

**Title: Genes with significantly altered expression by at least 1.4-fold in either MCF-7 or HepG2 cells after exposure to BPDE.**

Description: The data presented in each sheet are genes with expression significantly (Student's one-sample t-test p-value < 0.05) up-regulated (ratio > 1.4) or down-regulated (ratio < 0.714) (i.e. genes with a 1.4-fold change) in either MCF-7 (1081 genes) or HepG2 cells (95 genes) after exposure to 0.5 and 1  $\mu$ M BPDE for up to 24 h. The 45 expression changes common to both MCF-7 and HepG2 cells are shaded.

**MCF7 BPDE****Time (h)****Concentration (uM)**

<b>IMAGE Clone ID</b>	<b>Gene Symbol</b>	<b>Genbank</b>
214006		
714205	COMMD4	AK124968
812965	MYC	NM_002467
1461138	HIST1H4C	CD048335
21892	IARS	NM_013417
814615	MTHFD2	BC015062
22107	KIAA0280	D87470
704905	RAP1A	AK094737
220147		
725680	TFAP2C	NM_003222
278496	TRIM33	AF119043
53243	ASNS	NM_133436
33689	YARS	AK125213
1473211	HIST1H2BN	CA310244
789091	HIST1H2AC	CR608156
268891	HIST1H3D	BQ051491
66317	HIST1H1C	BQ940876
1842170	HIST1H4B	BX102654
1524557	HIST1H3E	BG676315
129467	HIST1H2BJ	BF983642
22379	CD59	NM_203330
381166	MYST4	AF217500
197520	NCOA3	NM_181659
213136	BTG2	NM_006763
261481		
23133	ZBTB5	NM_014872
824117	VRK2	BC036434
760231	USP9X	NM_004652
220054	HIPK1	NM_198268
814595	PRKCBP1	NM_183047
32234	XPOT	NM_007235
29022	RAI17	NM_020338
843158	NCOA3	NM_181659
2062620	TOP2A	NM_001067
53061	SLC22A15	BC026358
252272	CGGBP1	BC052980
1470048	LY6E	BF969813
220395	ARL6IP2	AK026946
41694	SNAPC3	CR624760
884655	GARS	NM_002047
179694	PTRF	NM_012232
251019	CDH1	NM_004360
122293		AA704763
361565	GLUD1	NM_005271
22170	HDHD1A	NM_012080
21790	WAC	AK091453
122933	NSUN3	NM_022072
271416	SP1	NM_138473

130242	CDK7	NM_001799
21899	SRPK2	U88666
43021	HARS	AK000498
417223	LOC399715	AK128185
781366	RBM8A	AK075009
143567	EIF2S3	NM_001415
362483	SPTBN1	NM_003128
726157	MGC10986	NM_030576
259364	XPO1	AL833550
203184	ATF1	CR624071
757787	KIAA1731	XM_374922
147924	SYPL	AK128299
113515	UBA2	AK124730
502333	NCOA3	NM_181659
39233	SLC38A2	NM_018976
592243	TCN1	NM_001062
417226	MYC	NM_002467
744047	PLK1	NM_005030
1493527	ASNS	NM_133436
376772	RPS27L	BC047648
856454	SLC3A2	AK025584
731750	TAF6L	BC008785
854668	CDKN1B	NM_004064
2163351	CASP2	NM_032982
129865	STK6	NM_198433
37947	OCIAD1	AK123529
755024	LOC284361	NM_175063
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34015		
1410444	AREG	AK023449
1645564	GSG1	AK075322
41477	TCEA2	BC050623
1870184	MGC14798	AL833427
23137	CRK	BC008506
245015	UBAP2L	NM_014847
240200	CDC10	BX648365
825013	ANP32B	BF683719
298362		
1646105	APG10L	NM_031482
325224	TAF9	BC033320
853938	DNCL1	BG165659
262920	H41	AK096865
40424	ATIC	CR606023
358125	EDD	NM_015902
344430	BMP7	AK094784
825312	ATP5J	CF993935
321706	KIAA1467	XM_370682
259649	IER3	BM994398

1693122	MGC45866	AK123612
823590	SIAT7B	BC038114
1472643	RPS15A	AK127316
46207	FLJ20366	AB195679
686172	DLG7	NM_014750
1641903	C10ORF53	AK091773
757143	C19ORF32	BC008201
757440	IL10RA	BC028082
364830	PARP11	BX648417
789182	PCNA	BE896331
162775	DDX5	BX571764
211482	UQCRC2	AK094006
768370		
755046		
42300	LOC93622	BC040997
30449	PLCB4	NM_000933
246474	RPL10	NM_006013
321693	TUBD1	NM_016261
814798	ALDH1A3	AF198444
1183990	GSK3B	BX640779
221551	FLJ10980	BC040548
281103	ASH1L	NM_018489
148379	IGF1R	BX640783
1704574	THEA	AB014607
788205	SOX4	NM_003107
773137	STK24	BC035578
293576	TARDBP	NM_007375
853570	SLC25A6	CR593822
166273	CDKN1A	NM_078467
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814306	TPD52	NM_005079
34849	EEF2	NM_001961
221476		BQ029067
471164	GARS	NM_002047
133323	LHFP	CR749848
152426		BF964783
275871	NAP1L1	AL162068
147527	OGFRL1	AK124833
128333	VPS26	BX647725
41750	NFE2L2	AK128852
174706	ATP4A	AL832971
127230	NDUFA5	BF576548
724893	GCS1	NM_006302
724104	ALS2CL	CR627258
27751	MAL2	AY007723
2578588	HIF1A	NM_001530
234312	GOLGA4	NM_002078
49591	STS	M16505
841641	CCND1	NM_053056
124824	RPL10A	BQ057538
46171	EIF4A1	BG033657
288991	METAP2	AK125296
127833	STX4A	CR590461

133173	PIP5K2C	AK125526
784504	MBTPS1	NM_003791
768622	G3BP	AK128316
210440	C11ORF23	NM_018312
171917	RPS16	AK055869
682555	IGF1R	BX640783
757941	NCBP1	D32002
487770	IRF6	NM_006147
36230	CCT6A	AB063318
147057		BM667064
753447	DDB2	BC050455
37753	SNX3	BC016863
39285	GLUD1	NM_005271
810506	STK3	CR627416
235155	FCER1G	CB529629
786680	ANXA5	BM994439
32529	ZNF207	AL834501
364975	LCHN	AF136629
509887	NONO	NM_007363
766876	MMP3	NM_002422
322452	CHGA	BC006459
162657	DARS	NM_001349
897596	RPL5	BX648424
814316		
813673	HDGF	NM_004494
21834		
898265	SFRS5	BX640605
198093	EIF2S2	BX648379
79739	TRIM33	AF119043
149203	CLIC4	AL117424
898286	CDC2	CR603310
760061		BX089736
1673711	GOLGA1	U51587
754538	DRAP1	BM994482
33346	ANKRD17	NM_032217
855910	LGALS3	AK091776
165857	INPP4B	BX649090
159285	LOC144501	BC065180
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210489	TMPO	AF113682
41922	TARS	NM_152295
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769921	UBE2C	BC032677
950690	CCNA2	CR604810
726791		
43977	KIAA0182	NM_014615
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768377		
625923	PCK2	AK129934

247149	DDX17	NM_006386
35630	CMKOR1	BC036661
949971	ATF4	NM_001675
22694	HNRPU	AF068846
755474	IARS	NM_013417
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163174	TCEA1	BX538034
131867	NET1	BX537509
34211	STK38	NM_007271
563451	TLK1	BX538296
207324	C2ORF25	BF572337
758467	NR2F2	BC042897
2338773	FOXA1	NM_004496
1926453	AREG	AK023449
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789011	AAMP	CR594232
897901	NUMA1	NM_006185
197176	GDI2	AK122841
950574	H3F3B	BX537379
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32706	SENP2	NM_021627
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279216	PPP1CC	NM_002710
293950	PIP5K1A	NM_003557
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300250	DKFZP451J0118	AL832637
277487	NECAP1	AK094805
270114	PAFAH1B2	BC021287
855521	KRT18	CR616919
897806	HIF1A	NM_001530
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470393	MMP7	BQ688566
591465	LOC348180	NM_014745
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197888	GNB2L1	AK124177
612274	TUBA1	AK054731
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52639	HRMT1L6	AY043278
34810	SIAHBP1	AF114818
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52933	SLC39A6	NM_012319
109385	DAZAP2	AK125855
1184257	LMNB1	BC052951
842825	GSPT1	AK095367
125278	CLDN4	AK126462
1566658	KCNK15	AF257081
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1472753	EIF4B	NM_001417
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795247	RPL24	CR608385
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361097	UBE2D3	AK127304
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293032	TFAP2A	BC017754
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248137	EP300	U01877
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195333	HECTD1	AY254380
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782406	ADSS	BX647502
32834	SQLE	BX647605
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273198	RHOBTB3	NM_014899
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1723558	LOC285989	BC050286
2314974	CD207	AJ242859
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840990	GSTM4	NM_000850
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124201	GCGR	NM_000160
2383393	FXVD6	AK092198
2374344	ADH1C	M12272
782760	CYP1B1	NM_000104
1692779	FSTL1	BX647421
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358544		BX116904
755498	PART1	AF163475
281580		BM906215
361798		AA054629
1417852	BTBD9	BX537534
1650770		
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1645979		AI031837
2404052	CP	NM_000096
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897751	TLK2	BC060511
23809	CLCN4	NM_001830
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1949445	NTRK2	AF410901
1647003	RLN2	NM_005059
120823	KLHL6	AF441792
147133		
731257	UNC13B	AF020202
1584142	GAGEB1	BU633662
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1868295	GEM	NM_005261
726149		BC036198
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788552	AMY2B	AK127047
417641	GYPC	CR609866
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44993	VEGFC	NM_005429
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229686	FLJ30681	AB075863
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1680226	NID2	BX648241
1626026	KIAA1465	AB040898
129131	SCFD2	AY299407
110220	NINJ2	CA431480
2390052	ZC3HDC1	BC081541
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120202	MGST3	BX537737
138745		N62146
205819	CPM	NM_001874
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207449	SLC37A1	AK127597
145154	MDS028	NM_018463
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2383157	CA5B	AK057568
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1390584	MIPEP	BC009934
1185901	BACH2	AJ271878
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809791	DATF1	AB002331
146520	EBF	CR627349
304975	KIAA0318	BX641152
1902522	CXCL10	BC010954
151248	SLC2A1	NM_006516
726929		CR740037
239754	SLC7A5	AF104032
1500825	ADRA2B	NM_000682
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137483	LOC91801	BX649085

668307	KIAA1199	AB103330
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742709	C14ORF50	AK130365
490763	IREB2	NM_004136
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21770	DENR	NM_003677
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44975	IDI1	BX537663
28775	PAK4	AB032968
51737	RBBP8	NM_002894
767994	STRN3	NM_014574
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47681	SFRS10	CR749214
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205445	H1FO	NM_005318
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814690	POLD3	NM_006591
756687	SCARB1	AK023485
79502		
729959	KIAA1324	AB037745
29161	MYST2	AK122932
365653		AW972055
39006	VGLL4	AK126479
978715	K-ALPHA-1	AK094717
2139081	PDCD10	BC002506
42739	PTP4A1	CR749458
884867	EIF5	NM_001969
28484	PYM	BC006135
563444	GNAS	NM_080425
266092	KIAA1033	NM_015275
320483	SPIRE1	AB032961
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268979	LOC374443	AK096274
214665	MRPL3	BM541805
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38926	POGZ	BX537838
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810802	RSN	NM_002956
292241	C20ORF129	AL832274
232837	TPX2	NM_012112
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785795	C6ORF211	AK022972
324254	RPL12	AK057602
207358	SLC2A1	NM_006516
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432486	NIPBL	AJ627032

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760224	XRCC1	CR591751
47559	RAB5A	NM_004162
40417	UBE3A	NM_130839
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306198	SRPRB	AK055102
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322002	SIAT8A	NM_003034
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23756	LRPPRC	AY289212
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214537	RFC1	NM_002913
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813823	LUM	BG114678
221092	GABPB2	BC036080
897997	SMC1L1	NM_006306
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124733	GA17	AK123310
113290	CANX	NM_001746
42352	SLC25A6	CR593822
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175103	CELSR2	AF234887
42648	TKT	BX649193
273714		
2346678	KIAA1324	AB037745
214990	GSN	AK125819
1631290	C6ORF199	AL832162
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197155	PRKWNK1	AJ296290
50614	SKIIP	AF045184
2311641	RPL3L	BC050413
41979	FLJ14525	BC066649
38123	ITM2B	BX537657
380851	RTN3	NM_201428
745402	CSNK1A1	BX647478
347223	LOC90321	BX648899
174776	TTBK1	XM_166453
25988	EIF4G1	NM_182917
320763	SP3	CR749323
40959	SLC25A5	AK092094
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141290		BE550129
43129	TOP1	NM_003286
23760	RIF1	AY727912
51865	CA2	AK123309
756831	MAPK6	NM_002748
322739	PTPN3	BX648253
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22594	PSMC6	AK127456
25980	SORCS2	NM_020777
768453	HAN11	NM_005828
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755752	PUM2	AF315591
268927	CCND1	NM_053056
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38736	CNAP1	D63880
29739	TTK	NM_003318
289143	ZCWCC3	NM_015358
298281	SNX13	BC050289
21652	CTNNA1	NM_001903
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814270		
884842	RPL36AL	BU902070
42076	TFG	NM_006070
1471829	RPL35A	AK096574
359956	MYOM3	AK125972
280633	PSITPTE22	BQ429561
362853	PTK9	NM_198974
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43138	DDX3X	NM_001356
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322555	EMP2	AK096403
307862	TOP2B	BX640880
120599	BCAS3	BX648103
128784	KIAA0182	NM_014615
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2095412		BU956222
1646820	SAP30L	AL833381
2569476	BAX	BF983096
760158	RIN2	NM_018993
759977	MRPL53	BM467462
2355503	IL18RAP	AF077346
741891	RGL2	BC040989
785851	FLJ35382	BC016290
151674	NA	XM_378976
229432	PCSK6	NM_002570
485096	VPS18	AL713725
123805	IL12RB2	NM_001559
148974	ATP10D	AJ441078
121373	SDCCAG8	AK023517
752640		
741815	RNF5	BM667062
149597	T1	BX647286
395609		AK125302
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486623	ZNF137	NM_003438
742578		BM552788
491113	CDH11	D21255
547058	CCNG1	NM_004060
785372	MR1	AF031469
322071	FLJ22104	BX648678
51448	ATF3	AK123699
124138	NXF1	BC028041
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48297	NPD014	NM_207035
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306810	SLC22A17	BX161416
278847	TNFAIP2	NM_006291
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Description	2		6		24	
	Ratio	t-test P-value	Ratio	t-test P-value	Ratio	t-test P-value
COMM domain containing 4	0.63	6.9E-03	0.66	1.2E-02	0.67	4.9E-03
V-myc myelocytomatosis viral oncogene homolog (avian)	1.15	1.1E-02	0.56	6.5E-03	0.60	4.0E-03
Histone 1, H4c	1.26	3.6E-02	0.57	3.3E-03	0.54	1.2E-03
Isoleucine-tRNA synthetase	0.80	1.4E-02	0.72	3.1E-03	0.68	7.7E-03
Methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	0.88	1.7E-01	0.76	3.8E-02	0.47	6.1E-03
KIAA0280 protein	0.83	2.6E-03	0.73	2.5E-02	0.40	7.0E-03
RAP1A, member of RAS oncogene family	0.87	2.9E-02	0.83	5.8E-03	0.74	9.4E-03
Transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	0.90	2.1E-02	0.76	5.1E-04	0.88	3.3E-02
Tripartite motif-containing 33	0.90	4.5E-04	0.96	5.3E-01	0.87	9.1E-03
Asparagine synthetase	0.75	2.2E-02	0.81	2.0E-03	1.05	6.1E-01
Tyrosyl-tRNA synthetase	0.71	2.9E-02	0.76	9.5E-03	0.93	1.3E-01
Histone 1, H2bn	0.86	1.4E-01	0.78	2.0E-02	0.34	8.9E-04
Histone 1, H2ac	0.92	1.2E-01	0.84	2.0E-03	0.69	7.5E-03
Histone 1, H3d	0.62	1.1E-03	0.60	6.9E-02	0.56	1.1E-02
Histone 1, H1c	0.65	1.1E-02	0.64	4.0E-02	0.64	3.0E-03
Histone 1, H4b	0.62	3.7E-03	0.60	1.2E-02	0.68	5.0E-02
Histone 1, H3e	0.63	7.6E-02	0.57	1.4E-02	0.57	4.9E-03
Histone 1, H2bj	0.69	5.7E-03	0.61	4.3E-02	0.66	1.5E-02
CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	0.71	4.6E-03	0.62	8.6E-02	0.65	1.7E-02
MYST histone acetyltransferase (monocytic leukemia) 4	0.64	3.6E-03	0.67	3.9E-02	0.64	2.8E-02
Nuclear receptor coactivator 3	0.88	1.4E-02	0.78	5.1E-03	0.97	5.2E-01
BTG family, member 2	0.74	1.7E-02	0.82	2.6E-01	0.97	6.7E-01
Zinc finger and BTB domain containing 5	0.73	8.3E-03	0.80	2.0E-01	1.06	7.8E-01
Vaccinia related kinase 2	1.20	4.6E-02	1.24	1.0E-01	1.10	4.0E-02
Ubiquitin specific protease 9, X-linked (fat facets-like, Drosophila)	0.80	3.8E-02	0.87	6.7E-03	0.94	3.1E-01
Homeodomain interacting protein kinase 1	0.93	1.0E-01	0.87	1.8E-02	0.82	4.2E-02
Protein kinase C binding protein 1	0.90	3.7E-02	0.88	3.4E-03	0.91	2.7E-03
Exportin, tRNA (nuclear export receptor for tRNAs)	0.91	2.5E-01	0.82	2.6E-02	0.99	9.0E-01
Retinoic acid induced 17	0.90	2.0E-02	0.89	1.9E-01	0.96	1.8E-01
Nuclear receptor coactivator 3	0.72	4.9E-02	0.69	3.5E-04	1.00	8.7E-01
Topoisomerase (DNA) II alpha 170kDa	0.89	8.9E-02	0.77	1.2E-02	0.55	1.6E-02
Solute carrier family 22 (organic cation transporter), member 15	0.77	3.9E-02	0.94	1.8E-01	0.98	7.7E-01
CGG triplet repeat binding protein 1	0.75	5.7E-02	0.69	2.6E-02	1.09	3.0E-01
Lymphocyte antigen 6 complex, locus E	0.97	1.1E-01	0.78	1.8E-02	0.63	4.8E-03
ADP-ribosylation factor-like 6 interacting protein 2	0.87	3.6E-02	0.79	1.0E-02	0.71	3.4E-02
Small nuclear RNA activating complex, polypeptide 3, 50kDa	0.90	6.0E-02	0.88	4.1E-02	0.71	1.7E-04
Glycyl-tRNA synthetase	1.23	7.3E-03	1.13	2.9E-01	1.20	7.0E-03
Polymerase I and transcript release factor	0.83	3.7E-02	0.86	2.5E-02	0.85	2.8E-02
Cadherin 1, type 1, E-cadherin (epithelial)	0.94	2.3E-01	0.90	5.8E-03	0.85	3.1E-02
Transcribed locus	0.96	3.2E-01	0.84	3.5E-02	0.62	1.3E-04
Glutamate dehydrogenase 1	1.01	4.6E-01	1.08	3.7E-01	1.10	3.9E-02
Haloacid dehalogenase-like hydrolase domain containing 1A	0.97	4.4E-01	0.78	3.4E-02	0.83	6.9E-03
WW domain containing adaptor with coiled-coil	0.94	2.4E-01	0.87	3.9E-02	0.69	2.0E-02
NOL1/NOP2/Sun domain family 3	1.00	9.7E-01	0.88	1.3E-02	0.77	3.7E-03
Sp1 transcription factor	0.84	4.9E-02	0.85	1.5E-02	0.85	1.0E-01
	0.87	1.2E-01	0.92	2.3E-01	0.87	2.4E-02
	0.98	1.8E-01	0.89	1.9E-01	0.69	1.0E-02
	0.90	2.2E-01	0.88	2.3E-02	0.85	2.2E-03

Cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase)	0.89	3.4E-02	0.94	3.0E-01	0.88	4.1E-02
SFRS protein kinase 2	0.81	9.5E-02	0.66	2.2E-03	0.85	1.8E-03
Histidyl-tRNA synthetase	0.86	2.9E-01	0.76	2.9E-02	0.87	1.4E-02
FLJ46311 protein	1.13	2.4E-01	1.32	3.3E-02	1.23	4.0E-03
RNA binding motif protein 8A	1.15	9.7E-02	1.05	2.8E-01	0.85	2.5E-02
Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	0.97	2.1E-02	0.89	1.2E-01	0.85	2.8E-02
Spectrin, beta, non-erythrocytic 1	0.92	1.6E-01	0.74	1.7E-02	0.85	1.9E-01
Hypothetical protein MGC10986	0.82	2.8E-02	0.65	3.4E-02	0.85	4.0E-01
Exportin 1 (CRM1 homolog, yeast)	0.87	9.7E-02	0.87	4.4E-03	0.90	4.9E-02
Activating transcription factor 1	0.88	3.9E-02	0.87	4.0E-03	0.92	1.6E-01
KIAA1731 protein	1.00	9.1E-01	1.05	2.0E-02	1.08	3.3E-02
Synaptophysin-like protein	0.95	3.7E-03	0.97	1.3E-01	0.85	2.8E-02
SUMO-1 activating enzyme subunit 2	0.87	6.2E-02	0.76	6.4E-03	0.82	7.5E-03
Nuclear receptor coactivator 3	0.71	3.7E-02	0.73	1.0E-01	1.06	7.5E-01
Solute carrier family 38, member 2	0.56	1.7E-02	0.68	1.5E-02	1.14	3.3E-01
Transcobalamin I (vitamin B12 binding protein, R binder family)	0.86	2.5E-02	0.76	1.7E-02	0.63	6.6E-03
V-myc myelocytomatosis viral oncogene homolog (avian)	1.14	2.2E-02	0.70	2.3E-02	0.70	3.7E-03
Polo-like kinase 1 ( <i>Drosophila</i> )	0.94	3.1E-01	0.70	1.6E-02	0.64	2.6E-03
Asparagine synthetase	0.89	3.7E-01	0.83	4.1E-02	0.38	1.5E-03
Ribosomal protein S27-like	1.09	1.5E-01	1.28	1.2E-02	1.88	1.1E-03
Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	0.89	4.2E-01	0.67	5.0E-02	0.59	5.9E-03
TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	0.75	2.9E-02	0.71	1.3E-01	0.76	5.0E-02
Cyclin-dependent kinase inhibitor 1B (p27, Kip1)	0.89	1.9E-01	0.70	1.0E-02	0.80	1.9E-02
Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)	1.06	1.3E-01	0.90	4.3E-01	0.55	6.2E-05
Serine/threonine kinase 6	0.86	2.5E-01	0.73	2.7E-02	0.58	2.8E-03
Ovarian carcinoma immunoreactive antigen	1.00	8.9E-01	0.89	9.7E-03	0.94	3.0E-02
Hypothetical protein LOC284361	0.97	7.2E-01	0.91	9.0E-03	0.62	3.5E-03
	1.13	2.2E-02	1.06	6.0E-01	0.84	3.2E-03
	0.78	6.8E-02	0.60	1.6E-02	0.77	9.7E-02
Amphiregulin (schwannoma-derived growth factor)	0.64	1.8E-02	0.45	7.0E-05	1.08	1.3E-01
Germ cell associated 1	1.04	4.7E-01	1.04	2.9E-02	1.16	3.6E-01
Transcription elongation factor A (SII), 2	0.80	2.1E-02	0.89	1.2E-02	0.97	6.6E-01
Similar to RIKEN cDNA 5730421E18 gene	1.00	8.7E-01	1.08	2.8E-01	1.16	3.9E-02
V-crk sarcoma virus CT10 oncogene homolog (avian)	0.90	9.7E-03	1.06	1.8E-02	0.97	6.7E-01
NICE-4 protein	1.09	3.2E-02	1.06	6.6E-01	1.00	9.8E-01
CDC10 cell division cycle 10 homolog ( <i>S. cerevisiae</i> )	1.15	4.6E-02	1.05	1.6E-01	0.85	5.1E-02
Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	1.05	2.1E-01	0.95	no replicates	0.71	3.3E-02
	1.06	1.2E-02	1.09	3.3E-02	1.12	3.3E-01
APG10 autophagy 10-like ( <i>S. cerevisiae</i> )	1.05	1.9E-02	1.02	5.1E-01	1.06	3.4E-01
TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	1.18	1.8E-03	1.11	4.1E-01	0.89	2.1E-01
Dynein, cytoplasmic, light polypeptide 1	1.25	1.5E-01	1.49	2.1E-02	1.16	1.4E-01
Hypothetical protein H41	1.00	9.1E-01	0.89	2.7E-02	0.77	1.3E-02
5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	0.98	5.5E-01	0.83	1.6E-01	0.87	1.7E-02
E3 identified by differential display	0.86	1.5E-02	0.87	3.9E-02	1.03	4.8E-01
Bone morphogenetic protein 7 (osteogenic protein 1)	1.07	2.2E-01	0.87	2.2E-02	0.96	5.9E-01
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	1.07	2.3E-01	1.11	7.7E-02	1.17	6.2E-03
Serotonin-7 receptor pseudogene	0.92	6.4E-03	1.00	8.7E-01	1.27	4.3E-02
Immediate early response 3	1.14	5.2E-02	0.96	6.0E-01	1.18	3.0E-02



Leucine-rich repeat kinase 1	0.96	3.8E-02	1.08	3.2E-01	1.11	8.3E-02
Sialyltransferase 7 ((alpha-N-acetylneuraminy-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) B	1.02	7.0E-01	0.96	4.6E-01	0.77	1.1E-03
Ribosomal protein S15a	1.14	6.8E-02	1.16	3.7E-02	0.95	3.3E-01
	1.09	8.6E-02	1.21	1.0E-01	1.17	1.8E-03
Discs, large homolog 7 (Drosophila)	0.96	4.1E-01	0.76	2.6E-01	0.69	1.4E-03
Chromosome 10 open reading frame 53	0.96	4.0E-01	0.86	2.3E-03	0.76	1.2E-02
Chromosome 19 open reading frame 32	1.06	3.8E-02	1.03	2.1E-01	1.03	2.0E-01
Interleukin 10 receptor, alpha	1.03	1.8E-01	1.09	1.2E-02	1.10	3.4E-01
Poly (ADP-ribose) polymerase family, member 11	0.88	2.8E-02	0.77	2.8E-02	1.00	9.8E-01
Proliferating cell nuclear antigen	1.17	2.1E-02	1.48	3.2E-02	0.95	1.1E-01
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	0.98	6.4E-01	0.74	1.2E-02	0.88	3.3E-01
Ubiquinol-cytochrome c reductase core protein II	1.05	3.5E-02	0.95	4.5E-01	0.80	3.3E-02
	0.91	4.0E-02	0.98	6.0E-01	0.97	5.8E-01
	0.97	4.0E-01	0.85	4.7E-02	0.73	1.1E-02
Hypothetical protein BC006130	1.01	7.6E-01	0.88	no replicates	0.89	1.5E-02
Phospholipase C, beta 4	0.89	6.3E-02	0.76	8.1E-03	0.86	1.0E-02
Ribosomal protein L10	1.15	9.0E-04	0.96	4.7E-01	0.93	5.8E-01
Tubulin, delta 1	0.98	3.6E-01	1.05	4.0E-02	1.26	4.6E-02
Aldehyde dehydrogenase 1 family, member A3	1.04	1.9E-01	1.23	2.7E-02	1.18	2.5E-02
Glycogen synthase kinase 3 beta	0.85	1.8E-02	0.86	5.4E-02	0.98	1.6E-01
Hypothetical protein FLJ10980	0.87	1.7E-01	0.93	6.4E-02	1.09	4.1E-02
Ash1 (absent, small, or homeotic)-like (Drosophila)	0.77	1.6E-02	0.85	1.2E-02	0.98	7.7E-01
Transcribed locus, moderately similar to XP_375099.1 hypothetical protein LOC283585 [Homo sapiens]	0.83	1.0E-01	0.74	1.5E-02	1.04	2.5E-01
Thioesterase, adipose associated	0.97	no replicates	1.18	1.6E-01	1.07	1.3E-02
SRY (sex determining region Y)-box 4	0.96	4.6E-01	0.86	3.5E-02	1.09	1.5E-01
Serine/threonine kinase 24 (STE20 homolog, yeast)	0.92	8.9E-02	0.79	5.2E-03	0.86	4.9E-03
TAR DNA binding protein	0.95	2.2E-02	0.82	2.6E-02	1.03	3.6E-01
Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	0.99	9.5E-01	0.91	1.5E-02	0.88	1.1E-02
Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.27	1.6E-01	2.46	1.1E-01	2.05	7.8E-02
Sp1 transcription factor	0.88	6.7E-02	0.90	3.3E-02	0.84	1.2E-02
Tumor protein D52	0.89	5.9E-02	0.82	9.9E-03	0.89	1.1E-01
Eukaryotic translation elongation factor 2	1.14	3.5E-01	0.89	1.9E-01	0.81	3.2E-02
Homo sapiens, Similar to neuronal thread protein, clone IMAGE:4102657, mRNA	1.05	9.2E-02	1.14	1.2E-02	1.13	2.8E-01
Glycyl-tRNA synthetase	0.87	7.1E-02	0.84	2.6E-02	0.60	5.5E-03
Lipoma HMGIC fusion partner	0.98	7.3E-01	1.08	2.0E-02	1.07	2.9E-01
Transcribed locus	1.06	3.7E-01	1.12	2.2E-01	1.19	8.8E-02
Nucleosome assembly protein 1-like 1	1.06	5.4E-02	1.03	7.1E-01	0.81	3.0E-02
Opioid growth factor receptor-like 1	1.02	6.5E-01	1.03	2.9E-02	1.09	2.9E-01
Vacuolar protein sorting 26 (yeast)	1.16	6.5E-03	1.23	1.7E-02	0.98	7.5E-01
Transcribed locus, weakly similar to NP_079012.2 gasdermin domain containing 1 [Homo sapiens]	0.93	1.5E-02	1.00	1.0E+00	0.91	1.6E-01
ATPase, H+/K+ exchanging, alpha polypeptide	1.02	6.3E-01	1.08	3.2E-01	1.06	1.5E-02
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	1.11	2.7E-02	1.00	9.8E-01	0.87	1.3E-01
Glucosidase I	1.00	1.0E+00	1.03	5.2E-03	1.18	1.1E-01
Hypothetical protein LOC259173	1.03	5.7E-01	1.08	2.5E-02	1.12	3.1E-01
Mal, T-cell differentiation protein 2	1.00	9.7E-01	0.87	5.5E-02	0.80	1.2E-02
Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	0.91	8.7E-03	0.93	6.2E-01	1.00	9.2E-01
Golgi autoantigen, golgin subfamily a, 4	0.91	1.4E-01	0.89	9.7E-03	0.91	4.5E-02
Steroid sulfatase (microsomal), arylsulfatase C, isozyme S	0.99	7.3E-01	0.81	6.2E-03	0.93	2.5E-01
Cyclin D1 (PRAD1: parathyroid adenomatosis 1)	0.90	2.8E-01	0.79	1.9E-03	1.09	2.6E-01
Ribosomal protein L10a	1.09	1.7E-02	1.00	9.7E-01	0.80	5.8E-02
Eukaryotic translation initiation factor 4A, isoform 1	1.05	2.8E-01	0.88	2.5E-01	0.81	9.1E-02
Methionyl aminopeptidase 2	0.95	4.7E-02	0.88	1.7E-01	0.86	1.1E-02
Syntaxin 4A (placental)	0.95	8.1E-02	0.82	1.9E-02	0.98	7.0E-01

Phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	1.06	1.3E-01	1.08	1.6E-01	1.14	2.4E-02
Membrane-bound transcription factor protease, site 1	0.91	7.1E-02	0.84	1.1E-02	0.94	5.0E-03
Ras-GTPase-activating protein SH3-domain-binding protein	0.97	1.8E-01	0.84	1.1E-01	0.84	3.0E-03
Chromosome 11 open reading frame 23	0.88	1.8E-01	0.85	9.4E-03	0.95	2.2E-01
Ribosomal protein S16	1.16	2.1E-02	1.10	3.7E-01	1.00	9.6E-01
Transcribed locus, moderately similar to XP_375099.1 hypothetical protein LOC283585 [Homo sapiens]	0.83	9.6E-02	0.76	1.1E-02	1.03	5.9E-01
Nuclear cap binding protein subunit 1, 80kDa	1.02	7.6E-01	1.10	3.0E-01	1.19	3.7E-02
Interferon regulatory factor 6	1.01	6.9E-01	1.09	2.4E-01	1.24	3.0E-02
	1.11	4.5E-02	1.22	1.1E-02	1.37	7.9E-02
Transcribed locus	0.99	8.3E-01	1.28	3.6E-02	1.16	2.3E-01
Damage-specific DNA binding protein 2, 48kDa	1.09	7.5E-03	1.42	4.9E-02	1.42	2.3E-02
Sorting nexin 3	1.00	9.1E-01	0.97	3.9E-01	0.90	1.4E-01
Glutamate dehydrogenase 1	0.96	3.7E-02	0.89	7.6E-02	0.78	2.0E-02
MRNA; cDNA DKFZp686O04121 (from clone DKFZp686O04121)	0.84	9.3E-02	0.78	1.8E-02	0.89	1.0E-02
Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	0.98	5.2E-01	1.09	2.1E-01	1.16	3.4E-02
Annexin A5	1.11	1.9E-02	1.10	3.7E-01	0.76	1.6E-02
Zinc finger protein 207	0.94	2.2E-01	0.92	2.2E-01	0.90	1.4E-02
LCHN protein	0.94	8.0E-02	0.84	2.3E-02	0.87	3.7E-02
Non-POU domain containing, octamer-binding	1.04	5.2E-01	0.87	3.4E-01	0.74	2.6E-02
Matrix metalloproteinase 3 (stromelysin 1, progelatinase)	1.02	7.8E-01	1.10	4.0E-03	1.17	2.6E-01
Chromogranin A (parathyroid secretory protein 1)	1.00	9.7E-01	1.08	2.9E-01	1.14	2.6E-02
Aspartyl-tRNA synthetase	0.99	8.9E-01	1.14	2.7E-01	1.14	1.3E-02
Ribosomal protein L5	1.14	8.0E-03	1.06	6.2E-01	0.84	6.3E-02
	1.22	4.5E-02	1.01	9.7E-01	0.90	1.1E-01
Hepatoma-derived growth factor (high-mobility group protein 1-like)	1.11	7.5E-03	0.96	5.6E-01	0.89	1.8E-01
	0.88	5.5E-02	0.79	5.4E-03	0.93	4.8E-01
Splicing factor, arginine/serine-rich 5	1.19	9.7E-03	0.79	7.9E-03	0.79	4.5E-02
Eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	0.98	5.9E-01	0.83	1.1E-01	0.69	6.9E-03
Tripartite motif-containing 33	0.74	4.0E-02	0.82	1.0E-02	0.95	5.1E-01
Chloride intracellular channel 4	0.91	1.2E-02	0.85	2.3E-01	0.60	3.8E-02
Cell division cycle 2, G1 to S and G2 to M	0.93	7.1E-02	0.92	2.3E-01	0.69	5.9E-04
Transcribed locus	0.99	7.8E-01	0.82	2.9E-02	0.67	6.5E-03
Golgi autoantigen, golgin subfamily a, 1	1.27	2.0E-02	1.09	3.5E-01	0.67	2.2E-02
DR1-associated protein 1 (negative cofactor 2 alpha)	1.08	1.6E-01	1.14	3.3E-03	1.13	3.5E-01
Ankyrin repeat domain 17	0.79	1.4E-02	0.69	1.8E-01	0.88	3.2E-01
Lectin, galactoside-binding, soluble, 3 (galectin 3)	1.06	3.4E-02	0.91	4.0E-02	0.71	5.9E-02
Inositol polyphosphate-4-phosphatase, type II, 105kDa	0.85	1.2E-01	0.70	3.5E-02	1.00	9.5E-01
Hypothetical protein LOC144501	0.90	2.3E-01	0.67	2.0E-04	1.48	2.9E-02
	0.99	6.4E-01	0.85	1.9E-01	0.60	3.3E-03
Neuronal cell adhesion molecule	0.78	8.7E-03	0.58	1.5E-02	0.94	5.0E-01
Thymopoietin	0.83	5.7E-03	0.74	8.9E-03	0.80	5.7E-02
Threonyl-tRNA synthetase	0.93	1.4E-01	0.79	1.2E-01	0.56	3.2E-03
Zinc finger protein 431	0.82	1.3E-01	0.70	3.2E-03	0.96	4.3E-02
Ubiquitin-conjugating enzyme E2C	0.99	8.2E-01	0.79	1.8E-02	0.58	3.3E-04
Cyclin A2	1.00	9.1E-01	0.78	3.5E-03	0.62	4.0E-03
	0.86	1.4E-01	0.76	3.7E-03	0.69	3.2E-02
KIAA0182 protein	0.73	4.2E-02	0.60	5.5E-05	0.77	2.7E-02
	0.99	8.9E-01	0.89	5.3E-01	0.71	2.0E-02
	0.71	3.1E-02	0.95	1.6E-01	1.05	3.7E-01
Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.97	6.1E-01	0.78	1.9E-02	0.55	6.7E-03

DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0.91	7.7E-02	0.66	7.0E-03	0.89	1.8E-01
Chemokine orphan receptor 1	0.80	1.2E-01	0.67	7.5E-03	0.96	3.7E-01
Activating transcription factor 4 (tax-responsive enhancer element B67)	1.04	4.6E-01	0.88	2.0E-01	0.59	3.0E-03
Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0.96	2.8E-01	0.82	8.1E-02	0.76	2.2E-03
Isoleucine-tRNA synthetase	0.90	5.6E-02	0.77	8.8E-03	0.49	2.6E-02
Splicing factor, arginine/serine-rich 3	0.83	1.1E-01	0.66	1.7E-02	0.87	3.6E-03
Transcription elongation factor A (SII), 1	0.88	4.8E-02	0.77	3.4E-02	0.71	3.2E-02
Neuroepithelial cell transforming gene 1	0.82	1.8E-01	0.68	2.3E-02	0.77	3.1E-02
Serine/threonine kinase 38	0.85	9.6E-02	0.64	3.0E-03	0.79	1.1E-01
Tousled-like kinase 1	0.84	8.9E-02	0.76	3.1E-02	0.88	2.5E-02
Chromosome 2 open reading frame 25	0.97	3.5E-01	0.88	1.1E-01	0.81	1.5E-02
Nuclear receptor subfamily 2, group F, member 2	0.71	1.6E-02	0.51	1.4E-03	0.82	2.1E-01
Forkhead box A1	0.82	6.5E-02	0.71	1.4E-02	0.89	2.8E-01
Amphiregulin (schwannoma-derived growth factor)	0.64	3.6E-02	0.48	2.0E-04	1.11	2.2E-01
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.03	4.5E-01	0.74	2.1E-03	0.84	7.9E-02
Angio-associated, migratory cell protein	1.11	4.7E-02	1.11	1.2E-02	1.11	1.9E-01
Nuclear mitotic apparatus protein 1	0.96	9.2E-02	0.78	1.7E-01	0.88	7.9E-02
GDP dissociation inhibitor 2	0.97	2.6E-01	0.87	2.4E-01	0.78	1.6E-02
H3 histone, family 3B (H3.3B)	0.98	8.5E-01	0.79	9.1E-02	0.73	3.4E-02
Chemokine orphan receptor 1	0.71	4.6E-02	0.54	1.9E-04	0.94	4.3E-01
Histone deacetylase 2	0.97	5.1E-01	0.89	5.6E-02	0.92	2.2E-02
SUMO1/sentrin/SMT3 specific protease 2	0.98	6.4E-01	0.95	4.3E-01	0.92	3.2E-01
Poly(rC) binding protein 2	1.00	9.8E-01	0.91	2.4E-01	0.81	2.1E-01
Guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	0.92	6.5E-02	0.86	1.4E-02	0.91	4.2E-01
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	0.99	6.9E-01	0.88	1.9E-01	0.81	6.7E-02
Twisted gastrulation homolog 1 (Drosophila)	1.00	6.9E-01	1.04	2.1E-01	1.16	1.3E-01
Full length insert cDNA clone ZC34E11	0.96	2.4E-01	1.20	1.6E-01	1.19	5.3E-02
Protein phosphatase 1, catalytic subunit, gamma isoform	0.93	1.7E-01	0.85	1.2E-01	0.92	6.2E-02
Phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	0.86	1.7E-01	1.08	2.4E-01	1.05	3.3E-01
Basic leucine zipper nuclear factor 1 (JEM-1)	0.82	4.0E-02	0.84	8.1E-03	0.98	8.1E-01
Taxilin	1.16	4.5E-02	1.03	5.3E-01	0.87	1.0E-01
DKFZP566B183 protein	0.92	4.8E-01	0.78	2.7E-02	0.81	1.8E-01
Platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kDa	0.97	6.3E-01	0.86	5.4E-02	0.93	3.1E-02
Keratin 18	1.15	1.8E-01	0.77	1.9E-01	1.19	5.0E-04
Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	0.86	5.5E-02	0.62	4.0E-02	1.03	6.0E-01
Ribosomal protein S9	1.11	9.3E-03	1.04	8.0E-01	0.90	1.0E-01
Histidyl-tRNA synthetase 2	1.07	2.7E-01	1.07	2.8E-02	1.14	2.1E-01
Matrix metalloproteinase 7 (matrilysin, uterine)	0.85	3.6E-02	0.95	1.1E-01	0.98	7.0E-01
Hypothetical protein LOC348180	1.02	6.1E-01	1.12	5.8E-02	1.18	1.7E-01
Ribosomal protein L24	1.02	2.8E-01	1.04	8.0E-01	1.03	7.4E-01
Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	1.12	3.2E-02	1.09	1.9E-01	0.98	8.1E-01
Tubulin, alpha 1 (testis specific)	1.05	6.3E-01	0.89	3.9E-01	0.85	1.3E-01
Zinc finger, DHHC domain containing 5	1.11	1.5E-01	0.99	9.5E-01	0.85	2.6E-01
Brain-derived neurotrophic factor	1.03	3.9E-01	1.04	3.1E-01	1.22	4.0E-02
Activity-dependent neuroprotector	0.98	5.6E-01	1.00	1.0E+00	1.04	3.3E-02
HMT1 hnRNP methyltransferase-like 6 (S. cerevisiae)	1.00	9.8E-01	1.03	5.5E-01	1.18	5.8E-02
Fuse-binding protein-interacting repressor	0.77	5.1E-02	0.97	5.7E-01	1.02	7.0E-01
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	0.96	1.6E-01	0.93	1.2E-01	1.00	9.6E-01
Beta 5-tubulin	1.02	2.1E-01	0.84	4.3E-02	0.96	5.2E-01
	1.06	2.1E-01	0.93	2.9E-01	0.91	3.5E-01
	1.05	1.1E-01	0.82	6.3E-02	0.80	1.2E-02

Importin 7	0.97	4.6E-01	0.87	2.7E-01	0.85	3.9E-02
Full-length cDNA clone CS0DI081YM02 of Placenta Cot 25-normalized of Homo sapiens (human)	0.99	6.0E-01	1.00	1.0E+00	0.72	5.1E-02
Solute carrier family 39 (zinc transporter), member 6	1.02	6.0E-01	0.95	6.3E-01	0.82	2.7E-01
DAZ associated protein 2	1.05	1.9E-01	0.95	4.9E-01	0.88	1.4E-02
Lamin B1	0.97	1.8E-01	0.77	1.5E-02	0.82	1.9E-01
G1 to S phase transition 1	1.05	1.3E-01	0.90	1.8E-01	0.96	3.6E-01
Claudin 4	1.07	3.4E-01	0.95	7.2E-01	1.10	1.4E-01
Potassium channel, subfamily K, member 15	1.05	1.3E-01	1.11	1.1E-01	1.10	2.4E-01
	1.06	2.2E-01	1.02	6.8E-01	0.86	2.2E-01
Cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	0.93	6.3E-02	0.94	4.9E-01	0.83	2.4E-02
Glycoprotein hormones, alpha polypeptide	1.00	9.1E-01	1.08	2.6E-01	1.20	1.1E-01
Heterogeneous nuclear ribonucleoprotein U-like 1	1.06	5.7E-01	0.80	6.4E-02	0.86	3.1E-02
Golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1	0.95	1.9E-01	1.11	3.5E-01	0.98	4.6E-01
Hypothetical protein MGC26733	1.00	9.3E-01	1.08	1.9E-01	1.09	4.4E-01
Eukaryotic translation initiation factor 4B	1.01	8.7E-01	0.88	2.0E-01	0.80	1.1E-01
RNA-binding region (RNP1, RRM) containing 2	0.84	2.2E-02	0.81	5.3E-02	0.90	1.1E-01
Ribosomal protein L24	1.06	1.0E-01	1.09	3.2E-01	0.88	1.0E-03
Calpain 3, (p94)	1.00	8.6E-01	1.05	1.9E-02	1.13	3.9E-01
Placenta-specific 4	0.95	4.2E-01	0.88	2.0E-02	1.00	9.8E-01
	0.95	8.4E-02	0.94	1.3E-01	0.74	8.7E-03
YY1 transcription factor	1.08	6.5E-02	1.00	1.0E+00	0.87	4.0E-01
Ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.99	6.9E-01	0.98	7.2E-01	0.91	2.4E-01
	1.02	6.9E-01	1.11	2.8E-01	1.20	4.4E-02
Transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	1.41	3.0E-01	0.89	7.0E-01	0.87	1.6E-02
Vacuolar protein sorting 35 (yeast)	0.79	4.4E-02	0.80	1.4E-05	0.90	1.1E-01
E1A binding protein p300	1.00	8.0E-01	1.03	4.8E-01	1.13	2.6E-01
Mitochondrial carrier triple repeat 1	1.03	5.4E-01	1.05	3.8E-02	1.15	4.0E-01
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	0.95	1.8E-01	0.83	1.5E-01	1.00	9.9E-01
Cullin 4B	1.02	1.1E-01	1.01	8.3E-01	1.02	1.4E-01
HECT domain containing 1	0.94	1.5E-01	0.93	1.7E-01	0.91	4.8E-02
Surfactant, pulmonary-associated protein B	0.99	7.4E-01	1.12	2.1E-01	1.16	1.2E-01
Annexin A5	1.06	3.9E-02	0.97	5.9E-01	0.78	1.3E-01
Hypothetical protein FLJ10618	0.99	8.0E-01	1.00	9.5E-01	1.13	1.5E-01
Adenylosuccinate synthase	0.94	2.0E-01	0.86	3.3E-02	0.90	6.9E-02
Squalene epoxidase	1.00	9.5E-01	0.96	2.7E-01	0.91	2.4E-01
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	0.93	1.4E-01	0.85	1.2E-01	0.84	3.6E-03
Matrin 3	0.97	4.2E-01	0.85	2.5E-02	1.00	9.6E-01
Zinc finger protein (C2H2 type) 277	0.96	1.2E-01	1.04	4.6E-01	1.10	1.2E-01
AT rich interactive domain 1A (SWI- like)	0.83	5.1E-02	0.95	4.4E-01	1.01	8.0E-01
PERP, TP53 apoptosis effector	1.12	7.6E-03	1.19	6.7E-02	0.96	7.0E-01
Bone morphogenetic protein 7 (osteogenic protein 1)	1.10	6.4E-03	0.88	2.1E-01	0.94	2.1E-01
MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	1.06	2.8E-01	1.08	3.0E-01	1.01	8.0E-02
HBxAg transactivated protein 2	0.86	7.8E-02	0.90	1.4E-01	0.95	8.8E-02
Prothymosin, alpha (gene sequence 28)	1.09	1.6E-01	0.94	7.1E-01	0.83	4.1E-02
Potassium voltage-gated channel, KQT-like subfamily, member 2	1.03	3.4E-01	1.11	2.2E-01	1.14	1.1E-01
DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	0.96	4.1E-03	0.93	2.7E-01	1.18	8.7E-02
Protein phosphatase 2, regulatory subunit B (B56), gamma isoform	0.95	1.0E-01	0.87	9.0E-02	0.91	2.3E-01
Regulating synaptic membrane exocytosis 4	1.04	6.2E-01	1.06	1.8E-01	1.15	2.2E-01
RAB5A, member RAS oncogene family	0.92	5.0E-03	0.96	2.4E-01	0.89	1.7E-01
Synaptotagmin-like 2	0.82	3.1E-02	0.75	8.6E-02	1.16	1.4E-01
Thrombospondin 1	0.89	3.0E-01	0.75	8.2E-03	0.93	6.5E-02

CASP2 and RIPK1 domain containing adaptor with death domain	1.03	6.5E-01	1.11	2.3E-01	1.13	4.9E-01
Ubiquitin C	1.07	5.4E-01	0.79	9.7E-02	0.96	3.5E-01
Cyclin-dependent kinase 2-interacting protein	0.78	1.1E-01	0.83	1.3E-01	0.89	8.7E-02
Rho-related BTB domain containing 3	0.90	5.8E-02	0.78	3.1E-02	1.06	3.1E-01
Chymotrypsin C (caldecrin)	1.03	1.2E-01	1.05	1.5E-01	1.07	4.6E-01
Hypothetical protein LOC285989	1.02	8.1E-01	1.06	5.4E-01	1.27	4.7E-02
CD207 antigen, langerin	1.04	1.1E-01	1.05	3.4E-01	1.11	2.5E-01
Transcribed locus	1.07	5.0E-02	1.10	2.8E-01	1.14	2.9E-01
	1.04	3.2E-01	1.09	1.1E-02	1.03	7.0E-01
WW domain containing adaptor with coiled-coil	1.00	9.8E-01	1.05	5.7E-01	1.13	2.9E-01
Glutathione S-transferase M4	0.96	4.2E-01	0.97	1.7E-03	1.07	2.0E-01
Beaded filament structural protein 2, phakinin	0.99	4.7E-01	1.10	1.3E-01	1.14	2.8E-01
Transcribed locus, highly similar to NP_116315.1 transcription elongation factor A (SII)-like 3 [Homo sapiens]	1.05	5.1E-01	1.03	4.8E-01	1.16	5.3E-02
Transcribed locus	0.99	6.4E-01	1.06	4.2E-01	1.20	8.7E-02
Troponin I, skeletal, slow	0.98	6.5E-01	1.08	5.1E-01	1.15	4.0E-01
Glucagon receptor	1.00	9.2E-01	1.02	5.5E-01	0.98	7.5E-01
FXVD domain containing ion transport regulator 6	1.06	3.0E-01	1.04	3.1E-01	1.09	4.0E-01
Alcohol dehydrogenase 1C (class I), gamma polypeptide	1.02	5.7E-01	1.08	1.5E-01	1.07	4.3E-01
Cytochrome P450, family 1, subfamily B, polypeptide 1	2.04	1.2E-02	1.91	4.1E-02	1.04	7.6E-01
Follistatin-like 1	1.03	4.4E-01	1.15	2.2E-01	1.20	3.8E-02
Cytochrome b-245, beta polypeptide (chronic granulomatous disease)	1.01	8.3E-01	1.09	2.5E-01	1.20	9.6E-02
Transcribed locus	1.05	5.6E-01	1.14	1.8E-01	1.22	1.5E-01
Prostate androgen-regulated transcript 1	1.01	5.7E-01	1.03	6.9E-01	1.16	1.5E-01
Similar to implantation-associated protein	1.00	9.3E-01	1.09	3.9E-02	1.14	2.5E-01
Transcribed locus	0.97	5.2E-01	1.08	4.2E-01	1.12	2.1E-02
BTB (POZ) domain containing 9	0.97	5.8E-01	1.01	9.0E-01	1.11	3.6E-01
	1.01	8.5E-01	1.07	3.8E-01	1.15	1.2E-01
Phosphatidylinositol glycan, class F	1.03	3.5E-01	1.42	5.6E-02	1.25	2.6E-02
Transcribed locus	1.07	2.8E-01	1.05	3.4E-01	1.17	4.9E-01
Ceruloplasmin (ferroxidase)	1.04	1.9E-01	1.04	2.5E-01	1.16	1.3E-01
Chemokine-like factor super family 4	1.00	9.5E-01	1.03	5.8E-01	1.15	9.0E-02
Tousled-like kinase 2	0.52	1.1E-02	0.82	4.4E-02	0.94	1.6E-01
Chloride channel 4	1.00	9.8E-01	1.11	4.8E-01	1.03	6.5E-01
	1.03	5.8E-01	1.07	3.9E-01	1.10	3.0E-01
Glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	1.01	7.5E-01	1.04	3.9E-02	1.07	1.9E-01
Neurotrophic tyrosine kinase, receptor, type 2	1.14	3.8E-01	1.06	9.2E-02	0.94	2.5E-01
Relaxin 2 (H2)	1.00	6.0E-01	1.03	1.0E-02	1.17	1.6E-01
Kelch-like 6 (Drosophila)	1.03	6.5E-01	1.09	8.3E-02	1.15	2.3E-01
	1.11	3.5E-01	1.23	2.7E-02	1.14	no replicates
Unc-13 homolog B (C. elegans)	1.02	no replicates	1.18	2.4E-02	1.35	1.6E-01
G antigen, family B, 1 (prostate associated)	1.01	8.8E-01	1.10	1.5E-02	1.12	2.3E-01
GATA binding protein 3	0.67	1.1E-01	0.65	5.1E-02	0.85	2.5E-01
GTP binding protein overexpressed in skeletal muscle	1.03	6.1E-01	1.09	1.4E-01	1.02	9.4E-01
Similar to RIKEN cDNA 0710001B24	0.99	2.2E-01	1.12	8.5E-02	1.10	1.6E-01
Parathyrosin	1.30	8.2E-03	1.22	2.7E-01	1.09	4.2E-02
Calcium/calmodulin-dependent protein kinase ID	0.96	3.4E-01	1.01	8.4E-01	1.15	3.3E-02
Transcribed locus	1.03	1.7E-01	1.09	2.3E-01	1.22	1.4E-02
Arachidonate 15-lipoxygenase, second type	1.02	2.9E-01	1.14	1.4E-01	1.09	2.3E-01
Amylase, alpha 2B; pancreatic	1.02	5.1E-01	1.11	5.7E-01	1.17	1.6E-01
Glycophorin C (Gerbich blood group)	0.99	5.4E-01	1.00	8.0E-01	1.13	5.0E-02
	0.96	3.3E-01	1.01	9.0E-01	1.11	2.5E-03
Transcribed locus	1.00	9.4E-01	1.14	1.5E-01	1.14	1.2E-01
Ras association (RalGDS/AF-6) domain family 1	1.03	6.8E-01	1.16	3.6E-01	1.10	4.3E-02
Family with sequence similarity 45, member A	0.97	5.7E-01	1.06	3.9E-01	1.10	5.6E-01

ROD1 regulator of differentiation 1 (S. pombe)	1.27	3.4E-02	1.30	3.0E-01	0.96	6.6E-01
KIAA0553 protein	1.06	3.3E-01	1.13	1.9E-01	1.24	4.4E-02
Hypothetical protein FLJ20265	0.99	5.0E-01	1.07	3.9E-01	1.09	1.3E-01
Vascular endothelial growth factor C	0.96	5.2E-01	1.03	5.3E-01	1.19	1.4E-02
Transcribed locus	0.99	7.7E-01	1.15	3.8E-01	1.07	1.3E-01
KIAA1983 protein	1.13	4.7E-01	1.06	4.7E-01	1.24	3.5E-02
	0.98	6.6E-01	1.08	4.0E-01	1.17	4.6E-03
Cytochrome P450, family 1, subfamily B, polypeptide 1	2.05	7.1E-03	1.82	4.3E-02	1.12	4.2E-01
Nidogen 2 (osteonidogen)	1.00	9.1E-01	1.08	3.0E-01	1.24	1.2E-01
KIAA1465 protein	1.07	2.7E-01	1.01	8.8E-01	1.19	2.1E-01
Sec1 family domain containing 2	0.99	8.9E-01	1.18	8.5E-02	1.13	3.9E-01
Ninjurin 2	1.00	9.7E-01	1.15	2.0E-01	1.20	6.5E-02
synonyms: FLJ22693, PARP12, PARP-12; Homo sapiens zinc finger CCCH type domain containing 1, mRNA (cDNA clone MGC:71625 IMAGE:5296560), complete cds.	1.02	6.4E-01	1.06	8.6E-02	1.19	1.1E-01
CDNA FLJ42255 fis, clone TKIDN2009889	1.02	6.3E-01	1.10	2.2E-01	1.16	3.2E-01
Transcribed locus	1.01	7.5E-01	1.09	3.6E-01	1.12	2.1E-01
	1.07	3.8E-01	1.02	6.8E-01	1.20	2.2E-01
	1.31	1.7E-02	1.30	1.7E-01	0.93	4.8E-01
	1.15	1.4E-01	1.13	4.4E-01	1.22	5.5E-02
	1.20	1.4E-01	1.47	2.5E-03	1.00	9.7E-01
Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	1.08	1.6E-01	2.13	1.1E-02	1.43	3.2E-02
Chaperonin containing TCP1, subunit 4 (delta)	1.06	2.1E-01	1.01	8.9E-01	0.82	1.7E-01
Caspase 7, apoptosis-related cysteine protease	0.86	2.0E-01	0.65	1.1E-01	1.04	7.8E-01
	1.01	9.5E-01	1.13	9.3E-02	1.20	1.6E-01
Growth differentiation factor 15	1.21	2.0E-02	1.40	7.7E-02	1.66	2.2E-03
	1.00	9.3E-01	1.07	5.4E-02	1.12	3.3E-01
Microsomal glutathione S-transferase 3	1.02	7.9E-01	1.09	2.2E-02	1.15	3.2E-01
Transcribed locus	1.03	3.9E-01	1.14	1.0E-01	1.17	1.7E-01
Carboxypeptidase M	0.92	3.8E-01	2.10	3.3E-02	1.48	1.8E-03
Zinc finger, DHHC domain containing 8	1.05	1.5E-01	1.15	2.8E-01	1.10	3.3E-01
Phorbol-12-myristate-13-acetate-induced protein 1	1.09	1.0E-01	1.27	5.0E-02	1.05	5.3E-01
Solute carrier family 37 (glycerol-3-phosphate transporter), member 1	0.99	8.5E-01	1.03	7.9E-02	1.05	5.9E-01
Uncharacterized hematopoietic stem/progenitor cells protein MDS028	1.03	6.1E-01	1.00	9.5E-01	1.04	7.5E-02
Carboxypeptidase A2 (pancreatic)	0.99	8.5E-01	1.02	4.6E-04	1.07	1.2E-01
Inactivation escape 2	1.08	5.1E-01	1.08	3.3E-01	1.21	5.2E-02
	0.98	1.5E-01	1.03	4.7E-01	1.05	6.0E-01
Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	0.84	1.0E-01	0.61	1.8E-03	0.87	1.1E-01
Mitochondrial intermediate peptidase	1.04	5.1E-01	1.08	2.4E-01	1.20	1.1E-01
BTB and CNC homology 1, basic leucine zipper transcription factor 2	1.07	4.0E-03	1.21	6.9E-02	1.15	3.4E-01
	1.06	2.5E-01	1.16	5.8E-02	1.10	3.0E-01
Sarcolemma associated protein	1.03	6.5E-01	1.10	1.9E-01	1.20	9.3E-02
Nasopharyngeal epithelium specific protein 1	1.01	8.2E-01	1.08	2.4E-01	1.20	8.3E-02
Death associated transcription factor 1	1.10	2.9E-01	1.17	1.1E-01	1.12	2.7E-01
Early B-cell factor	0.98	6.4E-01	1.07	5.3E-01	1.08	2.7E-02
RIM binding protein 2	1.02	5.1E-01	1.11	9.6E-03	0.97	no replicates
Chemokine (C-X-C motif) ligand 10	1.04	5.8E-01	1.10	1.9E-01	1.20	2.4E-01
Solute carrier family 2 (facilitated glucose transporter), member 1	1.00	9.7E-01	1.11	2.5E-02	1.13	1.7E-01
Transcribed locus	1.07	2.1E-01	1.11	4.0E-01	1.19	1.1E-01
Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	0.93	5.7E-01	0.67	1.6E-03	0.64	1.6E-02
Adrenergic, alpha-2B-, receptor	1.03	2.0E-01	1.06	4.6E-02	1.08	5.0E-01
RAB, member of RAS oncogene family-like 3	1.07	1.9E-01	1.17	1.2E-01	1.24	4.9E-02
RNA, U22 small nucleolar	1.23	1.7E-01	1.07	1.2E-01	0.93	3.4E-02
Hypothetical protein BC015183	1.02	5.7E-01	1.10	1.6E-01	1.16	1.8E-01

KIAA1199	0.84	1.3E-01	0.67	1.3E-02	0.83	1.2E-01
	1.10	2.1E-01	1.11	1.2E-02	1.18	1.0E-01
Chromosome 13 open reading frame 25	1.02	6.8E-01	1.04	5.2E-01	1.16	2.1E-01
	1.04	4.7E-01	1.04	6.9E-01	1.16	1.0E-01
Chromosome 14 open reading frame 50	1.05	3.5E-02	1.20	8.9E-02	1.17	2.6E-01
Iron-responsive element binding protein 2	0.83	6.9E-02	0.86	1.9E-02	0.96	6.1E-01
Protein kinase C, epsilon	0.97	4.3E-01	1.06	2.3E-01	1.08	1.7E-02
Cytochrome c oxidase subunit 8A (ubiquitous)	1.24	1.5E-01	0.98	9.3E-01	0.86	6.1E-03
Density-regulated protein	0.94	1.0E-01	0.85	1.6E-02	0.82	6.5E-02
	1.03	6.4E-01	1.09	3.7E-01	1.11	1.4E-01
PHD finger protein 3	0.86	8.2E-02	0.92	1.4E-01	0.91	1.5E-01
Isopentenyl-diphosphate delta isomerase	1.10	2.5E-01	1.12	3.7E-01	0.95	1.9E-02
P21(CDKN1A)-activated kinase 4	0.91	3.3E-01	0.74	5.0E-02	1.03	5.7E-01
Retinoblastoma binding protein 8	0.94	1.1E-01	0.91	3.4E-01	0.86	1.2E-02
Striatin, calmodulin binding protein 3	0.78	8.6E-02	1.02	4.8E-01	1.14	4.5E-02
Keratin 6B	1.00	9.7E-01	1.07	2.3E-01	1.16	2.2E-01
Splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	1.02	5.4E-01	0.97	5.5E-01	0.88	1.7E-01
Heterogeneous nuclear ribonucleoprotein R	0.94	8.6E-02	0.82	1.6E-02	0.82	7.8E-02
CD164 antigen, sialomucin	0.99	8.0E-01	1.03	6.2E-01	0.71	3.3E-02
H1 histone family, member 0	1.03	1.7E-01	0.90	1.5E-01	0.78	4.2E-03
Development and differentiation enhancing factor 2	0.83	6.1E-02	0.70	7.8E-02	0.85	1.4E-03
Caspase 9, apoptosis-related cysteine protease	1.01	6.8E-01	0.91	5.1E-01	0.99	no replicates
Polymerase (DNA-directed), delta 3, accessory subunit	0.92	1.8E-01	0.91	3.2E-02	0.99	9.2E-01
Scavenger receptor class B, member 1	1.03	6.7E-01	1.13	2.6E-01	1.18	2.9E-02
	1.16	8.9E-02	0.89	4.4E-02	0.87	2.3E-01
Maba1	0.98	2.2E-01	0.97	1.7E-01	0.85	2.3E-02
MYST histone acetyltransferase 2	0.91	4.6E-01	0.91	2.3E-01	0.90	2.3E-02
Transcribed locus	1.05	4.9E-01	1.13	3.2E-01	1.20	4.0E-02
Vestigial like 4 (Drosophila)	0.76	1.9E-01	0.91	1.3E-02	1.03	3.3E-01
Tubulin, alpha, ubiquitous	1.09	6.4E-01	1.00	1.0E+00	0.75	2.9E-02
Programmed cell death 10	0.95	2.1E-01	0.93	1.4E-01	0.88	3.7E-02
Protein tyrosine phosphatase type IVA, member 1	0.95	2.9E-01	1.16	2.6E-01	1.09	2.3E-01
Eukaryotic translation initiation factor 5	1.11	6.4E-02	1.13	1.6E-01	0.95	1.7E-01
PYM protein	0.94	2.1E-01	0.97	6.3E-01	0.96	3.0E-01
GNAS complex locus	1.24	4.6E-02	1.05	8.4E-01	0.98	5.3E-01
KIAA1033 protein	0.92	3.1E-01	0.89	2.1E-01	0.93	3.6E-02
Spire homolog 1 (Drosophila)	0.93	4.8E-02	0.92	3.7E-01	1.06	2.6E-01
	0.99	7.6E-01	1.23	6.6E-02	1.17	3.6E-01
Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.94	4.0E-01	0.88	8.6E-02	0.64	1.4E-02
CLR pseudogene	0.98	6.4E-01	0.95	4.5E-02	0.96	3.6E-01
Mitochondrial ribosomal protein L3	1.07	5.6E-02	0.89	1.6E-01	0.82	1.1E-01
Transcribed locus	1.05	3.4E-01	1.14	5.7E-02	1.18	3.0E-01
Pogo transposable element with ZNF domain	0.89	5.4E-02	0.94	1.2E-01	0.93	2.0E-01
	0.97	5.1E-01	0.80	9.0E-02	0.82	no replicates
Glioblastoma amplified sequence	1.06	1.1E-01	1.06	1.1E-01	1.08	3.6E-01
Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	0.86	8.8E-02	0.86	2.6E-02	0.95	2.3E-01
Chromosome 20 open reading frame 129	0.89	1.1E-01	0.88	7.2E-02	0.85	3.0E-02
TPX2, microtubule-associated protein homolog (Xenopus laevis)	0.96	2.6E-01	0.84	1.0E-01	0.70	5.1E-02
Fibroblast activation protein, alpha	0.92	1.4E-02	1.04	5.4E-01	1.11	2.0E-01
	1.01	7.6E-01	1.14	1.7E-01	1.15	4.0E-01
Protein tyrosine phosphatase, non-receptor type 12	0.78	1.0E-01	0.80	1.4E-01	0.94	1.7E-04
Chromosome 6 open reading frame 211	0.90	1.5E-01	0.69	1.7E-02	0.97	6.5E-01
Ribosomal protein L12	1.12	1.0E-01	1.13	2.4E-01	0.81	2.1E-01
Solute carrier family 2 (facilitated glucose transporter), member 1	0.90	4.0E-01	0.96	4.4E-03	1.09	7.6E-02
Chromosome 1 open reading frame 39	0.75	3.0E-02	0.78	1.7E-02	0.90	9.4E-02
Golgi phosphoprotein 3 (coat-protein)	0.79	8.6E-02	0.77	1.6E-02	0.85	1.2E-01
Nipped-B homolog (Drosophila)	0.80	7.6E-02	0.85	2.0E-01	0.97	5.5E-01

Transcribed locus, moderately similar to NP_078841.2 hypothetical protein FLJ14166 [Homo sapiens] GTP binding protein 4	1.01	8.6E-01	1.11	1.0E-01	1.20	2.5E-01
	0.91	2.5E-03	1.21	5.3E-02	1.14	1.5E-01
	1.02	7.6E-01	1.14	2.9E-01	1.30	1.2E-01
Hyperparathyroidism 2 (with jaw tumor)	0.89	4.9E-01	0.81	no replicates	0.92	3.5E-01
Golgi autoantigen, golgin subfamily a, 2	1.02	1.7E-01	1.14	2.1E-01	1.10	2.8E-01
X-ray repair complementing defective repair in Chinese hamster cells 1	0.98	5.8E-01	1.09	3.8E-01	1.19	4.0E-02
RAB5A, member RAS oncogene family	0.95	4.3E-01	0.95	6.5E-01	0.88	2.4E-02
Ubiquitin protein ligase E3A (human papilloma virus E6- associated protein, Angelman syndrome)	0.87	1.2E-01	0.91	1.3E-01	0.92	3.3E-02
Hypothetical protein MGC33887	0.96	3.6E-01	1.04	4.2E-01	1.15	7.0E-03
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.97	5.7E-01	0.90	3.7E-01	0.97	6.4E-01
Pre-B-cell leukemia transcription factor 3	0.92	1.5E-01	0.88	1.8E-01	0.88	4.5E-02
Transcribed locus, moderately similar to XP_375099.1 hypothetical protein LOC283585 [Homo sapiens]	0.80	3.3E-02	0.75	5.8E-02	0.97	6.5E-01
Glutamine-fructose-6-phosphate transaminase 1	0.92	1.5E-01	0.81	3.7E-02	0.77	2.4E-02
Sphingomyelin phosphodiesterase, acid-like 3A	0.99	9.3E-01	0.97	4.5E-01	1.01	8.9E-01
Signal recognition particle receptor, B subunit	1.01	5.6E-01	0.95	7.7E-02	1.13	3.6E-02
E74-like factor 1 (ets domain transcription factor)	0.78	1.1E-02	0.91	2.0E-01	1.03	5.1E-01
MAX dimerization protein 1	0.92	2.5E-01	0.83	1.8E-02	1.01	2.1E-01
Sialyltransferase 8A (alpha-N-acetylneuraminase: alpha- 2,8-sialyltransferase, GD3 synthase)	1.00	8.6E-01	1.04	6.4E-01	1.13	1.7E-01
HSPC128 protein	1.01	8.5E-01	1.12	1.9E-01	0.84	3.7E-02
Hypothetical protein FLJ11712	1.00	9.3E-01	0.99	9.1E-01	1.12	1.8E-01
UBX domain containing 2	0.97	2.3E-02	0.90	9.1E-02	0.92	1.7E-01
Leucine rich repeat transmembrane neuronal 1	0.96	2.8E-02	0.98	7.6E-01	1.01	9.7E-01
	0.96	4.3E-01	0.86	3.9E-02	0.90	1.3E-01
Insulin-like growth factor binding protein 5	1.00	9.9E-01	0.73	2.9E-02	1.02	3.8E-01
MutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	0.91	1.5E-01	0.95	5.4E-01	0.89	5.0E-02
Histone deacetylase 6	0.99	8.0E-01	0.80	1.8E-01	1.02	7.9E-01
Leucine-rich PPR-motif containing	0.91	6.9E-02	0.87	1.9E-01	0.92	3.7E-01
Ribosomal protein L10-like	1.03	4.5E-01	1.01	9.5E-01	0.82	4.3E-02
Replication factor C (activator 1) 1, 145kDa	0.92	1.7E-01	1.02	7.6E-01	0.96	1.4E-01
	0.99	9.0E-01	1.11	1.3E-01	0.98	9.0E-01
Lumican	1.02	4.6E-01	1.09	2.1E-01	1.15	2.1E-01
GA binding protein transcription factor, beta subunit 2, 47kDa	0.87	1.2E-01	1.00	9.7E-01	0.86	3.6E-02
SMC1 structural maintenance of chromosomes 1-like 1 (yeast)	0.92	2.3E-01	0.85	3.2E-01	0.84	1.1E-02
Jumonji, AT rich interactive domain 1B (RBP2-like)	0.91	2.3E-01	1.03	4.5E-02	0.99	5.9E-01
Tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, zeta polypeptide	1.10	5.1E-02	0.92	4.2E-01	0.78	no replicates
Dendritic cell protein	1.04	3.7E-01	0.98	6.4E-01	0.81	1.3E-02
Calnexin	0.95	2.4E-01	0.91	3.4E-01	0.81	3.8E-02
Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	1.08	2.1E-01	0.92	5.6E-01	0.79	7.9E-03
	1.05	2.6E-01	0.82	1.3E-01	0.95	4.4E-02
Cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	1.04	1.5E-01	0.88	1.2E-01	0.94	3.8E-01
Transketolase (Wernicke-Korsakoff syndrome)	1.10	3.6E-03	0.93	5.1E-01	1.06	2.3E-01
	0.94	2.1E-01	0.96	8.5E-01	0.83	no replicates
Maba1	1.03	7.0E-01	0.90	1.8E-01	0.80	1.3E-02
Gelsolin (amyloidosis, Finnish type)	1.03	3.4E-01	0.93	5.2E-02	1.32	3.9E-02
Chromosome 6 open reading frame 199	1.04	3.9E-01	1.11	6.4E-02	1.12	4.9E-01
Transcribed locus, moderately similar to NP_689573.2 zinc finger protein 573 [Homo sapiens]	0.99	8.4E-01	1.07	4.9E-01	1.20	4.6E-02



Similar to Kruppel-like factor 7 (ubiquitous); ubiquitous					
Kruppel-like transcription factor	1.02	7.5E-01	1.06	5.1E-01	0.67 1.2E-02
CCCTC-binding factor (zinc finger protein)	0.70	6.4E-02	0.84	3.6E-02	0.96 6.2E-02
Stearoyl-CoA desaturase (delta-9-desaturase)	0.96	4.7E-01	1.08	5.6E-01	0.68 1.8E-02
Elongation factor, RNA polymerase II, 2	0.93	3.3E-01	0.88	1.2E-01	0.79 1.2E-02
SRB7 suppressor of RNA polymerase B homolog (yeast)	1.05	2.5E-01	0.94	4.1E-01	0.95 4.3E-02
	1.05	5.8E-01	1.08	3.5E-01	1.18 1.8E-01
Butyrophilin-like 9	1.13	4.4E-02	1.04	6.5E-01	0.90 1.9E-01
DKFZP564M182 protein	1.14	7.1E-02	1.13	4.4E-01	0.86 1.8E-01
Protein kinase, lysine deficient 1	0.98	5.7E-01	0.90	2.0E-01	0.93 2.6E-03
SKI interacting protein	0.94	1.6E-01	0.90	2.6E-01	0.83 5.9E-02
Ribosomal protein L3-like	1.05	4.4E-01	0.86	2.9E-02	0.76 7.6E-03
Hypothetical protein FLJ14525	1.16	2.4E-02	1.00	9.6E-01	0.91 2.7E-01
Integral membrane protein 2B	1.10	1.3E-02	1.08	1.8E-01	1.01 9.1E-01
Reticulon 3	1.02	7.5E-01	1.07	5.9E-01	0.77 1.5E-02
Casein kinase 1, alpha 1	0.98	8.3E-01	0.82	7.2E-02	0.83 2.0E-02
Hypothetical protein LOC90321	0.98	4.0E-01	1.03	3.5E-03	1.22 1.9E-01
Tau tubulin kinase 1	0.97	7.2E-01	1.00	9.6E-01	1.14 3.8E-01
Eukaryotic translation initiation factor 4 gamma, 1	1.08	2.5E-01	0.95	6.3E-01	1.02 4.1E-02
Sp3 transcription factor	0.92	1.8E-01	0.97	4.6E-01	0.80 4.7E-02
Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	1.08	1.8E-01	0.96	5.4E-01	0.84 3.8E-02
Transcribed locus	0.97	4.9E-01	1.10	5.3E-02	1.21 2.0E-01
FCH domain only 1	1.07	2.4E-01	1.09	1.2E-02	1.14 5.1E-01
Unc-84 homolog A (C. elegans)	0.85	1.7E-02	0.74	1.4E-01	0.86 2.4E-01
CCCTC-binding factor (zinc finger protein)	0.85	2.1E-01	0.89	9.6E-02	0.86 1.8E-02
Serine hydroxymethyltransferase 2 (mitochondrial)	1.02	7.2E-01	0.91	2.6E-01	0.64 4.1E-04
ATP-binding cassette, sub-family F (GCN20), member 1	0.90	2.0E-01	0.87	1.1E-01	1.05 2.5E-01
Transcribed locus	1.02	5.3E-01	1.09	1.0E-01	1.11 3.4E-01
Topoisomerase (DNA) I	0.94	2.7E-02	0.96	7.3E-01	0.94 1.8E-01
	0.83	4.0E-03	0.90	3.5E-01	0.90 2.7E-01
Carbonic anhydrase II	0.95	1.3E-01	0.95	6.5E-01	0.65 1.4E-02
Mitogen-activated protein kinase 6	0.94	2.6E-01	1.05	2.9E-01	0.90 3.3E-01
Protein tyrosine phosphatase, non-receptor type 3	0.96	1.3E-01	1.08	3.5E-01	1.13 4.4E-01
RNA binding motif (RNP1, RRM) protein 3	1.03	7.2E-01	0.90	6.5E-01	0.63 2.5E-02
Proteasome (prosome, macropain) 26S subunit, ATPase, 6	0.97	2.1E-01	0.94	3.7E-01	0.88 8.2E-02
Sortilin-related VPS10 domain containing receptor 2	0.86	1.9E-01	0.89	7.3E-02	0.94 2.0E-01
WD-repeat protein	0.86	3.1E-02	0.98	7.3E-01	0.91 2.5E-01
	1.11	1.6E-01	1.09	1.1E-01	0.85 3.0E-01
Ribosomal protein L18	1.12	1.8E-01	1.02	8.3E-01	0.95 2.7E-01
Vacuolar protein sorting 35 (yeast)	0.82	no replicates	0.92	3.2E-02	0.90 7.7E-06
Cyclin D1 (PRAD1: parathyroid adenomatosis 1)	0.90	1.6E-01	0.75	6.9E-02	1.04 6.2E-01
Hypothetical protein DKFZp761O0113	0.98	3.9E-01	1.02	6.6E-01	1.18 1.3E-01
Chromosome condensation-related SMC-associated protein 1	0.91	3.6E-01	0.84	4.6E-02	0.93 2.6E-02
TTK protein kinase	0.90	2.5E-01	0.84	7.1E-02	0.70 3.7E-03
Zinc finger, CW-type with coiled-coil domain 3	1.00	1.0E+00	1.06	4.2E-01	1.08 4.3E-01
Sorting nexin 13	0.96	1.8E-01	1.05	1.5E-01	1.15 2.5E-01
Catenin (cadherin-associated protein), alpha 1, 102kDa	0.97	6.1E-01	0.79	1.3E-02	0.85 1.0E-01
	0.86	5.8E-02	0.63	2.1E-02	0.94 2.2E-01
	0.98	5.5E-01	0.88	3.2E-02	0.74 5.5E-04
Ribosomal protein L36a-like	1.15	1.2E-01	1.14	2.9E-02	0.99 9.2E-01
TRK-fused gene	1.05	6.5E-02	0.94	6.1E-01	0.87 2.4E-01
Ribosomal protein L35a	1.07	4.6E-01	1.05	3.4E-01	0.91 3.5E-01
Myomesin family, member 3	1.13	4.5E-02	1.14	6.6E-02	1.15 3.4E-01
TPTE pseudogene	1.03	6.0E-01	1.07	3.3E-01	1.14 1.7E-02
PTK9 protein tyrosine kinase 9	1.01	8.6E-01	0.99	8.9E-01	0.80 3.7E-02
Delta-like 1 homolog (Drosophila)	1.02	no replicates	0.96	3.8E-01	0.76 1.7E-02

DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	1.03	5.1E-01	0.90	3.2E-01	0.94	2.4E-01
Lipoma HMGIC fusion partner-like 3	1.00	9.1E-01	0.97	5.5E-01	0.87	8.6E-02
Epithelial membrane protein 2	0.97	4.9E-01	0.79	9.9E-02	0.73	2.7E-02
Topoisomerase (DNA) II beta 180kDa	0.92	4.7E-02	0.82	1.1E-01	1.05	3.5E-01
Breast carcinoma amplified sequence 3	1.08	9.5E-02	0.68	1.3E-02	1.01	8.7E-01
KIAA0182 protein	0.78	6.4E-02	0.74	1.3E-02	0.89	2.0E-01
	1.13	1.4E-02	0.99	8.9E-01	0.91	8.5E-02
Unactive progesterone receptor, 23 kD	0.94	8.3E-02	0.83	3.8E-02	0.75	4.9E-02
Similar to ribosomal protein L13a; 60S ribosomal protein L13a; 23 kD highly basic protein	1.16	2.4E-01	1.02	6.8E-01	1.00	9.7E-01
Sin3A associated protein p30-like	1.01	5.0E-01	1.07	5.5E-01	1.25	1.3E-01
BCL2-associated X protein	1.05	3.5E-01	1.26	1.8E-01	1.66	8.5E-02
Ras and Rab interactor 2	0.97	1.5E-01	1.01	7.9E-01	1.13	1.1E-01
Mitochondrial ribosomal protein L53	1.03	6.6E-01	1.03	8.6E-02	1.13	9.8E-02
Interleukin 18 receptor accessory protein	1.00	9.4E-01	1.08	5.8E-02	1.23	2.2E-01
Ral guanine nucleotide dissociation stimulator-like 2	1.08	5.5E-01	1.10	2.5E-01	1.31	9.7E-02
Hypothetical protein FLJ35382	1.03	4.4E-01	1.05	4.7E-01	1.17	1.8E-01
Hypothetical LOC400843	1.00	8.9E-01	0.98	7.1E-01	1.03	2.7E-01
Proprotein convertase subtilisin/kexin type 6	1.02	4.9E-01	1.05	7.1E-01	1.15	2.1E-01
Vacuolar protein sorting protein 18	1.01	7.5E-01	1.10	1.2E-01	1.29	3.8E-01
Interleukin 12 receptor, beta 2	1.03	6.6E-01	1.09	2.2E-01	1.10	2.0E-01
ATPase, Class V, type 10D	0.97	2.8E-01	1.10	2.8E-01	1.06	4.5E-01
Serologically defined colon cancer antigen 8	1.01	7.1E-01	1.05	6.8E-02	1.07	5.6E-01
	1.05	4.7E-01	1.01	9.0E-01	1.15	2.0E-01
Ring finger protein 5	1.00	9.2E-01	1.06	5.8E-01	1.07	3.3E-01
Transcribed locus, weakly similar to XP_375099.1						
hypothetical protein LOC283585 [Homo sapiens]	0.98	2.1E-01	1.09	2.3E-01	1.15	6.2E-02
CDNA FLJ43312 fis, clone NT2RI2012659	1.16	5.0E-02	1.25	6.4E-02	1.08	6.5E-01
	0.99	8.5E-01	1.21	2.4E-01	1.23	2.4E-01
Potassium voltage-gated channel, KQT-like subfamily, member 2	0.95	2.7E-01	1.04	4.7E-01	1.05	5.1E-02
Rearranged L-myc fusion sequence	1.05	6.5E-01	1.06	2.6E-01	1.25	1.6E-01
	1.11	2.4E-01	1.65	9.1E-02	1.30	3.2E-02
	1.17	9.3E-02	1.41	5.5E-02	1.09	2.6E-01
Glypican 5	0.97	6.7E-03	1.05	6.7E-01	1.05	7.8E-01
	1.08	2.8E-01	1.21	1.3E-01		
Zinc finger protein 137 (clone pHZ-30)	0.99	7.2E-01	1.08	2.9E-01	1.09	2.4E-01
LOC440900	1.04	no replicates	1.19	2.5E-01	1.22	1.3E-01
Cadherin 11, type 2, OB-cadherin (osteoblast)	0.99	8.4E-01	0.96	5.9E-01	1.19	5.2E-02
Cyclin G1	1.13	5.3E-01	1.59	1.6E-02	1.19	1.5E-01
Major histocompatibility complex, class I-related	1.03	7.1E-01	1.06	7.9E-02	1.11	1.2E-01
Hypothetical protein FLJ22104	0.93	4.8E-02	1.02	8.6E-01	1.09	3.9E-01
Activating transcription factor 3	1.01	7.9E-01	1.16	2.9E-01	0.96	5.1E-01
Nuclear RNA export factor 1	1.15	1.2E-01	1.28	4.6E-02	1.02	8.0E-01
Chromosome 9 open reading frame 47	1.00	9.3E-01	1.11	1.2E-01	1.07	1.5E-01
	1.11	2.8E-01	1.01	6.7E-01	1.09	6.7E-01
NPD014 protein	1.20	no replicates	1.12	2.0E-01	0.92	3.7E-02
Glycerol kinase 2	0.88	no replicates	1.06	3.5E-01	1.06	2.7E-01
Solute carrier family 22 (organic cation transporter), member 17	0.97	6.1E-01	1.14	2.5E-01	1.09	2.0E-01
Tumor necrosis factor, alpha-induced protein 2	1.02	8.1E-01	1.06	3.9E-01	1.09	5.6E-01
Hypothetical protein DKFZp313G1735	1.01	9.3E-01	1.07	2.9E-01	1.10	4.6E-01
DNA methyltransferase 1 associated protein 1	1.03	2.1E-01	1.10	9.6E-02	1.14	3.2E-01
ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1.07	2.2E-02	1.03	4.3E-01	1.04	2.0E-01
Transcribed locus	0.95	no replicates	1.00	9.9E-01	1.11	2.3E-02
Trophoblast-derived noncoding RNA	1.22	no replicates	1.26	no replicates	1.17	no replicates
Ets variant gene 5 (ets-related molecule)	0.90	no replicates	0.97	3.3E-01	1.18	2.1E-02
KIAA0152 gene product	1.20	2.0E-03	1.15	1.2E-01	0.94	5.1E-01
General transcription factor IIH, polypeptide 5	1.03	6.7E-01	1.12	7.8E-03	1.19	2.4E-01
Diablo homolog (Drosophila)	1.02	5.8E-01	1.07	2.9E-01	1.10	1.8E-01
Unc-119 homolog (C. elegans)	1.02	7.4E-01	1.07	6.8E-03	1.12	3.2E-01

Syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	0.94	4.4E-01	1.04	3.7E-01	1.04	4.2E-01
Hypothetical protein LOC285958	1.11	1.4E-01	1.06	1.8E-01	1.14	1.5E-01
Hypothetical protein FLJ30679	1.02	6.7E-01	1.08	1.6E-01	1.18	5.2E-02
Zinc finger protein 100	0.97	2.3E-01	1.04	9.2E-02	1.08	9.3E-02
Ornithine carbamoyltransferase	0.98	3.7E-01	1.02	5.8E-01	1.13	1.6E-01
Claudin 12	1.03	3.0E-01	1.05	2.8E-01	1.04	4.3E-01
VENT-like homeobox 2	1.11	6.0E-01	1.04	6.2E-01	1.07	3.4E-01
Adenosine kinase	1.06	2.5E-01	1.17	7.3E-02	1.09	4.0E-01
Neutral sphingomyelinase (N-SMase) activation associated factor	0.99	6.9E-01	1.12	1.4E-01	1.16	1.0E-01
	1.05	5.0E-01	1.18	7.2E-02	1.14	2.0E-01
Deleted in lymphocytic leukemia, 1	1.04	2.9E-01	1.08	2.5E-01	1.16	1.2E-01
KH domain containing, RNA binding, signal transduction associated 3	1.02	2.5E-01	0.95	1.6E-01	1.09	2.3E-01
Hypothetical protein FLJ20422	1.03	4.2E-01	1.00	1.0E+00	1.12	2.9E-01
Homo sapiens, clone IMAGE:5271023, mRNA	0.99	9.0E-01	1.10	3.6E-01	1.17	1.3E-01
Chromosome 18 open reading frame 43	1.00	8.9E-01	1.03	5.6E-01	1.15	3.1E-01
Fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)	1.01	4.5E-01	1.06	5.1E-01	1.15	5.8E-01
Thioredoxin	1.10	1.2E-01	1.10	2.3E-01	1.00	9.3E-01
Dedicator of cytokinesis 2	0.95	4.2E-01	1.11	3.2E-01	1.09	2.1E-01
Zinc finger protein 2 (A1-5)	0.99	8.7E-01	1.25	2.2E-01	1.17	1.4E-01
PRKR interacting protein 1 (IL11 inducible)	1.01	6.8E-01	1.06	1.0E-01	1.16	2.3E-01
Hypothetical gene supported by BC062741	1.10	2.5E-01	1.12	9.2E-02	1.17	3.1E-01
Hypothetical protein MGC40397	1.06	3.7E-01	1.16	1.4E-01	1.19	5.2E-02
KIAA1900	1.03	6.7E-01	1.01	7.7E-01	1.11	3.2E-01
BarH-like homeobox 1	1.04	4.4E-01	1.02	3.6E-01	1.10	2.2E-01
Cytochrome P450, family 2, subfamily R, polypeptide 1	0.98	7.3E-01	1.04	4.7E-01	1.11	4.6E-01
Hypothetical protein FLJ32499	0.96	5.3E-01	1.01	9.0E-01	1.07	2.9E-01
Biogenesis of lysosome-related organelles complex-1, subunit 1	0.96	3.6E-01	1.06	6.7E-01	1.14	4.6E-02
Zinc finger protein 318	0.97	6.1E-01	1.11	1.3E-01	1.11	3.8E-01
Hypothetical protein LOC285692	1.01	8.2E-01	1.13	8.5E-02	1.10	3.9E-01
Cell death-regulatory protein GRIM19	1.07	4.3E-01	1.17	3.3E-01	1.20	1.1E-01
EPS8-like 3	1.02	4.1E-01	1.03	4.1E-01	1.07	3.7E-01
Serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsin), member 2	0.99	4.9E-01	0.92	3.6E-01	1.11	3.8E-01
	1.05	1.5E-01	1.08	7.2E-02	1.17	2.9E-01
Mindbomb homolog 1 (Drosophila)	0.99	7.6E-01	1.02	5.4E-01	1.11	1.2E-01
Hypothetical protein FLJ21616	1.00	9.5E-01	0.96	3.8E-02	1.07	2.4E-01
Zinc finger, DHHC domain containing 4	1.01	8.8E-01	1.07	1.4E-01	1.16	7.7E-02
Chloride channel 3	1.02	7.1E-01	1.03	5.6E-01	1.04	3.2E-01
Phosphatase and actin regulator 4	1.02	7.7E-01	1.11	1.9E-01	1.14	4.1E-01
KIAA0141 gene product	0.98	5.6E-01	1.02	6.1E-01	1.15	2.1E-01
LIM domains containing 1	0.98	6.2E-01	1.03	7.2E-01	1.11	3.0E-01
Similar to hypothetical protein	0.98	8.0E-01	1.13	9.2E-02	1.10	4.3E-01
Heat shock transcription factor 2	1.03	5.1E-01	1.02	7.2E-01	1.15	1.5E-01
N-acylaminoacyl-peptide hydrolase	1.01	7.0E-01	1.08	1.6E-01	1.20	5.8E-02
PDZ domain containing 3	0.95	4.0E-01	1.10	4.3E-01	1.17	1.9E-01
Transcribed locus	1.05	1.4E-01	1.11	1.6E-01	1.13	2.6E-01
Cathepsin S	0.99	8.9E-01	1.09	3.4E-01	1.18	1.7E-01
Zinc finger, FYVE domain containing 20	0.99	6.9E-01	1.06	2.5E-01	1.21	1.4E-01
Hypothetical protein FLJ13150	1.01	9.0E-01	1.09	3.7E-01	1.08	1.1E-01
Suppression of tumorigenicity 7 like	0.97	5.8E-01	1.10	1.7E-01	1.13	3.1E-01
Major histocompatibility complex, class I-related	1.00	8.3E-01	1.12	2.1E-01	1.14	5.8E-01
Pancreatic lipase-related protein 1	1.02	2.3E-01	1.04	2.7E-01	1.05	2.6E-01
LEM domain containing 1	0.97	5.7E-02	1.11	2.6E-01	1.20	1.4E-01
Chromosome 18 open reading frame 1	0.96	4.9E-01	1.05	4.3E-01	1.12	2.3E-01
Frizzled homolog 10 (Drosophila)	1.06	1.9E-01	1.15	8.3E-02	1.15	2.3E-01
Zinc finger protein 202	0.99	6.7E-01	1.07	3.5E-01	1.06	4.2E-01
KIAA1961 protein	0.99	7.1E-01	1.06	4.2E-01	1.04	7.8E-01

Transcribed locus, moderately similar to NP_997349.1	1.00	9.4E-01	1.08	3.8E-01	1.17	2.7E-01
FLJ46489 protein [Homo sapiens]	1.01	9.0E-01	1.02	6.7E-01	1.06	3.8E-01
RNA binding protein with multiple splicing	1.07	6.6E-02	1.08	3.2E-01	1.18	1.7E-01
Hypothetical protein FLJ14082	1.00	9.1E-01	1.10	9.3E-02	1.18	1.9E-01
BTB (POZ) domain containing 5	0.96	6.4E-01	1.02	7.5E-01	1.16	2.6E-01
Calmegin	1.03	4.7E-01	0.98	3.9E-01	1.07	4.4E-01
Rap2 interacting protein x	1.05	4.5E-01	1.01	8.2E-01	1.14	2.1E-01
Hypothetical protein FLJ31166	1.03	5.9E-01	1.17	1.0E-01	1.08	6.0E-01
FLJ46385 protein	1.02	7.1E-01	1.11	4.2E-02	1.17	2.4E-01
Solute carrier organic anion transporter family, member 4A1	1.00	9.6E-01	1.09	2.8E-01	1.12	3.5E-01
Transcribed locus	0.98	8.4E-01	1.01	8.8E-01	1.06	3.4E-01
Matrix metalloproteinase 27	1.08	7.6E-02	1.10	2.8E-01	1.05	4.0E-01
Hypothetical protein FLJ21103	0.97	4.3E-01	0.97	3.5E-01	1.09	2.9E-01
KIAA1005 protein	1.04	3.5E-01	1.09	2.9E-01	1.25	1.5E-01
Hypothetical protein KIAA1434	0.95	4.1E-03	0.94	2.0E-01	1.04	4.5E-01
Nebulin-related anchoring protein	1.00	9.7E-01	1.09	2.5E-01	1.12	2.7E-01
TruB pseudouridine (psi) synthase homolog 1 (E. coli)	0.99	8.0E-01	1.00	9.5E-01	1.17	1.3E-02
Roundabout, axon guidance receptor, homolog 1 (Drosophila)	0.98	4.3E-01	1.04	5.9E-01	1.16	1.9E-01
DNA glycosylase hFPG2	0.99	8.3E-01	1.13	1.4E-01	1.04	6.8E-01
WAS protein family, member 1	0.98	7.2E-01	1.10	2.2E-01	1.09	4.0E-01
	0.97	5.1E-01	1.07	1.9E-01	1.18	3.1E-01
Hypothetical protein FLJ36665	1.07	1.4E-01	1.04	3.8E-01	1.18	8.6E-02
Hypothetical protein LOC283507	1.05	2.2E-01	1.10	1.5E-01	1.19	1.1E-01
MRNA; cDNA DKFZp761F1212 (from clone DKFZp761F1212)	1.03	6.9E-01	1.08	5.9E-02	1.11	3.3E-01
Caveolin 3	1.02	6.3E-01	1.05	1.9E-01	1.09	3.3E-01
Tetratricopeptide repeat domain 19	1.05	3.4E-01	1.09	2.6E-01	1.12	2.8E-01
Hypothetical protein MGC10986	1.00	9.2E-01	1.06	5.5E-01	1.16	2.8E-01
Fat-like cadherin FATJ	0.98	2.3E-01	1.00	7.7E-01	1.10	4.4E-01
Transmembrane protein 10	0.95	1.7E-01	1.00	9.8E-01	1.10	2.3E-01
	0.97	6.0E-01	1.08	3.0E-01	1.25	1.5E-01
Peroxisome proliferative activated receptor, gamma	1.04	1.4E-01	1.06	9.9E-02	1.19	1.9E-01
Scavenger receptor cysteine-rich type 1 protein M160	1.01	8.3E-01	1.10	3.8E-01	1.14	7.5E-02
Solute carrier family 9 (sodium/hydrogen exchanger), isoform 7	0.98	2.8E-01	0.98	7.9E-01	1.04	7.2E-01
Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	1.03	4.7E-01	1.05	4.2E-01	1.18	1.1E-01
Williams Beuren syndrome chromosome region 18	0.95	3.6E-01	1.03	6.4E-01	1.08	1.6E-01
Homeo box C13	1.01	7.7E-01	0.99	8.7E-01	1.13	9.5E-02
Hydroxyacyl-Coenzyme A dehydrogenase, type II	0.99	8.8E-01	1.00	8.7E-01	1.10	2.4E-01
	1.01	6.9E-01	1.03	2.0E-01	1.17	1.2E-01
Desmocollin 2	0.99	8.5E-01	1.04	2.3E-01	1.13	3.0E-01
TGFB inducible early growth response	0.99	7.7E-01	1.01	9.0E-01	1.08	4.7E-01
Transcribed locus	1.00	9.0E-01	1.02	4.8E-01	1.09	3.3E-01
	1.03	5.7E-01	1.14	8.5E-02	1.24	1.9E-01
Synaptogyrin 4	1.05	7.4E-02	1.06	1.5E-01	1.08	4.2E-01
Hypothetical protein FLJ40852	1.03	4.3E-01	1.02	1.4E-01	1.15	9.5E-02
Pim-1 oncogene	1.01	8.9E-01	1.01	8.5E-01	1.06	4.6E-01
	1.04	6.8E-01	1.07	3.7E-01	1.13	1.6E-01
Hypothetical LOC389188	0.97	1.8E-01	1.07	4.5E-01	1.15	1.0E-01
Likely ortholog of mouse monocyte macrophage 19	1.00	9.9E-01	1.02	4.2E-01	1.19	1.2E-01
CDNA FLJ23791 fis, clone HEP21711	1.03	2.9E-01	0.99	7.6E-01	1.07	5.2E-01
C1q and tumor necrosis factor related protein 3	1.00	8.7E-01	1.03	2.2E-01	1.13	2.8E-01
FYN binding protein (FYB-120/130)	1.00	9.8E-01	1.06	2.4E-01	1.18	1.4E-01
ATP-binding cassette, sub-family B (MDR/TAP), member 5	1.01	7.0E-01	1.08	2.4E-01	1.07	2.9E-01
Homeo box D8	1.05	2.9E-01	1.06	3.3E-01	1.08	4.2E-01
Transcribed locus	0.97	3.5E-01	0.99	7.9E-01	1.10	9.8E-02

Thioredoxin domain containing	0.95	4.2E-01	1.04	4.3E-01	1.11	8.8E-02
Transcribed locus	0.97	5.3E-01	1.06	2.3E-01	1.06	5.5E-01
Transcribed locus	1.03	5.1E-01	1.04	2.0E-01	1.15	2.9E-01
RNA-binding protein with multiple splicing 2	1.01	7.3E-01	1.02	8.4E-01	1.17	5.0E-02
Transcription factor 8 (represses interleukin 2 expression)	1.02	6.3E-01	1.14	1.6E-01	1.21	2.9E-01
	0.93	2.0E-01	1.11	4.4E-01	1.14	1.8E-01
Matrilin 3	0.99	8.3E-01	1.05	2.5E-01	1.22	1.3E-01
Hypothetical protein FLJ20668	1.07	2.1E-01	1.15	2.7E-01	1.09	1.4E-01
Caldesmon 1	1.06	3.6E-01	1.17	2.3E-01	1.13	2.7E-01
Chromogranin B (secretogranin 1)	1.02	6.0E-01	1.01	7.9E-01	1.11	7.6E-02
	1.05	4.5E-01	1.20	5.6E-02	1.18	3.0E-01
G patch domain containing 1	1.03	4.4E-01	1.15	1.6E-01	1.12	3.3E-01
	1.04	4.8E-01	1.10	1.1E-01	1.13	4.6E-01
Signal transducer and activator of transcription 1, 91kDa	0.97	1.1E-02	0.95	4.3E-01	1.18	5.9E-02
Neurotrophic tyrosine kinase, receptor, type 2	1.01	3.4E-01	1.02	6.8E-01	1.08	3.5E-01
IKK interacting protein	0.97	3.5E-01	1.04	6.4E-01	1.09	1.8E-01
KIAA1432	0.97	1.5E-01	1.11	1.8E-01	1.21	1.0E-01
Interferon regulatory factor 1	0.99	7.5E-01	1.00	9.5E-01	1.15	2.0E-01
InaD-like protein	0.95	1.8E-01	1.00	9.9E-01	1.10	4.6E-01
Transcribed locus	1.01	8.3E-01	1.08	1.3E-01	1.14	2.7E-01
Sodium channel, voltage-gated, type II, beta	0.98	4.0E-01	1.02	5.7E-01	1.18	2.6E-01
LOC440135	1.03	6.2E-01	1.03	3.9E-01	1.14	3.2E-01
Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	1.01	9.0E-01	1.03	7.1E-01	1.05	5.5E-01
Low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	1.02	7.4E-01	1.16	1.9E-01	1.15	2.0E-01
Protocadherin 20	1.03	5.8E-01	1.00	9.3E-01	1.22	6.6E-02
ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1	1.01	8.9E-01	1.04	3.3E-01	1.11	3.2E-01
Similar to Golgi autoantigen, golgin subfamily A member 6 (Golgin linked to PML) (Golgin-like protein)	1.02	6.3E-01	1.06	3.1E-01	1.18	1.8E-01
Hypothetical gene FLJ13072	1.03	1.6E-01	1.10	7.6E-02	1.16	3.0E-01
Transcribed locus	1.01	6.9E-01	1.08	2.6E-01	1.15	4.7E-01
Integrin, alpha 7	1.03	6.1E-01	1.01	2.6E-01	1.11	4.3E-01
5',3'-nucleotidase, mitochondrial	1.06	3.2E-01	1.03	5.5E-01	1.14	5.9E-02
TBC1 domain family, member 5	0.95	6.6E-02	0.98	5.2E-01	1.12	9.4E-02
Pseudouridylylase synthase 3	1.03	4.8E-01	1.08	2.6E-02	1.10	3.0E-01
Transcribed locus	1.00	9.8E-01	1.13	1.1E-01	1.17	2.8E-01
Discs, large (Drosophila) homolog-associated protein 4	1.00	9.5E-01	1.08	5.6E-01	0.98	6.1E-01
KIAA2026	1.00	9.5E-01	1.06	1.0E-01	1.17	1.5E-01
Hypothetical gene supported by BC040831	1.00	9.7E-01	1.12	2.7E-01	1.13	1.0E-01
TRAF and TNF receptor associated protein	0.88	7.0E-02	0.96	3.8E-01	0.97	5.9E-01
Golgi autoantigen, golgin subfamily a, 4	0.82	9.3E-02	0.95	6.6E-01	0.99	6.4E-01
RAB22A, member RAS oncogene family	0.91	9.7E-02	1.05	7.2E-01	1.01	9.0E-01
Protein tyrosine phosphatase, receptor type, C-associated protein	1.08	3.3E-01	1.14	1.8E-01	0.98	8.0E-01
Hypothetical protein FLJ11046	0.91	2.0E-01	0.94	1.2E-01	0.95	2.1E-02
High-mobility group box 1	1.14	2.3E-01	1.17	3.6E-01	0.81	2.0E-01
Basic transcription factor 3	1.02	3.6E-01	1.15	1.9E-01	0.81	1.8E-01
Coatomer protein complex, subunit beta	0.99	8.1E-01	0.92	4.0E-01	0.90	1.3E-01
Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	1.02	4.9E-01	0.97	4.8E-01	0.98	5.8E-01
GNAS complex locus	1.13	9.9E-02	1.03	7.7E-01	0.94	2.4E-01
Thyroid hormone receptor interactor 13	1.01	4.1E-01	0.90	1.2E-01	0.95	4.4E-01
H2A histone family, member Y2	0.89	3.6E-01	0.91	3.1E-01	0.93	1.2E-01
Hypothetical protein FLJ13955	1.04	6.3E-02	0.95	3.5E-01	0.79	1.8E-01
Adducin 3 (gamma)	0.79	1.5E-01	1.07	7.1E-01	0.88	4.0E-02
CCAAT/enhancer binding protein (C/EBP), gamma	0.91	1.8E-01	0.93	8.7E-03	0.80	6.8E-02
Poly(A) binding protein, cytoplasmic 1	1.14	5.0E-01	0.95	5.6E-01	0.80	1.2E-01

Forkhead box P1	0.89	2.2E-01	0.86	1.1E-01	0.89	6.7E-02
Homo sapiens, clone IMAGE:5299642, mRNA	0.84	2.8E-01	0.93	1.6E-01	0.95	2.8E-01
Runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	0.73	2.1E-01	0.86	1.0E-01	1.09	3.2E-02
	0.85	9.2E-02	0.82	5.8E-03	0.96	2.4E-01
Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	0.84	1.0E-01	0.92	4.2E-02	0.96	3.1E-01
Ring finger protein 4	0.89	9.0E-02	1.00	9.8E-01	0.88	1.0E-01
	0.84	1.6E-01	0.83	3.6E-02	0.95	3.8E-01
Pleckstrin homology domain containing, family C (with FERM domain) member 1	0.95	6.4E-01	0.88	1.1E-01	0.94	3.7E-02
Protein phosphatase 2, regulatory subunit B (B56), alpha isoform	0.94	2.6E-01	0.84	3.3E-02	0.93	4.1E-01
Ataxin 1	0.82	5.2E-01	0.76	3.5E-03	0.97	2.2E-01
Zinc finger protein, X-linked	0.77	no replicates	0.97	6.7E-01	0.88	3.1E-01
Metastasis suppressor 1	0.92	3.6E-01	0.81	no replicates	0.72	1.7E-02
Mastermind-like 1 (Drosophila)	0.85	7.3E-02	1.12	5.2E-01	0.95	1.6E-03
Pleckstrin homology domain containing, family F (with FYVE domain) member 2	0.85	3.3E-02	0.94	2.1E-01	0.97	5.5E-01
Adaptor-related protein complex 1, gamma 1 subunit	0.91	1.1E-01	0.89	2.6E-01	1.05	6.9E-01
PTK2 protein tyrosine kinase 2	0.83	no replicates	0.92	1.9E-02	0.99	7.9E-01
Ring finger protein 12	0.90	1.0E-01	0.96	4.5E-01	0.96	2.1E-01
Kinesin family member 5B	0.84	3.0E-03	0.85	1.1E-01	0.90	6.3E-02
Ubiquitin A-52 residue ribosomal protein fusion product 1	1.10	1.8E-02	1.04	8.0E-01	0.99	1.8E-01
Catenin (cadherin-associated protein), beta 1, 88kDa	1.05	3.0E-01	1.07	1.3E-01	0.99	8.8E-01
PABP1-dependent poly A-specific ribonuclease subunit PAN3	0.92	2.9E-01	0.96	4.6E-01	0.98	6.6E-01
Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	0.99	9.4E-01	1.02	7.3E-01	1.16	1.9E-03
Plakophilin 3	0.81	5.2E-02	0.76	8.0E-02	0.96	1.4E-01
Calpain, small subunit 1	1.09	4.0E-01	1.02	8.3E-01	0.92	2.0E-01
RGM domain family, member B	0.99	8.9E-01	0.87	4.0E-01	0.81	1.2E-01
High density lipoprotein binding protein (vigilin)	1.11	7.3E-02	0.94	1.5E-01	0.94	5.9E-02
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	1.02	6.9E-01	0.94	3.3E-01	0.96	6.4E-01
Programmed cell death 5	1.07	4.4E-02	0.92	4.0E-01	0.96	6.6E-01
Chromosome 12 open reading frame 8	1.00	8.3E-01	0.99	8.8E-01	0.89	3.7E-01
Cathepsin D (lysosomal aspartyl protease)	1.19	3.4E-01	0.90	5.0E-01	0.96	7.1E-01
Transcribed locus	1.09	1.2E-01	1.07	3.0E-01	0.84	7.1E-02
Full-length cDNA clone CS0DE008YL13 of Placenta of Homo sapiens (human)	0.95	1.2E-01	0.96	4.7E-01	1.00	9.4E-01
Eukaryotic translation initiation factor 4 gamma, 2	1.07	2.3E-01	0.95	6.6E-02	1.05	7.9E-01
Heat shock 70kDa protein 8	1.16	2.0E-01	0.95	6.3E-01	1.21	1.8E-01
Sulfatase 2	0.93	3.7E-01	0.87	1.1E-01	1.14	2.8E-01
Calnexin	0.98	7.6E-01	0.98	8.4E-01	0.81	7.4E-02
	1.04	5.6E-01	0.95	2.6E-01	0.60	3.2E-02
	1.08	5.5E-01	0.95	6.9E-01	0.94	4.5E-01
KIAA2010	0.86	1.1E-01	0.95	7.3E-02	1.05	6.3E-01
Cyclic AMP phosphoprotein, 19 kD	1.13	7.4E-03	1.13	2.1E-01	0.91	1.1E-01
Proteasome (prosome, macropain) 26S subunit, ATPase, 6	0.96	1.1E-01	0.97	5.7E-01	0.95	3.8E-01
Anterior gradient 2 homolog (Xenopus laevis)	1.10	1.7E-01	1.10	2.0E-01	0.97	4.7E-01
	1.02	5.6E-01	0.85	6.7E-02	0.88	1.6E-01
RAD23 homolog B (S. cerevisiae)	0.94	2.3E-01	0.86	7.8E-02	1.11	1.2E-01
	1.12	1.2E-01	1.12	1.1E-01	0.99	9.4E-01
Gem (nuclear organelle) associated protein 4	1.05	5.1E-01	0.88	1.4E-01	0.95	5.4E-02
Transducer of ERBB2, 1	1.03	4.4E-01	1.01	9.1E-01	0.97	7.7E-01
Gelsolin (amyloidosis, Finnish type)	1.07	3.0E-01	0.96	3.2E-01	1.13	2.3E-01
HLA-B associated transcript 2	0.95	2.8E-01	0.91	4.6E-01	0.99	9.3E-01

Ubiquitin specific protease 10	0.88	6.9E-02	0.87	2.4E-01	0.95	3.1E-01
SMT3 suppressor of mif two 3 homolog 2 (yeast)	0.99	6.4E-01	0.93	2.2E-01	0.93	5.1E-01
Actin, gamma 2, smooth muscle, enteric	1.14	2.7E-01	0.97	8.2E-01	0.96	6.4E-01
Cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	1.06	4.2E-01	0.88	2.5E-01	0.93	3.7E-01
ADP-ribosylation factor related protein 1	1.12	3.4E-03	0.95	8.1E-01	1.00	8.1E-01
Capping protein (actin filament) muscle Z-line, alpha 1	0.97	1.2E-01	0.91	1.3E-01	0.99	9.4E-01
	1.04	1.5E-01	0.96	5.0E-01	0.94	5.1E-01
Chromosome 1 open reading frame 35	1.02	6.1E-02	1.08	1.3E-01	1.08	3.7E-01
Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa	1.05	2.7E-01	0.86	3.0E-01	1.07	1.5E-01
Chloride intracellular channel 1	1.05	4.1E-01	0.95	5.3E-01	1.09	5.7E-01
CSE1 chromosome segregation 1-like (yeast)	0.93	4.8E-02	0.88	2.0E-02	1.00	9.7E-01
Filamin B, beta (actin binding protein 278)	0.95	3.3E-01	0.96	7.0E-01	0.92	2.7E-01
Kruppel-like factor 7 (ubiquitous)	0.98	8.2E-01	0.93	1.1E-01	0.93	3.1E-01
H3 histone, family 3B (H3.3B)	1.09	no replicates	0.82	3.4E-01	0.74	1.3E-01
	0.71	6.1E-02	0.75	5.1E-02	1.12	8.5E-02
Transducer of ERBB2, 1	0.98	7.2E-01	1.03	6.4E-01	1.00	9.9E-01
Cyclin B1	0.97	2.0E-01	0.83	1.3E-01	0.71	1.7E-02
Splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	1.03	2.3E-01	0.99	6.7E-01	0.90	1.1E-01
Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	0.79	1.5E-02	0.67	9.6E-02	1.04	4.4E-01
Nucleoporin 153kDa	0.78	1.0E-01	0.97	6.1E-01	1.05	4.1E-01
	0.95	1.4E-01	0.85	9.2E-02	0.98	6.1E-01
G1 to S phase transition 1	1.01	6.3E-01	0.85	1.7E-01	0.96	6.7E-01
Epstein-Barr virus induced gene 3	0.92	2.8E-01	0.96	5.0E-01	0.92	1.7E-01
Topoisomerase (DNA) II binding protein 1	0.90	2.9E-02	0.94	6.2E-01	0.94	2.9E-01
Protein phosphatase 2, regulatory subunit B (B56), gamma isoform	0.95	3.0E-01	0.85	1.2E-01	0.81	4.3E-02
Dickkopf homolog 1 (Xenopus laevis)	0.74	1.2E-01	0.93	2.1E-01	1.16	1.9E-01
Protein regulator of cytokinesis 1	0.94	2.5E-01	0.81	6.0E-02	0.66	1.2E-02
	0.93	4.1E-01	0.79	6.7E-02	1.04	7.0E-01
Zinc finger protein 217	0.80	7.2E-02	0.98	7.2E-01	1.28	1.0E-01
Nebulette	0.92	2.7E-01	0.63	6.2E-02	0.93	2.6E-03
Discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	0.85	1.1E-01	0.91	1.8E-01	0.88	1.9E-02
Quaking homolog, KH domain RNA binding (mouse)	0.81	2.5E-01	0.81	1.2E-01	0.98	6.1E-01
Exportin 1 (CRM1 homolog, yeast)	0.87	2.0E-01	0.86	5.5E-02	0.87	1.7E-01
Melanoma associated antigen (mutated) 1	1.03	3.5E-01	1.01	8.8E-01	0.65	1.3E-02
V-myb myeloblastosis viral oncogene homolog (avian)	0.84	1.2E-01	0.89	1.8E-01	0.91	2.8E-01
Solute carrier family 1 (neutral amino acid transporter), member 5	1.03	4.6E-01	0.85	5.0E-02	0.67	6.2E-02
Polymerase (DNA-directed), alpha (70kD)	0.91	1.3E-01	0.99	9.7E-01	0.61	1.8E-02
Ubiquitin specific protease 32	0.73	7.0E-02	0.68	5.9E-02	0.95	3.2E-01
Nuclear receptor interacting protein 1	0.67	3.8E-02	0.72	4.2E-02	1.00	9.9E-01
Insulin-like growth factor binding protein 3	0.87	2.1E-01	0.72	4.0E-02	0.87	9.8E-02
Topoisomerase (DNA) II alpha 170kDa	0.87	1.5E-01	0.77	5.8E-02	0.64	9.2E-03
Spindlin	0.78	3.6E-01	0.71	6.6E-02	1.01	8.7E-01
Reticulon 1	0.83	2.7E-01	0.94	2.9E-01	0.96	1.0E-01
CDNA FLJ43660 fis, clone SYNOV4004823	0.97	5.8E-01	0.97	6.8E-01	0.96	4.6E-01
Ribosomal protein S6 kinase, 70kDa, polypeptide 1	0.89	1.2E-01	0.89	1.4E-01	0.89	3.5E-01
Keratin 19	1.13	4.0E-01	0.70	5.9E-02	1.23	1.5E-01
Solute carrier family 16 (monocarboxylic acid transporters), member 6	0.86	1.6E-01	0.78	4.6E-02	1.13	1.8E-01
Par-6 partitioning defective 6 homolog beta (C. elegans)	0.93	2.9E-01	1.00	9.7E-01	1.03	8.0E-01
Protein tyrosine phosphatase, receptor type, K	0.80	5.1E-02	0.63	1.1E-01	1.04	3.6E-01
Zinc finger protein 364	0.90	1.2E-01	0.80	1.5E-01	0.91	3.0E-01
Fetal Alzheimer antigen	0.81	4.4E-02	0.86	6.0E-02	0.92	3.6E-01

Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	0.96	3.5E-01	1.00	9.7E-01	0.85	1.8E-01
Chromosome 2 open reading frame 30	0.93	no replicates	0.92	1.2E-01	0.91	7.9E-02
XTP3-transactivated protein A	1.06	2.3E-01	1.00	no replicates	1.03	5.1E-01
Histone deacetylase 7A	0.91	5.2E-01	0.88	1.0E-01	0.86	1.5E-01
	1.18	7.0E-02	1.13	1.1E-01	0.90	9.8E-02
Forkhead box K2	0.74	7.1E-02	0.90	2.8E-01	1.05	1.8E-01
REST corepressor 1	0.79	1.0E-01	0.95	4.9E-01	0.96	1.8E-01
Programmed cell death 4 (neoplastic transformation inhibitor)	0.95	1.9E-01	1.07	2.6E-01	1.01	8.6E-01
Signal recognition particle 19kDa	0.87	6.3E-02	0.90	1.3E-01	1.08	2.1E-01
	1.14	6.4E-02	1.03	7.8E-01	0.84	no replicates
RNA binding motif, single stranded interacting protein 1	0.87	8.8E-02	0.90	1.5E-01	0.98	3.8E-01
Glyceronephosphate O-acyltransferase	1.02	1.2E-01	1.04	5.4E-01	0.91	3.9E-03
Peripheral myelin protein 22	0.90	3.2E-02	0.82	8.7E-02	1.14	6.8E-02
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	0.86	9.1E-02	0.82	1.1E-01	0.85	5.1E-03
Fas (TNFRSF6)-associated via death domain	0.94	3.3E-03	0.96	2.9E-01	1.06	4.1E-01
RNA-binding protein pippin	0.95	3.4E-01	0.85	2.6E-02	0.89	3.3E-01
Potassium channel, subfamily K, member 1	0.81	1.1E-01	0.95	1.8E-01	1.06	1.7E-01
Hypothetical protein LOC253039	0.94	2.6E-01	1.00	9.7E-01	0.93	2.4E-01
Zinc finger protein 410	0.89	1.4E-01	0.94	3.2E-01	1.01	6.5E-01
Transcribed locus	1.07	6.9E-01	1.02	8.3E-01	0.93	no replicates
Transforming, acidic coiled-coil containing protein 2	1.16	2.4E-01	0.92	4.7E-01	1.11	4.7E-01
Solute carrier family 39 (zinc transporter), member 6	1.12	8.2E-02	1.05	6.7E-01	0.82	3.0E-01
Glutaryl-Coenzyme A dehydrogenase	0.87	2.0E-01	0.74	2.0E-03	0.85	1.5E-01
Lipoyltransferase 1	0.91	3.5E-01	0.95	2.6E-01	0.90	3.5E-02
Endoglin (Osler-Rendu-Weber syndrome 1)	1.09	6.9E-01	0.99	9.7E-01	0.84	2.8E-01
	0.91	2.9E-01	0.91	2.8E-01	1.01	9.2E-01
LOC441075	0.98	6.6E-01	1.02	4.5E-01	0.95	4.2E-01
Eukaryotic translation initiation factor 5B	0.95	1.2E-01	0.99	8.6E-01	0.98	7.6E-01
Stanniocalcin 2	1.13	6.5E-02	0.90	1.3E-01	1.10	3.6E-01
KIAA0924 protein	0.94	2.6E-01	1.12	2.4E-01	0.90	1.5E-01
Hypothetical protein LOC286505	1.00	9.9E-01	0.98	7.4E-01	0.96	1.7E-01
	0.85	6.3E-02	0.86	6.0E-02	1.03	6.1E-01
Trinucleotide repeat containing 15	0.83	4.0E-02	0.87	1.9E-01	0.95	5.6E-01
Primase, polypeptide 1, 49kDa	0.96	5.0E-01	0.91	5.7E-02	0.76	1.1E-02
	0.91	2.9E-01	0.99	7.6E-01	0.96	7.4E-02
RE1-silencing transcription factor	1.00	9.1E-01	1.13	3.9E-01	0.97	7.5E-01
PP784 protein	1.01	7.7E-01	1.05	4.1E-01	0.93	2.5E-01
Wiskott-Aldrich syndrome-like	0.87	1.5E-01	0.91	1.2E-01	0.89	7.7E-02
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	1.12	9.4E-02	0.99	9.5E-01	0.96	6.8E-01
Zinc finger protein 198	0.86	1.2E-01	0.89	1.4E-01	0.99	9.1E-01
KIAA0999 protein	1.00	9.0E-01	1.06	5.4E-01	1.02	9.5E-02
Microseminoprotein, beta-	1.00	1.0E+00	0.99	9.1E-01	1.40	2.7E-02
	1.02	6.7E-01	1.10	2.8E-01	1.16	3.4E-01
Normal mucosa of esophagus specific 1	0.97	4.2E-01	1.04	3.3E-01	1.15	8.2E-02
Melanoma antigen, family C, 1	1.03	6.5E-01	1.19	1.9E-01	1.21	2.3E-01
Transcribed locus	0.98	5.2E-01	1.09	4.6E-01	1.07	3.5E-01
Dedicator of cytokinesis 5	1.02	5.9E-01	1.24	1.9E-01	1.11	2.3E-01
AU RNA binding protein/enoyl-Coenzyme A hydratase	1.01	6.9E-01	1.10	1.3E-01	1.31	2.9E-01
Spermatogenesis associated 3	1.02	5.4E-01	1.01	9.2E-01	1.08	6.4E-01
	0.99	5.2E-01	1.03	2.2E-01	1.09	1.7E-01
Hypothetical protein FLJ38379	1.05	4.3E-01	1.07	1.1E-01	1.17	1.1E-01
	1.01	8.2E-01	1.12	2.1E-01	1.13	2.6E-01
Hypothetical protein LOC283337	1.04	2.7E-01	1.10	2.7E-01	1.10	3.6E-01
Chromosome 9 open reading frame 103	0.97	5.6E-01	1.04	6.1E-01	1.10	1.5E-02



Eukaryotic translation initiation factor 4E binding protein 3	0.97	5.6E-01	1.00	7.4E-01	1.18	8.8E-02
	1.03	1.5E-01	1.00	9.9E-01	1.14	3.6E-01
Carbonic anhydrase VB-like	1.01	7.0E-01	1.11	3.3E-01	1.14	2.8E-01
BCL2-associated X protein	1.02	3.6E-01	1.04	6.4E-01	1.31	2.5E-02
Chromosome 6 open reading frame 103	1.03	1.1E-01	1.01	7.7E-01	1.07	2.7E-01
Chromosome 20 open reading frame 75	1.01	8.6E-01	1.13	1.6E-01	1.16	3.4E-01
Transcribed locus	1.04	5.4E-01	1.05	4.9E-01	1.18	1.3E-01
Tumor necrosis factor receptor superfamily, member 6	0.99	7.7E-01	1.46	2.4E-02	1.15	1.1E-01
Selenocysteine lyase	1.05	1.2E-01	1.08	2.4E-01	1.19	1.1E-01
Zinc finger protein 84 (HPF2)	0.94	3.6E-01	0.99	9.3E-01	1.19	7.1E-02
Transcribed locus	1.04	4.2E-01	1.12	1.8E-01	1.17	3.6E-01
Potassium channel, subfamily T, member 1	1.02	6.4E-01	1.20	1.3E-01	1.10	3.9E-01
Hypothetical gene supported by BC062774	1.02	8.3E-01	1.10	2.2E-01	1.15	2.9E-01
IQ motif containing F3	1.07	3.7E-01	1.26	1.5E-01	1.14	6.3E-01
DKFZP434C153 protein	1.01	8.2E-01	1.10	1.8E-01	1.11	3.5E-01
MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)	0.99	7.8E-01	1.00	9.6E-01	1.22	2.0E-01
Homo sapiens, Similar to expressed sequence AI326115, clone IMAGE:5311838, mRNA	1.04	7.9E-01	1.29	1.2E-01	1.16	no replicates
DKFZP434B0335 protein	1.02	3.4E-01	1.01	6.6E-01	1.10	3.1E-01
Hypothetical protein LOC285690	1.02	4.9E-01	1.06	2.0E-01	1.10	3.4E-02
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	0.99	8.3E-01	1.07	4.5E-01	1.18	2.0E-01
	1.02	7.6E-01	1.11	1.5E-01		
MRNA of muscle specific gene M1.	0.98	6.9E-01	1.00	9.4E-01	1.13	7.2E-02
Hypothetical gene supported by AK126414	1.01	8.8E-01	1.17	1.2E-01	1.21	8.3E-02
EphA5	1.02	8.0E-01	1.15	2.1E-01	1.16	3.5E-01
Transcribed locus	0.91	no replicates	0.99	no replicates	1.10	8.3E-02
Histone 1, H4h	1.03	4.6E-01	1.06	4.9E-01	1.14	3.4E-01
	1.01	9.4E-01	1.12	2.6E-01	1.19	1.2E-01
Tetraspanin similar to uroplakin 1	1.03	7.6E-01	1.06	2.3E-01	1.15	9.6E-02
Transcribed locus	0.98	6.4E-01	1.18	1.9E-01	1.06	3.6E-01
Tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	0.99	9.0E-01	1.19	6.6E-02	1.17	4.2E-02
FK506 binding protein 9, 63 kDa	1.00	9.3E-01	1.05	5.1E-01	1.15	2.4E-01
	1.01	2.6E-01	1.06	3.0E-01	1.09	2.5E-01
	0.96	2.2E-01	1.08	3.1E-01	1.12	1.9E-01
Haloacid dehalogenase-like hydrolase domain containing 4	0.96	6.4E-01	1.11	2.5E-01	1.08	1.4E-01
Tripartite motif-containing 7	1.00	9.9E-01	1.03	6.2E-01	1.07	4.6E-01
Dystrophin (muscular dystrophy, Duchenne and Becker types)	0.98	6.0E-01	1.03	4.6E-01	1.11	6.4E-02
Hypothetical protein DKFZp434I2117	1.04	4.8E-01	1.04	2.5E-01	1.17	1.9E-01
Alkaline phosphatase, intestinal	1.06	1.3E-01	1.11	1.5E-02	1.21	3.2E-01
Type 1 protein phosphatase inhibitor	0.99	1.3E-01	1.05	7.6E-02	1.19	3.2E-01
Bassoon (presynaptic cytomatrix protein)	0.96	4.9E-01	1.02	6.8E-01	1.09	1.5E-01
	1.01	3.7E-01	1.05	6.5E-01	1.11	5.6E-02
Chromosome 18 open reading frame 21	1.02	7.0E-02	1.08	2.1E-01	1.20	1.7E-01
Acetylcholinesterase (YT blood group)	0.94	1.8E-01	0.98	5.1E-01	1.19	1.7E-01
Hypothetical protein MGC29875	0.98	8.1E-01	1.13	1.8E-01	1.05	5.4E-02
Thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	1.00	9.8E-01	1.09	1.9E-01	1.11	2.2E-01
Nidogen 2 (osteonidogen)	0.97	1.2E-01	1.02	6.3E-01	1.11	2.4E-01
DiGeorge syndrome critical region gene 5 (non-coding)	1.00	8.9E-01	1.08	1.8E-01	1.05	9.0E-02
Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	0.99	9.0E-01	1.08	3.6E-01	1.17	2.7E-01
Transcribed locus	1.08	1.6E-01	1.06	1.4E-01	1.18	3.6E-01
Receptor-interacting serine-threonine kinase 4	1.00	9.7E-01	1.05	1.5E-01	1.12	3.1E-01
EphB2	0.98	3.9E-01	1.04	3.8E-01	1.08	3.8E-01

POM121-like protein	1.01	7.3E-01	1.01	7.6E-01	1.15	1.1E-01
Tumor necrosis factor receptor superfamily, member 19 KIAA1217	1.01	9.1E-01	1.07	3.4E-01	1.22	1.8E-01
Milk fat globule-EGF factor 8 protein	1.03	6.4E-01	1.12	1.6E-01	1.13	2.5E-01
	0.94	9.7E-02	1.04	6.0E-01	1.14	1.4E-01
	0.96	3.0E-01	1.05	4.6E-01	1.11	8.8E-02
Hypothetical protein FLJ20344	1.02	8.0E-01	1.06	6.3E-01	1.09	8.8E-02
Suppressor of variegation 3-9 homolog 2 (Drosophila)	1.00	8.8E-01	1.03	4.3E-01	1.18	6.2E-02
Transcribed locus	1.01	7.9E-01	1.14	1.1E-01	1.17	7.4E-02
Transcribed locus	1.04	4.2E-01	1.10	4.4E-01	1.17	4.3E-01
CCCTC-binding factor (zinc finger protein)-like	1.00	8.4E-01	1.01	8.4E-01	1.06	4.3E-03
	1.02	3.6E-01	1.15	8.9E-02	1.13	3.9E-01
Zinc finger RNA binding protein	1.16	1.2E-01	1.15	1.2E-01	1.08	1.3E-01
Zinc finger protein 31 (KOX 29)	1.00	8.8E-01	1.03	3.3E-01	1.15	1.2E-01
Nicotinamide N-methyltransferase	1.08	5.7E-04	0.96	6.5E-01	0.86	8.1E-02
Oxidase (cytochrome c) assembly 1-like	1.07	1.1E-01	1.06	5.3E-01	0.86	1.2E-01
Protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	1.00	6.6E-01	0.93	2.7E-01	0.98	9.1E-01
Chromosome 12 open reading frame 8	1.04	1.0E-01	0.89	1.5E-01	0.88	1.1E-01
Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	0.92	3.0E-01	0.82	5.2E-02	0.95	6.5E-01
CDC5 cell division cycle 5-like (S. pombe)	0.95	1.5E-01	1.01	7.2E-01	0.95	1.1E-01
DKFZP586L0724 protein	0.94	2.1E-01	1.04	5.0E-01	0.98	4.3E-01
ADP-ribosylation factor-like 6 interacting protein	0.99	6.9E-01	1.03	4.4E-01	0.73	9.6E-02
NEL-like 1 (chicken)	1.25	1.8E-01	0.87	4.4E-01	0.92	4.0E-01
Annexin A7	0.97	3.4E-01	0.81	6.6E-02	0.91	4.1E-01
	0.84	7.6E-02	0.90	1.5E-01	0.71	1.0E-02
Hypothetical protein FLJ40869	0.91	2.0E-02	0.93	1.0E-01	1.06	4.3E-01
Hypothetical protein FLJ13910	0.93	1.7E-01	1.00	9.2E-01	0.92	6.2E-02
Aspartylglucosaminidase	1.19	8.3E-02	0.92	5.6E-01	1.00	2.4E-01
	0.88	9.1E-02	0.94	1.7E-01	1.01	8.1E-01
Hypothetical protein FLJ12443	0.91	3.9E-01	0.76	5.7E-03	1.06	5.9E-01
Mortality factor 4 like 2	1.05	3.6E-01	0.90	2.6E-01	0.96	6.3E-01
FK506 binding protein 4, 59kDa	1.17	7.7E-02	0.91	4.6E-01	1.24	2.7E-01
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide SET translocation (myeloid leukemia-associated)	0.99	4.4E-01	0.95	4.2E-01	0.93	8.8E-02
	1.05	3.7E-01	0.94	1.2E-01	0.85	1.5E-01
Proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	1.02	6.7E-01	1.11	2.6E-01	0.89	4.7E-01
KIAA1181 protein	0.96	2.6E-01	1.04	8.4E-01	0.80	5.8E-02
Heat shock 70kDa protein 8	1.24	1.8E-01	1.06	6.9E-01	0.94	4.7E-01
KIAA0460 protein	1.06	6.1E-01	1.18	1.6E-01	0.99	9.3E-01
ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	1.05	3.6E-01	0.95	5.0E-01	0.85	6.0E-02
Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	1.03	5.2E-01	0.92	1.4E-01	0.83	9.1E-02
Heterogeneous nuclear ribonucleoprotein A1	1.17	7.2E-02	1.03	8.8E-01	1.03	4.5E-01
MRNA; cDNA DKFZp686B1431 (from clone DKFZp686B1431)	1.07	9.7E-03	1.19	1.5E-01	1.12	1.6E-01
Nucleolin	1.16	1.1E-01	1.18	4.2E-01	0.93	2.3E-01
Stearoyl-CoA desaturase (delta-9-desaturase)	1.07	1.3E-01	1.17	5.7E-02	0.74	5.1E-02
Capping protein (actin filament) muscle Z-line, alpha 2	0.96	1.6E-01	0.93	1.5E-01	0.87	7.9E-02
Hypothetical protein MGC4368	1.12	2.7E-02	1.15	2.4E-01	1.00	9.5E-01
Actin related protein 2/3 complex, subunit 3, 21kDa	1.04	2.0E-01	1.05	3.0E-01	1.05	5.2E-01
Aspartate beta-hydroxylase	0.98	2.2E-01	0.80	1.8E-02	0.98	8.0E-01
Eukaryotic translation initiation factor 3, subunit 6 48kDa	1.04	4.6E-01	0.90	2.8E-01	0.84	2.5E-01
Electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	1.00	9.4E-01	0.87	8.5E-03	1.13	3.7E-01
Ribosomal protein L37a	1.08	1.2E-01	1.05	3.8E-01	0.84	9.1E-03

KIAA0179	0.97	6.9E-01	1.08	1.1E-01	1.01	8.2E-01
	1.10	3.5E-01	1.04	6.6E-01	0.88	2.8E-01
Phospholipase D1, phosphatidylcholine-specific	1.07	1.1E-01	1.13	5.3E-01	1.13	2.2E-01
Transcribed locus	1.00	9.9E-01	1.03	6.8E-01	1.19	2.3E-02
Transcribed locus	1.06	3.1E-01	1.11	5.6E-02	1.26	2.7E-01
Neuropeptide Y	1.03	7.8E-01	1.18	2.5E-01	1.10	4.7E-01
STAM binding protein	1.05	1.6E-01	1.12	1.6E-01	1.17	1.9E-01
Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	0.98	5.1E-01	1.06	2.4E-01	1.22	1.2E-01
CDNA FLJ25206 fis, clone REC05955	1.01	7.8E-01	1.11	7.3E-02	1.15	4.0E-01
Transcribed locus, moderately similar to XP_375099.1 hypothetical protein LOC283585 [Homo sapiens]	1.00	9.8E-01	1.15	2.2E-01	1.19	2.2E-01
Glucagon-like peptide 1 receptor	1.03	5.9E-01	1.20	1.4E-01	1.13	1.5E-01
Development and differentiation enhancing factor 1	1.02	6.2E-01	1.01	4.9E-01	1.23	8.4E-02
F-box and leucine-rich repeat protein 17	0.99	5.2E-01	1.09	2.9E-01	1.18	2.8E-01
Putative N-acetyltransferase Camello 2	1.05	4.8E-01	1.09	6.1E-02	1.23	2.0E-01
Transcribed locus	1.01	8.7E-01	1.08	2.7E-01	1.22	1.5E-01
Seizure related 6 homolog (mouse)-like	1.01	8.2E-01	1.02	7.5E-01	1.08	4.9E-01
	0.99	9.1E-01	1.08	5.2E-01	1.33	6.5E-02
Downregulated in ovarian cancer 1	1.06	3.0E-01	1.08	3.9E-01	1.18	1.4E-01
Cyclin D1 (PRAD1: parathyroid adenomatosis 1)	1.02	4.1E-01	1.16	7.3E-02	1.17	2.2E-01
Myotubularin related protein 9	1.02	6.9E-01	1.04	7.3E-01	1.18	1.2E-01
Hypothetical protein FLJ13105	0.99	8.5E-01	1.11	1.7E-01	1.17	3.8E-02
Non-POU domain containing, octamer-binding	1.07	3.0E-01	0.91	6.1E-02	0.86	1.1E-01
Myeloid cell leukemia sequence 1 (BCL2-related)	0.90	2.3E-01	0.99	8.9E-01	1.02	7.6E-01
Hypothetical protein LOC349236	0.99	8.6E-01	1.20	1.7E-01	1.21	5.9E-02
BTG family, member 2	1.53	2.3E-01	1.86	1.3E-01	1.15	1.5E-01
Zinc and ring finger 3	0.94	4.8E-01	0.90	1.8E-02	1.00	9.9E-01
Mitogen-activated protein kinase 6	0.92	1.4E-01	1.03	7.4E-01	0.91	5.5E-02
Transmembrane 4 superfamily member 13	1.04	3.7E-01	1.00	9.4E-01	0.81	6.7E-02
Hypothetical protein AY099107	1.12	2.9E-01	0.96	7.1E-01	0.98	5.8E-01
Sjogren syndrome antigen B (autoantigen La)	1.12	1.3E-01	1.15	3.4E-01	1.00	9.5E-01
CD9 antigen (p24)	0.93	1.1E-01	0.85	3.2E-03	0.91	6.2E-01
Hypothetical protein LOC283856	1.06	1.4E-01	1.15	1.2E-01	1.18	2.5E-01
CDNA FLJ43345 fis, clone NT2RI3008228	1.03	5.3E-01	1.08	1.3E-01	1.19	2.2E-01
	1.05	5.4E-01	1.04	3.6E-01	1.22	1.5E-01
Transcribed locus	1.01	6.7E-01	1.04	6.3E-01	1.19	1.1E-01
Tetratricopeptide repeat domain 6	1.02	7.2E-01	1.10	2.0E-01	1.16	2.0E-01
Biogenesis of lysosome-related organelles complex-1, subunit 2	1.09	2.2E-01	1.56	1.3E-01	1.43	6.8E-03
Serine/threonine kinase 17a (apoptosis-inducing)	1.03	3.2E-01	1.04	5.9E-01	1.16	6.7E-02
Haspin	1.00	9.4E-01	1.07	5.9E-02	1.07	6.2E-01
Transmembrane protein 27	1.05	1.3E-01	1.01	8.6E-01	1.13	1.7E-01
	1.00	9.4E-01	1.07	2.9E-01	1.26	1.3E-01

2			6			24		
1			1			1		
Ratio	t-test	P-value	Ratio	t-test	P-value	Ratio	t-test	P-value
0.46	1.3E-03		0.32	1.1E-02		0.34	3.9E-03	
0.83	1.0E-02		0.55	4.1E-03		0.56	6.6E-03	
0.81	1.9E-02		0.58	2.2E-03		0.47	7.7E-03	
0.69	5.7E-03		0.50	1.2E-02		0.42	6.2E-03	
0.78	8.2E-03		0.51	8.1E-03		0.43	1.0E-02	
0.85	8.0E-02		0.45	1.6E-03		0.45	3.9E-03	
0.86	6.9E-03		0.76	3.7E-02		0.64	9.5E-02	
0.91	2.2E-02		0.69	3.7E-04		0.62	4.6E-02	
0.85	2.2E-02		0.62	1.0E-03		0.71	2.1E-02	
0.61	2.4E-02		0.34	1.8E-04		0.47	3.2E-02	
0.69	2.3E-02		0.45	7.3E-05		0.63	2.9E-02	
0.73	7.3E-03		0.52	2.3E-03		0.44	1.1E-02	
0.86	8.2E-03		0.81	5.3E-03		0.70	4.2E-03	
0.45	1.0E-02		0.30	2.6E-04		0.25	7.9E-04	
0.46	3.5E-03		0.31	7.0E-05		0.35	5.8E-04	
0.49	1.8E-02		0.37	1.6E-03		0.34	3.3E-03	
0.45	1.3E-02		0.24	6.1E-04		0.37	5.0E-03	
0.49	1.3E-02		0.33	1.3E-03		0.30	3.1E-03	
0.53	7.1E-03		0.42	5.1E-03		0.35	6.2E-03	
0.46	1.3E-02		0.34	2.8E-03		0.32	3.1E-04	
0.85	1.9E-02		0.74	1.3E-02		0.68	2.4E-02	
0.78	2.2E-02		0.63	1.1E-02		0.60	3.1E-02	
0.75	3.6E-03		0.43	2.3E-03		0.50	1.1E-03	
1.10	5.1E-02		1.42	1.8E-02		1.11	2.3E-01	
0.84	3.3E-02		0.61	1.5E-02		0.83	1.3E-01	
0.87	4.0E-02		0.73	3.3E-02		0.62	4.3E-02	
0.94	1.5E-01		0.71	1.7E-02		0.83	7.8E-02	
0.90	5.2E-03		0.61	1.8E-02		0.79	2.5E-02	
0.84	1.6E-02		0.59	1.2E-02		0.65	1.8E-02	
0.74	1.8E-02		0.45	2.1E-03		0.74	1.2E-02	
0.88	1.7E-01		0.61	1.2E-02		0.56	1.2E-02	
0.70	1.4E-02		0.56	1.2E-02		0.67	3.5E-02	
0.76	1.8E-02		0.45	6.3E-04		0.50	7.0E-03	
0.94	2.9E-01		0.64	1.1E-03		0.61	8.9E-03	
0.87	6.1E-02		0.68	9.0E-03		0.61	9.7E-02	
0.82	2.5E-02		0.63	1.1E-02		0.68	2.5E-01	
1.22	4.6E-02		1.42	2.7E-02		1.00	1.0E+00	
0.79	7.2E-02		0.61	5.2E-03		0.79	1.8E-01	
0.97	6.3E-01		0.86	3.2E-02		0.70	2.0E-02	
0.93	2.1E-01		0.63	1.3E-02		0.58	8.9E-03	
0.92	4.2E-02		1.29	2.0E-02		1.67	2.9E-03	
0.94	2.4E-01		0.69	1.8E-03		0.49	1.2E-03	
0.96	4.7E-01		0.81	1.5E-02		0.75	2.3E-02	
0.98	4.2E-01		0.83	1.2E-02		0.66	1.6E-02	
0.74	1.3E-02		0.71	1.5E-02		0.62	2.8E-02	
0.85	2.9E-02		0.62	2.7E-03		0.69	3.7E-03	
0.91	4.0E-02		0.77	2.6E-02		0.56	3.7E-03	
0.85	5.6E-03		0.68	8.4E-03		0.85	2.3E-01	

0.90	5.8E-02	0.57	4.3E-03	0.76	2.4E-02
0.86	1.3E-02	0.60	2.6E-02	0.73	1.5E-01
0.89	1.1E-01	0.62	4.0E-03	0.41	2.1E-04
1.18	3.3E-02	1.55	9.5E-04	1.18	1.1E-01
1.09	2.8E-02	0.76	4.6E-03	0.69	2.7E-02
1.06	3.0E-01	0.85	1.3E-02	0.69	3.9E-02
0.94	2.5E-02	0.69	3.7E-03	0.59	3.8E-03
0.93	6.1E-02	0.72	6.9E-03	0.75	2.9E-02
0.82	1.2E-02	0.56	3.8E-04	0.75	2.3E-02
0.89	4.3E-01	0.63	2.3E-02	0.76	3.8E-02
0.97	3.1E-01	1.28	2.3E-02	1.47	3.5E-03
0.93	6.6E-02	0.69	3.7E-03	0.74	3.0E-02
0.85	7.7E-02	0.58	6.5E-03	0.73	2.0E-02
0.76	3.1E-02	0.32	4.5E-04	0.39	3.4E-03
0.44	1.2E-02	0.34	1.0E-03	0.54	1.4E-01
0.94	3.3E-01	0.68	2.8E-03	0.52	6.0E-02
0.89	2.2E-01	0.62	2.1E-03	0.72	6.4E-02
0.95	7.5E-02	0.64	4.7E-03	0.59	2.0E-03
0.86	2.1E-02	0.64	4.8E-03	0.58	8.3E-03
1.17	2.0E-02	1.26	3.0E-02	1.20	no replicates
0.79	3.2E-02	0.53	6.5E-03	0.64	7.2E-03
0.54	1.5E-02	0.51	7.1E-03	0.47	9.1E-04
0.76	2.3E-02	0.62	2.7E-02	0.58	no replicates
0.91	1.6E-02	0.68	3.2E-03	0.42	2.6E-04
0.78	6.1E-03	0.50	1.5E-02	0.60	1.1E-01
1.04	1.2E-01	0.79	2.9E-02	0.70	7.5E-03
0.94	2.4E-01	0.67	9.2E-03	0.65	1.0E-02
1.11	9.5E-02	1.06	5.4E-03	0.67	4.6E-04
0.78	3.1E-02	0.38	1.8E-04	0.35	1.1E-02
0.55	1.2E-02	0.30	9.1E-05	0.70	3.8E-02
1.01	9.1E-01	1.33	2.3E-02	1.60	5.0E-02
0.74	no replicates	0.64	4.7E-03	0.80	1.7E-01
1.01	4.8E-01	1.36	6.2E-02	1.74	8.0E-02
0.88	1.9E-01	0.70	5.9E-02	0.76	2.8E-02
1.04	5.0E-01	0.82	1.9E-03	0.66	6.9E-03
1.24	1.7E-02	0.95	1.7E-01	0.61	2.5E-02
1.10	1.1E-01	1.06	2.3E-02	0.79	7.3E-03
1.00	8.5E-01	1.39	3.2E-02	1.49	1.1E-01
0.95	3.5E-02	1.18	2.0E-01	1.45	5.6E-02
1.18	3.2E-02	1.07	3.9E-01	0.67	1.2E-02
1.26	4.8E-02	1.23	5.0E-02	0.91	4.3E-01
0.99	6.7E-01	0.73	2.2E-04	0.70	8.0E-02
1.01	2.9E-01	0.74	4.7E-03	0.63	3.7E-03
0.89	7.6E-02	0.68	2.6E-03	0.91	2.1E-01
1.03	1.1E-02	0.92	5.1E-01	0.67	5.3E-03
1.03	4.4E-01	1.27	3.3E-02	1.45	1.8E-03
0.95	6.3E-01	1.33	1.3E-01	1.78	4.7E-02
0.89	2.8E-01	1.05	3.6E-01	1.41	5.9E-02

1.02	4.9E-01	1.23	4.5E-02	1.44	5.7E-02
1.07	4.3E-02	0.84	5.0E-03	0.64	6.0E-02
1.28	4.3E-04	1.05	7.4E-01	0.65	1.0E-02
1.26	1.6E-02	1.47	1.8E-02	1.24	4.2E-01
0.97	3.5E-02	0.74	1.7E-02	0.73	3.7E-01
0.93	1.6E-01	0.70	6.7E-03	0.75	2.4E-01
0.97	5.5E-01	1.21	2.6E-02	1.48	1.6E-02
1.01	5.8E-01	1.39	1.7E-02	1.68	5.5E-03
0.92	1.6E-01	0.56	9.6E-03	0.56	2.6E-01
1.04	4.7E-01	0.91	9.5E-02	0.88	3.4E-02
1.00	9.8E-01	0.55	1.4E-04	0.43	7.3E-03
0.99	6.7E-01	0.84	2.9E-02	0.67	1.0E-01
0.84	9.7E-02	0.67	5.9E-03	0.63	4.6E-03
0.99	8.5E-01	0.70	4.6E-04	0.61	3.9E-03
0.91	2.0E-02	0.84	6.3E-03	0.70	no replicates
0.89	no replicates	0.80	6.8E-03	0.70	no replicates
1.22	1.4E-02	0.99	9.2E-01	0.53	3.4E-03
0.89	1.1E-01	1.36	2.0E-01	1.94	5.9E-02
1.17	no replicates	1.11	4.3E-03	1.44	3.6E-01
0.91	1.5E-01	0.66	1.4E-02	0.77	9.8E-03
0.82	2.3E-01	0.70	6.0E-03	1.02	3.1E-02
0.86	3.6E-01	0.65	1.1E-02	0.82	1.7E-01
0.87	9.0E-02	0.63	1.6E-02	0.73	8.1E-03
1.10	1.3E-01	1.25	1.5E-02	1.48	3.8E-03
0.84	1.6E-03	0.69	1.3E-01	0.92	1.9E-02
0.96	2.1E-01	0.71	5.3E-04	0.75	1.0E-01
0.97	8.9E-02	0.80	1.6E-02	0.70	3.2E-01
1.09	8.1E-02	1.04	3.9E-01	0.55	1.1E-02
1.06	3.6E-01	1.60	1.0E-02	1.68	4.4E-03
0.80	2.9E-02	0.52	6.0E-02	0.74	6.6E-02
0.96	2.5E-01	0.79	7.9E-03	0.70	3.0E-02
1.00	9.8E-01	0.80	2.0E-02	0.40	1.3E-03
1.01	7.7E-01	1.32	4.7E-02	1.79	5.0E-02
0.85	1.4E-01	0.78	1.6E-02	0.76	4.7E-02
0.99	8.1E-01	1.27	4.2E-02	1.42	2.5E-02
1.07	1.3E-02	1.44	2.3E-02	1.55	3.3E-02
1.07	4.0E-01	0.76	2.6E-03	0.45	5.9E-04
1.02	8.5E-01	1.40	3.5E-02	1.55	4.5E-02
1.21	1.3E-01	1.45	2.2E-02	1.29	1.9E-01
0.84	4.4E-02	0.68	7.7E-03	0.79	5.9E-02
1.03	6.4E-01	1.28	6.6E-03	1.47	4.9E-02
1.15	4.0E-03	1.01	8.2E-01	0.54	4.9E-03
0.97	3.6E-01	1.38	2.4E-02	1.60	7.5E-02
1.02	3.0E-02	1.34	4.9E-02	1.56	8.3E-02
1.05	3.7E-01	0.77	2.1E-02	0.61	1.6E-02
0.94	2.3E-01	0.82	2.3E-03	0.67	3.6E-03
0.92	1.8E-01	0.70	2.0E-03	0.89	7.0E-02
1.02	5.9E-01	0.69	1.0E-02	0.74	3.2E-02
0.87	2.9E-02	0.63	6.8E-03	0.77	9.8E-02
1.15	4.5E-02	0.88	5.0E-02	0.61	6.8E-03
1.08	1.6E-02	0.82	3.1E-02	0.50	1.1E-03
0.93	4.7E-02	0.67	1.4E-02	0.71	1.3E-01
0.90	1.4E-01	0.74	7.1E-03	0.70	1.6E-02

1.03	6.0E-01	1.23	2.1E-02	1.46	7.0E-03
0.99	6.1E-01	0.70	7.3E-03	0.76	7.4E-02
1.01	6.9E-01	0.82	4.7E-03	0.57	1.1E-02
0.92	4.4E-03	0.69	1.6E-02	0.90	1.9E-01
1.18	4.4E-02	1.02	7.4E-01	0.62	4.0E-03
0.92	1.1E-01	0.69	1.4E-02	0.72	4.9E-03
0.96	5.0E-01	1.45	4.0E-02	1.96	4.4E-02
1.01	8.2E-01	1.42	4.1E-02	1.74	3.6E-02
1.14	9.9E-02	1.55	2.9E-02	1.91	1.5E-01
1.04	2.6E-01	1.33	1.5E-03	1.63	5.5E-02
1.07	1.6E-01	1.05	2.8E-01	1.15	6.4E-02
1.08	3.9E-02	0.90	1.0E-02	0.69	2.2E-02
1.00	8.1E-01	0.88	2.3E-02	0.62	7.6E-02
0.93	2.4E-01	0.70	5.2E-04	0.82	2.6E-01
1.02	3.8E-01	1.31	4.0E-03	1.52	8.0E-03
1.10	5.5E-02	0.99	9.3E-01	0.71	2.5E-02
0.86	5.5E-02	0.68	7.5E-03	0.73	1.5E-02
0.97	3.4E-01	0.81	1.2E-02	0.65	1.1E-01
1.08	3.5E-01	0.81	6.8E-03	0.50	2.0E-04
1.02	3.6E-01	1.43	1.1E-02	1.60	2.5E-02
1.01	8.5E-01	1.42	6.0E-02	1.81	4.9E-03
1.08	4.1E-02	1.47	3.1E-03	1.47	1.7E-01
1.19	6.1E-04	0.89	2.3E-01	0.56	3.5E-03
1.14	6.8E-03	1.01	9.4E-01	0.63	1.1E-02
1.14	3.0E-02	0.94	3.3E-01	0.71	1.4E-02
0.93	1.6E-01	0.65	1.2E-02	0.68	2.5E-02
0.95	1.5E-01	0.60	6.0E-03	0.55	1.1E-01
0.96	5.3E-01	0.58	5.9E-03	0.53	1.2E-02
0.90	4.6E-01	0.49	1.1E-03	0.58	6.0E-02
0.97	5.7E-01	0.70	1.4E-02	0.72	1.3E-02
0.92	2.6E-02	0.61	1.1E-04	0.47	no replicates
0.98	no replicates	0.83	6.3E-03	0.71	1.2E-01
1.17	2.3E-01	0.96	6.8E-01	0.46	1.4E-04
1.02	7.4E-01	1.33	7.9E-03	1.45	3.3E-02
0.80	3.2E-02	0.52	1.1E-03	0.54	1.0E-01
0.99	7.5E-01	0.77	2.1E-02	0.68	1.2E-01
0.85	2.6E-02	0.64	1.4E-02	0.79	2.0E-01
0.88	1.1E-01	0.48	3.8E-03	1.14	3.3E-01
0.99	8.9E-01	0.66	2.9E-03	0.49	1.9E-02
0.95	no replicates	0.66	2.2E-04	0.57	8.4E-02
0.86	1.1E-01	0.56	6.3E-03	0.61	1.0E-01
0.88	1.3E-01	0.59	8.0E-04	0.49	7.6E-03
0.78	1.2E-01	0.52	2.0E-02	0.67	5.9E-02
1.02	3.4E-01	0.71	9.0E-03	0.64	6.6E-02
0.98	4.7E-01	0.64	3.7E-04	0.58	2.0E-01
0.90	1.1E-01	0.60	9.8E-03	0.54	1.5E-01
0.78	6.0E-02	0.42	1.0E-03	0.46	1.5E-01
0.93	1.4E-01	0.57	9.0E-04	0.47	2.6E-02
0.74	1.7E-01	0.50	7.5E-03	0.71	3.0E-02
0.95	4.2E-01	0.63	3.7E-03	0.54	1.1E-01

0.95	2.0E-02	0.48	3.1E-04	0.53	3.7E-02
0.76	8.5E-02	0.45	3.2E-03	0.60	2.2E-02
0.86	9.1E-02	0.68	2.9E-02	0.54	4.8E-03
0.98	6.5E-01	0.68	1.2E-02	0.55	7.8E-03
0.94	1.8E-01	0.61	8.3E-03	0.55	2.3E-02
0.97	4.6E-01	0.63	1.1E-03	0.59	1.0E-01
0.96	5.4E-01	0.63	5.0E-03	0.55	7.1E-02
0.86	1.5E-01	0.54	9.5E-03	0.57	1.6E-01
0.86	5.3E-02	0.52	3.0E-03	0.47	1.0E-02
0.82	2.0E-01	0.57	1.9E-03	0.61	1.4E-01
0.89	8.2E-02	0.59	1.4E-02	0.66	1.5E-02
0.69	8.3E-02	0.30	3.0E-05	0.40	3.1E-02
0.64	4.4E-02	0.33	1.0E-03	0.53	9.8E-03
0.60	3.3E-02	0.37	1.5E-03	0.79	4.5E-03
1.01	7.5E-01	0.62	3.4E-03	0.57	1.2E-02
1.00	9.7E-01	1.17	1.1E-01	1.51	2.0E-02
0.85	1.8E-03	0.70	5.3E-04	0.61	3.8E-02
0.97	4.8E-01	0.69	3.0E-03	0.47	1.9E-02
1.04	4.0E-01	0.63	1.3E-02	0.45	1.6E-03
0.62	1.9E-02	0.38	1.2E-03	0.43	5.8E-02
0.94	9.5E-02	0.71	2.5E-06	0.89	2.7E-01
1.00	9.8E-01	0.80	2.5E-02	0.69	6.3E-03
1.05	5.4E-02	0.82	2.7E-02	0.47	1.3E-02
0.92	1.5E-01	0.68	8.6E-04	0.68	2.0E-01
0.99	9.0E-01	0.83	3.7E-02	0.64	8.9E-04
0.98	6.4E-01	1.29	1.2E-02	1.40	2.0E-02
1.10	2.4E-02	1.33	7.2E-02	1.43	3.2E-01
0.96	2.0E-02	0.61	7.5E-03	0.69	8.8E-02
0.77	3.9E-02	0.52	6.1E-03	0.82	1.8E-02
0.85	9.9E-02	0.71	2.7E-03	0.82	9.6E-02
1.20	2.8E-01	0.95	4.5E-01	0.62	3.0E-03
1.02	7.5E-01	0.77	2.7E-02	0.63	1.2E-01
0.88	1.1E-01	0.69	3.0E-03	0.83	1.6E-01
1.15	1.1E-01	0.89	6.8E-02	0.42	6.5E-05
0.89	1.7E-01	0.46	1.9E-03	0.42	4.6E-03
1.08	4.2E-01	1.16	8.8E-02	0.66	2.4E-03
0.99	8.4E-01	1.30	4.0E-02	1.44	2.0E-01
0.87	2.5E-01	0.62	2.4E-04	0.76	1.2E-01
1.02	6.3E-01	1.31	4.4E-02	1.53	1.2E-02
1.00	9.6E-01	0.85	7.4E-03	0.67	8.2E-03
1.18	8.6E-02	0.98	7.8E-01	0.56	7.7E-04
1.14	4.6E-02	0.93	3.4E-01	0.53	3.1E-04
1.12	5.3E-02	0.94	4.5E-01	0.59	1.8E-02
0.97	3.2E-01	1.20	1.5E-01	1.61	6.9E-02
1.00	9.1E-01	1.03	4.0E-01	1.52	1.7E-02
0.95	1.4E-01	1.32	7.1E-03	1.44	4.3E-02
0.68	2.2E-02	0.55	2.1E-02	0.70	1.2E-01
0.93	3.2E-01	0.66	4.9E-03	0.63	1.5E-02
0.99	9.4E-01	0.86	7.1E-03	0.63	1.8E-02
1.08	3.6E-02	0.81	6.9E-02	0.65	1.9E-02
0.99	9.1E-01	0.78	2.9E-02	0.67	6.5E-02



0.91	7.6E-02	0.73	5.7E-02	0.70	6.2E-03
1.15	4.4E-01	0.86	1.7E-02	0.46	2.9E-05
1.05	1.4E-01	0.75	3.4E-02	0.40	8.1E-03
1.06	2.6E-01	0.95	2.6E-01	0.58	1.3E-03
0.96	3.8E-01	0.75	5.0E-03	0.69	2.4E-01
1.01	7.0E-01	0.75	2.1E-04	0.70	3.6E-04
0.92	2.4E-01	0.61	1.0E-02	0.62	2.3E-02
1.01	7.1E-01	1.35	4.5E-02	1.57	1.1E-02
1.20	1.1E-02	0.97	6.4E-01	0.60	3.8E-03
0.84	1.3E-01	0.62	1.9E-02	0.74	3.8E-02
0.92	3.8E-01	1.27	5.0E-02	1.40	3.6E-02
1.00	9.7E-01	0.88	2.4E-01	0.66	5.9E-03
0.92	6.1E-02	0.71	9.2E-04	0.84	1.6E-03
1.01	8.5E-01	1.29	4.6E-02	1.48	9.2E-03
0.97	3.8E-01	0.65	1.4E-02	0.40	5.7E-03
0.81	6.3E-02	0.54	4.1E-04	0.72	4.4E-02
1.05	8.5E-02	0.91	2.9E-01	0.69	7.2E-03
1.00	8.9E-01	1.15	1.1E-01	1.45	2.1E-02
0.91	1.6E-01	0.68	6.9E-03	0.93	6.9E-01
0.94	2.6E-02	0.66	3.8E-02	0.84	3.1E-01
1.00	8.5E-01	0.66	3.3E-02	0.64	9.5E-03
0.98	4.5E-01	0.69	3.7E-03	0.63	3.1E-03
1.00	9.0E-01	1.40	8.0E-02	1.55	2.6E-02
1.04	8.5E-01	0.97	8.2E-01	0.63	2.0E-02
0.86	1.8E-01	0.59	3.1E-03	0.70	1.4E-01
0.98	2.3E-01	1.34	3.6E-02	1.62	1.7E-02
0.96	1.9E-01	1.26	5.2E-02	1.47	2.3E-01
0.91	5.8E-01	0.65	2.4E-02	0.68	9.4E-03
1.00	9.4E-01	1.16	5.6E-02	1.42	4.5E-02
0.89	1.2E-01	0.69	2.0E-03	0.77	2.8E-04
1.08	3.2E-02	1.34	1.7E-02	1.64	8.6E-02
1.04	6.5E-01	0.95	5.6E-01	0.59	8.5E-03
1.01	9.0E-01	1.30	1.8E-02	1.51	4.9E-02
0.99	7.2E-01	0.71	1.4E-03	0.81	3.7E-01
0.86	8.7E-03	0.63	5.2E-03	0.53	4.7E-02
0.94	2.0E-01	0.72	2.3E-02	0.67	5.5E-02
1.03	4.6E-01	0.73	1.4E-02	0.71	1.8E-01
0.96	1.3E-02	1.32	5.6E-02	1.46	1.7E-01
0.82	3.2E-02	0.63	1.1E-02	0.88	2.7E-01
1.15	2.1E-01	1.00	9.9E-01	0.71	1.3E-02
1.07	9.5E-02	0.97	6.9E-01	0.62	7.7E-03
1.20	2.3E-02	0.99	8.3E-01	0.64	2.4E-02
0.90	1.4E-01	0.67	2.4E-02	0.77	2.1E-02
1.17	2.2E-01	0.91	7.4E-02	0.46	4.3E-03
1.06	3.6E-02	1.36	5.8E-02	1.43	8.0E-02
0.95	2.2E-01	1.05	7.0E-01	1.67	4.6E-03
1.03	4.4E-01	0.75	2.0E-03	0.70	9.1E-04
1.02	3.7E-01	1.40	1.7E-02	1.69	6.0E-02
0.90	6.9E-02	0.69	1.0E-02	0.77	1.9E-01
0.93	no replicates	0.55	3.9E-03	0.69	1.1E-01
0.82	1.1E-01	0.62	1.8E-02	0.80	2.5E-01

0.94	4.5E-01	1.37	5.2E-02	1.61	6.8E-02
0.96	6.9E-01	0.55	8.2E-03	0.53	3.9E-03
0.80	7.6E-03	0.56	2.8E-02	0.66	9.8E-02
1.03	4.5E-01	0.77	3.1E-03	0.67	6.9E-02
1.00	8.8E-01	1.21	2.1E-02	1.42	4.1E-02
1.02	7.3E-01	1.33	6.8E-02	1.57	3.6E-02
1.10	7.9E-02	1.31	3.2E-03	1.41	3.2E-02
0.97	4.0E-01	1.11	4.5E-01	1.46	2.0E-02
1.09	1.5E-01	1.34	1.2E-01	1.43	3.9E-02
0.99	8.8E-01	1.23	4.7E-02	1.63	9.4E-03
0.98	7.6E-01	1.00	9.9E-01	1.43	3.9E-02
1.00	9.5E-01	1.35	3.6E-02	1.45	2.0E-02

0.97	6.4E-01	1.23	3.2E-01	1.75	5.2E-02
0.99	7.8E-01	1.32	2.5E-02	1.93	2.4E-02
0.94	1.8E-02	1.28	5.0E-02	1.52	2.1E-01
0.95	1.6E-01	1.24	2.8E-02	1.41	3.1E-02
1.00	5.7E-01	1.24	5.4E-02	1.68	2.8E-02

1.01	8.6E-01	1.17	2.5E-02	1.52	3.1E-02
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1.13	3.8E-01	0.83	1.2E-01	1.30	1.2E-01
1.04	2.2E-01	1.41	8.8E-02	1.58	1.9E-02

0.98	7.0E-01	1.42	5.4E-03	1.59	4.4E-02
0.97	7.3E-01	1.53	3.0E-02	2.03	4.8E-02
0.98	8.0E-01	1.45	3.0E-02	1.67	5.3E-02
1.00	9.3E-01	1.45	4.7E-02	1.57	1.4E-01
1.01	7.5E-01	1.23	3.1E-02	1.48	1.1E-01
0.96	5.8E-01	1.18	5.6E-02	1.72	2.8E-02
1.00	9.6E-01	1.32	3.2E-02	1.77	6.8E-03
1.03	3.0E-01	1.04	3.6E-01	1.13	3.6E-01
0.99	8.1E-01	1.34	5.4E-02	1.80	5.3E-02
1.03	4.8E-01	1.32	4.7E-02	1.71	1.8E-02
0.94	4.9E-01	1.14	2.2E-02	1.41	4.3E-02
0.66	2.7E-01	0.42	4.7E-02	0.67	3.0E-03
1.06	3.3E-02	1.19	2.3E-01	1.65	6.1E-02
0.98	6.9E-01	1.39	5.2E-02	1.64	2.8E-02

1.04	1.5E-01	1.26	8.6E-02	1.40	4.8E-02
1.35	6.4E-02	1.44	3.9E-03	1.28	2.6E-01
1.00	9.4E-01	1.16	2.1E-01	1.45	1.2E-03
0.99	7.8E-01	1.36	2.7E-02	1.68	5.4E-02
1.12	4.7E-02	1.56	no replicates	1.20	3.0E-01
1.05	3.4E-01	1.35	1.6E-02	1.48	2.1E-01
0.99	8.3E-01	1.32	2.1E-01	1.54	5.3E-02
0.51	2.4E-02	0.25	1.1E-03	0.38	6.7E-03

1.05	4.4E-01	1.36	5.9E-02	1.52	3.6E-02
1.02	2.2E-01	1.14	3.3E-02	1.67	5.2E-02
1.22	2.2E-01	1.50	7.3E-02	1.03	8.4E-01
0.99	8.5E-01	1.22	2.6E-01	1.64	1.5E-02
1.07	5.7E-02	1.36	2.2E-02	1.41	1.7E-01
1.03	5.4E-01	1.25	5.1E-03	1.53	1.4E-02
0.98	7.3E-01	1.24	4.0E-02	1.57	9.4E-03
0.99	9.2E-01	1.25	1.5E-02	1.41	3.8E-01
0.98	7.1E-01	1.17	3.2E-01	1.62	3.2E-02
1.03	4.3E-01	1.32	4.5E-02	1.64	7.2E-02
1.03	1.3E-01	1.37	5.3E-02	1.42	1.7E-01
1.03	6.0E-01	1.36	4.0E-02	1.56	3.5E-02

1.17	3.3E-01	1.58	4.6E-02	1.10	4.7E-01
0.99	7.9E-01	1.34	1.8E-01	1.70	7.3E-02
0.99	7.0E-01	1.17	2.0E-02	1.69	3.1E-02
0.96	3.3E-01	1.34	9.7E-02	1.48	2.5E-02
0.97	2.3E-01	1.42	2.4E-02	1.66	7.0E-02
1.04	4.5E-01	1.44	2.1E-01	1.95	6.4E-02
1.02	2.5E-02	1.46	8.5E-02	1.57	1.1E-01
1.09	1.1E-01	0.96	6.1E-01	1.22	1.1E-01
0.99	8.8E-01	1.40	4.3E-02	1.84	2.6E-02
0.97	5.7E-01	1.41	2.7E-02	1.61	5.1E-02
1.05	1.6E-02	1.49	1.7E-02	1.61	7.8E-02
1.01	8.5E-01	1.48	2.8E-02	1.49	3.1E-02
0.98	7.7E-01	1.47	5.3E-02	1.96	2.9E-02
1.02	7.1E-01	1.40	1.0E-02	1.68	6.2E-02
1.03	5.7E-01	1.31	1.7E-02	1.48	4.8E-02
1.04	2.6E-01	1.24	2.2E-02	1.47	3.4E-02
1.13	4.2E-01	1.60	3.4E-02	1.16	4.1E-01
1.17	1.3E-01	1.15	1.4E-01	0.60	1.3E-03
1.35	3.0E-01	1.83	1.7E-02	1.67	2.7E-01
1.00	9.5E-01	1.34	1.6E-01	1.55	3.1E-01
0.94	3.0E-01	0.76	2.0E-03	0.58	2.3E-02
0.92	3.3E-01	0.49	2.4E-03	0.43	3.3E-03
0.95	4.8E-01	1.26	4.9E-02	1.46	5.3E-02
0.86	no replicates	1.07	3.1E-01	2.05	2.5E-01
1.01	6.6E-01	1.48	4.2E-02	1.55	2.7E-01
0.95	5.0E-01	1.52	7.3E-02	1.83	1.2E-01
0.98	6.0E-01	1.46	3.2E-02	1.69	1.1E-02
0.79	no replicates	0.97	5.9E-01	1.62	3.6E-01
1.08	1.8E-02	1.46	1.8E-02	1.47	2.0E-01
1.15	2.4E-01	1.57	5.7E-02	1.46	2.0E-01
0.93	3.5E-01	1.23	4.3E-02	1.50	1.1E-02
0.95	2.8E-01	1.29	1.4E-02	1.50	3.4E-02
0.95	1.8E-01	1.13	3.4E-01	1.40	5.3E-02
0.97	4.5E-01	1.56	9.5E-02	1.77	3.3E-02
0.96	1.7E-02	1.15	2.6E-02	1.42	1.5E-01
0.90	1.6E-01	0.57	1.1E-04	0.53	2.9E-02
1.00	8.8E-01	1.43	5.2E-02	1.62	2.2E-02
1.03	2.8E-01	1.47	6.3E-02	1.62	2.3E-01
1.12	7.3E-02	1.62	6.1E-02	1.41	4.5E-02
1.03	3.2E-01	1.48	4.5E-02	1.73	7.3E-02
1.01	7.3E-01	1.44	6.0E-02	1.72	2.1E-02
1.07	2.8E-02	1.43	4.1E-02	1.44	1.0E-01
1.05	5.0E-01	1.48	5.6E-02	1.20	4.1E-01
1.05	3.3E-01	1.42	no replicates	1.49	2.3E-02
0.97	3.4E-01	1.44	3.5E-03	1.76	2.8E-02
1.03	1.6E-01	1.41	4.4E-02	1.43	2.0E-01
1.01	7.6E-01	1.47	5.3E-02	1.53	5.7E-02
0.85	2.2E-01	0.54	1.4E-01	0.78	8.2E-02
1.01	9.3E-01	1.30	1.3E-01	1.66	2.2E-02
1.06	2.3E-01	1.43	4.1E-03	1.45	1.5E-01
1.42	1.3E-01	1.50	7.3E-02	1.14	4.1E-03
1.06	3.1E-01	1.32	2.0E-03	1.44	3.0E-02

0.92	2.4E-01	0.68	4.2E-02	0.61	2.5E-02
0.97	4.9E-01	1.42	1.1E-01	2.13	2.9E-02
1.03	3.2E-01	1.58	6.1E-02	1.45	4.7E-02
0.99	8.9E-01	1.44	3.1E-02	1.66	7.8E-02
1.10	9.5E-02	1.40	4.4E-02	1.61	2.9E-01
0.80	no replicates	0.64	4.8E-03	0.76	3.1E-01
0.99	8.8E-01	1.29	2.4E-02	1.40	1.4E-01
1.04	7.4E-01	1.00	9.8E-01	0.62	7.9E-03
0.91	7.3E-02	0.76	1.2E-02	0.67	1.3E-01
1.00	9.6E-01	1.27	4.6E-02	1.66	5.4E-02
0.88	2.0E-01	0.69	3.4E-02	0.85	4.4E-02
0.97	3.5E-01	0.80	4.0E-02	0.59	9.8E-02
0.86	1.3E-01	0.61	9.6E-03	0.45	4.2E-03
1.00	9.8E-01	0.70	6.8E-02	0.87	no replicates
0.88	3.1E-01	0.71	1.5E-02	1.00	9.8E-01
1.02	5.6E-01	1.35	4.6E-02	1.65	1.6E-02
0.93	1.1E-03	0.61	2.6E-03	0.52	7.3E-02
0.99	8.2E-01	0.74	2.2E-02	0.67	8.3E-02
0.99	5.3E-01	0.78	1.5E-02	0.55	4.8E-02
1.04	3.7E-01	0.85	1.2E-02	0.67	1.0E-01
0.96	1.8E-01	0.79	5.1E-02	0.78	2.1E-02
0.96	5.3E-01	0.72	1.2E-02	0.61	9.5E-04
0.88	6.5E-02	0.68	6.3E-03	0.82	3.2E-01
1.06	2.2E-01	1.35	2.6E-02	1.41	1.0E-01
1.05	7.0E-02	0.82	1.1E-02	0.68	1.4E-01
1.10	4.8E-02	1.02	6.4E-01	0.69	1.0E-01
0.81	2.4E-01	0.63	4.8E-03	0.81	3.0E-01
1.02	4.3E-01	1.30	4.6E-03	1.53	8.8E-02
0.88	1.1E-01	0.69	2.4E-02	0.84	4.2E-01
1.20	9.8E-02	1.08	6.6E-01	0.55	8.6E-03
0.89	no replicates	0.65	1.6E-03	0.81	2.8E-01
0.92	1.3E-02	0.64	3.2E-03	0.67	1.3E-01
1.22	4.4E-02	1.00	9.6E-01	0.67	1.7E-02
0.78	4.3E-02	0.67	4.7E-03	0.76	1.8E-01
1.29	2.1E-01	0.83	6.0E-02	0.63	1.1E-02
0.89	1.4E-02	0.67	7.2E-02	0.88	1.6E-01
0.98	1.1E-03	0.96	3.1E-01	1.40	7.6E-03
0.95	6.2E-01	1.38	4.4E-02	1.72	6.2E-02
0.94	5.9E-01	0.80	no replicates	0.68	6.0E-03
0.97	1.8E-01	0.83	3.0E-02	0.70	2.4E-01
1.07	5.3E-03	0.76	1.0E-02	0.62	7.1E-02
0.99	8.6E-01	1.34	3.5E-02	1.69	3.8E-02
0.78	3.1E-02	0.66	2.6E-02	0.72	1.3E-01
1.00	8.6E-01	0.69	1.9E-03	0.42	2.1E-02
1.02	6.4E-01	1.30	5.3E-02	1.52	4.2E-02
0.86	no replicates	0.71	1.8E-02	0.83	6.8E-02
0.87	1.6E-01	0.69	1.1E-02	0.74	2.2E-01
0.98	6.4E-01	0.72	6.0E-03	0.65	4.0E-02
0.89	8.7E-02	1.32	1.2E-01	1.80	1.7E-02
0.92	7.9E-02	1.33	4.9E-02	1.65	7.7E-02
0.92	no replicates	0.67	1.7E-02	0.87	2.9E-01
0.86	1.3E-01	0.63	1.4E-03	0.71	2.4E-01
1.19	9.6E-03	1.08	3.1E-01	0.67	1.2E-02
0.82	no replicates	0.69	3.5E-02	1.06	2.8E-01
0.78	no replicates	0.65	5.2E-02	0.77	1.3E-01
0.88	3.5E-01	0.47	3.3E-03	0.61	7.5E-02
0.81	8.0E-02	0.58	4.5E-03	0.82	4.0E-02

0.99	7.8E-01	1.36	3.7E-02	1.72	2.0E-02
0.80	no replicates	0.67	no replicates	0.91	1.8E-01
0.95	3.2E-01	1.20	5.5E-02	1.63	3.5E-02
0.78	no replicates	0.70	3.2E-02	0.73	6.8E-03
1.06	1.0E-02	1.27	1.4E-01	1.66	5.8E-02
0.97	3.8E-01	1.24	5.9E-02	1.43	1.4E-01
0.91	1.5E-01	0.55	3.7E-03	0.66	1.6E-01
0.81	1.6E-01	0.69	3.4E-02	0.80	2.1E-02
0.97	6.0E-01	1.34	8.8E-02	1.73	6.8E-02
0.98	7.1E-02	0.63	9.4E-03	0.73	2.1E-02
0.98	1.9E-01	0.81	1.9E-02	0.68	no replicates
0.89	1.9E-01	0.61	2.6E-03	0.61	7.9E-02
0.82	no replicates	0.83	1.3E-01	0.67	no replicates
0.95	3.4E-02	1.09	4.6E-01	1.44	5.5E-02
1.03	1.0E-01	1.13	6.9E-02	1.49	2.5E-02
0.79	4.5E-02	0.55	1.6E-04	0.77	6.5E-02
0.75	no replicates	0.64	7.0E-03	0.95	4.5E-01
1.00	9.7E-01	1.19	4.4E-02	1.76	5.2E-02
0.92	2.4E-01	0.66	1.2E-03	0.74	7.4E-02
0.99	6.8E-01	1.30	5.9E-02	1.63	7.1E-02
0.88	2.5E-01	0.79	2.6E-02	0.65	no replicates
0.93	3.5E-01	1.06	1.4E-01	1.61	6.5E-02
0.94	3.4E-01	0.66	6.7E-03	0.68	2.3E-01
1.01	8.9E-01	0.86	3.8E-02	0.52	5.5E-02
0.89	3.0E-02	0.80	3.3E-02	0.69	no replicates
0.96	1.2E-01	0.47	1.8E-03	0.54	1.0E-02
0.84	2.6E-02	0.65	9.5E-03	0.71	2.0E-01
1.04	2.1E-01	0.96	no replicates	0.52	6.6E-03
0.90	2.6E-02	0.67	no replicates	0.84	2.5E-02
1.04	2.0E-01	1.33	1.4E-02	1.53	4.1E-02
1.00	9.1E-01	1.32	3.2E-02	1.55	1.5E-02
0.89	3.8E-01	0.60	6.8E-03	0.81	1.1E-01
0.93	no replicates	0.79	2.2E-02	0.69	no replicates
0.88	1.2E-01	0.68	2.2E-03	0.73	2.7E-01
1.09	4.1E-01	0.85	2.2E-01	0.41	1.1E-02
1.01	8.9E-01	0.69	1.1E-02	0.70	6.8E-02
0.96	5.3E-01	0.89	2.0E-01	0.55	4.4E-03
0.99	8.1E-01	0.94	5.7E-01	0.50	3.0E-05
1.05	3.1E-01	1.03	6.3E-01	0.42	7.6E-04
0.98	4.9E-01	0.75	3.6E-03	0.63	1.6E-02
1.08	5.8E-01	0.89	3.2E-01	0.62	9.0E-03
0.93	1.5E-01	0.62	1.4E-02	0.30	1.9E-03
0.97	9.4E-02	0.98	7.0E-01	0.59	1.2E-02
1.02	5.8E-01	0.95	1.9E-01	0.71	1.0E-03
0.99	9.1E-01	1.28	4.9E-02	1.72	1.8E-02
1.02	7.7E-01	1.31	1.5E-01	1.41	3.5E-02

1.12	9.5E-02	0.94	3.1E-01	0.44	1.0E-04
0.81	9.8E-02	0.54	7.2E-03	0.78	8.9E-02
1.04	3.9E-01	1.10	1.3E-01	0.54	1.1E-02
0.94	7.8E-02	0.67	2.0E-02	0.63	6.2E-02
0.97	no replicates	0.74	1.2E-02	0.69	no replicates
0.95	5.0E-01	1.32	8.4E-03	1.78	3.3E-02
1.12	6.9E-02	0.94	3.3E-01	0.53	1.4E-02
0.96	9.2E-03	0.74	9.4E-02	0.63	9.8E-05
0.94	3.9E-01	0.66	3.0E-02	0.77	2.7E-01
0.89	4.7E-02	0.55	3.6E-03	0.71	1.1E-02
1.00	9.3E-01	0.93	1.3E-01	0.71	1.2E-01
1.25	2.3E-01	1.04	6.6E-01	0.55	1.5E-02
1.04	3.5E-01	0.90	7.8E-02	0.62	4.1E-03
1.09	1.7E-01	0.98	7.0E-01	0.59	1.1E-02
0.89	3.4E-02	0.68	8.0E-02	0.74	3.5E-01
0.97	3.6E-01	1.35	6.4E-02	1.48	7.7E-02
0.96	2.9E-02	1.33	1.4E-01	1.89	6.7E-02
0.95	3.0E-01	0.87	7.0E-02	0.64	2.0E-02
0.79	3.6E-03	0.56	1.2E-02	0.65	8.6E-02
1.12	8.7E-02	0.96	5.6E-01	0.58	1.9E-02
1.03	6.4E-01	1.28	2.7E-02	1.45	1.3E-01
0.98	8.3E-01	1.30	1.5E-01	1.70	3.9E-02
0.80	1.3E-01	0.68	5.2E-04	0.65	1.8E-01
0.83	1.2E-01	0.62	5.0E-03	0.76	1.6E-01
0.96	6.2E-01	0.85	6.0E-02	0.71	1.0E-02
0.81	1.6E-02	0.65	5.2E-03	0.90	1.5E-01
1.01	6.3E-01	1.23	3.0E-02	1.41	4.6E-02
0.90	6.6E-02	0.64	1.7E-03	0.72	5.3E-02
0.78	4.4E-02	0.69	1.3E-02	0.79	1.7E-01
1.02	5.4E-01	0.81	1.7E-02	0.74	2.2E-01
0.81	1.1E-01	0.51	7.2E-03	0.64	3.1E-02
0.95	4.7E-02	1.16	2.5E-01	1.41	4.1E-02
1.03	7.1E-01	0.82	8.3E-02	0.51	1.3E-02
0.84	1.8E-02	0.66	9.6E-03	0.67	1.1E-01
0.85	9.4E-02	0.69	1.6E-03	0.77	1.8E-02
0.84	6.5E-02	0.67	1.7E-03	0.71	1.7E-01
1.09	2.8E-02	0.89	1.9E-01	0.48	1.9E-02
1.15	9.9E-02	1.16	3.9E-02	0.65	1.7E-02
0.94	4.9E-01	0.56	no replicates	0.69	no replicates
0.80	5.4E-02	0.49	7.6E-03	0.47	3.0E-03
0.98	2.9E-01	1.30	4.7E-02	1.78	1.7E-02
1.01	3.6E-01	0.89	6.9E-02	0.58	2.0E-02
0.85	1.3E-01	0.68	7.0E-03	0.81	2.0E-01
0.96	3.4E-01	1.20	1.0E-02	1.42	3.9E-02
1.01	1.9E-01	1.15	2.3E-02	1.69	1.9E-02
0.98	6.4E-01	0.86	2.2E-01	0.61	1.5E-02
0.90	8.2E-02	0.62	3.2E-02	0.74	2.5E-02
0.94	no replicates	0.66	1.2E-01	0.64	no replicates
1.31	1.3E-01	0.94	4.0E-01	0.61	7.6E-03
0.96	1.5E-01	0.54	9.7E-03	0.60	4.9E-03
1.26	2.0E-02	0.92	1.5E-01	0.59	7.1E-03
1.02	6.2E-01	1.39	3.6E-02	1.66	1.1E-01
1.04	1.5E-01	1.21	4.4E-02	1.46	2.1E-01
1.03	1.9E-01	0.84	4.9E-02	0.64	2.4E-03
1.12	no replicates	0.76	3.2E-02	0.69	no replicates

0.84	1.4E-01	0.70	3.1E-03	0.68	3.9E-03
0.89	3.2E-02	0.62	1.2E-02	0.67	1.4E-01
0.97	4.4E-01	0.69	1.1E-02	0.56	6.8E-02
0.91	8.2E-02	0.62	4.6E-03	0.60	4.2E-02
1.10	3.1E-01	0.84	8.5E-02	0.37	2.6E-03
0.79	7.3E-02	0.63	6.1E-02	0.55	2.2E-02
1.13	1.2E-01	0.83	9.1E-02	0.65	2.0E-02
1.04	3.3E-01	0.71	9.5E-03	0.49	4.3E-02
1.17	2.4E-02	1.07	4.6E-01	0.57	7.5E-04
0.98	7.4E-01	1.28	1.0E-01	1.53	6.7E-02
1.10	4.7E-01	1.15	3.5E-01	1.25	3.6E-01
0.98	7.2E-01	1.29	4.8E-02	1.47	1.0E-01
1.05	1.1E-01	1.30	6.8E-02	1.51	4.7E-02
0.93	5.1E-01	1.34	2.0E-01	1.77	3.8E-02
1.01	8.6E-01	1.24	7.8E-02	1.44	5.0E-02
0.96	3.6E-02	1.31	2.0E-01	1.52	7.3E-02
0.96	5.3E-01	1.16	2.9E-01	1.40	4.9E-02
0.98	2.3E-01	1.32	1.9E-01	1.40	3.2E-02
0.96	5.3E-01	1.23	3.3E-01	1.53	1.8E-02
0.96	3.1E-01	1.19	1.6E-01	1.41	1.7E-02
0.97	4.7E-01	1.24	4.2E-01	1.57	4.2E-02
1.00	9.1E-01	1.26	1.2E-01	1.69	9.8E-03
0.97	3.4E-01	1.33	6.5E-02	1.55	6.2E-02
1.01	7.0E-01	1.22	7.9E-02	1.40	1.4E-02
1.01	7.6E-01	1.26	3.4E-01	1.61	2.5E-02
1.25	2.6E-01	1.41	1.3E-01	1.05	5.0E-01
1.01	7.3E-01	1.32	3.7E-02	1.56	8.7E-02
0.99	4.1E-01	1.06	5.9E-01	1.42	7.8E-02
0.97	6.4E-01	1.27	1.1E-01	1.51	6.6E-02
0.99	no replicates	1.35	3.3E-01	1.29	5.2E-01
1.09	5.6E-01	1.32	2.2E-01	1.28	no replicates
1.02	2.5E-01	1.19	1.1E-01	1.68	no replicates
1.05	no replicates	1.50	1.0E-01	1.39	1.5E-02
1.04	2.7E-01	1.23	2.6E-02	1.50	8.8E-02
1.14	3.6E-03	1.32	9.9E-02	1.44	2.9E-01
1.12	no replicates	1.24	2.5E-01	1.57	no replicates
1.02	8.9E-01	0.99	9.7E-01	0.87	5.6E-01
0.99	8.4E-01	1.34	5.3E-02	1.45	1.8E-01
0.90	1.9E-01	0.98	2.0E-01	1.66	6.1E-02
1.12	no replicates	1.26	2.2E-01	1.42	2.0E-02
1.17	no replicates	1.51	1.7E-01	1.22	2.6E-01
1.02	7.9E-01	1.14	1.9E-01	1.41	2.3E-02
0.98	5.1E-01	1.36	3.6E-03	1.55	1.2E-01
1.30	no replicates	1.49	6.6E-02	1.09	3.1E-01
1.09	4.0E-01			1.44	2.1E-02
1.05	4.7E-01	1.34	2.5E-02	1.52	1.7E-01
1.00	9.6E-01	1.35	5.4E-02	1.49	1.0E-01
0.99	8.2E-01	1.29	3.2E-02	1.45	9.9E-02
0.98	5.4E-01	1.25	4.4E-02	1.40	1.0E-01
1.05	3.5E-01	1.49	no replicates	1.04	no replicates
1.08	no replicates	1.25	no replicates	1.42	3.1E-01
1.27	7.7E-02	1.41	5.0E-02	1.24	4.4E-01
0.97	7.0E-01	1.14	5.1E-01	1.63	no replicates
1.07	4.3E-01	1.42	no replicates	0.97	no replicates
0.96	5.4E-01	1.25	6.4E-02	1.43	7.6E-02
0.96	1.9E-01	1.12	2.0E-01	1.47	1.7E-02
1.08	1.2E-01	1.37	2.4E-01	1.43	3.2E-01

0.98	7.7E-01	1.25	3.3E-02	1.43	2.5E-01
1.05	6.1E-02	1.28	1.9E-02	1.44	3.0E-01
0.98	6.1E-01	1.23	1.1E-01	1.60	7.7E-02
1.02	6.2E-01	1.05	2.7E-01	1.42	3.6E-02
1.05	5.2E-01	1.24	2.5E-01	1.64	1.5E-02
1.02	4.9E-01	1.19	1.1E-01	1.53	2.9E-02
1.01	5.1E-01	1.21	3.0E-01	1.53	2.4E-03
0.96	2.1E-01	1.24	9.9E-02	1.50	3.4E-02
1.04	3.6E-01	1.32	1.1E-02	1.45	1.1E-01
1.02	6.8E-01	1.41	3.0E-02	1.25	1.8E-01
0.95	2.0E-01	1.39	8.3E-02	1.67	3.6E-02
0.92	4.4E-01	1.16	1.6E-01	1.42	2.3E-02
0.96	3.4E-01	1.10	3.7E-01	1.41	6.0E-02
1.00	9.0E-01	1.28	5.7E-02	1.61	2.4E-01
0.98	5.8E-01	1.19	6.3E-02	1.73	3.8E-02
1.01	6.8E-01	1.29	3.7E-02	1.51	1.6E-01
1.21	1.9E-02	1.47	9.2E-02	1.08	7.1E-01
1.00	9.3E-01	1.29	2.5E-02	1.45	8.1E-02
1.16	1.8E-03	1.44	8.2E-02	1.29	3.4E-01
0.98	6.3E-01	1.24	8.3E-02	1.67	3.1E-02
1.02	7.2E-01	1.30	1.7E-01	1.64	6.1E-02
1.01	8.8E-01	1.33	2.0E-01	1.44	1.5E-01
0.99	8.1E-02	1.25	3.1E-02	1.55	1.2E-01
0.91	9.9E-02	1.09	4.8E-01	1.47	5.6E-02
1.04	5.5E-03	1.30	7.6E-02	1.47	2.2E-01
0.96	2.3E-01	1.14	2.3E-01	1.41	2.3E-02
1.00	9.9E-01	1.20	1.0E-01	1.43	7.4E-02
0.96	2.5E-01	1.35	6.1E-02	1.46	1.8E-01
0.99	8.4E-01	1.34	2.6E-02	1.43	2.1E-01
1.12	3.4E-02	1.42	1.3E-01	1.19	3.8E-01
0.96	4.4E-01	1.09	3.1E-01	1.43	6.8E-03
0.93	3.1E-01	1.10	2.1E-01	1.42	2.1E-02
0.94	5.7E-01	1.23	3.8E-03	1.49	8.7E-02
1.03	4.4E-01	1.11	8.2E-02	1.45	7.9E-03
0.97	3.8E-01	1.19	1.0E-01	1.44	1.2E-01
0.97	5.1E-01	1.20	2.7E-01	1.93	3.0E-02
0.95	1.6E-01	1.27	4.0E-02	1.42	7.5E-02
0.98	4.3E-01	1.36	2.3E-02	1.65	1.4E-01
0.97	5.9E-01	1.28	1.2E-01	1.54	4.2E-02
0.97	2.8E-01	1.33	5.8E-02	1.51	7.8E-02
1.05	1.6E-01	1.38	4.7E-02	1.49	8.5E-02
0.97	6.2E-01	1.27	1.7E-01	1.53	2.3E-02
0.96	6.8E-01	1.28	8.4E-02	1.57	7.5E-02
1.00	9.9E-01	1.31	7.0E-02	1.48	3.4E-02
1.01	7.5E-01	1.32	5.4E-02	1.49	1.3E-01
0.98	5.9E-01	1.27	1.3E-01	1.42	3.3E-03
0.96	5.2E-02	1.21	1.3E-01	1.62	4.7E-02
1.00	9.4E-01	1.24	1.1E-01	1.75	2.1E-02
0.94	3.3E-01	1.34	1.1E-01	1.63	2.6E-03
1.02	3.6E-01	1.31	8.7E-02	1.50	5.1E-02
0.99	7.7E-01	1.12	2.3E-01	1.40	2.8E-03
1.01	7.0E-01	1.38	3.3E-02	1.56	2.1E-01
0.93	3.9E-01	1.19	7.6E-02	1.59	3.3E-02
0.99	9.2E-01	1.33	2.4E-02	1.43	1.8E-01
1.02	8.8E-02	1.15	7.4E-02	1.46	4.1E-02
0.99	8.8E-01	1.09	2.0E-01	1.62	5.1E-02



0.99	7.8E-01	1.23	2.4E-01	1.48	2.1E-02
0.97	3.5E-01	1.19	1.0E-01	1.54	1.5E-03
0.99	8.9E-01	1.23	1.7E-01	1.43	4.7E-02
1.01	7.7E-01	1.34	3.9E-02	1.50	2.9E-01
0.98	3.1E-02	1.36	1.8E-01	1.42	1.6E-01
0.96	5.9E-01	1.16	9.2E-02	1.43	7.6E-02
0.98	6.6E-01	1.35	1.3E-01	1.63	4.1E-02
1.02	6.1E-01	1.33	3.2E-02	1.51	1.4E-01
0.97	5.9E-01	1.34	1.1E-01	1.49	8.3E-02
0.98	7.0E-01	1.39	7.5E-02	1.63	5.0E-02
0.98	6.5E-01	1.36	5.2E-02	1.44	1.2E-01
0.98	7.3E-01	1.22	2.6E-02	1.56	1.5E-01
0.94	1.0E-02	1.21	7.4E-02	1.54	1.4E-01
0.93	4.4E-01	1.38	6.8E-02	1.50	4.8E-02
0.95	3.2E-01	1.10	1.2E-01	1.46	8.0E-02
1.03	2.2E-01	1.37	6.4E-02	1.44	7.8E-02
0.90	1.8E-01	1.24	1.9E-01	1.57	8.9E-02
1.07	1.9E-01	1.33	2.1E-02	1.47	7.6E-02
0.98	2.4E-01	1.33	8.6E-02	1.58	1.6E-02
0.95	5.1E-01	1.09	5.4E-01	1.42	1.2E-04
1.02	8.4E-01	1.22	1.7E-01	1.47	2.0E-02
1.04	2.9E-01	1.37	3.9E-02	1.52	1.1E-01
1.02	4.0E-01	1.31	7.0E-02	1.48	5.7E-02
1.03	6.9E-03	1.38	1.3E-01	1.45	1.2E-01
0.93	1.2E-01	1.20	9.5E-02	1.55	3.3E-02
0.97	1.4E-01	1.29	7.9E-02	1.54	3.4E-02
1.06	1.3E-01	1.22	7.6E-03	1.48	8.1E-02
0.95	3.7E-01	1.31	1.7E-01	1.71	7.3E-02
0.91	9.5E-02	1.09	8.8E-04	1.45	8.0E-02
0.98	5.5E-01	1.40	1.7E-02	1.57	2.1E-01
1.02	6.8E-01	1.29	4.1E-02	1.46	7.9E-02
1.02	5.4E-01	1.38	2.3E-02	1.46	2.1E-01
1.00	9.7E-01	1.05	7.2E-02	1.53	1.6E-02
0.94	5.3E-01	1.33	7.2E-02	1.78	1.8E-02
0.95	3.0E-01	1.10	2.4E-01	1.42	6.7E-04
0.94	3.3E-01	1.13	6.3E-02	1.59	1.3E-03
0.92	1.9E-01	1.37	1.1E-01	1.78	3.1E-02
1.00	9.8E-01	1.30	1.3E-02	1.47	1.8E-01
0.99	8.0E-01	1.25	9.0E-02	1.65	1.6E-03
0.97	3.2E-01	1.16	1.8E-01	1.47	4.5E-04
0.95	2.4E-01	1.15	2.8E-01	1.41	6.1E-02
0.97	5.3E-01	1.25	2.3E-01	1.51	6.5E-02
0.96	7.4E-02	1.13	1.5E-01	1.47	6.4E-02
1.01	3.7E-01	1.21	1.4E-01	1.42	6.1E-02
1.00	9.9E-01	1.11	9.1E-02	1.45	4.9E-02
1.03	5.9E-01	1.44	5.0E-02	1.36	1.3E-01
0.93	1.8E-01	1.12	4.8E-01	1.55	4.8E-02
0.95	2.8E-01	1.27	8.7E-02	1.77	6.4E-02
0.99	8.9E-01	1.18	1.0E-01	1.43	2.0E-02
1.00	9.3E-01	1.26	5.0E-03	1.61	7.4E-02
1.05	2.3E-01	1.20	4.6E-02	1.46	1.2E-01
1.00	6.9E-01	1.18	1.1E-01	1.60	6.2E-02
1.03	5.3E-01	1.33	5.0E-02	1.43	1.9E-01
1.02	4.4E-01	1.18	1.9E-01	1.48	3.9E-02

0.90	8.8E-02	1.21	1.0E-01	1.53	6.5E-02
1.00	9.6E-01	1.12	2.6E-01	1.45	7.7E-03
0.98	5.9E-01	1.15	2.0E-01	1.45	3.3E-02
0.99	8.3E-01	1.36	6.8E-02	1.59	1.1E-01
1.02	3.8E-01	1.39	4.3E-02	1.65	1.9E-01
0.99	7.2E-01	1.23	8.2E-02	1.52	3.1E-02
0.99	8.7E-01	1.39	1.9E-02	1.69	1.1E-01
1.00	5.2E-01	1.19	3.5E-01	1.60	7.7E-03
1.06	2.8E-01	1.39	8.1E-03	1.46	3.7E-01
0.99	8.9E-01	1.14	9.1E-02	1.46	8.1E-02
1.08	3.5E-01	1.37	1.1E-01	1.48	2.1E-01
0.97	1.7E-01	1.29	5.3E-02	1.42	8.6E-02
0.98	6.7E-01	1.34	7.4E-02	1.84	5.2E-02
0.99	6.0E-01	1.14	2.8E-01	1.53	1.0E-01
0.99	6.9E-01	1.28	3.7E-02	1.49	2.3E-01
0.95	5.9E-01	1.24	5.3E-02	1.42	9.4E-02
1.05	3.8E-01	1.19	5.6E-02	1.43	8.4E-02
0.98	7.0E-01	1.31	8.1E-02	1.40	1.7E-02
0.93	2.2E-01	1.28	2.1E-02	1.57	1.1E-01
0.99	8.5E-01	1.36	8.4E-03	1.47	1.1E-01
0.92	1.4E-01	1.28	9.7E-03	1.57	1.9E-01
0.96	3.8E-01	1.39	1.8E-02	1.42	1.7E-01
0.93	2.5E-01	1.08	2.5E-01	1.43	9.8E-03
1.03	5.4E-01	1.26	5.2E-02	1.47	1.5E-01
0.96	4.8E-01	1.39	1.4E-01	1.89	3.3E-02
0.97	5.7E-01	1.26	1.0E-01	1.81	6.0E-02
0.97	4.5E-01	1.21	1.3E-01	1.43	6.6E-02
0.99	6.8E-01	1.32	5.2E-02	1.53	1.7E-01
1.01	8.6E-01	1.35	9.5E-02	1.46	2.6E-02
0.98	6.3E-01	1.22	8.4E-02	1.53	1.8E-02
0.95	5.0E-01	1.39	7.1E-02	1.75	6.3E-02
0.92	3.4E-01	1.21	9.7E-02	1.45	5.2E-03
0.93	1.1E-01	1.16	2.9E-01	1.60	1.4E-01
0.96	5.3E-01	1.31	1.2E-01	1.43	6.3E-02
1.00	9.4E-01	1.13	7.8E-02	1.42	6.2E-03
0.98	6.9E-01	1.13	2.1E-01	1.71	3.8E-02
1.03	6.4E-01	1.37	5.8E-02	1.54	1.4E-01
0.83	no replicates	0.66	2.2E-03	0.86	1.4E-01
0.92	4.1E-01	0.69	9.5E-03	0.82	1.8E-01
0.73	no replicates	0.70	6.9E-03	0.88	1.5E-01
0.87	2.9E-01	0.67	8.5E-03	1.03	1.3E-01
0.87	1.5E-01	0.68	6.0E-02	0.89	2.1E-01
1.33	3.1E-01	1.03	6.0E-01	0.57	3.8E-03
1.18	3.0E-02	1.00	1.0E+00	0.62	6.6E-02
0.93	1.2E-01	0.74	2.9E-02	0.66	4.7E-02
0.95	1.4E-01	0.96	2.3E-02	0.71	no replicates
1.18	2.7E-01	0.93	5.1E-01	0.59	1.5E-02
1.03	4.6E-01	1.05	1.1E-01	0.70	2.7E-02
0.84	5.4E-01	0.59	1.8E-02	0.83	6.4E-01
1.09	5.5E-02	0.88	1.2E-01	0.67	1.2E-02
0.96	6.1E-01	1.11	8.0E-02	0.57	3.0E-01
0.83	4.0E-01	0.65	5.3E-02	0.83	1.5E-01
1.09	5.7E-01	0.72	1.1E-01	0.43	1.0E-03

0.87	2.8E-01	0.71	5.0E-03	0.75	8.7E-02
0.79	4.1E-01	0.55	2.1E-02	0.81	2.7E-01
0.75	8.6E-02	0.64	4.7E-02	0.86	3.3E-01
0.83	no replicates	0.56	no replicates	0.76	no replicates
0.94	6.6E-01	0.71	no replicates	0.92	4.9E-01
0.71	no replicates			0.72	3.4E-02
0.87	no replicates	0.69	no replicates	0.76	2.2E-01
0.91	no replicates	0.66	no replicates	0.99	8.9E-01
1.00	no replicates	0.87	2.6E-01	0.69	no replicates
0.97	no replicates	0.52	no replicates	0.78	1.8E-01
0.81	1.0E-01	0.70	3.2E-02	0.81	no replicates
0.97	7.5E-01			0.63	2.4E-01
0.75	no replicates	0.68	no replicates	0.76	1.1E-01
0.76	3.0E-01	0.67	1.7E-01	0.82	1.3E-01
1.05	5.8E-01	0.71	3.2E-02	0.75	no replicates
0.85	3.6E-01	0.66	1.5E-01	0.77	5.0E-02
0.86	3.0E-01	0.70	5.1E-03	0.83	1.6E-01
0.87	4.1E-01	0.70	6.9E-02	0.86	2.8E-01
1.02	7.2E-01	0.91	6.1E-02	0.70	8.1E-02
1.04	no replicates	0.81	9.8E-03	0.71	1.5E-01
0.91	5.3E-01	0.69	3.6E-02	0.93	1.1E-01
0.85	2.2E-01	0.66	no replicates	0.96	4.1E-01
0.90	no replicates	0.70	3.1E-03	0.84	3.2E-01
1.04	2.0E-01	1.00	9.8E-01	0.70	5.4E-03
0.86	7.8E-02	0.94	3.2E-01	0.68	7.4E-04
1.03	5.3E-01	1.00	9.8E-01	0.71	9.4E-03
1.04	4.1E-01	0.92	1.1E-01	0.66	3.6E-03
1.01	3.3E-01	0.81	6.9E-02	0.69	1.2E-01
0.95	1.4E-01	0.88	1.7E-01	0.71	2.2E-02
1.13	1.7E-01	1.12	5.5E-01	0.62	8.5E-03
1.09	4.1E-02	1.02	8.4E-01	0.66	4.7E-02
0.97	4.3E-01	0.71	2.9E-03	0.88	2.4E-01
1.11	1.3E-01	0.85	1.4E-01	0.65	3.4E-02
1.35	1.4E-01	0.84	4.7E-02	0.33	7.1E-05
0.97	2.6E-01	0.67	1.7E-02	0.72	5.1E-02
1.01	7.3E-01	0.88	3.9E-02	0.60	3.6E-03
1.10	2.2E-01	1.04	3.3E-01	0.72	1.1E-03
1.04	3.3E-01	0.93	3.9E-01	0.66	1.0E-02
0.80	5.8E-02	0.66	2.3E-02	0.98	7.4E-01
1.08	1.2E-01	0.76	6.2E-02	0.70	3.7E-02
0.91	2.6E-01	0.67	9.7E-03	0.88	2.2E-01
1.14	2.1E-02	1.08	1.3E-01	0.65	9.6E-02
1.04	4.7E-01	0.71	2.6E-02	0.79	1.1E-01
0.97	5.1E-01	0.68	4.2E-03	0.81	1.3E-01
1.18	2.6E-02	0.90	3.4E-01	0.71	1.1E-01
1.02	6.8E-01	0.87	3.0E-01	0.68	1.3E-02
0.95	1.4E-01	0.81	1.3E-01	0.60	3.6E-03
1.01	7.9E-01	1.00	9.6E-01	0.61	1.5E-02
0.98	7.3E-01	0.88	1.8E-01	0.71	1.3E-02

0.87	4.8E-02	0.52	4.9E-03	0.73	4.6E-02
1.05	2.1E-01	0.86	8.9E-02	0.66	2.7E-02
1.11	1.7E-01	1.04	8.2E-01	0.67	2.9E-02
0.94	3.0E-01	0.90	2.5E-01	0.63	2.9E-02
1.07	6.8E-01	1.15	3.9E-01	0.63	9.7E-02
0.98	5.7E-01	0.70	1.9E-02	0.83	3.9E-01
1.06	2.3E-01	0.99	8.0E-01	0.69	1.9E-02
1.06	2.8E-01	1.10	1.4E-01	0.64	1.2E-02
1.01	8.7E-01	0.84	7.5E-02	0.64	2.8E-02
1.11	3.1E-01	1.00	9.7E-01	0.70	1.6E-02
0.91	7.2E-02	0.67	7.8E-02	1.01	8.5E-01
0.96	2.5E-01	0.91	3.8E-02	0.70	4.2E-02
0.99	8.7E-01	0.85	1.5E-01	0.66	1.4E-02
1.14	2.0E-01	0.63	1.3E-01	0.40	5.1E-03
0.74	no replicates	0.53	1.7E-02	0.79	3.4E-01
0.98	7.7E-01	0.69	1.4E-02	0.58	3.2E-02
1.01	no replicates	0.88	no replicates	0.70	no replicates
0.94	5.3E-02	0.65	4.1E-03	0.60	1.3E-01
0.89	1.6E-01	0.71	5.7E-02	0.78	2.7E-01
0.70	no replicates	0.54	6.5E-05	0.75	3.4E-02
0.69	no replicates	0.63	2.8E-02	0.83	7.1E-02
0.88	9.0E-02	0.70	6.8E-02	0.65	3.1E-03
0.88	9.8E-02	0.61	3.6E-04	0.68	no replicates
0.85	no replicates	0.59	1.1E-01	0.71	no replicates
0.91	1.0E-01	0.63	1.0E-02	0.65	9.4E-02
0.71	1.1E-01	0.57	6.0E-02	1.32	3.7E-02
0.97	2.4E-01	0.76	5.0E-02	0.65	1.4E-01
0.97	3.0E-01	0.66	1.4E-02	0.49	1.3E-01
0.64	5.8E-02	0.52	2.3E-04	0.76	1.1E-01
0.96	no replicates	0.82	3.0E-01	0.70	no replicates
0.91	no replicates	0.65	no replicates	0.62	no replicates
0.87	no replicates	0.63	1.8E-02	0.64	no replicates
0.92	1.6E-01	0.47	1.3E-03	0.57	4.1E-02
0.94	7.7E-02	0.99	8.2E-01	0.70	6.5E-02
0.86	1.0E-01	0.57	3.7E-02	0.64	7.1E-02
0.93	2.0E-01	0.76	9.1E-02	0.66	1.7E-02
0.93	4.2E-01	0.91	7.1E-01	0.70	1.9E-01
0.81	3.4E-01	0.51	2.5E-04	0.68	1.7E-01
0.50	no replicates	0.49	9.6E-02	0.71	9.4E-02
0.81	3.6E-01	0.56	5.9E-03	0.62	1.5E-01
0.81	7.4E-02	0.65	3.9E-02	0.68	2.7E-01
0.65	no replicates	0.59	2.7E-02	0.69	1.9E-01
0.71	3.1E-01	0.57	3.4E-03	0.73	3.9E-02
0.93	3.1E-01	0.67	2.2E-03	0.64	9.0E-02
0.90	2.5E-01	0.58	4.6E-03	0.61	3.5E-02
0.97	7.2E-01	0.72	4.6E-02	0.43	6.3E-05
0.67	no replicates	0.64	1.0E-02	0.88	3.7E-01
0.68	1.1E-01	0.47	5.9E-04	0.77	3.2E-01
0.83	no replicates	0.64	1.4E-02	0.83	3.3E-01
0.89	3.2E-01	0.61	2.7E-02	0.66	1.1E-01
0.84	8.4E-02	0.58	6.2E-04	0.65	1.4E-01

0.92	9.3E-02	0.63	7.8E-04	0.61	7.5E-02
0.88	2.1E-01	0.81	3.4E-03	0.71	no replicates
1.13	1.3E-01	1.15	8.7E-03	0.69	no replicates
1.00	9.7E-01	0.89	1.9E-01	0.67	1.7E-02
1.22	8.9E-02	1.05	no replicates	0.59	7.0E-03
0.80	no replicates	0.56	1.6E-02	0.76	8.9E-02
0.85	2.4E-01	0.62	2.9E-02	0.79	1.8E-01
0.95	no replicates	0.68	1.9E-02	0.81	3.9E-01
0.99	no replicates	0.64	5.2E-03	0.95	no replicates
1.11	1.4E-01	1.03	no replicates	0.53	1.5E-02
0.89	4.9E-02	0.69	1.1E-02	0.92	1.8E-01
1.12	2.5E-01			0.68	no replicates
0.89	no replicates	0.71	9.4E-02	0.84	1.6E-01
0.99	no replicates	0.80	1.3E-01	0.69	no replicates
0.63	no replicates	0.80	1.3E-01	0.87	no replicates
1.00	9.9E-01			0.66	2.8E-01
0.73	no replicates	0.66	3.8E-03	0.90	7.6E-02
0.94	3.4E-01	0.67	7.3E-03	0.79	6.1E-02
0.78	no replicates	0.58	4.6E-03	0.78	no replicates
1.07	2.1E-01	0.99	9.2E-01	0.59	1.5E-03
1.13	4.6E-01	0.87	2.1E-01	0.67	2.5E-02
1.16	2.1E-01	0.94	6.1E-01	0.45	1.1E-02
0.90	1.4E-01	0.71	5.7E-02	0.64	5.4E-02
0.88	6.9E-02	0.87	6.8E-02	0.63	3.2E-01
1.01	9.2E-01	1.00	9.6E-01	0.57	2.9E-02
0.94	4.6E-01	0.67	3.6E-03	0.76	1.9E-01
0.82	7.1E-02	0.66	7.8E-03	0.78	1.2E-01
0.84	2.5E-01	0.65	1.4E-02	0.80	1.2E-01
0.90	2.7E-01	0.80	2.9E-02	0.68	1.4E-01
0.80	7.6E-02	0.70	2.8E-02	0.74	2.9E-01
1.02	8.1E-01	0.71	2.7E-04	0.85	2.9E-01
0.87	1.5E-01	0.69	5.0E-03	0.87	1.0E-01
0.79	no replicates	0.71	5.2E-02	0.80	7.6E-02
0.93	4.5E-01	0.69	9.5E-02	0.86	2.9E-01
0.83	1.1E-01	0.66	3.0E-03	0.88	4.3E-01
0.92	3.0E-01	0.58	8.4E-03	0.80	2.1E-01
0.88	1.4E-01	0.65	6.8E-03	0.75	1.4E-01
0.81	5.1E-02	0.55	2.6E-02	0.82	2.0E-01
1.12	2.1E-01	0.96	5.7E-01	0.57	2.3E-03
0.94	5.1E-01	0.61	1.8E-03	0.71	2.2E-01
0.95	4.4E-01	0.97	5.6E-01	1.54	2.5E-02
0.98	3.7E-01	1.04	6.3E-01	1.02	5.4E-01
0.97	2.6E-01	1.22	1.6E-01	1.42	4.7E-02
0.79	3.8E-01	1.15	7.1E-02	1.43	3.2E-02
1.00	9.9E-01	1.28	2.7E-02	1.53	1.7E-01
0.91	3.6E-01	1.02	6.2E-01	1.43	6.3E-02
1.01	8.9E-01	1.32	1.9E-02	1.47	2.0E-01
0.96	3.6E-01	1.34	1.0E-01	1.44	4.8E-02
0.96	5.1E-01	1.19	9.9E-02	1.44	3.3E-02
1.01	5.3E-01	1.17	1.2E-01	1.55	1.3E-02
1.02	8.1E-01	1.36	5.6E-02	1.58	9.1E-02
0.96	4.2E-01	1.29	8.4E-02	1.60	2.6E-02
0.96	1.1E-01	1.13	2.0E-01	1.44	4.9E-02
0.99	6.4E-01	1.26	9.3E-02	1.41	1.8E-01

0.95	3.7E-01	1.10	2.7E-01	1.51	2.9E-02
0.95	4.3E-01	1.21	2.0E-01	1.63	4.5E-02
0.96	2.1E-01	1.16	1.4E-01	1.53	6.4E-02
1.02	3.3E-01	1.21	9.7E-02	1.43	1.1E-01
1.01	6.2E-01	1.14	6.3E-02	1.46	7.8E-03
1.08	3.0E-01	1.46	5.6E-02	1.73	1.6E-01
1.03	6.3E-01	1.40	5.1E-03	1.56	1.2E-01
1.07	1.8E-01	0.96	no replicates	1.46	2.0E-01
1.09	8.5E-02	1.41	9.5E-02	1.61	4.4E-03
1.00	9.4E-01	1.41	3.0E-02	1.44	2.7E-01
0.96	2.6E-01	1.42	3.1E-02	1.89	1.0E-01
1.02	4.7E-01	1.44	4.1E-02	1.65	2.1E-01
0.96	3.0E-01	1.51	4.3E-02	1.78	1.1E-01
1.08	no replicates	1.48	1.2E-03	1.69	no replicates
0.97	5.3E-01	1.43	7.2E-02	1.60	6.2E-02
0.96	6.4E-01	1.41	7.4E-02	1.82	7.9E-02
0.88	5.4E-01	1.52	9.4E-02	1.97	4.2E-02
1.01	8.5E-01	1.23	1.1E-02	1.42	1.3E-01
0.97	5.7E-01	1.41	8.5E-02	1.51	1.2E-01
0.97	7.0E-01	1.44	3.4E-02	1.41	9.3E-02
0.96	2.4E-01	1.50	4.7E-02	1.73	1.4E-01
1.03	5.4E-02	1.47	2.7E-02	1.69	1.1E-01
1.05	1.7E-01	1.52	3.0E-02	1.71	2.0E-01
1.00	9.5E-01	1.43	1.7E-02	1.91	1.5E-01
0.91	3.9E-01	1.43	no replicates	1.82	1.7E-02
0.98	7.4E-01	1.39	9.4E-02	1.58	2.0E-02
1.00	9.0E-01	1.40	3.1E-02	1.72	9.0E-02
0.95	3.1E-01	1.29	no replicates	1.68	2.6E-03
1.08	1.9E-01	1.26	4.8E-02	1.46	no replicates
1.03	7.4E-01	1.29	8.0E-02	1.61	1.1E-01
1.01	8.5E-01	1.23	1.7E-01	1.43	2.7E-02
0.98	6.9E-01	1.24	6.8E-02	1.56	4.7E-02
0.95	1.8E-01	1.39	3.5E-02	1.60	1.2E-01
1.02	4.4E-01	1.25	5.2E-02	1.49	9.8E-02
0.96	5.0E-01	1.16	2.7E-01	1.47	8.3E-03
1.07	2.6E-01	1.17	1.7E-01	1.58	4.8E-02
1.01	8.5E-01	1.33	no replicates	1.70	6.3E-02
1.00	9.7E-01	1.27	9.9E-02	1.53	9.0E-02
0.97	6.0E-01	1.22	5.0E-01	1.53	1.6E-02
1.06	2.2E-01	1.10	2.6E-01	1.55	2.4E-02
1.02	6.4E-01	1.21	2.2E-01	1.64	1.9E-02
1.02	7.1E-01	1.35	1.4E-01	1.67	3.2E-03
0.99	8.6E-01	1.35	1.9E-02	1.45	2.2E-01
1.13	2.3E-01	1.22	1.1E-01	1.44	6.0E-03
0.98	5.0E-01	1.28	7.5E-02	1.57	3.1E-02
0.98	7.2E-01	1.33	5.3E-02	1.57	1.6E-01
0.98	3.0E-01	1.20	8.9E-02	1.51	3.1E-02
0.97	3.7E-01	1.28	1.7E-01	1.49	3.2E-02
0.97	7.0E-01	1.35	2.0E-01	1.66	6.0E-02
0.94	3.3E-01	1.37	5.8E-02	1.69	1.6E-01
0.95	1.7E-01	1.14	5.9E-02	1.44	1.3E-02

0.98	5.8E-01	1.22	1.9E-01	1.52	3.3E-02
1.01	8.2E-01	1.37	9.2E-02	1.60	3.2E-02
1.00	9.5E-01	1.39	1.3E-02	1.64	2.5E-01
1.09	1.3E-01	1.32	4.3E-03	1.59	9.4E-02
0.99	8.5E-01	1.36	4.5E-02	1.53	9.2E-02
0.98	5.2E-01	1.35	1.8E-01	1.51	1.5E-02
0.99	6.9E-01	1.26	4.1E-02	1.56	1.1E-01
1.01	8.3E-01	1.37	6.8E-02	1.79	5.2E-02
0.98	3.1E-01	1.38	2.4E-02	1.78	1.4E-01
0.98	6.4E-01	1.13	2.0E-01	1.51	1.1E-01
1.08	1.4E-01	1.40	2.6E-02	1.35	2.0E-01
1.10	2.5E-01	1.47	1.6E-02	1.26	2.3E-01
0.97	5.0E-01	1.23	1.2E-01	1.49	1.0E-02
1.07	2.1E-01	0.94	6.6E-01	0.66	3.3E-02
0.96	5.4E-01	0.82	6.4E-02	0.62	7.8E-04
0.99	7.1E-02	0.77	4.4E-02	0.59	1.4E-02
1.01	6.9E-01	0.87	2.6E-01	0.67	3.2E-03
0.99	8.2E-01	0.73	8.6E-03	0.61	4.9E-02
0.87	1.0E-01	0.67	2.0E-03	0.93	2.1E-01
0.85	6.4E-02	0.62	7.4E-03	0.80	1.3E-01
1.09	7.1E-02	1.00	9.0E-01	0.44	1.7E-03
1.30	1.1E-01	1.05	6.2E-01	0.58	2.4E-03
0.98	6.9E-01	0.73	8.4E-03	0.71	1.9E-01
0.91	1.3E-01	0.76	3.8E-02	0.83	3.3E-01
1.04	5.1E-01	0.85	9.1E-02	0.70	2.0E-01
0.92	3.0E-01	0.70	3.3E-03	0.83	2.7E-01
1.14	1.3E-01	1.01	8.9E-01	0.67	1.9E-02
0.84	8.4E-02	0.70	2.1E-03	0.89	2.2E-01
0.93	3.3E-01	0.79	7.9E-02	0.68	4.6E-02
1.09	2.2E-01	0.77	1.8E-02	0.57	4.9E-02
1.15	1.4E-01	1.02	8.2E-01	0.63	2.6E-03
1.00	9.6E-01	0.83	6.8E-02	0.71	3.4E-02
1.08	4.2E-01	0.84	1.1E-01	0.62	3.5E-02
0.90	2.1E-01	0.69	2.9E-02	0.93	4.5E-01
1.12	3.7E-02	1.05	4.6E-01	0.62	5.7E-02
1.30	5.5E-02	0.72	6.0E-02	0.47	1.6E-01
1.22	1.3E-01	1.09	2.1E-01	0.65	2.6E-02
1.10	9.8E-02	1.06	4.0E-01	0.61	9.0E-03
1.04	2.2E-01	0.89	1.3E-01	0.54	3.2E-05
1.11	3.3E-01	1.23	1.8E-01	0.56	6.4E-03
1.12	2.3E-01	1.16	1.9E-01	0.68	5.1E-02
1.07	4.3E-01	0.86	1.4E-01	0.56	4.6E-03
1.08	3.5E-01	1.18	2.6E-01	0.66	1.2E-02
1.00	9.7E-01	0.90	1.0E-02	0.69	8.8E-02
1.08	2.2E-01	1.11	2.4E-01	0.70	4.5E-02
1.08	2.9E-02	0.92	3.9E-01	0.71	9.5E-02
1.06	2.7E-01	0.83	1.3E-01	0.63	1.3E-01
1.11	3.0E-01	0.72	1.8E-02	0.69	1.2E-01
1.05	1.2E-01	0.82	8.7E-02	0.67	6.3E-02
1.17	1.0E-01	0.92	2.7E-01	0.65	3.9E-02

0.92	1.5E-01	0.69	4.8E-02	0.94	4.2E-02
1.14	1.5E-01	0.94	4.4E-03	0.54	1.2E-01
1.10	7.7E-02	1.47	5.1E-02	1.74	3.8E-01
0.98	4.6E-01	1.51	8.3E-02	1.99	1.1E-01
1.00	9.8E-01	1.48	2.4E-02	1.96	9.6E-02
1.05	7.1E-02	1.42	6.1E-02	1.61	1.4E-01
1.12	1.1E-02	1.44	9.7E-02	1.54	1.2E-01
1.00	9.4E-01	1.41	1.2E-01	2.15	1.7E-02
1.01	4.4E-01	1.41	2.1E-02	1.42	3.0E-01
1.02	4.1E-01	1.41	5.0E-02	1.62	1.1E-01
1.05	3.3E-01	1.50	6.1E-02	1.53	2.0E-01
1.03	6.4E-02	1.53	3.5E-02	1.70	9.4E-02
1.06	1.2E-01	1.44	3.9E-02	1.43	2.6E-01
1.01	6.9E-01	1.57	1.1E-01	2.03	7.7E-02
0.94	6.4E-02	1.43	1.4E-01	1.81	3.9E-02
0.97	1.2E-01	1.41	5.1E-02	1.62	1.3E-01
0.91	4.1E-01	1.51	3.4E-02	2.51	no replicates
1.07	7.2E-03	1.43	7.5E-02	1.51	3.5E-01
0.98	7.0E-01	1.43	4.9E-02	1.75	9.6E-02
0.97	3.3E-01	1.50	9.6E-02	1.79	4.5E-02
1.03	5.8E-01	1.42	7.2E-02	2.07	2.9E-01
0.99	9.5E-01	0.81	2.9E-02	0.56	7.5E-02
0.78	4.8E-02	0.67	1.4E-03	0.78	1.9E-01
1.02	6.8E-01	1.45	6.3E-02	1.59	1.3E-01
1.03	no replicates	1.95	5.8E-02	1.50	3.5E-01
0.80	8.0E-02	0.63	2.0E-01	0.81	1.2E-01
0.81	8.1E-02	0.46	7.5E-07	0.75	5.6E-02
1.08	4.0E-01	0.96	6.1E-01	0.63	1.1E-02
1.12	4.7E-01	1.00	1.0E+00	0.54	5.5E-03
1.13	8.3E-02	0.76	5.2E-02	0.67	2.2E-02
1.00	8.1E-01	0.86	5.7E-02	0.50	1.0E-01
1.03	9.4E-02	1.50	4.5E-02	1.66	2.1E-01
1.00	9.9E-01	1.47	4.9E-02	1.65	1.4E-01
1.00	9.0E-01	1.50	5.4E-02	1.57	2.1E-01
1.01	9.1E-01	1.40	3.8E-02	1.46	1.9E-01
0.89	3.3E-01	1.42	1.2E-01	1.73	6.5E-02
1.08	3.4E-01	1.15	7.3E-02	1.22	5.3E-01
1.04	1.1E-01	1.40	5.8E-02	1.56	9.8E-02
0.98	6.5E-01	1.62	1.5E-02	1.61	1.5E-01
1.05	2.9E-01	1.43	3.2E-02	1.66	9.3E-02
1.01	8.2E-01	1.42	6.8E-02	1.89	5.1E-02



**HepG2 BPDE**
**Time (h)**
**Concentration (uM)**

IMAGE Clone ID	Gene Symbol	Genbank	Description
110931	PCNA	BE896331	Proliferating cell nuclear antigen
205819	CPM	NM_001874	Carboxypeptidase M
753447	DDB2	BC050455	Damage-specific DNA binding protein 2, 48kDa
789182	PCNA	BE896331	Proliferating cell nuclear antigen
233273	STOM	NM_004099	Stomatin
297832			
214006			
140997	GDF15	BQ883534	Growth differentiation factor 15
204148	RPS6KA3	NM_004586	Ribosomal protein S6 kinase, 90kDa, polypeptide 3
250821			
41452	SAT	BF680536	Spermidine/spermine N1-acetyltransferase
376772	RPS27L	BC047648	Ribosomal protein S27-like
502333	NCOA3	NM_181659	Nuclear receptor coactivator 3
359835	SAT	BF680536	Spermidine/spermine N1-acetyltransferase
42800		AI912163	Transcribed locus
166273	CDKN1A	NM_078467	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)
297136			
310493	ACSL3	NM_004457	Acyl-CoA synthetase long-chain family member 3
42062	PTPRK	CR749277	Protein tyrosine phosphatase, receptor type, K
			Transcribed locus, weakly similar to NP_079012.2
884438	NFE2L2	AK128852	gasdermin domain containing 1 [Homo sapiens]
130057	STC2	AK027663	Stanniocalcin 2
244307	SERPINE1	BX649164	Serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
2353276	CCL20	BG534134	Chemokine (C-C motif) ligand 20
788239	TOB1	BC031406	Transducer of ERBB2, 1
760246	BLOC1S2	NM_001001342	Biogenesis of lysosome-related organelles complex-1, subunit 2
66516	TNFRSF10D	NM_003840	Tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
265459			
1473211	HIST1H2BN	CA310244	Histone 1, H2bn
27548	NUP153	NM_005124	Nucleoporin 153kDa
221846	CHES1	NM_005197	Checkpoint suppressor 1
129865	STK6	NM_198433	Serine/threonine kinase 6
767994	STRN3	NM_014574	Striatin, calmodulin binding protein 3
268891	HIST1H3D	BQ051491	Histone 1, H3d
			Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)
243603	MDM2	M92424	
214990	GSN	AK125819	Gelsolin (amyloidosis, Finnish type)
137535	TIF1	NM_015905	Transcriptional intermediary factor 1
241530	EPHA2	NM_004431	EphA2
1842170	HIST1H4B	BX102654	Histone 1, H4b
810131	KRT19	BG292068	Keratin 19
178792	SYNPO	AB028952	Synaptopodin
1731368	LAMB2	NM_002292	Laminin, beta 2 (laminin S)
823940	TOB1	BC031406	Transducer of ERBB2, 1
810724	IER3	BM994398	Immediate early response 3
200774	FAM46A	AF350451	Family with sequence similarity 46, member A
859359	TP53I3	NM_004881	Tumor protein p53 inducible protein 3
29022	RAI17	NM_020338	Retinoic acid induced 17
789091	HIST1H2AC	CR608156	Histone 1, H2ac
1524557	HIST1H3E	BG676315	Histone 1, H3e
29629	STRN3	NM_014574	Striatin, calmodulin binding protein 3

284520	NUP153	NM_005124	Nucleoporin 153kDa
814595	PRKCBP1	NM_183047	Protein kinase C binding protein 1
141232	FAD104	NM_022763	FAD104
73531	ISCU	AK057251	Iron-sulfur cluster assembly enzyme
66317	HIST1H1C	BQ940876	Histone 1, H1c
39285	GLUD1	NM_005271	Glutamate dehydrogenase 1
138936	STOM	NM_004099	Stomatin
563451	TLK1	BX538296	Tousled-like kinase 1
25698	FLJ20296	BC068517	Hypothetical protein FLJ20296
1673711	GOLGA1	U51587	Golgi autoantigen, golgin subfamily a, 1
413733	TIMP1	BM994443	Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
788185	TNFRSF10B	NM_003842	Tumor necrosis factor receptor superfamily, member 10b
278146	RBM11	BC030196	RNA binding motif protein 11
243488	K-ALPHA-1	AK094717	Tubulin, alpha, ubiquitous
590369	SERPINE1	BX649164	Serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
259649	IER3	BM994398	Immediate early response 3
884641	ARFRP1	AL833084	ADP-ribosylation factor related protein 1
146123	PTPRK	CR749277	Protein tyrosine phosphatase, receptor type, K
590759	SC4MOL	CR623543	Sterol-C4-methyl oxidase-like
41750	NFE2L2	AK128852	Transcribed locus, weakly similar to NP_079012.2 gasdermin domain containing 1 [Homo sapiens]
39233	SLC38A2	NM_018976	Solute carrier family 38, member 2
32510	BTG2	NM_006763	BTG family, member 2
381166	MYST4	AF217500	MYST histone acetyltransferase (monocytic leukemia) 4
855624	ALDH1A1	NM_000689	Aldehyde dehydrogenase 1 family, member A1
270665			
785605	LOC23117	XM_290670	KIAA0220-like protein
196992	AKR1C1	AK095239	Aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
814615	MTHFD2	BC015062	Methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
744047	PLK1	NM_005030	Polo-like kinase 1 (Drosophila)
842849	POLA2	NM_002689	Polymerase (DNA-directed), alpha (70kD)
229602	BRE	CR627176	Brain and reproductive organ-expressed (TNFRSF1A modulator)
120188	ROD1	CR749471	ROD1 regulator of differentiation 1 (S. pombe)
24667	C13ORF1	AF334405	Chromosome 13 open reading frame 1
51448	ATF3	AK123699	Activating transcription factor 3
795317	LOC201243	NM_175734	Hypothetical protein LOC201243
1926446	E2F6	NM_198258	E2F transcription factor 6
810124	PAFAH1B3	BM904583	Platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 29kDa
49600	GLS	CR749593	Glutaminase
898062	CDC20	BM914120	CDC20 cell division cycle 20 homolog (S. cerevisiae)
143171	MBNL1	NM_021038	Muscleblind-like (Drosophila)
129467	HIST1H2BJ	BF983642	Histone 1, H2bj
324356	NQO1	NM_000903	NAD(P)H dehydrogenase, quinone 1
31471	GPM6A	NM_201591	Glycoprotein M6A
753104			
53243	ASNS	NM_133436	Asparagine synthetase
279721	LRRC3B	BC067784	Leucine rich repeat containing 3B

2		6		24		2		6		24	
0.5		0.5		0.5		1		1		1	
Ratio	t-test P-value	Ratio	t-test P-value	Ratio	t-test P-value	Ratio	t-test P-value	Ratio	t-test P-value	Ratio	t-test P-value
1.20	4.33E-02	1.40	5.22E-02	1.31	3.78E-02	1.25	3.67E-02	1.37	5.20E-02	1.34	
1.28	2.58E-02	1.56	1.12E-02	1.33	4.95E-02	0.86	1.41E-02	1.95	7.28E-02	1.65	
1.21	7.30E-03	1.17	8.57E-03	1.35	2.00E-02	1.14	8.30E-03	1.42	2.26E-02	1.48	
1.29	2.20E-02	1.19	1.56E-02	1.31	3.04E-03	1.10	9.08E-02	1.43	1.48E-02	1.56	
1.07	9.74E-03	1.32	3.76E-02	1.28	9.11E-02	1.11	3.54E-02	1.64	9.69E-02	1.67	
1.31	4.25E-02	1.28	1.28E-02	1.20	1.23E-01	1.34	8.33E-03	1.59	2.08E-01	1.20	
0.69	2.47E-02	0.79	2.24E-01	1.07	6.86E-01	0.80	3.72E-02	0.64	5.23E-03	1.21	
1.47	7.16E-02	1.51	3.59E-02	1.41	7.69E-02	1.50	2.77E-02	2.05	5.46E-02	1.54	
0.79	2.46E-02	0.80	2.02E-02	0.83	4.23E-02	0.80	1.32E-02	0.67	6.57E-02	0.88	
0.85	3.09E-03	0.71	6.46E-03	1.03	5.95E-01	0.86	7.36E-02	0.77	3.04E-02	1.24	
1.10	2.32E-01	1.11	1.44E-01	1.16	3.60E-02	1.13	5.16E-02	1.60	5.85E-02	1.31	
1.11	1.25E-01	1.15	2.19E-01	1.26	2.72E-02	1.08	2.33E-02	1.13	1.12E-02	1.62	
0.71	5.10E-03	0.84	1.22E-02	0.89	3.03E-01	0.70	1.81E-02	0.84	1.13E-01	0.91	
1.14	2.01E-01	1.17	9.15E-03	1.13	2.89E-02	1.10	2.90E-01	1.45	5.73E-02	1.28	
1.15	1.32E-01	0.96	1.79E-02	1.10	8.26E-02	1.44	9.64E-05	0.92	1.22E-02	0.89	
1.94	2.90E-02	1.72	1.01E-01	1.78	1.06E-01	1.91	4.08E-02	2.49	1.18E-01	1.73	
0.87	1.75E-02	0.66	2.17E-03	0.91	2.38E-01	0.87	1.22E-02	0.77	9.39E-02	0.98	
0.85	7.96E-02	1.03	1.95E-01	0.81	9.33E-03	0.80	2.07E-02	1.01	8.77E-01	0.71	
0.82	1.72E-03	0.80	2.34E-02	0.88	5.46E-02	0.86	9.18E-02	0.67	4.85E-02	0.92	
0.93	4.14E-02	0.83	6.45E-02	0.90	1.23E-01	0.60	1.96E-03	0.88	1.15E-01	0.85	
1.20	9.95E-02	0.92	2.33E-02	1.05	4.56E-01	1.49	6.95E-03	0.93	8.84E-02	0.86	
0.98	6.69E-01	1.18	1.87E-02	1.01	6.54E-01	1.05	1.58E-01	1.48	5.95E-02	1.27	
1.10	1.13E-02	1.40	3.90E-02	1.01	8.53E-01	0.91	2.66E-01	1.58	6.18E-03	0.89	
1.45	2.47E-02	1.24	1.52E-02	1.17	3.07E-01	1.87	9.21E-04	1.67	1.43E-01	1.00	
1.23	2.49E-02	1.31	4.50E-02	1.15	8.74E-02	1.22	2.45E-02	1.65	1.58E-01	1.31	
1.13	9.88E-02	1.16	4.24E-02	1.05	4.25E-03	1.12	1.71E-02	1.50	1.83E-01	1.04	
0.99	1.19E-01	1.07	3.02E-01	1.18	1.55E-01	0.84	5.24E-03	1.17	4.45E-02	1.60	
0.69	3.91E-02	0.79	2.49E-01	1.06	7.43E-01	0.76	2.23E-02	0.69	7.37E-04	1.19	
0.80	1.50E-04	0.95	2.66E-01	0.89	2.27E-01	0.62	1.17E-03	1.05	4.72E-01	0.90	
0.70	2.16E-03	0.83	3.73E-02	0.88	1.80E-01	0.71	3.39E-03	0.77	8.51E-02	0.98	
0.73	5.10E-02	0.68	6.23E-03	0.98	9.13E-01	0.61	1.28E-03	0.76	3.31E-02	1.00	
0.71	1.35E-02	0.96	5.94E-02	0.85	1.70E-01	0.64	3.01E-03	1.09	2.28E-02	1.08	
0.69	6.13E-02	0.82	3.56E-01	1.03	8.77E-01	0.78	2.40E-02	0.67	2.86E-03	1.11	
1.29	5.82E-02	1.10	4.82E-01	1.13	1.51E-01	0.99	7.01E-01	1.66	1.03E-01	1.38	
0.99	6.65E-01	1.10	5.34E-02	1.17	2.27E-01	1.11	1.25E-01	1.11	5.35E-02	1.40	
0.63	1.59E-03	1.00	9.92E-01	0.80	3.45E-01	0.59	1.37E-03	0.90	3.43E-01	1.03	
1.08	1.79E-01	1.24	3.29E-02	1.14	5.42E-02	1.03	1.48E-01	1.46	4.65E-02	1.17	
0.76	2.06E-02	0.83	3.18E-01	1.03	8.30E-01	0.82	5.34E-02	0.70	7.22E-04	1.18	
1.02	5.61E-01	0.88	4.55E-02	1.16	3.88E-02	1.08	2.24E-01	0.96	2.94E-01	1.44	
0.97	4.50E-03	1.42	3.33E-01	0.98	1.26E-01	1.12	4.26E-01	1.14	4.48E-02	1.05	
1.10	1.18E-01	1.19	1.87E-02	1.18	5.64E-02	1.14	1.58E-01	1.28	1.19E-01	1.48	
1.32	1.30E-02	1.03	5.55E-01	1.16	3.66E-01	1.60	3.10E-02	1.59	1.44E-01	1.04	
1.04	5.08E-01	1.20	1.71E-02	1.31	7.24E-02	1.09	3.70E-01	1.51	1.46E-01	1.25	
1.16	4.88E-01	1.17	1.13E-01	1.06	1.19E-01	1.19	3.62E-02	1.41	1.95E-01	1.08	
1.12	2.77E-02	1.11	1.15E-02	1.04	2.72E-01	1.00	9.92E-01	1.56	4.01E-01	1.24	
0.69	1.40E-02	0.91	2.58E-01	0.85	2.75E-01	0.71	5.19E-03	0.76	1.24E-01	0.91	
0.71	5.52E-02	0.71	1.08E-01	1.07	7.21E-01	0.71	1.59E-02	0.68	7.56E-03	1.27	
0.71	8.55E-02	0.82	3.78E-01	0.94	6.61E-01	0.81	8.61E-02	0.70	1.38E-03	1.16	
0.71	2.06E-03	1.10	2.61E-01	0.86	1.68E-01	0.75	1.91E-02	1.09	1.25E-01	0.98	

0.81	1.77E-02	1.01	7.29E-01	0.86	1.36E-01	0.67	7.66E-03	1.03	2.53E-01	0.93
0.76	5.29E-03	0.95	4.13E-01	0.93	5.03E-01	0.62	4.61E-03	0.91	1.49E-01	1.02
0.64	1.55E-02	1.03	5.17E-01	0.84	3.76E-01	0.66	9.87E-03	0.84	1.88E-01	0.95
1.16	9.95E-02	1.11	2.84E-02	1.10	2.84E-01	1.14	9.82E-02	1.45	1.46E-01	1.17
0.65	6.70E-02	0.69	1.69E-01	0.92	6.29E-01	0.64	2.19E-02	0.66	5.81E-03	1.16
0.97	7.15E-01	0.82	1.58E-01	0.80	1.01E-01	0.94	2.52E-01	0.84	2.28E-02	0.69
1.06	1.97E-02	1.12	1.57E-01	1.14	1.13E-01	0.99	8.27E-01	1.42	6.82E-02	1.35
0.78	8.54E-03	0.92	6.17E-02	0.88	8.08E-02	0.69	1.18E-02	0.86	1.65E-01	0.93
1.08	1.20E-01	1.20	5.37E-02	1.14	4.01E-02	1.34	6.78E-02	1.41	1.52E-01	1.15
0.91	6.37E-01	1.47	4.91E-01	1.01	7.21E-01	1.06	5.85E-01	1.22	1.92E-01	1.23
1.07	2.43E-01	0.99	4.00E-01	1.19	3.64E-02	1.03	1.03E-01	1.09	5.30E-01	1.48
1.00	8.55E-01	1.06	3.32E-01	0.99	8.34E-01	1.00	9.40E-01	1.45	4.46E-02	0.96
0.94	1.24E-02	1.19	4.42E-01	0.97	3.52E-01	1.48	4.83E-01	0.90	2.15E-01	1.11
1.04	5.11E-01	1.01	8.27E-01	1.28	1.85E-01	1.07	4.85E-01	0.91	1.09E-01	1.40
0.93	1.87E-01	1.26	7.74E-02	1.03	5.08E-01	1.19	9.52E-02	1.48	1.68E-01	1.33
1.11	5.61E-02	1.39	1.01E-01	1.34	1.56E-01	1.10	2.81E-01	1.40	6.90E-02	1.37
1.09	6.82E-01	1.21	4.25E-01	1.17	2.70E-01	1.47	1.95E-02	1.03	6.78E-01	1.10
0.84	3.62E-02	0.79	9.78E-02	0.89	8.05E-02	0.86	1.68E-01	0.71	1.21E-01	0.96
0.94	1.02E-01	0.71	1.48E-01	0.91	5.92E-02	0.86	1.53E-02	0.93	1.43E-01	0.89
0.96	2.60E-01	0.98	4.02E-01	0.93	1.01E-01	0.69	1.15E-02	0.88	1.69E-01	0.93
0.88	8.12E-02	1.13	1.04E-01	1.00	9.71E-01	0.68	6.92E-03	1.08	4.39E-01	0.98
1.49	3.76E-02	1.33	9.64E-02	1.80	no replicates	1.54	8.47E-02	2.12	3.00E-01	1.41
0.79	4.39E-02	0.87	7.72E-03	0.90	1.10E-01	0.71	no replicates	0.93	9.30E-02	0.94
1.01	5.56E-01	0.90	1.05E-01	0.84	1.47E-01	0.95	1.57E-01	0.89	8.73E-02	0.69
0.78	8.78E-04	1.07	2.08E-01	0.90	1.39E-01	0.70	4.10E-02	0.99	8.79E-01	1.05
0.83	6.22E-02	1.08	1.82E-01	0.93	1.81E-01	0.70	7.53E-03	1.11	7.36E-02	1.11
1.03	4.74E-01	1.01	8.82E-01	0.86	3.08E-01	1.02	8.11E-01	1.03	1.28E-01	0.66
1.03	5.42E-01	0.85	1.55E-01	0.91	4.30E-01	0.98	7.50E-01	0.91	3.01E-01	0.69
0.73	3.90E-02	0.71	1.92E-02	1.01	9.39E-01	0.89	1.07E-01	0.73	2.28E-01	0.95
0.96	5.13E-01	1.40	5.18E-01	0.85	9.68E-02	0.87	1.35E-01	0.80	7.99E-02	0.69
0.90	1.57E-01	0.79	1.74E-02	1.02	8.27E-01	1.00	9.67E-01	0.71	1.01E-01	1.01
0.94	3.24E-02	1.20	5.16E-01	1.02	7.88E-01	1.38	1.24E-01	1.24	2.03E-01	1.46
1.40	no replicates	0.99	9.15E-01			1.25	no replicates	0.93	2.35E-02	0.98
1.29	6.11E-03	0.97	5.83E-01	1.08	4.28E-01	1.47	3.13E-01	1.33	2.29E-01	0.99
1.03	9.02E-01	1.07	6.86E-01	1.04	8.77E-02	1.44	2.19E-02	1.03	6.45E-01	1.18
1.40	no replicates	1.31	1.20E-01	1.36	3.09E-02	1.12	no replicates	1.46	2.07E-01	1.26
1.18	1.59E-01	1.10	4.58E-02	1.09	4.04E-01	1.59	3.23E-01	1.01	7.78E-01	0.96
1.03	4.62E-01	1.16	7.55E-03	1.00	9.41E-01	1.14	no replicates	1.41	2.85E-01	1.04
0.90	1.18E-01	0.71	3.16E-02	0.94	1.89E-01	0.97	5.24E-01	0.85	7.55E-02	0.91
0.88	1.33E-02	1.04	3.61E-01	0.93	3.38E-01	0.70	no replicates	0.97	3.44E-01	1.02
0.72	5.50E-02	0.78	2.19E-01	1.01	9.57E-01	0.82	6.45E-02	0.68	9.76E-03	1.13
1.03	4.58E-01	0.91	1.14E-01	0.87	1.48E-01	0.96	4.67E-01	0.89	1.68E-01	0.66
0.96	1.93E-02	0.97	no replicates	0.93	1.05E-01			1.42	4.86E-01	0.91
0.98	6.77E-01	1.45	3.43E-01	1.06	1.92E-02	1.25	no replicates	1.07	no replicates	1.45
1.02	4.58E-01	0.95	7.21E-02	0.90	4.14E-01	1.17	1.00E-01	1.00	9.83E-01	0.70
1.41	2.07E-01	1.54	2.66E-02	1.01	8.30E-01	0.99	7.58E-01	0.96	2.13E-01	1.01

t-test P-value
2.26E-02
3.02E-02
2.59E-02
1.42E-04
2.88E-02
4.44E-02
3.35E-02
3.98E-02
5.21E-02
2.90E-02
1.47E-02
9.64E-03
3.00E-02
1.10E-02
1.81E-01
4.03E-02
3.69E-01
1.28E-03
1.50E-02
3.24E-02
2.16E-02
7.95E-03
1.76E-01
9.74E-01
6.31E-02
2.74E-01
5.45E-02
5.87E-02
1.48E-02
1.19E-01
4.88E-01
5.54E-02
1.67E-02
1.54E-02
1.27E-01
6.08E-01
5.89E-02
1.26E-01
1.62E-02
2.73E-01
2.25E-02
1.92E-01
1.29E-03
3.12E-02
9.06E-02
1.05E-01
9.57E-02
3.60E-02
2.75E-01

6.40E-02  
4.41E-01  
6.49E-02  
5.30E-02  
1.91E-01  
2.46E-03  
2.76E-02  
8.50E-02  
7.26E-02  
2.77E-02

1.31E-01  
2.53E-01  
4.92E-01  
3.67E-02

6.01E-03  
2.98E-02  
1.95E-01  
5.32E-01  
2.21E-01  
7.33E-02  
7.40E-01  
no replicates  
5.57E-01  
4.18E-03  
3.14E-01  
8.76E-02

4.20E-03  
3.52E-03  
5.27E-01  
6.46E-03

7.94E-01  
1.77E-01  
7.39E-01  
7.70E-01  
2.75E-01  
no replicates

5.99E-01  
4.85E-01

5.33E-01  
2.78E-01  
8.31E-02  
8.27E-03  
7.75E-02  
no replicates  
2.02E-03  
7.70E-01