

**Additional File 1. Heart Tissue: Alterations in Gene Expression due to Strain Effect and Rejection Effect (color coded based on Venn diagram, Figure 3A)**

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call				
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft	
<b>A. Strain Effect</b>												
1387011_at	lipocalin 2	Lcn2	170496	7.44	4.62	1.0E-01	7.9E-03	0.60	0.00	0.40	0.00	0.00
1388018_at	selectin, endothelial cell	Sele	25544	6.77	1.51	9.1E-02	1.9E-01	0.50	0.00	0.80	0.13	0.80
1369928_at	actin, alpha 1, skeletal muscle	Acta1	29437	5.45	0.69	2.0E-03	3.0E-01	1.00	1.00	1.00	1.00	1.00
1389673_at	Transcribed locus			5.12	0.48	1.2E-02	7.6E-03	1.00	1.00	0.80	1.00	1.00
1369152_at	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	Ppp3r1	29748	4.20	0.63	2.3E-02	2.0E-01	1.00	0.00	0.00	0.00	0.00
1372060_at				4.00	1.48	5.0E-03	3.5E-01	1.00	0.00	0.40	0.00	0.00
1389185_at	Adenylyate kinase 1	Ak1	24183	3.70	0.43	3.3E-03	1.7E-03	1.00	1.00	1.00	1.00	1.00
1389234_at	von Willebrand factor	Vwf	116669	3.51	0.94	3.8E-02	7.8E-01	1.00	1.00	1.00	1.00	1.00
1368128_at	phospholipase A2, group IIA (platelets, synovial fluid)	Pla2g2a	29692	3.16	2.25	4.9E-02	1.1E-01	1.00	1.00	1.00	0.63	1.00
1368681_at	insulin-like growth factor binding protein 3	Igfbbp3	24484	3.07	1.56	3.3E-03	1.7E-01	1.00	1.00	1.00	1.00	1.00
1368042_a_at	high mobility group box 1	Hmgb1	25459	0.31	0.84	4.8E-02	4.8E-02	1.00	1.00	1.00	1.00	1.00
1372577_at	actin related protein 2/3 complex, subunit 4 (predicted)	Arpe4_predicted	297518	0.30	1.43	4.8E-02	3.3E-02	1.00	1.00	1.00	1.00	1.00
1369716_s_at	lectin, galactose binding, soluble 5	Lgals5	25475	0.30	0.67	5.3E-02	2.0E-01	0.00	1.00	1.00	1.00	1.00
1374429_at	Transcribed locus			0.30	0.78	3.7E-02	1.9E-01	1.00	1.00	1.00	1.00	1.00
1386922_at	carbonic anhydrase 2	Ca2	54231	0.29	0.96	2.3E-02	8.2E-01	1.00	1.00	1.00	1.00	1.00
1375343_at	Transcribed locus			0.29	0.45	1.2E-02	8.6E-03	1.00	1.00	1.00	1.00	1.00
1370886_a_at	kinesin 2	Kns2	171041	0.28	0.59	3.3E-03	8.6E-02	1.00	1.00	1.00	1.00	1.00
1382778_at	Dual specificity phosphatase 6	Dusp6	116663	0.24	1.93	7.1E-02	1.5E-02	0.00	0.88	1.00	1.00	1.00
1377114_at				0.24	0.57	3.1E-03	7.2E-02	1.00	1.00	1.00	1.00	1.00
1375519_at	globin, alpha	LOC287167	287167	0.24	0.83	5.9E-02	7.1E-01	1.00	1.00	1.00	1.00	1.00
<b>B. Rejection Effect</b>												
1368266_at	arginase 1	Arg1	29221	1.10	84.50	9.5E-01	1.7E-05	0.20	0.00	1.00	0.00	0.00
1368521_at	napsin A aspartic peptidase	Napsa	365668	1.96	78.18	2.2E-01	4.4E-05	0.00	0.00	1.00	0.00	0.00
1370493_a_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Lilrb3	361493	4.65	54.39	3.9E-02	1.1E-03	0.20	0.00	1.00	0.00	0.00
1369191_at	interleukin 6	Il6	24498	1.54	41.53	6.8E-01	1.9E-03	0.00	0.00	1.00	0.00	0.00
1375917_at	glycoprotein 49b	Gp49b	292594	1.19	33.73	9.0E-01	2.9E-03	0.00	0.00	1.00	0.25	0.00
1369877_at	CD8 antigen, alpha chain	Cd8a	24930	0.96	32.01	9.8E-01	9.8E-04	0.00	0.00	1.00	0.00	0.00
1373525_at	Fc fragment of IgG, low affinity IIIa, receptor	Fcgr3a	304966	1.33	31.88	2.2E-01	1.3E-04	0.00	0.00	1.00	0.00	0.00
1387902_a_at	similar to IG KAPPA CHAIN N-V REGION K2 PRECURSOR	LOC590180	500180	1.01	26.98	9.9E-01	2.0E-04	0.00	0.00	1.00	0.00	0.00
1369290_at	chemokine (C-C motif) receptor 5	Ccr5	117029	1.22	26.71	8.7E-01	1.3E-03	0.00	0.00	1.00	0.00	0.00
1368519_at	serine (or cysteine) peptidase inhibitor, clade E, member 1	Serpine1	24617	1.27	26.62	7.4E-01	1.1E-03	0.00	0.00	1.00	0.25	0.00
1370628_at	granzyme B	Gzmb	171528	1.16	25.43	9.0E-01	5.1E-03	0.00	0.00	1.00	0.00	0.00
1388046_at	integrin alpha M	Itgam	25021	0.91	23.20	8.2E-01	4.4E-05	0.00	0.00	1.00	0.00	0.00
1371079_at	Fc receptor, IgG, low affinity IIb	Fcgr2b	289211	1.49	21.15	8.2E-01	1.3E-04	0.00	0.00	1.00	1.00	1.00
1387472_at	CD3 antigen delta polypeptide	Cd3d	25710	1.12	21.15	9.4E-01	7.5E-04	0.00	0.00	1.00	0.00	0.00
1387835_at	interleukin 1 receptor antagonist	Il1rn	60582	1.06	20.57	8.9E-01	6.8E-03	0.00	0.00	1.00	0.60	0.00
1376062_at	syndecan 1	Sdc1	25216	1.50	20.33	6.5E-01	1.9E-03	0.00	0.00	1.00	0.00	0.00
1367581_a_at	secreted phosphoprotein 1	Spp1	25353	1.18	19.21	7.0E-01	6.2E-04	0.00	0.00	1.00	1.00	1.00
1368965_at	solute carrier family 16 (monocarboxylic acid transporters), member 3	Slc16a3	80878	1.41	19.20	6.2E-01	1.3E-04	0.00	0.00	1.00	0.00	0.00
1372989_at	hypothetical LOC308081	LOC308081	308081	1.02	17.60	9.7E-01	2.5E-04	0.00	0.00	1.00	0.90	0.00
1390797_at	lymphocyte cytosolic protein 2	Lcp2	155918	1.43	16.85	3.5E-01	2.5E-03	0.00	0.00	1.00	0.00	0.00
1370902_at	aldo-keto reductase family 1, member B8	Akr1b8	286921	1.63	16.22	2.8E-01	2.8E-04	0.40	0.00	1.00	0.25	0.00
1387160_at	potassium voltage-gated channel, Isk-related subfamily, member 3	Kcnc3	63883	0.78	15.78	9.1E-01	1.5E-04	0.00	0.00	1.00	0.80	0.00
1398275_at	matrix metalloproteinase 9	Mmp9	81687	1.24	15.60	7.8E-01	1.4E-04	0.00	0.00	1.00	0.80	0.00
1370613_s_at	UDP glycosyltransferase 1 family, polypeptide A1	Ugt1a1	113992	1.11	15.38	9.3E-01	7.8E-04	0.00	0.00	1.00	0.00	0.00
1370080_at	heme oxygenase (decycling) 1	Hmox1	24451	1.29	14.78	4.9E-01	1.9E-04	1.00	1.00	1.00	1.00	1.00
1370090_at	lymphocyte cytosolic protein 2	Lcp2	155918	1.38	14.59	7.7E-01	1.5E-04	0.00	0.00	1.00	0.25	0.00
1383500_at	ribosome binding protein 1 homolog 180kDa (dog) (predicted)	Rrbp1_predicted	311483	0.91	13.91	9.6E-01	1.4E-03	0.00	0.00	1.00	0.60	0.00
1374779_at	Coagulation factor XIII, A1 subunit	F13a1	60327	1.40	13.71	2.8E-01	6.4E-05	1.00	0.63	1.00	1.00	1.00
1370904_at	major histocompatibility complex, class II, DM alpha	Hla-dma	294274	1.32	12.67	5.8E-01	1.3E-04	1.00	0.38	1.00	1.00	1.00
1371913_at	transforming growth factor, beta induced	Tgfb1	116487	1.01	12.42	9.9E-01	1.1E-04	1.00	1.00	1.00	1.00	1.00
1387017_at	squalene epoxidase	Sqle	29230	1.03	12.33	9.4E-01	2.2E-03	0.00	0.00	1.00	0.00	0.00
1370885_at	cathepsin Z	Ctsz	252929	1.14	12.13	6.8E-01	3.6E-04	1.00	1.00	1.00	1.00	1.00
1368930_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	Kcnn4	65506	0.55	12.01	4.9E-01	4.1E-04	0.00	0.00	1.00	0.00	0.00
1368134_a_at	interleukin 4 receptor, alpha	Il4ra	25084	2.57	11.97	4.9E-01	6.5E-03	0.00	0.00	1.00	0.00	0.00
1388436_at	small nuclear ribonucleoprotein polypeptide A	Snrpa	292729	1.24	11.95	8.6E-01	4.8E-04	0.00	0.00	1.00	0.00	0.00
1369964_at	coronin, actin binding protein 1A	Coro1a	155151	1.73	11.63	1.0E-01	2.0E-04	0.00	0.00	1.00	0.13	0.00
1387396_at	hepcidin antimicrobial peptide	Hamp	84604	1.01	11.55	9.9E-01	3.5E-04	1.00	1.00	1.00	1.00	1.00
1371209_at	RT1 class I, CE5	RT1-CE5	309607	1.92	11.50	1.4E-01	2.0E-04	1.00	0.75	1.00	1.00	1.00
1377698_at	tumor necrosis factor receptor superfamily, member 5	Tnfrsf5	171369	0.92	11.47	8.9E-01	2.4E-03	0.00	0.00	1.00	0.80	0.00
1370483_at	similar to transmembrane NK cell receptor 2B4	LOC679046	679046	0.90	11.34	9.0E-01	1.4E-03	0.80	0.75	1.00	0.63	1.00
1373889_at	similar to Cd300D antigen	LOC498022	498022	1.06	11.34	9.1E-01	3.7E-04	1.00	1.00	1.00	1.00	1.00
1371447_at	placenta-specific 8 (predicted)	Plac8_predicted	360914	2.89	11.33	1.5E-01	4.3E-04	1.00	0.88	1.00	1.00	1.00
1377163_at	inhibin beta-B	Inhb	25196	1.43	11.25	8.6E-01	4.7E-04	0.10	0.00	1.00	0.00	0.00
1367705_at	glutaredoxin 1 (thioltransferase)	Glxr1	64045	0.71	11.24	2.0E-01	2.2E-04	1.00	1.00	1.00	1.00	1.00
1376100_at	tubulin, beta 6	Tubb6	307351	1.05	11.18	9.5E-01	1.9E-04	0.20	0.00	1.00	1.00	1.00
1370964_at	argininosuccinate synthetase	Ass	25698	1.48	11.15	5.5E-01	1.4E-04	0.20	0.00	1.00	0.00	0.00
1369294_at	bone marrow stromal cell antigen 1	Bst1	81506	1.09	11.11	8.8E-01	2.8E-03	0.00	0.00	1.00	0.00	0.00
1374730_at	Thioredoxin reductase 3 (predicted)	Txnrd3_predicted	297437	1.12	11.10	6.5E-01	2.3E-04	1.00	1.00	1.00	1.00	1.00
1374775_at	antigen identified by monoclonal antibody Ki-67 (predicted)	Mki67_predicted	291234	2.06	11.09	4.7E-01	1.1E-02	0.00	0.00	1.00	0.50	0.00
1373932_at	Transcribed locus			3.21	10.89	2.5E-01	7.2E-04	1.00	0.25	1.00	1.00	1.00
1369665_a_at	interleukin 18	Il18	29197	1.41	10.78	4.9E-01	8.5E-05	0.00	0.00	1.00	0.63	0.00
1386998_at	aldolase C	Aldoc	24191	1.18	10.49	7.9E-01	2.7E-04	0.00	0.00	1.00	0.60	0.00

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call			
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1386052_at	Transcribed locus		0.82	10.48	7.8E-01	3.2E-03	0.00	0.00	1.00	0.00
1368674_at	liver glycogen phosphorylase	Pygl	64035	1.73	10.39	7.0E-01	3.7E-04	0.00	0.00	1.00
1368530_at	matrix metalloproteinase 12	Mmp12	117033	0.92	10.35	9.1E-01	6.9E-04	0.00	0.00	1.00
1370869_at	branched chain aminotransferase 1, cytosolic	Bcat1	29592	1.59	10.35	6.1E-01	6.4E-04	0.00	0.00	1.00
1388596_at	coactosin-like 1 (Dictyostelium) (predicted)	Cot1l_predicted	361422	1.11	10.29	7.8E-01	1.9E-04	0.40	0.00	1.00
1368518_at	CD53 antigen	Cd53	24251	1.24	10.15	4.2E-01	4.8E-04	1.00	1.00	1.00
1387675_at	Cystatin 10 (chondrocytes) (predicted)	Cst10_predicted	366219	0.52	10.08	4.8E-01	1.1E-04	0.00	0.00	1.00
1368482_at	B-cell leukemia/lymphoma 2 related protein A1	Bcl2l1	170929	1.13	9.99	7.2E-01	5.2E-04	0.00	0.00	1.00
1370382_at	RT1 class II, locus Bb	RT1-Bb	309622	1.08	9.98	9.7E-01	1.3E-03	0.00	0.00	1.00
1368490_at	CD14 antigen	Cd14	60350	1.29	9.75	5.3E-01	2.0E-04	0.80	0.50	1.00
1370371_a_at	CEA-related cell adhesion molecule 1	Ceacam1	287009	2.66	9.67	4.1E-01	6.7E-03	0.00	0.00	0.70
1392794_at	Transcribed locus		2.08	9.54	3.6E-01	1.1E-04	0.00	0.00	1.00	
1398287_at	plasminogen activator, urokinase	Plau	25619	0.65	9.53	5.2E-01	6.2E-03	0.00	0.00	1.00
1368541_at	embigin	Emb	114511	0.73	9.48	4.6E-01	1.5E-04	0.20	0.25	1.00
1368735_a_at	transient receptor potential cation channel, subfamily V, member 2	Trpv2	29465	1.16	9.44	9.1E-01	3.1E-03	0.00	0.00	1.00
1372886_at	transforming, acidic coiled-coil containing protein 3	Tacc3	360962	0.38	9.38	5.2E-01	2.8E-03	0.00	0.00	1.00
1387125_at	S100 calcium binding protein A9 (calgranulin B)	S100a9	94195	1.67	9.38	6.6E-01	5.4E-03	1.00	1.00	1.00
1393280_at	lymphocyte antigen 86 (predicted)	Ly86_predicted	291359	0.99	9.36	9.9E-01	3.2E-03	0.00	0.00	1.00
1388255_x_at	RT1 class I, CEs	RT1-CE5	309607	2.72	9.36	2.0E-01	8.2E-04	1.00	1.00	1.00
1387134_at	schlafen 3	Sln3	114247	1.27	9.25	4.7E-01	1.3E-04	0.00	0.00	1.00
1371146_at	transcription factor EC	Tfec	26296	0.97	9.19	9.8E-01	2.7E-03	0.00	0.00	0.60
1376390_at	membrane-spanning 4-domains, subfamily A, member 11 (predicted)	Ms4a11_predicted	361735	0.97	9.09	9.5E-01	5.3E-04	0.40	0.13	1.00
1370083_at	chemokine (C-C motif) receptor 1	Ccr1	57301	0.76	9.07	8.7E-01	6.4E-04	0.00	0.00	1.00
1374200_at	solute carrier family 29 (nucleoside transporters), member 3	Slc29a3	353307	1.33	8.95	7.4E-01	1.1E-02	0.00	0.00	1.00
1373722_at	kinesin family member 20A (predicted)	Kif20a_predicted	361308	0.20	8.94	6.3E-02	2.3E-02	0.00	0.00	0.60
1367849_at	syndecan 1	Sdc1	25216	1.07	8.93	8.7E-01	4.4E-04	0.40	0.75	1.00
1370682_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Lilrb3	361493	1.70	8.89	3.1E-01	1.4E-04	1.00	0.63	1.00
1370422_at	receptor-interacting serine-threonine kinase 3	Ripk3	246240	0.85	8.87	8.0E-01	2.0E-04	0.20	0.00	1.00
1386908_at	glutaredoxin 1 (thioltransferase)	Glxr1	64045	0.31	8.86	1.9E-01	1.1E-04	0.50	1.00	1.00
1390383_at	adipose differentiation related protein	Adfp	298199	1.18	8.86	2.1E-01	9.8E-05	1.00	1.00	1.00
1387715_at	extracellular peptidase inhibitor	Expi	171059	0.56	8.85	4.9E-01	2.2E-03	0.00	0.00	0.60
1392731_at	tumor necrosis factor receptor superfamily, member 1b	Tnfrsf1b	156767	1.25	8.81	8.6E-01	3.7E-04	0.00	0.00	0.70
1373025_at	complement component 1, q subcomponent, gamma polypeptide	C1aq	362634	1.41	8.78	4.4E-01	1.6E-04	1.00	1.00	1.00
1368760_at	chemokine (C-X-C motif) ligand 2	Cxcl2	114105	1.35	8.71	8.0E-01	1.0E-02	0.00	0.00	0.90
1390195_at	pleckstrin and Sec7 domain containing 4	Psd4	311785	0.54	8.65	5.5E-01	1.6E-03	0.00	0.00	0.90
1370119_at	leucocyte specific transcript 1	Lst1	64569	1.04	8.64	9.8E-01	3.2E-03	0.00	0.00	1.00
1368280_at	cathepsin C	Ctsc	25423	1.36	8.62	2.4E-01	1.6E-03	1.00	1.00	1.00
1385047_x_at	Complement component 6	C6	24237	1.42	8.55	6.4E-01	2.3E-04	0.00	0.00	1.00
1387799_at	FXRD domain-containing ion transport regulator 2	Fxyd2	29639	1.92	8.52	1.6E-01	3.0E-04	1.00	0.75	1.00
1368558_s_at	allograft inflammatory factor 1	Aif1	29427	1.04	8.45	9.4E-01	1.8E-04	0.60	0.50	1.00
1386938_at	alanyl (membrane) aminopeptidase	Anpep	81641	1.09	8.44	8.8E-01	1.6E-04	1.00	0.75	1.00
1370882_at	major histocompatibility complex, class II, DM beta	Hla-dmb	294273	1.26	8.41	4.3E-01	1.1E-04	1.00	1.00	1.00
1370383_s_at	RT1 class II, locus Db1	RT1-Db1	294270	1.11	8.39	8.5E-01	3.7E-04	1.00	1.00	1.00
1389210_at	lymphocyte cytosolic protein 1	Lcp1	306071	1.36	8.34	2.3E-01	1.1E-04	1.00	1.00	1.00
1369029_at	phospholipid scramblase 1	Plaer1	117540	1.76	8.18	5.9E-01	1.4E-04	0.80	0.25	1.00
1388340_at	Protocadherin beta 21 (predicted)	Pcdhb21_predicted	24189	1.78	8.15	6.6E-01	1.4E-04	0.80	0.50	1.00
1398540_at	regulator of G-protein signaling 1	Rgs1	54289	0.47	8.13	5.9E-01	7.1E-03	0.00	0.00	1.00
1375010_at	CD68 antigen	Cd68	287435	0.95	8.12	9.5E-01	4.9E-04	0.00	0.00	1.00
1398390_at	similar to Small inducible cytokine B13 precursor	L0C498335	498335	1.10	8.12	9.0E-01	1.2E-03	0.60	0.75	1.00
1372665_at	phosphoserine aminotransferase 1	Psat1	293820	1.10	8.03	9.7E-01	1.5E-02	0.00	0.00	1.00
1376296_at	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1	Pik3r1	25513	0.64	7.97	5.7E-01	3.0E-02	0.00	0.00	0.90
1398449_at	Protein tyrosine phosphatase, non-receptor type 7	Ptpn7	246781	0.88	7.96	9.2E-01	3.2E-04	0.00	0.00	1.00
1372321_at	lymphoblastic leukemia derived sequence 1	Ly11	304663	1.00	7.92	1.0E+00	2.5E-03	0.00	0.00	0.50
1369166_at	matrix metalloproteinase 9	Mmp9	81687	0.47	7.90	4.7E-01	7.8E-03	0.00	0.00	0.50
1377034_at	serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpinh1a	291091	1.66	7.89	1.8E-01	6.3E-05	0.00	0.00	1.00
1368332_at	guanylate nucleotide binding protein 2	Gbp2	171164	1.35	7.88	5.1E-01	3.3E-04	1.00	1.00	1.00
1374469_at	Similar to C20orf118 (predicted)	RGD1561343_predicted	502689	1.40	7.84	7.7E-01	2.9E-03	0.10	0.80	1.00
1367998_at	secretory leukocyte peptidase inhibitor	Slepi	296356	1.03	7.82	9.6E-01	2.2E-04	0.80	0.00	1.00
1390141_at	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (predicted)	Mthfd1l_predicted	361472	1.55	7.74	8.1E-01	5.7E-03	0.00	0.00	1.00
1368693_at	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	Fgr	79113	1.41	7.74	2.4E-01	1.5E-04	0.60	0.00	1.00
1370987_at	sialophorin	Spn	24796	2.36	7.62	4.8E-01	2.8E-03	0.10	0.00	1.00
1371210_s_at	RT1 class II, locus Aw2	RT1-Aw2	24737	3.69	7.59	2.0E-01	4.0E-03	0.80	0.00	0.38
1368487_at	serine (or cysteine) proteinase inhibitor, clade B, member 2	Serpinh2	60325	0.97	7.56	9.9E-01	8.3E-03	0.00	0.00	0.80
1388809_at	sphingomyelin phosphodiesterase, acid-like 3A	Smpd3a	294422	0.85	7.54	5.3E-01	1.4E-03	1.00	1.00	1.00
1388673_at	BCL2-like 12 (proline rich) (predicted)	Bcl2l12_predicted	361567	1.58	7.45	5.7E-01	4.9E-04	0.00	0.00	0.50
1370400_at	Cullin 2 (predicted)	Cul2_predicted	361258	1.15	7.37	9.5E-01	4.5E-03	0.00	0.00	1.00
1398256_at	interleukin 1 beta	Il1b	24494	0.90	7.36	9.3E-01	1.7E-04	0.40	0.25	1.00
1368006_at	lysosomal-associated protein transmembrane 5	Laptm5	89783	1.28	7.36	4.7E-01	1.7E-04	1.00	1.00	1.00
1388740_at	similar to cDNA sequence BC032204 (predicted)	RGD1310168_predicted	399186	1.14	7.35	9.5E-01	4.5E-04	0.00	0.00	1.00
1388924_at	angiotensin-like 4	Angptl4	362850	0.74	7.33	7.5E-01	3.7E-04	0.10	0.00	1.00
1371360_at	N-nuc downstream regulated gene 1	Ndrg1	299923	1.10	7.32	8.2E-01	2.0E-04	1.00	0.88	1.00
1371239_s_at	tropomyosin 3, gamma	Tpm3	117557	1.11	7.31	7.4E-01	8.6E-04	1.00	1.00	1.00
1390687_at	pleckstrin	Plek	364206	1.66	7.30	6.2E-01	5.4E-04	0.00	0.00	1.00
1376327_at	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	Tnfrsf14	366518	1.65	7.30	6.0E-01	5.1E-03	0.00	0.00	1.00
1398246_s_at	Fc receptor, IgG, low affinity III	Fcgr3	116591	1.10	7.30	6.8E-01	1.4E-03	1.00	1.00	1.00
1377064_at	dual specificity phosphatase 6	Dusp6	116663	0.98	7.29	9.7E-01	2.9E-04	1.00	0.50	1.00
1376255_at	mitogen activated protein kinase kinase kinase 1 (predicted)	Map4k1_predicted	292763	1.07	7.27	9.6E-01	5.0E-03	0.00	0.00	1.00

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call				
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isoraft	Native BN	Native DA	Allograft	Isoraft	
1387568_at	paired-Ig-like receptor B	Pirb	65146	1.05	7.21	9.7E-01	7.1E-04	0.00	0.00	1.00	0.25
1367786_at	proteasome (prosome, macropain) subunit, beta type 8	Psmh8	24968	1.34	7.18	3.5E-01	6.9E-04	1.00	1.00	1.00	1.00
1374976_a_at	Sterol O-acyltransferase 1	Soat1	81782	1.27	7.14	5.9E-01	1.0E-03	0.30	0.38	1.00	1.00
1369427_at	macrophage expressed gene 1	Mpeg1	64552	1.45	7.13	8.4E-01	1.2E-02	0.00	0.00	1.00	0.00
1378140_at	ADP-ribosylation factor-like 11	Ar11	364396	1.04	7.10	9.4E-01	4.3E-04	1.00	1.00	1.00	1.00
1369499_at	thymidylate synthase	Tyms	29261	0.75	7.08	8.7E-01	3.0E-03	0.00	0.00	0.80	0.00
1389696_at	Transcribed locus			2.11	7.05	5.0E-01	6.4E-04	0.00	0.00	1.00	0.25
1371033_at	RT1 class II, locus Bb	RT1-Bb	309622	0.92	7.02	8.4E-01	2.2E-04	1.00	1.00	1.00	1.00
1391505_x_at	Transcribed locus			0.76	6.93	6.7E-01	4.9E-04	0.20	0.75	1.00	1.00
1370463_x_at	RT1 class I, CEI6	RT1-CEI6	414819	2.61	6.90	2.2E-01	2.4E-03	1.00	0.00	1.00	0.75
1388054_a_at	chondroitin sulfate proteoglycan 2	Cspg2	114122	1.86	6.81	5.9E-01	2.7E-03	0.00	0.25	1.00	0.75
1388940_at	similar to Rho-GTPase-activating protein 25 (predicted)	RGD1562105_predicted	500246	0.28	6.81	1.3E-01	3.8E-03	0.00	0.00	1.00	0.00
1376652_at	complement component 1, q subcomponent, alpha polypeptide	C1qa	298566	1.19	6.80	5.7E-01	1.5E-04	1.00	1.00	1.00	1.00
1370215_at	complement component 1, q subcomponent, beta polypeptide	C1qb	29687	1.40	6.78	4.4E-01	1.5E-04	1.00	1.00	1.00	1.00
1374794_at	kinesin family member 15	Kif15	353302	0.65	6.77	6.4E-01	1.0E-02	0.00	0.00	1.00	0.00
1372685_at	cyclin-dependent kinase inhibitor 3 (predicted)	Cdkn3_predicted	289993	0.31	6.76	3.9E-01	9.6E-04	0.00	0.00	1.00	0.25
1373544_at	chemokine (C-X-C motif) ligand 9	Cxcl9	246759	1.27	6.76	5.0E-01	1.1E-03	1.00	1.00	1.00	1.00
1386494_at	S100 calcium binding protein A8 (calgranulin A)	S100a8	116547	1.11	6.71	9.4E-01	9.5E-03	0.70	0.50	1.00	0.50
1379497_at	Transcribed locus			0.85	6.69	4.5E-01	4.5E-04	0.10	0.25	1.00	0.88
1367942_at	acid phosphatase 5, tartrate resistant	Acp5	25732	1.16	6.67	8.3E-01	7.9E-04	0.00	0.00	1.00	0.63
1369953_a_at	CD24 antigen	Cd24	25145	1.89	6.67	4.9E-01	9.1E-03	0.30	0.00	0.80	0.00
1389408_at	ribonucleotide reductase M2 (mapped)	Rrm2	362720	0.89	6.65	9.2E-01	4.7E-04	0.30	0.00	1.00	0.50
1387831_at	Inhibitor of Bruton agammaglobulinemia tyrosine kinase (predicted)	Ibtk_predicted	315858	0.64	6.58	5.2E-01	1.9E-02	0.00	0.00	0.60	0.00
1367850_at	Fc receptor, IgG, low affinity III	Fcgr3	116591	1.11	6.55	7.8E-01	5.9E-04	1.00	1.00	1.00	1.00
1387687_at	immunoglobulin superfamily, member 6	Igsf6	171064	1.12	6.53	8.4E-01	4.0E-04	0.40	0.00	1.00	0.75
1389409_at	similar to Testis derived transcript	LOC500040	500040	1.64	6.50	7.9E-01	3.0E-04	0.00	0.00	1.00	0.00
1387627_at	cd86 antigen	Cd86	56822	0.76	6.42	8.2E-01	1.7E-03	0.00	0.00	0.80	0.00
1369190_at	CD2 antigen	Cd2	497761	1.32	6.42	5.8E-01	1.9E-03	0.00	0.00	0.70	0.00
1376130_a_at	dystrobrevin, beta	Dnb	362715	1.34	6.38	8.1E-01	2.2E-04	0.00	0.00	1.00	0.00
1387005_at	cathepsin S	Cts5	50654	0.88	6.37	5.5E-01	1.9E-04	1.00	1.00	1.00	1.00
1370394_at	gamma-2a immunoglobulin heavy chain	IgG-2a	367586	0.78	6.36	7.7E-01	9.0E-03	0.00	0.00	0.60	0.00
1376304_at	Transcribed locus			1.09	6.36	9.7E-01	2.0E-02	0.00	0.00	0.70	0.00
1388484_at	ubiquitin-conjugating enzyme E2C (predicted)	Ube2c_predicted	296368	0.79	6.31	6.0E-01	3.7E-04	0.00	0.25	1.00	0.50
1370281_at	fatty acid binding protein 5, epidermal	Fabp5	140868	0.95	6.31	8.6E-01	1.6E-04	1.00	1.00	1.00	1.00
1389553_at	dendritic cell inhibitory receptor 3	Dcir3	362431	0.99	6.30	9.9E-01	1.5E-03	0.50	0.50	1.00	1.00
1374902_at	IQ motif containing GTPase activating protein 3 (predicted)	Iqgap3_predicted	310621	0.88	6.28	8.6E-01	3.3E-03	0.00	0.00	1.00	0.00
1370265_at	arrestin, beta 2	Arrb2	25388	1.23	6.19	8.6E-01	8.1E-04	0.00	0.00	1.00	0.25
1390287_at	bridging integrator 2	Bin2	366988	0.89	6.14	9.3E-01	6.4E-04	0.00	0.00	1.00	0.63
1386859_at	transketolase	Tkt	64524	1.05	6.13	9.3E-01	1.4E-04	1.00	1.00	1.00	1.00
1387378_at	ficolin B	Fcnb	114091	2.26	6.11	2.2E-01	2.9E-03	0.00	0.00	1.00	0.00
1390798_at	protein tyrosine phosphatase, receptor type, C	Ptpcr	24699	1.50	6.09	1.2E-01	4.2E-04	0.80	0.75	1.00	1.00
1377351_at	sushi domain containing 3 (predicted)	Susd3_predicted	306810	0.73	6.04	8.5E-01	1.6E-03	0.00	0.00	1.00	0.00
1371960_at	YTH domain family 2 (predicted)	Ythdf2_predicted	313053	7.13	6.04	1.2E-01	1.1E-03	1.00	0.25	1.00	1.00
1387269_s_at	plasminogen activator, urokinase receptor	Plaur	50692	1.10	6.04	9.3E-01	3.7E-04	0.00	0.00	1.00	0.00
1387992_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Lilrb3	361493	2.28	6.02	5.2E-02	1.8E-03	0.40	0.13	0.80	0.00
1377239_at	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	Apbb1ip	307171	2.35	6.01	4.8E-01	3.7E-04	0.30	0.00	1.00	0.63
1370928_at	LPS-induced TN factor	Ltaif	65161	1.58	5.99	1.1E-01	1.6E-04	1.00	1.00	1.00	1.00
1368247_at	heat shock 70kD protein 1A	Hspa1a	24472	1.07	5.98	7.8E-01	3.7E-04	0.80	0.88	1.00	1.00
1374961_at	similar to polyamine-modulated factor 1	LOC681050	681050	0.77	5.97	5.8E-01	2.5E-03	0.00	0.00	0.50	0.00
1387608_at	indoleamine-pyrrole 2,3 dioxygenase	Indo	66029	0.74	5.95	7.0E-01	3.8E-02	0.00	0.00	0.80	0.00
1370848_at	solute carrier family 2 (facilitated glucose transporter), member 1	Slc2a1	24778	0.65	5.93	1.5E-01	5.2E-04	0.60	1.00	1.00	1.00
1388337_at	nucleoside phosphorylase (mapped)	Np	290029	1.14	5.93	5.8E-01	6.1E-04	1.00	1.00	1.00	1.00
1387984_at	chemokine-like factor	Klif	245978	1.63	5.92	7.4E-01	1.6E-02	0.00	0.00	1.00	0.00
1369688_s_at	protein tyrosine kinase 2 beta	Ptk2b	50646	1.37	5.91	7.4E-01	1.6E-03	0.00	0.00	1.00	0.00
1371016_at	similar to RIKEN cDNA A430107P09 gene	LOC290071	290071	0.98	5.89	9.8E-01	1.3E-03	1.00	1.00	1.00	1.00
1389092_at	interleukin 2 receptor, gamma (severe combined immunodeficiency)	Il2rg	140924	1.17	5.87	5.5E-01	1.4E-04	1.00	1.00	1.00	1.00
1373528_at		Hck	25734	1.05	5.87	9.5E-01	4.8E-03	0.00	0.00	0.70	0.00
1371074_a_at	minichromosome maintenance deficient 6 (MISS homolog, S. pombe) (S. cerevisiae)	Mcm6	29685	1.84	5.85	6.7E-01	1.1E-03	0.00	0.00	0.80	0.00
1373611_at	interleukin 17 receptor (predicted)	Il17r_predicted	312679	1.82	5.83	2.2E-01	5.2E-05	1.00	0.75	1.00	1.00
1389911_at	meteorin, glial cell differentiation regulator-like	Metnl	316842	0.89	5.83	4.1E-01	7.2E-04	1.00	1.00	1.00	1.00
1390137_at	TRAF4 associated factor 1	Traf4af1	311325	0.92	5.82	9.5E-01	4.2E-03	0.00	0.00	0.50	0.00
1371774_at	spermidine/spermine N1-acetyl transferase (mapped)	Sat	302642	1.32	5.82	2.9E-01	1.7E-04	1.00	1.00	1.00	1.00
1392785_at	Potassium channel tetramerisation domain containing 12 (predicted)	Kctd12_predicted	364458	3.12	5.80	1.6E-01	3.4E-03	0.50	0.00	1.00	0.75
1369186_at	caspase 1	Casp1	25166	1.14	5.80	7.7E-01	6.9E-04	1.00	0.75	1.00	1.00
1376709_at	solute carrier family 39 (metal ion transporter), member 8	Slc39a8	295455	1.69	5.76	1.2E-01	1.6E-04	1.00	0.50	1.00	1.00
1389248_at	galactokinase 1	Galk1	287835	0.82	5.73	5.7E-01	2.4E-03	0.00	0.00	0.80	0.00
1373490_at	Similar to chromosome 14 open reading frame 21 (predicted)	RGD1308396_predicted	290235	1.18	5.72	4.9E-01	3.0E-04	0.90	0.88	1.00	1.00
1389566_at	cyclin B2	Ccnb2	363088	0.93	5.71	9.3E-01	1.2E-03	0.00	0.00	1.00	0.00
1376089_at	Low density lipoprotein receptor-related protein 5 (predicted)	Lrp5_predicted	293649	1.70	5.70	1.2E-01	1.2E-03	0.50	0.00	1.00	1.00
1369204_at	hemopoietic cell kinase	Hck	25734	1.21	5.69	2.8E-01	6.4E-04	1.00	1.00	1.00	1.00
1374805_at	similar to hypothetical protein MGC5528 (predicted)	RGD1561749_predicted	299933	0.76	5.67	7.3E-01	1.2E-02	0.20	0.25	0.80	0.00
1376073_at	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	Sel1h	314352	2.25	5.66	4.2E-01	6.5E-03	0.00	0.00	1.00	0.00
1376026_at	downstream neighbor of SON	Donson	288257	0.67	5.65	4.6E-01	4.8E-02	0.00	0.00	1.00	0.00
1384787_at	CD3 antigen, gamma polypeptide	Cd3g	300678	1.39	5.65	7.6E-01	2.5E-03	0.00	0.00	1.00	0.00
1369724_at	coagulation factor XIII, A1 subunit	F13a1	60327	1.33	5.64	7.0E-01	1.1E-03	0.70	0.25	1.00	0.63
1389030_a_at	Rous sarcoma oncogene	Src	83805	1.42	5.62	8.6E-01	1.7E-02	0.00	0.00	0.70	0.00
1370603_a_at	protein tyrosine phosphatase, receptor type, C	Ptpcr	24699	0.86	5.62	9.0E-01	2.0E-02	0.00	0.00	1.00	0.00

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1377058_at	similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 2 (predicted)	RGD1564160_predicted	500973	0.36	5.60	5.0E-01	2.8E-03	0.00	0.00	1.00	0.00
1376076_at	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (predicted)	Mpp5_predicted	314259	0.96	5.56	9.1E-01	2.8E-04	1.00	0.75	1.00	1.00
1387759_s_at	UDP glycosyltransferase 1 family, polypeptide A1	Ugt1a1	113992	1.61	5.56	1.4E-01	7.9E-04	0.60	0.00	1.00	0.75
1398303_s_at	tropomyosin 3, gamma	Tpm3	117557	1.55	5.54	1.6E-01	3.1E-03	0.70	0.00	1.00	1.00
1370469_at	protein tyrosine phosphatase, non-receptor type 7	Ptpn7	246781	0.92	5.53	9.6E-01	9.6E-03	0.00	0.00	0.90	0.00
1373746_at	similar to HSPC049 protein (predicted)	RGD1306697_predicted	312225	0.53	5.53	6.8E-01	7.9E-04	0.20	0.00	1.00	0.00
1389695_at	similar to cDNA sequence BC040444	RGD1311980	304334	1.01	5.53	9.9E-01	1.1E-04	0.20	0.25	1.00	1.00
1377185_at	similar to RIKEN cDNA 6330442E10 gene (predicted)	RGD1562622_predicted	503035	0.86	5.52	7.9E-01	9.7E-03	0.00	0.00	0.70	0.00
1370024_at	Similar to RIKEN cDNA 4931400A14 (predicted)	RGD1307234_predicted	316732	0.96	5.52	9.9E-01	4.8E-02	0.00	0.00	1.00	0.00
1376231_at	similar to Hypothetical UPF0080 protein KIAA0186 (predicted)	RGD1562246_predicted	499914	1.43	5.51	7.9E-01	1.4E-02	0.00	0.00	0.50	0.00
1377023_at	dual specificity phosphatase 2	Dusp2	311406	1.15	5.49	7.7E-01	2.5E-04	0.50	0.63	1.00	0.38
1387742_at	chemokine (C-C motif) receptor 2	Ccr2	60463	1.13	5.49	9.1E-01	8.2E-03	0.00	0.00	0.60	0.00
1388272_at	immunoglobulin heavy chain 1a (serum IgG2a)	Igh-1a	299352	1.09	5.47	9.6E-01	1.1E-02	0.00	0.00	0.80	0.00
1369815_at	chemokine (C-C motif) ligand 3	Ccl3	25542	0.84	5.47	8.5E-01	3.7E-04	0.00	0.00	1.00	0.38
1375428_at	cellular repressor of E1A-stimulated genes (predicted)	Creg_predicted	289185	1.61	5.45	3.8E-01	4.3E-04	1.00	0.75	1.00	0.38
1367955_at	RAB4B, member RAS oncogene family	Rab4b	50866	1.61	5.44	4.8E-01	1.5E-02	0.00	0.00	0.60	0.00
1370234_at	fibronectin 1	Fn1	25661	1.65	5.41	2.5E-01	1.5E-03	1.00	1.00	1.00	1.00
1387180_at	interleukin 1 receptor, type II	Il1r2	117022	1.63	5.39	6.3E-01	5.6E-02	0.20	0.00	1.00	0.00
1386879_at	lectin, galactose binding, soluble 3	Lgals3	83781	1.24	5.39	6.5E-01	4.1E-04	1.00	1.00	1.00	1.00
1370942_at	RAS p21 protein activator 3	Rasa3	29372	2.06	5.37	5.4E-01	1.0E-02	0.00	0.00	1.00	1.00
1370883_at	RTI class II, locus Da	RT1-Da	294269	0.89	5.34	6.9E-01	4.3E-04	1.00	1.00	1.00	1.00
1368527_at	prostaglandin-endoperoxide synthase 2	Ptgs2	29527	0.73	5.34	8.5E-01	1.2E-02	0.10	0.13	1.00	0.75
1369181_at	cytochrome b-245, beta polypeptide	Cybb	66021	1.01	5.33	9.9E-01	7.1E-04	0.20	0.25	1.00	0.50
1383426_at	proline-serine-threonine phosphatase-interacting protein 1 (predicted)	Pstpip1_predicted	300732	1.11	5.33	7.6E-01	4.4E-05	0.60	0.75	1.00	0.88
1369683_at	BH3 interacting domain death agonist	Bid	64625	2.09	5.33	4.5E-01	3.3E-02	0.00	0.00	0.80	0.00
1388265_x_at	chondroitin sulfate proteoglycan 2	Cspg2	114122	0.64	5.30	6.1E-01	1.5E-02	0.00	0.00	1.00	0.13
1387101_at	acyl-CoA synthetase long-chain family member 4	Acsl4	113976	1.16	5.27	3.6E-01	2.4E-04	1.00	1.00	1.00	1.00
1368742_at	complement component 5, receptor 1	C5r1	113959	1.15	5.27	6.7E-01	3.2E-04	1.00	1.00	1.00	1.00
1367856_at	glucose-6-phosphate dehydrogenase X-linked	G6pdx	24377	2.20	5.26	3.3E-01	4.4E-05	1.00	0.25	1.00	1.00
1370967_at	Claudin 10 (predicted)	Cldn10_predicted	290485	2.07	5.25	5.5E-01	1.3E-02	0.00	0.00	1.00	0.50
1368260_at	aurora kinase B	Aurkb	114592	1.14	5.24	8.8E-01	6.3E-04	0.60	0.00	1.00	0.50
1368407_at	heparinase	Hpsa	64537	3.26	5.23	4.1E-01	2.0E-02	0.00	0.00	1.00	0.00
1370832_at	Alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	246284	0.84	5.22	4.7E-01	9.9E-04	1.00	1.00	1.00	1.00
1389123_at	chemokine (C-C motif) ligand 6	Ccl6	287910	1.73	5.22	2.7E-01	8.9E-04	1.00	1.00	1.00	1.00
1387969_at	chemokine (C-X-C motif) ligand 10	Cxcl10	245920	1.54	5.21	4.7E-02	9.4E-03	0.80	0.13	1.00	0.75
1370585_a_at	protein kinase C, beta 1	Prkcb1	25023	1.32	5.20	5.4E-01	4.6E-04	1.00	1.00	1.00	1.00
1379766_at	Src-like adaptor	Sla	338477	1.59	5.14	6.7E-01	3.0E-04	0.00	0.00	1.00	0.63
1390659_at	Transcribed locus			1.43	5.13	3.8E-01	1.5E-04	1.00	1.00	1.00	1.00
1390389_at	C-mer proto-oncogene tyrosine kinase	Merik	65037	0.92	5.10	9.1E-01	9.7E-04	0.00	0.00	1.00	0.00
1390674_at	Transcribed locus			0.56	5.08	3.7E-01	1.3E-02	0.00	0.00	0.60	0.00
1372200_at	G-protein signalling modulator 3 (AGS3-like, C. elegans)	Gpsm3	406163	1.05	5.08	9.8E-01	1.3E-03	0.00	0.00	1.00	0.25
1389413_at	similar to ecotropic viral integration site 2A	LOC685433	685433	0.67	5.06	5.0E-01	2.0E-04	0.00	0.00	1.00	0.50
1389006_at	Transcribed locus			1.38	5.03	4.9E-01	7.9E-04	0.70	0.00	1.00	1.00
1368921_a_at	CD44 antigen	Cd44	25406	1.33	5.02	6.4E-01	1.2E-04	0.80	0.38	1.00	1.00
1388142_at	chondroitin sulfate proteoglycan 2	Cspg2	114122	1.13	5.01	8.6E-01	6.7E-03	0.40	0.25	1.00	0.75
1369672_at	archidonate 5-lipoxygenase activating protein	Alox5ap	29624	1.18	4.99	7.6E-01	1.1E-03	1.00	0.38	1.00	1.00
1368027_at	thromboxane A synthase 1	Tbxas1	24886	0.99	4.99	9.8E-01	1.3E-04	0.00	0.13	1.00	0.88
1370186_at	proteasome (prosome, macropain) subunit, beta type 9	Psmb9	24967	0.92	4.97	7.7E-01	1.3E-03	1.00	1.00	1.00	1.00
1377867_at	similar to Glutaminy-peptide cyclotransferase precursor (QC) (predicted)	RGD1562284_predicted	313837	0.64	4.97	2.9E-01	7.8E-04	0.20	0.88	1.00	0.88
1368000_at	complement component 3	C3	24232	1.53	4.95	3.6E-01	2.9E-03	1.00	0.88	1.00	1.00
1368412_a_at	protein tyrosine phosphatase, receptor type, O	Ptpro	50677	0.77	4.93	4.6E-01	9.9E-04	0.00	0.00	1.00	1.00
1368179_at	thymic stromal-derived lymphopoietin, receptor	Tslpr	171499	1.64	4.92	6.2E-01	5.7E-03	0.00	0.00	1.00	0.00
1376675_at	similar to CD300A antigen	LOC501736	501736	0.97	4.92	9.6E-01	9.8E-04	0.00	0.00	1.00	0.75
1370097_a_at	chemokine (C-X-C motif) receptor 4	Cxcr4	60628	1.43	4.92	3.0E-01	6.5E-04	1.00	0.75	1.00	1.00
1368799_at	baculoviral IAP repeat-containing 5	Birc5	64041	1.28	4.91	8.4E-01	1.5E-02	0.00	0.00	0.60	0.00
1368046_at	solute carrier family 31 (copper transporters), member 1	Slc31a1	171135	2.87	4.90	2.9E-01	3.3E-02	0.00	0.00	0.60	0.00
1389440_at	Transcribed locus			1.03	4.88	9.9E-01	4.3E-03	0.00	0.00	0.90	0.00
1369031_at	interleukin 18 binding protein	Il18bp	84388	0.83	4.87	4.3E-01	1.3E-03	0.90	1.00	1.00	1.00
1388650_at	topoisomerase (DNA) 2 alpha	Top2a	360243	1.01	4.87	9.9E-01	2.4E-03	0.00	0.00	1.00	0.50
1371961_at	phospholipase D family, member 3	Pld3	361527	1.04	4.87	9.4E-01	1.7E-03	0.80	0.63	1.00	1.00
1387952_a_at	CD44 antigen	Cd44	25406	2.43	4.85	1.1E-01	2.4E-03	0.00	0.00	1.00	0.50
1373207_at	Transcribed locus			0.63	4.83	4.5E-01	7.2E-04	0.00	0.25	1.00	1.00
1387956_s_at	chemokine-like factor	Klfl	245978	0.90	4.81	9.5E-01	1.6E-02	0.00	0.00	0.80	0.00
1376914_at	DEP domain containing 1a (predicted)	Depdc1a_predicted	295538	0.87	4.81	9.2E-01	7.5E-02	0.00	0.00	0.70	0.00
1379387_at	Regulator of G-protein signaling 18	Rgs18	289076	1.07	4.77	9.6E-01	7.2E-03	0.00	0.00	1.00	0.50
1376784_at	Formin binding protein 1	Fnbp1	192348	1.89	4.76	5.9E-01	1.3E-02	0.00	0.00	0.90	0.00
1372064_at	similar to chemokine (C-X-C motif) ligand 16	Cxcl16	497942	0.94	4.75	8.7E-01	3.3E-04	1.00	1.00	1.00	1.00
1393688_at	Complement component 6	C6	24237	1.22	4.75	9.0E-01	4.2E-04	0.00	0.00	1.00	0.25
1370339_at				0.89	4.75	4.2E-01	2.0E-04	1.00	1.00	1.00	1.00
1370740_at	killer cell lectin-like receptor, subfamily A, member 5	Klra5	297666	1.10	4.75	9.7E-01	1.4E-02	0.00	0.00	1.00	0.13
1376943_at				1.09	4.73	8.6E-01	4.8E-04	0.90	0.50	1.00	0.75
1387808_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Slc7a7	83509	1.20	4.72	5.8E-01	3.7E-04	1.00	1.00	1.00	1.00
1388460_at	capping protein (actin filament), gelsolin-like	Capg	297339	0.98	4.72	9.5E-01	2.8E-04	1.00	1.00	1.00	1.00
1373504_at	GL1 pathogenesis-related 1 (glioma)	Glipr1	299783	1.06	4.71	7.9E-01	5.1E-04	1.00	1.00	1.00	1.00
1374544_at	hypothetical protein LOC679150	LOC679150	679150	1.29	4.71	4.8E-01	1.2E-04	0.00	0.00	1.00	0.63
1387048_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	Ddx39	89827	1.03	4.70	9.4E-01	6.4E-04	0.80	0.38	1.00	1.00
1388149_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	Tap1	24811	1.66	4.70	6.7E-01	4.4E-04	0.00	0.00	1.00	0.00

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call				
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Iso graft	Native BN	Native DA	Allograft	Iso graft	
1368207_at	FXVD domain-containing ion transport regulator 5	Fxyd5	60338	1.27	4.69	5.7E-01	4.1E-04	1.00	0.75	1.00	1.00
1387834_at	megakaryocyte-associated tyrosine kinase	Matk	60450	1.39	4.69	8.6E-01	1.4E-02	0.00	0.00	1.00	0.00
1373575_at	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	LOC498279	498279	1.31	4.69	1.5E-01	5.5E-04	1.00	1.00	1.00	1.00
1368808_at	CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	64185	1.67	4.69	1.3E-01	1.3E-03	1.00	0.50	1.00	1.00
1368975_at	CD38 antigen	Cd38	25668	0.90	4.68	8.8E-01	8.4E-04	0.00	0.50	1.00	0.75
1368826_at	catechol-O-methyltransferase	Comt	24267	0.95	4.68	7.9E-01	3.9E-04	1.00	1.00	1.00	1.00
1368464_at	macrophage galactose N-acetyl-galactosamine specific lectin 1	Mgl1	64195	0.92	4.67	8.8E-01	1.4E-03	0.00	0.00	1.00	1.00
1375211_at	ribonuclease T2 (predicted)	Rnaset2_predicted	292306	1.02	4.67	9.6E-01	2.8E-04	1.00	1.00	1.00	1.00
1373823_at	similar to Cyclin-dependent kinases regulatory subunit 2 (CKS-2) (predicted)	RGD1562047_predicted	498709	1.45	4.67	8.2E-01	3.0E-03	0.00	0.00	1.00	0.38
1371803_at	GM2 ganglioside activator protein	Gm2a	282838	1.07	4.65	9.2E-01	5.3E-04	0.90	0.63	1.00	1.00
1390850_at	Adipose differentiation related protein	Adfp	298199	2.43	4.65	4.9E-01	4.4E-04	0.00	0.00	1.00	0.00
1372082_at	NECAP endocytosis associated 2	Necap2	298598	1.03	4.65	9.7E-01	2.5E-04	1.00	1.00	1.00	1.00
1388848_at	similar to hypothetical protein MGC13251	RGD1308350	362790	0.80	4.64	5.5E-01	3.7E-03	0.00	0.00	1.00	0.00
1369173_at	complement component 3a receptor 1	C3ar1	84007	1.78	4.63	6.2E-01	6.5E-04	1.00	0.25	1.00	0.63
1372852_at	similar to protein tyrosine phosphatase, receptor type, C polypeptide-associated protein	LOC499300	499300	0.69	4.63	7.4E-01	1.5E-03	0.00	0.00	1.00	0.25
1371184_x_at	tropomyosin 3, gamma	Tpm3	117557	0.79	4.62	7.3E-01	5.6E-03	1.00	0.75	1.00	1.00
1370393_at	coiled-coil domain containing 5	Ccdc5	192228	1.88	4.60	6.6E-01	1.2E-02	0.00	0.00	0.70	0.00
1377153_a_at	kelch-like 6 (Drosophila) (predicted)	Klhl6_predicted	287974	1.38	4.60	4.3E-01	4.6E-04	1.00	0.75	1.00	1.00
1371782_at	nipsnap homolog 3A (C. elegans)	Nipsnap3a	313211	0.75	4.60	7.6E-01	2.7E-04	0.00	0.00	1.00	0.75
1389997_at	CD3 antigen, epsilon polypeptide (predicted)	Cd3e_predicted	315609	0.76	4.60	7.7E-01	1.3E-03	0.00	0.00	1.00	0.00
1387202_at	intercellular adhesion molecule 1	Icam1	25464	1.82	4.58	4.3E-01	5.7E-03	0.00	0.00	1.00	0.25
1368455_at	natural killer cell group 7 sequence	Nkg7	171062	1.20	4.58	6.8E-01	3.6E-03	0.80	0.75	1.00	1.00
1371646_at	phosphogluconate dehydrogenase (mapped)	Pgd	362660	1.11	4.57	8.0E-01	3.0E-04	1.00	1.00	1.00	1.00
1388275_at	T-cell receptor beta chain	Terb	24820	1.12	4.57	9.5E-01	1.7E-03	0.00	0.13	1.00	0.50
1369814_at	chemokine (C-C motif) ligand 20	Ccl20	29538	1.07	4.55	9.5E-01	1.1E-02	0.20	0.00	1.00	0.00
1376006_at	Transcribed locus			1.06	4.53	8.5E-01	2.2E-04	0.60	0.13	1.00	1.00
1377340_at	tissue factor pathway inhibitor 2	Tfpi2	286926	1.29	4.52	6.2E-01	1.7E-03	1.00	0.75	1.00	1.00
1383684_at	ASF1 anti-silencing function 1 homolog B (S. cerevisiae) (predicted)	Asf1b_predicted	304648	1.10	4.51	9.2E-01	1.2E-03	0.20	0.25	1.00	0.50
1372516_at	kinesin family member 22	Kif22	293502	1.36	4.51	5.4E-01	3.6E-04	0.00	0.00	1.00	0.00
1387667_at	nitric oxide synthase 2, inducible	Nos2	24599	1.15	4.50	8.9E-01	3.6E-03	0.00	0.13	1.00	0.00
1377832_at	polo-like kinase 4 (Drosophila) (predicted)	Plk4_predicted	310344	0.52	4.50	4.3E-01	3.6E-03	0.20	1.00	1.00	0.25
1390325_at	CD38 antigen	Cd38	25668	0.88	4.49	4.3E-01	1.4E-04	1.00	1.00	1.00	1.00
1387483_at	phospholipase C, gamma 2	Plcg2	29337	1.09	4.48	9.6E-01	1.7E-02	0.00	0.00	0.70	0.00
1368679_a_at	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	Lyn	81515	1.13	4.48	8.1E-01	8.5E-04	1.00	1.00	1.00	1.00
1368187_at	glycoprotein (transmembrane) nmh	Gpnmh	113955	1.77	4.46	2.2E-01	7.4E-03	1.00	0.00	1.00	1.00
1370912_at	heat shock 70kD protein 1B (mapped)	Hspa1b	294254	1.45	4.46	1.1E-01	2.8E-04	1.00	1.00	1.00	1.00
1368258_at	apelin, AGTRL1 ligand	Apln	58812	0.78	4.45	5.4E-01	3.7E-04	1.00	1.00	1.00	0.63
1386925_at	actin related protein 2/3 complex, subunit 1B	Arpc1b	54227	1.43	4.45	8.1E-02	1.3E-04	1.00	1.00	1.00	1.00
1368379_at	scavenger receptor class B, member 2	Scarb2	117106	0.72	4.45	3.5E-01	5.1E-04	0.40	0.63	1.00	1.00
1387154_at	neuropeptide Y	Npy	24604	0.67	4.43	1.9E-01	1.8E-03	1.00	1.00	1.00	1.00
1372585_at	RGD1566254 (predicted)	RGD1566254_predicted	499318	1.17	4.42	6.3E-01	1.0E-03	1.00	1.00	1.00	1.00
1367905_at	ectonucleotide pyrophosphatase/phosphodiesterase 3	Enpp3	54410	1.83	4.39	8.7E-02	3.8E-04	1.00	0.75	1.00	1.00
1367632_at	glutamate-ammonia ligase (glutamine synthase)	Glul	24957	1.49	4.36	2.7E-01	1.3E-04	1.00	1.00	1.00	1.00
1368010_at	protein tyrosine phosphatase, non-receptor type 6	Ptpn6	116689	0.98	4.36	9.3E-01	4.8E-04	0.00	0.25	1.00	1.00
1367676_at	high mobility group box 2	Hmgb2	29395	1.47	4.35	1.9E-01	6.3E-04	1.00	1.00	1.00	1.00
1387076_at	hypoxia inducible factor 1, alpha subunit	Hif1a	29560	1.02	4.35	9.6E-01	4.4E-05	1.00	1.00	1.00	1.00
1371946_at	kidney predominant protein NCU-G1	RGD1303130	295231	1.10	4.33	8.0E-01	2.7E-04	1.00	1.00	1.00	1.00
1390226_at	similar to hypothetical protein LOC340061 (predicted)	RGD1562552_predicted	498840	1.81	4.33	6.4E-01	5.4E-04	0.00	0.00	1.00	0.00
1369979_at	src family associated phosphoprotein 2	Scap2	155183	1.26	4.32	6.0E-01	2.7E-03	0.00	0.00	1.00	0.50
1367776_at	cell division cycle 2 homolog A (S. pombe)	Cdc2a	54237	0.89	4.32	9.0E-01	2.8E-03	0.00	0.00	1.00	0.38
1370531_a_at	phospholipase D1	Pld1	25096	1.03	4.31	9.9E-01	1.7E-02	0.00	0.00	1.00	0.00
1374778_at	Similar to GA binding protein transcription factor, beta subunit 2 (GABPB2) (predicted)	RGD1560391_predicted	499883	1.28	4.29	5.4E-01	2.2E-04	1.00	1.00	1.00	1.00
1367633_at	glutamate-ammonia ligase (glutamine synthase)	Glul	24957	1.42	4.26	1.3E-01	1.5E-03	1.00	1.00	1.00	1.00
1368420_at	ceruloplasmin	Cp	24268	1.24	4.26	7.2E-01	7.6E-04	0.90	0.50	1.00	1.00
1387918_at	tropomyosin 3, gamma	Tpm3	117557	1.74	4.26	5.7E-01	3.2E-03	0.00	0.00	0.80	0.00
1388784_at	colony stimulating factor 1 receptor	Csf1r	307403	1.34	4.25	4.6E-01	1.2E-04	1.00	1.00	1.00	1.00
1373661_a_at	chemokine (C-X-C motif) receptor 4	Cxcr4	60628	1.05	4.25	9.2E-01	6.2E-04	1.00	1.00	1.00	1.00
1372890_at	Transcribed locus			0.53	4.24	1.7E-01	4.9E-04	0.00	0.00	1.00	0.25
1370177_at	poliovirus receptor	PVR	25066	1.74	4.21	3.4E-01	1.1E-03	0.30	0.00	1.00	0.00
1372056_at	CKLF-like MARVEL transmembrane domain containing 6	Cntm6	316035	1.11	4.19	7.7E-01	1.9E-04	1.00	1.00	1.00	1.00
1373850_at	sphingomyelin phosphodiesterase, acid-like 3B	Smpd3b	362619	1.20	4.19	7.9E-01	1.5E-03	0.00	0.00	0.90	0.00
1372404_at	RAS-related C3 botulinum substrate 2	Rac2	366957	1.02	4.19	9.2E-01	3.5E-03	1.00	1.00	1.00	1.00
1372478_at	similar to chemokine-like factor super family 7	LOC501065	501065	1.10	4.18	4.9E-01	5.4E-04	1.00	0.50	1.00	1.00
1376151_a_at	Similar to novel protein similar to human oligophrenin 1 (OPHN1) (predicted)	RGD1564081_predicted	500943	1.18	4.17	5.5E-01	4.6E-03	1.00	1.00	1.00	1.00
1389250_at	Transcribed locus			1.11	4.14	9.4E-01	1.9E-03	0.00	0.00	1.00	0.25
1377385_at	Rho GTPase activating protein 27	Arhgap27	303583	3.29	4.14	2.5E-01	1.1E-02	0.00	0.00	1.00	0.38
1368073_at	interferon regulatory factor 1	Irf1	24508	1.40	4.14	3.5E-01	1.2E-03	1.00	1.00	1.00	1.00
1370219_at	cytochrome b-245, alpha polypeptide	Cyba	79129	0.99	4.13	9.8E-01	1.2E-03	1.00	1.00	1.00	1.00
1372303_at	similar to 0910001 A06Rk protein (predicted)	RGD1307697_predicted	299909	0.99	4.13	9.9E-01	1.8E-03	1.00	0.88	1.00	1.00
1387057_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	Slc7a8	192117	1.46	4.12	6.5E-01	3.3E-03	0.00	0.00	0.80	0.00
1371529_at	receptor (TNFRSF)-interacting serine-threonine kinase 1 (predicted)	Ripk1_predicted	306886	1.56	4.12	7.7E-01	9.3E-04	0.00	0.00	1.00	0.25
1367677_at	peroxiredoxin 5	Prdx5	113898	0.96	4.11	9.5E-01	3.7E-04	1.00	1.00	1.00	1.00
1387354_at	signal transducer and activator of transcription 1	Stat1	25124	1.36	4.10	3.4E-01	2.2E-04	1.00	1.00	1.00	1.00
1383320_at	lymphocyte protein tyrosine kinase (mapped)	Lck	313050	0.99	4.08	9.8E-01	3.2E-04	1.00	1.00	1.00	1.00
1369387_at	vav 1 oncogene	Vav1	25156	0.87	4.07	7.8E-01	9.8E-04	1.00	0.00	1.00	0.50
1368605_at	adaptor protein with pleckstrin homology and src homology 2 domains	Aps	114203	0.86	4.07	8.2E-01	1.6E-03	0.00	0.25	1.00	0.50
1391946_at	selectin, platelet	Selp	25651	0.50	4.07	5.3E-01	2.8E-03	0.00	0.00	1.00	0.00

Probe Set ID	Gene Title	Fold Change		False Discovery Rate		Average Present Call				
		Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft	
		Entrez Gene ID	Native BN / DA	Allograft / Isograft	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1368270_at	apolipoprotein B editing complex 1	Apohec1	25383	4.06	4.8E-01	4.7E-03	0.00	0.00	1.00	0.50
1370340_x_at	tropomyosin 3, gamma	Tpm3	117557	1.36	4.04	3.7E-01	3.2E-03	0.00	0.00	1.00
1387982_at	toll-like receptor 4	Tlr4	29260	0.89	4.03	8.2E-01	5.6E-03	0.60	0.88	1.00
1374518_at	transmembrane protein 77	Tmem77	362011	1.20	4.03	2.5E-01	4.3E-04	1.00	1.00	1.00
1389732_at	Similar to CG4025-PA	LOC679937	679937	0.97	4.02	9.2E-01	6.5E-04	1.00	1.00	1.00
1374033_at	proteasome (prosome, macropain) subunit, beta type 10	Psmh10	291983	0.84	4.02	6.6E-01	3.6E-03	1.00	1.00	1.00
1368811_at	lamin B1	Lmb1	116685	0.70	4.00	8.1E-01	4.2E-04	0.00	0.00	1.00
1371040_at	solute carrier family 1 (neutral amino acid transporter), member 5	Slc1a5	292657	0.72	4.00	8.3E-01	5.3E-04	0.00	0.00	1.00
1387739_at	CD8 antigen, beta chain	Cd8b	24931	0.49	3.98	6.0E-01	2.7E-03	0.00	0.00	1.00
1371194_at	tumor necrosis factor alpha induced protein 6	Tnfaip6	84397	1.73	3.97	5.4E-01	6.1E-02	0.00	0.00	1.00
1398523_a_at	interferon (alpha and beta) receptor 1 (predicted)	Ifnar1_predicted	288264	0.93	3.97	9.2E-01	1.2E-04	0.60	0.50	1.00
1371970_at	similar to expressed sequence AW413625 (predicted)	RGD1560913_predicted	499322	1.20	3.96	8.8E-01	3.0E-04	0.00	0.00	1.00
1387221_at	GTP cyclohydrolase 1	Gch	29244	1.03	3.94	9.5E-01	1.3E-02	0.00	0.25	1.00
1368809_at	CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	64185	0.86	3.94	5.9E-01	2.5E-04	1.00	1.00	1.00
1373250_at	similar to Anillin (predicted)	RGD1566097_predicted	307056	0.87	3.94	9.5E-01	1.4E-02	0.00	0.00	1.00
1371932_at	similar to hypothetical protein FLJ38482	RGD1309341	361137	0.82	3.93	4.6E-01	5.7E-04	0.00	0.00	1.00
1373494_at	breakpoint cluster region (predicted)	Bcr_predicted	309696	1.69	3.89	7.7E-01	8.8E-02	0.00	0.00	1.00
1373613_at	similar to RIKEN cDNA 4930570C03	LOC300191	300191	1.00	3.89	9.9E-01	2.0E-04	1.00	1.00	1.00
1387432_at	ROD1 regulator of differentiation 1 (S. pombe)	Rod1	83515	1.32	3.88	8.7E-01	5.5E-02	0.00	0.00	1.00
1377116_at	Cation channel, sperm associated 3 (predicted)	Catsper3_predicted	290989	1.01	3.86	9.7E-01	6.0E-04	1.00	1.00	1.00
1374388_at	EF hand domain containing 2	Efh2	298609	1.28	3.86	4.1E-01	1.4E-04	1.00	1.00	1.00
1374392_at	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b (predicted)	Ptplb_predicted	288058	1.40	3.85	7.8E-01	1.4E-04	0.40	0.00	1.00
1390348_at	folate receptor 2 (fetal) (predicted)	Folr2_predicted	293154	1.07	3.85	8.0E-01	4.6E-04	0.00	0.00	1.00
1373818_at	Potassium channel tetramerisation domain containing 12 (predicted)	Kctd12_predicted	364548	1.22	3.84	5.4E-01	2.6E-04	1.00	1.00	1.00
1399148_s_at	glycosyltransferase 25 domain containing 1 (predicted)	Gl25d1_predicted	290637	1.35	3.84	8.4E-01	5.6E-02	0.00	0.00	1.00
1387074_at	regulator of G-protein signaling 2	Rgs2	84583	1.86	3.82	5.3E-02	3.5E-04	1.00	1.00	1.00
1371123_x_at	RT1 class Ib, locus S3	RT1-S3	294228	1.76	3.81	1.5E-01	2.5E-03	1.00	1.00	1.00
1373514_at	similar to chromosome 17 open reading frame 27	LOC688296	688296	0.93	3.80	9.3E-01	4.0E-03	0.00	0.00	1.00
1390510_at	membrane-spanning 4-domains, subfamily A, member 6B	Ms4a6b	293749	0.97	3.80	9.5E-01	7.7E-04	1.00	1.00	1.00
1388282_s_at	killer cell lectin-like receptor, subfamily A, member 5	Klra5	297666	2.73	3.80	3.6E-01	9.9E-03	0.00	0.00	1.00
1388667_at	mannosidase 2, alpha 1	Man2a1	25478	1.98	3.79	5.5E-01	1.7E-03	0.00	0.00	1.00
1373897_at	Ubiquitin carboxyl-terminal hydrolase L5	UchL5	360853	1.03	3.79	9.8E-01	2.8E-04	0.00	0.88	1.00
1376795_at	Phosphoinositide-3-kinase adaptor protein 1 (predicted)	Plk3ap1_predicted	294048	1.66	3.79	2.9E-01	1.6E-04	1.00	0.00	1.00
1372070_at	interferon gamma inducible protein 30	Ifl30	290644	1.13	3.79	5.6E-01	9.2E-04	1.00	1.00	1.00
1388213_a_at	RT1 class Ib, locus S3	RT1-S3	294228	1.81	3.78	2.9E-01	5.3E-03	1.00	1.00	1.00
1389244_x_at	chemokine (C-X-C motif) receptor 4	Cxcr4	60628	1.18	3.77	5.7E-01	7.9E-04	1.00	1.00	1.00
1387947_at	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	Matb	54264	0.63	3.77	6.7E-01	5.8E-03	0.00	0.00	1.00
1374678_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Sema4b	293042	2.06	3.76	5.9E-01	1.1E-02	0.00	0.70	0.25
1372889_at	Transcribed locus			1.84	3.76	4.2E-01	5.7E-03	0.00	0.00	0.50
1373658_at	Rac GTPase-activating protein 1 (predicted)	Racgap1_predicted	315298	1.49	3.75	6.2E-01	1.0E-03	0.20	0.00	0.63
1373026_at	spindle pole body component 24 homolog (S. cerevisiae) (predicted)	Spbc24_predicted	363028	0.49	3.75	6.4E-01	1.1E-03	0.00	0.00	0.80
1372893_at	Yip1 domain family, member 1	Yip1	298312	1.16	3.74	6.8E-01	1.5E-04	1.00	0.75	1.00
1368655_at	proteoglycan peptide core protein	Pgsg	56782	0.99	3.74	9.9E-01	3.5E-04	1.00	1.00	1.00
1381968_at	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (predicted)	Sema6d_predicted	311384	0.95	3.72	8.4E-01	8.1E-04	1.00	1.00	1.00
1373992_at	similar to interferon-inducible GTPase	MGC108823	307414	1.07	3.72	9.2E-01	3.0E-03	1.00	1.00	1.00
1376109_at	Transcribed locus			1.19	3.71	6.0E-01	1.3E-03	1.00	1.00	1.00
1367721_at	syndecan 4	Sdc4	24771	1.00	3.71	1.0E+00	1.6E-04	0.50	0.00	1.00
1389227_at	Ras homolog gene family, member G	Rhog	308875	1.17	3.71	5.2E-01	1.7E-04	1.00	1.00	1.00
1373685_at	similar to low density lipoprotein receptor-related protein binding protein (predicted)	RGD1565715_predicted	361149	0.67	3.71	6.9E-01	1.7E-03	0.00	0.00	0.80
1372043_at	similar to ribosomal protein P0-like protein; 60S acidic ribosomal protein PO; ribosomal protein, large, P0-like (predicted)	RGD1311709_predicted	298586	1.13	3.70	9.3E-01	2.0E-03	0.20	0.00	1.00
1374799_at	similar to mKIAA0159 protein (predicted)	RGD1562596_predicted	362438	0.82	3.68	6.2E-01	4.3E-02	0.20	0.00	1.00
1387087_at	CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	24253	1.08	3.68	8.5E-01	7.4E-04	1.00	1.00	1.00
1368430_at	legumain	Lgmn	63865	1.21	3.68	3.6E-01	2.1E-04	1.00	1.00	1.00
1376728_at	Hypothetical RNA binding protein RGD1359713	RGD1359713	305340	0.88	3.68	6.9E-01	5.7E-04	0.40	0.13	1.00
1375422_at				1.81	3.67	3.3E-01	3.9E-03	1.00	1.00	1.00
1390022_at	actin related protein 2/3 complex, subunit 5	Arpc5	360854	1.25	3.67	2.1E-01	4.4E-04	1.00	1.00	1.00
1371248_at	similar to Cornifin A (Small proline-rich protein 1A) (SPR1A) (SPRR1)	LOC499660	499660	1.86	3.66	4.1E-01	5.8E-02	0.00	0.00	0.50
1386870_at	glutamate-ammonia ligase (glutamine synthase)	GluI	24957	1.15	3.65	6.4E-01	2.0E-04	1.00	1.00	1.00
1369792_a_at	melanoma cell adhesion molecule	Mcam	78967	1.59	3.65	3.1E-01	3.0E-03	1.00	0.63	1.00
1373949_at	ATPase type 13A2 (predicted)	Atp13a2_predicted	362645	1.07	3.63	8.4E-01	2.9E-03	0.00	0.00	1.00
1376850_a_at	chemokine (C-C motif) ligand 27 (predicted)	Ccl27_predicted	362505	1.22	3.63	8.3E-01	1.6E-02	0.00	0.00	1.00
1371402_at	ATPase, H transporting, lysosomal V1 subunit B2	Atp6v1b2	117596	1.02	3.63	9.5E-01	3.1E-04	1.00	1.00	1.00
1373554_at	splA/ryanodine receptor domain and SOCS box containing 1 (predicted)	Spsb1_predicted	313722	0.94	3.63	9.7E-01	2.5E-04	0.00	0.00	1.00
1387135_at	a disintegrin and metalloproteinase domain 15 (metargidin)	Adam15	57025	0.97	3.62	9.2E-01	1.2E-04	1.00	1.00	1.00
1389525_at	ring finger protein 149	Rnf149	363222	0.95	3.62	8.6E-01	1.5E-04	1.00	1.00	1.00
1374529_at	Thrombospondin 1	Tbs1	445442	1.31	3.62	7.3E-01	3.3E-03	1.00	1.00	1.00
1389668_at	spindle pole body component 25 homolog (S. cerevisiae)	Spbc25	295661	1.00	3.62	1.0E+00	1.4E-03	0.00	0.50	1.00
1370530_a_at	phospholipase D1	Pld1	25096	1.19	3.62	7.6E-01	4.6E-04	0.40	0.50	1.00
1384934_at	Clone GDY20 unknown mRNA			0.91	3.62	7.3E-01	1.5E-03	0.00	0.25	1.00
1368754_at	pyrimidinergic receptor P2Y, G-protein coupled, 6	P2ry6	117264	0.98	3.60	9.4E-01	2.6E-03	0.50	0.00	0.75
1370073_at	Dual (Hsp40) homolog, subfamily C, member 3	Dnajc3	63880	0.92	3.60	8.5E-01	1.6E-03	1.00	1.00	1.00
1369562_at	hippocalcin-like 1	Hpcal1	50871	1.89	3.60	3.6E-01	7.1E-03	0.20	0.00	1.00
1368976_at	CD38 antigen	Cd38	25668	0.99	3.60	9.7E-01	5.3E-03	1.00	0.50	1.00
1368045_at	solute carrier family 31 (copper transporters), member 1	Slc31a1	171135	1.43	3.59	6.9E-01	4.5E-03	0.00	0.00	0.60
1373262_at	similar to 2310014H01Rik protein (predicted)	RGD1309543_predicted	361790	1.07	3.59	9.2E-01	4.8E-04	0.00	0.00	1.00
1377002_at	Interferon (alpha and beta) receptor 1 (predicted)	Ifnar1_predicted	288264	0.91	3.59	8.1E-01	1.6E-03	0.00	0.00	1.00
1368647_at	G protein-coupled receptor kinase 6	Gprk6	59076	1.13	3.58	9.4E-01	3.7E-03	0.00	0.00	1.00

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Native BN / DA	Allograft / Isoraft	Native BN / DA	Allograft / Isoraft	Native BN	Native DA	Allograft	Isoraft
1388762_at	IQ motif containing GTPase activating protein 1 (predicted)	Iqgap1_predicted	361598	1.05	3.58	8.0E-01	2.0E-04	1.00	1.00	1.00	1.00
1377172_at	similar to Pins (predicted)	RGD1560967_predicted	362021	1.28	3.58	8.4E-01	8.3E-02	0.00	0.00	0.70	0.00
1392407_at	similar to RIKEN cDNA 6030405P05 gene (predicted)	RGD1561419_predicted	498282	1.01	3.57	9.9E-01	1.5E-03	0.80	0.25	1.00	1.00
1373881_at	Rho, GDP dissociation inhibitor (GDI) beta	Arhgdib	362456	0.87	3.56	5.0E-01	1.4E-04	1.00	1.00	1.00	1.00
1368555_at	CD37 antigen	Cd37	29185	1.15	3.56	8.1E-01	3.8E-03	0.10	0.00	1.00	0.75
1368186_a_at	spleen tyrosine kinase	Syk	25155	1.50	3.56	3.0E-01	1.8E-04	0.00	0.00	1.00	0.50
1385903_at	Zinc finger, SWIM domain containing 6	Zswim6	310062	0.71	3.56	7.8E-01	5.7E-04	0.00	0.00	0.50	0.00
1373657_at	solute carrier family 31, member 2	Slc31a2	298091	1.05	3.55	9.2E-01	1.5E-03	1.00	1.00	1.00	1.00
1377759_at	Transcribed locus			0.94	3.54	8.8E-01	3.4E-04	1.00	0.63	1.00	1.00
1368683_at	oxidized low density lipoprotein (lectin-like) receptor 1	Oxidrl1	140914	0.64	3.54	7.1E-01	7.0E-03	0.00	0.00	1.00	0.25
1373672_at	Biotinidase	Bid	306262	0.97	3.54	9.5E-01	9.2E-04	0.80	1.00	1.00	1.00
1368878_at	isopentenyl-diphosphate delta isomerase	Idi1	89784	1.54	3.52	2.5E-01	1.1E-03	1.00	0.75	1.00	0.75
1387198_at	inositol polyphosphate-5-phosphatase D	Inpp5d	54259	1.02	3.50	9.6E-01	1.1E-02	1.00	1.00	1.00	1.00
1399050_at	adenylosuccinate synthetase, non muscle (predicted)	Adss_predicted	289276	0.95	3.50	8.6E-01	2.0E-04	1.00	1.00	1.00	1.00
1373224_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	St3gal4	363040	1.72	3.49	5.3E-01	2.2E-03	0.00	0.00	1.00	0.00
1375857_at	similar to Myoferlin (Fer-1 like protein 3) (predicted)	RGD1564216_predicted	309499	1.56	3.49	6.4E-01	7.9E-04	0.00	0.00	1.00	0.50
1370516_at	solute carrier family 15, member 3	Slc15a3	246239	0.76	3.48	2.7E-01	1.2E-03	1.00	1.00	1.00	1.00
1374468_at	myeloid differentiation primary response gene 88	Myd88	301059	1.09	3.48	8.6E-01	1.8E-04	1.00	1.00	1.00	1.00
1372032_at	Transcribed locus			0.80	3.48	6.9E-01	2.9E-03	1.00	1.00	1.00	1.00
1389496_at	A kinase (PRKA) anchor protein 7	Akap7	361458	0.82	3.47	2.7E-01	6.5E-04	1.00	1.00	1.00	1.00
1388482_at	similar to RIKEN cDNA 9130404D14	RGD1307018	362115	1.12	3.47	8.4E-01	1.6E-04	1.00	1.00	1.00	1.00
1370043_at	activated leukocyte cell adhesion molecule	Alcam	79559	1.00	3.46	1.0E+00	1.0E-03	1.00	1.00	1.00	1.00
1370365_at	glutathione synthetase	Gss	25458	1.17	3.45	8.7E-01	1.3E-02	0.00	0.00	1.00	0.00
1372097_at	Transcribed locus, strongly similar to NP_543171.1 apoptotic inhibitory molecule [Rattus norvegicus]			1.27	3.45	6.3E-01	1.5E-03	1.00	0.38	1.00	1.00
1369268_at	activating transcription factor 3	Atf3	25389	1.04	3.44	9.8E-01	1.2E-02	0.00	0.00	1.00	0.75
1377092_at	Transcribed locus			1.68	3.44	3.1E-01	1.4E-03	1.00	1.00	1.00	1.00
1370348_at	ninjurin 1	Ninj1	25338	0.94	3.43	8.3E-01	1.9E-04	1.00	1.00	1.00	1.00
1371539_at	nucleolar protein family A, member 2 (predicted)	Nola2_predicted	287273	1.16	3.43	7.4E-01	9.6E-04	1.00	1.00	1.00	1.00
1370347_at	PDZ and LIM domain 7	Pdlim7	286908	0.99	3.43	9.9E-01	1.1E-03	0.30	0.00	1.00	1.00
1389756_at	maternal embryonic leucine zipper kinase (predicted)	Melk_predicted	362510	1.20	3.43	7.5E-01	3.7E-03	0.00	0.13	1.00	0.50
1368066_at	BCL2-antagonist/killer 1	Bak1	116502	0.67	3.40	4.6E-01	1.5E-03	0.20	0.25	1.00	0.75
1368762_at	ubiquitin D	Ubd	29168	0.62	3.40	2.8E-01	3.6E-02	0.30	0.50	1.00	1.00
1374556_at	spermine oxidase (predicted)	Smox_predicted	308652	0.77	3.40	3.3E-01	5.3E-04	1.00	1.00	1.00	1.00
1391880_at	tumor protein D52 (predicted)	Tpd52_predicted	294900	1.35	3.40	4.6E-01	2.4E-04	1.00	1.00	1.00	1.00
1367973_at	chemokine (C-C motif) ligand 2	Ccl2	24770	0.80	3.39	6.2E-01	7.4E-04	0.10	0.00	1.00	1.00
1388182_at	DNA primase, p49 subunit	Prim1	246327	1.34	3.37	5.1E-01	5.2E-04	0.40	0.00	1.00	1.00
1369940_at	transaldolase 1	Taldo1	83688	1.15	3.37	6.5E-01	2.9E-03	1.00	0.75	1.00	1.00
1376481_at	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (predicted)	Adams9_predicted	312566	1.76	3.37	7.4E-01	2.2E-03	0.00	0.00	1.00	0.00
1371977_at	actin related protein 2/3 complex, subunit 3 (predicted)	Arcp3_predicted	288669	0.98	3.36	9.6E-01	1.9E-04	1.00	1.00	1.00	1.00
1373959_at	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Ppp2r1b	315648	2.12	3.36	3.5E-01	7.6E-04	0.00	0.00	1.00	0.00
1376636_at	transforming growth factor, beta receptor 1	Tgfbri	29591	1.21	3.35	6.3E-01	9.9E-04	1.00	0.88	1.00	1.00
1373138_at	nudix (nucleoside diphosphate linked moiety X)-type motif 5	Nudt5	361274	2.09	3.34	2.7E-01	1.9E-04	0.00	0.00	1.00	0.50
1376693_at	similar to OEF2 (predicted)	RGD1563091_predicted	500011	1.07	3.34	8.8E-01	7.5E-03	1.00	0.50	1.00	1.00
1394316_a_at	tetraspanin 5	Tspan5	362048	0.72	3.34	7.7E-01	3.0E-02	0.00	0.00	1.00	0.00
1369456_at	5-hydroxytryptamine (serotonin) receptor 2B	Htr2b	29581	1.54	3.34	6.6E-01	4.0E-03	0.60	0.25	1.00	0.75
1373869_at	sterol O-acyltransferase 1	Soa1	81782	1.44	3.33	4.3E-01	1.2E-03	0.00	0.00	1.00	0.25
1374626_at	leucine-rich alpha-2-glycoprotein 1	Lrg1	367455	1.18	3.33	5.8E-01	9.9E-04	1.00	0.25	1.00	0.75
1373592_at	similar to SPI6	MGC94010	361241	1.21	3.33	5.0E-01	1.8E-03	0.80	1.00	1.00	1.00
1398349_at	adenylate kinase 2	Ak2	24184	0.69	3.32	2.5E-01	2.8E-04	1.00	1.00	1.00	1.00
1376637_at	Transcribed locus			1.07	3.32	9.7E-01	9.7E-02	0.00	0.25	0.80	0.00
1375170_at	S100 calcium binding protein A11 (calizzarin)	S100a11	445415	1.12	3.31	7.0E-01	3.7E-04	1.00	1.00	1.00	1.00
1367712_at	tissue inhibitor of metalloproteinase 1	Timp1	116510	1.37	3.31	5.7E-01	2.6E-02	0.80	0.63	1.00	1.00
1368914_at	runt related transcription factor 1	Runx1	50662	2.39	3.30	2.1E-01	3.3E-02	0.00	0.00	0.80	0.25
1388071_x_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	1.65	3.29	1.9E-01	7.5E-04	1.00	1.00	1.00	1.00
1371537_at	Transcribed locus			1.15	3.29	7.6E-01	7.9E-04	0.90	1.00	1.00	1.00
1374578_at	Transcribed locus			1.24	3.29	3.3E-01	4.2E-04	0.80	0.88	1.00	1.00
1374449_at	Solute carrier family 35, member E1 (predicted)	Slc35e1_predicted	306328	0.85	3.28	5.9E-01	1.5E-03	0.60	1.00	0.88	1.00
1373536_at				0.90	3.28	8.4E-01	4.5E-04	1.00	0.75	1.00	1.00
1368948_at	moesin	Msn	81521	1.55	3.28	2.7E-01	3.2E-02	0.50	0.25	1.00	0.50
1370294_a_at	cell division cycle 20 homolog (S. cerevisiae)	Cdc20	64515	0.86	3.28	7.8E-01	3.7E-04	0.00	0.00	1.00	0.25
1389873_at	PYD and CARD domain containing	Pycard	282817	1.07	3.27	6.6E-01	1.9E-03	1.00	1.00	1.00	1.00
1371922_at	Transcribed locus			0.86	3.27	7.7E-01	3.1E-02	0.00	0.88	1.00	0.13
1367914_at	epithelial membrane protein 3	Emp3	81505	0.82	3.27	6.1E-01	1.8E-04	1.00	1.00	1.00	1.00
1367936_at	serine/threonine kinase 10	Stk10	29398	1.22	3.27	5.2E-01	1.9E-03	1.00	1.00	1.00	1.00
1371232_a_at	chondroitin sulfate proteoglycan 2	Cspg2	114122	0.98	3.27	9.9E-01	3.7E-02	0.00	0.00	1.00	0.50
1376842_at	Transcribed locus			1.32	3.27	5.4E-01	2.0E-03	0.80	0.25	1.00	0.50
1390391_at	Transcribed locus			1.13	3.26	7.2E-01	1.1E-03	0.80	1.00	1.00	1.00
1374458_at	Transcribed locus, strongly similar to XP_001060531.1 similar to serum/glucocorticoid regulated kinase 3			1.18	3.25	8.2E-01	6.6E-04	1.00	1.00	1.00	1.00
1370972_x_at	RT1 class I, CE5	RT1-CE5	309607	0.71	3.25	3.6E-01	1.4E-02	0.00	0.00	1.00	0.00
1389742_at	Transcribed locus			1.22	3.25	8.2E-01	1.0E-02	0.20	0.25	1.00	0.50
1367780_at	pituitary tumor-transforming 1	Pttg1	64193	0.99	3.24	9.9E-01	1.2E-03	0.00	0.00	0.60	0.00
1372132_at	CNDP dipeptidase 2 (metallopeptidase M20 family)	Cndp2	291394	1.12	3.23	6.7E-01	2.1E-04	1.00	1.00	1.00	1.00
1374431_at	similar to ATPase, H+ transporting, V1 subunit A, isoform 1	LOC685232	685232	1.22	3.23	6.5E-01	4.7E-04	1.00	1.00	1.00	1.00
1392819_at	Transcribed locus			1.31	3.22	7.0E-01	1.2E-03	0.10	0.00	1.00	0.63
1375696_at	interferon (alpha and beta) receptor 1 (predicted)	Ifnar1_predicted	288264	1.22	3.21	7.5E-01	5.8E-03	1.00	1.00	1.00	1.00
1388440_at	anterior pharynx defective 1b homolog (C. elegans)	Aph1b	300802	0.88	3.21	4.2E-01	2.4E-04	1.00	1.00	1.00	1.00
1388203_x_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	1.01	3.21	9.8E-01	2.7E-04	1.00	1.00	1.00	1.00

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call					
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft		
1370539_at	RAB8B, member RAS oncogene family	Rab8b	266688	1.67	3.21	1.00	1.5E-01	4.2E-03	1.00	1.00	1.00	1.00
1387946_at	lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp	245955	0.91	3.20	7.7E-01	5.0E-04	1.00	1.00	1.00	1.00	1.00
1370184_at	cofilin 1, non-muscle	Cfl1	29271	0.94	3.19	9.1E-01	1.9E-03	1.00	1.00	1.00	1.00	1.00
1390386_at	caspace 3, apoptosis related cysteine protease	Casp3	25402	1.20	3.18	9.2E-01	1.5E-03	0.00	0.00	1.00	0.00	0.00
1371644_at	protein tyrosine kinase 9	Ptk9	315265	0.62	3.17	7.4E-01	1.7E-04	0.00	0.00	1.00	1.00	1.00
1369122_at	Bcl2-associated X protein	Bax	24887	0.99	3.17	9.7E-01	2.8E-03	0.10	0.50	1.00	1.00	1.00
1376793_at	similar to RIKEN cDNA 5730414C17 (predicted)	RGD1308377_predicted	306687	0.89	3.16	6.2E-01	3.3E-04	1.00	1.00	1.00	1.00	1.00
1370082_at	transforming growth factor, beta 1	Tgfb1	59086	1.30	3.16	5.8E-01	7.7E-04	0.00	0.00	1.00	0.00	0.00
1374565_at	NIMA (never in mitosis gene a)-related expressed kinase 6	Nek6	360161	1.17	3.16	6.4E-01	6.8E-04	1.00	0.00	1.00	1.00	0.75
1372691_at	uridine phosphorylase 1	Upp1	289801	0.91	3.16	8.3E-01	5.0E-04	1.00	1.00	1.00	1.00	1.00
1371618_s_at	tubulin, beta 3	Tubb3	246118	0.99	3.15	9.9E-01	7.3E-03	0.00	0.00	1.00	1.00	1.00
1373751_at	Transcribed locus			1.49	3.15	1.8E-01	4.4E-04	1.00	0.50	1.00	1.00	1.00
1375020_at	Ras and Rab interactor 3 (predicted)	Rin3_predicted	314397	1.21	3.14	3.0E-01	2.6E-03	0.00	0.00	1.00	0.50	1.00
1374615_at				1.61	3.14	4.9E-01	1.3E-02	0.60	0.50	1.00	1.00	1.00
1372513_at	ras-related C3 botulinum toxin substrate 1	Rac1	363875	1.70	3.14	7.3E-02	3.8E-03	1.00	1.00	1.00	1.00	1.00
1375420_at	tumor protein p53 inducible protein 11 (predicted)	Tp53i11_predicted	311209	0.98	3.13	9.7E-01	1.9E-04	0.40	0.13	1.00	0.88	1.00
1373198_at	similar to RIKEN cDNA 2810451A06	RGD1311098	362998	1.46	3.13	2.0E-01	2.5E-03	0.20	0.00	1.00	0.00	0.00
1383912_at	similar to Protein C6orf115	LOC684848	684848	0.84	3.13	3.1E-01	6.9E-03	1.00	1.00	1.00	1.00	1.00
1367745_at	diacylglycerol kinase zeta	Dgkz	81821	1.09	3.12	8.4E-01	7.0E-03	0.20	0.00	1.00	0.00	0.00
1390563_at	ATP-binding cassette, sub-family A (ABC1), member 3	Abcc3	302973	1.54	3.12	6.2E-01	2.8E-03	0.00	0.00	1.00	1.00	1.00
1376722_at	nucleoporin 205Da (predicted)	Nup205_predicted	362335	1.47	3.12	3.3E-01	1.9E-04	0.90	0.00	1.00	1.00	1.00
1371368_at	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	80843	1.42	3.12	4.9E-01	4.6E-04	0.70	0.25	1.00	1.00	1.00
1372156_at	transmembrane protein 97	Tmem97	303330	1.11	3.12	6.9E-01	5.7E-04	0.00	0.00	1.00	1.00	1.00
1370499_at	killer cell lectin-like receptor subfamily B, member 1A (mapped)	Klrb1a	362443	0.86	3.12	8.1E-01	6.6E-02	0.80	0.75	1.00	0.50	1.00
1387402_at	myosin, heavy polypeptide 9, non-muscle	Myh9	25745	0.99	3.12	9.9E-01	8.5E-02	0.00	0.75	1.00	0.60	0.00
1374912_at	Alpha-2u globulin PGCL1	LOC259246	259246	0.92	3.12	9.4E-01	4.9E-02	0.00	0.00	1.00	0.60	0.00
1370096_at	perforin 1 (pore forming protein)	Prfl	50669	1.16	3.12	9.4E-01	1.4E-03	0.00	0.00	1.00	0.60	0.00
1374933_at	melanoma cell adhesion molecule	Mcam	78967	1.84	3.12	4.0E-01	1.3E-03	1.00	1.00	1.00	1.00	1.00
1372182_at	phosphofruktokinase, platelet	Pfkp	60416	1.17	3.11	6.7E-01	5.7E-03	1.00	1.00	1.00	1.00	1.00
1370954_at	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	P4ha1	64475	1.04	3.11	9.3E-01	1.8E-04	1.00	1.00	1.00	1.00	1.00
1388857_at	SEC23B (S. cerevisiae) (predicted)	Sec23b_predicted	362226	1.34	3.11	3.6E-01	6.5E-04	1.00	1.00	1.00	1.00	1.00
1386976_at	CD82 antigen	Cd82	83628	1.10	3.11	8.2E-01	1.4E-03	0.60	0.38	1.00	1.00	1.00
1368437_at	carbonic anhydrase 4	Ca4	29422	0.34	3.10	2.2E-01	7.2E-03	0.00	0.00	0.90	0.00	0.00
1388745_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	Sema4a	310630	1.01	3.10	9.7E-01	9.3E-04	1.00	0.75	1.00	1.00	1.00
1388913_at	phosphatidic acid phosphatase type 2c	Ppap2c	246115	1.24	3.10	8.8E-01	7.2E-02	0.00	0.00	0.70	0.00	0.00
1375424_at	ARP2 actin-related protein 2 homolog (yeast)	Actr2	289820	1.25	3.10	4.9E-01	1.3E-04	1.00	1.00	1.00	1.00	1.00
1367740_at	creatine kinase, brain	Ckb	24264	1.23	3.10	5.3E-01	2.9E-03	1.00	1.00	1.00	1.00	1.00
1383906_at	similar to lung inducible neuralized-related C3HC4 RING finger protein	LOC316326	316326	1.63	3.09	5.3E-01	5.2E-04	0.00	0.00	1.00	0.00	0.00
1380546_at	similar to hypothetical protein FLJ10986	LOC298250	298250	0.72	3.09	4.1E-01	4.0E-03	1.00	1.00	1.00	1.00	1.00
1388600_at	CDNA clone IMAGE:7320582			1.51	3.08	3.3E-01	1.5E-03	1.00	0.88	1.00	1.00	1.00
1377353_a_at	tumor necrosis factor (ligand) superfamily, member 13	Tnfrsf13	287437	1.04	3.08	8.5E-01	2.7E-03	0.20	0.13	1.00	0.75	1.00
1388347_at	similar to lymphocyte antigen 6 complex, locus E	LOC62934	362934	0.72	3.08	2.8E-01	2.1E-03	1.00	1.00	1.00	1.00	1.00
1389380_at	similar to Folylpolylglutamate synthase, mitochondrial precursor	LOC687266	687266	1.36	3.08	7.3E-01	4.2E-03	0.00	0.00	1.00	0.00	0.00
1373043_at	similar to stromal cell-derived factor 2-like 1	LOC680945	680945	1.06	3.08	9.0E-01	7.2E-04	1.00	1.00	1.00	1.00	1.00
1368305_at	caspace 6	Casp6	83584	1.39	3.07	5.5E-01	4.7E-02	0.00	0.00	0.60	0.00	0.00
1370631_at	regenerating islet-derived 3 gamma	Reg3g	24620	4.48	3.07	1.1E-01	6.5E-02	1.00	0.75	1.00	1.00	1.00
1376624_at	Transcribed locus			1.02	3.07	9.6E-01	3.6E-04	1.00	0.75	1.00	1.00	1.00
1377821_at	Transcribed locus			0.92	3.07	9.2E-01	4.4E-05	1.00	1.00	1.00	1.00	1.00
1388416_at	low density lipoprotein receptor-related protein 1	Lrp1	299858	2.73	3.07	3.0E-01	3.4E-03	1.00	0.25	1.00	1.00	1.00
1373221_at	diaphanous homolog 1 (Drosophila) (predicted)	Diap1_predicted	307483	1.28	3.06	6.3E-01	6.4E-04	1.00	0.75	1.00	1.00	1.00
1398892_at	Niemann Pick type C2	Npc2	286898	1.02	3.06	9.7E-01	1.3E-03	1.00	1.00	1.00	1.00	1.00
1398319_at	Nclone10 mRNA			1.12	3.06	7.8E-01	2.1E-03	1.00	0.88	1.00	1.00	1.00
1372770_at				1.55	3.05	1.9E-01	5.3E-04	1.00	1.00	1.00	1.00	1.00
1398360_at	similar to Elongation of very long chain fatty acids protein 1	LOC679532	679532	0.87	3.04	7.4E-01	1.4E-04	1.00	1.00	1.00	1.00	1.00
1387871_at	cofilin 1, non-muscle	Cfl1	29271	0.92	3.04	8.8E-01	2.5E-03	0.70	0.75	1.00	1.00	1.00
1374939_at	cytoplasmic FMR1 interacting protein 2 (predicted)	Cyfp2_predicted	303073	0.80	3.04	5.4E-01	5.2E-03	0.60	0.63	1.00	0.75	1.00
1373164_at	Transcribed locus			1.10	3.04	8.6E-01	3.3E-04	1.00	1.00	1.00	1.00	1.00
1370999_at	sperm associated antigen 5	Spag5	252918	1.71	3.04	5.5E-01	1.4E-02	0.00	0.00	0.50	0.00	0.00
1376697_at	carbohydrate sulfotransferase 12	Cst12	304322	0.86	3.03	8.3E-01	6.5E-04	0.00	0.00	1.00	0.00	0.00
1388393_at	proteolipid protein 2 (mapped)	Plp2	302562	1.14	3.03	5.6E-01	1.8E-04	1.00	1.00	1.00	1.00	1.00
1377260_at	Transcribed locus			0.74	3.03	4.5E-01	8.6E-03	0.00	0.13	1.00	0.25	1.00
1371027_at	Casitas B-lineage lymphoma b	Cblb	171136	0.95	3.03	9.1E-01	2.5E-03	1.00	1.00	1.00	1.00	1.00
1370822_at	RT1 class II, locus Ba	RT1-Ba	309621	1.08	3.03	9.3E-01	8.3E-03	0.00	0.00	1.00	1.00	1.00
1369262_at	caspace 8	Casp8	64044	0.90	3.02	9.3E-01	3.6E-04	0.00	0.00	1.00	0.00	0.00
1374876_at	leptin receptor overlapping transcript-like 1	Leprotl1	361160	0.84	3.02	4.8E-01	2.6E-03	0.90	0.88	1.00	1.00	1.00
1387195_at	suppression of tumorigenicity 14 (colon carcinoma)	St14	114093	1.05	3.02	9.3E-01	1.4E-03	1.00	0.75	1.00	1.00	1.00
1370297_at	polo-like kinase 1 (Drosophila)	Pkl1	25515	1.04	3.02	9.4E-01	3.2E-02	0.00	0.00	0.60	0.00	0.00
1376657_at	immunoglobulin superfamily, member 4A	Igsf4a	363058	0.61	3.02	5.9E-01	2.4E-02	0.00	0.00	1.00	0.25	1.00
1372459_at	vasodilator-stimulated phosphoprotein (predicted)	Vasp_predicted	361517	1.12	3.02	7.2E-01	2.6E-04	1.00	1.00	1.00	1.00	1.00
1376317_at	origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	291927	0.89	3.02	8.6E-01	1.3E-03	0.00	0.00	1.00	0.00	0.00
1370051_at	transglutaminase 1	Tgm1	60335	2.92	3.01	3.3E-01	2.9E-02	0.00	0.00	0.70	0.00	0.00
1379598_at	Transcribed locus			1.13	3.01	9.4E-01	1.6E-03	0.00	0.00	1.00	0.75	1.00
1371936_at	eukaryotic translation initiation factor 4A1	Eif4a1	287436	0.98	3.01	9.6E-01	2.4E-04	1.00	1.00	1.00	1.00	1.00
1388566_at	LIM and SH3 protein 1	Lasp1	29278	1.18	3.01	2.9E-01	3.8E-04	1.00	1.00	1.00	1.00	1.00
1373831_at	hypothetical protein LOC619574	LOC619574	619574	0.85	3.01	8.2E-01	4.4E-04	1.00	1.00	1.00	0.00	0.00
1388750_at	transferrin receptor	Tfrc	64678	0.59	3.00	3.2E-01	2.1E-04	1.00	1.00	1.00	1.00	1.00
1388151_at	coronin 7	Coro7	192276	0.96	3.00	9.3E-01	1.9E-04	0.40	0.13	1.00	1.00	0.75



Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Iso graft	Native BN	Native DA	Allograft	Iso graft
				Native BN / DA	Allograft / Iso graft	Native BN / DA	Allograft / Iso graft	Native BN	Native DA	Allograft	Iso graft
1374320_at	coagulation factor 5 (mapped)	F5	304929	1.30	3.00	3.4E-01	3.9E-04	1.00	1.00	1.00	1.00
1367938_at	UDP-glucose dehydrogenase	Ugdh	83472	1.27	3.00	3.0E-01	9.5E-03	1.00	1.00	1.00	1.00
1376169_at	similar to PHD finger protein 20-like 1 isoform 1	LOC314964	314964	1.02	0.33	9.8E-01	5.5E-02	1.00	1.00	0.70	1.00
1368252_at	kelch repeat and BTB (POZ) domain containing 10	Kbtd10	117537	1.21	0.33	3.4E-01	4.3E-03	1.00	1.00	1.00	1.00
1370918_a_at	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Atp5c1	116550	0.89	0.33	7.4E-01	5.0E-03	1.00	1.00	1.00	1.00
1377054_at	Transcribed locus			1.02	0.33	9.8E-01	1.3E-03	1.00	1.00	0.00	1.00
1375540_at	FK506 binding protein 9	Fkbp9	297123	0.96	0.33	9.0E-01	5.2E-04	0.80	1.00	1.00	1.00
1388112_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	Slc25a4	85333	0.85	0.33	6.3E-01	2.8E-03	1.00	1.00	1.00	1.00
1373249_at	Transcribed locus			0.86	0.33	6.5E-01	1.3E-03	1.00	1.00	1.00	1.00
1372054_at	Transcribed locus			1.08	0.33	8.1E-01	5.2E-03	1.00	1.00	1.00	1.00
1383175_a_at	similar to C11orf17 protein (predicted)	RGD1306959_predicted	361624	1.24	0.33	5.5E-01	9.9E-03	1.00	1.00	1.00	1.00
1389805_at	Transcribed locus			0.17	0.33	7.6E-02	1.5E-02	0.00	0.00	0.00	0.50
1376066_at	fat tumor suppressor homolog (Drosophila)	Fath	83720	0.90	0.33	8.7E-01	2.5E-04	1.00	1.00	1.00	1.00
1367654_at	Transcribed locus			1.52	0.33	1.8E-01	9.9E-04	1.00	1.00	1.00	1.00
1376584_at	Transcribed locus			1.35	0.33	3.6E-01	1.0E-03	1.00	1.00	1.00	1.00
1375197_at	Transcribed locus			0.81	0.33	2.8E-01	2.5E-03	1.00	1.00	1.00	1.00
1371293_at	similar to Myosin light polypeptide 4 (Myosin light chain 1, atrial isoform)	LOC688228	688228	1.25	0.33	4.6E-01	2.8E-03	1.00	1.00	0.00	1.00
1367726_at	thyroid hormone receptor alpha	Thra	81812	0.91	0.33	7.7E-01	1.4E-03	0.90	0.75	0.00	1.00
1373239_at	SH3 and PX domain containing 3 (predicted)	Sh3px3_predicted	315696	0.74	0.33	4.8E-01	6.1E-03	0.30	0.50	0.00	1.00
1371793_at	Acetylcholinesterase	Ache	83817	0.94	0.33	8.5E-01	1.9E-03	1.00	1.00	0.80	1.00
1370060_at	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	Slc25a11	64201	0.97	0.33	9.3E-01	1.4E-03	1.00	1.00	1.00	1.00
1372612_at	dynein light chain LC8-type 2	Dynll2	140734	0.84	0.33	3.8E-01	1.1E-03	1.00	1.00	1.00	1.00
1370447_at	phospholipase B	Phlph	192259	1.22	0.33	7.4E-01	3.9E-02	1.00	1.00	0.80	1.00
1372296_at	similar to putative SH3BGR protein (predicted)	RGD1563599_predicted	498066	0.82	0.33	4.7E-01	1.3E-02	1.00	1.00	1.00	1.00
1387898_at	heat shock protein, alpha-crystallin-related, B6	Hspb6	192245	1.03	0.33	9.5E-01	3.8E-02	1.00	1.00	1.00	1.00
1389918_at	Similar to AL023001 protein (predicted)	RGD1305001_predicted	304714	0.53	0.33	4.1E-03	1.0E-03	0.90	1.00	1.00	1.00
1373134_at	fumarylacetoacetyl hydrolase domain containing 2A (predicted)	Fahd2a_predicted	296131	0.99	0.33	9.8E-01	3.2E-03	1.00	1.00	0.60	1.00
1375411_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)	Ndufa7_predicted	299643	0.74	0.33	1.7E-01	1.0E-02	1.00	1.00	1.00	1.00
1375628_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 (predicted)	Ndufb8_predicted	293991	0.75	0.32	4.8E-01	1.2E-02	1.00	1.00	0.50	1.00
1376924_a_at	palmdelphin	Palmd	310811	0.90	0.32	8.3E-01	7.7E-03	1.00	1.00	0.10	1.00
1371871_at	RAB12, member RAS oncogene family	Rab12	25530	1.04	0.32	8.7E-01	1.2E-03	1.00	1.00	1.00	1.00
1388936_at	cadherin 11	Cdh11	84407	1.43	0.32	2.7E-01	1.1E-02	1.00	1.00	0.80	1.00
1388437_at	Transcribed locus			1.25	0.32	4.1E-01	2.0E-04	1.00	1.00	1.00	1.00
1371346_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (predicted)	Ndufb6_predicted	297990	0.79	0.32	4.0E-01	8.5E-03	1.00	1.00	1.00	1.00
1388200_at	myosin regulatory light chain 2, ventricular/cardiac muscle isoform	Mlc2	363925	0.84	0.32	6.6E-01	2.6E-02	1.00	1.00	1.00	1.00
1368818_at	proteasome (prosome, macropain) activator subunit 4	Psme4	498433	1.18	0.32	2.8E-01	7.6E-04	1.00	1.00	1.00	1.00
1373967_at	Transcribed locus			1.01	0.32	9.9E-01	2.5E-03	1.00	1.00	0.20	1.00
1399130_at	similar to RIKEN cDNA 261002G08	LOC502782	502782	0.83	0.32	5.2E-01	1.7E-03	1.00	1.00	1.00	1.00
1368281_at	dipeptidase 1 (renal)	Dpep1	94199	0.48	0.32	2.3E-02	4.8E-04	0.60	0.88	0.60	1.00
1387768_at	myoglobin	Mb	59108	0.84	0.32	5.6E-01	2.5E-02	1.00	1.00	1.00	1.00
1372586_at	Ubiquitin-conjugating enzyme E2D 3 (UBCA5 homolog, yeast)	Ubc2d3	81920	0.78	0.32	3.4E-01	5.6E-03	1.00	1.00	1.00	1.00
1390706_at	spectrin beta 2	Spnb2	305614	1.52	0.32	1.2E-01	4.3E-03	1.00	1.00	1.00	1.00
1371371_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	Ndufb4	288088	0.81	0.32	5.6E-01	2.6E-03	1.00	1.00	1.00	1.00
1371989_at	high mobility group nucleosomal binding domain 3	Hmg3	113990	0.60	0.32	2.3E-01	6.7E-04	1.00	1.00	1.00	1.00
1371786_at	triptarin motif protein 35	Trim35	498538	0.88	0.32	5.8E-01	4.8E-04	1.00	1.00	1.00	1.00
1383192_at	spasin (predicted)	Spast_predicted	362700	0.94	0.32	9.0E-01	8.9E-02	0.40	0.13	0.00	0.75
1370642_s_at	platelet derived growth factor receptor, beta polypeptide	Pdgfrb	24629	1.24	0.32	6.2E-01	1.0E-02	1.00	0.75	1.00	1.00
1367604_at	cysteine-rich protein 2	Crip2	338401	0.88	0.32	6.4E-01	1.6E-03	1.00	1.00	1.00	1.00
1372799_at	deoxyguanosine kinase (predicted)	Dguok_predicted	297389	0.60	0.32	1.9E-01	2.6E-03	1.00	1.00	1.00	1.00
1375642_at	ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)	Ubc2b	81816	1.04	0.32	9.3E-01	2.0E-03	1.00	1.00	1.00	1.00
1370238_at	RAB12, member RAS oncogene family	Rab12	25530	0.77	0.32	2.4E-01	8.0E-03	1.00	1.00	1.00	1.00
1370288_a_at	tropomyosin 1, alpha	Tpm1	24851	0.92	0.32	7.0E-01	1.9E-02	1.00	1.00	1.00	1.00
1369927_at	malate dehydrogenase 2, NAD (mitochondrial)	Mdh2	81829	0.90	0.32	7.8E-01	2.5E-03	1.00	1.00	1.00	1.00
1371738_at	similar to hypothetical protein FLJ10375 (predicted)	RGD1308260_predicted	301111	0.99	0.32	9.9E-01	2.9E-03	1.00	1.00	1.00	1.00
1388603_a_at	HESB like domain containing 2	Hbid2	290985	0.96	0.32	8.5E-01	8.9E-04	1.00	1.00	1.00	1.00
1388955_at	Transcribed locus			1.21	0.32	5.3E-01	1.6E-03	1.00	1.00	0.60	1.00
1383161_a_at				0.83	0.32	6.6E-01	7.7E-03	1.00	1.00	1.00	1.00
1367764_at	cyclin G1	Cng1	25405	0.97	0.32	7.7E-01	2.5E-03	1.00	1.00	1.00	1.00
1370006_at	Receptor-interacting serine-threonine kinase 3	Ripk3	246240	0.95	0.32	8.9E-01	6.6E-03	1.00	1.00	1.00	1.00
1372149_at	AU RNA binding protein/enoyl-coenzyme A hydratase (predicted)	Auh_predicted	361215	0.78	0.32	2.8E-01	1.3E-03	1.00	1.00	1.00	1.00
1373142_at	Growth hormone inducible transmembrane protein	Ghltm	290596	0.94	0.32	8.3E-01	2.0E-03	1.00	1.00	1.00	1.00
1368814_at	aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	81708	1.73	0.32	2.1E-01	7.7E-04	1.00	1.00	0.70	1.00
1372934_at	similar to 1700019E19Rik protein (predicted)	RGD1307392_predicted	299209	0.91	0.32	6.4E-01	9.5E-03	1.00	1.00	1.00	1.00
1369817_at	heart and neural crest derivatives expressed transcript 2	Hand2	64637	1.08	0.32	7.7E-01	9.5E-04	1.00	1.00	0.10	1.00
1387873_at	WAP four-disulfide core domain 1	Wfdc1	171112	0.68	0.32	2.1E-01	1.4E-03	1.00	1.00	0.30	1.00
1372590_at	C1q and tumor necrosis factor related protein 1	C1qtnf1	303701	0.89	0.32	7.8E-01	6.4E-02	0.50	0.13	0.00	0.75
1369636_at	sorbitol dehydrogenase	Sord	24788	0.80	0.32	4.5E-01	2.1E-03	1.00	1.00	0.20	1.00
1373487_at	Spondin 1	Spon1	64456	2.64	0.32	1.1E-01	1.1E-02	1.00	0.38	1.00	1.00
1372299_at	cyclin-dependent kinase inhibitor 1C (P57)	Cdkn1c	246060	1.22	0.32	5.8E-01	2.6E-03	0.90	0.20	0.20	1.00
1389287_at	CDNA clone IMAGE7193711			1.36	0.32	2.3E-01	4.0E-04	1.00	1.00	1.00	1.00
1373848_at	similar to RIKEN cDNA 5730449L18 (predicted)	RGD1308584_predicted	289083	0.72	0.31	5.0E-01	9.0E-02	1.00	1.00	0.50	1.00
1388111_at	elastin	Eln	25043	0.93	0.31	9.0E-01	6.5E-03	0.80	0.75	0.40	1.00
1371542_at	tubulin, alpha 4	Tuba4	316531	0.81	0.31	4.0E-01	1.5E-02	1.00	1.00	1.00	1.00
1370166_at	syndecan 2	Sdc2	25615	1.29	0.31	4.7E-01	1.3E-02	1.00	1.00	1.00	1.00
1373158_at	Transcribed locus			0.76	0.31	3.2E-01	1.5E-03	1.00	1.00	1.00	1.00
1373582_at	similar to CLIP-170-related protein (predicted)	RGD1306245_predicted	308493	1.32	0.31	5.4E-01	8.2E-02	0.00	0.00	0.20	0.75
1388167_at	nuclear factor 1B	Nf1b	29227	1.06	0.31	8.7E-01	3.2E-04	1.00	1.00	0.80	1.00

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call				
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft	
1372144_at	Dnal (Hsp40) homolog, subfamily B, member 5 (predicted)	Dnajb5_predicted	315811	1.49	0.31	1.2E-01	2.1E-02	1.00	1.00	0.20	1.00
1371607_at	microtubule-associated protein 4	LOC367171	367171	1.29	0.31	6.0E-01	2.5E-03	1.00	1.00	1.00	1.00
1372849_at	Transcribed locus			0.90	0.31	8.7E-01	3.0E-02	1.00	1.00	0.70	1.00
1371349_at	procollagen, type VI, alpha 1 (predicted)	Col6a1_predicted	294337	1.06	0.31	8.7E-01	6.5E-02	1.00	1.00	1.00	1.00
1368137_at	microtubule-associated protein tau	Mapt	29477	1.06	0.31	8.3E-01	1.6E-03	0.90	0.63	0.00	1.00
1389562_at	Transcribed locus			0.79	0.31	5.6E-01	3.7E-04	0.00	0.38	0.00	1.00
1387919_at	mitofusin 2	Mfn2	64476	0.92	0.31	6.6E-01	1.6E-03	1.00	1.00	1.00	1.00
1376861_at	similar to RIKEN cDNA 1810018L05	LOC317312	317312	1.12	0.31	8.0E-01	1.1E-03	1.00	1.00	1.00	1.00
1387773_at	cytochrome c, somatic	Cytc	25309	0.84	0.31	5.2E-01	5.8E-03	1.00	1.00	1.00	1.00
1389816_at	Procollagen, type XI, alpha 2 (mapped)	Col11a2_mapped	294279	1.10	0.31	6.7E-01	1.4E-03	1.00	1.00	1.00	1.00
1370855_at	cystatin C	Cst3	25307	0.78	0.31	2.5E-01	2.4E-03	1.00	1.00	1.00	1.00
1375018_at	similar to hypothetical protein D630003M21 (predicted)	RGD1563354_predicted	311592	0.78	0.31	2.0E-01	8.8E-02	0.00	0.63	0.00	1.00
1376320_at	Transcribed locus			0.79	0.31	4.8E-01	3.5E-02	1.00	0.50	0.00	1.00
1367599_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Atp5g1	29754	0.81	0.31	4.5E-01	2.4E-03	1.00	1.00	1.00	1.00
1371691_at	retinoic acid receptor responder (tazarotene induced) 2	Rarres2	297073	1.47	0.31	3.6E-01	2.5E-02	1.00	1.00	1.00	1.00
1384240_at	angiotensin II receptor, type 1 (AT1A)	Agtr1a	24180	0.65	0.31	6.8E-01	5.5E-02	0.00	0.00	0.10	1.00
1373092_at	Transcribed locus			1.29	0.31	1.8E-01	3.0E-03	1.00	1.00	1.00	1.00
1376646_at	popeye domain containing 2	Popdc2	360718	0.81	0.31	4.8E-01	5.6E-03	1.00	1.00	1.00	1.00
1387224_at	diacylglycerol kinase, beta	Dgkb	54248	0.48	0.31	7.6E-02	1.1E-04	0.20	0.10	0.80	1.00
1374636_at	PHD finger protein 17 (predicted)	Phf17_predicted	310352	0.86	0.31	4.9E-01	3.5E-04	1.00	1.00	1.00	1.00
1367959_a_at	sodium channel, voltage-gated, type I, beta	Scn1b	29866	1.30	0.31	4.7E-01	2.1E-02	1.00	1.00	1.00	1.00
1373270_at	WD repeat domain, phosphoinositide interacting 1 (predicted)	Wip1_predicted	303630	0.94	0.31	8.8E-01	6.9E-04	1.00	1.00	1.00	1.00
1371593_at	Proliferating cell nuclear antigen	Pcna	25737	0.98	0.31	9.7E-01	1.1E-03	1.00	1.00	1.00	1.00
1392530_at	similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	LOC679398	679398	0.70	0.31	2.6E-01	4.0E-03	1.00	1.00	1.00	1.00
1368544_a_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	No3	85383	1.71	0.31	1.1E-01	9.3E-04	1.00	1.00	1.00	1.00
1373839_at	Neighbor of Punc E11 (predicted)	Nope_predicted	363081	1.17	0.31	5.1E-01	3.2E-03	1.00	1.00	0.60	1.00
1374520_at	similar to heart alpha-kinase (predicted)	RGD1564431_predicted	498875	1.30	0.31	4.8E-01	6.3E-03	1.00	1.00	1.00	1.00
1388323_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	362440	0.83	0.31	4.6E-01	1.1E-03	1.00	1.00	1.00	1.00
1388361_at	similar to NADH-ubiquinone oxidoreductase PDSW subunit (Complex I-PDSW) (CI-PDSW)	LOC681418	681418	0.73	0.31	3.1E-01	3.1E-03	1.00	1.00	1.00	1.00
1376750_at	Transcribed locus			0.83	0.31	8.4E-01	5.4E-03	0.00	0.00	0.00	0.50
1389159_at	Transcribed locus			0.86	0.31	7.0E-01	2.3E-03	1.00	0.88	0.00	1.00
1376465_at	Sim ilar to glucocorticoid induced gene 1 (predicted)	RGD1563869_predicted	310233	0.99	0.30	9.9E-01	1.7E-03	1.00	1.00	0.90	1.00
1376302_at	Coilin	Coil	50998	1.14	0.30	5.1E-01	1.2E-03	1.00	0.75	0.00	1.00
1389652_at	Similar to 2700029M09Rik protein (predicted)	RGD1311747_predicted	290706	0.82	0.30	4.8E-01	1.7E-03	1.00	1.00	1.00	1.00
1372684_at	Similar to ovary-specific MOB-like protein (predicted)	RGD1562983_predicted	499288	1.25	0.30	5.6E-01	4.0E-04	1.00	1.00	1.00	1.00
1373167_at	Transcribed locus			0.75	0.30	5.2E-01	8.8E-03	1.00	1.00	0.30	1.00
1373836_at	Forty-two-three domain containing 1	Fyttd1	360726	1.14	0.30	6.9E-01	3.7E-04	1.00	1.00	1.00	1.00
1372440_at	serine (or cysteine) proteinase inhibitor, clade E, member 2	Serpine2	29366	1.12	0.30	8.4E-01	4.5E-03	1.00	1.00	1.00	1.00
1373151_at	similar to RIKEN cDNA 2810489O06 (predicted)	RGD1560177_predicted	499615	0.97	0.30	9.3E-01	1.6E-04	1.00	1.00	1.00	1.00
1377462_at	Transcribed locus			1.24	0.30	7.7E-01	2.5E-02	0.20	0.00	0.00	0.50
1373883_at	Similar to PDZ-domain protein scribble (predicted)	RGD1565055_predicted	362938	0.89	0.30	5.2E-01	3.4E-03	1.00	1.00	0.20	1.00
1375545_at	RNA binding motif protein 9 (predicted)	Rbm9_predicted	362950	1.02	0.30	9.7E-01	1.7E-04	1.00	0.50	0.40	1.00
1368053_at	par-3 (partitioning defective 3) homolog (C, elegans)	Par3	81918	0.91	0.30	8.2E-01	2.6E-03	1.00	0.88	0.00	1.00
1388870_at	similar to RNA-binding protein Musashi2-5 (predicted)	RGD1560397_predicted	366596	0.82	0.30	3.2E-01	1.0E-03	1.00	1.00	1.00	1.00
1368298_at	adenylyl cyclase 5	Adcy5	64532	0.99	0.30	9.7E-01	2.1E-03	1.00	1.00	0.40	1.00
1371475_at	ribonuclease, RNase A family 4	Rnase4	56759	1.36	0.30	1.4E-01	3.4E-02	1.00	1.00	1.00	1.00
1390126_at	Similar to protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	LOC690040	266708	0.93	0.30	8.2E-01	3.2E-03	1.00	1.00	0.50	1.00
1383176_at	similar to C11orf17 protein (predicted)	RGD1306959_predicted	361624	1.14	0.30	8.0E-01	1.2E-02	1.00	1.00	1.00	1.00
1373193_at	Hypothetical protein LOC690089	LOC690089	690089	0.71	0.30	4.9E-01	8.2E-03	1.00	1.00	1.00	1.00
1376770_at	similar to EF hand domain containing 1 (predicted)	RGD1559565_predicted	501181	0.59	0.30	1.0E-01	1.5E-02	1.00	1.00	0.00	1.00
1394234_x_at	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	289181	0.80	0.30	6.7E-01	7.3E-04	0.80	1.00	1.00	1.00
1390711_at				1.03	0.30	9.8E-01	3.9E-02	0.60	0.50	0.00	1.00
1369960_at	GATA binding protein 4	Gata4	54254	0.69	0.30	2.9E-01	8.0E-03	1.00	1.00	1.00	1.00
1390255_at	similar to mKIAA0843 protein (predicted)	RGD1565118_predicted	307395	0.63	0.30	1.4E-01	1.4E-03	1.00	1.00	1.00	1.00
1371202_a_at	nuclear factor I/B	Nf1b	29227	1.08	0.30	8.3E-01	2.2E-04	1.00	1.00	1.00	1.00
1370178_at	calcium channel, voltage-dependent, beta 2 subunit	Caacb2	116600	0.83	0.30	3.3E-01	2.4E-03	1.00	1.00	1.00	1.00
1370816_at	nuclear receptor subfamily 1, group D, member 1	Nr1d1	25297	0.80	0.30	4.0E-01	8.3E-04	1.00	1.00	1.00	1.00
1389333_at	similar to F-box only protein 3 isoform 1	LOC687307	687307	1.11	0.30	7.0E-01	6.2E-04	1.00	1.00	1.00	1.00
1386993_at	myosin, heavy polypeptide 7, cardiac muscle, beta	Myl7	29557	1.93	0.30	5.2E-02	1.8E-02	1.00	1.00	1.00	1.00
1375295_at	Citrate synthase	Cs	170587	1.20	0.30	6.6E-01	4.3E-03	1.00	1.00	1.00	1.00
1388975_at	succinate-Coenzyme A ligase, ADP-forming, beta subunit (predicted)	Sucla2_predicted	361071	0.98	0.30	9.7E-01	1.1E-03	1.00	1.00	1.00	1.00
1375685_at	cytoplasmic linker associated protein 1	Clasp1	304740	0.93	0.30	8.9E-01	1.7E-04	1.00	1.00	1.00	1.00
1387709_at	c-fos induced growth factor	Figf	360457	0.61	0.30	7.3E-02	5.8E-02	0.00	0.00	0.00	0.63
1389332_at	Transcribed locus			1.82	0.30	8.4E-02	2.1E-04	1.00	1.00	1.00	1.00
1373937_at	FYVE and coiled-coil domain containing 1 (predicted)	Fyco1_predicted	301085	1.14	0.29	6.8E-01	1.9E-03	1.00	1.00	1.00	1.00
1388489_at	similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9)	LOC683547	683547	0.78	0.29	5.2E-01	9.9E-03	1.00	1.00	1.00	1.00
1389354_at	similar to semaF cytoplasmic domain associated protein 2	LOC365960	365960	0.69	0.29	2.5E-01	2.7E-03	1.00	1.00	1.00	1.00
1374173_at	Hexosaminidase B	Hexb	294673	0.79	0.29	7.1E-01	1.7E-02	0.80	1.00	0.10	1.00
1388925_at	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	Sirt5	30840	0.92	0.29	7.9E-01	1.6E-03	1.00	1.00	1.00	1.00
1376572_a_at	supervillin (predicted)	Svil_predicted	361256	1.32	0.29	1.8E-01	4.1E-04	1.00	1.00	1.00	1.00
1371634_at	similar to RIKEN cDNA 1810020E01	RGD1305677	295113	0.82	0.29	4.9E-01	3.5E-03	1.00	1.00	1.00	1.00
1372338_at	similar to CG9240-PA	LOC687395	687395	1.06	0.29	9.0E-01	2.5E-03	1.00	1.00	1.00	1.00
1376125_at	Activity and neurotransmitter-induced early gene 11 (ania-11) mRNA, 3' UTR			1.10	0.29	7.0E-01	5.7E-04	1.00	1.00	1.00	1.00
1367828_at	acetyl-Coenzyme A dehydrogenase, short chain	Acads	64304	0.90	0.29	7.9E-01	2.5E-03	1.00	1.00	1.00	1.00
1388908_at	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	Peci	291075	0.86	0.29	5.6E-01	1.4E-03	1.00	1.00	1.00	1.00
1388403_at	similar to NADP+-specific isocitrate dehydrogenase	LOC361596	361596	0.86	0.29	6.1E-01	4.4E-03	1.00	1.00	1.00	1.00
1372762_at	HD domain containing 3 (predicted)	Hddc3_predicted	308758	0.82	0.29	4.0E-01	9.1E-04	1.00	1.00	1.00	1.00

Probe Set ID	Gene Title	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call				
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft	
1374275_at	carbonic anhydrase 11	Car11	308588	0.75	0.29	4.8E-01	8.9E-02	0.80	0.13	0.00	0.75
1377807_a_at	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	289181	1.26	0.29	3.9E-01	8.7E-03	1.00	1.00	1.00	1.00
1375001_at	Transcribed locus			0.50	0.29	9.5E-02	1.2E-02	0.40	1.00	0.00	1.00
1388799_at	kelch-like 7 (Drosophila)	Kih7	362303	1.43	0.29	6.4E-02	1.2E-03	1.00	1.00	1.00	1.00
1372733_at	similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma (predicted)	RGD1311444_predicted	314075	0.99	0.29	9.9E-01	1.2E-03	1.00	1.00	1.00	1.00
1368008_at	prominin 1	Prom1	60357	0.52	0.29	9.8E-02	1.4E-03	1.00	1.00	1.00	1.00
1388569_at	serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpin1	287526	1.55	0.29	2.9E-01	7.6E-02	1.00	1.00	0.80	1.00
1375898_at	similar to RNA binding protein gene with multiple splicing (predicted)	RGD1561067_predicted	498642	1.06	0.29	8.2E-01	1.7E-03	1.00	1.00	1.00	1.00
1372603_at	protein kinase C and casein kinase substrate in neurons 3	Pascin3	311187	1.29	0.29	3.7E-01	2.8E-03	1.00	1.00	1.00	1.00
1373892_at	F-box and leucine-rich repeat protein 17 (predicted)	Fbxl17_predicted	316663	0.89	0.29	6.7E-01	1.4E-03	1.00	1.00	1.00	1.00
1388546_at				1.18	0.29	6.0E-01	2.4E-03	1.00	1.00	1.00	1.00
1367907_a_at	clathrin, light polypeptide (Lcb)	Cltb	116561	1.05	0.29	8.8E-01	2.0E-03	1.00	1.00	1.00	1.00
1372273_at	glycophorin C (Gerbich blood group)	Gypc	364837	0.85	0.29	5.2E-01	3.6E-03	1.00	1.00	1.00	1.00
1374969_at	similar to phosphoglucomutase 5	LOC679990	679990	1.37	0.29	3.0E-01	1.4E-03	1.00	1.00	0.60	1.00
1376785_at	Synaptonemal complex protein 3	Sycp3	25561	0.88	0.29	8.0E-01	3.8E-02	1.00	1.00	0.20	1.00
1368371_at	potassium voltage-gated channel, subfamily Q, member 1	Kcnq1	84020	0.78	0.29	5.0E-01	5.0E-03	0.60	1.00	0.00	0.75
1374278_at	Transcribed locus			0.71	0.29	4.9E-02	3.2E-03	1.00	1.00	0.40	1.00
1377456_at				0.57	0.29	4.7E-01	1.7E-03	1.00	1.00	0.10	1.00
1389527_at	promethin	LOC378467	378467	0.81	0.29	2.3E-01	1.0E-03	1.00	1.00	1.00	1.00
1388343_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (predicted)	Ndufv7_predicted	361385	0.64	0.29	2.3E-01	7.0E-03	1.00	1.00	1.00	1.00
1376200_at	Unknown (protein for MGC:72974)	MGC72974	316976	1.10	0.29	7.9E-01	1.2E-03	1.00	1.00	1.00	1.00
1374171_at	Transcribed locus			1.19	0.28	5.4E-01	1.5E-03	1.00	1.00	1.00	1.00
1369989_at	pyridoxine 5'-phosphate oxidase	Pnpo	64533	0.41	0.28	1.2E-01	7.0E-03	1.00	1.00	0.60	1.00
1388118_at	3-hydroxyisobutyrate dehydrogenase	Hibadh	63938	0.87	0.28	4.3E-01	1.6E-03	1.00	1.00	1.00	1.00
1379380_at	sprouty homolog 1 (Drosophila) (predicted)	Spry1_predicted	294981	1.04	0.28	9.4E-01	2.2E-04	1.00	1.00	0.00	1.00
1373351_at	ankyrin 2, neuronal	Ank2	362036	0.69	0.28	3.8E-01	1.9E-03	1.00	1.00	1.00	1.00
1390664_at	hypothetical protein LOC687361	LOC687361	687361	0.95	0.28	8.9E-01	2.6E-03	1.00	1.00	1.00	1.00
1388465_at	Transcribed locus			1.02	0.28	9.0E-01	3.3E-03	1.00	1.00	1.00	1.00
1386981_at	solute carrier family 16 (monocarboxylic acid transporters), member 1	Slc16a1	25027	1.45	0.28	2.6E-01	1.9E-04	1.00	1.00	1.00	1.00
1385548_at	similar to ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog	LOC687789	687789	0.82	0.28	2.8E-01	4.6E-04	1.00	1.00	0.00	1.00
1367897_at	acyl-Coenzyme A dehydrogenase, very long chain	Acadvl	25363	0.96	0.28	9.2E-01	2.6E-04	1.00	1.00	1.00	1.00
1376692_at	homeodomain interacting protein kinase 2 (predicted)	Hipk2_predicted	362342	1.17	0.28	6.8E-01	1.1E-03	1.00	0.50	0.20	1.00
1398417_at	feminization 1 homolog a (C. elegans)	Fem1a	316131	1.09	0.28	6.7E-01	1.0E-03	1.00	1.00	1.00	1.00
1398265_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	Abcx9	25560	1.46	0.28	2.9E-01	1.7E-03	1.00	1.00	0.60	1.00
1377011_at	similar to hypothetical protein CG003 (predicted)	RGD1307034_predicted	304244	0.85	0.28	6.6E-01	4.8E-04	1.00	1.00	1.00	1.00
1370333_a_at	insulin-like growth factor 1	Igf1	24482	1.37	0.28	3.1E-01	1.2E-03	0.70	0.00	0.80	1.00
1389650_at	Transcribed locus, strongly similar to XP_238535.3 similar to hypothetical protein DKFZp547K1113 [Rattus norvegicus]			0.41	0.28	3.3E-03	1.0E-02	1.00	1.00	0.20	1.00
1387010_s_at	sodium channel, voltage-gated, type I, beta	Scn1b	29686	1.00	0.28	9.9E-01	4.4E-03	1.00	1.00	1.00	1.00
1390480_at	Transcribed locus			0.30	0.28	2.8E-01	5.4E-04	0.00	1.00	0.30	1.00
1374004_at	similar to RIKEN cDNA D030028O16	RGD1310143	298771	1.37	0.28	3.0E-01	2.9E-03	1.00	1.00	1.00	1.00
1370276_at	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Atp5o	192241	0.63	0.28	1.5E-01	4.8E-03	1.00	1.00	1.00	1.00
1377072_at	Transcribed locus, weakly similar to XP_238535.3 similar to ankyrin repeat domain 25 [Rattus norvegicus]			1.08	0.28	7.6E-01	6.1E-04	0.60	0.50	0.00	1.00
1372568_at	EPM2A (laforin) interacting protein 1 (predicted)	Epm2aip1_predicted	316021	1.11	0.28	5.9E-01	1.1E-03	1.00	1.00	1.00	1.00
1371482_at	NADH dehydrogenase (ubiquinone) Fe-S protein 2	Ndufs2	289218	0.90	0.28	6.5E-01	1.7E-03	1.00	1.00	1.00	1.00
1374060_at	Transcribed locus			1.09	0.28	8.6E-01	1.1E-03	1.00	1.00	1.00	1.00
1367678_at	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	Sdha	157074	1.01	0.28	9.8E-01	3.6E-03	1.00	1.00	1.00	1.00
1371554_at	similar to Teletthonin (Ttin cap protein)	LOC688173	688173	0.80	0.28	5.0E-01	1.2E-02	1.00	1.00	1.00	1.00
1383222_at	FERM-domain-containing protein 163SCII	LOC257646	257646	0.95	0.28	8.6E-01	1.7E-03	1.00	1.00	1.00	1.00
1374685_at	Transcribed locus			1.69	0.28	2.6E-01	3.0E-03	1.00	1.00	0.80	1.00
1374466_at	Transcribed locus			1.42	0.28	6.6E-01	1.2E-03	1.00	1.00	0.90	1.00
1390253_at	ankyrin repeat domain 9	Ankrd9	314457	1.13	0.28	7.3E-01	2.4E-02	0.40	0.13	0.00	0.50
1390203_at	Transcribed locus, strongly similar to XP_580018.1 hypothetical protein XP_580018 [Rattus norvegicus]			1.10	0.28	7.7E-01	3.3E-03	1.00	1.00	1.00	1.00
1369127_a_at	prostaglandin F receptor	Ptgfr	25652	0.89	0.28	8.1E-01	1.0E-02	0.50	0.13	0.00	1.00
1387398_at	protein kinase inhibitor, alpha	Pkia	114906	1.36	0.28	2.0E-01	8.1E-03	1.00	1.00	0.00	1.00
1372110_at	Transcribed locus			1.43	0.28	1.8E-01	1.2E-03	1.00	1.00	1.00	1.00
1382446_at	mitochondrial ATP synthase regulatory component factor B	Atp5b	362749	0.85	0.28	6.6E-01	4.0E-04	1.00	1.00	1.00	1.00
1390996_at	SH3-domain GRB2-like B1 (endophilin)	Sh3gbl	29255	0.81	0.28	6.2E-01	1.8E-03	1.00	1.00	1.00	1.00
1390592_at	similar to SH3-domain binding protein 3	LOC688018	688018	0.66	0.28	2.2E-01	2.3E-03	1.00	1.00	1.00	1.00
1373362_at	ubiquinol cytochrome c reductase core protein 2	Uqcrc2	293448	1.08	0.28	8.0E-01	2.0E-03	1.00	1.00	1.00	1.00
1370164_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Hadh	170670	0.89	0.28	7.0E-01	1.5E-03	1.00	1.00	1.00	1.00
1367818_at	coenzyme Q3 homolog, methyltransferase (yeast)	Coq3	29309	0.87	0.28	7.1E-01	8.1E-04	1.00	1.00	0.80	1.00
1372524_at	Transcribed locus			1.03	0.28	9.4E-01	2.2E-04	1.00	1.00	1.00	1.00
1367653_a_at	malate dehydrogenase 1, NAD (soluble)	Mdh1	24551	0.91	0.28	7.9E-01	1.2E-03	1.00	1.00	1.00	1.00
1389610_at	Transcribed locus			1.12	0.28	7.5E-01	2.7E-02	1.00	1.00	0.40	1.00
1386934_at	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Slc6a8	50690	1.79	0.27	1.3E-02	2.7E-03	1.00	1.00	1.00	1.00
1386867_at	brain protein 44-like	Brp44l	171087	0.91	0.27	7.2E-01	4.1E-03	1.00	1.00	1.00	1.00
1377463_at	Mannosidase 2, alpha 2 (predicted)	Man2a2_predicted	308757	0.93	0.27	9.1E-01	7.1E-03	1.00	0.75	0.80	1.00
1374959_at	NAD(P)H dehydrogenase, quinone 2	Nqo2	291084	0.63	0.27	1.3E-01	1.3E-03	1.00	1.00	1.00	1.00
1367869_at	oxidation resistance 1	Oxr1	117520	0.54	0.27	1.3E-01	2.2E-03	1.00	1.00	1.00	1.00
1371388_at	pyruvate dehydrogenase (lipoamide) beta	Pdhb	289950	0.89	0.27	6.2E-01	6.4E-04	1.00	1.00	1.00	1.00
1382061_at	lactate dehydrogenase D	Ldh	307858	0.96	0.27	8.0E-01	1.1E-03	1.00	1.00	0.70	1.00
1390259_at	similar to ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog	LOC687789	687789	0.75	0.27	1.8E-01	4.3E-03	1.00	1.00	1.00	1.00
1373922_at	Transcribed locus			1.76	0.27	2.4E-01	2.9E-04	1.00	1.00	0.70	1.00
1371416_at	NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	293655	0.95	0.27	7.9E-01	1.2E-03	1.00	1.00	1.00	1.00
1371369_at	procollagen, type VI, alpha 2	Col6a2	361821	1.36	0.27	3.7E-01	9.9E-02	0.50	0.25	0.80	1.00
1387059_at	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	54348	0.77	0.27	4.9E-01	2.8E-03	1.00	1.00	1.00	1.00
1369679_a_at	nuclear factor 1A	Nfia	25492	1.25	0.27	5.1E-01	2.2E-03	1.00	1.00	0.60	1.00

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call				
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft	
1373074_at	similar to RIKEN cDNA 2700002I20	RGD1307279	0.83	0.27	5.4E-01	8.1E-04	1.00	1.00	1.00	1.00	
1371323_at	General transcription factor IIIC, polypeptide 5 (predicted)	Gtf3e5_predicted	0.85	0.27	6.6E-01	1.9E-03	1.00	1.00	1.00	1.00	
1388160_a_at	isocitrate dehydrogenase 3 (NAD+) beta	ldh3b	0.92	0.27	7.4E-01	2.1E-03	1.00	1.00	1.00	1.00	
1374698_at	similar to Cytochrome c oxidase polypeptide VIIa-heart, mitochondrial precursor (Cytochrome c oxidase subunit VIIa-H) (COX VIIa-M)	LOC687508	0.89	0.27	7.4E-01	3.2E-04	1.00	1.00	1.00	1.00	
1389253_at	vanin 1	Vnn1	1.57	0.27	3.8E-02	4.3E-04	1.00	1.00	0.00	1.00	
1388304_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (predicted)	Ndufb5_predicted	0.81	0.27	4.1E-01	2.7E-03	1.00	1.00	1.00	1.00	
1369633_at	chemokine (C-X-C motif) ligand 12	Cxcl12	24772	1.81	0.27	1.4E-02	9.1E-03	1.00	1.00	0.90	1.00
1376180_at	Similar to RIKEN cDNA 1700012B09 (predicted)	RGD1561795_predicted	500945	0.58	0.27	3.9E-01	2.6E-03	1.00	1.00	0.10	1.00
1373934_at			0.66	0.27	9.8E-02	1.3E-03	1.00	1.00	1.00	1.00	
1376380_at	Transcribed locus		1.11	0.27	8.7E-01	5.6E-02	0.70	0.75	0.00	1.00	
1371436_at	dimethylarginine dimethylaminohydrolase 2	Ddah2	294239	0.84	0.27	5.4E-01	3.0E-03	0.90	0.50	0.00	1.00
1374710_at	Transcribed locus		0.94	0.27	7.7E-01	7.5E-03	1.00	1.00	1.00	1.00	
1388462_at	similar to SH3-binding kinase	LOC292603	292603	0.93	0.27	7.9E-01	2.8E-02	0.80	0.50	0.00	1.00
1392890_at	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit 45kDa	Pafah1b1	83572	1.21	0.27	8.6E-01	1.6E-02	0.40	0.25	0.00	0.88
1375517_at	tumor protein p53 inducible nuclear protein 2	Trp53inp2	362246	1.09	0.27	6.6E-01	3.7E-04	1.00	1.00	1.00	1.00
1384217_at	zinc fingers and homeobox 2	Zfx2	314988	1.06	0.27	9.5E-01	6.4E-04	1.00	1.00	1.00	1.00
1373223_at	Transcribed locus		0.77	0.26	5.2E-01	3.3E-03	0.00	0.00	0.20	1.00	
1389601_at	nuclear factor 1B	Nf1b	29227	0.89	0.26	6.6E-01	1.3E-03	1.00	1.00	0.90	1.00
1372159_at	Transcribed locus		0.81	0.26	4.0E-01	1.6E-03	1.00	1.00	1.00	1.00	
1377015_at	Transcribed locus		0.75	0.26	3.3E-01	6.9E-04	1.00	1.00	0.20	1.00	
1389180_at	Transcribed locus		0.89	0.26	7.8E-01	2.2E-03	1.00	1.00	0.60	1.00	
1389024_at	similar to Sec1 family domain containing protein 2 (Syntaxin binding protein 1-like 1) (Neuronal Sec1)	LOC498353	498353	0.83	0.26	4.8E-01	1.2E-03	1.00	1.00	0.00	1.00
1373581_at	Similar to KIAA0672 gene product	RGD1305664	303222	1.62	0.26	6.4E-02	3.5E-04	1.00	1.00	0.30	1.00
1386974_at	pleckstrin homology-like domain, family B, member 1	Phldb1	171434	1.22	0.26	8.3E-01	4.4E-03	0.30	0.00	0.00	1.00
1387441_at	potassium channel, subfamily K, member 3	Kenk3	29553	1.35	0.26	2.9E-01	4.0E-03	1.00	1.00	0.70	1.00
1387053_at	flavin containing monooxygenase 1	Fmo1	25256	1.13	0.26	8.0E-01	8.3E-04	1.00	1.00	0.10	1.00
1376184_at	Ly6/neurotoxin 1 (predicted)	Lynx1_predicted	300018	0.56	0.26	2.3E-01	9.5E-04	1.00	1.00	0.20	1.00
1388469_at	Insulin-like growth factor 1	Igf1	24482	1.52	0.26	3.7E-01	8.8E-03	1.00	1.00	1.00	1.00
1398378_at	glutathione S-transferase kappa 1	Gstk1	297029	0.82	0.26	4.3E-01	2.0E-03	1.00	1.00	1.00	1.00
1371576_at	mitochondrial ribosomal protein S36 (predicted)	Mrps36_predicted	294696	0.72	0.26	3.5E-01	2.1E-03	1.00	1.00	1.00	1.00
1387914_at	cytochrome P450, family 27, subfamily a, polypeptide 1	Cyp27a1	301517	0.77	0.26	5.3E-01	1.8E-03	1.00	1.00	1.00	1.00
1388611_at	transcription elongation factor A (SID), 3	Tea3	298559	0.67	0.26	2.8E-01	3.1E-03	1.00	1.00	1.00	1.00
1399056_at	similar to CG10585-PA	LOC365592	365592	0.74	0.26	3.3E-01	4.0E-02	0.80	1.00	0.00	1.00
1398249_at	solute carrier family 25 (mitochondrial carnitine/aclycarnitine translocase), member 20	Slc25a20	117035	0.70	0.26	2.5E-01	3.0E-04	1.00	1.00	1.00	1.00
1390020_at	Similar to HORMA domain containing 2	LOC498400	305479	1.04	0.26	9.2E-01	1.2E-03	1.00	1.00	1.00	1.00
1370068_at	phospholipase A2, group V	Pla2g5	29354	0.76	0.26	3.8E-01	3.1E-04	1.00	1.00	0.00	1.00
1375916_at	protein-L-isospartate (D-aspartate) O-methyltransferase domain containing 2 (predicted)	Pcmtd2_predicted	311726	1.02	0.26	9.8E-01	4.6E-04	1.00	1.00	1.00	1.00
1368358_a_at	protein tyrosine phosphatase, receptor type, R	Ptprr	94202	1.47	0.26	2.3E-01	8.0E-03	1.00	1.00	1.00	1.00
1374179_at			1.00	0.26	9.9E-01	2.5E-03	1.00	1.00	1.00	1.00	
1367572_at	myosin, light polypeptide 3	My13	24585	0.86	0.26	6.7E-01	3.8E-03	1.00	1.00	1.00	1.00
1374635_at	Hypothetical protein LOC689663	LOC689663	689663	1.42	0.26	3.5E-01	6.3E-02	0.20	0.13	0.00	0.50
1367680_at	acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	50681	1.00	0.26	9.9E-01	1.3E-03	1.00	1.00	1.00	1.00
1370865_at	isocitrate dehydrogenase 3 (NAD), gamma	ldh3g	25179	0.75	0.26	2.9E-01	2.2E-03	1.00	1.00	1.00	1.00
1373564_at	3-hydroxyisobutyryl-Coenzyme A hydrolase	Hibch	301384	1.15	0.26	7.7E-01	9.1E-04	1.00	1.00	1.00	1.00
1371864_at	Transcribed locus		0.93	0.26	7.7E-01	4.3E-04	1.00	1.00	1.00	1.00	
1388692_at	similar to spermatogenesis associated 11	LOC679944	679944	0.57	0.26	1.0E-01	2.8E-03	1.00	1.00	1.00	1.00
1368059_at	crystallin, mu	Crym	117024	0.70	0.26	2.8E-01	4.2E-04	1.00	1.00	1.00	1.00
1372109_at	Pre-B-cell leukemia transcription factor interacting protein 1	Pbixp1	310644	0.65	0.25	3.5E-01	4.1E-03	1.00	1.00	1.00	1.00
1376214_at	Transcribed locus		1.15	0.25	5.7E-01	1.9E-03	1.00	1.00	1.00	1.00	
1372248_at	sestrin 1 (predicted)	Sesn1_predicted	294518	0.84	0.25	6.3E-01	2.5E-03	1.00	1.00	1.00	1.00
1368013_at	DNA-damage-inducible transcript 4-like	Ddit4l	140582	0.72	0.25	4.8E-01	1.2E-02	1.00	1.00	0.00	1.00
1377381_at	Transcribed locus		0.83	0.25	5.1E-01	2.0E-04	1.00	1.00	0.90	1.00	
1388688_at	Transcribed locus		0.75	0.25	2.1E-01	1.7E-03	1.00	1.00	1.00	1.00	
1374160_at	similar to RIKEN cDNA 1110063G11 (predicted)	RGD1311960_predicted	305095	0.49	0.25	4.9E-02	3.7E-04	1.00	1.00	1.00	1.00
1371736_at	hypothetical protein LOC679333	LOC679333	679333	0.65	0.25	2.3E-01	1.3E-03	1.00	1.00	1.00	1.00
1389964_at	TBC1 domain family, member 19 (predicted)	Tbc1d19_predicted	289657	0.80	0.25	5.4E-01	7.4E-03	1.00	1.00	1.00	1.00
1372507_at	T-cell leukemia translocation altered gene	Teia	306587	0.79	0.25	5.9E-01	1.1E-03	1.00	1.00	0.80	1.00
1390852_x_at	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	289181	1.36	0.25	4.2E-01	2.7E-03	1.00	1.00	1.00	1.00
1389015_at	similar to FUN14 domain containing 2 (predicted)	RGD1560916_predicted	361288	0.56	0.25	2.1E-02	9.8E-04	1.00	1.00	1.00	1.00
1372639_at	triptartite motif-containing 54	Trim54	362708	1.59	0.25	1.8E-01	6.0E-03	1.00	1.00	1.00	1.00
1371041_at	NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	81728	0.85	0.25	5.6E-01	1.3E-03	1.00	1.00	1.00	1.00
1398343_at	similar to Dnaj (Hsp40) homolog, subfamily A, member 4	Ndufv2	498996	0.89	0.25	5.8E-01	5.7E-04	1.00	1.00	1.00	1.00
1377773_at	Transcribed locus, weakly similar to NP_766020.1 cDNA C030002O17 [Mus musculus]		0.65	0.25	4.5E-01	4.6E-02	0.40	0.50	0.00	0.50	
1374515_at	similar to RIKEN cDNA 6330409N04	RGD1306437	290303	0.82	0.25	6.0E-01	1.3E-03	1.00	1.00	1.00	1.00
1368618_at	growth factor receptor bound protein 14	Grb14	58844	1.16	0.25	6.3E-01	6.7E-04	1.00	1.00	1.00	1.00
1389966_at	procollagen, type VI, alpha 3 (predicted)	Col6a3_predicted	367313	1.10	0.25	8.0E-01	4.8E-02	1.00	1.00	1.00	1.00
1387039_at	glypican 1	Gpc1	58920	0.98	0.25	9.4E-01	3.3E-04	1.00	1.00	1.00	1.00
1389572_at	malic enzyme 3, NADP(+)-dependent, mitochondrial (predicted)	Me3_predicted	361602	1.03	0.25	9.3E-01	2.5E-03	1.00	1.00	0.80	1.00
1376194_at	Transcribed locus		1.21	0.25	7.1E-01	1.1E-03	1.00	0.88	1.00	1.00	
1373186_at	similar to RIKEN cDNA 5033405K12 (predicted)		0.80	0.25	3.2E-01	1.1E-03	1.00	1.00	1.00	1.00	
1374726_at	fibronectin type III domain containing 1	Fndc1	308099	1.07	0.25	9.2E-01	2.0E-02	0.00	0.25	0.20	1.00
1388447_at	similar to limb-bud and heart	LOC683626	683626	1.00	0.25	9.9E-01	3.9E-04	1.00	1.00	1.00	1.00
1388194_at	dihydropyrimidine S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Diat	81654	1.24	0.25	2.9E-01	3.2E-03	1.00	1.00	1.00	1.00
1373659_at	hypothetical protein LOC688257	LOC688257	688257	1.23	0.25	7.7E-01	5.7E-03	1.00	1.00	0.00	1.00
1373312_at	Transcribed locus		0.77	0.25	6.5E-01	1.1E-02	1.00	1.00	0.00	1.00	
1372583_at	Transcribed locus		1.38	0.25	4.0E-01	8.1E-04	1.00	1.00	1.00	1.00	
1368827_at	GATA binding protein 6	Gata6	29300	1.24	0.25	2.9E-01	2.0E-04	1.00	1.00	0.00	1.00

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1368064_a_at	dopa decarboxylase	Ddc	24311	1.17	0.25	6.2E-01	1.1E-03	1.00	1.00	0.60	1.00
1373790_at				0.87	0.25	7.6E-01	2.9E-03	1.00	1.00	0.00	1.00
1380854_at	R3H domain containing 1	R3hdm1	304763	0.99	0.24	9.9E-01	1.0E-03	1.00	1.00	1.00	1.00
1371995_at	kelch-like 21 (Drosophila) (predicted)	Kihl21_predicted	313743	1.07	0.24	8.6E-01	1.5E-02	1.00	0.88	0.00	1.00
1370541_at	nuclear receptor subfamily 1, group D, member 2	Nr1d2	259241	1.06	0.24	9.2E-01	8.6E-03	1.00	1.00	1.00	1.00
1388902_at	lysyl oxidase-like 1	Lox1l	315714	0.23	0.24	2.5E-01	2.4E-02	0.00	0.00	0.30	1.00
1377563_at	similar to leiomodin 3 (fetal) (predicted)	RGD1564924_predicted	500267	1.33	0.24	4.7E-01	8.8E-04	1.00	1.00	0.00	1.00
1372084_at	protein tyrosine phosphatase 4a3 (predicted)	Ptp4a3_predicted	362930	1.13	0.24	7.0E-01	1.1E-03	1.00	1.00	1.00	1.00
1374705_at	collagen, type IV, alpha 5 (predicted)	Col4a5_predicted	363457	0.97	0.24	9.7E-01	1.7E-04	1.00	1.00	1.00	1.00
1370312_at	spondin 1	Spon1	64456	2.40	0.24	5.2E-02	1.0E-02	1.00	1.00	1.00	1.00
1368132_at	transducer of ErbB-2.1	Tob1	170842	0.86	0.24	6.2E-01	1.3E-03	1.00	1.00	1.00	1.00
1376672_at	Transcribed locus			1.19	0.24	4.5E-01	5.8E-04	1.00	1.00	1.00	1.00
1373278_at	nuclear factor, erythroid derived 2,-like 1 (predicted)	Nfe2l1_predicted	360610	0.37	0.24	3.1E-03	5.2E-04	1.00	1.00	1.00	1.00
1372727_at	Transcribed locus			0.86	0.24	6.8E-01	5.3E-04	1.00	1.00	1.00	1.00
1374235_at	Down syndrome critical region gene 1-like 1	Dscr11	140666	0.87	0.24	7.2E-01	1.3E-03	1.00	1.00	0.10	1.00
1390430_at	Nuclear receptor subfamily 1, group D, member 2	Nr1d2	259241	0.75	0.24	3.3E-01	1.3E-03	1.00	1.00	1.00	1.00
1367694_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Hadhb	171155	0.85	0.24	5.2E-01	9.3E-04	1.00	1.00	1.00	1.00
1377423_at	Transcribed locus			0.86	0.24	6.6E-01	1.9E-02	0.90	0.63	0.20	1.00
1370258_at	basic leucine zipper and W2 domains 2	Bzw2	171439	0.80	0.24	5.4E-01	2.2E-04	1.00	1.00	1.00	1.00
1373016_at	dihydropyrimidine dehydrogenase	Dhl	298942	0.94	0.24	9.3E-01	1.0E-03	1.00	1.00	1.00	1.00
1374218_at	similar to IQ motif and Sec7 domain 2	LOC683475	683475	0.87	0.24	6.8E-01	1.4E-03	1.00	1.00	1.00	1.00
1368892_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	Cap2	116653	1.03	0.24	9.3E-01	4.6E-03	1.00	1.00	0.60	1.00
1368114_at	fibroblast growth factor 13	Fgf13	84488	0.96	0.24	8.8E-01	8.8E-04	1.00	1.00	1.00	1.00
1387669_a_at	epoxide hydrolase 1, microsomal	Ephx1	25315	0.83	0.24	4.8E-01	3.7E-03	0.60	1.00	0.00	1.00
1387795_at	polymerase (DNA directed), alpha 2	Pola2	85242	1.39	0.24	3.6E-01	2.7E-02	1.00	1.00	0.00	0.75
1370389_at	glycoprotein m6b	Gpm6b	192179	1.40	0.24	4.9E-01	4.2E-02	0.60	0.50	0.20	1.00
1367687_a_at	peptidylglycine alpha-amidating monooxygenase	Pam	25508	0.95	0.24	8.2E-01	4.1E-03	1.00	1.00	1.00	1.00
1371414_at	gelsoin	Gsn	296654	1.14	0.24	7.1E-01	3.7E-04	1.00	1.00	1.00	1.00
1389521_at	Transcribed locus, strongly similar to NP_445868.1 perinuclear RNA-binding protein [Rattus norvegicus]	Mnab_predicted	311909	0.86	0.24	5.4E-01	4.9E-04	1.00	1.00	1.00	1.00
1373212_at	mitochondrial ATP synthase regulatory component factor B	Atp5b	362749	0.76	0.24	2.9E-01	2.4E-03	1.00	1.00	0.20	1.00
1389376_at	Transcribed locus			0.97	0.24	9.3E-01	3.7E-04	1.00	1.00	0.80	1.00
1369949_at	basal cell adhesion molecule	Beam	78958	0.99	0.24	9.9E-01	8.0E-04	1.00	1.00	0.00	1.00
1373371_a_at	similar to RIKEN cDNA 1110001J03	MGC112899	500087	0.66	0.24	2.1E-01	1.5E-03	1.00	1.00	1.00	1.00
1375223_at				0.74	0.24	5.3E-01	2.4E-02	1.00	1.00	0.20	1.00
1372925_at	sirtuin 3 (silent mating type information regulation 2, homolog 3 (S. cerevisiae)) (predicted)	Sirt3_predicted	293615	0.87	0.23	3.5E-01	1.4E-03	1.00	1.00	0.60	1.00
1370814_at	dehydrogenase/reductase (SDR family) member 4	Dhrs4	266686	0.95	0.23	8.2E-01	3.7E-04	1.00	1.00	1.00	1.00
1372695_at	Fibronectin type III domain containing 5	Fndc5	260327	0.84	0.23	2.6E-01	2.0E-03	1.00	1.00	1.00	1.00
1371954_at	tensin	Tns	29136	1.07	0.23	8.3E-01	1.9E-03	1.00	1.00	1.00	1.00
1376498_at	similar to 2900002H16Rik protein (predicted)	RGD1307973_predicted	304469	0.76	0.23	5.3E-02	1.2E-03	1.00	1.00	1.00	1.00
1367813_at	protein phosphatase 1, regulatory (inhibitor) subunit 14A	Ppp1r14a	114004	1.07	0.23	8.5E-01	9.2E-02	0.20	0.00	0.10	1.00
1372044_at	similar to Ser-Thr-rich protein T10 in DGCR region (predicted)	RGD1310348_predicted	360738	0.82	0.23	6.2E-01	1.0E-03	1.00	1.00	1.00	1.00
1375297_at	similar to RIKEN cDNA 0610008C08 (predicted)	RGD1565289_predicted	363474	1.09	0.23	8.6E-01	6.3E-04	1.00	1.00	1.00	1.00
1370656_a_at	homer homolog 1 (Drosophila)	Homer1	29546	1.03	0.23	9.6E-01	3.5E-02	0.80	0.50	0.00	0.50
1372864_at	Transcribed locus			0.85	0.23	5.9E-01	5.0E-04	1.00	1.00	1.00	1.00
1375092_at	Transcribed locus, moderately similar to XP_620246.2 myosin XVIIIb [Mus musculus]			0.92	0.23	8.9E-01	7.4E-04	1.00	1.00	0.10	1.00
1398396_at	Transcribed locus			0.91	0.23	6.6E-01	1.3E-02	0.20	0.50	0.00	1.00
1372856_at	Transcribed locus			1.46	0.23	1.1E-01	1.6E-03	1.00	1.00	0.60	1.00
1368154_at	guanylate cyclase 1, soluble, alpha 3	Gucyl1a3	497757	1.02	0.23	9.7E-01	4.0E-03	0.40	0.38	0.00	1.00
1389020_at	similar to immunoglobulin superfamily containing leucine-rich repeat	LOC686539	686539	0.64	0.23	2.8E-01	3.7E-04	1.00	1.00	1.00	1.00
1368574_at	adrenergic receptor, alpha 1b	Adra1b	24173	0.46	0.23	1.1E-01	2.7E-03	1.00	1.00	1.00	1.00
1390449_at	CDNA clone IMAGE:7309127			1.46	0.23	2.4E-01	1.2E-03	1.00	1.00	1.00	1.00
1372168_s_at	insulin-like growth factor binding protein 6	Igfbp6	25641	0.49	0.23	1.0E-01	2.4E-03	0.80	1.00	0.70	1.00
1389543_at	mannan-binding lectin serine peptidase 1	Masp1	64023	1.04	0.23	9.3E-01	6.7E-04	1.00	1.00	1.00	1.00
1376170_at				0.92	0.23	9.0E-01	2.0E-02	0.00	0.25	0.00	1.00
1371253_at	electron transferring flavoprotein, alpha polypeptide	Erf1a	300726	0.84	0.23	4.8E-01	4.6E-04	1.00	1.00	1.00	1.00
1370342_at	potassium channel, subfamily K, member 2	Kenk2	170899	0.37	0.23	5.3E-02	1.9E-03	1.00	1.00	0.00	1.00
1388143_at	tensin XA	Tnsx	25602	1.51	0.23	3.1E-01	2.8E-03	1.00	1.00	0.30	1.00
1374039_at	lchyl homolog E3 ubiquitin protein ligase (mouse)	Lch	311567	0.77	0.23	5.0E-01	1.5E-03	1.00	1.00	0.00	1.00
1388804_at	Transcribed locus			1.37	0.23	4.8E-01	6.2E-02	0.70	0.50	0.00	1.00
1372199_at	PTEN induced putative kinase 1 (predicted)	Pink1_predicted	298575	0.94	0.23	7.6E-01	1.3E-03	1.00	1.00	1.00	1.00
1368429_at	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	Taf9l	171152	1.07	0.23	9.2E-01	1.9E-03	1.00	0.75	0.30	1.00
1372289_at	similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (predicted)	RGD1561141_predicted	311122	0.82	0.23	3.3E-01	3.7E-04	1.00	1.00	1.00	1.00
1390420_at	carboxypeptidase X 1 (M14 family) (predicted)	Cpxm1_predicted	296156	0.79	0.23	5.3E-01	2.0E-03	0.00	0.25	0.00	1.00
1372720_at	BTB (POZ) domain containing 1	Btb1	293060	0.73	0.23	5.2E-02	5.5E-04	1.00	1.00	1.00	1.00
1377060_at	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mccc2	361884	1.01	0.23	9.6E-01	1.7E-03	1.00	1.00	1.00	1.00
1369674_at	purinergic receptor P2X, ligand-gated ion channel, 5	P2rx5	113995	0.99	0.23	9.9E-01	6.9E-04	1.00	1.00	1.00	1.00
1370165_at	small muscle protein, X-linked	Smpx	84416	0.92	0.23	8.4E-01	1.1E-02	1.00	1.00	1.00	1.00
1372979_at	Transcribed locus			1.06	0.23	8.0E-01	5.8E-03	1.00	1.00	1.00	1.00
1374352_at	actin alpha cardiac 1	Act1	29275	0.94	0.22	8.3E-01	1.1E-02	1.00	1.00	1.00	1.00
1386914_at	guanosine monophosphate reductase	Gmpr	117533	0.95	0.22	9.0E-01	8.9E-04	1.00	1.00	1.00	1.00
1389386_at				0.82	0.22	5.5E-01	3.2E-04	1.00	1.00	0.60	1.00
1376912_at	hypothetical LOC287388 (predicted)	RGD1310324_predicted	287388	0.84	0.22	5.1E-01	3.5E-02	1.00	1.00	0.40	1.00
1379936_at	Tropomyosin 1, alpha	Tpm1	24851	1.26	0.22	6.6E-01	4.1E-02	1.00	0.88	0.20	1.00
1389704_at	Transcribed locus			1.26	0.22	2.0E-01	3.9E-04	1.00	1.00	0.00	1.00
1384309_at	Transcribed locus			1.00	0.22	1.0E+00	1.8E-03	1.00	1.00	0.20	1.00
1368772_at	solute carrier family 4, member 3	Slc4a3	24781	0.81	0.22	2.8E-01	5.2E-05	1.00	1.00	1.00	1.00
1368440_at	solute carrier family 3, member 1	Slc3a1	29484	0.16	0.22	1.7E-01	8.6E-04	0.00	1.00	0.60	1.00

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Strain Effect		Fold Change		Rejection Effect		False Discovery Rate		Average Present Call		
				Native BN / DA	Allograft / Isograft	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft			
1377448_at	transmembrane protein 38a (predicted)	Tmem38a_predicted	306327	1.03	0.22	9.6E-01	3.5E-02	1.00	1.00	0.00	0.75			
1388617_at	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	361239	0.54	0.22	1.5E-01	7.3E-03	1.00	1.00	0.10	1.00			
1368673_at	discoidin domain receptor family, member 2	Ddr2	83573	1.60	0.22	7.0E-01	2.5E-02	0.00	0.00	0.00	0.88			
1386921_at	carboxypeptidase E	Cpe	25669	0.80	0.22	4.5E-01	7.3E-03	1.00	1.00	1.00	1.00			
1370981_at	retinoid X receptor gamma	Rxrg	83574	0.94	0.22	8.6E-01	4.6E-04	1.00	1.00	0.20	1.00			
1375549_at	Transcribed locus			0.71	0.22	4.8E-01	1.8E-03	1.00	1.00	0.00	1.00			
1386880_at	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacetyl-Coenzyme A thiolase)	Acat2	170465	0.81	0.22	7.0E-01	1.3E-03	1.00	1.00	1.00	1.00			
1388305_at	v-rat murine sarcoma 3611 viral oncogene homolog	Araf	64363	0.71	0.22	5.8E-01	4.1E-04	1.00	1.00	1.00	1.00			
1387370_at	tropomodulin 1	Tmod1	25566	1.51	0.22	2.1E-01	3.1E-03	1.00	1.00	0.50	1.00			
1367913_at	cytoglobin	Cygb	170520	1.04	0.22	9.4E-01	2.1E-03	1.00	1.00	0.70	1.00			
1388423_at	hypothetical protein MGC:15854	RGD1302996	294231	0.88	0.22	6.5E-01	2.8E-03	1.00	1.00	1.00	1.00			
1368642_at	cadherin 2	Cdh2	83501	0.99	0.22	9.9E-01	1.7E-03	1.00	1.00	1.00	1.00			
1384466_at	notch1-induced protein	LOC493574	493574	1.15	0.22	7.8E-01	4.8E-04	1.00	1.00	1.00	1.00			
1387814_at	caveolin 3	Cav3	29161	1.04	0.22	9.3E-01	1.1E-02	1.00	1.00	0.50	1.00			
1373178_at	Transcribed locus			1.28	0.22	4.9E-01	5.9E-04	1.00	1.00	0.50	1.00			
1389334_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10	314071	0.58	0.22	6.9E-02	2.7E-03	1.00	1.00	1.00	1.00			
1368317_at	aquaporin 7	Aqp7	29171	0.51	0.22	1.2E-01	9.9E-04	1.00	1.00	1.00	1.00			
1377266_at	Transcribed locus					9.5E-01	2.6E-03	0.40	0.13	0.00	0.75			
1388471_at	-complex 11 (mouse) like 2	Tsp112	314683	1.35	0.22	2.4E-01	6.7E-04	1.00	1.00	1.00	1.00			
1388364_at	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (predicted)	Ndufs3_predicted	295923	0.75	0.22	3.6E-01	1.1E-03	1.00	1.00	1.00	1.00			
1387018_at	Arg/Abi-interacting protein ArgBP2	Argbp2	114901	1.03	0.22	8.6E-01	7.2E-03	1.00	1.00	1.00	1.00			
1389256_at	Transcribed locus			1.44	0.22	7.4E-02	4.0E-04	1.00	1.00	1.00	1.00			
1370419_a_at	SH3-domain kinase binding protein 1	Sh3kbp1	84357	0.89	0.22	7.8E-01	3.7E-04	1.00	1.00	1.00	1.00			
1377452_at	Transcribed locus			1.99	0.21	1.4E-01	6.1E-02	0.60	0.00	0.00	0.75			
1368700_at	phospholipase C-like 1	Plcl1	84587	1.00	0.21	9.9E-01	2.9E-02	0.20	0.50	0.10	0.75			
1389423_at	Discoidin domain receptor family, member 2	Ddr2	83573	1.22	0.21	5.9E-01	7.8E-03	1.00	1.00	1.00	1.00			
1369926_at	glutathione peroxidase 3	Gpx3	64317	1.27	0.21	5.7E-01	8.6E-03	1.00	1.00	1.00	1.00			
1375698_at	Transcribed locus			0.75	0.21	3.6E-01	6.2E-04	1.00	1.00	0.00	1.00			
1390339_at	Transcribed locus			0.97	0.21	9.3E-01	9.3E-04	1.00	1.00	1.00	1.00			
1372736_at	amylase-1, 6-glucosidase, 4-alpha-glucanotransferase	Agl_predicted	362029	1.12	0.21	7.1E-01	3.7E-04	1.00	1.00	1.00	1.00			
1374062_x_at	microtubule-associated protein, RPB family, member 3	Mapr3	298848	0.87	0.21	5.7E-01	7.2E-04	1.00	1.00	0.40	1.00			
1398354_at	catenin (cadherin associated protein), alpha-like 1 (predicted)	Ctnna1_predicted	298019	0.71	0.21	2.3E-01	2.7E-03	1.00	1.00	0.80	1.00			
1373810_at	phospholipase A2, group X1A (predicted)	Pla2g12a_predicted	362039	0.46	0.21	5.9E-02	5.3E-02	1.00	1.00	0.00	0.75			
1376441_at	similar to RIKEN cDNA 1810048J11 (predicted)	RGD1305147_predicted	314219	0.66	0.21	4.1E-01	1.2E-03	0.80	1.00	0.00	1.00			
1367735_at	acetyl-Coenzyme A dehydrogenase, long-chain	Acatd	25287	0.90	0.21	6.6E-01	1.1E-03	1.00	1.00	1.00	1.00			
1369876_at	guanine nucleotide binding protein, beta 3	Gnb3	60449	0.98	0.21	9.7E-01	1.4E-03	1.00	1.00	0.30	1.00			
1372266_at	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	Rev3l	309812	0.82	0.21	6.4E-01	1.0E-03	1.00	1.00	1.00	1.00			
1390130_at	Transcribed locus			1.02	0.21	9.6E-01	4.9E-04	1.00	1.00	1.00	1.00			
1373921_at	similar to enoyl Coenzyme A hydratase domain containing 3	LOC684538	684538	0.95	0.21	9.6E-01	2.3E-03	1.00	1.00	0.50	1.00			
1369065_a_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	29693	0.89	0.21	7.1E-01	4.1E-03	1.00	1.00	1.00	1.00			
1371412_a_at	Neuronal regeneration related protein	Nrep	338475	0.68	0.21	4.4E-01	6.5E-04	1.00	1.00	1.00	1.00			
1370678_s_at	monoamine oxidase A	Maoa	29253	1.28	0.21	5.8E-01	1.2E-03	1.00	1.00	1.00	1.00			
1374353_x_at	actin alpha cardiac 1	Actc1	29275	1.04	0.21	9.0E-01	1.0E-02	1.00	1.00	1.00	1.00			
1388133_at	cold shock domain containing C2, RNA binding	Cskc2	266600	0.79	0.21	3.8E-01	7.5E-04	1.00	1.00	0.00	1.00			
1387197_at	osteomodulin	Omd	83717	0.87	0.21	7.4E-01	1.7E-03	0.80	1.00	0.20	1.00			
1370301_at	matrix metalloproteinase 2	Mmp2	81866	1.23	0.21	6.0E-01	4.4E-02	1.00	1.00	1.00	1.00			
1377808_at	Similar to IQ motif and WD repeats 1 (predicted)	RGD1561961_predicted	289181	1.38	0.21	4.1E-01	5.9E-03	1.00	1.00	1.00	1.00			
1389179_at	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (predicted)	Cidea_predicted	291541	0.82	0.21	5.8E-01	4.8E-04	1.00	1.00	1.00	1.00			
1370018_at	heat shock 27kDa protein 2	Hspb2	161476	0.85	0.21	4.8E-01	2.2E-02	1.00	1.00	0.90	1.00			
1370328_at	dickkopf homolog 3 (Xenopus laevis)	Dkk3	171548	1.30	0.20	5.2E-01	1.8E-03	1.00	1.00	0.20	1.00			
1398326_at	similar to Nur77 downstream protein 2	MGC105647	361824	0.84	0.20	5.6E-01	2.5E-03	1.00	1.00	1.00	1.00			
1374389_at	guanylate cyclase 1, soluble, beta 3	Gucylb3	25202	0.76	0.20	5.4E-01	6.8E-02	0.50	0.25	0.20	0.88			
1371886_at	carnitine acetyltransferase	Crat	311849	0.63	0.20	8.4E-02	3.4E-03	1.00	1.00	1.00	1.00			
1376015_at				1.14	0.20	5.9E-01	2.0E-02	1.00	1.00	0.20	1.00			
1371609_at	homolog of zebrafish ES1	RGD1303003	294326	0.86	0.20	5.1E-01	1.6E-03	1.00	1.00	1.00	1.00			
1387957_a_at	SH3-domain kinase binding protein 1	Sh3kbp1	84357	1.02	0.20	9.7E-01	1.2E-03	1.00	1.00	1.00	1.00			
1388783_at	transcription factor 21	Tcf21	252856	1.19	0.20	7.0E-01	2.7E-02	1.00	1.00	0.20	1.00			
1374454_at	protein-L-isospartate (D-aspartate) O-methyltransferase domain containing 2 (predicted)	Pemt2_predicted	311726	1.12	0.20	7.9E-01	2.3E-04	1.00	1.00	1.00	1.00			
1368098_a_at	small nuclear ribonucleoprotein N	Snrpn	81781	0.72	0.20	3.6E-01	3.7E-03	1.00	1.00	0.00	1.00			
1370930_at	Active BCR-related gene (predicted)	Abr_predicted	287537	0.99	0.20	9.6E-01	9.9E-04	1.00	1.00	1.00	1.00			
1368894_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	Cap2	116653	1.07	0.20	8.4E-01	1.1E-03	1.00	1.00	0.60	1.00			
1369625_at	aquaporin 1	Aqp1	25240	0.95	0.20	9.1E-01	1.1E-03	1.00	1.00	1.00	1.00			
1376537_at	Protein tyrosine phosphatase, non-receptor type 3	Ptpn3	362524	0.38	0.20	1.2E-02	5.3E-04	0.80	1.00	0.40	1.00			
1373684_at	Transcribed locus			1.22	0.20	4.2E-01	2.3E-03	1.00	1.00	0.80	1.00			
1388697_at	inositol polyphosphate-5-phosphatase A (predicted)	Inpp5a_predicted	365382	0.91	0.20	7.0E-01	7.9E-04	1.00	1.00	1.00	1.00			
1398248_s_at	myosin, heavy polypeptide 6, cardiac muscle, alpha	Myh6	29556	1.13	0.20	6.7E-01	1.4E-02	1.00	1.00	1.00	1.00			
1386951_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	Ndufa5	25488	0.59	0.20	2.9E-01	1.1E-03	1.00	1.00	1.00	1.00			
1371965_at	similar to Propionyl-CoA carboxylase alpha chain, mitochondrial precursor	LOC687008	687008	0.84	0.20	4.7E-01	8.2E-04	1.00	1.00	0.80	1.00			
1371358_at	glycoprotein, synaptic 2	Gpsn2	191576	1.10	0.20	7.2E-01	1.6E-03	1.00	1.00	1.00	1.00			
1389757_at	Metadherin	Muh	170910	0.77	0.20	4.4E-01	2.7E-02	1.00	1.00	0.00	1.00			
1370550_at	limbic system-associated membrane protein	Lsamp	29561	0.74	0.20	3.4E-01	6.9E-03	0.70	1.00	0.00	0.75			
1370209_at	Kruppel-like factor 9	Klf9	117560	0.78	0.20	4.4E-01	3.9E-04	1.00	1.00	1.00	1.00			
1388583_at	chemokine (C-X-C motif) ligand 12	Cxcl12	24772	1.14	0.20	5.9E-01	1.7E-03	1.00	1.00	1.00	1.00			
1371577_at	NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	301458	1.04	0.20	7.9E-01	2.8E-04	1.00	1.00	1.00	1.00			
1371483_at	nicotinamide nucleotide transhydrogenase (mapped)	Nnt	310378	0.78	0.20	2.5E-01	1.2E-03	1.00	1.00	1.00	1.00			
1387401_at	calsequestrin 2	Casq2	29209	0.93	0.20	7.6E-01	5.8E-04	1.00	1.00	1.00	1.00			
1371625_at	brain glycogen phosphorylase	Pygb	25739	0.94	0.19	9.0E-01	4.0E-04	1.00	1.00	1.00	1.00			

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1388718_at	tropomodulin 1	Tmod1	25566	1.23	0.19	4.0E-01	1.00	1.00	1.00	1.00	1.00
1368272_at	glutamate oxaloacetate transaminase 1	Got1	24401	1.16	0.19	6.8E-01	4.8E-04	1.00	1.00	1.00	1.00
1389772_at	Transcribed locus			0.86	0.19	3.6E-01	2.8E-02	1.00	1.00	1.00	1.00
1368322_at	superoxide dismutase 3, extracellular	Sod3	25352	1.15	0.19	6.0E-01	4.8E-04	1.00	1.00	0.30	1.00
1376222_at	similar to HCD1 protein (predicted)	RGD1309307_predicted	361044	0.83	0.19	5.8E-01	1.3E-03	1.00	1.00	0.00	0.88
1388358_at	electron-transfer-flavoprotein, beta polypeptide	Etfb	292845	0.88	0.19	7.0E-01	6.2E-04	1.00	1.00	1.00	1.00
1367589_at	aconitase 2, mitochondrial	Aco2	79250	0.97	0.19	9.4E-01	4.5E-04	1.00	1.00	1.00	1.00
1370390_at	coronin, actin binding protein 6	Coro6	245982	1.14	0.19	5.4E-01	1.2E-03	1.00	1.00	1.00	1.00
1369085_s_at	small nuclear ribonucleoprotein N	Snrp	113938	1.03	0.19	9.6E-01	7.9E-04	1.00	1.00	1.00	1.00
1367777_at	2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	117543	0.83	0.19	4.8E-01	1.0E-03	1.00	1.00	1.00	1.00
1373604_at	hypothetical protein LOC680199	LOC680199	680199	0.79	0.19	2.3E-01	1.0E-02	1.00	1.00	0.00	1.00
1370237_at	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	Hadhs	113965	1.01	0.19	9.7E-01	5.6E-04	1.00	1.00	1.00	1.00
1367763_at	acetyl-coenzyme A acetyltransferase 1	Acat1	25014	1.01	0.19	9.8E-01	3.7E-04	1.00	1.00	1.00	1.00
1376927_at	similar to LOC432779 protein (predicted)	RGD1564978_predicted	502225	1.02	0.19	9.6E-01	1.0E-03	1.00	1.00	1.00	1.00
1388604_at	similar to Calsequestrin-1 precursor (Calsequestrin, skeletal muscle isoform)	LOC679341	679341	0.89	0.19	7.8E-01	3.3E-04	1.00	1.00	1.00	1.00
1388961_at	integrin beta 1 binding protein 2 (predicted)	Igb1bp2_predicted	317258	0.90	0.19	6.6E-01	2.4E-03	1.00	1.00	0.60	1.00
1371389_at	hypothetical LOC306766	LOC306766	306766	0.43	0.19	4.4E-02	7.6E-04	1.00	1.00	1.00	1.00
1373911_at	perostin, osteoblast specific factor (predicted)	Postn_predicted	361945	0.63	0.19	7.3E-01	9.2E-02	1.00	1.00	1.00	1.00
1374088_at	myopalladin (predicted)	Mypn_predicted	309760	1.03	0.19	9.4E-01	1.7E-02	1.00	1.00	0.60	1.00
1371942_at	similar to Citrullione S-transferase, theta 3 (predicted)	RGD1562732_predicted	499422	0.90	0.19	6.5E-01	5.3E-03	0.70	1.00	0.00	1.00
1372641_at	Alpha-kinase 3 (predicted)	Alpk3_predicted	365298	1.00	0.19	9.9E-01	5.1E-04	1.00	1.00	1.00	1.00
1375349_at	similar to sorbin and SH3 domain containing 1 isoform 3	LOC678826	678826	1.11	0.19	7.6E-01	3.1E-03	1.00	1.00	1.00	1.00
1372103_at	similar to DnaJ (Hsp40) homolog, subfamily A, member 4	LOC498996	498996	0.86	0.19	4.2E-01	3.8E-04	1.00	1.00	1.00	1.00
1375476_at	muscle glycogen phosphorylase	Pygm	24701	1.52	0.19	2.4E-01	3.8E-04	1.00	1.00	0.00	1.00
1368038_at	synaptotagmin 2 binding protein	Synj2bp	64531	0.78	0.19	3.8E-01	7.4E-04	1.00	1.00	1.00	1.00
1372240_at	sarcoglycan, alpha (dystrophin-associated glycoprotein) (predicted)	Sgca_predicted	303468	0.85	0.19	5.5E-01	6.7E-04	1.00	1.00	1.00	1.00
1368566_a_at	NADH dehydrogenase (ubiquinone) flavoprotein 3-like	Ndufv3l	64539	0.74	0.19	3.7E-01	3.1E-03	1.00	1.00	1.00	1.00
1376852_at	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mcc1	294972	1.13	0.19	7.9E-01	3.1E-03	1.00	1.00	0.80	1.00
1368716_at	protein phosphatase 1, regulatory (inhibitor) subunit 14c	Ppp1r14c	171010	1.05	0.19	9.3E-01	3.2E-03	1.00	1.00	0.00	1.00
1370956_at	decorin	Den	29139	1.18	0.19	5.8E-01	2.5E-02	1.00	1.00	1.00	1.00
1371421_at	similar to 3-oxoacid CoA transferase 1	LOC678860	678860	1.12	0.18	6.0E-01	3.0E-03	1.00	1.00	1.00	1.00
1372256_at	Transcribed locus			0.09	0.18	2.3E-02	7.9E-04	0.00	0.38	0.00	1.00
1389411_at	Transcribed locus			1.53	0.18	8.4E-02	4.5E-03	1.00	1.00	0.60	1.00
1374017_at	Similar to tripartite motif protein 50 (predicted)	RGD1562778_predicted	365377	1.76	0.18	4.9E-02	8.8E-04	1.00	1.00	1.00	1.00
1367829_at	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	Ech1s	140547	1.14	0.18	6.4E-01	1.2E-03	1.00	1.00	0.60	1.00
1376495_at	Transcribed locus			1.19	0.18	7.5E-01	2.4E-03	1.00	1.00	0.00	1.00
1371794_at	similar to SH3-domain binding protein 3	LOC688018	688018	1.01	0.18	9.8E-01	4.8E-04	1.00	1.00	1.00	1.00
1370854_at	nexilin	Nexn	246172	1.09	0.18	6.6E-01	4.1E-03	1.00	1.00	1.00	1.00
1371519_at	electron-transferring-flavoprotein dehydrogenase	Etfhd	295143	1.10	0.18	7.6E-01	3.4E-04	1.00	1.00	1.00	1.00
1369948_at	nerve growth factor receptor (TNFRSF16) associated protein 1	Ngfrap1	117089	1.06	0.18	9.1E-01	4.1E-03	1.00	1.00	0.40	1.00
1387893_at	complement component 1, s subcomponent	C1s	192262	1.70	0.18	2.3E-01	7.0E-03	1.00	1.00	1.00	1.00
1370697_a_at	nexilin	Nexn	246172	1.28	0.18	1.9E-01	7.6E-03	1.00	1.00	1.00	1.00
1372157_at	bolA-like 1 (E. coli) (predicted)	BolA1_predicted	365875	0.61	0.18	1.5E-01	1.4E-03	1.00	1.00	0.50	1.00
1389460_at	Transcribed locus			1.61	0.18	2.2E-01	5.5E-04	1.00	1.00	0.40	1.00
1373188_at	sodium channel, voltage-gated, type IV, beta	Scn4b	315611	0.79	0.18	1.2E-01	1.2E-03	1.00	1.00	1.00	1.00
1372158_at	LRP16 protein	Lrp16	246233	0.81	0.18	5.8E-01	1.3E-03	1.00	1.00	0.30	1.00
1373674_at	microfibrillar associated protein 5 (predicted)	Mfap5_predicted	362429	0.58	0.18	2.9E-01	1.8E-02	0.20	1.00	0.80	1.00
1375518_at	titin	Tin	84015	1.17	0.18	5.2E-01	1.7E-03	1.00	1.00	1.00	1.00
1388211_s_at	cytosolic acyl-CoA thioesterase 1	Cte1	192272	1.06	0.18	8.9E-01	6.3E-02	0.90	0.50	0.00	1.00
1374496_at	similar to RIKEN cDNA 1200009022; EST AI316813	RGD1310827	362364	0.81	0.18	5.6E-01	5.5E-04	1.00	1.00	0.30	1.00
1389774_at	Transcribed locus			0.78	0.18	1.8E-01	1.8E-02	0.60	1.00	0.30	1.00
1388570_at	similar to RIKEN cDNA 2310005014	LOC498909	498909	0.91	0.18	7.4E-01	6.7E-04	1.00	1.00	1.00	1.00
1390033_at	Transcribed locus			1.18	0.18	7.5E-01	1.1E-02	0.80	0.25	0.00	0.75
1372848_at	Transcribed locus			0.94	0.18	8.6E-01	1.0E-03	1.00	1.00	0.00	1.00
1370036_at	sulfite oxidase	Suox	81805	1.03	0.18	9.5E-01	6.0E-03	1.00	1.00	0.00	1.00
1367799_at	eukaryotic translation elongation factor 1 alpha 2	Eef1a2	24799	1.11	0.18	7.3E-01	1.5E-04	1.00	1.00	1.00	1.00
1376128_at	Transcribed locus			1.49	0.18	2.9E-01	4.7E-03	1.00	1.00	0.00	1.00
1373953_at	solute carrier family 4 (anion exchanger), member 1, adaptor protein (predicted)	Slc4a1ap_predicted	298805	1.01	0.18	9.8E-01	1.6E-03	1.00	1.00	1.00	1.00
1388916_at	Similar to novel protein (predicted)	RGD1564074_predicted	500514	1.04	0.17	9.2E-01	1.3E-03	1.00	1.00	1.00	1.00
1385704_at	tensin	Tns	29136	1.69	0.17	3.3E-01	2.4E-03	1.00	0.63	0.00	1.00
1372475_at	PTEN induced putative kinase 1 (predicted)	Pink1_predicted	298575	0.92	0.17	8.1E-01	1.2E-03	1.00	1.00	1.00	1.00
1368988_at	calsequestrin 2	Casq2	29209	0.84	0.17	5.7E-01	8.6E-04	1.00	1.00	1.00	1.00
1374307_at	Transcribed locus			0.93	0.17	8.6E-01	6.4E-03	1.00	1.00	0.40	1.00
1389449_at	similar to CG10671-like (predicted)	RGD1306911_predicted	290223	0.79	0.17	5.2E-01	1.4E-04	1.00	1.00	0.80	1.00
1374796_at	similar to Beta-sarcoglycan (Beta-SG) (43 kDa dystrophin-associated glycoprotein) (43DAG)	LOC687025	687025	0.81	0.17	4.5E-01	9.9E-04	1.00	1.00	1.00	1.00
1390227_at	hypothetical protein LOC678810	LOC678810	678810	0.49	0.17	7.6E-02	5.0E-02	0.80	1.00	0.00	1.00
1369698_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	Abcc3	140668	0.92	0.17	7.9E-01	4.1E-03	0.50	0.75	0.00	0.50
1372400_at	similar to cullin 4A (predicted)	RGD1563853_predicted	361181	0.98	0.17	9.8E-01	4.0E-04	1.00	1.00	1.00	1.00
1392633_at	Transcribed locus			0.85	0.17	7.5E-01	4.8E-04	1.00	1.00	0.00	1.00
1367749_at	lumican	Lum	81682	0.84	0.17	6.2E-01	5.1E-02	1.00	1.00	1.00	1.00
1376175_at	similar to NipSnap2 protein (Glioblastoma amplified sequence)	LOC498174	498174	0.74	0.17	6.5E-01	1.9E-04	1.00	1.00	1.00	1.00
1367885_at	peroxisomal membrane protein 2	Pmp2	29533	1.00	0.17	1.0E+00	2.5E-03	1.00	1.00	1.00	1.00
1373011_at	hypothetical protein LOC619558	LOC619558	619558	1.01	0.17	9.8E-01	1.0E-03	1.00	1.00	1.00	1.00
1379747_at	Protease, serine, 35	Prss35	315866	0.77	0.17	9.0E-01	2.6E-03	0.00	0.00	0.20	1.00
1370232_at	isovaleryl coenzyme A dehydrogenase	Ivd	24513	1.16	0.17	5.1E-01	1.9E-03	1.00	1.00	1.00	1.00
1373920_at	Similar to CG10084-PA	RGD1308297	306137	0.71	0.17	2.8E-01	2.9E-03	1.00	1.00	1.00	1.00
1368924_at	growth hormone receptor	Ghr	25235	1.77	0.17	3.0E-01	1.5E-03	1.00	1.00	0.60	1.00

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isoraft	Native BN	Native DA	Allograft	Isoraft
1370648_a_at	SH3 domain binding protein CR16	Cr16	259242	0.80	0.17	5.3E-01	6.5E-03	1.00	1.00	0.60	1.00
1376619_at	similar to protein tyrosine phosphatase, receptor type, D (predicted)	RGD1561090_predicted	313278	1.70	0.17	7.3E-01	4.6E-04	0.60	0.25	0.00	1.00
1387373_at	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	64183	1.44	0.17	3.5E-01	3.0E-04	1.00	1.00	1.00	1.00
1372595_at	actinin alpha 2 (predicted)	Actn2_predicted	291245	0.96	0.17	9.1E-01	4.5E-03	1.00	1.00	1.00	1.00
1370259_a_at	parathyroid hormone receptor 1	Pthr1	56813	1.07	0.17	9.0E-01	4.9E-02	0.00	0.25	0.00	1.00
1372423_at	PERP, TP53 apoptosis effector (predicted)	Perp_predicted	292949	1.21	0.17	7.6E-01	9.9E-04	1.00	1.00	0.30	1.00
1374648_at	Transcribed locus			0.41	0.17	8.4E-02	6.9E-04	0.80	1.00	0.00	1.00
1389694_at	Transcribed locus			0.82	0.17	8.0E-01	1.8E-02	1.00	1.00	0.00	1.00
1372457_at	mitochondrial tumor suppressor 1	Mtst1	306487	0.93	0.16	7.2E-01	2.0E-04	1.00	1.00	1.00	1.00
1375849_at	RGM domain family, member A (predicted)	Rgma_predicted	308739	0.76	0.16	6.6E-01	3.3E-03	1.00	1.00	0.20	1.00
1367702_at	acetyl-Coenzyme A dehydrogenase, medium chain	Acadm	24158	0.99	0.16	9.9E-01	9.5E-04	1.00	1.00	1.00	1.00
1370952_at	glutathione S-transferase, mu 2	Gstm2	24424	1.44	0.16	4.5E-01	4.3E-04	1.00	1.00	1.00	1.00
1372452_at	Transcribed locus			0.54	0.16	1.7E-01	4.8E-04	1.00	1.00	0.80	1.00
1388456_at	S100 calcium binding protein A1	S100a1	295214	1.10	0.16	8.4E-01	1.2E-02	1.00	1.00	0.00	1.00
1375182_at	Solute carrier family 3, member 1	Slc3a1	29484	1.29	0.16	5.1E-01	3.4E-04	1.00	1.00	1.00	1.00
1373082_at	Transcribed locus			0.72	0.16	1.1E-01	1.6E-03	1.00	1.00	1.00	1.00
1377133_at	Hypothetical protein LOC680687	LOC680687	680687	0.14	0.16	1.3E-01	4.0E-03	0.00	1.00	0.00	1.00
1378625_at	insulin-like growth factor binding protein 6	Igfbp6	25641	0.38	0.16	6.9E-02	1.9E-03	0.00	1.00	0.20	1.00
1374925_at	Transcribed locus			1.18	0.16	5.7E-01	4.8E-04	1.00	1.00	1.00	1.00
1370109_at	sulfotransferase family 1A, phenol-preferring, member 1	Sult1a1	83783	0.59	0.16	3.6E-01	6.0E-04	1.00	1.00	0.60	1.00
1374335_at	GATA binding protein 6	Gata6	29300	0.88	0.16	8.1E-01	4.4E-05	1.00	1.00	1.00	1.00
1370061_at	RAB3B, member RAS oncogene family	Rab3b	81755	0.94	0.16	8.6E-01	2.4E-03	1.00	1.00	0.00	1.00
1373915_at	dystrophia myotonica-protein kinase (predicted)	Dmpk_predicted	308405	0.85	0.16	6.2E-01	6.2E-04	1.00	1.00	1.00	1.00
1386965_at	lipoprotein lipase	Lpl	24539	1.15	0.16	4.0E-01	1.0E-03	1.00	1.00	1.00	1.00
1367659_s_at	dodecenoyl-coenzyme A delta isomerase	Dei	29740	0.70	0.16	2.1E-01	6.1E-04	1.00	1.00	1.00	1.00
1383169_at	Transcribed locus			1.33	0.16	4.6E-01	1.3E-03	1.00	1.00	1.00	1.00
1367739_at	Cytochrom c oxidase subunit VIII-H (heart/muscle)	Cox8b	25250	0.80	0.16	5.4E-01	1.1E-02	1.00	1.00	1.00	1.00
1369957_at	regulator of G-protein signaling 5	Rgs5	54294	1.23	0.15	6.3E-01	1.9E-03	1.00	1.00	0.60	1.00
1372820_at	Transcribed locus			1.03	0.15	9.4E-01	5.2E-02	1.00	1.00	4.00	1.00
1375638_at	serum deprivation response protein	Sdpr	316384	1.07	0.15	9.0E-01	3.2E-04	1.00	1.00	1.00	1.00
1384178_at	leucine rich repeat containing 4B (predicted)	Lrrc4b_predicted	308571	0.72	0.15	3.8E-01	2.0E-04	1.00	1.00	1.00	1.00
1388300_at	microsomal glutathione S-transferase 3 (predicted)	Mgst3_predicted	289197	0.98	0.15	9.8E-01	7.3E-04	1.00	1.00	1.00	1.00
1373427_at	Ras-related GTP binding D (predicted)	Rragd_predicted	297960	0.60	0.15	1.3E-01	8.1E-03	1.00	1.00	0.00	1.00
1374172_at	Transcribed locus			1.54	0.15	2.9E-01	5.5E-04	0.60	0.00	0.20	1.00
1390766_at	similar to Tubulin alpha-8 chain (Alpha-tubulin 8)	LOC500377	500377	0.88	0.15	4.8E-01	2.7E-03	1.00	1.00	0.70	1.00
1372646_at	similar to RIKEN cDNA 1500015O10 (predicted)	RGD1305645_predicted	363225	0.33	0.15	2.9E-01	3.7E-03	0.00	0.00	0.00	0.75
1374989_at	ankyrin repeat and SOCS box-containing protein 12	Asb12	503446	0.78	0.15	4.0E-01	1.4E-02	1.00	1.00	0.00	1.00
1376575_at	Transcribed locus			0.74	0.15	4.9E-01	4.5E-04	1.00	1.00	0.80	1.00
1376105_at	procollagen, type XIV, alpha 1 (predicted)	Col14a1_predicted	314981	1.09	0.15	8.6E-01	7.6E-03	1.00	1.00	0.50	1.00
1367892_at	pyruvate dehydrogenase kinase, isoenzyme 2	Pdk2	81530	0.92	0.15	8.1E-01	2.7E-04	1.00	1.00	0.60	1.00
1374029_at	Transcribed locus			0.78	0.15	3.1E-01	2.5E-02	1.00	1.00	0.00	1.00
1388497_at	thioesterase superfamily member 2 (predicted)	Them2_predicted	291135	0.65	0.15	1.6E-01	7.7E-04	1.00	1.00	1.00	1.00
1392939_at	solute carrier family 41, member 3	Slc41a3	641603	1.34	0.15	3.8E-01	4.1E-04	1.00	1.00	1.00	1.00
1389583_at	similar to Hypothetical protein MGCS37938 (predicted)	RGD1566169_predicted	298605	0.73	0.15	2.7E-01	2.2E-03	1.00	1.00	0.20	1.00
1383058_at	Transcribed locus			0.95	0.15	8.7E-01	2.8E-04	1.00	1.00	1.00	1.00
1387004_at	neuroblastoma, suppression of tumorigenicity 1	Nbl1	50594	0.79	0.15	5.4E-01	6.0E-03	0.10	0.00	0.00	1.00
1370973_at	sodium channel, voltage-gated, type VII, alpha	Scn7a	64155	1.07	0.15	9.0E-01	2.5E-02	1.00	1.00	0.50	1.00
1388506_at	desmoplakin	Dsp	306871	1.46	0.15	1.2E-01	5.5E-04	1.00	1.00	1.00	1.00
1370906_at	branched chain keto acid dehydrogenase E1, beta polypeptide	Bckdhb	29711	1.04	0.15	9.4E-01	1.0E-03	1.00	1.00	0.00	1.00
1372390_at	Transcribed locus			0.96	0.14	9.7E-01	3.7E-04	1.00	1.00	0.00	1.00
1377275_at	ADP-ribosyltransferase 1 (predicted)	Art1_predicted	308873	2.64	0.14	6.4E-02	2.5E-02	1.00	0.50	0.00	0.50
1389171_at	transmembrane protein 38a (predicted)	Tmem38a_predicted	306327	0.94	0.14	7.7E-01	1.2E-03	1.00	1.00	1.00	1.00
1371677_at	similar to Esophagus cancer-related gene-2 protein precursor (ECRG-2) (predicted)	RGD1307150_predicted	301016	0.58	0.14	1.3E-01	1.7E-03	1.00	1.00	1.00	1.00
1371356_at	tensin like C1 domain containing phosphatase (predicted)	Tenc1_predicted	315326	0.94	0.14	9.4E-01	1.6E-02	1.00	0.50	0.00	1.00
1373803_a_at	growth hormone receptor	Ghr	25235	1.18	0.14	6.4E-01	3.2E-04	1.00	1.00	0.40	1.00
1386927_at	carnitine palmitoyltransferase 2	Cpt2	25413	0.98	0.14	9.7E-01	7.3E-04	1.00	1.00	0.00	1.00
1386931_at	troponin I type 3 (cardiac)	Tnni3	29248	0.84	0.14	7.0E-01	6.7E-03	1.00	1.00	1.00	1.00
1372297_at	glutathione S-transferase, alpha 4	Gsta4	300850	0.53	0.14	1.1E-01	7.9E-04	1.00	1.00	1.00	1.00
1386962_at	phospholipase C, beta 4	Plc4	25031	1.02	0.14	9.6E-01	2.9E-04	1.00	1.00	1.00	1.00
1370229_at	N-myc downstream regulated gene 4	Ndr4	64457	1.23	0.14	3.4E-01	3.7E-04	1.00	1.00	1.00	1.00
1374038_at	Transcribed locus			1.11	0.14	8.5E-01	2.1E-04	1.00	1.00	1.00	1.00
1374444_at	plexin B1 (predicted)	Plexb1_predicted	316009	2.10	0.14	4.9E-02	7.8E-03	1.00	1.00	0.00	1.00
1371951_at	Transcribed locus			1.00	0.14	9.9E-01	1.3E-03	1.00	1.00	1.00	1.00
1387344_at	aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	81708	1.23	0.14	6.2E-01	4.6E-04	1.00	1.00	1.00	1.00
1388432_at	optineurin	Optn	246294	1.29	0.14	4.3E-01	7.0E-04	1.00	1.00	0.70	1.00
1371672_at	chromobox homolog 7	Chx7	362962	0.91	0.14	9.2E-01	3.0E-03	0.80	0.38	0.00	0.50
1370157_at	Similar to RIKEN cDNA 2600005C20 (predicted)	RGD1305633_predicted	309673	0.89	0.14	5.5E-01	3.2E-04	1.00	1.00	1.00	1.00
1367673_at	selenium binding protein 2	Selenbp1	140927	1.04	0.14	9.5E-01	1.5E-04	1.00	1.00	0.00	1.00
1388422_at	LIM and senescent cell antigen like domains 2	Lims2	361303	1.28	0.14	5.8E-01	4.5E-03	1.00	1.00	0.80	1.00
1374056_at	similar to RNA binding motif protein 24	LOC681858	681858	1.03	0.13	9.5E-01	1.4E-03	1.00	1.00	1.00	1.00
1374166_at	Transcribed locus			0.90	0.13	7.6E-01	4.9E-03	1.00	1.00	0.60	1.00
1369968_at	pleiotrophin	Ptn	24924	1.59	0.13	3.1E-01	3.3E-02	1.00	0.88	0.60	1.00
1372613_at	3-hydroxybutyrate dehydrogenase, type 2 (predicted)	Bdh2_predicted	295458	0.61	0.13	2.8E-01	1.8E-02	1.00	1.00	0.00	1.00
1372536_at	chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1	360887	0.69	0.13	2.1E-01	1.2E-03	1.00	1.00	1.00	1.00
1387703_a_at	ubiquitin specific peptidase 2	Usp2	115771	0.85	0.13	6.2E-01	9.6E-04	1.00	1.00	0.80	1.00
1377271_at	unc-45 homolog B (C. elegans) (predicted)	Unc45b_predicted	303373	1.19	0.13	5.8E-01	1.4E-04	1.00	1.00	0.20	1.00
1367864_at	phosphofructokinase, muscle	Pfkfb	65152	0.90	0.13	6.2E-01	1.2E-04	1.00	1.00	1.00	1.00



Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1372527_at	reticulon 2 (Z-band associated protein)	Rtn2	308410	0.72	0.13	2.4E-01	6.8E-04	1.00	1.00	0.00	1.00
1370897_at	branched chain ketoacid dehydrogenase E1, alpha polypeptide	Bckdha	25244	0.95	0.13	8.9E-01	5.2E-04	1.00	1.00	0.40	1.00
1376789_at	Similar to Myosin light chain kinase 2, skeletal/cardiac muscle (MLCK2) (predicted)	RGD1305801_predicted	291926	0.76	0.13	2.5E-01	1.0E-03	1.00	1.00	1.00	1.00
1388527_at	Transcribed locus			0.84	0.13	8.8E-01	1.0E-03	0.60	0.63	0.40	1.00
1371500_at	latent transforming growth factor beta binding protein 4	Ltbp4	292734	1.06	0.13	8.8E-01	4.1E-03	1.00	1.00	0.80	1.00
1373947_at	dermatopontin (predicted)	Dpt_predicted	289178	2.04	0.13	7.2E-02	9.5E-04	1.00	1.00	1.00	1.00
1390404_at	laminin, alpha 2 (predicted)	Lama2_predicted	309368	0.83	0.13	5.0E-01	2.9E-04	1.00	1.00	0.20	1.00
1380883_at	Transcribed locus, strongly similar to XP_001061572.1 hypothetical protein [Rattus norvegicus]			1.40	0.13	4.5E-01	3.8E-03	1.00	0.50	0.00	1.00
1388597_at	myosin binding protein C, cardiac (predicted)	Mybpc3_predicted	295929	1.31	0.13	2.7E-01	9.1E-04	1.00	1.00	1.00	1.00
1376892_at	CDNA clone IMAGE:7313785			0.88	0.13	7.7E-01	1.7E-03	1.00	1.00	0.60	1.00
1376590_at	Transcribed locus			0.81	0.13	5.5E-01	7.4E-04	1.00	1.00	0.00	1.00
1387047_at	heat shock 27kDa protein 3	Hspb3	78951	0.80	0.13	4.9E-01	5.8E-04	1.00	1.00	0.30	1.00
1383188_at	Transcribed locus			1.13	0.12	7.1E-01	8.7E-03	1.00	1.00	0.00	1.00
1384202_at	similar to Tescalcin (predicted)	RGD1566317_predicted	288689	0.82	0.12	6.3E-01	3.5E-03	1.00	1.00	1.00	1.00
1385924_at	Transcribed locus			0.37	0.12	4.7E-01	2.8E-02	0.00	0.88	0.00	0.63
1376905_at	Transcribed locus			0.70	0.12	8.3E-01	6.5E-03	0.00	0.00	0.00	0.75
1386885_at	enoyl coenzyme A hydratase 1, peroxisomal	Ech1	64526	0.72	0.12	3.6E-01	1.8E-04	1.00	1.00	1.00	1.00
138918_at	Transcribed locus			1.14	0.12	7.8E-01	1.4E-04	1.00	1.00	0.60	1.00
1371566_at	similar to F-box protein FBL2 (predicted)	RGD1311830_predicted	363083	1.11	0.12	8.2E-01	1.5E-02	1.00	1.00	0.60	1.00
1387804_at	tripartite motif protein 63	Trimf3	140930	1.04	0.12	8.9E-01	4.8E-04	1.00	1.00	0.60	1.00
1370161_at	steroid sensitive gene 1	Ssg1	64387	1.38	0.12	5.0E-01	3.5E-03	1.00	1.00	1.00	1.00
1388689_at	similar to Acylphosphatase, muscle type isozyme (Acylphosphate phosphohydrolase)	LOC682245	682245	1.13	0.12	8.5E-01	4.7E-04	1.00	1.00	1.00	1.00
1390112_at	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	Efemp1	305604	1.62	0.12	2.8E-01	2.5E-02	1.00	0.75	0.20	1.00
1388866_at	Transcribed locus			0.71	0.12	2.1E-01	2.8E-04	1.00	1.00	1.00	1.00
1388349_at	Transcribed locus			0.97	0.12	9.3E-01	3.6E-03	1.00	1.00	1.00	1.00
1387121_a_at	N-myc downstream regulated gene 2	Ndrg2	171114	1.09	0.12	6.8E-01	1.6E-03	1.00	1.00	1.00	1.00
1374667_at	CDNA clone IMAGE:7302289			0.99	0.12	9.9E-01	6.3E-04	1.00	1.00	0.60	1.00
1370941_at	platelet derived growth factor receptor, alpha polypeptide	Pdgfra	25267	1.12	0.12	8.3E-01	6.2E-02	1.00	1.00	0.40	1.00
1373130_at	Transcribed locus			1.23	0.12	4.9E-01	2.2E-03	1.00	1.00	1.00	1.00
1371933_at	Glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein	LOC246295	246295	1.09	0.12	7.5E-01	4.2E-04	1.00	1.00	1.00	1.00
1389727_at	leucine-rich repeat-containing 10 (predicted)	Lrrc10_predicted	314848	1.28	0.11	2.0E-01	7.2E-04	1.00	1.00	1.00	1.00
1383072_at	muscle glycogen phosphorylase	Pygm	24701	1.61	0.11	2.5E-01	2.0E-04	1.00	1.00	1.00	1.00
1398445_at	Transcribed locus			3.64	0.11	1.6E-01	1.9E-02	1.00	0.25	0.00	0.88
1387022_at	aldehyde dehydrogenase family 1, member A1	Aldh1a1	24188	0.70	0.11	2.5E-01	5.6E-04	1.00	1.00	0.20	1.00
1374311_at	similar to tripartite motif-containing 56	LOC691246	691246	0.96	0.11	9.3E-01	2.5E-02	1.00	1.00	0.20	1.00
1373648_at	similar to Protein C6orf142 homolog	LOC681849	681849	0.75	0.11	2.4E-01	9.9E-04	1.00	1.00	1.00	1.00
1372383_at	G-protein signalling modulator 1 (AGS3-like, C. elegans)	Gpsm1	246254	0.97	0.11	9.4E-01	3.7E-04	1.00	1.00	1.00	1.00
1375990_a_at	Transcribed locus			0.91	0.11	7.3E-01	3.7E-04	1.00	1.00	1.00	1.00
1374099_at	nebulin-related anchoring protein (predicted)	Nrap_predicted	307982	1.63	0.11	1.8E-01	1.5E-03	1.00	1.00	1.00	1.00
1372790_at	Malate dehydrogenase 1, NAD (soluble)	Mdh1	24551	0.86	0.11	5.8E-01	1.9E-04	1.00	1.00	1.00	1.00
1372162_at	acyl-CoA synthetase short-chain family member 1 (predicted)	Acs1_predicted	296259	1.22	0.11	6.5E-01	2.7E-03	1.00	1.00	0.70	1.00
1367742_at	carnitine palmitoyltransferase 1b, muscle	Cpt1b	25756	0.96	0.11	9.5E-01	2.1E-04	1.00	1.00	1.00	1.00
1375031_at	Transcribed locus, moderately similar to XP_342453.2 titin [Rattus norvegicus]			1.08	0.11	8.1E-01	4.6E-04	1.00	1.00	0.70	1.00
1387271_at	phytanoyl-CoA hydroxylase	Phyh	114209	0.69	0.10	2.9E-01	4.9E-04	1.00	1.00	1.00	1.00
1369313_at	four and a half LIM domains 2	Fhl2	63839	1.16	0.10	6.2E-01	2.9E-04	1.00	1.00	1.00	1.00
1369126_at	prostaglandin F receptor	Ptgrf	25652	0.50	0.10	6.5E-01	2.4E-02	0.00	0.25	0.00	0.50
1370982_at	muscle glycogen phosphorylase	Pygm	24701	1.15	0.10	5.9E-01	8.1E-04	1.00	1.00	0.60	1.00
1383060_at	G kinase anchoring protein 1	Gkap1	361202	1.22	0.10	6.2E-01	9.2E-03	0.40	0.00	0.00	0.75
1374148_at	Microtubule-associated protein tau	Mapt	29477	0.61	0.10	1.4E-01	4.8E-04	0.60	1.00	0.00	0.63
1387071_a_at	microtubule-associated protein tau	Mapt	29477	1.11	0.10	8.0E-01	1.9E-02	0.90	0.88	0.20	1.00
1374190_at	citrate lyase beta like	Clybl	306198	0.93	0.10	8.2E-01	8.9E-03	1.00	1.00	0.00	1.00
1373882_at	Transcribed locus			0.96	0.10	9.5E-01	1.6E-02	0.10	0.25	0.40	1.00
1388153_at	acyl-CoA synthetase long-chain family member 1	Acs1	25288	0.87	0.10	6.6E-01	3.9E-04	1.00	1.00	0.80	1.00
1386911_at	ATPase, Na+/K+ transporting, alpha 2 polypeptide	Atp1a2	24212	0.81	0.10	3.6E-01	5.6E-04	1.00	1.00	1.00	1.00
1390365_at	leukocyte receptor cluster (LRC) member 1 (predicted)	Leng1_predicted	292535	0.64	0.10	4.8E-01	2.9E-04	0.20	0.50	0.00	0.75
1374816_at	similar to hypothetical protein FLJ30973	LOC363091	363091	1.07	0.10	8.4E-01	1.1E-04	1.00	1.00	1.00	1.00
1385249_at	Kruppel-like factor 15	Klf15	85497	0.87	0.10	6.3E-01	1.1E-03	1.00	1.00	0.50	1.00
1388876_at	Transcribed locus			0.83	0.10	5.0E-01	1.0E-03	1.00	1.00	1.00	1.00
1368542_at	zinc finger protein 423	Zfp423	94188	0.96	0.09	9.4E-01	1.9E-02	0.90	1.00	0.00	1.00
1374616_at	platelet-derived growth factor receptor-like	Pdgfrl	290771	0.79	0.09	8.4E-01	4.0E-02	0.00	0.00	0.00	0.63
1374895_at	myomesin 1 (sklemin) 18kDa	Myom1	316740	1.09	0.09	8.7E-01	1.2E-03	1.00	1.00	1.00	1.00
1367626_at	creatine kinase, muscle	Ckm	24265	1.00	0.09	9.9E-01	4.1E-04	1.00	1.00	1.00	1.00
1386907_at	Carboxypeptidase D	Cpd	25306	1.29	0.09	6.2E-01	9.3E-04	1.00	1.00	1.00	1.00
1367880_at	laminin, beta 2	Lamb2	25473	1.06	0.09	8.8E-01	3.5E-04	1.00	1.00	1.00	1.00
1371801_at	myozenin 2 (predicted)	Myoz2_predicted	295426	0.87	0.09	6.1E-01	1.1E-03	1.00	1.00	1.00	1.00
1367660_at	fatty acid binding protein 3	Fabp3	79131	0.68	0.09	2.5E-01	1.0E-03	1.00	1.00	1.00	1.00
1386961_at	phosphofructokinase, muscle	Pfkm	65152	1.42	0.09	3.9E-01	1.6E-04	1.00	1.00	0.00	1.00
1389532_at	Nebulette (predicted)	Neb1_predicted	307189	1.32	0.09	3.7E-01	1.1E-03	1.00	1.00	0.00	1.00
1370739_x_at	triadin	Trdn	59299	1.26	0.09	3.7E-01	6.5E-04	1.00	0.80	0.80	1.00
1391428_at	Transcribed locus			0.52	0.09	3.4E-01	1.7E-05	1.00	1.00	0.70	1.00
1389488_at	Transcribed locus			1.06	0.09	9.0E-01	2.7E-04	1.00	1.00	1.00	1.00
1389548_at	alcohol dehydrogenase, iron containing, 1	Adh1e1	362474	0.86	0.09	6.6E-01	3.8E-03	1.00	1.00	0.00	0.75
1388712_at	pleckstrin homology, Sec7 and coiled-coil domains 3	Pscd3	116693	0.71	0.09	8.5E-01	2.4E-03	0.40	0.25	0.00	1.00
1387023_at	glutathione S-transferase, mu type 3	Gstm3	81869	0.82	0.09	6.7E-01	1.8E-03	1.00	1.00	0.20	1.00
1369210_at	sodium channel, voltage-gated, type 1, alpha	Scn1a	81574	1.10	0.09	8.5E-01	9.1E-03	1.00	0.50	0.00	1.00
1370939_at	acyl-CoA synthetase long-chain family member 1	Acs1	25288	0.88	0.09	5.9E-01	2.0E-04	1.00	1.00	1.00	1.00
1371746_at	Transcribed locus			0.77	0.09	2.7E-01	8.7E-04	1.00	1.00	1.00	1.00

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1367989_at	solute carrier family 2 (facilitated glucose transporter), member 4	Slc2a4	25139	0.85	0.09	5.1E-01	8.8E-04	1.00	1.00	1.00	1.00
1376716_at	Transcribed locus			0.64	0.09	3.0E-01	8.1E-04	0.40	0.75	0.00	1.00
1387138_at	tachykinin 2	Tac2	29191	0.36	0.09	1.9E-01	9.2E-03	0.00	0.00	0.00	0.75
1372565_at	HraA serine peptidase 3 (predicted)	HraA_predicted	360959	1.27	0.09	5.4E-01	1.9E-03	1.00	1.00	0.20	1.00
1382954_at	Corin	Corin	289596	1.59	0.09	2.1E-01	3.0E-04	1.00	1.00	0.60	1.00
1367949_at	proenkephalin 1	Penk1	29237	0.61	0.09	2.9E-01	1.5E-03	1.00	1.00	0.60	1.00
1390716_at	Transcribed locus			0.85	0.09	7.2E-01	5.2E-04	1.00	1.00	0.20	1.00
1388802_at	brain expressed X-linked 1	Bex1	501625	2.00	0.09	2.2E-01	6.4E-04	1.00	1.00	0.10	1.00
1369326_at	A kinase (PRKA) anchor protein 6	Akap6	64553	1.63	0.08	4.8E-01	9.4E-04	1.00	0.00	0.00	1.00
1389095_at	bi-regional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein (predicted)	Boc_predicted	360715	0.80	0.08	8.5E-01	7.8E-04	0.20	0.00	0.00	1.00
1381504_at	similar to asporin precursor	LOC306805	306805	0.78	0.08	5.4E-01	1.7E-02	0.40	0.25	0.10	1.00
1398458_at	similar to protein kinase, lysine deficient 1; kinase deficient protein (predicted)	RGD1307284_predicted	306811	1.05	0.08	9.0E-01	3.0E-03	1.00	1.00	0.00	1.00
1386943_at	plasma membrane protolipid	Plp	64364	0.38	0.08	9.8E-02	5.8E-04	0.80	1.00	0.00	1.00
1374217_at	similar to chromosome 16 open reading frame 5	RGD1310686	360480	0.77	0.08	6.5E-01	1.3E-03	1.00	1.00	0.00	1.00
1379884_at	Aspartate-beta-hydroxylase (predicted)	Asph_predicted	312981	0.94	0.08	8.7E-01	4.4E-04	1.00	1.00	0.80	1.00
1389066_at	Down syndrome critical region gene 1-like 1	Dscr11	140666	0.93	0.08	8.0E-01	7.4E-04	1.00	1.00	1.00	1.00
1388778_at	Transcribed locus			0.66	0.08	1.2E-01	2.0E-03	1.00	1.00	1.00	1.00
1373755_at	similar to leucine rich repeat containing 39 isoform 2	LOC686192	686192	0.83	0.08	5.5E-01	7.0E-04	1.00	1.00	1.00	1.00
1370310_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	Hmgcs2	24450	0.73	0.08	7.9E-01	1.1E-03	0.00	0.00	0.00	0.75
1373696_at	Biconical C homology 1 (Drosophila) (predicted)	Bicc1_predicted	361832	0.73	0.08	8.4E-02	3.6E-04	1.00	1.00	0.00	1.00
1389362_at	protein tyrosine phosphatase, non-receptor type 3	Ptpn3	362524	0.68	0.08	1.4E-01	3.6E-04	1.00	1.00	1.00	1.00
1386865_at	SPARC-like 1 (mast9, hevjin)	Spnc1	25434	1.60	0.08	1.5E-01	1.9E-04	1.00	1.00	1.00	1.00
1372372_at	similar to Ab2-225	RGD1306952	310201	0.60	0.07	1.8E-01	4.8E-04	1.00	1.00	0.60	1.00
1376746_at	lactate dehydrogenase D	Ldh	307858	0.84	0.07	7.9E-01	1.8E-03	1.00	1.00	0.00	1.00
1372615_at	amine oxidase, copper containing 3	Aoc3	29473	1.28	0.07	5.2E-01	6.5E-04	1.00	1.00	0.00	1.00
1374677_at	similar to Adenylosuccinate synthetase isozyme 1	LOC684425	684425	0.76	0.07	4.7E-01	2.1E-04	1.00	1.00	1.00	1.00
1370738_a_at	triadin	Trdn	59299	0.78	0.07	7.2E-01	7.0E-03	1.00	1.00	0.00	1.00
1389908_at	Transcribed locus			1.43	0.07	6.3E-01	3.4E-03	0.80	0.38	0.00	1.00
1369654_at	protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	78975	1.74	0.07	6.2E-02	3.6E-02	1.00	1.00	0.20	1.00
1371472_at	Transcribed locus			0.96	0.07	8.8E-01	1.8E-04	1.00	1.00	1.00	1.00
1389398_at	ankyrin 1, erythroid	Ank1	306570	0.85	0.07	5.6E-01	1.3E-04	1.00	1.00	0.10	1.00
1373778_at	Transcribed locus			1.06	0.07	9.4E-01	4.9E-03	1.00	0.00	0.00	1.00
1372280_at	ankyrin repeat and SOCS box-containing protein 2	Axb2	299266	1.07	0.07	8.6E-01	1.7E-04	1.00	1.00	0.80	1.00
1373436_at	similar to RIKEN cDNA 1700040L02 (predicted)	RGD1306739_predicted	361834	0.64	0.06	2.8E-01	5.6E-03	1.00	1.00	0.00	1.00
1374814_at				0.57	0.06	6.7E-02	9.5E-04	1.00	1.00	0.70	1.00
1388741_at	similar to cardiomyopathy associated 5	LOC683555	683555	1.72	0.06	3.3E-01	1.0E-03	1.00	1.00	0.20	1.00
1382775_at	ryanodine receptor 2, cardiac	Ryr2	498783	1.19	0.06	7.7E-01	1.4E-02	1.00	1.00	0.40	1.00
1375983_at	MAM domain containing 2	Mamdc2	309410	0.67	0.06	7.0E-01	2.9E-04	0.20	0.25	0.00	1.00
1372737_at	Similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	498587	1.42	0.06	3.1E-01	6.4E-04	1.00	1.00	0.00	1.00
1377499_a_at	histidine rich calcium binding protein	Hrc	292905	0.95	0.06	8.4E-01	8.6E-04	1.00	1.00	0.80	1.00
1390461_at	Transcribed locus			0.34	0.06	2.0E-01	1.1E-04	0.00	0.00	0.00	1.00
1368380_at	vitronectin	Vtn	29169	0.82	0.06	5.2E-01	1.7E-03	1.00	1.00	0.00	1.00
1371984_at	similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	498587	1.10	0.06	5.9E-01	5.7E-04	1.00	1.00	1.00	1.00
1374672_at	cardiac ankyrin repeat kinase	CarK	295531	1.15	0.06	6.3E-01	1.6E-04	1.00	1.00	0.20	1.00
1389707_at	Transcribed locus			3.94	0.06	1.5E-01	2.3E-04	0.20	0.00	0.00	0.75
1388557_at	complement component 7	C7	117517	1.25	0.06	5.4E-01	2.9E-03	1.00	1.00	1.00	1.00
1390473_at	potassium voltage-gated channel, subfamily G, member 2	Kcng2	307234	0.83	0.05	6.6E-01	7.6E-03	1.00	1.00	0.00	1.00
1371732_at	dermatopontin (predicted)	Dpt_predicted	289178	0.90	0.05	5.4E-01	8.6E-04	1.00	1.00	1.00	1.00
1373108_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	309513	1.43	0.05	2.1E-01	5.4E-03	1.00	1.00	0.00	1.00
1373987_at	Kv channel-interacting protein 2	Kenip2	56817	1.30	0.05	4.9E-01	1.8E-03	1.00	1.00	0.70	1.00
1377065_at	Transcribed locus, strongly similar to XP_573855.1 similar to chromosome 10 open reading frame 71			0.90	0.05	6.5E-01	1.5E-03	1.00	1.00	0.00	1.00
1389808_at	hypothetical protein LOC688274	LOC688274	688274	0.53	0.05	2.4E-01	1.5E-03	1.00	1.00	0.00	1.00
1389306_at	Transcribed locus, weakly similar to XP_001073995.1 similar to Prostatic steroid-binding protein C1 chain precursor	Cd151	64315	1.13	0.05	9.4E-01	2.8E-04	1.00	0.13	0.00	1.00
1376884_a_at	ribosomal protein L3-like (predicted)	Rpl3_predicted	287122	0.93	0.05	7.9E-01	6.2E-04	1.00	1.00	0.60	1.00
1389079_at	dehydrogenase/reductase (SDR family) member 7C (predicted)	Dhrs7c_predicted	287411	0.64	0.05	2.9E-01	2.5E-03	1.00	1.00	0.50	1.00
1370363_at	carboxylesterase 3	Ces3	113902	0.83	0.05	6.4E-01	3.8E-03	1.00	1.00	0.00	1.00
1392652_at	Transcribed locus			0.85	0.05	7.9E-01	4.4E-03	0.80	1.00	0.00	1.00
1389095_at				1.58	0.05	1.7E-01	2.4E-03	1.00	1.00	0.00	1.00
1390450_a_at	osteglycin (predicted)	Ogn_predicted	291015	1.12	0.04	8.6E-01	3.1E-03	1.00	1.00	0.40	1.00
1375303_at	similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	498587	0.96	0.04	9.3E-01	1.9E-04	1.00	1.00	1.00	1.00
1374168_at	Transcribed locus			0.41	0.04	1.4E-02	1.3E-03	1.00	1.00	0.00	1.00
1385248_a_at	osteglycin (predicted)	Ogn_predicted	291015	1.98	0.04	2.8E-01	2.9E-03	1.00	1.00	0.00	1.00
1389448_at	septin 4	Sept4	287606	0.71	0.04	5.0E-01	6.7E-04	1.00	1.00	0.00	1.00
1375982_at	similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	498587	0.83	0.04	5.6E-01	8.4E-04	1.00	1.00	0.60	1.00
1371700_at	microfibrillar-associated protein 4	Mfap4	287382	0.55	0.03	3.2E-01	4.9E-03	0.90	1.00	0.40	1.00
1368093_at	myosin, heavy polypeptide 6, cardiac muscle, alpha	Myh6	29556	0.60	0.03	1.8E-01	3.1E-03	1.00	1.00	1.00	1.00
1391007_s_at	potassium inwardly rectifying channel, subfamily J, member 11	Kcnj11	83535	0.79	0.02	5.5E-01	1.3E-04	1.00	1.00	0.00	1.00
1389464_at	ligand of numb-protein X 1 (predicted)	Lnx1_predicted	360926	0.71	0.02	1.2E-01	4.4E-05	1.00	1.00	0.00	1.00
1383263_at	osteglycin (predicted)	Ogn_predicted	291015	0.46	0.01	9.8E-02	9.5E-04	0.50	1.00	0.00	1.00
1367951_at	phosphoglycerate mutase 2	Pgam2	24959	0.61	0.01	3.3E-01	1.1E-03	1.00	1.00	0.00	1.00
1387049_at	Sideroflexin 2	Sfxn2	294011	1.24	0.01	7.0E-01	4.4E-05	1.00	1.00	0.00	1.00
<b>C. Overlap</b>											
1370428_x_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	42.93	57.55	3.1E-03	4.4E-05	1.00	0.25	1.00	0.75
1367928_at	myosin, heavy polypeptide 7, cardiac muscle, beta	Myh7	29557	9.20	0.17	2.6E-02	1.3E-02	1.00	1.00	1.00	1.00
1371237_a_at	metallothionein 1a	Mt1a	24567	4.65	6.04	3.9E-02	4.1E-04	1.00	1.00	1.00	1.00
1370773_a_at	Kv channel-interacting protein 2	Kenip2	56817	3.82	0.10	4.4E-02	2.5E-03	1.00	1.00	0.00	1.00

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call				
			Strain Effect	Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft	
1369050_at	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide	Pik3c2g	116720	0.30	0.23	2.5E-03	5.1E-03	0.00	1.00	0.20	1.00
1368304_at	flavin containing monooxygenase 3	Fmo3	84493	0.26	0.06	8.5E-02	1.1E-03	0.00	1.00	0.00	1.00
1376749_at	osteglycin (predicted)	Ogn_predicted	291015	0.23	0.03	8.4E-03	1.4E-04	1.00	1.00	0.80	1.00
1370176_at	trafficking protein, kinesin binding 2	Trak2	171086	0.22	0.22	4.4E-04	2.3E-04	1.00	1.00	1.00	1.00
1375861_at	similar to nucleosome assembly protein 1-like 5	LOC682844	682844	0.17	0.17	3.8E-02	1.3E-03	0.30	1.00	0.00	1.00
1371245_a_at	beta-globin	LOC689064	689064	0.08	0.16	9.1E-03	1.3E-02	1.00	1.00	1.00	1.00
1374527_at	enoyl Coenzyme A hydratase domain containing 2 (predicted)	Echdc2_predicted	298381	0.01	0.15	9.3E-06	2.1E-03	0.00	1.00	0.00	1.00
1368637_at	caspase recruitment domain family, member 9	Cad9	64171	0.02	0.09	1.0E-02	2.9E-03	0.00	1.00	0.00	1.00
1393130_at	Regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	Rchb1	361050	0.02	0.07	4.4E-04	1.4E-04	0.00	1.00	0.20	1.00