

Table S1. Complete list of candidate genes identified by the microarray analysis

Affymetrix probe set ID	RefSeq transcript ID	Gene symbol	Gene title	Control #1	Control #2	Delta #1	Delta #2	Wnt2b #1	Wnt2b #2
GgaAffx.24672.1.S1_s_at	XM_416641	PROS1	protein S (alpha)	-0.92	-0.7	-0.57	-0.25	1.61	0.82
GgaAffx.12737.1.S1_at	NM_001007917	MPP1	membrane protein, palmitoylated 1, 55 kDa	-0.62	-0.8	-0.31	-0.56	1.83	0.46
Gga.17369.1.S1_at	-	-	Finished cDNA, clone ChEST33o12	-0.81	-0.87	-0.34	-0.34	1.71	0.65
GgaAffx.6955.1.S1_s_at	XM_418721	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	-0.59	-1.04	-0.42	-0.34	1.64	0.77
Gga.8094.1.S1_a_at	XM_416182	ARHGDI3	Rho GDP dissociation inhibitor (GDI) beta	-0.43	-0.63	-0.58	-0.82	1.67	0.79
Gga.2136.1.S1_a_at	XM_001234310	LOC770992	similar to DNA polymerase gamma	-0.49	-0.37	-0.72	-0.86	1.65	0.8
Gga.2136.1.S1_at	XM_427270	LOC429716	similar to GTP-binding protein SB128	-0.47	-0.41	-0.67	-0.87	1.7	0.72
Gga.17545.1.S1_at	-	-	Finished cDNA, clone ChEST992c8	-0.25	-0.87	-0.77	-0.47	1.72	0.64
Gga.4726.1.S1_at	NM_001005618	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	-0.59	-0.72	-0.66	-0.5	1.69	0.77
GgaAffx.8655.1.S1_s_at	XM_420680	FAT	FAT tumor suppressor homolog 1 (Drosophila)	-0.41	-0.74	-0.75	-0.57	1.66	0.81
Gga.13110.1.S1_at	-	-	Finished cDNA, clone ChEST110n14	-0.19	-0.75	-0.32	-1.07	1.62	0.71
GgaAffx.6670.1.S1_at	XM_419515	LOC421466	similar to cytochrome P450 1B1	-0.41	-0.56	-0.39	-0.87	1.87	0.36
GgaAffx.20575.1.S1_at	-	-	Finished cDNA, clone ChEST1019k13	-0.77	-0.14	-0.78	-0.7	0.72	1.66
GgaAffx.43.1.S1_at	-	-	-	-0.15	-0.53	-1.18	-0.57	1.25	1.19
Gga.5920.1.S1_a_at	-	-	Finished cDNA, clone ChEST375n15	-0.52	-0.44	-1.21	-0.28	1.32	1.13
Gga.9776.1.S1_at	-	-	Finished cDNA, clone ChEST573k5	-0.38	-0.34	-1.19	-0.54	1.39	1.06
Gga.3869.1.S1_at	XM_420664	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	-0.05	-0.18	-1.15	-0.95	1.25	1.08
Gga.15918.1.S1_at	XM_419669	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	-0.49	-0.39	-0.77	-0.87	1.42	1.11
Gga.7473.1.S1_at	XM_413689	STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	-0.36	-0.35	-0.95	-0.83	1.36	1.13
GgaAffx.23883.1.S1_at	XM_419669	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	-0.39	-0.34	-0.91	-0.85	1.47	1.02
Gga.16698.1.S1_at	-	-	Finished cDNA, clone ChEST875h18	-0.05	-0.6	-0.86	-0.91	1.47	0.95
Gga.1322.1.S1_at	XM_420664	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	-0.16	-0.54	-0.87	-0.91	1.36	1.12
Gga.1322.1.S1_a_at	XM_426665	TTC4	Tetratricopeptide repeat domain 4	-0.22	-0.4	-0.82	-1	1.45	1
Gga.1322.2.S1_x_at	XM_420664	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	-0.12	-0.43	-0.8	-1.07	1.36	1.07
GgaAffx.23779.1.S1_at	XM_421441	LOC423548	similar to chromosome 14 open reading frame 108	-0.55	-0.06	-1.11	-0.69	1.37	1.05
Gga.4932.1.S1_at	XM_001235688	JAG2	jagged 2	-0.36	-0.3	-0.89	-0.93	1.11	1.37
Gga.17769.1.S1_at	-	-	Finished cDNA, clone ChEST847b13	-0.34	-0.26	-0.96	-0.91	1.18	1.29
Gga.1241.1.S1_s_at	XM_421441	LOC423548	similar to chromosome 14 open reading frame 108	-0.62	-0.18	-0.97	-0.71	1.09	1.4
Gga.3074.1.S1_a_at	NM_206905	C-16	galectin CG-16	-0.6	-0.33	-0.73	-0.87	1.29	1.25
Gga.14870.1.S1_at	NM_204112	LMO4	LIM domain only 4	-0.71	-0.1	-0.83	-0.85	1.24	1.25
GgaAffx.23665.1.S1_x_at	NM_001079721	LOC417957	similar to histone H2B	-0.18	-0.26	-1.18	-0.64	0.62	1.64
Gga.17329.1.S1_at	-	-	Finished cDNA, clone ChEST757g6	-0.09	-0.8	-0.83	-0.68	0.8	1.6
Gga.2669.1.S1_at	-	-	Transcribed locus	-0.06	-0.62	-0.86	-0.87	0.89	1.52
Gga.11321.1.S1_at	NM_205506	P11	cellular ligand of annexin II	-0.12	-0.49	-0.9	-0.88	0.83	1.57

GgaAffx.7456.1.S1_at	-	-	-	-0.16	-0.44	-1	-0.8	0.87	1.54
Gga.5225.1.S1_at	-	-	Finished cDNA, clone ChEST412b10	0.17	-0.69	-0.98	-0.85	1.06	1.3
Gga.8797.1.S1_at	-	-	Finished cDNA, clone ChEST189k11	-0.03	-0.37	-0.94	-1.05	1.04	1.34
Gga.3077.1.S1_at	-	-	Finished cDNA, clone ChEST148h22	-0.54	-0.84	-0.15	-0.89	0.86	1.56
GgaAffx.21540.1.S1_at	-	-	Finished cDNA, clone ChEST569n13	-0.15	-1.02	-0.26	-0.91	0.8	1.55
Gga.17014.1.S1_at	-	-	Finished cDNA, clone ChEST973g12	-0.29	-0.97	0.03	-1.02	0.7	1.56
Gga.4919.1.S1_at	NM_204260	CUGBP2	CUG triplet repeat, RNA binding protein 2	-0.65	-1.07	-0.18	-0.38	0.56	1.72
Gga.8445.1.S1_at	NM_204354	DUSP6	dual specificity phosphatase 6	-0.39	-0.94	-0.22	-0.7	0.45	1.8
GgaAffx.12137.1.S1_s_at	NM_001031245	RCJMB04_9I13	LanC lantibiotic synthetase component C-like 1 (bacterial)	-0.47	-0.57	-0.95	-0.53	1.01	1.5
Gga.1030.1.S1_at	NM_001030952	MYC	v-myc myelocytomatosis viral oncogene	-0.49	-0.82	-0.86	-0.29	0.87	1.59
Gga.14140.1.S1_at	-	-	Finished cDNA, clone ChEST443k14	-0.47	-0.74	-0.96	-0.3	0.94	1.53
Gga.4974.1.S2_at	NM_204787	VCAN	versican	-0.6	-0.56	-0.85	-0.37	0.63	1.75
Gga.3412.1.S1_at	NM_204718	CITED4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	-0.72	-0.54	-0.75	-0.3	0.5	1.81
Gga.4990.1.S1_at	NM_001100911	COL9A1	collagen, type IX, alpha 1	-0.62	-0.63	-0.73	-0.39	0.58	1.79
Gga.9891.1.S1_at	XM_426107	FLRT3	fibronectin leucine rich transmembrane protein 3	-0.65	-0.64	-0.72	-0.33	0.54	1.8
Gga.3280.1.S1_at	XM_001233212	LOC771265	similar to Cerebellin precursor (Precerebellin)	-0.73	-0.42	-0.99	-0.26	0.75	1.64
Gga.153.1.S2_at	-	-	-	-0.84	-0.59	-0.82	-0.12	0.71	1.66
Gga.11765.1.S1_at	-	-	Finished cDNA, clone ChEST1012h22	-0.81	-0.55	-0.8	-0.19	0.62	1.73
GgaAffx.1518.1.S1_s_at	XM_001234811	NOC4L	nucleolar complex associated 4 homolog (<i>S. cerevisiae</i>)	-0.63	-0.46	-0.81	-0.58	0.83	1.65
Gga.4440.1.S1_at	NM_204814	CHRNA4	cholinergic receptor, nicotinic, alpha 4	-0.6	-0.6	-0.76	-0.48	0.73	1.71
Gga.514.1.S1_at	NM_205022	F10	coagulation factor X	-0.66	-0.55	-0.71	-0.55	0.79	1.68
Gga.3974.1.S2_at	NM_204213	CCND2	cyclin D2	-0.64	-0.63	-0.63	-0.54	0.72	1.73
GgaAffx.24674.1.S1_at	XM_001233072	STX19	syntaxin 19	-0.64	-0.61	-0.64	-0.58	0.79	1.69
Gga.4517.1.S1_at	NM_001030965	RCJMB04_13p19	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	-0.7	-0.63	-0.59	-0.58	0.87	1.63
Gga.11119.1.S1_at	XM_001233072	STX19	syntaxin 19	-0.66	-0.6	-0.57	-0.65	0.8	1.68
GgaAffx.12575.1.S1_s_at	NM_001006262	ASB9	ankyrin repeat and SOCS box-containing 9	-0.85	-0.54	-0.48	-0.64	0.95	1.56
Gga.19264.1.S1_at	-	-	Finished cDNA, clone ChEST392I14	-0.61	-0.6	-0.67	-0.65	0.95	1.58
GgaAffx.2357.1.S1_s_at	XM_414094	NKD1	naked cuticle homolog 1 (<i>Drosophila</i>)	-0.61	-0.7	-0.56	-0.67	0.98	1.55
Gga.1444.1.S1_at	-	-	-	-0.62	-0.67	-0.6	-0.67	1.03	1.52
GgaAffx.12380.1.S1_s_at	NM_001030965	RCJMB04_13p19	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	-0.83	-0.51	-0.67	-0.53	1.08	1.47
Gga.7716.2.S1_a_at	-	-	Finished cDNA, clone ChEST419o13	-0.77	-0.58	-0.67	-0.51	0.96	1.56
GgaAffx.3989.1.S1_at	NM_001030600	RCJMB04_3k20	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	-0.73	-0.57	-0.64	-0.6	0.99	1.55
Gga.17542.1.S1_at	-	-	Finished cDNA, clone ChEST196k16	-0.71	-0.56	-0.73	-0.54	1.06	1.49
Gga.1869.1.S1_at	XM_419958	LOC421946	similar to NSE1	-0.74	-0.62	-0.71	-0.47	1.03	1.51
GgaAffx.22332.1.S1_at	XM_420297	LOC422321	similar to Ras11c protein	-0.73	-0.67	-0.7	-0.45	1.09	1.46
Gga.15367.1.S1_at	-	-	Finished cDNA, clone ChEST662I8	-0.69	-0.7	-0.43	-0.59	0.65	1.75
Gga.11918.1.S1_at	XM_416643	NSUN3	NOL1/NOP2/Sun domain family, member 3	-0.81	-0.72	-0.4	-0.44	0.62	1.75
Gga.4146.1.S1_at	NM_204737	LOC395489	EURL	-0.89	-0.56	-0.56	-0.47	0.86	1.62
Gga.14349.1.S1_at	-	-	Finished cDNA, clone ChEST326d3	-0.95	-0.58	-0.53	-0.37	0.75	1.67

Gga.11876.1.S1_a_at	XM_419085	LOC420999	similar to chromosome 9 open reading frame 19; 17kD fetal brain protein	-0.97	-0.33	-0.64	-0.47	0.76	1.66
GgaAffx.9020.1.S1_at	XM_001233939	KCTD8	potassium channel tetramerisation domain containing 8	-0.86	-0.48	-0.67	-0.41	0.71	1.7
Gga.13358.1.S1_at	-	-	Finished cDNA, clone ChEST115n18	-0.74	-0.77	-0.59	-0.35	0.79	1.67
GgaAffx.6997.1.S1_at	XM_422027	LOC424181	hypothetical LOC424181	-0.86	-0.63	-0.59	-0.29	0.64	1.74
Gga.17354.1.S1_at	XM_001233456	ZNF503	zinc finger protein 503	-0.47	-0.65	-0.76	-0.62	0.9	1.6
Gga.14051.1.S1_at	-	-	Finished cDNA, clone ChEST489n5	-0.38	-0.78	-0.69	-0.63	0.85	1.63
GgaAffx.25672.1.S1_s_at	XM_415639	LOC417384	similar to Alveolar soft part sarcoma chromosome region, candidate 1 (human)	-0.33	-0.7	-0.73	-0.72	0.88	1.6
Gga.12419.1.S1_at	-	-	Finished cDNA, clone ChEST100h19	-0.45	-0.72	-0.6	-0.61	0.58	1.79
Gga.19075.1.S1_at	XM_419931	PXDN	peroxidasin homolog (Drosophila)	-0.39	-0.71	-0.75	-0.54	0.63	1.76
Gga.1046.1.S1_at	XM_414601	RNF130	ring finger protein 130	-0.85	-0.47	-0.97	-0.18	1.31	1.16
Gga.253.1.S1_at	NM_205192	CBF-2	brain factor-2	-0.8	-0.56	-0.84	-0.34	1.2	1.34
Gga.16172.1.S1_s_at	XM_001232621	LOC426155	hypothetical gene supported by CR385555	-0.72	-0.51	-0.86	-0.45	1.25	1.3
Gga.9476.1.S1_at	NM_204509	ROR1	receptor tyrosine kinase-like orphan receptor 1	-0.66	-0.73	-0.76	-0.35	0.96	1.54
Gga.2694.1.S2_s_at	NM_205013	LEF1	lymphoid enhancer-binding factor 1	-0.72	-0.75	-0.77	-0.26	1.02	1.49
Gga.17441.1.S1_at	XM_001235027	LOC771797	similar to MGC84049 protein	-0.88	-0.63	-0.81	-0.16	1.03	1.45
Gga.5591.1.S1_at	-	-	Transcribed locus, moderately similar to XP_001099261.1	-0.9	-0.65	-0.66	-0.3	1.02	1.48
Gga.7239.1.S1_at	-	-	Finished cDNA, clone ChEST65819	-0.74	-0.86	-0.8	-0.07	1.26	1.22
Gga.7467.1.S1_at	NM_204839	PDLIM4	PDZ and LIM domain 4	-0.94	-0.68	-0.76	-0.1	1.16	1.31
Gga.718.3.S1_at	NM_205299	DMD	dystrophin	-0.88	-0.76	-0.71	-0.16	1.19	1.31
Gga.718.3.S1_x_at	NM_205299	DMD	dystrophin	-0.92	-0.71	-0.72	-0.15	1.18	1.31
Gga.16710.2.S1_a_at	XM_417583	LOC419422	hypothetical LOC419422	-0.86	-0.75	-0.7	-0.21	1.26	1.26
Gga.718.1.S1_at	NM_205299	DMD	dystrophin	-0.8	-0.74	-0.71	-0.29	1.18	1.35
Gga.718.2.S1_a_at	NM_205299	DMD	dystrophin	-0.84	-0.77	-0.68	-0.23	1.18	1.34
Gga.8266.1.S1_at	-	-	Finished cDNA, clone ChEST835a14	-0.76	-0.79	-0.8	-0.02	0.75	1.61
Gga.13556.1.S1_at	-	-	Finished cDNA, clone ChEST432p5	-0.67	-0.6	-1.08	-0.1	1.12	1.33
GgaAffx.230.1.S1_at	XM_418066	LOC419945	similar to degenerin channel MDEG	-0.72	-0.74	-0.94	-0.05	1.04	1.41
Gga.4993.1.S1_at	NM_204127	RCJMB04_23c5	actinin, alpha 1	-0.82	-0.76	-0.92	0.12	1	1.37
GgaAffx.24103.1.S1_at	XM_416405	EPS8	epidermal growth factor receptor pathway substrate 8	-0.77	-0.83	-0.82	0.02	0.95	1.46
Gga.5475.1.S1_at	XM_416083	SLC35E3	solute carrier family 35, member E3	-0.73	-0.57	-1.07	-0.03	0.94	1.46
GgaAffx.8313.1.S1_s_at	XM_416405	EPS8	epidermal growth factor receptor pathway substrate 8	-0.56	-0.6	-1.13	-0.1	0.85	1.53
Gga.10549.1.S1_s_at	XM_417330	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	-0.63	-0.68	-0.97	-0.15	0.88	1.55
Gga.718.3.S1_a_at	NM_205299	DMD	dystrophin	-0.59	-0.77	-0.96	-0.1	0.92	1.51
GgaAffx.11732.1.S1_at	NM_001006385	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	-1.18	-0.65	-0.22	-0.37	1.38	1.05
GgaAffx.2399.2.S1_at	XM_425066	TRPM1	transient receptor potential cation channel, subfamily M, member 1	-1.06	-0.44	-0.5	-0.48	1.48	1.01
GgaAffx.8725.1.S1_s_at	NM_001006385	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	-1.32	-0.44	-0.47	-0.13	1.25	1.11
GgaAffx.2399.3.S1_s_at	XM_425066	TRPM1	transient receptor potential cation channel, subfamily M, member 1	-0.99	-0.54	-0.58	-0.42	1.3	1.23
Gga.10157.2.S1_at	XM_416641	PROS1	protein 5 (alpha)	-1.14	-0.63	-0.44	-0.25	1.23	1.24

Gga.10157.2.S1_s_at	XM_416641	PROS1	protein S (alpha)	-1.21	-0.39	-0.51	-0.35	1.18	1.27
GgaAffx.21336.1.S1_s_at	NM_001012574	SH3BGR1	SH3 domain binding glutamic acid-rich protein like	-0.82	-1.02	-0.29	-0.35	1.16	1.32
GgaAffx.3525.1.S1_at	XM_426640	F3	coagulation factor III (thromboplastin, tissue factor)	-0.74	-1	-0.26	-0.5	1.24	1.27
GgaAffx.21613.1.S1_s_at	-	-	Finished cDNA, clone ChEST790114	-0.68	-0.83	-0.47	-0.57	1.11	1.44
Gga.4744.3.S1_a_at	NM_001006197	PMPCA	peptidase (mitochondrial processing) alpha	-0.7	-0.83	-0.48	-0.52	1.02	1.51
Gga.3374.1.S1_at	NM_204800	SPRY2	sprouty homolog 2 (Drosophila)	-0.9	-0.88	-0.32	-0.39	1.08	1.41
GgaAffx.13076.1.S1_at	NM_001079756	RCJMB04_31i7	leucine rich repeat containing 45	-0.88	-0.73	-0.43	-0.47	1.03	1.49
Gga.17574.1.S1_s_at	XM_414630	SEC24A	SEC24 related gene family, member A (S. cerevisiae)	-0.45	-0.63	-0.91	-0.56	1.43	1.11
Gga.13573.1.S1_at	XM_415249	DEPDC5	DEP domain containing 5	-0.6	-0.55	-0.9	-0.5	1.34	1.22
Gga.1644.1.S1_a_at	XM_414365	MGLL	monoglyceride lipase	-0.64	-0.61	-0.79	-0.52	1.44	1.12
Gga.2906.1.S1_at	-	-	Transcribed locus	-0.57	-0.64	-0.82	-0.54	1.37	1.2
Gga.1322.2.A1_at	XM_420664	PPP3CA	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	-0.27	-0.66	-0.85	-0.75	1.21	1.32
Gga.15268.1.S1_at	NM_001030600	RCJMB04_3k20	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6	-0.4	-0.74	-0.78	-0.64	1.19	1.36
Gga.16594.1.S1_at	-	-	Transcribed locus	-0.37	-0.8	-0.8	-0.59	1.28	1.27
Gga.8470.1.S1_at	-	-	Finished cDNA, clone ChEST752o10	-0.48	-0.61	-0.71	-0.74	1.07	1.48
Gga.2136.3.S1_at	XM_427270	LOC429716	similar to GTP-binding protein SB128	-0.45	-0.61	-0.69	-0.81	1.21	1.36
Gga.12227.1.S1_at	XM_001233786	LOC770452	hypothetical protein LOC770452	-0.65	-0.51	-0.58	-0.82	1.2	1.37
Gga.2644.1.S1_at	-	-	-	-0.61	-0.55	-0.73	-0.68	1.31	1.27
Gga.558.1.S1_at	-	-	Domesticus, peripheral Retina, embryonal stage E6-cDNA, PEV16/8	-0.68	-0.63	-0.67	-0.59	1.18	1.39
Gga.19655.1.S1_at	XM_415640	NOTUM	notum pectinacetyltransferase homolog (Drosophila)	-0.68	-0.64	-0.62	-0.64	1.26	1.32
Gga.3477.1.S1_at	NM_205319	FGFR2	fibroblast growth factor receptor 2	-0.66	-0.52	-0.7	-0.66	1.53	1.02
Gga.19242.1.S1_at	-	-	Finished cDNA, clone ChEST763a23	-0.64	-0.62	-0.7	-0.58	1.56	0.98
Gga.170.1.S1_at	NM_204336	WNT2B	wingless-type MMTV integration site family, member 2B	-0.64	-0.64	-0.64	-0.64	1.47	1.09
Gga.2974.1.S1_at	NM_204660	LOC395378	IPR328-like protein	-0.73	-0.69	-0.56	-0.57	1.47	1.09
Gga.5205.1.S1_at	XM_418037	BZRPL1	benzodiazapine receptor (peripheral)-like 1	-0.7	-0.63	-0.56	-0.62	1.62	0.88
Gga.3477.1.S2_at	NM_205319	FGFR2	fibroblast growth factor receptor 2	-0.65	-0.48	-0.57	-0.81	1.6	0.9
Gga.3154.1.S1_at	NM_204461	RHOQ	ras homolog gene family, member Q	-0.64	-0.51	-0.66	-0.7	1.61	0.91
GgaAffx.10806.1.S1_at	XM_416971	CLYBL	citrate lyase beta like	-0.67	-0.53	-0.52	-0.84	1.37	1.19
GgaAffx.25775.1.S1_at	NM_001030920	RCJMB04_3p2	BCL2-antagonist/killer 1	-0.85	-0.67	-0.39	-0.63	1.43	1.11
Gga.446.1.S1_at	XM_418106	ETV4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	-0.7	-0.8	-0.31	-0.72	1.44	1.09
Gga.17521.1.S1_s_at	NM_001006453	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	-0.71	-0.78	-0.22	-0.79	1.45	1.05
Gga.4320.1.S1_a_at	XM_001232006	LOC769341	hypothetical protein LOC769341	-0.78	-0.7	-0.28	-0.77	1.24	1.3
Gga.6191.1.S1_at	-	-	Transcribed locus	-0.56	-0.86	-0.37	-0.76	1.29	1.26
Gga.10296.1.S1_a_at	-	-	Finished cDNA, clone ChEST357f6	-0.66	-0.82	-0.45	-0.63	1.28	1.29
GgaAffx.3568.1.S1_at	XM_414180	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	-0.63	-0.75	-0.57	-0.62	1.27	1.31
Gga.661.1.S1_at	NM_001012767	FGF8	fibroblast growth factor 8 (androgen-induced)	-0.86	-0.9	-0.28	-0.45	1.45	1.04
GgaAffx.20528.1.S1_at	XM_416641	PROS1	protein S (alpha)	-0.88	-0.82	-0.48	-0.31	1.51	0.98

GgaAffx.3789.1.S1_at	XM_420222	GPC4	glypican 4	-0.95	-0.81	-0.42	-0.32	1.39	1.1
Gga.8095.1.S1_at	-	-	-	-0.66	-0.86	-0.59	-0.44	1.22	1.34
Gga.12955.1.S1_at	NM_001030920	RCJMB04_3p2	BCL2-antagonist/killer 1	-0.72	-0.86	-0.57	-0.41	1.24	1.31
Gga.9686.2.S1_a_at	XM_418296	RDH10	retinol dehydrogenase 10 (all-trans)	-0.73	-0.76	-0.63	-0.4	1.52	1.01
GgaAffx.20423.1.S1_at	-	-	Finished cDNA, clone ChEST770i7	-0.81	-0.75	-0.67	-0.29	1.4	1.13
Gga.2606.1.S1_at	-	-	Finished cDNA, clone ChEST380k16	-0.73	-0.74	-0.63	-0.47	1.41	1.15
Gga.2606.1.S1_x_at	-	-	Finished cDNA, clone ChEST380k16	-0.74	-0.74	-0.62	-0.47	1.31	1.26
Gga.9558.1.S1_at	XM_424808	RCL1	RNA terminal phosphate cyclase-like 1	-1.43	-0.62	-0.31	0.22	0.8	1.34
Gga.11904.1.S1_a_at	XM_001233489	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand	-1.32	-0.63	-0.38	0.01	1	1.31
Gga.5761.1.S1_at	NM_001031773	EFHD1	EF-hand domain family, member D1	-1.34	-0.77	-0.26	0.11	1.05	1.2
GgaAffx.408.1.S1_at	-	-	-	-1.24	-0.81	-0.26	-0.01	0.96	1.35
GgaAffx.24044.3.S1_s_at	XM_416363	YARS2	tyrosyl-tRNA synthetase 2, mitochondrial	-1.17	-0.59	-0.54	0.01	0.75	1.55
GgaAffx.24214.1.S1_at	XM_001232621	LOC426155	hypothetical gene supported by CR385555	-1.27	-0.57	-0.46	-0.01	0.87	1.45
GgaAffx.20849.1.S1_at	XM_001234219	LOC417139	Similar to pancreatitis-induced protein 49	-1.29	-0.5	-0.56	0	1.11	1.24
Gga.6597.1.S1_at	XM_419972	SDC1	syndecan 1	-1.17	-0.48	-0.72	0	1.01	1.37
Gga.5825.1.S1_at	-	-	Finished cDNA, clone ChEST190j19	-0.78	-1.19	-0.45	0.13	0.88	1.41
Gga.4108.4.S1_a_at	NM_205401	TPM1	tropomyosin 1 (alpha)	-1	-0.99	-0.59	0.3	1.11	1.16
Gga.4108.4.S1_x_at	NM_205401	TPM1	tropomyosin 1 (alpha)	-1.02	-0.96	-0.58	0.29	1.01	1.26
Gga.3754.2.S1_at	NM_001005848	HES1	hairy and enhancer of split 1, (Drosophila)	-0.93	-1.07	-0.5	0.18	1.21	1.11
Gga.13545.1.S1_at	XM_421940	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	-1.04	-1.11	-0.34	0.23	1.11	1.14
Gga.485.1.S1_a_at	NM_001001337	TEAD4	TEA domain family member 4	-1.11	-0.84	-0.43	-0.03	1.24	1.16
GgaAffx.11425.1.S1_s_at	NM_001031260	RCJMB04_1g10	uridine monophosphate synthetase	-1	-0.97	-0.41	-0.02	1.22	1.18
GgaAffx.24299.1.S1_at	XM_419129	CEP192	centrosomal protein 192kDa	-0.9	-0.95	-0.63	0.07	1.17	1.24
Gga.181.1.S1_at	NM_204203	PCBD2	pterin-4 alpha-carbinolamine dehydratase	-1.13	-0.77	-0.55	0.07	1.16	1.21
Gga.8360.1.S1_at	XM_001234979	ATOH8	Atonal homolog 8 (Drosophila)	-1	-0.79	-0.69	0.07	1.11	1.29
GgaAffx.11356.2.S1_s_at	XM_001234127	RCJMB04_15k6	similar to hypothetical protein FLJ13089	-1.11	-0.94	-0.33	0.13	0.82	1.44
Gga.5673.1.S1_at	-	-	Transcribed locus	-1.07	-0.94	-0.41	0.14	0.83	1.45
Gga.4108.5.S1_x_at	NM_205401	TPM1	tropomyosin 1 (alpha)	-1.04	-0.91	-0.52	0.23	0.75	1.49
Gga.4759.1.S1_at	XM_001232212	LOC769030	similar to multisynthetase complex p38 auxiliary component	-0.94	-0.96	-0.52	0.09	0.89	1.45
Gga.4108.1.S1_at	NM_205401	TPM1	tropomyosin 1 (alpha)	-1.02	-0.92	-0.52	0.17	0.84	1.45
GgaAffx.20738.1.S1_s_at	NM_205401	TPM1	tropomyosin 1 (alpha)	-1.05	-0.89	-0.51	0.14	0.88	1.43
Gga.4108.4.S1_s_at	NM_205401	TPM1	tropomyosin 1 (alpha)	-1.03	-0.86	-0.57	0.14	0.87	1.45
Gga.4108.1.S2_at	NM_205401	TPM1	tropomyosin 1 (alpha)	-1.02	-0.87	-0.37	-0.02	0.67	1.61
GgaAffx.20685.1.S1_at	-	-	Finished cDNA, clone ChEST663c11	-1	-1.05	-0.28	0.04	0.79	1.49
Gga.4704.2.S1_a_at	NM_001001469	GART	phosphoribosylglycinamide formyltransferase	-1.03	-1.06	-0.17	-0.07	1.01	1.32
Gga.4704.1.S1_at	NM_001001469	GART	phosphoribosylglycinamide formyltransferase	-1.04	-0.99	-0.28	-0.06	1.09	1.29
Gga.1377.1.S1_at	XM_417547	LOC419384	similar to hypothetical protein LOC127262	-1	-0.87	-0.45	-0.14	1.12	1.33
Gga.17132.1.S1_at	-	-	Finished cDNA, clone ChEST120n19	-1.07	-0.77	-0.49	-0.08	0.96	1.45
Gga.7101.1.S1_at	XM_421630	NOLC1	nucleolar and coiled-body phosphoprotein 1	-1.05	-0.74	-0.4	-0.27	0.99	1.46
Gga.11895.1.S1_at	XM_419411	LYPLAL1	lysophospholipase-like 1	-1.02	-0.61	-0.18	-0.51	0.61	1.71

Gga.19378.1.S1_at	–	–	Finished cDNA, clone ChEST761o6	–0.9	–0.7	–0.09	–0.65	0.65	1.69
Gga.9580.2.S1_a_at	XM_416402	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	–1.18	–0.87	0.19	–0.34	0.72	1.48
Gga.107.1.S1_at	NM_204220	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	–1.02	–0.77	–0.28	–0.34	0.81	1.59
Gga.1906.1.S2_at	NM_204654	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1	–1.18	–0.8	–0.09	–0.26	0.88	1.45
Gga.7606.1.S1_at	XM_419580	LOC421539	similar to Protein KIAA0133	–1.19	–0.79	–0.08	–0.26	0.85	1.47
GgaAffx.25111.1.S1_s_at	XM_416978	RANBP5	RAN binding protein 5	–0.86	–0.99	–0.08	–0.45	0.84	1.54
GgaAffx.21790.1.S1_s_at	NM_204586	GJA1	gap junction protein, alpha 1, 43kDa	–0.96	–0.83	0	–0.59	0.9	1.49
Gga.4772.1.S1_at	–	–	Finished cDNA, clone ChEST662i24	–1.08	–0.66	–0.07	–0.62	0.99	1.43
Gga.19230.1.S1_s_at	NM_001006525	EAF2	ELL associated factor 2	–1.48	–0.33	–0.01	–0.32	0.69	1.45
Gga.51.1.S1_at	NM_204646	BCHE	butyrylcholinesterase	–1.08	–0.31	–0.49	–0.55	0.87	1.56
GgaAffx.6997.2.S1_s_at	XM_422027	LOC424181	hypothetical LOC424181	–1.02	–0.42	–0.4	–0.57	0.76	1.65
Gga.2869.1.S1_at	NM_204555	KCNIP4	Kv channel interacting protein 4	–1.37	–0.24	–0.48	–0.26	1.03	1.31
Gga.8312.1.S1_s_at	XM_001232057	LOC415787	similar to LOC443703 protein /// similar to thioesterase B	–1.25	–0.13	–0.65	–0.26	0.76	1.53
Gga.15236.1.S1_at	–	–	Finished cDNA, clone ChEST411o13	–0.17	–1.07	–0.64	–0.56	1.47	0.96
Gga.11303.1.S1_at	–	–	Finished cDNA, clone ChEST982p8	–0.34	–1.35	–0.55	0.02	1.5	0.71
Gga.6941.1.S1_at	XM_001234452	LOC771156	Similar to guanine nucleotide exchange factor Lbc	–0.61	–1.28	–0.29	–0.21	1.28	1.11
Gga.1477.1.S1_at	–	–	Finished cDNA, clone ChEST662n13	–0.33	–1.19	–0.66	–0.21	1.45	0.94
Gga.13522.2.S1_a_at	–	–	Finished cDNA, clone ChEST398i23	–0.46	–1.28	–0.36	–0.28	1.41	0.98
Gga.4498.1.S1_s_at	NM_001030749	RCJMB04_1j13	ELK3, ETS-domain protein (SRF accessory protein 2)	–0.51	–1.17	–0.49	–0.26	1.43	1.01
GgaAffx.12581.1.S1_s_at	NM_001079725	RCJMB04_18j24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	–0.41	–1.25	–0.49	–0.26	1.43	0.97
Gga.13323.2.S1_s_at	NM_001006359	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	–0.54	–1.45	–0.27	0.05	0.88	1.33
Gga.4039.1.S1_s_at	NM_001006359	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	–0.42	–1.44	–0.32	–0.12	1.13	1.17
Gga.7514.1.S1_at	XR_027188	LOC428659	similar to carbamoyl-phosphate synthetase 2	–0.39	–1.5	–0.31	–0.04	1.1	1.13
GgaAffx.12756.1.S1_at	XM_001233434	BAG3	BCL2-associated athanogene 3	–0.34	–1.05	–0.64	–0.41	0.86	1.57
Gga.7126.2.S1_a_at	–	–	Transcribed locus, weakly similar to XP_001106440.1	–0.3	–1.1	–0.63	–0.41	0.95	1.49
Gga.6208.1.S1_at	–	–	Finished cDNA, clone ChEST37n24	–0.2	–1.12	–0.48	–0.64	1.04	1.4
Gga.19054.1.S1_at	–	–	Finished cDNA, clone ChEST1001h1	–0.29	–0.95	–0.6	–0.65	0.98	1.51
Gga.18082.1.S1_at	–	–	Finished cDNA, clone ChEST866d15	0	–1.13	–0.87	–0.36	1.11	1.26
Gga.5227.1.S1_at	–	–	Finished cDNA, clone ChEST313k1	–0.36	–1.07	–0.75	–0.29	1.1	1.37
Gga.6897.1.S1_at	–	–	Transcribed locus	–0.26	–0.99	–0.91	–0.28	1.01	1.43
Gga.11731.1.S1_at	XM_420309	AMOT	angiominin	–0.27	–0.98	–0.86	–0.38	1.3	1.18
GgaAffx.5942.1.S1_at	XM_001232291	FOXP2	forkhead box P2	–0.49	–1.05	–0.74	–0.21	1.3	1.18
Gga.7514.2.S1_at	XR_027188	LOC428659	similar to carbamoyl-phosphate synthetase 2	–0.39	–1.14	–0.58	–0.37	1.29	1.18
Gga.2289.2.S1_a_at	–	–	Transcribed locus	–0.37	–1.13	–0.97	0.2	1.05	1.23
GgaAffx.21588.1.S1_at	XR_027119	LOC426499	similar to importin beta subunit	–0.32	–1.29	–0.77	0.14	0.87	1.37
Gga.5191.1.S1_at	–	–	Transcribed locus	–0.17	–1.23	–0.97	0.2	0.82	1.35
GgaAffx.11856.1.S1_s_at	NM_001030601	RCJMB04_1j11	IMP (inosine monophosphate) dehydrogenase 2	–0.56	–1.15	–0.69	0.06	0.87	1.46

GgaAffx.7006.1.S1_s_at	XM_426585	FIGN	fidgetin	-0.53	-1.04	-0.76	0	0.74	1.59
GgaAffx.4625.1.S1_at	XM_421717	PPRC1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	-0.49	-1.27	-0.57	-0.02	0.98	1.37
Gga.110.1.S3_at	NM_204221	FZD7	frizzled homolog 7 (Drosophila)	-0.31	-1.23	-0.67	-0.11	0.82	1.5
Gga.1548.1.S1_at	-	-	Finished cDNA, clone ChEST321k8	-0.2	-1.27	-0.65	-0.23	0.98	1.38
GgaAffx.21208.1.S1_s_at	-	-	Finished cDNA, clone ChEST192f6	-0.62	-1.11	-0.47	-0.28	1.17	1.3
Gga.7271.1.S1_s_at	NM_001007917	MPP1	membrane protein, palmitoylated 1, 55kDa	-0.64	-1.19	-0.45	-0.13	1.06	1.35
Gga.17449.1.S1_at	-	-	Finished cDNA, clone ChEST266m15	-0.7	-1.09	-0.53	-0.12	1.11	1.34
Gga.9465.1.S1_at	NM_204473	OPTC	opticin	-0.68	-1.07	-0.73	0.09	1.27	1.12
GgaAffx.6693.1.S1_s_at	XM_419519	STRN	striatin, calmodulin binding protein	-0.66	-1.05	-0.79	0.16	1.01	1.34
Gga.5548.1.S1_at	XM_001233763	NPM3	nucleophosmin/nucleoplasmin, 3	-0.76	-1.06	-0.67	0.13	1.08	1.29
GgaAffx.22228.1.S1_at	XM_413904	PUNC	putative neuronal cell adhesion molecule	-0.74	-1.06	-0.71	0.16	1.04	1.31
Gga.13254.1.S1_at	-	-	Finished cDNA, clone ChEST361a6	-0.65	-0.8	-0.86	-0.14	1.53	0.92
Gga.7716.1.S1_at	-	-	Finished cDNA, clone ChEST419o13	-0.84	-0.83	-0.72	-0.07	1.42	1.04
Gga.4821.2.S1_s_at	NM_001006513	SLC19A1	solute carrier family 19 (folate transporter), member 1	-0.93	-0.88	-0.58	0.01	1.48	0.91
Gga.14853.1.S1_at	-	-	Finished cDNA, clone ChEST32g2	-0.75	-0.7	-1	0.05	1.4	0.99
Gga.5309.1.S1_at	XM_001235037	LOC771811	hypothetical protein LOC771811	-0.9	-0.73	-0.89	0.15	1.31	1.06
Gga.3667.1.S1_at	NM_204839	PDLIM4	PDZ and LIM domain 4	-0.8	-0.8	-0.94	0.28	1.43	0.84
Gga.15991.1.S1_at	XM_418603	LOC420501	similar to KIAA1217 protein	-0.86	-0.92	-0.77	0.23	1.35	0.97
GgaAffx.21035.1.S1_s_at	XM_422690	EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	-0.53	-0.86	-0.97	-0.1	1.21	1.25
Gga.207.1.S1_at	-	-	ZIC2 gene, partial 3'UTR	-0.37	-0.9	-1.17	0.12	1.2	1.11
GgaAffx.7403.3.S1_at	XM_416173	SLC5A8	solute carrier family 5 (iodide transporter), member 8	-0.36	-0.74	-1.27	0.05	1.14	1.18
GgaAffx.2399.1.S1_s_at	XM_425066	TRPM1	transient receptor potential cation channel, subfamily M, member 1	-1.07	-0.67	-0.01	-0.66	1.37	1.05
Gga.2461.1.S1_at	-	-	Transcribed locus	-0.99	-0.79	0.18	-0.73	1.41	0.92
Gga.11604.3.S1_at	-	-	-	-0.57	-1.48	0.15	-0.25	1.31	0.83
Gga.8127.1.S1_at	XM_415954	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	-0.88	-1.28	0.14	-0.2	1.3	0.92
Gga.19802.1.S1_at	-	-	Finished cDNA, clone ChEST733c10	-0.81	-1.24	-0.08	-0.22	1.26	1.08
Gga.3828.1.S1_at	NM_204557	EMB	embigin homolog (mouse)	-0.62	-1.06	0.09	-0.8	1.12	1.26
Gga.9134.1.S1_at	XM_419722	IFNGR1	interferon gamma receptor 1	-0.62	-0.78	0.13	-1.09	1.08	1.28
Gga.9268.1.S1_at	-	-	Finished cDNA, clone ChEST473f3	-0.55	-1.2	-0.08	-0.58	1.18	1.23
Gga.1855.1.S1_at	-	-	-	-0.49	-1.26	-0.26	-0.4	1.14	1.28
Gga.13519.1.S1_s_at	NM_001030579	RCJMB04_25m5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	-0.37	-1.14	0.05	-0.84	1.46	0.85
GgaAffx.12896.1.S1_at	NM_001030579	RCJMB04_25m5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	-0.4	-1.27	0.05	-0.7	1.31	1.01

The ten transcription factors we studied and the CMZ marker genes are labeled in yellow and green, respectively. The expression levels for each gene are shown as standardized values to have mean 0 and standard deviation 1 using dChip software.