

Decreased expression: 102

Increased expression: 677

Total: 779

Table S1
Transgenerational Male Whole Brain Regulated Genes

Apoptosis

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Aven_predi	97	63	0.65	AA899459	apoptosis, caspase activation inhibitor (predicted)
Pycard	43	81	1.88	BI282953	apoptosis-associated speck-like protein containing a C
Cflar	69	126	1.84	AI578435	CASP8 and FADD-like apoptosis regulator
Casp1	43	108	2.52	D85899	caspase 1
Higd1b_pre	48	116	2.44	AI576009	HIG1 domain family, member 1B (predicted)
Stk17b	171	276	1.62	AI012590	serine/threonine kinase 17b (apoptosis-inducing)

Cell Cycle

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Arrdc3	163	339	2.07	AA818910	Arrestin domain containing 3
Cdc14a_pre	42	78	1.86	AW915083	CDC14 cell division cycle 14 homolog A (S. cerevisiae)
Cdc73	168	285	1.70	BI290578	Cell division cycle 73, Paf1/RNA polymerase II complex
Ccnd1	70	191	2.75	BI295861	cyclin D1
Gadd45b_p	48	138	2.88	BI287978	growth arrest and DNA-damage-inducible 45 beta (pre
Pak4_predi	57	87	1.52	BE098920	P21 (CDKN1A)-activated kinase 4 (predicted)

Cytoskeleton-ECM

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Als2cr3	152	284	1.86	BG378620	amyotrophic lateral sclerosis 2 (juvenile) chromosome 1
Cdh1	15	121	7.96	NM_031334	cadherin 1
Cdh11	118	71	0.61	BF419584	Cadherin 11
Cdh5_predi	111	204	1.84	BE110616	Cadherin 5 (predicted)
Cldn5	412	690	1.68	BI281680	claudin 5
Col3a1	108	357	3.30	BI275716	collagen, type III, alpha 1
Col4a5_pre	102	196	1.92	AA891834	Collagen, type IV, alpha 5 (predicted)
Col5a2	134	231	1.73	AI179399	collagen, type V, alpha 2
Coro1c_pre	45	80	1.78	BE108221	coronin, actin binding protein 1C (predicted)
Clec14a	10	134	12.99	BI295930	C-type lectin domain family 14, member a
Dcn	95	180	1.90	BM390253	decorin
Dsp	43	127	2.99	AW144509	Desmoplakin (predicted)
Dncl2b_pre	126	251	1.98	AI144946	dynein, cytoplasmic, light chain 2B (predicted)
DLP2	49	80	1.65	AI409460	Dynein-like protein 2
Eml1	273	458	1.68	BI289642	Echinoderm microtubule associated protein like 1 (pred
RGD:13032	125	217	1.73	BF285026	endothelial cell adhesion molecule
Emp2	14	489	35.53	AA818807	epithelial membrane protein 2
Eva_predic	39	97	2.51	BI282616	epithelial V-like antigen (predicted)
Xlkd1_pred	27	254	9.32	AI179260	extra cellular link domain-containing 1 (predicted)
Ecm1	58	169	2.92	AI407838	extracellular matrix protein 1
Fgg	4	128	29.41	NM_012559	fibrinogen, gamma polypeptide
Fgl2	39	175	4.50	BG663284	fibrinogen-like 2
Fn1	147	303	2.07	AA893484	fibronectin 1
Flna_predic	129	334	2.59	BI283060	filamin, alpha (predicted)
Gsn	573	1281	2.24	BI285576	gelsolin
Icam1	12	419	35.37	NM_012967	intercellular adhesion molecule 1
Icam2	56	225	4.00	AI410467	intercellular adhesion molecule 2

F11r	93	288	3.10	NM_053796	junctional adhesion molecule 1
Krt1-18	44	152	3.43	BI286012	keratin complex 1, acidic, gene 18
Krt1-19	16	253	16.09	BI279605	keratin complex 1, acidic, gene 19
Krt2-7_prec	27	109	4.09	BI284344	keratin complex 2, basic, gene 7 (predicted)
Krt2-8	41	138	3.37	BF281337	keratin complex 2, basic, gene 8
Lamc2	32	95	2.99	BM385282	lamimin, gamma 2
Lamb2	126	202	1.60	NM_012974	laminin, beta 2
Lamb3	45	105	2.33	BE101834	Laminin, beta 3
Lgals3	63	454	7.15	NM_031832	lectin, galactose binding, soluble 3
Lgals3bp	82	151	1.83	AF065438	lectin, galactoside-binding, soluble, 3 binding protein
Lmcd1_pre	52	83	1.58	AI602501	LIM and cysteine-rich domains 1 (predicted)
LMO7	352	968	2.75	AI598833	LIM domain only protein 7
Lamp3_pre	8	568	70.52	BF283924	lysosomal-associated membrane protein 3 (predicted)
Mgp	383	1179	3.08	NM_012862	matrix Gla protein
Mxra8	71	110	1.55	AA946351	matrix-remodelling associated 8
Mfap5_prec	18	76	4.22	BI283094	microfibrillar associated protein 5 (predicted)
Mfap4_prec	22	479	21.84	AI177059	microfibrillar-associated protein 4 (predicted)
Msn	151	738	4.88	BF281185	moesin
Muc1	13	155	11.87	BI274326	mucin 1
Myh11	111	166	1.50	X16262	myosin heavy chain 11
Myh6	38	112	2.91	NM_017239	myosin heavy chain, polypeptide 6
Myo1c	41	82	2.02	NM_023092	myosin IC
Mrlcb	323	874	2.71	X05566	myosin regulatory light chain
Myo5c_pre	41	108	2.64	BM386808	Myosin VC (predicted)
Myh14_pre	201	346	1.72	AI578120	myosin, heavy polypeptide 14 (predicted)
Myh9	181	291	1.61	BM392410	myosin, heavy polypeptide 9
Myl7_predic	8	100	13.31	AA891242	myosin, light polypeptide 7, regulatory (predicted)
Myl9_predic	106	180	1.70	BI279044	myosin, light polypeptide 9, regulatory (predicted)
Mylk_predic	153	360	2.35	AI177055	Myosin, light polypeptide kinase (predicted)
Nid	99	155	1.57	AI235948	nidogen (entactin)
Ogn_predic	164	349	2.13	AA945955	osteoglycin (predicted)
Plunc	8	377	44.83	BF546645	palate, lung, and nasal epithelium expressed transcript
Pdlim1	50	139	2.78	NM_017365	PDZ and LIM domain protein 1 (Elfin) (LIM domain prot
Col4a1_pre	85	187	2.20	AI176393	procollagen, type IV, alpha 1 (predicted)
Col6a1_pre	59	100	1.68	AI598402	procollagen, type VI, alpha 1 (predicted)
Col6a3_pre	55	109	2.00	AI176126	procollagen, type VI, alpha 3 (predicted)
Col12a1	48	78	1.63	BE108345	procollagen, type XII, alpha 1
Pgsg	298	475	1.60	NM_020074	proteoglycan peptide core protein
Plp2	55	194	3.54	BM385031	proteolipid protein 2
LOC31595	25	546	22.22	BF290699	Similar to claudin-18A1.2
Lrp16	154	93	0.60	AW524615	Similar to fibronectin leucine rich transmembrane prote
RGD15631	104	582	5.58	AI237685	Similar to osteoclast inhibitory lectin
MGC10951	24	101	4.18	AA012755	similar to tropomyosin 1, embryonic fibroblast - rat
Stom_predi	33	102	3.14	BI295949	stomatin (predicted)
Svll_predic	94	170	1.81	AI045848	supervillin (predicted)
Sdc1	108	179	1.66	NM_013026	syndecan 1
Tln_predic	110	194	1.77	BI283756	talin (predicted)
Thbd	41	411	10.12	AA818521	thrombomodulin
Tagln	43	151	3.53	NM_031549	transgelin
Tmod3	127	232	1.83	BG378269	tropomodulin 3
Tpm1	287	437	1.52	M23764	tropomyosin 1, alpha
Tpm4	211	553	2.61	BI281955	Tropomyosin 4
Tnnt2	23	86	3.74	NM_012676	troponin T2

Vil2	220	395	1.80	AA851304	villin 2
Vill_predicte	96	145	1.51	BE099937	villin-like (predicted)
Vim	454	881	1.94	NM_031140	vimentin

Development

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Adfp	42	85	2.03	BG673602	Adipose differentiation related protein
ADRP	54	138	2.55	BI285616	adipose differentiation-related protein
Jub	33	87	2.64	BI284400	ajuba homolog (Xenopus laevis)
Amotl2	161	275	1.71	BF418582	Angiomotin like 2
Amotl1_pre	152	239	1.57	BI277433	Angiomotin-like 1 (predicted)
Angpt1	43	88	2.03	AI639162	angiopoietin 1
Ace	24	167	7.00	AA926148	angiotensin 1 converting enzyme 1
Apeg1	152	101	0.67	AI072733	Aortic preferentially expressed gene 1
Bk	75	35	0.47	U30831	Brain and kidney protein
Crygs_pred	123	45	0.37	AI408238	crystallin, gamma S (predicted)
Dpt_predict	36	252	6.95	BI285485	dermatopontin (predicted)
Evi1_predic	64	168	2.61	BE107033	ecotropic viral integration site 1 (predicted)
Elav1_prec	123	188	1.53	BF559812	ELAV (embryonic lethal, abnormal vision, Drosophila)-li
Emcn	64	159	2.49	AI172271	endomucin
Emp1	32	77	2.42	BI275741	epithelial membrane protein 1
Fbn1	62	96	1.54	BM389019	fibrillin-1
Fhl1	78	119	1.52	BI298356	four and a half LIM domains 1
Glpr1_prec	39	105	2.65	BF287967	GLI pathogenesis-related 1 (glioma) (predicted)
Gmfg	78	192	2.46	BG666787	glia maturation factor, gamma
Gpnmb	76	382	5.02	NM_133298	glycoprotein (transmembrane) nmb
Gp38	147	701	4.76	NM_019358	glycoprotein 38
Gpc3	45	118	2.62	NM_012774	Glypican 3
Heca_predi	70	125	1.79	BM390524	Headcase homolog (Drosophila) (predicted)
IAG2	117	223	1.90	AI575519	implantation-associated protein
lrx1_predici	55	184	3.35	BF543574	Iroquois related homeobox 1 (Drosophila) (predicted) //
lrx3_predici	55	128	2.32	AI030203	Iroquois related homeobox 3 (Drosophila) (predicted)
Kirrel3_pre	193	106	0.55	BF402633	Kin of IRRE like 3 (Drosophila) (predicted)
Mvp	75	132	1.75	NM_022715	major vault protein
Mog	71	122	1.72	BF410306	myelin oligodendrocyte glycoprotein
Mcl1	182	302	1.66	AI172056	myeloid cell leukemia sequence 1
Myadm	137	222	1.62	BI296048	myeloid-associated differentiation marker
Nedd9	115	267	2.32	BM392374	neural precursor cell expressed, developmentally down
Nedd9_pre	27	91	3.39	BF555968	neural precursor cell expressed, developmentally down
Net1	125	229	1.83	AI180187	Neuroepithelial cell transforming gene 1
Nrp1	149	359	2.41	AF016296	neuropilin 1
Npc2	898	1716	1.91	BI287960	Niemann Pick type C2
Odz2 /// LO	168	111	0.66	NM_020088	odd Oz/ten-m homolog 2 (Drosophila) /// hypothetical g
Pard6b_pre	50	115	2.32	BF525012	par-6 (partitioning defective 6) homolog beta (C. elegar
Prx	13	96	7.49	NM_023976	periaxin
Postn_pred	19	260	13.57	BM389026	periostin, osteoblast specific factor (predicted)
Pmp22	452	839	1.86	AA943163	peripheral myelin protein 22
Plac8_pred	52	217	4.17	BG378630	placenta-specific 8 (predicted)
Plac9_pred	61	152	2.48	BI276313	placenta-specific 9 (predicted)
Pivap	87	523	5.99	NM_020086	plasmalemma vesicle associated protein
Prg-2	136	88	0.65	AI711557	plasticity-related protein PRG-2
Retnla	41	198	4.80	NM_053333	resistin like alpha

S100a10	252	445	1.77	NM_031114	S-100 related protein, clone 42C
Spa17	67	113	1.68	NM_053482	sperm autoantigenic protein 17
Sox17_prec	79	138	1.75	AI031004	SRY-box containing gene 17 (predicted)
Sox18	56	100	1.78	AW528157	SRY-box containing gene 18
Sox4_predi	140	234	1.68	AA956294	SRY-box containing gene 4 (predicted)
Sftpc	18	5858	321.89	AI009659	surfactant associated protein C
Sftpa1	7	745	111.13	NM_017329	surfactant, pulmonary-associated protein A1
Sftpb	5	1190	255.87	X14778	surfactant, pulmonary-associated protein B
Syn3	535	854	1.60	AI599265	Synapsin III
Syng2	75	114	1.52	BF285314	synaptogyrin 2
Vamp8	106	316	2.98	NM_031827	vesicle-associated membrane protein 8 (endobrevin)

Electron Transport

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Cybrd1_pre	33	95	2.91	BF419070	cytochrome b reductase 1 (predicted)
Cybasc3	43	77	1.80	AI179227	Cytochrome b, ascorbate dependent 3
Cyb5r3	217	354	1.63	J03867	Cytochrome b5 reductase 3
Cyp2b2	14	635	45.67	AI454613	Cytochrome P450, family 2, subfamily b, polypeptide 2
Cyp2f2	23	93	4.12	NM_019303	cytochrome P450, family 2, subfamily f, polypeptide 2
Cyp4b1	18	526	29.37	M29853	cytochrome P450, subfamily 4B, polypeptide 1
Glrx2	152	247	1.62	BG671304	Glutaredoxin 2 (thioltransferase) (predicted)
Gpx1	787	1182	1.50	S41066	glutathione peroxidase 1
Gpx2	10	202	20.33	AA800587	glutathione peroxidase 2
Gpx3	118	569	4.80	NM_022525	glutathione peroxidase 3
Prdx6	42	130	3.06	BF398290	Peroxiredoxin 6

Growth Factors, Cyto-, Chemokines

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Bmp4	40	106	2.62	NM_012827	bone morphogenetic protein 4
Ccl5	46	153	3.36	NM_031116	chemokine (C-C motif) ligand 5
Ccl6	2	467	217.16	BE095824	chemokine (C-C motif) ligand 6
Cxcl4	88	313	3.56	AI169104	Chemokine (C-X-C motif) ligand 4
Cxcr4	46	94	2.05	AA945737	Chemokine receptor (LCR1)
Cklfsf6	77	170	2.22	AI406687	Chemokine-like factor super family 6 (predicted)
F3	144	222	1.54	NM_013057	coagulation factor 3
Ctgf	177	453	2.56	NM_022266	connective tissue growth factor
Egfl7	73	177	2.42	AF223678	EGF-like domain 7
Eps8l2_pre	112	199	1.77	BI285918	EPS8-like 2 (predicted)
Fgf1	86	132	1.53	BI289840	fibroblast growth factor 1
Igf1	94	180	1.92	M15481	insulin-like growth factor 1
Il18	64	147	2.29	AJ222813	interleukin 18
Ogn_predic	55	100	1.82	AA945955	osteoglycin (predicted)
Pdgfa	41	83	2.05	AA866419	platelet derived growth factor, alpha
Scgb3a1	3	468	180.13	AI011836	secretoglobin, family 3A, member 1
Cxcl16	53	134	2.54	BI296385	similar to chemokine (C-X-C motif) ligand 16
Vegf	324	563	1.74	AI175732	vascular endothelial growth factor
Wfdc1	85	130	1.53	BI279661	wap four-disulfide core domain 1

Golgi Apparatus

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		

Gla	123	77	0.62	BM385090	galactosidase, alpha
Gcnt2 /// LC	93	143	1.54	AI234819	glucosaminyl (N-acetyl) transferase 2, l-branching enzy
Hs2st1_pre	105	68	0.65	AW530083	heparan sulfate 2-O-sulfotransferase 1 (predicted)
Man2a1	84	184	2.19	AI178793	Mannosidase 2, alpha 1
Pomt2	55	91	1.65	AI180194	Protein-O-mannosyltransferase 2
RGD15636	100	231	2.30	BF410842	Similar to chondroitin sulfate GalNAcT-2 (predicted)
LOC69048!	43	118	2.77	AA944162	Similar to cis-Golgi matrix protein GM130
RGD15662	571	33	0.06	AT005664	similar to Coatomer gamma-2 subunit (Gamma-2 coat
St3gal4	51	97	1.91	BI295550	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
B4galt1_ma	52	85	1.63	BF282414	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, p

Immune Response

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio	Genbank	Gene Title
B2m	2504	3766	1.50	NM_012512	beta-2 microglobulin
Cd36	31	301	9.70	NM_031561	Cd36 antigen
Cd36 /// LO	11	89	8.34	AF072411	cd36 antigen /// similar to fatty acid translocase/CD36
Cd44	49	137	2.80	BI302830	CD44 antigen
Cd48	129	272	2.11	X13016	CD48 antigen
Cd53	103	195	1.90	NM_012523	CD53 antigen
Cd68_predi	17	92	5.45	AI177761	CD68 antigen (predicted)
Cd74	158	939	5.96	NM_013069	CD74 antigen (invariant polypeptide of major histocon
Cd9	410	677	1.65	AI227627	CD9 antigen
Cd97_predi	38	182	4.83	BI296525	CD97 antigen (predicted)
Cd99	103	201	1.96	AI235284	CD99 antigen
HA11_RAT	192	569	2.97	M24024	Class I histocompatibility antigen, Non-RT1.A alpha-1 c
---	18	936	52.27	U07886	Polymeric immunoglobulin receptor AATTA-containing
F2r	185	363	1.97	NM_012950	coagulation factor II receptor
C1s	62	121	1.95	D88250	complement component 1, s subcomponent
C2	51	109	2.11	AI716125	Complement component 2
C3	175	316	1.81	NM_016994	complement component 3
C4a /// C4-	85	334	3.92	BI285347	complement component 4a /// complement component
C7	82	355	4.33	BF284922	Complement component 7
Crry	175	325	1.86	D42115	complement receptor related protein
Fcgr3	143	360	2.51	NM_053843	Fc gamma receptor II beta
Fcgr3 /// LC	137	380	2.78	NM_053843	Fc receptor, IgG, low affinity III /// Fc gamma receptor II
IgG-2a /// L	23	300	12.99	L22654	gamma-2a immunoglobulin heavy chain /// similar to ga
LOC28716!	401	839	2.09	AI237401	globin, alpha
Gbp2	41	96	2.34	NM_133624	guanylate binding protein 2, interferon-inducible
LOC68032!	7	441	65.36	BG374683	Ig active lambda2-like chain mRNA, 3' end
Igha	42	749	17.82	AI412189	immunoglobulin heavy chain (alpha polypeptide)
Igh-1a_pre	5	568	107.15	AI411947	immunoglobulin heavy chain 1a (serum IgG2a) (predict
Igj_predicte	22	285	13.16	AA817898	immunoglobulin joining chain (predicted)
Ifnar1_pred	57	86	1.51	AA799711	interferon (alpha and beta) receptor 1 (predicted)
Ifi30_predic	122	194	1.60	BM389261	interferon gamma inducible protein 30 (predicted)
Ifitm1_pred	68	202	2.99	BG380285	interferon induced transmembrane protein 1 (predicted
Ifitm2	104	233	2.24	NM_030833	interferon induced transmembrane protein 2 (1-8D)
Irf2_predict	50	77	1.53	BI302791	interferon regulatory factor 2 (predicted)
Ifit2	44	86	1.96	BE118697	interferon-induced protein with tetratricopeptide repeats
Ly6b	10	333	34.47	M30689	Ly6-B antigen gene
Ly6c	50	214	4.24	NM_020103	Ly6-C antigen
C1qr1	49	163	3.31	BI282932	Lymphocyte antigen 68
RT1-CE12	130	262	2.02	M24026	RT1 class I, CE12

RT1-Aw2	170	370	2.17	AI012221	RT1 class Ib, locus Aw2
RT1-Aw2 ///	96	329	3.45	BI282965	RT1 class Ib, locus Aw2 /// RT1 class I, CE12 /// RT1 cl
RT1-Aw2 ///	215	463	2.15	AJ249701	RT1 class Ib, locus Aw2 /// RT1 class Ia, locus A2 /// RT
RT1-S3	56	153	2.76	AJ243974	RT1 class Ib, locus S3
RT1-Ba	20	181	9.04	BG378249	RT1 class II, locus Ba
RT1-Da	93	583	6.25	Y00480	RT1 class II, locus Da
RT1-Db1	19	137	7.21	BI279526	RT1 class II, locus Db1
LOC498989	61	98	1.62	BG664827	similar to Ab2-143
LOC680404	321	208	0.65	BG374818	Similar to Complement C1q-like protein 3 precursor (GI
LOC500180	6	2341	368.59	L22655	similar to IG KAPPA CHAIN V-V REGION K2 PRECUR
LOC299357	33	115	3.50	AI411693	similar to Igh-6 protein /// similar to Ig H-chain V-region
LOC498022	26	105	4.12	BF387360	similar to immunoglobulin superfamily, member 7
LOC686326	43	98	2.27	BI294409	similar to Interferon-alpha/beta receptor beta chain pre
LOC314509	28	87	3.11	AA996557	similar to single chain Fv antibody fragment scFv 7-10A
RGD15634	207	395	1.91	BM391860	Similar to T-cell activation leucine repeat-rich protein (p
Tiam1_prec	75	42	0.56	BM389265	T-cell lymphoma invasion and metastasis 1 (predicted)
Thbd	13	103	7.77	BG666306	thrombomodulin

Metabolism & Transport

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Synt	Raw	Raw	Ratio		
Acs15	175	282	1.61	NM_053607	acyl-CoA synthetase long-chain family member 5
Aytl2_predi	186	429	2.31	BG380281	Acyltransferase like 2 (predicted)
Arf4l_predic	30	89	2.95	AI030650	ADP-ribosylation factor 4-like (predicted)
Aldh2	195	327	1.68	NM_032416	aldehyde dehydrogenase 2
Aldh1a1	286	631	2.21	NM_022407	aldehyde dehydrogenase family 1, member A1
Aldh9a1	200	329	1.65	BI294750	Aldehyde dehydrogenase family 9, subfamily A1
Akr1c11_pre	45	262	5.83	AW522526	aldo-keto reductase family 1, member C-like 1 (predicte
Accn1	78	45	0.58	Y14635	amiloride-sensitive cation channel 1
Aoc3	11	187	17.11	AI070137	amine oxidase, copper containing 3
Alas2	159	244	1.53	NM_013197	aminolevulinic acid synthase 2
Ace	75	259	3.45	AF201331	angiotensin 1 converting enzyme 1
Aqp1	30	171	5.78	AA891661	aquaporin 1
Aqp5	35	232	6.67	NM_012779	aquaporin 5
Atp6v1c2	13	185	14.15	BF283053	ATPase, H+ transporting, V1 subunit C, isoform 2
Ca3	46	114	2.49	AB030829	carbonic anhydrase 3
Ces3	17	543	32.31	L46791	carboxylesterase 3
Comt	113	251	2.23	NM_012531	catechol-O-methyltransferase
Chia	1	210	167.76	AI639227	chitinase, acidic
Clic2_predi	28	95	3.33	BI293548	chloride intracellular channel 2 (predicted)
Clic3_predi	4	169	42.18	AI234249	chloride intracellular channel 3 (predicted)
Colec12	114	182	1.60	BI284441	collectin sub-family member 12
Cngb1	77	24	0.31	AJ224680	cyclic nucleotide-gated channel beta subunit 1
RGD:13029	551	898	1.63	NM_022501	cysteine-rich protein 2
Cyp27a1	40	111	2.75	M73231	cytochrome P450, family 27, subfamily a, polypeptide 1
Dguok_pre	82	52	0.64	BF285179	deoxyguanosine kinase (predicted)
Dpysl4	308	204	0.66	BF413467	dihydropyrimidinase-like 4
Acbd3	88	57	0.65	BF419134	DMT1-associated protein
Cybb	13	75	5.64	AI176057	endothelial type gp91-phox gene
Ephx1	105	167	1.58	NM_012844	epoxide hydrolase 1
Ftl1	1000	1596	1.60	L01122	ferritin light chain 1
Fmo1	59	296	5.05	NM_012792	flavin containing monooxygenase 1
Fmo2	13	117	8.73	BM389350	flavin containing monooxygenase 2

Galm	91	165	1.81	AA997048	galactose mutarotase (aldose 1-epimerase)
Gja4	25	81	3.25	NM_021654	gap junction membrane channel protein alpha 4
Gja5	38	87	2.29	NM_019280	gap junction membrane channel protein alpha 5
Gpt2_predi	110	57	0.52	AA955605	Glutamic pyruvate transaminase (alanine aminotransferase)
Gstm2	33	100	3.06	AI169331	glutathione S-transferase, mu 2
Gpd1	79	193	2.46	BF399697	Glycerol-3-phosphate dehydrogenase 1 (soluble)
Gpd2	137	60	0.44	U08027	glycerol-3-phosphate dehydrogenase 2
Gypc_predi	57	107	1.89	AA944212	glycophorin C (Gerbich blood group) (predicted) /// similar
Ggta1	60	118	1.95	AI178222	Glycoprotein galactosyltransferase alpha 1, 3
Gimap5	19	86	4.46	BI294743	GTPase, IMAP family member 5
Gmps_prec	66	110	1.67	BI283031	guanine monophosphate synthetase (predicted)
Hk1	104	58	0.55	_Rat_Hexokinase	hexokinase 1
Hsd11b1	360	540	1.50	NM_017080	hydroxysteroid 11-beta dehydrogenase 1
Ltbp1	33	89	2.71	NM_021587	LanC (bacterial lantibiotic synthetase component C)-like
Lta4h	283	472	1.67	AW918009	Leukotriene A4 hydrolase
Lpl	167	266	1.59	NM_012598	lipoprotein lipase
Lcp1_predi	151	333	2.20	BE109711	lymphocyte cytosolic protein 1 (predicted)
Lyz	521	5571	10.70	L12458	lysozyme
Loxl1_predi	43	101	2.34	AI599031	lysyl oxidase-like 1 (predicted)
Mettl7a	270	500	1.85	AA946026	Methyltransferase like 7A
Mgst1	252	723	2.87	NM_134349	microsomal glutathione S-transferase 1
Mgst2_prec	38	130	3.45	BI290559	microsomal glutathione S-transferase 2 (predicted)
Mgl1	208	130	0.62	AY081195	monoglyceride lipase
Gnptg	100	56	0.56	AW522848	N-acetylglucosamine-1-phosphotransferase, gamma subunit
Asah1_pred	62	235	3.80	AI412627	N-acylsphingosine amidohydrolase (acid ceramidase)-like
Asah3l_pre	65	149	2.27	AI137826	N-acylsphingosine amidohydrolase 3-like (predicted)
Pon3	33	355	10.65	BM385409	paraoxonase 3
Pnpla2_pre	84	132	1.57	BI278288	Patatin-like phospholipase domain containing 2 (predicted)
Pi4k2b	44	121	2.77	BM383435	Phosphatidylinositol 4-kinase type-II beta
Pspla1	32	87	2.73	D88666	phosphatidylserine-specific phospholipase A1
Pik3ap1_pr	34	84	2.48	AW916092	phosphoinositide-3-kinase adaptor protein 1 (predicted)
Pla2g1b	23	160	6.97	AI234860	phospholipase A2, group IB
Pla2g2a	7	87	12.06	NM_031598	phospholipase A2, group IIA (platelets, synovial fluid)
Pla2g2d	7	108	16.68	AI044869	phospholipase A2, group IID
Plscr1	10	78	7.47	NM_057194	phospholipid scramblase 1
Ppcdc_prec	81	39	0.48	AI411422	Phosphopantothienoylcysteine decarboxylase (predicted)
Kcnk15	105	68	0.65	BF405604	potassium channel, subfamily K, member 15
Kcnj16	241	152	0.63	AI411366	potassium inwardly-rectifying channel, subfamily J, member 16
Kcnma1	113	74	0.65	BF386160	potassium large conductance calcium-activated channel
Selenbp1	54	175	3.26	NM_080892	selenium binding protein 2
Shmt1_pre	60	106	1.77	AI010087	serine hydroxymethyl transferase 1 (soluble) (predicted)
LOC500358	96	179	1.86	BM391516	similar to Deoxyribose-phosphate aldolase-like
LOC368066	45	182	4.03	AI232716	similar to thioether S-methyltransferase
LOC361871	89	55	0.62	AW433978	similar to Vacuolar ATP synthase subunit S1 precursor
Scnn1a	13	84	6.50	NM_031548	sodium channel, nonvoltage-gated, type I, alpha polypeptide
Scn7a	48	289	6.09	BF285019	sodium channel, voltage-gated, type 6, alpha polypeptide
Slc13a5	105	66	0.63	BG381311	solute carrier family 13 (sodium-dependent citrate transporter)
Slc25a24_pr	49	106	2.18	BM385894	Solute carrier family 25 (mitochondrial carrier, phosphate carrier)
Slc29a1	56	183	3.25	NM_031684	solute carrier family 29, member 1
Slc34a2	3	1161	368.63	NM_053380	solute carrier family 34 (sodium phosphate), member 2
Slc39a4_pr	33	104	3.19	AI556941	solute carrier family 39 (zinc transporter), member 4 (platelet)
Slc4a8	52	82	1.57	BM385244	solute carrier family 4 (anion exchanger), member 8
Slc44a2_pr	229	344	1.50	AI408306	Solute carrier family 44, member 2 (predicted)

Slc9a3r2	89	155	1.75	BI277485	solute carrier family 9 (sodium/hydrogen exchanger), is
Slco2a1	7	240	35.00	AI407489	Solute carrier organic anion transporter family, member
Scd2	127	62	0.49	BI850137	stearoyl-Coenzyme A desaturase 2
Sqrdl	113	178	1.57	AI013361	sulfide quinone reductase-like (yeast)
Sult1a1	159	362	2.27	AF394783	sulfotransferase family 1A, phenol-preferring, member
Syt4	403	236	0.59	L38247	synaptotagmin 4
Tpmt	101	165	1.63	AI638971	thiopurine methyltransferase
Tgm2	112	321	2.87	NM_019386	tissue-type transglutaminase
Tmc4_pred	70	149	2.14	AI556940	transmembrane channel-like gene family 4 (predicted)
Unc93b_pr	74	131	1.77	AI234533	unc-93 homolog B (C. elegans) (predicted)
Vat1_predic	77	117	1.52	BI284849	vesicle amine transport protein 1 homolog (T californica)
Xdh	70	199	2.86	NM_017154	xanthine dehydrogenase

Proteolysis

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Adam17	147	240	1.64	NM_020306	a disintegrin and metalloproteinase domain 17
Anpep	31	186	6.05	NM_031012	alanyl (membrane) aminopeptidase
Ctsc	56	162	2.87	AI409046	cathepsin C
Ctsh	341	662	1.94	NM_012939	cathepsin H
Dpp4	20	106	5.36	J02997	dipeptidylpeptidase 4
Laptm5	69	165	2.38	BF406601	lysosomal-associated protein transmembrane 5
Napsa	3	221	67.09	NM_031670	napsin A aspartic peptidase
Osgepl1_pr	94	61	0.65	BF393066	O-sialoglycoprotein endopeptidase-like 1 (predicted)
Psme1	287	460	1.60	NM_017264	protease (prosome, macropain) 28 subunit, alpha
Prss23	125	432	3.45	AI177099	protease, serine, 23
Psmb8	57	112	1.98	NM_080767	proteasome (prosome, macropain) subunit, beta type 8
Serping1	92	224	2.43	AW915763	serine (or cysteine) peptidase inhibitor, clade G, memb
Serpinb10	4	96	26.99	BF399855	serine (or cysteine) proteinase inhibitor, clade B (ovalbu
Serpinb6	96	223	2.33	AA997359	serine (or cysteine) proteinase inhibitor, clade B (ovalbu
Serpinb1a_	80	210	2.62	BF411331	serine (or cysteine) proteinase inhibitor, clade B, memb
Serpinh1	118	201	1.71	BI285495	serine (or cysteine) proteinase inhibitor, clade H, memb
Spint2	175	370	2.11	AI412117	serine protease inhibitor, Kunitz type 2
Siah1a	52	79	1.51	NM_080905	seven in absentia 1A
LOC49869(27	87	3.21	AI230591	similar to ctla-2-beta protein (141 AA)
Senp5_pre	137	210	1.53	BE105606	SUMO/sentrin specific protease 5 (predicted) /// similar
Timp1	39	77	1.95	NM_053819	tissue inhibitor of metalloproteinase 1
Timp2	456	704	1.54	NM_021989	tissue inhibitor of metalloproteinase 2
Timp3	221	386	1.75	AA893169	tissue inhibitor of metalloproteinase 3 (Sorsby fundus d
Ube3a_pre	61	96	1.56	BG376442	ubiquitin protein ligase E3A (predicted)
Ube1dc1_p	103	190	1.85	AI408025	ubiquitin-activating enzyme E1-domain containing 1 (pr

Receptor & Binding Proteins

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Admr	15	86	5.69	BF551274	adrenomedullin receptor
Ager	32	882	27.90	NM_053336	advanced glycosylation end product-specific receptor
Apbb1ip_pr	79	126	1.60	BM386169	amyloid beta (A4) precursor protein-binding, family B, n
Abca3	189	303	1.61	BE096678	ATP-binding cassette, sub-family A (ABC1), member 3
Abcc10_pre	126	81	0.64	AI577346	ATP-binding cassette, sub-family C (CFTR/MRP), mem
Bzrp	90	196	2.19	AI008680	benzodiazepin receptor
Bmpr2	189	304	1.61	BF398206	Bone morphogenic protein receptor, type II (serine/thre
Calcrl	108	703	6.53	AA945708	calcitonin receptor-like

Dlgap1	196	84	0.43	BF413506	Discs, large (Drosophila) homolog-associated protein 1
Dlgap1	464	275	0.59	BE116953	Disks large-associated protein 1 (DAP-1) (Guanylate ki
Eng	59	153	2.60	BF288089	Endoglin
Edg5	25	79	3.17	NM_017192	endothelial differentiation, sphingolipid G-protein-coupl
Ednra	23	104	4.45	BF414702	Endothelin receptor type A
Epha8	113	73	0.64	C06786	Eph receptor A8
Esrrg	194	98	0.51	AA996810	Estrogen-related receptor gamma
Fubp3	108	71	0.66	BF282112	Far upstream element (FUSE) binding protein 3 (predic
Grik2	148	70	0.48	AW527501	Glutamate receptor, ionotropic, kainate 2
Igfbp7_prec	795	1454	1.83	AI233246	insulin-like growth factor binding protein 7 (predicted)
Il13ra1	60	106	1.76	BF282650	interleukin 13 receptor, alpha 1
Il17r_predic	75	122	1.63	BI279744	interleukin 17 receptor (predicted)
Kdr	97	345	3.54	U93307	kinase insert domain protein receptor
Ltbp4_pred	97	186	1.91	BG375362	latent transforming growth factor beta binding protein 4
Ltbr_predic	56	95	1.69	AI705656	lymphotoxin B receptor (predicted)
Mrc1_predi	30	161	5.44	BI294018	mannose receptor, C type 1 (predicted)
Mrvldc1_pr	52	179	3.42	AI176583	MARVEL (membrane-associating) domain containing 1
Nucb2	125	214	1.71	NM_021663	NEFA precursor
Nrp2	59	105	1.77	BM386520	neuropilin 2
Osbp1a	104	60	0.58	BM384713	Oxysterol binding protein-like 1A
Osbp15_pre	94	153	1.62	BG372522	oxysterol binding protein-like 5 (predicted)
Pvrl3_predi	48	95	1.96	AW525315	poliovirus receptor-related 3 (predicted)
Ptbp1	124	199	1.60	X60790	polypyrimidine tract binding protein 1
Rbp1	76	124	1.62	NM_012733	retinol binding protein 1
S100a11	101	1257	12.49	BG378926	S100 calcium binding protein A11 (calizzarin)
S100a6	74	1215	16.37	AF140232	S100 calcium binding protein A6 (calcyclin)
S100g	8	315	39.41	NM_012521	S100 calcium binding protein G
S100a4	85	454	5.31	NM_012618	S100 calcium-binding protein A4
S100a8	32	111	3.48	NM_053822	S100 calcium-binding protein A8 (calgranulin A)
S100a9	81	276	3.42	NM_053587	S100 calcium-binding protein A9 (calgranulin B)
Sec14I3	39	171	4.41	AA925062	SEC14-like 3 (S. cerevisiae)
Sec14I3	14	565	39.92	AJ132352	SEC14-like protein 3 (45 kDa secretory protein) (rsec4)
LOC305633	27	79	2.94	AI013888	similar to Antxr2 [anthrax toxin receptor] protein
LOC287847	832	554	0.67	BG380409	similar to ataxin 2-binding protein 1 isoform 2
LOC498433	56	114	2.02	BM385804	similar to ATP-binding cassette, subfamily G, member 3
LOC690976	108	181	1.67	AI230762	Similar to Calponin-2 (Calponin H2, smooth muscle) (N
RGD15651	88	1111	12.70	AA817993	Similar to dendritic cell-derived immunoglobulin(Ig)-like
LOC296462	162	56	0.34	BI292232	similar to GTP binding protein 5
LOC316130	59	99	1.69	BI281957	similar to mannose-6-phosphate receptor binding prote
Sftpd	21	625	30.13	NM_012878	surfactant associated protein D
Sftpa1	18	1949	110.76	BI295853	surfactant, pulmonary-associated protein A1
Tax1bp3	85	179	2.12	BI274159	Tax1 (human T-cell leukemia virus type I) binding prote
Thra	115	71	0.62	M18028	thyroid hormone receptor alpha
Trip10	53	80	1.50	NM_053920	thyroid hormone receptor interactor 10
Tgfbr2	257	580	2.26	AI408571	transforming growth factor, beta receptor II
Tyrobp	72	143	1.97	AI102519	Tyro protein tyrosine kinase binding protein
Vipr1	64	479	7.54	BI301509	vasoactive intestinal peptide receptor 1
LOC679357	179	277	1.55	AI103026	similar to interferon regulatory factor 2 binding protein 2

Signaling

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
Akap13	110	217	1.97	AI599048	A kinase (PRKA) anchor protein 13

Akap2	44	81	1.86	BF398063	A kinase (PRKA) anchor protein 2
Akap5	66	143	2.15	NM_133515	A kinase (PRKA) anchor protein 5
Acvr1	30	170	5.64	NM_022441	activin A receptor type II-like 1
Acvr1c	134	63	0.47	U35025	activin receptor-like kinase 7
Arc	200	313	1.57	NM_019361	activity regulated cytoskeletal-associated protein
Enpep	27	108	4.04	AF214568	aminopeptidase A
Anxa1	78	778	9.91	NM_012904	annexin 1
Anxa5	329	633	1.92	NM_013132	annexin 5
Anxa2	197	557	2.83	NM_019905	Annexin A2
Anxa8_prec	34	355	10.33	BM389254	annexin A8 (predicted)
Alox5ap	24	85	3.46	NM_017260	arachidonate 5-lipoxygenase activating protein
Btg2	101	242	2.40	NM_017259	B-cell translocation gene 2, anti-proliferative
Bf	58	283	4.92	AI639117	B-factor, properdin
Bgn	103	216	2.10	NM_017087	biglycan
Bst2	73	329	4.54	BM385476	bone marrow stromal cell antigen 2
Camk2d	88	53	0.60	NM_012519	calcium/calmodulin-dependent protein kinase II, delta
Crem	135	202	1.50	AW529408	CAMP responsive element modulator
Csnk1g3	76	45	0.59	NM_022855	casein kinase 1 gamma 3 isoform
Cav	158	947	6.01	BI285449	Caveolin
Cav2	167	631	3.77	BE349669	caveolin 2
Cdc42ep3_	138	231	1.67	AA874943	CDC42 effector protein (Rho GTPase binding) 3 (predic
Defb3	3	1034	382.91	AF068861	defensin beta 3
Dab2	137	239	1.75	AI407821	disabled homolog 2, mitogen-responsive phosphoprote
Dusp1	367	770	2.10	U02553	dual specificity phosphatase 1
Dusp6	322	554	1.72	NM_053883	dual specificity phosphatase 6
Dyrk2_pred	101	171	1.69	AI501693	Dual-specificity tyrosine-(Y)-phosphorylation regulated
Eld1	92	140	1.52	NM_022294	EGF, latrophilin seven transmembrane domain containi
Ehd2	72	291	4.04	BE110691	EH-domain containing 2
Ehd4	73	155	2.11	BI284307	EH-domain containing 4
Epas1	1085	2151	1.98	AI598434	endothelial PAS domain protein 1
Tek	108	349	3.24	AI710931	Endothelial-specific receptor tyrosine kinase
Efna1	33	92	2.83	AW531877	ephrin A1
Efnb2_pred	209	350	1.67	BF389666	ephrin B2 (predicted)
Egfl6	23	116	5.09	BF418373	epidermal growth factor-like protein 6
Fos	197	506	2.57	BF415939	FBJ murine osteosarcoma viral oncogene homolog
Flt1	130	204	1.56	AI059968	FMS-like tyrosine kinase 1
Fxyd3	63	133	2.12	AI009597	FXYD domain-containing ion transport regulator 3
Fgd5_predi	49	91	1.87	AI555744	FYVE, RhoGEF and PH domain containing 5 (predicte
Gpr116	134	424	3.16	BI295477	G protein-coupled receptor 116
Gprc5a	40	354	8.81	BI276110	G protein-coupled receptor, family C, group 5, member
Gm2a	168	259	1.54	AI717483	GM2 ganglioside activator protein
Gng11	102	188	1.84	NM_022396	guanine nucleotide binding protein gamma subunit 11
Hspb1	118	535	4.54	NM_031970	heat shock 27kDa protein 1
Hspa1a	67	327	4.90	BI278231	heat shock 70kD protein 1A
Hspa1a /// l	45	389	8.70	NM_031971	heat shock 70kD protein 1A /// heat shock 70kD protein
Homer1	45	213	4.72	AF030088	homer, neuronal immediate early gene, 1
Itga1	57	150	2.64	NM_030994	integrin alpha 1
Itgal	43	110	2.58	BI289767	Integrin alpha L
Itgb1	230	591	2.58	AI177366	integrin beta 1
Itgb2	67	160	2.40	AI177292	integrin beta 2
Itga6	297	196	0.66	BE110753	integrin, alpha 6
Itgb6	18	106	5.94	AI070686	integrin, beta 6
Igtp	69	123	1.80	AI407953	interferon gamma induced GTPase

Ifitm3	146	509	3.47	BI285494	interferon induced transmembrane protein 3
lrf7_predict	67	128	1.91	BF411036	interferon regulatory factor 7 (predicted)
lqgap1_pre	138	369	2.67	BM387072	IQ motif containing GTPase activating protein 1 (predic
Lcn2	3	234	73.20	NM_130741	lipocalin 2
Lu	71	243	3.44	NM_031752	Lutheran blood group (Auberger b antigen included)
Met	14	99	6.99	BG378920	met proto-oncogene
Map2k3_pr	78	117	1.52	BI283843	mitogen activated protein kinase kinase 3 (predicted)
Parva	94	155	1.65	AA686007	parvin, alpha
Phactr2	89	148	1.67	AW527533	Phosphatase and actin regulator 2
Pcyt1b	102	58	0.57	AI175443	Phosphorylase kinase alpha 1
Plekhf2_pre	108	194	1.79	AI103367	pleckstrin homology domain containing, family F (with F
RGD:72785	3	83	31.87	AW530225	prepro-Neuropeptide W polypeptide
Pacsin1	289	179	0.62	NM_017294	protein kinase C and casein kinase substrate in neuron
Prkch	78	118	1.50	AA799981	protein kinase C-eta
Ptprc	45	105	2.36	BF288130	Protein tyrosine phosphatase, receptor type, C
Ptpnf	228	409	1.80	M60103	protein tyrosine phosphatase, receptor type, F
isg12(b)	30	144	4.83	AA819034	putative ISG12(b) protein
Rab2l	98	218	2.21	BI295991	RAB2, member RAS oncogene family-like
Rab27a	54	107	1.97	BM389524	RAB27A, member RAS oncogene family
Rab3d	51	80	1.55	M83681	RAB3D, member RAS oncogene family
Rab5b_pre	138	91	0.66	BF560790	RAB5B, member RAS oncogene family (predicted)
Rab8b	169	270	1.60	BF398743	RAB8B, member RAS oncogene family
Rin2_predict	190	353	1.85	BM392293	Ras and Rab interactor 2 (predicted)
Rassf7_pre	58	89	1.54	BM385768	Ras association (RalGDS/AF-6) domain family 7 (predi
Rhoj_predict	53	108	2.02	BM389644	ras homolog gene family, member J (predicted)
Rasip1_pre	75	149	2.00	AA848597	Ras interacting protein 1 (predicted)
Rac2_predi	53	167	3.17	AI010476	RAS-related C3 botulinum substrate 2 (predicted)
Ramp2	210	556	2.64	NM_031646	receptor (calcitonin) activity modifying protein 2
Rims2	76	49	0.64	NM_053945	regulating synaptic membrane exocytosis 2
Arhgdib_pr	138	304	2.21	BF285771	Rho, GDP dissociation inhibitor (GDI) beta (predicted)
Rgnef_prec	48	90	1.90	AW521384	Rho-guanine nucleotide exchange factor (predicted)
Scgb1a1	18	5790	318.15	NM_013051	secretoglobin, family 1A, member 1
Sgk	360	654	1.82	NM_019232	serum/glucocorticoid regulated kinase
Shc1	53	107	2.03	BF548525	SHC (Src homology 2 domain-containing) transforming
RGD15627	70	117	1.67	BG669292	Similar to ABI gene family, member 3 (NESH) binding p
RGD15635	87	50	0.58	BF401477	similar to AP2 associated kinase 1 (predicted)
LOC688297	130	85	0.65	BG371889	similar to Retinal rod rhodopsin-sensitive cGMP 3,5-cyc
Snf1lk	41	78	1.89	NM_021693	SNF1-like kinase
Snx4_predi	374	242	0.65	AI029221	Sorting nexin 4 (predicted)
Scap2	103	203	1.98	NM_130413	src family associated phosphoprotein 2
Socs2	140	220	1.57	BM384088	Suppressor of cytokine signaling 2
Tns	84	382	4.57	BF290193	Tensin
Tenc1_prec	92	151	1.65	BI294836	tensin like C1 domain containing phosphatase (predicte
Tspan8	52	392	7.58	NM_133526	Tetraspanin 8
Tagln2_pre	82	454	5.53	BI285865	transgelin 2 (predicted)
Tacstd2	20	122	6.02	AA891826	tumor-associated calcium signal transducer 2
Vasp_predi	102	213	2.10	AW520792	vasodilator-stimulated phosphoprotein (predicted)
Wif1	52	139	2.68	NM_053738	Wnt inhibitory factor 1
Anxa4	82	228	2.78	BM385237	ZAP 36/annexin IV

Transcription

Sample	F3-Cont	F3-Vinc	Vin/Con
Gene Symt	Raw	Raw	Ratio

Genbank	Gene Title
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Aebp1_pre	93	203	2.20	BI278482	AE binding protein 1 (predicted)
Ahnak	274	1327	4.85	AI407114	AHNAK nucleoprotein (desmoyokin)
Rai14	48	124	2.58	AI234852	Ankyrin repeat and coiled-coil structure-co
Bcl11b_pre	421	190	0.45	BM390227	B-cell leukemia/lymphoma 11B (predicted)
Bcor_predic	53	87	1.62	BI289386	Bcl6 interacting corepressor (predicted)
Cebpb	24	104	4.39	NM_024125	CCAAT/enhancer binding protein (C/EBP), beta
Copeb	90	233	2.60	NM_031642	core promoter element binding protein
Ddx58_pre	42	75	1.80	AI575264	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)
Dnajc1_pre	82	140	1.70	BI295806	DnaJ (Hsp40) homolog, subfamily C, member 1 (predicted)
Elf1	45	76	1.70	AA818055	E74-like factor 1 (ets domain transcription factor)
Ebf	119	65	0.55	AI406967	Early B-cell factor 1
Egr2	92	162	1.76	NM_053633	early growth response 2
Egr4	74	123	1.66	NM_019137	early growth response 4
Elk3_predic	74	145	1.96	BM392135	ELK3, member of ETS oncogene family (predicted)
Fos	197	506	2.57	BF415939	FBJ murine osteosarcoma viral oncogene homolog
FoxA1	6	76	12.63	BM383972	Forkhead box A1
Fhl1	620	996	1.61	BG673187	four and a half LIM domains 1
Gata2	37	107	2.91	NM_033442	GATA binding protein 2
Gata6	7	170	25.34	AA800786	GATA binding protein 6
Hes1	48	126	2.63	NM_024360	hairy and enhancer of split 1 (Drosophila)
Hmgb2 /// L	55	132	2.40	NM_017187	high mobility group box 2 /// similar to High mobility gro
Hoxa5	22	77	3.44	BE107303	homeo box A5
Hod	317	1216	3.84	NM_133621	homeobox only domain
Nr4a1	192	431	2.24	NM_024388	immediate early gene transcription factor NGFI-B
Id1	167	386	2.31	M86708	Inhibitor of DNA binding 1, helix-loop-helix protein (spli
Junb	91	144	1.57	NM_021836	Jun-B oncogene
Klf2	102	654	6.45	BM385790	Kruppel-like factor 2
Klf4	50	307	6.20	NM_053713	Kruppel-like factor 4 (gut)
Klf5	58	133	2.28	NM_053394	Kruppel-like factor 5 (intestinal)
Lrrfip1	21	102	5.00	BM387864	Leucine rich repeat (in FLII) interacting protein 1
Mfhas1_pre	109	170	1.55	AI136864	malignant fibrous histiocytoma amplified sequence 1 (p
Mgea6_pre	143	237	1.65	AI177180	meningioma expressed antigen 6 (coiled-coil proline-ric
Mcl1	308	606	1.97	AI102618	Myeloid cell leukemia sequence 1
Nfe2l2	182	295	1.62	NM_031789	NF-E2-related factor 2
Nfix	1251	2557	2.04	AI555855	nuclear factor I/X
Nfkbia	114	326	2.87	AW672589	nuclear factor of kappa light chain gene enhancer in B-
Nr4a3	167	329	1.98	NM_031628	nuclear receptor subfamily 4, group A, member 3
Ptrf_predict	566	1369	2.42	AA899937	Polymerase I and transcript release factor (predicted)
Runx1	39	92	2.34	NM_017325	runt related transcription factor 1
Stat1	118	182	1.54	AW434718	signal transducer and activator of transcription 1
LOC687536	20	81	3.99	AA817785	similar to Forkhead box protein F1 (Forkhead-related p
MGC72578	84	137	1.62	BF420059	similar to immediate early response 2
LOC499497	992	1768	1.78	BE104219	similar to MADS box transcription enhancer factor 2, pc
RGD15631	739	285	0.39	BF414312	similar to MADS box transcription enhancer factor 2, pc
RGD13063	44	100	2.26	AI407047	similar to Zinc finger protein 198 (Fused in myeloprolife
Sp110_prec	68	117	1.73	AI411381	SP110 nuclear body protein (predicted)
Sox13_prec	55	102	1.86	BM383170	SRY (sex determining region Y)-box 13 (predicted)
Ssg1	69	125	1.81	AI235465	steroid sensitive gene 1
Tnks_predic	99	169	1.70	BM388725	tankyrase, TRF1-interacting ankyrin-related ADP-ribose
Tiparp_prec	109	165	1.51	AI179464	TCDD-inducible poly(ADP-ribose) polymerase (predicte
Titf1	17	217	12.77	BF389361	thyroid transcription factor 1
Tcf21	12	97	8.25	BE113336	transcription factor 21
Tacstd1	20	217	10.97	BG376410	tumor-associated calcium signal transducer 1

Txnip	237	789	3.33	U30789	upregulated by 1,25-dihydroxyvitamin D-3
Ets1	69	175	2.53	NM_012555	v-ets erythroblastosis virus E26 oncogene homolog 1 (
Erg	31	85	2.76	NM_133397	v-ets erythroblastosis virus E26 oncogene like (avian)
Jun	253	544	2.15	BI288619	v-jun sarcoma virus 17 oncogene homolog (avian)
Zfp36	67	242	3.62	AB025017	zinc finger protein 36
Zfp3611	316	488	1.54	NM_017172	zinc finger protein 36, C3H type-like 1
Zfp628_pre	118	60	0.51	BE097029	Zinc finger protein 628 (predicted)
RGD:62867	109	68	0.62	AF277900	zinc finger protein HIT-4
Zcchc8_pre	123	82	0.66	AA894084	zinc finger, CCHC domain containing 8 (predicted)
Zfyve28_pr	95	60	0.63	BF403058	Zinc finger, FYVE domain containing 28 (predicted)

Translation_Protein Modification

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio	Genbank	Gene Title
Ear11	2	100	40.80	D88586	eosinophil-associated, ribonuclease A family, member 1
Dcps	44	76	1.74	AI535521	mRNA decapping enzyme
Dcps	121	64	0.53	BI288131	mRNA decapping enzyme
Paip1_pred	338	520	1.54	AA963084	Polyadenylate binding protein-interacting protein 1 (pre
Slfn2_predi	42	122	2.94	AW915529	schlafen 2 (predicted)
Slfn3	31	125	4.06	NM_053687	schlafen 3
Slfn5_predi	63	172	2.75	AI072951	schlafen 5 (predicted)
Cugbp2	67	117	1.74	BF390754	CUG triplet repeat, RNA binding protein 2

Miscellaneous & Unknown

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio	Genbank	Gene Title
Lrrc4c_prec	209	112	0.53	AA819053	leucine rich repeat containing 4C (predicted)
Angel1_pre	79	38	0.49	AI578461	angel homolog 1 (Drosophila) (predicted)
---	47	106	2.24	BM386869	CDNA clone IMAGE:7366335
Cttnbp2nl_f	141	232	1.64	BM383195	CTTNBP2 N-terminal like (predicted)
Fam38a_pr	23	75	3.20	BI274438	family with sequence similarity 38, member A (predicted)
Gm1960	11	276	24.89	AW917501	gene model 1960, (NCBI)
Gm1960	4	958	228.15	D21095	gene model 1960, (NCBI)
RGD13115:	100	163	1.62	BF288207	hypothetical LOC315055 (predicted)
LOC49854:	367	1672	4.55	AA800750	hypothetical protein LOC498544
Kirrel3_prec	347	211	0.61	BF399121	kin of IRRE like 3 (Drosophila) (predicted)
Lims2_prec	30	75	2.51	BI275904	LIM and senescent cell antigen like domains 2 (predicte
Mtac2d1	35	194	5.57	BI302544	membrane targeting (tandem) C2 domain containing 1
Perc64	35	103	2.93	BM384701	PE responsive protein c64
Perc64	63	176	2.78	BI278571	PE responsive protein c64
Pqlc3	66	115	1.75	AW915795	PQ loop repeat containing 3
Sema3g	210	387	1.84	BE108859	Sema domain, immunoglobulin domain (Ig), short basic
Sema3c_pr	103	238	2.30	BM390322	sema domain, immunoglobulin domain (Ig), short basic
Sdpr	82	802	9.79	AI009714	serum deprivation response protein
Sh2d4a_pr	21	97	4.69	AA800626	SH2 domain containing 4A (predicted)
Stac2_pred	81	48	0.60	BF406342	SH3 and cysteine rich domain 2 (predicted)
Spn	34	126	3.74	BF550890	sialophorin
---	51	84	1.65	AA858591	similar HORMA domain containing 1 (predicted)
MGC10949	44	93	2.10	AI071166	similar to 1110007F12Rik protein
---	69	232	3.35	BM385779	Similar to 1300014I06Rik protein (predicted)
RGD13095:	47	77	1.63	AI102745	Similar to 2310014H01Rik protein (predicted)
RGD13069	34	81	2.38	AA819788	similar to 5830458K16Rik protein (predicted)
RGD13048	123	81	0.66	AI044301	similar to 6430573F11Rik protein (predicted)

---	29	162	5.67	BE109323	Similar to 9530046H09Rik protein (predicted)
LOC309112	59	115	1.96	AI178948	similar to BC026645 protein
LOC680229	334	145	0.43	AI413058	Similar to Beta-sarcoglycan (Beta-SG) (43 kDa dystrop
RGD15594	98	148	1.51	BF291168	Similar to BH3-only member B protein (predicted)
LOC679937	25	316	12.85	BM386323	similar to CG4025-PA
RGD13081	53	85	1.59	AA899109	similar to chromosome 17 open reading frame 27 (pred
RGD15651	16	179	10.93	AI045955	similar to Clecsf12 protein (predicted)
LOC304138	150	475	3.17	AA818900	similar to cysteine and tyrosine-rich protein 1
RGD15663	37	95	2.59	AA946147	Similar to cysteine-rich glycoprotein (predicted)
LOC691657	37	315	8.43	BF550246	Similar to Cysteine-rich protein 1 (Cysteine-rich intestin
RGD13080	118	190	1.61	AI408727	similar to DNA segment, Chr 4, Brigham & Womens Ge
LOC499322	13	226	17.06	AA799328	similar to expressed sequence AW413625
LOC687266	29	103	3.50	AI072658	similar to Folylpolyglutamate synthase, mitochondrial p
LOC291964	51	84	1.64	BI281796	similar to Formin homology 2 domain containing 1
RGD13075	41	91	2.23	AI231799	similar to Friedreich ataxia region gene X123 (predicte
RGD13105	67	116	1.74	BG375354	similar to hypothetical protein FLJ14146 (predicted)
RGD131131	90	158	1.77	BI294811	similar to hypothetical protein FLJ20037 (predicted)
RGD15596	399	247	0.62	BE101933	similar to hypothetical protein FLJ25477 isoform 2 (pre
LOC363097	5	128	24.46	AI103939	similar to hypothetical protein FLJ30973
RGD13058	36	102	2.85	BI288939	similar to hypothetical protein FLJ40283 (predicted)
LOC500300	41	109	2.68	BM390487	similar to hypothetical protein MGC6835
MGC12488	138	253	1.83	AI176611	Similar to Mob4B protein
RGD15619	48	87	1.82	BM390809	similar to Muc5b protein (predicted)
LOC309498	34	88	2.57	AW917760	similar to Myoferlin (Fer-1 like protein 3)
RGD15616	174	327	1.88	AA997745	similar to nemo like kinase (predicted)
LOC686753	28	250	8.87	AA851385	similar to nephronectin isoform a
LOC287346	56	177	3.16	BF284080	similar to novel protein
LOC287346	47	144	3.09	AA957487	similar to novel protein
LOC315733	31	75	2.46	BI276339	similar to Nuclear membrane binding protein NUCLING
B130017107	145	319	2.20	AI407483	Similar to Parg1-pending protein (predicted)
LOC684877	19	129	6.88	AI230625	similar to Protein C8orf4 (Thyroid cancer protein 1) (TC
MGC10877	91	459	5.03	BM391248	similar to RIKEN cDNA 1810057C19
LOC498643	42	95	2.28	AW252379	similar to RNA binding protein gene with multiple splicir
LOC690777	38	78	2.04	BF404935	Similar to RUN and FYVE domain-containing 2
LOC362057	70	143	2.03	BF285490	similar to semaF cytoplasmic domain associated protei
RGD15625	72	110	1.53	AW142608	similar to SH3-containing guanine nucleotide exchange
LOC686543	84	53	0.63	AW527248	similar to slit homolog 1
MGC94010	187	338	1.80	BM384419	Similar to SPI6
RGD15621	269	162	0.60	AW521222	Similar to TAF5
LOC500040	127	199	1.57	BI288769	similar to Testis derived transcript
LOC315843	46	114	2.49	BE107185	similar to WD repeat domain 11 protein
Slitrk1_prec	157	94	0.60	AW523107	SLIT and NTRK-like family, member 1 (predicted)
Spsb1_prec	80	49	0.61	BE106389	SplA/ryanodine receptor domain and SOCS box contain
Samd8	85	50	0.59	BI295733	sterile alpha motif domain containing 8
Tmem10_p	487	324	0.67	AI717253	transmembrane protein 10 (predicted)
Tmem123	94	169	1.81	AI171651	transmembrane protein 123//transmembrane protein 12
Tnrc6_pred	578	872	1.51	BI294732	Trinucleotide repeat containing 6 (predicted)
Trim23	135	87	0.64	L04760	tripartite motif protein 23
Trim_predic	61	105	1.73	BI280655	Tripartite motif protein 34 (predicted)
RGD:73507	76	163	2.16	AI009530	Unknown (protein for MGC:72614)
Wfdc2	26	265	10.10	AI411527	WAP four-disulfide core domain 2

EST

Sample	F3-Cont	F3-Vinc	Vin/Con	Genbank	Gene Title
Gene Symt	Raw	Raw	Ratio		
---	138	222	1.61	AI031032	Transcribed locus, weakly similar to XP_341951.1 PRE
---	123	222	1.80	AI598401	Transcribed locus, weakly similar to NP_002639.1 pim-
---	49	76	1.55	BM385157	Transcribed locus, strongly similar to XP_001058445.1
---	270	429	1.59	BI289625	Transcribed locus, strongly similar to NP_035333.2 pro
---	131	79	0.60	BF403401	Transcribed locus, moderately similar to XP_580018.1
---	91	215	2.36	BI278962	Transcribed locus, moderately similar to NP_795929.1
---	26	128	4.89	BM389422	Transcribed locus, moderately similar to NP_694996.2
---	127	79	0.62	BF403165	Transcribed locus
---	68	117	1.73	AI175779	Transcribed locus
---	65	106	1.64	AI408264	Transcribed locus
---	150	92	0.62	BF549454	Transcribed locus
---	95	57	0.61	BF391706	Transcribed locus
---	27	103	3.86	AI233857	Transcribed locus
---	106	201	1.90	AI411809	Transcribed locus
---	179	478	2.68	BF283404	Transcribed locus
---	63	101	1.60	BE116601	Transcribed locus
---	45	118	2.62	BM384377	Transcribed locus
---	52	175	3.36	BF407452	Transcribed locus
---	112	237	2.11	BI283685	Transcribed locus
---	67	107	1.60	AI169118	Transcribed locus
---	134	215	1.60	AI709424	Transcribed locus
---	104	161	1.54	AA900322	Transcribed locus
---	761	501	0.66	AA925373	Transcribed locus
---	40	129	3.25	AI058292	Transcribed locus
---	36	300	8.39	BE107090	Transcribed locus
---	106	166	1.56	BE103875	Transcribed locus
---	84	54	0.64	AA924955	Transcribed locus
---	182	279	1.53	BF545309	Transcribed locus
---	29	78	2.72	AA818143	Transcribed locus
---	220	398	1.81	BF563716	Transcribed locus
---	67	147	2.20	AI178627	Transcribed locus
---	45	106	2.37	AI410262	Transcribed locus
---	13	206	15.76	AA859079	Transcribed locus
---	107	65	0.61	BE099664	Transcribed locus
---	162	100	0.62	BE117653	Transcribed locus
---	340	20	0.06	AA964506	Transcribed locus
---	77	116	1.51	AW918368	Transcribed locus
---	311	587	1.89	AI144865	Transcribed locus
---	288	504	1.75	AI071538	Transcribed locus
---	73	143	1.96	AI228481	Transcribed locus
---	162	99	0.61	AW531387	Transcribed locus
---	747	466	0.62	AI100827	Transcribed locus
---	46	120	2.64	BE115859	Transcribed locus
---	120	181	1.51	AI502604	Transcribed locus
---	27	81	3.03	BF389682	Transcribed locus
---	48	110	2.30	BI277619	Transcribed locus
---	49	77	1.55	AA818282	Transcribed locus
---	427	278	0.65	AA955175	Transcribed locus
---	57	105	1.84	AI408734	Transcribed locus
---	171	281	1.64	BI279751	Transcribed locus
---	485	914	1.89	BE107419	Transcribed locus

---	43	116	2.67	BE101285	Transcribed locus
---	124	221	1.79	BF551377	Transcribed locus
RGD13052	39	77	1.95	BF393865	similar to RIKEN cDNA C130022K22 gene (predicted)
LOC362898	105	170	1.61	AA859508	similar to RIKEN cDNA 9330161F08
RGD131118	297	562	1.89	AI716248	similar to RIKEN cDNA 9230117N10 (predicted)
RGD13070	150	276	1.85	BM384306	similar to RIKEN cDNA 9130404D14 (predicted)
LOC313518	41	121	2.95	AW915484	similar to RIKEN cDNA 5330440M15 /// similar to hypot
RGD131158	80	49	0.61	BF407634	similar to RIKEN cDNA 5033405K12 (predicted)
LOC49980	102	171	1.68	BE328914	similar to RIKEN cDNA 4933404M02
RGD13064	117	67	0.58	BF396478	similar to RIKEN cDNA 4930556P03 (predicted)
RGD13050	143	408	2.84	AI171466	similar to RIKEN cDNA 2700055K07 (predicted)
Rod1	212	389	1.84	BI280285	Similar to RIKEN cDNA 2610207I16 (predicted)
RGD15630	95	150	1.57	BF291140	similar to RIKEN cDNA 2010106G01 (predicted)
LOC363068	5	113	22.77	AI599133	similar to RIKEN cDNA 1600029D21
---	46	89	1.94	AA924459	Similar to RIKEN cDNA 1200013B08
RGD13103	107	182	1.70	H33457	similar to RIKEN cDNA 1200004M23 (predicted)
LOC500840	84	219	2.61	AI178214	LOC500840
LOC500719	29	92	3.16	AW919728	LOC500719 /// LOC500720 /// LOC500721
LOC500488	53	250	4.76	BM387041	LOC500488
LOC499318	175	353	2.02	BM388445	LOC499318
LOC498261	30	102	3.44	AI177743	LOC498261
LOC497957	49	97	1.98	BF399335	LOC497957
---	112	69	0.62	BI273954	---
---	614	326	0.53	BF393011	---
---	90	495	5.50	BF542239	---
---	81	49	0.60	AW527725	---
---	111	182	1.64	BE102708	---
---	69	118	1.72	BF390648	---
---	317	165	0.52	BI303277	---
---	46	97	2.10	AW528011	---
---	81	247	3.03	AI101416	---
---	53	120	2.28	AI071755	---
---	51	197	3.91	AI575277	---
---	107	70	0.65	AA998001	---
---	22	82	3.66	AI043711	---
---	321	167	0.52	AI555608	---
---	105	168	1.60	BE329364	---
---	96	61	0.64	AI013683	---
---	88	57	0.64	AW529368	---
---	168	109	0.65	AI029275	---
---	88	28	0.32	BI297481	---
---	12	95	7.93	AA893192	---
LOC498278	283	479	1.69	BE111722	---
---	260	129	0.49	AI169620	---
---	61	118	1.94	BM388957	---
---	168	302	1.80	AI012566	---
---	125	259	2.08	BE103242	Transcribed locus
LOC679818	63	148	2.34	AA963975	similar to GLI pathogenesis-related 2
---	78	117	1.50	AW253907	Transmembrane 9 superfamily protein member 4 (pred
LOC291318	310	474	1.53	AA900781	N-myristoyltransferase 2