Figure S1. Representative gating scheme for flow cytometric analysis of the tumor-splenocyte co-cultures.
Naïve, unfractionated splenocytes from WT C57BL/6J mice were co-cultured with irradiated RMAS cells as described in the Materials and Methods for 5 days. Cells were harvested from the co-cultures and stained with primary-conjugated antibodies against CD4, CD8, and Foxp3 to assess yields of various T cell compartments by flow cytometry.

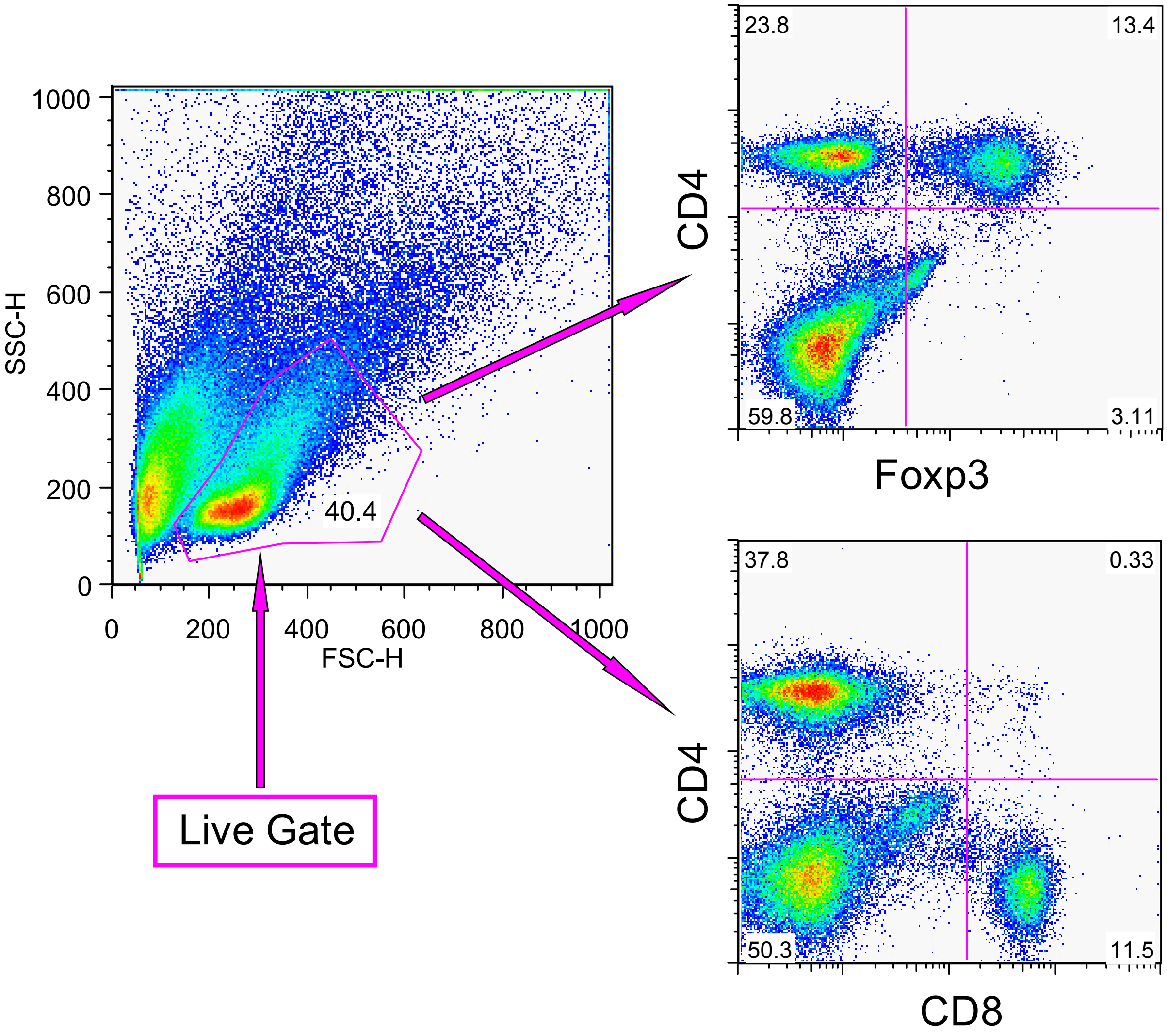


Figure S2. Non-T accessory splenocytes and IL-2 are required for Treg expansion. **A.** 1 x 10^6 Pan T cells were isolated from the resting spleens of WT 129/SvPas or C57BL/6J mice, and cultured in 2 ml of standard K10 medium only, or in the presence of 3 x 10^6 T cell depleted (TcD) splenocytes, or 1.2 x 10^5 irradiated RMAS tumor cells, or both, for 5 days. **B.** Instead of RMAS cells, cryopreserved primary APL cells harvested from the spleens of 3 independent leukemic mCG-PML-RARα transgenic mice were irradiated (3,000 Rads) and used at the same doses in the co-cultures. **C.** 4 x 10^6 unfractionated splenocytes were cultured with 1.2 x 10^5 irradiated RMAS tumor cells for 5 days. At the beginning of the culture, a TGF-β neutralizing antibody (1D11) or its isotype control (11711.11), or an IL-2 neutralizing antibody (JES6-5H4) or its isotype control (R35-95) were added to a final concentration of 10 μg/ml. **D.** Identical to Panel C, except that primary APL cells were irradiated and used in the cultures. At the beginning and the end of co-cultures, $CD4^+Foxp3^+$ Treg cell numbers were assessed as described in the Materials and Methods. Treg cell expansion is presented as fold-change of the final yield over initial input. Shown are summaries of 2 independent experiments. Data points are shown as mean ± SD; Two-tailed t-tests were used to determine statistical significance (*P<0.05, **P<0.01, ***P<0.001).

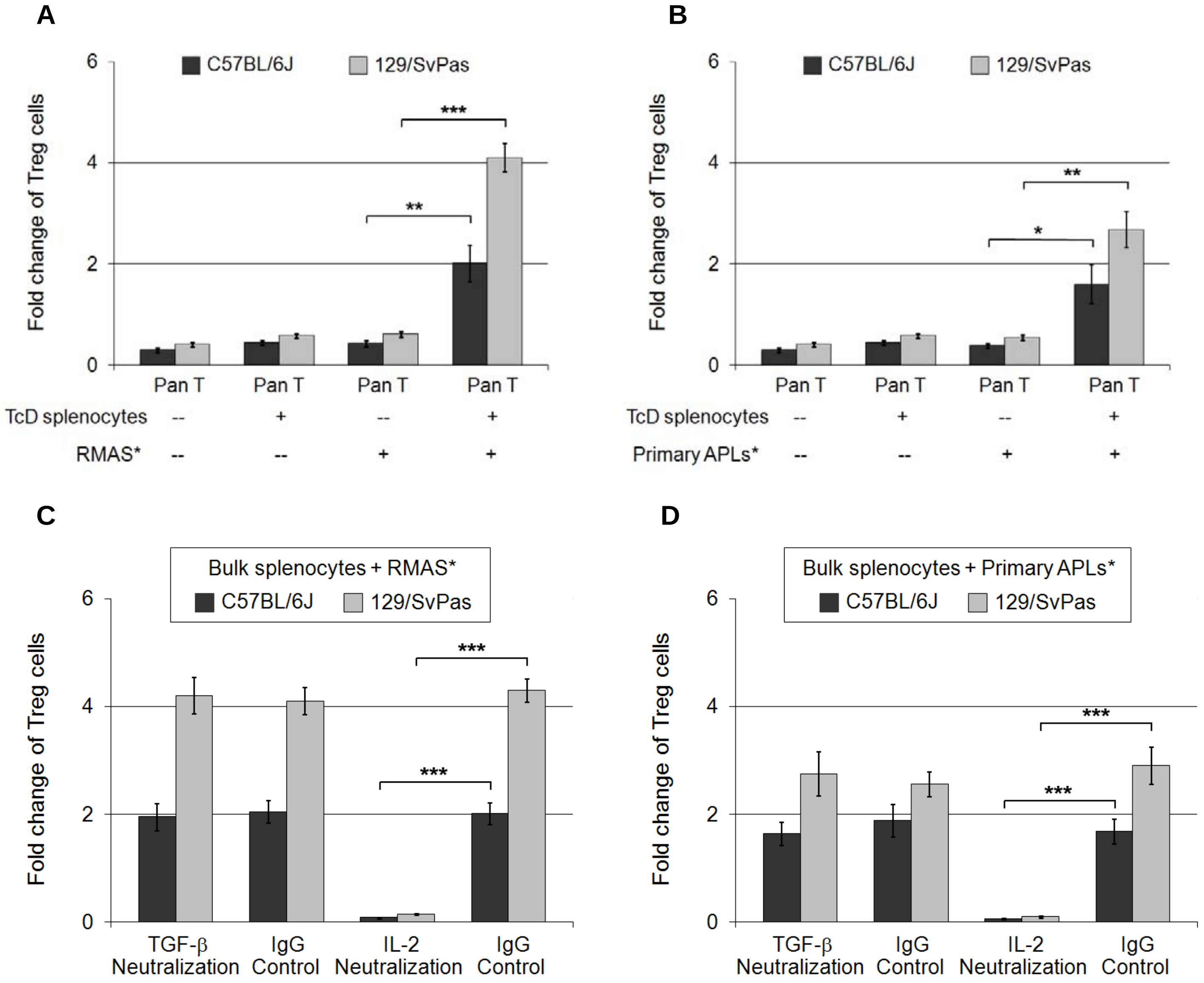


Figure S3. Cytokine receptor expression profiles of naïve and tumor-associated Treg cells.

Naïve Treg cells were purified from the resting spleens of FoxP3-GFP knock-in mice made in the 129/SvJ strain. Ascites Treg cells are tumor-associated FoxP3-GFP$^+$ cells that were sorted from the tumor ascites of 129/SvJ mice IP-injected with 1 x 10^6 RMAS cells 5 days earlier; Spleen^T Treg cells were purified from the spleens of the same tumor-bearing mice. The purity of the sorted Treg cells is >99%. Affymetrix MOE430v2 arrays were used to perform gene expression studies. Shown here is absolute abundance of selected cytokine receptor gene mRNAs. The complete set of Treg gene expression data is deposited in Gene Expression Omnibus (GEO) microarray database (http://www.ncbi.nlm.nih.gov/geo/), accession number GSE13409. Two-tailed t-tests were used to determine statistical significance (*P<0.05, **P<0.01, ***P<0.001; ∇ indicates below detection limits of MAPs; Open ο indicates an "absent" call on the Affymetrix arrays).

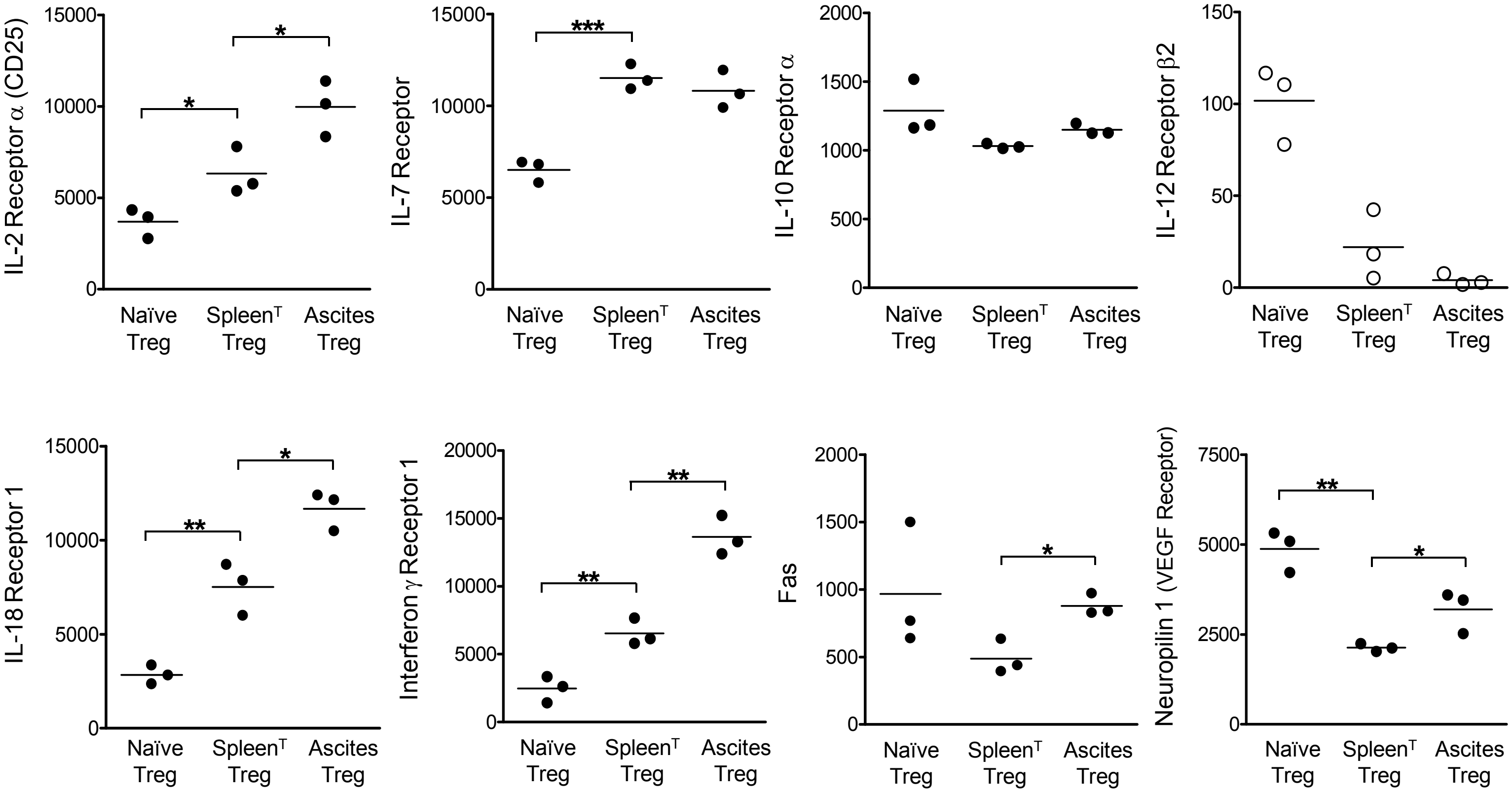


Figure S4. CFSE-labeled Treg cells proliferated differentially.

MACS-purified $CD4^+CD25^+$ Treg cells were labeled with CFSE and mixed with WT splenocytes and irradiated RMAS cells for 4 days. Representative histograms of $CFSE^+$ $CD4^+Foxp3^+$ Treg cells are shown at day 0 and day 4. A subset of Treg cells retained high levels of CFSE, while other subpopulations of Treg cells diluted CFSE signal to lower levels by proliferating more extensively.

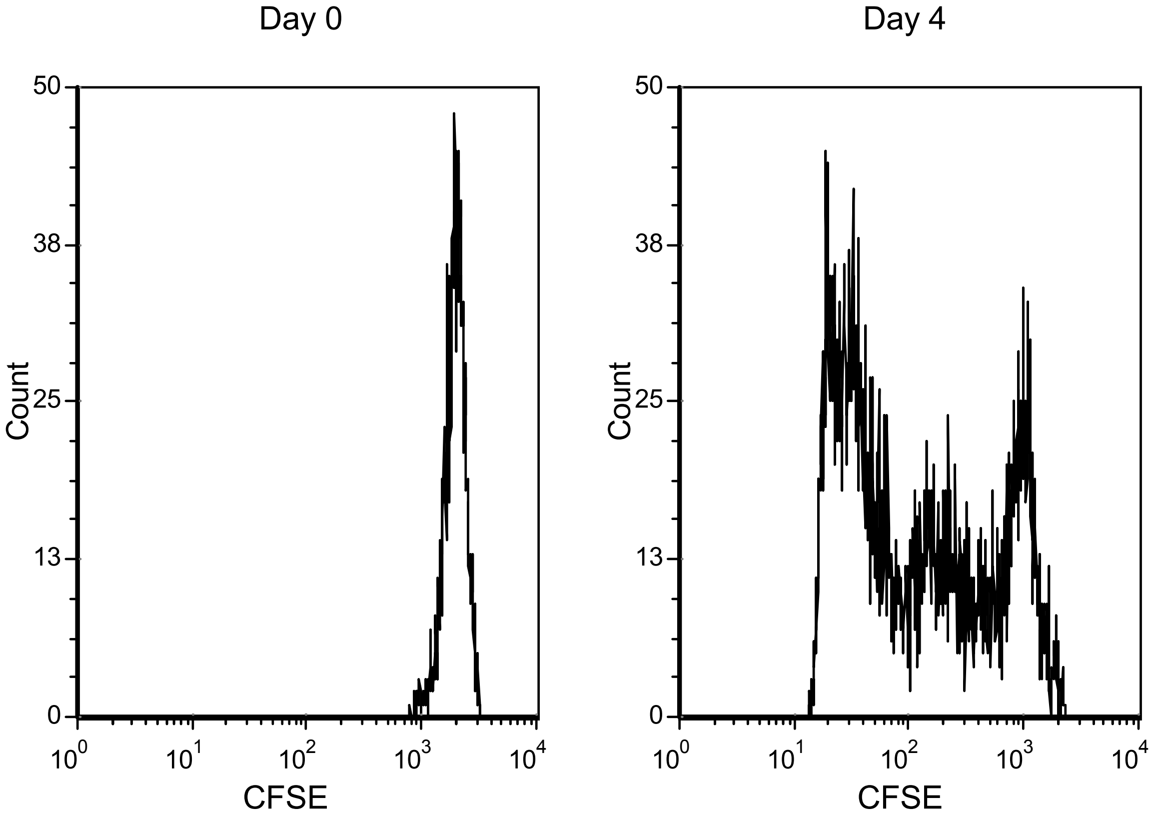
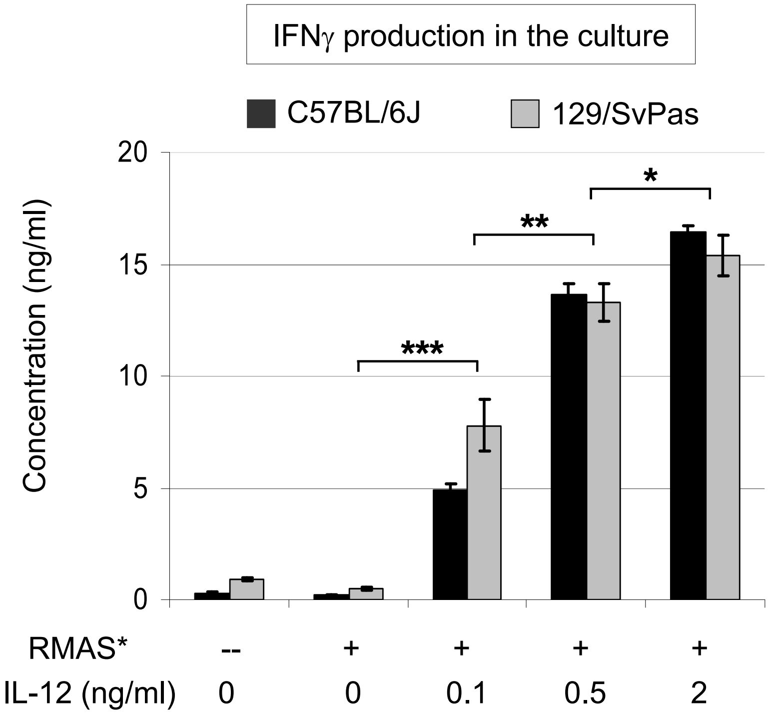


Figure S5. IL-12 treatment increases IFNγ secretion, and decreases IL-2 secretion. Naïve, unfractionated splenocytes from WT mice were cultured alone or with irradiated RMAS cells for 5 days in the presence of the indicated doses of IL-12, as described in the Materials and Methods. IFNγ and IL-2 concentrations were measured by performing ELISA assays (e-Bioscience) using the cell-free media harvested from the cultures. Shown are representative data from 1 of 3 independent experiments performed with similar results. Data points are shown as mean ± SD; Two-tailed t-tests were used to determine statistical significance (*P<0.05, **P<0.01, ***P<0.001).

A



B

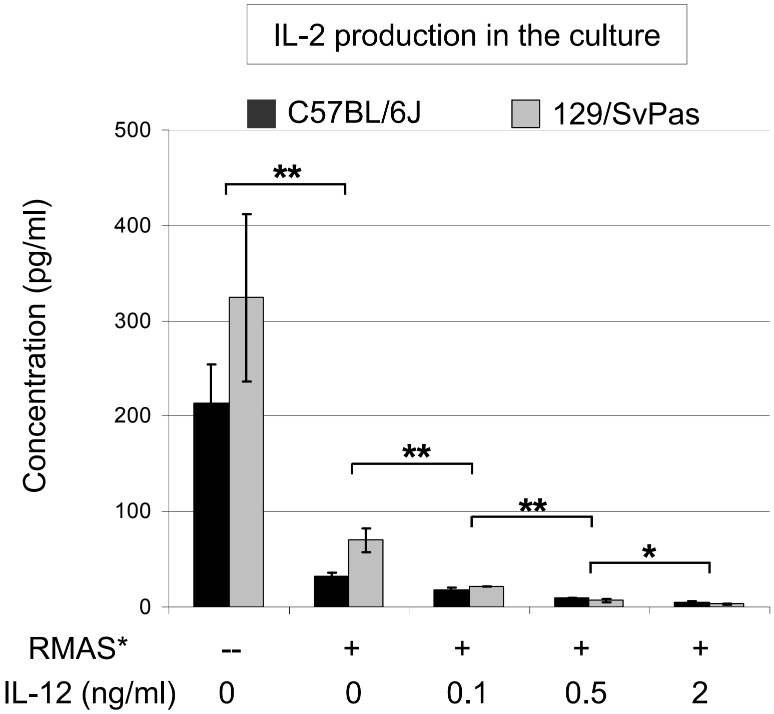


Figure S6. IL-12 treatment enhances tumor clearance more efficiently than Treg cell depletion *in vivo*. Four days prior to RMAS injection, 129/SvJ WT mice received a single IP injection of 400 μg PC61 CD25 antibody to deplete Treg cells (TrD), or were injected with an isotype control antibody. From day 0 to day 7 after IP injection of 2 x 10^6 luciferase-expressing RMAS cells, these mice were injected IP daily with equal volumes of PBS, while a third set of mice received 100 ng of IL-12 IP daily. Bioluminescence imaging was performed to monitor tumor burden. Representative images (**A**) and summary data (**B**) of 2 independent experiments are shown. Data points are shown as mean ± SD; Two-tailed t-tests were used to determine statistical significance (*P<0.05, **P<0.01, ***P<0.001).

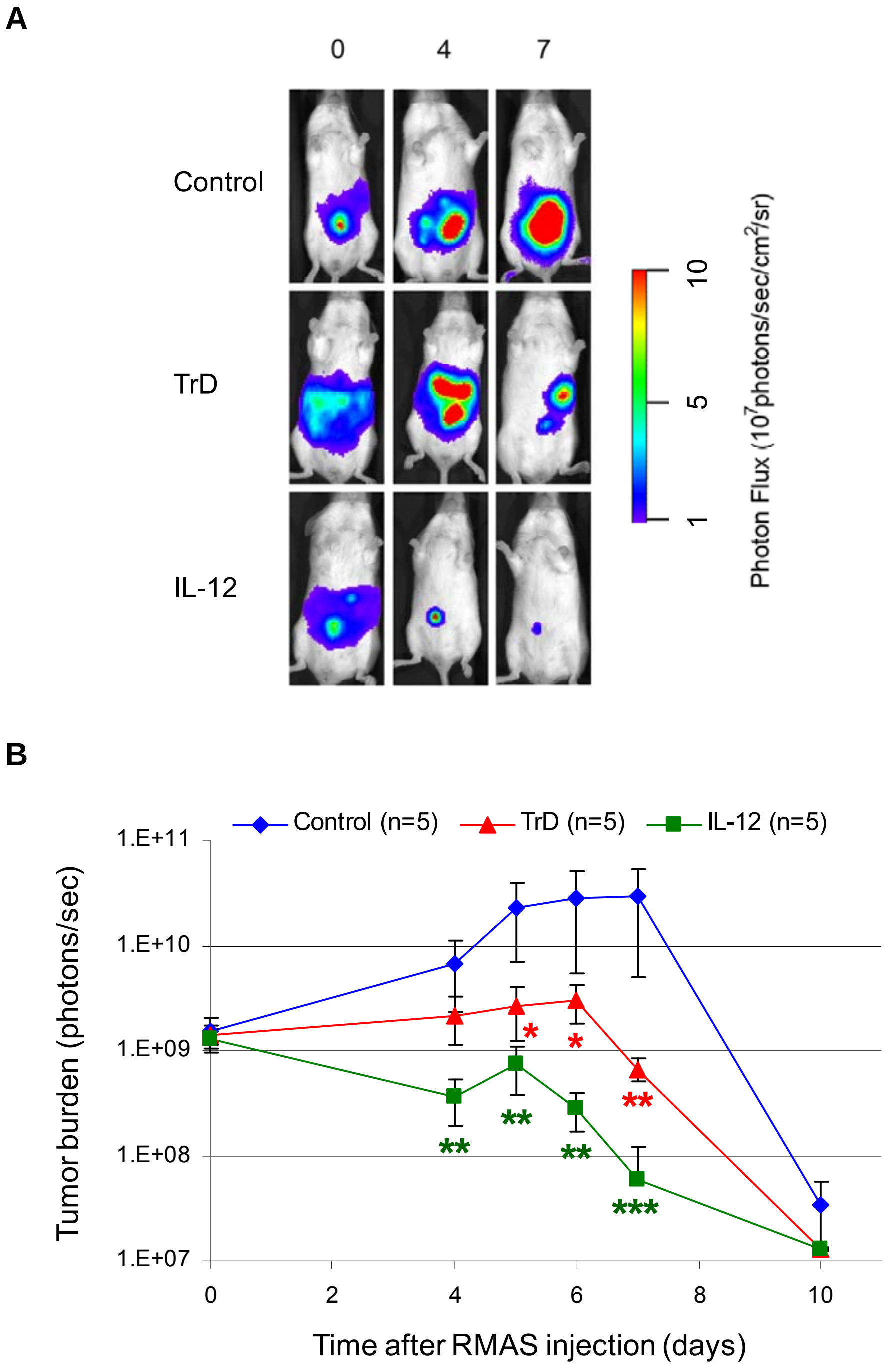


Figure S7. IL-12 treatment does not cause significant cell death in the Treg cell compartment.
Naïve, unfractionated splenocytes from Foxp3-GFP knock-in mice were co-cultured with irradiated RMAS cells as described in the Materials and Methods for 4 days. Lymphocytes were harvested from the co-cultures and stained with primary-conjugated antibody against CD4 and 7-AAD to assess cell death in the GFP+ Treg and GFP- non-Treg compartments by flow cytometry. Shown here are representative data from two independent experiments.

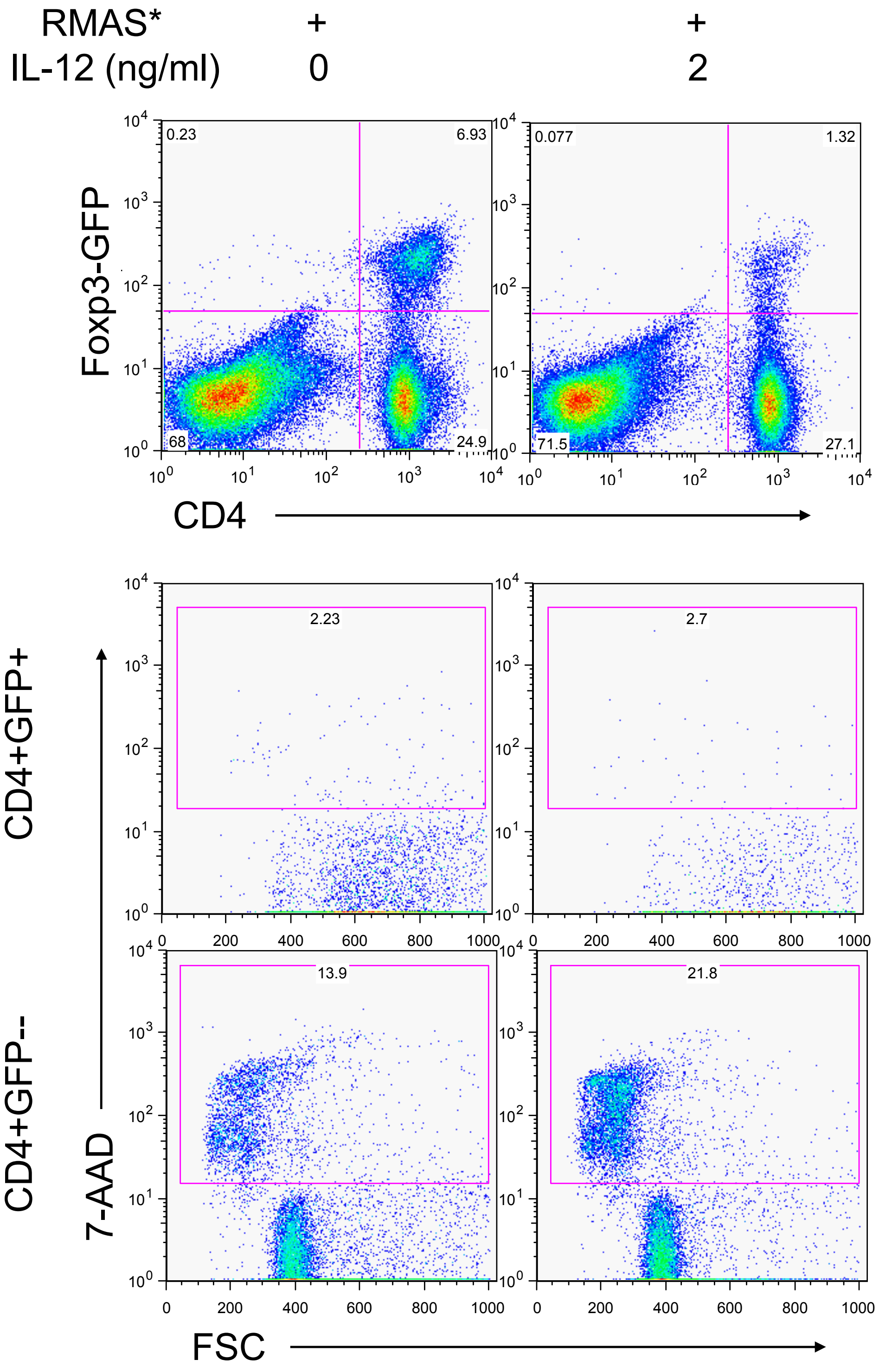
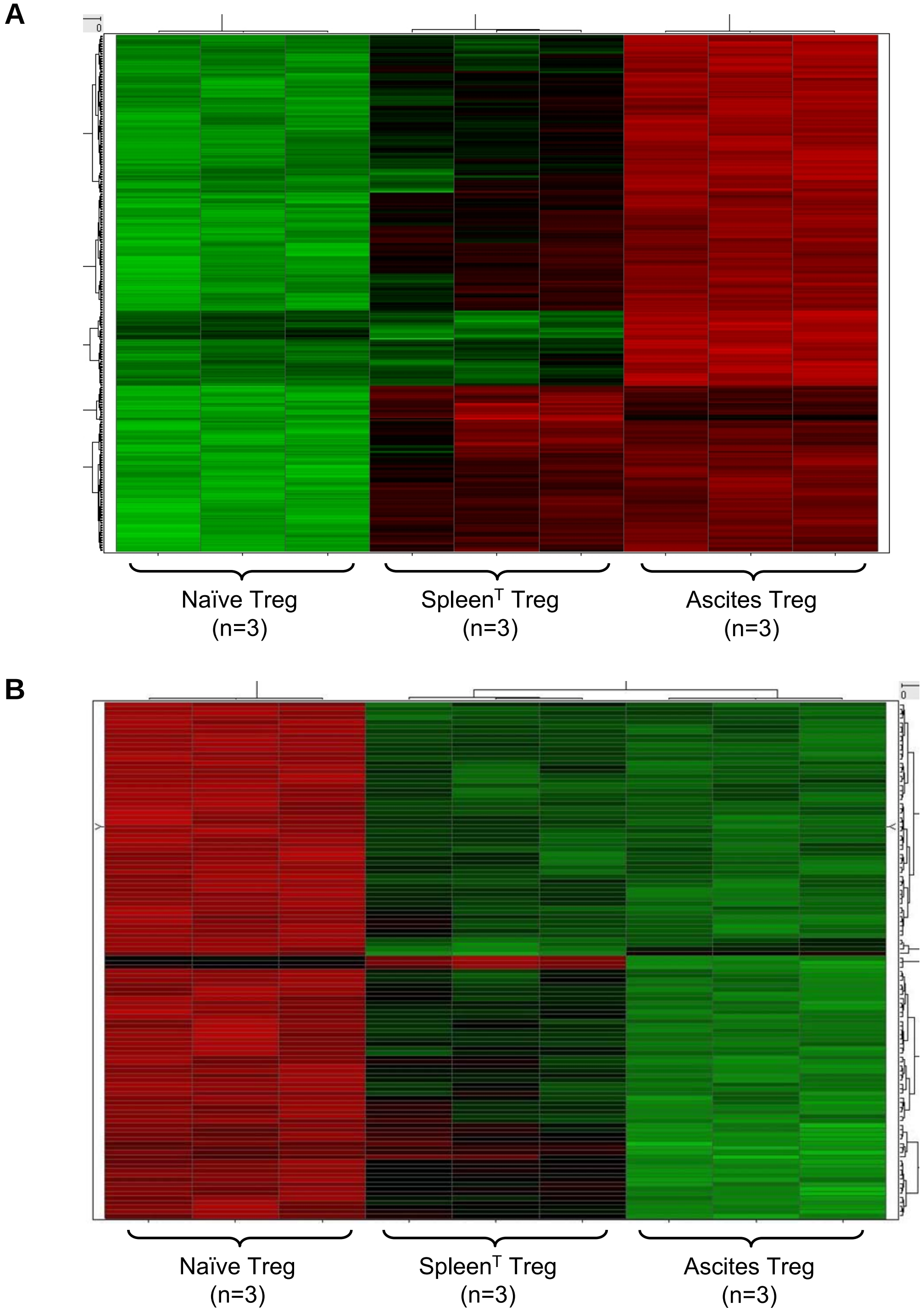


Figure S8. Gene expression profiles of naïve versus tumor-associated Treg cells. Naïve, Spleen^{T}, and Ascites Treg cells were purified and Affymetrix MOE430v2 arrays were performed as described in Figure S3. RMA normalization was performed for all microarray data. 2-group comparison (t-test) of Ascites vs. Naïve samples, with multiple test corrections (adjusted p-value/FDR(false discovery rate) = q-value) was performed. **A.** Shown is a heat map of 419 probesets with $q<0.005$ and linear fold change ≥ 2 (Ascites:Naïve) **B.** Shown is a heat map of 114 probesets with $q<0.005$ and linear fold change ≤ 0.5 (Ascites:Naïve). Red indicates relatively increased expression; green indicates relatively decreased expression. Gene titles and fold changes of the 419 up-regulated and 114 down-regulated probesets are shown in the Supplement Table on next page.



Supplemental Table. Gene titles and fold changes of the 419 up-regulated and 114 down-regulated probesets. Naïve, Spleen^T, and Ascites Treg cells were purified and Affymetrix MOE430v2 arrays were performed as described in Figure S3. Data analysis was performed as described in Figure S8. Shown here are the 419 probesets with q<0.005 and linear fold change ≥ 2 (Ascites:Naïve) and the 114 probesets with q<0.005 and linear fold change ≤ 0.5 (Ascites:Naïve). The GO annotations for these probesets are shown in the attached supplemental Excel file. The complete set of Treg gene expression data is deposited in Gene Expression Omnibus (GEO) microarray database (http://www.ncbi.nlm.nih.gov/geo/), accession number GSE13409.

Figure S5 Probeset ID	Gene Title	Gene Symbol	Ascites Average (linear)	Naive Average (linear)	Linear Fold Change (Ascites: Naive)	q-value
1436996_x_at	lysozyme 1	Lyz1	4913.833753	26.46725492	185.6571	0.003202
1425923_at	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	Mycn	6107.219573	89.46842204	68.26117	0.004591
1419060_at	granzyme B	Gzmb	7644.465941	194.8585376	39.23085	0.004591
1448226_at	ribonucleotide reductase M2	Rrm2	1941.020985	51.67782095	37.56004	0.004149
1421811_at	similar to thrombospondin 1 /// thrombospondin 1	LOC640441 /// Thbs1	405.1540261	11.40715145	35.51755	0.004679
1426642_at	fibronectin 1	Fn1	1328.424021	44.7807463	29.66507	0.003976
1424046_at	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	Bub1	419.805328	14.77783821	28.40776	0.004149
1429295_s_at	thyroid hormone receptor interactor 13	Trip13	1103.21378	40.77774241	27.05431	0.004458
1417019_a_at	cell division cycle 6 homolog (S. cerevisiae)	Cdc6	763.9670823	29.08580509	26.26598	0.002488
1415810_at	ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	1810.95293	69.44633563	26.07701	0.003202
1428304_at	establishment of cohesion 1 homolog 2 (S. cerevisiae)	Esco2	206.5904852	8.006804977	25.80186	0.004405
1426774_at	poly (ADP-ribose) polymerase family, member 12	Parp12	1007.350479	40.99842738	24.57047	0.004701
1424727_at	chemokine (C-C motif) receptor 5	Ccr5	937.4231849	39.9458392	23.46735	0.003166
1434437_x_at	ribonucleotide reductase M2	Rrm2	2815.547939	124.3066786	22.65001	0.004304
1416343_a_at	lysosomal-associated membrane protein 2	Lamp2	297.6720592	13.16744322	22.60667	0.002488
1422430_at	fidgetin-like 1	Fignl1	646.8347305	29.77094957	21.72704	0.004461
1421186_at	chemokine (C-C motif) receptor 2	Ccr2	2943.873574	136.8043221	21.51886	0.004149
1454694_a_at	topoisomerase (DNA) II alpha	Top2a	3435.807121	159.9673132	21.47818	0.004304
1450194_a_at	myeloblastosis oncogene	Myb	898.4804693	42.55706248	21.11237	0.004591
1417266_at	chemokine (C-C motif) ligand 6	Ccl6	641.3686382	32.10538365	19.97698	0.004304
1416802_a_at	cell division cycle associated 5	Cdca5	938.5848305	47.09830821	19.92821	0.004304
1417719_at	sin3 associated polypeptide	Sap30	706.4482151	36.90667851	19.14147	0.004304
1424278_a_at	baculoviral IAP repeat-containing 5	Birc5	478.0938376	25.19536876	18.97546	0.004304
1417910_at	cyclin A2	Ccna2	572.4847027	30.88982944	18.53311	0.004922
1436847_s_at	cell division cycle associated 8	Cdca8	1898.397864	105.256827	18.03586	0.004963
1451313_a_at	RIKEN cDNA 1110067D22 gene	1110067D22Rik	526.4392816	29.51923304	17.83377	0.003976
1436203_a_at	RIKEN cDNA 1110059G02 gene	1110059G02Rik	787.6385971	45.5234082	17.30184	0.003976
1452912_at	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	Dscc1	348.389339	20.21419248	17.23489	0.004864
1417898_a_at	granzyme A	Gzma	718.8747729	43.26944367	16.61391	0.004591
1448466_at	cell division cycle associated 5	Cdca5	332.3815902	20.33382893	16.34624	0.004405
1448627_s_at	PDZ binding kinase	Pbk	835.7224029	53.70768628	15.56057	0.004304

1418322_at	cAMP responsive element modulator	Crem	1162.821014	75.63191972	15.37474	0.004681
1424128_x_at	aurora kinase B	Aurkb	365.6940475	24.14796985	15.14388	0.004681
1419082_at	serine (or cysteine) peptidase inhibitor, clade B, member 2	Serpinb2	199.5043878	13.22971429	15.08002	0.004405
1448213_at	annexin A1	Anxa1	812.3400705	54.13000689	15.0072	0.004681
1451246_s_at	aurora kinase B	Aurkb	339.1555599	22.64294962	14.97842	0.004581
1428104_at	TPX2, microtubule-associated protein homolog (Xenopus laevis)	Tpx2	425.6301876	28.44454305	14.96351	0.004663
1420338_at	arachidonate 15-lipoxygenase	Alox15	376.5401772	25.29867637	14.88379	0.004304
1435327_at	lysophosphatidylglycerol acyltransferase 1	Lpgat1	394.2426368	26.53031684	14.86008	0.002697
1417541_at	helicase, lymphoid specific	Hells	612.0489938	41.69695133	14.67851	0.004149
1417926_at	non-SMC condensin II complex, subunit G2	Ncapg2	490.5704985	33.88786088	14.47629	0.004174
1427707_a_at	Scl/Tal1 interrupting locus	Stil	226.5182271	15.74618032	14.3856	0.004701
1449037_at	cAMP responsive element modulator	Crem	2089.439108	146.8585381	14.22756	0.004591
1421855_at	fibrinogen-like protein 2	Fgl2	782.3588427	55.1602338	14.18339	0.004681
1416579_a_at	epithelial cell adhesion molecule	Epcam	1288.767825	90.95388349	14.16946	0.004591
1434695_at	denticleless homolog (Drosophila)	Dtl	603.3020468	43.13518784	13.98631	0.004304
1416120_at	ribonucleotide reductase M2	Rrm2	909.0694254	66.81622947	13.60552	0.003976
1436325_at	RAR-related orphan receptor alpha	Rora	1032.230894	77.49439167	13.32007	0.004304
1447363_s_at	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	Bub1b	518.4352484	40.19525598	12.89792	0.004922
1434427_a_at	ring finger protein 157	Rnf157	979.7772615	76.69921994	12.77428	0.003976
1416076_at	cyclin B1 /// predicted gene, EG434175 /// predicted gene, EG667005	Ccnb1 /// EG434175 /// EG667005	434.5856317	34.05378687	12.76174	0.004965
1440408_at	RIKEN cDNA B830008J18 gene	B830008J18Rik	391.1875558	31.33927717	12.48234	0.004304
1448314_at	cell division cycle 2 homolog A (S. pombe)	Cdc2a	485.2092801	39.27746732	12.35337	0.004405
1428369_s_at	Rho GTPase activating protein 21	Arhgap21	425.5436559	34.48076792	12.34148	0.003057
1426817_at	antigen identified by monoclonal antibody Ki 67	Mki67	4152.41043	338.4651146	12.26836	0.004304
1424176_a_at	annexin A4	Anxa4	396.4018815	32.80142682	12.0849	0.004701
1416318_at	serine (or cysteine) peptidase inhibitor, clade B, member 1a	Serpinb1a	394.2080243	32.75674273	12.03441	0.004591
1427615_at	integrin alpha 4	Itga4	159.5056075	13.29919177	11.99363	0.004048
1450744_at	elongation factor RNA polymerase II 2	Ell2	642.6116534	54.10424925	11.87729	0.004591
1435306_a_at	kinesin family member 11	Kif11	170.7434786	14.40492256	11.85313	0.003976
1450920_at	cyclin B2	Ccnb2	995.6466378	84.89807871	11.72755	0.004911
1438288_x_at	RIKEN cDNA 1110059G02 gene	1110059G02Rik	375.2816659	32.22987452	11.64391	0.004174
1428094_at	lysosomal-associated membrane protein 2	Lamp2	2095.04667	180.8838758	11.58227	0.004461
1435264_at	elastin microfibril interfacer 2	Emilin2	481.9033433	41.8827229	11.50602	0.00423
1424629_at	breast cancer 1	Brca1	433.7460071	37.82225127	11.46801	0.004304
1448167_at	interferon gamma receptor 1	Ifngr1	9109.145434	806.1810156	11.29913	0.004461
1424895_at	G-protein signalling modulator 2 (AGS3-like, C. elegans)	Gpsm2	400.6874	36.07531283	11.10697	0.004304
1416698_a_at	CDC28 protein kinase 1b	Cks1b	3784.446683	341.98123	11.06624	0.004304
1452011_a_at	UDP-glucuronate decarboxylase 1	Uxs1	528.1424644	47.81009388	11.04667	0.004681
1417063_at	complement component 1, q subcomponent, beta polypeptide	C1qb	197.7334768	17.97711988	10.99917	0.003976
1455030_at	protein tyrosine phosphatase, receptor type, J	Ptprj	142.5182964	13.03079621	10.93704	0.004681
1419943_s_at	cyclin B1	Ccnb1	465.1342395	43.49698001	10.69348	0.004174
1450484_a_at	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	Cmpk2	448.1661885	42.12398444	10.63922	0.004304
1419042_at	interferon inducible GTPase 1	Iigp1	2259.36243	216.675166	10.42742	0.004591
1434316_at	chondroitin sulfate synthase 1 /// similar to mKIAA0990 protein	Chsy1 /// LOC100047	902.8421729	86.97145108	10.3809	0.004304

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1424704_at	runt related transcription factor 2	Runx2	1358.312767	131.3434094	10.34169	0.002608
1423804_a_at	isopentenyl-diphosphate delta isomerase	Idi1	896.6244311	87.23347764	10.27844	0.004304
1449708_s_at	checkpoint kinase 1 homolog (S. pombe)	Chek1	382.6097956	37.45491995	10.21521	0.003202
1418264_at	centromere protein K	Cenpk	223.8114446	22.03314193	10.15795	0.004922
1443481_at	epsilon-tubulin 1	Tube1	155.9139999	15.47552735	10.07487	0.004343
1436004_at	ubiquitin specific peptidase 27, X chromosome	Usp27x	322.1353853	32.05453703	10.0496	0.002608
1424083_at	ROD1 regulator of differentiation 1 (S. pombe)	Rod1	547.8422291	55.13347638	9.936653	0.00477
1450862_at	RAD54 like (S. cerevisiae)	Rad54l	443.7582097	45.66594131	9.717487	0.004864
1429658_a_at	structural maintenance of chromosomes 2	Smc2	360.8728174	37.51502636	9.619421	0.00477
1420897_at	synaptosomal-associated protein 23	Snap23	1089.378814	114.5282744	9.511877	0.004304
1449207_a_at	kinesin family member 20A	Kif20a	199.4592195	21.40515929	9.318278	0.004343
1421968_a_at	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	Nipa2	594.1733136	64.87571672	9.15864	0.003665
1426205_at	similar to protein phosphatase 1 /// protein phosphatase 1, catalytic subunit, b	LOC100044953 /// Ppp1cb	3336.454236	366.1709001	9.111741	0.004688
1433428_x_at	transglutaminase 2, C polypeptide	Tgm2	228.8782666	25.25901834	9.061249	0.004304
1433696_at	hematological and neurological expressed 1-like	Hn1l	248.964575	27.58566141	9.025144	0.004149
1434951_at	armadillo repeat containing 8	Armc8	175.6484051	19.49037576	9.012058	0.004701
1418203_at	phorbol-12-myristate-13-acetate-induced protein 1	Pmaip1	755.2113657	84.5482702	8.93231	0.004461
1428433_at	homeodomain interacting protein kinase 2	Hipk2	2536.517385	285.7804336	8.875756	0.003665
1434503_s_at	lysosomal-associated membrane protein 2	Lamp2	3684.619682	427.4780897	8.619435	0.004304
1433445_x_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 /// similar to Hmgcs1 protein	Hmgcs1 /// LOC100040592	2120.173577	246.1351119	8.613861	0.004701
1430569_at	tetratricopeptide repeat domain 9C	Ttc9c	119.2492735	13.85613833	8.606242	0.004922
1450871_a_at	branched chain aminotransferase 1, cytosolic	Bcat1	303.9963096	35.81329447	8.488365	0.004591
1439943_at	vacuolar protein sorting 54 (yeast)	Vps54	688.3030058	81.65711357	8.429186	0.004405
1435575_at	kinetochore associated 1	Kntc1	320.6057893	38.04144124	8.427803	0.004922
1436058_at	radical S-adenosyl methionine domain containing 2	Rsad2	626.5344378	74.60721931	8.397772	0.00424
1452534_a_at	high mobility group box 2	Hmgb2	2583.65908	308.5919605	8.372412	0.003976
1420731_a_at	cysteine and glycine-rich protein 2	Csrp2	429.6803525	51.97694733	8.266749	0.004343
1450677_at	checkpoint kinase 1 homolog (S. pombe)	Chek1	195.5147083	23.78538271	8.219952	0.004304
1429095_at	centromere protein P	Cenpp	203.9375087	24.8664732	8.201304	0.004174
1452040_a_at	cell division cycle associated 3	Cdca3	318.8107943	39.15957856	8.141323	0.004681
1435597_at	ATPase family, AAA domain containing 5	Atad5	546.953105	67.44969433	8.109052	0.004864
1452007_at	vesicle-associated membrane protein 7	Vamp7	228.3505836	28.43107347	8.031726	0.004304
1421317_x_at	myeloblastosis oncogene	Myb	2594.606429	323.5780645	8.018487	0.004701
1433444_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 /// similar to Hmgcs1 protein	Hmgcs1 /// LOC100040592	1801.105116	224.948354	8.006749	0.004922
1423971_at	THO complex 3	Thoc3	452.95063	56.70038659	7.988493	0.00477
1417190_at	nicotinamide phosphoribosyltransferase	Nampt	932.5194458	116.7374244	7.988179	0.004304
1450646_at	cytochrome P450, family 51	Cyp51	832.334715	105.228377	7.909793	0.004304
1452608_at	c-myc binding protein	Mycbp	457.2005514	58.04044464	7.877275	0.004681
1417696_at	sterol O-acyltransferase 1	Soat1	460.8701972	60.23583027	7.651097	0.004304
1434278_at	X-linked myotubular myopathy gene 1	Mtm1	469.109205	61.5548232	7.620998	0.00477
1425521_at	polyadenylate binding protein-interacting protein 1	Paip1	354.7822445	48.83724797	7.264583	0.003665
1417400_at	retinoic acid induced 14	Rai14	252.3379411	35.07416046	7.194411	0.004304
1435975_at	DENN/MADD domain containing 4A	Dennd4a	716.718773	99.6991984	7.188812	0.004591
1416529_at	epithelial membrane protein 1	Emp1	973.7133646	136.0217298	7.158513	0.003976

1423774_a_at	protein regulator of cytokinesis 1	Prc1	271.6013173	38.2454619	7.101531	0.004304
1436456_at	solute carrier family 38, member 9	Slc38a9	422.8933313	59.9341624	7.055965	0.004304
1428487_s_at	coenzyme Q10 homolog B (S. cerevisiae)	Coq10b	444.3614953	63.21200482	7.029701	0.004245
1457070_at	---	---	174.0848284	25.00850076	6.961026	0.004174
1425537_at	protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a	229.1110662	33.44843177	6.84968	0.004304
1443602_at	---	---	2522.898878	368.3738054	6.848747	0.00477
1450724_at	family with sequence similarity 126, member A	Fam126a	1053.786339	154.580372	6.817077	0.004591
1440866_at	eukaryotic translation initiation factor 2-alpha kinase 2	Eif2ak2	91.77504426	13.50994597	6.793147	0.002783
1438852_x_at	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	Mcm6	1944.88167	289.6024505	6.715695	0.00477
1448191_at	polo-like kinase 1 (Drosophila)	Plk1	374.9791753	56.30820801	6.659405	0.004405
1437743_at	AE binding protein 2	Aebp2	1050.902662	157.8444801	6.657836	0.00424
1434294_at	---	---	242.7476188	36.64700349	6.623942	0.004591
1423463_a_at	DNA segment, Chr 2, ERATO Doi 750, expressed	D2Ertd750e	84.67260285	12.80894723	6.610426	0.004304
1448061_at	macrophage scavenger receptor 1	Msr1	121.1426725	18.3596502	6.59831	0.00424
1419552_at	enoyl Coenzyme A hydratase domain containing 1	Echdc1	288.7866018	43.90327527	6.577792	0.003202
1435679_at	optineurin	Optn	198.1153242	30.28119007	6.542521	0.004591
1428281_at	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	Trub1	388.8500193	59.56721759	6.52792	0.004361
1453024_at	WD repeat domain 37	Wdr37	278.7684214	42.74202435	6.522116	0.004343
1433739_at	nucleolar protein 10	Nol10	105.601023	16.20312299	6.517325	0.00424
1427940_s_at	c-myc binding protein	Mycbp	114.6606591	17.74113822	6.462982	0.004405
1437495_at	similar to zinc finger, X-linked, duplicated B /// membrane-bound transcription	LOC100047187 /// Mbtps2 /// Yy2	331.2040873	51.40024508	6.443629	0.004922
1448710_at	chemokine (C-X-C motif) receptor 4	Cxcr4	1489.831374	234.7351367	6.346861	0.004461
1424711_at	transmembrane protein 2	Tmem2	97.60095325	15.47506252	6.306983	0.004922
1428336_at	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransf	Agpat4	608.0108815	96.79607655	6.281359	0.004343
1442350_at	---	---	134.0109118	21.74914326	6.161664	0.00477
1449095_at	vacuolar protein sorting 54 (yeast)	Vps54	3734.933049	609.4384302	6.128483	0.003976
1455990_at	kinesin family member 23	Kif23	562.0442856	91.73709599	6.126685	0.00477
1447217_at	ubiquitin-like, containing PHD and RING finger domains 2	Uhrf2	452.3032859	74.11601112	6.102639	0.004304
1416035_at	hypoxia inducible factor 1, alpha subunit	Hif1a	1903.052966	314.9727773	6.04196	0.004405
1452352_at	cytotoxic T lymphocyte-associated protein 2 beta	Ctla2b	97.93368961	16.22140263	6.037313	0.004304
1448721_at	DNA segment, Chr 1, ERATO Doi 622, expressed	D1Ertd622e	380.021351	63.01922031	6.030245	0.004174
1419598_at	membrane-spanning 4-domains, subfamily A, member 6D	Ms4a6d	87.86926168	14.73086252	5.964977	0.004922
1453035_at	limb and neural patterns	Lnp	182.7574828	30.70553142	5.95194	0.004174
1418507_s_at	suppressor of cytokine signaling 2	Socs2	1424.263139	240.9010158	5.912234	0.004256
1418152_at	nucleosome binding protein 1	Nsbp1	1603.675652	272.9135093	5.876131	0.00477
1441955_s_at	similar to poly(A) binding protein interacting protein 1 /// polyadenylate bindi	LOC676674 /// Paip1	104.6880771	17.84766375	5.865646	0.004304
1438750_at	Alpha thalassemia/mental retardation syndrome X-linked homolog (human) (Atrx), m	Atrx	260.7102209	44.46279286	5.863559	0.003976
1429058_at	transmembrane protein 107	Tmem107	379.2573509	64.94965692	5.839251	0.004922
1423347_at	SEC23A (S. cerevisiae)	Sec23a	923.1641141	158.9798377	5.8068	0.002931
1426240_at	chromatin modifying protein 4B /// similar to zinc finger protein 341	Chmp4b /// LOC674706	1781.611014	307.0777133	5.801825	0.004591
1433585_at	transportin 1	Tnpo1	1074.718666	185.8296201	5.783355	0.00424

1427061_at	retinoblastoma binding protein 8	Rbbp8	1281.425006	225.0689662	5.693477	0.004405
1455486_at	protein inhibitor of activated STAT 1	Pias1	349.932617	61.51003962	5.689033	0.004963
1428796_at	bobby sox homolog (Drosophila)	Bbx	418.6768484	73.88041167	5.666953	0.004174
1420028_s_at	similar to DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzym	LOC100045677 /// Mcm3	1939.317543	344.2612523	5.633273	0.004174
1437539_at	protein kinase, AMP-activated, alpha 1 catalytic subunit	Prkaa1	200.5961352	35.61294898	5.632674	0.004965
1452598_at	GINS complex subunit 1 (Psf1 homolog)	Gins1	480.0297467	85.69129007	5.60185	0.004701
1418206_at	stromal cell-derived factor 2-like 1	Sdf2l1	605.0623477	108.3661225	5.583501	0.004174
1426416_a_at	Yip1 domain family, member 4	Yipf4	1735.016098	310.7620808	5.583101	0.004149
1449140_at	NudC domain containing 2	Nudcd2	358.6600715	64.50757448	5.559968	0.00424
1454739_at	cell division cycle 27 homolog (S. cerevisiae)	Cdc27	641.719939	116.3617697	5.514869	0.003976
1460359_at	armadillo repeat containing, X-linked 3 /// hypothetical protein LOC100044266	Armcx3 /// LOC100044266	367.1425886	67.6949668	5.423484	0.004304
1425048_a_at	predicted gene, ENSMUSG00000060128 /// high mobility group box 1 /// similar to	ENSMUSG00000060128 /// Hmgb1 /// LOC100045876 /// LOC100045972 /// LOC100048378	5082.537831	952.9499716	5.333478	0.003976
1431037_a_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	Elavl1	392.378813	74.53709392	5.264209	0.004591
1424020_at	ADP-ribosylation factor-like 6 interacting protein 6	Arl6ip6	1208.470606	230.2812811	5.247802	0.004591
1425166_at	retinoblastoma-like 1 (p107)	Rbl1	504.0908649	96.19788921	5.240145	0.004304
1418895_at	src family associated phosphoprotein 2	Skap2	2301.140462	445.1506956	5.169352	0.002608
1437478_s_at	EF hand domain containing 2	Efhd2	1737.101895	339.757911	5.112764	0.004679
1435702_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon	Ywhae	512.421311	100.4604153	5.100729	0.00477
1431050_at	ribosomal protein S6 kinase, polypeptide 5	Rps6ka5	75.77797417	14.91973494	5.079043	0.004343
1455156_at	striatin, calmodulin binding protein	Strn	590.717005	117.8793064	5.011202	0.004701
1417471_s_at	DNA segment, Chr 1, ERATO Doi 622, expressed	D1Ertd622e	540.483463	109.3412022	4.943091	0.002608
1424902_at	plexin domain containing 1	Plxdc1	330.8010492	67.61040262	4.892754	0.004681
1424243_at	RWD domain containing 4A	Rwdd4a	384.7159944	78.63211021	4.892607	0.004591
1457321_at	RIKEN cDNA D130037M23 gene	D130037M23Rik	193.174832	39.67568794	4.868846	0.004405
1424924_at	SEC63-like (S. cerevisiae)	Sec63	322.6389189	66.34120599	4.863326	0.002536
1428976_at	thymopoietin	Tmpo	1105.053115	227.704659	4.853011	0.004405
1452247_at	fragile X mental retardation gene 1, autosomal homolog	Fxr1	123.4782673	25.46393251	4.849144	0.004784
1418622_at	RAB2A, member RAS oncogene family	Rab2a	1087.095774	225.2463628	4.826252	0.004343
1434408_at	ataxin 3	Atxn3	216.3280101	44.95802226	4.811778	0.004304
1448441_at	CDC28 protein kinase 1b	Cks1b	253.0712833	52.94221559	4.780142	0.003808
1448571_a_at	glia maturation factor, beta	Gmfb	593.9633075	124.3259232	4.77747	0.004922
1451315_at	transmembrane protein 101	Tmem101	183.9733944	38.57203436	4.769606	0.003976
1424105_a_at	pituitary tumor-transforming gene 1	Pttg1	648.3459437	136.2120003	4.75983	0.004911
1455488_at	RIKEN cDNA 6230416J20 gene	6230416J20Rik	418.2408013	88.37542442	4.732546	0.004304
1434884_at	metadherin	Mtdh	300.6261436	63.81999837	4.710532	0.004467
1415945_at	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	Mcm5	1183.354543	254.9893768	4.640799	0.004304

1421077_at	SERTA domain containing 3	Sertad3	779.6791079	168.9169157	4.615755	0.004304
1429712_at	RIKEN cDNA 6230416C02 gene /// ethanol induced 1 /// KRAB box and zinc finger, C	6230416C02Rik /// Etohi1 /// RP24-87L14.2	116.3547798	25.2999039	4.599021	0.004681
1418334_at	DBF4 homolog (S. cerevisiae)	Dbf4	1050.727853	229.5991249	4.576358	0.004681
1431087_at	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc24	340.5162884	74.45671183	4.573346	0.004681
1416868_at	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	Cdkn2c	1264.27974	276.5551376	4.571529	0.004591
1422554_at	necdin-like 2	Ndnl2	377.6222598	83.30974364	4.53275	0.004405
1448883_at	legumain	Lgmn	554.5575337	123.7787631	4.480232	0.004974
1429897_a_at	DNA segment, Chr 16, ERATO Doi 472, expressed	D16Ertd472e	990.4200199	221.2162158	4.477158	0.004681
1425098_at	zinc finger protein 106	Zfp106	84.66614713	18.92506915	4.473756	0.004405
1437904_at	RNA binding motif protein 45	Rbm45	1440.84557	322.4578244	4.468323	0.004304
1435167_at	RAN binding protein 6	Ranbp6	156.4795157	35.039736	4.465773	0.003956
1421895_at	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x /// LOC100048746	345.2027147	77.46664387	4.456147	0.004922
1430996_at	ethanolamine kinase 1	Etnk1	99.24734934	22.36943119	4.43674	0.004645
1423531_a_at	heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	1741.321246	393.310984	4.427339	0.004965
1420898_at	synaptosomal-associated protein 23	Snap23	283.7329715	64.24356287	4.41652	0.004405
1434225_at	SWA-70 protein	Swap70	1432.97726	326.5446964	4.388304	0.002608
1436204_at	RIKEN cDNA 1110059G02 gene	1110059G02Rik	1326.185312	302.458487	4.384685	0.004304
1418565_at	Serpine1 mRNA binding protein 1	Serbp1	116.7123431	26.63835951	4.381364	0.004974
1444437_at	ubiquitin specific peptidase 34	Usp34	98.39342448	22.50712691	4.371656	0.004304
1447640_s_at	pre B-cell leukemia transcription factor 3	Pbx3	160.141491	36.72210021	4.360902	0.004701
1420916_at	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	Prpf40a	359.7755495	82.60897734	4.355163	0.002569
1454955_at	importin 7	Ipo7	837.0248628	192.2282641	4.354328	0.002488
1452717_at	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	Slc25a24	1154.591398	265.5666181	4.347653	0.004591
1455698_at	SEC62 homolog (S. cerevisiae)	Sec62	182.9983292	42.48701256	4.307159	0.004405
1423520_at	lamin B1	Lmnb1	410.3231287	95.54620499	4.294499	0.004701
1440459_at	senataxin	Setx	130.633702	30.58473774	4.271206	0.003665
1423744_x_at	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	2073.281074	488.9060112	4.240654	0.004591
1421644_at	schlafen 3	Slfn3	47.57384304	11.2373244	4.233556	0.002931
1434242_at	ubiquitin specific peptidase 37	Usp37	363.5878047	86.1291686	4.221425	0.004807
1434068_s_at	expressed sequence AI662270	AI662270	3038.478427	726.6851763	4.181286	0.004149
1451122_at	isopentenyl-diphosphate delta isomerase	Idi1	1097.034615	264.7242717	4.144065	0.004405
1450012_x_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma po	Ywhag	1309.590458	317.5786243	4.123673	0.004681
1442656_at	Myelination associated SUR4-like protein (Masr)	Elovl6	350.1865831	85.16763205	4.111733	0.004405
1455634_at	Son DNA binding protein	Son	735.4941213	178.9339501	4.110422	0.004688
1439790_at	serine (or cysteine) peptidase inhibitor, clade B, member 9	Serpinb9	68.56323771	16.72143396	4.10032	0.002488
1426269_at	vesicle-associated membrane protein 7	Vamp7	469.7675772	114.7756931	4.092919	0.004591
1416832_at	solute carrier family 39 (metal ion transporter), member 8	Slc39a8	105.2614478	25.75576226	4.086909	0.004304
1433531_at	acyl-CoA synthetase long-chain family member 4	Acsl4	614.832663	151.1817307	4.066845	0.004681
1438855_x_at	tumor necrosis factor, alpha-induced protein 2	Tnfaip2	53.83751816	13.33821157	4.036337	0.003976
1437747_at	ubiquitination factor E4A, UFD2 homolog	Ube4a	245.960585	61.07415107	4.027245	0.003665

	(S. cerevisiae)					
1434468_at	OTU domain containing 4	Otud4	1969.208286	491.3407208	4.007826	0.003976
1418656_at	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Lsm5	1046.896666	262.0121675	3.995603	0.004405
1460431_at	glucosaminyl (N-acetyl) transferase 1, core 2	Gcnt1	75.55402277	18.9621415	3.984467	0.004304
1451064_a_at	phosphoserine aminotransferase 1	Psat1	999.6666855	250.9089286	3.984181	0.004467
1439487_at	ligase IV, DNA, ATP-dependent	Lig4	220.5288102	55.42378499	3.978956	0.004591
1416034_at	CD24a antigen /// predicted gene, EG621324	Cd24a /// EG621324	218.5273435	55.30609847	3.951234	0.004974
1433571_at	serine incorporator 5	Serinc5	313.2389919	79.54356587	3.937955	0.002931
1448958_at	interferon alpha responsive gene	Ifrg15	317.5500088	80.98334522	3.921177	0.004681
1434076_at	WD repeat domain 37	Wdr37	1396.919658	358.577213	3.895729	0.004149
1424202_at	SEH1-like (S. cerevisiae	Seh1l	513.3788318	132.6342906	3.870634	0.004343
1415975_at	calcium regulated heat stable protein 1	Carhsp1	339.6291942	87.82765221	3.866996	0.004681
1452059_at	solute carrier family 35, member F5	Slc35f5	87.12994133	22.6522115	3.846421	0.004591
1423795_at	splicing factor proline/glutamine rich (polypyrimidine tract binding protein ass	Sfpq	2270.613859	591.8536491	3.836445	0.004591
1455059_at	helicase with zinc finger domain	Helz	166.6433573	43.50361348	3.830564	0.004174
1443733_x_at	polymerase (DNA-directed), delta 3, accessory subunit	Pold3	173.9276309	45.43671619	3.827909	0.00424
1423445_at	Rho-associated coiled-coil containing protein kinase 1	Rock1	994.1639641	259.8970894	3.825222	0.004304
1435081_at	synaptophysin-like protein	Sypl	339.7304369	89.35583275	3.801995	0.004174
1434079_s_at	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	Mcm2	1842.522685	487.273065	3.781294	0.004591
1418399_at	potassium channel tetramerisation domain containing 9	Kctd9	169.3890337	45.01300578	3.763113	0.004174
1424343_a_at	eukaryotic translation initiation factor 1A	Eif1a	607.850755	161.7983778	3.756841	0.004701
1421188_at	chemokine (C-C motif) receptor 2	Ccr2	162.7871863	43.35490545	3.754758	0.004867
1416011_x_at	EH-domain containing 1	Ehd1	391.2924147	104.5307311	3.743324	0.004523
1416556_at	tetraspanin 31	Tspan31	1356.65045	363.267041	3.734582	0.004681
1422946_a_at	DNA methyltransferase (cytosine-5) 1	Dnmt1	1679.520085	450.3220571	3.729598	0.003976
1438814_at	---	---	1772.905593	475.7335627	3.726678	0.003202
1433897_at	expressed sequence AI597468	AI597468	861.0779292	231.4965153	3.719615	0.003202
1431320_a_at	myosin Va	Myo5a	215.4660363	58.46872933	3.68515	0.004405
1438578_a_at	BTB (POZ) domain containing 10 /// similar to BTB (POZ) domain containing 10	Btbd10 /// LOC100047893	652.2856138	177.7538092	3.669601	0.004864
1423207_at	transmembrane protein 167	Tmem167	346.8352368	94.65848979	3.664069	0.003665
1425186_at	LMBR1 domain containing 1	Lmbrd1	111.5976884	30.52332029	3.656145	0.004461
1454671_at	insulin induced gene 1	Insig1	347.489763	95.23214128	3.648871	0.004701
1426914_at	MARVEL (membrane-associating) domain containing 2	Marveld2	68.78601311	18.88946584	3.641501	0.004922
1460536_at	RIKEN cDNA 2310079F09 gene	2310079F09Rik	531.5273065	146.3710742	3.631368	0.00477
1452655_at	zinc finger, DHHC domain containing 2	Zdhhc2	268.998938	74.45361533	3.612973	0.004304
1438951_x_at	nucleoporin 54	Nup54	487.6379737	135.0918347	3.609678	0.004304
1423369_at	fragile X mental retardation syndrome 1 homolog	Fmr1	726.5575835	201.3255782	3.608869	0.004304
1423885_at	laminin, gamma 1	Lamc1	374.0550159	103.7686375	3.604702	0.004701
1427098_at	WW domain containing E3 ubiquitin protein ligase 1	Wwp1	116.2373575	32.29785987	3.598918	0.00496
1416873_a_at	cyclin-dependent kinase 2	Cdk2	555.4089699	154.415097	3.596857	0.004532
1455278_at	WD repeat domain 37	Wdr37	219.6490831	61.32457109	3.581747	0.00477
1417398_at	related RAS viral (r-ras) oncogene homolog 2	Rras2	947.710974	265.7998843	3.565506	0.00477
1429775_a_at	G protein-coupled receptor 137B /// G protein-coupled receptor 137B, pseudogene	Gpr137b /// Gpr137b-ps ///	255.4552307	71.75230799	3.560237	0.004922

1450028_a_at	LanC (bacterial lantibiotic synthetase component C)-like 2 /// similar to testis	LOC100044979 Lancl2 /// LOC100045439	282.1991828	79.96554812	3.52901	0.004591
1436400_at	fragile X mental retardation gene 1, autosomal homolog	Fxr1	127.8448292	36.41985651	3.510306	0.004304
1425193_at	RIKEN cDNA 2010106G01 gene	2010106G01Rik	723.6542052	206.2575806	3.508497	0.004304
1429491_s_at	Rap1 interacting factor 1 homolog (yeast)	Rif1	626.4562722	179.2533992	3.494808	0.003808
1460623_at	src family associated phosphoprotein 2	Skap2	440.7112761	126.2258282	3.491451	0.004591
1434310_at	bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	600.3666383	172.6579954	3.477201	0.004547
1447784_x_at	solute carrier family 38, member 9	Slc38a9	323.3844878	93.32381201	3.465187	0.004174
1436448_a_at	prostaglandin-endoperoxide synthase 1	Ptgs1	52.56485644	15.21694314	3.454364	0.004681
1426395_s_at	eukaryotic translation initiation factor 3, subunit J	Eif3j	347.8657102	100.8658037	3.448797	0.004304
1435390_at	exonuclease domain containing 1	Exod1	255.4959596	74.40236971	3.433976	0.004304
1436128_at	pleckstrin homology domain containing, family A (phosphoinositide binding specif	Plekha8	91.47548999	26.83517392	3.408791	0.004304
1416681_at	ubiquitin protein ligase E3A	Ube3a	68.05629307	19.97268887	3.407468	0.00424
1426356_at	RIKEN cDNA 6330578E17 gene	6330578E17Rik	295.5878857	86.98330775	3.398214	0.004922
1423723_s_at	TAR DNA binding protein	Tardbp	2587.482399	761.6019347	3.397421	0.004681
1424500_at	UTP6, small subunit (SSU) processome component, homolog (yeast)	Utp6	785.2037939	231.2506056	3.395467	0.004784
1415963_at	heterogeneous nuclear ribonucleoprotein H2	Hnrnph2	3451.162444	1016.710575	3.394439	0.00424
1428103_at	a disintegrin and metallopeptidase domain 10	Adam10	2543.971277	749.9306268	3.392275	0.004922
1442348_at	---	---	102.575094	30.34029764	3.38082	0.004405
1433505_a_at	leucine rich repeat containing 8D	Lrrc8d	719.9402328	213.2260657	3.376418	0.004591
1439127_at	expressed sequence AI314180	AI314180	133.2002826	39.87695468	3.340282	0.004965
1455079_at	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	Dcun1d4	315.9436223	94.62700114	3.338832	0.004591
1433756_at	S100P binding protein	S100pbp	723.1460968	217.1919266	3.329526	0.004922
1449194_at	mitochondrial ribosomal protein S25	Mrps25	530.9271102	159.474285	3.329233	0.004304
1455094_s_at	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	Ube2g1	411.5593453	123.668706	3.327918	0.004149
1431295_a_at	syntaxin 18	Stx18	65.62271295	19.76879916	3.319509	0.004591
1449348_at	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	Mpp6	550.3376931	165.8555332	3.318175	0.004304
1436942_at	RIKEN cDNA A930035D04 gene	A930035D04Rik	59.9811246	18.11944256	3.310318	0.004882
1433955_at	bromodomain and WD repeat domain containing 1	Brwd1	214.3706124	65.16656293	3.28958	0.004304
1453064_at	Ewing's tumor-associated antigen 1	Etaa1	271.682281	82.65575306	3.286913	0.004701
1430029_a_at	tetraspanin 31	Tspan31	849.8964896	258.6104327	3.286397	0.002488
1424589_s_at	RNA-binding region (RNP1, RRM) containing 3	Rnpc3	152.4416516	46.39004477	3.286085	0.004174
1448844_at	cytochrome b5 type B	Cyb5b	829.0986728	253.8472229	3.266133	0.003976
1435834_at	Fanconi anemia, complementation group F	Fancf	162.1284353	50.08557783	3.237028	0.004965
1433930_at	heparanase	Hpse	209.1460103	64.73556685	3.230774	0.004681
1443628_at	---	---	310.5941112	96.33423377	3.22413	0.00492
1428386_at	acyl-CoA synthetase long-chain family member 3	Acsl3	67.58978562	21.05634801	3.209948	0.002931
1437177_at	La ribonucleoprotein domain family, member 4	Larp4	274.9203708	85.70178413	3.207872	0.004591
1460352_s_at	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150	Pik3r4	506.129703	157.904302	3.205294	0.004681
1436770_x_at	proteasome (prosome, macropain)	Psma1	73.2024485	23.00241344	3.182381	0.004591

	subunit, alpha type 1					
1439428_x_at	GDP-mannose 4, 6-dehydratase	Gmds	45.82448197	14.41857483	3.178156	0.004225
1416155_at	high mobility group box 3	Hmgb3	948.357149	299.0687446	3.171034	0.004304
1416308_at	UDP-glucose dehydrogenase	Ugdh	846.1658588	266.9199509	3.170111	0.004149
1435366_at	RIKEN cDNA D430042O09 gene	D430042O09Rik	63.60536995	20.18259811	3.151496	0.00424
1428930_at	transmembrane protein 29	Tmem29	234.093327	74.82093036	3.128714	0.003168
1417172_at	ubiquitin-conjugating enzyme E2L 6	Ube2l6	92.22738794	29.49877896	3.126482	0.00477
1419276_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	Enpp1	228.447683	73.07233143	3.126323	0.004922
1451559_a_at	dehydrogenase/reductase (SDR family) member 4	Dhrs4	415.6177137	132.9715074	3.125615	0.004681
1434174_at	LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	624.3768916	200.0481301	3.121133	0.004681
1419585_at	retinitis pigmentosa 2 homolog (human)	Rp2h	91.48056261	29.36644384	3.115139	0.004701
1454905_at	inhibitor of Bruton agammaglobulinemia tyrosine kinase	Ibtk	683.8423686	219.7902126	3.111341	0.004965
1434630_at	ankyrin repeat domain 28	Ankrd28	387.2979353	125.0140701	3.098035	0.004174
1438517_at	WW domain-containing oxidoreductase	Wwox	87.26855476	28.29496276	3.084243	0.004405
1418402_at	a disintegrin and metallopeptidase domain 19 (meltrin beta) /// similar to metal	Adam19 /// LOC100045780	2052.073467	665.5131365	3.083445	0.004304
1425059_at	protein arginine N-methyltransferase 6	Prmt6	209.6816304	68.41970601	3.064638	0.004681
1454741_s_at	transmembrane protein 164	Tmem164	632.1646997	206.5327369	3.060845	0.003976
1435548_at	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	Mrs2	149.9090149	49.01608433	3.058364	0.003976
1442599_at	solute carrier family 12 (potassium/chloride transporters), member 9	Slc12a9	135.4324834	44.65180735	3.03308	0.00477
1437296_at	protein kinase N2	Pkn2	153.4636681	50.62225958	3.031545	0.004922
1456918_at	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	Raph1	642.6903499	212.5919757	3.023117	0.0042
1422503_s_at	poly (ADP-ribose) polymerase family, member 1	Parp1	865.9360452	286.6367936	3.021022	0.004304
1453332_at	RIKEN cDNA 2410002O22 gene /// hypothetical protein LOC100044479	2410002O22Rik /// LOC100044479	223.7323401	74.14067441	3.017673	0.004663
1429698_at	mitochondrial transcription termination factor	Mterf	271.8467933	90.14215279	3.015757	0.004461
1432374_a_at	DNA segment, Chr 5, Wayne State University 178, expressed	D5Wsu178e	83.66428589	27.94787459	2.993583	0.004149
1435637_at	integrin alpha FG-GAP repeat containing 1	Itfg1	193.3731036	65.17108009	2.967161	0.004304
1418258_s_at	dynein light chain LC8-type 2	Dynll2	517.5388422	174.6032577	2.964085	0.004681
1428069_at	cell division cycle associated 7	Cdca7	523.7338348	177.0905396	2.957435	0.004405
1423521_at	lamin B1	Lmnb1	557.0629927	188.5687327	2.954164	0.004591
1419763_at	NFKB activating protein	Nkap	30.4111823	10.40356925	2.923149	0.004304
1430274_a_at	STARD3 N-terminal like	Stard3nl	349.0443786	119.5010927	2.920847	0.004405
1444746_at	---	---	732.3028837	251.2529398	2.914604	0.004663
1448126_at	family with sequence similarity 60, member A	Fam60a	372.9219744	129.0780609	2.88912	0.00477
1439256_x_at	G protein-coupled receptor 137B, pseudogene	Gpr137b-ps	242.8845087	84.2649055	2.882392	0.004681
1448026_at	chromodomain helicase DNA binding protein 7	Chd7	307.4703177	106.9552384	2.874757	0.004149
1460583_at	golgi transport 1 homolog B (S. cerevisiae)	Golt1b	41.78857525	14.57169367	2.867791	0.004802
1436714_at	LIM domain containing preferred translocation partner in lipoma	Lpp	285.6022101	99.69320937	2.864811	0.00477
1437009_a_at	ring finger protein 115	Rnf115	2335.58246	818.2890105	2.854227	0.004681
1419235_s_at	helicase (DNA) B	Helb	1405.986149	494.9480625	2.840674	0.002488

1448301_s_at	serine (or cysteine) peptidase inhibitor, clade B, member 1a	Serpinb1a	33.21723308	11.83586576	2.80649	0.00424
1431921_a_at	similar to Stromal antigen 1 /// stromal antigen 1	LOC100045442 /// Stag1	896.908291	320.1342743	2.801663	0.004911
1455351_at	RIKEN cDNA 2610101N10 gene	2610101N10Rik	252.9683937	90.80060468	2.785977	0.004304
1429911_at	microcephaly, primary autosomal recessive 1	Mcph1	215.6508113	77.45787406	2.784104	0.004922
1433718_a_at	chromobox homolog 1 (Drosophila HP1 beta)	Cbx1	437.9897609	157.3801742	2.783005	0.004827
1426999_at	zinc finger CCCH type containing 14	Zc3h14	1409.531496	512.0910969	2.752501	0.004461
1424222_s_at	RAD23b homolog (S. cerevisiae)	Rad23b	1225.73665	445.337925	2.752374	0.004701
1417454_at	cullin 4B	Cul4b	1554.354651	565.4582377	2.748841	0.004304
1416925_at	karyopherin (importin) beta 1	Kpnb1	1383.813047	512.0283921	2.70261	0.004149
1423076_at	sorting nexin 9	Snx9	466.7447549	172.7609486	2.70168	0.004701
1428323_at	glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	179.9888009	66.71410918	2.697912	0.004701
1438767_at	oncostatin M	Osm	609.3342396	226.3142055	2.692426	0.004864
1437362_at	coiled-coil domain containing 76	Ccdc76	207.1343962	77.07903831	2.687299	0.003913
1416998_at	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	Rrs1	566.3303356	211.9729946	2.67171	0.004591
1439802_at	serine/threonine kinase 35	Stk35	63.93157215	23.96156113	2.668089	0.00477
1418039_at	RAB, member of RAS oncogene family-like 3	Rabl3	427.3961198	161.0446213	2.653899	0.002783
1459977_x_at	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferas	Cox10	27.41771938	10.35027121	2.648986	0.00424
1436297_a_at	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (gluta	Grina	956.0970998	361.7811256	2.64275	0.002488
1441212_at	family with sequence similarity 92, member A	Fam92a	35.44221014	13.4312034	2.638796	0.004304
1452831_s_at	phosphoribosyl pyrophosphate amidotransferase	Ppat	688.7691266	263.1357272	2.617543	0.004864
1426933_at	oxidative-stress responsive 1	Oxsr1	540.688302	207.5746804	2.604789	0.004405
1460711_at	DnaJ (Hsp40) homolog, subfamily C, member 21	Dnajc21	748.7239015	288.9207479	2.591451	0.004922
1453045_at	coiled-coil domain containing 41	Ccdc41	586.4170879	226.8728247	2.584783	0.004681
1428287_at	cullin 5	Cul5	235.3199786	91.13752792	2.582032	0.004922
1420472_at	myotrophin	Mtpn	148.6885763	57.7090896	2.576519	0.004591
1428582_at	methyltransferase like 10	Mettl10	612.9660386	238.4384902	2.570751	0.004405
1432304_a_at	RIKEN cDNA 9030624J02 gene	9030624J02Rik	38.40751363	14.95397029	2.568382	0.004304
1425498_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	812.7117825	316.5888568	2.567089	0.00424
1452937_s_at	coiled coil domain containing 28B	Ccdc28b	136.7701891	53.62151217	2.550659	0.00424
1416376_at	transmembrane protein 97	Tmem97	141.2339712	55.39536382	2.549563	0.004405
1460551_at	similar to RAN, member RAS oncogene family /// RAN, member RAS oncogene family	LOC100045999 /// Ran	1024.717132	403.7355084	2.53809	0.004679
1434821_at	bromodomain containing 1 /// similar to bromodomain containing 1	Brd1 /// LOC100045983	580.3059858	228.7899706	2.536414	0.004304
1426275_a_at	UDP-glucuronate decarboxylase 1	Uxs1	229.5460824	90.87679183	2.525904	0.004922
1416665_at	demethyl-Q 7	Coq7	512.6628926	203.8150346	2.515334	0.004965
1447442_at	---	---	224.2856228	89.56997717	2.504027	0.004461
1424377_at	cDNA sequence BC003885 /// predicted gene, EG623867	BC003885 /// EG623867	639.396336	259.5832229	2.463165	0.004795
1415881_at	growth hormone inducible transmembrane protein	Ghitm	971.7221199	396.4101245	2.451305	0.004974
1430133_at	TBC1 domain family, member 8B	Tbc1d8b	487.3744011	201.3632598	2.420374	0.004681

1426460_a_at	UDP-glucose pyrophosphorylase 2	Ugp2	187.9154661	78.48055469	2.394421	0.004581
1456846_at	predicted gene, EG382639	EG382639	802.8759751	337.0393745	2.382143	0.004681
1445402_at	---	---	43.94407234	18.45538591	2.381097	0.004304
1454680_at	DNA segment, Chr 5, ERATO Doi 579, expressed	D5Ertd579e	402.1379462	169.759284	2.368872	0.004405
1430258_at	RIKEN cDNA 2810422J05 gene	2810422J05Rik	67.59056646	28.53854742	2.368395	0.00488
1419924_at	Folliculin interacting protein 1, mRNA (cDNA clone MGC:100017 IMAGE:30543296)	Fnip1	30.49815365	12.89068181	2.365907	0.003323
1448033_at	TatD DNase domain containing 1	Tatdn1	105.9221132	44.8072413	2.363951	0.004681
1428693_at	RIKEN cDNA 2610044O15 gene	2610044O15Rik	36.57324335	15.50082754	2.359438	0.004681
1424390_at	nucleoporin like 1	Nupl1	707.8991339	300.3248409	2.357111	0.004461
1439074_a_at	Son DNA binding protein	Son	131.0487698	57.09819891	2.295147	0.004304
1451343_at	vacuolar protein sorting 36 (yeast)	Vps36	647.5225685	287.9138405	2.249015	0.004405
1436828_a_at	tumor protein D52-like 2	Tpd52l2	433.5836866	193.2350958	2.243814	0.004827
1416031_s_at	minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	1368.708968	615.0230482	2.22546	0.00477
1419253_at	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofola	Mthfd2	1090.318059	490.932205	2.220914	0.004304
1438510_a_at	histidyl-tRNA synthetase	Hars	2663.609115	1215.780161	2.190864	0.004591
1438032_at	leucine-rich repeats and calponin homology (CH) domain containing 1	Lrch1	367.0263927	169.0891173	2.170609	0.004922
1455611_at	protein inhibitor of activated STAT 1	Pias1	271.7306197	125.3941876	2.167011	0.00477
1417200_at	transmembrane protein 183A	Tmem183a	737.3197884	353.6291356	2.085009	0.004591
1449661_at	Suppressor of zeste 12 homolog (Drosophila), mRNA (cDNA clone IMAGE:3485208)	Suz12	26.29074891	12.64308533	2.079457	0.004304
1419193_a_at	glia maturation factor, gamma	Gmfg	1017.528391	492.1724182	2.067423	0.004304
1419996_s_at	aryl hydrocarbon receptor nuclear translocator	Arnt	273.426008	133.7560186	2.044215	0.004174
1419819_s_at	SEC63-like (S. cerevisiae)	Sec63	438.1749908	214.350306	2.0442	0.003976
1448816_at	prostaglandin I2 (prostacyclin) synthase	Ptgis	101.388485	49.83750708	2.034381	0.004965
1445220_at	---	---	35.20251665	17.37703458	2.025807	0.00424
1429759_at	ribosomal protein S6 kinase polypeptide 6	Rps6ka6	44.78353995	22.16851152	2.020142	0.004762
1449770_x_at	transmembrane protein 191C	Tmem191c	214.7280223	106.6320018	2.01373	0.004681
1438204_at	Histone cluster 1, H1c (Hist1h1c), mRNA	Hist1h1c	44.46885439	89.82779404	0.495046	0.004304
1434640_at	neurensin 2	Nrsn2	21.77554115	44.05793585	0.494248	0.004965
1418783_at	transient receptor potential cation channel, subfamily M, member 5	Trpm5	10.70154111	21.67239468	0.493787	0.004965
1430728_at	keratin associated protein 5-5	Krtap5-5	16.13058288	32.72580253	0.492901	0.004701
1450196_s_at	glycogen synthase 1, muscle	Gys1	17.09658965	34.79086555	0.49141	0.004405
1447346_s_at	RIKEN cDNA 5530400B01 gene	5530400B01Rik	61.40056389	125.7899919	0.48812	0.004461
1441017_at	zinc finger, CCHC domain containing 14	Zcchc14	46.99384801	96.3484799	0.487749	0.002608
1448662_at	frizzled homolog 6 (Drosophila)	Fzd6	10.80856681	22.19408511	0.487002	0.004974
1436768_x_at	RIKEN cDNA E130112L23 gene	E130112L23Rik	56.46271772	116.3832799	0.485145	0.004174
1453363_at	calcium channel, voltage-dependent, gamma subunit 2	Cacng2	60.95319754	126.8007967	0.4807	0.004655
1439529_at	RIKEN cDNA A430110N23 gene	A430110N23Rik	53.31082734	111.0608603	0.480015	0.004701
1432107_at	RIKEN cDNA 2310010M20 gene	2310010M20Rik	11.87863096	24.74794224	0.479985	0.004304
1420001_at	DNA segment, Chr 7, ERATO Doi 1, expressed	D7Ertd1e	28.67304729	60.02271476	0.477703	0.004304
1450556_at	spectrin beta 1	Spnb1	40.60137459	85.0808967	0.477209	0.004596
1432410_a_at	bone morphogenetic protein 7	Bmp7	13.76529223	28.86561384	0.476875	0.004645
1430078_a_at	8-oxoguanine DNA-glycosylase 1	Ogg1	122.8831534	257.7246405	0.4768	0.004304

1425439_a_at	solute carrier family 41, member 3	Slc41a3	127.4667068	267.8608639	0.475869	0.004304
1427987_at	scaffold attachment factor B2	Safb2	302.1595367	635.440544	0.475512	0.004681
1421081_a_at	barrier to autointegration factor 1	Banf1	241.4114009	507.9690074	0.475248	0.004681
1422940_x_at	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B /// ser	Serpinb3b /// Serpinb3c	9.776038725	20.81661137	0.469627	0.004807
1437094_x_at	dynein, axonemal, intermediate chain 1	Dnaic1	19.08838754	40.97361655	0.46587	0.004681
1447743_x_at	exostoses (multiple) 2	Ext2	36.54984374	78.48019204	0.465721	0.004591
1450795_at	luteinizing hormone beta	Lhb	21.10003275	45.42065692	0.464547	0.003202
1437604_x_at	adenomatosis polyposis coli down-regulated 1	Apcdd1	38.44275965	82.85766925	0.463961	0.004591
1457463_at	Down syndrome cell adhesion molecule-like 1	Dscaml1	38.5955693	83.7056635	0.461087	0.004461
1440227_at	solute carrier family 5 (inositol transporters), member 3	Slc5a3	92.43025982	201.571333	0.458549	0.004405
1437929_at	dapper homolog 2, antagonist of beta-catenin (xenopus)	Dact2	28.23481617	61.62184615	0.458195	0.002488
1431561_a_at	DEAH (Asp-Glu-Ala-His) box polypeptide 34	Dhx34	256.0544225	560.913048	0.456496	0.004458
1430937_at	RIKEN cDNA A930016O22 gene	A930016O22Rik	41.70273216	91.53511103	0.455593	0.004681
1457823_at	cysteine rich protein 61	Cyr61	9.532557534	20.99528305	0.454033	0.004149
1426338_a_at	netrin G1	Ntng1	16.06040831	35.39613667	0.453733	0.002488
1457004_at	DNA segment, Chr 15, Wayne State University 169, expressed	D15Wsu169e	59.69355763	131.7814352	0.452974	0.00477
1428717_at	secernin 1	Scrn1	40.44165127	89.33518956	0.452696	0.004591
1456571_at	decapping enzyme, scavenger	Dcps	21.3649396	47.33197882	0.451385	0.004149
1421226_at	triggering receptor expressed on myeloid cells 2	Trem2	59.30560955	132.1070211	0.448921	0.004304
1445054_at	---	---	27.89155892	62.35355887	0.447313	0.004304
1428434_at	zinc finger, CCHC domain containing 12	Zcchc12	40.81742689	91.35087652	0.44682	0.004149
1424392_at	alcohol dehydrogenase, iron containing, 1	Adhfe1	12.3240682	27.73649018	0.444327	0.004681
1428707_at	parathymosin	Ptms	290.8779244	658.3556461	0.441825	0.004304
1420606_at	neuropeptide FF-amide peptide precursor	Npff	83.46483937	189.3616012	0.44077	0.004405
1422574_at	Max dimerization protein 4	Mxd4	74.23151973	168.585113	0.440321	0.004922
1451815_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	B3gnt4	16.02215907	36.90556998	0.434139	0.004405
1428708_x_at	parathymosin	Ptms	292.0159443	680.3625873	0.429206	0.003976
1439838_a_at	transmembrane inner ear	Tmie	29.13611601	67.99735232	0.428489	0.004304
1438393_at	---	---	18.26926473	42.65668654	0.428286	0.004149
1421659_at	adrenergic receptor, alpha 1a	Adra1a	17.91206794	42.12612569	0.425201	0.004174
1421388_at	myocyte enhancer factor 2D	Mef2d	114.0413595	269.8043877	0.422682	0.004461
1455125_at	centaurin, beta 1	Centb1	140.3887318	332.7542617	0.421899	0.004405
1424566_s_at	polymerase (RNA) III (DNA directed) polypeptide D	Polr3d	99.33337788	236.0643978	0.420789	0.004718
1459858_x_at	cartilage acidic protein 1	Crtac1	9.768587709	23.42455929	0.417023	0.004405
1453724_a_at	serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1	65.01211421	156.5684809	0.415231	0.004566
1456291_x_at	scleraxis	Scx	12.41767638	30.05917135	0.413108	0.004591
1459911_at	cerebellar degeneration-related protein 2-like	Cdr2l	45.63313926	110.6282989	0.412491	0.00477
1421150_at	human immunodeficiency virus type I enhancer binding protein 3	Hivep3	32.11131853	77.85403998	0.412455	0.003976
1450810_at	follicle stimulating hormone receptor	Fshr	16.57354137	40.20909611	0.412184	0.004304
1420598_x_at	defensin related cryptdin, related sequence 2	Defcr-rs2	116.1675514	281.9665082	0.411991	0.004304
1426305_at	uroplakin 1A	Upk1a	31.46116087	77.32787521	0.406854	0.004461
1433147_at	caldesmon 1	Cald1	16.13442211	40.0067076	0.403293	0.004591
1421380_at	insulin receptor	Insr	19.93856948	50.07481682	0.398176	0.004149
1442042_at	---	---	111.626055	280.3677631	0.398142	0.004701

1433084_at	RIKEN cDNA 4930402C16 gene	4930402C16Rik	19.77432668	50.57561314	0.390985	0.004701
1442264_at	RAS, guanyl releasing protein 2	Rasgrp2	92.29880089	236.1260388	0.390888	0.004965
1427350_a_at	GTP binding protein 6 (putative)	Gtpbp6	273.1349271	702.5871271	0.388756	0.004304
1424268_at	spermine oxidase	Smox	78.55529764	202.3735126	0.38817	0.004802
1420266_at	predicted gene, ENSMUSG00000074106	ENSMUSG00000074106	90.3101769	232.7886109	0.387949	0.004591
1447524_at	adaptor-related protein complex 3, mu 2 subunit	Ap3m2	39.60251094	102.8432526	0.385076	0.004681
1439778_at	CDK5 and Abl enzyme substrate 1 (Cables1), mRNA	Cables1	10.74830057	28.00592162	0.383787	0.004701
1431227_at	---	---	44.01001627	114.941821	0.382889	0.004756
1456167_at	expressed sequence AA619741	AA619741	72.87573716	191.1078637	0.381333	0.004461
1452975_at	alanine-glyoxylate aminotransferase 2-like 1	Agxt2l1	15.41236835	42.13517854	0.365784	0.004922
1441762_at	---	---	88.5483386	242.2965412	0.365454	0.00496
1447833_x_at	microfibrillar-associated protein 2	Mfap2	54.28531218	148.6387709	0.365216	0.004405
1440328_at	nuclear autoantigenic sperm protein (histone-binding)	Nasp	85.90359878	236.5464993	0.363157	0.004304
1427385_s_at	actinin, alpha 1	Actn1	20.84356288	57.62634713	0.361702	0.004591
1429261_at	RIKEN cDNA 2210411K11 gene	2210411K11Rik	97.08613239	273.327473	0.355201	0.00477
1421541_a_at	myocyte enhancer factor 2B	Mef2b	38.74110861	109.7740572	0.352917	0.00424
1450512_at	netrin 4	Ntn4	23.91753272	68.287045	0.35025	0.004304
1441698_at	---	---	123.3462462	359.6508824	0.342961	0.004681
1420183_at	Loricrin, mRNA (cDNA clone IMAGE:4190845)	Lor	35.35657609	103.530593	0.341508	0.004591
1431734_a_at	DnaJ (Hsp40) homolog, subfamily B, member 4	Dnajb4	45.57086973	133.5679444	0.341181	0.004591
1458991_at	---	---	57.45604037	169.4661515	0.339041	0.004591
1416006_at	midkine	Mdk	60.19882127	183.777542	0.327564	0.004591
1455071_at	zinc finger and BTB domain containing 7B	Zbtb7b	193.8974473	593.1843258	0.326876	0.004304
1422377_at	vomeronasal 1 receptor, B4	V1rb4	72.7171289	223.1912513	0.325806	0.004405
1447748_x_at	solute carrier family 29 (nucleoside transporters), member 2	Slc29a2	22.22117706	69.42162994	0.32009	0.002488
1455903_at	TBC1 domain family, member 4	Tbc1d4	106.2861645	332.1037032	0.320039	0.004591
1420047_at	MAF1 homolog (S. cerevisiae) (Maf1), mRNA	Maf1	26.85644918	85.0235151	0.315871	0.002488
1440565_at	---	---	49.43336919	158.1226249	0.312627	0.004461
1429719_at	forkhead box P4	Foxp4	76.45982537	250.5972316	0.30511	0.004688
1425167_a_at	guanine nucleotide binding protein (G protein), gamma transducing activity polyp	Gngt1	12.76159427	44.80744835	0.28481	0.004591
1420037_at	CDNA fis, clone TRACH2013369,highly similar to ATP SYNTHASE ALPHA CHAIN, MITOCHO	Atp5a1	63.7485225	226.0868596	0.281965	0.004681
1428669_at	brain expressed myelocytomatosis oncogene	Bmyc	148.6312156	530.3729303	0.280239	0.004149
1440930_a_at	scratch homolog 2, zinc finger protein (Drosophila)	Scrt2	29.51166338	107.2363344	0.275202	0.004922
1419757_at	phosphatidylinositol transfer protein, membrane-associated 2	Pitpnm2	66.01018182	241.8060727	0.272988	0.004304
1420570_x_at	T-cell leukemia/lymphoma 1B, 3	Tcl1b3	573.8036493	2192.609736	0.261699	0.004174
1448346_at	cofilin 1, non-muscle	Cfl1	652.0445224	2618.999375	0.248967	0.004681
1457933_at	Gene model 1964, (NCBI) (Gm1964), mRNA	Gm1964	30.98282237	126.7360664	0.244467	0.004149
1426816_at	coiled-coil domain containing 64	Ccdc64	88.77941723	366.602632	0.242168	0.004304
1420735_at	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 2	Gabrr2	30.66894569	130.4720223	0.235061	0.002488
1447772_at	pleckstrin homology domain-containing, family A (phosphoinositide binding specif	Plekha3	26.53068463	113.9776124	0.232771	0.004591

1451046_at	similar to FOG /// zinc finger protein, multitype 1	LOC100047651 /// Zfpm1	111.3975222	510.7959703	0.218086	0.004304
1427725_a_at	POU domain, class 2, transcription factor 2	Pou2f2	62.80060997	300.2637841	0.209151	0.00424
1424518_at	apolipoprotein L 9a /// apolipoprotein L 9b	Apol9a /// Apol9b	32.59148839	158.3127164	0.205868	0.004304
1438291_x_at	predicted gene, 100043481 /// predicted gene, OTTMUSG00000009529 /// ribosomal p	100043481 /// OTTMUSG00000009529 /// Rpl37	290.2414986	1423.868304	0.20384	0.004304
1416521_at	selenoprotein W, muscle 1	Sepw1	163.4659867	837.9923906	0.195069	0.004304
1417163_at	dual specificity phosphatase 10	Dusp10	28.50875898	149.2051304	0.191071	0.004591
1420089_at	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, al	Nfkbia	127.0714985	761.0390471	0.166971	0.002931
1422632_at	cathepsin W	Ctsw	119.7285443	924.3572102	0.129526	0.004304
1449381_a_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1	47.62102164	414.112804	0.114995	0.004397
1419117_at	solute carrier family 22 (organic cation transporter), member 2	Slc22a2	23.1624614	209.4380849	0.110593	0.004681
1416368_at	glutathione S-transferase, alpha 4	Gsta4	51.0542798	492.6365982	0.103635	0.002569
1426043_a_at	calpain 3	Capn3	40.46137193	411.0452276	0.098435	0.004701
1435872_at	---	---	107.5149397	1273.073501	0.084453	0.004591
1442434_at	DNA segment, Chr 8, ERATO Doi 82, expressed	D8Ertd82e	66.71087227	947.6058753	0.070399	0.004405