,209	NM_008392	16365
0,710	-0,452	-0,511	0,481	NM_021334	16411
0,655	2,021	*0,151*	1,980	NM_011888	24047
-1,927	-1,862	*-2,527*	-0,959		
-1,949	-1,795	-2,452	1,336		
4,008	3,490	4,213	4,551	NM_008373	16198
1,684	1,404	1,174	*0,857*	NM_008179	14853
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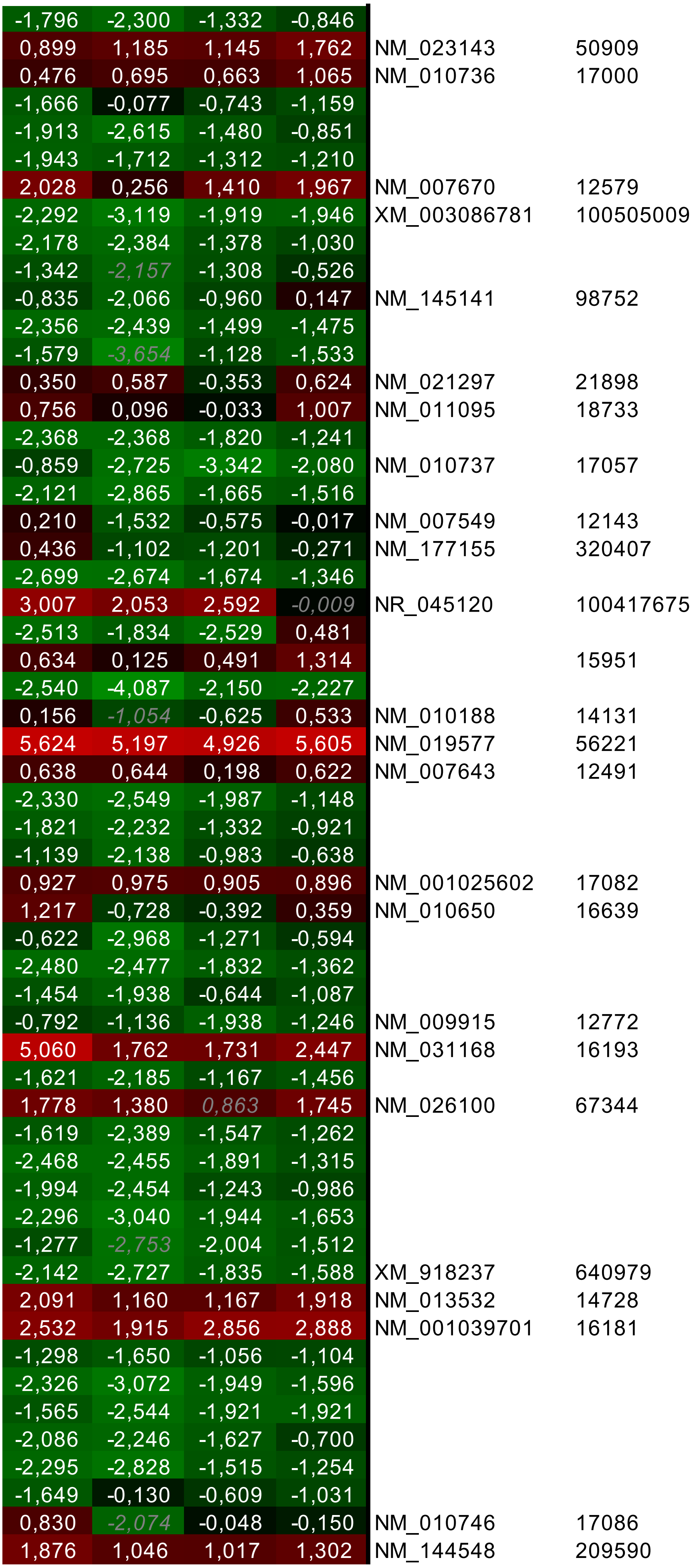

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0,899	1,185	1,145	1,762	NM_023143	50909
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-0,835	-2,066	-0,960	0,147	NM_145141	98752
-2,356	-2,439	-1,499	-1,475		
-1,579	*-3,654*	-1,128	-1,533		
0,350	0,587	-0,353	0,624	NM_021297	21898
0,756	0,096	-0,033	1,007	NM_011095	18733
-2,368	-2,368	-1,820	-1,241		
-0,859	-2,725	-3,342	-2,080	NM_010737	17057
-2,121	-2,865	-1,665	-1,516		
0,210	-1,532	-0,575	-0,017	NM_007549	12143
0,436	-1,102	-1,201	-0,271	NM_177155	320407
-2,699	-2,674	-1,674	-1,346		
3,007	2,053	2,592	*-0,009*	NR_045120	100417675
-2,513	-1,834	-2,529	0,481		
0,634	0,125	0,491	1,314		15951
-2,540	-4,087	-2,150	-2,227		
0,156	*-1,054*	-0,625	0,533	NM_010188	14131
5,624	5,197	4,926	5,605	NM_019577	56221
0,638	0,644	0,198	0,622	NM_007643	12491
-2,330	-2,549	-1,987	-1,148		
-1,821	-2,232	-1,332	-0,921		
-1,139	-2,138	-0,983	-0,638		
0,927	0,975	0,905	0,896	NM_001025602	17082
1,217	-0,728	-0,392	0,359	NM_010650	16639
-0,622	-2,968	-1,271	-0,594		
-2,480	-2,477	-1,832	-1,362		
-1,454	-1,938	-0,644	-1,087		
-0,792	-1,136	-1,938	-1,246	NM_009915	12772
5,060	1,762	1,731	2,447	NM_031168	16193
-1,621	-2,185	-1,167	-1,456		
1,778	1,380	*0,863*	1,745	NM_026100	67344
-1,619	-2,389	-1,547	-1,262		
-2,468	-2,455	-1,891	-1,315		
-1,994	-2,454	-1,243	-0,986		
-2,296	-3,040	-1,944	-1,653		
-1,277	*-2,753*	-2,004	-1,512		
-2,142	-2,727	-1,835	-1,588	XM_918237	640979
2,091	1,160	1,167	1,918	NM_013532	14728
2,532	1,915	2,856	2,888	NM_001039701	16181
-1,298	-1,650	-1,056	-1,104		
-2,326	-3,072	-1,949	-1,596		
-1,565	-2,544	-1,921	-1,921		
-2,086	-2,246	-1,627	-0,700		
-2,295	-2,828	-1,515	-1,254		
-1,649	-0,130	-0,609	-1,031		
0,830	*-2,074*	-0,048	-0,150	NM_010746	17086
1,876	1,046	1,017	1,302	NM_144548	209590

2,177	0,986	1,404	1,954	NM_013532	14728
-1,751	-2,307	-1,228	-0,949		
-1,112	-1,364	-1,644	-0,263	NM_028728	74039
-3,331	-2,902	-1,544	-0,742		
-2,216	-2,311	-1,527	-1,326		
-1,977	-3,782	-0,951	-1,221		
-2,117	-3,417	-1,662	-1,510		16061
1,582	1,488	1,675	2,401	NM_009877	12578
0,165	-0,011	0,613	1,809	NM_009844	12478
-1,544	-2,382	-1,265	-0,911		
-2,311	-2,563	-1,834	-1,363		
2,139	0,930	1,384	2,179	NM_007670	12579
-2,309	-2,296	-1,474	-1,009		
-1,987	-3,384	-1,286	-0,645		
-2,080	*-1,626*	-0,536	-0,344		
2,620	1,858	1,556	1,823	NM_016971	50929
-2,497	-2,339	-2,164	-1,156	NM_152839	16069
-2,323	-2,012	-1,682	0,245		
4,728	4,000	4,589	4,713	NM_008355	16163
-2,590	-2,250	-1,786	-1,427		
-2,206	-2,363	-1,346	-0,830		
-2,488	-2,553	-1,946	-0,966		
-2,431	-2,500	-1,650	-1,024		
-2,512	-2,331	-1,935	-0,814		
3,768	3,935	3,683	4,673	NM_008599	17329
-1,671	-1,590	-1,451	0,589		
1,762	1,014	1,231	1,710	NM_011617	21948
-2,431	-2,571	-1,457	-1,312		
2,643	2,925	2,289	2,202	NM_203320	330122
1,225	-0,753	0,361	0,681	NM_001110323	16638
0,079	-0,252	-0,931	0,570	NM_009396	21928
2,264	1,893	1,980	2,690	NM_011611	21939
-2,637	-3,200	-2,271	-1,435		
1,093	-0,691	-0,280	-0,029	NM_010650	16639
-2,584	-3,366	-2,101	-1,854		
-2,390	-2,293	-2,008	-0,785		
-1,714	-2,491	-1,198	-0,976		
0,129	-0,614	-0,367	0,152	NM_022021	63955
2,371	1,655	1,691	2,242	NM_010215	14204
3,069	2,552	2,639	2,721	NM_011332	20295
4,489	3,224	3,205	3,724	NM_010556	16187
2,667	0,804	1,535	1,464	NM_011338	20308
-1,375	-1,607	-1,976	-1,475	NM_015790	50723
0,492	0,323	-0,074	0,760	NM_020044	56743
-0,522	-1,530	-0,781	-1,222	NM_007640	12480
-2,496	-2,683	-2,105	-0,467		
-2,095	-3,140	-1,894	-1,869		
1,673	1,275	1,196	1,951	NM_010555	16178
-0,845	-0,566	-0,558	*-0,866*	NM_001134458	16199
1,489	0,982	1,268	1,344	NM_008337	15978
-2,254	-1,933	-1,256	-0,716		
1,468	-0,340	0,251	0,414	NM_014194	16638
2,912	1,611	1,954	2,270	NM_013542	14939
-2,813	-3,366	-3,284	-2,926	NM_013653	20304
0,064	-0,149	-0,064	1,060	NM_001042605	16149
0,293	-0,230	-0,489	0,056	NM_010580	16419

-3,210	-3,753	-3,006	0,243	XM_001476673	100046710
-2,078	*-2,746*	-1,239	-1,612		
0,610	0,330	0,550	1,265	NM_021274	15945
1,108	-0,677	-0,357	-0,059	NM_030599	80782
3,038	2,863	3,007	3,804	NM_008599	17329
0,583	-0,638	-0,513	-0,217	NM_030599	80782
1,845	1,409	1,633	1,784	NM_009401	21941
-1,452	-2,407	-1,035	-0,882		
1,193	-0,143	-0,081	0,394	NM_010185	14127
-2,021	-3,161	-1,875	-1,018		
0,601	-0,039	0,412	0,797	NM_009142	20312
-1,121	-0,725	-0,885	0,325	NM_007655	12518
0,534	0,081	0,337	0,010	NM_023158	66102
0,604	-0,044	0,238	0,632	NM_012057	27056
-0,772	-1,497	-1,564	-1,093	NM_008329	15951
-1,089	-1,162	-1,103	-0,064	NM_008339	15985
1,104	-0,291	-0,005	0,374	NM_010651	16640
-2,214	-1,574	-2,207	-1,038		
-0,024	-0,034	*-1,143*	0,677	NM_008795	18557
-0,001	-0,519	-0,029	-0,099	NM_010652	16641
-0,088	-0,014	0,585	1,772	NM_001169153	246746
-0,282	0,030	0,111	1,188	NM_028075	72049
1,766	1,100	1,063	1,370	NM_019465	54698
1,776	0,575	0,701	0,692	NM_008362	16177
-0,936	-1,270	-0,755	-0,021	NM_133211	170743
-1,520	-1,550	-1,440	-0,047		12518
0,084	-0,348	-0,321	0,329	NM_024124	79221
1,785	1,564	1,697	1,488	NM_021782	60505
0,141	-0,567	-0,823	-0,758	NM_001034031	57890
0,361	-0,020	0,492	1,849	NM_008370	16192
0,259	-0,503	0,110	0,070	NM_008510	16963
-2,042	-1,529	-1,964	-1,049		
-0,865	-1,970	-1,408	-0,964	NM_010553	16174
3,225	2,416	2,888	2,717		20290
2,003	*0,598*	1,013	1,228	NM_001079876	237436
-1,395	-1,424	-1,702	-0,429	NM_010871	17952
-1,479	-1,873	-1,803	-0,486	NM_026976	69169
0,312	0,123	0,168	0,635	NM_007609	12363
0,865	0,020	0,130	0,455	NM_001025602	17082
2,341	1,843	2,286	2,210	NM_021283	16189