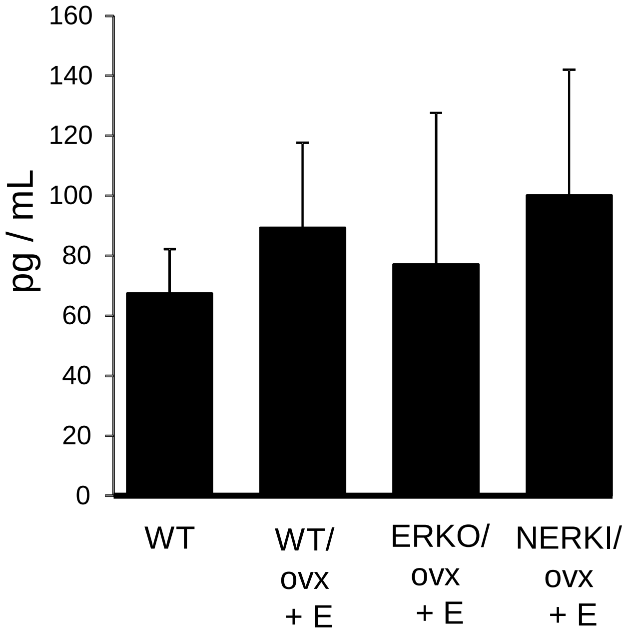
Supplemental Figure 1



Supplemental Figure 1. Serum estradiol levels measured in a subset (n = 7-8 per group) of the experimental mice relative to WT control mice. Data are mean SEM.

Supplemental Table 1: Complete microarray dataset for genes commonly regulated in ERKO and NERKI bones (both relative to wildtype; WT). The p-value (p-val), q-value (q-val) and fold change (FC) are indicated along with the available information on description of the transcript with the RefSeq ID (when available).

			ERKO vs WT			**NERKI vs WT**		
Gene Symbol	**Description**	**RefSeq ID**	**FC**	**p-val**	**q-val**	**FC**	**p-val**	**q-val**
1500015O10Rik	RIKEN cDNA 1500015O10 gene	NM_024283	1.86	0.0208	0.08245	2.89	0.001	0.0459
2010007H06Rik	RIKEN cDNA 2010007H06 gene		1.80	0.0011	0.01974	1.66	0.0042	0.084
2510008P16Rik			-1.87	0.0018	0.02523	-1.78	0.0046	0.0876
2510042H12Rik	RIKEN cDNA 2510042H12 gene		1.57	0.0022	0.02797	1.78	0.0005	0.0379
4833424O15Rik	RIKEN cDNA 4833424O15 gene	NM_029425	-3.27	0.0000	0.00286	-3.32	0	0.0093
4933404M02Rik	RIKEN cDNA 4933404M02 gene	NM_025744	2.81	0.0045	0.03901	2.86	0.0055	0.0961
4933411D12Rik	RIKEN cDNA 4933411D12 gene		1.61	0.0002	0.00992	1.65	0.0002	0.0267
5430406J06Rik	RIKEN cDNA 5430406J06 gene		1.95	0.0022	0.02799	1.87	0.0048	0.0897
5430417J04Rik			-2.85	0.0018	0.02523	-2.78	0.0031	0.0713
5430435G22Rik	RIKEN cDNA 5430435G22 gene		-1.56	0.0000	0.00355	-1.66	0	0.0065
A130047F11Rik			1.62	0.0045	0.03902	1.79	0.0017	0.0584
A430070A22Rik			1.56	0.0062	0.04539	1.60	0.0062	0.0997
A530024C08Rik			1.58	0.0024	0.02914	1.52	0.0062	0.0997
A630034E16Rik			1.58	0.0004	0.0136	1.70	0.0002	0.025
A630098G22Rik			-1.59	0.0011	0.01988	-1.64	0.001	0.0463
A830055I09Rik			1.75	0.0001	0.00801	1.70	0.0003	0.0308
A930004J17Rik	RIKEN cDNA A930004J17 gene		2.05	0.0002	0.01056	1.74	0.0027	0.0682
Adss	Adenylosuccinate synthetase, non muscle	NM_007422	-2.07	0.0016	0.0242	-2.07	0.0024	0.065
Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	NM_145542	-1.53	0.0000	0.00464	-1.58	0	0.0106
AI607873	Expressed sequence AI607873		-2.10	0.0005	0.01378	-1.88	0.0023	0.0637
AK157302	CDNA sequence AK157302		-1.97	0.0005	0.01475	-1.85	0.0018	0.0595
Aldh1a2	Aldehyde dehydrogenase family 1, subfamily A2	NM_009022	-2.28	0.0000	0.00193	-2.16	0	0.0087
Alox15	Arachidonate 15-lipoxygenase	NM_009660	1.65	0.0000	0.00257	1.51	0.0001	0.0187
Ambp	Alpha 1 microglobulin/bikunin	NM_007443	-1.98	0.0026	0.02972	-2.07	0.0024	0.065
Angpt4	Angiopoietin 4	NM_009641	-2.12	0.0003	0.01183	-2.10	0.0006	0.0381
Atp6a1	ATPase, H+ transporting, lysosomal V1 subunit A	NM_001690	-1.85	0.0002	0.00986	-1.71	0.001	0.0463
B130064I06Rik			1.55	0.0009	0.01877	1.58	0.001	0.0459
B230208H17Rik	RIKEN cDNA B230208H17 gene	NM_001024616	1.58	0.0007	0.01622	1.60	0.0008	0.0438

B930036M14Rik			1.59	0.0024	0.02901	1.60	0.003	0.0711
Bach2	BTB and CNC homology 2	NM_001109661	3.54	0.0000	0.00242	2.68	0.0001	0.0216
Blk	B lymphoid kinase	NM_007549	1.89	0.0000	0.00468	1.54	0.0014	0.0514
C330006D17Rik	RIKEN cDNA C330006D17 gene		1.55	0.0009	0.01844	1.50	0.0023	0.0637
C330021F23Rik	RIKEN cDNA C330021F23 gene	NM_001024728	2.63	0.0009	0.01794	2.61	0.0014	0.0515
C430014G13Rik			2.11	0.0000	0.00227	2.24	0	0.0048
C4a	complement component 4A (Rodgers blood group)	NM_011413	-1.85	0.0001	0.00642	-1.67	0.0005	0.0381
C730026O12Rik			1.70	0.0039	0.03644	1.70	0.0055	0.096
Capn2	Calpain 2	NM_009794	-1.94	0.0002	0.00908	-1.68	0.0018	0.0595
Capza1	Capping protein (actin filament) muscle Z-line, alpha 1	NM_009797	-1.88	0.0005	0.01446	-1.71	0.0024	0.0653
Casq1	Calsequestrin 1	NM_009813	-1.74	0.0001	0.00771	-1.61	0.0007	0.0405
Ccdc3	Coiled-coil domain containing 3	NM_028804	2.17	0.0017	0.02512	2.75	0.0003	0.0308
Cd19	CD19 antigen	NM_009844	1.99	0.0000	0.00193	1.65	0.0001	0.0202
Cd300lg	CD300 antigen like family member G	NM_001160711	1.58	0.0031	0.0329	1.57	0.0046	0.0878
Cd72	CD72 antigen	NM_001110320	2.00	0.0000	0.00401	1.87	0.0001	0.0187
Ch25h	Cholesterol 25-hydroxylase	NM_009890	-1.58	0.0002	0.00895	-1.56	0.0003	0.0308
Chst3	Carbohydrate (chondroitin 6/keratan) sulfotransferase 3		2.11	0.0000	0.0048	1.68	0.0013	0.0508
Col2a1	Collagen, type II, alpha 1	NM_001113515	-3.96	0.0001	0.00649	-4.02	0.0001	0.0193
Col8a1	Collagen, type VIII, alpha 1	NM_007739	-3.93	0.0000	0.00435	-3.23	0.0002	0.0236
Cpa3	Carboxypeptidase A3, mast cell	NM_007753	1.58	0.0001	0.00607	1.65	0	0.0132
Cpm	Carboxypeptidase M	NM_027468	2.35	0.0001	0.00642	1.88	0.0014	0.052
Csf1r	Colony stimulating factor 1 receptor	NM_001037859	-2.08	0.0002	0.00918	-1.90	0.0008	0.0436
Cyp2e1	Cytochrome P450, family 2, subfamily e, polypeptide 1	NM_021282	-2.55	0.0018	0.02519	-2.65	0.0019	0.0612
D030069G17Rik			1.62	0.0022	0.02774	1.58	0.0043	0.0853
D130032J17Rik			2.13	0.0032	0.03329	2.08	0.0056	0.0966
D230047F17Rik			1.95	0.0001	0.00607	1.80	0.0003	0.0304
D6Mit97	DNA segment, Chr 6, Massachusetts Institute of Technology 97		-3.05	0.0007	0.01665	-2.65	0.0029	0.0693
Dnm3os	Dynamin 3, opposite strand		1.75	0.0028	0.03108	1.86	0.0019	0.0621
E330018D03Rik	RIKEN cDNA E330018D03 gene		1.53	0.0012	0.02108	1.62	0.0006	0.0392

E330019D12Rik			1.53	0.0073	0.04894	1.71	0.0021	0.0629
Ear10	Eosinophil-associated, ribonuclease A family, member 10	NM_053112	2.86	0.0003	0.01059	2.54	0.001	0.0463
Ear12	Eosinophil-associated, ribonuclease A family, member 12	NM_001012766	3.04	0.0005	0.01441	2.57	0.0025	0.0661
Ear2	Eosinophil-associated, ribonuclease A family, member 2	NM_007895	4.02	0.0007	0.01652	3.44	0.0025	0.0655
Ear3		NM_017388	3.33	0.0002	0.00959	3.01	0.0006	0.039
Ear6	Eosinophil-associated, ribonuclease A family, member 6	NM_053111	5.23	0.0018	0.02548	4.42	0.0053	0.0943
Eef2	Eukaryotic translation elongation factor 2	NM_007907	-1.99	0.0023	0.02841	-1.94	0.0042	0.0831
Epx	Eosinophil peroxidase	NM_007946	4.00	0.0009	0.01877	3.35	0.0036	0.0779
Evx1	Even skipped homeotic gene 1 homolog	NM_007966	-1.57	0.0001	0.00649	-1.51	0.0003	0.0304
F730045P10Rik			2.07	0.0000	0.00033	1.53	0.0001	0.0151
F830002E14Rik			-2.56	0.0002	0.00892	-2.37	0.0005	0.0376
Fcrls		NM_030707	-4.31	0.0000	0.00197	-3.45	0	0.0124
Fn1	Fibronectin 1	NM_010233	-2.49	0.0003	0.01059	-2.38	0.0006	0.0389
Gdf3	Growth differentiation factor 3	NM_008108	-2.47	0.0000	0.00197	-2.58	0	0.0048
Gdpd2	Glycerophosphodiester phosphodiesterase domain containing 2	NM_023608	-2.36	0.0001	0.00744	-2.05	0.0007	0.0414
Gpr88	G-protein coupled receptor 88	NM_022427	1.94	0.0000	0.00401	1.73	0.0002	0.0248
Greb1	Gene regulated by estrogen in breast cancer protein	NM_001252071	-2.02	0.0000	0.00193	-2.09	0	0.0048
Grn	Granulin	NM_008175	-1.51	0.0001	0.00664	-1.51	0.0001	0.0202
Gsn	Gelsolin		-1.69	0.0001	0.00771	-1.75	0.0001	0.0193
Hnrpk	Heterogeneous nuclear ribonucleoprotein K		-1.61	0.0020	0.02637	-1.55	0.0046	0.088
Ibsp	Integrin binding sialoprotein	NM_008318	-3.33	0.0000	0.00359	-2.79	0.0001	0.0203
Id4	Inhibitor of DNA binding 4	NM_031166	-1.51	0.0010	0.01902	-1.54	0.001	0.0459
IGHV10S3_AF064446_Ig_heavy_variable_10S3_9			-2.88	0.0008	0.01752	-3.14	0.0007	0.0398
Igh-V11	Immunoglobulin heavy chain (V11 family)		-2.17	0.0002	0.00998	-1.92	0.0013	0.0508
IGHV12S1_M22439_Ig_heavy_variable_12S1_339			-2.03	0.0003	0.01059	-1.86	0.0011	0.0481
IGHV1S119_L33961_Ig_heavy_variable_1S119_14			-4.04	0.0002	0.00892	-3.66	0.0005	0.0376

IGHV1S120_AF025443_Ig_heavy_variable_1S120_8			-4.72	0.0005	0.0139	-4.89	0.0006	0.0389
IGHV1S124_AF025449_Ig_heavy_variable_1S124_11			-2.68	0.0025	0.0295	-2.82	0.0026	0.0662
IGHV1S135_AF304556_Ig_heavy_variable_1S135_43			-2.00	0.0023	0.02841	-2.06	0.0024	0.0653
IGHV1S14_K00707$X00161_Ig_heavy_variable_1S14_164			-1.69	0.0000	0.00401	-1.69	0	0.0123
IGHV1S28_X02460_Ig_heavy_variable_1S28_13			-2.78	0.0004	0.0126	-2.52	0.0013	0.0508
IGHV1S30_X02462_Ig_heavy_variable_1S30_12			-2.63	0.0000	0.00489	-2.92	0	0.0106
IGHV1S31_X02463_Ig_heavy_variable_1S31_40			-2.52	0.0003	0.01068	-2.62	0.0003	0.0304
IGHV1S34_X02467_Ig_heavy_variable_1S34_71			-2.36	0.0002	0.00986	-2.19	0.0007	0.0405
IGHV1S35_M12376_Ig_heavy_variable_1S35_13			-4.39	0.0008	0.01739	-4.80	0.0008	0.0422
IGHV1S36_M13788_Ig_heavy_variable_1S36_40			-3.90	0.0005	0.01406	-4.27	0.0004	0.0374
IGHV1S59_L17134_Ig_heavy_variable_1S59_150			-1.55	0.0013	0.02227	-1.51	0.0031	0.0714
IGHV5S18_AF290972_Ig_heavy_variable_5S18_125			-1.61	0.0017	0.02454	-1.62	0.0022	0.0637
IGHV8S6_U23021_Ig_heavy_variable_8S6_61			-3.34	0.0002	0.01056	-3.23	0.0005	0.0376
IGHV8S7_U23022_Ig_heavy_variable_8S7_163			-4.58	0.0001	0.0083	-3.81	0.0006	0.0398
IGKV2-137_AJ231263_Ig_kappa_variable_2-137_15			-3.66	0.0003	0.01141	-3.59	0.0005	0.0379
IGKV9-120_V00804$J00566_Ig_kappa_variable_9-120_12			-2.83	0.0161	0.07265	-4.22	0.0031	0.0725
Il8ra	Interleukin 8 receptor, alpha		-1.86	0.0001	0.00642	-1.89	0.0001	0.0187
Irf4	Interferon regulatory factor 4	NM_013674	2.00	0.0000	0.00278	1.56	0.0009	0.0443
Irx3	Iroquois related homeobox 3 (Drosophila)	NM_001253822	-1.75	0.0019	0.02573	-1.94	0.0008	0.043
Itm2a	Integral membrane protein 2A	NM_008409	-1.80	0.0006	0.01521	-1.72	0.0016	0.056
Jakmip1	Janus kinase and microtubule interacting protein 1	NM_178394	2.21	0.0000	0.00563	1.60	0.0049	0.0899
Kcnc4	Potassium voltage gated channel, Shaw-related subfamily, member 4		2.01	0.0119	0.06146	2.65	0.0021	0.0629
Kcnk1	Potassium channel, subfamily K, member 1	NM_008430	-1.86	0.0050	0.04117	-1.95	0.0043	0.085

Kng1	Kininogen 1	NM_001102411	-2.10	0.0003	0.01177	-1.79	0.003	0.0713
Kpna2	Karyopherin (importin) alpha 2	NM_010655	-2.01	0.0007	0.01626	-1.89	0.002	0.0622
Lgi2	Leucine-rich repeat LGI family, member 2	NM_144945	-1.87	0.0003	0.01156	-1.85	0.0005	0.0381
Lifr	Leukemia inhibitory factor receptor	NM_001113386	-1.94	0.0001	0.00763	-1.77	0.0006	0.039
Limch1	LIM and calponin homology domains 1	NM_001001980	1.91	0.0003	0.01185	1.65	0.0034	0.0756
LOC100043991	similar to Immunogloblin heavy chain		-1.70	0.0028	0.03101	-1.73	0.0032	0.073
LOC100044696	similar to cysteine-rich PAK1inhibitor		-1.73	0.0038	0.03557	-1.73	0.0054	0.0951
LOC100046136	hypothetical protein LOC100046136		-1.64	0.0010	0.01947	-1.70	0.0008	0.0438
LOC100046275	ig heavy chain V-II region SESS-like		-2.09	0.0006	0.01569	-2.14	0.0007	0.0415
LOC100046320	similar to Matrin 3		-1.69	0.0006	0.01554	-1.63	0.0016	0.0562
LOC100046496	Ig kappa V-region 24B-like		-2.51	0.0008	0.01708	-2.49	0.0012	0.0497
LOC100046546	similar to IgM (kappa)light-chain		-1.75	0.0056	0.04324	-1.81	0.0052	0.0935
LOC100047012	similar to ubiquitin-conjugating enzyme UbcM2		-2.25	0.0013	0.02242	-2.04	0.0047	0.0886
LOC100047815	similar to CD79A antigen (immunoglobulin-associated alpha)		2.80	0.0001	0.00607	1.93	0.0035	0.0768
LOC100048461	similar to dendritic cell-associated C-type lectin-1; DECTIN-1		-1.52	0.0035	0.034	-1.52	0.0049	0.09
LOC100048770	Ig heavy chain V region 108A-like		-3.45	0.0001	0.0083	-3.80	0.0001	0.0193
LOC232067	similar to immunoglobulin light chain variable region		-4.40	0.0039	0.03617	-4.94	0.0033	0.0748
LOC331102	similar to 14-3-3 PROTEIN TAU (14-3-3 PROTEIN THETA)		-2.92	0.0008	0.01739	-2.83	0.0015	0.0537
LOC380799	similar to Igh-VJ558 protein		-3.16	0.0004	0.0136	-2.87	0.0013	0.0508
LOC380801	similar to VH283 protein		-1.74	0.0012	0.02168	-1.69	0.0026	0.0662
LOC380805	similar to idiotypic anti-NP IgG(1) heavy chain V-D-J		-2.58	0.0032	0.03329	-2.83	0.0025	0.0653
LOC380862			2.25	0.0015	0.02318	2.60	0.0006	0.0392
LOC381285			-1.81	0.0005	0.01468	-1.71	0.0017	0.0574
LOC381739	hypothetical LOC381739		1.84	0.0010	0.01942	1.66	0.0051	0.093
LOC384538	similar to serine/threonine kinase AIE1		3.04	0.0002	0.00998	3.05	0.0003	0.0317
LOC544904	similar to Ig heavy chain V region 186-1 precursor		-2.94	0.0019	0.02585	-3.36	0.0012	0.0496
LOC630242	similar to Ig heavy chain V region MC101 precursor		-2.08	0.0008	0.01736	-2.06	0.0013	0.0508
LOC630284	similar to Ig heavy chain V region 5-84 precursor		-1.82	0.0003	0.01117	-1.75	0.0008	0.0429

LOC630337	similar to Ig heavy chain V region 1B43 precursor		-3.37	0.0000	0.00519	-3.30	0.0001	0.0179
LOC637082	similar to Traf2 binding protein		1.84	0.0000	0.00401	1.57	0.0005	0.0379
LOC637337	ig heavy chain V-III region VH26-like		-2.30	0.0023	0.02817	-2.46	0.0019	0.061
LOC637785	Ig heavy chain V region 3-like		-5.41	0.0004	0.01316	-5.19	0.0008	0.0424
LOC669660	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein)		-2.20	0.0003	0.01059	-1.85	0.0025	0.0661
LOC674089	similar to Ig heavy chain V region 345 precursor		-1.54	0.0086	0.05277	-1.66	0.0042	0.084
LOC674094	similar to Ig heavy chain V region MC101 precursor		-1.66	0.0010	0.0196	-1.66	0.0015	0.0544
LOC674147	similar to Ig heavy chain V-I region HG3 precursor		-1.64	0.0018	0.02519	-1.59	0.0041	0.0821
LOC677369	hypothetical protein LOC677369		-6.57	0.0000	0.00132	-5.77	0	0.0048
LOC677648	Ig heavy chain V-II region SESS-like		-2.79	0.0001	0.00753	-2.91	0.0001	0.0195
Lpl	Lipoprotein lipase	NM_008509	1.84	0.0015	0.02362	1.71	0.005	0.0911
Lrp4	Low density lipoprotein receptor-related protein 4	NM_001145857	-1.57	0.0098	0.05592	-1.81	0.0024	0.065
Lrrc15	Leucine rich repeat containing 15	NM_028973	2.30	0.0251	0.08955	3.81	0.0021	0.0629
Ly6d	Lymphocyte antigen 6 complex, locus D	NM_010742	1.85	0.0004	0.01323	1.57	0.0058	0.0976
Mcpt8	Mast cell protease 8	NM_008572	2.01	0.0031	0.03259	2.55	0.0005	0.0376
Mdk	Midkine	NM_001012335	2.12	0.0001	0.00753	2.31	0.0001	0.017
Megf10	Multiple EGF-like-domains 10	NM_001001979	1.58	0.0050	0.0414	1.74	0.002	0.0623
Mgl1	Macrophage galactose N-acetyl-galactosamine specific lectin 1		-1.74	0.0044	0.03879	-1.95	0.0018	0.06
Mgl2	Macrophage galactose N-acetyl-galactosamine specific lectin 2	NM_145137	-3.18	0.0002	0.00959	-2.91	0.0006	0.0389
Mmd2	Monocyte to macrophage differentiation-associated 2	NM_175217	-1.81	0.0001	0.00649	-1.93	0.0001	0.0148
Mt3	Metallothionein 3	NM_013603	-1.88	0.0016	0.0241	-1.88	0.0022	0.0637
Mup1	Major urinary protein 1	NM_001163010	-3.91	0.0000	8.64E-06	-3.88	0	0
Mup2	Major urinary protein 2	NM_001045550	-11.83	0.0000	5.81E-06	-11.71	0	0
Myl4	Myosin, light polypeptide 4	NM_010858	3.06	0.0003	0.01185	2.63	0.0015	0.0547
Mylc2pl	Myosin light chain 2, precursor lymphocyte-specific		-3.77	0.0001	0.00602	-3.51	0.0002	0.0216
Ncoa4	Nuclear receptor coactivator 4	NM_001033988	-1.90	0.0034	0.03383	-1.89	0.005	0.0917

Oasl2	2'-5' oligoadenylate synthetase-like 2	NM_011854	-2.08	0.0000	0.00464	-1.57	0.0027	0.0676
Olfm4	Olfactomedin 4		-3.09	0.0051	0.04144	-3.32	0.0047	0.0883
Panx3	Pannexin 3	NM_172454	-5.48	0.0000	0.00242	-5.93	0	0.0074
Papd4	PAP associated domain containing 4	NM_133905	-1.62	0.0005	0.01406	-1.51	0.0023	0.0641
Pappa	Pregnancy-associated plasma protein A	NM_021362	1.76	0.0010	0.0196	1.71	0.0023	0.0637
Pdap1	PDGFA associated protein 1	NM_001033313	1.76	0.0002	0.00959	1.60	0.0014	0.052
Phospho1	Phosphatase, orphan 1	NM_153104	-1.96	0.0006	0.01554	-1.71	0.0045	0.0867
Ppp1cb	Protein phosphatase 1, catalytic subunit, beta isoform	NM_172707	-2.83	0.0012	0.02137	-2.39	0.0058	0.0974
Ppp1r12a	Protein phosphatase 1, regulatory (inhibitor) subunit 12A	NM_027892	1.51	0.0001	0.00642	1.52	0.0001	0.0193
Prss34	Protease, serine, 34	NM_178372	1.64	0.0144	0.06849	2.17	0.0011	0.0475
Psmb8	Proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	NM_010724	-3.26	0.0021	0.02694	-2.88	0.0061	0.0997
Rag1	Recombination activating gene 1	NM_009019	2.77	0.0000	0.00197	1.75	0.0016	0.0563
Ranbp3l	RAN binding protein 3-like	NM_198024	1.92	0.0003	0.01076	1.74	0.0015	0.0544
Rbbp7	Retinoblastoma binding protein 7		-2.06	0.0001	0.00602	-2.09	0.0001	0.0178
Rerg	RAS-like, estrogen-regulated, growth-inhibitor	NM_001164212	-1.87	0.0048	0.04005	-2.23	0.0012	0.0496
Saps1	SAPS domain family, member 1		1.56	0.0000	0.00181	1.65	0	0.003
scl0001487.1_50			-1.73	0.0004	0.01269	-1.78	0.0004	0.0357
scl0002547.1_9			1.55	0.0051	0.04164	1.61	0.0039	0.0816
scl0002975.1_346			2.20	0.0003	0.01059	2.32	0.0002	0.0274
scl0003476.1_2802			1.85	0.0000	0.00311	1.57	0.0004	0.0345
Sdc3	Syndecan 3	NM_011520	-1.52	0.0019	0.02548	-1.54	0.0023	0.0637
Serpinf1	Serine (or cysteine) peptidase inhibitor, clade F, member 1	NM_011340	1.90	0.0020	0.02665	1.94	0.0023	0.0637
Sfrp2	Secreted frizzled-related protein 2	NM_009144	-1.92	0.0014	0.02263	-2.07	0.0009	0.0448
Shox2	Short stature homeobox 2	NM_013665	-1.57	0.0005	0.01455	-1.55	0.0011	0.0471
Siglec1	Sialic acid binding Ig-like lectin 1, sialoadhesin	NM_011426	-1.61	0.0005	0.0139	-1.55	0.0013	0.0508
Siglecg	Sialic acid binding Ig-like lectin G	NM_172900	1.65	0.0008	0.01785	1.52	0.0044	0.0866
Sirpb1	Signal-regulatory protein beta 1		-1.61	0.0054	0.04286	-1.74	0.0026	0.067
Snx30	Sorting nexin family member 30	NM_172468	1.54	0.0036	0.03452	1.54	0.0049	0.0908
Socs2	Suppressor of cytokine signaling 2		-2.25	0.0000	0.0047	-1.87	0.0005	0.0379

Socs3	Suppressor of cytokine signaling 3	NM_007707	-1.69	0.0001	0.00757	-1.52	0.0011	0.0486
Sox4	SRY-box containing gene 4	NM_009238	2.14	0.0000	0.00538	1.84	0.0005	0.0376
Sox9	SRY-box containing gene 9	NM_011448	2.15	0.0007	0.01662	1.82	0.0058	0.0983
St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_001035228	1.57	0.0002	0.00858	1.65	0.0001	0.0187
Syngr2	Synaptogyrin 2	NM_009304	-2.06	0.0011	0.01988	-1.84	0.005	0.0916
Thbs1	Thrombospondin 1	NM_011580	-1.74	0.0009	0.01859	-1.69	0.0019	0.061
Tmed2	Transmembrane emp24 domain trafficking protein 2	NM_019770	-2.36	0.0001	0.00642	-2.26	0.0002	0.0236
Tmed7	Transmembrane emp24 protein transport domain containing 7	NM_025698	-1.80	0.0002	0.00895	-1.84	0.0002	0.0247
Tmem38b	Transmembrane protein 38B	NM_028053	-1.52	0.0052	0.04223	-1.61	0.003	0.0709
Tmem86a	Transmembrane protein 86A	NM_026436	-3.43	0.0000	0.00181	-3.09	0	0.0079
Tnfrsf1a	Tumor necrosis factor receptor superfamily, member 1a	NM_011609	-1.82	0.0013	0.02247	-1.70	0.0046	0.0875
Tpm3	Tropomyosin 3, gamma	NM_001253738	-2.49	0.0008	0.01762	-2.06	0.006	0.0992
Trpc6	Transient receptor potential cation channel, subfamily C, member 6	NM_013838	-1.57	0.0002	0.00983	-1.58	0.0003	0.0304
Tsc22d1	TSC22 domain family, member 1	NM_001177751	-3.85	0.0001	0.00649	-3.93	0.0001	0.0193
Tspan3	Tetraspanin 3	NM_019793	-2.27	0.0000	0.00341	-2.19	0	0.0131
Ube2v1	Ubiquitin-conjugating enzyme E2 variant 1	NM_023230	-1.74	0.0015	0.02348	-1.60	0.0059	0.099
Vit	Vitrin	NM_001197028	1.79	0.0009	0.01785	1.67	0.003	0.0713
Vpreb1	Pre-B lymphocyte gene 1	NM_016982	2.10	0.0002	0.0095	1.83	0.0015	0.0529
Vpreb3	Pre-B lymphocyte gene 3	NM_009514	3.91	0.0000	0.00128	2.77	0	0.012
Wisp2	WNT1 inducible signaling pathway protein 2	NM_016873	-4.36	0.0000	0.0011	-2.87	0	0.012
Zubr1			1.71	0.0005	0.01406	1.60	0.0019	0.061

Supplemental Table 2: Complete microarray dataset for genes regulated in NERKI bones (relative to wildtype; WT). The p-value (p-val), q-value (q-val) and fold change (FC) are indicated along with the available information on description of the transcript with the RefSeq ID (when available).

Illumina Search Key	Gene Symbol	Description	RefSeq ID	FC	p-val	q-val
ILMN_193252	0610037M15Rik			-2.24	0.0002	0.0267
ILMN_196382	1100001F19Rik			-2.28	0.0061	0.0997
ILMN_204598	1300006C19Rik			-1.72	0.0009	0.0451
ILMN_186408	2010001H16Rik	RIKEN cDNA 2010001H16 gene		-1.61	0.0021	0.0629
ILMN_218953	2310005G13Rik	RIKEN cDNA 2310005G13 gene	NM_183281	-1.81	0.0014	0.0523
ILMN_220011	2410019A14Rik	RIKEN cDNA 2410019A14 gene	NM_001081094	-1.51	0.002	0.0622
ILMN_201765	2500004H21Rik			1.52	0.0038	0.0807
ILMN_193245	4632427E13Rik	RIKEN cDNA 4632427E13 gene		1.52	0	0.012
ILMN_205813	4833425P12Rik			1.55	0.0001	0.0171
ILMN_189952	4930445K14Rik	RIKEN cDNA 4930445K14 gene		1.68	0.0001	0.0165
ILMN_220780	4930513E20Rik	RIKEN cDNA 4930513E20 gene		1.55	0.0038	0.0807
ILMN_184143	5530400B01Rik	RIKEN cDNA 5530400B01 gene		1.64	0.0033	0.0751
ILMN_218048	6430510M02Rik	RIKEN cDNA 6430510M02 gene	NM_176932	1.64	0.0005	0.0376
ILMN_204800	6430573H23Rik			1.73	0.0061	0.0997
ILMN_191889	8030474H12Rik	RIKEN cDNA 8030474H12 gene		1.50	0.0001	0.0193
ILMN_206918	A430096A09Rik			1.54	0.0001	0.0178
ILMN_222725	B230380D07Rik	RIKEN cDNA B230380D07 gene	NM_172772	1.68	0.0013	0.0508
ILMN_204740	B930037B01Rik			1.58	0.0038	0.0806
ILMN_212436	BC030863	cDNA sequence BC030863		1.50	0.0006	0.0384
ILMN_192092	C030002B11Rik	RIKEN cDNA C030002B11 gene		-1.51	0.0005	0.0381
ILMN_191384	C030014K22Rik	RIKEN cDNA C030014K22 gene	NM_175461	-1.92	0	0.0074
ILMN_210294	C130067A03Rik			1.57	0.0038	0.0807
ILMN_209356	Cldn10	Claudin 10	NM_021386 NM_023878	2.49	0.0002	0.0216
ILMN_188288	D030017L14Rik			1.56	0.0022	0.0632
ILMN_217188	D0H4S114	DNA segment, human D4S114	NM_001109988 NM_001109989 NM_001109990 NM_053078	2.05	0.0046	0.0876
ILMN_222493	D630048P19Rik			1.54	0	0.0048
ILMN_218073	Dpysl3	Dihydropyrimidinase-like 3	NM_009468	1.81	0.0016	0.0561
ILMN_223889	Drctnnb1a	Down-regulated by Ctnnb1, a	NM_053090	1.67	0.004	0.0818
ILMN_215523	Dusp8	Dual specificity phosphatase 8	NM_008748	1.61	0.0043	0.0842
ILMN_206779	E030007N04Rik			1.61	0.002	0.0623

ILMN_233946	EG434858			-3.47	0.0005	0.0376
ILMN_210527	EG633692			-2.44	0.0036	0.0779
ILMN_213378	Hoxa5	Homeo box A5	NM_010453	-1.55	0.0006	0.0381
ILMN_203312	HPBRII4			1.57	0.0003	0.0308
ILMN_184287	IGHV10S1_AF064442_Ig_heavy_variable_10S1_100			-1.67	0.0046	0.0879
ILMN_216381	Igk-V33	Immunoglobulin kappa chain variable 33 (V33)		-3.80	0.0021	0.0629
ILMN_186543	Igl-5			2.11	0.0004	0.0357
ILMN_186467	Igsf3	Immunoglobulin superfamily, member 3	NM_207205	1.84	0.0004	0.036
ILMN_211329	Kcnk2	Potassium channel, subfamily K, member 2	NM_010607	-1.60	0.0057	0.0971
ILMN_206227	LOC100041569			1.76	0.0018	0.059
ILMN_201525	LOC100046393	similar to Protein phosphatase 2, regulatory subunit B (B56), alpha		-1.82	0.0039	0.0816
ILMN_214618	LOC100046918	similar to Electron transferring flavoprotein, alpha polypeptide		-3.69	0.0054	0.0949
ILMN_223933	LOC100048556	similar to monocyte chemoattractant protein-5		-2.62	0	0.0093
ILMN_198435	LOC209281			-1.87	0.0028	0.0683
ILMN_218449	LOC238447			-4.59	0.0001	0.0187
ILMN_198486	LOC269859			-1.80	0.0005	0.0376
ILMN_215850	LOC333331			-1.65	0.0001	0.0193
ILMN_198427	LOC381219	hypothetical LOC381219		1.53	0.0018	0.059
ILMN_211083	LOC383196			-3.40	0.002	0.0623
ILMN_199705	LOC383850			1.55	0.003	0.0707
ILMN_190076	LOC432709			-1.72	0.0003	0.0318
ILMN_200478	LOC545208			-3.15	0	0.0106
ILMN_234960	LOC620807			-3.81	0	0
ILMN_190903	LOC630347			-1.57	0.0035	0.0775
ILMN_196641	LOC632684	similar to La-related protein 4 (La ribonucleoprotein domain family member 4)		1.55	0.0025	0.0655
ILMN_193885	LOC640696	ig heavy chain V region 108A-like		-2.42	0.001	0.0464
ILMN_197393	LOC667005			-1.96	0.002	0.0622
ILMN_211990	LOC668549			-2.03	0.0005	0.0376
ILMN_212697	LOC675759	ig heavy chain V-III region J606-like		-1.95	0.0007	0.0398
ILMN_185836	LOC676974	glucose-6-phosphate isomerase-like		-1.53	0.0028	0.0691
ILMN_210701	LOC677643	ig heavy chain V region 3-like		-5.24	0.0011	0.0475
ILMN_212683	Matn4	Matrilin 4	NM_013592	1.53	0.0011	0.0475

ILMN_210134	Mgst3	Microsomal glutathione S-transferase 3	NM_025569	1.54	0.0017	0.0575
ILMN_211445	Mmp8	Matrix metallopeptidase 8	NM_008611	-1.54	0.0021	0.0629
ILMN_212438	Msr2	Macrophage scavenger receptor 2	NM_030707	-1.96	0.0001	0.0181
ILMN_212812	Nme7	Non-metastatic cells 7, protein expressed in	NM_138314 NM_178071	1.69	0.0016	0.0551
ILMN_205762	P38ip-pending			1.51	0.006	0.0992
ILMN_219297	Pnck	Pregnancy upregulated non-ubiquitously expressed CaM kinase	NM_012040.2	1.52	0.0008	0.0429
ILMN_198467	Prkg1	Protein kinase, cGMP-dependent, type I	NM_001013833 NM_011160	1.76	0.0026	0.0668
ILMN_218286	Slc25a39	Solute carrier family 25, member 39		1.52	0.0002	0.0247
ILMN_215945	Spon1	Spondin 1, (f-spondin) extracellular matrix protein	NM_145584	1.63	0.0034	0.076
ILMN_240633	Tnfsf12-tnfsf13			-1.50	0.0039	0.0812
ILMN_214163	Tprkb	Tp53rk binding protein	NM_176842	1.52	0	0.012
ILMN_229647	Whrn	Whirlin	NM_001008791 NM_001008792 NM_001008793 NM_001008794 NM_001008795 NM_001008796 NM_001008797 NM_001008798 NM_028640	-1.53	0.0029	0.0691

Supplemental Table 3: Complete microarray dataset for genes regulated in ERKO bones (relative to wildtype; WT). The p-value (p-val), q-value (q-val) and fold change (FC) are indicated along with the available information on description of the transcript with the RefSeq ID (when available).

Illumina Search Key	**Gene Symbol**	**Description**	**RefSeq ID**	**p-val**	**q-val**	**FC**
ILMN_184190	Ifi27	Interferon, alpha-inducible protein 27	NM_029803	0.012679	0.0636446	-1.73676
ILMN_205627	1190012C08Rik			0.0036069	0.0345365	1.56422
ILMN_219204	1700030K09Rik	RIKEN cDNA 1700030K09 gene	NM_028170	0.0291171	0.0960102	1.70061
ILMN_227745	1700109H08Rik	RIKEN cDNA 1700109H08 gene	NM_029843	0.0107516	0.0586125	1.59963
ILMN_222236	1810013D10Rik	RIKEN cDNA 1810013D10 gene	NM_001145433	0.009242	0.0547814	1.56463
ILMN_186537	2010004M13Rik	RIKEN cDNA 2010004M13 gene		0.0031851	0.0332701	1.56907
ILMN_218797	2310046A06Rik	RIKEN cDNA 2310046A06 gene	NM_027150	0.0313743	0.099409	-1.73735
ILMN_218359	2410076I21Rik	RIKEN cDNA 2410076I21 gene	NM_028598	0.006555	0.0465791	1.63672
ILMN_190342	2610319H10Rik	RIKEN cDNA 2610319H10 gene		0.0004926	0.014267	1.50889
ILMN_189076	2810455B08Rik	RIKEN cDNA 2810455B08 gene		0.0085831	0.0527602	1.57154
ILMN_203092	3830430K15Rik			0.0263576	0.0916207	-1.55569
ILMN_203114	4930418I18Rik			0.0277256	0.0939705	1.53416
ILMN_202319	4930426D05Rik	RIKEN cDNA 4930426D05 gene		2.49E-05	0.0041369	1.78712
ILMN_215095	4930519L02Rik	RIKEN cDNA 4930519L02 gene		0.0101958	0.0571315	1.66003
ILMN_195320	4930533K18Rik	RIKEN cDNA 4930533K18 gene		0.00033	0.011848	-2.01009
ILMN_216350	4931429I11Rik	RIKEN cDNA 4931429I11 gene	NM_001081121	2.52E-06	0.0018118	2.18495
ILMN_203384	4932410M19Rik			0.0018546	0.0254843	1.50257
ILMN_188842	5330403D14Rik	RIKEN cDNA 5330403D14 gene		0.0018677	0.0254843	1.81511
ILMN_189730	5430434G16Rik	RIKEN cDNA 5430434G16 gene		0.0029312	0.0317629	1.57386
ILMN_216779	5730437N04Rik			0.0257661	0.0907105	-2.31845
ILMN_188077	5830427D02Rik	RIKEN cDNA 5830427D02 gene		0.0045235	0.0390671	1.60803
ILMN_203520	5830496L11Rik			0.0073087	0.0488619	1.73518
ILMN_203009	5930437C20Rik			0.0068426	0.0474756	1.59986
ILMN_202862	6330403E01Rik			0.010802	0.0587953	1.56216
ILMN_187875	6330509M05Rik	RIKEN cDNA 6330509M05 gene		0.0020208	0.0264779	1.57028
ILMN_203250	6430407L02Rik			0.0085526	0.0526654	1.50496
ILMN_203479	6430524C05Rik			0.0074005	0.0492549	1.8238
ILMN_203481	6430562A12Rik			0.0125708	0.0634971	1.56794
ILMN_188686	6720418B01Rik	RIKEN cDNA 6720418B01 gene		0.0026314	0.0301413	1.63151
ILMN_207187	6820437F20Rik			0.0237232	0.0874567	1.79009
ILMN_192598	9430064K01Rik	RIKEN cDNA 9430064K01 gene		0.0012707	0.0219974	-1.50722
ILMN_204270	9530082I15Rik			0.0118628	0.061458	1.52081
ILMN_192234	9626100_15			0.0161123	0.0726478	1.94824
ILMN_187760	9626100_224			0.0143739	0.0684973	2.24942
ILMN_190851	9626958_317			0.0094874	0.0553312	2.30437
ILMN_205726	9830141J12Rik			0.0145432	0.0687223	1.50079

ILMN_205725	9830141K10Rik			0.0040695	0.0372276	1.56964
ILMN_202852	A130004B21Rik			0.0189474	0.0786791	1.5845
ILMN_204390	A130017C09Rik			0.003474	0.0340595	1.63862
ILMN_203926	A130020K16Rik			6.35E-06	0.0022133	1.74225
ILMN_203758	A130026C10Rik			0.0136743	0.0663767	1.56375
ILMN_195241	A130038J17Rik	RIKEN cDNA A130038J17 gene		0.0265862	0.0920786	1.67789
ILMN_204052	A130039H09Rik			0.0003665	0.0124013	1.56359
ILMN_202876	A130052C08Rik			0.001302	0.0222805	1.55515
ILMN_204872	A130096D14Rik			0.0256394	0.0904777	1.51851
ILMN_204870	A230021I18Rik			0.0159605	0.0722125	1.57127
ILMN_203950	A430090G16Rik			0.0007107	0.0165214	1.50733
ILMN_195915	A430106G13Rik	RIKEN cDNA A430106G13 gene		0.0015653	0.0239988	1.96229
ILMN_191455	A430110M15Rik	RIKEN cDNA A430110M15 gene		0.00201	0.0263693	1.5087
ILMN_205464	A530065H22Rik			0.0275738	0.0937254	-1.82274
ILMN_204063	A630072J24Rik			0.0168201	0.0740637	1.54018
ILMN_205576	A630076G18Rik			0.0069185	0.0476952	1.54721
ILMN_204025	A630097D09Rik			0.0097345	0.0558334	1.65423
ILMN_204301	A830091E24Rik			0.002458	0.0291721	1.64015
ILMN_204252	A830092P18Rik			0.0118175	0.0613829	1.53212
ILMN_254698	Acaa2	Acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	NM_177470	4.44E-05	0.0053797	-1.61961
ILMN_223620	Adfp	Adipose differentiation related protein		0.0304376	0.0978739	-1.54477
ILMN_223121	Adi1	Acireductone dioxygenase 1	NM_134052	0.0292083	0.0961254	-1.60234
ILMN_217418	Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	NM_026212	0.0128904	0.0641301	-2.3309
ILMN_221723	Ahi1	Abelson helper integration site		0.01119	0.0598173	1.5346
ILMN_206936	Akap12	A kinase (PRKA) anchor protein (gravin) 12	NM_031185	0.0024333	0.0291352	1.71485
ILMN_241430	Amica1	Adhesion molecule, interacts with CXADR antigen 1	NM_001005421	0.0039701	0.0367033	1.7058
ILMN_217348	Anp32b-ps1	Bacidic (leucine-rich) nuclear phosphoprotein 32 family, member B, pseudogene 1		0.0138254	0.0668324	-1.50953
ILMN_216245	Apod	Apolipoprotein D	NM_007470	0.0117389	0.0611851	-1.65459
ILMN_217368	Apoe	Apolipoprotein E	NM_009696	0.0052018	0.0421583	-1.75692
ILMN_216978	Arf5	ADP-ribosylation factor 5	NM_007480	0.0153492	0.0707321	-2.19208
ILMN_218774	Arl2bp	ADP-ribosylation factor-like 2 binding protein		0.0140907	0.0676768	-1.71794
ILMN_218211	Arl5a	ADP-ribosylation factor-like 5A	NM_182994	0.0112265	0.0599511	-1.86754
ILMN_218211	Arl5a	ADP-ribosylation factor-like 5A	NM_182994	0.0139207	0.0671688	-1.85682

ILMN_213701	Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	NM_022992	0.0300955	0.0974539	-1.72911
ILMN_214532	Arrdc4	Arrestin domain containing 4	NM_001042592	0.0024474	0.0291352	-1.87593
ILMN_218764	Asprv1	Aspartic peptidase, retroviral-like 1	NM_026414	0.0100646	0.0568081	-1.8922
ILMN_223681	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	NM_009721	0.0284981	0.0950482	1.77646
ILMN_201616	Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	NM_009725	0.0047242	0.0398677	-2.47675
ILMN_220358	Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	NM_025494	0.0088427	0.0535265	-1.73388
ILMN_222537	Atp6v1g1	ATPase, H+ transporting, lysosomal V1 subunit G1	NM_024173	0.0086101	0.052802	-2.14761
ILMN_204453	B130008O17Rik			0.008786	0.0534106	1.69604
ILMN_203212	B230205C01Rik			0.0133904	0.0654568	1.58862
ILMN_204511	B230337C21Rik			0.0037428	0.0355124	1.54717
ILMN_204524	B230363H02Rik			0.0070053	0.0477834	1.53702
ILMN_204535	B230386D16Rik			0.002831	0.0312901	1.5051
ILMN_204525	B230387C07Rik			0.0004013	0.0129302	1.66774
ILMN_216317	B3gat2	Beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)	NM_172124	0.0130716	0.0645005	-1.56506
ILMN_222923	B3gnt5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5		0.0045183	0.0390671	1.57699
ILMN_203218	B430109P06Rik			0.0063076	0.0459599	1.58822
ILMN_204550	B930008G03Rik			0.0234437	0.0870481	1.53951
ILMN_204753	B930044G13Rik			0.0221802	0.0845153	1.53132
ILMN_209456	BC005537	CDNA sequence BC005537	NM_024473	0.0041431	0.0375173	-1.74427
ILMN_215495	Bcl2a1b	B-cell leukemia/lymphoma 2 related protein A1b	NM_007534	0.0052434	0.0422709	-1.59717
ILMN_188537	Bcl7a	B-cell CLL/lymphoma 7A	NM_029850	6.08E-05	0.0060164	1.98408
ILMN_221165	Bfsp2	Beaded filament structural protein 2, phakinin		0.0006778	0.0163286	1.80557
ILMN_211373	Bst2	Bone marrow stromal cell antigen 2	NM_198095	0.0010072	0.0194656	-1.65596
ILMN_192205	C130045I22Rik			0.0243473	0.0883022	1.5021
ILMN_224197	C1qa	Complement component 1, q subcomponent, alpha polypeptide	NM_007572	0.0009383	0.018829	-1.7799
ILMN_211795	C1qb	Complement component 1, q subcomponent, beta polypeptide	NM_009777	0.009854	0.0560576	-1.83825
ILMN_219967	C1qc	Complement component 1, q subcomponent, C chain	NM_007574	0.0079182	0.050991	-1.96767
ILMN_217653	C230071H18Rik	RIKEN cDNA C230071H18 gene		0.0006659	0.016193	1.59701
ILMN_188891	C230075M21Rik	RIKEN cDNA C230075M21 gene		0.005423	0.0429078	1.85877
ILMN_206258	C230091E03Rik			0.0037038	0.035238	-2.2079
ILMN_196664	C330018D20Rik	RIKEN cDNA C330018D20 gene	NM_029909	0.006043	0.0448994	-1.54208

ILMN_205312	C430002D13Rik			0.0241213	0.0879095	1.68388
ILMN_218857	Calr	Calreticulin	NM_007591	0.0231077	0.0862922	-1.60834
ILMN_223956	Capns1	Calpain, small subunit 1	NM_009795	0.0227315	0.0853986	-2.72995
ILMN_223468	Capsl	Calcyphosine-like	NM_029341	2.22E-06	0.0018118	1.9268
ILMN_210229	Car2	Carbonic anhydrase 2	NM_009801	0.0042219	0.0378922	-2.51768
ILMN_212767	Car3	Carbonic anhydrase 3	NM_007606	0.0017507	0.0251929	-5.52297
ILMN_223809	Cbln1	Cerebellin 1 precursor protein	NM_019626	0.0186768	0.0778957	1.69095
ILMN_229007	Cbx3	Chromobox homolog 3 (Drosophila HP1 gamma)	NM_007624	0.0118542	0.0614514	-1.92653
ILMN_196616	Cc1			0.0013285	0.0224724	1.52277
ILMN_223933	Ccl12	Chemokine (C-C motif) ligand 12	NM_011331	2.51E-06	0.0018118	-3.00915
ILMN_216555	Ccna2	Cyclin A2	NM_009828	0.0011159	0.0204705	1.72099
ILMN_191206	Ccne2	Cyclin E2	NM_001037134	0.0232411	0.0866033	-1.64721
ILMN_221922	Cd14	CD14 antigen	NM_009841	4.15E-05	0.0051928	-1.8287
ILMN_218570	Cd3d	CD3 antigen, delta polypeptide	NM_013487	0.0039767	0.0367319	2.35807
ILMN_222081	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	NM_010581	0.0097472	0.0558756	1.50834
ILMN_210940	Cd79b	CD79B antigen	NM_008339	0.0025687	0.0297769	1.93807
ILMN_209396	Cdk4	Cyclin-dependent kinase 4	NM_009870	0.0045113	0.0390482	-1.81255
ILMN_219392	Cdkn1c	Cyclin-dependent kinase inhibitor 1C (P57)	NM_001161624	0.0098767	0.0560949	2.04581
ILMN_190329	Celf2		NM_001110228	0.0048737	0.0404436	1.79018
ILMN_213056	Cep152	Centrosomal protein 152	NM_001081091	0.0155064	0.0710184	1.58344
ILMN_216300	Cfl1	Cofilin 1, non-muscle	NM_007687	0.0021523	0.0274444	1.5604
ILMN_213309	Cgrrf1	Cell growth regulator with ring finger domain 1	NM_026832	0.0006103	0.015543	-1.52887
ILMN_218521	Chpt1	Choline phosphotransferase 1	NM_001146690	0.0054338	0.0429078	-1.51276
ILMN_217790	Ckap2	Cytoskeleton associated protein 2	NM_001004140	0.0056304	0.0435119	-1.83554
ILMN_210718	Clasp2	CLIP associating protein 2	NM_001081960	0.01048	0.0579782	1.53118
ILMN_210305	Clec4e	C-type lectin domain family 4, member e	NM_019948	0.0078498	0.0506651	-1.61456
ILMN_184708	Cnih	Cornichon homolog (Drosophila)	NM_009919	0.0074404	0.0493637	-2.096
ILMN_222860	Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	NM_001146318	0.0001304	0.0079094	1.59139
ILMN_208637	Cntn2	Contactin 2	NM_177129	0.0077642	0.0503299	2.66641
ILMN_223214	Col1a2	Collagen, type I, alpha 2	NM_007743	0.0240285	0.0877855	1.50061
ILMN_211069	Cox4i2	Cytochrome c oxidase subunit IV isoform 2	NM_053091	0.0065843	0.0466429	1.94053
ILMN_219945	Cplx2	Complexin 2	NM_009946	8.70E-05	0.0068415	1.69765
ILMN_218575	Cst7	Cystatin F (leukocystatin)	NM_009977	0.0010192	0.0195169	1.66776

ILMN_218498	Ctnnb1	Catenin (cadherin associated protein), beta 1	NM_001165902	0.0169637	0.0742709	1.56621
ILMN_189442	Cxcl16	Chemokine (C-X-C motif) ligand 16	NM_023158	0.0019059	0.0257336	-1.58712
ILMN_217785	Cxcr7	Chemokine (C-X-C motif) receptor 7	NM_007722	0.0087591	0.0533092	1.75431
ILMN_210012	Cyb5r4	Cytochrome b5 reductase 4	NM_024195	0.0262081	0.0913877	-2.18494
ILMN_218995	Cyp2f2	Cytochrome P450, family 2, subfamily f, polypeptide 2	NM_007817	0.0059897	0.0447213	1.77086
ILMN_205970	D130062J21Rik	RIKEN cDNA D130062J21 gene		0.0109531	0.0593397	1.66971
ILMN_204935	D230005E09Rik			0.0011845	0.0212429	1.95308
ILMN_206057	D330001D04Rik			0.0024421	0.0291352	1.56972
ILMN_206065	D330012P07Rik			0.0069366	0.0476952	1.82097
ILMN_206504	D630035D13Rik			0.0123909	0.0628877	1.73824
ILMN_203436	D730006F06Rik			0.0052811	0.042444	1.72567
ILMN_208662	D930015E06Rik	RIKEN cDNA D930015E06 gene	NM_172681	0.0017644	0.0251929	1.52389
ILMN_205388	D930049D10Rik			0.001293	0.0222004	1.60882
ILMN_218436	Ddit4l	DNA-damage-inducible transcript 4-like	NM_030143	0.0177171	0.0757754	2.12988
ILMN_216603	Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	NM_001040187	0.0008309	0.017623	1.54368
ILMN_195752	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	NM_172689	0.0032498	0.0332897	-1.57201
ILMN_218091	Depp			0.0211604	0.0829052	1.56581
ILMN_188868	Dgkg	Diacylglycerol kinase, gamma	NM_138650	0.0100495	0.0568081	1.65583
ILMN_214861	Dlg7	Discs, large homolog 7 (Drosophila)		0.0036868	0.0351402	1.53779
ILMN_188938	Dlst	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	NM_030225	0.0076556	0.0501236	1.75246
ILMN_218325	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	NM_019795	5.61E-05	0.0060164	1.82936
ILMN_203087	Dpp4	Dipeptidylpeptidase 4	NM_001159543	8.97E-06	0.0024215	1.90726
ILMN_214164	Dtl	Denticleless homolog (Drosophila)	NM_029766	0.0015249	0.0236568	1.62856
ILMN_212470	Dusp2	Dual specificity phosphatase 2	NM_010090	0.0035438	0.0343414	1.60774
ILMN_218093	Dusp7	Dual specificity phosphatase 7	NM_153459	0.0052684	0.0423742	1.70225
ILMN_205792	E030020A01Rik			0.0040139	0.0369449	-1.5087
ILMN_206892	E030038D23Rik			0.0288633	0.0957397	1.56094
ILMN_203538	E130202F10Rik			0.0058363	0.0441304	1.63014
ILMN_207230	E130301F21Rik			0.0124275	0.0629564	-1.52684
ILMN_214463	E2f4	E2F transcription factor 4	NM_148952	0.0026423	0.0301609	1.87158
ILMN_205261	E330013M12Rik			4.11E-05	0.0051928	1.7282
ILMN_206618	E330031M19Rik			0.0001173	0.007666	1.50505
ILMN_237050	Ear4	Eosinophil-associated, ribonuclease A family, member 4	NM_001017422	0.0148788	0.0696075	2.66472

ILMN_213475	Ecm1	Extracellular matrix protein 1	NM_001252653	0.0016357	0.0243281	-1.62337
ILMN_217037	Efr3a		NM_133766	0.0026101	0.0300893	-1.5311
ILMN_216453	Eif3b	Eukaryotic translation initiation factor 3, subunit B	NM_133916	0.0209368	0.0827031	-1.79389
ILMN_216646	Eif4ebp2	Eukaryotic translation initiation factor 4E binding protein 2	NM_010124	0.0039026	0.0363685	1.58776
ILMN_202214	Emb	Embigin	NM_010330	0.0240687	0.0878709	-2.14062
ILMN_212810	Emd	Emerin	NM_007927	0.010087	0.0568081	-1.58839
ILMN_227395	Eprs	Glutamyl-prolyl-tRNA synthetase	NM_029735	0.0070595	0.0479623	-1.59409
ILMN_220172	Evi2a	Ecotropic viral integration site 2a	NM_001033711	0.0117341	0.0611851	-2.01887
ILMN_191021	Fads6	Fatty acid desaturase domain family, member 6	NM_178035	0.0006421	0.0159091	1.5514
ILMN_220304	Faim3	Fas apoptotic inhibitory molecule 3	NM_026976	0.001603	0.0241801	1.99741
ILMN_223889	FAM126A	family with sequence similarity 126, member A	NM_053090	0.0078304	0.0506335	1.55023
ILMN_210354	Fam133b	family with sequence similarity 133, member B	NM_001042501	0.0032246	0.0332897	1.5025
ILMN_220048	Fam3c	family with sequence similarity 3, member C	NM_138587	0.0025849	0.0299313	1.51486
ILMN_222725	Fam63b	family with sequence similarity 63, member B	NM_172772	0.0001227	0.0077089	1.92826
ILMN_191384	Fam78b	family with sequence similarity 78, member B	NM_001160261	1.46E-05	0.0031072	-1.81615
ILMN_219622	Fcgr1	Fc receptor, IgG, high affinity I	NM_010186	5.78E-07	0.0010971	-1.62824
ILMN_211779	Fcrla	Fc receptor-like A	NM_001160215	0.0082826	0.0521075	1.82753
ILMN_212438	Fcrls	Fc receptor-like S, scavenger receptor	NM_030707	1.08E-05	0.0027452	-2.20162
ILMN_217290	Fech	Ferrochelatase	NM_007998	0.0187108	0.0780064	-1.66076
ILMN_214571	Fermt3	fermitin family homolog 3 (Drosophila)	NM_153795	0.0138239	0.0668324	-1.68281
ILMN_204362	Fkbp15	FK506 binding protein 15	NM_001045528	0.0210438	0.0828342	1.71567
ILMN_192281	Fkbp1a	FK506 binding protein 1a	NM_008019	3.16E-05	0.004642	-1.55843
ILMN_214651	Foxc1	Forkhead box C1	NM_008592	0.0012859	0.0221497	-1.76148
ILMN_194758	Foxo1	Forkhead box O1	NM_019739	9.42E-05	0.0070855	1.53116
ILMN_209602	Fryl	Furry homolog-like (Drosophila)	NM_028194	0.0001309	0.0079094	1.63638
ILMN_209602	Fryl	Furry homolog-like (Drosophila)	NM_028194	0.0111684	0.0598173	1.80601
ILMN_210866	Fxyd6	FXYD domain-containing ion transport regulator 6	NM_022004	0.0272094	0.0931856	2.0738
ILMN_190245	Gatad2b	GATA zinc finger domain containing 2B	NM_139304	0.0003986	0.0129302	1.5163
ILMN_219053	Gbas	Glioblastoma amplified sequence	NM_008095	0.0001334	0.0079227	-1.55946
ILMN_199021	Gm10233	predicted pseudogene 10233		0.0018619	0.0254843	-2.18502
ILMN_197716	Gm10705	predicted gene 10705		0.0246642	0.0887741	-2.07586

ILMN_244723	Gm11428	predicted gene 11428	NM_001081957	0.0188365	0.0784312	-1.90961
ILMN_197470	Gm14044	predicted gene 14044		0.0276264	0.0937254	-1.52624
ILMN_216067	Gm14085	In multiple Geneids		0.0190802	0.0790388	-1.64434
ILMN_184683	Gm14680	predicted gene 14680		0.0023934	0.0289977	1.64193
ILMN_195867	Gm14698	predicted gene 14698		0.0005995	0.0154784	-1.5779
ILMN_198304	Gm15596	predicted gene 15596		0.0106406	0.0583114	-2.23534
ILMN_200058	Gm16372	predicted pseudogene 16372		0.0028126	0.0311536	-2.50931
ILMN_210809	Gm16971	predicted gene, 16971		0.0052332	0.0422292	-2.10082
ILMN_190417	Gm2423	predicted gene 2423		0.0264333	0.0917618	-2.47975
ILMN_196255	Gm2589	predicted gene 2589		0.0286592	0.0953422	-1.98929
ILMN_214618	Gm2893	predicted gene 2893		0.0024438	0.0291352	-4.04995
ILMN_206227	Gm3411	predicted gene 3411		0.0027576	0.0309782	1.65613
ILMN_199332	GM3758	predicted gene 3758		0.0134603	0.0657054	-1.72806
ILMN_184725	GM4353	predicted gene 4353		0.0110368	0.0594849	-1.90898
ILMN_198435	Gm4757	predicted gene 4757		0.0009458	0.0188359	-1.9877
ILMN_197091	Gm4788	predicted gene 4788	NM_001029977	0.0018525	0.0254843	-3.71452
ILMN_198486	Gm5052	predicted gene 5052		0.0001064	0.0074658	-1.93988
ILMN_215850	Gm5131	predicted gene 5131		5.20E-06	0.0019724	-1.92088
ILMN_197687	Gm5150	predicted gene 5150	NM_001081687	0.0276232	0.0937254	-1.59606
ILMN_211083	Gm5222	predicted gene 5222		0.0018925	0.025677	-3.23066
ILMN_200808	Gm5328	predicted gene 5328		0.0122936	0.0626728	1.66958
ILMN_200810	Gm5330	predicted gene 5330		0.00657	0.0466075	1.64564
ILMN_198488	Gm5521	predicted gene 5521		0.0008603	0.0178482	-1.63581
ILMN_197915	Gm5552	predicted gene 5552		0.0293547	0.09633	-1.91107
ILMN_200277	Gm5564	predicted gene 5564		0.0263017	0.0914872	-1.57535
ILMN_200679	Gm5578	predicted pseudogene 5578		0.014173	0.0677918	1.71111
ILMN_200751	Gm5586	predicted gene 5586		0.0211085	0.0828916	-2.80361
ILMN_233946	Gm5643	predicted gene 5643		0.0003758	0.0125503	-3.3991
ILMN_200478	Gm5814	predicted pseudogene 5814		8.58E-06	0.0024215	-3.36827
ILMN_210322	Gm5815	predicted pseudogene 5815		0.0008548	0.0178482	1.59649
ILMN_198318	Gm6663	predicted gene 6663		0.0095618	0.0554419	-3.44491
ILMN_198083	Gm6705	predicted gene 6705		0.0005228	0.0146151	-1.61874
ILMN_199989	Gm6745	predicted gene 6745		0.024523	0.0886548	1.59033
ILMN_196888	Gm6969	predicted pseudogene 6969		0.0039898	0.0367614	-2.68434
ILMN_197711	Gm7083	predicted gene 7083		0.026284	0.0914872	-2.17266
ILMN_210527	Gm7122	predicted pseudogene 7122		0.0010252	0.0195617	-2.75045
ILMN_197393	Gm8416	predicted gene 8416		0.0013207	0.0224169	-1.95836
ILMN_247624	Gm8909	predicted gene 8909	NM_001081032	0.000692	0.0164058	-2.94121
ILMN_207496	Gm9391	predicted gene 9391		0.0091722	0.0545579	1.91654
ILMN_220727	Gm9574			0.028894	0.0957577	-2.23881

ILMN_215032	Gp38			0.0275317	0.0937254	1.71155
ILMN_185836	Gpi1	Glucose phosphate isomerase 1	NM_008155	0.0002762	0.0107598	-1.73225
ILMN_211323	Gpnmb	Glycoprotein (transmembrane) nmb	NM_053110	0.0139873	0.0673288	1.70671
ILMN_211662	Gpr171	G protein-coupled receptor 171	NM_173398	0.0028677	0.0314965	1.76673
ILMN_219947	Gpx3	Glutathione peroxidase 3	NM_008161	6.36E-05	0.0060733	-2.49393
ILMN_210612	Grit	Rho GTPase-activating protein		0.0114691	0.0608626	1.54692
ILMN_258260	Gstp2	Glutathione S-transferase, pi 2	NM_181796	0.0162156	0.0728477	-1.82593
ILMN_208621	H2-K2			0.0313312	0.0993929	-2.3394
ILMN_193997	H2-Ob	Histocompatibility 2, O region beta locus	NM_010389	0.0054174	0.0429078	1.56154
ILMN_216783	H2-Q6			0.0066376	0.0468356	-2.46727
ILMN_216783	H2-Q6			0.0001138	0.0075762	-2.28778
ILMN_223897	H2-Q8	Histocompatibility 2, Q region locus 8	NM_023124	0.0061702	0.0453375	-1.66392
ILMN_223761	Hdac7		NM_001204275	0.0003141	0.0115449	1.67247
ILMN_218025	Hey1	Hairy/enhancer-of-split related with YRPW motif 1	NM_010423	0.0063781	0.0461446	1.54629
ILMN_195878	Hk1	Hexokinase 1	NM_001146100	0.0070215	0.0477975	-1.57183
ILMN_219962	Hmga1	High mobility group AT-hook 1	NM_001025427	0.0007495	0.0169259	1.51007
ILMN_217580	Hmha1	Histocompatibility (minor) HA-1	NM_001142701	0.0173415	0.0747723	1.60247
ILMN_211433	Hnrnpa2b1	Heterogeneous nuclear ribonucleoprotein A2/B1	NM_016806	0.0151427	0.0703115	-1.63225
ILMN_217576	Hnrph1	Heterogeneous nuclear ribonucleoprotein H1		0.0063347	0.0460609	-2.5509
ILMN_223593	Hspa2	Heat shock protein 2	NM_001002012	2.95E-06	0.0018118	1.55428
ILMN_222238	Htra1	HtrA serine peptidase 1	NM_019564	0.0047066	0.0398158	-1.96814
ILMN_217646	Htra3	HtrA serine peptidase 3	NM_001042615	0.0141478	0.0677534	-1.5361
ILMN_186902	Idh1	Isocitrate dehydrogenase 1 (NADP+), soluble	NM_001111320	0.0169548	0.0742709	-2.63707
ILMN_209421	Idh2	Isocitrate dehydrogenase 2 (NADP+), mitochondrial		0.0107269	0.0585252	1.6909
ILMN_214979	Ifit3	Interferon-induced protein with tetratricopeptide repeats 3	NM_010501	0.0014242	0.0229105	-1.71379
ILMN_217958	Igfbp6	Insulin-like growth factor binding protein 6	NM_008344	0.0229563	0.0859095	-1.66356
ILMN_218449	Igha			4.18E-05	0.0051928	-4.85564
ILMN_192751	IGHA_J00475$V00785_Ig_heavy_constant_alpha_135			0.0081522	0.0516291	-1.57519
ILMN_222723	Ighg	Immunoglobulin heavy chain (gamma polypeptide)		0.0095514	0.0554419	-2.17337
ILMN_195481	Ighg1			0.0010919	0.0201009	-2.40016
ILMN_187077	IGHG1_J00453$V00793_Ig_heavy_constant_gamma_1_792			0.0003634	0.012374	-2.92562
ILMN_193885	Ighv1-20	immunoglobulin heavy variable V1-20		0.0003704	0.0124528	-2.60777

ILMN_210701	Ighv1-62	immunoglobulin heavy variable V1-62		0.0008595	0.0178482	-5.06891
ILMN_211990	Ighv1-62-3	immunoglobulin heavy variable 1-62-3		0.0015205	0.0236226	-1.77975
ILMN_215902	Ighv5-12-4	immunoglobulin heavy variable 5-12-4		0.0068058	0.0474043	-1.63392
ILMN_213335	Ighv5-16	immunoglobulin heavy variable 5-16		0.0001788	0.0092109	-1.50965
ILMN_212697	Ighv6-3	immunoglobulin heavy variable 6-3		0.000185	0.0093923	-2.09242
ILMN_190076	Ighv8-9	immunoglobulin heavy variable V8-9		0.0001563	0.0087869	-1.76233
ILMN_190903	Ighvhs107.a3.106	Ig heavy chain V region VHS107.a3.106		0.0037509	0.0355247	-1.53318
ILMN_223600	Igkv10-95	immunoglobulin kappa variable 10-95		0.0303845	0.0978014	-3.20095
ILMN_211208	Igkv1-133	immunoglobulin kappa variable 1-133		0.0204856	0.0817547	-2.86178
ILMN_222830	Igkv12-41			0.0033851	0.0338347	-4.64369
ILMN_219649	Igkv12-46	immunoglobulin kappa variable 12-46		0.0028087	0.0311536	-4.18172
ILMN_185365	Igkv12-67	immunoglobulin kappa chain variable 12-67		0.0029119	0.0316491	-2.53948
ILMN_217861	Igkv12-89	immunoglobulin kappa chain variable 12-89		0.0031933	0.0332897	-2.60101
ILMN_216381	Igkv13-84	immunoglobulin kappa chain variable 13-84		0.0009436	0.018829	-4.10403
ILMN_210508	Igkv14-126	immunoglobulin kappa variable 14-126		0.0109986	0.059463	-3.19488
ILMN_191930	Igkv15-103	immunoglobulin kappa chain variable 15-103		0.0253557	0.0900847	-2.40111
ILMN_193298	IGKV1-88_AJ231206_Ig_kappa_variable_1-88_289			0.026042	0.0910563	-1.62898
ILMN_192326	IGKV1-99_AJ231207_Ig_kappa_variable_1-99_1			0.0129168	0.0641301	-2.3642
ILMN_187862	Igkv2-116	immunoglobulin kappa variable 2-116		0.0007235	0.0165462	-1.53856
ILMN_185385	IGKV3-2_X16954_Ig_kappa_variable_3-2_18			0.0160775	0.0725756	-3.9423
ILMN_217531	Igkv3-4			0.0203632	0.0817028	-2.10696
ILMN_189280	IGKV4-53_AJ231231_Ig_kappa_variable_4-53_12			0.0008103	0.01747	-2.4906
ILMN_210750	Igkv4-54			0.009811	0.0560462	-3.84291
ILMN_201508	Igkv4-60			0.0033486	0.0337587	-2.78195
ILMN_194801	Igkv4-62			0.0040247	0.0370119	-6.14983
ILMN_192727	Igkv4-68			0.0109014	0.0591038	-3.91348
ILMN_195194	IGKV4-71_AJ231218_Ig_kappa_variable_4-71_20			0.003397	0.0338347	-5.13339
ILMN_211147	Igkv4-72			0.0105228	0.0580614	-4.35146
ILMN_188601	IGKV4-73_AJ231216_Ig_kappa_variable_4-73_18			0.0061157	0.0450954	-4.85363
ILMN_189696	Igkv4-74			0.0105641	0.0581218	-5.92739
ILMN_195045	Igkv4-77			0.0316041	0.0997743	-2.57318
ILMN_222174	Igkv4-79			0.0047395	0.0399167	-4.95582

ILMN_189593	IGKV4-80_AJ231213_Ig_kappa_variable_4-80_91			0.0044794	0.039018	-1.61517
ILMN_193923	IGKV4-91_AJ231229_Ig_kappa_variable_4-91_29			0.0296189	0.0967152	-1.95694
ILMN_212878	Igk-V5			0.0206645	0.0821551	-3.24699
ILMN_191857	Igkv5-48			0.0002178	0.0099812	-5.93831
ILMN_220501	Igkv6-23			0.0122476	0.0625615	-6.2353
ILMN_216293	Igk-V8	Immunoglobulin kappa chain variable 8 (V8)		0.0229267	0.0858294	-2.873
ILMN_189603	Igkv8-16			0.0178312	0.0760061	-1.70556
ILMN_212982	Igkv8-19			0.0085392	0.0526654	-3.58653
ILMN_214561	Igkv9-124			0.0096902	0.0556811	-4.00106
ILMN_187173	IGKV9-128_AJ231245_Ig_kappa_variable_9-128_15			0.007075	0.0480055	-4.17136
ILMN_219509	Igkvk33-85			0.0060652	0.0448994	-1.79959
ILMN_196028	Igl			0.0086	0.0527708	-2.29238
ILMN_186543	Igll1	Immunoglobulin lambda-like polypeptide 1	NM_001190325	4.76E-06	0.0019724	3.13501
ILMN_216227	Il13ra1	Interleukin 13 receptor, alpha 1	NM_133990	0.0282862	0.0946957	-1.5942
ILMN_221311	Il4i1	Interleukin 4 induced 1	NM_010215	0.0242262	0.0880769	1.59014
ILMN_204884	Il7r	Interleukin 7 receptor	NM_008372	0.0001079	0.0074684	1.74528
ILMN_212867	Isg15	ISG15 ubiquitin-like modifier		0.0067622	0.0472319	-1.90784
ILMN_220885	Ism1		NM_001126490	0.0005487	0.0147496	1.88422
ILMN_213333	Kbtbd5	Kelch repeat and BTB (POZ) domain containing 5	NM_028202	0.0087999	0.0534568	-1.6574
ILMN_208819	Kctd20	Potassium channel tetramerisation domain containing 20	NM_025888	0.0081605	0.0516499	-1.50012
ILMN_218823	Kctd3	Potassium channel tetramerisation domain containing 3	NM_172650	0.0071632	0.0483458	1.62417
ILMN_201976	Kif23	Kinesin family member 23	NM_024245	0.0157059	0.0715118	-2.7633
ILMN_201976	KIF23	Kinesin family member 23	NM_024245	0.025422	0.0902315	1.57003
ILMN_218058	Klhl14	Kelch-like 14 (Drosophila)	NM_001081403	7.62E-06	0.0024215	1.61892
ILMN_228856	Klhl32	Kelch-like 32 (Drosophila)	NM_001033531	6.10E-05	0.0060164	1.53746
ILMN_211787	Klhl6	Kelch-like 6 (Drosophila)	NM_183390	0.000691	0.0164058	1.53572
ILMN_216774	Klk8	Kallikrein related-peptidase 8	NM_008940	0.0013841	0.0226262	1.58392
ILMN_199376	Kng2	Kininogen 2	NM_001102409	0.0006602	0.0161054	-2.1638
ILMN_212848	Krit1	KRIT1, ankyrin repeat containing	NM_001170552	0.0014868	0.0234831	1.68997
ILMN_212848	Krit1	KRIT1, ankyrin repeat containing	NM_001170552	0.017296	0.0747302	1.55184
ILMN_201338	Larp1	La ribonucleoprotein domain family, member 1	NM_028451	0.0039296	0.0364437	-1.91583
ILMN_215964	Ldhc	Lactate dehydrogenase C	NM_013580	0.0012547	0.0217919	1.62554
ILMN_209512	Ldoc1l	Leucine zipper, down-regulated in cancer 1-like	NM_177630	0.0012837	0.0221491	1.6019
ILMN_209652	Lgmn	Legumain	NM_011175	0.0221096	0.084464	-2.53787
ILMN_201677	LOC100040243	hypothetical protein LOC100040243		0.0201016	0.0810576	1.57349

ILMN_190047	LOC100044566	similar to Nuclear receptor coactivator 1 (NCoA-1) (Steroid receptor coactivator 1) (SRC-1) (Nuclear receptor coactivator protein 1) (mNRC-1)		0.0169604	0.0742709	1.62967
ILMN_188063	LOC100045617	similar to Eukaryotic translation initiation factor 4A2		0.0110348	0.0594849	-2.5039
ILMN_221594	LOC100045882	hypothetical protein LOC100045882		0.0024534	0.0291507	1.57943
ILMN_186715	LOC100047132	similar to monoclonal antibody 17-1A, light chain		0.0129094	0.0641301	-3.12752
ILMN_186243	LOC100047162	similar to immunoglobulin kappa-chain		0.0212041	0.0829446	-5.47982
ILMN_202556	LOC100047273	hypothetical protein LOC100047273		0.026538	0.0919726	1.60417
ILMN_209887	LOC100047316	similar to anti-MOG Z12 variable light chain		0.0043587	0.0385303	-5.3641
ILMN_188128	LOC100047628	similar to Chain L, Structural Basis Of Antigen Mimicry In A Clinically Relevant Melanoma Antigen System		0.0070029	0.0477834	-1.64717
ILMN_186258	LOC100048346	similar to ubiquitin specific protease UBP43		0.000729	0.0166061	-1.84124
ILMN_197504	LOC219145	similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed)		0.0268907	0.0926117	-1.7811
ILMN_215575	LOC232060	similar to monoclonal antibody kappa light chain		0.0128413	0.0639679	-4.07342
ILMN_198956	LOC234360	similar to hypothetical protein FLJ20445		0.00563	0.0435119	-2.28058
ILMN_198324	LOC271490	similar to pendulin		0.0133198	0.0653245	-2.34689
ILMN_199267	LOC272683	similar to variable region of immunoglobulin kappa light chain		0.0167053	0.0737629	-3.14814
ILMN_198234	LOC333744	similar to Archain 1		0.0067039	0.047044	-1.92703
ILMN_197335	LOC381398			0.0281255	0.0944684	-2.63044
ILMN_197754	LOC381501	similar to ubiquitin-conjugating enzyme E2 variant 1 isoform b; DNA-binding protein		0.0007722	0.0170803	-1.50377
ILMN_199932	LOC381578	similar to protein 40kD		0.0278869	0.0941776	-1.61222
ILMN_221711	LOC381774			0.0209247	0.0826866	-4.20156
ILMN_200884	LOC381889			0.0065574	0.0465791	-1.81015
ILMN_199844	LOC383077			9.12E-05	0.0070449	1.5418
ILMN_199630	LOC383775	similar to 40S ribosomal protein S16		0.0042031	0.037788	2.39598
ILMN_212905	LOC384415			0.0117348	0.0611851	-4.93703
ILMN_200229	LOC386005	similar to hypothetical protein		0.004574	0.0391048	1.59818

ILMN_200392	LOC386405	similar to hypothetical protein MGC37588		0.0024437	0.0291352	-1.6131
ILMN_217925	LOC630302	similar to Ig heavy chain V region 5-84 precursor		0.0042488	0.0380028	-1.88235
ILMN_199322	LOC674004	similar to gonadotropin inducible ovarian transcription factor 2		0.0152464	0.0705824	-1.67162
ILMN_221529	LOC674110	similar to Ig heavy chain V region 7-39 precursor		0.0040343	0.0370317	-1.89669
ILMN_210939	LOC674706	similar to zinc finger protein 341		0.0195771	0.0800854	-1.6001
ILMN_195977	Loxl1	Lysyl oxidase-like 1	NM_010729	0.0016061	0.0241801	-1.66189
ILMN_237934	Lrmp	Lymphoid-restricted membrane protein	NM_008511	9.16E-05	0.0070449	1.68844
ILMN_194484	Lrrc29	Leucine rich repeat containing 29	NM_177449	0.0058894	0.0443658	1.59712
ILMN_222498	Ltb	Lymphotoxin B	NM_008518	0.0081442	0.0516095	-1.59191
ILMN_209150	Ly6a	Lymphocyte antigen 6 complex, locus A		0.0054751	0.043108	-1.63687
ILMN_184595	MALT1	Mucosa associated lymphoid tissue lymphoma translocation gene 1	NM_172833	0.0046829	0.0397487	1.54056
ILMN_213057	Map4k1	Mitogen activated protein kinase kinase kinase kinase 1	NM_008279	0.0257085	0.0905404	1.52963
ILMN_215807	Map4k3	Mitogen-activated protein kinase kinase kinase kinase 3		0.0221789	0.0845153	-1.68646
ILMN_213080	Mcm3	Minichromosome maintenance deficient 3 (S. cerevisiae)	NM_008563	0.0166711	0.073643	-1.91397
ILMN_208709	Med18	Mediator of RNA polymerase II transcription, subunit 18 homolog (yeast)	NM_026039	0.0017164	0.0249637	1.51181
ILMN_192108	Mela	Melanoma antigen		0.0084629	0.0524841	1.96598
ILMN_221807	Mical2	Microtubule associated monoxygenase, calponin and LIM domain containing 2	NM_001193305	0.0139925	0.0673288	-1.79074
ILMN_211739	Mical3	Microtubule associated monoxygenase, calponin and LIM domain containing 3	NM_153396	0.0001662	0.0089511	1.56435
ILMN_192319	Mll1	Myeloid/lymphoid or mixed-lineage leukemia 1	NM_001081049	0.0162263	0.0728477	1.65728
ILMN_219045	Mmadhc	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	NM_133839	0.0083362	0.0522246	-2.17811
ILMN_217083	Mppe1	Metallophosphoesterase 1	NM_172630	0.0170501	0.0744846	-1.54515
ILMN_213874	Mrpl48	Mitochondrial ribosomal protein L48	NM_198831	0.0275962	0.0937254	-1.53263
ILMN_215402	Ms4a3	Membrane-spanning 4-domains, subfamily A, member 3	NM_133246	0.0280269	0.0942887	-1.61876
ILMN_208807	Ms4a6d	Membrane-spanning 4-domains, subfamily A, member 6D	NM_026835	0.0015179	0.0236226	-1.8531

ILMN_203016	Msi2h			0.0062975	0.0459499	1.52502
ILMN_234960	Mup6		NM_001081285	1.11E-09	5.81E-06	-3.86999
ILMN_214832	Myl9	Myosin, light polypeptide 9, regulatory	NM_172118	0.0303899	0.0978014	-1.75651
ILMN_210294	Mysm1	Myb-like, SWIRM and MPN domains 1	NM_177239	5.88E-05	0.0060164	2.05798
ILMN_209679	Nckap1	NCK-associated protein 1	NM_016965	0.0156316	0.0712983	-2.38476
ILMN_195057	Nd4l	NADH dehydrogenase subunit 4L		0.0161998	0.0728477	-3.10361
ILMN_194230	Nd5	NADH dehydrogenase subunit 5		0.0051559	0.0419315	1.71355
ILMN_238643	Ndfip1	Nedd4 family interacting protein 1	NM_022996	0.0012171	0.0216055	-2.09432
ILMN_238643	Ndfip1	Nedd4 family interacting protein 1	NM_022996	0.0006168	0.0156234	-1.54629
ILMN_209531	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	NM_153064	0.0169695	0.0742709	-2.3131
ILMN_219985	Nipbl	Nipped-B homolog (Drosophila)	NM_027707	0.0018608	0.0254843	1.93447
ILMN_203322	Nktr	Natural killer tumor recognition sequence	NM_010918	0.0127772	0.0638616	1.59885
ILMN_235165	Nlrc3	NLR family, CARD domain containing 3	NM_001081280	0.0058287	0.0441304	1.83268
ILMN_185152	Nmd3	NMD3 homolog (S. cerevisiae)	NM_133787	0.0179334	0.0760392	1.54506
ILMN_212812	Nme7	Non-metastatic cells 7, protein expressed in	NM_138314	0.0005149	0.0145487	1.77613
ILMN_217099	Nola2	Nucleolar protein family A, member 2		0.0293615	0.09633	-2.31511
ILMN_218567	Notch3	Notch gene homolog 3 (Drosophila)	NM_008716	0.0010714	0.019883	1.61552
ILMN_221287	Nrm	Nurim (nuclear envelope membrane protein)	NM_134122	0.0043951	0.0387356	1.70004
ILMN_221796	Nsbp1	Nucleosome binding protein 1		0.0216825	0.0836843	-1.74104
ILMN_215517	Nt5dc2	5'-nucleotidase domain containing 2	NM_027289	0.0265177	0.0919632	-1.5512
ILMN_212179	Oas1g	2'-5' oligoadenylate synthetase 1G	NM_011852	2.27E-05	0.0040083	-1.74977
ILMN_216357	Oas2	2'-5' oligoadenylate synthetase 2	NM_145227	0.0007177	0.0165462	-1.99476
ILMN_221386	Olfml1	Olfactomedin-like 1	NM_172907	0.0051223	0.0417773	1.86981
ILMN_187890	Oxa1l	Oxidase assembly 1-like	NM_026936	0.0047623	0.040028	-1.59396
ILMN_215489	P2rx3	Purinergic receptor P2X, ligand-gated ion channel, 3		9.85E-05	0.0073355	1.93878
ILMN_194028	P2ry6	Pyrimidinergic receptor P2Y, G-protein coupled, 6	NM_183168	0.0098679	0.0560754	-1.57322
ILMN_213804	Pafah1b3	Platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	NM_008776	0.0073845	0.0492114	2.00328
ILMN_188937	Parp12	Poly (ADP-ribose) polymerase family, member 12	NM_172893	0.0012828	0.0221491	-1.5757
ILMN_222572	Pbk	PDZ binding kinase	NM_023209	0.0018981	0.025677	1.52151
ILMN_204318	Pde4b	Phosphodiesterase 4B, cAMP specific	NM_001177980	0.00327	0.0333574	1.54506

ILMN_213240	Pdhb	Pyruvate dehydrogenase (lipoamide) beta	NM_024221	0.0136561	0.0663767	-1.56721
ILMN_215714	Pdia4	Protein disulfide isomerase associated 4	NM_009787	0.0172437	0.074634	-1.56667
ILMN_221690	Pex7	Peroxisome biogenesis factor 7	NM_001161825	0.0054328	0.0429078	-1.75748
ILMN_217699	Phex	Phosphate regulating gene with homologies to endopeptidases on the X chromosome (hypophosphatemia, vitamin D resistant rickets)	NM_011077	0.00316	0.0331734	-2.16559
ILMN_205821	Phf20l1	PHD finger protein 20-like 1	NM_001081409	0.0131881	0.0649079	1.64219
ILMN_221026	Pigu	Phosphatidylinositol glycan anchor biosynthesis, class U	NM_001004721	0.0240028	0.0877682	-1.73891
ILMN_252909	Pira11	Paired-Ig-like receptor A11	NM_011088	0.0222936	0.0846412	-1.58746
ILMN_190986	Pitpnc1	Phosphatidylinositol transfer protein, cytoplasmic 1	NM_145823	0.0016754	0.0246734	-1.59756
ILMN_209036	Plekha2	Pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	NM_031257	8.02E-06	0.0024215	1.53333
ILMN_218871	Plscr1	Phospholipid scramblase 1		0.03172	0.0999591	-1.57859
ILMN_217787	Pou2f2	POU domain, class 2, transcription factor 2	NM_001163554	0.0277193	0.0939705	1.67584
ILMN_259833	Ppapdc1b	POU domain, class 2, transcription factor 2	NM_028000	0.0165101	0.0733364	-1.61669
ILMN_190255	Ppp1r2-ps2	phosphatidic acid phosphatase type 2 domain containing 1B		0.0193442	0.0795997	-1.56913
ILMN_201525	Ppp2r5a	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform	NM_144880	0.001172	0.0210839	-1.96481
ILMN_221477	Ppt1	Palmitoyl-protein thioesterase 1	NM_008917	0.0113871	0.0606539	-1.62544
ILMN_211235	Prg2	Proteoglycan 2, bone marrow	NM_008920	0.011848	0.0614497	3.09238
ILMN_219970	Prg3	Proteoglycan 3	NM_016914	0.0041108	0.0374607	3.45831
ILMN_238017	Prm1	Protamine 1	NM_013637	0.008427	0.0524486	1.63486
ILMN_214926	Prok2	Prokineticin 2	NM_001037539	0.0079247	0.050991	-1.70367
ILMN_221097	Psme2	Proteasome (prosome, macropain) 28 subunit, beta	NM_001029855	0.0111785	0.0598173	-1.98849
ILMN_213298	Pthr1	Parathyroid hormone receptor 1		0.0066888	0.0470158	-1.61359
ILMN_215638	Qrsl1	Glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	NM_001081054	0.0004974	0.014327	1.52893
ILMN_208686	Rab14	RAB14, member RAS oncogene family	NM_026697	0.0025166	0.0294986	1.51368
ILMN_221923	Rab43	RAB43, member RAS oncogene family	NM_001039394	0.0033183	0.0336591	1.50099
ILMN_223403	Rab4a	RAB4A, member RAS oncogene family	NM_009003	0.0004829	0.0140661	1.52319

ILMN_214788	Rab5a	RAB5A, member RAS oncogene family		0.0041854	0.0376937	-2.16852
ILMN_211132	Rad21	RAD21 homolog (S. pombe)	NM_009009	0.0035862	0.034524	1.77477
ILMN_238709	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	NM_001159965	0.0061968	0.0454376	1.51395
ILMN_217907	Ranbp9	RAN binding protein 9	NM_019930	0.0149435	0.0696647	-2.06805
ILMN_212357	Rapgefl1	Rap guanine nucleotide exchange factor (GEF)-like 1	NM_001080925	0.0001012	0.0073504	1.6896
ILMN_188488	Rcor1	REST corepressor 1	NM_198023	0.0066326	0.0468356	1.5275
ILMN_217614	Rdh14	Retinol dehydrogenase 14 (all-trans and 9-cis)	NM_023697	0.0163562	0.0730232	-1.95301
ILMN_223820	Reck	Reversion-inducing-cysteine-rich protein with kazal motifs	NM_016678	0.0228243	0.0856915	-1.64384
ILMN_187635	Refbp2	RNA and export factor binding protein 2		0.0105156	0.0580523	1.5801
ILMN_209775	Rexo2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	NM_024233	0.0094933	0.0553312	-1.85219
ILMN_216035	Rhag	Rhesus blood group-associated A glycoprotein	NM_011269	0.010292	0.0574751	-2.47141
ILMN_218398	Rhbdl2	Rhomboid, veinlet-like 2 (Drosophila)		0.0262536	0.0914872	1.65811
ILMN_210173	Rnase4	Ribonuclease, RNase A family 4	NM_021472	0.0180315	0.0762383	-1.77579
ILMN_193392	Rnf13	Ring finger protein 13	NM_001113413	0.00213	0.0272932	-1.56937
ILMN_210478	Rnf181	Ring finger protein 181	NM_025607	0.0036503	0.0348248	-1.73567
ILMN_209890	Rnf4	Ring finger protein 4	NM_011278	0.0238277	0.0876028	-1.99838
ILMN_199705	Rpl23a-ps5	ribosomal protein L23A, pseudogene 5		0.0028794	0.0315185	1.5205
ILMN_199029	Rpl27a-ps1	ribosomal protein L27A, pseudogene 1		0.0297891	0.0969119	-1.5067
ILMN_234979	Rpl7a	Ribosomal protein L7a		0.0214875	0.0833358	-4.48113
ILMN_221551	Rps4y2	Ribosomal protein S4, Y-linked 2		0.0047735	0.0400526	-1.52772
ILMN_201538	Rps6-ps3	ribosomal protein S6, pseudogene 3		0.0004212	0.0131871	1.56584
ILMN_214605	Rsad2	Radical S-adenosyl methionine domain containing 2	NM_021384	0.0236718	0.0873367	-1.55961
ILMN_187143	Rsph1	Radial spoke head 1 homolog (Chlamydomonas)	NM_025290	0.0002537	0.0105907	1.98919
ILMN_242897	Rsph9		NM_029338	0.0048854	0.0405091	1.74257
ILMN_186120	Rtn4	Reticulon 4	NM_024226	0.0001074	0.0074684	-1.60784
ILMN_222481	Rybp	RING1 and YY1 binding protein	NM_019743	0.014437	0.0686364	-2.60731
ILMN_220623	Sbk			0.0007665	0.0170528	2.04085
ILMN_219254	Scara3	Scavenger receptor class A, member 3	NM_172604	0.0048667	0.0404175	1.58523
ILMN_218062	Scd1	Stearoyl-Coenzyme A desaturase 1	NM_009127	0.004605	0.0392738	2.08244
ILMN_195140	scl0001905.1_3			5.82E-05	0.0060164	-1.50208

ILMN_188988	scl0002368.1_75			0.0278538	0.0941776	1.7254
ILMN_184713	scl0002624.1_576			0.0172666	0.0746648	-1.5271
ILMN_193137	scl0002791.1_134			0.0063284	0.046056	-1.88849
ILMN_186828	scl0003799.1_2			0.0033527	0.0337587	-1.59533
ILMN_188130	scl0004020.1_31			0.0233432	0.08686	-1.96334
ILMN_190146	scl000416.1_19			0.0009233	0.0187464	-1.8387
ILMN_222018	Sdf2l1	Stromal cell-derived factor 2-like 1	NM_022324	0.0055293	0.0432438	-1.7551
ILMN_184862	Sec23a	SEC23A (S. cerevisiae)	NM_009147	0.0002349	0.010221	-1.50137
ILMN_219302	Sec24d	SEC24 related gene family, member D (S. cerevisiae)	NM_027135	0.0043148	0.0383344	-1.51882
ILMN_210845	Sec61b	Sec61 beta subunit	NM_024171	0.0214404	0.0833177	-1.92927
ILMN_209357	Sep15	Selenoprotein	NM_053102	0.0080448	0.0515104	-2.75
ILMN_214926	Sfr1	SWI5 dependent recombination repair 1	NM_026377	0.0123959	0.0628877	-1.70367
ILMN_214616	Sfrs5	Splicing factor, arginine/serine-rich 5 (SRp40, HRS)		0.0099869	0.0566284	-2.06117
ILMN_185390	Slamf6	SLAM family member 6	NM_030710	0.0003765	0.0125503	1.74422
ILMN_207184	Slc6a4	Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	NM_010484	0.0004806	0.0140595	-1.60042
ILMN_221451	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	NM_001174078	0.0013504	0.0224779	1.69714
ILMN_228402	Smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	NM_134034	0.0001986	0.0095924	1.57482
ILMN_192585	Snhg10	Small nucleolar RNA host gene (non-protein coding) 10		0.0125152	0.063278	1.64758
ILMN_195167	Snhg5	small nucleolar RNA host gene 5		0.0268278	0.092456	-1.76956
ILMN_201536	Snn	Stannin	NM_009223	0.0003355	0.011862	1.80601
ILMN_215357	Snx29	sorting nexin 29	NM_028964	0.0010338	0.0195819	1.52172
ILMN_218435	Snx7	Sorting nexin 7	NM_001190156	0.0101389	0.0569625	-1.56445
ILMN_217542	Srpk3	Serine/arginine-rich protein specific kinase 3	NM_019684	0.0144003	0.0685342	1.81098
ILMN_220427	Srpr	Signal recognition particle receptor ('docking protein')	NM_026130	0.0040385	0.0370317	-1.51223
ILMN_202257	Srsf11		NM_001093752	0.0098509	0.0560576	1.75593
ILMN_220254	Stap1	Signal transducing adaptor family member 1	NM_019992	0.0101493	0.0569625	-1.72404
ILMN_209686	Stk25	Serine/threonine kinase 25 (yeast)	NM_021537	0.0157331	0.0715863	-1.51974
ILMN_218897	Strbp	Spermatid perinuclear RNA binding protein	NM_009261	4.19E-06	0.0019724	2.20538
ILMN_218897	Strbp	Spermatid perinuclear RNA binding protein	NM_009261	0.0249048	0.0892775	1.518
ILMN_203452	Strn3	Striatin, calmodulin binding protein 3	NM_001172098	0.0184115	0.0774068	1.59614

ILMN_210817	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	NM_024222	0.0002992	0.0111734	-1.80257
ILMN_211084	Stx18	Syntaxin 18	NM_026959	0.006823	0.0474291	-1.61668
ILMN_205316	Stxbp3			0.0013624	0.0225395	1.85091
ILMN_215684	Sumo3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	NM_019929	0.0081309	0.0515811	-1.8232
ILMN_223539	Supt16h	Suppressor of Ty 16 homolog (S. cerevisiae)	NM_033618	0.0032312	0.0332897	1.95893
ILMN_216821	Tbc1d10c	TBC1 domain family, member 10c	NM_178650	0.0003092	0.0114222	1.62891
ILMN_223469	Tceal8	Transcription elongation factor A (SII)-like 8	NM_001168578	0.0214734	0.0833334	-1.70603
ILMN_195510	Tcrb-V8.2	T-cell receptor beta, variable 8.2		0.0115473	0.0609483	-1.51557
ILMN_217992	Tespa1		NM_183264	0.0004563	0.0138285	1.63974
ILMN_240795	Tgfbr3	Transforming growth factor, beta receptor III	NM_011578	0.005437	0.0429078	-1.67127
ILMN_221308	Tlr2	Toll-like receptor 2	NM_011905	0.0162138	0.0728477	-1.52284
ILMN_229771	Tm6sf1	Transmembrane 6 superfamily member 1		0.0084446	0.052464	-1.90134
ILMN_195093	Tmcc1	Transmembrane and coiled coil domains 1	NM_177412	0.0146167	0.0689365	1.59784
ILMN_192442	TMED1	Transmembrane emp24 domain containing 1	NM_010744	0.0019799	0.0261421	-1.65425
ILMN_214664	Tmed3	Transmembrane emp24 domain containing 3	NM_025360	0.0258168	0.0907105	-1.58051
ILMN_223572	Tmem100	Transmembrane protein 100	NM_026433	0.0278096	0.0941026	-1.52224
ILMN_217129	Tmem132e	Transmembrane protein 132E	NM_023438	0.0016706	0.0246369	1.63913
ILMN_214193	Tmem16a	Transmembrane protein 16A		0.0049647	0.0409716	-1.56246
ILMN_184478	Tmem181a	transmembrane protein 181A	NM_001033178	0.0065366	0.046494	1.63873
ILMN_219321	Tmem188	Transmembrane protein 188	NM_029074	0.0179049	0.0760392	-1.82282
ILMN_216276	Tmem41a	Transmembrane protein 41a	NM_025693	0.0283795	0.0948362	-1.52375
ILMN_184824	Tmpo	Thymopoietin	NM_001080129	0.0192909	0.0794829	-1.86714
ILMN_186905	Tmprss3	Transmembrane protease, serine 3	NM_001163776	0.0005989	0.0154784	1.61252
ILMN_191673	Tnfrsf13c	Tumor necrosis factor receptor superfamily, member 13c	NM_028075	0.0010742	0.019883	1.79442
ILMN_188500	Top2b	Topoisomerase (DNA) II beta	NM_009409	0.0004203	0.0131871	1.5763
ILMN_217774	Tra2a	Transformer 2 alpha homolog (Drosophila)		0.0070892	0.0480706	1.57699
ILMN_186732	Trappc2	Trafficking protein particle complex 2	NM_025432	0.0050021	0.0411744	-1.53332
ILMN_220866	Tspo	Translocator protein	NM_009775	0.0182756	0.0770523	-1.74744
ILMN_187652	Tssc8	Tumor-suppressing subchromosomal transferable fragment 8		0.0110624	0.0594951	1.72174

ILMN_187427	Ttc39b		NM_027238	0.0023318	0.0286161	1.60884
ILMN_255437	Tuba1a	Tubulin, alpha 1A	NM_011653	0.0109638	0.0593669	-1.597
ILMN_189979	Twistnb	TWIST neighbor	NM_172253	0.0034083	0.0338347	1.66141
ILMN_194776	Uba5	tetratricopeptide repeat domain 39B	NM_025692	0.0233797	0.086919	-1.50808
ILMN_187391	Ube2d3	Ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	NM_025356	0.0030532	0.0325422	-2.39363
ILMN_251929	Ube2f	Ubiquitin-conjugating enzyme E2F (putative)	NM_026454	0.0084562	0.0524841	-1.6787
ILMN_214968	Ubr4	Ubiquitin protein ligase E3 component n-recognin 4	NM_001160319	0.0004814	0.0140595	1.70696
ILMN_217393	Ufsp2	UFM1-specific peptidase 2	NM_138668	0.0078424	0.0506651	-1.70738
ILMN_186258	Usp18	Ubiquitin specific peptidase 18	NM_011909	0.0023463	0.0286715	-1.6472
ILMN_203488	Vdac3	Voltage-dependent anion channel 3	NM_001198998	0.0239823	0.0877638	-2.37979
ILMN_216014	Vezt	Vezatin, adherens junctions transmembrane protein	NM_172538	0.0069801	0.0477834	1.52407
ILMN_187199	Vim	Vimentin	NM_011701	0.0197761	0.0805385	-2.63284
ILMN_208893	Wnk1	WNK lysine deficient protein kinase 1	NM_001185020	0.0015358	0.0237551	1.88875
ILMN_195108	Wnt4	Wingless-related MMTV integration site 4	NM_009523	0.0005839	0.0153795	-1.58662
ILMN_187626	Xist	Inactive X specific transcripts		0.0010308	0.0195819	2.12041
ILMN_230389	Xlr4a	X-linked lymphocyte-regulated 4A	NM_001081642	0.002544	0.0295886	1.7184
ILMN_210641	Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	NM_010247	0.0006334	0.0157679	1.66699
ILMN_184863	Zdhhc21	Zinc finger, DHHC domain containing 21	NM_026647	0.0016392	0.0243463	1.50674
ILMN_237439	Zfp157	Zinc finger protein 157	NM_028130	0.0001379	0.0081008	1.51216
ILMN_223660	Zfp420	Zinc finger protein 420	NM_172740	0.0097163	0.0557808	1.64412
ILMN_185725	Zfp433	RIKEN cDNA 1700123A16 gene	NM_001243067	0.011109	0.059567	-1.75437
ILMN_189126	Zfp592	Zinc finger protein 592	NM_178707	0.0249414	0.0893639	1.5634
ILMN_188634	Zfp943	zinc finger with KRAB and SCAN domains 3	NM_001025373	0.0018983	0.025677	1.57403
ILMN_192808	Zkscan3	Zinc finger with KRAB and SCAN domains 3	NM_001145778	0.0236832	0.087348	1.50421
ILMN_220011	Znhit6	zinc finger, HIT type 6	NM_001081094	0.0010126	0.0194718	-1.53588