



Supplementary Figure 1. The variation in transcript values between unrelated individuals versus discordant MZ twin pairs. Results are graphed as Δ CT comparing each transcript (*CLIC2* or *PIN4*) to β 2-microglobulin (B2M) control. The average healthy control for each transcript was the calibrator, set to 1.0. A population of 20 healthy females demonstrate the normal population range compared to the pool of their sisters with PBC (also unrelated within the population). The differences in Δ CT values for both transcripts is most apparent between MZ twin set samples, but the variation in the transcript appear to fall within the normal range for both health and PBC populations. A higher Δ CT value is indicative of lower transcript levels in this assay.

Supplementary Table 1. Primers and gene descriptions

#	\$ orien- tation	Gene	Alias	Gene Product	& Y homology	Accession	PRIMER 1	PRIMER2
1	+	UBQLN2		Ubiquilin 2		Hs.4552	CACCTAGTGAACCACGAGT	GGTTTAAAGACCCATTGCG
2	+	FLJ31204		Hypothetical protein with mRNA & EST support		Hs.57876	GGAGGACCTTCTGCAAGGTTA	TCCCAGCTTGTCTCTGCT
3	-	FAM9C		Family with sequence similarity 9, member C	Y homology by BLAST	Hs.276694	CACAGAGCCAAACCTAAAAC	GCCACAGCAGTTTCTATGATC
4		AW448933		EST		AW448933	GGGCATAAATCTTCAGGGC	GCAGCATTGTGATTACCAGCA
5	+	PDZK10		PDZ domain containing 10		Hs.12308	AGCTCTGATTTTGTGTCC	ACCTGTTGTAATGTC
6	+	REPS2	POB1	RALBP1 associated Eps domain containing 2		Hs.334168	ACGAATTGCATTGGAAAACC	TTTGTCTGCACAGCTTTTG
7	+	CDKL5	STK9	Cyclin-dependent kinase-like 5		Hs.50905	AAATGGCGGAGCCAGTAC	TGGCTACTGTCCATGTGCTC
8		Hs.435570		ESTs		Hs.435570	AGCATTACCTCCAAAATGTAG	ACCTGCCAAGCTCTCAC
9		Hs.446513		ESTs		Hs.446513	CAGCAAGGGCAATGGCTC	ACCCACATCTCAATATCCCAC
10	+	RS1		Retinoschisis (X-linked, juvenile) 1		Hs.149376	CAGAGTTGTGCAACCATTATCA	GTAGACAGTCCAGAAAGGCA
11	-	PHKA2		Phosphorylase kinase alpha 2		Hs.54941	TGCAATAGGGTCTCACCTGG	TCCTCAGCTCTATCTGTGGC
12		N53651		EST		N53651	AGACAGGGCTTCACTCTGTCA	ATGCATGGTGTGCTGTG
13		Hs.444490		ESTs		Hs.444490	TTGACAAGTTGAAAATGCCCC	TGGTCAACCAAGTCACTTCC
14	-	ACATE2	MT-ACT48	Mitochondrial Acyl-CoA Thioesterase		Hs.298885	TGTGAGGACACGAAGCAACTACT	GGCAGCGCATTTC
15	-	TAB3	NAP1	TAK1-binding protein 3	Y pseudogene	Hs.371135	TGGCACAAAGTTTATCTGTGC	CCATTCCAAAATCCATTGG
16		Hs.177986		ESTs		Hs.177986	TCTTTGGCTCAAGGATAATCC	CCTTTTGGCTCATTTCTGG
17	+	BCoR		BCL6 co-repressor	Y pseudogene	Hs.186424	CCGGTTTGATGCGTGA AAC	CGGCCAGGTAAAATGCTAT
18	-	SYP		Synaptophysin		Hs.75667	GGGTTCCAGACAGGGTG	CCGTTCCAAAGTCGTAGC
19	+	CCNB3		Cyclin B3		Hs.130310	CAAGGGAAACACCAAGGAGA	AGAATGGCCCTCATGTAC
20	-	LOC51248		Hypothetical protein with mRNA & EST support		Hs.11042	TTTCTGCCCGAACCATCA	CTATGTGCCATCCAGAGTCA
21	-	FLJ20105		Hypothetical protein with mRNA and EST support		Hs.89306	ATCCTTGGCCCATATTTC	CACAACCCCTGCTTTGGAAT
22		Hs.37464		ESTs		Hs.37464	ACATGCCCAAAGCGATTGTA	GACTGACAAAGTTGTCACAGTTAG
23	-	ABCB7		ABC transporter 7, sub-family B, member		Hs.370480	AAAGTGTGAGCCTGGAAAGC	AAAGCTTGTGCTCTGTTCC
24		Hs.182171		ESTs		Hs.182171	AATCACAAAACCTTCTCAACA	TCCTATTCAAGTGAGTCCAGATAGC
25	-	BTK		Bruton agammaglobulinemia tyrosine kinase		Hs.159494	AAGAGGTGCATTCCAGATG	TACTTCTCTTCCACAAGGCC
26	+	RPL36A		Ribosomal protein L36a		Hs.454495	AGAGCAACCCAATCTTGCC	TGCTTGGCACACTTCTTACA
27	-	GLA		Galactosidase, alpha		Hs.69089	ATGGTCTCAGAAGGCTGGAA	GCTTCAGTCTTGTGCTGTA
28	-	BEX1		Brain expressed, X-linked 1		Hs.334370	TTTTTTTGGCTTTTAAAGTGC	TTACGTGGAGTCTCCTATTACCA
29	+	FLJ21174		Hypothetical protein with mRNA & EST support		Hs.194329	GCTAAGGTGCAGGATGAGAA	GCCAGGGACACTACACATAA
30	+	NXT2	P15-2	NTF2-related export protein 2		Hs.25010	CAGTCTAGTCTTATACGAGTAG	AACTAGCAATAACTACATTGAAC
31	+	FLJ2679		Hypothetical protein with mRNA & EST support		Hs.5472	CATTATAACAGTAAGCCCATGG	CGCCTTTGGAATAAATGGT
32		Hs.425072		ESTs		Hs.425072	AAGGGGTTTCTCTACATATGG	GTCAATAAGTAGAGGGTGGG
33	-	AMMECR1		Protein of unknown function		Hs.433256	GCTCCAAAATGCTCCCAAGT	GGTATCTCTCATCCAGC
34		Hs.61094		ESTs		Hs.61094	AAGAGCATTGCAACATGCAG	CTCTATTTTCGTGACAAGCGC
35	+	PAK3		p21-activated kinase 3		Hs.390616	GCCTATCCTTCGAGTACAAA	TGGATTCAACACAGAGACGCA
36	-	LHFPL1		lipoma HMGIC fusion partner-like 1		Hs.297420	CAACTGGCAAGTCGTGCTAA	GTGGTAGGAACCCAGCTGTC
37	-	FLJ22965		Hypothetical protein with mRNA & EST support		Hs.248572	GTTAGAGAATTGCCATGAGG	GTCGTTCAATGCCTTCAGT
38	-	UPF3B		Homolog of UPF3 regulator of nonsense transcripts		Hs.103832	GCCTCTCTCTTCTCGAAGT	GCTGCTCAAGAAGCCAGAAA
39	+	MCTS1		Malignant T cell amplified sequence 1		Hs.102696	CTCGTTTTCCGGATAACGA	CTATATGTTTCATGGCATCGGACT
40	-	GPC4		Glypican 4		Hs.58367	GATCCCACTAATTTTACCG	CCATTTTGACCACTCTGC
41	+	PHF6		PHD finger protein 6		Hs.356501	AAGAGGCACGAAGCTGATGT	TGCTTCGGAGTTATGTGCAG
42	-	MOSPD1	DJ473B4	motile sperm domain containing 1		Hs.57549	TTCAGGTCAAATTTCTGTTATTT	TGTTTAAACCATGTGAGGAGCC
43	+	Hs.436787		Hypothetical protein with mRNA & EST support		Hs.436787	GACTTCCAATTCGAATGCA	CATGTTTGGCTTCCITTTCTT
44	-	CDR1		Cerebellar degeneration-related protein 1		Hs.446675	TGGTGGAAAGACCAAGTATGTC	AGACAATCCAGTCTTCCGG
45	+	SLITRK2	CXORF2	SLIT and NTRK-like family, member 2		Hs.320368	GTCTGTTTTGGGGCTGGTTT	CGTGAGTCTCAGTGTGTAAG
46		LOC347512~		Hypothetical protein with EST support		Hs.278078	TCTGAGGAGCCTTCTCACTCC	GGCTACTACTGGATGGAAAGG
47	+	ZNF185		Zinc finger protein 185		Hs.16622	AGTATGATTAGAAACACTAAGCA	TTCAAGGTATAGTCTGCC
48		M78874		EST		M78874	CCTGTACGTGTCAACTTTGA	GGACAGACATCAAACCGTA
49	+	23809		Hypothetical protein with mRNA & EST support		AF052117	TTAATAAGGTGTCAACGTTTAC	CAGACCTATTTTCACTG
50		Hs.122516		ESTs		Hs.122516	ATTCAGCAGAGCAATAAGAGGC	GGTGAAGGAAGATCAGAGAGG
51	+	MSL3L1		Male-specific lethal 3-like 1 (Drosophila)		Hs.371233	AAGATAGCACTTTAATTTGTAGC	CTGTATGTAAGTGGTTAATAAG
52	-	ASB11		Ankyrin repeat and SOCS box-containing 11		Hs.352183	AGGTCATCCACCTGTAAACC	GCCTTCACGGAGCAAGAGT
53	+	NHS		Nance-Horan syndrome protein		Hs.21470	CTCAGTGTTTCTCCTACTGTG	CTAATTCAGACCCGCTACCG
54	+	PHEX	PEX	Phosphate regulating neutral endopeptidase		Hs.72874	CACATTCACCAACAACAGC	CTGGCCTGTGCAACTGTCT
55	+	TIMP1		Tissue inhibitor of metalloproteinase 1		Hs.446641	AGATCAGCGCCAGAGAGA	CCCTGATGACGAGGTTCGGAA
56	+	MLL7	AFX 1	Trithorax homolog translocated in certain leukemias		Hs.512585	TGAAGACTGGCAGGAATGTG	TCTAGTCTATGATCGCGGC
57	-	PIN4		Parvulin		Hs.11774	TGTAAGAGAGGGTGGGGCTA	TCCCTGAAGATGGTTTCTG
58	+	COX7B		Cytochrome c oxidase subunit VIIb		Hs.432170	AGCCACCAAGAACTACACC	TTTGGGGTAACTCTGCAAC
59	-	RAB40A		RAS oncogene family member		Hs.27453	TTATTTCTTCTTACTGAAATGGC	GGAGGAAAACGCCAAAGATA
60	-	COL4A6		Collagen, type IV, alpha 6		Hs.408	CTGCCTCATGTCAACATAGC	TGAAGCTGCACAGTGTGGT
61	-	FLJ36576		Hypothetical protein with mRNA & EST support		Hs.442518	TCTTCAGCATAAATGGAGATGG	CAATCACAATACGCCCTGT

62	+	UTP14A	SDCCAG16	U3 small nucleolar ribonucleoprotein, homolog A		Hs.271926	TGCTCATCAGGTACGAGTGC	TGACGTGTGGTGATTGCTTT
63	-	COVA1	APK1	Cytosolic ovarian carcinoma antigen 1		Hs.155185	CAACCGTCGTAGCGCCAATA	CTTGTTTGCACCACACGCTG
64	-	PLAC1		Placenta-specific 1		Hs.13026	AAAAGGCTTAATTCATGAAGTTGC	TCCTAGTTTGGGGTCTC
65	-	LOC159090		Hypothetical protein with mRNA & EST support		Hs.404706	CAAGCAAGAGAATTTCTGATCA	TCTTAGTGCCCTAAAACACCC
66	+	MAGEA8		Melanoma antigen, family A, 8		Hs.37109	TCAGGAAGCTGCTCAACC	CTCCTGTCCCAAAGCCTCTT
67	+	ABCD1		ATP-binding cassette D1		Hs.159546	GTCACTTCAAGAGGCCAGG	ACACCACCGTACGTGGGC
68	+	C6.1A		C6.1A gene		Hs.458371	CCCAGCAGTTGTGCTCCT	TTCAITCCAGAGCAGTATTTCCA
69	-	CLIC2		Chloride intracellular channel 2		Hs.54570	CCAATTGATCTTGACTCTTCC	TCACCCTGCTCCTTAGAAAACA
70	-	SH3KBP1	CIN85	SH3-domain kinase binding protein 1		Hs.153260	CCAGTCCCTCACATCTTCA	CAGCTGTTCCTCAAAGAGGAT
71	+	USP11	UHX	Ubiquitin specific protease 11		Hs.171501	GGTATAAGCAGTGGGAGGCA	GTGCGCAATACTAGGCCAAT
72	+	WAS		Wiskott-Aldrich syndrome		Hs.2157	ACTTGCTGCCCTGTGCTC	AGGCAAGGATAACAGCATTG
73	+	XEDAR		Ectodysplasin A2 isoform receptor		Hs.302017	CTCCTCGCAGGTACAAAAGC	ACTGGAAGGCACATTGAACC
74	+	MAGEE1		Melanoma antigen, family E, 1		Hs.8453	TCATACAATAGCAGACAGAAAGGG	CTTGAAGCTTGAAAAAATTTCG
75	+	ATP7A		ATPase, Cu++ transporting, alpha polypeptide		Hs.606	GACACAGCATTCATGATGTTACC	TGTTGTAAACCTCACTGCTTACC
76	-	Hs.445729		EST		Hs.445729	TAGCCATTTTCATTTGACACAA	CGTGGTGGTTTGTGTTAGGA
77	-	NXF3		Nuclear RNA export factor 3		Hs.60386	GGATCCTGGGGTAACAGG	GGATCTGTAACAAACAAAGCC
78	+	LOC340544		Hypothetical protein with mRNA & EST support		Hs.441076	ACTTCAAAAATACACAAAAGTAGG	CTGGGAATGATAAAAATATGC
79	+	PLS3		plastin 3, T isoform		Hs.430166	GCAGACAGTTTGTACCCT	GTTACCGAAGGTTCTTTCTTCC
80	-	CUL4B	KIAA0695	Cullin 4B		Hs.155976	GTTAAGGAGAACACTGCAGTC	CTGGTTGTACACTTCTGA AAC
81		Hs.108029		ESTs		Hs.108029	TACTAAGGATAATTTGGTGGTCTG	GATAAAGGTACATGTTCTGCATTCT
82	+	CLCN4		Chloride channel 4		Hs.417091	ATAGTAGAGAATTTAATCCT	ACACCAACACTAACATTAAG
83		Hs.157695		ESTs		Hs.157695	TTCCAGGTACACAACCTCACAGG	TGTGGGATCACAGTCTTCA
84	-	MORF4L2		Mortality factor 4 like 2		Hs.411358	AATATCAACTTTTCCAGAAAACCG	ATTGTTTCATGGTTTTTGATTTG
85	+	MYCL2		v-myc myelocytomatosis viral oncogene homolog 2		Hs.72931	TCCTCATCTGTA AAACTGGTGG	CCTTGGCGTATGACAACT
86	-	BRS3		Bombesin-like receptor 3		Hs.121484	TGCGTAAACCCCTTTGCG	TACACCAGTGAACGAGGTC
87	-	ARD1	TE2	N-acetyltransferase		Hs.433291	GACCTAATGAACATGCAGCACTG	GCACCCAGCACCACGCTGCTT
88	+	CXORF12	ITBA1	Protein of unknown function		Hs.23119	CGGAAATCACGAAATCACGG	GTAGTGCTCATAGCCCCTAT
89	+	FLJ23018		Hypothetical protein with mRNA & EST support		Hs.169078	ATCTAAAGCAGAGAACCATGTGC	CAAGAGCCTTTGCTTCTGGA
90	+	GRPR		Gastrin releasing peptide receptor		Hs.73883	CCAGAGTGTTCACATCTTCC	CACCTACACACTCAGGAG
91	-	CHM	REP1	Choroideremia		Hs.416244	TCAGCCTGTTGACTGCA	ACAGTCCAGCAGAGGAA
92		HEIL2		Hypothetical protein with mRNA & EST support		AB027122	GGGATCATTTTCAGCAGCAT	CGGAAGGGACTGAGAGTGAG
93	-	HCFC1		host cell factor C1		Hs.83634	AGAAGAGGTGGGAGCAGAAA	:GAAAGCGCTCCCTCTTGG
94	+	RIBC1	FLJ32783	RIB43A domain with coiled-coils 1		Hs.351743	AAGAGTTCAGAAAACCTGCCG	GCTGCTTCCCTTTGGTATC
95	-	Hs.86443		mRNA of unknown function		Hs.86443	AGCATGGAGATGCATTTTCC	TTGCTTGCTGTTGAAAGCC
96	+	TBL1X		Transducin (beta) like 1	Y orthologue	Hs.76536	TGTAAGGGTCTGCTTTGTTCT	TCTTCAAAGAGCGTGAGGTT
97	-	GPR143	OA1	G protein-coupled receptor 143	Y pseudogene	Hs.74124	ACTGCCGAAGTGTAGCGG	TGGACTTACACTTACTTTACAGCC
98	-	SMC1L1		Structural maintenance of chromosomes 1-like 1		Hs.211602	AGGCATAGTGATGCTCCTGT	CGATGTTTTGAGATCTGTGC
99		Hs.258828		ESTs		Hs.258828	AATGAATAGCACCCAGCCAC	CCAGACAAGTTGCTCTGCAA
100	-	FLJ38564		Hypothetical protein with mRNA & EST support		Hs.447808	ACTCTTTAGGACTTTAGACAAAAGGC	GAAGTAGTTTCTGAGATTGTCAGCC
101		NAP1L3	NPL	Nucleosome assembly protein 1-like 3		Hs.21365	GTGAAGCAGATTCATACAGCC	TCACAGCTACAGTCTAACAGA
102	+	ZD89B07		full-length mRNA of unknown function		Hs.58670	AGGGGAGAGGAATAGGCAGG	ACAGCCAGACCAAAGGGCTA
103	-	SYTL4		Synaptotagmin-like 4		Hs.376981	AGTTACAGCCCGGATCC	AACTGATTTCTATAAGCACACTGG
104		Hs.527551~		ESTs		Hs.527551	GCATAGGACCAAGGCAGAAA	TTAAAGGTGCGTTGACGTGG
105	-	ARHGAP4		Rho GTPase activating protein 4		Hs.3109	TAGACACGACCCCAAGCCAC	CTGGACAGGGCTGGAGAGAAG
106	-	RENBP		Renin-binding protein		Hs.158331	TGCATTCGGAAAGGCAC	TGGGGCAGAAAGTATACGCATC
107		Hs.404298		ESTs		Hs.404298	AGGTTTTAGTGAGCCCTACTTC	CAATTAAGAGAGCTTTGGAGAG
108	+	ARMCX4		Armadillo repeat containing, X-linked 4		Hs.546509	GGTGTTCATAAAATGGTCCAGC	TTGCACCTCTGGAAGTAATGCA
109	-	FLJ11016		Hypothetical protein with mRNA & EST support		Hs.139053	TGTACAAGCCCTTTGGGAAG	TCAGGATTTGCCCTCAGTTT
110		Hs.333016		ESTs		Hs.333016	CTAGCGTTAGACTTTGGAAGG	ACTGTCTAGGATTTTGAGAGG
111	+	DOCK11		Dedicator of cytokinesis 11		Hs.107513	CTTTCCCGCAGAAGTCAAAG	CGCAGCCTCTGAAAATCTC
112	+	LOC203427	FLJ33985	Hypothetical protein with mRNA & EST support		Hs.294799	CGGCACCTGAACATTTAGGAA	GCGGATATCATGGGCATAGT
113	+	HSU24186	DIAPH2	Replication protein A 34 kd subunit homolog Rpa4		Hs.226483	TGGGTTGCACCTCTTCCCT	CACCTCCAACTGGCCATAAA
114		Hs.271686		ESTs		Hs.271686	GGTCTGAGGACTGAAATCTGA	TTCTGATGTTGGTCAGGT
115	+	WBP5		WW domain binding protein 1		Hs.15984	GA AAAATCATTATAATCCC	GGCTAAGTAATATGTGAATA
116	-	TRPC5		Transient receptor potential channel 5		Hs.247868	CACCTATTTTACTTTTCTGGCC	CATTAGCAGAAAGTTTCTCTCA
117	+	TNFSF5		Tumor necrosis factor superfamily member 5		Hs.652	CACCCCTGTTAACTGCCTA	CTGGATGTCTGCATCAGTGG
118	-	ITM2A		Integral membrane protein 2A		Hs.17109	CAAGGCACTCTATCTGTTGCC	ACTGGCAGTGGCAGATATC
119	+	SRPX2		sushi-repeat-containing protein, X-linked 2		Hs.306339	ATCTCCATCTTCCATGCAG	ACTGAGCTTGCCACTTGGTT
120	+	KIAA1817	CAG24	Protein of unknown function		Hs.157549	GTCCACAGCCCGTAACCT	CTCATAACAGTCCGCGAAG
121	+	MDS031		Hematopoietic stem/progenitor cell protein		Hs.110853	AGTTTTACATTAGGCAGATT	TGGATATGCTCTGTGAATGA
122		AA348446		ESTs	Y homology by BLAST	Hs.546242	AGGGATGGAACAAAAGACCC	ATCTATGAAAATCCTCTGCTG
123	-	DKFZP564I1922		Adican	Y pseudogene	Hs.72157	AGCAGCCACTTAGACCAGA	TGAAAGCTGTGCTCAGAGGA
124	-	PRKX		Protein kinase, X-linked	Y orthologue	Hs.147996	CTTACGGCATAAGGCATCTC	TTCAAACACTTCTACAGTGTGG
125		Hs.431292		ESTs		Hs.431292	CCTGCAATTTAAAAAATGTT	CGTGAACATGACATGAAGACA

Linearized Values

Weakest Normalized Calibrator

Twin ID	23809	AA 348446	ABCB7	ABCD1	ACATE2	AMME CR1	ARD1	ARH GAP4
ID1	5.278	4.228	2.313	9.580	9.714	3.074	3.531	4.469
ID2	5.242	2.445	2.908	1.932	11.551	2.732	2.129	3.458
ID52	3.182	3.580	6.916	3.580	20.393	8.634	4.595	4.659
ID9	2.056	3.655	2.549	1.141	27.096	2.908	3.095	2.848
ID54	10.928	11.236	5.352	6.498	10.339	4.028	5.063	6.821
ID55	3.630	-	2.362	3.340	16.679	3.010	2.770	4.891
ID18	1.079	-	1.301	-	7.781	1.729	2.585	2.445
ID19	-	2.313	2.085	1.569	8.225	2.129	2.928	2.235
ID24	1.625	-	1.892	-	9.254	2.868	3.364	3.138
ID57	4.595	-	4.757	-	20.678	2.445	5.502	3.482
Twin ID	ASB11	ATP7A	AW 448933	BCoR	BEX1	BRS3	BTK	C6.1A
ID1	-	60.548	7.516	3.864	7.111	-	2.676	4.170
ID2	-	63.119	--	1.932	3.074	-	2.158	2.462
ID52	-	120.259	18.765	7.013	8.694	-	3.732	4.891
ID9	5.242	70.522	6.498	2.479	15.455	-	2.532	2.603
ID54	-	135.298	-	3.681	-	-	4.563	3.317
ID55	14.221	57.680	11.472	2.250	-	-	3.095	2.694
ID18	-	128.890	-	1.376	-	-	1.693	1.000
ID19	-	--	10.196	1.000	3.972	-	2.346	1.815
ID24	-	140.070	8.056	2.514	-	-	1.790	3.918
ID57	-	81.008	-	4.790	-	-	3.434	4.257
Twin ID	CCNB3	CDKL5	CDR1	CHM	CLCN4	CLIC2	COL4A6	COVA1
ID1	6.774	5.938	6.190	3.364	3.117	5.579	-	4.000
ID2	--	5.205	1.866	2.809	2.266	3.458	-	2.412
ID52	6.453	6.821	29.446	4.317	3.182	5.502	-	7.013
ID9	4.500	1.932	11.794	2.828	1.729	2.732	-	2.990
ID54	-	2.099	6.727	3.605	6.681	3.918	-	3.272
ID55	14.026	2.462	7.062	2.445	4.500	1.879	-	4.170
ID18	4.408	3.458	3.095	1.790	1.110	--	-	1.214
ID19	5.426	2.158	3.605	1.986	10.853	2.114	-	2.129
ID24	1.385	6.453	3.340	3.531	1.197	6.727	-	2.676
ID57	-	-	6.681	5.816	1.197	8.168	-	1.840
Twin ID	COX7B	CUL4B	CXORF 12	DKFZP 564I1922	DOCK11	FAM9C	FLJ 11016	FLJ 20105
ID1	3.117	3.010	22.316	-	22.162	16.000	14.825	2.585
ID2	2.028	1.705	19.027	-	7.621	11.959	9.063	3.272
ID52	2.639	3.655	59.302	-	30.696	17.030	22.316	3.434
ID9	1.717	2.114	19.293	-	13.269	12.295	11.314	2.532

ID54	1.853	3.031	24.933	-	6.869	41.355	14.221	4.659
ID55	1.464	2.479	31.125	-	7.516	5.502	11.632	1.580
ID18	1.434	1.125	10.853	-	9.714	8.056	--	2.042
ID19	-	5.540	5.776	-	4.857	7.362	5.242	1.240
ID24	2.297	1.464	7.311	-	2.949	8.340	12.729	1.945
ID57	3.117	3.891	-	-	50.213	213.783	38.586	9.126
Twin ID	FLJ 21174	FLJ 22679	FLJ 22965	FLJ 23018	FLJ 31204	FLJ 36576	FLJ 38564	GLA
ID1	6.233	9.580	2.848	5.618	5.856	3.580	3.434	2.514
ID2	6.233	8.225	1.972	4.757	3.811	2.532	4.857	2.713
ID52	14.221	5.979	2.479	8.515	5.897	2.497	6.453	3.732
ID9	4.469	3.182	2.173	1.959	4.112	1.670	2.828	3.681
ID54	7.413	17.509	6.320	6.320	5.134	4.347	6.190	4.595
ID55	5.897	9.714	1.778	1.945	1.945	1.670	3.918	2.639
ID18	1.602	7.362	--	1.670	1.647	1.117	2.346	2.028
ID19	2.056	7.062	1.310	2.204	1.495	2.250	5.816	2.282
ID24	6.774	14.825	1.682	--	3.053	2.297	4.891	2.514
ID57	26.723	12.295	3.891	33.591	11.876	4.563	1.705	4.170
Twin ID	GPC4	GPR143	GRPR	HCFC1	HEIL2	Hs. 108029	Hs. 122516	Hs. 157695
ID1	31.559	4.595	3.506	8.398	4.408	2.158	1.526	10.196
ID2	27.474	3.272	3.317	5.028	3.074	2.235	-	6.916
ID52	8.515	-	4.500	22.162	2.395	3.182	7.516	9.000
ID9	5.579	4.627	3.364	4.500	3.010	2.219	3.506	5.579
ID54	32.900	-	3.434	2.567	5.776	3.227	2.014	13.269
ID55	56.493	-	2.514	4.000	2.158	2.129	8.574	5.352
ID18	3.918	2.158	--	1.157	1.197	2.297	8.000	2.828
ID19	4.257	-	1.803	1.057	2.770	1.414	-	2.585
ID24	3.706	-	1.485	3.294	2.235	2.114	18.765	6.320
ID57	33.591	-	3.387	4.691	4.724	1.705	-	23.918
Twin ID	Hs. 177986	Hs. 182171	Hs. 258828	Hs. 37464	Hs. 404298	Hs. 425072	Hs. 431292	Hs. 435570
ID1	5.242	2.789	9.580	2.445	4.500	11.713	-	10.126
ID2	7.621	2.532	13.454	2.071	3.074	6.821	-	7.835
ID52	3.945	4.377	12.553	5.134	3.117	3.160	-	8.398
ID9	3.706	2.173	15.455	2.789	2.751	5.540	-	5.169
ID54	56.103	3.630	22.943	4.532	5.502	12.996	-	12.295
ID55	19.160	2.514	22.627	2.479	2.099	28.443	-	10.483
ID18	24.933	1.647	14.420	1.338	1.424	13.737	-	1.972
ID19	19.835	1.853	5.426	2.250	2.694	9.849	-	3.317
ID24	5.618	2.282	7.311	1.765	2.235	23.264	-	5.776
ID57	-	6.589	12.295	7.260	7.013	-	-	8.398
Twin ID	Hs. 436787	Hs. 444490	Hs. 445729	Hs. 446513	Hs. 527551	Hs. 61094	Hs. 86443	HSU 24186

ID1	2.868	-	2.250	2.585	2.250	-	3.053	3.340
ID2	2.428	2.809	2.789	18.252	1.613	-	--	2.497
ID52	3.138	-	6.774	4.757	4.857	-	-	2.071
ID9	2.099	-	2.639	10.629	1.778	-	3.227	2.412
ID54	4.959	4.084	4.823	-	4.317	-	-	7.160
ID55	1.485	-	3.074	31.779	2.297	-	-	1.558
ID18	1.240	35.506	1.613	-	1.376	-	-	2.532
ID19	1.231	-	-	5.579	1.424	-	-	2.144
ID24	1.853	-	1.613	6.916	1.558	-	-	3.340
ID57	6.727	-	3.605	-	4.438	-	-	2.969
Twin ID	ITM2A	KIAA 1817	LHFPL1	LOC 159090	LOC 203427	LOC 340544	LOC 347512	LOC 51248
ID1	5.856	10.411	11.392	3.160	4.317	3.605	-	4.377
ID2	3.249	37.014	9.318	2.144	6.498	1.892	-	4.724
ID52	12.042	109.896	15.889	3.010	10.056	2.585	-	11.794
ID9	4.659	13.929	6.635	2.603	7.260	1.778	-	3.972
ID54	6.233	66.257	7.413	2.173	23.918	2.949	-	7.413
ID55	5.063	24.251	22.162	2.789	-	--	-	3.506
ID18	3.732	24.251	5.657	2.129	-	1.050	-	2.603
ID19	4.595	30.484	10.056	1.659	-	1.157	-	2.639
ID24	3.482	1.569	8.398	2.621	1.892	2.362	-	3.117
ID57	4.857	-	-	2.848	-	7.413	-	6.727
Twin ID	M78874	MAGEA8	MAGEE1	MCTS1	MDS031	MLL7	MORF4L2	MOSPD1
ID1	-	18.896	71.506	3.272	2.621	2.639	6.821	31.125
ID2	-	10.703	48.503	2.412	3.010	1.815	17.268	36.758
ID52	--	22.943	162.017	3.630	3.160	4.823	23.752	56.886
ID9	-	7.568	44.942	2.514	1.778	2.713	12.126	51.625
ID54	-	27.284	85.627	4.500	4.000	3.294	12.295	49.867
ID55	-	-	95.010	1.591	1.248	1.197	14.520	29.041
ID18	-	-	34.060	1.266	1.647	4.595	8.398	22.471
ID19	-	15.137	--	1.803	1.840	-	2.567	25.281
ID24	-	-	39.671	1.945	1.892	4.532	1.000	15.562
ID57	-	-	62.250	5.028	7.674	4.823	17.753	53.076
Twin ID	MSL3L1	MYCL2	N53651	NAP1L3	NHS	NXF3	NXT2	PAK3
ID1	27.474	1.853	22.627	5.134	5.856	10.196	2.144	9.580
ID2	26.909	2.000	14.420	4.438	11.158	3.758	2.071	5.389
ID52	38.319	-	11.713	9.254	14.723	-	6.869	14.825
ID9	23.752	-	10.196	4.563	7.413	12.996	1.959	5.897
ID54	36.504	-	25.813	8.815	20.678	7.013	4.170	16.912
ID55	22.943	-	14.420	3.506	6.727	8.754	3.945	-
ID18	12.126	-	6.869	4.563	4.438	-	2.189	7.727

ID19	-	-	9.580	1.959	-	--	2.014	5.897
ID24	2.428	-	11.551	4.757	5.979	-	1.434	5.169
ID57	32.672	-	20.678	-	-	-	1.189	-
Twin ID	PDZK10	PHEX	PHF6	PHKA2	PIN4	PLAC1	PLS3	PRKX
ID1	-	1.079	7.111	3.074	16.111	-	4.993	2.990
ID2	-	-	5.696	2.751	21.112	-	3.605	3.387
ID52	-	5.352	16.450	2.990	22.471	-	12.641	9.000
ID9	3.758	1.181	6.148	1.840	8.112	-	5.205	4.000
ID54	4.563	10.483	8.815	4.028	39.397	-	40.504	4.959
ID55	-	8.000	6.916	1.972	17.268	-	5.205	3.811
ID18	-	-	5.098	--	10.056	-	18.765	1.986
ID19	-	-	3.945	1.424	-	-	2610.300	1.682
ID24	-	5.540	4.724	2.219	7.210	-	4.959	2.809
ID57	-	61.820	8.754	3.458	5.856	-	-	2.888
Twin ID	RAB40A	RENBP	REPS2	RIBC1	RPL36A	RS1	SH3KBP1	SLITRK2
ID1	4.959	3.160	108.383	3.434	3.555	--	3.117	-
ID2	6.727	1.613	116.162	6.727	2.603	4.170	2.158	-
ID52	5.657	1.866	121.938	2.428	7.062	-	4.257	-
ID9	11.876	1.729	113.772	3.117	2.888	-	2.549	-
ID54	35.753	3.182	205.074	9.448	3.630	-	3.249	-
ID55	12.641	2.144	124.500	--	1.790	-	2.809	-
ID18	12.126	1.035	156.498	4.469	2.204	-	1.035	-
ID19	-	--	93.701	4.056	2.266	-	1.516	-
ID24	10.339	3.555	168.897	1.173	3.758	-	2.219	-
ID57	-	5.897	198.088	-	8.877	-	3.317	-
Twin ID	SMC1L1	SRPX2	SYP	SYTL4	TAB3	TBL1X	TIMP1	TNFRSF5
ID1	4.532	1.014	-	2.250	2.297	2.751	3.531	7.945
ID2	3.160	3.434	-	4.056	1.717	1.376	2.412	5.464
ID52	5.816	2.129	-	4.000	5.205	2.868	2.639	19.427
ID9	3.506	-	-	3.095	2.282	2.000	1.959	7.945
ID54	2.639	-	-	10.196	2.532	3.204	4.056	5.315
ID55	4.724	-	-	5.205	1.434	2.395	4.112	5.856
ID18	--	-	-	1.636	--	1.231	1.464	1.892
ID19	1.157	2.378	-	2.189	1.347	1.021	-	3.732
ID24	2.445	-	-	--	5.242	3.784	1.972	2.713
ID57	8.938	-	-	6.681	3.364	2.694	2.479	13.737
Twin ID	TRPC5	UBQLN2	UPF3B	USP11	UTP14A	WAS	WBP5	XEDAR
ID1	-	5.315	2.990	3.031	3.580	3.706	3.160	4.993
ID2	-	3.053	2.514	2.532	3.249	2.621	4.257	2.549
ID52	-	4.823	3.272	6.916	5.618	2.282	2.694	2.657

ID9	-	2.603	2.189	2.313	3.317	2.235	2.949	1.102
ID54	-	2.949	3.811	2.969	3.706	2.657	5.389	2.099
ID55	-	2.549	2.028	3.031	3.482	2.282	3.482	-
ID18	-	1.042	1.000	1.404	1.347	1.035	3.732	-
ID19	-	1.347	2.235	7.210	3.204	1.434	1.828	107.635
ID24	-	2.868	2.751	3.227	3.249	2.888	1.149	-
ID57	-	2.428	6.105	2.266	6.916	4.563	5.736	-
Twin ID	ZD89B07	ZNF185						
ID1	-	7.890						
ID2	-	6.727						
ID52	-	9.918						
ID9	-	7.210						
ID54	-	14.026						
ID55	-	11.236						
ID18	-	7.674						
ID19	-	6.233						
ID24	-	1.602						
ID57	-	12.126						