Gene Name	Fold Change	P-value (Based on log2)	Control Mean Expression	Cuprizone Mean Expression	P Call % of control	P Call % of cuprizone	Affymetrix Probe Set	Entrez Gene ID or UniGene ID	Myelin Marker
Adpgk: ADP-dependent glucokinase	-1.32	0.001	319	242	100	100	1374958_at	315722	
Adpgk: ADP-dependent glucokinase	-1.47	0.001	236	161	100	100	1377952_at	315722	
Adprhl1: ADP-ribosylhydrolase like 1	-1.45	0.018	162	111	100	100	1379392_at	290880	
Apln: apelin, AGTRL1 ligand	-1.43	0.013	285	199	100	100	1368258_at	58812	
Apln: apelin, AGTRL1 ligand	-1.37	0.005	639	465	100	100	1389651_at	58812	
Apod: apolipoprotein D	-1.52	0.001	1668	1099	100	100	1398258_at	25239	
Aps: adaptor protein with pleckstrin homology and src homology 2 domains	-1.2	0.025	60	50	100	100	1368605_at	114203	
Arpc4: actin related protein 2/3 complex, subunit 4	-1.22	0.048	2432	1995	100	100	1372577_at	297518	
Aspa: aspartoacylase	-1.36	0.000	242	178	100	100	1368563_at	79251	x
Bdh1: 3-hydroxybutyrate dehydrogenase, type 1	-1.32	0.002	186	142	100	100	1382260_at	117099	
Bspry: B-box and SPRY domain containing	-1.36	0.000	101	74	100	100	1379366_a_at	64027	
Ca2: carbonic anhydrase 2	-1.2	0.025	1525	1272	100	100	1367733_at	54231	
Ca5b: carbonic anhydrase VB, mitochondrial	-1.2	0.005	60	50	100	100	1390807_at	302669	
Carhsp1: calcium regulated heat stable protein 1	-1.23	0.002	317	257	100	100	1371536_at	260416	
Carhsp1: calcium regulated heat stable protein 1	-1.2	0.004	283	235	100	100	1388659_at	260416	
Cd82: CD82 antigen	-1.26	0.001	257	203	100	100	1386976_at	83628	
Cd9: CD9 antigen	-1.27	0.012	896	704	100	100	1371499_at	24936	x
Cdc42ep1: CDC42 effector protein (Rho GTPase binding) 1	-1.2	0.001	270	225	100	100	1389157_at	315121	
Cdc42ep2: CDC42 effector protein (Rho GTPase binding) 2	-1.26	0.000	475	377	100	100	1389145_at	309175	
Cdw92: CDW92 antigen	-1.33	0.000	462	347	100	100	1368480_at	85254	
Cldn11: claudin 11	-1.85	0.031	882	477	100	100	1369609_at	84588	x
Cldn11: claudin 11	-1.48	0.003	3639	2458	100	100	1376711_at	84588	x
Cnp1: cyclic nucleotide phosphodiesterase 1	-1.76	0.007	1014	576	100	100	1370693_a_at	25275	
Cnp1: cyclic nucleotide phosphodiesterase 1	-1.55	0.001	3455	2223	100	100	1387897_at	25275	
Col11a2: procollagen, type XI, alpha 2	-1.26	0.005	287	227	100	100	1389891_at	294279	
Col9a3: procollagen, type IX, alpha 3	-1.52	0.001	202	133	100	100	1377631_at	362285	
Csrp1: cysteine and glycine-rich protein 1	-1.41	0.000	1289	916	100	100	1370057_at	29276	
Cyp3a13: cytochrome P450, family 3, subfamily a, polypeptide 13	-1.49	0.001	94	63	100	80	1370387_at	171352	
Dapk1: death associated protein kinase 1	-1.27	0.007	667	523	100	100	1379911_at	306722	
Edg2: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	-1.8	0.003	659	366	100	100	1370048_at	116744	
Edg2: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	-1.55	0.000	480	310	100	100	1374016_at	116744	
Enpp2: ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.29	0.013	1092	848	100	100	1368536_at	84050	
Erbb3:-erb-b2 erythroblastic leukemia viral oncogene homolog 3	-1.58	0.004	157	99	100	100	1377821_at	29496	x
Etv5: ets variant gene 5 (ets-related molecule)	-1.31	0.047	519	396	100	100	1383447_at	303828	
Fam31b: Family with sequence similarity 31, member B	-1.3	0.001	58	44	100	80	1379398_at	289051	
Gamt: guanidinoacetate methyltransferase	-1.39	0.000	551	397	100	100	1368253_at	25257	
Gja12: gap junction protein, alpha 12, 47kDa	-1.63	0.004	158	97	100	40	1377485_at	497913	
Gng8: guanine nucleotide binding protein (G protein), gamma 8 subunit	-1.23	0.033	109	89	100	100	1370843_at	245986	
Gpr37: G protein-coupled receptor 37	-1.41	0.000	1056	748	100	100	1387182_at	117549	
Gsn: gelsolin	-1.37	0.001	992	721	100	100	1371414_at	296654	x
Hapln2: hyaluronan and proteoglycan link protein 2	-1.43	0.004	210	147	100	100	1370849_at	64057	
Hapln2: Hyaluronan and proteoglycan link protein 2	-1.29	0.004	23	18	100	60	1394952_at	64057	
Kcna1: potassium voltage-gated channel, shaker-related subfamily, member 1	-1.26	0.008	1036	820	100	100	1370545_at	24520	
Kdelr3: KDEL endoplasmic reticulum protein retention receptor 3	-1.27	0.016	59	46	100	60	1372870_at	315131	
Klk6: kallikrein 6	-2.84	0.000	230	81	100	40	1368384_at	29245	x
Large: Like-glycosyltransferase	-1.21	0.025	22	18	66	80	1391993_at	361368	
Lgi3: leucine-rich repeat LGI family, member 3	-1.23	0.012	337	275	100	100	1381369_at	306013	
Lgi3: leucine-rich repeat LGI family, member 3	-1.29	0.000	694	538	100	100	1383459_at	306013	
Lmcd1: LIM and cysteine-rich domains 1	-1.25	0.017	143	114	100	100	1376632_at	494021	
LOC361016: similar to RIKEN cDNA 4933406L09	-1.88	0.000	888	471	100	100	1382956_at	361016	
LOC679462: similar to Tetraspanin-15 (Tspan-15)	-1.22	0.003	252	206	100	80	1389656_at	679462	
LOC679532: similar to Elongation of very long chain fatty acids protein 1	-1.25	0.001	399	321	100	100	1398360_at	679532	
LOC681021; LOC686392: similar to progestin and adipoQ receptor family member VI	-1.22	0.008	157	129	100	100	1373642_at	681021; 686392	
LOC681190, LOC681501: similar to potassium voltage-gated channel, member 1-like	-1.39	0.004	264	190	100	100	1374015_at	681190; 681501	
LOC683713: similar to Cerebroside sulfotransferase	-1.2	0.001	90	75	100	100	1385432_at	683713	
LOC685433; LOC688044: similar to ecotropic viral integration site 2A	-1.3	0.003	546	421	100	100	1389413_at	685433; 688044	
Mag: myelin-associated glycoprotein	-1.78	0.000	740	415	100	100	1368861_a_at	29409	x
Mal: myelin and lymphocyte protein, T-cell differentiation protein	-3.76	0.000	1541	409	100	100	1387040_at	25263	x
Mbp: myelin basic protein	-1.39	0.000	12245	8793	100	100	1368810_a_at	24547	x
Mbp: myelin basic protein	-1.8	0.025	5017	2782	100	100	1387341_a_at	24547	x
Mobp: myelin-associated oligodendrocytic basic protein	-2.08	0.000	1164	559	100	100	1368263_a_at	25037	x
Mobp: myelin-associated oligodendrocytic basic protein	-3.38	0.000	3014	892	100	100	1370434_a_at	25037	x
Mobp: myelin-associated oligodendrocytic basic protein	-3.45	0.002	1361	395	100	100	1370500_a_at	25037	x
Mog: Myelin oligodendrocyte glycoprotein	-1.27	0.011	60	47	100	60	1377352_at	24558	x
Mog: myelin oligodendrocyte glycoprotein	-1.99	0.000	901	452	100	100	1398257_at	24558	x
Myo1d: myosin ID	-1.36	0.002	86	63	100	100	1388917_at	25485	
Ndrg1: N-myc downstream regulated gene 1	-1.25	0.001	470	376	100	100	1371360_at	299923	
Nr4a2: nuclear receptor subfamily 4, group A, member 2	-1.25	0.025	124	99	100	100	1387410_at	54278	
Olig1: oligodendrocyte transcription factor 1	-1.31	0.001	1646	1259	100	100	1387200_at	60394	x
P2rx4: purinergic receptor P2X, ligand-gated ion channel 4	-1.21	0.044	247	204	100	100	1369743_a_at	29659	
Papss2: 3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.23	0.011	127	103	100	100	1376047_at	294103	
Papss2: 3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.35	0.011	56	41	100	80	1395721_at	294103	
Plekhb1: pleckstrin homology domain containing, family B (evectins) member 1	-1.43	0.001	1242	867	100	100	1370334_at	64471	
Plekhh1: pleckstrin homology domain containing, family H member 1	-1.52	0.000	526	347	100	100	1384277_at	314262	
Plk4: polo-like kinase 4 (Drosophila)	-1.22	0.033	45	37	100	100	1377832_at	310344	
Pllp: plasma membrane proteolipid	-1.25	0.014	661	529	100	100	1386943_at	64364	x
Plp: proteolipid protein	-1.6	0.001	8132	5082	100	100	1387112_at	24943	x
Plxna4: Plexin A4	-1.22	0.003	83	68	66	60	1381249_at	312213	
Ppap2c: phosphatidic acid phosphatase type 2c	-1.23	0.012	81	66	100	80	1388913_at	246115	
Ppp1r14a: protein phosphatase 1, regulatory subunit 14A	-2.2	0.000	259	118	100	100	1367813_at	114004	
Recc1: replication factor C 1	-1.2	0.017	351	293	100	100	1391078_at	89809	
Rgc32: response gene to complement 32	-1.25	0.000	1850	1474	100	100	1368080_at	117183	x
RGD1305713: similar to RIKEN cDNA 3110040N11	-1.22	0.029	358	293	100	100	1373833_at	293059	
RGD1305755: Similar to RIKEN cDNA 5033406L14	-1.39	0.046	228	165	100	100	1389444_at	305923	
RGD1308089: similar to common-site lymphoma leukemia guanine nucleotide exchange factor like	-1.23	0.010	211	172	100	100	1375767_at	314249	
RGD1308367: similar to KIAA1189 protein	-1.84	0.001	433	235	100	100	1382382_at	295619	
RGD1308367: similar to KIAA1189 protein	-1.69	0.005	210	124	100	100	1385547_at	295619	
RGD1309969: similar to RIKEN cDNA 2600010E01	-1.33	0.006	77	58	100	100	1376775_at	362171	
RGD1311937: similar to hypothetical protein MGC17299	-1.34	0.030	191	143	100	100	1394653_at	313545	
RGD1359634: Similar to RIKEN cDNA 1700088E04	-1.27	0.000	318	251	100	100	1389187_at	315126	
RGD1561238: Similar to ring finger protein 122 homolog	-1.27	0.006	56	44	100	60	1373485_at	502091	
RGD1562732: similar to Glutathione S-transferase, theta 3	-1.45	0.007	685	473	100	100	1371942_at	499422	
RGD1562969: similar to Tweety homolog 2	-1.2	0.027	455	377	100	100	1384238_at	287803	
RGD1563215: similar to cytochrome P450, family 2, subfamily J, polypeptide 4	-1.66	0.000	65	39	100	80	1396327_at	313373	
RGD1564108: similar to hedgehog-interacting protein	-1.42	0.000	215	152	100	100	1385038_at	291936	
RGD1564108: Similar to hedgehog-interacting protein	-1.77	0.000	127	71	100	80	1393064_at	291936	
RGD1564490: similar to Coronin, actin binding protein 1C	-1.26	0.006	116	92	100	100	1396250_at	501841	
RGD1564797: similar to empty spiracles-like protein 2	-1.27	0.017	118	93	100	100	1377311_at	499380	
RGD1566097: similar to Anillin	-1.82	0.000	180	99	100	100	1373250_at	307056	
Rn.1448.1	-1.24	0.001	374	302	100	100	1371444_at	Rn.1448.1	
Rn.15543.1	-1.3	0.000	94	72	100	100	1379108_at	Rn.15543.1	
Rn.18592.1	-1.29	0.011	1179	912	100	100	1375247_at	Rn.18592.1	
Rn.18819.1	-1.33	0.017	302	227	100	100	1390174_at	Rn.18819.1	
Rn.19213.1	-1.34	0.000	777	581	100	100	1380405_at	Rn.19213.1	
Rn.23887.1	-1.39	0.013	113	81	66	40	1391656_at	Rn.23887.1	
Rn.34703.1	-1.27	0.008	168	133	100	100	1381775_at	Rn.34703.1	
Rn.38978.1	-1.32	0.002	846	639	100	100	1383218_at	Rn.38978.1	
Rn.46031.1	-1.21	0.021	248	205	100	100	1377403_at	Rn.46031.1	
Rn.49196.2	-1.2	0.021	56	47	100	100	1394258_at	Rn.49196.2	

Gene Name	Fold Change	P-value (Based on log2)	Control Mean Expression	Cuprizone Mean Expression	P Call % of control	P Call % of cuprizone	Affymetrix Probe Set	Entrez Gene ID or UniGene ID	Myelin Marker
Rn.61646.1	-1.48	0.000	26	18	50	40	1378956_at	Rn.61646.1	
Rn.9408.1	-1.33	0.012	132	99	100	100	1373790_at	Rn.9408.1	
Scrg1: scrapie responsive gene 1	-1.33	0.005	450	337	100	100	1368978_at	64458	
Sept4: septin 4	-1.35	0.000	1314	976	100	100	1389448_at	287606	
Slc25a18: solute carrier family 25 member 18	-1.66	0.001	804	486	100	100	1390537_at	681896	
Slc4a8: Solute carrier family 4 (anion exchanger), member 8	-1.2	0.001	46	38	100	60	1374095_at	315311	
Sox10: SRY-box containing gene 10	-1.25	0.034	276	221	100	100	1368439_at	29361	
St3gal6: ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-1.29	0.006	136	105	100	100	1395389_at	304023	
Thrb: thyroid hormone receptor beta	-1.38	0.023	340	246	100	100	1370474_at	24831	
Tmbim1: transmembrane BAX inhibitor motif containing 1	-1.2	0.027	126	104	100	100	1376102_at	316516	
Tmem10: transmembrane protein 10	-2.71	0.000	490	181	100	100	1380329_at	361757	
Tmem63a: transmembrane protein 63a	-1.26	0.007	131	104	50	40	1377102_at	289318	
Tmem98: transmembrane protein 98	-1.21	0.008	145	120	100	100	1373161_at	303356	
Tnnc2: troponin C type 2	-2.85	0.000	277	97	100	100	1372195_at	296369	
Tpo1: developmentally regulated protein TPO1	-1.2	0.048	217	181	100	100	1386979_at	170907	x
Transcribed locus	-1.22	0.014	106	87	100	100	1374410_at	Rn.17013.1	
Transcribed locus	-2.38	0.005	215	91	100	100	1376011_at	Rn.38649.1	
Transcribed locus	-1.4	0.035	451	322	100	100	1376685_at	Rn.40821.1	
Transcribed locus	-1.21	0.037	313	259	100	100	1377054_at	Rn.41884.1	
Transcribed locus	-1.44	0.035	308	214	100	100	1378303_at	Rn.51713.1	
Transcribed locus	-1.2	0.018	95	79	83	60	1379470_at	Rn.24370.1	
Transcribed locus	-1.2	0.014	98	82	100	100	1381057_at	Rn.67784.1	
Transcribed locus	-1.39	0.000	50	36	100	100	1381865_at	Rn.43397.1	
Transcribed locus	-1.23	0.024	216	176	100	100	1382081_at	Rn.9379.1	
Transcribed locus	-1.2	0.004	1180	983	100	100	1383086_at	Rn.16489.1	
Transcribed locus	-1.33	0.001	131	98	100	100	1385729_at	Rn.51583.1	
Transcribed locus	-1.25	0.003	351	281	100	100	1393178_at	Rn.72652.1	
Transcribed locus	-1.79	0.001	411	229	100	100	1393730_at	Rn.77698.1	
Transcribed locus	-1.49	0.001	73	49	100	40	1394410_at	Rn.46692.1	
Transcribed locus	-1.22	0.047	15	13	33	80	1395664_at	Rn.51186.1	
Transcribed locus	-1.29	0.049	201	156	100	100	1395819_at	Rn.46093.1	
Transcribed locus	-1.25	0.004	25	20	100	80	1395979_at	Rn.57708.1	
Transcribed locus	-1.26	0.043	310	247	100	100	1398411_at	Rn.7594.1	
Transcribed locus	-1.27	0.004	75	59	66	40	1398566_at	Rn.67780.1	
transferrin	-1.64	0.003	1626	989	100	100	1370228_at	24825	x
Tspan2: tetraspanin 2	-1.53	0.000	1681	1098	100	100	1368104_at	64521	x
Tspan2: tetraspanin 2	-1.4	0.001	1204	862	100	100	1368105_at	64521	x
Ugt8: UDP galactosyltransferase 8	-2.28	0.000	669	293	100	100	1368858_at	50555	x
Wdr59: WD repeat domain 59	-1.98	0.000	482	243	100	80	1393808_at	307855	
Zfp608: Zinc finger protein 608	-1.2	0.007	58	49	100	40	1384535_at	307296	
upregulated transcripts	**upregulated transcripts**	**upregulated transcripts**	**upregulated transcripts**	**upregulated transcripts**	**upregulated transcripts**	**upregulated transcripts**	**upregulated transcripts**		
A2m: alpha-2-macroglobulin	2.4	0.031	59	142	66	100	1367794_at	24153	
Abcg3: ATP-binding cassette, sub-family G (WHITE), member 3	1.24	0.007	58	72	100	100	1393217_at	289453	
Abhd4: abhydrolase domain containing 4	1.25	0.010	815	1017	100	100	1399019_at	364380	
Adhfe1: alcohol dehydrogenase, iron containing, 1	1.25	0.025	482	600	100	100	1389548_at	362474	
Agt: angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	1.37	0.023	293	400	100	100	1387811_at	24179	
Aif1: allograft inflammatory factor 1	1.22	0.004	393	477	100	100	1368558_s_at	29427	
Aqp9: aquaporin 9	1.27	0.047	157	199	100	100	1368621_at	65054	
Atf5: activating transcription factor 5	2.85	0.000	465	1327	100	100	1372601_at	282840	
B2m: Beta-2 microglobulin	1.21	0.001	1135	1369	100	100	1371440_at	24223	
C1qa: complement component 1, q subcomponent, alpha polypeptide	1.3	0.005	746	966	100	100	1376652_at	298566	
C1qb: complement component 1, q subcomponent, beta polypeptide	1.24	0.002	277	342	100	100	1370215_at	29687	
Calca: calcitonin/calcitonin-related polypeptide, alpha	1.56	0.046	135	211	100	100	1370775_a_at	24241	
Casp4: caspase 4, apoptosis-related cysteine peptidase	1.31	0.006	58	76	66	100	1387818_at	114555	
Ccr5: chemokine (C-C motif) receptor 5	1.31	0.035	150	196	100	100	1369290_at	117029	
Cd48: CD48 antigen	1.23	0.032	330	406	100	100	1370891_at	245962	
Cdkn1a: cyclin-dependent kinase inhibitor 1A	1.2	0.038	276	331	100	100	1388674_at	114851	
Cebpd: CCAAT/enhancer binding protein (C/EBP), delta	1.48	0.000	94	139	100	100	1387343_at	25695	
Cenpj: centromere protein J	1.28	0.023	67	86	100	100	1379538_at	305909	
Cfd: complement factor D (adipsin)	1.3	0.009	45	59	50	80	1388602_at	54249	
Chpt1: choline phosphotransferase 1	1.27	0.019	307	389	100	100	1393887_at	362866	
Chrdl1: kohjirin	1.22	0.041	38	47	100	100	1393579_at	363455	
Cib1: calcium and integrin binding 1 (calmyrin)	1.2	0.007	245	293	100	100	1367675_at	81823	
Col6a3: procollagen, type VI, alpha 3	1.23	0.050	103	128	100	100	1389966_at	367313	
Cp: ceruloplasmin	1.27	0.005	95	121	100	100	1368419_at	24268	
Cth: cystathionase (cystathionine gamma-lyase)	1.21	0.027	101	122	100	100	1367838_at	24962	
Ctsh: cathepsin H	1.25	0.003	781	978	100	100	1386899_at	25425	
Cyp2j9: cytochrome P450, family 2, subfamily j, polypeptide 9	1.46	0.006	89	130	100	100	1370706_a_at	313375	
Cyp4f2: cytochrome P450, family 4, subfamily F, polypeptide 2	1.34	0.000	57	77	100	100	1368467_at	56266	
Cyp4f4: cytochrome P450, family 4, subfamily f, polypeptide 4	1.4	0.003	84	118	100	100	1387973_at	286904	
Ddit4: DNA-damage-inducible transcript 4	1.2	0.041	669	802	100	100	1368025_at	140942	
Dusp6: dual specificity phosphatase 6	1.32	0.008	788	1038	100	100	1377064_at	116663	
Egfl6: EGF-like-domain, multiple 6	1.43	0.004	37	53	100	100	1393335_at	317470	
Eif4ebp1: eukaryotic translation initiation factor 4E binding protein 1	1.38	0.003	193	266	100	100	1386888_at	116636	
Emr1: EGF-like module containing, mucin-like, hormone receptor-like sequence 1	1.2	0.013	41	49	100	100	1381311_at	316137	
Entpd2: ectonucleoside triphosphate diphosphohydrolase 2	1.23	0.012	243	299	100	100	1370845_at	64467	
Eprs: glutamyl-prolyl-tRNA synthetase	1.23	0.001	801	981	100	100	1373418_at	289352	
Fads1: fatty acid desaturase 1	1.23	0.009	1456	1794	100	100	1367857_at	84575	
Fgl2: fibrinogen-like 2	1.29	0.041	85	110	66	100	1392894_at	84586	
Fmo1: flavin containing monooxygenase 1	1.39	0.012	154	214	100	100	1387053_at	25256	
Gas5: growth arrest specific 5	1.21	0.000	570	693	100	100	1373499_at	81714	
Gatm: glycine amidinotransferase (L-arginine:glycine amidinotransferase)	1.33	0.003	876	1166	100	100	1367627_at	81660	
Gcsh: glycine cleavage system protein H (aminomethyl carrier)	1.22	0.005	1055	1286	100	100	1367908_at	171133	
Gfap: glial fibrillary acidic protein	1.43	0.013	3192	4553	100	100	1368353_at	24387	GFAP
Gjb2: gap junction membrane channel protein beta 2	1.69	0.033	352	594	100	100	1373386_at	394266	
Gjb6: gap junction membrane channel protein beta 6	1.47	0.002	610	895	100	100	1368577_at	84403	
Gng11: guanine nucleotide binding protein (G protein), gamma 11	1.23	0.002	42	52	100	100	1398530_at	64199	
Gpc3: glypican 3	1.26	0.014	112	141	100	100	1368395_at	25236	
Heph: hephaestin	1.32	0.006	32	42	100	100	1368533_at	117240	
Hes1: hairy and enhancer of split 1 (Drosophila)	1.26	0.044	163	206	100	100	1387036_at	29577	
Hey2: hairy/enhancer-of-split related with YRPW motif 2	1.22	0.001	454	552	100	100	1384515_at	155430	
Hist1h2bh: Histone cluster 1, H2bh	1.28	0.008	861	1103	100	100	1381428_a_at	306945	
Hist1h2bh: histone cluster 1, H2bh	1.31	0.001	218	286	100	100	1390021_at	306945	
Hist1h4b: histone cluster 1, H4b	1.36	0.004	133	181	100	100	1374600_at	64627	
Hist1h4b: histone cluster 1, H4b	1.53	0.000	157	239	100	100	1372726_at	64627	
Hnrpa2b1: heterogeneous nuclear ribonucleoprotein A2/B1	1.21	0.031	182	221	100	100	1378543_at	362361	
Hnrpa2b1: heterogeneous nuclear ribonucleoprotein A2/B1	1.21	0.046	354	430	100	100	1373540_at	362361	
Hrsp12: heat-responsive protein 12	1.2	0.001	331	397	100	100	1368060_at	65151	
Ier5l: immediate early response 5-like	1.28	0.009	373	476	100	100	1391026_at	499772	
Ifi30: interferon gamma inducible protein 30	1.24	0.001	248	308	100	100	1372070_at	290644	
Igfbp5: insulin-like growth factor binding protein 5	1.37	0.004	390	536	100	100	1370960_at	25285	
Igsf1: Immunoglobulin superfamily, member 1	1.47	0.000	75	110	83	100	1370594_at	302822	
Igsf1: immunoglobulin superfamily, member 1	1.54	0.009	284	437	100	100	1370410_at	302822	
Igtp: interferon gamma induced GTPase	1.34	0.006	46	61	100	100	1397304_at	303163	
Isg20: interferon stimulated exonuclease 20	1.2	0.001	33	40	50	100	1390507_at	293052	
Kcnj16: potassium inwardly-rectifying channel, subfamily J, member 16	1.26	0.007	71	89	100	100	1370076_at	29719	
Kcnj16: Potassium inwardly-rectifying channel, subfamily J, member 16	1.83	0.000	113	207	100	100	1373991_at	29719	
Klhl5: kelch-like 5 (Drosophila)	1.34	0.008	77	103	100	100	1380784_at	305351	

Gene Name	Fold Change	P-value (Based on log2)	Control Mean Expression	Cuprizone Mean Expression	P Call % of control	P Call % of cuprizone	Affymetrix Probe Set	Entrez Gene ID or UniGene ID	Myelin Marker
Lama2: laminin, alpha 2	1.22	0.006	123	149	100	100	1390404_at	309368	
Lcat: lecithin cholesterol acyltransferase	1.58	0.048	273	432	100	100	1367887_at	24530	
LOC305633: similar to Antxr2 protein	1.2	0.019	65	79	83	100	1389017_at	305633	
LOC360997: similar to ATP-binding cassette, sub-family G (WHITE), member 3	1.28	0.015	97	125	83	100	1379717_at	360997	
LOC361596: similar to NADP+-specific isocitrate dehydrogenase	1.22	0.001	687	836	100	100	1388403_at	361596	
LOC363251: similar to 1700029B21Rik protein	1.62	0.000	37	59	66	100	1374245_at	363251	
LOC500013: similar to sterile alpha motif domain containing 9-like	1.3	0.013	102	132	100	100	1376920_at	500013	
LOC501039: Similar to solute carrier family 25, member 36	1.23	0.013	171	212	100	100	1380084_at	501039	
LOC679869: LOC683733: similar to transcription factor 7-like 2, T-cell specific, HMG-box	1.23	0.003	328	404	100	100	1377156_at	679869; 683733	
LOC683529: similar to ADAMTS-like 1 isoform 1	1.25	0.015	116	144	100	100	1391139_at	683529	
LOC691966: similar to Sulfide:quinone oxidoreductase, mitochondrial precursor	1.31	0.006	185	243	100	100	1389142_at	691966	
Lrrc23: leucine rich repeat containing 23	1.22	0.019	156	191	100	100	1378864_at	312707	
Lxn: latexin	1.41	0.001	572	806	100	100	1367768_at	59073	
Maob: monoamine oxidase B	1.22	0.014	1047	1272	100	100	1368514_at	25750	
March7: Membrane-associated ring finger (C3HC4) 7	1.23	0.011	32	40	83	100	1381651_at	311059	
Mdk: midkine	1.26	0.005	356	448	100	100	1367682_at	81517	
MGC108778: similar to RIKEN cDNA 1810057C19	1.43	0.000	387	554	100	100	1389467_at	497979	
MGC108823; RGD1559715: similar to interferon-inducible GTPase	1.26	0.022	38	48	100	100	1373992_at	307414; 498871	
Mgst1: microsomal glutathione S-transferase 1	1.42	0.019	103	146	100	100	1367612_at	171341	
Mycn: v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	1.2	0.005	174	208	100	100	1376648_at	298894	
Ndrg2: N-myc downstream regulated gene 2	1.23	0.000	5115	6277	100	100	1387121_a_at	171114	
Ntf3: neurotrophin 3	1.23	0.005	78	96	100	100	1387267_at	81737	
Ogn: osteoglycin	2.04	0.047	106	217	100	100	1385248_a_at	291015	
Pax6: paired box gene 6	1.24	0.007	144	179	100	100	1369242_at	25509	
Pcf11: cleavage and polyadenylation factor subunit homolog	1.21	0.006	218	264	100	100	1377670_at	361605	
Pdpn: podoplanin	1.43	0.001	390	557	100	100	1386913_at	54320	
Phgdh: 3-phosphoglycerate dehydrogenase	1.39	0.003	643	894	100	100	1367811_at	58835	
Phyhd1: phytanoyl-CoA dioxygenase domain containing 1	1.22	0.039	293	357	100	100	1371974_at	296621	
Pros1: protein S (alpha)	1.28	0.003	185	235	100	100	1371037_at	81750	
Psmb8: proteosome (prosome, macropain) subunit, beta type 8	1.24	0.008	77	95	66	100	1367786_at	24968	
Psmb9: proteosome (prosome, macropain) subunit, beta type 9	1.2	0.033	82	98	83	80	1370186_at	24967	
Ptprc: protein tyrosine phosphatase, receptor type, C	1.22	0.025	42	52	100	100	1390798_at	24699	
Ptprz1: protein tyrosine phosphatase, receptor-type, Z polypeptide 1	1.33	0.001	1150	1525	100	100	1368350_at	25613	
Rarres1: retinoic acid receptor responder 1	1.29	0.001	155	201	100	100	1382274_at	310486	
RGD1304579: similar to 9230105E10Rik protein	1.2	0.001	164	196	100	100	1372112_at	308906	
RGD1307393: similar to hypothetical protein MGC9907	1.24	0.040	64	80	100	100	1390653_at	314243	
RGD1307658: similar to 3000004N20Rik protein	1.23	0.030	185	227	100	100	1377187_at	313069	
RGD1310725: hypothetical LOC297077	1.27	0.007	691	875	100	100	1373204_at	297077	
RGD1311381: similar to hypothetical protein FLJ20037	1.35	0.004	69	92	100	100	1394940_at	300870	
RGD1311723: similar to KIAA1731 protein	1.21	0.011	58	70	100	100	1398460_at	363018	
RGD1559605: similar to hypothetical protein FLJ25477 isoform 2	1.26	0.048	179	225	100	100	1383390_at	498529	
RGD1560155: Similar to mKIAA0934 protein	1.33	0.038	100	133	100	100	1380399_at	307067	
RGD1560646: similar to Myosin VI	1.21	0.008	276	335	100	100	1376804_at	315840	
RGD1560744: Similar to ring finger protein 111	1.24	0.025	116	144	100	100	1381636_at	307251	
RGD1562092: similar to regulatory factor X 4 variant	1.22	0.000	212	259	100	100	1392189_at	500818	
RGD1564089: similar to peroxisomal long chain acyl-CoA thioesterase Ia	1.29	0.038	35	46	50	100	1378169_at	314304	
RGD1564993: Similar to cofactor required for Sp1 transcriptional activation subunit 8	1.2	0.005	56	68	50	80	1381552_at	296612	
RGD1565715: similar to low density lipoprotein receptor-related protein binding protein	1.21	0.009	118	143	100	100	1373685_at	361149	
RGD1565845: similar to 5730537D05Rik protein	1.41	0.007	111	156	100	100	1394625_at	361968	
Rn.12355.1	1.2	0.003	132	158	100	100	1383120_at	Rn.12355.1	
Rn.15937.1	1.27	0.033	59	74	66	100	1393551_at	Rn.15937.1	
Rn.23744.1	1.2	0.048	44	53	83	100	1384010_at	Rn.23744.1	
Rn.29107.1	1.23	0.006	188	231	100	100	1382500_at	Rn.29107.1	
Rn.43880.1	1.27	0.032	64	82	100	100	1391654_at	Rn.43880.1	
Rn.53140.1	1.29	0.003	50	65	33	80	1378944_at	Rn.53140.1	
Rn.55366.1	1.23	0.036	126	155	100	100	1394793_at	Rn.55366.1	
Rn.64231.1	1.6	0.000	96	153	100	100	1397917_at	Rn.64231.1	
Rn.6719.1	1.2	0.035	108	129	100	100	1384087_at	Rn.6719.1	
Rn.6766.1	1.24	0.043	366	456	100	100	1383659_a_at	Rn.6766.1	
Rnaset2: ribonuclease T2	1.21	0.002	576	700	100	100	1375211_at	292306	
RT1-Aw2: RT1 class Ib, locus Aw2	1.21	0.050	21	25	66	100	1379818_at	24737	
Rtp4: receptor transporter protein 4	1.2	0.021	103	124	100	100	1379285_at	360733	
Scd1: stearoyl-Coenzyme A desaturase 1	1.24	0.036	254	314	100	100	1370355_at	246074	
Sdc4: syndecan 4	1.21	0.001	1054	1276	100	100	1367721_at	24771	
Serpinh1: serine (or cysteine) proteinase inhibitor, clade H, member 1	1.34	0.004	504	676	100	100	1371310_s_at	29345	
Sfxn5: Sideroflexin 5	1.23	0.033	53	65	33	80	1376322_at	261737	
Siah1a: seven in absentia 1A	1.2	0.004	304	366	100	100	1387266_at	140941	
Slc3a2: solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	1.47	0.000	1898	2788	100	100	1398771_at	50567	
Slc6a13: solute carrier family 6 (neurotransmitter transporter, GABA), member 13	1.44	0.018	118	170	83	100	1387372_at	171163	
Slc7a3: solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	1.28	0.000	241	309	100	100	1368582_at	29485	
Slc7a5: solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	1.47	0.000	436	640	100	100	1387280_a_at	50719	
Smpdl3a: sphingomyelin phosphodiesterase, acid-like 3A	1.43	0.002	204	291	100	100	1388809_at	294422	
Srebf1: sterol regulatory element binding factor 1	1.21	0.025	468	568	100	100	1388426_at	78968	
Sult1d1: sulfotransferase family 1D, member 1	1.28	0.018	23	29	100	100	1369047_at	60393	
Svil: supervillin	1.22	0.027	137	168	100	100	1376572_a_at	361256	
Thrsp: thyroid hormone responsive protein	1.27	0.011	167	212	100	100	1387852_at	25357	
Thrsp: thyroid hormone responsive protein	1.33	0.024	298	395	100	100	1371400_at	25357	
Thrsp: thyroid hormone responsive protein	1.38	0.027	236	327	100	100	1370150_a_at	25357	
Transcribed locus	1.2	0.003	327	391	100	100	1398430_at	Rn.8814.1	
Transcribed locus	1.2	0.040	62	75	33	60	1393602_at	Rn.47209.1	
Transcribed locus	1.2	0.044	338	406	100	100	1393308_at	Rn.25047.1	
Transcribed locus	1.2	0.050	322	387	100	100	1373651_at	Rn.45576.1	
Transcribed locus	1.21	0.003	145	175	100	100	1371450_at	Rn.19036.1	
Transcribed locus	1.21	0.004	522	634	100	100	1374622_at	Rn.9546.1	
Transcribed locus	1.21	0.025	29	36	100	100	1396775_at	Rn.57462.1	
Transcribed locus	1.21	0.031	600	727	100	100	1384814_at	Rn.26735.1	
Transcribed locus	1.21	0.037	116	141	100	100	1397300_at	Rn.42112.1	
Transcribed locus	1.21	0.043	98	119	83	100	1383601_at	Rn.17704.1	
Transcribed locus	1.22	0.028	336	410	100	100	1393007_at	Rn.15063.1	
Transcribed locus	1.22	0.034	260	318	100	100	1385098_at	Rn.46170.1	
Transcribed locus	1.22	0.042	294	358	100	100	1394135_at	Rn.43903.1	
Transcribed locus	1.23	0.007	71	87	100	100	1385078_at	Rn.9329.1	
Transcribed locus	1.24	0.001	105	131	100	100	1377142_at	Rn.23617.1	
Transcribed locus	1.24	0.026	229	285	100	100	1388866_at	Rn.6181.1	
Transcribed locus	1.24	0.034	57	71	100	100	1374868_at	Rn.13827.1	
Transcribed locus	1.25	0.006	105	131	100	100	1398189_at	Rn.62531.1	
Transcribed locus	1.25	0.032	26	32	100	100	1382619_at	Rn.19933.1	
Transcribed locus	1.25	0.034	14	18	33	100	1392619_at	Rn.22011.1	
Transcribed locus	1.26	0.008	328	412	100	100	1389554_at	Rn.3836.1	
Transcribed locus	1.26	0.010	276	348	100	100	1377389_at	Rn.28553.1	
Transcribed locus	1.27	0.005	226	286	100	100	1390170_at	Rn.40912.1	
Transcribed locus	1.27	0.027	224	284	100	100	1378350_at	Rn.811.1	
Transcribed locus	1.28	0.027	19	25	33	100	1384226_at	Rn.16010.1	
Transcribed locus	1.29	0.000	1359	1758	100	100	1389586_at	Rn.23464.1	
Transcribed locus	1.29	0.023	518	667	100	100	1380822_at	Rn.21416.1	
Transcribed locus	1.3	0.020	120	157	100	100	1394101_at	Rn.19284.1	
Transcribed locus	1.33	0.001	132	175	100	100	1382613_at	Rn.24594.1	
Transcribed locus	1.33	0.007	59	79	100	100	1380831_at	Rn.39250.1	
Transcribed locus	1.34	0.001	694	930	100	100	1372479_at	Rn.8739.1	

Gene Name	Fold Change	P-value (Based on log2)	Control Mean Expression	Cuprizone Mean Expression	P Call % of control	P Call % of cuprizone	Affymetrix Probe Set	Entrez Gene ID or UniGene ID	Myelin Marker
Transcribed locus	1.34	0.032	182	244	100	100	1397348_at	Rn.52992.1	
Transcribed locus	1.36	0.012	429	581	100	100	1379259_at	Rn.22140.1	
Transcribed locus	1.46	0.004	569	833	100	100	1383058_at	Rn.4287.1	
Transcribed locus	1.53	0.010	144	221	100	100	1371861_at	Rn.19802.1	
Transcribed locus	1.59	0.002	103	165	100	100	1396000_at	Rn.40801.1	
Transcribed locus	1.79	0.000	44	79	100	100	1374752_at	Rn.18295.1	
Transcribed locus	1.88	0.000	700	1313	100	100	1378133_at	Rn.38677.1	
Transcribed locus, similar to XP_580072.1 hypothetical protein XP_580072	1.21	0.040	90	109	100	100	1373302_at	Rn.6387.1	
Trim34: tripartite motif protein 34	1.25	0.006	159	199	100	100	1385252_at	293294	
Txnip: thioredoxin interacting protein	1.59	0.003	344	546	100	100	1371131_a_at	117514	
Vamp5: vesicle-associated membrane protein 5	1.22	0.030	94	114	100	100	1398840_at	89818	
Vcam1: vascular cell adhesion molecule 1	1.26	0.001	655	827	100	100	1368474_at	25361	