

Additional File 2. Peripheral Blood Mononuclear Cells: Alterations in Gene Expression due to Strain Effect and Strain + Rejection Effect (color coded based on Venn diagram, Figure 3B)

Probe Set ID	Gene Title	Gene Symbol	Fold Change		False Discovery Rate		Average Present Call					
			Strain Effect	Strain+Rejection Effect	Strain Effect	Strain+Rejection Effect	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	
A. Strain Effect												
1368053_at	par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	81918	24.70	13.34	3.0E-02	8.7E-05	1.00	0.00	0.20	0.00	
1375497_at	Transcribed locus			21.16	2.99	2.8E-02	2.6E-02	0.50	0.00	0.10	0.00	
1394841_at	Translocase of inner mitochondrial membrane 9 homolog (yeast)	Timm9	171139	17.91	2.20	4.8E-02	1.5E-01	0.67	0.00	0.00	0.00	
1371621_at	Transcribed locus			10.39	2.18	4.6E-02	2.8E-01	1.00	0.00	0.60	0.00	
1375842_at	similar to Glycoporin	LOC688972	688972	10.07	0.55	7.1E-02	4.2E-01	1.00	0.33	1.00	1.00	
1378865_at	Transcribed locus			9.24	0.80	4.1E-02	6.2E-01	0.50	0.00	0.00	0.00	
1371527_at	epithelial membrane protein 1	Emp1	25314	6.72	3.00	2.5E-02	2.2E-04	1.00	1.00	1.00	1.00	
1381532_at	Lymphoid enhancer binding factor 1	Lef1	161452	6.25	7.42	7.8E-02	1.6E-02	1.00	0.00	0.00	0.00	
1398365_at	similar to RIKEN cDNA 2700055K07	RGDI1305061	291966	5.80	2.34	3.9E-02	1.4E-03	1.00	0.00	1.00	0.11	
1369555_at	chemokine (C-C motif) receptor 4	Ccr4	171054	5.56	3.33	5.1E-02	1.8E-03	1.00	0.00	0.00	0.00	
1371947_at	necln	Ndn	308690	5.00	1.71	6.1E-02	3.7E-01	0.67	0.00	0.00	0.00	
1386420_at	Transcribed locus			5.00	1.99	3.3E-02	3.0E-01	1.00	0.00	1.00	0.50	
1390119_at	secreted frizzled-related protein 2	Sfrp2	310552	4.99	2.06	3.8E-02	3.4E-02	1.00	0.67	1.00	0.00	
1395337_at	microtubule-associated protein 1b	Map1b	29456	4.99	2.26	5.3E-02	1.7E-01	0.50	0.00	0.40	0.00	
1378419_at	pre-ecsinophil-associated ribonuclease-2	LOC474169	474169	4.82	1.15	3.2E-02	6.5E-01	1.00	1.00	1.00	0.89	
1383365_at	procollagen, type XVII, alpha 1 (predicted)	Col17a1_predicted	294027	4.60	2.68	3.6E-02	3.4E-05	1.00	0.67	1.00	0.00	
1374519_at	Gamma-glutamyl carboxylase	Ggcx	81716	4.58	2.10	6.8E-02	2.2E-04	1.00	0.17	1.00	0.00	
1382153_at	C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6	Clecsf6	474143	4.58	2.10	4.0E-02	4.8E-02	1.00	0.50	1.00	0.78	
1368491_at	deoxyribonuclease II beta	Dnase2b	59296	4.24	1.54	7.2E-02	2.2E-01	1.00	0.17	1.00	0.56	
1385465_at	Sialic acid binding Ig-like lectin 5 (predicted)	Siglec5_predicted	292843	4.23	2.99	6.9E-02	1.6E-02	1.00	0.67	1.00	0.67	
1392648_at	mannose receptor, C type 1 (predicted)	Mrc1_predicted	291327	4.18	2.38	9.7E-02	9.8E-03	1.00	0.67	1.00	0.44	
1369086_a_at	calcium channel, voltage-dependent, L type, alpha 1D subunit	Cacna1d	29716	4.08	1.96	6.9E-02	1.9E-02	1.00	0.00	0.40	0.06	
1396713_at	Similar to RIKEN cDNA 2610110G12	RGDI1303066	361789	4.02	2.38	3.3E-02	1.7E-02	1.00	0.00	1.00	0.17	
1386009_at	Colony stimulating factor 3 receptor (granulocyte) (predicted)	Csf3r_predicted	298518	3.88	1.93	6.9E-02	5.4E-03	1.00	1.00	1.00	1.00	
1393227_at				3.87	2.74	5.0E-02	1.2E-03	1.00	1.00	1.00	1.00	
1369736_at	epithelial membrane protein 1	Emp1	25314	3.78	4.67	7.9E-02	1.9E-02	1.00	0.00	0.40	0.00	
1370613_x_at	UDP glycosyltransferase 1 family, polypeptide A1	Ugt1a1	113992	3.78	2.70	4.6E-02	1.0E-02	1.00	1.00	1.00	0.89	
1396672_at				3.66	1.30	9.7E-02	1.7E-01	1.00	1.00	1.00	0.78	
1388728_at	lysosomal-associated protein transmembrane 4B	Laptm4b	315047	3.66	2.40	5.5E-02	5.3E-05	1.00	1.00	1.00	1.00	
1377671_at	Transcribed locus			3.55	2.43	2.7E-02	3.8E-03	1.00	1.00	1.00	1.00	
1387947_at	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	Mafb	54264	3.53	1.83	6.3E-02	9.6E-03	1.00	1.00	1.00	1.00	
1388416_at	low density lipoprotein receptor-related protein 1	Lrp1	299858	3.52	1.85	5.0E-02	2.1E-03	1.00	1.00	1.00	1.00	
1368000_at	complement component 3	C3	24232	3.51	1.73	2.7E-02	3.6E-02	1.00	1.00	1.00	1.00	
1375055_at	similar to JP-45 protein	LOC686460	686460	3.43	4.86	9.3E-02	4.8E-02	1.00	0.00	0.00	0.00	
1382201_at	unc-5 homolog C (C. elegans)	Unc5c	362049	3.42	1.11	9.5E-02	7.4E-01	0.83	0.00	1.00	0.89	
1383936_at	Elastin microfibril interactor 2 (predicted)	Emilin2_predicted	316736	3.40	2.05	3.7E-02	1.3E-03	1.00	1.00	1.00	1.00	
1395301_x_at	Transcribed locus, strongly similar to XP_580064.1 hypothetical protein XP_580064 [Rattus norvegicus]	Fbxh4_predicted	313101	3.38	2.19	3.3E-02	7.9E-04	1.00	1.00	1.00	1.00	
1395788_at	Transcribed locus			3.35	2.31	6.3E-02	3.2E-01	1.00	0.00	0.00	0.00	
1394611_at				3.30	1.66	6.3E-02	2.7E-02	1.00	0.00	1.00	0.61	
1372691_at	uridine phosphorylase 1	Upp1	289801	3.29	2.36	3.8E-02	4.5E-03	1.00	0.50	1.00	1.00	
1376771_at	Transcribed locus			3.27	1.35	4.8E-02	6.3E-01	1.00	0.00	0.60	0.22	
1369375_a_at	calpain 3	Capn3	29155	3.26	1.55	5.8E-02	1.1E-01	1.00	1.00	1.00	0.67	
1388272_at	immunoglobulin heavy chain 1a (serum IgG2a)	Igh-1a	299352	3.21	0.46	4.1E-02	1.7E-01	1.00	1.00	1.00	1.00	
1382905_at	Collagen-binding factor Endo180	Endo180	498011	3.21	1.28	2.8E-02	4.0E-01	1.00	1.00	1.00	1.00	
1378285_at	natural cytotoxicity triggering receptor 3	Ncr3	294251	3.20	1.97	3.6E-02	5.5E-03	1.00	1.00	1.00	1.00	
1387029_at	complement component factor H	Chf	155012	3.19	2.32	7.8E-02	1.2E-03	1.00	1.00	1.00	1.00	
1368393_at	complement component 1, q subcomponent, receptor 1	C1qr1	84398	3.17	2.25	6.0E-02	1.0E-02	1.00	1.00	1.00	1.00	
1390102_at	disrupted in renal carcinoma 2 homolog (human)	Dirc2	303902	3.15	2.44	3.3E-02	9.4E-05	1.00	1.00	1.00	1.00	
1377064_at	dual specificity phosphatase 6	Dusp6	116663	3.12	1.93	6.1E-02	2.7E-02	1.00	1.00	1.00	1.00	
1374794_at	kinesin family member 15	Kif15	353302	3.12	2.36	3.0E-02	3.9E-04	1.00	1.00	1.00	0.78	
1373204_at	hypothetical LOC297077	RGDI1310725	297077	3.06	2.34	4.6E-02	6.4E-04	1.00	1.00	1.00	1.00	
1378418_at	similar to MGC37193 protein	RGDI1311681	364674	3.06	2.54	6.3E-02	4.9E-04	1.00	1.00	1.00	1.00	
1379625_at	Transcribed locus			3.06	1.50	3.8E-02	2.1E-01	1.00	0.00	0.80	0.72	
1370491_a_at	histidine decarboxylase	Hdc	24443	3.04	2.30	8.3E-02	1.2E-02	1.00	0.00	0.50	0.00	
1369089_at	protein kinase C, gamma	Pkcc	24681	3.04	1.19	9.1E-02	5.0E-01	0.83	0.00	0.00	0.00	
1385129_at	similar to mitochondrial glycerol 3-phosphate acyltransferase (predicted)	RGDI1304904_predicted	296130	3.02	2.30	3.8E-02	1.2E-01	1.00	0.50	0.80	0.17	
1379642_at	Transcribed locus			3.02	2.28	7.7E-02	4.2E-04	1.00	1.00	1.00	1.00	
1373082_at	Transcribed locus			0.33	0.36	6.8E-02	4.2E-04	0.00	0.67	0.00	1.00	
1384180_at	interferon-induced protein with tetratricopeptide repeats 2	Ifit2	294091	0.33	0.66	8.9E-02	8.7E-02	1.00	1.00	1.00	1.00	
1371951_at	Transcribed locus			0.33	0.57	3.4E-02	2.7E-02	1.00	1.00	1.00	1.00	
1391495_at	Similar to RIKEN cDNA 2010012005 (predicted)	RGDI1311783_predicted	294012	0.33	0.78	1.9E-02	1.5E-01	1.00	1.00	0.40	1.00	
1393887_at	choline phosphotransferase 1	Chpt1	362866	0.33	0.43	8.1E-02	2.5E-03	0.00	1.00	0.50	0.61	
1387831_at	Inhibitor of Bruton agammaglobulinemia tyrosine kinase (predicted)	Ibk_predicted	315858	0.32	0.34	2.9E-02	3.3E-03	1.00	1.00	1.00	1.00	
1394154_at	Transcribed locus			0.32	0.87	6.8E-02	6.2E-01	0.17	1.00	0.30	0.44	
1389832_at	glutathione S-transferase omega 1	Gsto1	114846	0.32	0.47	3.0E-02	1.8E-04	1.00	1.00	1.00	1.00	
1383503_at	Transcribed locus			0.32	0.67	5.5E-02	3.7E-02	0.33	1.00	0.20	1.00	
1377697_at	similar to amyloid beta (A4) precursor protein-binding, family B, member 2 (predicted)	RGDI1562438_predicted	305338	0.32	0.36	2.5E-02	1.0E-03	1.00	1.00	1.00	1.00	
1379285_at	receptor transporter protein 4 (predicted)	Rtp4_predicted	360733	0.31	0.64	3.5E-02	1.1E-01	1.00	1.00	1.00	1.00	
1383393_at	Transcribed locus			0.31	0.62	4.4E-02	1.5E-02	1.00	1.00	1.00	1.00	
1398664_at	GRAM domain containing 3	Grand3	307288	0.31	0.34	7.8E-02	1.2E-03	1.00	1.00	0.80	1.00	
1385643_at	Transcribed locus			0.31	0.47	7.7E-02	2.6E-02	1.00	1.00	0.20	1.00	
1397907_at	Hypothetical protein LOC501546	LOC501546	501546	0.31	0.42	6.4E-02	1.2E-02	1.00	1.00	0.80	1.00	
1377133_at	Hypothetical protein LOC680687	LOC680687	680687	0.31	0.43	3.2E-02	2.1E-03	1.00	1.00	0.80	1.00	
1370628_at	granzyme B	Gzmb	171528	0.30	0.75	6.1E-02	1.8E-01	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	Strain+Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1369857_at	solute carrier family 14 (urea transporter), member 1	Scl14a1	54301	0.30	0.62	8.2E-02	1.1E-01	1.00	1.00	0.10	0.67
1384933_at	Transcribed locus			0.30	0.35	8.3E-02	9.1E-03	0.17	1.00	0.30	1.00
1383564_at	interferon regulatory factor 7	Irf7	293624	0.30	0.35	5.1E-02	7.6E-05	1.00	1.00	1.00	1.00
1394500_at	Transcribed locus			0.29	0.62	7.6E-02	5.4E-03	0.33	1.00	1.00	1.00
1392745_at	similar to RIKEN cDNA 3110040N11	RGD1305713	293059	0.29	0.49	2.6E-02	2.7E-02	1.00	1.00	0.00	1.00
1380415_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.29	0.41	4.2E-02	1.1E-05	1.00	1.00	1.00	1.00
1395116_at	Procollagen, type IX, alpha 1	Col9a1	305104	0.29	0.52	4.0E-02	2.1E-04	1.00	1.00	1.00	1.00
1373028_at	receptor-like tyrosine kinase	Ryk	140585	0.29	0.40	3.3E-02	2.3E-04	0.00	1.00	0.00	1.00
1397300_at	Transcribed locus			0.29	0.54	2.5E-02	1.3E-02	1.00	1.00	1.00	1.00
1383097_at	similar to RIKEN cDNA 201002C05 (predicted)	RGD1311783_predicted	294012	0.29	0.51	3.5E-02	6.1E-03	1.00	1.00	1.00	1.00
1395274_at	dystonin (predicted)	Dst_predicted	316313	0.28	0.38	4.0E-02	5.9E-02	1.00	1.00	0.40	0.78
1371152_a_at	2',5'-oligoadenylate synthetase 1, 40/46kDa	Oas1	192281	0.28	1.33	4.5E-02	2.0E-01	1.00	1.00	1.00	1.00
1384067_at	FCH domain only 2 (predicted)	Fcho2_predicted	309129	0.28	0.34	5.0E-02	2.2E-04	0.67	1.00	0.90	1.00
1371101_at	receptor-like tyrosine kinase	Ryk	140585	0.28	0.61	7.3E-02	8.1E-02	1.00	1.00	0.90	1.00
1380888_at	similar to CG31613-PA	LOC684841	684841	0.28	0.36	9.8E-02	4.3E-03	0.33	1.00	0.00	1.00
1370013_at	cyclic nucleotide gated channel alpha 1	Cnga1	85259	0.28	0.39	6.6E-02	4.9E-04	0.17	1.00	0.00	1.00
1368762_a_at	ubiquitin D	UblD	29168	0.27	0.40	4.3E-02	1.3E-05	0.33	1.00	0.40	1.00
1387995_a_at	interferon induced transmembrane protein 3	Ifim3	361673	0.27	0.89	7.7E-02	5.9E-01	1.00	1.00	1.00	1.00
1380094_at	Zinc finger protein 212	Zfp212	297066	0.27	0.50	2.9E-02	2.3E-03	0.83	1.00	0.40	1.00
1382314_at	interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted	298693	0.27	0.39	6.0E-02	5.5E-04	1.00	1.00	0.90	1.00
1368409_at	glutathione S-transferase, theta 2	Gst2	29487	0.27	0.29	2.7E-02	2.2E-04	0.00	1.00	0.00	0.22
1371017_at	Glycerol-3-phosphate acyltransferase, mitochondrial	Gpam	29653	0.27	0.35	1.4E-02	1.4E-04	1.00	1.00	1.00	1.00
1389470_at	complement factor B	Cfb	294257	0.27	0.91	6.9E-02	7.3E-01	0.00	1.00	1.00	1.00
1373833_at	similar to RIKEN cDNA 3110040N11	RGD1305713	293059	0.26	0.38	3.8E-02	5.4E-05	1.00	1.00	1.00	1.00
1387739_at	CD8 antigen, beta chain	Cd8b	24931	0.26	0.55	1.4E-02	1.4E-03	1.00	1.00	1.00	1.00
1369877_at	CD8 antigen, alpha chain	Cd8a	24930	0.26	0.41	2.5E-02	3.0E-04	1.00	1.00	1.00	1.00
1375724_at	similar to testhymin (predicted)	RGD1563612_predicted	500026	0.26	0.34	2.6E-02	1.4E-04	1.00	1.00	1.00	1.00
1385414_at	CD8 antigen, alpha chain	Cd8a	24930	0.25	0.39	2.5E-02	4.0E-04	1.00	1.00	1.00	1.00
1387283_at	myxovirus (influenza virus) resistance 2	Mx2	286918	0.25	0.46	7.3E-02	1.2E-03	1.00	1.00	1.00	1.00
1385314_at	Transcribed locus			0.25	0.81	5.0E-02	1.6E-01	1.00	1.00	1.00	1.00
1398706_at	interleukin enhancer binding factor 3	Ilf3	84472	0.24	0.60	2.5E-02	7.4E-03	1.00	1.00	1.00	1.00
1387366_at	similar to Nucleoprotein G2 (predicted)	RGD1564353_predicted	300923	0.24	0.60	1.9E-02	2.2E-02	1.00	1.00	1.00	1.00
1394027_at	similar to CG3996-PA (predicted)	RGD1305255_predicted	299824	0.24	0.26	3.9E-02	4.7E-02	0.00	0.83	0.00	0.06
1397538_at	Transcribed locus			0.23	0.47	6.1E-02	7.0E-02	1.00	1.00	0.80	1.00
1396771_at	granzyme A	Gzma	266708	0.23	0.70	3.0E-02	1.9E-01	1.00	1.00	1.00	1.00
1376899_at	coagulation factor II (thrombin) receptor	F2r	25439	0.23	0.41	2.6E-02	5.9E-04	1.00	1.00	1.00	1.00
1393245_at	Phytanoyl-CoA hydroxylase	Phyh	114209	0.23	0.36	2.3E-02	9.9E-06	1.00	1.00	1.00	1.00
1380638_at	nuclear receptor coactivator 3	Ncoa3	84584	0.23	0.67	4.7E-02	9.9E-03	1.00	1.00	1.00	1.00
1382155_at	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	309391	0.23	0.87	2.9E-02	6.0E-01	1.00	1.00	0.80	1.00
1372002_at	gap junction membrane channel protein alpha 1	Gja1	24392	0.22	0.46	2.5E-02	1.2E-03	0.33	1.00	0.10	1.00
1382024_at	Similar to RIKEN cDNA 2010315L10 (predicted)	RGD1306660_predicted	290627	0.22	0.61	3.2E-02	3.9E-02	1.00	1.00	1.00	1.00
1397146_at	Transcribed locus			0.22	0.41	3.3E-02	1.6E-03	0.00	0.60	1.00	0.00
1392716_at	granzyme B	Gzmb	171528	0.21	0.64	4.5E-02	4.4E-02	1.00	1.00	1.00	1.00
1379794_at	prolycarboxypeptidase (angiotensinase C) (predicted)	Prep_predicted	293118	0.21	1.02	3.2E-02	9.7E-01	0.00	1.00	1.00	1.00
1393657_at	Transcribed locus			0.20	0.36	8.9E-02	3.4E-04	1.00	1.00	0.60	1.00
1379436_a_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.20	0.40	3.2E-02	1.4E-04	1.00	1.00	0.70	1.00
1368598_at	somatostatin receptor 3	Sstr3	171044	0.17	0.39	7.9E-02	4.8E-04	1.00	1.00	1.00	1.00
1374708_at	similar to Rho guanine nucleotide exchange factor (GEF) 10 (predicted)	RGD1565043_predicted	306618	0.17	0.39	4.8E-02	1.9E-06	1.00	1.00	1.00	1.00
1368042_a_at	high mobility group box 1	Hmgb1	25459	0.17	0.68	2.7E-02	9.4E-03	1.00	1.00	1.00	1.00
1374015_at	similar to potassium voltage-gated channel, Isk-related family, member 1-like	LOC681190	681190	0.17	0.35	2.6E-02	3.5E-04	1.00	1.00	1.00	1.00
1370822_at	RT1 class II, locus Ba	RT1-Ba	309621	0.17	0.60	3.2E-02	8.8E-02	1.00	1.00	1.00	1.00
1380084_at	Similar to solute carrier family 25, member 36	LOC501039	501039	0.16	0.33	7.0E-02	2.1E-04	0.67	1.00	0.80	1.00
1378233_at	Transcribed locus			0.15	0.16	9.5E-02	1.5E-04	0.00	1.00	0.00	0.17
1397146_at	Transcribed locus, weakly similar to XP_917161.1 hypothetical protein XP_912068 [Mus musculus]			0.12	0.65	2.1E-02	3.9E-01	0.00	0.67	0.00	0.00
1392707_at	Similar to CG33154-PB (predicted)	RGD1310270_predicted	314798	0.12	0.58	7.3E-02	3.1E-01	0.00	0.50	0.00	0.00
1396551_at	Transcribed locus			0.11	0.37	5.9E-02	4.0E-02	0.00	1.00	0.00	0.22
1398468_at	Transcribed locus			0.11	0.41	2.5E-02	2.7E-02	0.00	0.67	0.00	0.00
1394277_at	interferon-induced protein with tetratricopeptide repeats 3	Ifi3	309526	0.11	0.72	8.3E-02	6.7E-01	0.00	0.67	0.00	0.00
1376908_at	Transcribed locus			0.11	0.35	3.6E-02	4.0E-03	1.00	1.00	1.00	1.00
1380119_at	Transcribed locus			0.10	0.34	3.1E-02	1.3E-01	0.00	0.67	0.00	0.00
1397473_at	distrobrein binding protein 1	Dtnbp1	641528	0.10	0.75	9.7E-02	3.6E-01	0.00	1.00	0.00	0.00
1393397_at	carboxypeptidase A2 (pancreatic) (predicted)	Cpa2_predicted	296959	0.09	0.15	4.3E-02	1.5E-04	0.00	0.83	0.00	0.00
1379846_at	Transcribed locus			0.07	0.23	9.8E-02	1.2E-02	0.00	1.00	0.00	0.00
1375030_at	Transcribed locus			0.07	0.17	7.3E-02	1.5E-03	0.00	1.00	0.00	0.17
1395942_at	Transcribed locus			0.07	0.69	5.0E-02	9.3E-02	0.00	1.00	0.00	0.72
1376892_at	CDNA clone IMAGE:7313785			0.05	0.42	3.2E-02	6.1E-04	0.00	1.00	0.30	1.00
1395888_at	Thyroid hormone receptor associated protein 6 (predicted)	Thrap6_predicted	299905	0.04	0.27	2.6E-02	1.5E-02	0.00	0.67	0.00	0.00
1390911_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.03	0.03	2.6E-02	4.5E-06	0.00	1.00	0.00	0.00
1378193_at	membrane-spanning 4-domains, subfamily A, member 7 (predicted)	Msa47_predicted	293744	0.03	0.91	2.9E-02	9.3E-01	0.00	1.00	0.80	0.83
1380651_at	ring finger protein (CSH2C3 type) 6 (predicted)	Rnf6_predicted	304271	0.01	0.40	9.6E-03	1.1E-03	0.00	1.00	1.00	1.00

B. Strain+Rejection Effect											
1371081_at	Rap guanine nucleotide exchange factor (GEF) 4	Rapgef4	252857	9.34	21.28	2.5E-01	8.6E-04	1.00	0.00	1.00	0.00
1391018_at	Transcribed locus			5.52	15.12	2.2E-01	3.5E-03	0.67	0.00	1.00	0.00
1382788_at	Major histocompatibility complex, class II, DM beta	Hla-dmb	294273	4.29	9.91	1.6E-01	8.3E-03	0.17	0.00	0.60	0.00
1370215_at	complement component 1, q subcomponent, beta polypeptide	C1qb	29687	0.39	9.82	6.9E-01	3.6E-02	0.00	0.00	0.80	0.00

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Strain+Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1394673_at	similar to Myeloid cell surface antigen CD33 precursor (Siglec-3)	LOC687856	687856	2.25	9.76	3.8E-02	1.4E-02	1.00	0.33	1.00	0.00
1387835_at	interleukin 1 receptor antagonist	Il1rn	60582	2.40	8.15	6.2E-01	3.8E-02	0.67	0.33	1.00	0.33
1378733_at	Transcribed locus			5.56	7.46	3.9E-01	9.0E-03	1.00	0.00	1.00	0.00
1385205_at	Transcribed locus			6.87	7.02	1.4E-01	1.4E-04	1.00	0.00	1.00	0.00
1396420_at	Bromodomain adjacent to zinc finger domain protein 1B	Baz1b	368002	15.86	6.15	1.1E-01	3.0E-02	1.00	0.33	0.80	0.11
1376652_at	complement component 1, q subcomponent, alpha polypeptide	C1qa	298566	0.44	5.59	5.7E-01	6.1E-02	0.00	0.00	0.80	0.06
1376100_at	tubulin, beta 6	Tubb6	307351	5.50	5.45	2.2E-01	2.0E-02	0.00	0.00	0.50	0.00
1387742_at	chemokine (C-C motif) receptor 2	Ccr2	60463	4.47	5.42	1.3E-01	2.8E-03	1.00	1.00	1.00	0.78
1372060_at				16.09	5.04	1.2E-01	2.6E-02	1.00	0.33	1.00	0.00
1368266_at	arginase 1	Arg1	29221	1.59	4.64	7.7E-01	7.6E-04	0.00	0.00	0.80	0.00
1382601_at	Similar to scavenger receptor type A SR-A (predicted)	RGD1564316_predicted	498638	1.63	4.60	5.7E-01	3.0E-02	0.33	0.00	1.00	0.33
1396133_at	Integrin, beta 5	Igb5	257645	9.10	4.59	1.7E-01	1.0E-02	0.67	0.00	0.80	0.00
1387314_at	sulfotransferase family 1B, member 1	Sult1b1	64305	2.22	4.48	1.2E-01	2.3E-02	0.00	0.00	0.80	0.00
1393252_at	Transcribed locus			2.57	4.45	2.6E-01	1.6E-02	1.00	0.33	1.00	0.33
1384466_at	notch1-induced protein	LOC493574	493574	5.53	4.36	3.4E-01	1.4E-02	0.67	0.00	0.80	0.11
1397730_at	similar to RIKEN cDNA 231003C23 (predicted)	RGD1307235_predicted	309053	1.63	4.23	7.2E-01	1.7E-02	1.00	0.67	1.00	0.22
1367860_a_at	matrix metalloproteinase 14 (membrane-inserted)	Mmp14	81707	0.59	4.22	6.4E-01	1.5E-02	0.00	0.00	0.90	0.00
1388142_at	chondroitin sulfate proteoglycan 2	Cspg2	114122	1.86	4.18	2.1E-01	3.4E-04	1.00	1.00	1.00	1.00
1373025_at	complement component 1, q subcomponent, gamma polypeptide	C1qg	362634	0.46	4.07	6.2E-01	1.9E-02	0.00	0.00	0.80	0.00
1393682_at	G-protein-coupled receptor GPR34 (predicted)	GPR34_predicted	554353	3.01	4.07	1.0E-01	5.0E-04	0.67	0.50	1.00	1.00
1369665_a_at	interleukin 18	Il18	29197	2.77	4.04	3.8E-02	3.4E-05	1.00	1.00	1.00	1.00
1369290_at	chemokine (C-C motif) receptor 5	Ccr5	117029	1.44	3.96	6.1E-01	5.3E-03	1.00	1.00	1.00	0.78
1388054_a_at	chondroitin sulfate proteoglycan 2	Cspg2	114122	2.30	3.95	2.2E-01	1.2E-03	1.00	0.33	1.00	0.78
1370728_at	interleukin 13 receptor, alpha 1	Il13ra1	252963	2.62	3.92	1.9E-01	4.1E-02	1.00	0.67	1.00	0.33
1394630_at	LIM domain only 4	Lmo4	362051	1.27	3.90	7.4E-01	8.1E-02	1.00	0.00	0.50	0.00
1368494_at	S100 calcium binding protein A8 (calgranulin A)	S100a8	116547	1.78	3.90	2.1E-01	1.9E-02	1.00	1.00	1.00	1.00
1371146_at	transcription factor EC	Tec	26296	1.72	3.73	4.8E-01	7.5E-03	1.00	0.33	1.00	0.22
1390364_at	Transcribed locus			1.10	3.70	9.1E-01	5.9E-04	1.00	1.00	1.00	1.00
1383105_at	hypothetical protein LOC681292	LOC681292	681292	2.54	3.68	7.4E-02	2.1E-04	1.00	1.00	1.00	0.67
1378428_at	Transcribed locus			1.62	3.66	3.6E-01	9.2E-03	1.00	1.00	1.00	1.00
1383743_at	leucine rich repeat containing 16 (predicted)	Lrrc16_predicted	306941	6.08	3.58	2.1E-01	2.0E-03	1.00	0.33	1.00	0.22
1381613_at	Similar to farnesyl diphosphate synthetase	LOC501976	501976	2.27	3.51	7.7E-02	4.0E-02	1.00	0.00	1.00	0.00
1372031_at	Transcribed locus			1.07	3.51	8.4E-01	4.6E-04	0.00	0.00	1.00	0.00
1371232_a_at	chondroitin sulfate proteoglycan 2	Cspg2	114122	1.62	3.47	1.2E-01	1.4E-03	1.00	1.00	1.00	1.00
1391774_at	Transcribed locus			2.89	3.41	1.1E-01	1.5E-05	1.00	1.00	1.00	1.00
1368597_at	SNF1-like kinase	Snf1lk	59329	18.46	3.31	1.6E-01	1.2E-03	1.00	0.00	1.00	0.00
1394490_at	ATP-binding cassette, sub-family A (ABC1), member 1	Abca1	313210	1.73	3.31	1.8E-01	1.5E-04	1.00	0.67	1.00	1.00
1368187_at	glycoprotein (transmembrane) nmb	Gpmb	113955	2.04	3.30	2.1E-01	2.6E-04	1.00	1.00	1.00	1.00
1397222_at	Tripartite motif protein 39	Trim39	309591	2.87	3.29	1.3E-01	6.4E-02	1.00	0.67	0.80	0.22
1377698_at	tumor necrosis factor receptor superfamily, member 5	Tnfrsf5	171369	2.67	3.25	3.9E-02	2.4E-04	1.00	1.00	1.00	0.56
1394861_at	POU domain, class 6, transcription factor 1	Pou6f1	116545	3.61	3.23	1.3E-01	4.0E-02	0.83	0.33	1.00	0.00
1392043_at	Insulin receptor	Insr	24954	2.21	3.21	4.0E-01	3.1E-03	1.00	0.00	1.00	0.56
1375003_at	serine (or cysteine) peptidase inhibitor, clade B, member 6a	Serpinh6a	291085	2.94	3.20	7.8E-02	1.4E-04	1.00	1.00	1.00	1.00
1394451_at	annexin A1	Anxa1	25380	2.84	3.19	3.6E-02	1.3E-05	1.00	0.33	1.00	0.00
1385892_at	Transcribed locus			1.00	3.14	9.9E-01	7.5E-02	1.00	0.83	0.90	0.17
1384479_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	Galnt3	366061	2.69	3.13	1.5E-01	8.9E-02	1.00	0.00	1.00	0.00
1382129_at	Guanine nucleotide binding protein, alpha stimulating, olfactory type	Gnal	24611	2.24	3.11	3.8E-01	5.1E-02	1.00	0.67	1.00	0.61
1383506_at	B-cell CLL/lymphoma 11A (zinc finger protein)	Bcl11a	305589	2.74	3.11	9.8E-02	4.5E-02	1.00	1.00	1.00	0.06
1370382_at	RT1 class II, locus Bb	RT1-Bb	309622	1.99	3.08	5.1E-01	8.2E-03	1.00	0.67	1.00	1.00
1385759_at	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10	Serpinh10	266775	2.39	3.08	1.8E-01	4.9E-04	1.00	1.00	1.00	1.00
1385871_at	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted	310461	1.48	3.07	5.8E-01	7.1E-03	1.00	1.00	1.00	1.00
1391219_at	Transcribed locus			2.36	3.05	3.0E-01	3.3E-05	1.00	0.33	1.00	0.56
1390412_at	Pre-B lymphocyte gene 3 (predicted)	Vpreb3_predicted	365550	0.45	0.33	2.2E-01	7.6E-05	1.00	1.00	1.00	1.00
1387112_at	proteolipid protein	Pip	24943	0.57	0.33	3.6E-01	9.0E-05	1.00	1.00	1.00	1.00
1378738_at	potassium voltage-gated channel, shaker-related subfamily, beta member 1	Kcnab1	29737	0.41	0.33	1.4E-01	3.0E-05	1.00	1.00	1.00	1.00
1390807_at	carbonic anhydrase VB, mitochondrial	CaSb	302669	0.34	0.33	4.7E-02	1.2E-05	1.00	1.00	1.00	1.00
1380831_at	Transcribed locus			0.45	0.33	1.4E-01	2.6E-05	1.00	1.00	1.00	1.00
1369097_s_at	guanylate cyclase 1, soluble, beta 3	Gucyl1b3	25202	0.57	0.32	3.4E-01	3.3E-04	1.00	1.00	1.00	1.00
1382853_at	ring finger protein 11 (predicted)	Rnf11_predicted	316552	0.53	0.32	8.3E-02	5.6E-05	1.00	1.00	1.00	1.00
1384045_at				0.50	0.32	2.2E-01	8.4E-02	0.33	1.00	0.40	0.56
1395967_at	Transcribed locus			0.70	0.32	1.6E-01	8.4E-04	1.00	1.00	0.00	0.94
1384273_at	carbohydrate kinase-like	Carkl	287479	0.66	0.32	5.2E-01	3.3E-04	1.00	1.00	0.60	1.00
1371541_at	myosin, light polypeptide kinase (predicted)	Mylk_predicted	288057	0.51	0.32	1.7E-01	1.4E-04	1.00	1.00	1.00	1.00
1386275_at	Transcribed locus			0.39	0.32	6.8E-02	8.8E-05	1.00	1.00	1.00	1.00
1392817_at	Transcribed locus			0.28	0.32	5.1E-01	2.6E-02	0.00	0.00	0.40	0.94
1370418_s_at	brain and kidney protein	Bk	192189	0.39	0.32	7.2E-02	1.6E-05	0.00	0.00	0.00	1.00
1392801_at	similar to novel protein (predicted)	RGD1561145_predicted	498580	0.37	0.32	7.2E-02	1.1E-04	1.00	1.00	1.00	1.00
1377309_at	Transcribed locus			0.34	0.32	1.9E-01	3.7E-05	1.00	1.00	0.90	1.00
1376546_at	similar to hypothetical protein (predicted)	RGD1565432_predicted	499157	0.72	0.32	3.6E-01	1.7E-02	1.00	0.80	1.00	1.00
1387130_at	solute carrier family 39 (iron-regulated transporter), member 1	Slc40a1	170840	0.51	0.32	3.6E-01	7.1E-05	1.00	1.00	1.00	1.00
1394386_s_at	vacuolar protein sorting 52 (yeast)	Vps52	25218	0.52	0.32	5.6E-02	1.5E-02	1.00	1.00	0.00	0.67
1383240_at	integrin, alpha 6	Iga6	114517	0.44	0.32	6.1E-02	1.2E-04	1.00	1.00	1.00	1.00
1380600_at	similar to Integrin alpha-IIb precursor (Platelet membrane glycoprotein IIb) (GPIIb) (GPIIb) (CD41 antigen)	LOC685269	685269	0.48	0.31	2.0E-01	1.9E-04	1.00	1.00	1.00	1.00
1368348_at	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	Slc6a4	25553	0.79	0.30	6.3E-01	1.4E-04	1.00	1.00	1.00	1.00
1388432_at	optineurin	Optn	246294	0.44	0.30	3.4E-02	3.8E-04	1.00	1.00	1.00	1.00
1388804_at	Transcribed locus			0.52	0.30	2.0E-01	2.3E-02	1.00	1.00	0.00	0.61
1369732_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	St3gal2	64442	0.76	0.30	5.2E-01	3.4E-05	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	Strain+Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1370548_at	solute carrier family 16 (monocarboxylic acid transporters), member 10	Slc16a10	170566	0.55	0.30	1.7E-01	7.8E-03	1.00	1.00	0.40	1.00
1398420_at	SMAD specific E3 ubiquitin protein ligase 2 (predicted)	Smurf2_predicted	303614	0.54	0.30	1.8E-01	1.1E-03	1.00	1.00	1.00	1.00
1370518_a_at	syntaxin binding protein 1	Sixbp1	25558	0.21	0.30	1.2E-01	3.3E-05	0.00	1.00	0.10	1.00
1374529_at	Thrombospondin 1	Tbhs1	445442	0.54	0.30	1.4E-01	9.6E-06	1.00	1.00	1.00	1.00
1377029_at	RAR-related orphan receptor alpha (predicted)	Rora_predicted	300807	1.03	0.30	9.0E-01	8.5E-02	0.00	0.17	0.00	0.56
1377646_at	Transcribed locus			0.70	0.29	7.4E-01	3.7E-02	0.00	0.00	0.10	0.67
1370913_at	Best5 protein	Best5	65190	0.39	0.29	3.6E-01	1.7E-02	1.00	1.00	1.00	1.00
1381780_at	Transcribed locus			1.09	0.29	8.6E-01	2.1E-02	1.00	1.00	1.00	1.00
1379325_at	Fatty acid amide hydrolase	Faah	29347	0.52	0.29	2.0E-01	5.6E-04	1.00	1.00	1.00	1.00
1374139_at	cerebellar degeneration-related 2	Cdr2	308958	1.15	0.29	6.5E-01	2.6E-02	1.00	1.00	1.00	1.00
1379496_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.34	0.29	3.3E-02	3.4E-04	1.00	1.00	1.00	1.00
1394621_at	Similar to genetic suppressor element 1 (predicted)	RGD1562686_predicted	307913	0.36	0.29	3.6E-02	2.2E-06	1.00	1.00	1.00	1.00
1370138_at	lymphoid enhancer binding factor 1	Lef1	161452	0.61	0.29	3.6E-02	1.3E-04	1.00	1.00	1.00	1.00
1370163_at	ornithine decarboxylase 1	Odc1	24609	0.42	0.29	7.7E-02	2.6E-06	1.00	1.00	1.00	1.00
1383933_at	Similar to KIAA0564 protein (predicted)	RGD1308772_predicted	290381	0.60	0.29	2.1E-01	8.8E-06	1.00	1.00	1.00	1.00
1380100_at	similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted)	RGD1561817_predicted	294917	0.46	0.28	6.5E-02	8.9E-06	1.00	1.00	0.10	1.00
1389654_at	Plastin 1 (I isoform) (predicted)	Pls1_predicted	315926	0.53	0.28	3.9E-01	1.2E-05	1.00	1.00	0.20	1.00
1390579_at	similar to RIKEN cDNA 1810029B16 (predicted)	RGD1305222_predicted	290686	0.58	0.28	5.5E-02	8.1E-05	1.00	1.00	0.60	1.00
1370152_at	glycoprotein 5, platelet	Gp5	25259	0.80	0.28	6.7E-01	3.2E-04	1.00	1.00	1.00	1.00
1372455_at	transmembrane 4 superfamily member 12	Tms4f12	362326	0.57	0.28	3.1E-01	7.1E-05	1.00	1.00	1.00	1.00
1368755_at	C-type lectin domain family 4, member f	Clec4f	114598	0.37	0.28	2.1E-01	4.9E-04	1.00	1.00	0.50	1.00
1383399_at	synaptic vesicle glycoprotein 2a	Sv2a	117559	0.40	0.28	4.8E-02	2.1E-06	1.00	1.00	1.00	1.00
1373356_at				0.58	0.28	2.0E-01	1.0E-03	1.00	1.00	0.30	1.00
1370624_at	coagulation factor II (thrombin) receptor-like 2	F2r2	29636	0.21	0.27	1.2E-01	1.3E-05	1.00	1.00	1.00	1.00
1387905_at	J domain protein 1	LOC619393	619393	0.41	0.27	6.3E-02	5.5E-06	1.00	1.00	1.00	1.00
1389398_at	ankyrin 1, erythroid	Ank1	306570	1.13	0.27	9.5E-01	6.8E-02	0.00	0.00	0.00	0.67
1378843_at	DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	362293	0.36	0.27	1.9E-01	3.1E-03	1.00	1.00	0.80	1.00
1388544_at	2,3-bisphosphoglycerate mutase	Bpgm	296973	1.04	0.27	8.8E-01	1.2E-02	1.00	1.00	1.00	1.00
1390388_at	ferrochelatase (predicted)	Fchc_predicted	361338	1.06	0.27	8.2E-01	3.1E-02	1.00	1.00	1.00	1.00
1395222_at	FCH domain only 2 (predicted)	Fcho2_predicted	309129	0.19	0.27	2.8E-01	6.9E-05	0.00	1.00	0.00	1.00
1398622_at	cysteine-rich motor neuron 1 (predicted)	Crim1_predicted	298744	0.45	0.27	1.5E-01	8.3E-05	1.00	1.00	1.00	1.00
1386212_at	spectrin alpha 1	Spm1	289257	1.20	0.26	8.6E-01	6.1E-02	0.00	0.00	0.40	0.89
1383551_at	2,3-bisphosphoglycerate mutase	Bpgm	296973	1.00	0.26	1.0E+00	5.4E-02	1.00	1.00	0.80	1.00
1377423_at	Transcribed locus			1.37	0.26	8.8E-01	1.6E-02	0.00	0.00	0.00	0.61
1394109_at	Thrombospondin 1	Tbhs1	445442	0.68	0.26	4.0E-01	2.3E-05	1.00	1.00	1.00	1.00
1391448_at	cysteine-rich motor neuron 1 (predicted)	Crim1_predicted	298744	0.44	0.26	2.0E-01	6.9E-05	1.00	1.00	1.00	1.00
1379203_at	transcription factor Dp 2 (predicted)	Tcfdp2_predicted	300947	0.80	0.25	5.2E-01	4.9E-02	1.00	1.00	0.60	1.00
1370176_at	trafficking protein, kinesin binding 2	Trak2	171086	0.45	0.25	9.8E-02	1.4E-03	1.00	1.00	0.90	1.00
1386463_at	Transcribed locus			0.15	0.25	1.7E-01	7.4E-05	0.00	1.00	0.20	1.00
1383853_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	Dyrk3	304775	0.60	0.25	7.6E-01	4.2E-02	0.00	0.00	0.00	0.61
1392359_at	Cytoskeleton associated protein 5	Ckap5	311191	0.29	0.25	5.7E-01	2.2E-02	0.00	0.00	0.00	0.89
1384805_at	defensin beta 24	Defb24	641632	0.24	0.24	1.1E-01	8.6E-05	0.00	0.33	0.00	0.50
1382106_at	Chemokine (C-C motif) ligand 6	Ccl6	287910	0.29	0.24	2.2E-01	7.8E-05	0.17	1.00	0.80	1.00
1377114_at				0.34	0.24	2.7E-02	1.1E-07	1.00	1.00	1.00	1.00
1368338_at	CD52 antigen	Cd52	117054	0.71	0.24	4.0E-01	7.2E-02	0.00	0.00	0.40	0.94
1373093_at	ERBB receptor feedback inhibitor 1	Errf1	313729	0.62	0.23	1.3E-01	3.4E-02	1.00	1.00	0.20	0.56
1387756_s_at	hemogen	Hemgn	113882	0.73	0.23	4.9E-01	3.0E-02	1.00	0.67	1.00	1.00
1390991_at	hemoglobin, theta 1 (predicted)	Hbq1_predicted	303007	0.95	0.23	9.6E-01	3.2E-02	0.33	0.33	1.00	1.00
1368682_at	synaptic vesicle glycoprotein 2a	Sv2a	117559	0.47	0.23	9.1E-02	8.7E-03	1.00	1.00	0.20	0.94
1389353_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (predicted)	Sema6d_predicted	311384	0.39	0.23	1.2E-01	3.8E-04	1.00	1.00	0.80	1.00
1386922_at	carbonic anhydrase 2	Ca2	54231	0.72	0.23	1.1E-01	1.1E-02	1.00	1.00	1.00	1.00
1392405_at	transcription factor Dp 2 (predicted)	Tcfdp2_predicted	300947	1.94	0.22	9.5E-02	2.5E-02	1.00	1.00	1.00	1.00
1367912_at	latent transforming growth factor beta binding protein 1	Ltbp1	59107	0.49	0.22	1.9E-01	1.4E-05	1.00	1.00	1.00	1.00
1387656_at	solute carrier family 4, member 1	Slc4a1	24779	1.28	0.22	8.5E-01	3.6E-02	0.67	1.00	1.00	1.00
1378520_at	B-cell leukemia/lymphoma 11B (predicted)	Bcl11b_predicted	314423	0.62	0.22	2.3E-01	1.0E-02	1.00	1.00	0.10	0.89
1382472_at				0.43	0.22	9.2E-02	5.3E-05	1.00	1.00	1.00	1.00
1374330_at	similar to Kell protein (predicted)	RGD1565470_predicted	297025	1.13	0.22	7.3E-01	2.2E-02	0.00	0.00	0.40	1.00
1389160_at	erythroid associated factor (predicted)	Eraf_predicted	293522	3.65	0.21	6.6E-01	5.2E-02	0.00	0.00	1.00	1.00
1398577_at	similar to RIKEN cDNA 1300017J02	RGD1310507	315963	0.39	0.20	2.5E-01	8.1E-03	0.00	0.00	0.30	1.00
1383557_at	Transcribed locus			0.38	0.20	5.7E-02	1.9E-06	1.00	1.00	1.00	1.00
1367673_at	selenium binding protein 2	Selenbp1	140927	1.24	0.20	8.6E-01	7.6E-03	0.00	0.00	0.60	1.00
1390800_a_at	caveolin 2	Cav2	363425	0.08	0.19	2.1E-01	7.6E-03	0.33	1.00	0.40	1.00
1389783_s_at	similar to Fc fragment of IgG binding protein; IgG Fc binding protein	RGD1311906	292746	0.68	0.18	6.0E-01	2.6E-02	0.67	1.00	0.00	0.50
1368052_at	hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1 // Tspan8	171048	1.67	0.18	7.1E-01	5.5E-02	0.00	0.00	0.80	1.00
1391735_at	Transcribed locus			0.34	0.18	6.4E-02	2.1E-05	1.00	1.00	0.20	1.00
1369716_s_at	lectin, galactose binding, soluble 5	Lgals5 // Lgals9	25475	1.36	0.18	1.9E-01	2.8E-03	1.00	1.00	1.00	1.00
1368751_at	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	Kcns3	83588	0.37	0.17	5.0E-02	1.4E-05	1.00	1.00	1.00	1.00
1381160_at	Transcribed locus			0.16	0.15	1.3E-01	2.2E-06	0.00	1.00	0.00	1.00
1381487_at	angiopoietin 1	Angpt1	89807	0.50	0.14	6.5E-01	1.1E-02	0.33	0.67	0.00	0.50
1368753_at	calcium/calmodulin-dependent protein kinase kinase 2, beta	Camkk2	83506	0.59	0.14	8.3E-01	1.1E-04	0.00	0.33	0.00	1.00
1382618_at	erythrocyte protein band 4.2 (predicted)	Epb4_2_predicted	362202	0.71	0.14	7.7E-01	1.8E-02	0.00	0.00	0.10	0.89
1372374_at	carbonic anhydrase 1 (predicted)	Car1_predicted	310218	0.20	0.12	3.4E-01	2.6E-02	0.00	0.33	0.00	0.72
1395198_at	Zinc finger protein 313	Zfp313	362277	0.30	0.11	3.1E-01	5.6E-05	0.00	0.67	0.00	0.78
1392361_at	Transcribed locus			0.12	0.11	1.4E-02	5.9E-04	0.00	0.00	0.00	0.78
1374160_at	similar to RIKEN cDNA 1110063G11 (predicted)	RGD1311960_predicted	305095	0.97	0.09	9.6E-01	2.1E-04	0.83	1.00	1.00	1.00
1380183_at	pancreatic trypsin 1	Pss1	24691	0.91	0.08	9.2E-01	3.5E-04	0.00	0.00	0.00	0.78
1390216_a_at	Transcribed locus			0.15	0.05	8.4E-02	5.4E-05	0.00	0.00	0.00	0.78

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Strain+Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1369142_at	bone gamma-carboxylglutamate protein 2	Bglap2	25295	0.05	0.02	1.3E-01	6.5E-09	0.00	1.00	0.00	1.00
C. Overlap											
1370428_x_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	116.65	97.43	1.4E-02	9.6E-08	1.00	1.00	1.00	0.78
1381593_x_at	RT1 class II, locus Ba	RT1-Ba	309621	88.70	45.16	2.5E-02	5.4E-07	1.00	1.00	1.00	0.00
1374959_at	NAD(P)H dehydrogenase, quinone 2	Nqo2	291084	21.08	53.10	3.3E-02	9.1E-07	1.00	0.00	1.00	0.00
1392334_at	RT1 class II, locus Ba	RT1-Ba	309621	51.80	27.39	1.4E-02	6.5E-09	1.00	0.00	1.00	0.00
1387992_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Lilrb3	361493	41.82	27.88	2.5E-02	1.6E-04	1.00	0.00	1.00	0.00
1374924_at	UPF3 regulator of nonsense transcripts homolog B (yeast) (predicted)	Ulp3b_predicted	313449	39.15	21.02	8.9E-02	1.4E-04	1.00	0.00	1.00	0.00
1392172_at	chemokine (C-C motif) ligand 9	Ccl9	360579	19.87	6.65	7.8E-02	6.0E-04	1.00	0.00	1.00	0.00
1387839_at	Cullin 2 (predicted)	Cul2_predicted	361258	18.16	9.63	2.8E-02	2.7E-03	1.00	0.00	0.80	0.00
1377655_at	Similar to zinc finger protein 40	LOC690661	690661	17.37	9.77	2.7E-02	1.2E-03	1.00	0.00	0.50	0.00
1370964_at	argininosuccinate synthetase	Ass	25698	13.75	15.39	3.2E-02	2.8E-05	1.00	0.00	1.00	0.00
1367974_at	annexin A3	Anxa3	25291	15.04	13.64	1.5E-02	4.0E-07	1.00	0.17	1.00	0.72
1395366_at	Transcribed locus		12.55	7.53	9.0E-03	1.4E-03	1.00	0.33	1.00	0.00	0.00
1380948_at	Transcribed locus		12.51	9.15	2.3E-02	5.2E-03	1.00	1.00	1.00	0.44	0.00
1394846_at	similar to killer activatory receptor-like protein p91D (predicted)	RGD1562625_predicted	502291	4.63	12.02	9.3E-02	3.7E-05	1.00	0.00	0.80	0.00
1382257_at	Uridine monophosphate synthetase	Umps	288051	11.60	7.34	2.3E-02	1.9E-06	1.00	1.00	1.00	0.94
1387799_at	FXVD domain-containing ion transport regulator 2	Fxyd2	29639	8.85	9.88	3.8E-02	9.3E-07	1.00	1.00	1.00	1.00
1370493_a_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Lilrb3	361493	8.79	9.34	6.8E-02	5.7E-05	1.00	1.00	1.00	1.00
1374298_at	Transcribed locus		9.21	7.27	3.2E-02	5.9E-04	1.00	0.00	1.00	0.67	0.00
1383331_at	Transcribed locus		9.10	4.68	3.0E-02	2.4E-03	1.00	0.33	1.00	0.00	0.00
1370682_at	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Lilrb3	361493	9.02	8.52	3.8E-03	1.1E-07	1.00	1.00	1.00	1.00
1377539_at	Immunoglobulin superfamily, member 4B (predicted)	Igsf4b_predicted	360882	8.14	4.53	9.4E-02	1.6E-02	1.00	0.00	1.00	0.06
1388102_at	leukotriene B4 12-hydroxydehydrogenase	Ltd4dh	192227	3.80	8.07	5.6E-02	2.0E-04	1.00	0.00	1.00	0.00
1380346_at	serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpib1a	291091	3.19	7.81	5.6E-02	1.9E-04	1.00	1.00	1.00	1.00
1372293_at	Transcribed locus		7.74	4.88	3.3E-02	3.8E-05	1.00	1.00	1.00	1.00	0.00
1381336_at	Transcribed locus		7.66	3.14	7.7E-02	1.7E-03	1.00	0.33	1.00	0.61	0.00
1398358_a_at	similar to integrin beta-5 (predicted)	RGD1563276_predicted	498091	3.44	7.36	7.2E-02	1.2E-03	1.00	0.00	0.70	0.00
1385397_at	Abi-219	LOC499991	499991	7.35	6.50	2.6E-02	1.5E-03	1.00	0.67	1.00	1.00
1372069_at	ankyrin repeat domain 15	Ankrd15	309429	7.19	3.53	1.8E-02	6.1E-05	1.00	0.50	1.00	0.89
1377851_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	3.51	6.84	4.6E-02	1.6E-03	1.00	0.00	1.00	0.00
1368700_at	phospholipase C-like 1	Pcl1	84587	6.67	3.08	9.8E-02	8.1E-02	1.00	0.00	0.60	0.00
1385842_at	interleukin 1 family, member 8 (predicted)	Il1l8_predicted	362076	6.13	5.63	3.4E-02	7.4E-05	1.00	0.33	1.00	1.00
1391399_at	Transcribed locus		3.09	5.62	3.0E-02	5.2E-05	1.00	1.00	1.00	1.00	0.00
1379223_x_at	Transcribed locus		3.32	5.24	2.9E-02	7.8E-06	1.00	1.00	1.00	1.00	0.00
1367627_at	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Gatm	81660	3.65	5.23	5.7E-02	6.7E-06	1.00	1.00	1.00	1.00
1383561_at	ligase IV, DNA, ATP-dependent (predicted)	Lig4_predicted	290907	5.19	4.32	3.4E-02	7.6E-05	1.00	1.00	1.00	1.00
1385047_x_at	Complement component 6	C6	24237	5.02	3.92	4.9E-02	3.0E-07	1.00	1.00	1.00	1.00
1375080_at	similar to mitochondrial hepatocellular carcinoma-downregulated carrier protein	LOC684556	684556	4.98	4.73	3.2E-02	1.7E-05	1.00	0.67	1.00	0.44
1380546_at	similar to hypothetical protein FLJ10986	LOC298250	298250	3.05	4.86	2.5E-02	1.0E-05	1.00	0.50	1.00	0.06
1386938_at	alanyl (membrane) aminopeptidase	Anpep	81641	4.57	4.04	3.1E-02	1.2E-05	1.00	1.00	1.00	1.00
1383117_at	peroxisomal membrane protein 4	Pxmp4	282634	4.57	4.48	2.6E-02	1.9E-06	1.00	1.00	1.00	0.94
1393688_at	Complement component 6	C6	24237	4.55	3.63	5.8E-02	3.7E-06	1.00	1.00	1.00	1.00
1382926_s_at	Transcribed locus	Pum2	298874	3.31	4.34	8.3E-02	6.9E-05	1.00	1.00	1.00	1.00
1386064_at	Transcribed locus		4.34	3.12	3.3E-02	1.3E-04	1.00	1.00	1.00	1.00	0.00
1379306_at	Retinoblastoma-like 2	Rbl2	81758	4.30	3.60	3.9E-02	5.2E-05	1.00	0.67	1.00	0.39
1377034_at	serine (or cysteine) proteinase inhibitor, clade B, member 1a	Serpib1a	291091	3.62	4.01	5.1E-02	1.6E-04	1.00	1.00	1.00	1.00
1367614_at	annexin A1	Anxa1	25380	3.13	3.81	6.7E-02	3.0E-05	1.00	1.00	1.00	1.00
1378347_at	Transcribed locus		3.77	3.45	9.4E-02	2.7E-02	1.00	0.33	1.00	0.44	0.00
1387125_at	S100 calcium binding protein A9 (calgranulin B)	S100a9	94195	0.32	3.55	6.1E-02	7.1E-02	1.00	1.00	1.00	1.00
1370904_at	major histocompatibility complex, class II, DM alpha	Hla-dma	294274	3.20	3.46	5.6E-02	3.5E-05	1.00	1.00	1.00	1.00
1380768_at	Transcribed locus		3.44	3.04	3.5E-02	3.7E-05	1.00	1.00	1.00	1.00	0.00
1374626_at	leucine-rich alpha-2-glycoprotein 1	Lrg1	367455	3.23	3.20	6.7E-02	1.9E-03	1.00	0.67	1.00	1.00
1373270_at	WD repeat domain, phosphoinositide interacting 1 (predicted)	Wipi1_predicted	303630	3.06	3.04	7.8E-02	7.6E-05	1.00	0.00	1.00	0.78
1392778_at	Transcribed locus, weakly similar to XP_001056676.1 similar to Discs large homolog 5		3.06	3.01	2.7E-02	6.5E-05	1.00	1.00	1.00	1.00	0.00
1385551_at	Transcribed locus		0.33	0.25	4.1E-02	8.7E-05	1.00	1.00	1.00	0.00	0.00
1381646_at	ATPase, H transporting, lysosomal V1 subunit B2	Atp6v1b2	117596	0.21	0.33	1.8E-02	1.5E-04	0.67	1.00	1.00	1.00
1381893_at	Transcribed locus, weakly similar to XP_573972.1 similar to RIKEN cDNA 843042hH19 [Rattus norvegicus]		0.28	0.33	6.0E-02	2.4E-02	0.00	0.00	0.00	0.89	0.00
1392702_at	Transcribed locus		0.25	0.33	3.3E-02	4.0E-06	1.00	1.00	1.00	1.00	0.00
1380740_at	Asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase) (predicted)	Alg12_predicted	315212	0.25	0.33	7.3E-02	1.1E-03	0.00	1.00	0.20	1.00
1374280_at	cerebellin 2 precursor protein	Cbin2	291388	0.25	0.33	5.0E-02	2.2E-04	1.00	1.00	0.60	1.00
1384743_at	Transcribed locus		0.32	0.17	7.0E-02	3.7E-06	1.00	1.00	1.00	1.00	0.00
1375573_at	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	Mll5	311968	0.32	0.30	7.7E-02	1.1E-04	1.00	1.00	1.00	1.00
1395067_at	Transcribed locus		0.29	0.32	4.3E-02	1.6E-04	1.00	1.00	0.60	1.00	0.00
1374429_at	Transcribed locus		0.18	0.32	9.8E-03	1.1E-04	1.00	1.00	1.00	1.00	0.00
1370464_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Acbcb1a	170913	0.20	0.30	5.0E-02	1.7E-04	0.33	1.00	0.00	1.00
1380531_at	Synaptobrevin-like 1	Sybl1	85491	0.24	0.30	2.8E-02	8.0E-05	0.83	1.00	0.40	1.00
1397589_at	Transcribed locus		0.23	0.30	2.7E-02	3.5E-04	1.00	1.00	1.00	1.00	0.00
1369926_at	glutathione peroxidase 3	Gpx3	64317	0.19	0.30	5.0E-02	1.2E-04	1.00	1.00	0.60	1.00
1386679_at	Transcribed locus		0.29	0.25	3.9E-02	1.2E-05	1.00	1.00	1.00	1.00	0.00
1367857_at	fatty acid desaturase 1	Fads1	84575	0.29	0.18	7.5E-02	1.3E-05	1.00	1.00	1.00	1.00
1376071_at	Transcribed locus		0.20	0.29	2.9E-02	1.1E-04	1.00	1.00	1.00	1.00	0.00
1371171_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.14	0.29	2.5E-02	1.4E-05	1.00	1.00	1.00	1.00
1371078_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.28	0.24	3.5E-02	1.2E-04	1.00	1.00	0.60	1.00
1398330_at	syntaxin binding protein 1	Sixbp1	25558	0.28	0.27	3.6E-02	5.5E-06	1.00	1.00	1.00	1.00
1395436_at	Protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	24674	0.18	0.28	3.9E-02	1.4E-04	0.00	1.00	0.20	0.94

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	Fold Change		False Discovery Rate		Average Present Call			
				Strain Effect	Strain+Rejection Effect	Native BN / DA	Allograft / Isograft	Native BN	Native DA	Allograft	Isograft
1379150_at	Cytoplasmic FMR1 interacting protein 2 (predicted)	Cyfp2_predicted	303073	0.27	0.23	3.6E-02	3.5E-04	1.00	1.00	0.30	1.00
1394805_at	Exportin 6	Xpo6	293476	0.22	0.27	3.0E-02	3.5E-04	0.00	1.00	0.00	0.61
1395166_at	EH-domain containing 2	Ehd2	361512	0.11	0.27	6.3E-02	3.0E-04	0.17	1.00	0.00	1.00
1385166_at	Transcribed locus			0.26	0.25	3.0E-02	5.4E-05	1.00	1.00	0.30	1.00
1384165_at	Coagulation factor II (thrombin) receptor-like 2	F2rl2	29636	0.26	0.21	9.4E-02	1.4E-06	1.00	1.00	1.00	1.00
1372923_at	peroxisomal biogenesis factor 11b	Pex11b	310682	0.22	0.26	2.5E-02	1.7E-07	1.00	1.00	1.00	1.00
1378887_at	Transcribed locus			0.23	0.25	9.7E-02	5.4E-05	0.33	1.00	0.00	1.00
1374557_at	CG6210-like	LOC362065	362065	0.25	0.24	7.6E-02	2.3E-04	0.00	1.00	0.00	0.56
1373267_at	Sh3 domain YSC-like 1 (predicted)	Sh3yl1_predicted	362724	0.12	0.24	2.8E-02	1.3E-04	1.00	1.00	1.00	1.00
1398598_at	dystonia (predicted)	Dst_predicted	316313	0.24	0.23	7.2E-02	7.8E-05	1.00	1.00	1.00	1.00
1377479_at	Transcribed locus			0.22	0.19	2.8E-02	1.5E-04	1.00	1.00	1.00	1.00
1369836_at	interferon-induced protein with tetratricopeptide repeats 1	Ifit1	56824	0.15	0.21	3.5E-02	8.5E-04	0.00	1.00	0.10	1.00
1392972_at	triple functional domain (PTPRF interacting)	Trio	310192	0.11	0.21	4.4E-03	8.7E-06	1.00	1.00	0.80	1.00
1388276_at	histone cluster 1, H4a (predicted)	Hist1h4a_predicted	364716	0.19	0.17	3.3E-02	2.7E-05	1.00	1.00	0.70	1.00
1383977_a_at				0.19	0.17	9.8E-03	1.1E-03	0.00	1.00	0.00	1.00
1373810_at	phospholipase A2, group X11A (predicted)	Pla2g12a_predicted	362039	0.19	0.11	1.9E-02	1.9E-06	0.33	1.00	0.00	1.00
1376193_at	Kohjirin	Chrd1	363455	0.11	0.18	3.0E-02	5.5E-06	1.00	1.00	1.00	1.00
1381036_at	Transcribed locus			0.14	0.18	7.2E-03	5.2E-03	0.83	1.00	0.00	1.00
1377334_at	RT1 class II, locus Ba	RT1-Ba	309621	0.05	0.18	3.2E-02	1.6E-05	0.67	1.00	0.60	1.00
1383272_at	ankyrin repeat and SOCS box-containing protein 11 (predicted)	Ash11_predicted	302666	0.16	0.08	6.3E-02	8.3E-04	0.00	1.00	0.00	0.78
1391791_at	N-acylsphingosine amidohydrolase 3-like (predicted)	Asah3l_predicted	313339	0.06	0.16	2.3E-02	1.1E-07	0.00	1.00	0.10	1.00
1377642_at	caveolin 2	Cav2	363425	0.06	0.13	2.6E-02	2.1E-05	0.33	1.00	0.80	1.00
1392860_at				0.09	0.13	4.3E-02	2.7E-07	0.33	1.00	0.00	1.00
1368150_at	solute carrier family 27 (fatty acid transporter), member 2	Slc27a2	65192	0.11	0.13	3.3E-02	6.6E-06	0.83	1.00	0.80	1.00
1388955_at	EH-domain containing 2	Ehd2	361512	0.08	0.13	3.2E-02	2.7E-06	0.83	1.00	0.40	1.00
1373302_at	Transcribed locus, strongly similar to XP_580072.1 hypothetical protein XP_580072 [Rattus norvegicus]			0.07	0.12	3.4E-02	1.1E-07	0.33	1.00	0.40	1.00
1384380_at	Zinc finger, CCHC domain containing 7 (predicted)	Zcfc7_predicted	298086	0.10	0.08	3.3E-02	7.2E-06	0.33	1.00	0.00	1.00
1388176_at	camello-like 5	Cml5	114020	0.10	0.07	8.3E-02	1.8E-04	0.00	1.00	0.00	1.00
1384191_at	Cdc42 GTPase-activating protein (predicted)	Cdgap_predicted	288093	0.10	0.10	2.6E-02	2.7E-07	0.67	1.00	1.00	1.00
1372809_at	hypothetical gene supported by AF152002	LOC290595	290595	0.05	0.10	6.5E-02	4.6E-07	0.33	1.00	0.80	1.00
1369202_at	myxovirus (influenza virus) resistance 2	Mx2	286918	0.02	0.09	2.5E-02	5.2E-06	0.33	1.00	1.00	1.00
1387770_at	putative ISG12(a) protein	ig12(a)	360415	0.04	0.09	3.8E-03	3.4E-07	1.00	1.00	1.00	1.00
1396304_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.04	0.08	4.0E-02	2.7E-07	1.00	1.00	1.00	1.00
1387522_at	Rhesus blood group-associated A glycoprotein	Rhag	65207	0.02	0.08	7.9E-02	3.9E-04	0.00	1.00	0.00	1.00
1392954_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.08	0.06	3.1E-02	6.5E-05	0.00	1.00	0.00	1.00
1394620_at				0.08	0.06	7.9E-02	3.5E-05	0.00	1.00	0.00	0.78
1369110_x_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.05	0.06	9.0E-03	6.4E-08	1.00	1.00	1.00	1.00
1374915_at	GH regulated TBC protein 1	Grtp1	361180	0.04	0.06	1.8E-02	8.5E-08	0.00	1.00	0.00	1.00
1382437_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.03	0.05	6.3E-02	4.4E-05	0.00	1.00	0.00	0.78
1370429_at	RT1 class Ib, locus Aw2	RT1-Aw2	24737	0.02	0.04	4.4E-03	1.1E-07	0.33	1.00	0.50	1.00
1379435_at	deoxyguanosine kinase (predicted)	Dguok_predicted	297389	0.03	0.04	2.6E-02	4.0E-08	0.00	1.00	0.00	0.89
1398692_at	Transcribed locus			0.01	0.04	3.8E-02	1.8E-07	0.00	1.00	0.10	1.00
1398576_at				0.03	0.01	2.8E-02	6.5E-09	0.00	1.00	0.00	1.00
1392714_at	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11 (predicted)	Serpib11_predicted	304689	0.02	0.01	1.8E-02	6.6E-06	0.00	1.00	0.00	1.00
1397859_x_at	RT1 class I, A3	RT1-A3	309627	0.01	0.02	4.4E-03	6.5E-09	1.00	1.00	1.00	1.00
1393347_at	integrin alpha L	Igal	308995	0.01	0.01	3.8E-03	6.5E-09	0.83	1.00	0.80	1.00