Supplemental Table 1

Genes that show significant differences in their expression across MN cell types. Supplemental Table S1 is a 10 page table. The data in supplement 1 represent the 813 genes that are differentially expressed among cell types. The data are displayed in spreadsheet format with the probe sets listed alphabetically, according to class as defined in Figure 5. Each row represents one probe set, except for probe set 99056_at, whose name is too long to fit on one line. The information in the columns is as indicated. Statistically significant fold changes are shown in orange ink. Some genes are represented by multiple probe sets (highlighted with violet), and in 18 cases, each of the 2 probe sets for a single gene fell into a different class. When this occurred, the probe sets were moved to the same class if the distribution of signal intensities across cell types was the same for the 2 probe sets. These probe sets are indicated with asterisks (4930553; cyba; mgs; mmp9; nde1; zpf275; atp5c1; Ncam1; ndr4; rex3). While multiple probe sets for a given gene usually produced consistent results, the probe sets for 8 genes produced dissimilar signal distributions and were not moved to the same class. These sixteen probe sets (2 for each of the 8 genes) are indicated by red ink. These discrepancies could represent an alternately spliced and differentially expressed transcript. On the other hand, in many of these cases (5/8) one probe set in the pair reported a strong signal intensity, while the other probe set reported a very low, and perhaps inaccurate, signal.

In some cases, the genes in the list do not appear to be expressed in the LCM population. For example, the transglutaminase 3 gene (class V) is thought to be specifically expressed in the epidermis. The signal intensity associated with the probe set representing this gene is always at or below 20, and it is called absent. Therefore, the inclusion of this gene in the data set most likely represents a false positive (type II) error or some basal expression level. Because it is impossible to establish a criterion for measuring background noise that can be applied to all probe sets on an array, no genes were omitted from the list. Thus, we expect that we have excluded false negative (type I) errors from our data set at the expense of including false positive (type II) errors.

The abbreviations are: G, golgi; N, nucleus; ER, endoplasmic reticulum; EC, extracellular; M, membrane; IC, intracellular; CySk, cytoskeleton; lys, lysosome; mit, mitochondria; mic, microsome

Class I: Genes that are uniquely expressed in all cell types (12)

									Average Signal Intensities & Standard Deviations					
						Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**Probeset**	**location**	**Description**	**Function**	**IML/LMN**	**IML/MMN**	**LMN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
AW125626	Cnn3	160150_f_at	CySk	calponin 3, acidic	actin binding protein	1.71	1.28	0.75	1178.00	88.00	1566.71	274.84	2013.12	189.38
X15052	Ncam1	100153_at	M; EC	neural cell adhesion molecule 1	cell adhesion, synaptic transmission, plasticity	2.50	1.83	0.73	459.98	81.79	629.06	93.95	1148.35	178.60
AV324706	**Ncam1	161750_f_at				1.76	1.55	0.89	131.59	17.33	148.67	16.09	231.11	54.27
AI852470	Nme3	94981_i_at	EC	nucleoside diphosphate kinase DR-nm23	nucleotide biosynthesis	1.43	1.18	0.83	324.74	18.36	391.93	23.46	462.84	55.10
AI852470	Nme3	94982_f_at				1.60	1.23	0.77	603.27	39.26	785.07	75.76	963.32	140.90
AB007136	Psme1; PA28a	101510_at	IC	proteosome activator PA28a	proteolysis	2.34	1.59	0.68	83.03	20.08	121.67	29.82	193.94	24.73
AW121600	**Ndr4	160819_at	IC	N-myc downstream regulated 4	unknown	0.82	0.89	1.08	9487.97	535.66	8819.17	331.97	7810.90	657.43
AV329719	**Ndr4	161998_f_at				0.79	0.95	1.20	1544.27	244.94	1288.05	56.27	1217.22	51.53
AA790008	Rex3	93021_at	IC, N	reduced expression 3	unknown	2.04	1.58	0.77	211.07	15.58	273.13	40.72	431.14	66.48
AF051347	**Rex3	93020_at				2.05	1.73	0.84	39.20	5.60	46.44	5.79	80.38	21.95
AV105022	Rpl10	161657_f_at	IC	ribosomal protein 10	protein biosynthesis	1.31	1.15	0.88	835.51	43.39	951.92	69.16	1096.31	83.20
AV150997	Slc16a2	162219_f_at	M	solute carrier family 16 , member 2	monocarboxylic acid transport	1.37	1.15	0.84	44.55	3.43	53.13	4.96	60.99	3.85
X13986	Spp1	97519_at	EC	secreted phosphoprotein 1	cell adhesion, cytokine activity	0.51	0.69	1.36	3754.97	328.59	2758.02	340.15	1902.64	425.02
AI153693	Zfp275	104002_at	IC, N	Zinc finger protein 275	transcription factor	1.31	1.16	0.89	113.41	9.86	127.99	7.41	149.00	7.14
AV124943	**Zfp275	161503_f_at				1.19	1.12	0.94	21.17	1.70	22.44	1.95	25.16	2.60
AI838836	6330403K07Rik	95559_at		RIKEN cDNA 6330403K07 gene	unknown	2.75	1.74	0.63	1431.69	442.50	2271.21	335.95	3941.51	1238.17
AV161034	6330403K07Rik	161354_f_at				1.94	1.46	0.75	188.45	15.87	249.97	35.97	365.17	66.46
AI834976	C330011J09	104413_at		hypothetical protein C330011J09	unknown	1.42	1.16	0.82	159.90	14.05	195.38	21.47	226.52	15.52

Class II: Genes that are uniquely expressed in IML (149)

									Average Signal Intensities & Standard Deviations					
						Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**Probeset**	**location**	**Description**	**Function**	**IML/LMN**	**IML/MMN**	**LMN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
AA690434	Ace2	160986_r_at	M, EC	angiotensin I converting enzyme	proteolysis and peptidolysis	1.15	1.18	1.02	13.34	1.10	13.08	0.40	15.40	1.26
AB009673	Adam23	92357_at	M	disintegrin & metalloprotease domain 23	proteolysis and peptidolysis	0.76	0.78	1.03	470.07	30.15	456.37	68.81	355.94	53.01
U12919	Adcy7	103392_at	M	adenylate cyclase 7	signal transduction	1.72	1.76	1.02	161.23	28.96	158.30	42.21	278.05	43.15
AB010149	Adcyap1; PACAP	92200_at	EC	PACAP ligand precursor	neuropeptide hormone	3.60	3.08	0.86	211.08	190.76	246.59	102.66	760.66	389.44
AF004326	Agpt2	92210_at	EC	angiopoietin 2	promotes angiogenesis	1.54	1.41	0.92	42.12	9.12	45.87	9.63	64.72	13.39
AW061337	Ak4	99959_at	mit	adenylate kinase 4	nucleotide transport & metabolism	1.38	1.37	1.00	56.10	10.76	56.34	10.53	77.15	10.82
AB020239	Ak4	99521_at				1.14	1.14	1.00	40.39	2.12	40.36	3.69	45.93	3.66
AF020313	Apbb1ip	102710_at	N	amyloid β (A4) precursor protein-binding protein	signal transduction, transcription factor	1.83	1.72	0.94	35.86	2.41	38.01	5.60	65.48	30.49
AW215551	Arhgap9	103365_s_at		Rho GTPase activating protein 9	signal transduction	0.76	0.80	1.05	135.86	10.01	129.76	8.71	103.82	12.96
AI117236	Arhgap9	103366_at				0.83	0.89	1.07	147.37	11.76	137.55	7.58	122.30	14.66
AA870675	Atp5c1	92799_g_at	mit	ATP synthase, F1 gamma polypeptide 1	ATP synthesis; proton transport	0.83	0.76	0.92	2814.53	266.68	3058.26	448.28	2322.67	219.90
AI836694	**Atp5c1	92800_i_at				0.87	0.85	0.98	4897.43	509.41	5021.02	440.49	4265.96	140.02
M64298	Atp6v0c	96919_at	lys	ATPase, V0 subunit C	proton pump	0.81	0.87	1.08	8609.77	495.68	8001.62	566.38	6959.80	746.94
AI843029	Atp6v1b2	92598_at	lys	ATPase, V1 subunit B	proton pump	0.89	0.90	1.00	6109.35	223.91	6088.81	189.09	5466.73	492.64
AW107884	AW107884	93829_at	IC	ROD1 homolog [Rattus norvegicus],	RNA processing & modification	2.28	2.00	0.88	30.18	5.46	34.32	12.25	68.69	27.48
X01838	B2m	93088_at	M, EC	beta-2 microglobulin	small subunit MHC I receptor	2.10	1.53	0.73	662.22	113.37	910.26	287.76	1388.77	275.21
AI844631	Baiap2	99337_at		angiogenesis inhibitor 1-associated protein 2	Rho protein signal transduction	1.37	1.33	0.97	61.88	5.03	63.99	7.07	85.03	17.62
U42443	Bcat1	100026_at	IC	branched chain aminotransferase 1	amino acid metabolism	0.63	0.75	1.18	2598.70	152.63	2201.62	380.81	1647.20	297.39
M22531	C1qb	96020_at	EC	complement component 1q beta polypeptide	complement activity	1.46	1.33	0.91	58.84	6.66	64.50	14.16	85.78	10.18
K02782	C3	93497_at	EC	complement component 3	complement activity	2.61	1.81	0.70	97.18	18.14	139.77	47.79	253.45	69.08
AW125070	C630022N07Rik	96147_at	IC, N	RIKEN cDNA C630022N07 gene	predicted transcription factor	0.83	0.88	1.06	202.99	15.20	191.75	10.34	169.31	6.63
AJ010949	Cacna2d3	98300_at	M	calcium channel, alpha2/delta subunit 3	Ca channel regulatory subunit	0.56	0.67	1.20	696.07	100.17	579.00	74.09	386.42	49.73
U49513	Ccl9	104388_at	EC	chemokine (C-C motif) ligand 9	signal transduction	1.39	1.28	0.92	57.47	3.38	62.55	6.38	79.82	7.79
U56819	Ccr2	93397_at	M	chemokine (C-C) receptor 2	signal transduction	1.27	1.30	1.02	31.32	2.43	30.68	3.55	39.86	5.74
AV370035	Ccr5	161968_f_at	M	chemokine (C-C motif) receptor 5	signal transduction	1.51	1.70	1.13	39.85	13.13	35.28	3.48	59.98	16.88
X97227	Cd53	94939_at	M	CD53 antigen	modulates cell-ECM interaction	2.24	1.99	0.89	39.68	8.11	44.76	14.83	89.01	53.01
U60473	Cd59a	101516_at	M, EC	CD59a antigen	complement activity	0.78	0.80	1.03	2333.06	192.37	2257.15	205.82	1810.77	161.36
AF011644	Cdkap1	98532_at	IC	CDK2-associated protein 1	cell growth and/or maintenance	0.78	0.79	1.01	793.06	63.54	784.33	92.13	619.54	73.28
AF012708	Cenpc	98770_at	N	centromere protein C (Cenp-c)	chromosome organization & biogenesis	1.23	1.21	0.98	136.80	14.95	139.33	16.95	168.37	11.73
AF011450	Col15a1	99637_at	EC	procollagen, type XV	ECM structural constituent	1.46	1.28	0.88	95.13	9.71	108.00	21.04	138.69	12.32
AW049031	Copeb	98083_at	N	core promoter element binding protein	transcription factor coactivator	1.55	1.40	0.90	489.10	60.66	541.95	96.69	759.39	149.86
AI020792	Copg1	96936_at	ER, G	coatomer protein, subunit gamma 1	intracellular protein transport	0.76	0.81	1.06	780.64	90.44	736.29	58.83	595.39	104.21
X06368	Csf1r	104354_at	M	colony stimulating factor 1 receptor	signal transduction	1.48	1.34	0.90	169.83	18.30	188.50	30.00	251.72	51.16
X15591	Ctla2a	96912_s_at		cytotoxic T lymphocyte-associated protein 2α	unknown	1.73	1.77	1.02	88.30	29.77	86.32	21.14	152.77	44.43
U74683	Ctsc	101019_at	lys, EC	cathepsin C preprotein	proteolysis and peptidolysis	2.06	1.66	0.81	46.57	19.13	57.78	28.55	96.08	17.39
AJ223208	Ctss	98543_at	lys, EC	cathepsin S preprotein	proteolysis and peptidolysis	1.92	1.69	0.88	624.07	123.03	710.46	236.09	1201.30	355.01
AW046124	Cyba	97013_f_at	mit	cytochrome b-245, alpha polypeptide	electron transport	1.45	1.35	0.93	70.78	5.26	76.00	14.46	102.88	23.76
M31775	**Cyba	100059_at				1.30	1.19	0.91	239.22	20.20	261.72	32.13	310.26	65.72
AB011678	Dcx	102307_at	CySk	doublecortin	cytoskeletal complex constituent	1.27	1.26	0.99	91.95	15.34	92.56	14.08	116.43	6.79
AB009376	Dffa	99485_at	IC	DNA fragmentation factor, alpha subunit	apoptosis regulator	0.43	0.58	1.35	540.16	145.93	400.47	107.89	234.18	75.78
AI182272	Dffa	160866_at				0.49	0.59	1.19	2643.32	668.43	2218.30	654.46	1299.17	254.02
AI846152	Dscr1	100555_at	IC, N	Down syndrome critical region homolog 1	calcium-mediataed signaling	0.74	0.78	1.06	784.07	125.10	741.25	65.58	579.01	99.97
AV122030	Dscr3	162486_f_at	IC	Down syndrome critical region gene 3	intracellular protein transport	0.84	0.89	1.06	879.30	70.82	829.89	45.37	738.35	39.51
AA624336	Dtymk	98618_at		deoxythymidylate kinase	nucleotide biosynthesis	0.87	0.89	1.02	154.03	2.58	150.85	16.03	133.89	3.45
AW212878	Edem-pending	104065_at	ER	ER degradation enhancer, mannosidase	ER-associated protein catabolism	1.14	1.11	0.97	12.65	0.81	13.00	0.17	14.43	0.38
AW123850	F2r	95474_at	M	thrombin receptor	signal transduction	2.03	1.78	0.88	662.17	193.49	752.40	146.20	1341.07	321.28
X59398	Flt3	95295_s_at	M	FMS-like tyrosine kinase 3	signal transduction	0.63	0.70	1.11	1044.99	108.49	938.68	143.52	659.30	106.42
AA960459	Fnbp2, srGap3	96516_at	IC	formin binding protein 2	signal transduction	0.75	0.81	1.07	118.65	8.63	110.45	8.56	89.54	7.82
L13204	Foxj1	98831_at	N	forkhead box J1	transcription factor	0.85	0.81	0.96	421.04	38.05	440.07	40.85	357.49	28.53
AI839918	Gars	93270_at	IC	glycyl-tRNA synthetase	protein biosynthesis	0.73	0.71	0.98	865.12	138.73	881.10	99.01	627.65	115.65
U85414	Gclc	99649_at	IC	glutamate-cysteine ligase, catalytic subunit	glutathione biosynthesis	0.86	0.88	1.02	555.67	38.33	546.43	40.60	480.19	31.58
Y17851	Gdap2	104134_at		ganglioside-induced differentiation-assoc.-pr 2	unknown	0.70	0.77	1.10	664.00	68.34	602.48	72.73	466.12	88.16
U10551	Gem	92534_at	IC	monomeric G protein	signal transduction	0.50	0.63	1.27	132.42	25.84	104.14	37.26	65.88	9.75
AW125649	Gna12	97226_at	M	trimeric G protein, alpha 12 subunit	signal transdiction	1.36	1.22	0.90	202.96	25.01	225.97	29.21	276.57	29.72
X83577	Gpc4	102886_at	M, EC	glypican 4	signal transdiuction, ECM interactions	1.42	1.26	0.89	80.82	8.85	90.78	12.18	114.65	11.73
U13705	Gpx3	101676_at	EC	glutathione peroxidase 3	response to oxidative stress	1.50	1.43	0.96	239.10	53.58	250.15	83.75	357.50	40.44
AC002397	Grcc3f	98965_at		gene rich cluster	unknown	1.35	1.26	0.93	103.85	7.33	111.89	14.32	140.63	17.67
AI836554	Hdlbp	96359_at	N	high density lipoprotein binding protein	lipid transport	0.82	0.84	1.02	1414.90	143.98	1392.31	68.54	1165.35	115.41
Y11666	Hk2; HKII	94375_at	M	hexokinase II	glycolysis	1.39	1.26	0.90	62.72	4.05	69.50	7.50	87.25	13.29
AF054670	Hmox2	101062_at	M	heme oxygenase (decycling) 2	heme oxidation	0.80	0.81	1.02	204.30	12.32	200.63	18.46	163.50	26.92

AF023482	Hs1bp1	101096_s_at	mit, ER	HS1 binding protein	signal transduction	0.76	0.77	1.02	587.91	69.12	578.68	56.57	448.09	99.03
AI574278	Ide	160290_at	EC	insulin degrading enzyme	proteolysis and peptidolysis	0.74	0.78	1.05	86.68	7.83	82.79	12.92	64.28	7.43
Y15001	Irx3	99034_at	N	Iroquois related homeobox 3 (Drosophila)	transcription factor	0.46	0.51	1.09	170.47	73.72	155.92	41.34	79.01	12.20
Y16518	Lancl1	103656_at	M	LanC-like protein 1, GPCR 69	GPCR, signal transduction	0.71	0.78	1.09	1623.74	156.32	1486.32	216.49	1160.92	141.39
AW123934	Laptm4b	100571_at	lys	lysosomal associated protein	lysosome transmembrane protein	0.64	0.71	1.12	4575.58	554.55	4089.53	418.61	2914.02	456.15
U29539	Laptm5	100012_at	lys	lysosomal associated protein	lysosome transmembrane protein	1.45	1.40	0.96	340.45	25.75	353.28	25.00	493.37	135.37
AA726364	lpl	95611_at	EC	lipoprotein lipase	lipid metabolism	2.75	2.18	0.79	59.35	7.37	74.69	31.28	162.93	109.02
AF045573	Lrrfip1	92563_at		leucine rich repeat interacting protein 1	unknown	0.85	0.88	1.04	583.59	56.97	562.22	21.00	494.83	32.33
U72644	Lst1	103571_at		leukocyte specific transcript 1	unknown	1.55	1.43	0.92	190.20	3.64	206.28	13.55	295.38	79.58
M21050	lys	100611_at	EC, mit	lysozyme	carbohydrate metabolism	4.49	2.82	0.63	44.54	16.27	71.04	37.29	200.10	188.88
AJ243608	Magel2	92681_at		melanoma antigen	unknown	1.45	1.33	0.92	61.27	4.75	66.36	2.04	88.55	6.33
AW259500	Map3k7ip2	160309_at	IC	MAPKKK 7 interacting protein 2	signal transduction	1.53	1.43	0.94	496.70	61.13	530.47	109.53	757.49	134.23
Y13439	Mapk12	92323_at	IC	mitogen-activated protein kinase 12		0.84	0.82	0.97	377.30	14.36	389.23	31.90	317.83	44.60
M60474	MARCKS	96865_at	M	myristoylated alanine rich PKC substrate	actin & calmodulin binding	2.59	1.74	0.67	277.09	71.64	413.22	145.09	718.12	87.82
X72795	Mmp9	99957_at	EC	matrix metalloproteinase 9	proteolysis and peptidolysis	0.51	0.68	1.35	393.23	104.18	291.36	26.91	198.85	44.93
AV239570	**Mmp9	162369_f_at				0.70	0.91	1.30	26.40	7.08	20.35	2.22	18.52	3.62
L20315	Mpeg1	99071_at		macrophage expressed gene 1	unknown	1.35	1.29	0.96	225.81	14.63	236.12	19.93	304.21	56.42
AJ223362	Myh7	98616_f_at	CySk	myosin, heavy polypeptide 7	cytoskeletal organization	1.52	1.44	0.95	84.79	7.50	89.36	8.53	128.78	33.19
AW047320	Ndel1	98882_s_at	IC	nuclear distribution gene E-like homolog 1	retrograde axon transport, CySk interacting protein	0.75	0.84	1.13	1633.64	41.33	1444.58	139.72	1217.07	149.68
AI837311	**Ndel1	98884_r_at				0.66	0.90	1.37	926.55	289.74	676.97	91.17	610.32	93.35
AW046205	Ndufa4	160477_at	mit	NADH dehydrogenase 1 alpha subcomplex, 4	electron transport chain	0.86	0.89	1.04	33.09	1.65	31.95	1.91	28.56	2.41
M35131	Nefh	103234_at	CySk	neurofilament, heavy polypeptide	cytoskeleton organization & biogenesis	0.49	0.64	1.32	6286.97	1515.16	4778.15	796.94	3080.17	637.30
AI846534	Nek6	160846_at		NIMA-related expressed kinase 6	signal transduction	0.87	0.85	0.99	185.95	11.00	188.72	16.35	161.16	16.78
M17298	Ngfb	102298_at	EC	nerve growth factor, beta	growth & maintenance, signal transduction	0.87	0.89	1.01	32.01	2.59	31.56	2.19	27.93	1.44
AV372577	Npy2r	162037_f_at	M	neuropeptide Y receptor Y2	neuropeptide signal transduction	1.91	1.89	0.99	234.17	27.65	235.89	14.57	446.90	174.57
D86238	Npy2r	100703_at				1.38	1.41	1.02	49.00	2.00	48.00	5.52	67.51	12.70
D13664	Osf2-pending	92593_at	EC	periostin	cell adhesion, transcription factor	3.07	2.67	0.87	36.42	12.52	41.88	19.12	111.72	78.27
AW046590	Pcbd	99056_at	IC, N	6-pyruvoyl-tetrahydropterin synthase/ dimerization cofactor of hepatocyte nuclear factor 1α	L-phenylalanine metabolism/ transcription coactivator	1.45	1.35	0.93	331.52	66.89	354.71	82.96	480.38	30.31
AA755004	Pdir-pending	96831_at		protein disulfide isomerase-related		1.26	1.32	1.05	58.64	3.21	55.93	7.41	73.62	9.95
AI842259	Pdk3	92810_at	mit	pyruvate dehydrogenase kinase, isoenzyme 3	phosphorylates pyruvate dehydr.	0.61	0.75	1.23	666.71	88.68	540.48	117.78	405.10	45.21
M55181	Penk1	94516_f_at	EC	preproenkephalin 1	neuropeptide signal transduction	3.15	2.43	0.77	1506.34	665.99	1950.34	586.98	4748.73	1129.00
M55181	Penk1	94517_r_at				1.74	1.51	0.87	139.27	14.63	159.78	8.72	241.80	60.47
M68915	Pgr	98726_at	IC, N	progesterone receptor	steroid hormone signal transduction	0.90	0.89	0.99	22.09	0.63	22.35	0.70	19.97	0.99
AJ242864	Phtf	94406_at		putative homeodomain transcription factor	transcription regulation	0.83	0.84	1.01	334.29	40.82	329.95	34.56	277.28	19.99
AV378129	Ppfibp2	162129_f_at	IC	tyrosine phosphatase receptor F interacting protein	signal transduction	1.15	1.09	0.95	11.30	0.41	11.88	0.49	12.98	0.72
AV261930	Prm2	161229_at		protamine 2		0.84	0.85	1.01	19.91	1.83	19.66	1.91	16.66	0.63
AW122465	Prp19, snev	97395_at	N	PRP19/PSO4 homolog (S. cerevisiae)	nuclear matrix protein	0.73	0.75	1.03	1730.46	226.76	1677.50	309.27	1264.62	236.32
AB007696	Ptger2	98768_at	M	prostaglandin E receptor 2	eicosanoid hormone signal transduction	1.10	1.13	1.03	19.48	0.83	18.99	1.04	21.49	0.76
D10204	Ptger3	96588_at	M	prostaglandin E receptor 3	eicosanoid hormone signal transduction	1.18	1.16	0.98	10.49	0.56	10.68	0.72	12.40	1.16
U37465	Ptpro	100427_at	M	protein tyrosine phosphatase, receptor type, O	signal transduction	1.36	1.24	0.91	176.83	12.45	194.75	24.45	240.63	28.83
AI891912	Pvrl3	99062_at	M	poliovirus receptor-related 3	cell adhesion	1.28	1.22	0.95	16.19	1.51	17.04	1.31	20.71	1.31
AB030505	Rdh11	99592_f_at	M	retinol dehydrogenase 11	retinoid metabolism	1.23	1.15	0.93	994.46	40.44	1064.57	74.03	1219.77	79.49
AI835968	Rin2	160827_at	IC	Ras and Rab interactor 2	secretion, vesicular transport, signaling	1.82	1.39	0.76	317.55	40.33	416.24	120.04	578.20	85.36
L08651	Rpl29	94240_i_at	IC	ribosomal protein L29	protein biosynthesis	1.62	1.45	0.90	194.34	36.69	216.07	17.41	313.92	79.27
U41341	S100a11	98600_at	IC, N	S100 calcium binding protein A11 (calizzarin)	cytokine activity	4.05	2.22	0.55	107.52	28.22	195.99	83.90	435.39	225.18
X68837	Scg2; Chgc; SgII	92981_at	EC	secretogranin II	calcium binding	1.43	1.44	1.01	598.54	128.03	592.51	76.28	855.68	90.06
X91144	Selpl	103488_at	M	selectin, platelet (p-selectin) ligand	cell adhesion	1.16	1.14	0.98	199.26	12.36	202.96	20.52	230.67	13.25
AJ239082	Sh3bgr	96204_at		SH3-binding domain glutamic acid-rich protein	unknown	0.69	0.77	1.12	241.69	19.84	216.27	11.03	167.39	20.06
AW048272	Sh3bgr	96205_at				0.49	0.54	1.09	1308.13	140.05	1197.38	143.16	641.77	91.45
AF038848	Sin3b	93789_s_at	N	transcriptional regulator, SIN3B (yeast)	regulates transcription	1.23	1.16	0.95	238.06	23.77	251.70	25.01	293.20	20.41
U73521	Slc1a1	104747_at		solute carrier family 1, member 1		0.66	0.72	1.10	290.25	24.58	264.32	35.92	191.53	27.83
U70859	Slc7a3	93133_at	M	cationic amino acid transporter, y+ system	glutamate symporter	1.23	1.25	1.01	127.00	12.78	125.27	11.30	156.03	15.10
AW120567	Snx9	160593_at	IC	sorting nexin 9	intracellular protein transport, endocytosis	1.24	1.21	0.98	915.91	25.75	935.24	100.99	1131.83	129.00
AF008914	Sstr2	98350_at	M	somatostatin receptor 2	signal transduction	1.71	1.60	0.94	53.62	2.70	57.30	4.95	91.86	23.09
D86639	Stac	94731_at	IC	SH3 and cysteine rich domain	intracellular signaling cascade	1.70	1.65	0.97	63.86	10.99	65.71	5.62	108.63	51.73
AV378535	Sult1a1	162130_r_at		sulfotransferase family 1A, phenol-preferring, member 1	steroid metabolism	1.08	1.08	1.00	11.57	0.31	11.62	0.49	12.50	0.55
AB026806	Syt5	104269_at	IC	synaptotagmin 5	synaptc vessicle & secretory granule exocytosis	1.43	1.39	0.97	321.25	33.69	332.33	52.61	460.96	62.90
D17584	Tac1	102726_at	EC	tachykinin 1	neuropeptide signal transduction	6.31	5.41	0.86	67.04	29.24	78.17	72.89	422.82	503.80
X95279	Thrsp	160306_at	N	thyroid hormone-responsive protein	unknown	0.46	0.59	1.29	513.72	123.46	398.27	50.31	235.53	17.30
AI848685	Timm13a	94012_at	mit	translocase of inner mitochondrial membrane 13	protein-mitochondrial targeting	0.86	0.85	0.99	93.83	6.43	94.52	7.33	80.45	5.68
U38967	Tmsb4x; Ptmb4	96426_at	CySk	thymosin beta 4	cytoskeleton organization and biogenesis	1.32	1.32	1.00	1297.34	183.81	1297.78	158.37	1715.36	245.37
AF011543	Trpc4	94100_s_at	M	transient receptor potential cation channel C4	signal transduction	1.33	1.48	1.11	70.01	6.95	62.97	2.68	93.16	18.01
AF024637	Tyrobp	100397_at	M	TYRO protein tyrosine kinase binding protein	signal transduction	2.02	1.66	0.82	98.85	11.20	120.39	9.98	200.13	82.68
U16818	Ugt1a6	99580_s_at		UDP glycosyltransferase 1 family, polypeptide A6	glucuronate metabolism	1.51	1.41	0.93	226.02	21.80	241.90	50.29	341.84	56.80
AF079565	Usp2	92821_at	IC	ubiquitin specific protease 2	ubiquitin-dependent protein catabolism	0.83	0.75	0.91	191.25	12.16	210.50	10.15	158.57	16.34
AW012491	Vkorc1	95709_at	ER	vitamin K epoxide reductase, subunit 1	vitamen K biosynthesis	1.37	1.25	0.91	493.57	36.63	541.01	120.54	677.60	29.15
AW050287	Wdr6	95643_at		WD repeat domain 6	unknown	2.05	1.46	0.71	229.19	50.79	321.28	54.95	470.13	121.63
AF076956	Ykt6-pending	104400_at		prenylated SNARE protein	unknown	0.56	0.65	1.15	213.81	51.17	186.01	36.60	120.12	13.88
AI643393		104641_f_at		Similar to RIKEN cDNA 9030624G23		0.81	0.81	0.99	868.95	117.02	874.14	88.03	705.91	66.01
C80836		96391_at		ESTs		1.36	1.52	1.12	116.40	19.90	104.23	24.21	158.60	19.94
AI643731		95377_at		ESTs		0.63	0.68	1.07	723.57	129.95	676.71	135.09	458.87	55.29
AA873956		102862_at		ESTs		0.62	0.67	1.08	1025.48	157.20	953.37	252.74	639.01	59.52
AV099015		161498_at				1.26	1.15	0.92	486.39	28.76	529.53	17.93	611.34	73.51
AW123823		104252_at		RIKEN A630040D01		1.40	1.20	0.86	75.66	5.13	87.83	5.70	105.83	14.27
AW227650	0610038P07Rik	104248_at		RIKEN cDNA 0610038P07 gene		0.85	0.89	1.05	509.67	26.60	487.13	38.82	435.69	16.91
AI854264	0710001C05Rik	96021_at		RIKEN cDNA 0710001C05 gene		0.79	0.78	0.99	996.11	95.77	1004.27	120.87	788.17	164.32
AW047874	1110020K19Rik	103773_at		RIKEN cDNA 1110020K19 gene		0.78	0.83	1.06	535.77	39.15	506.60	64.74	419.61	26.69
AI841858	1500036F01Rik	97297_at		RIKEN cDNA 1500036F01 gene		0.60	0.74	1.22	1057.29	224.28	864.06	105.13	637.18	101.19
AI840191	2210409B22Rik	97425_at		RIKEN cDNA 2210409B22 gene		1.57	1.29	0.82	275.84	18.06	335.89	26.48	432.98	90.21
AW046552	2310042M24Rik	96649_at		RIKEN cDNA 2310042M24 gene		0.74	0.76	1.02	3253.01	246.03	3176.20	102.54	2402.38	330.40
AI853129	2310057G13Rik	160659_at		RIKEN cDNA 2310057G13 gene		0.79	0.77	0.98	77.92	11.26	79.35	13.14	61.35	6.71
AI846893	2400004O09Rik	160991_at		RIKEN cDNA 2400004O09 gene		0.68	0.72	1.07	3848.69	538.98	3602.62	777.30	2608.13	414.44
AI854043	2600013G09Rik	96941_at		RIKEN cDNA 2600013G09 gene		0.88	0.86	0.98	350.17	8.19	357.78	20.04	308.47	28.89
AI595313	2610019F01Rik	161011_at		RIKEN cDNA 2610019F01 gene		1.28	1.27	0.99	48.30	2.33	48.61	8.66	61.63	8.53
AI846549	2610019F03Rik	100902_at		RIKEN cDNA 2610019F03 gene		0.68	0.69	1.02	564.47	48.92	552.31	51.07	382.66	68.97
AV375886	2700038P16Rik	161071_at		RIKEN cDNA 2700038P16 gene		0.84	0.84	1.00	359.61	25.83	358.45	27.74	301.38	22.65
AA607767	3110001K13Rik	104212_at		RIKEN cDNA 3110001K13 gene		0.79	0.77	0.98	2101.42	330.03	2136.40	300.12	1653.35	208.35
AI043090	3110018A08Rik	93913_at		RIKEN cDNA 3110018A08 gene		1.67	1.51	0.90	123.25	8.16	136.54	23.69	205.91	41.53
AI843267	3110056M06Rik	103356_at		RIKEN cDNA 3110056M06 gene		1.28	1.17	0.91	19.72	1.33	21.58	1.99	25.24	1.99

AA733594	4632428N09Rik	160286_at		RIKEN cDNA 4632428N09 gene		1.57	1.59	1.01	148.49	21.39	146.40	39.09	232.48	72.49
AI552922	4633402N23Rik	97370_at		RIKEN cDNA 4633402N23 gene		0.79	0.83	1.04	471.61	24.90	452.25	25.27	374.88	35.19
AI464596	4930553M18Rik	104639_i_at		mz66c12.y1 S		1.38	1.28	0.93	257.82	24.13	277.59	44.65	355.03	57.18
AI464596	**4930553M18Rik	104640_f_at				1.61	1.41	0.88	237.83	33.67	271.70	58.24	382.41	105.92
AI842353	AI842353	160971_at		unknown		0.71	0.75	1.05	412.00	65.63	393.71	61.08	294.28	39.26
AI844839	6330442E10Rik	103424_at		RIKEN cDNA 6330442E10 gene		0.66	0.68	1.04	748.09	96.08	719.81	144.11	490.57	153.23
AI850713	8430420C20Rik	103916_at		RIKEN cDNA 8430420C20 gene		1.87	1.54	0.83	112.46	20.85	136.22	40.19	210.09	29.09
AA592069	9130025P16Rik	104215_at		RIKEN cDNA 9130025P16 gene		0.74	0.73	0.98	184.43	27.35	187.38	32.17	136.31	29.36
AW060889	BC005662	160897_at		cDNA sequence BC005662		1.33	1.27	0.95	78.57	5.28	82.57	6.11	104.74	5.99
AI852661	D430019H16Rik	95397_at		RIKEN cDNA D430019H16 gene		2.26	1.88	0.83	191.06	20.05	229.02	31.91	431.21	97.09

Class III: Genes that are uniquely expressed in LMN (73)

									Average Signal Intensities & Standard Deviations					
						Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**Probeset**	**location**	**Description**	**Function**	**IML/LMN**	**IML/MMN**	**LMN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
AW125884	Acas2l	160921_at	mit	acetyl-Coenzyme A synthetase 2	metabolism	1.50	1.01	0.67	150.65	35.63	223.41	58.77	226.19	55.46
AJ130977	Arih1	95563_at		ariadne ubiquitin-conjugating enzyme E2 binding protein	ubiquitin-dependent protein catabolism	0.82	0.98	1.18	204.89	11.21	173.08	9.27	168.91	10.74
AW121246	Atp6v1g1	96281_at	lys	ATPase, H+ transporting, V1 subunit G isoform 1	proton pump	0.79	0.94	1.19	3257.24	321.78	2729.22	329.60	2558.92	214.25
AV356510	AW491445	161578_r_at	mit	expressed sequence AW491445	transport	0.86	1.04	1.21	116.13	11.12	95.99	5.66	99.67	9.25
AV102186	Bad	161500_i_at	mit	Bcl-associated death promoter	integrates glucose metabolism & apoptosis	0.85	1.01	1.19	341.73	27.63	286.48	19.95	290.40	22.95
AA863928	Baz1b	103081_at	N	bromodomain adjacent to zinc finger domain, 1B	transcription regulation	1.23	1.08	0.87	858.10	32.52	983.51	58.88	1059.08	87.84
L18888	Canx	94886_at	ER	calnexin	ER chaperone	0.88	1.01	1.15	667.31	61.50	580.77	34.46	584.94	16.60
Y11896	Chic1	98316_at	G	cysteine-rich hydrophobic domain 1	Golgi to plasma membrane transport	0.80	0.92	1.16	98.19	11.29	84.87	3.52	78.33	1.25
AI840975	Cltc	160252_at	IC	clathrin, heavy polypeptide (Hc)	coat protein for intracellular transport	0.85	1.00	1.17	4798.22	170.52	4097.58	450.09	4077.26	227.01
M13018	Crip	94061_at		cysteine rich intestinal protein	unknown	1.32	1.00	0.75	76.93	9.45	102.25	11.91	101.84	16.21
AV218205	Cst3	161522_i_at	EC	cystatin C	cysteine protease inhibitor activity	1.59	1.18	0.74	327.66	33.81	440.51	20.46	520.65	149.06
U10098	Cst3	99586_at				1.49	1.15	0.77	2499.38	371.94	3242.08	388.66	3733.85	394.84
Y14004	Cte1	103581_at	IC	cytosolic acyl-CoA thioesterase 1	lipid metabolism	1.17	1.01	0.86	117.98	11.58	136.73	4.83	137.81	13.14
AW049573	D5Bwg0860e	161062_r_at		rap2 interacting protein x	signal transduction	0.81	0.97	1.21	2776.58	194.06	2304.00	274.86	2239.34	144.82
AW047343	Dbp	160841_at	N	D site albumin promoter binding protein	transcription regulator, circadian rhythm	1.42	1.08	0.76	113.29	8.67	149.64	18.73	161.23	16.84
X77952	Eng	100134_at	M	endoglin	constituent of TGF-beta signaling complex	1.56	1.07	0.69	543.31	88.88	789.78	112.17	847.13	184.77
AF079765	Epc1	103263_at	N	enhancer of polycomb homolog 1 (Drosophila)	transcription factor	1.28	1.08	0.85	438.32	37.68	518.54	64.23	559.03	45.15
L11333	Es31	99941_at	ER,EC	esterase 31	carboxylesterase activity	0.89	1.01	1.14	65.86	2.86	58.02	4.23	58.42	3.10
AV251191	Foxc2	162016_f_at	N	forkhead box C2	transcription factor	1.56	1.02	0.65	82.74	13.21	126.63	31.06	129.28	19.34
AF091390	Fxyd1; PLM; PML	93040_at	M	FXYD domain-containing ion transport regulator 1	accessory protein of Na,K-ATPase	1.50	1.20	0.80	546.78	49.50	682.24	90.24	820.28	114.16
AI046826	Gab1	160714_at	IC	growth factor receptor bound protein 2-associated protein 1	signal transduction	1.65	1.09	0.66	313.46	50.75	473.00	56.21	516.46	81.88
X65128	Gas1	94813_at	M	growth arrest specific 1	growth regulation	2.01	1.25	0.62	311.55	63.70	503.46	127.66	627.42	214.01
AV062425	Gast	161639_f_at	EC	gastrin	peptide hormone	0.78	1.03	1.32	44.90	3.67	34.05	3.55	35.08	3.28
AV381947	Glul	161826_r_at	mit	glutamate-ammonia ligase	glutamine synthetase	0.90	1.01	1.12	721.82	45.09	643.90	32.13	650.13	41.95
D29802	Gnb2-rs1	99340_at	IC	guanine nucleotide binding protein, beta 2	signal transduction	1.37	1.05	0.77	995.00	136.22	1297.15	123.32	1359.88	80.60
J03952	Gstm1	93543_f_at		glutathione S-transferase, mu 1	metabolism	1.18	0.98	0.83	3052.33	252.33	3684.24	406.36	3614.40	245.60
AI841270	Gstm1	102094_f_at				1.31	1.00	0.76	1478.87	244.54	1933.58	94.86	1935.07	209.72
U43715	Hand2	99914_at	N	heart and neural crest derivatives expressed transcript 2	transcription factor	0.92	1.05	1.14	44.20	1.91	38.68	1.42	40.50	2.14
Y09517	Hsd17b2	101891_at	M	hydroxysteroid (17-beta) dehydrogenase 2	steroid biosynthesis	0.58	0.78	1.35	113.46	26.60	83.96	14.98	65.67	7.05
M58567	Hsd3b1	103072_at	ER, mit	hydroxysteroid dehydrogenase-1, delta<5>-3-beta	steroid hormone bisynthesis	0.89	1.01	1.13	86.53	3.59	76.60	2.02	76.99	1.64
AI844520	Ifi30	97444_at	EC, lys	interferon gamma inducible protein 30	antigen processing for MHC II presentation	1.39	1.12	0.80	38.16	3.10	47.47	8.97	52.98	3.13
AB012886	Igfbp7	160527_at	EC	insulin-like growth factor binding protein 7	regulationof growth & metabolism	1.15	0.99	0.86	119.44	8.53	138.68	13.30	137.00	5.50
AW047808	Immt	100589_at	mit	inner membrane protein, mitochondrial		0.82	0.92	1.12	135.55	3.72	121.17	9.22	111.50	3.34
AI047617	Itsn	104522_at	IC	intersectin (SH3 domain protein 1A)	endocytic adaptor protein	1.22	1.04	0.85	714.68	48.56	839.91	28.82	873.75	73.69
AA986344	Kcnj1	103973_at	M	K inwardly-rectifying channel, subfamily J, member 1	potassium channel	0.88	1.05	1.19	36.46	2.41	30.67	2.04	32.11	1.39
X64070	M6pr	92846_at	lys	mannose-6-phosphate receptor, cation dependent	intracellular protein transport	0.80	0.98	1.23	36.17	2.86	29.44	2.41	28.84	2.83
AJ005532	Magea8	103291_at		melanoma antigen family A, 8	unknown	0.84	0.95	1.13	178.84	11.82	158.17	9.45	149.56	11.03
AV345275	Matn2	161776_at	EC	matrilin 2	non-collagenous extracellular matrix protein	0.90	1.02	1.13	95.50	5.40	84.21	5.47	86.09	4.85
AF079366	Mpp3	103247_at	M	MAGUK p55 subfamily member 3	signal transduction	1.36	1.05	0.78	186.29	27.51	239.94	31.87	252.47	32.42
AF073997	Mtmr1	103264_at	IC, M	myotubularin related protein 1	phosphatase, signal transduction	0.83	0.94	1.14	108.30	7.23	94.97	6.37	89.68	6.11
Z11886	Notch1	97497_at	M	Notch gene homolog 1 (Drosophila)	transcription factor, signal transduction	1.47	1.10	0.75	253.47	22.58	338.22	51.77	372.38	44.20
AB008180	Pcdha13	101771_r_at	M	protocadherin alpha 13	cell adhesion	0.87	0.98	1.12	4045.65	159.81	3607.67	280.98	3518.39	184.09
AV149007	Pdlim1	161348_r_at	IC	PDZ and LIM domain 1 (elfin)	adaptor, signal transduction, CySk interactions	0.85	0.96	1.14	454.49	32.25	399.01	35.08	384.86	23.35
AV318045	Pvrl3	161415_r_at	M	poliovirus receptor-related 3	cell adhesion	0.75	0.89	1.18	33.90	4.41	28.67	2.22	25.39	0.56
U73199	Rgnef	92710_at		Rho-guanine nucleotide exchange factor	signal transduction	1.24	1.03	0.83	170.92	17.36	205.65	21.28	211.56	16.08
X15962	Rps12	102126_at	IC	ribosomal protein S12	protein biosynthesis	1.76	1.30	0.74	1439.57	215.79	1949.57	393.91	2530.88	368.21
AF100956	Rps18	98333_at	IC	ribosomal protein subunit S18	protein biosynthesis	1.47	1.10	0.75	920.88	74.51	1233.85	270.76	1352.71	191.64
AI836446	Rrbp1	92850_at	IC	ribosome binding protein 1	protein biosynthesis	1.57	1.21	0.78	198.44	17.01	255.85	47.83	310.62	32.27
AI840996	Sepr	160275_at		selenoprotein R	methionine sulfoxide reductase	0.66	0.87	1.31	686.54	14.69	523.68	70.10	456.09	83.40
AB030836	Siat7e	92403_at	G	sialyltransferase 7E	protein amino acid glycosylation	1.28	0.92	0.72	53.44	5.96	74.35	5.57	68.46	10.05
U10531	Skil; sno; Skir	94752_s_at	N	SNO proto-oncogene	cell growth and maintenance	0.88	1.00	1.13	82.17	2.75	72.64	2.88	72.61	5.42
X81633	Spag5	92412_s_at	N	sperm associated antigen 5	microtubule (mitotic spindle) associated protein	0.86	1.00	1.16	25.61	3.24	22.06	1.29	22.11	1.18
U10355	syt4	160190_at	IC	synaptotagmin 4	vesicular trafficking and exocytosis	0.56	1.04	1.87	55.29	18.40	29.61	6.14	30.86	10.34
AV220470	Tbx2	161146_r_at	N	T-box 2	transcription factor	0.76	0.99	1.30	47.91	3.96	36.90	2.13	36.59	1.78
D38410	Tff3	100106_at	EC	trefoil factor 3, intestinal	peptide signal transduction	0.91	1.00	1.09	295.52	15.01	270.28	11.28	269.31	7.76
L34169	Thpo	97734_at	EC	thrombopoietin	hormone/cytokine, cell growth & maintenance	0.92	0.99	1.08	97.41	5.75	90.56	2.84	89.24	1.61
AW210080	Ube2n	96959_at	IC	ubiquitin-conjugating enzyme E2N	ubiquitin-dependent protein catabolism	0.77	0.97	1.27	800.92	69.61	629.18	123.41	613.02	38.55
AI850362	Uck2-pending	94367_at		uridine-cytidine kinase 2	carbohydrate metabolism	0.70	0.95	1.36	225.47	27.69	166.13	18.50	157.02	33.71
AF035643	Vamp5	92496_at	M	vesicle-associated membrane protein 5	vesicular trafficking & transport, secretion	1.44	1.12	0.77	222.48	24.34	287.19	51.93	320.96	40.05
AV157222	Vapa	161516_r_at	IC	vesicle-associated membrane protein A	vesicular trafficking & transport	0.81	0.97	1.19	20.16	1.91	16.95	2.38	16.37	0.46
X60671	Vil2	100084_at	CySk	villin 2	actin filament-plasma membrane linker	1.43	1.05	0.73	123.47	5.70	168.05	29.09	175.96	18.67
U47024	Vps35	92640_at		vacuolar protein sorting 35	lysosomal protein-sorting pathway	0.77	0.96	1.25	1844.55	180.76	1471.02	290.11	1418.19	162.95
AV008160	1110008H02Rik	161635_f_at		RIKEN cDNA 1110008H02 gene		0.88	1.05	1.19	17.01	1.43	14.26	0.93	15.04	0.75
AW045753	1110015E22Rik	104217_at		RIKEN cDNA 1110015E22 gene		1.85	1.18	0.64	392.97	110.25	614.53	143.23	726.69	171.53
AW125347	1810037I17Rik	95406_at		RIKEN cDNA 1810037I17 gene		1.33	1.08	0.81	1176.57	68.11	1448.27	106.37	1564.07	290.64
AV329607	2210013I18Rik	161997_f_at		RIKEN cDNA 2210013I18 gene		1.75	1.17	0.67	233.59	56.56	348.85	59.60	409.22	103.72
AA407120	2210418O10Rik	100321_f_at		RIKEN cDNA 2210418O10 gene		0.89	1.03	1.16	17.59	1.35	15.20	1.21	15.67	0.61
AV370769	4833412C19Rik	161887_r_at		RIKEN cDNA 4833412C19 gene		0.88	0.98	1.12	72.73	6.17	65.03	1.71	63.65	4.80
AI157260	4833420O05Rik	160605_s_at		RIKEN cDNA 4833420O05 gene		0.77	0.94	1.22	82.05	8.06	67.09	5.41	62.89	9.74
AI845273	4933402J24Rik	161015_at		RIKEN cDNA 4933402J24 gene		0.44	0.70	1.60	227.55	63.69	142.39	40.09	99.29	19.55
AI561567	5730481H23Rik	93464_at		RIKEN cDNA 5730481H23 gene		0.81	0.99	1.22	28.16	4.37	22.99	1.78	22.72	2.39
AI845886	MGC18745	98608_at		hypothetical protein MGC18745		0.84	0.96	1.15	577.56	49.98	503.80	37.85	485.05	35.79
AV363068	MGC28888	161785_f_at		hypothetical protein MGC28888		0.89	1.03	1.16	70.51	4.95	60.84	2.41	62.65	4.25
AJ011565	MGC6694	93600_at		hypothetical protein MGC6694		1.30	1.09	0.84	260.97	34.35	310.04	14.83	339.34	40.19

AI156978	D12Ertd7e	160957_at		DNA segment, Chr 12, ERATO Doi 7, expressed		1.23	1.01	0.82	107.27	6.58	130.11	11.55	131.99	16.98

Class IV: Genes that are uniquely expressed in MMN (4)

									Average Signal Intensities & Standard Deviations					
						Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**Probeset**	**location**	**Description**	**Function**	**IML/LMN**	**IML/MMN**	**LMN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
X61448	Cbln1	92932_at	EC	cerebellin 1 precursor protein	neuropeptide	0.85	0.44	0.52	464.56	76.34	895.38	258.83	395.70	37.93
AF059735	Ctbp2	92554_at	N	C-terminal binding protein 2	transcriptional regulation	0.86	0.71	0.83	192.13	22.86	231.96	19.57	165.07	8.79
D26186	Srms	98794_at		src-related kinase	signal transduction	1.00	1.05	1.05	34.10	0.68	32.35	0.73	34.06	0.74
AF011420	V2r10	94722_f_at	M	vomeronasal 2, receptor, 10	signal transduction	0.96	1.11	1.16	124.12	2.60	107.44	7.69	119.32	4.76

Class V: Genes that are differentially expressed between LMN and IML (472)

									Average Signal Intensities & Standard Deviations					
						Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**Probeset**	**location**	**Description**	**Function**	**IML/LMN**	**IML/MMN**	**LMN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
AA967624	Abcc8	103274_at		sulfonylurea receptor	component of potassium ATP channel	0.89	0.92	1.03	132.32	6.85	128.74	8.58	118.15	4.61
M12347	Acta1; Acts	100381_at	CySk	skeletal alpha-actin gene	structural constituent of cytoskeleton	1.42	1.29	0.91	54.25	4.98	59.67	15.13	76.91	16.69
AA791742	Actr2	104168_at	CySk	ARP2 actin-related protein 2 homolog (yeast)	structural constituent of cytoskeleton	0.80	0.89	1.12	111.20	14.32	99.26	8.91	88.66	11.84
AF006196	Adam15	103588_at	M, EC	a disintegrin and metalloproteinase domain 15	membrane surface & ECM proteolysis, cell adhesion	0.83	0.92	1.10	179.21	20.29	162.53	9.92	149.58	12.35
AA036065	Adcy2	103241_at	M	adenylate cyclase 2	signal transduction	1.25	1.17	0.94	1090.99	78.54	1165.27	194.09	1364.39	183.56
M93422	Adcy6	102321_at	M	adenylate cyclase 6	signal transduction	1.19	1.03	0.87	215.72	18.21	249.33	32.09	256.74	24.24
Z50190	Adcy9	92527_at	M	adenylate cyclase 9	signal transduction	0.73	0.84	1.16	132.05	15.86	114.05	16.92	95.88	9.24
AV355809	Admr	162449_f_at	M	adrenomedullin receptor	neuropeptide signal transduction	1.31	0.99	0.75	21.52	2.02	28.67	6.36	28.24	2.72
AJ007780	Adprtl2	100903_at	N	poly(ADP-ribose) polymerase-2	DNA repair	1.50	1.31	0.88	206.87	17.51	235.96	31.96	309.38	91.61
AB016592	Agr2	101075_f_at	EC	anterior gradient 2 (Xenopus laevis)	survival factor	0.84	0.97	1.15	56.02	6.39	48.69	3.52	47.26	3.92
AF045887	Agt; Aogen	101887_at	EC	angiotensinogen	local & circulating hormone	1.65	1.16	0.70	346.27	56.61	495.47	100.82	572.68	210.40
AB020203	Ak3l	92492_at	mit	adenylate kinase 3 alpha-like	ATP metabolism	0.83	0.91	1.09	30.43	2.10	27.90	1.92	25.30	2.95
AW050387	Aldh1a3	98372_at	IC	retinaldehyde dehydrogenase type 3	retinoic acid production	1.21	1.08	0.89	29.68	2.44	33.32	1.10	36.00	3.97
U89906	Amacr	95588_at	mit	alpha-methylacyl-CoA racemase	metabolism	0.89	0.94	1.05	129.68	9.45	123.00	9.08	115.16	5.54
U73478	Anp32a	93372_at	N	acidic nuclear phosphoprotein 32, family member A	Regulation of histone acetylation & transcription	0.80	0.86	1.07	75.28	4.45	70.33	5.34	60.39	8.75
AI842771	Anp32b	96891_at	N	acidic nuclear phosphoprotein 32 family, member B	cell cycle progression	1.54	1.35	0.87	422.53	22.17	484.39	97.56	651.89	153.96
AV003419	Anxa1; lpc1	161703_f_at	EC, M, IC	annexin A 1, lipocortin 1	Ca- & phospholipid-binding protein, multiple functions	5.95	2.37	0.40	90.78	49.43	227.72	137.75	540.17	661.66
M69260	Anxa1; Lpc1	93038_f_at				5.84	2.15	0.37	83.07	56.53	225.95	146.54	485.07	551.50
X13460	Anxa6	94304_at	EC, M, IC	annexin A6	Ca- & phospholipid-binding protein, multiple functions	0.60	0.67	1.10	1393.51	314.44	1261.77	462.23	839.86	233.55
U22262	Apobec1	98398_s_at	IC	apolipoprotein B editing complex 1	mRNA editing	1.29	1.19	0.92	57.68	2.81	62.61	6.52	74.55	14.86
D00466	Apoe	95356_at	EC	apolipoprotein,	lipid transport, lipoprotein metabolism	2.13	1.35	0.63	2898.04	825.71	4594.10	1631.17	6182.09	1664.78
M13071	Araf; A-Raf	102286_at	IC, mit	A-raf peptide	signal transduction	1.22	1.09	0.90	134.29	15.40	149.88	21.63	163.63	10.85
AW212775	Arpc1b	96357_at	Cysk	actin related protein 2/3 complex, subunit 1B	cytoskeletal organization	1.24	1.16	0.93	328.40	33.43	351.79	49.38	407.25	36.92
U48797	Astn1	92702_at	M	astrotactin 1	cell adhesion	1.23	1.10	0.89	801.13	71.36	897.52	118.66	986.26	107.57
AB012276	Atf5	103006_at	N	activating transcription factor 5	regulataes transcription	1.34	1.16	0.87	87.24	5.63	100.61	6.82	116.95	17.50
AV348528	Atp1b1	161467_f_at	M	ATPase, Na+/K+ transporting, beta 1 polypeptide	Na-K exchange	0.76	0.86	1.13	701.21	21.36	622.20	107.81	535.47	88.45
U29530	Atp5f1	96898_at	mit	ATP synthase, F0 complex	ATP synthesis	0.88	0.90	1.02	106.03	3.85	104.22	9.40	93.83	6.54
U13840	Atp6v0d1	92603_at	lys	ATPase, H+ transporting, V0 subunit D isoform 1	proton pump	0.78	0.82	1.06	1578.13	80.68	1494.12	114.80	1228.13	260.87
AI843269	Atp6v0e	94301_at	lys	ATPase, H+ transporting, V0 subunit	proton pump	1.22	1.01	0.83	233.35	30.72	280.62	38.14	283.82	19.38
AV303935	AW146116	162226_r_at	M	SM-11044 binding protein	channel, small molecule transporter or receptor	0.80	0.93	1.15	147.49	21.75	128.21	11.07	118.60	6.31
X63535	Axl	99136_at	M	AXL receptor tyrosine kinase	signal transduction	1.17	1.09	0.93	96.14	4.43	103.32	10.37	112.89	10.22
AW124185	B230114J08Rik	96340_at		predicited membrane protein	unknown	0.84	0.87	1.03	2525.25	343.32	2452.01	167.41	2127.54	174.02
AI643420	Bag3	96167_at	M	Bcl2-associated athanogene 3	regulation of apoptosis	0.52	0.79	1.54	679.96	236.62	442.53	74.35	351.47	157.80
AW124113	Basp1	95673_s_at	N, M	brain abundant, membrane attached signal protein 1	transcriptional cosuppressor, signal transduction	1.62	1.33	0.83	1271.05	333.61	1539.62	568.63	2053.11	430.89
U41465	Bcl6	103015_at	N	B-cell leukemia/lymphoma 6	transcription factor	0.35	0.47	1.32	603.42	281.81	458.51	278.94	213.26	44.20
X53928	Bgn	96049_at	EC	biglycan	glycoprotein, binds collagen	2.82	1.60	0.57	403.42	157.52	711.40	431.96	1136.95	646.38
U76371	Bop	101903_at	IC, N	CD8beta opposite strand	transcription factor	0.88	0.92	1.04	89.73	5.97	85.99	5.75	79.25	3.79
Z16410	Btg1	93104_at	IC	B-cell translocation gene 1	antiproliferative	1.52	1.27	0.83	102.84	21.00	123.52	38.34	156.43	17.41
D83745	Btg3	96146_at	IC	B-cell translocation gene 3	antiproliferative	2.12	1.56	0.73	67.09	25.77	91.57	30.07	142.51	19.19
AF007802	Bysl	96644_at	IC	bystin-like	cell adhesion	0.87	0.94	1.08	21.60	1.88	19.92	1.72	18.82	0.80
X66295	C1qg	92223_at	EC	complement component 1q gamma	complement activity	1.28	1.23	0.96	200.32	26.15	208.95	33.14	257.01	28.74
AI132585	C1r	95415_f_at	EC	complement component 1, r subcomponent	complement activity	1.43	1.23	0.86	107.38	10.42	125.36	30.94	153.62	26.18
X06454	C4	103033_at	EC	complement component 4 (within H-2S)	complement activity	1.89	1.47	0.78	120.05	32.18	153.87	57.37	226.44	55.29
X73985	Calb2	95036_at	IC	calbindin 2	'fast' Ca(2+)-buffer	0.56	0.63	1.12	1720.84	570.00	1538.51	521.17	970.53	268.32
AI847646	Calml4	96203_at	IC	calmodulin-like 4	signal transduction	1.47	1.04	0.71	114.20	6.77	161.47	52.54	168.14	27.98
X54511	Capg	160106_at	CySk	capping protein (actin filament), gelsolin-like	cytoskeletal organization	1.24	1.14	0.92	105.82	9.38	114.51	18.60	130.96	12.90
AI847631	Carhsp1	96884_at		calcium regulated heat stable protein 1	transcriptional regulation	1.23	1.16	0.94	280.00	19.50	297.50	39.96	345.19	34.20
D28492	Casp2	99049_at	IC, N	caspase 2	proteolysis and peptidolysis	1.14	1.08	0.95	228.05	6.12	240.82	17.27	260.80	16.71
Y13087	Casp6	94458_at		caspase 6	proteolysis and peptidolysis	1.30	1.12	0.86	35.63	2.94	41.49	8.04	46.47	3.75
D86353	Casp7	98498_at		caspase 7	proteolysis and peptidolysis	1.21	1.05	0.87	110.38	6.39	127.40	12.18	133.17	12.16
AB026997	Cast	95062_at		calpastatin	protease inhibitor	0.52	0.71	1.37	250.90	73.57	183.28	49.34	131.01	26.74
L03279	Cbfb	93547_at	N	core binding factor beta	transcriptional regulator	1.71	1.43	0.84	2358.21	357.11	2819.27	318.59	4042.24	1467.87
AI852086	Cbx5	95614_at	N	chromobox homolog 5 (Drosophila HP1a)	chromatin assembly/disassembly	1.15	1.09	0.95	119.62	6.61	126.45	9.83	137.73	4.21
M58004	Ccl6	92849_at	EC	chemokine (C-C motif) ligand 6	signal transduction	1.31	1.21	0.92	89.51	15.07	96.99	8.03	117.22	23.28
AV174603	Ccs	162351_f_at		copper chaperone for superoxide dismutase	incorporation of copper into SOD1	1.12	1.07	0.95	64.70	3.58	67.77	4.06	72.73	1.69
AI847784	Cd34	160358_at	M	CD34 antigen	cell adhesion	1.35	1.19	0.88	109.23	10.75	123.55	22.53	147.00	26.54
X68273	Cd68	103016_s_at	M, Lys	CD68 antigen	scavenger receptor	1.25	1.12	0.90	90.66	5.54	100.90	12.54	113.21	19.00
L08115	Cd9	95661_at	M	CD9 antigen	cell adhesion	2.16	1.70	0.79	474.03	132.60	601.11	246.58	1021.92	559.12
AI844806	Cdc42ep4	94036_at	IC, CySk	CDC42 effector protein (Rho GTPase binding) 4	signal transduction	1.36	1.20	0.88	209.62	17.05	238.17	53.92	286.05	36.02
AI853217	Cdh5	104083_at	M	cadherin 5	cell adhesion	1.56	1.15	0.74	59.33	4.03	80.14	21.41	92.47	16.02
M29009	Cfh	94743_f_at	EC	complement component factor h	complement activity	2.18	1.25	0.57	61.16	23.73	106.38	67.00	133.15	46.79
M29008	Cfhl1	92291_f_at	EC	complement component factor h-like 1	complement activity	1.71	1.28	0.75	92.37	25.95	123.78	46.98	158.01	34.68
AI838398	Cic	96725_at		capicua homolog (Drosophila)	transcription factor	0.88	0.96	1.10	290.90	16.99	265.01	16.30	255.27	17.59
AF109905	Clic1	95654_at	M, IC	chloride intracellular channel 1	state-dependent voltage-gated chloride channel	2.11	1.36	0.64	68.85	24.23	106.94	36.55	145.49	47.94
U30292	Col13a1	102262_r_at	EC	procollagen, type XIII, alpha 1	structural constituent of ECM	1.11	1.04	0.93	29.48	1.61	31.55	2.26	32.86	1.61
U30292	Col13a1	102261_f_at				1.32	1.14	0.87	136.52	12.91	157.43	19.98	179.94	24.11
D17546	Col18a1	99638_at	EC	procollagen, type XVIII, alpha 1	structural constituent of ECM	1.30	1.09	0.84	309.16	33.95	369.33	56.76	402.43	44.33
AB000636	Col19a1	99842_at	EC	procollagen, type XIX, alpha 1	structural constituent of ECM	0.71	0.80	1.13	80.36	10.98	70.94	12.29	56.87	3.56
U03419	Col1a1	94305_at	EC	procollagen, type I, alpha 1	structural constituent of ECM	1.77	1.65	0.93	94.29	36.22	100.92	29.89	166.89	65.57
AV234303	Col3a1	161984_f_at	EC	procollagen, type III, alpha 1	structural constituent of ECM	3.96	1.99	0.50	34.39	18.35	68.49	39.97	136.16	88.17
X52046	Col3a1; Col3a-1	98331_at				3.42	1.82	0.53	156.33	73.58	293.99	185.30	535.11	316.15
X66405	Col6a1	95493_at	EC	procollagen, type VI, alpha 1	structural constituent of ECM	1.59	1.31	0.83	330.96	42.84	400.37	127.69	526.04	162.82
AV010209	Col6a1	162459_f_at				2.24	1.54	0.69	48.95	12.18	71.29	30.78	109.44	54.08

AI843212	Copz2	104143_at	IC	coatomer protein complex, subunit zeta 2	intracellular protein transport	1.30	1.04	0.80	159.79	20.74	199.69	44.31	207.98	15.03
U49430	Cp	92851_at	EC	ceruloplasmin	ferroxidase regulating iron efflux	2.39	1.26	0.53	53.84	19.60	102.14	55.50	128.50	19.25
AF017175	Cpt1a	93320_at	mit	carnitine palmitoyltransferase 1, liver	fatty acid metabolism	0.62	0.78	1.26	1262.84	353.79	1003.48	253.56	778.17	140.94
AF017639	Cpxm2	102226_at	EC	carboxypeptidase X 2 (M14 family)	proteolysis and peptidolysis; cell adhesion	2.01	1.43	0.71	145.28	20.02	204.70	65.60	292.39	70.91
AF084524	Creg	160502_at	N, IC	cellular repressor of E1A-stimulated genes	transcription factor	0.80	0.90	1.13	235.88	27.29	208.22	11.92	188.25	14.07
AJ006469	Crtap	103817_at	EC	cartilage associated protein	constiuent of the ECM	1.43	1.03	0.72	244.42	36.71	341.42	90.02	350.66	53.29
D14485	Csda	95755_at	N	cold shock domain protein A	transcription factor	1.32	1.20	0.91	372.38	24.24	408.63	43.51	489.88	106.34
M55219	Csprs	101845_s_at	N	component of Sp100-rs	signal transduction	0.85	0.98	1.15	21.85	2.26	19.04	1.82	18.59	1.15
X15592	Ctla2b	103518_at		cytotoxic T lymphocyte-associated protein 2 beta	cysteine protease inhibitor	1.44	1.34	0.93	41.61	6.92	44.73	7.75	59.93	16.54
U49350	Ctps	103341_at		cytidine 5'-triphosphate synthase	pyrimidine biosynthesis; glutamine metabolism	0.89	0.98	1.10	2172.46	52.78	1970.21	152.46	1925.79	130.84
AJ242663	Ctsz	92633_at	EC, Lys	cathepsin Z	proteolysis and peptidolysis	1.53	1.38	0.90	114.13	29.71	127.04	39.50	175.02	32.34
L12029	Cxcl12	160511_at	EC	chemokine (C-X-C motif) ligand 12	signal transduction; growth factor	2.58	1.68	0.65	57.12	14.39	87.88	27.86	147.51	80.49
AF047529	Cyp2b19	102690_at		cytochrome P450, family 2, subfamily b, polypeptide 19	arachidonic acid epoxygenase	0.91	0.98	1.08	167.44	6.91	155.15	10.73	152.42	7.33
AA212964	Cyp4v3	160611_at		cytochrome P450, family 4, subfamily v, polypeptide 3	lipid metabolism	1.76	1.32	0.75	122.40	31.40	163.16	49.25	215.96	47.84
AV039198	Dab1	161291_at	IC	disabled homolog 1 (Drosophila)	adaptor protein, signal tansduction	0.73	0.75	1.03	26.89	5.02	26.21	5.07	19.63	1.70
AF098508	Dctn3	94522_at	CySk	dynactin 3	intracellular transport	0.74	0.77	1.03	1485.05	66.47	1439.10	264.65	1105.54	246.28
AF004106	Ddah2	92887_at		dimethylarginine dimethylaminohydrolase 2	nitric oxide mediated signal transduction	1.36	1.18	0.87	314.04	30.06	361.36	67.02	427.99	56.30
AF016697	Dfy; FY;	93412_at	M	chemokine receptor	signal transduction	0.76	0.83	1.10	311.46	39.97	284.31	45.12	236.08	41.09
AW124813	Dlat	96746_at	mit	E2 component of pyruvate dehydrogenase complex	acetyl-CoA biosynthesis from pyruvate	0.77	0.86	1.12	692.39	67.43	620.72	116.94	536.27	29.53
AJ242625	Dmp1; PP	99903_at	IC, N, EC	dentin matrix protein	transcription factor & mineralization of ECM	0.45	0.70	1.55	93.62	50.90	60.31	18.44	41.95	13.17
AF032115	Dnajc5	93211_at	M	DnaJ (Hsp40) homolog, subfamily C, member 5	protein folding	0.90	0.97	1.08	180.78	15.63	168.09	6.74	162.84	4.89
AF063229	Dncic1	103809_r_at	CySk	dynein, cytoplasmic, intermediate chain 1	microtubule-based movement	0.82	0.89	1.08	3046.25	323.57	2818.23	169.04	2503.33	345.42
AA717826	Dpt	96742_at	EC	dermatopontin	cell adhesion	2.15	1.72	0.80	42.05	9.32	52.49	21.36	90.23	40.82
AW228162	Dsc2	103506_f_at	M	desmocollin 2	cell adhesion	1.25	1.17	0.94	12.74	1.69	13.51	1.32	15.87	1.51
AW121709	Dtymk	98619_at		deoxythymidylate kinase	nucleotide biosynthesis	1.19	1.11	0.94	86.78	6.82	92.76	8.63	102.98	10.09
L12147	Ebf1	92535_at	N	early B-cell factor 1	transcription factor	1.19	1.11	0.94	43.10	2.27	46.05	2.59	51.15	4.32
U13370	Edg2	100435_at	M	lysophosphatidic acid G-protein-coupled receptor, 2	signal transduction	1.70	1.27	0.74	490.22	138.96	660.17	148.71	835.69	90.86
M17878	Eef1a1-ps1	94766_at	IC	elongation factor Tu	translation	1.94	1.36	0.70	3421.27	2055.72	4874.56	2335.27	6625.60	2116.85
U57686	Efs	96195_at		embryonal Fyn-associated substrate	cell adhesion	1.13	1.06	0.94	136.14	7.64	144.78	9.73	153.31	7.78
M27347	Ela1	93783_at		elastase 1, pancreatic	serine-type endopeptidase activity	0.75	0.88	1.17	690.86	41.86	590.91	93.52	519.90	69.13
U65735	Elavl1	94001_at	IC	embryonic lethal, abnormal vision, -like 1	regulates stability & movement of mRNAs	1.52	1.21	0.79	73.42	5.95	92.59	16.10	111.84	17.65
U19617	Elf1	160721_at	N	E74-like factor 1	transcription regulator	1.21	1.09	0.90	17.40	0.66	19.29	1.75	21.08	2.94
AF049702	Elf5	103283_at	N	E74-like factor 5	transcription regulator	0.77	0.87	1.13	29.70	4.02	26.39	2.05	22.98	2.21
AA919594	Eln	92836_at	EC	elastin	constituent of ECM	1.69	1.25	0.74	320.45	37.79	432.25	121.00	541.22	80.38
J02700	Enpp1	104174_at	M	ectonucleotide pyrophosphatase/phosphodiesterase 1	nucleotide mediated signal transduction	1.31	1.09	0.83	66.36	2.72	79.84	6.50	86.64	15.15
AV378405	Entpd2	161821_f_at	M	ectonucleoside triphosphate diphosphohydrolase 2	nucleotide mediated signal transduction	1.26	1.09	0.87	80.51	8.67	92.98	7.11	101.44	11.71
X79083	Epha7	92906_at	M	Eph receptor A7	cell adhesion	1.53	1.33	0.87	75.71	7.93	87.34	14.15	115.77	35.12
AI836140	Eplin-pending	94561_at	CySk	epithelial protein lost in neoplasm	cytoskelatal organization	1.37	1.17	0.86	228.24	15.28	266.63	45.98	312.34	42.64
AI835644	Erp29	98076_at	ER	endoplasmic reticulum protein 29	stress unresponsive reticuloplasmin	1.17	1.07	0.91	584.05	48.67	638.71	59.06	685.88	47.92
J04103	Ets2	94246_at	IC, N	E26 avian leukemia oncogene 2, 3' domain	transcription factor	1.20	1.07	0.89	161.31	7.80	180.71	11.22	193.04	19.32
U04827	Fabp7; B-FABP	98967_at		brain fatty acid-binding protein	regulates Schwann cell-axon interactions	3.01	1.89	0.63	628.02	217.67	998.40	613.73	1891.67	788.72
AB033887	Facl4	104017_at	M	fatty acid-Coenzyme A ligase, long chain 4	fatty acid metabolism	0.79	0.93	1.17	28.74	1.87	24.47	2.78	22.70	3.18
L29454	Fbn1	101090_at	EC	fibrillin 1	constituent of the ECM	1.85	1.40	0.75	56.28	10.05	74.58	28.18	104.23	31.09
M31312	Fcgr2b; CD32; Fcr	102337_s_at	M	beta Fc receptor type II precursor;	signal transduction	1.27	1.16	0.91	32.83	2.39	36.01	5.04	41.76	6.20
L17022	Fcgrt	97533_at	M	Fc receptor, IgG, alpha chain transporter	signal transduction	1.20	1.07	0.89	10.96	0.84	12.33	1.83	13.19	0.67
D49920	Fdxr	92754_at	mit	ferredoxin reductase	electron tansport	0.93	0.96	1.03	110.36	4.54	106.94	3.43	102.49	2.08
AI196896	Fgb	96868_at	EC	fibrinogen, B beta polypeptide	blood clotting	0.90	0.95	1.06	20.66	1.43	19.48	1.06	18.50	0.72
M30641	Fgf1	100494_at	EC	fibroblast growth factor 1	signal transduction, cell growth	0.53	0.71	1.33	237.45	93.48	178.88	50.23	126.74	27.89
AW125390	Fgls; Ifitm3	160253_at		fragilis, interferon induced transmembrane protein 3	signal transduction	1.51	1.07	0.71	193.79	38.72	273.36	92.21	293.14	54.86
AF040252	Fkbp7	104746_at	ER	FK506 binding protein 7	chaperone	1.30	1.12	0.86	47.87	4.89	55.54	11.35	62.04	6.62
AF090334	Fkbp9	93731_at	ER	FK506 binding protein 9	chaperone	2.17	1.41	0.65	316.47	155.54	485.83	301.65	685.40	219.65
D16215	Fmo1	101991_at	M	flavin containing monooxygenase 1	electron transport	2.17	1.53	0.70	94.00	12.41	133.59	46.16	203.96	70.61
X94998	Fmod	99152_at	EC	fibromodulin	ECM organization	2.39	1.34	0.56	271.71	123.95	484.18	305.30	649.78	289.05
M18194	Fn1	92852_at	EC	fibronectin 1	ECM, cell adhesion	1.82	1.18	0.65	302.33	114.75	467.86	129.90	551.28	153.05
AF045017	Foxc1	160604_at	N	forkhead box C1	transcription factor	1.13	1.02	0.90	9.90	0.38	10.95	0.66	11.21	0.87
L38607	Foxd1	160996_at	N	forkhead box D1	transcription factor	1.34	1.07	0.80	66.34	6.74	83.15	16.54	88.92	13.09
U72680	Fxyd5	103394_at	M	FXYD domain-containing ion transport regulator 5	regulates ion transport	1.45	1.05	0.72	99.87	13.68	138.00	37.03	144.83	28.78
D38557	Galc	93131_at	lys	galactosylceramidase	carbohydrate metabolism	0.88	0.94	1.07	39.08	4.02	36.64	0.93	34.34	1.91
U18975	Galgt1	103367_at	G	beta-1,4-N-acetylgalactosaminyltransferase	glycosylation	0.69	0.73	1.06	301.78	27.41	284.52	79.43	207.47	43.43
AW121380	Galnt9	102352_at	G	N-acetylgalactosaminyltransferase 9	glycosylation	1.19	1.09	0.91	120.29	7.44	131.51	10.95	143.54	15.26
AI841303	Gap43	102389_s_at	M	growth associated protein 43	regulation of growth, synaptic plasticity and release	2.64	2.01	0.76	562.79	324.58	740.97	168.10	1487.40	228.11
AI849615	Gas5	98531_g_at		growth arrest specific 5	unkown	1.73	1.26	0.73	1673.16	222.57	2303.50	526.87	2901.23	537.49
X59846	Gas6	99067_at	EC	growth arrest specific 6	vitamin K-dependent growth factor	0.66	0.73	1.10	597.88	68.90	543.80	181.23	395.07	123.52
AI844626	Gatm	96336_at	mit	glycine amidinotransferase	creatine biosynthesis	1.38	1.29	0.94	1152.51	173.36	1230.49	254.75	1591.93	250.98
AW210370	Gbe1	96803_at	IC	glucan (1,4-alpha-), branching enzyme 1	glycogen metabolism	0.50	0.77	1.55	89.90	25.09	57.97	22.46	44.72	15.24
U95053	Gclm	160335_at	IC	glutamate-cysteine ligase , modifier subunit	glutathione biosynthesis	0.59	0.71	1.21	390.83	102.34	322.13	66.85	230.29	61.07
C79210	Ggps1	104222_f_at	IC	geranylgeranyl diphosphate synthase 1	isoprenoid biosynthesis	0.89	0.94	1.05	149.50	7.56	141.88	6.16	133.75	11.68
M85153	Ggta1	102993_at	G	glycoprotein galactosyltransferase alpha 1, 3	carbohydrate metabolism	1.60	1.26	0.79	139.21	9.06	176.54	48.37	222.62	37.71
M63801	Gja1	100064_f_at	M	gap junction membrane channel protein alpha 1	constituent of connexon complex	1.47	1.19	0.81	3549.05	748.90	4393.59	933.97	5214.19	967.84
L46651	Gla; Ags	102341_at	lys	alpha-D-galactosidase	carbohydrate metabolism	0.86	0.92	1.07	42.43	2.94	39.63	2.36	36.60	1.31
X81202	Glrb	104449_at	M	glycine receptor, beta subunit	synaptic transmission	0.71	0.96	1.35	3932.12	426.83	2914.62	700.03	2809.71	652.86
AI841629	Gnai2	99598_g_at	M	guanine nucleotide binding protein, alpha inhibiting 2	signal transduction	1.48	1.27	0.85	725.97	39.22	851.18	229.70	1077.61	205.94
M13963	Gnai2	99596_f_at				1.90	1.42	0.75	2528.44	456.79	3386.31	661.22	4815.15	1254.95
AF107848	Gnas	93271_s_at	M	guanine nucleotide binding protein, alpha stimulating	signal transduction	1.15	1.04	0.91	9826.37	835.40	10823.89	877.25	11264.78	662.57
AI843937	Gng5	94042_f_at	M	guanine nucleotide binding protein gamma 5 subunit	signal transduction	1.57	1.26	0.80	819.29	116.14	1018.43	150.28	1286.56	263.33
AI843313	Gpc3	160158_at	EC	glypican 3	growth control	1.83	1.28	0.70	171.64	52.92	245.78	106.00	314.69	62.38
AW123852	Gphn	99441_at	IC	gephyrin	clusters glycine receptor & other synaptic proteins	0.70	0.83	1.19	599.89	85.21	506.12	83.51	421.63	81.31
AF110818	Gpr49	98297_at	M	G protein-coupled receptor 49	signal transduction	0.82	0.90	1.09	40.10	4.14	36.68	3.66	32.85	2.19
Y15798	Gprk6	102040_at	IC	G protein-coupled receptor kinase 6	signal transduction, receptor endocytosis	1.32	1.18	0.90	278.81	28.69	311.47	36.16	367.82	49.89
M94450	Grb7	103095_at	IC	growth factor receptor bound protein 7	signal transduction	0.87	0.96	1.10	336.12	26.21	305.31	20.53	293.12	12.56
X66117	Grik2	98863_at	M	glutamate receptor, ionotropic, kainate 2 (beta 2)	synaptic transmission	0.82	0.87	1.05	44.81	6.24	42.48	4.18	36.85	2.07
D16195	Grn; epithelin	93066_at	EC,	granulin	growth factor, signal transduction	1.50	1.25	0.83	161.43	22.26	193.33	42.72	241.51	22.04
J04953	Gsn; MGC28083	93750_at	CySk	gelsolin	cytoskeletal organization	2.85	1.57	0.55	259.83	139.08	471.13	244.94	739.86	331.42
X98055	Gstt1	95019_at	N	glutathione S-transferase, theta 1	glutathione metabolism	1.32	1.13	0.85	140.25	14.49	164.04	15.73	185.62	16.69
AV239949	Gtpbp1	161683_r_at	IC	GTP binding protein 1	putatve elongation factor	0.84	1.00	1.19	929.88	96.26	782.77	81.85	780.86	71.51
M19279	Gus	97538_at	lys	beta-glucuronidase	carbohydrate metabolism	1.50	1.25	0.83	68.44	12.42	82.11	22.57	102.57	14.61
AI853078	H2afy	97452_at	N	H2A histone family, member Y	chromatin remodeling	1.20	1.15	0.95	219.51	16.67	230.01	17.35	264.10	35.05
Y00629	H2-T23; H-2T23	98472_at	M	Murine gene 37 for pot. membrane bound protein.	MHC class I receptor, antigen presentation	2.22	1.38	0.62	45.41	14.30	73.18	25.11	100.62	30.45
AV003378	Hba-a1	162457_f_at	IC	hemoglobin alpha, adult chain 1	oxygen transporter	2.14	1.86	0.87	641.39	45.84	738.73	149.27	1374.75	980.46
V00714	Hba-a1; Hba1	94781_at				2.55	2.02	0.79	991.76	241.67	1250.82	505.81	2524.31	1771.49

AJ225123	Hcn1	99902_at	M	hyperpolarization-activated, cyclic nucleotide-gated K+ 1	ion channel	0.55	0.76	1.38	122.64	30.32	88.96	12.19	67.59	8.70
M68902	Hcph	102851_s_at	IC	hemopoietic cell phosphatase	signal transduction	1.15	1.12	0.97	25.06	2.06	25.75	1.95	28.83	2.62
AB013095	Hebp1	103085_at	IC	heme binding protein 1	heme metabolism	1.30	1.23	0.95	131.05	13.51	138.01	12.88	170.19	28.20
AB017132	Hhex; Hex; Prh	98408_at	N	Hex (Prh)	transcription factor	1.19	1.07	0.90	67.68	7.30	75.22	3.69	80.21	8.56
AW123564	Hop-pending	96672_at	N	homeodomain only protein	transcription factor	1.50	1.34	0.89	884.78	192.19	990.42	131.04	1325.30	304.42
AV279579	Hoxa4	162402_r_at	N	homeo box A4	transcription factor	0.85	0.97	1.14	16.82	1.22	14.77	1.43	14.32	1.16
AF030065	Hpn	160639_at	M	hepsin	proteolysis and peptidolysis	0.79	0.91	1.15	73.24	10.99	63.54	8.86	57.55	3.29
AA824102	Hsd3b7	160104_at		HSD5D, 3 beta- and steroid delta-isomerase 7	steroid metabolism	1.27	1.13	0.89	224.98	18.06	253.51	16.61	285.95	28.62
M31885	Idb1	100050_at	N	inhibitor of DNA binding 1	transcription factor	1.40	1.15	0.82	78.98	13.21	96.44	25.27	110.89	17.35
M60523	Idb3	92614_at	N	inhibitor of DNA binding 3	transcription factor	1.69	1.26	0.75	138.36	19.13	185.35	67.19	233.91	65.17
U51167	Idh2	95693_at	mit	isocitrate dehydrogenase	tricarboxylic acid cycle	1.39	1.06	0.76	214.29	25.72	282.53	61.51	298.68	56.49
AI838061	Idh3b	95676_at	mit	isocitrate dehydrogenase 3 (NAD+) beta	tricarboxylic acid cycle	0.91	0.98	1.08	65.68	4.37	60.62	2.50	59.49	3.41
X67644	Ier3	94384_at	M	immediate early response 3	stress signal transduction	0.77	0.88	1.14	232.18	23.21	203.28	23.86	179.28	22.57
U43085	Ifit2	103639_at		interferon-induced protein with tetratricopeptide repeats 2	unknown	1.62	1.27	0.78	57.26	13.91	73.33	20.13	92.99	21.16
Y09864	Ifnar2	101014_at	M	interferon (alpha and beta) receptor 2	signal transduction	1.20	1.12	0.93	58.65	4.06	63.08	7.55	70.55	4.98
X71922	Igf2; Mpr; M6pr	98623_g_at	EC	insulin-like growth factor 2	growth factor, signal transduction	2.87	1.50	0.52	2416.06	1432.42	4632.00	1996.58	6937.16	1150.94
AI838737	Igfbp4	94222_at	EC	insulin-like growth factor binding protein 4	cell growth, signal transduction	1.18	1.07	0.91	310.28	17.62	341.01	17.12	364.62	34.79
X76066	Igfbp4; IGFBP-4	101571_g_at				1.24	1.09	0.88	157.80	15.03	179.79	14.48	195.22	25.01
L12447	Igfbp5	100566_at	EC	insulin-like growth factor binding protein 5	cell growth, signal transduction	4.36	1.48	0.34	256.86	178.61	757.23	699.65	1119.62	410.93
U53696	Il10rb	99491_at	M	interleukin 10 receptor, beta	cell surface receptor linked signal transduction	1.65	1.34	0.81	570.21	103.84	703.19	205.97	938.78	198.67
AA608387	Il13ra1	103723_at	M	interleukin 13 receptor, alpha 1	cell surface receptor linked signal transduction	1.72	1.25	0.72	38.06	7.45	52.55	17.22	65.54	12.06
M26271	IL2R	101917_at	M	Mouse interleukin 2 receptor gene, 5' end.	cell surface receptor linked signal transduction	0.85	0.93	1.10	25.86	2.65	23.43	2.05	21.89	1.19
X06271	Il5; Il-5	98374_at	EC	interleukin 5 (eosinophil differentiation factor).	cell surface receptor linked signal transduction	0.90	0.99	1.10	73.47	3.06	66.50	3.28	66.01	6.25
U00978	Impdh1	98390_at	IC	inosine 5'-phosphate dehydrogenase 1	purine nucleotide biosynthesis	0.73	0.88	1.21	207.65	41.08	172.05	32.30	151.16	12.52
AW120756	Inpp5e	96848_at	G	inositol polyphosphate-5-phosphatase	lipid metabolism	0.91	0.93	1.02	50.58	1.81	49.81	3.63	46.22	1.16
AI837528	Jak1	98911_at	IC	Janus kinase 1	signal transduction	0.69	0.72	1.04	898.86	202.04	861.74	202.34	618.69	155.17
L16956	Jak2	101457_at	IC	Janus kinase 2	signal transduction	1.27	1.17	0.92	96.37	10.34	104.82	12.37	122.41	15.87
L22218	Kcna5	102295_at	M	voltage-gated K channel, shaker subfamily, member 5	ion channel subunit	1.51	1.24	0.82	34.16	1.08	41.80	5.35	51.74	7.93
AV335854	Kcnab1	162087_f_at	IC	voltage-gated K channel, shaker subfamily, beta member 1	ion channel subunit	0.68	0.76	1.12	251.06	45.50	224.75	42.81	171.78	11.48
U65593	Kcnab3	102577_at	IC	voltage-gated K channel, shaker subfamily, beta member 3	ion channel subunit	0.82	0.86	1.04	137.54	17.44	131.77	13.57	113.15	6.76
D45022	Kcnj3	101188_at	M	inward-rectifying K channel, subfamily J, member 3	ion channel subunit	0.91	0.94	1.04	29.76	1.92	28.60	1.02	26.95	1.25
AI642389	Kdelr3	104464_s_at	ER	KDEL ER protein retention receptor 3	intracellular protein transport	1.60	1.19	0.74	67.19	16.98	90.27	31.66	107.68	20.61
AF055665	Kns2	93565_at	IC	kinesin 2	microtubule-based movement	0.78	0.93	1.19	3500.63	427.70	2929.70	128.78	2729.79	383.05
D89902	Krtap6-2; HGTpII.4	92253_at	CySk	high-glycine tyrosine keratin type II.4	intermediate filament of cytoskeleton	0.87	0.98	1.12	123.74	13.17	110.61	3.14	107.85	7.69
AV357656	Lamb1-1	162263_f_at	EC	laminin B1 subunit 1	ECM component	2.32	1.61	0.69	101.45	43.27	146.01	77.91	235.20	89.93
AW122780	Lasp1	93793_at	IC	LIM and SH3 protein 1	adaptor in signal transduction	1.38	1.13	0.82	207.96	31.98	252.98	27.34	286.94	41.36
X99347	Lbp	96123_at	EC	lipopolysaccharide binding protein	lipopolysaccharide transport	1.80	1.16	0.64	347.57	79.43	540.32	199.45	625.84	112.29
D37837	Lcp1	94278_at	CySk	lymphocyte cytosolic protein 1	actin cross-linker	0.41	0.56	1.35	1368.27	729.13	1014.84	325.61	566.04	228.93
X86569	Limk1	102889_r_at	IC	LIM-domain containing, protein kinase	cytoskeletal regulation	0.92	0.97	1.06	1631.60	113.93	1539.20	55.55	1493.29	31.39
AI852632	Litaf	93753_at	N	LPS-induced TNF-alpha factor	transcription factor	1.51	1.20	0.79	198.95	44.97	250.93	45.32	299.96	35.46
AI152966	C1qdc1	92208_at	IC	C1q domain containing 1	unknown	0.72	0.88	1.23	293.32	46.12	238.76	30.37	210.69	32.46
AV232133	Lox	161177_f_at	EC	lysyl oxidase	oxidoreductase activity	1.22	1.06	0.87	68.74	4.51	79.07	6.33	84.16	9.62
D49691	Lsp1	104093_at	CySk	lymphocyte specific 1	filamentous-actin binding protein	1.48	1.27	0.86	74.70	6.84	86.76	15.92	110.43	27.31
AF022889	Ltbp1	103209_at	EC	latent transforming growth factor beta binding protein 1	TGF beta receptor signal transduction	1.55	1.23	0.80	44.96	4.15	56.32	11.38	69.47	13.93
AI849993	Ly6h	103487_at	M	lymphocyte antigen 6 complex, locus H	cell surface glycoprotein, growth regulation	1.42	1.23	0.86	369.25	32.02	427.75	66.57	524.09	59.88
AI875934	Lypla1	97207_f_at	mit	lysophospholipase 1	lipid metabolism	0.83	0.94	1.14	935.25	99.06	818.82	101.03	772.56	72.10
X51547	Lzp-s	101753_s_at	EC	P lysozyme structural	carbohydrate metabolism	2.03	1.76	0.87	65.45	9.21	75.49	17.14	132.74	84.84
X61172	Man2a1	104628_at	G	mannosidase 2, alpha 1	carbohydrate metabolism	1.32	1.19	0.90	197.21	21.35	219.80	40.21	261.13	34.08
AV317327	Mapk1	161583_at	IC, N	mitogen activated protein kinase 1	signal transduction	0.83	0.94	1.13	38.14	2.60	33.85	2.98	31.65	3.26
AB005664	Mapk9	101362_at	IC	mitogen activated protein kinase 9	signal transduction	0.79	0.94	1.20	133.03	18.65	111.22	6.95	104.82	19.94
U51196	Mapre1	93306_at	CySk	microtubule-associated protein, RP/EB family, member 1	regulates microtubule dynamics	1.25	1.14	0.91	1352.11	115.63	1489.44	159.97	1694.15	207.29
U69262	Matn2	98475_at	EC	matrilin 2	non-collagenous extracellular matrix protein	2.21	1.68	0.76	26.12	10.95	34.30	18.69	57.78	19.05
AJ010984	Matn4; matrilin-4	96835_at	EC	matrilin 4	non-collagenous extracellular matrix protein	1.40	1.15	0.82	132.42	17.81	160.74	38.96	185.30	36.36
AI853261	Mcam	160458_at	M	melanoma cell adhesion molecule	cell adhesion	0.50	0.64	1.27	1477.70	643.83	1162.50	305.31	744.24	203.34
AI852838	Meg3	160173_at		maternally expressed gene 3	growth suppressor	0.75	0.85	1.13	111.93	18.26	98.68	10.00	84.00	7.21
U33629	Meis1	98790_s_at	N	myeloid ecotropic viral integration site 1	transcription factor	1.39	1.14	0.82	61.15	6.84	74.67	17.02	85.16	7.70
Z16406	Meox2	99937_at	N	mesenchyme homeobox 2	transcription factor	1.90	1.38	0.73	11.14	0.97	15.35	6.16	21.17	5.93
AF017994	Mest; Peg1	92607_at	EC	mesoderm specific transcript	proteolysis and peptidolysis	0.42	0.85	2.05	157.67	92.87	76.86	30.46	65.57	24.84
AB003144	Metap2	93505_at		methionine aminopeptidase 2	proteolysis and peptidolysis	0.88	0.93	1.06	23.21	1.12	21.95	1.64	20.39	1.80
AI957146	Mfhas1	93195_at	EC	malignant fibrous histiocytoma amplified sequence 1	signal transduction	1.56	1.16	0.74	479.17	137.62	648.11	65.74	748.64	198.74
D00613	Mglap	93866_s_at		matrix gamma-carboxyglutamate (gla) protein	calcium binding protein	2.52	0.99	0.40	88.38	53.02	223.58	170.16	222.37	93.84
AW124337	Mgst1	93026_at	mit, mic	microsomal glutathione S-transferase 1	glutathione metabolism	1.34	1.20	0.90	38.83	5.28	43.37	7.99	52.05	4.48
AW050035	Mic2l1	160435_at	M	MIC2-like 1	unknown	0.78	0.83	1.06	1468.95	120.88	1383.71	164.43	1149.68	217.94
AV316101	Mizf-pending	161581_r_at	N	MBD2 -interacting zinc finger protein	DNA methylation and transcription repression	0.85	0.87	1.03	136.99	18.29	133.08	7.10	116.05	8.77
AF100171	Mlf1	102061_at	N	myeloid leukemia factor 1	cell differentiation	1.28	1.12	0.88	19.21	1.78	21.95	1.69	24.57	2.48
AF010135	Mllt10	93878_at	N	MLT 10 homolog	regulation of transcription	0.91	0.97	1.06	95.10	2.37	89.41	6.68	86.33	2.92
X61399	Mlp	97203_at		MARCKS-like protein	signal transduction	1.40	1.27	0.91	180.89	11.58	198.54	33.22	252.52	62.71
Z11974	Mrc1	103226_at	M	mannose receptor, C type 1	endocytosis	1.88	1.43	0.76	30.74	8.25	40.39	19.43	57.85	11.61
U84903	Mrpl23; Rpl23	92646_at	mit	L23 mitochondrial-related protein	mitochondrial large ribosomal subunit	1.25	1.04	0.83	395.72	24.61	474.20	56.63	494.71	64.03
AI853575	Mrps2	160423_at	mit	mitochondrial ribosomal protein S2	constituent of mitochondrial ribosome	0.71	0.77	1.08	242.59	47.78	223.60	44.93	172.50	24.86
AI504305	Ms4a6b	102104_f_at	M	membrane-spanning 4-domains, subfamily A, member 6B	signal transduction	1.25	1.14	0.92	20.91	1.45	22.82	3.16	26.05	2.23
AI835093	Ms4a6b	97322_at				1.17	1.07	0.92	9.95	0.42	10.80	0.75	11.59	0.81
AI875598	Mtif2	93859_at	mit	mitochondrial translational initiation factor 2	mitochondrial protein synthesis	0.72	0.85	1.17	290.75	56.70	247.71	42.67	210.50	32.09
AJ001616	Myadm	96285_at	M	myeloid-associated differentiation marker	unknown	1.37	1.20	0.87	1491.10	179.86	1708.95	204.42	2049.81	333.77
AB015858	Mycbp	102766_at	N	c-myc binding protein	transcriptional regulator	0.86	0.87	1.01	25.02	1.08	24.75	3.20	21.46	1.45
X56182	Myf5	101162_at	N	myogenic factor 5	transcription factor	1.11	1.07	0.96	11.32	0.25	11.81	0.98	12.60	0.70
AF041335	Myoc; TIGR	94122_at	EC	trabecular meshwork induced glucocorticoid protein	inhibitor of neurite outgrowth	1.41	1.15	0.82	37.87	3.64	46.43	9.49	53.51	12.46
AW125874	Nars	95070_at	IC	asparaginyl-tRNA synthetase	protein biosynthesis	0.68	0.87	1.28	3117.49	491.20	2426.77	422.87	2109.68	466.54
U64828	Ncoa1	103229_at	N	nuclear receptor coactivator 1	transcriptional regulator	0.87	0.93	1.06	209.87	16.27	197.80	13.93	182.99	15.04
U35312	Ncor1	101536_at	N	nuclear receptor co-repressor 1	transcriptional regulator	1.39	1.18	0.85	361.32	38.46	425.39	56.32	500.72	69.51
X92397	Ndph	92976_at	EC	Norrie disease homolog	receptor for Norrin-Fz4 signal transduction	1.25	1.11	0.89	206.01	30.60	231.80	29.56	257.70	26.84
AV367714	Nedd8	162180_r_at	N	neural precursor cell expressed, developmentally down-regulated 8	transcriptional regulator	0.87	0.92	1.06	78.41	2.91	73.89	1.56	68.27	5.44
AJ010045	Net1	94223_at	IC, N	neuroepithelial cell transforming gene 1	Rho GEF, signal transduction	0.62	0.95	1.52	114.53	30.48	75.54	20.30	71.45	23.96
U70475	Nfe2l2; Nrf2	92562_at	N	CNC basic leucine zipper DNA binding protein	transcriptional regulator	1.86	1.38	0.74	237.00	64.32	320.45	118.78	441.39	118.31
AI642048	Nfkbia	104149_at	IC, N	nuclear factor of κ light chain gene enhancer in B-cells inhibitor, α	regulation of cell proliferation	1.37	1.08	0.79	166.62	14.47	210.72	34.29	227.78	43.86
M55424	NF-L	103575_at	CySk	neurofilament, light polypeptide	intermediate filament of cytoskeletal	0.74	0.86	1.16	541.09	63.88	464.87	84.08	399.66	73.40
AW050346	Ngef	93178_at		neuronal guanine nucleotide exchange factor	signal transduction	1.45	1.38	0.95	529.99	126.69	558.54	103.52	770.96	164.27
M35970	Nme1	92794_f_at	N	expressed in non-metastatic cells 1, protein	nucleotide biosynthesis	0.76	0.82	1.08	1086.11	83.48	1008.92	135.88	828.92	113.03
AV216468	Nme1	161161_r_at				0.74	0.87	1.18	120.14	13.24	102.03	6.96	88.61	8.67
M12731	Nmyc1; N-mycc	103048_at	IC, N	N-myc proto-oncogene	transcription factor	1.25	1.11	0.89	53.35	2.50	60.06	3.99	66.51	7.82

Y09257	Nov	100507_at	EC	nephroblastoma overexpressed gene	insulin-like growth factor binding activity	3.05	1.92	0.63	123.24	69.56	195.19	103.05	375.33	172.45
AA592182	Npnt	103721_at	EC	nephronectin	cell-matrix adhesion	1.27	1.14	0.90	55.48	4.47	61.79	6.71	70.50	13.52
AF004927	Oprs1	94828_at	M, ER	opioid receptor, sigma 1	opiod signal transduction, lipid biosynthesis	0.71	0.84	1.19	466.56	54.52	392.24	80.55	330.22	64.27
AI553463	Orc4l	103500_at	N	origin recognition complex, subunit 4-like (S. cerevisiae)	DNA replication	1.59	1.27	0.80	83.59	15.44	104.64	12.92	133.18	9.89
AI842377	P5-pending	94207_at	ER	protein disulfide isomerase-related protein		1.22	1.14	0.94	235.42	32.08	250.16	20.63	286.18	26.26
D16580	Padi2	103526_at		peptidyl arginine deiminase, type II	Ca-dependent protein modification	1.45	1.15	0.79	374.66	41.97	472.76	73.30	542.93	75.66
U39738	Pak3	161021_at		p21 (CDKN1A)-activated kinase 3	signal transduction	0.71	0.86	1.21	184.68	28.67	152.96	26.88	131.51	33.88
AI323533	Papss1	102122_f_at		3'-phosphoadenosine 5'-phosphosulfate synthase 1	sulfate assimilation	0.86	0.92	1.06	301.29	19.40	283.84	18.78	260.01	20.16
AI847661	Papss1	102374_at				1.49	1.23	0.83	523.17	48.18	633.79	41.48	777.26	181.01
AF052453	Papss2	96713_at		3'-phosphoadenosine 5'-phosphosulfate synthase 2	sulfate assimilation	1.47	1.22	0.83	23.84	3.25	28.74	5.88	34.94	8.24
AA260005	Pawr	93439_f_at	IC, N	PRKC, apoptosis, WT1, regulator	signal transduction	1.86	1.09	0.59	12.13	3.21	20.64	8.74	22.52	5.72
AW124044	Pcmt1	94348_f_at		protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	protein modification	0.81	0.85	1.06	4957.21	470.69	4688.57	412.61	4005.07	551.57
M69196	Pcsk1	94694_at	EC	proprotein convertase subtilisin/kexin type 1	proteolysis and peptidolysis	1.40	1.31	0.94	99.19	14.61	105.97	11.33	138.40	26.81
AV138382	Pdcd6	162490_f_at	IC	programmed cell death 6	apoptotic response	0.77	0.92	1.19	32.63	3.25	27.39	3.25	25.18	3.08
AJ005073	Pdcd6ip	96252_at	IC	programmed cell death 6 interacting protein	signal transduction	0.76	0.90	1.19	458.46	52.32	384.08	39.25	346.26	49.62
AF042491	Pgrmc1	101585_at	M	progesterone receptor membrane component 1	signal transduction	1.76	1.47	0.84	853.39	247.25	1021.10	360.45	1505.12	283.24
AI850079	Pib5pa	103732_at	IC	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	signal modifying enzyme	0.74	0.81	1.10	612.18	87.18	556.58	114.84	452.05	71.63
AB008791	Pik3c2g	94108_at	M	phosphatidylinositol 3-kinase, C2, gamma polypeptide	phosphatidylinositol metabolism, signal transduction	0.80	0.84	1.05	41.03	2.69	38.98	6.00	32.84	4.05
D86176	Pip5k1a	103573_at		phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	phosphatidylinositol metabolism, signal transduction	0.61	0.77	1.27	266.85	50.29	210.63	33.76	162.54	27.91
U71206	Pitx1	92920_at	N	paired-like homeodomain transcription factor 1	transcriptional regulation	0.89	0.96	1.08	315.22	22.48	290.90	17.31	279.00	20.28
D30779	Pla2g1br	98853_at	M	phospholipase A2, group IB, pancreas, receptor	lipid metabolism, signal transduction	1.26	1.18	0.94	17.44	1.42	18.62	1.61	21.96	2.65
U85713	Plcb1	92465_at	IC	phospholipase C, beta 1	signal transduction	0.91	0.96	1.06	43.44	3.51	40.94	1.73	39.34	0.94
AB031292	Plp2	93323_at	M	proteolipid protein 2	unknown	1.40	1.16	0.83	597.27	72.73	719.82	104.68	834.74	119.59
D78354	Plscr1	102839_at	M	phospholipid scramblase 1	membrane lipid organization	1.37	1.27	0.93	76.11	5.54	82.26	10.38	104.54	22.26
AB023027	Pnck	93910_at		pregnancy upregulated non-ubiquitously expressed CaM kinase	signal transduction	1.69	1.40	0.83	124.34	33.77	149.82	33.72	210.24	67.05
X68363	Pou2f1	102894_g_at	N	POU domain, class 2, transcription factor 1	transcription factor	0.88	0.94	1.06	96.74	6.18	90.85	6.63	85.45	4.47
D84376	Ppap2a	98508_s_at	M	phosphatidic acid phosphatase 2a	lipid metabolism, signal transduction	0.69	0.82	1.18	682.51	97.39	576.10	47.40	469.90	95.01
AI842675	Ppif	99159_at	mit	peptidylprolyl isomerase F (cyclophilin F)	protein folding	0.80	0.87	1.09	331.26	26.07	305.01	24.76	265.20	32.32
AW124336	Ppp6c	160821_r_at		protein phosphatase 6, catalytic subunit	signal transduction	0.80	0.86	1.08	379.19	43.83	352.31	36.75	301.69	31.27
M28723	Prdx3	96256_at	mit	peroxiredoxin 3	peroxidase reaction	0.80	0.90	1.13	1583.84	36.55	1403.88	65.24	1268.76	202.86
J04148	Prf1	93932_at	EC	perforin 1 (pore forming protein)	cytolysis	0.79	0.89	1.13	76.02	7.71	67.20	6.25	60.10	4.37
L27439	Pros1	104728_at	EC	protein S (alpha)	blood coagulation	2.16	1.42	0.66	109.50	30.86	166.37	76.61	236.16	74.31
AW125478	Prss11	96920_at	EC	protease, serine, 11 (Igf binding)	proteolysis and peptidolysis	0.57	0.65	1.15	2573.57	1023.22	2229.81	361.56	1456.53	377.21
Y18723	Prss18	92353_at	EC	protease, serine, 18	proteolysis and peptidolysis	2.04	1.24	0.61	167.51	45.62	274.92	79.33	341.73	139.26
AW121166	Prss8	160566_at	M	protease, serine, 8 (prostasin)	proteolysis and peptidolysis	0.93	0.99	1.07	40.91	2.33	38.10	1.36	37.89	1.61
U65636	Psmb4	98558_r_at	IC	proteasome (prosome, macropain) subunit, beta type 4	ubiquitin-dependent protein catabolism	0.92	0.97	1.05	11.60	0.39	11.02	0.20	10.73	0.77
AB000121	Psmc3ip	102970_at	IC	proteasome 26S subunit, ATPase 3, interacting protein	ubiquitin-dependent protein catabolism	0.81	0.91	1.12	80.77	8.51	71.83	7.45	65.68	6.09
AV248657	Psmd3	161674_i_at	IC	proteasome 26S subunit, non-ATPase, 3	ubiquitin-dependent protein catabolism	0.85	0.93	1.09	114.24	10.75	104.36	4.91	97.36	5.95
AI839158	Psmd8	98522_at	IC	proteasome 26S subunit, non-ATPase, 8	ubiquitin-dependent protein catabolism	0.81	0.84	1.04	419.94	39.34	404.47	50.28	338.82	49.02
D83966	Ptpn13	98424_at	IC, CySk	protein tyrosine phosphatase, non-receptor type 13	signal transduction	1.61	1.33	0.82	98.83	11.04	119.84	33.50	159.26	33.21
D31898	Ptprr	92303_at	M	protein tyrosine phosphatase, receptor type, R	signal transduction	1.27	1.22	0.96	557.34	36.01	582.06	58.12	708.69	121.77
U36488	Ptprv	92661_at	M	protein tyrosine phosphatase, receptor type	signal transduction	0.88	0.96	1.09	25.71	0.86	23.59	2.22	22.75	1.50
AI837010	Pum2	93580_at		pumilio 2 (Drosophila)	translational regulation	1.50	1.22	0.81	1006.10	337.86	1238.74	234.98	1511.37	248.47
AA798971	Rab3ip	95539_at	IC	RAB3A interacting protein	signal transduction	0.80	0.84	1.05	192.84	26.07	183.47	23.19	153.95	10.31
AW047017	Rab14	95686_at	IC	RAB14, member RAS oncogene family	G protein, signal transduction	0.83	0.96	1.16	58.79	5.70	50.76	4.28	48.91	5.88
AI835712	Rab34	160317_at	G	RAB34, member of RAS oncogene family	G protein, signal transduction	1.25	1.11	0.89	218.61	17.28	246.92	42.43	273.95	24.97
AF034955	Rad51l3	101924_at	N	RAD51-like 3 (S. cerevisiae)	DNA repair & recombination	0.91	0.97	1.07	93.51	4.37	87.65	3.93	84.68	5.44
AW124597	Rap1gds1	96733_at		RAP1, GTP-GDP dissociation stimulator 1	signal transduction	0.70	0.81	1.17	3970.40	879.55	3407.16	513.19	2759.54	544.29
AW049415	Rassf1	102379_at		Ras association (RalGDS/AF-6) domain family 1	signal transduction	1.20	1.07	0.89	115.89	13.35	129.66	11.36	138.56	9.15
D13003	Rcn	160896_at	ER	reticulocalbin	ER resident Ca-binding protein	2.40	1.67	0.70	106.36	36.81	152.89	69.92	254.87	87.52
X67812	Ret	101828_at	M	ret proto-oncogene	protein kinase receptor, signal transduction	0.76	0.83	1.10	115.11	11.80	104.92	11.22	87.25	15.17
AV335997	Rgs10	161765_f_at		regulator of G-protein signalling 10	signal transduction	1.75	1.44	0.82	170.75	29.88	207.46	13.95	298.41	124.39
AF061934	Rgs11	102650_at		regulator of G-protein signaling 11	signal transduction	0.70	0.80	1.14	547.07	82.82	478.12	83.75	380.49	57.03
U12403	Rpl10a	100711_at	IC	ribosomal protein L10A	translation	1.39	1.19	0.86	321.67	35.57	375.29	62.07	445.74	15.86
U28917	Rpl13	102109_at	IC	ribosomal protein L13	translation	1.45	1.13	0.78	686.45	67.45	876.20	214.70	994.23	173.03
AB020237	Rpl27a; L27A	101573_f_at	IC	ribosomal protein L27A	translation	1.52	1.23	0.81	802.94	118.33	993.10	189.15	1220.18	224.09
K02928	Rpl30	98119_at	IC	ribosomal protein L30	translation	1.38	1.23	0.88	4567.81	578.59	5163.62	916.66	6325.97	906.57
AW047116	Rpl37	92577_f_at	IC	ribosomal protein L37	translation	1.51	1.16	0.77	1241.10	268.40	1608.82	313.60	1871.42	295.80
U29402	Rplp1	100694_at	IC	ribosomal protein, large, P1	translation	1.32	1.11	0.84	3252.91	305.21	3854.58	182.18	4283.77	660.20
M11408	Rps16	97647_at	IC	S16 ribosomal protein	translation	1.25	1.08	0.86	947.52	55.00	1097.66	189.72	1187.64	86.89
AW048899	Rps19	94068_at	IC	ribosomal protein S19	translation	1.41	1.19	0.84	428.55	61.97	507.78	52.34	602.32	50.50
AI837403	Rps23	96358_at	IC	ribosomal protein S23	translation	1.51	1.28	0.85	1041.42	83.70	1226.10	221.59	1568.91	249.66
AI854238	Rps27	96300_f_at	IC	ribosomal protein S27	translation	1.63	1.28	0.78	1051.91	232.46	1344.24	251.31	1717.66	446.78
X73829	Rps8	100732_at	IC	ribosomal protein S8	translation	1.29	1.04	0.81	1117.45	79.37	1377.55	198.18	1436.39	204.25
M21019	Rras	94394_at	IC	Harvey rat sarcoma oncogene, subgroup R	G protein signal transduction	1.36	1.20	0.88	95.31	9.72	107.99	19.00	129.63	29.68
L21707	Ryk	160453_at	M	receptor-like tyrosine kinase	signal transduction	1.18	1.03	0.87	306.41	25.24	352.65	18.89	362.46	46.83
AV007820	S100a13	161121_f_at		S100 calcium binding protein A13	cell growth and/or maintenance	1.92	1.34	0.70	352.57	28.25	505.90	75.51	677.77	233.71
X99921	S100a13	100959_at				1.85	1.30	0.70	509.36	75.56	723.12	161.15	942.88	234.95
X66449	S100a6	92770_at		S100 calcium binding protein A6 (calcyclin)	cell growth and/or maintenance	5.62	2.74	0.49	139.12	43.57	285.30	137.65	782.38	787.07
U15635	Samhd1	103080_at	IC	SAM domain and HD domain, 1	signal transduction	1.19	1.11	0.93	96.48	4.18	104.10	11.03	115.15	11.58
AW048916	Sc65-pending	100471_at	N	SC65 synaptonemal complex protein	alignment of mitotic chromasomes	1.15	1.08	0.94	75.94	4.28	80.79	7.60	87.65	4.37
AW046162	Scamp2	104365_at	IC	secretory carrier membrane protein 2	protein transport	1.17	1.03	0.89	170.35	15.38	192.10	14.94	198.49	6.11
M21285	Scd1; ab; SCD	94057_g_at	ER, M	stearoyl-CoA desaturase	fatty acid biosynthesis	1.59	1.36	0.86	1890.70	350.77	2205.34	401.11	3001.01	821.89
M21285	Scd1; ab; SCD	94056_at				1.39	1.26	0.90	3104.48	525.43	3432.20	389.14	4328.81	557.87
X97817	Sema5a	103766_at	M	semaphorin 5A	axon guidance receptor activity	1.16	1.09	0.94	22.28	1.57	23.76	1.23	25.86	1.92
AF036164	Serpinf1	93574_at	EC	serine (or cysteine) proteinase inhibitor, clade F), member 1	serine-type endopeptidase inhibitor activity	1.73	1.38	0.79	154.46	44.25	194.40	57.41	267.41	59.57
AF010254	Serping1	99081_at	EC	serine (or cysteine) proteinase inhibitor, clade G, member 1	complement activation, classical pathway	2.87	1.23	0.43	334.57	213.62	780.54	697.30	958.55	353.26
AI846308	Sfxn1	92831_at	mit	sideroflexin 1	cation transporter	1.54	1.26	0.82	157.70	32.42	192.54	33.72	242.58	41.99
D28941	Siat4c	95599_at	G	sialyltransferase 4C	protein amino acid glycosylation	1.33	1.14	0.86	328.73	24.79	384.01	56.37	437.88	13.52
X84235	Siat8a	94164_at	G	sialyltransferase 8 (alpha-2, 8-sialyltransferase) A	protein amino acid glycosylation	0.84	0.92	1.09	69.41	4.19	63.64	2.92	58.50	5.06
AW212397	Ski	104576_at	IC, N	Sloan-Kettering viral oncogene homolog	transcriptional regulation	1.42	1.12	0.79	335.80	62.13	424.13	72.26	476.28	21.09
D83262	Slc1a6	99845_at	M	solute carrier family 1, member 6	dicarboxylic acid transport	1.21	1.06	0.87	180.26	15.89	206.10	17.66	218.52	27.46
L42115	Slc1a7	92582_at	M	solute carrier family 1, member 7	dicarboxylic acid transport	1.27	1.18	0.93	40.03	3.43	43.00	6.61	50.78	4.64
AI853978	Slc21a11	161006_at	M	solute carrier family 21, member 11	organic anion transporter	0.84	0.91	1.08	749.99	52.78	693.52	68.34	630.70	65.66
AI848354	Slc25a1	94807_at	mit	solute carrier family 25 (mitochondrial carrier; c), member 1	citrate transporter	0.67	0.77	1.16	1729.87	290.88	1487.05	325.73	1150.60	143.63
U51112	Slc9a1	99922_at	M	solute carrier family 9 , member 1	sodium/hydrogen exchanger	0.79	0.81	1.02	443.53	32.03	432.87	73.37	351.37	35.08
AF002719	Slpi; SLPI	92858_at	EC	secretory leukoprotease inhibitor	serine-type endopeptidase inhibitor	1.32	1.22	0.93	77.93	1.82	84.18	8.22	102.88	26.45
AI838691	Snx4	97818_at	IC	sorting nexin 4	endocytosis and intracellular trafficking	1.46	1.18	0.81	618.15	126.33	761.79	117.09	902.49	133.72
AA189890	Soat2	97132_at	ER	sterol O-acyltransferase 2	cholesterol metabolism	0.89	0.97	1.09	258.96	20.00	237.35	14.59	229.96	8.27
AW214439	Sparc	97017_f_at	EC	secreted acidic cysteine rich glycoprotein	ECM organization	1.23	1.13	0.92	299.27	15.60	326.71	24.52	367.85	45.56

M25529	Spi1-2	101575_i_at		serine protease inhibitor 1-2	regulator of proteolysis	1.66	1.08	0.65	107.68	33.89	164.73	35.54	178.56	42.64
AI838923	Serpinb9	102125_f_at	IC	serine (or cysteine) proteinase inhibitor, clade B, member 9	regulator of intracellular proteolysis	1.42	1.20	0.84	60.50	9.01	71.80	6.38	86.01	13.05
X92864	Spock1	161054_at	EC	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	regulates cell shape & growth and ECM production	0.65	0.76	1.17	480.69	135.95	411.63	81.70	314.75	36.25
AJ005563	Sprr2e	100723_f_at		small proline-rich protein 2E	unknown	0.79	0.88	1.11	2108.67	278.96	1901.55	247.12	1668.92	101.15
AI837107	Ssbp2	103504_at	N	single-stranded DNA binding protein 2	transcriptional regulation	0.63	0.76	1.21	1732.78	360.07	1430.08	193.50	1086.20	219.79
U02487	Sspn	102378_at	M	sarcospan	cell growth and/or maintenance	1.59	1.24	0.78	78.85	27.53	100.99	18.30	125.26	23.10
AW122911	Ssx2ip	96724_r_at	CySk	synovial sarcoma, X breakpoint 2 interacting protein	cytoskeletalprotein at cell-cell adherins junction	0.70	0.86	1.24	620.11	122.68	501.98	74.79	434.20	66.26
AW060556	Stab1	96886_at	M	stabilin 1	cell adhesion	1.58	1.21	0.77	81.48	6.77	106.45	27.34	128.91	9.12
L47650	Stat6	94331_at	IC, N	signal transducer and activator of transcription 6	transcription factor	1.65	1.34	0.81	43.61	5.45	53.68	13.41	72.06	28.10
AA667323	Stau1	103872_r_at	IC	staufen (RNA binding protein) homolog 1 (Drosophila)	somatodendritic transport of mRNA in neurons	0.83	0.95	1.14	64.39	6.41	56.56	4.10	53.56	4.18
AA822531	Stk2	96130_at	IC, N	serine/threonine kinase 2	signal transduction	1.23	1.16	0.94	556.75	81.51	590.14	73.51	687.10	51.53
AI838080	Stmn1	97909_at	CySk	stathmin 1	tubulin binding protein, maintenance of axonal integrity	1.58	1.24	0.78	3319.71	750.83	4244.50	857.73	5254.97	540.08
AF105222	Stmn4	98486_at	CySk	stathmin-like 4	tubulin binding protein	1.49	1.28	0.86	859.08	109.32	1000.82	137.06	1278.05	253.71
D37793	Syt2	101183_at	IC	synaptotagmin 2	synaptic vessicle membrane, Ca-binding protein	0.84	0.95	1.12	78.81	8.26	70.07	3.76	66.39	5.41
Z47088	Tceb1l	99607_at	IC	transcription elongation factor B (SIII), polypeptide 1-like	constituent of SCF ubiquitin ligase complex	0.77	0.94	1.23	3039.05	230.22	2479.91	256.75	2337.46	460.38
AJ223069	Tcf3	160780_at	IC, N	transcription factor 3	transcriptional regulation	1.21	1.09	0.91	180.40	7.73	199.21	32.72	217.45	11.05
AF032714	Tdpx-ps1	100331_g_at		type II peroxiredoxin protein 2		0.79	0.83	1.06	3822.93	336.87	3613.66	410.75	3016.82	586.56
X72310	Tfdp1	101959_r_at	IC, N	transcription factor Dp 1	transcriptional regulation	1.36	1.19	0.88	154.33	10.00	176.01	21.88	210.24	41.65
AF039601	Tgfbr3	102637_at	M	transforming growth factor, beta receptor III	signal transduction	0.81	0.84	1.04	135.54	11.61	130.17	16.02	109.79	9.57
L10385	Tgm3	96566_at	EC	transglutaminase 3, E polypeptide	cross-linking epidermal protein	0.86	0.95	1.10	20.87	2.25	18.95	1.63	18.03	0.92
M62470	Thbs1; TSP1	160469_at	EC	thrombospondin	cell adhesion	4.21	1.94	0.46	41.56	23.91	90.21	59.55	174.88	134.49
U26437	Timp3; TIMP-3	160519_at	EC	tissue inhibitor of metalloproteinases-3	metalloendopeptidase inhibitor	1.99	1.28	0.64	918.63	247.64	1425.62	481.30	1831.61	276.97
AW125880	Tmem4	100039_at	M	transmembrane protein 4	regulates neurite outgrowth	1.30	1.05	0.81	157.77	28.05	195.17	28.47	205.33	27.69
AI846797	Tmod3	99013_f_at	CySk	tropomodulin 3	actin filament organization	1.59	1.15	0.72	1405.34	323.17	1948.56	668.69	2237.73	554.87
AV230686	Tnc	162362_f_at	EC	tenascin C	ECM component, determinant of synaptic plasticity	1.97	1.81	0.92	13.04	3.39	14.20	4.29	25.70	16.14
X87128	Tnfrsf1b; p75	94928_at	M	p75 TNF receptor	signal transduction, neurotransmitter release,apoptosis	1.31	1.19	0.91	72.35	3.31	79.84	13.56	94.75	15.63
D38046	Top2b	99462_at	N	topoisomerase (DNA) II beta	DNA topological change	1.58	1.42	0.90	77.46	24.03	86.28	18.35	122.18	20.77
AF004428	Tpd52l1	101446_at	IC	tumor protein D52-like 1	(dis)assembly of endosomal SNARE complexes	0.26	0.49	1.86	256.77	181.92	138.38	77.75	67.58	10.80
AI835858	Tpm4	95542_at	CySk	tropomyosin 4	actin organization	2.17	1.55	0.71	375.75	120.52	527.02	133.91	815.36	283.61
AW060819	Twg-pending	102032_at	EC	twisted gastrulation protein	signal transduction	1.76	1.32	0.75	186.04	35.20	247.34	102.36	326.68	90.52
M63649	Twist1; Pde; M-Twis	98028_at	N	Mouse M-twist gene, complete cds.	transcriptional regulation	1.46	1.20	0.82	45.12	4.01	54.73	9.30	65.74	13.42
AW125643	Ubce7ip5-pending	104157_at	IC	ubiquitin conjugating enzyme 7 interacting protein 5	ubiquitin-dependent protein catabolism	0.85	0.87	1.02	62.58	5.81	61.48	6.32	53.23	3.87
U82627	Ube2i	97530_at	IC	ubiquitin-conjugating enzyme E2I	ubiquitin-dependent protein catabolism	1.18	1.04	0.88	297.94	17.33	339.79	39.75	352.10	13.39
AW125420	Ubqln1	95601_at	IC	ubiquilin 1	ubiquitin-dependent protein catabolism	0.74	0.87	1.19	287.67	34.87	242.23	9.91	211.44	32.76
AF115848	Unc13h1	92498_at	IC	unc13 homolog (C. elegans) 1	regulates SNARE complex assembly	1.19	1.12	0.94	15.70	1.37	16.76	2.28	18.73	1.13
AF053724	Vamp8	93305_f_at	IC	vesicle-associated membrane protein 8	functions as vesicle SNARE in vessicle trafficking	1.54	1.10	0.71	125.43	25.47	176.33	61.44	193.64	28.74
W65964	Vamp8	100345_f_at				1.47	1.10	0.75	763.58	85.78	1018.72	304.50	1120.30	133.21
AF019045	VAT; VAChT	101354_at	M	vesicular acetylcholine transporter	neurotransmitter transport	0.27	0.37	1.35	541.45	391.16	400.26	315.44	147.44	28.89
M84487	Vcam1	92558_at	M, EC	vascular cell adhesion molecule 1	cell adhesion; signal transduction	2.30	1.47	0.64	158.34	45.33	248.22	116.25	364.60	136.38
U12884	Vcam1	92559_at				2.19	1.50	0.68	21.60	2.32	31.59	11.55	47.40	26.30
AI843063	Vwf	103499_at	EC	Von Willebrand factor homolog	blood coagulation	3.28	1.68	0.51	168.21	106.58	327.83	189.37	552.33	238.94
AF071186	Wbp11	98617_at	IC, N	WW domain binding protein 11	mRNA splicing factor, protein phosphatase-1 interactions	0.86	0.94	1.09	532.15	40.70	487.49	35.45	459.02	45.54
AF084482	Wfs1	103824_at	ER	Wolfram syndrome 1 homolog (human)	unknown	0.48	0.54	1.14	1700.79	831.68	1493.53	375.81	813.85	211.16
M89800	Wnt6	103735_at	EC	wingless-related MMTV integration site 6	signaling peptide	1.30	1.06	0.81	68.05	8.36	83.81	14.10	88.75	12.29
AA880988	Xlkd1	160583_at	M	extra cellular link domain-containing 1	glycosaminoglycan catabolism, cell adhesion, signaling	1.43	1.21	0.85	39.10	6.25	46.27	10.34	55.94	10.43
X80508	Yap	160520_at	IC	yes-associated protein	TGF-beta growth factor signal transducton	1.65	1.17	0.71	251.13	59.14	355.55	130.72	415.59	62.64
AI842472	Zdhhc14	104299_at		zinc finger, DHHC domain containing 14	unknown	1.38	1.17	0.85	113.94	8.72	134.82	16.71	157.31	35.12
M58566	Zfp36l1	93324_at	N	zinc finger protein 36, C3H type-like 1	putative transcription factor, immediate early response gene	1.99	1.26	0.63	201.06	61.41	318.14	93.10	400.01	121.97
C77776		101226_at		ESTs		0.86	0.96	1.12	140.78	15.97	125.27	6.94	120.86	9.34
AI573367		104056_at		Mus musculus, clone IMAGE:5322989, mRNA		1.53	1.20	0.78	462.17	132.94	589.45	135.09	708.73	115.71
AI463656		98849_at		ESTs		1.29	1.16	0.90	128.08	21.04	142.87	21.71	165.29	22.47
AI845854		96305_at		Mus musculus, IMAGE:3594956, mRNA		0.90	0.91	1.02	96.84	7.13	95.10	5.75	86.96	4.21
AV115928		161659_f_at		ESTs		0.87	0.93	1.07	49.51	2.90	46.18	4.48	43.12	3.15
AI848479		98524_f_at		Mus musculus cDNA clone UI-M-AP1-agf-a-10-0-UI		1.37	1.19	0.86	86.05	9.50	99.68	16.08	118.18	23.21
AV251613		96481_at		A330078N12, hypothetical Na+/H+ exchanger		1.35	1.28	0.95	49.78	7.79	52.67	5.34	67.24	12.19
AA684508		97838_at		clone:A730062M15		1.47	1.23	0.84	194.59	32.77	232.72	46.74	286.49	52.50
AI835315		94823_at		clone IMAGE:3586350,		1.34	1.16	0.87	978.98	112.99	1130.23	143.95	1313.27	190.35
AI843358		103565_at		clone:A930010M14 product:PRP31		1.24	1.10	0.89	234.64	18.41	264.66	17.00	290.12	35.53
AA960603		160273_at		Mus musculus Brf2 gene, 3' UTR		2.09	1.43	0.69	297.03	57.68	432.56	136.28	620.13	209.02
AI117936		104300_at		clone:6230409N14		2.09	1.39	0.67	168.30	31.00	252.65	100.05	352.41	128.97
AA795285		104255_at		ESTs		0.68	0.81	1.19	314.01	51.67	264.68	38.73	214.99	28.45
AA209597		161096_at		Similar to zinc finger protein, clone MGC:51479 IMAGE:4012958		1.20	1.08	0.90	136.88	9.40	152.29	13.34	164.81	9.03
AI835359	0610038P07Rik	96007_at		RIKEN cDNA 0610038P07 gene		1.38	1.19	0.86	1088.24	177.72	1266.18	263.73	1503.19	200.90
AI853364	0710001O03Rik	160391_at		RIKEN cDNA 0710001O03 gene		1.47	1.14	0.78	533.17	138.17	684.35	148.67	782.17	69.44
AW121947	1100001I22Rik	96307_s_at		RIKEN cDNA 1100001I22 gene		1.33	1.22	0.91	3301.40	432.63	3619.64	439.86	4403.08	628.17
AI837621	1100001I23Rik	95120_at		RIKEN cDNA 1100001I23 gene		0.66	0.92	1.40	454.45	122.61	323.76	82.50	298.10	61.99
AW047554	1110001I14Rik	104605_at		RIKEN cDNA 1110001I14 gene		1.30	1.08	0.83	522.10	107.41	628.48	67.69	679.85	75.86
AI848584	1110002B05Rik	96862_at		RIKEN cDNA 1110002B05 gene		2.01	1.54	0.77	638.77	199.53	832.11	335.04	1284.74	327.31
AI846118	1110014K08Rik	98910_at		RIKEN cDNA 1110014K08 gene		1.19	1.10	0.92	607.71	38.65	659.93	36.71	725.41	84.75
AW230977	1110017N23Rik	103739_at		RIKEN cDNA 1110017N23 gene		1.88	1.42	0.75	161.87	41.75	214.95	50.37	304.96	87.72
AI836568	1110018O08Rik	95138_at		RIKEN cDNA 1110018O08 gene		1.27	1.11	0.87	226.00	31.76	258.38	28.32	288.07	22.34
AI843359	1110025J15Rik	99161_at		RIKEN cDNA 1110025J15 gene		0.66	0.73	1.12	4771.99	259.45	4267.59	1097.27	3131.37	744.02
AA690218	1110030N17Rik	98569_at		RIKEN cDNA 1110030N17 gene		0.75	0.80	1.07	1694.66	53.62	1581.62	322.45	1272.32	238.00
AW124316	1110032A10Rik	103092_at		RIKEN cDNA 1110032A10 gene		0.75	0.84	1.12	655.64	67.90	586.35	113.21	491.31	52.35
AW046496	1110033J19Rik	98149_s_at		RIKEN cDNA 1110033J19 gene		1.35	1.12	0.83	78.23	6.84	94.21	20.66	105.79	10.19
AI839150	1110035L05Rik	95052_at		RIKEN cDNA 1110035L05 gene		1.19	1.18	0.99	44.93	6.72	45.61	4.73	53.66	3.43
AI853900	1110055L24Rik	160387_at		RIKEN cDNA 1110055L24 gene		1.37	1.26	0.92	87.50	7.97	95.15	19.71	119.83	20.07
AA681807	1110061O17Rik	94790_at		RIKEN cDNA 1110061O17 gene		0.74	0.77	1.04	56.67	9.16	54.67	8.05	42.02	6.55
AI852734	1190007F10Rik	93467_at		RIKEN cDNA 1190007F10 gene		1.34	1.06	0.79	774.56	138.61	980.17	160.18	1036.69	122.60
AW048159	1200017E04Rik	95664_at		RIKEN cDNA 1200017E04 gene		0.82	0.91	1.11	62.56	5.39	56.52	7.69	51.20	3.85
AW124151	1500004O14Rik	104303_i_at				0.68	0.78	1.15	305.38	45.55	264.68	62.12	207.25	13.50
AI836143	1500036F01Rik	160264_s_at		RIKEN cDNA 1500036F01 gene		0.57	0.64	1.13	1359.45	459.76	1200.21	250.51	773.13	179.31
AI848201	1700008H23Rik	160634_at		RIKEN cDNA 1700008H23 gene		0.58	0.70	1.21	266.45	76.55	220.98	55.18	154.87	31.30
AW226968	1700023M09Rik	94249_at		RIKEN cDNA 1700023M09 gene		0.89	0.93	1.05	524.93	23.94	500.62	32.38	466.46	34.51
AI837771	1810003N24Rik	97237_at		RIKEN cDNA 1810003N24 gene		0.73	0.82	1.12	673.85	92.69	601.16	108.43	492.46	94.19
AB031386	1810009M01Rik	97885_at		RIKEN cDNA 1810009M01 gene		1.77	1.36	0.77	464.85	72.70	604.77	138.93	823.31	176.15
AI844179	1810015M01Rik	97277_at		RIKEN cDNA 1810015M01 gene		0.65	0.72	1.11	573.22	98.42	517.54	137.96	373.75	116.48
AI159700	1810028B20Rik	97118_at		RIKEN cDNA 1810028B20 gene		0.72	0.79	1.10	1708.26	246.31	1557.15	275.19	1234.21	93.99
AA168418	1810054D07Rik	93462_at		RIKEN cDNA 1810054D07 gene		0.77	0.89	1.17	18.45	3.00	15.82	0.89	14.15	1.25
AI120671	2010001M06Rik	103355_at		RIKEN cDNA 2010001M06 gene		1.30	1.14	0.88	97.91	6.43	110.97	9.60	127.02	17.23

AW048347	2210023F24Rik	93187_at		RIKEN cDNA 2210023F24 gene		1.14	1.02	0.90	140.82	14.73	156.82	11.33	160.46	9.83
AI852704	2210402G22Rik	97484_at		RIKEN cDNA 2210402G22 gene		1.39	1.07	0.77	578.87	145.91	749.39	141.47	805.10	58.74
AI834777	2210419D22Rik	93877_at		RIKEN cDNA 2210419D22 gene		1.29	1.12	0.87	361.11	24.22	416.56	80.99	465.19	60.89
AF034580	2310008H09Rik	160872_f_at		RIKEN cDNA 2310008H09 gene		0.67	0.79	1.19	135.89	23.08	114.66	20.68	91.03	11.37
AI131744	2310009E04Rik	102783_at		RIKEN cDNA 2310009E04 gene		0.90	0.95	1.06	439.24	34.34	414.34	19.75	393.13	17.89
AI661590	2310010J17Rik	161018_at		RIKEN cDNA 2310010J17 gene		1.26	1.14	0.90	81.55	4.71	90.58	5.33	103.10	18.84
AI834895	2310021M12Rik	99142_at		RIKEN cDNA 2310021M12 gene		0.83	0.86	1.03	932.32	53.85	903.54	109.08	776.18	60.27
AW125284	2310032D16Rik	98942_r_at		RIKEN cDNA 2310032D16 gene		0.60	0.81	1.35	491.02	131.11	362.82	83.21	295.54	70.60
AI841777	2310036D04Rik	104320_at		RIKEN cDNA 2310036D04 gene		1.50	1.19	0.80	489.62	71.73	614.85	119.22	732.15	223.24
AV369210	2310046B19Rik	162034_r_at		RIKEN cDNA 2310046B19 gene		1.16	1.11	0.95	12.04	0.50	12.62	0.78	14.02	1.00
AW125329	2310057D15Rik	160067_at		RIKEN cDNA 2310057D15 gene		1.39	1.33	0.95	306.71	68.29	321.26	62.72	426.53	82.97
AF003352	2400010D15Rik	160433_at		RIKEN cDNA 2400010D15 gene		0.81	0.91	1.12	333.84	40.25	298.92	37.01	271.75	18.27
AI849500	2410004C24Rik	97891_at		RIKEN cDNA 2410004C24 gene		0.80	0.96	1.20	320.55	33.95	267.31	38.42	256.18	32.99
AV207612	2410004C24Rik	161135_f_at		RIKEN cDNA 2410004C24 gene		0.69	0.89	1.29	351.86	70.25	273.14	38.24	243.73	49.43
AI853219	2410012H22Rik	93138_at		RIKEN cDNA 2410012H22 gene		0.76	0.80	1.06	217.67	16.30	205.68	31.13	164.64	27.27
AW124778	2610034N03Rik	97247_at		RIKEN cDNA 2610034N03 gene		0.62	0.81	1.29	1640.75	449.22	1268.31	476.22	1021.19	153.25
AW045664	2810026P18Rik	104089_at		RIKEN cDNA 2810026P18 gene		1.74	1.45	0.83	65.73	17.05	78.98	20.75	114.19	32.28
AI845988	2810404F18Rik	95153_at		RIKEN cDNA 2810404F18 gene		1.30	1.11	0.85	350.21	75.44	409.65	36.98	455.70	33.29
AI853616	2810422B04Rik	160400_at		RIKEN cDNA 2810422B04 gene		0.75	0.84	1.12	470.61	47.14	419.39	70.07	353.81	23.86
AI414025	2900016D05Rik	104502_f_at		RIKEN cDNA 2900016D05 gene		1.27	1.12	0.88	217.85	14.06	247.27	17.94	276.05	50.52
AI844890	2900053E13Rik	160284_at		RIKEN cDNA 2900053E13 gene		0.84	0.89	1.06	382.83	30.84	361.07	28.92	321.58	24.72
AA833293	3110052D19Rik	104415_at		RIKEN cDNA 3110052D19 gene		1.18	1.03	0.87	108.01	4.30	123.74	9.24	127.92	14.62
AA930526	4833411B01Rik	104427_at		RIKEN cDNA 4833411B01 gene		1.55	1.21	0.78	385.13	43.54	495.13	71.29	598.03	106.72
AV254726	4921513E08Rik	98326_f_at		RIKEN cDNA 4921513E08 gene		0.87	0.94	1.08	28.22	1.07	26.15	1.87	24.53	1.05
AI647612	5031439A09Rik	101001_at		RIKEN cDNA 5031439A09 gene		2.12	1.25	0.59	315.25	131.09	535.86	233.58	669.71	158.45
AI846906	5033414D02Rik	98495_at		RIKEN cDNA 5033414D02 gene		1.15	1.10	0.95	114.84	7.96	120.32	3.17	132.62	12.78
AI843709	5133400A03Rik	94345_at		RIKEN cDNA 5133400A03 gene		1.87	1.30	0.69	178.51	53.22	256.97	120.33	333.22	61.64
AI426400	5430401D19Rik	97357_at		RIKEN cDNA 5430401D19 gene		1.28	1.23	0.96	29.14	2.89	30.43	6.14	37.28	2.63
AI851345	5730591C18Rik	160385_at		RIKEN cDNA 5730591C18 gene		0.77	0.85	1.10	331.56	25.56	300.82	42.47	256.14	23.44
AW048944	6330514M23Rik	97496_f_at		RIKEN cDNA 6330514M23 gene		1.39	1.08	0.77	229.92	21.76	297.28	70.61	319.95	28.44
AI842002	6530413N01Rik	99553_f_at		RIKEN cDNA 6530413N01 gene		1.40	1.17	0.84	155.78	15.96	186.25	18.67	217.96	50.50
AA790291	9130208G10	103786_at		hypothetical protein 9130208G10		0.86	0.96	1.11	89.27	6.63	80.51	5.44	76.92	5.17
AI854482	9130229H14Rik	103295_at		RIKEN cDNA 9130229H14 gene		0.75	0.88	1.18	607.49	106.03	513.82	49.67	453.67	71.25
AW215585	9130422G05Rik	102920_at		RIKEN cDNA 9130422G05 gene		0.65	0.69	1.07	968.59	240.73	907.88	207.86	629.85	115.02
AW046661	9330140I15Rik	94991_at		RIKEN cDNA 9330140I15 gene		1.80	1.38	0.77	35.24	6.72	46.02	14.44	63.32	21.32
AI593759	9530051K01Rik	98346_at		RIKEN cDNA 9530051K01 gene		1.11	1.07	0.96	84.38	1.86	87.89	2.20	93.88	6.43
AI839880	A230070D14Rik	93147_f_at		RIKEN cDNA A230070D14 gene		1.45	1.31	0.91	844.53	216.04	929.52	192.11	1221.46	247.90
AA623587	AA536743	97918_at		expressed sequence AA536743		1.80	1.28	0.71	103.31	15.75	145.95	37.96	186.27	50.32
AA657044	AA589382	160255_at		expressed sequence AA589382		3.31	1.73	0.52	784.71	517.96	1503.67	1048.40	2594.26	783.76
AI553536	E030024M05Rik	99366_at		RIKEN cDNA E030024M05 gene		3.47	2.02	0.58	78.65	20.82	135.29	76.12	273.05	256.09
AA711773	E430013J17Rik	103200_at		RIKEN cDNA E430013J17 gene		1.42	1.35	0.95	40.28	5.37	42.48	8.18	57.35	14.45
AW120628	D10Ertd73e	95161_at		DNA segment, Chr 10, ERATO Doi 73, expressed		1.22	1.09	0.90	372.80	30.18	416.25	51.31	455.52	26.19
AA915342	D11Ertd603e	96932_at		DNA segment, Chr 11, ERATO Doi 603, expressed		0.88	0.94	1.08	325.85	14.43	302.98	29.41	285.94	15.26
AW125724	D13Wsu50e	94502_at		DNA segment, Chr 13, Wayne State University 50		0.70	0.83	1.18	254.22	39.78	216.25	13.94	178.73	39.60
AW047083	D19Wsu162e	96829_at		DNA segment, Chr 19, Wayne State University 162		1.25	1.07	0.86	228.84	25.78	267.62	29.60	285.54	15.19
C77922	D1Ertd75e	97140_at		ESTs		0.91	0.96	1.05	45.16	2.91	43.12	1.99	41.23	1.46
N28141	D6Bwg1452e	99779_at		ESTs		0.86	0.91	1.06	96.23	6.33	90.54	5.75	82.47	4.46
AV230529	D7Ertd743e	161979_f_at		DNA segment, Chr 7, ERATO Doi 743, expressed		0.90	0.96	1.07	14.33	0.60	13.35	0.90	12.88	0.57
AW125274	D8Ertd354e	97863_at		cDNA clone UI-M-BH2.1-aps-h-08-0-UI		0.78	0.83	1.06	887.04	79.92	833.28	68.27	688.54	109.76
AI841487	C330016O16Rik	102702_at		RIKEN cDNA C330016O16 gene		1.35	1.16	0.86	85.22	7.38	98.68	12.30	114.74	24.26
AI840339	C730049F20Rik	96038_at		RIKEN cDNA C730049F20 gene		1.81	1.28	0.71	42.05	9.78	59.45	30.91	76.05	16.15
AI835706	MGC18837	95442_at		hypothetical protein MGC18837		0.82	0.90	1.10	1045.72	58.59	949.53	108.65	855.08	83.89

Class VI: Genes that are differentially expressed between MMN and IML (42)

									Average Signal Intensities & Standard Deviations					
						Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**Probeset**	**location**	**Description**	**Function**	**IML/LMN**	**IML/MMN**	**LMN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
U96401	Aldh1a7	94778_at		aldehyde dehydrogenase family 1, subfamily A7	metabolism	0.78	0.67	0.87	112.25	13.96	129.72	34.62	87.20	9.62
M31690	Ass1	97521_at		argininosuccinate synthetase 1	arginine biosynthesis	1.07	1.23	1.15	235.60	28.87	204.15	16.35	251.97	31.36
AF068182	Blnk	100772_g_at	M	B-cell linker	signal transduction	1.17	1.21	1.04	16.13	0.90	15.52	0.65	18.80	2.98
X62502	Ccl4; Act-2; Mip1b	94146_at	EC	chemokine (C-C motif) ligand 4	signal transduction	1.03	1.08	1.05	116.68	2.92	111.55	3.04	120.69	5.58
L34808	Chx10	101127_at	N	C. elegans ceh-10 homeo domain containing homolog	transcription factor	1.12	1.26	1.12	120.55	16.60	107.71	7.41	135.28	18.92
U92702	Ebf3	104492_at	N	early B-cell factor 3	transcription factor	1.13	1.21	1.07	100.09	6.31	93.41	11.95	112.62	11.18
L38580	Gal; Galn	100407_at	EC	galanin neuropeptide	neuropeptide signal transduction	1.21	1.28	1.06	214.48	10.75	202.41	6.20	259.99	52.94
U68564	Idh3g	93029_at	mit	isocitrate dehydrogenase 3 (NAD+), gamma	TCA cycle	0.79	0.73	0.93	1028.78	122.01	1111.88	151.23	815.45	222.91
U53219	Igtp	160933_at	IC	interferon gamma induced GTPase	G protein signal transduction	1.09	1.16	1.06	41.62	1.62	39.11	3.85	45.25	3.69
D13695	Il1rl1	98500_at	M	interleukin 1 receptor-like 1	signal transduction, synaptic plasticity	1.14	1.24	1.09	18.46	1.25	16.99	0.80	21.10	4.27
M29697	Il7r	99030_at	M	interleukin 7 receptor	cell surface receptor linked signal transduction	1.14	1.20	1.05	20.22	2.09	19.20	1.31	22.99	3.12
AJ001373	Itgb1bp1	100989_at	IC	integrin beta 1 binding protein 1	integrin depended cell-matrix adhesion	0.91	0.85	0.94	485.02	15.89	517.71	49.39	439.27	31.24
AW120557	Lsm4	93008_at	N	U6 snRNA-associated SM-like protein 4	component of the spliceosome complex	0.87	0.77	0.89	376.43	34.42	422.81	69.16	326.76	36.14
AI843685	Mrpl15	96296_at	mit	mitochondrial ribosomal protein L15	mitochondrial protein biosynthesis	0.87	0.83	0.96	225.16	23.69	233.77	29.63	195.01	14.93
L00039	Myc; Myc2; Nird	104712_at	N	c-myc (Myc) gene	transcriptional regulation	1.14	1.17	1.02	13.03	1.05	12.73	0.41	14.87	1.68
AI848871	Ndufb10	101525_at	mit	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	electron transport	0.79	0.75	0.95	591.41	58.71	623.05	128.70	466.93	71.83
X76653	Nr2f2	103052_r_at	N	nuclear receptor subfamily 2, group F, member 2	steroid hormone receptor, transcription factor	1.19	1.53	1.28	103.50	22.96	80.56	24.78	123.20	14.37
X80937	Ralbp1	93255_at		ralA binding protein 1	Ral G protein effector, regulates receptor endocytosis	1.13	1.20	1.06	889.23	38.87	841.76	66.19	1008.02	151.95
AB026583	Rbms2	92517_at	IC	RNA binding motif, single stranded interacting protein 2	transcriptional and/or translational regulator	0.86	0.82	0.95	137.54	13.72	144.50	16.15	118.62	10.23
U85055	Rgs14	102711_at		regulator of G-protein signaling 14	G protein signal transduction	1.08	1.12	1.04	217.03	10.01	207.87	7.07	233.55	21.41
U66918	Shox2	99042_s_at	N	short stature homeobox 2	transcription factor	1.20	1.26	1.05	65.47	6.34	62.58	5.06	78.82	14.29
U10404	Slc25a5	100617_at	mit	solute carrier family 25 , member 5	adenine nucleotide translocator	0.92	0.89	0.97	115.25	4.61	118.72	6.28	105.67	8.14
U79550	Snai2	99552_at	N	snail homolog 2 (Drosophila)	transcription factor	1.20	1.24	1.03	231.19	20.76	224.08	13.26	277.30	48.40
AF068748	Sphk1	103839_at	IC, M	sphingosine kinase 1	sphingolipid metabolism	0.90	0.80	0.89	181.72	17.76	204.15	21.66	162.96	14.42
Y09972	Taf1a	92339_at	N	TATA box binding protein -associated factor, RNA Pol I, A	transcriptional regulator for Pol I	0.88	0.87	1.00	324.37	38.37	325.79	10.24	284.45	19.42
D86081	Tcea2	104622_at	N	transcription elongation factor A (SII), 2	regulation of transcription	0.83	0.73	0.88	258.88	54.90	294.32	28.47	216.10	42.24
X57349	Trfr	103958_g_at	M, IC, EC	transferrin receptor	iron transpoerter	1.14	1.16	1.02	1400.28	124.31	1370.41	66.15	1593.16	146.68
AA138192	Trim21	92942_at	IC, N	tripartite motif protein 21	unknown	1.05	1.10	1.04	191.78	8.11	183.61	8.32	201.87	4.84
AA522008		101124_at		IMAGE:893086		1.10	1.18	1.07	60.83	4.49	57.01	2.08	67.06	8.76
AI639614		104457_at		ESTs		1.12	1.16	1.03	19.66	1.31	19.10	1.26	22.09	2.22
AF109906		101546_at				0.80	0.78	0.98	379.65	43.30	386.35	70.58	303.10	26.50
C78246		101863_at		clone J0044H11 3'		1.14	1.17	1.03	18.67	1.59	18.16	0.82	21.30	2.38

AW061299	Igsf8	160820_at		clone UI-M-BH1-anw-c-06-0-UI		1.29	1.20	0.93	876.77	91.08	945.47	131.81	1132.49	129.17
AW120867	1700013H19Rik	95561_at		RIKEN cDNA 1700013H19 gene		1.05	1.08	1.03	9.91	0.43	9.65	0.41	10.43	0.53
AW049360	1700017B05Rik	104389_at		clone UI-M-BH1-ane-a-10-0-UI		0.90	0.88	0.98	117.97	5.90	120.40	9.65	106.43	7.06
L04848	1700029H17Rik	103847_at		RIKEN cDNA 1700029H17 gene		1.07	1.16	1.08	35.43	1.68	32.87	1.67	38.06	2.89
AI835060	1810013D10Rik	97265_at		RIKEN cDNA 1810013D10 gene		0.84	0.82	0.98	533.59	57.27	546.25	53.42	447.33	58.93
AV364118	9430015G03Rik	161792_f_at		RIKEN cDNA 9430015G03 gene		1.10	1.15	1.04	10.68	0.75	10.27	0.49	11.79	1.05
AI843294	C330006A16Rik	95604_at		RIKEN cDNA C330006A16 gene		0.95	0.88	0.92	1932.13	158.52	2089.64	148.59	1833.68	96.81
AW123987	D15Ertd785e	160292_at		clone UI-M-BH2.3-aqc-g-08-0-UI		0.85	0.81	0.95	360.64	29.22	380.82	52.56	307.14	42.73
AA407378	D8Wsu26e	94657_at		ESTs		1.06	1.07	1.01	10.60	0.40	10.50	0.42	11.19	0.42
AW048729	E430023I20	104200_at		hypothetical protein E430023I20		0.90	0.80	0.89	517.10	45.58	580.58	77.71	463.53	46.27
AA881294	LOC218699	97325_at		similar to CG8726 gene product		0.84	0.78	0.92	496.24	28.15	538.49	96.57	417.82	60.54
AV366522	LOC231430	162029_r_at		hypothetical protein LOC231430		1.04	1.10	1.05	13.08	0.72	12.42	0.62	13.64	0.58

Class VII: Genes that are differentially expressed between LMN and MMN (61)

									Average Signal Intensities & Standard Deviations					
							Fold changes*		LMN		MMN		IML	
Genbank	**Common**	**Probeset**	**location**	**Description**	**Function**	**IML/LMN**	**IML/MMN**	**LMN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
AF004108	Aanat	92512_g_at		arylalkylamine N-acetyltransferase	acyltransferase, penultimate enzyme in melatonin synthesis	0.93	1.01	1.09	904.34	38.22	829.91	34.47	841.62	53.59
X13297	Acta2	93100_at	CySk	actin, alpha 2, smooth muscle, aorta	structural constituent of cytoskeleton	3.47	0.73	0.21	178.52	213.79	841.89	582.42	618.77	789.78
M92850	Aeg2	94730_at	IC, EC	acidic epididymal glycoprotein 2	unknown	1.05	0.97	0.93	8.68	0.22	9.35	0.34	9.10	0.41
AF103809	Ap3b1	103878_at	G	adaptor-related protein complex 3, beta 1 subunit	traficking in endomembrane system	1.24	0.93	0.75	485.32	78.73	649.88	75.97	603.31	63.98
D87899	Arf2	100518_at	G	ADP-ribosylation factor 2	traficking in endomembrane system	0.91	1.04	1.14	137.58	8.54	120.53	5.77	124.76	12.77
X97991	Calca	92533_at	EC	calcitonin/calcitonin-related polypeptide, alpha	peptide signal transduction	0.93	1.02	1.10	117.83	6.75	106.82	5.41	109.17	5.06
AB019600	Casp9	100367_g_at	IC	caspase 9	proteolysis and peptidolysis	0.89	1.02	1.14	180.07	16.39	157.80	11.22	160.35	6.93
AF022990	Ccr5; CCR5	102718_at	M	chemokine receptor-5 (CCR5)	signal transduction	0.99	1.11	1.12	21.10	1.10	18.81	1.20	20.80	1.26
U34881	Cd8a	102975_at	M	CD8 antigen, alpha chain	antigen recognition, signal transduction	0.95	1.04	1.09	26.40	1.20	24.23	1.53	25.15	0.60
M17640	Chrna1	100021_at	M	cholinergic receptor, nicotinic, alpha polypeptide 1	synaptic transmission	0.95	1.04	1.10	31.37	0.97	28.50	1.76	29.77	0.85
AV339532	Ckb	162257_i_at	IC	creatine kinase, brain	energy homeostasis	0.90	1.06	1.18	25.11	2.13	21.36	0.90	22.59	2.20
AF012822	Cpsf2	160542_at	N	cleavage and polyadenylation specific factor 2	transcript processing	0.95	1.04	1.09	506.90	19.83	464.75	27.27	481.11	21.67
AJ010338	Cubn	95000_g_at	M	cubilin (intrinsic factor-cobalamin receptor)	endocytic receptors	1.13	0.73	0.65	77.28	5.94	119.49	31.34	87.06	14.83
M20625	Cyct	92929_at	mit	cytochrome c, testis	electron transport	0.96	1.05	1.10	97.36	6.13	88.84	3.15	93.29	3.82
U75530	Eif4ebp2	94353_at	IC	eukaryotic translation initiation factor 4E binding protein 2	protein biosynthesis	0.98	1.07	1.09	275.71	13.94	252.47	11.68	270.14	13.34
L12703	En1	96523_at	N	engrailed 1	TF	0.75	1.11	1.48	197.67	54.42	133.34	16.78	147.98	11.97
AF030001	Fkbpl	102206_at		FK506 binding protein like	protein folding and trafficking	0.97	1.04	1.07	110.90	5.14	103.34	4.08	107.45	3.90
AV309794	Gkap42-pending	161833_r_at	G	cGMP-dependent protein kinase anchoring protein	signal transduction	0.98	1.13	1.16	41.88	2.93	36.26	2.52	40.98	4.17
M96688	Kcna6	94719_at	M	voltage-gated K channel, shaker-related, subfamily, member 6	potassium channel	0.94	1.06	1.12	29.65	1.56	26.50	0.80	27.99	0.81
AB028071	Keg1	96938_at	mit	kidney expressed gene 1	unknown	0.93	1.05	1.14	29.89	2.40	26.32	1.51	27.72	1.45
AV330502	Kpnb1	161936_at	IC, N	karyopherin (importin) beta 1	nuclear transport	0.95	1.07	1.12	51.96	3.43	46.38	2.88	49.43	2.20
X03491	Krt2-4	100421_at	CySk	keratin complex 2, basic, gene 4	intermediate filament of cytoskelton	0.89	1.01	1.13	420.59	35.98	373.56	23.64	375.73	21.54
AV295836	Lt1	162111_r_at		lurcher transcript 1		0.90	1.08	1.19	17.92	1.71	15.01	1.02	16.16	1.12
M17015	Lta; LT; Ltx	100327_at	EC	lymphotoxin	TNF-receptor ligand, cell growth and/or maintenance	0.95	1.09	1.15	315.84	24.11	274.97	21.51	298.66	20.43
U19033	Mageb3; Smage3	95783_g_at		melanoma antigen, family B, 3	unknown	0.92	1.03	1.13	67.28	5.15	59.59	3.46	61.60	4.53
AV339603	Mrps18a	161767_r_at	mit	mitochondrial ribosomal protein S18A	mitochondrial protein translation	0.89	1.03	1.15	1023.33	73.16	887.99	74.27	911.93	62.65
AW125634	Mrs3/4-pending	104560_at	mit	putative mitochondrial solute carrier	mitochondrial transport	1.06	0.90	0.85	241.12	11.99	284.44	34.72	256.09	21.37
U31566	Nkx2-2	92747_at	N	NK2 transcription factor related, locus 2 (Drosophila)	transcription factor	1.22	0.91	0.75	70.70	7.12	94.88	10.08	86.54	19.07
AV320040	Nmyc1	161417_r_at	N	neuroblastoma myc-related oncogene 1	transcription factor	0.97	1.05	1.09	9.80	0.30	8.99	0.38	9.47	0.32
U12961	Nqo1	94351_r_at	IC	NAD(P)H dehydrogenase, quinone 1	oxidoreductase activity	0.99	1.07	1.08	40.63	1.74	37.47	1.60	40.12	1.64
AV320880	Nr5a1	161418_r_at	N	nuclear receptor subfamily 5, group A, member 1	transcription regulation	0.88	1.06	1.21	40.69	2.10	33.67	3.01	35.78	4.09
X53257	Ntf3; NT3	92420_at	EC	neurotrophin-3 peptide	growth and/or maintenance	1.06	0.90	0.85	38.51	3.09	45.08	3.44	40.75	2.26
U51908	Ntsr2	93137_at	M	neurotensin receptor 2	signal transduction, neuromodulation	1.17	0.99	0.85	893.37	66.75	1046.40	93.86	1041.15	107.83
Y16386	Orc4l	104096_at	N	origin recognition complex, subunit 4-like (S. cerevisiae)	DNA replication	0.80	1.09	1.37	470.82	50.09	344.70	85.57	374.67	22.61
X60664	Pde6a	100696_at	IC	phosphodiesterase 6A, cGMP-specific, rod, alpha	signal transduction	0.91	1.05	1.16	123.31	8.70	106.73	5.29	112.56	10.46
U70209	Pkd1	97375_at	M	polycystic kidney disease 1 homolog	ion channel, signaling, cell adhesion, Ca homostasis	1.05	0.96	0.91	215.00	9.42	235.29	15.61	226.72	4.26
AJ250489	Ramp1	104680_at	M	receptor (calcitonin) activity modifying protein 1	receptor transport and activity	1.03	0.83	0.80	436.50	36.06	543.29	50.16	449.28	73.30
AV076835	Rgs11	161309_r_at		regulator of G protein	signal transduction	0.91	1.07	1.17	17.75	0.83	15.14	1.15	16.20	0.97
AV148041	Rpo1-1	161347_r_at	N	RNA polymerase 1-1	rRNA transcription	0.91	1.08	1.18	466.26	35.87	394.14	25.20	426.15	47.34
AV293396	S100a14	162428_i_at		S100 calcium binding protein A14		0.88	1.01	1.15	1057.33	100.03	916.15	80.72	927.98	46.28
AA189555	Sfxn2	160967_at	mit	sideroflexin 2	cation transport	0.93	1.02	1.10	77.73	5.95	70.73	1.77	72.47	3.88
U40576	Sim2	92896_s_at	N	single-minded 2	transcriptioin factor	0.96	1.08	1.12	23.83	1.84	21.25	1.35	22.86	0.77
U95132	Slc10a1	100341_g_at	M	solute carrier family 10 , member 1	sodium/bile acid cotransporter	0.93	1.06	1.14	19.18	1.22	16.84	1.41	17.90	0.92
D49473	Sox17	92996_at	N	SRY-box containing gene 17	transcription factor	1.00	0.87	0.87	127.39	11.84	146.65	12.10	127.49	9.50
AF096285	Strap	94292_at		serine/threonine kinase receptor associated protein	signal transduction	0.74	1.06	1.43	386.86	76.83	269.90	73.44	284.77	30.50
AV102624	Upp	161325_at		uridine phosphorylase	nucleoside metabolism	0.90	1.04	1.16	503.35	44.47	435.69	34.02	452.60	21.40
AF011412	V2r2	101630_f_at	M	vomeronasal 2, receptor, 2	putative pheromone receptor	0.95	1.07	1.13	113.83	6.51	100.88	5.19	108.03	4.08
AV245272	Vim	162379_r_at	CySk	vimentin	intermediate filament of the cytoskelton	0.94	1.08	1.15	252.09	15.26	219.41	20.21	236.29	15.61
AL078630		98779_at		CT7-BM573K1 on chromosome 17		0.98	1.08	1.10	147.14	9.59	133.24	3.24	143.61	10.34
						0.95	1.02	1.08	26.81	0.53	24.87	0.68	25.35	1.40
AA516942		94684_at		ESTs		0.92	1.06	1.15	42.06	3.51	36.72	2.34	38.76	1.36
AA536953	vj86c09.r	101125_at		IMAGE:943984		0.95	1.05	1.11	26.51	1.26	23.86	1.00	25.09	1.50
AI854813		160993_at		clone UI-M-BH0-aka-h-03-0-UI		0.95	1.06	1.12	23.66	1.60	21.21	1.14	22.44	0.59
AW229141	2310006I24Rik	95075_at		RIKEN cDNA 2310006I24 gene		0.84	1.04	1.24	68.75	5.82	55.58	6.70	57.63	7.07
AI846338	2400006G15Rik	95517_i_at		RIKEN cDNA 2400006G15 gene		1.21	0.98	0.80	638.95	87.35	794.68	97.63	775.01	94.37
AV115721	2410017E24Rik	161334_r_at		RIKEN cDNA 2410017E24 gene		0.95	1.09	1.15	116.88	11.42	101.40	2.48	110.99	9.03
AA795841	2410080P20Rik	100917_at		RIKEN cDNA 2410080P20 gene		1.05	0.93	0.89	146.56	6.98	165.17	10.17	153.38	12.18
AV379830	5033402L14Rik	162135_r_at		RIKEN cDNA 5033402L14 gene		1.12	1.00	0.89	8.39	0.20	9.40	0.44	9.37	0.94
AI843141	AA437972	97281_at		EST AA437972		0.88	1.02	1.16	117.08	12.97	101.02	8.04	103.32	5.66
AW120832	B230313N05Rik	94869_at		RIKEN cDNA B230313N05 gene		0.93	1.03	1.11	175.28	11.50	158.02	5.68	163.15	9.98
C80892	C530030P08Rik	97147_at		RIKEN cDNA C530030P08 gene		0.95	1.07	1.13	19.67	1.58	17.45	1.21	18.70	0.70

Supplemental Table 2

Mean Expression Profiles for developmentally important transcription factors in three MN cell types. The members of several classes of developmentally relevant transcription factors that are included on the microarray are listed. Their average normalized signal intensities in each cell type are shown (5 animals per cell type, ten chips per cell type). Note that some genes are represented by multiple probe sets. Genes showing significantly different expression values across the three cell types are red. The last column indicates the class of each significantly different gene, as designated in Supplemental Table S1 and Figure 5.

affy ID	Name	Ave IML	Ave LMN	Ave MMN	Class (in Suppl. 1)
HomeoDomain (HD) containing proteins					
a. Iroquois related					
99034_at	Irx3	79.01	170.47	155.92	II
b. Engrailed					
96523_at	**En1**	147.98	197.67	133.34	VII
98338_at	**En2**	121.32	117.17	121.14	
c. Hox					
95297_at	Hoxa1	56.2	59.4	57.7	
92970_at	Hoxa10	36.2	47.3	47.9	
104021_at	Hoxa11	44.8	47.6	50.5	
93873_s_at	Hoxa11s	54.9	58.8	61.1	
161670_f_at	Hoxa11s	170.7	190.1	179.2	
94636_at	Hoxa13	86.5	84.1	84.1	
102643_at	Hoxa2	111.6	116.0	111.8	
102087_at	Hoxa3	62.6	68.0	64.3	
97747_r_at	Hoxa4	682.0	677.6	691.4	
97746_f_at	Hoxa4	11.8	11.0	11.4	
97745_at	Hoxa4	144.5	144.9	136.9	
162402_r_at	Hoxa4	14.3	16.8	14.8	V
103086_at	Hoxa5	419.6	388.8	450.3	
102580_r_at	Hoxa6	132.9	130.6	133.5	
102864_at	Hoxa7	360.2	469.2	429.0	
102579_f_at	Hoxa7	65.4	76.9	74.7	
92745_at	Hoxa9	243.6	297.1	277.6	
93888_at	Hoxb1	52.6	50.6	52.0	
99808_at	Hoxb13	98.7	96.4	98.9	
98780_at	Hoxb3	80.0	82.1	79.8	
92255_at	Hoxb4	60.2	63.7	61.6	
103666_at	Hoxb5	413.7	391.8	429.3	
103445_at	Hoxb6	347.2	333.3	324.7	
92915_s_at	Hoxb7	288.5	295.6	286.1	
92914_at	Hoxb7	267.7	261.6	257.1	
96418_r_at	Hoxb8	379.5	420.4	387.7	
96417_s_at	Hoxb8	46.1	49.1	45.9	
103952_at	Hoxb9	54.6	49.8	52.7	
102660_at	Hoxc4	84.5	87.3	84.1	
95312_at	Hoxc5	145.1	155.1	157.9	
99980_at	Hoxc6	136.1	134.4	122.1	
93378_at	Hoxc8	123.0	146.4	118.0	
92891_f_at	Hoxc9	159.7	164.6	159.6	
98820_g_at	Hoxd1	66.8	12.9	14.3	
98819_at	Hoxd1	127.0	87.9	81.4	
103741_at	Hoxd10	113.1	125.6	132.3	
92951_at	Hoxd11	104.8	119.4	121.9	
99427_at	Hoxd12	30.4	32.0	29.0	
102567_at	Hoxd13	93.9	92.3	95.1	
98367_at	Hoxd3	26.9	27.8	26.2	
102380_s_at	Hoxd4	103.8	111.9	104.4	

93221_at	Hoxd8	137.3	144.2	153.4	
160460_at	Hoxd8	828.8	802.7	939.7	
99426_at	Hoxd9	121.4	128.4	127.8	
d. Paired box Proteins					
100697_at	Pax3	66.28	66.83	64.92	
99908_at	Pax4	264.98	287.89	278.95	
92271_at	Pax6	92.89	95.58	90.27	
e. NKx Proteins					
98337_at	Nkx1-2	170.94	164.87	161.58	
92747_at	Nkx2-2	86.54	70.70	94.88	VII
101334_at	Nkx2-3	72.53	71.07	74.73	
97777_at	Nkx2-5	94.74	98.44	95.36	
99873_at	Nkx2-6	70.12	72.60	68.62	
96422_at	Nkx2-9	200.96	195.52	199.99	
97157_at	Nkx3-1	28.83	30.28	31.27	
93182_at	Nkx6-2	291.31	243.77	275.16	
f. Paired-like Homeobox Proteins					
92980_at	Phox2a	91.38	91.22	93.47	
g. Lim-HD Proteins					
93644_at	Lhx9	30.0	30.4	30.2	
93643_at	Lhx9	23.3	22.3	22.8	
94176_at	Lhx6	68.0	69.1	68.6	
94754_at	Lhx8	27.7	28.6	28.1	
92515_at	Isl1	54.4	49.2	51.8	
101775_at	Lmx1b	155.9	171.3	163.6	
102902_at	Lhx3	112.1	127.5	119.8	
101192_at	Lhx5	65.5	64.4	65.0	
92961_at	Lhx1	162.3	170.2	166.2	
Lim domain proteins					
a. Lim domain only proteins					
102413_at	Lmo1	349.3	399.5	374.4	
96810_at	Lmo2	312.0	230.1	271.0	
93666_at	Lmo2	135.9	122.3	129.1	
98122_at	Lmo4	957.9	1129.3	1043.6	
93451_at	Lmo7	378.7	217.4	298.1	
97500_g_at	Fhl1	281.4	315.7	298.5	
97499_at	Fhl1	13.8	13.8	13.8	
97498_at	Fhl1	1061.1	1017.0	1039.1	
100986_at	Fhl2	153.8	145.1	149.5	
b. Lim and SH3 domain proteins					
93930_at	Lasp1	135.5	145.0	140.2	
93793_at	Lasp1	286.9	208.0	247.5	V
c. Lim kinase protein					
102889_r_at	Limk1	1493.3	1631.6	1562.4	V
102888_s_at	Limk1	426.9	443.0	435.0	
99606_at	Limk2	480.5	504.8	492.7	
d. PDZ and Lim domain					
161348_r_at	Pdlim1	384.9	454.5	419.7	III

100554_at	Pdlim1	145.5	125.8	135.6	
101089_at	Pdlim3	23.1	24.1	23.6	
162494_at	Pdlim4	20.9	21.4	21.2	
104094_at	Pdlim4	93.8	91.7	92.8	
98413_at	Pdlim7	14.3	15.1	14.7	
160837_at	Pdlim7	465.6	488.7	477.2	
160367_at	Pdlim7	29.8	28.1	28.9	
102845_at	Pdlim7	198.4	203.3	200.8	

Forkhead Domain Proteins

92697_at	Foxa1	21.73	21.40	22.41	
93950_at	Foxa2	128.18	132.39	131.80	
98324_at	Foxa3	41.40	44.33	39.91	
94687_at	Foxb1	16.15	14.44	15.12	
94618_at	Foxb2	188.75	192.80	190.06	
160604_at	Foxc1	11.21	9.90	10.95	V
102800_at	Foxc2	174.47	130.32	172.62	
162016_f_at	Foxc2	129.28	82.74	126.63	III
160996_at	Foxd1	88.92	66.34	83.15	V
94621_at	Foxd2	297.53	297.24	295.47	
92889_r_at	Foxd3	19.15	19.67	18.25	
101648_at	Foxd4	32.67	32.37	31.22	
93704_at	Foxf1a	42.59	48.78	44.37	
99846_at	Foxf2	24.67	22.91	26.88	
161049_at	Foxg1	12.95	12.90	13.14	
97789_at	Foxh1	354.98	346.55	341.72	
98831_at	Foxj1	357.49	421.04	440.07	II
160969_at	Foxk1	166.16	169.62	166.28	
101185_at	Foxl1	200.21	215.03	202.77	
98305_at	Foxm1	219.82	228.30	219.14	
98306_g_at	Foxm1	576.53	576.46	551.50	
92674_at	Foxn1	109.87	114.81	108.77	
92958_at	Foxo3	579.71	453.55	512.21	
96183_at	Foxp1	72.39	72.47	72.72	
104415_at	Foxp1	127.92	108.01	123.74	V
92658_at	Foxq1	82.49	78.72	83.59	

ETS Proteins

92927_at	ER81/Etv1	251.37	201.19	183.09	
161842_r_at	Pea3/Etv4	492.63	515.28	490.83	
92979_at	Pea3/Etv4	129.01	135.17	140.56	
94332_at	Ets1	29.52	27.09	27.55	
94720_at	Ets1	104.45	104.38	103.73	
94246_at	Ets2	193.04	161.31	180.71	
160721_at	Elf1	21.08	17.40	19.29	V
161584_r_at	Elf1	8.85	8.34	8.78	

basic Helix-loop-Helix Proteins

102238_at	Mash1/Ascl	53.8654	56.325	49.72938

161069_at	Neurog1	13.472	13.3833	14.08956
93230_at	Neurog1	104.918	100.713	105.5938
97792_at	Neurog2	44.0113	45.2759	45.74502
99814_at	Neurog3	93.523	97.1659	93.63582
102569_at	Math1/Atoh	109.594	115.259	113.4677

(A) extracellular

					Fold changes*			Average Signal Intensities & Standard Deviations					
								LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	IML/MMN	MN/MMN	Average	SD	Average	SD	Average	SD
AI852470	Nme3	EC	nucleoside diphosphate kinase DR-nm23	nucleotide biosynthesis	1.60	1.23	0.77	603.27	39.26	785.07	75.76	963.32	140.90
X13986	Spp1	EC	secreted phosphoprotein 1	cell adhesion, cytokine activity	0.51	0.69	1.36	3754.97	328.59	2758.02	340.15	1902.64	425.02
AA690434	Ace2	M, EC	angiotensin I converting enzyme	proteolysis and peptidolysis	1.15	1.18	1.02	13.34	1.10	13.08	0.40	15.40	1.26
AF004326	Agpt2	EC	angiopoietin 2	promotes angiogenesis	1.54	1.41	0.92	42.12	9.12	45.87	9.63	64.72	13.39
M22531	C1qb	EC	complement component 1q beta polypeptide	complement activity	1.46	1.33	0.91	58.84	6.66	64.50	14.16	85.78	10.18
K02782	C3	EC	complement component 3	complement activity	2.61	1.81	0.70	97.18	18.14	139.77	47.79	253.45	69.08
U49513	Ccl9	EC	chemokine (C-C motif) ligand 9	signal transduction	1.39	1.28	0.92	57.47	3.38	62.55	6.38	79.82	7.79
U60473	Cd59a	M, EC	CD59a antigen	complement activity	0.78	0.80	1.03	2333.06	192.37	2257.15	205.82	1810.77	161.36
AF011450	Col15a1	EC	procollagen, type XV	ECM structural constituent	1.46	1.28	0.88	95.13	9.71	108.00	21.04	138.69	12.32
U74683	Ctsc	lys, EC	cathepsin C	proteolysis and peptidolysis	2.06	1.66	0.81	46.57	19.13	57.78	28.55	96.08	17.39
AJ223208	Ctss	lys, EC	cathepsin S preprotein	proteolysis and peptidolysis	1.92	1.69	0.88	624.07	123.03	710.46	236.09	1201.30	355.01
X83577	Gpc4	M, EC	glypican 4	signal transdiuction, ECM interactions	1.42	1.26	0.89	80.82	8.85	90.78	12.18	114.65	11.73
U13705	Gpx3	EC	glutathione peroxidase 3	response to oxidative stress	1.50	1.43	0.96	239.10	53.58	250.15	83.75	357.50	40.44
AI574278	Ide	EC	insulin degrading enzyme	proteolysis and peptidolysis	0.74	0.78	1.05	86.68	7.83	82.79	12.92	64.28	7.43
AA726364	lpl	EC	lipoprotein lipase	lipid metabolism	2.75	2.18	0.79	59.35	7.37	74.69	31.28	162.93	109.02
M21050	lys	EC, mit	lysozyme	carbohydrate metabolism	4.49	2.82	0.63	44.54	16.27	71.04	37.29	200.10	188.88
X72795	Mmp9	EC	matrix metalloproteinase 9	proteolysis and peptidolysis	0.51	0.68	1.35	393.23	104.18	291.36	26.91	198.85	44.93
M17298	Ngfb	EC	nerve growth factor, beta	growth & maintenance, signal transduction	0.87	0.89	1.01	32.01	2.59	31.56	2.19	27.93	1.44
D13664	Osf2-pending	EC	periostin	cell adhesion, transcription factor	3.07	2.67	0.87	36.42	12.52	41.88	19.12	111.72	78.27
M55181	Penk1	EC	preproenkephalin 1	neuropeptide signal transduction	3.15	2.43	0.77	1506.34	665.99	1950.34	586.98	4748.73	1129.00
X68837	Scg2; Chgc; SgII	EC	secretogranin II	calcium binding	1.43	1.44	1.01	598.54	128.03	592.51	76.28	855.68	90.06
D17584	Tac1	EC	tachykinin 1	neuropeptide signal transduction	6.31	5.41	0.86	67.04	29.24	78.17	72.89	422.82	503.80
AV218205	Cst3	EC	cystatin C	cysteine protease inhibitor activity	1.59	1.18	0.74	327.66	33.81	440.51	20.46	520.65	149.06
L11333	Es31	ER,EC	esterase 31	carboxylesterase activity	0.89	1.01	1.14	65.86	2.86	58.02	4.23	58.42	3.10
AV062425	Gast	EC	gastrin	peptide hormone	0.78	1.03	1.32	44.90	3.67	34.05	3.55	35.08	3.28
AB012886	Igfbp7	EC	insulin-like growth factor binding protein 7	regulationof growth & metabolism	1.15	0.99	0.86	119.44	8.53	138.68	13.30	137.00	5.50
AV345275	Matn2	EC	matrilin 2	non-collagenous extracellular matrix protein	0.90	1.02	1.13	95.50	5.40	84.21	5.47	86.09	4.85
L34169	Thpo	EC	thrombopoietin	hormone/cytokine, cell growth & maintenance	0.92	0.99	1.08	97.41	5.75	90.56	2.84	89.24	1.61
D38410	Tff3	EC	trefoil factor 3, intestinal	peptide signal transduction	0.91	1.00	1.09	295.52	15.01	270.28	11.28	269.31	7.76
X61448	Cbln1	EC	cerebellin 1 precursor protein	neuropeptide, unknown function	0.85	0.44	0.52	464.56	76.34	895.38	258.83	395.70	37.93
AB016592	Agr2	EC	anterior gradient 2 (Xenopus laevis)	survival factor	0.84	0.97	1.15	56.02	6.39	48.69	3.52	47.26	3.92
AF006196	Adam15	M, EC	a disintegrin and metalloproteinase domain 15	membrane surface & ECM proteolysis, cell adhesion	0.83	0.92	1.10	179.21	20.29	162.53	9.92	149.58	12.35
AF045887	Agt; Aogen	EC	angiotensinogen	local & circulating hormone	1.65	1.16	0.70	346.27	56.61	495.47	100.82	572.68	210.40
M29008	Cfhl1	EC	complement component factor h-like 1	complement activity	1.71	1.28	0.75	92.37	25.95	123.78	46.98	158.01	34.68
M29009	Cfh	EC	complement component factor h	complement activity	2.18	1.25	0.57	61.16	23.73	106.38	67.00	133.15	46.79
AV003419	Anxa1; lpc1	EC, M, IC	annexin A 1, lipocortin 1	Ca- & phospholipid-binding protein, multiple functions	5.95	2.37	0.40	90.78	49.43	227.72	137.75	540.17	661.66
X13460	Anxa6	EC, M, IC	annexin A6	Ca- & phospholipid-binding protein, multiple functions	0.60	0.67	1.10	1393.51	314.44	1261.77	462.23	839.86	233.55
D00466	Apoe	EC	apolipoprotein,	lipid transport, lipoprotein metabolism	2.13	1.35	0.63	2898.04	825.71	4594.10	1631.17	6182.09	1664.78
X53928	Bgn	EC	biglycan	glycoprotein, binds collagen	2.82	1.60	0.57	403.42	157.52	711.40	431.96	1136.95	646.38
X66295	C1qg	EC	complement component 1q gamma	complement activity	1.28	1.23	0.96	200.32	26.15	208.95	33.14	257.01	28.74
AI132585	C1r	EC	complement component 1, r subcomponent	complement activity	1.43	1.23	0.86	107.38	10.42	125.36	30.94	153.62	26.18
X06454	C4	EC	complement component 4 (within H-2S)	complement activity	1.89	1.47	0.78	120.05	32.18	153.87	57.37	226.44	55.29
M29009	Cfh	EC	complement component factor h	complement activity	2.18	1.25	0.57	61.16	23.73	106.38	67.00	133.15	46.79
M29008	Cfhl1	EC	complement component factor h-like 1	complement activity	1.71	1.28	0.75	92.37	25.95	123.78	46.98	158.01	34.68
U30292	Col13a1	EC	procollagen, type XIII, alpha 1	structural constituent of ECM	1.11	1.04	0.93	29.48	1.61	31.55	2.26	32.86	1.61
D17546	Col18a1	EC	procollagen, type XVIII, alpha 1	structural constituent of ECM	1.30	1.09	0.84	309.16	33.95	369.33	56.76	402.43	44.33
AB000636	Col19a1	EC	procollagen, type XIX, alpha 1	structural constituent of ECM	0.71	0.80	1.13	80.36	10.98	70.94	12.29	56.87	3.56
U03419	Col1a1	EC	procollagen, type I, alpha 1	structural constituent of ECM	1.77	1.65	0.93	94.29	36.22	100.92	29.89	166.89	65.57
AV234303	Col3a1	EC	procollagen, type III, alpha 1	structural constituent of ECM	3.96	1.99	0.50	34.39	18.35	68.49	39.97	136.16	88.17
X66405	Col6a1	EC	procollagen, type VI, alpha 1	structural constituent of ECM	1.59	1.31	0.83	330.96	42.84	400.37	127.69	526.04	162.82
AV010209	Col6a1		procollagen, type VI, alpha 1		2.24	1.54	0.69	48.95	12.18	71.29	30.78	109.44	54.08
U49430	Cp	EC	ceruloplasmin	ferroxidase regulating iron efflux	2.39	1.26	0.53	53.84	19.60	102.14	55.50	128.50	19.25
AF017639	Cpxm2	EC	carboxypeptidase X 2 (M14 family)	proteolysis and peptidolysis; cell adhesion	2.01	1.43	0.71	145.28	20.02	204.70	65.60	292.39	70.91
AJ006469	Crtap	EC	cartilage associated protein	constiuent of the ECM	1.43	1.03	0.72	244.42	36.71	341.42	90.02	350.66	53.29
AJ242663	Ctsz	EC, Lys	cathepsin Z	proteolysis and peptidolysis	1.53	1.38	0.90	114.13	29.71	127.04	39.50	175.02	32.34
L12029	Cxcl12	EC	chemokine (C-X-C motif) ligand 12	signal transduction; growth factor	2.58	1.68	0.65	57.12	14.39	87.88	27.86	147.51	80.49
AJ242625	Dmp1; PP	IC, N, EC	dentin matrix protein	transcription factor & mineralization of ECM	0.45	0.70	1.55	93.62	50.90	60.31	18.44	41.95	13.17
AA717826	Dpt	EC	dermatopontin	cell adhesion	2.15	1.72	0.80	42.05	9.32	52.49	21.36	90.23	40.82
AA919594	Eln	EC	elastin	constituent of ECM	1.69	1.25	0.74	320.45	37.79	432.25	121.00	541.22	80.38
X79083	Epha7	M	Eph receptor A7	cell adhesion	1.53	1.33	0.87	75.71	7.93	87.34	14.15	115.77	35.12
L29454	Fbn1	EC	fibrillin 1	constituent of the ECM	1.85	1.40	0.75	56.28	10.05	74.58	28.18	104.23	31.09
AI196896	Fgb	EC	fibrinogen, B beta polypeptide	blood clotting	0.90	0.95	1.06	20.66	1.43	19.48	1.06	18.50	0.72
M30641	Fgf1	EC	fibroblast growth factor 1	signal transduction, cell growth	0.53	0.71	1.33	237.45	93.48	178.88	50.23	126.74	27.89
X94998	Fmod	EC	fibromodulin	ECM organization	2.39	1.34	0.56	271.71	123.95	484.18	305.30	649.78	289.05
M18194	Fn1	EC	fibronectin 1	ECM, cell adhesion	1.82	1.18	0.65	302.33	114.75	467.86	129.90	551.28	153.05
X59846	Gas6	EC	growth arrest specific 6	vitamin K-dependent growth factor	0.66	0.73	1.10	597.88	68.90	543.80	181.23	395.07	123.52
X59846	Gas6	EC	growth arrest specific 6	vitamin K-dependent growth factor	0.66	0.73	1.10	597.88	68.90	543.80	181.23	395.07	123.52
AI843313	Gpc3	EC	glypican 3	growth control	1.83	1.28	0.70	171.64	52.92	245.78	106.00	314.69	62.38
D16195	Grn; epithelin	EC,	granulin	growth factor, signal transduction	1.50	1.25	0.83	161.43	22.26	193.33	42.72	241.51	22.04
X06271	Il5; Il-5	EC	interleukin 5 (eosinophil differentiation factor).	cell surface receptor linked signal transduction	0.90	0.99	1.10	73.47	3.06	66.50	3.28	66.01	6.25
L12447	Igfbp5	EC	insulin-like growth factor binding protein 5	cell growth, signal transduction	4.36	1.48	0.34	256.86	178.61	757.23	699.65	1119.62	410.93
X71922	Igf2; Mpr; M6pr	EC	insulin-like growth factor 2	growth factor, signal transduction	2.87	1.50	0.52	2416.06	1432.42	4632.00	1996.58	6937.16	1150.94
AI838737	Igfbp4	EC	insulin-like growth factor binding protein 4	cell growth, signal transduction	1.18	1.07	0.91	310.28	17.62	341.01	17.12	364.62	34.79
X76066	Igfbp4; IGFBP-4		insulin like growth factor binding protein 4.		1.24	1.09	0.88	157.80	15.03	179.79	14.48	195.22	25.01
AV357656	Lamb1-1	EC	laminin B1 subunit 1	ECM component	2.32	1.61	0.69	101.45	43.27	146.01	77.91	235.20	89.93
X99347	Lbp	EC	lipopolysaccharide binding protein	lipopolysaccharide transport	1.80	1.16	0.64	347.57	79.43	540.32	199.45	625.84	112.29
AV232133	Lox	EC	lysyl oxidase	oxidoreductase activity	1.22	1.06	0.87	68.74	4.51	79.07	6.33	84.16	9.62
AF022889	Ltbp1	EC	latent transforming growth factor beta binding protein 1	TGF beta receptor signal transduction	1.55	1.23	0.80	44.96	4.15	56.32	11.38	69.47	13.93
AI849993	Ly6h	M	lymphocyte antigen 6 complex, locus H	cell surface glycoprotein, growth regulation	1.42	1.23	0.86	369.25	32.02	427.75	66.57	524.09	59.88
X51547	Lzp-s	EC	P lysozyme structural	carbohydrate metabolism	2.03	1.76	0.87	65.45	9.21	75.49	17.14	132.74	84.84
AJ010984	Matn4; matrilin-4	EC	Mus musculus matn4 partial gene, exon 3.	non-collagenous extracellular matrix protein	1.40	1.15	0.82	132.42	17.81	160.74	38.96	185.30	36.36
AF017994	Mest; Peg1	EC	mesoderm specific transcript	proteolysis and peptidolysis	0.42	0.85	2.05	157.67	92.87	76.86	30.46	65.57	24.84
AF041335	Myoc; TIGR	EC	trabecular meshwork induced glucocorticoid protein	inhibitor of neurite outgrowth	1.41	1.15	0.82	37.87	3.64	46.43	9.49	53.51	12.46

X92397	Ndph	EC	Norrie disease homolog	receptor for Norrin-Fz4 signal transduction	1.25	1.11	0.89	206.01	30.60	231.80	29.56	257.70	26.84
Y09257	Nov	EC	nephroblastoma overexpressed gene	insulin-like growth factor binding activity	3.05	1.92	0.63	123.24	69.56	195.19	103.05	375.33	172.45
AA592182	Npnt	EC	nephronectin	cell-matrix adhesion	1.27	1.14	0.90	55.48	4.47	61.79	6.71	70.50	13.52
M69196	Pcsk1	EC	proprotein convertase subtilisin/kexin type 1	proteolysis and peptidolysis	1.40	1.31	0.94	99.19	14.61	105.97	11.33	138.40	26.81
J04148	Prf1	EC	perforin 1 (pore forming protein)	cytolysis	0.79	0.89	1.13	76.02	7.71	67.20	6.25	60.10	4.37
L27439	Pros1	EC	protein S (alpha)	blood coagulation	2.16	1.42	0.66	109.50	30.86	166.37	76.61	236.16	74.31
AW125478	Prss11	EC	protease, serine, 11 (Igf binding)	proteolysis and peptidolysis	0.57	0.65	1.15	2573.57	1023.22	2229.81	361.56	1456.53	377.21
Y18723	Prss18	EC	protease, serine, 18	proteolysis and peptidolysis	2.04	1.24	0.61	167.51	45.62	274.92	79.33	341.73	139.26
AF002719	Slpi; SLPI	EC	secretory leukoprotease inhibitor	serine-type endopeptidase inhibitor	1.32	1.22	0.93	77.93	1.82	84.18	8.22	102.88	26.45
AW214439	Sparc	EC	secreted acidic cysteine rich glycoprotein	ECM organization	1.23	1.13	0.92	299.27	15.60	326.71	24.52	367.85	45.56
X92864	Spock1	EC	arc/osteonectin, cwcv and kazal-like domains proteoglycan	regulates cell shape & growth and ECM production	0.65	0.76	1.17	480.69	135.95	411.63	81.70	314.75	36.25
AW060556	Stab1	M	stabilin 1	cell adhesion	1.58	1.21	0.77	81.48	6.77	106.45	27.34	128.91	9.12
M62470	Thbs1; TSP1	EC	thrombospondin	cell adhesion	4.21	1.94	0.46	41.56	23.91	90.21	59.55	174.88	134.49
U26437	Timp3; TIMP-3	EC	tissue inhibitor of metalloproteinases-3	metalloendopeptidase inhibitor	1.99	1.28	0.64	918.63	247.64	1425.62	481.30	1831.61	276.97
AV230686	Tnc	EC	tenascin C	ECM component, determinant of synaptic plasticity	1.97	1.81	0.92	13.04	3.39	14.20	4.29	25.70	16.14
AW060819	Twg-pending	EC	twisted gastrulation protein	signal transduction	1.76	1.32	0.75	186.04	35.20	247.34	102.36	326.68	90.52
M84487	Vcam1	M, EC	vascular cell adhesion molecule 1	cell adhesion; signal transduction	2.30	1.47	0.64	158.34	45.33	248.22	116.25	364.60	136.38
AI843063	Vwf	EC	Von Willebrand factor homolog	blood coagulation	3.28	1.68	0.51	168.21	106.58	327.83	189.37	552.33	238.94
M89800	Wnt6	EC	wingless-related MMTV integration site 6	signaling peptide	1.30	1.06	0.81	68.05	8.36	83.81	14.10	88.75	12.29
X62502	Ccl4; Act-2; Mip1b	EC	chemokine (C-C motif) ligand 4	signal transduction	1.03	1.08	1.05	116.68	2.92	111.55	3.04	120.69	5.58
L38580	Gal; Galn	EC	galanin neuropeptide	neuropeptide signal transduction	1.21	1.28	1.06	214.48	10.75	202.41	6.20	259.99	52.94
M92850	Aeg2	IC, EC	acidic epididymal glycoprotein 2	unknown	1.05	0.97	0.93	8.68	0.22	9.35	0.34	9.10	0.41
X97991	Calca	EC	calcitonin/calcitonin-related polypeptide, alpha	peptide signal transduction	0.93	1.02	1.10	117.83	6.75	106.82	5.41	109.17	5.06
M17015	Lta; LT; Ltx	EC	lymphotoxin	TNF-receptor ligand, cell growth and/or maintenance	0.95	1.09	1.15	315.84	24.11	274.97	21.51	298.66	20.43
X53257	Ntf3; NT3	EC	neurotrophin-3 peptide	growth and/or maintenance	1.06	0.90	0.85	38.51	3.09	45.08	3.44	40.75	2.26

(B) growth

					Fold changes*			Average Signal Intensities & Standard Deviations					
								LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	IML/MMN	LMN/MMN	Average	SD	Average	SD	Average	SD
AF011644	Cdkap1	IC	CDK2-associated protein 1	cell growth and/or maintenance	0.78	0.79	1.01	793.06	63.54	784.33	92.13	619.54	73.28
U49513	Ccl9	EC	chemokine (C-C motif) ligand 9	signal transduction	1.39	1.28	0.92	57.47	3.38	62.55	6.38	79.82	7.79
U56819	Ccr2	M	chemokine (C-C) receptor 2	signal transduction	1.27	1.30	1.02	31.32	2.43	30.68	3.55	39.86	5.74
AV370035	Ccr5	M	chemokine (C-C motif) receptor 5	signal transduction	1.51	1.70	1.13	39.85	13.13	35.28	3.48	59.98	16.88
AB016592	Agr2	EC	anterior gradient 2 (Xenopus laevis)	survival factor	0.84	0.97	1.15	56.02	6.39	48.69	3.52	47.26	3.92
X77952	Eng	M	endoglin	constituent of TGF-beta signaling complex	1.56	1.07	0.69	543.31	88.88	789.78	112.17	847.13	184.77
AI046826	Gab1	IC	growth factor receptor bound protein 2-associated protein 1	signal transduction	1.65	1.09	0.66	313.46	50.75	473.00	56.21	516.46	81.88
X65128	Gas1	M	growth arrest specific 1	growth regulation	2.01	1.25	0.62	311.55	63.70	503.46	127.66	627.42	214.01
AB012886	Igfbp7	EC	insulin-like growth factor binding protein 7	regulationof growth & metabolism	1.15	0.99	0.86	119.44	8.53	138.68	13.30	137.00	5.50
U10531	Skil; sno; Skir	N	SNO proto-oncogene	cell growth and maintenance	0.88	1.00	1.13	82.17	2.75	72.64	2.88	72.61	5.42
L34169	Thpo	EC	thrombopoietin	hormone/cytokine, cell growth & maintenance	0.92	0.99	1.08	97.41	5.75	90.56	2.84	89.24	1.61
X53928	Bgn	EC	biglycan	glycoprotein, binds collagen, growth anad survival	2.82	1.60	0.57	403.42	157.52	711.40	431.96	1136.95	646.38
Z16410	Btg1	IC	M.musculus btg1 mRNA.	antiproliferative	1.52	1.27	0.83	102.84	21.00	123.52	38.34	156.43	17.41
D83745	Btg3	IC	B-cell translocation gene 3	antiproliferative	2.12	1.56	0.73	67.09	25.77	91.57	30.07	142.51	19.19
L12029	Cxcl12	EC	chemokine (C-X-C motif) ligand 12	signal transduction; growth factor	2.58	1.68	0.65	57.12	14.39	87.88	27.86	147.51	80.49
M58004	Ccl6	EC	chemokine (C-C motif) ligand 6	signal transduction	1.31	1.21	0.92	89.51	15.07	96.99	8.03	117.22	23.28
AF016697	Dfy; FY;	M	chemokine receptor	signal transduction	0.76	0.83	1.10	311.46	39.97	284.31	45.12	236.08	41.09
U04827	Fabp7; B-FABP		brain fatty acid-binding protein	regulates Schwann cell-axon interactions	3.01	1.89	0.63	628.02	217.67	998.40	613.73	1891.67	788.72
M30641	Fgf1	EC	fibroblast growth factor 1	signal transduction, cell growth	0.53	0.71	1.33	237.45	93.48	178.88	50.23	126.74	27.89
AW125390	Fgls; Ifitm3		fragilis, interferon induced transmembrane protein 3	signal transduction	1.51	1.07	0.71	193.79	38.72	273.36	92.21	293.14	54.86
AI841303	Gap43	IC, M	growth associated protein 43	regulation of growth, plasticity, synaptic release	2.64	2.01	0.76	562.79	324.58	740.97	168.10	1487.40	228.11
X59846	Gas6	EC	growth arrest specific 6	vitamin K-dependent growth factor	0.66	0.73	1.10	597.88	68.90	543.80	181.23	395.07	123.52
M94450	Grb7	IC	growth factor receptor bound protein 7	signal transduction	0.87	0.96	1.10	336.12	26.21	305.31	20.53	293.12	12.56
D16195	Grn; epithelin	EC	granulin	growth factor, signal transduction	1.50	1.25	0.83	161.43	22.26	193.33	42.72	241.51	22.04
X71922	Igf2; Mpr; M6pr	EC	insulin-like growth factor 2	growth factor, signal transduction	2.87	1.50	0.52	2416.06	1432.42	4632.00	1996.58	6937.16	1150.94
X76066	Igfbp4; IGFBP-4		insulin-like growth factor binding protein 4	cell growth, signal transduction	1.24	1.09	0.88	157.80	15.03	179.79	14.48	195.22	25.01
L12447	Igfbp5	EC	insulin-like growth factor binding protein 5	cell growth, signal transduction	4.36	1.48	0.34	256.86	178.61	757.23	699.65	1119.62	410.93
Y09864	Ifnar2	M	interferon (alpha and beta) receptor 2	signal transduction	1.20	1.12	0.93	58.65	4.06	63.08	7.55	70.55	4.98
U53696	Il10rb	M	interleukin 10 receptor, beta	cell surface receptor linked signal transduction	1.65	1.34	0.81	570.21	103.84	703.19	205.97	938.78	198.67
AA608387	Il13ra1	M	interleukin 13 receptor, alpha 1	cell surface receptor linked signal transduction	1.72	1.25	0.72	38.06	7.45	52.55	17.22	65.54	12.06
M26271	IL2R	M	Mouse interleukin 2 receptor gene, 5' end.	cell surface receptor linked signal transduction	0.85	0.93	1.10	25.86	2.65	23.43	2.05	21.89	1.19
X06271	Il5; Il-5	EC	interleukin 5 (eosinophil differentiation factor).	cell surface receptor linked signal transduction	0.90	0.99	1.10	73.47	3.06	66.50	3.28	66.01	6.25
AF022889	Ltbp1	EC	latent transforming growth factor beta binding protein 1	TGF beta receptor signal transduction	1.55	1.23	0.80	44.96	4.15	56.32	11.38	69.47	13.93
AI849993	Ly6h	M	lymphocyte antigen 6 complex, locus H	cell surface glycoprotein, growth regulation	1.42	1.23	0.86	369.25	32.02	427.75	66.57	524.09	59.88
AI852838	Meg3		maternally expressed gene 3	growth suppressor	0.75	0.85	1.13	111.93	18.26	98.68	10.00	84.00	7.21
AF041335	Myoc; TIGR	EC	trabecular meshwork induced glucocorticoid protein	inhibitor of neurite outgrowth	1.41	1.15	0.82	37.87	3.64	46.43	9.49	53.51	12.46
AI642048	Nfkbia	IC, N	clear factor of κ light chain gene enhancer in B-cells inhibitor, α	regulation of cell proliferation	1.37	1.08	0.79	166.62	14.47	210.72	34.29	227.78	43.86
Y09257	Nov	EC	nephroblastoma overexpressed gene	insulin-like growth factor binding activity	3.05	1.92	0.63	123.24	69.56	195.19	103.05	375.33	172.45
AW125478	Prss11	EC	protease, serine, 11 (Igf binding)	proteolysis and peptidolysis, cell growth	0.57	0.65	1.15	2573.57	1023.22	2229.81	361.56	1456.53	377.21
AV007820	S100a13		S100 calcium binding protein A13	cell growth and/or maintenance	1.92	1.34	0.70	352.57	28.25	505.90	75.51	677.77	233.71
X66449	S100a6		S100 calcium binding protein A6 (calcyclin)	cell growth and/or maintenance	5.62	2.74	0.49	139.12	43.57	285.30	137.65	782.38	787.07
X92864	Spock1	EC	parc/osteonectin, cwcv and kazal-like domains proteoglycan 1	regulates cell shape & growth and ECM production	0.65	0.76	1.17	480.69	135.95	411.63	81.70	314.75	36.25
U02487	Sspn	M	sarcospan	cell growth and/or maintenance	1.59	1.24	0.78	78.85	27.53	100.99	18.30	125.26	23.10
X97817	Sema5a	M	semaphorin 5A	axon guidance receptor activity	1.16	1.09	0.94	22.28	1.57	23.76	1.23	25.86	1.92
AV230686	Tnc	EC	tenascin C	ECM component, determinant of synaptic plasticity	1.97	1.81	0.92	13.04	3.39	14.20	4.29	25.70	16.14
AF039601	Tgfbr3	M	transforming growth factor, beta receptor III	signal transduction	0.81	0.84	1.04	135.54	11.61	130.17	16.02	109.79	9.57
X87128	Tnfrsf1b; p75	M	p75 TNF receptor	signal transduction, neurotransmitter release,apoptosis	1.31	1.19	0.91	72.35	3.31	79.84	13.56	94.75	15.63
X62502	Ccl4; Act-2; Mip1	EC	chemokine (C-C motif) ligand 4	signal transduction	1.03	1.08	1.05	116.68	2.92	111.55	3.04	120.69	5.58
D13695	Il1rl1	M	interleukin 1 receptor-like 1	signal transduction, synaptic plasticity	1.14	1.24	1.09	18.46	1.25	16.99	0.80	21.10	4.27
M29697	Il7r	M	interleukin 7 receptor	cell surface receptor linked signal transduction	1.14	1.20	1.05	20.22	2.09	19.20	1.31	22.99	3.12
M17015	Lta; LT; Ltx	EC	lymphotoxin	TNF-receptor ligand, cell growth and/or maintenance	0.95	1.09	1.15	315.84	24.11	274.97	21.51	298.66	20.43
X53257	Ntf3; NT3	EC	neurotrophin-3 peptide	growth and/or maintenance	1.06	0.90	0.85	38.51	3.09	45.08	3.44	40.75	2.26

(C) cell adhesion

Genbank	Common	location	Description	Function	Fold changes*			SD
					IML/LM	ML/MM	MN/MMN	
X15052	Ncam1	M; EC	neural cell adhesion molecule 1	cell adhesion, synaptic transmission, plasticity	2.50	1.83	0.73	178.60
X13986	Spp1	EC	secreted phosphoprotein 1	cell adhesion, cytokine activity	0.51	0.69	1.36	425.02
AB009673	Adam23	M	disintegrin & metalloprotease domain 23	proteolysis and peptidolysis	0.76	0.78	1.03	53.01
X97227	Cd53	M	CD53 antigen	modulates cell-ECM interaction	2.24	1.99	0.89	53.01
D13664	Osf2-pending	EC	periostin	cell adhesion, transcription factor	3.07	2.67	0.87	78.27
AV378129	Ppfibp2	IC	tyrosine phosphatase receptor F interacting protei	signal transduction	1.15	1.09	0.95	0.72
AI891912	Pvrl3	M	poliovirus receptor-related 3	cell adhesion	1.28	1.22	0.95	1.31
X91144	Selpl	M	selectin, platelet (p-selectin) ligand	cell adhesion	1.16	1.14	0.98	13.25
AB008180	Pcdha13	M	protocadherin alpha 13	cell adhesion	0.87	0.98	1.12	184.09
AF006196	Adam15	M, EC	a disintegrin and metalloproteinase domain 15	membrane surface & ECM proteolysis, cell adhesion	0.83	0.92	1.10	12.35
X63535	Axl	M	AXL receptor tyrosine kinase	signal transduction	1.17	1.09	0.93	10.22
U48797	Astn1	M	astrotactin 1	cell adhesion	1.23	1.10	0.89	107.57
AF007802	Bysl	IC	bystin-like	cell adhesion	0.87	0.94	1.08	0.80
AI847784	Cd34	M	CD34 antigen	cell adhesion	1.35	1.19	0.88	26.54
L08115	Cd9	M	CD9 antigen	cell adhesion	2.16	1.70	0.79	559.12
AI853217	Cdh5	M	cadherin 5	cell adhesion	1.56	1.15	0.74	16.02
AF017639	Cpxm2	EC	carboxypeptidase X 2 (M14 family)	proteolysis and peptidolysis; cell adhesion	2.01	1.43	0.71	70.91
AA717826	Dpt	EC	dermatopontin	cell adhesion	2.15	1.72	0.80	40.82
AW228162	Dsc2	M	desmocollin 2	cell adhesion	1.25	1.17	0.94	1.51
U57686	Efs		embryonal Fyn-associated substrate	cell adhesion	1.13	1.06	0.94	7.78
X79083	Epha7	M	Eph receptor A7	cell adhesion	1.53	1.33	0.87	35.12
M18194	Fn1	EC	fibronectin 1	ECM, cell adhesion	1.82	1.18	0.65	153.05
AI841303	Gap43	IC, M	growth associated protein 43	regulation of growth, synaptic plasticity and release	2.64	2.01	0.76	228.11
AI853261	Mcam	M	melanoma cell adhesion molecule	cell adhesion	0.50	0.64	1.27	203.34
AA592182	Npnt	EC	nephronectin	cell-matrix adhesion	1.27	1.14	0.90	13.52
X97817	Sema5a	M	semaphorin 5A	axon guidance receptor activity	1.16	1.09	0.94	1.92
M62470	Thbs1; TSP1	EC	thrombospondin	cell adhesion	4.21	1.94	0.46	134.49
AV230686	Tnc	EC	tenascin C	ECM component, determinant of synaptic plasticity	1.97	1.81	0.92	16.14
AW125880	Tmem4	M	transmembrane protein 4	regulates neurite outgrowth, CySk interactions	1.30	1.05	0.81	27.69
AF039601	Tgfbr3	M	transforming growth factor, beta receptor III	signal transduction	0.81	0.84	1.04	9.57
M84487	Vcam1	M, EC	vascular cell adhesion molecule 1	cell adhesion; signal transduction	2.30	1.47	0.64	136.38
AA880988	Xlkd1	M	extra cellular link domain-containing 1	glycosaminoglycan catabolism, cell adhesion, signaling	1.43	1.21	0.85	10.43
AJ001373	Itgb1bp1	IC	integrin beta 1 binding protein 1	integrin depended cell-matrix adhesion	0.91	0.85	0.94	31.24
U70209	Pkd1	M	polycystic kidney disease 1 homolog	ion channel, signaling, cell adhesion, Ca homostasis	1.05	0.96	0.91	4.26

(D) CySk

								Average Signal Intensities & Standard Deviatio					
					Fold changes*			LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	ML/MMN	MN/MMN	Average	SD	Average	SD	Average	SD
AW125626	Cnn3	CySk	calponin 3, acidic	actin binding protein	1.71	1.28	0.75	1178.00	88.00	1566.71	274.84	2013.12	189.38
AB011678	Dcx	CySk	doublecortin	cytoskeletal complex constituent	1.27	1.26	0.99	91.95	15.34	92.56	14.08	116.43	6.79
AJ223362	Myh7	CySk	myosin, heavy polypeptide 7	cytoskeletal organization	1.52	1.44	0.95	84.79	7.50	89.36	8.53	128.78	33.19
AW047320	Ndel1	IC	nuclear distribution gene E-like homolog 1	retrograde axon transport, CySk interacting protein	0.75	0.84	1.13	1633.64	41.33	1444.58	139.72	1217.07	149.68
M35131	Nefh	CySk	neurofilament, heavy polypeptide	cytoskeleton organization & biogenesis	0.49	0.64	1.32	6286.97	1515.16	4778.15	796.94	3080.17	637.30
M60474	Marcks	M	myristoylated alanine rich PKC substrate	actin & calmodulin binding	2.59	1.74	0.67	277.09	71.64	413.22	145.09	718.12	87.82
U38967	Tmsb4x; Ptmb4	CySk	thymosin beta 4	cytoskeleton organization and biogenesis	1.32	1.32	1.00	1297.34	183.81	1297.78	158.37	1715.36	245.37
AV149007	Pdlim1	IC	PDZ and LIM domain 1 (elfin)	adaptor, signal transduction, CySk interactions	0.85	0.96	1.14	454.49	32.25	399.01	35.08	384.86	23.35
X60671	Vil2	CySk	villin 2	actin filament-plasma membrane linker	1.43	1.05	0.73	123.47	5.70	168.05	29.09	175.96	18.67
M12347	Acta1; Acts	CySk	skeletal alpha-actin gene	structural constituent of cytoskeleton	1.42	1.29	0.91	54.25	4.98	59.67	15.13	76.91	16.69
AA791742	Actr2	CySk	ARP2 actin-related protein 2 homolog (yeast)	structural constituent of cytoskeleton	0.80	0.89	1.12	111.20	14.32	99.26	8.91	88.66	11.84
AW212775	Arpc1b	Cysk	actin related protein 2/3 complex, subunit 1B	cytoskeletal organization	1.24	1.16	0.93	328.40	33.43	351.79	49.38	407.25	36.92
AW124113	Basp1	N, M	brain abundant, membrane attached signal protein 1	transcriptional regulation, signal transduction	1.62	1.33	0.83	1271.05	333.61	1539.62	568.63	2053.11	430.89
AI844806	Cdc42ep4	IC, CySk	CDC42 effector protein (Rho GTPase binding) 4	signal transduction	1.36	1.20	0.88	209.62	17.05	238.17	53.92	286.05	36.02
AF098508	Dctn3	CySk	dynactin 3	intracellular transport	0.74	0.77	1.03	1485.05	66.47	1439.10	264.65	1105.54	246.28
AF063229	Dncic1	CySk	dynein, cytoplasmic, intermediate chain 1	microtubule-based movement	0.82	0.89	1.08	3046.25	323.57	2818.23	169.04	2503.33	345.42
AI836140	Eplin-pending	CySk	epithelial protein lost in neoplasm	cytoskelatal organization	1.37	1.17	0.86	228.24	15.28	266.63	45.98	312.34	42.64
AW123852	Gphn	IC, CySk	gephyrin	clusters glycine receptor & other synaptic proteins	0.70	0.83	1.19	599.89	85.21	506.12	83.51	421.63	81.31
J04953	Gsn; MGC28083	CySk	gelsolin	cytoskeletal organization	2.85	1.57	0.55	259.83	139.08	471.13	244.94	739.86	331.42
AF055665	Kns2	IC, CySk	kinesin 2	microtubule-based movement	0.78	0.93	1.19	3500.63	427.70	2929.70	128.78	2729.79	383.05
D89902	Krtap6-2; HGTpII.4	CySk	high-glycine tyrosine keratin type II.4	intermediate filament of cytoskeleton	0.87	0.98	1.12	123.74	13.17	110.61	3.14	107.85	7.69
AW122780	Lasp1	IC	LIM and SH3 protein 1	signal transduction, actin binding, CySk organization	1.38	1.13	0.82	207.96	31.98	252.98	27.34	286.94	41.36
X86569	Limk1	IC	LIM-domain containing, protein kinase	cytoskeletal regulation	0.92	0.97	1.06	1631.60	113.93	1539.20	55.55	1493.29	31.39
D49691	Lsp1	CySk	lymphocyte specific 1	filamentous-actin binding protein	1.48	1.27	0.86	74.70	6.84	86.76	15.92	110.43	27.31
U51196	Mapre1	CySk	icrotubule-associated protein, RP/EB family, member	regulates microtubule dynamics	1.25	1.14	0.91	1352.11	115.63	1489.44	159.97	1694.15	207.29
M55424	NF-L	CySk	neurofilament, light polypeptide	intermediate filament of cytoskeletal	0.74	0.86	1.16	541.09	63.88	464.87	84.08	399.66	73.40
D83966	Ptpn13	IC, CySk	protein tyrosine phosphatase, non-receptor type 13	signal transduction	1.61	1.33	0.82	98.83	11.04	119.84	33.50	159.26	33.21
AW122911	Ssx2ip	CySk	synovial sarcoma, X breakpoint 2 interacting protein	cytoskeletalprotein at cell-cell adherins junction	0.70	0.86	1.24	620.11	122.68	501.98	74.79	434.20	66.26
AI838080	Stmn1	CySk	stathmin 1	tubulin binding protein, maintenance of axonal integrity	1.58	1.24	0.78	3319.71	750.83	4244.50	857.73	5254.97	540.08
AF105222	Stmn4	CySk	stathmin-like 4	tubulin binding protein	1.49	1.28	0.86	859.08	109.32	1000.82	137.06	1278.05	253.71
AW125880	Tmem4	M	transmembrane protein 4	regulates neurite outgrowth, CySk interactions	1.30	1.05	0.81	157.77	28.05	195.17	28.47	205.33	27.69
AI846797	Tmod3	CySk	tropomodulin 3	actin filament organization	1.59	1.15	0.72	1405.34	323.17	1948.56	668.69	2237.73	554.87
AI835858	Tpm4	CySk	tropomyosin 4	actin organization	2.17	1.55	0.71	375.75	120.52	527.02	133.91	815.36	283.61
X13297	Acta2	CySk	actin, alpha 2, smooth muscle, aorta	structural constituent of cytoskeleton	3.47	0.73	0.21	178.52	213.79	841.89	582.42	618.77	789.78
X03491	Krt2-4	CySk	keratin complex 2, basic, gene 4	intermediate filament of cytoskelton	0.89	1.01	1.13	420.59	35.98	373.56	23.64	375.73	21.54
AV245272	Vim	CySk	vimentin	intermediate filament of the cytoskelton	0.94	1.08	1.15	252.09	15.26	219.41	20.21	236.29	15.61

(E) endomembrane

					Fold changes*			Average Signal Intensities & Standard Deviati					
								LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	ML/MMN	MN/MMN	Average	SD	Average	SD	Average	SD
AI020792	Copg1	ER, G	coatomer protein, subunit gamma 1	intracellular protein transport	0.76	0.81	1.06	780.64	90.44	736.29	58.83	595.39	104.21
AV122030	Dscr3	IC	Down syndrome critical region gene 3	intracellular protein transport	0.84	0.89	1.06	879.30	70.82	829.89	45.37	738.35	39.51
AW047320	Ndel1	IC	nuclear distribution gene E-like homolog	etrograde axon transport, CySk interacting protei	0.75	0.84	1.13	1633.64	41.33	1444.58	139.72	1217.07	149.68
AI835968	Rin2	IC	Ras and Rab interactor 2	secretion, vesicular transport, signaling	1.82	1.39	0.76	317.55	40.33	416.24	120.04	578.20	85.36
U70859	Slc7a3	M	cationic amino acid transporter, y+ system	glutamate symporter	1.23	1.25	1.01	127.00	12.78	125.27	11.30	156.03	15.10
AW120567	Snx9	IC	sorting nexin 9	intracellular protein transport, endocytosis	1.24	1.21	0.98	915.91	25.75	935.24	100.99	1131.83	129.00
Y11896	Chic1	G	cysteine-rich hydrophobic domain 1	Golgi to plasma membrane transport	0.80	0.92	1.16	98.19	11.29	84.87	3.52	78.33	1.25
AI840975	Cltc	IC	clathrin, heavy polypeptide (Hc)	coat protein for intracellular transport	0.85	1.00	1.17	4798.22	170.52	4097.58	450.09	4077.26	227.01
X64070	M6pr	lys	nnose-6-phosphate receptor, cation deper	intracellular protein transport	0.80	0.98	1.23	36.17	2.86	29.44	2.41	28.84	2.83
AF035643	Vamp5	M	vesicle-associated membrane protein 5	vesicular trafficking & transport, secretion	1.44	1.12	0.77	222.48	24.34	287.19	51.93	320.96	40.05
AF053724	Vamp8	IC	vesicle-associated membrane protein 8	functions as vesicle SNARE in vessicle trafficking	1.54	1.10	0.71	125.43	25.47	176.33	61.44	193.64	28.74
AV157222	Vapa	ER	vesicle-associated membrane protein A	vesicular trafficking & transport	0.81	0.97	1.19	20.16	1.91	16.95	2.38	16.37	0.46
U47024	Vps35		vacuolar protein sorting 35	lysosomal protein-sorting pathway	0.77	0.96	1.25	1844.55	180.76	1471.02	290.11	1418.19	162.95
AI843212	Copz2	IC	coatomer protein complex, subunit zeta 2	intracellular protein transport	1.30	1.04	0.80	159.79	20.74	199.69	44.31	207.98	15.03
AW046162	Scamp2	IC	secretory carrier membrane protein 2	protein transport	1.17	1.03	0.89	170.35	15.38	192.10	14.94	198.49	6.11
AF019045	VAT; VAChT	M	vesicular acetylcholine transporter	neurotransmitter transport	0.27	0.37	1.35	541.45	391.16	400.26	315.44	147.44	28.89
AJ250489	Ramp1	M	receptor (calcitonin) activity modifying protein	receptor transport and activity	1.03	0.83	0.80	436.50	36.06	543.29	50.16	449.28	73.30

(F) synaptic transmisssoin

								Average Signal Intensities & Standard Deviatio					
					Fold changes*			LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	ML/MMN	MN/MMN	Average	SD	Average	SD	Average	SD
AB010149	Adcyap1; PACAP	EC	PACAP ligand precursor	neuropeptide hormone	3.60	3.08	0.86	211.08	190.76	246.59	102.66	760.66	389.44
M55181	Penk1	EC	preproenkephalin 1	neuropeptide signal transduction	3.15	2.43	0.77	1506.34	665.99	1950.34	586.98	4748.73	1129.00
D17584	Tac1	EC	tachykinin 1	neuropeptide signal transduction	6.31	5.41	0.86	67.04	29.24	78.17	72.89	422.82	503.80
X61448	Cbln1	EC	cerebellin 1 precursor protein	neuropeptide, unknown function	0.85	0.44	0.52	464.56	76.34	895.38	258.83	395.70	37.93
L38580	Gal; Galn	EC	galanin neuropeptide	neuropeptide signal transduction	1.21	1.28	1.06	214.48	10.75	202.41	6.20	259.99	52.94
X97991	Calca	EC	calcitonin/calcitonin-related polypeptide, alpha	peptide signal transduction	0.93	1.02	1.10	117.83	6.75	106.82	5.41	109.17	5.06
M17640	Chrna1	M	cholinergic receptor, nicotinic, alpha polypeptide 1	synaptic transmission	0.95	1.04	1.10	31.37	0.97	28.50	1.76	29.77	0.85
AV372577	Npy2r	M	neuropeptide Y receptor Y2	neuropeptide signal transduction	1.91	1.89	0.99	234.17	27.65	235.89	14.57	446.90	174.57
AF008914	Sstr2	M	somatostatin receptor 2	signal transduction	1.71	1.60	0.94	53.62	2.70	57.30	4.95	91.86	23.09
U51908	Ntsr2	M	neurotensin receptor 2	signal transduction, neuromodulation	1.17	0.99	0.85	893.37	66.75	1046.40	93.86	1041.15	107.83
X66117	Grik2	M	glutamate receptor, ionotropic, kainate 2 (beta 2)	synaptic transmission	0.82	0.87	1.05	44.81	6.24	42.48	4.18	36.85	2.07
AF004927	Oprs1	M, ER	opioid receptor, sigma 1	opiod signal transduction, lipid biosynthesis	0.71	0.84	1.19	466.56	54.52	392.24	80.55	330.22	64.27
AI841303	Gap43	IC, M	growth associated protein 43	regulation of growth, synaptic plasticity and release	2.64	2.01	0.76	562.79	324.58	740.97	168.10	1487.40	228.11
X81202	Glrb	M	glycine receptor, beta subunit	synaptic transmission	0.71	0.96	1.35	3932.12	426.83	2914.62	700.03	2809.71	652.86
AW123852	Gphn	IC	gephyrin	clusters glycine receptor & other synaptic proteins	0.70	0.83	1.19	599.89	85.21	506.12	83.51	421.63	81.31
X87128	Tnfrsf1b; p75	M	p75 TNF receptor	signal transduction, neurotransmitter release,apoptosis	1.31	1.19	0.91	72.35	3.31	79.84	13.56	94.75	15.63
Y15798	Gprk6	IC	G protein-coupled receptor kinase 6	signal transduction, receptor endocytosis	1.32	1.18	0.90	278.81	28.69	311.47	36.16	367.82	49.89
D13695	Il1rl1	M	interleukin 1 receptor-like 1	signal transduction, synaptic plasticity	1.14	1.24	1.09	18.46	1.25	16.99	0.80	21.10	4.27
X15052	Ncam1	M	neural cell adhesion molecule 1	cell adhesion, synaptic transmission, plasticity	2.50	1.83	0.73	459.98	81.79	629.06	93.95	1148.35	178.60
AB026806	Syt5	IC	synaptotagmin 5	synaptc vessicle & secretory granule exocytosis	1.43	1.39	0.97	321.25	33.69	332.33	52.61	460.96	62.90
U10355	syt4	IC	synaptotagmin 4	vesicular trafficking and exocytosis	0.56	1.04	1.87	55.29	18.40	29.61	6.14	30.86	10.34
D37793	Syt2	IC	synaptotagmin 2	synaptic vessicle membrane, Ca-binding protein	0.84	0.95	1.12	78.81	8.26	70.07	3.76	66.39	5.41
AV157222	Vapa	IC	vesicle-associated membrane protein A	vesicular trafficking & transport	0.81	0.97	1.19	20.16	1.91	16.95	2.38	16.37	0.46
AF004428	Tpd52l1	IC	tumor protein D52-like 1	(dis)assembly of endosomal SNARE complexes	0.26	0.49	1.86	256.77	181.92	138.38	77.75	67.58	10.80
AF115848	Unc13h1	IC	unc13 homolog (C. elegans) 1	regulates SNARE complex assembly	1.19	1.12	0.94	15.70	1.37	16.76	2.28	18.73	1.13
AF019045	VAT; VAChT	M	vesicular acetylcholine transporter	neurotransmitter transport	0.27	0.37	1.35	541.45	391.16	400.26	315.44	147.44	28.89

(G) ion channel

					Fold changes*			Average Signal Intensities & Standard Deviatic					
								LMN		MMN		IML	
Genbank	**Common**	**location**	**Description**	**Function**	**IML/LMN**	**ML/MMN**	**MN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
AJ010949	Cacna2d3	M	calcium channel, alpha2/delta subunit 3	Ca channel regulatory subunit	0.56	0.67	1.20	696.07	100.17	579.00	74.09	386.42	49.73
AF011543	Trpc4	M	transient receptor potential cation channel C4	signal transduction	1.33	1.48	1.11	70.01	6.95	62.97	2.68	93.16	18.01
AJ225123	Hcn1	M	hyperpolarization-activated, cyclic nucleotide-gated K+ 1	ion channel	0.55	0.76	1.38	122.64	30.32	88.96	12.19	67.59	8.70
L22218	Kcna5	M	voltage-gated K channel, shaker subfamily, member 5	ion channel subunit	1.51	1.24	0.82	34.16	1.08	41.80	5.35	51.74	7.93
AV335854	Kcnab1	IC	voltage-gated K channel, shaker subfamily, beta member 1	ion channel subunit	0.68	0.76	1.12	251.06	45.50	224.75	42.81	171.78	11.48
U65593	Kcnab3	IC	voltage-gated K channel, shaker subfamily, beta member 3	ion channel subunit	0.82	0.86	1.04	137.54	17.44	131.77	13.57	113.15	6.76
M96688	Kcna6	M	oltage-gated K channel, shaker-related, subfamily, member	potassium channel	0.94	1.06	1.12	29.65	1.56	26.50	0.80	27.99	0.81
D45022	Kcnj3	M	inward-rectifying K channel, subfamily J, member 3	ion channel subunit	0.91	0.94	1.04	29.76	1.92	28.60	1.02	26.95	1.25
AA986344	Kcnj1	M	K inwardly-rectifying channel, subfamily J, member 1	potassium channel	0.88	1.05	1.19	36.46	2.41	30.67	2.04	32.11	1.39
AA967624	Abcc8		sulfonylurea receptor	component of potassium ATP channel	0.89	0.92	1.03	132.32	6.85	128.74	8.58	118.15	4.61
AF109905	Clic1	M, IC	chloride intracellular channel 1	state-dependent voltage-gated chloride channel	2.11	1.36	0.64	68.85	24.23	106.94	36.55	145.49	47.94
U70209	Pkd1	M	polycystic kidney disease 1 homolog	ion channel, signaling, cell adhesion, Ca homostas	1.05	0.96	0.91	215.00	9.42	235.29	15.61	226.72	4.26

(H) Transcription

								Average Signal Intensities & Standard Deviation					
					Fold changes*			LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	ML/MMN	MN/MMN	Average	SD	Average	SD	Average	SD
AI153693	Zfp275	IC, N	Zinc finger protein 275	transcription factor	1.31	1.16	0.89	113.41	9.86	127.99	7.41	149.00	7.14
AF020313	Apbb1ip	N	amyloid β (A4) precursor protein-binding protein	signal transduction, transcription factor	1.83	1.72	0.94	35.86	2.41	38.01	5.60	65.48	30.49
L13204	Foxj1	N	forkhead box J1	transcription factor	0.85	0.81	0.96	421.04	38.05	440.07	40.85	357.49	28.53
Y15001	Irx3	N	Iroquois related homeobox 3 (Drosophila)	transcription factor	0.46	0.51	1.09	170.47	73.72	155.92	41.34	79.01	12.20
D13664	Osf2-pending	EC	periostin	cell adhesion, transcription factor	3.07	2.67	0.87	36.42	12.52	41.88	19.12	111.72	78.27
AJ242864	Phtf		putative homeodomain transcription factor	transcription regulation	0.83	0.84	1.01	334.29	40.82	329.95	34.56	277.28	19.99
AA863928	Baz1b	N	bromodomain adjacent to zinc finger domain, 1B	transcription regulation	1.23	1.08	0.87	858.10	32.52	983.51	58.88	1059.08	87.84
AW047343	Dbp	N	D site albumin promoter binding protein	transcription regulator, circadian rhythm	1.42	1.08	0.76	113.29	8.67	149.64	18.73	161.23	16.84
AF079765	Epc1	N	enhancer of polycomb homolog 1 (Drosophila)	transcription factor	1.28	1.08	0.85	438.32	37.68	518.54	64.23	559.03	45.15
AV251191	Foxc2	N	forkhead box C2	transcription factor	1.56	1.02	0.65	82.74	13.21	126.63	31.06	129.28	19.34
U43715	Hand2	N	heart and neural crest derivatives expressed transcript 2	transcription factor	0.92	1.05	1.14	44.20	1.91	38.68	1.42	40.50	2.14
Z11886	Notch1	M	Notch gene homolog 1 (Drosophila)	transcription factor, signal transduction	1.47	1.10	0.75	253.47	22.58	338.22	51.77	372.38	44.20
AV220470	Tbx2	N	T-box 2	transcription factor	0.76	0.99	1.30	47.91	3.96	36.90	2.13	36.59	1.78
AF059735	Ctbp2	N	C-terminal binding protein 2	transcriptional regulation	0.86	0.71	0.83	192.13	22.86	231.96	19.57	165.07	8.79
AB012276	Atf5	N	activating transcription factor 5	regulataes transcription	1.34	1.16	0.87	87.24	5.63	100.61	6.82	116.95	17.50
AW124113	Basp1	N, M	brain abundant, membrane attached signal protein 1	transcriptional regulation, signal transduction	1.62	1.33	0.83	1271.05	333.61	1539.62	568.63	2053.11	430.89
U41465	Bcl6	N	B-cell leukemia/lymphoma 6	transcription factor	0.35	0.47	1.32	603.42	281.81	458.51	278.94	213.26	44.20
U76371	Bop	IC, N	CD8beta opposite strand	transcription factor	0.88	0.92	1.04	89.73	5.97	85.99	5.75	79.25	3.79
AI847631	Carhsp1		calcium regulated heat stable protein 1	transcriptional regulation	1.23	1.16	0.94	280.00	19.50	297.50	39.96	345.19	34.20
L03279	Cbfb	N	core binding factor beta	transcriptional regulator	1.71	1.43	0.84	2358.21	357.11	2819.27	318.59	4042.24	1467.87
AI838398	Cic		capicua homolog (Drosophila)	transcription factor	0.88	0.96	1.10	290.90	16.99	265.01	16.30	255.27	17.59
AF084524	Creg	N, IC	cellular repressor of E1A-stimulated genes	transcription factor	0.80	0.90	1.13	235.88	27.29	208.22	11.92	188.25	14.07
D14485	Csda	N	cold shock domain protein A	transcription factor	1.32	1.20	0.91	372.38	24.24	408.63	43.51	489.88	106.34
AJ242625	Dmp1; PP	IC, N, EC	dentin matrix protein	transcription factor & mineralization of ECM	0.45	0.70	1.55	93.62	50.90	60.31	18.44	41.95	13.17
L12147	Ebf1	N	early B-cell factor 1	transcription factor	1.19	1.11	0.94	43.10	2.27	46.05	2.59	51.15	4.32
U19617	Elf1	N	E74-like factor 1	transcription regulator	1.21	1.09	0.90	17.40	0.66	19.29	1.75	21.08	2.94
AF049702	Elf5	N	E74-like factor 5	transcription regulator	0.77	0.87	1.13	29.70	4.02	26.39	2.05	22.98	2.21
J04103	Ets2	IC, N	E26 avian leukemia oncogene 2, 3' domain	transcription factor	1.20	1.07	0.89	161.31	7.80	180.71	11.22	193.04	19.32
AF045017	Foxc1	N	forkhead box C1	transcription factor	1.13	1.02	0.90	9.90	0.38	10.95	0.66	11.21	0.87
L38607	Foxd1	N	forkhead box D1	transcription factor	1.34	1.07	0.80	66.34	6.74	83.15	16.54	88.92	13.09
AB017132	Hhex; Hex; Prh	N	Hex (Prh)	transcription factor	1.19	1.07	0.90	67.68	7.30	75.22	3.69	80.21	8.56
AW123564	Hop-pending	N	homeodomain only protein	transcription factor	1.50	1.34	0.89	884.78	192.19	990.42	131.04	1325.30	304.42
AV279579	Hoxa4	N	homeo box A4	transcription factor	0.85	0.97	1.14	16.82	1.22	14.77	1.43	14.32	1.16
M31885	Idb1	N	inhibitor of DNA binding 1	transcription factor	1.40	1.15	0.82	78.98	13.21	96.44	25.27	110.89	17.35
M60523	Idb3	N	inhibitor of DNA binding 3	transcription factor	1.69	1.26	0.75	138.36	19.13	185.35	67.19	233.91	65.17
AI852632	Litaf	N	LPS-induced TNF-alpha factor	transcription factor	1.51	1.20	0.79	198.95	44.97	250.93	45.32	299.96	35.46
U33629	Meis1	N	myeloid ecotropic viral integration site 1	transcription factor	1.39	1.14	0.82	61.15	6.84	74.67	17.02	85.16	7.70
Z16406	Meox2	N	mesenchyme homeobox 2	transcription factor	1.90	1.38	0.73	11.14	0.97	15.35	6.16	21.17	5.93
AV316101	Mizf-pending	N	MBD2 -interacting zinc finger protein	DNA methylation and transcription repression	0.85	0.87	1.03	136.99	18.29	133.08	7.10	116.05	8.77
AF010135	Mllt10	N	MLT 10 homolog	regulation of transcription	0.91	0.97	1.06	95.10	2.37	89.41	6.68	86.33	2.92
AB015858	Mycbp	N	c-myc binding protein	transcriptional regulator	0.86	0.87	1.01	25.02	1.08	24.75	3.20	21.46	1.45
X56182	Myf5	N	myogenic factor 5	transcription factor	1.11	1.07	0.96	11.32	0.25	11.81	0.98	12.60	0.70
U64828	Ncoa1	N	nuclear receptor coactivator 1	transcriptional regulator	0.87	0.93	1.06	209.87	16.27	197.80	13.93	182.99	15.04
U35312	Ncor1	N	nuclear receptor co-repressor 1	transcriptional regulator	1.39	1.18	0.85	361.32	38.46	425.39	56.32	500.72	69.51
AV367714	Nedd8	N	eural precursor cell expressed, developmentally down-regulated	transcriptional regulator	0.87	0.92	1.06	78.41	2.91	73.89	1.56	68.27	5.44
U70475	Nfe2l2; Nrf2	N	CNC basic leucine zipper DNA binding protein	transcriptional regulator	1.86	1.38	0.74	237.00	64.32	320.45	118.78	441.39	118.31
M12731	Nmyc1; N-mycc	IC, N	N-myc proto-oncogene	transcription factor	1.25	1.11	0.89	53.35	2.50	60.06	3.99	66.51	7.82
U71206	Pitx1	N	paired-like homeodomain transcription factor 1	transcriptional regulation	0.89	0.96	1.08	315.22	22.48	290.90	17.31	279.00	20.28
X68363	Pou2f1	N	POU domain, class 2, transcription factor 1	transcription factor	0.88	0.94	1.06	96.74	6.18	90.85	6.63	85.45	4.47
AW212397	Ski	IC, N	Sloan-Kettering viral oncogene homolog	transcriptional regulation	1.42	1.12	0.79	335.80	62.13	424.13	72.26	476.28	21.09
AI837107	Ssbp2	N	single-stranded DNA binding protein 2	transcriptional regulation	0.63	0.76	1.21	1732.78	360.07	1430.08	193.50	1086.20	219.79
L47650	Stat6	IC, N	signal transducer and activator of transcription 6	transcription factor	1.65	1.34	0.81	43.61	5.45	53.68	13.41	72.06	28.10
AJ223069	Tcf3	IC, N	transcription factor 3	transcriptional regulation	1.21	1.09	0.91	180.40	7.73	199.21	32.72	217.45	11.05
X72310	Tfdp1	IC, N	transcription factor Dp 1	transcriptional regulation	1.36	1.19	0.88	154.33	10.00	176.01	21.88	210.24	41.65
M63649	Twist1; Pde; M-Twis	N	Mouse M-twist gene, complete cds.	transcriptional regulation	1.46	1.20	0.82	45.12	4.01	54.73	9.30	65.74	13.42
M58566	Zfp36l1	N	zinc finger protein 36, C3H type-like 1	utative transcription factor, immediate early response ger	1.99	1.26	0.63	201.06	61.41	318.14	93.10	400.01	121.97
L34808	Chx10	N	C. elegans ceh-10 homeo domain containing homolog	transcription factor	1.12	1.26	1.12	120.55	16.60	107.71	7.41	135.28	18.92
U92702	Ebf3	N	early B-cell factor 3	transcription factor	1.13	1.21	1.07	100.09	6.31	93.41	11.95	112.62	11.18
L00039	Myc; Myc2; Nird	N	c-myc (Myc) gene	transcriptional regulation	1.14	1.17	1.02	13.03	1.05	12.73	0.41	14.87	1.68
X76653	Nr2f2	N	nuclear receptor subfamily 2, group F, member 2	steroid hormone receptor, transcription factor	1.19	1.53	1.28	103.50	22.96	80.56	24.78	123.20	14.37
AB026583	Rbms2	IC	RNA binding motif, single stranded interacting protein 2	transcriptional and/or translational regulator	0.86	0.82	0.95	137.54	13.72	144.50	16.15	118.62	10.23
U66918	Shox2	N	short stature homeobox 2	transcription factor	1.20	1.26	1.05	65.47	6.34	62.58	5.06	78.82	14.29
U79550	Snai2	N	snail homolog 2 (Drosophila)	transcription factor	1.20	1.24	1.03	231.19	20.76	224.08	13.26	277.30	48.40
U31566	Nkx2-2	N	NK2 transcription factor related, locus 2 (Drosophila)	transcription factor	1.22	0.91	0.75	70.70	7.12	94.88	10.08	86.54	19.07
AV320880	Nr5a1	N	nuclear receptor subfamily 5, group A, member 1	transcription regulation	0.88	1.06	1.21	40.69	2.10	33.67	3.01	35.78	4.09
D49473	Sox17	N	SRY-box containing gene 17	transcription factor	1.00	0.87	0.87	127.39	11.84	146.65	12.10	127.49	9.50

(I) signal transduction

								Average Signal Intensities & Standard Deviati					
					Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**location**	**Description**	**Function**	**IML/LMN**	**ML/MMN**	**MN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
U12919	Adcy7	M	adenylate cyclase 7	signal transduction	1.72	1.76	1.02	161.23	28.96	158.30	42.21	278.05	43.15
AB010149	Adcyap1; PACAP	EC	PACAP ligand precursor	neuropeptide hormone	3.60	3.08	0.86	211.08	190.76	246.59	102.66	760.66	389.44
AF020313	Apbb1ip		amyloid β (A4) precursor protein-binding protein	signal transduction, transcription factor	1.83	1.72	0.94	35.86	2.41	38.01	5.60	65.48	30.49
AW215551	Arhgap9		Rho GTPase activating protein 9	signal transduction	0.76	0.80	1.05	135.86	10.01	129.76	8.71	103.82	12.96
AI844631	Baiap2		angiogenesis inhibitor 1-associated protein 2	Rho protein signal transduction	1.37	1.33	0.97	61.88	5.03	63.99	7.07	85.03	17.62
U49513	Ccl9	EC	chemokine (C-C motif) ligand 9	signal transduction	1.39	1.28	0.92	57.47	3.38	62.55	6.38	79.82	7.79
U56819	Ccr2	M	chemokine (C-C) receptor 2	signal transduction	1.27	1.30	1.02	31.32	2.43	30.68	3.55	39.86	5.74
AV370035	Ccr5	M	chemokine (C-C motif) receptor 5	signal transduction	1.51	1.70	1.13	39.85	13.13	35.28	3.48	59.98	16.88
X06368	Csf1r	M	colony stimulating factor 1 receptor	signal transduction	1.48	1.34	0.90	169.83	18.30	188.50	30.00	251.72	51.16
AW123850	F2r	M	thrombin receptor	signal transduction	2.03	1.78	0.88	662.17	193.49	752.40	146.20	1341.07	321.28
X59398	Flt3	M	FMS-like tyrosine kinase 3	signal transduction	0.63	0.70	1.11	1044.99	108.49	938.68	143.52	659.30	106.42
AA960459	Fnbp2, srGap3	IC	formin binding protein 2	signal transduction	0.75	0.81	1.07	118.65	8.63	110.45	8.56	89.54	7.82
U10551	Gem	IC	monomeric G protein	signal transduction	0.50	0.63	1.27	132.42	25.84	104.14	37.26	65.88	9.75
AW125649	Gna12	M	trimeric G protein, alpha 12 subunit	signal transdiction	1.36	1.22	0.90	202.96	25.01	225.97	29.21	276.57	29.72
X83577	Gpc4	M, EC	glypican 4	signal transdiuction, ECM interactions	1.42	1.26	0.89	80.82	8.85	90.78	12.18	114.65	11.73
AF023482	Hs1bp1	mit, ER	HS1 binding protein	signal transduction	0.76	0.77	1.02	587.91	69.12	578.68	56.57	448.09	99.03
Y16518	Lancl1	M	LanC-like protein 1, GPCR 69	GPCR, signal transduction	0.71	0.78	1.09	1623.74	156.32	1486.32	216.49	1160.92	141.39
AW259500	Map3k7ip2	IC	MAPKKK 7 interacting protein 2	signal transduction	1.53	1.43	0.94	496.70	61.13	530.47	109.53	757.49	134.23
Y13439	Mapk12	IC	mitogen-activated protein kinase 12	signal transduction	0.84	0.82	0.97	377.30	14.36	389.23	31.90	317.83	44.60
AI846534	Nek6		NIMA-related expressed kinase 6	signal transduction	0.87	0.85	0.99	185.95	11.00	188.72	16.35	161.16	16.78
M17298	Ngfb	EC	nerve growth factor, beta	growth & maintenance, signal transduction	0.87	0.89	1.01	32.01	2.59	31.56	2.19	27.93	1.44
AV372577	Npy2r	M	neuropeptide Y receptor Y2	neuropeptide signal transduction	1.91	1.89	0.99	234.17	27.65	235.89	14.57	446.90	174.57
M55181	Penk1	EC	preproenkephalin 1	neuropeptide signal transduction	1.74	1.51	0.87	139.27	14.63	159.78	8.72	241.80	60.47
M68915	Pgr	IC, N	progesterone receptor	steroid hormone signal transduction	0.90	0.89	0.99	22.09	0.63	22.35	0.70	19.97	0.99
AV378129	Ppfibp2	IC	tyrosine phosphatase receptor F interacting protein	signal transduction	1.15	1.09	0.95	11.30	0.41	11.88	0.49	12.98	0.72
AB007696	Ptger2	M	prostaglandin E receptor 2	eicosanoid hormone signal transduction	1.10	1.13	1.03	19.48	0.83	18.99	1.04	21.49	0.76
D10204	Ptger3	M	prostaglandin E receptor 3	eicosanoid hormone signal transduction	1.18	1.16	0.98	10.49	0.56	10.68	0.72	12.40	1.16
U37465	Ptpro	M	protein tyrosine phosphatase, receptor type, O	signal transduction	1.36	1.24	0.91	176.83	12.45	194.75	24.45	240.63	28.83
AI835968	Rin2	IC	Ras and Rab interactor 2	secretion, vesicular transport, signaling	1.82	1.39	0.76	317.55	40.33	416.24	120.04	578.20	85.36
AF008914	Sstr2	M	somatostatin receptor 2	signal transduction	1.71	1.60	0.94	53.62	2.70	57.30	4.95	91.86	23.09
D86639	Stac	IC	SH3 and cysteine rich domain	intracellular signaling cascade	1.70	1.65	0.97	63.86	10.99	65.71	5.62	108.63	51.73
D17584	Tac1	EC	tachykinin 1	neuropeptide signal transduction	6.31	5.41	0.86	67.04	29.24	78.17	72.89	422.82	503.80
X77952	Eng	M	endoglin	constituent of TGF-beta signaling complex	1.56	1.07	0.69	543.31	88.88	789.78	112.17	847.13	184.77
AF079366	Mpp3	M	MAGUK p55 subfamily member 3	signal transduction	1.36	1.05	0.78	186.29	27.51	239.94	31.87	252.47	32.42
AF073997	Mtmr1	IC, M	myotubularin related protein 1	phosphatase, signal transduction	0.83	0.94	1.14	108.30	7.23	94.97	6.37	89.68	6.11
Z11886	Notch1	M	Notch gene homolog 1 (Drosophila)	transcription factor, signal transduction	1.47	1.10	0.75	253.47	22.58	338.22	51.77	372.38	44.20
AV149007	Pdlim1	IC	PDZ and LIM domain 1 (elfin)	adaptor, signal transduction	0.85	0.96	1.14	454.49	32.25	399.01	35.08	384.86	23.35
U73199	Rgnef		Rho-guanine nucleotide exchange factor	signal transduction	1.24	1.03	0.83	170.92	17.36	205.65	21.28	211.56	16.08
D38410	Tff3	EC	trefoil factor 3, intestinal	peptide signal transduction	0.91	1.00	1.09	295.52	15.01	270.28	11.28	269.31	7.76
D26186	Srms		src-related kinase	signal transduction	1.00	1.05	1.05	34.10	0.68	32.35	0.73	34.06	0.74
AF011420	V2r10	M	vomeronasal 2, receptor, 10	signal transduction	0.96	1.11	1.16	124.12	2.60	107.44	7.69	119.32	4.76
AA036065	Adcy2	M	adenylate cyclase 2	signal transduction	1.25	1.17	0.94	1090.99	78.54	1165.27	194.09	1364.39	183.56
M93422	Adcy6	M	adenylate cyclase 6	signal transduction	1.19	1.03	0.87	215.72	18.21	249.33	32.09	256.74	24.24
Z50190	Adcy9	M	adenylate cyclase 9	signal transduction	0.73	0.84	1.16	132.05	15.86	114.05	16.92	95.88	9.24
AV355809	Admr	M	adrenomedullin receptor	neuropeptide signal transduction	1.31	0.99	0.75	21.52	2.02	28.67	6.36	28.24	2.72
AF045887	Agt; Aogen	EC	angiotensinogen	local & circulating hormone	1.65	1.16	0.70	346.27	56.61	495.47	100.82	572.68	210.40
M13071	Araf; A-Raf	IC, mit	A-raf peptide	signal transduction	1.22	1.09	0.90	134.29	15.40	149.88	21.63	163.63	10.85
X63535	Axl	M	AXL receptor tyrosine kinase	signal transduction	1.17	1.09	0.93	96.14	4.43	103.32	10.37	112.89	10.22
AW124113	Basp1	N, M	brain abundant, membrane attached signal protein 1	transcriptional regulation, signal transduction	1.62	1.33	0.83	1271.05	333.61	1539.62	568.63	2053.11	430.89
AI847646	Calml4	IC	calmodulin-like 4	signal transduction	1.47	1.04	0.71	114.20	6.77	161.47	52.54	168.14	27.98
M58004	Ccl6	EC	chemokine (C-C motif) ligand 6	signal transduction	1.31	1.21	0.92	89.51	15.07	96.99	8.03	117.22	23.28
AI844806	Cdc42ep4	IC, CySk	CDC42 effector protein (Rho GTPase binding) 4	signal transduction	1.36	1.20	0.88	209.62	17.05	238.17	53.92	286.05	36.02
M55219	Csprs	N	component of Sp100-rs	signal transduction	0.85	0.98	1.15	21.85	2.26	19.04	1.82	18.59	1.15
L12029	Cxcl12	EC	chemokine (C-X-C motif) ligand 12	signal transduction; growth factor	2.58	1.68	0.65	57.12	14.39	87.88	27.86	147.51	80.49
AF016697	Dfy; FY;	M	chemokine receptor	signal transduction	0.76	0.83	1.10	311.46	39.97	284.31	45.12	236.08	41.09
U13370	Edg2	M	lysophosphatidic acid G-protein-coupled receptor, 2	signal transduction	1.70	1.27	0.74	490.22	138.96	660.17	148.71	835.69	90.86
J02700	Enpp1	M	ectonucleotide pyrophosphatase/phosphodiesterase 1	nucleotide mediated signal transduction	1.31	1.09	0.83	66.36	2.72	79.84	6.50	86.64	15.15
AV378405	Entpd2	M	ectonucleoside triphosphate diphosphohydrolase 2	nucleotide mediated signal transduction	1.26	1.09	0.87	80.51	8.67	92.98	7.11	101.44	11.71
M31312	Fcgr2b; CD32; Fcr-2;	M	beta Fc receptor type II precursor;	signal transduction	1.27	1.16	0.91	32.83	2.39	36.01	5.04	41.76	6.20
L17022	Fcgrt	M	Fc receptor, IgG, alpha chain transporter	signal transduction	1.20	1.07	0.89	10.96	0.84	12.33	1.83	13.19	0.67
M30641	Fgf1	EC	fibroblast growth factor 1	signal transduction, cell growth	0.53	0.71	1.33	237.45	93.48	178.88	50.23	126.74	27.89
AW125390	Fgls; Ifitm3		fragilis, interferon induced transmembrane protein 3	signal transduction	1.51	1.07	0.71	193.79	38.72	273.36	92.21	293.14	54.86
AI841629	Gnai2	M	guanine nucleotide binding protein, alpha inhibiting 2	signal transduction	1.48	1.27	0.85	725.97	39.22	851.18	229.70	1077.61	205.94
AF107848	Gnas	M	guanine nucleotide binding protein, alpha stimulating	signal transduction	1.15	1.04	0.91	9826.37	835.40	10823.89	877.25	11264.78	662.57
AI843937	Gng5	M	guanine nucleotide binding protein gamma 5 subunit	signal transduction	1.57	1.26	0.80	819.29	116.14	1018.43	150.28	1286.56	263.33
AF110818	Gpr49	M	G protein-coupled receptor 49	signal transduction	0.82	0.90	1.09	40.10	4.14	36.68	3.66	32.85	2.19
Y15798	Gprk6		G protein-coupled receptor kinase 6	signal transduction	1.32	1.18	0.90	278.81	28.69	311.47	36.16	367.82	49.89
M94450	Grb7	IC	growth factor receptor bound protein 7	signal transduction	0.87	0.96	1.10	336.12	26.21	305.31	20.53	293.12	12.56
D16195	Grn; epithelin	EC,	granulin	growth factor, signal transduction	1.50	1.25	0.83	161.43	22.26	193.33	42.72	241.51	22.04
M68902	Hcph	IC	hemopoietic cell phosphatase	signal transduction	1.15	1.12	0.97	25.06	2.06	25.75	1.95	28.83	2.62
X67644	Ier3	M	immediate early response 3	stress signal transduction	0.77	0.88	1.14	232.18	23.21	203.28	23.86	179.28	22.57
Y09864	Ifnar2	M	interferon (alpha and beta) receptor 2	signal transduction	1.20	1.12	0.93	58.65	4.06	63.08	7.55	70.55	4.98

(I) signal transduction

					Fold changes*			Average Signal Intensities & Standard Deviati					
								LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	ML/MMN	MN/MMN	Average	SD	Average	SD	Average	SD
X71922	Igf2; Mpr; M6pr	EC	insulin-like growth factor 2	growth factor, signal transduction	2.87	1.50	0.52	2416.06	######	4632.00	######	6937.16	#####
AI838737	Igfbp4	EC	insulin-like growth factor binding protein 4	cell growth, signal transduction	1.18	1.07	0.91	310.28	17.62	341.01	17.12	364.62	34.79
L12447	Igfbp5	EC	insulin-like growth factor binding protein 5	cell growth, signal transduction	4.36	1.48	0.34	256.86	178.61	757.23	699.65	1119.62	410.93
U53696	Il10rb	M	interleukin 10 receptor, beta	cell surface receptor linked signal transduction	1.65	1.34	0.81	570.21	103.84	703.19	205.97	938.78	198.67
AA608387	Il13ra1	M	interleukin 13 receptor, alpha 1	cell surface receptor linked signal transduction	1.72	1.25	0.72	38.06	7.45	52.55	17.22	65.54	12.06
M26271	IL2R	M	Mouse interleukin 2 receptor gene, 5' end.	cell surface receptor linked signal transduction	0.85	0.93	1.10	25.86	2.65	23.43	2.05	21.89	1.19
X06271	Il5; Il-5	EC	interleukin 5 (eosinophil differentiation factor).	cell surface receptor linked signal transduction	0.90	0.99	1.10	73.47	3.06	66.50	3.28	66.01	6.25
AI837528	Jak1	IC	Janus kinase 1	signal transduction	0.69	0.72	1.04	898.86	202.04	861.74	202.34	618.69	155.17
L16956	Jak2	IC	Janus kinase 2	signal transduction	1.27	1.17	0.92	96.37	10.34	104.82	12.37	122.41	15.87
AF022889	Ltbp1	EC	latent transforming growth factor beta binding protein 1	TGF beta receptor signal transduction	1.55	1.23	0.80	44.96	4.15	56.32	11.38	69.47	13.93
AV317327	Mapk1	IC, N	mitogen activated protein kinase 1	signal transduction	0.83	0.94	1.13	38.14	2.60	33.85	2.98	31.65	3.26
AB005664	Mapk9	IC	mitogen activated protein kinase 9	signal transduction	0.79	0.94	1.20	133.03	18.65	111.22	6.95	104.82	19.94
AI957146	Mfhas1	EC	malignant fibrous histiocytoma amplified sequence 1	signal transduction	1.56	1.16	0.74	479.17	137.62	648.11	65.74	748.64	198.74
X61399	Mlp		MARCKS-like protein	signal transduction	1.40	1.27	0.91	180.89	11.58	198.54	33.22	252.52	62.71
AI504305	Ms4a6b	M	embrane-spanning 4-domains, subfamily A, member 6	signal transduction	1.25	1.14	0.92	20.91	1.45	22.82	3.16	26.05	2.23
X92397	Ndph	EC	Norrie disease homolog	receptor for Norrin-Fz4 signal transduction	1.25	1.11	0.89	206.01	30.60	231.80	29.56	257.70	26.84
AW050346	Ngef		neuronal guanine nucleotide exchange factor	signal transduction	1.45	1.38	0.95	529.99	126.69	558.54	103.52	770.96	164.27
AF004927	Oprs1	M	opioid receptor, sigma 1	opiod signal transduction	0.71	0.84	1.19	466.56	54.52	392.24	80.55	330.22	64.27
U39738	Pak3		p21 (CDKN1A)-activated kinase 3	signal transduction	0.71	0.86	1.21	184.68	28.67	152.96	26.88	131.51	33.88
AJ005073	Pdcd6ip	IC	programmed cell death 6 interacting protein	signal transduction	0.76	0.90	1.19	458.46	52.32	384.08	39.25	346.26	49.62
AF042491	Pgrmc1	M	progesterone receptor membrane component 1	signal transduction	1.76	1.47	0.84	853.39	247.25	1021.10	360.45	1505.12	283.24
AI850079	Pib5pa	IC	hosphatidylinositol (4,5) bisphosphate 5-phosphatase,	signal modifying enzyme	0.74	0.81	1.10	612.18	87.18	556.58	114.84	452.05	71.63
AB008791	Pik3c2g	M	phosphatidylinositol 3-kinase, C2, gamma polypeptide	phosphatidylinositol metabolism, signal transduction	0.80	0.84	1.05	41.03	2.69	38.98	6.00	32.84	4.05
D86176	Pip5k1a		phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	phosphatidylinositol metabolism, signal transduction	0.61	0.77	1.27	266.85	50.29	210.63	33.76	162.54	27.91
D30779	Pla2g1br	M	phospholipase A2, group IB, pancreas, receptor	lipid metabolism, signal transduction	1.26	1.18	0.94	17.44	1.42	18.62	1.61	21.96	2.65
U85713	Plcb1	IC	phospholipase C, beta 1	signal transduction	0.91	0.96	1.06	43.44	3.51	40.94	1.73	39.34	0.94
AB023027	Pnck		pregnancy upregulated non-ubiquitously expressed CaM ki	signal transduction	1.69	1.40	0.83	124.34	33.77	149.82	33.72	210.24	67.05
D84376	Ppap2a	M	phosphatidic acid phosphatase 2a	lipid metabolism, signal transduction	0.69	0.82	1.18	682.51	97.39	576.10	47.40	469.90	95.01
AW124336	Ppp6c		protein phosphatase 6, catalytic subunit	signal transduction	0.80	0.86	1.08	379.19	43.83	352.31	36.75	301.69	31.27
D83966	Ptpn13	IC, CySk	protein tyrosine phosphatase, non-receptor type 13	signal transduction	1.61	1.33	0.82	98.83	11.04	119.84	33.50	159.26	33.21
D31898	Ptprr	M	protein tyrosine phosphatase, receptor type, R	signal transduction	1.27	1.22	0.96	557.34	36.01	582.06	58.12	708.69	121.77
U36488	Ptprv	M	protein tyrosine phosphatase, receptor type	signal transduction	0.88	0.96	1.09	25.71	0.86	23.59	2.22	22.75	1.50
AA798971	Rab3ip	IC	RAB3A interacting protein	signal transduction	0.80	0.84	1.05	192.84	26.07	183.47	23.19	153.95	10.31
AW047017	Rab14	IC	RAB14, member RAS oncogene family	G protein, signal transduction	0.83	0.96	1.16	58.79	5.70	50.76	4.28	48.91	5.88
AI835712	Rab34	G	RAB34, member of RAS oncogene family	G protein, signal transduction	1.25	1.11	0.89	218.61	17.28	246.92	42.43	273.95	24.97
AW124597	Rap1gds1		RAP1, GTP-GDP dissociation stimulator 1	signal transduction	0.70	0.81	1.17	3970.40	879.55	3407.16	513.19	2759.54	544.29
AW049415	Rassf1		Ras association (RalGDS/AF-6) domain family 1	signal transduction	1.20	1.07	0.89	115.89	13.35	129.66	11.36	138.56	9.15
AV335997	Rgs10		regulator of G-protein signalling 10	signal transduction	1.75	1.44	0.82	170.75	29.88	207.46	13.95	298.41	124.39
AF061934	Rgs11		regulator of G-protein signaling 11	signal transduction	0.70	0.80	1.14	547.07	82.82	478.12	83.75	380.49	57.03
M21019	Rras	IC	Harvey rat sarcoma oncogene, subgroup R	G protein signal transduction	1.36	1.20	0.88	95.31	9.72	107.99	19.00	129.63	29.68
L21707	Ryk	M	receptor-like tyrosine kinase	signal transduction	1.18	1.03	0.87	306.41	25.24	352.65	18.89	362.46	46.83
U15635	Samhd1	IC	SAM domain and HD domain, 1	signal transduction	1.19	1.11	0.93	96.48	4.18	104.10	11.03	115.15	11.58
AA822531	Stk2	IC, N	serine/threonine kinase 2	signal transduction	1.23	1.16	0.94	556.75	81.51	590.14	73.51	687.10	51.53
AF039601	Tgfbr3	M	transforming growth factor, beta receptor III	signal transduction	0.81	0.84	1.04	135.54	11.61	130.17	16.02	109.79	9.57
X87128	Tnfrsf1b; p75	M	M.musculus p75 TNF receptor DNA.	signal transduction	1.31	1.19	0.91	72.35	3.31	79.84	13.56	94.75	15.63
AW060819	Twg-pending	EC	twisted gastrulation protein	signal transduction	1.76	1.32	0.75	186.04	35.20	247.34	102.36	326.68	90.52
M89800	Wnt6	EC	wingless-related MMTV integration site 6	signaling peptide	1.30	1.06	0.81	68.05	8.36	83.81	14.10	88.75	12.29
AA880988	Xlkd1	M	extra cellular link domain-containing 1	glycosaminoglycan catabolism, cell adhesion, signaling	1.43	1.21	0.85	39.10	6.25	46.27	10.34	55.94	10.43
X80508	Yap	IC	yes-associated protein	TGF-beta growth factor signal transducton	1.65	1.17	0.71	251.13	59.14	355.55	130.72	415.59	62.64
AF068182	Blnk	M	B-cell linker	signal transduction	1.17	1.21	1.04	16.13	0.90	15.52	0.65	18.80	2.98
X62502	Ccl4; Act-2; Mip1b	EC	chemokine (C-C motif) ligand 4	signal transduction	1.03	1.08	1.05	116.68	2.92	111.55	3.04	120.69	5.58
L38580	Gal; Galn	EC	galanin neuropeptide	neuropeptide signal transduction	1.21	1.28	1.06	214.48	10.75	202.41	6.20	259.99	52.94
U53219	Igtp	IC	interferon gamma induced GTPase	G protein signal transduction	1.09	1.16	1.06	41.62	1.62	39.11	3.85	45.25	3.69
D13695	Il1rl1	M	interleukin 1 receptor-like 1	cell surface receptor linked signal transduction	1.14	1.24	1.09	18.46	1.25	16.99	0.80	21.10	4.27
M29697	Il7r	M	interleukin 7 receptor	cell surface receptor linked signal transduction	1.14	1.20	1.05	20.22	2.09	19.20	1.31	22.99	3.12
X80937	Ralbp1		ralA binding protein 1	Ral G protein effector, regulates receptor endocytosis	1.13	1.20	1.06	889.23	38.87	841.76	66.19	1008.02	151.95
U85055	Rgs14		regulator of G-protein signaling 14	G protein signal transduction	1.08	1.12	1.04	217.03	10.01	207.87	7.07	233.55	21.41
X97991	Calca	EC	calcitonin/calcitonin-related polypeptide, alpha	peptide signal transduction	0.93	1.02	1.10	117.83	6.75	106.82	5.41	109.17	5.06
AF022990	Ccr5; CCR5	M	chemokine receptor-5 (CCR5)	signal transduction	0.99	1.11	1.12	21.10	1.10	18.81	1.20	20.80	1.26
U34881	Cd8a	M	CD8 antigen, alpha chain	antigen recognition, signal transduction	0.95	1.04	1.09	26.40	1.20	24.23	1.53	25.15	0.60
AV309794	Gkap42-pending	G	cGMP-dependent protein kinase anchoring protein	signal transduction	0.98	1.13	1.16	41.88	2.93	36.26	2.52	40.98	4.17
U51908	Ntsr2	M	neurotensin receptor 2	signal transduction	1.17	0.99	0.85	893.37	66.75	1046.40	93.86	1041.15	107.83
X60664	Pde6a	IC	phosphodiesterase 6A, cGMP-specific, rod, alpha	signal transduction	0.91	1.05	1.16	123.31	8.70	106.73	5.29	112.56	10.46
AF096285	Strap		serine/threonine kinase receptor associated protein	signal transduction	0.74	1.06	1.43	386.86	76.83	269.90	73.44	284.77	30.50

(J) ribosome

								Average Signal Intensities & Standard Deviatic					
					Fold changes*			LMN		MMN		IML	
Genbank	**Common**	**location**	**Description**	**Function**	**IML/LMN**	**ML/MMN**	**MN/MMN**	**Average**	**SD**	**Average**	**SD**	**Average**	**SD**
AV105022	Rpl10	IC	ribosomal protein 10	protein biosynthesis	1.31	1.15	0.88	835.51	43.39	951.92	69.16	1096.31	83.20
L08651	Rpl29	IC	ribosomal protein L29	protein biosynthesis	1.62	1.45	0.90	194.34	36.69	216.07	17.41	313.92	79.27
X15962	Rps12	IC	ribosomal protein S12	protein biosynthesis	1.76	1.30	0.74	1439.57	215.79	1949.57	393.91	2530.88	368.21
AF100956	Rps18	IC	ribosomal protein subunit S18	protein biosynthesis	1.47	1.10	0.75	920.88	74.51	1233.85	270.76	1352.71	191.64
AI836446	Rrbp1	IC	ribosome binding protein 1	protein biosynthesis	1.57	1.21	0.78	198.44	17.01	255.85	47.83	310.62	32.27
U12403	Rpl10a	IC	ribosomal protein L10A	translation	1.39	1.19	0.86	321.67	35.57	375.29	62.07	445.74	15.86
U28917	Rpl13	IC	ribosomal protein L13	translation	1.45	1.13	0.78	686.45	67.45	876.20	214.70	994.23	173.03
AB020237	Rpl27a; L27A	IC	ribosomal protein L27A	translation	1.52	1.23	0.81	802.94	118.33	993.10	189.15	1220.18	224.09
K02928	Rpl30	IC	ribosomal protein L30	translation	1.38	1.23	0.88	4567.81	578.59	5163.62	916.66	6325.97	906.57
AW047116	Rpl37	IC	ribosomal protein L37	translation	1.51	1.16	0.77	1241.10	268.40	1608.82	313.60	1871.42	295.80
U29402	Rplp1	IC	ribosomal protein, large, P1	translation	1.32	1.11	0.84	3252.91	305.21	3854.58	182.18	4283.77	660.20
M11408	Rps16	IC	S16 ribosomal protein	translation	1.25	1.08	0.86	947.52	55.00	1097.66	189.72	1187.64	86.89
AW048899	Rps19	IC	ribosomal protein S19	translation	1.41	1.19	0.84	428.55	61.97	507.78	52.34	602.32	50.50
AI837403	Rps23	IC	ribosomal protein S23	translation	1.51	1.28	0.85	1041.42	83.70	1226.10	221.59	1568.91	249.66
AI854238	Rps27	IC	ribosomal protein S27	translation	1.63	1.28	0.78	1051.91	232.46	1344.24	251.31	1717.66	446.78
X73829	Rps8	IC	ribosomal protein S8	translation	1.29	1.04	0.81	1117.45	79.37	1377.55	198.18	1436.39	204.25

(K) mitochondria

									Average Signal Intensities & Standard Deviati				
					Fold changes*			LMN		MMN		IML	
Genbank	Common	location	Description	Function	IML/LMN	ML/MMN	LMN/MMN	Average	SD	Average	SD	Average	SD
AW061337	Ak4	mit	adenylate kinase 4	nucleotide transport & metabolism	1.38	1.37	1.00	56.10	10.76	56.34	10.53	77.15	10.82
AA870675	Atp5c1	mit	ATP synthase, F1 gamma polypeptide 1	ATP synthesis; proton transport	0.83	0.76	0.92	2814.53	266.68	3058.26	448.28	2322.67	219.90
AW046124	Cyba	mit	cytochrome b-245, alpha polypeptide	electron transport	1.45	1.35	0.93	70.78	5.26	76.00	14.46	102.88	23.76
AF023482	Hs1bp1	mit, ER	HS1 binding protein	signal transduction	0.76	0.77	1.02	587.91	69.12	578.68	56.57	448.09	99.03
M21050	lys	EC, mit	lysozyme	carbohydrate metabolism	4.49	2.82	0.63	44.54	16.27	71.04	37.29	200.10	188.88
AW046205	Ndufa4	mit	NADH dehydrogenase 1 alpha subcomplex, 4	electron transport chain	0.86	0.89	1.04	33.09	1.65	31.95	1.91	28.56	2.41
AI842259	Pdk3	mit	pyruvate dehydrogenase kinase, isoenzyme 3	phosphorylates pyruvate dehydr.	0.61	0.75	1.23	666.71	88.68	540.48	117.78	405.10	45.21
AI848685	Timm13a	mit	translocase of inner mitochondrial membrane 13	protein-mitochondrial targeting	0.86	0.85	0.99	93.83	6.43	94.52	7.33	80.45	5.68
AW125884	Acas2l	mit	acetyl-Coenzyme A synthetase 2	metabolism	1.50	1.01	0.67	150.65	35.63	223.41	58.77	226.19	55.46
AV356510	AW491445	mit	expressed sequence AW491445	transport	0.86	1.04	1.21	116.13	11.12	95.99	5.66	99.67	9.25
AV102186	Bad	mit	Bcl-associated death promoter	integrates glucose metabolism & apoptosis	0.85	1.01	1.19	341.73	27.63	286.48	19.95	290.40	22.95
AV381947	Glul	mit	glutamate-ammonia ligase	glutamine synthetase	0.90	1.01	1.12	721.82	45.09	643.90	32.13	650.13	41.95
M58567	Hsd3b1	ER, mit	hydroxysteroid dehydrogenase-1, delta<5>-3-beta	steroid hormone bisynthesis	0.89	1.01	1.13	86.53	3.59	76.60	2.02	76.99	1.64
AW047808	Immt	mit	inner membrane protein, mitochondrial		0.82	0.92	1.12	135.55	3.72	121.17	9.22	111.50	3.34
AB020203	Ak3l	mit	adenylate kinase 3 alpha-like	ATP metabolism	0.83	0.91	1.09	30.43	2.10	27.90	1.92	25.30	2.95
U89906	Amacr	mit	alpha-methylacyl-CoA racemase	metabolism	0.89	0.94	1.05	129.68	9.45	123.00	9.08	115.16	5.54
M13071	Araf; A-Raf	IC, mit	A-raf peptide	signal transduction	1.22	1.09	0.90	134.29	15.40	149.88	21.63	163.63	10.85
U29530	Atp5f1	mit	ATP synthase, F0 complex	ATP synthesis	0.88	0.90	1.02	106.03	3.85	104.22	9.40	93.83	6.54
AF017175	Cpt1a	mit	carnitine palmitoyltransferase 1, liver	fatty acid metabolism	0.62	0.78	1.26	1262.84	353.79	1003.48	253.56	778.17	140.94
AW124813	Dlat	mit	E2 component of pyruvate dehydrogenase complex	acetyl-CoA biosynthesis from pyruvate	0.77	0.86	1.12	692.39	67.43	620.72	116.94	536.27	29.53
D49920	Fdxr	mit	ferredoxin reductase	electron tansport	0.93	0.96	1.03	110.36	4.54	106.94	3.43	102.49	2.08
AI844626	Gatm	mit	glycine amidinotransferase	creatine biosynthesis	1.38	1.29	0.94	1152.51	173.36	1230.49	254.75	1591.93	250.98
U51167	Idh2	mit	isocitrate dehydrogenase	tricarboxylic acid cycle	1.39	1.06	0.76	214.29	25.72	282.53	61.51	298.68	56.49
AI838061	Idh3b	mit	isocitrate dehydrogenase 3 (NAD+) beta	tricarboxylic acid cycle	0.91	0.98	1.08	65.68	4.37	60.62	2.50	59.49	3.41
AI875934	Lypla1	mit	lysophospholipase 1	lipid metabolism	0.83	0.94	1.14	935.25	99.06	818.82	101.03	772.56	72.10
AW124337	Mgst1	mit, mic	microsomal glutathione S-transferase 1	glutathione metabolism	1.34	1.20	0.90	38.83	5.28	43.37	7.99	52.05	4.48
U84903	Mrpl23; Rpl23	mit	L23 mitochondrial-related protein	mitochondrial large ribosomal subunit	1.25	1.04	0.83	395.72	24.61	474.20	56.63	494.71	64.03
AI853575	Mrps2	mit	mitochondrial ribosomal protein S2	constituent of mitochondrial ribosome	0.71	0.77	1.08	242.59	47.78	223.60	44.93	172.50	24.86
AI875598	Mtif2	mit	mitochondrial translational initiation factor 2	mitochondrial protein synthesis	0.72	0.85	1.17	290.75	56.70	247.71	42.67	210.50	32.09
AI842675	Ppif	mit	peptidylprolyl isomerase F (cyclophilin F)	protein folding	0.80	0.87	1.09	331.26	26.07	305.01	24.76	265.20	32.32
M28723	Prdx3	mit	peroxiredoxin 3	peroxidase reaction	0.80	0.90	1.13	1583.84	36.55	1403.88	65.24	1268.76	202.86
AI846308	Sfxn1	mit	sideroflexin 1	cation transporter	1.54	1.26	0.82	157.70	32.42	192.54	33.72	242.58	41.99
AI848354	Slc25a1	mit	olute carrier family 25 (mitochondrial carrier; c), member 1	citrate transporter	0.67	0.77	1.16	1729.87	290.88	1487.05	325.73	1150.60	143.63
U68564	Idh3g	mit	isocitrate dehydrogenase 3 (NAD+), gamma	TCA cycle	0.79	0.73	0.93	1028.78	122.01	1111.88	151.23	815.45	222.91
AI843685	Mrpl15	mit	mitochondrial ribosomal protein L15	mitochondrial protein biosynthesis	0.87	0.83	0.96	225.16	23.69	233.77	29.63	195.01	14.93
AI848871	Ndufb10	mit	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	electron transport	0.79	0.75	0.95	591.41	58.71	623.05	128.70	466.93	71.83
U10404	Slc25a5	mit	solute carrier family 25 , member 5	adenine nucleotide translocator	0.92	0.89	0.97	115.25	4.61	118.72	6.28	105.67	8.14
M20625	Cyct	mit	cytochrome c, testis	electron transport	0.96	1.05	1.10	97.36	6.13	88.84	3.15	93.29	3.82
AB028071	Keg1	mit	kidney expressed gene 1	unknown	0.93	1.05	1.14	29.89	2.40	26.32	1.51	27.72	1.45
AV339603	Mrps18a	mit	mitochondrial ribosomal protein S18A	mitochondrial protein translation	0.89	1.03	1.15	1023.33	73.16	887.99	74.27	911.93	62.65
AW125634	Mrs3/4-pending	mit	putative mitochondrial solute carrier	mitochondrial transport	1.06	0.90	0.85	241.12	11.99	284.44	34.72	256.09	21.37
AA189555	Sfxn2	mit	sideroflexin 2	cation transport	0.93	1.02	1.10	77.73	5.95	70.73	1.77	72.47	3.88