

Supplemental table 1.

Probe Name	Gene	Gene Name	Control MI	UO MI	FC	p	FDR
A_43_P11590	Mmp7	matrix metalloproteinase 7	-9.256	0.518	875.8	5.000E-04	3.200E-02
A_44_P318318	Mmp3	matrix metalloproteinase 3	-6.299	1.637	244.8	1.000E-04	2.100E-02
A_44_P975250	UNKNOWN		-5.777	1.751	184.5	6.000E-04	3.500E-02
A_44_P332790	Trh	thyrotropin releasing hormone	-5.876	0.948	113.3	0.000E+00	1.100E-02
A_42_P592385	Aoc1	amiloride binding protein 1	-6.318	0.399	105.2	0.000E+00	1.100E-02
A_44_P229338	Il19	interleukin 19 (predicted)	-5.657	0.972	98.9	0.000E+00	1.700E-02
A_44_P555271	Mmp12	matrix metalloproteinase 12	-5.132	1.421	93.9	5.000E-04	3.300E-02
A_44_P552738	Dmbt1	deleted in malignant brain tumors 1	-6.272	0.234	90.9	0.000E+00	1.100E-02
A_43_P15489	Il24	interleukin 24	-6.039	0.455	90.1	0.000E+00	1.800E-02
A_43_P11861	Dio3	deiodinase, iodothyronine, type III	-5.912	0.560	88.7	1.000E-04	2.200E-02
A_43_P11443	C4bpa	complement component 4 binding protein, alpha	-4.622	1.241	58.2	2.000E-04	2.300E-02
A_44_P233786	Vgf	VGF nerve growth factor inducible	-5.429	0.230	50.6	0.000E+00	8.000E-03
A_43_P11672	Il1rl1	interleukin 1 receptor-like 1	-4.551	1.048	48.5	1.300E-03	4.500E-02
A_44_P252517	Havcr1	kidney injury molecule 1	-4.583	1.013	48.4	2.000E-04	2.500E-02
A_44_P372254	Slpi	secretory leukocyte peptidase inhibitor	-5.063	0.526	48.1	0.000E+00	1.100E-02
A_44_P271658	Reg3b	pancreatitis-associated protein	-4.193	1.355	46.8	5.000E-04	3.200E-02
A_44_P739541	Cxcl6	chemokine (C-X-C motif) ligand 6	-4.182	1.348	46.2	5.000E-04	3.300E-02
A_42_P735417	Fcgr2b	Fc receptor, IgG, low affinity IIb	-4.720	0.720	43.4	1.000E-04	2.200E-02
A_44_P372261	Slpi	secretory leukocyte peptidase inhibitor	-4.894	0.541	43.3	0.000E+00	1.100E-02
A_42_P473594	Egr2	early growth response 2	-5.062	0.217	38.8	0.000E+00	8.000E-03
A_44_P404861	Mmp10	matrix metalloproteinase 10	-4.160	1.105	38.5	1.200E-03	4.300E-02
A_43_P13004	Cdh17	cadherin 17	-4.713	0.534	38.0	3.000E-04	3.000E-02
A_44_P1023538	C3	complement component 3	-4.195	0.964	35.7	1.000E-04	2.100E-02
A_44_P623953	Wnt7a	wingless-type MMTV integration site family, member 7A	-4.350	0.739	34.0	1.000E-04	2.100E-02
A_42_P501233	Adra1d	adrenergic receptor, alpha 1d	-4.779	0.193	31.4	0.000E+00	1.000E-02

A_44_P428673	C7	complement component 7 (predicted)	-4.331	0.639	31.3	1.000E-04	2.200E-02
A_44_P377266	Oldlr1	oxidized low density lipoprotein (lectin-like) receptor 1	-4.371	0.512	29.5	3.000E-04	2.700E-02
A_43_P19561	Lypd1	Ly6/Plaur domain containing 1	-4.056	0.801	29.0	2.000E-04	2.300E-02
A_44_P930681	Unknown		-4.460	0.371	28.5	0.000E+00	9.000E-03
A_44_P330783	Z27087	T-cell receptor gamma chain	-4.393	0.381	27.4	0.000E+00	1.800E-02
A_44_P144232	Fgl2	fibrinogen-like 2	-4.227	0.481	26.1	1.000E-04	2.100E-02
A_43_P14597	Sgcg	gamma sarcoglycan	-3.641	1.025	25.4	9.000E-04	3.900E-02
A_42_P602724	Ubd	ubiquitin D	-4.472	0.174	25.0	0.000E+00	1.800E-02
A_44_P393235	Has1	hyaluronan synthase1	-3.023	1.609	24.8	1.400E-03	4.600E-02
A_44_P452245	Serpine1	serine (or cysteine) proteinase inhibitor, clade E, member 1	-3.799	0.812	24.4	3.000E-04	3.000E-02
A_44_P318662	Tac3	tachykinin 2	-3.988	0.603	24.1	1.000E-04	1.900E-02
A_43_P13203	Expi	extracellular peptidase inhibitor	-3.636	0.943	23.9	1.000E-03	4.100E-02
A_44_P306439	Fcgr3a	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	-3.905	0.640	23.3	2.000E-04	2.600E-02
A_44_P462661	Il1m	interleukin 1 receptor antagonist	-3.970	0.529	22.6	0.000E+00	1.700E-02
A_44_P363116	Cxcl3	gene model 1960, (NCBI)	-3.708	0.733	21.7	7.000E-04	3.600E-02
A_42_P466362	Adcy8	adenylyl cyclase 8	-3.558	0.858	21.3	1.200E-03	4.400E-02
A_44_P313507	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-3.193	1.210	21.1	8.000E-04	3.900E-02
A_44_P550748	Lrat	lecithin-retinol acyltransferase	-3.727	0.671	21.1	2.000E-04	2.500E-02
A_44_P405858	Sectm1a	secreted and transmembrane 1A	-4.054	0.314	20.7	1.100E-03	4.200E-02
A_42_P638620	Lcn2	lipocalin 2	-3.902	0.431	20.2	0.000E+00	1.100E-02
A_44_P248105	Pira2_	paired-Ig-like receptor A2 (predicted)	-3.205	1.122	20.1	9.000E-04	3.900E-02
A_42_P509314	Tubb3	tubulin, beta 3	-3.371	0.941	19.9	5.000E-04	3.300E-02
A_44_P515197	Cxcl2	chemokine (C-X-C motif) ligand 2	-3.772	0.525	19.7	0.000E+00	1.700E-02
A_44_P294838	Il1a	interleukin 1 alpha	-3.499	0.796	19.6	3.000E-04	2.700E-02
A_44_P178252	Ccl21	chemokine (C-C motif) ligand 21b (serine) (predicted)	-2.920	1.344	19.2	1.400E-03	4.600E-02
A_44_P160841	Calcb	calcitonin-related polypeptide, beta	-3.793	0.423	18.6	1.000E-04	2.200E-02
A_44_P225952	AW142932	Unknown	-3.172	1.041	18.5	1.200E-03	4.400E-02
A_44_P828142	Il7r	interleukin 7 receptor	-3.844	0.274	17.4	2.000E-04	2.500E-02

A_44_P670272	Unknown	TC625415	-3.364	0.740	17.2	7.000E-04	3.700E-02
A_44_P118475	Unknown		-2.824	1.280	17.2	6.000E-04	3.500E-02
A_42_P475885	Ptprz1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	-3.846	0.213	16.7	0.000E+00	9.000E-03
A_44_P294965	RT1-DOb	RT1 class II, locus DOb	-2.880	1.133	16.1	4.000E-04	3.100E-02
A_43_P10020	Lyz2	lysozyme	-3.532	0.473	16.0	1.000E-04	2.100E-02
A_44_P402750	Gda	guanine deaminase	-3.302	0.695	16.0	5.000E-04	3.300E-02
A_44_P421727	ENSRNOT00000065894	caspase recruitment domain family, member 11 (predicted)	-3.431	0.553	15.8	1.000E-04	2.100E-02
A_44_P522760	Fcamr	Fc receptor, IgA, IgM, high affinity (predicted)	-3.113	0.824	15.3	1.000E-03	4.100E-02
A_44_P169124	BF558918	Unknown	-3.554	0.349	15.0	0.000E+00	1.400E-02
A_42_P732259	Fam26f	family with sequence similarity 26, member F	-3.521	0.350	14.6	2.000E-04	2.500E-02
A_44_P273839	Reg3g	regenerating islet-derived 3 gamma	-3.473	0.378	14.4	0.000E+00	1.800E-02
A_43_P15819	Prss22	protease, serine, 22 (predicted)	-3.246	0.588	14.3	3.000E-04	2.800E-02
A_44_P1027971	Gpr84	G protein-coupled receptor 84	-3.396	0.436	14.2	3.000E-04	2.900E-02
A_43_P14036	Ifi27l2b	putative ISG12(b) protein	-3.295	0.518	14.0	0.000E+00	1.700E-02
A_44_P352538	Sectm1a	secreted and transmembrane 1A	-3.590	0.214	14.0	0.000E+00	1.100E-02
A_44_P602702	CO555173	AABR07006310.1	-3.362	0.438	13.9	2.000E-04	2.600E-02
A_43_P15515	Ccr5	chemokine (C-C) receptor 5	-3.439	0.350	13.8	4.000E-04	3.100E-02
A_42_P693821	Fosl1	fos-like antigen 1	-3.559	0.226	13.8	7.000E-04	3.600E-02
A_44_P885679	Bnc1	basonuclin 1	-2.948	0.836	13.8	1.500E-03	4.700E-02
A_43_P11875	Grik1	glutamate receptor, ionotropic, kainate 1	-2.977	0.806	13.8	5.000E-04	3.300E-02
A_44_P916210	TC629545	Unknown	-3.325	0.429	13.5	0.000E+00	1.000E-02
A_44_P928825	Msr1	macrophage scavenger receptor 1	-3.100	0.643	13.4	3.000E-04	2.900E-02
A_44_P463899	LOC360777	similar to paired immunoglobulin-like type 2 receptor beta	-3.277	0.461	13.3	1.000E-04	2.100E-02
A_42_P473398	Cxcl1	chemokine (C-X-C motif) ligand 1	-3.020	0.715	13.3	2.000E-04	2.400E-02
A_44_P520175	Masp1	mannan-binding lectin serine peptidase 1	-2.890	0.837	13.2	4.000E-04	3.100E-02
A_44_P130516	RT1-Db1	RT1 class II, locus Db1	-3.317	0.399	13.1	0.000E+00	1.700E-02
A_44_P1017206	Podnl1	similar to podocan protein (predicted)	-3.238	0.478	13.1	1.000E-04	2.200E-02
A_44_P494274	Trpv6	transient receptor potential cation channel, subfamily V, member 6	-3.403	0.279	12.8	8.000E-04	3.800E-02

A_44_P633489	DV723525	Unknown	-2.835	0.829	12.7	4.000E-04	3.000E-02
A_42_P518855	Bcl2a1	B-cell leukemia/lymphoma 2 related protein A1	-3.213	0.449	12.7	3.000E-04	2.700E-02
A_42_P693316	Cfi	complement factor I	-3.281	0.356	12.4	0.000E+00	1.100E-02
A_43_P21634	C4a	complement component 4a	-2.945	0.683	12.4	2.000E-04	2.400E-02
A_44_P993328	Ms4a6a	membrane-spanning 4-domains, subfamily A, member 11 (predicted)	-2.767	0.848	12.3	4.000E-04	3.100E-02
A_42_P800916	Tdo2	tryptophan 2,3-dioxygenase	-3.283	0.331	12.2	1.000E-04	2.100E-02
A_44_P110120	RGD1563818	similar to secretory leukocyte protease inhibitor	-2.969	0.642	12.2	4.000E-04	3.100E-02
A_44_P522580	Slc34a2	solute carrier family 34 (sodium phosphate), member 2	-3.272	0.339	12.2	1.000E-04	1.900E-02
A_44_P330565	Unknown		-2.891	0.718	12.2	1.000E-04	2.100E-02
A_44_P492373	Rgs20	similar to regulator of G-protein signaling Z1	-3.170	0.434	12.2	2.000E-04	2.600E-02
A_44_P340587	CB548303	Unknown	-3.189	0.413	12.1	2.000E-04	2.500E-02
A_42_P820657	Il1r2	interleukin 1 receptor, type II	-3.197	0.396	12.1	1.000E-04	1.900E-02
A_44_P575946	TC584577	Unknown	-2.539	1.049	12.0	1.000E-03	4.200E-02
A_42_P565621	Slamf9	SLAM family member 9 (predicted)	-3.019	0.559	11.9	2.000E-04	2.600E-02
A_44_P113088	Slc34a2	solute carrier family 34 (sodium phosphate), member 2	-3.326	0.251	11.9	0.000E+00	1.100E-02
A_44_P376900	Gpr171	G protein-coupled receptor 171	-3.256	0.318	11.9	1.000E-04	2.100E-02
A_44_P367688	RT1-Da	RT1 class II, locus Da	-3.244	0.325	11.9	1.000E-04	2.100E-02
A_44_P311126	Clu	clusterin	-3.414	0.130	11.7	0.000E+00	8.000E-03
A_44_P237715	Lcn2	lipocalin 2	-2.870	0.659	11.5	1.100E-03	4.300E-02
A_44_P130513	RT1-Db1	RT1 class II, locus Db1	-3.107	0.407	11.4	1.000E-04	1.900E-02
A_44_P630174	Trim15	tripartite motif containing 15	-3.067	0.445	11.4	1.000E-04	1.800E-02
A_44_P247923	Stmn4	stathmin-like 4	-3.160	0.350	11.4	1.000E-04	2.000E-02
A_44_P431296	Gpr18	G protein-coupled receptor 18 (predicted)	-2.803	0.706	11.4	4.000E-04	3.100E-02
A_44_P594136	Sall4	spalt-like transcription factor 4	-3.362	0.128	11.2	0.000E+00	8.000E-03
A_44_P161121	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-2.678	0.801	11.1	4.000E-04	3.100E-02
A_43_P19776	LOC681325	hypothetical protein LOC681325	-2.843	0.633	11.1	1.000E-04	2.200E-02
A_44_P915860	RT1-T18	Unknown	-2.771	0.689	11.0	2.000E-04	2.500E-02
A_43_P15552	Ccr2	chemokine (C-C motif) receptor 2	-3.158	0.290	10.9	4.000E-04	3.100E-02

A_42_P781919	C1qb	complement component 1, q subcomponent, beta polypeptide	-2.819	0.620	10.8	3.000E-04	2.800E-02
A_44_P991532	RT1-Da	RT1 class II, locus Da	-3.072	0.367	10.8	1.000E-04	2.100E-02
A_44_P330828	MGC105649	hypothetical LOC302884	-2.826	0.603	10.8	4.000E-04	3.100E-02
A_44_P941248	BF286677	RGIFR91	-2.484	0.942	10.7	8.000E-04	3.800E-02
A_44_P746420	Arl11	ADP-ribosylation factor-like 11	-2.695	0.730	10.7	1.400E-03	4.600E-02
A_43_P16707	Ccl6	chemokine (C-C motif) ligand 6	-2.645	0.777	10.7	6.000E-04	3.400E-02
A_42_P832728	Cst7	cystatin F (leukocystatin) (predicted)	-2.934	0.482	10.7	1.500E-03	4.700E-02
A_44_P487764	C1qa	complement component 1, q subcomponent, alpha polypeptide (predicted)	-2.723	0.685	10.6	4.000E-04	3.100E-02
A_44_P318861	Wdfy4	WDFY family member 4	-3.159	0.237	10.5	0.000E+00	1.800E-02
A_44_P602351	Pld4	phospholipase D family, member 4	-3.016	0.379	10.5	1.000E-03	4.100E-02
A_44_P210921	RT1-Db2	arrestin, beta 2, pseudogene	-3.187	0.204	10.5	0.000E+00	1.800E-02
A_44_P960765	Chodl	chondrolectin	-3.074	0.311	10.4	0.000E+00	1.000E-02
A_44_P395788	Wnt7a	wingless-related MMTV integration site 7A	-2.810	0.575	10.4	1.100E-03	4.200E-02
A_44_P459144	Inhba	inhibin beta-A	-2.679	0.697	10.4	8.000E-04	3.800E-02
A_44_P487761	C1qa	complement component 1, q subcomponent, alpha polypeptide (predicted)	-2.703	0.662	10.3	4.000E-04	3.100E-02
A_44_P499129	RGD1311300	similar to T cell receptor V delta 6 (predicted)	-2.509	0.845	10.2	4.000E-04	3.100E-02
A_44_P372587	Cx3cr1	chemokine (C-X3-C) receptor 1	-3.121	0.232	10.2	2.000E-04	2.300E-02
A_44_P108304	Slc41a2	solute carrier family 41, member 2 (predicted)	-2.624	0.713	10.1	8.000E-04	3.900E-02
A_44_P104630	Wbscr5	Williams-Beuren syndrome chromosome region 5 homolog (human)	-2.468	0.855	10.0	3.000E-04	2.800E-02
A_44_P414258	Ptpnc	protein tyrosine phosphatase, receptor type, C	-2.887	0.430	10.0	1.000E-04	2.200E-02
A_44_P464045	Arl11	ADP-ribosylation factor-like 11	-2.809	0.495	9.9	5.000E-04	3.300E-02
A_44_P500708	C1qc	complement component 1, q subcomponent, gamma polypeptide (predicted)	-2.436	0.868	9.9	1.000E-03	4.100E-02
A_44_P470430	Fap	fibroblast activation protein	-2.203	1.093	9.8	1.600E-03	4.800E-02
A_44_P552452	RT1-Bb	RT1 class II, locus Bb	-2.964	0.328	9.8	2.000E-04	2.300E-02
A_44_P715283	Fyb	FYN binding protein	-2.789	0.502	9.8	1.000E-04	2.000E-02
A_44_P700588	TC638908	Unknown	-2.943	0.346	9.8	1.000E-04	1.900E-02
A_44_P500803	RT1-Bb	RT1 class II, locus Bb	-2.850	0.424	9.7	1.000E-04	2.200E-02

A_44_P152395	Rnd1	Rho family GTPase 1	-3.039	0.217	9.6	0.000E+00	1.000E-02
A_44_P1042360	Clec4a3	dendritic cell inhibitory receptor 3	-2.539	0.705	9.5	8.000E-04	3.800E-02
A_44_P174992	Ifi47	interferon gamma inducible protein	-3.015	0.226	9.5	0.000E+00	1.300E-02
A_44_P177724	Trac	T cell receptor alpha constant	-2.755	0.484	9.4	1.000E-04	2.100E-02
A_44_P558641	Fgg	fibrinogen, gamma polypeptide	-2.275	0.955	9.4	1.300E-03	4.500E-02
A_44_P252756	Flt3	fms-related tyrosine kinase 3	-2.794	0.425	9.3	5.000E-04	3.200E-02
A_44_P230320	Il1b	interleukin 1 beta	-2.764	0.454	9.3	1.000E-04	2.200E-02
A_44_P363291	Kcnk10	potassium channel, subfamily K, member 10	-3.082	0.135	9.3	0.000E+00	1.000E-02
A_44_P115116	Mpeg1	macrophage expressed gene 1	-2.570	0.637	9.2	1.500E-03	4.800E-02
A_44_P428824	Unknown		-2.698	0.493	9.1	6.000E-04	3.500E-02
A_44_P157314	Clec4d	C-type lectin domain family 4, member D	-2.302	0.888	9.1	1.100E-03	4.200E-02
A_42_P457756	Pkib	protein kinase (cAMP dependent, catalytic) inhibitor beta	-3.039	0.150	9.1	0.000E+00	1.100E-02
A_44_P231564	Cbln2	cerebellin 2 precursor	-2.858	0.330	9.1	1.000E-04	2.100E-02
A_43_P14911	Il1b	interleukin 1 beta	-2.468	0.707	9.0	4.000E-04	3.200E-02
A_43_P22080	Lcp1	lymphocyte cytosolic protein 1 (predicted)	-2.722	0.452	9.0	3.000E-04	2.800E-02
A_44_P325772	NP516920	MHC class II antigen	-2.834	0.338	9.0	0.000E+00	1.400E-02
A_44_P1010416	P2ry13	purinergic receptor P2Y, G-protein coupled, 13	-2.569	0.603	9.0	1.400E-03	4.700E-02
A_44_P573545	Unknown		-2.754	0.405	8.9	1.000E-04	1.900E-02
A_44_P144188	Syt12	synaptotagmin 12	-2.777	0.381	8.9	1.000E-04	1.800E-02
A_44_P482128	Ptprz1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	-2.959	0.198	8.9	0.000E+00	1.000E-02
A_44_P464111	RGD1308694	similar to hypothetical protein MGC47256 (predicted)	-2.726	0.426	8.9	1.000E-04	1.900E-02
A_44_P792845	TC601188	Unknown	-2.499	0.650	8.9	3.000E-04	2.900E-02
A_44_P255817	Pram1	similar to PML-RAR alpha-regulated adaptor molecule-1	-2.510	0.629	8.8	7.000E-04	3.600E-02
A_44_P517958	Lilrb3	leukocyte immunoglobulin-like receptor, subfamily B, member 3 (predicted)	-2.291	0.841	8.8	1.400E-03	4.700E-02
A_44_P531414	Il18	interleukin 18	-2.709	0.422	8.8	1.600E-03	4.800E-02
A_42_P598602	Cd3g	CD3 antigen, gamma polypeptide (predicted)	-2.501	0.626	8.7	1.200E-03	4.400E-02
A_44_P450786	Ccr5	chemokine (C-C motif) receptor 5	-2.514	0.604	8.7	1.000E-03	4.100E-02
A_43_P19712	Gpr65	G-protein coupled receptor 65 (predicted)	-2.704	0.402	8.6	2.000E-04	2.300E-02

A_44_P175530	Plek	pleckstrin	-2.820	0.278	8.6	0.000E+00	1.200E-02
A_43_P11621	Cd44	CD44 antigen	-2.656	0.441	8.6	1.000E-04	1.800E-02
A_42_P762150	LOC305501	similar to DNA-binding protein Ikaros form 1 - mouse	-2.724	0.372	8.6	1.000E-04	2.200E-02
A_44_P958894	LOC298795	similar to 14-3-3 protein sigma	-2.729	0.359	8.5	1.200E-03	4.400E-02
A_44_P838920	Unknown		-2.269	0.815	8.5	1.700E-03	5.000E-02
A_44_P235892	Cyp24a1	cytochrome P450, subfamily 24	-2.102	0.981	8.5	1.300E-03	4.600E-02
A_44_P177169	Fgl2	fibrinogen-like 2	-2.564	0.517	8.5	1.000E-04	2.100E-02
A_43_P11616	Atf3	activating transcription factor 3	-2.937	0.135	8.4	0.000E+00	8.000E-03
A_42_P745356	Sox9	SRY (sex determining region Y)-box 9	-2.884	0.187	8.4	1.000E-04	2.200E-02
A_43_P12384	Birc3	inhibitor of apoptosis protein 1	-2.786	0.282	8.4	0.000E+00	1.000E-02
A_43_P22739	RGD1565785	similar to chromosome X open reading frame 21	-2.417	0.650	8.4	3.000E-04	2.900E-02
A_44_P525969	Cybb	cytochrome b-245, beta polypeptide	-2.590	0.472	8.4	8.000E-04	3.700E-02
A_44_P283839	Unknown		-2.346	0.715	8.3	5.000E-04	3.200E-02
A_44_P290022	Lrg1	similar to leucine-rich alpha-2-glycoprotein	-2.532	0.517	8.3	4.000E-04	3.100E-02
A_43_P11522	Cd4	CD4 antigen	-2.655	0.383	8.2	6.000E-04	3.400E-02
A_44_P182020	Psmb8	proteasome (prosome, macropain) subunit, beta type 8	-2.872	0.156	8.2	0.000E+00	1.000E-02
A_44_P1004840	Tnfsf9	tumor necrosis factor (ligand) superfamily, member 9	-2.342	0.674	8.1	2.000E-04	2.600E-02
A_44_P574914	Sox9	SRY (sex determining region Y)-box 9	-2.846	0.167	8.1	7.000E-04	3.600E-02
A_43_P19543	Cyp24a1	cytochrome P450, subfamily 24	-2.036	0.967	8.0	6.000E-04	3.500E-02
A_44_P510436	Myr8	myosin heavy chain Myr 8	-1.975	1.020	8.0	9.000E-04	3.900E-02
A_43_P16181	RT1-Db	SHR/NCrIbR MHC class II antigen	-2.282	0.712	8.0	4.000E-04	3.100E-02
A_44_P168405	Fcgr3	Fc receptor, IgG, low affinity III	-2.405	0.588	8.0	1.000E-03	4.100E-02
A_44_P463749	Rasd1	RAS, dexamethasone-induced 1	-2.586	0.402	7.9	1.000E-04	2.100E-02
A_44_P492025	Oasl	2'-5' oligoadenylate synthetase-like 1 (predicted)	-2.444	0.542	7.9	5.000E-04	3.200E-02
A_42_P538670	Cybb	cytochrome b-245, beta polypeptide	-2.398	0.587	7.9	7.000E-04	3.600E-02
A_42_P774527	Gzmc	granzyme C	-2.312	0.667	7.9	9.000E-04	3.900E-02
A_43_P19999	Fcrl2	macrophage scavenger receptor 2 (predicted)	-2.613	0.352	7.8	1.000E-04	1.900E-02
A_44_P652293	Ly49i8	Ly49 inhibitory receptor 8	-2.474	0.490	7.8	2.000E-04	2.500E-02

A_44_P189909	Syndig1	synapse differentiation inducing 1	-2.232	0.720	7.7	3.000E-04	2.900E-02
A_44_P151834	Tagap	T-cell activation GTPase activating protein (predicted)	-2.617	0.334	7.7	1.000E-04	2.200E-02
A_44_P187246	ENSRNOT00000050242	similar to cell surface receptor FDFACT	-2.448	0.503	7.7	8.000E-04	3.700E-02
A_44_P685189	Unknown		-2.468	0.482	7.7	3.000E-04	2.600E-02
A_44_P687814	TC586436	Unknown	-2.378	0.571	7.7	5.000E-04	3.200E-02
A_44_P466636	Cd72	Cd72 molecule	-2.510	0.434	7.7	5.000E-04	3.300E-02
A_44_P592899	Ccdc69	coiled-coil domain containing 69	-2.641	0.297	7.7	1.000E-04	2.100E-02
A_43_P16166	Cd69	Cd69 molecule	-2.414	0.518	7.6	7.000E-04	3.600E-02
A_44_P540511	Pkib	protein kinase (cAMP dependent, catalytic) inhibitor beta	-2.816	0.115	7.6	2.000E-04	2.500E-02
A_44_P515548	Pilra	similar to paired immunoglobulin-like type 2 receptor alpha	-2.460	0.468	7.6	2.000E-04	2.500E-02
A_44_P359684	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	-2.703	0.223	7.6	0.000E+00	1.000E-02
A_44_P436181	Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	-2.201	0.724	7.6	3.000E-04	2.700E-02
A_44_P914868	CO567020	Unknown	-2.449	0.459	7.5	2.000E-04	2.600E-02
A_44_P221245	Sox9	SRY (sex determining region Y)-box 9	-2.542	0.364	7.5	5.000E-04	3.200E-02
A_43_P15357	Bhlhb3	basic helix-loop-helix domain containing, class B3	-2.471	0.433	7.5	2.000E-04	2.500E-02
A_44_P1053605	Hcn1	hyperpolarization-activated, cyclic nucleotide-gated potassium channel 1	-2.305	0.595	7.5	7.000E-04	3.600E-02
A_44_P355928	Ctss	cathepsin S	-2.406	0.494	7.5	6.000E-04	3.500E-02
A_44_P816448	CV076973	Unknown	-2.549	0.344	7.4	1.000E-04	2.100E-02
A_44_P113974	Ccr5	chemokine (C-C) receptor 5	-2.165	0.725	7.4	9.000E-04	3.900E-02
A_44_P975868	Cd44	CD44 molecule (Indian blood group)	-2.372	0.507	7.4	1.000E-04	2.000E-02
A_44_P468879	Btk	Bruton agammaglobulinemia tyrosine kinase	-2.489	0.390	7.4	2.000E-04	2.500E-02
A_44_P335776	Chodl	chondrolectin (predicted)	-2.214	0.665	7.4	5.000E-04	3.200E-02
A_44_P780510	Unknown		-2.015	0.864	7.4	1.700E-03	5.000E-02
A_44_P452222	Itgal	integrin alpha L	-2.272	0.602	7.3	4.000E-04	3.100E-02
A_44_P311136	Vav1	vav 1 oncogene	-2.238	0.630	7.3	1.400E-03	4.600E-02
A_44_P189496	Fcgr1a	Fc fragment of IgG receptor Ia	-2.377	0.491	7.3	4.000E-04	3.100E-02
A_44_P412290	C1qg	complement component 1, q subcomponent, gamma polypeptide (predicted)	-2.067	0.796	7.3	1.400E-03	4.700E-02

A_44_P588937	Unknown		-2.547	0.307	7.2	7.000E-04	3.700E-02
A_44_P855088	Gpr114	adhesion G protein-coupled receptor G5	-2.428	0.417	7.2	1.000E-04	1.900E-02
A_44_P340236	Clec4a1	dendritic cell inhibitory receptor 4	-2.284	0.549	7.1	5.000E-04	3.200E-02
A_44_P745407	TC627879	Unknown	-2.250	0.583	7.1	1.000E-03	4.200E-02
A_44_P436008	Lamc2	laminin, gamma 2 (predicted)	-2.370	0.459	7.1	1.100E-03	4.200E-02
A_44_P399249	Tgm1	transglutaminase 1	-2.534	0.291	7.1	1.000E-04	2.000E-02
A_42_P736315	Rtp4	similar to 5830458K16Rik protein (predicted)	-2.502	0.319	7.1	7.000E-04	3.600E-02
A_42_P686427	Clic6	chloride intracellular channel 6	-1.991	0.826	7.0	1.100E-03	4.200E-02
A_44_P933121	Cybb	cytochrome b-245, beta polypeptide	-2.477	0.340	7.0	5.000E-04	3.200E-02
A_44_P562894	Rnd1	Rho family GTPase 1	-2.612	0.200	7.0	0.000E+00	9.000E-03
A_44_P525953	CB547650	Unknown	-2.316	0.496	7.0	4.000E-04	3.100E-02
A_44_P309097	Sctr	secretin receptor	-2.290	0.516	7.0	3.000E-04	3.000E-02
A_42_P660129	Casp12	caspase 12	-2.237	0.561	7.0	2.000E-04	2.500E-02
A_44_P219026	Bdnf	brain derived neurotrophic factor	-2.540	0.254	6.9	2.000E-04	2.300E-02
A_44_P1057055	Ccl12	chemokine (C-C motif) ligand 12 (predicted)	-2.469	0.322	6.9	0.000E+00	1.100E-02
A_43_P12403	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	-2.314	0.470	6.9	4.000E-04	3.100E-02
A_44_P372823	XM_342309_	similar to novel protein	-2.361	0.420	6.9	4.000E-04	3.000E-02
A_44_P105034	Alox5	arachidonate 5-lipoxygenase	-2.439	0.341	6.9	2.000E-04	2.300E-02
A_44_P1004731	Ctss	cathepsin S	-2.234	0.542	6.9	7.000E-04	3.700E-02
A_42_P750340	Ifitm10	similar to RIKEN cDNA 6330512M04 gene	-2.040	0.730	6.8	7.000E-04	3.600E-02
A_43_P21641	Hcls1	hematopoietic cell specific Lyn substrate 1 (predicted)	-2.479	0.288	6.8	1.000E-04	1.800E-02
A_44_P332429	C1s	complement component 1, s subcomponent	-2.024	0.741	6.8	1.000E-03	4.200E-02
A_44_P548126	Socs3	suppressor of cytokine signaling 3	-2.199	0.562	6.8	2.000E-04	2.500E-02
A_44_P572818	Unknown		-2.371	0.380	6.7	5.000E-04	3.300E-02
A_44_P315437	Unknown		-2.091	0.658	6.7	6.000E-04	3.400E-02
A_44_P335219	Il21r	interleukin 21 receptor (predicted)	-2.280	0.464	6.7	3.000E-04	2.900E-02
A_44_P260072	Tbxas1	thromboxane A synthase 1	-2.367	0.376	6.7	5.000E-04	3.200E-02
A_44_P478340	Msc	musculin (predicted)	-2.409	0.333	6.7	1.000E-04	2.000E-02

A_44_P130898	Ly86	lymphocyte antigen 86 (predicted)	-2.402	0.338	6.7	1.000E-04	2.200E-02
A_42_P588738	Igsf6	immunoglobulin superfamily, member 6	-2.229	0.495	6.6	8.000E-04	3.800E-02
A_44_P1038296	Cd68	CD68 antigen (predicted)	-2.181	0.538	6.6	1.400E-03	4.700E-02
A_44_P105304	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (predicted)	-2.310	0.408	6.6	1.000E-03	4.100E-02
A_44_P489862	Tnfaip8l2	tumor necrosis factor, alpha-induced protein 8-like 2	-2.265	0.451	6.6	4.000E-04	3.100E-02
A_42_P679371	Coro1a	coronin, actin binding protein 1A	-2.327	0.389	6.6	2.000E-04	2.500E-02
A_44_P317250	Ifi27l2b	interferon, alpha-inducible protein 27 like 2B	-2.294	0.420	6.6	1.000E-04	2.200E-02
A_44_P551075	Nfam1	NFAT activating protein with ITAM motif 1	-2.246	0.466	6.6	1.300E-03	4.500E-02
A_44_P560973	Lamc2	laminin, gamma 2 (predicted)	-2.553	0.158	6.6	1.000E-04	2.100E-02
A_44_P549494	Cd74	CD74 antigen	-2.328	0.376	6.5	2.000E-04	2.600E-02
A_44_P435955	Pilra	similar to cell surface receptor FDFACT	-2.295	0.408	6.5	2.000E-04	2.400E-02
A_42_P814235	P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	-2.142	0.551	6.5	4.000E-04	3.100E-02
A_44_P668359	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-2.062	0.621	6.4	5.000E-04	3.300E-02
A_44_P961127	ENSRNOT00000036132	pan hematopoietic expression (predicted)	-2.013	0.669	6.4	8.000E-04	3.800E-02
A_44_P715645	Pou2f2	POU class 2 homeobox 2	-2.014	0.665	6.4	1.600E-03	4.900E-02
A_44_P214857	Gpr141	G protein-coupled receptor 141	-2.231	0.435	6.3	6.000E-04	3.500E-02
A_44_P437896	Bdnf	brain derived neurotrophic factor	-2.469	0.198	6.3	7.000E-04	3.600E-02
A_44_P311541	Ccr6	chemokine (C-C motif) receptor 6	-2.083	0.583	6.3	3.000E-04	3.000E-02
A_42_P591344	Itgb2	integrin beta 2 (predicted)	-2.170	0.490	6.3	9.000E-04	3.900E-02
A_42_P826221	Dpysl4	dihydropyrimidinase-like 4	-2.205	0.453	6.3	1.000E-04	2.100E-02
A_44_P482476	Fcgr3	Unknown	-2.111	0.545	6.3	1.400E-03	4.600E-02
A_42_P577136	Fcer2a	Fc receptor, IgE, low affinity II, alpha polypeptide	-1.922	0.729	6.3	1.100E-03	4.200E-02
A_44_P668363	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-2.008	0.639	6.3	6.000E-04	3.400E-02
A_44_P482710	Spnb4	spectrin beta 4 (predicted)	-2.085	0.553	6.2	3.000E-04	2.600E-02
A_44_P550590	Rinl	similar to RIKEN cDNA 5830482F20 gene (predicted)	-2.461	0.173	6.2	0.000E+00	1.000E-02
A_44_P242059	Unknown		-2.333	0.298	6.2	9.000E-04	3.900E-02
A_44_P563447	Wnt10a	wingless related MMTV integration site 10a (predicted)	-2.389	0.241	6.2	0.000E+00	1.000E-02
A_44_P478144	LOC290595	hypothetical gene supported by AF152002	-2.422	0.205	6.2	1.000E-04	1.800E-02

A_44_P898168	Slamf7	SLAM family member	-2.133	0.491	6.2	2.000E-04	2.400E-02
A_44_P421534	Aif1	allograft inflammatory factor 1	-2.108	0.514	6.2	5.000E-04	3.200E-02
A_43_P22811	Cd6	CD6 antigen	-2.043	0.575	6.1	1.400E-03	4.700E-02
A_44_P438060	Gna15	guanine nucleotide binding protein, alpha 15	-2.161	0.453	6.1	9.000E-04	4.000E-02
A_43_P15464	Capn8	calpain 8	-2.399	0.210	6.1	9.000E-04	3.900E-02
A_44_P1004886	Fam198b	Unknown (protein for MGC:72614)	-1.778	0.825	6.1	1.600E-03	4.900E-02
A_44_P426638	Osmr	oncostatin M specific receptor	-2.301	0.300	6.1	3.000E-04	3.000E-02
A_42_P607092	Glipr1	GLI pathogenesis-related 1 (glioma) (predicted)	-2.178	0.418	6.0	9.000E-04	4.000E-02
A_43_P14764	Nrxn1	neurexin 1	-1.805	0.790	6.0	5.000E-04	3.400E-02
A_44_P233080	Egr1	early growth response 1	-1.873	0.716	6.0	4.000E-04	3.100E-02
A_44_P961443	Trpv6	transient receptor potential cation channel, subfamily V, member 6	-2.035	0.552	6.0	1.000E-04	2.200E-02
A_44_P228942	Runx1	runt related transcription factor 1	-2.045	0.540	6.0	9.000E-04	3.900E-02
A_42_P653257	Ptpn7	protein tyrosine phosphatase, non-receptor type 7	-2.340	0.245	6.0	2.000E-04	2.400E-02
A_44_P281510	Tlr7	similar to toll-like receptor 7	-2.079	0.505	6.0	3.000E-04	2.800E-02
A_44_P389132	Rgs18	regulator of G-protein signaling 18 (predicted)	-2.197	0.382	6.0	2.000E-04	2.600E-02
A_42_P749449	Nckap1l	hematopoietic protein 1 (predicted)	-2.122	0.456	6.0	6.000E-04	3.500E-02
A_42_P577431	Bcl3	B-cell leukemia/lymphoma 3 (predicted)	-2.531	0.045	6.0	0.000E+00	1.700E-02
A_44_P487313	LOC363890	similar to cell surface receptor FDFACT	-2.136	0.437	5.9	5.000E-04	3.300E-02
A_44_P766678	Pik3r5	phosphoinositide-3-kinase, regulatory subunit 5	-1.887	0.685	5.9	1.000E-03	4.100E-02
A_43_P11236	Laptn5	lysosomal-associated protein transmembrane 5	-2.006	0.562	5.9	3.000E-04	2.900E-02
A_44_P211679	BM299612	Unknown	-2.012	0.556	5.9	2.000E-04	2.300E-02
A_43_P12125	Junb	Jun-B oncogene	-2.186	0.379	5.9	2.000E-04	2.400E-02
A_44_P517012	Rac2	RAS-related C3 botulinum substrate 2 (predicted)	-2.002	0.552	5.9	5.000E-04	3.300E-02
A_44_P763036	TC608341	Unknown	-2.047	0.504	5.9	1.100E-03	4.200E-02
A_44_P290204	Dnm3	dynammin 3	-2.199	0.348	5.8	3.000E-04	2.700E-02
A_44_P1058966	Apbb1ip	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (predicted)	-2.076	0.457	5.8	1.300E-03	4.600E-02
A_42_P824217	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (predicted)	-2.263	0.270	5.8	2.000E-04	2.400E-02
A_43_P15904	Fcgr1a	Fc receptor, IgG, high affinity I (predicted)	-1.988	0.541	5.8	5.000E-04	3.300E-02

A_44_P361454	Lrrc2	leucine rich repeat containing 2 (predicted)	-2.172	0.355	5.8	1.000E-04	1.900E-02
A_44_P715240	Pilra	Unknown	-2.006	0.511	5.7	6.000E-04	3.500E-02
A_44_P452632	Irf8	interferon regulatory factor 8	-2.074	0.441	5.7	1.400E-03	4.700E-02
A_42_P807697	Tyrobp	Tyro protein tyrosine kinase binding protein	-2.036	0.476	5.7	8.000E-04	3.800E-02
A_42_P520349	Clec10a	macrophage galactose N-acetyl-galactosamine specific lectin 1	-1.988	0.520	5.7	2.000E-04	2.500E-02
A_44_P482519	Itgb7	integrin, beta 7	-1.939	0.567	5.7	3.000E-04	2.800E-02
A_44_P102481	Sox9	SRY-box containing gene 9	-2.114	0.390	5.7	1.200E-03	4.400E-02
A_44_P217744	Ms4a4a	membrane-spanning 4-domains, subfamily A, member 4 (predicted)	-2.151	0.352	5.7	6.000E-04	3.500E-02
A_44_P974862	Pld4	phospholipase D family, member 4	-2.226	0.270	5.6	2.000E-04	2.600E-02
A_44_P986010	Il1r1	interleukin 1 receptor, type I	-1.790	0.702	5.6	1.300E-03	4.500E-02
A_42_P572521	C5r1	complement component 5, receptor 1	-1.872	0.619	5.6	1.100E-03	4.200E-02
A_44_P311054	Unknown		-2.299	0.184	5.6	1.000E-04	2.200E-02
A_44_P402445	Nefh	neurofilament, heavy polypeptide	-2.016	0.466	5.6	6.000E-04	3.400E-02
A_44_P871423	TC598531	Unknown	-2.145	0.333	5.6	0.000E+00	1.300E-02
A_44_P853694	BG709676	Unknown	-2.240	0.230	5.5	6.000E-04	3.500E-02
A_44_P210173	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	-2.250	0.216	5.5	0.000E+00	1.000E-02
A_44_P139939	Cp	ceruloplasmin	-2.192	0.267	5.5	0.000E+00	1.700E-02
A_44_P311096	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	-1.931	0.521	5.5	9.000E-04	3.900E-02
A_44_P356391	Blk	BLK proto-oncogene, Src family tyrosine kinase	-1.750	0.700	5.5	8.000E-04	3.700E-02
A_43_P11840	Xdh	xanthine dehydrogenase	-1.880	0.563	5.4	5.000E-04	3.400E-02
A_44_P283909	LOC296811	Unknown	-2.249	0.192	5.4	0.000E+00	1.100E-02
A_44_P251008	Efhb	similar to hypothetical protein 4921525D22	-2.097	0.343	5.4	5.000E-04	3.300E-02
A_44_P262382	Batf3	Jun dimerization protein 1	-2.181	0.257	5.4	1.000E-04	1.800E-02
A_44_P506980	Kcnk13	potassium channel, subfamily K, member 13	-1.952	0.483	5.4	9.000E-04	3.900E-02
A_44_P180717	Pstpip1	proline-serine-threonine phosphatase-interacting protein 1 (predicted)	-1.960	0.474	5.4	2.000E-04	2.500E-02
A_42_P689631	Ephb6	Eph receptor B6 (predicted)	-1.931	0.496	5.4	2.000E-04	2.600E-02
A_42_P576953	Pla1a	phosphatidylserine-specific phospholipase A1	-2.061	0.366	5.4	1.000E-03	4.100E-02
A_44_P230879	Spidr	scaffolding protein involved in DNA repair	-1.742	0.684	5.4	3.000E-04	2.800E-02

A_44_P458855	Ptpn	protein tyrosine phosphatase, receptor type, N	-2.038	0.386	5.4	6.000E-04	3.400E-02
A_44_P139869	Tmem176b	LR8 protein	-2.024	0.386	5.3	1.000E-04	1.900E-02
A_44_P463805	Cd3z	CD3 antigen, zeta polypeptide	-1.767	0.634	5.3	6.000E-04	3.500E-02
A_44_P801735	Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	-1.922	0.476	5.3	3.000E-04	3.000E-02
A_44_P358235	Ccr1	macrophage inflammatory protein-1 alpha receptor gene	-1.843	0.551	5.3	8.000E-04	3.800E-02
A_44_P986952	Irf8	interferon regulatory factor 8	-2.036	0.356	5.2	5.000E-04	3.400E-02
A_44_P108217	Nrbp2	nuclear receptor binding protein 2	-1.975	0.416	5.2	1.000E-04	2.100E-02
A_44_P1038028	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	-2.092	0.297	5.2	0.000E+00	1.500E-02
A_44_P1045986	Erp27	similar to RIKEN cDNA 1810033M07	-1.866	0.515	5.2	5.000E-04	3.300E-02
A_44_P419898	Cldn9	claudin 9 (predicted)	-2.003	0.371	5.2	1.700E-03	5.000E-02
A_44_P332422	C1s	complement component 1, s subcomponent	-1.934	0.431	5.2	4.000E-04	3.000E-02
A_44_P578061	Mab21l3	mab-21-like 3 (C. elegans)	-1.792	0.568	5.1	4.000E-04	3.000E-02
A_44_P463745	Fas	Tumor necrosis factor receptor superfamily, member 6	-1.783	0.574	5.1	2.000E-04	2.400E-02
A_44_P791638	TC623018	Unknown	-1.682	0.675	5.1	8.000E-04	3.900E-02
A_44_P257582	Csf1r	colony stimulating factor 1 receptor	-2.005	0.342	5.1	8.000E-04	3.800E-02
A_44_P197350	Traf3ip3	TRAF3 interacting protein 3	-1.721	0.625	5.1	1.000E-03	4.100E-02
A_44_P419746	Dennd1c	similar to RIKEN cDNA 4432409M07	-1.844	0.497	5.1	5.000E-04	3.400E-02
A_43_P13117	Lcp2	lymphocyte cytosolic protein 2	-1.808	0.532	5.1	1.000E-03	4.100E-02
A_44_P961280	TC601928	unknown	-1.785	0.547	5.0	5.000E-04	3.300E-02
A_44_P904810	Nckap1	NCK associated protein 1 like	-1.912	0.419	5.0	6.000E-04	3.500E-02
A_43_P18738	Mrc1	mannose receptor, C type 1 (predicted)	-2.035	0.295	5.0	4.000E-04	3.100E-02
A_44_P960804	Rgs16	regulator of G-protein signaling 16	-1.941	0.385	5.0	2.000E-04	2.600E-02
A_44_P404836	Cp	ceruloplasmin	-1.955	0.360	5.0	0.000E+00	1.800E-02
A_44_P384404	Ms4a6a	membrane-spanning 4-domains, subfamily A, member 11 (predicted)	-1.860	0.454	5.0	6.000E-04	3.500E-02
A_44_P168348	Unknown		-1.796	0.517	5.0	1.500E-03	4.800E-02
A_43_P16070	Axl	Axl receptor tyrosine kinase	-1.537	0.775	5.0	1.200E-03	4.400E-02
A_42_P473314	RT1-DMa	major histocompatibility complex, class II, DM alpha	-2.030	0.281	5.0	2.000E-04	2.300E-02
A_44_P669519	Mir142	microRNA 142	-1.787	0.519	4.9	4.000E-04	3.100E-02

A_44_P519251	Cd14	CD14 antigen	-1.984	0.318	4.9	2.000E-04	2.600E-02
A_44_P777359	Unknown		-2.082	0.220	4.9	7.000E-04	3.600E-02
A_44_P360907	Unknown		-1.884	0.416	4.9	8.000E-04	3.800E-02
A_42_P678430	Card9	caspase recruitment domain family, member 9	-1.875	0.424	4.9	4.000E-04	3.100E-02
A_44_P466118	Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	-1.881	0.415	4.9	6.000E-04	3.500E-02
A_44_P232508	Ptpn7	protein tyrosine phosphatase, non-receptor type 7	-1.919	0.357	4.8	6.000E-04	3.400E-02
A_44_P700638	Unknown		-1.855	0.419	4.8	3.000E-04	2.800E-02
A_44_P900584	Unknown		-1.931	0.338	4.8	1.400E-03	4.700E-02
A_44_P390172	RT1-Aw2	RT1 class Ib, locus Aw2	-1.675	0.587	4.8	7.000E-04	3.600E-02
A_44_P508379	Cd37	CD37 antigen	-1.706	0.556	4.8	1.200E-03	4.400E-02
A_44_P100301	Selpl	selectin, platelet (p-selectin) ligand (predicted)	-1.695	0.564	4.8	1.600E-03	4.900E-02
A_42_P822726	Myo1g	myosin IG (predicted)	-1.690	0.568	4.8	1.400E-03	4.600E-02
A_44_P184659	Fam65b	similar to mKIAA0386 protein (predicted)	-1.930	0.325	4.8	3.000E-04	2.900E-02
A_44_P388650	Camk4	calcium/calmodulin-dependent protein kinase IV	-1.638	0.613	4.8	5.000E-04	3.300E-02
A_44_P258225	Ly6h	lymphocyte antigen 6 complex, locus H (predicted)	-1.551	0.699	4.8	1.400E-03	4.600E-02
A_44_P565432	Unknown		-2.055	0.194	4.8	2.000E-04	2.500E-02
A_44_P313652	RATMHC1	RT1 class Ib, locus Aw2	-1.821	0.426	4.7	5.000E-04	3.200E-02
A_44_P576822	Inhbb	inhibin beta-B	-2.035	0.204	4.7	0.000E+00	1.800E-02
A_42_P596050	Cdhr1	MT-protocadherin	-1.914	0.325	4.7	2.000E-04	2.600E-02
A_44_P590505	LOC102546864	uncharacterized LOC102546864	-1.752	0.476	4.7	1.200E-03	4.400E-02
A_44_P792446	Scube1	signal peptide, CUB domain, EGF-like 1 (predicted)	-1.920	0.305	4.7	6.000E-04	3.500E-02
A_44_P156462	Ren1	renin 1	-1.930	0.289	4.7	1.000E-03	4.100E-02
A_44_P852790	Unknown		-2.005	0.192	4.6	0.000E+00	1.200E-02
A_42_P588944	Mgp	matrix Gla protein	-1.838	0.359	4.6	2.000E-04	2.600E-02
A_44_P236761	Rasal3	RAS protein activator like 3	-1.586	0.602	4.6	7.000E-04	3.600E-02
A_44_P550662	LOC100912573	membrane-spanning 4-domains, subfamily A, member 6A (predicted)	-1.758	0.428	4.5	4.000E-04	3.100E-02
A_42_P623358	Ren1	renin 1	-1.960	0.224	4.5	8.000E-04	3.900E-02
A_44_P866312	Unknown		-1.741	0.442	4.5	7.000E-04	3.600E-02

A_44_P484889	Ifitm3	interferon induced transmembrane protein 3	-1.865	0.317	4.5	3.000E-04	2.800E-02
A_44_P267706	Apol11a	similar to Apolipoprotein L3 (predicted)	-1.742	0.439	4.5	2.000E-04	2.600E-02
A_43_P12315	P2ry12	purinergic receptor P2Y, G-protein coupled 12	-1.937	0.240	4.5	1.000E-04	1.800E-02
A_42_P762829	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	-1.975	0.188	4.5	0.000E+00	1.000E-02
A_43_P19907	Loxl1	lysyl oxidase-like 1 (predicted)	-1.575	0.586	4.5	5.000E-04	3.300E-02
A_44_P691232	Unknown		-1.798	0.357	4.5	1.000E-04	2.100E-02
A_44_P1053404	Fcer1g	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	-1.697	0.454	4.4	1.600E-03	4.900E-02
A_42_P640700	Tmem176a	hypothetical LOC297077 (predicted)	-1.796	0.348	4.4	0.000E+00	1.700E-02
A_44_P791276	Unknown		-1.685	0.459	4.4	9.000E-04	4.000E-02
A_43_P18268	Axl	Axl receptor tyrosine kinase	-1.474	0.669	4.4	8.000E-04	3.800E-02
A_42_P652897	Fas	Tumor necrosis factor receptor superfamily, member 6	-1.699	0.443	4.4	1.000E-04	2.100E-02
A_44_P348922	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	-1.786	0.337	4.4	1.000E-04	1.900E-02
A_44_P166581	Ifitm7	interferon induced transmembrane protein 7 (predicted)	-1.781	0.341	4.4	1.000E-04	2.100E-02
A_43_P11448	Cp	ceruloplasmin	-1.902	0.215	4.3	0.000E+00	1.000E-02
A_44_P536275	Adamts4	a disintegrin and metallopeptidase with thrombospondin motifs 4	-1.394	0.720	4.3	1.200E-03	4.300E-02
A_44_P304190	Tifa	TRAF-interacting protein with forkhead-associated domain	-1.608	0.503	4.3	6.000E-04	3.500E-02
A_42_P772157	Il6r	interleukin 6 receptor	-1.804	0.307	4.3	1.100E-03	4.300E-02
A_43_P15253	Icam1	intercellular adhesion molecule 1	-1.895	0.205	4.3	0.000E+00	9.000E-03
A_44_P286788	Ncf4	neutrophil cytosolic factor 4 (predicted)	-1.743	0.355	4.3	8.000E-04	3.700E-02
A_43_P19806	Traf3ip3	similar to RIKEN cDNA 6030423D04 (predicted)	-1.574	0.524	4.3	1.100E-03	4.200E-02
A_44_P342821	Cd300lf	Cd300 molecule-like family member F	-1.543	0.554	4.3	9.000E-04	4.000E-02
A_43_P21322	Hcls1	hematopoietic cell specific Lyn substrate 1 (predicted)	-1.721	0.376	4.3	2.000E-04	2.600E-02
A_44_P319979	AA859954	Unknown	-1.687	0.404	4.3	2.000E-04	2.500E-02
A_44_P443220	Frzb	frizzled-related protein (predicted)	-1.747	0.340	4.2	1.000E-04	2.100E-02
A_42_P536266	Unknown		-1.743	0.339	4.2	1.000E-04	2.100E-02
A_44_P869736	TC614184	Unknown	-1.477	0.595	4.2	1.600E-03	4.900E-02
A_44_P492104	Fermt3	similar to cDNA sequence BC032204 (predicted)	-1.664	0.408	4.2	1.300E-03	4.500E-02
A_44_P635138	Mrc1	mannose receptor, C type 1	-1.706	0.363	4.2	6.000E-04	3.400E-02

A_44_P362749	Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	-1.778	0.286	4.2	5.000E-04	3.400E-02
A_42_P633664	Niban	niban protein	-1.792	0.272	4.2	3.000E-04	2.900E-02
A_44_P306930	LOC361140	similar to hypothetical protein FLJ20035	-1.928	0.128	4.2	0.000E+00	1.700E-02
A_44_P533794	Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b	-1.557	0.472	4.1	1.600E-03	4.900E-02
A_42_P773606	Ppm1n	similar to expressed sequence C79127	-1.724	0.302	4.1	2.000E-04	2.600E-02
A_44_P1057690	Dnase1l3	deoxyribonuclease I-like 3	-1.723	0.287	4.0	4.000E-04	3.100E-02
A_42_P550914	Ltb	lymphotoxin B	-1.681	0.326	4.0	9.000E-04	4.000E-02
A_44_P546338	Loxl1	lysyl oxidase-like 1 (predicted)	-1.361	0.643	4.0	9.000E-04	3.900E-02
A_44_P625026	Tbc1d10c	TBC1 domain family, member 10C	-1.602	0.393	4.0	9.000E-04	4.000E-02
A_44_P489721	LOC308742	similar to multiple C2-domains with two transmembrane regions 2	-1.796	0.196	4.0	2.000E-04	2.600E-02
A_44_P628055	Unknown		-1.580	0.409	4.0	6.000E-04	3.400E-02
A_44_P342047	Rgs10	regulator of G-protein signalling 10	-1.647	0.335	4.0	8.000E-04	3.700E-02
A_44_P428455	Cygb	cytoglobin	-1.759	0.222	3.9	1.000E-04	2.200E-02
A_44_P415193	Apobec3f	apolipoprotein B editing complex 3 (predicted)	-1.302	0.667	3.9	1.000E-03	4.100E-02
A_43_P17697	Ms4a6bl	membrane-spanning 4-domains, subfamily A, member 6B	-1.417	0.545	3.9	1.200E-03	4.400E-02
A_44_P479899	Myocd	transcription factor myocardin	-1.255	0.704	3.9	1.400E-03	4.700E-02
A_42_P685287	Fxyd5	FXYD domain-containing ion transport regulator 5	-1.667	0.291	3.9	1.000E-03	4.100E-02
A_44_P491883	Unknown		-1.398	0.559	3.9	6.000E-04	3.500E-02
A_44_P126061	Oasl2	2'-5' oligoadenylate synthetase-like 2 (predicted)	-1.564	0.390	3.9	3.000E-04	2.800E-02
A_44_P134143	Hspb8	heat shock 22kDa protein 8	-1.464	0.488	3.9	3.000E-04	2.700E-02
A_43_P16847	Spsb1	similar to SPRY domain-containing SOCS box protein SSB-1 (predicted)	-1.551	0.395	3.9	7.000E-04	3.600E-02
A_44_P471182	Cfp	properdin factor, complement	-1.568	0.371	3.8	5.000E-04	3.300E-02
A_44_P265709	Il2rb	interleukin 2 receptor, beta chain	-1.405	0.533	3.8	1.100E-03	4.300E-02
A_44_P1021630	Akr1cl1	aldo-keto reductase family 1, member C-like 1 (predicted)	-1.297	0.642	3.8	1.600E-03	4.900E-02
A_44_P301963	Psmb9	proteosome (prosome, macropain) subunit, beta type 9	-1.773	0.165	3.8	0.000E+00	1.000E-02
A_43_P21130	Sh3bp2	SH3-domain binding protein 2 (predicted)	-1.427	0.502	3.8	1.400E-03	4.600E-02
A_44_P960755	Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	-1.610	0.319	3.8	6.000E-04	3.500E-02
A_44_P370774	Irak3	interleukin-1 receptor-associated kinase 3 (predicted)	-1.525	0.395	3.8	7.000E-04	3.600E-02

A_42_P562617	Irf5	interferon regulatory factor 5 (predicted)	-1.580	0.339	3.8	1.400E-03	4.700E-02
A_42_P466321	Matk	megakaryocyte-associated tyrosine kinase	-1.700	0.219	3.8	7.000E-04	3.600E-02
A_44_P708169	Unknown		-1.555	0.362	3.8	1.100E-03	4.200E-02
A_44_P530253	Adam23	ADAM metallopeptidase domain 23	-1.479	0.433	3.8	1.100E-03	4.200E-02
A_44_P509138	Rab37	RAB37, member of RAS oncogene family (predicted)	-1.650	0.261	3.8	6.000E-04	3.500E-02
A_44_P393551	Gja1	gap junction membrane channel protein alpha 1	-1.659	0.249	3.8	2.000E-04	2.600E-02
A_44_P468258	Casp1	caspase 1	-1.666	0.242	3.8	1.000E-04	2.200E-02
A_44_P544063	Irgm	interferon inducible protein 1 (predicted)	-1.683	0.217	3.7	1.000E-04	1.900E-02
A_44_P469584	Cd14	CD14 antigen	-1.665	0.227	3.7	1.000E-04	2.100E-02
A_44_P463980	Ifitm3	interferon induced transmembrane protein 3	-1.618	0.264	3.7	4.000E-04	3.100E-02
A_44_P410348	Nlrc4	NLR family, CARD domain containing 4	-1.683	0.199	3.7	3.000E-04	2.800E-02
A_44_P587550	Unknown		-1.781	0.090	3.7	0.000E+00	8.000E-03
A_43_P19763	Tlr2	toll-like receptor 2	-1.498	0.369	3.6	4.000E-04	3.100E-02
A_42_P458530	Ripk3	receptor-interacting serine-threonine kinase 3	-1.451	0.414	3.6	5.000E-04	3.300E-02
A_44_P135531	RGD1304929	similar to chromosome 13 open reading frame 18 (predicted)	-1.366	0.483	3.6	1.500E-03	4.800E-02
A_44_P220325	Dynlrb2	dynein, cytoplasmic, light chain 2B (predicted)	-1.574	0.268	3.6	7.000E-04	3.600E-02
A_42_P768355	Hrk	BH3 interacting (with BCL2 family) domain, apoptosis agonist	-1.375	0.460	3.6	7.000E-04	3.600E-02
A_44_P1031571	Map1b	microtubule-associated protein 1b	-1.375	0.450	3.5	1.300E-03	4.600E-02
A_44_P461154	Timp1	tissue inhibitor of metalloproteinase 1	-1.483	0.338	3.5	6.000E-04	3.500E-02
A_44_P642946	Ak5	adenylate kinase 5	-1.278	0.541	3.5	1.500E-03	4.700E-02
A_44_P226597	Pycard	apoptosis-associated speck-like protein containing a CARD	-1.430	0.386	3.5	5.000E-04	3.300E-02
A_44_P469113	Slfn2	schlafen 2 (predicted)	-1.468	0.347	3.5	2.000E-04	2.500E-02
A_44_P217049	BF289650	Unknown	-1.445	0.365	3.5	2.000E-04	2.500E-02
A_44_P115142	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-1.257	0.552	3.5	1.300E-03	4.600E-02
A_44_P272201	LOC362442	similar to ovostatin-2	-1.593	0.215	3.5	4.000E-04	3.000E-02
A_44_P552830	A3galt2	iGb3 synthase	-1.588	0.220	3.5	1.000E-04	1.900E-02
A_44_P622992	Tuba8	tubulin, alpha 8	-1.404	0.403	3.5	7.000E-04	3.600E-02
A_42_P621642	Lsp1	lymphocyte specific 1 (predicted)	-1.617	0.187	3.5	3.000E-04	3.000E-02

A_44_P523355	Unknown		-1.592	0.211	3.5	5.000E-04	3.200E-02
A_44_P161233	Il18	interleukin 18	-1.476	0.317	3.5	6.000E-04	3.400E-02
A_44_P1042952	Bid3	BH3 interacting (with BCL2 family) domain, apoptosis agonist	-1.590	0.201	3.5	1.000E-04	2.200E-02
A_43_P11577	Anxa3	annexin A3	-1.409	0.382	3.5	2.000E-04	2.400E-02
A_42_P472133	Slc2a6	solute carrier family 2 (facilitated glucose transporter), member 6 (predicted)	-1.646	0.136	3.4	0.000E+00	1.800E-02
A_42_P817417	PVR	poliovirus receptor	-1.532	0.246	3.4	0.000E+00	1.100E-02
A_44_P405066	Scn1b	sodium channel, voltage-gated, type I, beta polypeptide	-1.407	0.368	3.4	2.000E-04	2.300E-02
A_44_P510738	Pigr	polymeric immunoglobulin receptor	-1.496	0.278	3.4	2.000E-04	2.400E-02
A_42_P750683	Cyr61	cysteine rich protein 61	-1.268	0.500	3.4	6.000E-04	3.400E-02
A_44_P965173	Unknown		-1.371	0.393	3.4	6.000E-04	3.400E-02
A_42_P631122	Cd302	CD302 molecule	-1.526	0.237	3.4	7.000E-04	3.600E-02
A_44_P264915	B4galnt4	beta-1,4-N-acetyl-galactosaminyl transferase 4	-1.300	0.454	3.4	9.000E-04	4.000E-02
A_44_P1035483	BF559836	Unknown	-1.508	0.240	3.4	1.000E-04	2.200E-02
A_44_P494259	Eif5a2	eukaryotic translation initiation factor 5A2	-1.380	0.350	3.3	7.000E-04	3.600E-02
A_44_P233702	Clc	cardiotrophin-like cytokine	-1.516	0.207	3.3	0.000E+00	1.000E-02
A_42_P510386	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	-1.393	0.325	3.3	9.000E-04	4.000E-02
A_44_P252545	Grik2	glutamate receptor, ionotropic, kainate 2	-1.468	0.249	3.3	2.000E-04	2.400E-02
A_44_P1007215	Upp1	uridine phosphorylase 1	-1.545	0.172	3.3	0.000E+00	1.600E-02
A_44_P1023058	March11	membrane-associated ring finger (C3HC4) 11	-1.518	0.198	3.3	2.000E-04	2.400E-02
A_43_P11683	F3	coagulation factor 3	-1.288	0.428	3.3	3.000E-04	2.900E-02
A_44_P130740	Trim6	tripartite motif containing 6	-1.380	0.334	3.3	7.000E-04	3.600E-02
A_43_P17298	Asahl_	N-acylsphingosine amidohydrolase (acid ceramidase)-like (predicted)	-1.327	0.374	3.3	1.400E-03	4.700E-02
A_44_P480817	Mmp19	matrix metalloproteinase 19 (predicted)	-1.249	0.452	3.3	8.000E-04	3.900E-02
A_44_P700209	Unknown		-1.381	0.308	3.2	5.000E-04	3.200E-02
A_44_P731699	TC606209	Unknown	-1.371	0.317	3.2	4.000E-04	3.100E-02
A_42_P773675	S1pr5	sphingosine-1-phosphate receptor 5	-1.092	0.595	3.2	1.500E-03	4.700E-02
A_44_P402948	Unknown		-1.394	0.293	3.2	1.100E-03	4.300E-02
A_42_P672907	Tspan8	transmembrane 4 superfamily member 3	-1.479	0.201	3.2	2.000E-04	2.300E-02

A_44_P516017	Efh2	EF hand domain containing 2 (predicted)	-1.213	0.463	3.2	6.000E-04	3.400E-02
A_44_P1037041	Map3k6	mitogen-activated protein kinase kinase kinase 6 (predicted)	-1.348	0.327	3.2	1.200E-03	4.400E-02
A_44_P193959	Rgs14	regulator of G-protein signaling 14	-1.490	0.184	3.2	5.000E-04	3.300E-02
A_44_P452370	SAAL1	serum amyloid A 3 (predicted)	-1.536	0.137	3.2	5.000E-04	3.300E-02
A_44_P306602	Irf1	interferon regulatory factor 1	-1.397	0.270	3.2	3.000E-04	2.900E-02
A_42_P639047	RGD1309350	similar to transthyretin (4L369)	-1.484	0.159	3.1	6.000E-04	3.500E-02
A_44_P340261	RGD1305807	hypothetical LOC298077	-1.483	0.146	3.1	0.000E+00	1.100E-02
A_44_P398729	Sbno2	similar to KIAA0963 protein (predicted)	-1.375	0.253	3.1	1.000E-04	1.900E-02
A_44_P440885	Dcdc2	doublecortin domain containing 2 (predicted)	-1.411	0.216	3.1	1.000E-04	2.100E-02
A_44_P540126	Pros1	protein S (alpha)	-1.184	0.441	3.1	7.000E-04	3.600E-02
A_43_P18101	Elf3	E74-like factor 3	-1.490	0.133	3.1	8.000E-04	3.700E-02
A_44_P823212	Unknown		-1.515	0.102	3.1	4.000E-04	3.100E-02
A_43_P17833	Kel	Kell blood group, metallo-endopeptidase	-1.349	0.263	3.1	7.000E-04	3.500E-02
A_44_P510826	Stx11	syntaxin 11	-1.417	0.193	3.1	1.000E-04	1.800E-02
A_44_P290987	Cd70	Cd70 molecule	-1.192	0.414	3.0	6.000E-04	3.500E-02
A_44_P209638	Unknown		-1.203	0.399	3.0	1.100E-03	4.300E-02
A_42_P840729	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	-1.459	0.141	3.0	1.000E-04	1.800E-02
A_44_P393696	LOC308990	hypothetical protein LOC308990	-1.247	0.351	3.0	1.100E-03	4.300E-02
A_43_P20861	RGD1305779	similar to NSE1 (predicted)	-1.371	0.224	3.0	0.000E+00	1.300E-02
A_44_P164192	RGD1310490	similar to hypothetical protein MGC29390 (predicted)	-1.403	0.188	3.0	2.000E-04	2.500E-02
A_43_P17969	ENSRNOT00000059737	neuron-glia-CAM-related cell adhesion molecule	-1.353	0.228	3.0	1.300E-03	4.500E-02
A_44_P164188	Parp14	similar to hypothetical protein MGC29390 (predicted)	-1.371	0.204	3.0	6.000E-04	3.500E-02
A_44_P185470	LOC301556	similar to Dedicator of cytokinesis protein 10 (Protein zizimin 3)	-1.334	0.240	3.0	1.300E-03	4.600E-02
A_44_P388720	Fstl3	follistatin-like 3	-1.187	0.378	3.0	7.000E-04	3.600E-02
A_44_P762342	Unknown		-1.257	0.300	2.9	1.100E-03	4.300E-02
A_43_P15907	Pp2d1	protein phosphatase 2C-like domain containing 1	-1.206	0.346	2.9	8.000E-04	3.900E-02
A_44_P582557	Gpr153	Unknown	-1.236	0.312	2.9	6.000E-04	3.400E-02
A_44_P427814	Ighm	immunoglobulin heavy constant mu	-1.154	0.389	2.9	7.000E-04	3.600E-02

A_42_P677623	Copeb	core promoter element binding protein	-1.192	0.348	2.9	1.400E-03	4.600E-02
A_44_P534478	LOC296404	hypothetical LOC296404	-1.313	0.227	2.9	1.500E-03	4.700E-02
A_44_P290539	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-1.056	0.482	2.9	1.300E-03	4.600E-02
A_44_P491796	Spp1	secreted phosphoprotein 1	-1.260	0.277	2.9	6.000E-04	3.500E-02
A_44_P301936	Anxa3	annexin A3	-1.295	0.239	2.9	0.000E+00	1.500E-02
A_42_P813840	Tapbpl	TAP binding protein-like (predicted)	-1.420	0.098	2.9	0.000E+00	8.000E-03
A_43_P19437	Rhbdl2	rhomboid, veinlet-like 2 (Drosophila) (predicted)	-1.334	0.181	2.9	1.100E-03	4.200E-02
A_44_P110400	Aloxe3	arachidonate lipoxygenase 3	-1.354	0.159	2.9	1.300E-03	4.500E-02
A_44_P409840	Ccl17	small inducible cytokine subfamily A (Cys-Cys), member 17	-1.379	0.128	2.8	1.000E-04	2.100E-02
A_43_P10571	RGD1311848	similar to prolyl-4-hydroxylase-alpha NE2 CG9720-PA (predicted)	-1.092	0.415	2.8	1.200E-03	4.400E-02
A_44_P856419	Arrdc4	arrestin domain containing 4	-1.108	0.393	2.8	1.500E-03	4.800E-02
A_44_P931922	Unknown		-1.245	0.243	2.8	9.000E-04	3.900E-02
A_44_P1042473	Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	-1.125	0.357	2.8	1.000E-03	4.100E-02
A_44_P112527	LOC691521	similar to MEGF11 protein	-1.271	0.211	2.8	1.000E-04	1.900E-02
A_44_P270468	Slc15a3	peptide/histidine transporter PHT2	-1.270	0.211	2.8	5.000E-04	3.300E-02
A_44_P217541	Vmp1	vacuole membrane protein 1	-1.326	0.153	2.8	0.000E+00	1.300E-02
A_44_P127294	Unknown		-1.197	0.280	2.8	4.000E-04	3.100E-02
A_44_P101700	Stx11	syntaxin 11	-1.098	0.377	2.8	5.000E-04	3.200E-02
A_44_P222166	Cd86	cd86 antigen	-1.061	0.411	2.8	7.000E-04	3.600E-02
A_44_P793692	Dtx3l	deltex 3 like, E3 ubiquitin ligase	-1.239	0.229	2.8	6.000E-04	3.500E-02
A_42_P557394	Isg20	interferon-stimulated protein (predicted)	-0.940	0.520	2.8	1.500E-03	4.800E-02
A_44_P496864	Sema4a	semaphorin 4A (predicted)	-1.373	0.083	2.7	1.000E-04	1.900E-02
A_44_P506609	Stra6	stimulated by retinoic acid 6	-1.171	0.285	2.7	6.000E-04	3.500E-02
A_44_P807649	Unknown		-1.198	0.255	2.7	1.000E-03	4.100E-02
A_44_P152144	Psmb10	proteasome subunit beta 10	-1.104	0.346	2.7	3.000E-04	2.800E-02
A_44_P334736	Edn1	endothelin 1	-1.221	0.229	2.7	7.000E-04	3.600E-02
A_44_P353978	v-rel	similar to Avian reticuloendotheliosis viral (v-rel) oncogene related B	-1.240	0.209	2.7	4.000E-04	3.100E-02
A_44_P746478	Unknown		-1.074	0.370	2.7	1.100E-03	4.200E-02

A_44_P809374	Clcf1	cardiotrophin-like cytokine factor 1	-1.402	0.036	2.7	0.000E+00	1.200E-02
A_44_P393442	Mtap6	microtubule-associated protein 6	-1.002	0.436	2.7	1.400E-03	4.700E-02
A_42_P797295	Sulf2	sulfatase 2	-1.043	0.393	2.7	5.000E-04	3.200E-02
A_44_P618385	Efhd2	EF hand domain containing 2 (predicted)	-1.088	0.344	2.7	3.000E-04	2.900E-02
A_42_P840836	Nmt	neurotrimin	-1.155	0.274	2.7	7.000E-04	3.600E-02
A_44_P457548	Parp9	similar to B aggressive lymphoma (predicted)	-1.018	0.410	2.7	4.000E-04	3.100E-02
A_44_P219046	CF110435		-1.109	0.319	2.7	1.200E-03	4.400E-02
A_44_P137677	Rhov	ras homolog gene family, member V	-1.127	0.296	2.7	9.000E-04	3.900E-02
A_44_P762190	Unknown		-1.111	0.309	2.7	2.000E-04	2.600E-02
A_44_P451916	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-1.197	0.214	2.7	2.000E-04	2.300E-02
A_44_P296155	RT1-A2	RT1 class Ia, locus A2	-1.091	0.313	2.6	6.000E-04	3.400E-02
A_42_P556829	Wif1	Wnt inhibitory factor 1	-1.274	0.127	2.6	1.000E-04	2.200E-02
A_44_P358358	RT1-T18	RT1 class Ib, locus T18	-1.035	0.364	2.6	8.000E-04	3.800E-02
A_44_P323754	Serpnb1b	similar to serine (or cysteine) proteinase inhibitor, clade B, member 1b	-1.194	0.204	2.6	8.000E-04	3.700E-02
A_44_P325508	Anxa3	annexin A3	-1.249	0.145	2.6	0.000E+00	1.500E-02
A_44_P745749	Unknown		-1.169	0.222	2.6	1.600E-03	4.900E-02
A_42_P821581	LOC100912012	tetranectin-like	-1.215	0.168	2.6	1.200E-03	4.400E-02
A_43_P10742	CB547617		-1.131	0.241	2.6	2.000E-04	2.300E-02
A_44_P480267	Asns	asparagine synthetase	-1.228	0.140	2.6	3.000E-04	2.800E-02
A_44_P327492	Anxa3	annexin A3	-1.145	0.218	2.6	3.000E-04	2.900E-02
A_44_P201295	Mybpc2	myosin binding protein C, fast-type (predicted)	-1.197	0.167	2.6	1.000E-04	2.200E-02
A_43_P10008	Aig1	similar to Aig1 protein	-1.013	0.348	2.6	3.000E-04	2.700E-02
A_44_P277026	Apol3	apolipoprotein L, 3	-1.048	0.302	2.5	8.000E-04	3.800E-02
A_43_P19662	Unknown		-1.169	0.174	2.5	1.000E-03	4.100E-02
A_44_P557338	Mfsd8	similar to 2810423E13Rik protein (predicted)	-0.976	0.366	2.5	1.200E-03	4.300E-02
A_44_P128147	Tf	Transferrin	-0.993	0.349	2.5	1.600E-03	4.900E-02
A_44_P221434	Dtx4	deltex 4 homolog (Drosophila) (predicted)	-0.976	0.361	2.5	1.200E-03	4.400E-02
A_44_P556989	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	-1.151	0.182	2.5	1.000E-04	2.100E-02

A_44_P564274	Ccdc3	coiled-coil domain containing 3	-0.867	0.464	2.5	1.300E-03	4.500E-02
A_44_P235679	Unknown		-1.104	0.217	2.5	1.600E-03	4.900E-02
A_44_P174624	Zfp365	zinc finger protein 365	-1.001	0.318	2.5	1.200E-03	4.300E-02
A_44_P948250	Il13ra1	interleukin 13 receptor, alpha 1	-1.090	0.227	2.5	0.000E+00	1.800E-02
A_44_P501639	Man1a1	similar to mannosyl-oligosaccharide alpha-1,2-mannosidase	-1.144	0.170	2.5	2.000E-04	2.600E-02
A_44_P536676	B3galt3	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	-1.142	0.169	2.5	1.000E-04	2.200E-02
A_44_P777016	Ypel4		-1.061	0.244	2.5	6.000E-04	3.500E-02
A_43_P14890	Ptpns1	protein tyrosine phosphatase, non-receptor type substrate 1	-1.073	0.220	2.5	7.000E-04	3.600E-02
A_44_P325744	Nap1l1	nucleosome assembly protein 1-like 1	-1.103	0.181	2.4	1.000E-04	1.800E-02
A_43_P11114	TC621252		-1.150	0.128	2.4	1.000E-04	2.100E-02
A_44_P184505	Dtr	diphtheria toxin receptor	-1.111	0.164	2.4	3.000E-04	2.800E-02
A_44_P560285	Unknown		-1.133	0.137	2.4	1.100E-03	4.200E-02
A_44_P883191	Unknown		-1.150	0.119	2.4	1.000E-04	1.900E-02
A_44_P128195	Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	-1.026	0.242	2.4	5.000E-04	3.300E-02
A_42_P493380	Myc	myelocytomatosis viral oncogene homolog (avian)	-0.932	0.332	2.4	1.500E-03	4.800E-02
A_44_P324707	RT1-EC2	RT1 class Ib, locus Aw2	-0.936	0.311	2.4	1.000E-03	4.100E-02
A_43_P17239	Aig1	androgen-induced 1	-0.987	0.258	2.4	6.000E-04	3.400E-02
A_42_P704967	Arid5a	AT rich interactive domain 5A (Mrf1 like)	-1.043	0.202	2.4	1.600E-03	4.900E-02
A_44_P490484	Unknown		-1.069	0.173	2.4	1.500E-03	4.700E-02
A_42_P711464	Cfap45		-1.155	0.087	2.4	1.200E-03	4.300E-02
A_44_P362915	Il13ra1	interleukin 13 receptor, alpha 1	-1.085	0.155	2.4	1.000E-04	1.900E-02
A_43_P23262	Pscdbp	pleckstrin homology, Sec7 and coiled-coil domains, binding protein (predicted)	-1.087	0.150	2.4	1.000E-04	1.900E-02
A_43_P12974	F2rl1	coagulation factor II (thrombin) receptor-like 1	-1.141	0.094	2.4	6.000E-04	3.400E-02
A_44_P1018447	Micall2	similar to FLJ23471 protein (predicted)	-0.945	0.289	2.4	1.000E-03	4.100E-02
A_44_P330197	Srpk3	serine/threonine kinase 23	-0.930	0.302	2.3	9.000E-04	3.900E-02
A_43_P13426	Ceacam10	CEA-related cell adhesion molecule 10	-0.870	0.358	2.3	1.400E-03	4.600E-02
A_43_P15259	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	-1.118	0.092	2.3	1.000E-04	1.900E-02

A_44_P309800	Vwa5a	loss of heterozygosity, 11, chromosomal region 2, gene A homolog (human)	-1.047	0.162	2.3	4.000E-04	3.100E-02
A_43_P13172	Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	-0.822	0.387	2.3	1.500E-03	4.700E-02
A_44_P501637	LOC294410	similar to mannosyl-oligosaccharide alpha-1,2-mannosidase	-0.996	0.211	2.3	4.000E-04	3.000E-02
A_44_P344346	Arpc1b	actin related protein 2/3 complex, subunit 1B	-0.933	0.275	2.3	5.000E-04	3.300E-02
A_44_P277167	Unknown		-0.987	0.219	2.3	1.200E-03	4.400E-02
A_44_P298210	Casp8	caspase 8	-0.815	0.377	2.3	1.200E-03	4.400E-02
A_44_P271423	Zc3hav1	zinc finger CCCH type, antiviral 1	-0.925	0.266	2.3	1.000E-03	4.100E-02
A_44_P250579	LOC290282	similar to actin-related protein complex 1b	-0.899	0.291	2.3	1.400E-03	4.700E-02
A_44_P503147	Unknown		-0.982	0.207	2.3	6.000E-04	3.500E-02
A_44_P369399	Rab38	Rab38, member of RAS oncogene family	-0.804	0.384	2.3	9.000E-04	3.900E-02
A_44_P1001517	Tgfb2	transforming growth factor, beta 2	-0.885	0.301	2.3	1.600E-03	4.900E-02
A_44_P475181	Sla	src-like adaptor	-0.873	0.308	2.3	1.000E-03	4.100E-02
A_44_P128350	Lad1	ladinin (predicted)	-0.815	0.360	2.3	1.600E-03	4.900E-02
A_43_P20282	Kpna4	karyopherin subunit alpha 4	-1.013	0.157	2.2	2.000E-04	2.300E-02
A_44_P668233	Unknown		-0.906	0.263	2.2	9.000E-04	4.000E-02
A_44_P417916	Myd88	myeloid differentiation primary response gene 88	-0.858	0.309	2.2	7.000E-04	3.600E-02
A_43_P15854	Noct	nocturnin	-0.978	0.186	2.2	1.000E-03	4.100E-02
A_44_P490490	Unknown		-0.962	0.201	2.2	1.300E-03	4.600E-02
A_42_P598365	Colec12	collectin sub-family member 12	-0.879	0.281	2.2	7.000E-04	3.600E-02
A_44_P428507	Nfkbie	solute carrier family 35, member B2	-0.877	0.280	2.2	8.000E-04	3.800E-02
A_43_P10650	Tmem181	Rattus norvegicus transmembrane protein 181	-0.881	0.273	2.2	4.000E-04	3.100E-02
A_44_P326147	Blvrb	biliverdin reductase B	-0.894	0.260	2.2	1.500E-03	4.700E-02
A_44_P365379	Gadd45g	growth arrest and DNA-damage-inducible, gamma	-0.956	0.191	2.2	1.000E-03	4.100E-02
A_44_P960871	Unknown		-0.924	0.219	2.2	1.000E-04	2.200E-02
A_44_P547954	RT1-CE6	RT1-CE6 gene	-0.781	0.358	2.2	8.000E-04	3.900E-02
A_44_P380182	Mthfd2	similar to methylenetetrahydrofolate dehydrogenase precursor	-0.800	0.335	2.2	1.000E-03	4.100E-02
A_44_P493980	Nptxr	neuronal pentraxin receptor	-0.883	0.253	2.2	7.000E-04	3.600E-02
A_44_P532270	Herc6	potential ubiquitin ligase	-0.899	0.230	2.2	8.000E-04	3.800E-02

A_44_P497863	Neud4	neuronal d4 domain family member	-0.888	0.237	2.2	1.000E-03	4.100E-02
A_43_P12333	RT1-M3	RT1 class Ib, locus M3	-0.876	0.247	2.2	1.400E-03	4.600E-02
A_44_P335175	RGD1311892	similar to hypothetical protein FLJ10901	-1.049	0.067	2.2	0.000E+00	1.100E-02
A_43_P11442	B2m	beta-2 microglobulin	-0.754	0.361	2.2	1.600E-03	4.900E-02
A_43_P12768	Bhlhe40	basic helix-loop-helix domain containing, class B2	-0.860	0.250	2.2	4.000E-04	3.100E-02
A_42_P741027	Jun	v-jun sarcoma virus 17 oncogene homolog (avian)	-0.919	0.188	2.2	1.000E-04	2.100E-02
A_44_P590748	Ifih1	Interferon induced with helicase C domain 1	-0.682	0.424	2.2	1.400E-03	4.600E-02
A_44_P201028	Nfil3	nuclear factor, interleukin 3 regulated	-1.039	0.064	2.1	0.000E+00	9.000E-03
A_44_P330971	Plin2	adipose differentiation-related protein	-0.943	0.156	2.1	2.000E-04	2.300E-02
A_44_P506817	Unknown		-0.687	0.411	2.1	1.600E-03	4.900E-02
A_44_P451434	Ipo5	similar to RAN binding protein 5	-0.861	0.232	2.1	2.000E-04	2.400E-02
A_44_P278659	Unknown		-0.938	0.153	2.1	1.000E-03	4.100E-02
A_44_P623856	Dkk2	dickkopf WNT signaling pathway inhibitor 2	-0.775	0.308	2.1	7.000E-04	3.700E-02
A_44_P392201	Reep2		-0.896	0.185	2.1	1.600E-03	4.900E-02
A_44_P273734	FQ227170		-0.906	0.170	2.1	3.000E-04	2.800E-02
A_43_P23014	Lpxn	leupaxin (predicted)	-0.843	0.230	2.1	6.000E-04	3.500E-02
A_44_P390495	Gch	GTP cyclohydrolase 1	-0.801	0.271	2.1	1.500E-03	4.700E-02
A_44_P365516	Tsc22d1	transforming growth factor beta 1 induced transcript 4	-0.785	0.284	2.1	4.000E-04	3.100E-02
A_44_P227174	Sh2d4a	SH2 domain containing 4A	-0.805	0.261	2.1	1.500E-03	4.700E-02
A_44_P806840	Apol3	apolipoprotein L, 3	-0.817	0.247	2.1	5.000E-04	3.200E-02
A_42_P816479	Glr1	glutaredoxin 1 (thioltransferase)	-0.884	0.178	2.1	5.000E-04	3.300E-02
A_44_P389072	Il13ra1	interleukin 13 receptor, alpha 1	-1.015	0.042	2.1	0.000E+00	1.400E-02
A_44_P125273	Unknown		-0.894	0.163	2.1	1.500E-03	4.700E-02
A_44_P480573	Cytip	pleckstrin homology, Sec7 and coiled-coil domains, binding protein (predicted)	-0.775	0.277	2.1	1.100E-03	4.200E-02
A_43_P11838	Csrp1	cysteine and glycine-rich protein 1	-0.688	0.358	2.1	9.000E-04	3.900E-02
A_44_P543473	Ppp1r13l	protein phosphatase 1, regulatory subunit 13 like	-0.942	0.102	2.1	2.000E-04	2.400E-02
A_44_P863933	Traf1	TNF receptor-associated factor 1	-0.857	0.184	2.1	1.200E-03	4.400E-02
A_44_P200116	Pde10a	phosphodiesterase 10A	-0.846	0.193	2.1	3.000E-04	2.700E-02

A_43_P17175	Serpinb1a	serine (or cysteine) proteinase inhibitor, clade B, member 1a	-0.910	0.127	2.1	4.000E-04	3.100E-02
A_44_P373285	Unknown		-0.915	0.120	2.0	1.000E-04	1.900E-02
A_44_P975601	Phf11b	PHD finger protein 11B	-0.712	0.322	2.0	1.600E-03	4.900E-02
A_44_P649871	Unknown		-0.688	0.344	2.0	1.300E-03	4.500E-02
A_42_P541872	B3galnt1		-0.821	0.208	2.0	3.000E-04	3.000E-02
A_43_P13241	Ctsd	cathepsin D	-0.754	0.274	2.0	1.300E-03	4.600E-02
A_44_P134213	Tpm1	tropomyosin 1, alpha	-0.680	0.347	2.0	1.600E-03	4.900E-02
A_42_P540711	Rasd2	RASD family, member 2	-0.887	0.140	2.0	1.000E-03	4.200E-02
A_44_P462306	Unknown		-0.888	0.138	2.0	1.000E-04	2.200E-02
A_44_P850918	Unknown		-0.678	0.346	2.0	1.000E-03	4.200E-02
A_44_P513029	RT1-CE1	RT1 class I, CE1	-0.841	0.182	2.0	4.000E-04	3.100E-02
A_44_P522847	Pik3ap1	phosphoinositide-3-kinase adaptor protein 1 (predicted)	-0.698	0.314	2.0	1.600E-03	4.800E-02
A_44_P220575	Irak4	interleukin-1 receptor-associated kinase 4 (predicted)	-0.820	0.190	2.0	1.300E-03	4.500E-02
A_44_P456769	Ncr1	lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46)	-0.892	0.115	2.0	1.500E-03	4.800E-02
A_44_P377625	RGD1311294	similar to Hypothetical protein C6orf60 (predicted)	-0.877	0.127	2.0	1.000E-04	1.800E-02
A_44_P788634	Mum1l1		0.841	-0.161	-2.0	5.000E-04	3.300E-02
A_44_P172449	Unknown		0.890	-0.114	-2.0	8.000E-04	3.700E-02
A_44_P210852	Sh3rf2	SH3 domain containing ring finger 2 (predicted)	0.850	-0.157	-2.0	1.500E-03	4.800E-02
A_44_P324878	Unknown		0.922	-0.088	-2.0	0.000E+00	1.000E-02
A_43_P20474	Ptprb	protein tyrosine phosphatase, receptor type, B	0.954	-0.056	-2.0	6.000E-04	3.400E-02
A_44_P561902	NIRP2	nuclear receptor interacting protein 2	0.928	-0.085	-2.0	1.000E-04	2.200E-02
A_44_P608780	Unknown		0.933	-0.083	-2.0	1.000E-04	1.900E-02
A_44_P905337	Unknown		0.719	-0.299	-2.0	1.600E-03	4.900E-02
A_44_P512679	Unknown		0.829	-0.194	-2.0	5.000E-04	3.200E-02
A_43_P12613	Apln	apelin, AGTRL1 ligand	0.781	-0.246	-2.0	6.000E-04	3.500E-02
A_44_P477866	Slc6a4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	0.730	-0.298	-2.0	1.200E-03	4.400E-02
A_44_P378845	Rasgrp3		0.952	-0.078	-2.0	3.000E-04	3.000E-02
A_44_P451198	Unknown		0.795	-0.255	-2.1	1.200E-03	4.500E-02

A_44_P1008867	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	0.924	-0.131	-2.1	1.000E-04	2.200E-02
A_44_P263186	Unknown		0.758	-0.298	-2.1	1.200E-03	4.400E-02
A_44_P121547	Unknown		0.863	-0.205	-2.1	8.000E-04	3.800E-02
A_44_P592757	Sema5a	semaphorin 5A	0.968	-0.100	-2.1	7.000E-04	3.600E-02
A_44_P538970	Ptpdc1	protein tyrosine phosphatase domain containing 1 (predicted)	0.813	-0.257	-2.1	4.000E-04	3.100E-02
A_44_P280898	Dbp	D site albumin promoter binding protein	0.850	-0.223	-2.1	4.000E-04	3.100E-02
A_44_P326078	Fam149a	family with sequence similarity 149, member A	0.831	-0.248	-2.1	9.000E-04	3.900E-02
A_44_P624391	Unknown		0.907	-0.175	-2.1	4.000E-04	3.000E-02
A_44_P960530	Unknown		0.944	-0.139	-2.1	8.000E-04	3.800E-02
A_44_P118970	Il12a	interleukin 12a	0.969	-0.115	-2.1	1.000E-03	4.100E-02
A_44_P961053	Unknown		0.889	-0.199	-2.1	3.000E-04	2.800E-02
A_44_P608917	Unknown		0.996	-0.096	-2.1	1.000E-04	1.900E-02
A_42_P807826	Syne1		0.946	-0.146	-2.1	1.000E-04	1.900E-02
A_44_P271678	Dag1	dystroglycan 1	0.695	-0.397	-2.1	1.300E-03	4.600E-02
A_44_P431572	Rasgrp3	RAS, guanyl releasing protein 3 (predicted)	0.974	-0.125	-2.1	1.000E-04	2.200E-02
A_43_P14961	Unknown		0.946	-0.153	-2.1	1.600E-03	4.900E-02
A_44_P231859	Chd1l	chromodomain helicase DNA binding protein 1-like	0.909	-0.202	-2.2	1.200E-03	4.300E-02
A_44_P234854	Unknown		0.999	-0.113	-2.2	1.000E-04	2.200E-02
A_43_P23391	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	0.963	-0.151	-2.2	1.000E-04	2.100E-02
A_44_P1058692	Angpt1	angiopoietin 1	0.821	-0.297	-2.2	1.100E-03	4.200E-02
A_44_P432470	Unknown		0.812	-0.314	-2.2	1.400E-03	4.700E-02
A_44_P449108	Unknown		0.981	-0.148	-2.2	1.000E-04	2.200E-02
A_43_P18922	Sema5a	semaphorin 5A	0.969	-0.170	-2.2	9.000E-04	4.000E-02
A_44_P303009	Unknown		0.956	-0.193	-2.2	1.600E-03	4.900E-02
A_42_P544898	Bcl6b	similar to BAZF	0.978	-0.171	-2.2	2.000E-04	2.300E-02
A_44_P279337	Slc22a5	solute carrier family 22 (organic cation/carnitine transporter), member 5	0.957	-0.194	-2.2	1.000E-03	4.100E-02
A_44_P780848	Chst9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (predicted)	0.873	-0.289	-2.2	7.000E-04	3.600E-02
A_43_P14796	Apcdd1	adenomatosis polyposis coli down-regulated 1	0.852	-0.310	-2.2	1.500E-03	4.800E-02

A_43_P14838	Alx1	cartilage homeo protein 1	1.100	-0.067	-2.2	4.000E-04	3.100E-02
A_44_P1032042	Tmem35	spinal cord expression protein 4	1.100	-0.072	-2.3	2.000E-04	2.400E-02
A_44_P263740	RGD1305749	similar to RIKEN cDNA 1810054O13 (predicted)	1.051	-0.123	-2.3	1.000E-04	1.900E-02
A_44_P1043926	Acad9	acyl-Coenzyme A dehydrogenase family, member 9	1.049	-0.128	-2.3	0.000E+00	1.800E-02
A_44_P475144	Unknown		0.930	-0.248	-2.3	8.000E-04	3.800E-02
A_44_P297872	St3gal1		1.016	-0.163	-2.3	2.000E-04	2.300E-02
A_44_P482859	Sema5a	semaphorin 5A	1.004	-0.176	-2.3	1.000E-04	2.100E-02
A_44_P187403	Unknown		0.919	-0.264	-2.3	1.100E-03	4.300E-02
A_44_P499634	Lztr1_	leucine-zipper-like transcriptional regulator, 1 (predicted)	0.863	-0.324	-2.3	1.500E-03	4.700E-02
A_44_P1002452	Nt5dc2	similar to hypothetical protein FLJ12442 (predicted)	1.003	-0.198	-2.3	2.000E-04	2.300E-02
A_44_P563844	Unknown		0.964	-0.242	-2.3	2.000E-04	2.400E-02
A_44_P435103	Grhl2	grainyhead-like transcription factor 2	1.005	-0.203	-2.3	9.000E-04	4.000E-02
A_44_P126730	Cml2	Camello-like 2	1.023	-0.189	-2.3	1.200E-03	4.300E-02
A_43_P11122	Unknown		1.000	-0.215	-2.3	1.000E-04	1.900E-02
A_44_P154793	Iqcg		0.878	-0.351	-2.3	9.000E-04	4.000E-02
A_44_P697832	Unknown		1.122	-0.125	-2.4	0.000E+00	1.700E-02
A_44_P267465	Hsf4	heat shock transcription factor 4 (predicted)	0.928	-0.336	-2.4	1.200E-03	4.300E-02
A_44_P169012	Unknown		1.191	-0.083	-2.4	1.300E-03	4.600E-02
A_44_P169917	Unknown		0.845	-0.434	-2.4	1.400E-03	4.700E-02
A_44_P405290	Fras1	Fraser extracellular matrix complex subunit 1	1.063	-0.219	-2.4	4.000E-04	3.100E-02
A_44_P307718	BF281946		1.151	-0.131	-2.4	4.000E-04	3.200E-02
A_44_P254373	Epha7	Eph receptor A7	1.170	-0.114	-2.4	1.000E-04	2.100E-02
A_44_P638093	TC596726		1.077	-0.211	-2.4	1.000E-04	2.200E-02
A_44_P848759	Unknown		0.988	-0.301	-2.4	3.000E-04	2.700E-02
A_44_P901064	Unknown		1.052	-0.239	-2.4	1.000E-04	2.100E-02
A_43_P13457	Slc35g2	solute carrier family 35, member G2	0.863	-0.436	-2.5	1.600E-03	4.900E-02
A_42_P768685	Negr1	neuronal growth regulator 1	1.252	-0.052	-2.5	0.000E+00	1.000E-02
A_44_P346913	XM_219543	similar to Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	1.007	-0.298	-2.5	1.100E-03	4.200E-02

A_44_P148888	Unknown		1.018	-0.288	-2.5	1.200E-03	4.400E-02
A_43_P11350	Nt5dc2	similar to hypothetical protein FLJ12442 (predicted)	1.197	-0.115	-2.5	0.000E+00	1.000E-02
A_44_P322910	Pdgfa	platelet derived growth factor, alpha	0.971	-0.343	-2.5	9.000E-04	4.000E-02
A_44_P609103	Unknown		0.973	-0.346	-2.5	4.000E-04	3.100E-02
A_42_P572948	Prosapip1	ProSAPiP1 protein	1.188	-0.136	-2.5	3.000E-04	3.000E-02
A_44_P203596	LOC100909600	PI-PLC X domain-containing protein 1-like	1.000	-0.330	-2.5	9.000E-04	4.000E-02
A_44_P409835	Plvap	plasmalemma vesicle associated protein	1.071	-0.263	-2.5	1.400E-03	4.600E-02
A_44_P156846	Lamc3	laminin gamma 3 (predicted)	1.019	-0.322	-2.5	1.600E-03	4.900E-02
A_44_P824467	Unknown		1.095	-0.251	-2.5	6.000E-04	3.400E-02
A_43_P21969	Aff3	lymphoid nuclear protein related to AF4 (predicted)	1.049	-0.303	-2.6	6.000E-04	3.500E-02
A_44_P185719	RGD1308772	similar to KIAA0564 protein (predicted)	0.977	-0.377	-2.6	1.300E-03	4.500E-02
A_44_P297633	Irx3	Iroquois related homeobox 3 (Drosophila) (predicted)	1.067	-0.297	-2.6	4.000E-04	3.000E-02
A_44_P380384	Ripply3	Down syndrome critical region gene 6 (predicted)	0.914	-0.455	-2.6	1.600E-03	4.900E-02
A_44_P392129	Spg7	spastic paraplegia 7 homolog (human)	1.107	-0.268	-2.6	1.600E-03	4.900E-02
A_44_P484579	Nos1ap	C-terminal PDZ domain ligand of neuronal nitric oxide synthase	1.075	-0.306	-2.6	4.000E-04	3.100E-02
A_44_P483358	Spg7	spastic paraplegia 7 homolog (human)	1.000	-0.398	-2.6	8.000E-04	3.800E-02
A_44_P651304	AW142782		1.299	-0.101	-2.6	0.000E+00	1.600E-02
A_44_P547586	AW915407		1.007	-0.404	-2.7	1.200E-03	4.300E-02
A_44_P995716	Ccna1	Rattus norvegicus cyclin A1	1.278	-0.133	-2.7	1.100E-03	4.200E-02
A_44_P423365	AW143634		1.198	-0.227	-2.7	7.000E-04	3.600E-02
A_43_P19751	RGD1565975	hypothetical LOC291903	1.003	-0.423	-2.7	9.000E-04	4.000E-02
A_43_P21504	Slick	sodium- and chloride-activated ATP-sensitive potassium channel	1.159	-0.269	-2.7	6.000E-04	3.500E-02
A_43_P17262	Tmod4	tropomodulin 4 (predicted)	1.368	-0.060	-2.7	0.000E+00	8.000E-03
A_44_P244338	Doc2a	double C2, alpha	0.988	-0.450	-2.7	1.300E-03	4.500E-02
A_44_P419123	Angpt2	angiopoietin 2	1.143	-0.306	-2.7	8.000E-04	3.800E-02
A_44_P222726	Slc31a2	solute carrier family 31, member 2 (predicted)	1.220	-0.229	-2.7	3.000E-04	2.900E-02
A_44_P312122	Wscd1	Rattus norvegicus WSC domain containing 1 (Wscd1), mRNA	1.145	-0.308	-2.7	4.000E-04	3.100E-02
A_43_P16274	Chma7	cholinergic receptor, nicotinic, alpha polypeptide 7	1.133	-0.338	-2.8	1.000E-03	4.100E-02

A_44_P553526	Unknown		1.122	-0.352	-2.8	5.000E-04	3.300E-02
A_44_P403545	Unknown		1.326	-0.153	-2.8	3.000E-04	2.800E-02
A_42_P667292	Trim63	tripartite motif-containing 63	1.261	-0.225	-2.8	4.000E-04	3.000E-02
A_44_P161846	Hist3h2ba	histone cluster 3, H2ba	1.085	-0.411	-2.8	1.500E-03	4.800E-02
A_44_P1017013	Ndufa7	NADH dehydrogenase 1 alpha subcomplex (predicted)	1.069	-0.438	-2.8	1.400E-03	4.700E-02
A_44_P824489	Unknown		1.189	-0.338	-2.9	8.000E-04	3.800E-02
A_44_P160688	Unknown		1.335	-0.198	-2.9	0.000E+00	1.800E-02
A_44_P253393	Tm7sf4	transmembrane 7 superfamily member 4 (predicted)	1.100	-0.437	-2.9	1.300E-03	4.600E-02
A_44_P547771	Cited1	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	1.248	-0.297	-2.9	3.000E-04	2.900E-02
A_42_P704429	Fgf13	fibroblast growth factor 13	1.134	-0.422	-2.9	7.000E-04	3.600E-02
A_44_P593612	TC594548		1.362	-0.201	-3.0	5.000E-04	3.300E-02
A_44_P685517	Unknown		0.950	-0.614	-3.0	1.500E-03	4.800E-02
A_42_P670631	RGD1305645	similar to RIKEN cDNA 1500015O10 (predicted)	1.404	-0.179	-3.0	1.000E-04	2.000E-02
A_43_P15980	Angpt2	angiopoietin 2	1.334	-0.260	-3.0	2.000E-04	2.500E-02
A_44_P104870	Crygd	crystallin, gamma D	1.029	-0.568	-3.0	1.400E-03	4.700E-02
A_44_P1039213	Cpa2	carboxypeptidase A2 (pancreatic) (predicted)	1.234	-0.378	-3.1	3.000E-04	2.900E-02
A_44_P793873	Sema5a	semaphorin 5A	1.527	-0.100	-3.1	0.000E+00	1.800E-02
A_44_P960581	Unknown		1.307	-0.321	-3.1	1.600E-03	4.900E-02
A_44_P729029	Ssmem1	serine-rich single-pass membrane protein 1	1.230	-0.399	-3.1	1.500E-03	4.700E-02
A_44_P1039205	Cpa2	carboxypeptidase A2 (pancreatic)	1.148	-0.487	-3.1	7.000E-04	3.600E-02
A_44_P172251	Unknown		1.266	-0.384	-3.1	1.400E-03	4.700E-02
A_44_P300612	Dpp6	dipeptidylpeptidase 6	1.440	-0.211	-3.1	9.000E-04	3.900E-02
A_44_P538086	Oact2	O-acyltransferase (membrane bound) domain containing 2 (predicted)	1.488	-0.165	-3.1	1.500E-03	4.700E-02
A_44_P670563	TC608471		1.350	-0.305	-3.1	1.000E-04	1.800E-02
A_44_P647689	Unknown		1.114	-0.550	-3.2	1.000E-03	4.100E-02
A_44_P257953	Rnf165	similar to ring finger protein 111	1.315	-0.354	-3.2	1.700E-03	5.000E-02
A_44_P126545	Lrriq1	similar to leucine-rich repeats and IQ motif containing 1	1.097	-0.606	-3.3	1.200E-03	4.400E-02
A_42_P755894	BF556567		1.391	-0.328	-3.3	3.000E-04	2.800E-02

A_44_P255424	Hpse2	similar to heparanase-like protein HPA2a	1.631	-0.120	-3.4	0.000E+00	1.000E-02
A_44_P281549	Unknown		1.123	-0.635	-3.4	1.400E-03	4.600E-02
A_43_P19435	Egfl6	epidermal growth factor-like protein 6	1.526	-0.234	-3.4	0.000E+00	1.100E-02
A_43_P13233	Slc25a21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	1.210	-0.584	-3.5	1.200E-03	4.400E-02
A_44_P798023	Trem1	triggering receptor expressed on myeloid cells-like 1	1.376	-0.465	-3.6	4.000E-04	3.100E-02
A_44_P792166	Angpt2		1.727	-0.151	-3.7	0.000E+00	1.000E-02
A_43_P11502	Slc4a1	solute carrier family 4, member 1	1.158	-0.732	-3.7	1.400E-03	4.600E-02
A_44_P398612	Slc26a7	solute carrier family 26, member 7 (predicted)	1.601	-0.290	-3.7	1.300E-03	4.500E-02
A_44_P456197	Crrh1	corticotropin releasing hormone receptor 1	1.563	-0.366	-3.8	1.200E-03	4.300E-02
A_42_P841255	Igdc3	immunoglobulin superfamily, DCC subclass, member 3	1.378	-0.594	-3.9	1.500E-03	4.800E-02
A_42_P799390	Cdkn1c		1.536	-0.469	-4.0	2.000E-04	2.500E-02
A_42_P455025	Unknown		1.640	-0.371	-4.0	1.500E-03	4.800E-02
A_43_P15314	P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3	1.893	-0.156	-4.1	1.500E-03	4.700E-02
A_44_P245835	RGD1310110	similar to 3632451O06Rik protein (predicted)	1.802	-0.259	-4.2	2.000E-04	2.400E-02
A_44_P358743	LOC361113	hypothetical LOC361113	1.722	-0.373	-4.3	7.000E-04	3.600E-02
A_44_P223978	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	1.321	-0.779	-4.3	1.200E-03	4.400E-02
A_44_P407761	RGD1309567_	similar to hypothetical protein FLJ20300 (predicted)	1.742	-0.378	-4.3	8.000E-04	3.700E-02
A_44_P527325	Unknown		1.958	-0.169	-4.4	0.000E+00	1.100E-02
A_43_P20954	Cfap43	cilia and flagella associated protein 43	1.414	-0.723	-4.4	1.500E-03	4.800E-02
A_44_P215383	Hpse2	heparanase 2 (predicted)	1.784	-0.366	-4.4	1.000E-04	2.100E-02
A_42_P671800	Car5a	carbonic anhydrase 5	1.639	-0.532	-4.5	1.000E-03	4.100E-02
A_44_P531758	Cryab	crystallin, alpha B	1.770	-0.421	-4.6	1.000E-03	4.100E-02
A_44_P374618	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	1.640	-0.557	-4.6	4.000E-04	3.000E-02
A_44_P374620	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	1.542	-0.667	-4.6	1.000E-03	4.100E-02
A_44_P123965	Slc8a3	solute carrier family 8 (sodium/calcium exchanger), member 3	1.690	-0.531	-4.7	1.500E-03	4.700E-02
A_44_P819726	Aqp4		2.184	-0.043	-4.7	6.000E-04	3.400E-02
A_44_P934428	Aqp4	aquaporin 4	2.006	-0.268	-4.8	1.700E-03	5.000E-02
A_42_P756334	Myh6	myosin heavy chain, polypeptide 6	1.759	-0.523	-4.9	5.000E-04	3.300E-02

A_44_P669476	Unknown		1.665	-0.640	-4.9	7.000E-04	3.700E-02
A_44_P389904	Kcnq3	potassium voltage-gated channel, subfamily Q, member 3	1.900	-0.416	-5.0	5.000E-04	3.200E-02
A_44_P561166	Aqp4	aquaporin 4	1.889	-0.456	-5.1	8.000E-04	3.800E-02
A_43_P19532	Dpp10	dipeptidylpeptidase 10 (predicted)	2.012	-0.343	-5.1	4.000E-04	3.000E-02
A_44_P528667	B3gat1	beta-1,3-glucuronyltransferase 1	1.720	-0.674	-5.3	4.000E-04	3.100E-02
A_44_P306162	Ugt8	UDP-glucuronosyltransferase 8	1.943	-0.473	-5.3	1.000E-03	4.100E-02
A_44_P1046787	Sbspon	similar to RPE-spondin	1.543	-0.875	-5.3	1.600E-03	4.900E-02
A_44_P664280	Unknown		1.962	-0.515	-5.6	1.600E-03	4.900E-02
A_44_P576815	Unknown		2.038	-0.458	-5.6	0.000E+00	1.800E-02
A_42_P762508	Nptx2	neuronal pentraxin II	2.105	-0.403	-5.7	1.300E-03	4.600E-02
A_44_P239044	LOC362480	similar to lipoxygenase homology domains 1	1.967	-0.542	-5.7	6.000E-04	3.500E-02
A_44_P370065	Nptx2	neuronal pentraxin II	2.231	-0.309	-5.8	6.000E-04	3.400E-02
A_44_P511552	Unknown		2.179	-0.402	-6.0	8.000E-04	3.800E-02
A_43_P22805	Unc5d	unc-5 netrin receptor D	1.874	-0.747	-6.2	6.000E-04	3.500E-02
A_44_P510442	Trim50	tripartite motif protein 50	1.902	-0.734	-6.2	1.100E-03	4.200E-02
A_43_P11794	Tacr3	tachykinin receptor 3	1.970	-0.666	-6.2	6.000E-04	3.400E-02
A_43_P11983	Rgs9	regulator of G-protein signaling 9	2.370	-0.280	-6.3	1.700E-03	5.000E-02
A_44_P823383	Unknown		1.770	-0.888	-6.3	7.000E-04	3.700E-02
A_44_P271405	Pxmp4	peroxisomal membrane protein 4	2.324	-0.340	-6.3	4.000E-04	3.100E-02
A_44_P173289	Pkd2l2	polycystic kidney disease 2-like 2 (predicted)	2.210	-0.483	-6.5	1.600E-03	4.900E-02
A_42_P734395	Scml4	sex comb on midleg-like 4 (Drosophila)	2.185	-0.550	-6.7	3.000E-04	3.000E-02
A_44_P545966	Cfap43	cilia and flagella associated protein 43	1.890	-0.872	-6.8	7.000E-04	3.700E-02
A_44_P332674	Myh13	myosin, heavy polypeptide 13, skeletal muscle	2.063	-0.766	-7.1	7.000E-04	3.600E-02
A_44_P597401	Unknown		2.251	-0.613	-7.3	1.300E-03	4.500E-02
A_44_P1040494	Tle6	transducin-like enhancer of split 6	2.212	-0.654	-7.3	6.000E-04	3.500E-02
A_44_P285423	Sphkap	SPHK1 interactor, AKAP domain containing	2.609	-0.272	-7.4	0.000E+00	1.800E-02
A_44_P208102	Lrrc66	leucine rich repeat containing 66	2.038	-0.874	-7.5	1.700E-03	5.000E-02
A_44_P210250	Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	2.124	-0.791	-7.5	3.000E-04	3.000E-02

A_44_P541244	LOC290078	similar to RIKEN cDNA A430107P09 gene	2.283	-0.672	-7.8	1.000E-03	4.100E-02
A_44_P347299	Unknown		2.466	-0.501	-7.8	2.000E-04	2.600E-02
A_43_P12609	Kcnj10	potassium inwardly-rectifying channel, subfamily J, member 10	2.325	-0.671	-8.0	8.000E-04	3.900E-02
A_44_P961911	Unknown		2.488	-0.541	-8.2	3.000E-04	2.700E-02
A_44_P332675	Myh13	myosin, heavy polypeptide 13, skeletal muscle	2.418	-0.663	-8.5	6.000E-04	3.400E-02
A_44_P584408	Unknown		2.368	-0.728	-8.6	5.000E-04	3.400E-02
A_44_P224403	Gcm1	glial cells missing homolog 1 (Drosophila)	2.155	-1.077	-9.4	1.500E-03	4.700E-02
A_44_P1021535	Mlana	melan-A	2.540	-0.814	-10.2	1.200E-03	4.400E-02
A_44_P370005	Spna1_	spectrin alpha 1 (predicted)	2.981	-0.403	-10.4	1.000E-04	2.200E-02
A_44_P499156	LOC361943	similar to OL-protocadherin isoform	3.207	-0.251	-11.0	2.000E-04	2.500E-02
A_44_P775989	Vwc2	von Willebrand factor C domain containing 2	2.879	-0.633	-11.4	4.000E-04	3.100E-02
A_42_P464434	Ranbp3l	similar to Hypothetical protein FLJ25422 (predicted)	2.714	-0.800	-11.4	1.400E-03	4.600E-02
A_44_P358194	Fmo3	flavin containing monooxygenase 3	2.961	-0.644	-12.2	5.000E-04	3.300E-02
A_44_P653949	Unknown		3.428	-0.290	-13.2	2.000E-04	2.300E-02
A_44_P125710	Pex5l	peroxin 2	3.287	-0.581	-14.6	0.000E+00	1.700E-02
A_44_P828432	Unknown		3.526	-0.453	-15.8	4.000E-04	3.100E-02
A_44_P328062	Edn3		3.774	-0.914	-25.8	4.000E-04	3.000E-02
A_44_P159091	LOC290195	similar to T cell receptor V delta 2	3.480	-1.248	-26.5	1.200E-03	4.400E-02

Supplemental table 1. List of the transcripts showing significant alteration in the kidney of newborn rats underwent UO compared to those of sham-operated controls. Abbreviations used in the letterhead of the supplemental Table 1.: MI - Mean Intensity; FC-fold change; p-p value calculated with T test (two tailed unpaired); FDR-Multiple test correction controlled with the Bonferroni-Hochberg method.

Supplemental table 2.

GO term and name	Count	Genes	Pop Hits	Pop Total	Enrichment	Occurance	p	FDR
GO:0006955 immune response	47	CXCL1, RT1-DB2, CXCL3, RT1-DB1, CCR1, CXCL2, IL19, TLR2, CD70, RT1-DMA, CXCL6, RT1-DOB, RT1-DA, RT1-BB, TNFRSF1A, TNFRSF1B, IL1B, FAS, FCGR3A, NFIL3, LTB, IL1A, SBSPON, FYB, RT1-CE1, COLEC12, C4BPA, RT1-EC2, IL24, CTSS, GZMC, TNFSF9, SECTM1A, VAV1, RT1-A2, C1QB, TNFSF10, CCR6, CCR5, FCGR2B, TNFSF13B, CCR2, IRF8, IL12A, SLPI, NGFR, LCP2	266	17126	6.651	0/10	0.000E+00	0.000E+00
GO:0006954 inflammatory response	41	ELF3, AIF1, C3, CCR1, IL18, CXCL3, IL19, CXCL2, F2RL1, TLR2, KCNJ10, CXCL6, CCL6, TNFRSF1A, SLC11A1, TNFRSF1B, FGG, MYD88, CD44, CCL21, PYCARD, IL1B, FAS, IL1A, SPP1, CSF1R, HCN1, NFKBIZ, C4A, AXL, IL24, CCL17, CCL12, CYBB, CCR5, CAMK4, CCR2, NTRK2, NGFR, ALOX5, CD14	264	17126	5.846	0/10	0.000E+00	0.000E+00
GO:0032496 response to lipopolysaccharide	34	CXCL1, CXCL3, EDN1, TLR2, CXCL6, MMP3, CITED1, TNFRSF1A, SLC11A1, TNFRSF1B, MYD88, CASP8, SERPINE1, IL1B, FAS, CD6, CASP1, LOXL1, IL1A, ICAM1, CEBPB, SOCS3, IL1RN, IL6R, JUNB, CD86, CCR5, F3, JUN, IL12A, SLPI, NGFR, PROS1, CD14	269	17126	4.757	0/10	0.000E+00	0.000E+00
GO:0045087 innate immune response	32	TNFAIP8L2, IFIH1, FGR, ZC3HAV1, BLK, F2RL1, TLR2, C1S, TRIM15, TLR7, C1QC, B2M, BTK, OASL2, FCER1G, CFI, CLEC4D, CSF1R, MATK, CARD9, C4A, IRGM, AXL, SERPING1, C4BPA, LCN2, C1QA, C1QB, OASL, CYBB, SLPI, CD14	239	17126	5.040	0/10	0.000E+00	0.000E+00
GO:0071347 cellular response to interleukin-1	19	ICAM1, CEBPB, CXCL2, EDN1, AQP4, MMP3, SOX9, PSMB9, CCL17, CCL6, LCN2, INHBB, CCL12, CCL21, SERPINE1, IRF1, PYCARD, FAS, MYC	88	17126	8.127	0/10	0.000E+00	0.000E+00
GO:0019221 cytokine-mediated signaling pathway	23	IL1R2, IL2RB, IL1R1, PODNL1, OSMR, SOCS3, IL1RL1, IL21R, IL1RN, IL6R, PTPRN, IL7R, IRAK4, TNFRSF1A, MYD88, IRF5, CD44, F3, CCR2, CX3CR1, IL1B, IL1A, CSF1R	139	17126	6.228	0/10	0.000E+00	0.000E+00

GO:0030593 neutrophil chemotaxis	16	CXCL1, EDN3, CXCL3, CXCL2, EDN1, NCKAP1L, ITGB2, VAV1, TGFB2, CCL6, CCL17, CCL12, CCL21, FCER1G, IL1B, SPP1	58	17126	10.383	0/10	0.000E+00	0.000E+00
GO:0071222 cellular response to lipopolysaccharide	24	MRC1, ICAM1, SBNO2, CEBPB, IL18, CXCL3, CXCL2, AXL, CXCL6, IL24, B2M, LCN2, CD86, TNFRSF1B, CCR5, FCGR2B, IRF8, CX3CR1, SERPINE1, IL12A, PYCARD, IL1B, FCGR3A, CD14	188	17126	4.805	0/10	0.000E+00	0.000E+00
GO:0001666 response to hypoxia	27	TF, ICAM1, CRYAB, PDGFA, SOCS3, IL18, SLC6A4, EDN1, TLR2, MMP3, TRH, TGFB2, CRHR1, TNFRSF1A, BDNF, MYOCD, DIO3, P2RX3, CCR2, IL1B, CHRNA7, CYGB, ANGPT1, FAS, CASP1, ANGPT2, IL1A	258	17126	3.939	0/10	0.000E+00	0.000E+00
GO:0070098 chemokine-mediated signaling pathway	13	CXCL1, CXCL3, CCR1, CXCL2, CXCL6, CCL17, CCL6, CCL12, CCR6, CCR5, CCL21, CCR2, CX3CR1	56	17126	8.738	0/10	0.000E+00	0.000E+00
GO:0032355 response to estradiol	21	CXCL1, TACR3, PDGFA, C3, CRYAB, SOCS3, MAP1B, CXCL2, SLC6A4, MMP3, SLC34A2, TGFB2, REG3B, FCGR2B, FCGR1A, F3, CASP8, IL1B, CD4, WNT7A, MYC	189	17126	4.182	0/10	0.000E+00	0.000E+00
GO:0090023 positive regulation of neutrophil chemotaxis	9	CXCL1, RAC2, CCL21, CXCL3, EDN1, CXCL2, IL1B, NCKAP1L, CD74	25	17126	13.550	0/10	0.000E+00	0.000E+00
GO:0034097 response to cytokine	15	AIF1, OSMR, SOCS3, IL6R, MMP3, JUNB, CITED1, TIMP1, TGFB2, CORO1A, CDKN2B, JUN, SERPINE1, FAS, FOSL1	98	17126	5.761	0/10	0.000E+00	1.000E-04
GO:0042102 positive regulation of T cell proliferation	12	PTPRC, ITGAL, CD86, CORO1A, TNFSF13B, AIF1, IL12A, IL1B, NCKAP1L, CD4, SLC4A1, CD6	62	17126	7.285	0/10	0.000E+00	1.000E-04
GO:0032755 positive regulation of interleukin-6 production	11	MYD88, CARD9, CCR5, PYCARD, TLR2, IL1B, FCER1G, IL6R, TNFSF9, TLR7, IL1A	50	17126	8.281	0/10	0.000E+00	1.000E-04
GO:0009617 response to bacterium	10	LCN2, SLC11A1, FCGR2B, SOCS3, FCGR1A, IRF8, PYCARD, TLR2, CASP1, CD14	39	17126	9.651	0/10	0.000E+00	1.000E-04
GO:0070374 positive regulation of ERK1 and ERK2 cascade	19	ICAM1, PDGFA, C3, CCR1, F2RL1, TLR2, CD74, CCL17, CCL6, CCL12, FGG, CD44, CCL21, JUN, PYCARD, IL1B, ANGPT1, IL1A, CSF1R	171	17126	4.182	0/10	0.000E+00	1.000E-04
GO:0032729 positive regulation of interferon-gamma production	11	SLC11A1, IL18, CCR2, IRF8, PYCARD, IL12A, IL1B, BCL3, RUNX1, TNFSF9, CD14	51	17126	8.118	0/10	0.000E+00	1.000E-04
GO:0042060 wound healing	16	EGR1, PDGFA, CXCL2, IL24, MMP3, TPM1, MMP12, TIMP1, TGFB2, SLC11A1,	123	17126	4.896	0/10	0.000E+00	1.000E-04

		BNC1, SERPINE1, IL1B, FCGR3A, WNT7A, IL1A						
GO:0032760 positive regulation of tumor necrosis factor production	11	TNFRSF1A, MYD88, CARD9, CCR5, IL18, CCR2, CLU, PYCARD, TLR2, FCER1G, CD14	54	17126	7.667	0/10	0.000E+00	2.000E-04
GO:0007568 aging	25	TACR3, CLU, MMP7, ITGB2, TIMP1, TGFB2, TNFRSF1B, CDKN2B, FAS, HCN1, SOCS3, CRYAB, BCL2A1, SERPING1, SLC34A2, CDKN1C, C1QB, CD86, CCR5, F3, JUN, NTRK2, CASP12, CP, ADRA1D	298	17126	3.158	0/10	0.000E+00	2.000E-04
GO:0051384 response to glucocorticoid	16	CXCL1, AIF1, C3, SOCS3, IL1RN, CXCL2, AQP4, MGP, KCNJ10, IL6R, TRIM63, ANXA3, ABCB4, C1QB, IL1B, FAS	131	17126	4.597	0/10	0.000E+00	2.000E-04
GO:0071260 cellular response to mechanical stimulus	14	EGR1, IL18, MMP7, GJA1, SOX9, TLR7, TNFRSF1A, MYD88, SERPINE1, CASP8, IRF1, IL1B, FAS, CASP1	101	17126	5.217	0/10	0.000E+00	3.000E-04
GO:0071346 cellular response to interferon-gamma	11	MRC1, CCL12, AIF1, CCL21, IL18, EDN1, AQP4, MYC, RT1-BB, CCL6, CCL17	59	17126	7.018	0/10	0.000E+00	3.000E-04
GO:0042127 regulation of cell proliferation	21	CXCL1, FGR, BLK, CXCL3, CXCL2, MMP7, CXCL6, TNFSF9, SOX9, JUNB, TGFB2, BTK, TNFRSF1A, TNFRSF1B, MYD88, SERPINE1, IRF1, FAS, NGFR, WNT7A, MATK	229	17126	3.452	0/10	0.000E+00	3.000E-04
GO:0045766 positive regulation of angiogenesis	15	C3, ITGB2, ANXA3, SEMA5A, TNFRSF1A, LRG1, F3, CX3CR1, SERPINE1, IL1B, CHRNA7, RUNX1, ANGPT2, IL1A, CYR61	120	17126	4.705	0/10	0.000E+00	4.000E-04
GO:0006958 complement activation, classical pathway	9	C1QA, C1QB, C4A, C3, SERPING1, CFI, C4BPA, C1S, C1QC	36	17126	9.410	0/10	0.000E+00	3.000E-04
GO:0006909 phagocytosis	9	SLC11A1, CORO1A, IRF8, PLD4, AXL, MYO1G, CD302, VAV1, ANXA3	36	17126	9.410	0/10	0.000E+00	3.000E-04
GO:0002504 antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	6	RT1-DB2, RT1-DB1, RT1-DMA, RT1-DOB, RT1-DA, RT1-BB	12	17126	18.820	0/10	0.000E+00	8.000E-04
GO:0071356 cellular response to tumor necrosis factor	14	ICAM1, IL18, EDN1, CCL6, CCL17, LCN2, REG3B, CCL12, BDNF, CCL21, NTRK2, IRF1, PYCARD, FAS	114	17126	4.622	0/10	0.000E+00	9.000E-04
GO:0009615 response to virus	12	LCN2, BATF3, OASL, IFIH1, MYD88, ZC3HAV1, OASL2, IFITM3, CLU, IL12A, BCL3, ISG20	82	17126	5.508	0/10	0.000E+00	9.000E-04

GO:0042493 response to drug	32	PDGFA, EDN1, SLC6A4, MMP7, B2M, TGFB2, BDNF, PLIN2, IL1B, FAS, CASP1, FOSL1, MYC, EGR1, ICAM1, CARD9, HAVCR1, SOCS3, IL1RN, MAP1B, NCKAP1L, MMP12, JUNB, PSMB9, ABCB4, LCN2, INHBA, CD86, CYBB, JUN, CASP12, AOC1	504	17126	2.390	0/10	0.000E+00	1.100E-03
GO:0051607 defense response to virus	14	PTPRC, CARD9, ZC3HAV1, IFITM3, F2RL1, TLR7, NCR1, ISG20, CD86, OASL, IRF5, OASL2, PYCARD, IRF1	118	17126	4.466	0/10	0.000E+00	1.200E-03
GO:0019886 antigen processing and presentation of exogenous peptide antigen via MHC class II	6	FCGR2B, RT1-DB1, FCER1G, RT1-DMA, CD74, RT1-BB	14	17126	16.131	0/10	0.000E+00	1.600E-03
GO:0010332 response to gamma radiation	9	CXCL1, PTPRC, SOCS3, CXCL2, IL1B, IL6R, CXCL6, MYC, IL1A	46	17126	7.364	0/10	0.000E+00	1.900E-03
GO:0043123 positive regulation of I-kappaB kinase/NF-kappaB signaling	15	CARD9, ZC3HAV1, F2RL1, GJA1, IRAK4, APOL3, TNFRSF1A, TNFSF10, MYD88, CCL21, CASP8, UBD, IL1B, CASP1, IL1A	147	17126	3.841	0/10	0.000E+00	2.700E-03
GO:0006898 receptor-mediated endocytosis	12	SBSPON, MRC1, LGALS3BP, MSR1, FCGR2B, FCGR1A, IFITM3, FCRL2, CFI, CD6, CD14, DMBT1	97	17126	4.656	0/10	1.000E-04	3.600E-03
GO:0050830 defense response to Gram-positive bacterium	11	REG3B, LYZ2, MYD88, CARD9, FGR, TLR2, MMP7, IL12A, LOC290595, REG3G, B2M	81	17126	5.112	0/10	1.000E-04	3.700E-03
GO:0001774 microglial cell activation	6	JUN, CLU, CX3CR1, TLR2, CASP1, TLR7	17	17126	13.285	1/10	1.000E-04	4.100E-03
GO:0071407 cellular response to organic cyclic compound	13	MSR1, CEBPB, IL18, P2RY12, INHBB, P2RY13, RGS20, P2RY6, SERPINE1, CASP8, IL1B, FAS, MYC	117	17126	4.182	0/10	1.000E-04	4.200E-03
GO:0007229 integrin-mediated signaling pathway	11	ITGAL, PLEK, FGR, CDH17, FERMT3, PRAM1, ITGB7, FCER1G, ITGB2, VAV1, TYROBP	84	17126	4.929	0/10	1.000E-04	4.700E-03
GO:0097191 extrinsic apoptotic signaling pathway	8	INHBA, TNFRSF1B, TNFRSF12A, CASP8, IL12A, CD70, FAS, TGFB2	41	17126	7.344	0/10	1.000E-04	5.600E-03
GO:0043066 negative regulation of apoptotic process	30	AIF1, BLK, CLU, ASNS, SOX9, CD74, TIMP1, TGFB2, TSC22D1, REG3B, TNFRSF1A, BDNF, CD44, BCL3, ANGPT1, FAS, CSF1R, CYR61, IL2RB, CRYAB, SOCS3, IL1RN, BCL2A1, AXL, NCKAP1L, IL24, BIRC3, JUN, NGFR, WNT7A	507	17126	2.227	0/10	1.000E-04	5.600E-03
GO:0050766 positive regulation of phagocytosis	8	SLC11A1, FCGR2B, C3, FCGR1A, PYCARD, IL1B, FCER1G, PROS1	42	17126	7.169	0/10	1.000E-04	6.300E-03
GO:0050829 defense response to Gram-negative bacterium	8	REG3B, SLC11A1, LYZ2, SERPINE1, PYCARD, MMP7, CD4, B2M	42	17126	7.169	0/10	1.000E-04	6.300E-03

GO:0007613 memory	11	CRHR1, SLC8A3, CEBPB, SLC6A4, IL1RN, CX3CR1, IL1B, FGF13, CHRNA7, CASP1, KCNK10	88	17126	4.705	0/10	1.000E-04	6.400E-03
GO:0043065 positive regulation of apoptotic process	22	TNFRSF12A, IL18, BCL2A1, CLU, HRK, IL24, FRZB, TGFB2, TSC22D1, EPHA7, TNFSF10, IRF5, JUN, CASP12, PYCARD, UBD, IL1B, FAS, NGFR, CASP1, FOSL1, CYR61	318	17126	2.604	0/10	1.000E-04	7.000E-03
GO:0050729 positive regulation of inflammatory response	9	CCL12, TNFRSF1A, CCR5, IL1RL1, SERPINE1, CCR2, TLR2, CTSS, CCL6	58	17126	5.841	0/10	1.000E-04	7.600E-03
GO:0042742 defense response to bacterium	13	TNFRSF1A, SLC11A1, LY2Z, CEBPB, CCR5, FCGR1A, IRF8, MMP7, FCER1G, BCL3, CLEC4D, ANXA3, ADAMTS4	128	17126	3.823	0/10	2.000E-04	8.300E-03
GO:0007166 cell surface receptor signaling pathway	16	EDN3, ITGAL, CD3G, EDN1, TSPAN8, SCTR, CRHR1, TNFRSF1A, CD37, TNFRSF1B, MYD88, FCGR2B, CLCF1, FCGR1A, FCER1G, CD4	191	17126	3.153	0/10	2.000E-04	9.500E-03
GO:0045576 mast cell activation	5	FYB, FCGR2B, SERPINE1, FCER1G, LCP2	12	17126	15.683	0/10	2.000E-04	1.060E-02
GO:0051092 positive regulation of NF-kappaB transcription factor activity	12	TRAF1, ICAM1, MYD88, CARD9, CLU, PYCARD, TLR2, RIPK3, IL1B, ITGB2, TRIM15, IL6R	114	17126	3.962	0/10	2.000E-04	1.130E-02
GO:0042981 regulation of apoptotic process	16	EGR1, CARD9, NOS1AP, BIRC3, SOX9, TGFB2, INHBB, TNFRSF1A, INHBA, TNFRSF1B, CASP12, PYCARD, BCL3, FAS, CASP1, MYC	195	17126	3.088	0/10	2.000E-04	1.130E-02
GO:0010628 positive regulation of gene expression	23	EGR1, WNT10A, IL18, SLC6A4, TLR2, GJA1, SOX9, IL7R, CITED1, TGFB2, LCN2, TNFRSF1A, INHBA, SLC11A1, ATF3, CCR5, CD44, NTRK2, SERPINE1, IL1B, NFIL3, WNT7A, IL1A	357	17126	2.425	0/10	2.000E-04	1.120E-02
GO:0009416 response to light stimulus	7	BDNF, SYNE1, NTRK2, CLU, ASNS, BHLHE40, JUNB	34	17126	7.749	0/10	2.000E-04	1.150E-02
GO:0014068 positive regulation of phosphatidylinositol 3-kinase signaling	9	FGR, PDGFA, HCLS1, F2RL1, NTRK2, ANGPT1, PIK3AP1, SOX9, TGFB2	64	17126	5.293	0/10	3.000E-04	1.300E-02
GO:0007612 learning	9	SLC8A3, BDNF, JUN, NTRK2, FGF13, STRA6, NRXN1, FOSL1, RGS14	65	17126	5.212	0/10	3.000E-04	1.420E-02
GO:0007204 positive regulation of cytosolic calcium ion concentration	13	CRHR1, CXCL1, GNA15, CCR6, CCR5, CCR1, CXCL3, F2RL1, EDN1, CXCL2, IL1B, GJA1, ADRA1D	138	17126	3.546	0/10	3.000E-04	1.410E-02
GO:0006952 defense response	7	TNFRSF1A, CCR5, FCGR2B, IRGM, TAP1, IFI47, CD74	36	17126	7.319	0/10	3.000E-04	1.480E-02
GO:0016064 immunoglobulin mediated immune response	5	MYD88, FCGR2B, FCER1G, RT1-DMA, CD74	14	17126	13.443	0/10	4.000E-04	1.720E-02

GO:0043627 response to estrogen	11	C3, SERPINE1, ANGPT1, RGS9, FAS, PTPRN, WNT7A, CITED1, SLC34A2, TGFB2, DMBT1	103	17126	4.020	0/10	4.000E-04	1.740E-02
GO:0043525 positive regulation of neuron apoptotic process	9	EGR1, TNFRSF1A, EPHA7, GRIK2, IL18, JUN, HRK, IL1B, TGFB2	68	17126	4.982	0/10	4.000E-04	1.780E-02
GO:0032481 positive regulation of type I interferon production	5	MYD88, ZC3HAV1, IRF1, TRIM15, CD14	15	17126	12.547	0/10	5.000E-04	2.180E-02
GO:0002244 hematopoietic progenitor cell differentiation	10	SLC8A3, PTPRC, INHBA, ARL11, PLEK, CEBPD, PTPRZ1, PLD4, HERC6, FSTL3	89	17126	4.229	0/10	6.000E-04	2.370E-02
GO:0050727 regulation of inflammatory response	8	SBNO2, IL1R1, MYD88, CASP12, PYCARD, CHRNA7, PIK3AP1, CASP1	56	17126	5.377	0/10	7.000E-04	2.660E-02
GO:0071310 cellular response to organic substance	7	EGR1, ICAM1, CD68, EGR2, SLC6A4, IL1B, CASP1	41	17126	6.426	0/10	7.000E-04	2.710E-02
GO:0009968 negative regulation of signal transduction	6	RGS10, SOCS3, IL1RN, RGS18, RGS9, RGS16	28	17126	8.066	0/10	8.000E-04	2.940E-02
GO:0034341 response to interferon-gamma	6	SLC11A1, CD86, IFITM3, RT1-DB1, UBD, CITED1	28	17126	8.066	0/10	8.000E-04	2.940E-02
GO:0008285 negative regulation of cell proliferation	22	PTPRZ1, IL1RL1, IFITM3, TLR2, GJA1, IL24, SOX9, FRZB, TGFB2, SLFN2, INHBA, CD37, MYOCD, CDKN2B, JUN, IRF1, IL1B, RIPPLY3, RUNX1, FOSL1, IL1A, CSF1R	365	17126	2.269	0/10	8.000E-04	2.960E-02
GO:0008284 positive regulation of cell proliferation	27	EDN3, OSMR, PDGFA, EDN1, CLU, SOX9, TIMP1, TGFB2, TSC22D1, REG3B, MYOCD, HPSE2, RAC2, CLCF1, CHRNA7, HSF4, MYC, APLN, CSF1R, HCLS1, IL24, IL6R, MYCN, ATF3, JUN, NTRK2, WNT7A	496	17126	2.049	0/10	8.000E-04	2.980E-02
GO:0014070 response to organic cyclic compound	18	TF, ICAM1, ADCY8, SOCS3, IL1RN, TRH, MMP12, JUNB, INHBB, CDKN2B, CD44, PLIN2, JUN, IL1B, CASP1, FOSL1, ANGPT2, IL1A	267	17126	2.537	0/10	8.000E-04	3.000E-02
GO:0051591 response to cAMP	9	JUN, MMP19, C1S, IL6R, PTPRN, VGF, FOSL1, CITED1, JUNB	75	17126	4.517	0/10	8.000E-04	2.980E-02
GO:0009408 response to heat	9	CXCL1, SOCS3, P2RX3, CXCL2, IRF1, IL1B, MYH6, IL1A, CD14	76	17126	4.457	0/10	9.000E-04	3.210E-02
GO:0032494 response to peptidoglycan	4	MYD88, CARD9, IRF5, TLR2	8	17126	18.820	0/10	9.000E-04	3.320E-02
GO:0030335 positive regulation of cell migration	15	FGR, AIF1, PTPRZ1, PDGFA, FERMT3, CCR1, EDN1, F2RL1, MMP3, TGFB2, SEMA5A, CORO1A, SEMA4A, CSF1R, CYR61	201	17126	2.809	0/10	1.000E-03	3.390E-02
GO:0009611 response to wounding	9	TNFRSF1A, PDGFA, F3, CLU, MAP1B, NGFR, MYC, TGFB2, DMBT1	77	17126	4.399	0/10	1.000E-03	3.350E-02
GO:0043524 negative regulation of neuron apoptotic process	13	CEBPB, GRIK2, AXL, CITED1, REG3B, BDNF, CORO1A, CLCF1, JUN, NTRK2, ANGPT1, NGFR, NRBP2	157	17126	3.117	0/10	1.000E-03	3.360E-02

GO:0009612 response to mechanical stimulus	10	INHBB, F3, P2RX3, JUN, MAP1B, MGP, ASNS, ANGPT2, FOSL1, JUNB	97	17126	3.880	0/10	1.100E-03	3.630E-02
GO:0048661 positive regulation of smooth muscle cell proliferation	9	IRAK4, EGR1, MYD88, AIF1, IL18, JUN, EDN1, IL6R, MYC	79	17126	4.288	0/10	1.200E-03	3.800E-02
GO:0007249 I-kappaB kinase/NF-kappaB signaling	6	CARD9, IRF1, RIPK3, TIFA, BCL3, BTK	31	17126	7.285	0/10	1.200E-03	4.010E-02
GO:2001238 positive regulation of extrinsic apoptotic signaling pathway	6	PTPRC, TNFSF10, TNFRSF12A, CASP8, PYCARD, FAS	32	17126	7.057	0/10	1.400E-03	4.570E-02

Supplemental table 2. List of gene ontology (GO) terms in the biological function domain showing significant alteration in the kidney of newborn rats underwent UUO compared to those of sham-operated controls. Abbreviations used in the letterhead of the supplemental Table 2.: Count-number of entities in our list associated with the term; Genes-associated gens in our list; Pop Hits-genes associated with the term in the whole rat genome; Pop Total-total number of genes (with GO annotation) of the whole rat genome; Enrichment-ratio of the expected and identified number of associated genes; Occurance-Occurance in random sets (bootstrap value without replacement); p-p value calculated with Fisher's exact test; FDR-Multiple test correction controlled with the Bonferroni-Hochberg method

Supplemental table 3.

GO term and name	Count	Genes	Pop Hits	Pop Total	Enrichment	Occurance	p	FDR
GO:0042803 protein homodimerization activity	46	PVR, XDH, GRIK1, SYNDIG1, MASP1, GRIK2, PDGFA, SLC6A4, ASNS, PLVAP, TPM1, CITED1, TGFB2, SLC11A1, FAP, TAP1, PYCARD, CHRNA7, CD4, SLC4A1, BHLHE40, RUNX1, CSF1R, ALX1, ZFP365, CARD9, CEBPB, PLEK, CRYAB, CEBPD, BCL2A1, MYH7, IL6R, MYH6, LCN2, INHBB, C1QB, CORO1A, SYNE1, ATF3, JUN, CCR2, CLIC6, NTRK2, NGFR, AOC1	779	16276	2.288	0/10	3.000E-07	2.000E-04
GO:0005125 cytokine activity	18	IL18, IL1RN, IL19, EDN1, IL24, TNFSF9, TIMP1, TGFB2, INHBB, INHBA, TNFSF10, CLCF1, IL12A, IL1B, WNT7A, LTB, IL1A, SPP1	151	16276	4.620	0/10	4.000E-07	1.000E-04
GO:0005515 protein binding	69	GRIK1, ZC3HAV1, ADCY8, GRIK2, IL18, DPP10, SLC6A4, F2RL1, TLR2, GJA1, KCNJ10, RHOV, MYD88, MYOCD, CD44, CASP8, CPA2, CHRNA7, FAS, CASP1, DPP6, MYC, NOS1AP, CRYAB, HRK, NRXN1, CRHR1, RT1-A2, CCR5, JUN, LAMC2, NGFR, RASD1, RASD2, IL1R1, SCN1B, FGR, C3, CLU, DAG1, STK17B, SOX9, TNFRSF1A, FCGR1A, TAP1, PYCARD, VMP1, TYROBP, HCN1, PTPRC, DNM3, CEBPB, PTPRZ1, MAP1B, DPYSL4, RGS14, ABCB4, NCKAP1, CDKN1C, CYBB, EPHA7, SYNE1, NTRK2, CASP12, IRF8, IRF1, ALOX5, WNT7A, CD14	1514	16276	1.766	0/10	3.700E-06	8.000E-04
GO:0002020 protease binding	13	LCN2, TNFRSF1A, IL1R1, NOS1AP, F3, FAP, CASP12, SERPINE1, PYCARD, CD70, FAS, TIMP1, ADAMTS4	105	16276	4.798	0/10	1.630E-05	2.500E-03
GO:0004896 cytokine receptor activity	8	IL2RB, CD44, OSMR, F3, IL21R, CX3CR1, IL7R, CD74	33	16276	9.395	0/10	1.710E-05	2.100E-03
GO:0008009 chemokine activity	8	CXCL1, CCL12, CCL21, CXCL3, CXCL2, CXCL6, CCL6, CCL17	36	16276	8.612	0/10	3.120E-05	3.200E-03
GO:0005102 receptor binding	24	PVR, FGR, BLK, EDN1, GJA1, KCNJ10, CD70, NRXN1, RT1-EC2, TNFSF9, TGFB2, BTK, INHBA, CD86, SYNE1, FGG, MYD88, RND1, CLCF1, SERPINE1, ANGPT1, WNT7A, MATK, TYROBP	352	16276	2.642	0/10	4.430E-05	3.900E-03
GO:0046982 protein heterodimerization activity	30	ITGAL, PDGFA, TLR2, ITGB2, SOX9, TGFB2, RT1-BB, CLCF1, CASP8, TAP1, NEFH, BHLHE40, RUNX1, MYC, ALX1, BATF3, CEBPB, CD3G, CEBPD, SCUBE1,	541	16276	2.149	0/10	1.649E-04	1.270E-02

		BCL2A1, AXL, MYH7, MYH6, INHBB, INHBA, CYBB, ATF3, JUN, IL12A						
GO:0005164 tumor necrosis factor receptor binding	7	TRAF1, TNFSF10, TNFSF13B, CASP8, CD70, TNFSF9, LTB	34	16276	7.978	0/10	2.049E-04	1.400E-02
GO:0032403 protein complex binding	22	HCN1, FYB, ICAM1, ITGAL, HCLS1, MAP1B, DAG1, NCKAP1L, ITGB2, MMP3, NCKAP1, CRHR1, TNFRSF1A, NPTXR, CASP8, RIPK3, RGS9, FAS, TAPBPL, AOC1, MYC, PROS1	356	16276	2.395	0/10	3.829E-04	2.350E-02
GO:0023026 MHC class II protein complex binding	5	RT1-DB1, RT1-DMA, RT1-DOB, RT1-DA, CD74	16	16276	12.110	0/10	6.162E-04	3.420E-02
GO:0005149 interleukin-1 receptor binding	5	IRAK4, MYD88, IL1RN, IL1B, IL1A	16	16276	12.110	0/10	6.162E-04	3.420E-02
GO:0042605 peptide antigen binding	7	RT1-A2, RT1-CE1, RT1-DB1, TAP1, RT1-EC2, RT1-DA, RT1-BB	43	16276	6.309	0/10	7.641E-04	3.880E-02

Supplemental table 3. List of gene ontology (GO) terms in the molecular function domain showing significant alteration in the kidney of newborn rats underwent UUO compared to those of sham-operated controls. Abbreviations used in the letterhead of the supplemental Table 3.: Count-number of entities in our list associated with the term; Genes-associated gens in our list; Pop Hits-genes associated with the term in the whole rat genome; Pop Total-total nuber of genes (with GO annotation) of the whole rat genome; Enrichment-ratio of the expected and identified number of associated genes; Occurance-Occurance in random sets (bootstrap value without replacement); p-p value calculated with Fisher's exact test; FDR-Multiple test correction controlled with the Bonferroni-Hochberg method

Supplemental table 4.

GO term and name	Count	Genes	Pop Hits	Pop Total	Enrichment	Occurance	p	FDR
GO:0005615 extracellular space	93	EDN3, MASP1, PDGFA, IL18, RT1-DB1, EDN1, IL19, FSTL3, MMP7, MMP3, VGF, C1QC, B2M, TGFB2, REG3B, MTHFD2, BDNF, FAP, SERPINE1, RGD1305645, CPA2, IL1B, ANGPT1, FAS, CFI, ANGPT2, APLN, LTB, IL1A, WNT10A, ICAM1, C4A, SCUBE1, MGP, SERPING1, IL6R, IL24, PIGR, CTSS, INHBB, INHBA, CBLN2, NPTXR, F3, IL12A, CTSD, SLPI, LAMC2, PROS1, AOC1, SEMA4A, LCP1, ADAMTS4, XDH, CXCL1, TF, IL1R1, C3, CXCL3, CXCL2, CLU, DAG1, CXCL6, SERPINB1B, TIMP1, CCL6, IRAK4, TNFRSF1A, LGALS3BP, FGG, LRG1, CCL21, VWC2, SPP1, LYZ2, HAVCR1, PTPRZ1, IL1RL1, IL1RN, AXL, C4BPA, FRZB, TNFSF9, CCL17, DKK2, LCN2, CCL12, TNFSF10, CP, ALOX5, WNT7A, CD14, DMBT1	1247	18143	2.837	0/10	0.000E+00	0.000E+00
GO:0009986 cell surface	60	PVR, PDGFA, RT1-DB1, TLR2, MMP7, RT1-DMA, RT1-DA, TGFB2, KCNQ3, CD44, FAP, FAS, SLC4A1, DPP6, FCGR3A, IL1A, ICAM1, CRYAB, SCUBE1, IL6R, NRXN1, CTSS, CD86, CCR6, CCR5, F3, NGFR, TF, ITGAL, IL1R1, TNFRSF12A, IFITM3, CLU, ITGB2, PLVAP, CD74, RT1-BB, TNFRSF1A, SLC11A1, FGG, EPHB6, ITGB7, FCER1G, CD4, CSF1R, TYROBP, HCN1, MRC1, PTPRC, IL2RB, HAVCR1, IL1RL1, AXL, P2RY12, FCGR2B, CDH17, NTRK2, TREML1, WNT7A, CD14	598	18143	3.816	0/10	0.000E+00	0.000E+00
GO:0009897 external side of plasma membrane	33	ITGAL, OSMR, RT1-DB1, CCR1, TLR2, AQP4, IL7R, CD74, B2M, RT1-BB, FGG, CD44, CD69, FCGR1A, FCER1G, CHRNA7, CD4, FAS, FCGR3A, PTPRC, ICAM1, IL2RB, IL1RL1, SCUBE1, SLAMF7, RT1-A2, P2RY12, CD86, CCR5, FCGR2B, CCR2, NGFR, CD14	263	18143	4.773	1/10	0.000E+00	0.000E+00

GO:0045121 membrane raft	27	SLC6A4, TLR2, DAG1, GJA1, ITGB2, BTK, EFHD2, TNFRSF1A, TNFRSF1B, KCNQ3, FCGR1A, CASP8, ANGPT1, CD4, CHRNA7, FAS, PTPRC, ICAM1, BIRC3, RGS16, ABCB4, RT1-A2, FCGR2B, P2RX3, CTSD, NGFR, CD14	257	18143	3.996	0/10	0.000E+00	0.000E+00
GO:0005576 extracellular region	43	TF, IL1R2, EDN3, DAG1, LOC290595, FGF13, C1S, TRH, C1QC, TGFB2, TAC3, CALCB, BDNF, NPTX2, CLCF1, GLIPR1, SERPINE1, CPA2, PYCARD, IL1B, FAS, REG3G, APOL11A, CASP1, CYR61, LYZ2, C4A, IL1RN, C4BPA, IL6R, PIGR, CTSS, IL24, FRZB, LCN2, INHBB, INHBA, APOL3, SLPI, LAMC2, WIF1, RGD1563818, DMBT1	696	18143	2.350	1/10	0.000E+00	0.000E+00
GO:0042613 MHC class II protein complex	7	RT1-DB2, RT1-DB1, RT1-DMA, RT1-DOB, RT1-DA, CD74, RT1-BB	14	18143	19.018	0/10	0.000E+00	0.000E+00
GO:0031012 extracellular matrix	19	SBSPON, MMP19, CLU, MGP, MMP3, MMP12, TIMP1, TGFB2, CFP, MMP10, LGALS3BP, F3, SERPINE1, SLPI, CTSD, LOXL1, CYR61, ADAMTS4, DMBT1	177	18143	4.083	0/10	0.000E+00	0.000E+00
GO:0072562 blood microparticle	14	TF, C4A, C3, CLU, SERPING1, C1S, C4BPA, C1QC, C1QB, LGALS3BP, FGG, SLC4A1, CP, PROS1	118	18143	4.513	0/10	0.000E+00	6.000E-04
GO:0043025 neuronal cell body	31	SLC8A3, GRIK1, GRIK2, CCR1, VGF, TGFB2, RGS10, TNFRSF1B, BDNF, KCNQ3, PPP1R1B, PYCARD, CHRNA7, CYGB, FAS, DPP6, NEGR1, TUBB3, HCN1, PTPRZ1, MAP1B, PDE10A, NRXN1, PTPRN, ANXA3, CRHR1, EPHA7, CYBB, P2RX3, CCR2, NTRK2	515	18143	2.290	0/10	0.000E+00	1.600E-03
GO:0005887 integral component of plasma membrane	40	PVR, SLC8A3, GPR84, SYNDIG1, GRIK2, SLC6A4, F2RL1, GJA1, AQP4, TSPAN8, KCNJ10, KCNK13, CD72, FXD5, KCNK10, TNFRSF1A, TNFRSF1B, EPHB6, LAPTM5, FCER1G, FAS, SLC4A1, PILRA, HCN1, PTPRC, ICAM1, CDHR1, GPR171, P2RY12, P2RY13, CYBB, CD37, EPHA7, HAS1, SLC26A7, P2RX3, NTRK2, NGFR, ADRA1D, FAM26F	778	18143	1.956	0/10	1.000E-04	3.000E-03

GO:0070062 extracellular exosome	100	PVR, GDA, IL18, MMP7, RT1-DMA, TSPAN8, C1QC, B2M, ST3GAL1, CD44, SERPINE1, PLA1A, IL1B, CFI, SLC4A1, FAS, NEGR1, C4A, LAD1, CRYAB, MGP, SERPING1, COLEC12, C1QA, ARPC1B, C1QB, CD37, CAMK4, F3, IQCG, DYNLRB2, ITGAL, FGR, IFITM3, CLU, DAG1, ITGB2, CD70, CD74, TIMP1, SEMA5A, LGALS3BP, FGG, RAC2, ITGB7, FGL2, SPP1, IL1RN, MYO1G, NCKAP1L, CSRP1, PSMB8, NCKAP1, PSMB9, ABCB4, LCN2, CORO1A, TNFSF10, LYVE1, MYH13, RT1-DB1, FERMT3, GJA1, RT1-DA, CLCF1, ANGPT1, TRPV6, FCGR3A, DPP6, TUBB3, ICAM1, MAN1A1, PIGR, CD86, CLIC6, SLPI, CTSD, KPNA4, AOC1, PROS1, LCP1, TF, C7, C3, MUM1L1, PLVAP, C1S, TAC3, SPHKAP, LRG1, TGM1, PTPRC, DNM3, LYZ2, AXL, ANXA3, BLVRB, CP, CD14, DMBT1	2645	18143	1.438	0/10	1.000E-04	3.900E-03
GO:0030424 axon	23	HCN1, IRX3, DNM3, IL1R1, SPG7, CRYAB, PTPRZ1, GRIK2, MAP1B, STMN4, FGF13, ANXA3, TGFB2, TNFRSF1A, TNFRSF1B, CORO1A, BDNF, P2RX3, NTRK2, NEFH, CHRNA7, MYC, TUBB3	357	18143	2.450	0/10	2.000E-04	5.700E-03
GO:0005578 proteinaceous extracellular matrix	18	WNT10A, PTPRZ1, EGFL6, IL1RL1, MMP7, MMP3, MMP12, TIMP1, MMP10, LGALS3BP, HPSE2, VWC2, LAMC2, LOXL1, WNT7A, CYR61, ADAMTS4, DMBT1	248	18143	2.761	0/10	3.000E-04	8.200E-03
GO:0043197 dendritic spine	13	SLC8A3, DNM3, SYNDIG1, CRYAB, PTPRZ1, MAP1B, RGS14, CRHR1, RGS10, SYNE1, P2RX3, NTRK2, CHRNA7	146	18143	3.387	0/10	5.000E-04	1.160E-02
GO:0005771 multivesicular body	6	CRHR1, LRAT, GJA1, RT1-DMA, CD74, RT1-BB	27	18143	8.452	0/10	6.000E-04	1.380E-02
GO:0005604 basement membrane	10	TF, LAMC3, EGFL6, DAG1, VWC2, LAMC2, RUNX1, LOXL1, TIMP1, TGFB2	91	18143	4.180	0/10	6.000E-04	1.360E-02
GO:0043204 perikaryon	12	SLC8A3, BDNF, AIF1, CRYAB, GRIK2, CCR2, NTRK2, MAP1B, NEFH, PDE10A, NGFR, PTPRN	134	18143	3.406	1/10	8.000E-04	1.640E-02

GO:0030670 phagocytic vesicle membrane	5	SLC11A1, CORO1A, IRGM, ANXA3, DMBT1	18	18143	10.565	0/10	1.100E-03	2.020E-02
GO:0001891 phagocytic cup	5	CORO1A, AIF1, IRGM, MYO1G, LCP1	19	18143	10.009	0/10	1.300E-03	2.370E-02
GO:0016020 membrane	78	GNA15, TACR3, GRIK1, ADCY8, GRIK2, PDGFA, FERMT3, RT1-DB1, DPP10, IL21R, NAP1L1, FCRL2, AQP4, GJA1, RT1-DMA, RHOV, B2M, ST3GAL1, CHRNA7, PIK3AP1, SLC4A1, CFI, DPP6, ICAM1, EGFL6, NCF4, IFI47, PDE10A, MAN1A1, CTSS, PTPRN, PKD2L2, CRHR1, CD37, RND1, HAS1, PARP14, IPO5, LAMC2, TF, ITGAL, IL1R1, KEL, DAG1, ITGB2, CD74, RT1-BB, SEMA5A, TNFRSF1B, LGALS3BP, LPXN, LAPTM5, HPSE2, RAC2, ITGB7, GLIPR1, TAP1, PSTPIP1, SLC31A2, STX11, PTPRC, IL2RB, TBC1D10C, PLEK, PTPRZ1, IL1RL1, MYO1G, AXL, NCKAP1L, ANXA3, ABCB4, APOL3, OASL, CORO1A, PARP9, P2RX3, RAB38, CD302	2157	18143	1.375	0/10	3.000E-03	4.980E-02

Supplemental table 4. List of gene ontology (GO) terms in the cellular localisation domain showing significant alteration in the kidney of newborn rats underwent UUO compared to those of sham-operated. Abbreviations used in the letterhead of the supplemental Table 4.: Count-number of entities in our list associated with the term; Genes-associated genes in our list; Pop Hits-genes associated with the term in the whole rat genome; Pop Total-total number of genes (with GO annotation) of the whole rat genome; Enrichment-ratio of the expected and identified number of associated genes; Occurance-Occurance in random sets (bootstrap value without replacement); p-p value calculated with Fisher's exact test; FDR-Multiple test correction controlled with the Bonferroni-Hochberg method

Supplemental table 5.

Reactome Pathway	Ratio of protein in pathway	Number of protein in pathway	Protein from gene set	p	FDR	Hit genes
Cytokine Signaling in Immune system	0.069	489	44	6.350E-08	1.980E-05	OSMR, B2M, ISG20, IL1R2, IL1R1, IL1RN, ANGPT1, IL6R, IL12A, IL7R, IL18, IL1B, IL1A, TNFRSF12A, IFITM3, VAV1, CLCF1, CASP1, TNFSF13B, MYD88, CD44, CD70, OASL, ICAM1, FCGR1A, BIRC3, PDGFA, SOCS3, IRAK4, IRAK3, RASAL3, PSMB8, PSMB9, LTB, EGR1, KPNA4, PSMB10, TNFRSF1A, TNFRSF1B, RASGRP3, IL2RB, IRF5, IRF8, IRF1
Innate Immune System	0.113	806	61	6.460E-08	1.980E-05	MASP1, BTK, B2M, C4A, JUN, ANGPT1, C7, C3, NLRC4, IL1B, ARPC1B, FGR, VAV1, CASP8, CASP1, LCP2, CD4, C4BPA, ADCY8, C1QC, MYD88, CFI, CLEC4D, CD3G, C1QA, C1QB, CCR6, CAMK4, CCR2, FCER1G, TYROBP, NCKAP1L, NCKAP1, LY86, FCGR3A, FCGR1A, BIRC3, CD14, PDGFA, TLR2, TLR7, RIPK3, IFIH1, ITGB2, IRAK4, IRAK3, RASAL3, CARD9, PSMB8, PSMB9, CTSS, CD86, PROS1, PSMB10, C1S, RASGRP3, PSTPIP1, PYCARD, DTX4, IL2RB, IRF1
Chemokine receptors bind chemokines	0.008	55	11	9.370E-06	1.920E-03	CCL21, CCL17, CCR6, CCR5, CX3CR1, CCR2, CXCL1, CXCL3, CCR1, CXCL2, CXCL6
Class A/1 (Rhodopsin-like receptors)	0.043	304	27	3.510E-05	5.270E-03	C3, GPR65, CCL21, CCL17, P2RY12, P2RY13, P2RY6, ADRA1D, APLN, GPR18, TAC3, EDN3, EDN1, S1PR5, CCR6, CCR5, CX3CR1, CCR2, KEL, CXCL1, CXCL3, CCR1, CXCL2, CXCL6, F2RL1, TRH, TACR3
Peptide ligand-binding receptors	0.027	191	20	4.280E-05	5.270E-03	C3, CCL21, CCL17, APLN, TAC3, EDN3, EDN1, CCR6, CCR5, CX3CR1, CCR2, KEL, CXCL1, CXCL3, CCR1, CXCL2, CXCL6, F2RL1, TRH, TACR3
Signaling by Interleukins	0.039	280	25	6.360E-05	5.910E-03	OSMR, IL1R2, IL1R1, IL1RN, ANGPT1, IL6R, IL12A, IL7R, IL18, IL1B, IL1A, VAV1, CLCF1, CASP1, MYD88, PDGFA, SOCS3, IRAK4, IRAK3, RASAL3, PSMB8, PSMB9, PSMB10, RASGRP3, IL2RB
Degradation of the extracellular matrix	0.011	81	12	6.790E-05	5.910E-03	ADAMTS4, SPP1, MMP19, MMP12, MMP10, TIMP1, CD44, LAMC2, MMP7, MMP3, CTSS, CTSD
GPCR ligand binding	0.055	389	30	1.600E-04	1.170E-02	C3, GPR65, CCL21, CCL17, P2RY12, P2RY13, P2RY6, ADRA1D, APLN, GPR18, TAC3, EDN3, EDN1, S1PR5, CRHR1, CCR6, CCR5, CX3CR1, CCR2, KEL, CXCL1, CXCL3, CCR1, CXCL2, CXCL6, F2RL1, SCTR, TRH, TACR3, CALCB
G alpha (i) signalling events	0.030	212	20	1.720E-04	1.170E-02	C3, CCL21, P2RY12, P2RY13, APLN, GPR18, ADCY8, S1PR5, CCR6, CCR5, CCR2, CXCL1, CXCL3, CCR1, CXCL2, CXCL6, RGS10, RGS18, RGS14, RGS20
Regulation of Complement cascade	0.003	22	6	2.050E-04	1.250E-02	C4A, C7, C3, C4BPA, CFI, PROS1

Platelet activation, signaling and aggregation	0.029	203	19	2.750E-04	1.260E-02	SERPINE1, SERPING1, RAC2, APBB1IP, P2RY12, GNA15, TGFB2, TIMP1, FGG, VAV1, LCP2, FCER1G, TF, PLEK, PDGFA, CLU, PROS1, PIK3R5, IL2RB
RIPK1-mediated regulated necrosis	0.002	15	5	2.830E-04	1.260E-02	FAS, TNFSF10, CASP8, BIRC3, RIPK3
Regulated Necrosis	0.002	15	5	2.830E-04	1.260E-02	FAS, TNFSF10, CASP8, BIRC3, RIPK3
Interleukin-1 signaling	0.006	44	8	2.930E-04	1.260E-02	IL1R2, IL1R1, IL1RN, IL1B, IL1A, MYD88, IRAK4, IRAK3
Antagonism of Activin by Follistatin	0.001	4	3	4.940E-04	2.030E-02	FSTL3, INHBB, INHBA
Toll-Like Receptors Cascades	0.019	132	14	5.340E-04	2.030E-02	BTk, JUN, CASP8, MYD88, LY86, BIRC3, CD14, TLR2, TLR7, RIPK3, ITGB2, IRAK4, IRAK3, CTSS
Other semaphorin interactions	0.003	19	5	8.170E-04	2.800E-02	CD72, SEMA5A, TYROBP, SEMA4A, PTPRC
Platelet degranulation	0.011	78	10	8.240E-04	2.800E-02	SERPINE1, SERPING1, TGFB2, TIMP1, FGG, TF, PLEK, PDGFA, CLU, PROS1
Interferon alpha/beta signaling	0.009	66	9	9.740E-04	3.120E-02	ISG20, IFITM3, OASL, SOCS3, PSMB8, EGR1, IRF5, IRF8, IRF1
Response to elevated platelet cytosolic Ca ²⁺	0.012	83	10	1.310E-03	3.920E-02	SERPINE1, SERPING1, TGFB2, TIMP1, FGG, TF, PLEK, PDGFA, CLU, PROS1
Toll Like Receptor 4 (TLR4) Cascade	0.016	114	12	1.400E-03	3.950E-02	BTk, JUN, CASP8, MYD88, LY86, BIRC3, CD14, TLR2, RIPK3, ITGB2, IRAK4, IRAK3
Regulation of necroptotic cell death	0.002	13	4	1.560E-03	3.950E-02	FAS, TNFSF10, CASP8, BIRC3
CLEC7A/inflammasome pathway	0.001	6	3	1.580E-03	3.950E-02	IL1B, CASP8, PYCARD
Interleukin-1 processing	0.001	6	3	1.580E-03	3.950E-02	IL18, IL1B, CASP1
Interferon gamma signaling	0.010	74	9	2.110E-03	5.070E-02	B2M, CD44, OASL, ICAM1, FCGR1A, SOCS3, IRF5, IRF8, IRF1
Beta defensins	0.001	7	3	2.440E-03	5.290E-02	CCR6, CCR2, TLR2
Adaptive Immune System	0.086	609	37	2.450E-03	5.290E-02	IGHM, BTk, B2M, NCF4, NFKBIE, PIK3AP1, C3, DAPP1, TRAC, VAV1, LCP2, CD4, CYBB, PVR, CD3G, CD74, TYROBP, FCGR3A, ICAM1, FCGR1A, FYB, FCGR2B, PDGFA, ITGAL, BLK, ITGB2, ITGB7, PSMB8, PSMB9, CTSS, NCR1, CD86, CTSD, PSMB10, RASGRP3, TAP1, PTPRC
Antigen processing-Cross presentation	0.011	76	9	2.520E-03	5.290E-02	B2M, NCF4, CYBB, FCGR1A, PSMB8, PSMB9, CTSS, PSMB10, TAP1

Defensins	0.002	15	4	2.600E-03	5.470E-02	CD4, CCR6, CCR2, TLR2
Interleukin-6 family signaling	0.004	26	5	3.180E-03	6.170E-02	OSMR, IL6R, IL12A, CLCF1, SOCS3
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) pathways	0.005	38	6	3.330E-03	6.170E-02	NLRC4, CASP8, CASP1, CARD9, PSTPIP1, PYCARD
Integrin cell surface interactions	0.009	65	8	3.430E-03	6.170E-02	SPP1, FGG, CD44, DAG1, ICAM1, ITGAL, ITGB2, ITGB7
Semaphorin interactions	0.009	65	8	3.430E-03	6.170E-02	RAC2, DPYSL4, RND1, CD72, SEMA5A, TYROBP, SEMA4A, PTPRC
TNFR2 non-canonical NF-kB pathway	0.014	96	10	3.680E-03	6.420E-02	TNFRSF12A, TNFSF13B, CD70, BIRC3, PSMB8, PSMB9, LTB, PSMB10, TNFRSF1A, TNFRSF1B
Collagen degradation	0.006	39	6	3.780E-03	6.420E-02	MMP19, MMP12, MMP10, MMP7, MMP3, CTSD
Inflammasomes	0.002	17	4	4.060E-03	6.490E-02	NLRC4, CASP1, PSTPIP1, PYCARD
Ligand-dependent caspase activation	0.002	17	4	4.060E-03	6.490E-02	FAS, TNFSF10, CASP8, CD14
TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway	0.002	17	4	4.060E-03	6.490E-02	TNFRSF12A, TNFSF13B, BIRC3, LTB
The AIM2 inflammasome	0.000	3	2	5.830E-03	8.740E-02	CASP1, PYCARD
Death Receptor Signalling	0.006	43	6	6.010E-03	9.010E-02	FAS, TRAF1, TNFSF10, CASP8, BIRC3, TNFRSF1A
Interferon Signaling	0.025	174	14	6.480E-03	9.170E-02	B2M, ISG20, IFITM3, CD44, OASL, ICAM1, FCGR1A, SOCS3, PSMB8, EGR1, KPNA4, IRF5, IRF8, IRF1
TRIF-mediated programmed cell death	0.001	10	3	6.550E-03	9.170E-02	CASP8, CD14, RIPK3
Activated TLR4 signalling	0.015	107	10	7.670E-03	1.018E-01	BTK, JUN, CASP8, MYD88, BIRC3, CD14, TLR2, RIPK3, IRAK4, IRAK3
Class I MHC mediated antigen processing & presentation	0.013	91	9	7.920E-03	1.018E-01	B2M, NCF4, CYBB, FCGR1A, PSMB8, PSMB9, CTSS, PSMB10, TAP1
TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling	0.002	11	3	8.490E-03	1.018E-01	MYD88, TLR7, IRAK4
Regulation by c-FLIP	0.002	11	3	8.490E-03	1.018E-01	FAS, TNFSF10, CASP8
CASP8 activity is inhibited	0.002	11	3	8.490E-03	1.018E-01	FAS, TNFSF10, CASP8

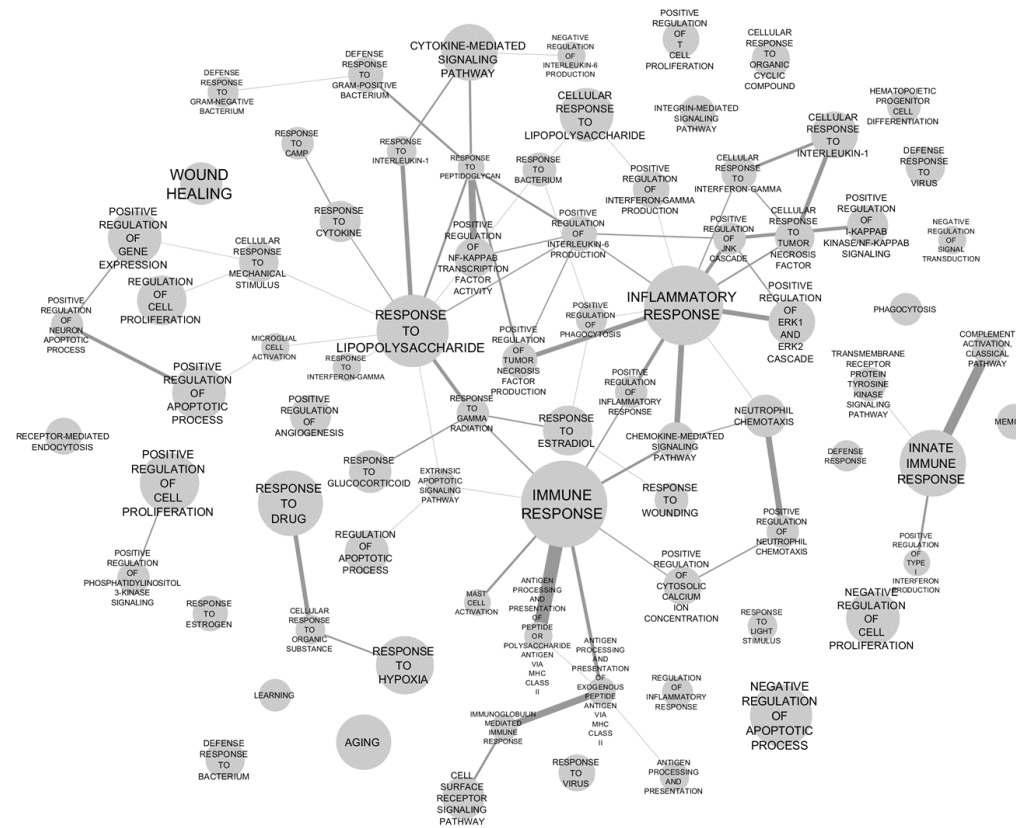
Dimerization of procaspase-8	0.002	11	3	8.490E-03	1.018E-01	FAS, TNFSF10, CASP8
The NLRP3 inflammasome	0.002	12	3	1.070E-02	1.287E-01	CASP1, PSTPIP1, PYCARD
P2Y receptors	0.002	12	3	1.070E-02	1.287E-01	P2RY12, P2RY13, P2RY6
GPVI-mediated activation cascade	0.007	49	6	1.100E-02	1.315E-01	RAC2, VAV1, LCP2, FCER1G, PIK3R5, IL2RB
RHO GTPases Activate NADPH Oxidases	0.002	13	3	1.330E-02	1.460E-01	NCF4, RAC2, CYBB
Signaling by Activin	0.002	13	3	1.330E-02	1.460E-01	FSTL3, INHBB, INHBA
Generation of second messenger molecules	0.005	38	5	1.480E-02	1.507E-01	TRAC, LCP2, CD4, CD3G, FYB
Caspase activation via extrinsic apoptotic signalig pathway	0.004	25	4	1.510E-02	1.507E-01	FAS, TNFSF10, CASP8, CD14
TNFs bind their physiological receptors	0.004	25	4	1.510E-02	1.507E-01	TNFSF13B, CD70, TNFRSF1A, TNFRSF1B
Tachykinin receptors bind tachykinins	0.001	5	2	1.540E-02	1.541E-01	TAC3, TACR3
FasL/ CD95L signaling	0.001	5	2	1.540E-02	1.541E-01	FAS, CASP8
Regulation of TNFR1 signaling	0.004	26	4	1.710E-02	1.714E-01	TRAF1, CASP8, BIRC3, TNFRSF1A
Activation of Matrix Metalloproteinases	0.004	27	4	1.940E-02	1.937E-01	MMP10, TIMP1, MMP7, MMP3
Activation of C3 and C5	0.001	6	2	2.170E-02	1.960E-01	C4A, C3
Phosphorylation of CD3 and TCR zeta chains	0.004	28	4	2.180E-02	1.960E-01	TRAC, CD4, CD3G, PTPRC
Nucleotide-like (purinergic) receptors	0.002	16	3	2.280E-02	2.053E-01	P2RY12, P2RY13, P2RY6
Purine catabolism	0.001	7	2	2.880E-02	2.590E-01	GDA, XDH
Organic cation transport	0.001	7	2	2.880E-02	2.590E-01	SLC22A5, RUNX1
TRAIL signaling	0.001	7	2	2.880E-02	2.590E-01	TNFSF10, CASP8

Metal ion SLC transporters	0.003	18	3	3.080E-02	2.770E-01	CP, SLC41A2, SLC11A1
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	0.005	32	4	3.320E-02	2.820E-01	SERPINE1, MYC, CDKN2B, JUNB
IL-6-type cytokine receptor ligand interactions	0.003	19	3	3.520E-02	2.820E-01	OSMR, IL12A, CLCF1
Scavenging by Class A Receptors	0.003	19	3	3.520E-02	2.820E-01	MASP1, COLEC12, MSR1
Cell surface interactions at the vascular wall	0.014	100	8	3.610E-02	2.885E-01	ANGPT1, ANGPT2, CD44, CD74, FCER1G, ITGAL, ITGB2, PROS1
Cross-presentation of particulate exogenous antigens (phagosomes)	0.001	8	2	3.670E-02	2.935E-01	NCF4, CYBB
Organic cation/anion/zwitterion transport	0.001	8	2	3.670E-02	2.935E-01	SLC22A5, RUNX1
Progressive trimming of alpha-1,2-linked mannose residues from Man9/8/7GlcNAc2	0.000	1	1	3.670E-02	2.937E-01	MAN1A1
C-type lectin receptors (CLRs)	0.017	119	9	3.670E-02	2.938E-01	IL1B, CASP8, CLEC4D, FCER1G, CARD9, PSMB8, PSMB9, PSMB10, PYCARD
TCR signaling	0.017	120	9	3.840E-02	3.070E-01	TRAC, LCP2, CD4, CD3G, FYB, PSMB8, PSMB9, PSMB10, PTPRC
TNFR1-induced NFkappaB signaling pathway	0.003	21	3	4.510E-02	3.089E-01	TRAF1, BIRC3, TNFRSF1A
IKK complex recruitment mediated by RIP1	0.003	21	3	4.510E-02	3.089E-01	BIRC3, CD14, RIPK3
Dectin-2 family	0.001	9	2	4.530E-02	3.089E-01	CLEC4D, FCER1G
TNFR1-induced proapoptotic signaling	0.001	9	2	4.530E-02	3.089E-01	CASP8, TNFRSF1A
Endosomal/Vacuolar pathway	0.001	9	2	4.530E-02	3.089E-01	B2M, CTSS
Toll Like Receptor TLR6:TLR2 Cascade	0.012	87	7	4.690E-02	3.089E-01	BTK, JUN, MYD88, CD14, TLR2, IRAK4, IRAK3
MyD88:Mal cascade initiated on plasma membrane	0.012	87	7	4.690E-02	3.089E-01	BTK, JUN, MYD88, CD14, TLR2, IRAK4, IRAK3
Toll Like Receptor 2 (TLR2) Cascade	0.012	87	7	4.690E-02	3.089E-01	BTK, JUN, MYD88, CD14, TLR2, IRAK4, IRAK3
Toll Like Receptor TLR1:TLR2 Cascade	0.012	87	7	4.690E-02	3.089E-01	BTK, JUN, MYD88, CD14, TLR2, IRAK4, IRAK3

TNF signaling	0.005	36	4	4.740E-02	3.089E-01	TRAF1, CASP8, BIRC3, TNFRSF1A
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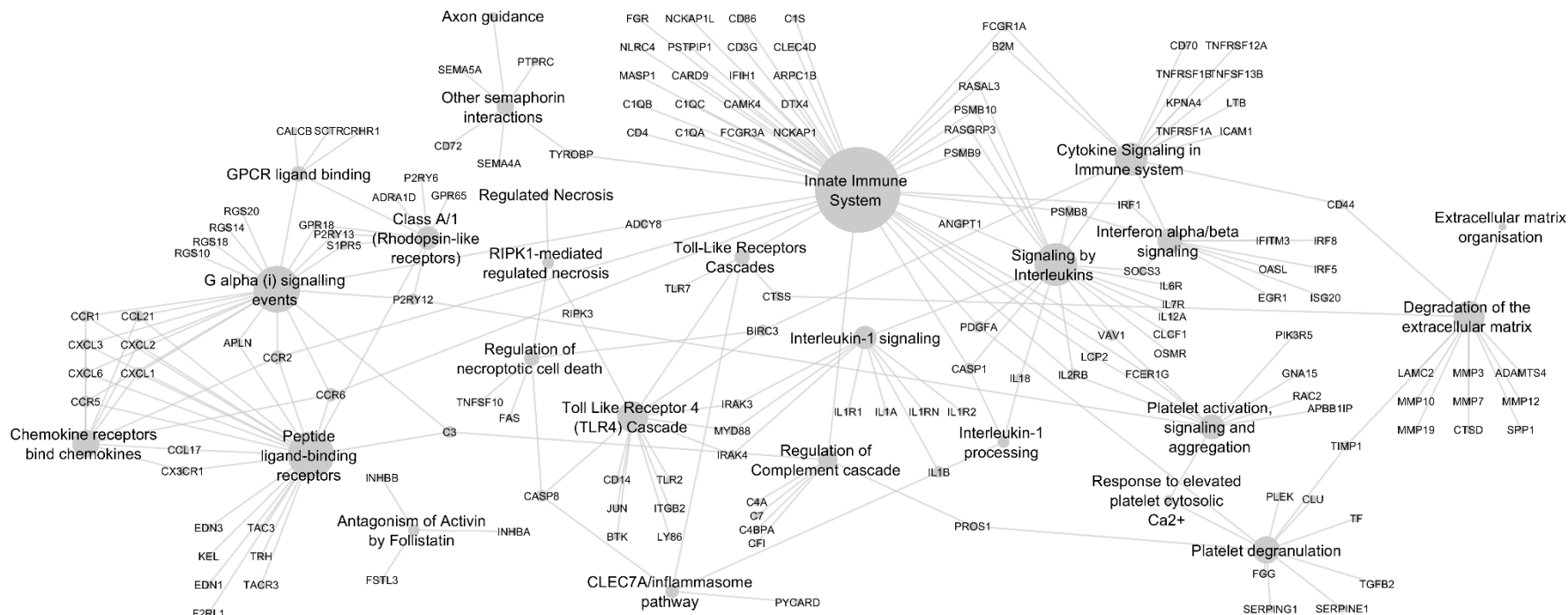
Supplemental table 5. List of pathways based on Reactome database showing significant alteration in the kidney of newborn rats underwent UUO compared to those of sham-operated. Abbreviations used in the letterhead of the supplemental Table 5.: p-p value calculated with Fisher's exact test; FDR-Multiple test correction controlled with the Bonferroni-Hochberg method

Supplemental figure 1.



Supplemental figure 1. Visualization of the gene ontology (GO) terms in the biological function domain showing significant alteration in the kidney of newborn rats underwent UUO compared to those of sham-operated controls. The main representative GO terms are shown as grey circles. The diameter of the circles or the width of the links is proportional with the number of the altered genes or the overlap between GO terms, respectively.

Supplemental figure 2.



Supplemental figure 2. Network representation of the Reactome database-derived pathway involvements of differentially expressed molecules in the kidney of newborn rats following unilateral ureteral obstruction. The diameter of the circles is proportional with the number of the proteins mapped to pathways.