MacQuarrie Supplemental Material List

Supplemental Figures

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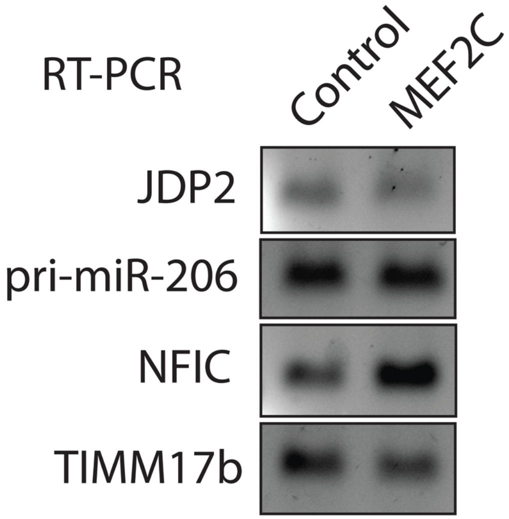

Figure S1. MEF2C expression does not increase the microRNA miR-206 or the transcription factor JDP2. RT-PCR for transcripts as indicated from RD cells either infected with an empty retrovirus (control) or one expressing MEF2C and placed in differentiation media for 36 h. TIMM17b serves as the internal control.

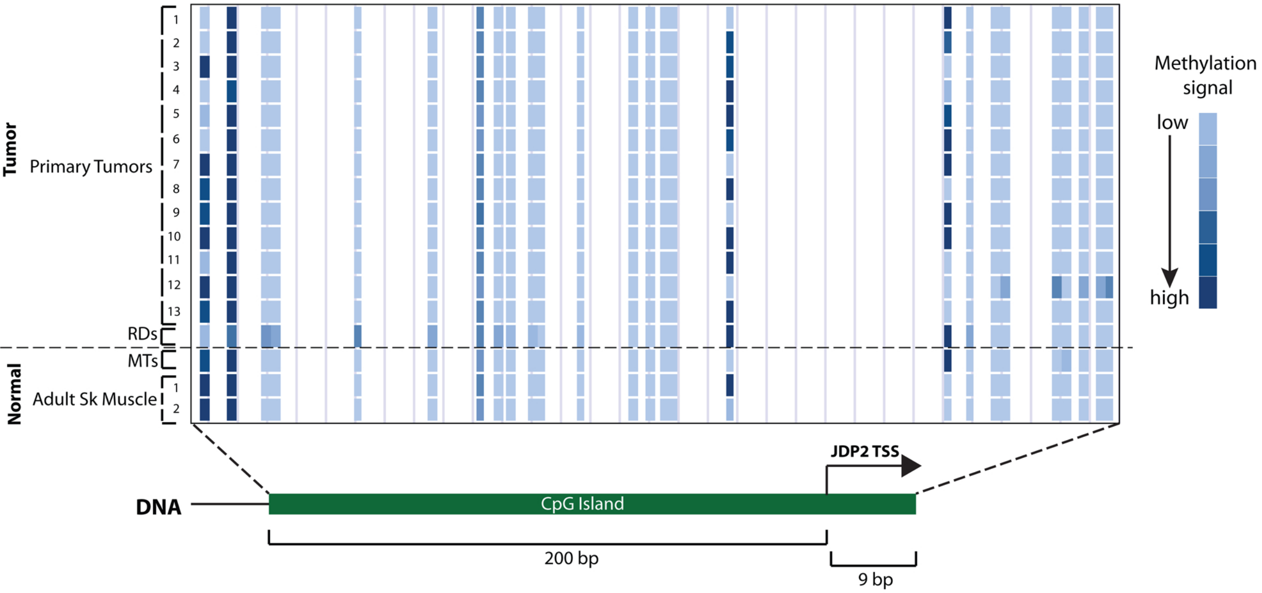

Figure S2. The CpG island located at the transcription start site of *JDP2* is not differentially methylated between rhabdomyosarcoma cells and normal muscle cells. RRBS data as in Figure 6 from the 5' portion of the CpG island located at the *JDP2* transcription start site. As in Figure 6, a darker shade of blue coloration indicates a higher level of methylation. Genomic distances are indicated at the bottom of the figure.

Supplemental Table S1. Genes regulated during myogenesis.

Entrez ID	Symbol	Gene Name	Myoblast value[a]	Myotube value[b]	Fold change[c]	p-value	FDR
29895	MYLPF	myosin light chain, phosphorylatable, fast skeletal muscle	6.26	14.56	7.57	9.95 E-32	2.15 E-27
4621	MYH3	myosin, heavy chain 3, skeletal muscle, embryonic	6.49	14.54	7.40	1.04 E-29	8.54 E-26
845	CASQ2	calsequestrin 2 (cardiac muscle)	6.49	13.80	6.61	1.19 E-29	8.54 E-26
4635	MYL4	myosin, light chain 4, alkali; atrial, embryonic	7.09	13.99	6.48	3.38 E-29	1.46 E-25
4632	MYL1	myosin, light chain 1, alkali; skeletal, fast	6.43	13.60	6.46	3.08 E-29	1.46 E-25
7134	TNNC1	troponin C type 1 (slow)	7.93	14.56	6.41	1.50 E-27	4.64 E-24
58	ACTA1	actin, alpha 1, skeletal muscle	6.44	12.88	5.83	2.96 E-27	6.40 E-24
4626	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	6.30	12.73	5.78	7.63 E-27	1.27 E-23
7125	TNNC2	troponin C type 2 (fast)	6.27	12.43	5.49	4.31 E-26	4.91 E-23
7139	TNNT2	troponin T type 2 (cardiac)	8.59	14.24	5.49	2.19 E-25	1.75 E-22
4608	MYBPH	myosin binding protein H	7.98	13.67	5.44	1.11 E-24	6.49 E-22
7140	TNNT3	troponin T type 3 (skeletal, fast)	6.44	12.26	5.21	9.54 E-26	9.82 E-23
348	APOE	apolipoprotein E	6.30	12.09	5.14	2.17 E-25	1.75 E-22
7169	TPM2	tropomyosin 2 (beta)	8.28	13.52	5.06	4.14 E-27	8.13 E-24
3270	HRC	histidine rich calcium binding protein	6.55	12.10	4.99	4.95 E-27	8.91 E-24
8988	HSPB3	heat shock 27kDa protein 3	8.40	13.58	4.99	4.27 E-26	4.91 E-23
4656	MYOG	myogenin (myogenic factor 4)	6.73	12.06	4.86	1.48 E-24	8.00 E-22
55502	HES6	hairy and enhancer of split 6 (Drosophila)	8.59	13.32	4.60	2.30 E-25	1.77 E-22
6588	SLN	sarcolipin	6.56	11.65	4.55	1.36 E-24	7.53 E-22
6345	SRL	sarcalumenin	6.51	11.61	4.55	2.01 E-26	2.90 E-23
58494	JAM2	junctional adhesion molecule 2	7.58	12.27	4.49	8.85 E-25	5.62 E-22

786	CACNG1	calcium channel, voltage-dependent, gamma subunit 1	6.56	11.56	4.47	7.56 E-24	2.94 E-21
347273	MURC	muscle-related coiled-coil protein	6.91	11.73	4.45	1.01 E-25	9.88 E-23
389827	TMEM8C	transmembrane protein 8C	6.70	11.60	4.43	3.73 E-24	1.61 E-21
1158	CKM	creatine kinase, muscle	7.13	11.83	4.40	1.06 E-25	9.95 E-23
4320	MMP11	matrix metallopeptidase 11 (stromelysin 3)	7.41	11.90	4.26	4.04 E-25	2.81 E-22
80303	EFHD1	EF-hand domain family, member D1	7.82	12.21	4.22	1.15 E-21	1.90 E-19
2027	ENO3	enolase 3 (beta, muscle)	8.15	12.45	4.18	5.76 E-25	3.89 E-22
64397	ZFP106	zinc finger protein 106 homolog (mouse)	8.85	13.04	4.10	2.43 E-19	2.04 E-17
4208	MEF2C	myocyte enhancer factor 2C	7.56	11.80	4.06	9.42 E-25	5.82 E-22
5919	RARRES 2	retinoic acid receptor responder (tazarotene induced) 2	7.92	12.12	4.05	1.25 E-21	2.07 E-19
4625	MYH7	myosin, heavy chain 7, cardiac muscle, beta	6.40	11.01	4.04	5.02 E-23	1.49 E-20
10777	ARPP21	cAMP-regulated phosphoprotein, 21kDa	6.50	11.01	3.98	7.90 E-25	5.18 E-22
2162	F13A1	coagulation factor XIII, A1 polypeptide	6.56	11.02	3.95	9.31 E-22	1.65 E-19
56961	SHD	Src homology 2 domain containing transforming protein D	7.14	11.32	3.92	3.93 E-25	2.81 E-22
8470	SORBS2	sorbin and SH3 domain containing 2	7.36	11.49	3.91	8.19 E-24	3.01 E-21
65055	REEP1	receptor accessory protein 1	6.47	10.89	3.87	6.24 E-24	2.59 E-21
10930	APOBEC 2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	6.32	10.80	3.86	2.14 E-22	4.53 E-20
3488	IGFBP5	insulin-like growth factor binding protein 5	6.88	11.05	3.81	1.30 E-20	1.59 E-18
252995	FNDC5	fibronectin type III domain containing 5	8.06	11.99	3.81	3.41 E-20	3.78 E-18
114907	FBXO32	F-box protein 32	7.27	11.24	3.76	9.18 E-21	1.20 E-18
5239	PGM5	phosphoglucomutase 5	6.53	10.83	3.75	3.04 E-24	1.43 E-21
222166	C7orf41	chromosome 7 open reading frame 41	8.76	12.52	3.71	1.86 E-22	4.10 E-20

6319	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	9.68	13.43	3.66	1.56 E-23	5.11 E-21
10324	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	8.50	12.22	3.65	2.44 E-24	1.20 E-21
8537	BCAS1	breast carcinoma amplified sequence 1	6.38	10.59	3.62	6.41 E-24	2.59 E-21
8736	MYOM1	myomesin 1, 185kDa	6.62	10.71	3.60	1.29 E-23	4.50 E-21
7138	TNNT1	troponin T type 1 (skeletal, slow)	6.60	10.69	3.57	1.53 E-21	2.44 E-19
150572	SMYD1	SET and MYND domain containing 1	6.48	10.60	3.57	1.50 E-20	1.82 E-18
23676	SMPX	small muscle protein, X-linked	6.28	10.47	3.57	2.63 E-23	8.37 E-21
55615	PRR5	proline rich 5 (renal)	7.19	10.99	3.55	1.21 E-23	4.28 E-21
1396	CRIP1	cysteine-rich protein 1 (intestinal)	7.13	10.95	3.55	1.33 E-20	1.63 E-18
3316	HSPB2	heat shock 27kDa protein 2	8.53	12.13	3.53	2.97 E-22	6.00 E-20
23294	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	7.82	11.47	3.52	1.29 E-22	2.91 E-20
1339	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	6.48	10.56	3.52	4.59 E-21	6.48 E-19
6711	SPTBN1	spectrin, beta, non-erythrocytic 1	6.44	10.53	3.51	1.13 E-21	1.89 E-19
169611	OLFML2A	olfactomedin-like 2A	7.62	11.27	3.50	5.94 E-21	8.18 E-19
207107	SFTA1P	surfactant associated 1 (pseudogene)	8.14	11.72	3.49	1.99 E-22	4.30 E-20
274	BIN1	bridging integrator 1	9.87	13.35	3.40	3.46 E-22	6.86 E-20
10457	GPNMB	glycoprotein (transmembrane) nmb	7.77	11.27	3.38	2.04 E-19	1.78 E-17
6261	RYR1	ryanodine receptor 1 (skeletal)	6.49	10.42	3.38	2.62 E-22	5.39 E-20
83937	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	6.69	10.50	3.35	6.16 E-23	1.67 E-20
4619	MYH1	myosin, heavy chain 1, skeletal muscle, adult	6.30	10.26	3.34	9.58 E-23	2.38 E-20
1837	DTNA	dystrobrevin, alpha	6.72	10.49	3.33	1.44 E-21	2.34 E-19
4633	MYL2	myosin, light chain 2, regulatory, cardiac, slow	7.04	10.66	3.31	1.09 E-21	1.84 E-19
7111	TMOD1	tropomodulin 1	6.45	10.32	3.29	1.49	5.04

						E-23	E-21
79805	VASH2	vasohibin 2	7.32	10.85	3.29	2.42 E-20	2.79 E-18
64084	CLSTN2	calsyntenin 2	6.40	10.26	3.26	1.25 E-22	2.91 E-20
2034	EPAS1	endothelial PAS domain protein 1	8.02	11.36	3.26	1.35 E-18	8.96 E-17
79933	SYNPO2L	synaptopodin 2-like	7.01	10.59	3.26	3.11 E-20	3.47 E-18
83543	AIF1L	allograft inflammatory factor 1-like	6.85	10.49	3.25	1.29 E-22	2.91 E-20
633	BGN	biglycan	7.09	10.63	3.25	1.08 E-19	1.01 E-17
2348	FOLR1	folate receptor 1 (adult)	6.48	10.29	3.25	5.19 E-23	1.51 E-20
84466	MEGF10	multiple EGF-like-domains 10	7.00	10.57	3.24	4.49 E-20	4.83 E-18
2889	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	9.11	12.38	3.22	6.23 E-21	8.41 E-19
4130	MAP1A	microtubule-associated protein 1A	7.72	11.07	3.21	4.79 E-21	6.72 E-19
9518	GDF15	growth differentiation factor 15	7.36	10.78	3.20	1.54 E-18	1.00 E-16
1917	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	6.55	10.27	3.18	1.13 E-19	1.05 E-17
8912	CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	6.31	10.11	3.17	3.45 E-21	4.94 E-19
9235	IL32	interleukin 32	9.16	12.35	3.17	5.36 E-21	7.48 E-19
4703	NEB	nebulin	6.42	10.17	3.16	1.73 E-20	2.05 E-18
6664	SOX11	SRY (sex determining region Y)-box 11	8.93	12.14	3.15	6.58 E-21	8.78 E-19
1400	CRMP1	collapsin response mediator protein 1	7.85	11.11	3.14	1.97 E-20	2.31 E-18
4620	MYH2	myosin, heavy chain 2, skeletal muscle, adult	6.73	10.30	3.11	6.63 E-21	8.80 E-19
148738	HFE2	hemochromatosis type 2 (juvenile)	6.27	10.01	3.11	1.89 E-22	4.12 E-20
30812	SOX8	SRY (sex determining region Y)-box 8	7.03	10.45	3.11	9.71 E-23	2.39 E-20
440	ASNS	asparagine synthetase (glutamine-hydrolyzing)	10.01	13.17	3.09	4.26 E-18	2.46 E-16
134	ADORA1	adenosine A1 receptor	7.71	10.94	3.08	5.89 E-23	1.65 E-20
88	ACTN2	actinin, alpha 2	6.65	10.18	3.04	2.20	1.88

						E-19	E-17
114299	PALM2	paralemmin 2	6.85	10.27	3.03	8.41 E-22	1.53 E-19
134265	AFAP1L1	actin filament associated protein 1-like 1	7.52	10.72	3.02	6.24 E-19	4.59 E-17
3911	LAMA5	laminin, alpha 5	8.13	11.19	3.00	4.61 E-19	3.51 E-17
5730	PTGDS	prostaglandin D2 synthase 21kDa (brain)	7.42	10.61	2.99	2.17 E-21	3.28 E-19
29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	6.59	10.09	2.98	6.23 E-23	1.67 E-20
245806	VGLL2	vestigial like 2 (Drosophila)	6.82	10.20	2.97	3.49 E-19	2.81 E-17
5129	CDK18	cyclin-dependent kinase 18	6.46	10.00	2.97	7.76 E-20	7.66 E-18
80206	FHOD3	formin homology 2 domain containing 3	7.82	10.90	2.96	2.67 E-20	3.04 E-18
116496	FAM129 A	family with sequence similarity 129, member A	7.13	10.35	2.94	1.53 E-13	3.04 E-12
113451	ADC	arginine decarboxylase	6.88	10.18	2.91	1.04 E-21	1.80 E-19
859	CAV3	caveolin 3	7.92	10.93	2.91	2.98 E-19	2.46 E-17
140465	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle	11.33	14.38	2.90	2.90 E-22	5.91 E-20
84886	C1orf198	chromosome 1 open reading frame 198	8.50	11.42	2.88	3.83 E-20	4.18 E-18
22924	MAPRE3	microtubule-associated protein, RP/EB family, member 3	6.94	10.18	2.88	3.76 E-18	2.22 E-16
57761	TRIB3	tribbles homolog 3 (Drosophila)	7.82	10.79	2.84	1.45 E-10	1.50 E-09
7130	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	7.41	10.43	2.81	2.47 E-17	1.18 E-15
58528	RRAGD	Ras-related GTP binding D	6.39	9.78	2.80	2.38 E-19	2.01 E-17
30061	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	6.87	10.03	2.77	1.44 E-21	2.34 E-19
256691	MAMDC 2	MAM domain containing 2	9.67	12.46	2.76	1.52 E-17	7.73 E-16
1028	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	6.53	9.82	2.75	2.39 E-18	1.47 E-16
5947	RBP1	retinol binding protein 1, cellular	7.03	10.10	2.75	3.03 E-20	3.40 E-18
127294	MYOM3	myomesin family, member 3	6.45	9.76	2.74	2.67	3.04

						E-20	E-18
11145	PLA2G16	phospholipase A2, group XVI	8.23	11.01	2.72	9.43 E-21	1.21 E-18
158471	PRUNE2	prune homolog 2 (Drosophila)	8.63	11.37	2.72	6.45 E-16	2.23 E-14
23439	ATP1B4	ATPase, Na+/K+ transporting, beta 4 polypeptide	6.42	9.72	2.72	9.46 E-20	9.21 E-18
221914	GPC2	glypican 2	7.91	10.72	2.70	3.27 E-21	4.71 E-19
7102	TSPAN7	tetraspanin 7	6.66	9.84	2.69	1.26 E-20	1.55 E-18
131377	KBTBD5	kelch repeat and BTB (POZ) domain containing 5	6.61	9.80	2.68	1.59 E-18	1.03 E-16
9260	PDLIM7	PDZ and LIM domain 7 (enigma)	10.25	12.96	2.66	6.34 E-22	1.20 E-19
9459	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	9.09	11.78	2.66	1.16 E-20	1.45 E-18
26471	NUPR1	nuclear protein, transcriptional regulator, 1	8.45	11.15	2.66	1.76 E-18	1.12 E-16
488	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	9.11	11.77	2.65	1.46 E-17	7.48 E-16
477	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	6.29	9.53	2.62	1.60 E-21	2.48 E-19
25890	ABI3BP	ABI family, member 3 (NESH) binding protein	8.78	11.41	2.62	1.21 E-18	8.18 E-17
83729	INHBE	inhibin, beta E	6.50	9.66	2.61	1.01 E-10	1.09 E-09
1346	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	9.85	12.46	2.59	2.70 E-20	3.05 E-18
9891	NUAK1	NUAK family, SNF1-like kinase, 1	10.16	12.77	2.57	3.61 E-19	2.88 E-17
80144	FRAS1	Fraser syndrome 1	6.72	9.75	2.57	3.69 E-17	1.63 E-15
6641	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	8.08	10.74	2.56	1.06 E-20	1.34 E-18
254102	EHBP1L1	EH domain binding protein 1-like 1	8.62	11.19	2.56	1.32 E-18	8.84 E-17
7857	SCG2	secretogranin II	7.07	9.92	2.54	1.52 E-19	1.38 E-17
10912	GADD45G	growth arrest and DNA-damage-inducible, gamma	6.47	9.56	2.53	2.13 E-19	1.83 E-17
10611	PDLIM5	PDZ and LIM domain 5	7.48	10.21	2.52	1.39	1.27

						E-19	E-17
3983	ABLIM1	actin binding LIM protein 1	7.01	9.85	2.51	2.96E-19	2.45E-17
55608	ANKRD10	ankyrin repeat domain 10	7.53	10.23	2.50	4.81E-18	2.71E-16
9289	GPR56	G protein-coupled receptor 56	7.32	10.07	2.50	1.15E-18	7.88E-17
3482	IGF2R	insulin-like growth factor 2 receptor	9.34	11.85	2.49	1.09E-15	3.57E-14
54510	PCDH18	protocadherin 18	7.43	10.13	2.49	9.92E-18	5.30E-16
7412	VCAM1	vascular cell adhesion molecule 1	6.66	9.60	2.46	2.02E-13	3.90E-12
782	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	6.37	9.42	2.46	2.07E-19	1.79E-17
56997	ADCK3	aarF domain containing kinase 3	7.31	10.00	2.45	1.16E-18	7.88E-17
59285	CACNG6	calcium channel, voltage-dependent, gamma subunit 6	6.78	9.64	2.44	8.53E-19	6.06E-17
8082	SSPN	sarcospan (Kras oncogene-associated gene)	7.10	9.83	2.43	2.47E-16	9.20E-15
1152	CKB	creatine kinase, brain	7.99	10.54	2.43	6.98E-18	3.85E-16
5106	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	8.10	10.62	2.43	2.88E-13	5.33E-12
64115	C10orf54	chromosome 10 open reading frame 54	6.71	9.60	2.43	8.26E-16	2.78E-14
2065	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	6.59	9.52	2.43	2.17E-18	1.36E-16
10966	RAB40B	RAB40B, member RAS oncogene family	8.54	10.99	2.42	4.79E-20	5.13E-18
6840	SVIL	supervillin	7.73	10.30	2.41	1.75E-19	1.56E-17
5413	5-Sep	septin 5	8.98	11.39	2.40	3.15E-17	1.44E-15
90441	ZNF622	zinc finger protein 622	9.97	12.38	2.39	6.13E-19	4.52E-17
28514	DLL1	delta-like 1 (Drosophila)	6.74	9.56	2.38	1.52E-18	9.98E-17
54937	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	6.83	9.61	2.38	1.84E-16	7.06E-15
64207	IRF2BPL	interferon regulatory factor 2 binding protein-like	9.26	11.65	2.38	6.74E-20	6.87E-18
160622	GRASP	GRP1 (general receptor for phosphoinositides 1)-	6.72	9.55	2.38	7.51	4.11

		associated scaffold protein				E-18	E-16
22808	MRAS	muscle RAS oncogene homolog	7.65	10.19	2.37	1.61E-16	6.24E-15
9024	BRSK2	BR serine/threonine kinase 2	6.85	9.61	2.37	3.77E-19	2.97E-17
768211	RELL1	RELT-like 1	7.95	10.42	2.36	1.12E-19	1.05E-17
10486	CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	10.34	12.75	2.36	2.23E-19	1.89E-17
8326	FZD9	frizzled homolog 9 (Drosophila)	6.73	9.53	2.35	1.99E-19	1.75E-17
1306	COL15A1	collagen, type XV, alpha 1	6.38	9.32	2.35	1.63E-14	4.09E-13
4684	NCAM1	neural cell adhesion molecule 1	8.10	10.54	2.35	3.85E-19	3.01E-17
27242	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	7.84	10.30	2.33	8.30E-19	5.92E-17
7004	TEAD4	TEA domain family member 4	9.05	11.38	2.33	5.35E-20	5.64E-18
1410	CRYAB	crystallin, alpha B	10.91	13.32	2.32	9.50E-19	6.61E-17
26353	HSPB8	heat shock 22kDa protein 8	7.66	10.14	2.31	1.16E-19	1.07E-17
377007	KLHL30	kelch-like 30 (Drosophila)	7.47	9.97	2.30	2.21E-18	1.38E-16
79007	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	7.95	10.36	2.30	9.86E-20	9.47E-18
8497	PPFIA4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	7.31	9.84	2.29	9.86E-18	5.28E-16
4088	SMAD3	SMAD family member 3	8.61	10.92	2.28	3.16E-17	1.44E-15
9201	DCLK1	doublecortin-like kinase 1	6.84	9.51	2.28	3.18E-19	2.61E-17
347733	TUBB2B	tubulin, beta 2B	7.00	9.59	2.27	2.12E-19	1.83E-17
8553	BHLHE40	basic helix-loop-helix family, member e40	9.60	11.88	2.27	2.12E-16	8.12E-15
26576	SRPK3	SRSF protein kinase 3	7.21	9.73	2.26	1.66E-19	1.49E-17
5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	8.06	10.42	2.26	3.94E-15	1.12E-13
23095	KIF1B	kinesin family member 1B	8.42	10.71	2.24	2.82	8.29

						E-15	E-14
3157	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	9.24	11.47	2.23	8.57 E-11	9.35 E-10
8821	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	8.45	10.72	2.22	3.47 E-18	2.08 E-16
8365	HIST1H4H	histone cluster 1, H4h	6.69	9.38	2.22	1.25 E-17	6.56 E-16
28227	PPP2R3B	protein phosphatase 2, regulatory subunit B", beta	7.63	10.01	2.22	1.55 E-19	1.40 E-17
1674	DES	desmin	9.89	12.12	2.21	9.71 E-20	9.37 E-18
57159	TRIM54	tripartite motif containing 54	6.36	9.15	2.20	4.19 E-19	3.23 E-17
8028	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	6.65	9.34	2.20	1.62 E-18	1.05 E-16
19	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	6.48	9.22	2.20	1.94 E-14	4.75 E-13
8908	GYG2	glycogenin 2	7.51	9.90	2.19	4.52 E-19	3.46 E-17
221662	RBM24	RNA binding motif protein 24	8.14	10.42	2.19	5.07 E-16	1.79 E-14
23433	RHOQ	ras homolog gene family, member Q	9.78	11.98	2.19	2.64 E-18	1.61 E-16
26227	PHGDH	phosphoglycerate dehydrogenase	10.72	12.95	2.18	4.23 E-18	2.45 E-16
8349	HIST2H2BE	histone cluster 2, H2be	7.18	9.61	2.17	2.88 E-16	1.07 E-14
9242	MSC	musculin	7.42	9.79	2.17	1.74 E-17	8.64 E-16
11155	LDB3	LIM domain binding 3	6.58	9.25	2.16	4.13 E-16	1.50 E-14
2318	FLNC	filamin C, gamma	11.25	13.50	2.14	3.31 E-15	9.56 E-14
22801	ITGA11	integrin, alpha 11	7.51	9.85	2.14	7.69 E-16	2.62 E-14
11214	AKAP13	A kinase (PRKA) anchor protein 13	7.89	10.16	2.14	5.55 E-14	1.24 E-12
56911	C21orf7	chromosome 21 open reading frame 7	10.46	12.60	2.14	3.59 E-19	2.88 E-17
7453	WARS	tryptophanyl-tRNA synthetase	9.46	11.61	2.14	1.63 E-13	3.22 E-12
5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-	7.69	9.97	2.12	1.47 E-16	5.81 E-15

		catalytic subunit					
1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	7.18	9.56	2.12	6.53E-17	2.76E-15
94241	TP53INP1	tumor protein p53 inducible nuclear protein 1	7.37	9.69	2.10	3.44E-17	1.54E-15
414325	DEFB103A	defensin, beta 103A	7.00	9.41	2.09	4.32E-13	7.67E-12
57801	HES4	hairy and enhancer of split 4 (Drosophila)	7.77	10.01	2.09	8.80E-19	6.19E-17
875	CBS	cystathionine-beta-synthase	8.14	10.32	2.09	9.11E-15	2.40E-13
8816	DCAF5	DDB1 and CUL4 associated factor 5	7.78	10.00	2.08	3.91E-18	2.29E-16
404217	CTXN1	cortexin 1	8.50	10.61	2.07	6.67E-17	2.81E-15
55714	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)	8.64	10.74	2.06	6.26E-16	2.17E-14
58476	TP53INP2	tumor protein p53 inducible nuclear protein 2	7.61	9.83	2.05	3.36E-17	1.52E-15
11341	SCRG1	stimulator of chondrogenesis 1	6.37	8.98	2.04	9.23E-16	3.09E-14
6720	SREBF1	sterol regulatory element binding transcription factor 1	6.99	9.36	2.03	4.69E-17	2.05E-15
57568	SIPA1L2	signal-induced proliferation-associated 1 like 2	6.47	9.05	2.03	1.07E-16	4.34E-15
10962	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	10.83	12.92	2.03	9.76E-19	6.76E-17
89795	NAV3	neuron navigator 3	7.66	9.85	2.03	5.16E-16	1.82E-14
55616	ASAP3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	8.08	10.19	2.00	1.86E-17	9.07E-16
4134	MAP4	microtubule-associated protein 4	7.44	9.64	2.00	3.58E-14	8.41E-13
10193	RNF41	ring finger protein 41	7.86	9.99	1.99	3.71E-17	1.64E-15
80032	ZNF556	zinc finger protein 556	7.31	9.53	1.99	1.29E-17	6.72E-16
157285	SGK223	homolog of rat pragma of Rnd2	8.65	10.68	1.98	2.10E-17	1.01E-15
23499	MACF1	microtubule-actin crosslinking factor 1	9.17	11.14	1.98	7.47E-11	8.24E-10
10217	CTDSPL	CTD (carboxy-terminal	9.13	11.10	1.98	1.44	9.50

		domain, RNA polymerase II, polypeptide A) small phosphatase-like				E-18	E-17
22982	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	7.23	9.45	1.97	2.43 E-16	9.12 E-15
27254	CSDC2	cold shock domain containing C2, RNA binding	6.63	9.07	1.97	2.12 E-17	1.02 E-15
27295	PDLIM3	PDZ and LIM domain 3	10.67	12.65	1.96	4.18 E-17	1.84 E-15
4861	NPAS1	neuronal PAS domain protein 1	6.86	9.20	1.96	3.41 E-17	1.53 E-15
389136	VGLL3	vestigial like 3 (Drosophila)	7.62	9.74	1.96	3.33 E-15	9.62 E-14
10579	TACC2	transforming, acidic coiled-coil containing protein 2	8.41	10.42	1.96	3.01 E-17	1.39 E-15
1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	12.70	14.72	1.95	2.68 E-18	1.63 E-16
8140	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	10.76	12.76	1.95	3.28 E-15	9.52 E-14
79412	KREMEN2	kringle containing transmembrane protein 2	6.84	9.18	1.95	1.69 E-18	1.09 E-16
3898	LAD1	ladinin 1	6.71	9.09	1.94	5.60 E-18	3.14 E-16
54972	TMEM132A	transmembrane protein 132A	7.60	9.70	1.94	1.50 E-17	7.61 E-16
388551	CEACAM16	carcinoembryonic antigen-related cell adhesion molecule 16	6.46	8.93	1.93	8.43 E-18	4.56 E-16
1307	COL16A1	collagen, type XVI, alpha 1	7.77	9.84	1.93	4.98 E-17	2.16 E-15
51706	CYB5R1	cytochrome b5 reductase 1	10.41	12.35	1.92	1.79 E-17	8.81 E-16
7421	VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor	6.77	9.11	1.92	5.89 E-18	3.28 E-16
22809	ATF5	activating transcription factor 5	9.75	11.68	1.92	3.68 E-11	4.28 E-10
10188	TNK2	tyrosine kinase, non-receptor, 2	9.10	11.01	1.91	1.67 E-17	8.37 E-16
10630	PDPN	podoplanin	7.15	9.33	1.91	9.65 E-16	3.20 E-14
196740	C10orf72	chromosome 10 open reading frame 72	6.84	9.13	1.91	5.14 E-17	2.23 E-15
246329	STAC3	SH3 and cysteine rich domain 3	6.69	9.04	1.90	1.68 E-17	8.37 E-16

6733	SRPK2	SRSF protein kinase 2	6.84	9.13	1.90	1.21 E-16	4.86 E-15
10867	TSPAN9	tetraspanin 9	10.31	12.23	1.89	5.71 E-17	2.45 E-15
22885	ABLIM3	actin binding LIM protein family, member 3	8.61	10.55	1.89	4.74 E-18	2.69 E-16
3636	INPPL1	inositol polyphosphate phosphatase-like 1	9.24	11.12	1.89	7.85 E-16	2.66 E-14
26137	ZBTB20	zinc finger and BTB domain containing 20	7.45	9.53	1.88	8.39 E-12	1.12 E-10
9839	ZEB2	zinc finger E-box binding homeobox 2	7.87	9.88	1.88	1.04 E-14	2.71 E-13
116138	KLHDC3	kelch domain containing 3	10.18	12.05	1.87	1.44 E-17	7.42 E-16
2170	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	6.54	8.92	1.87	4.90 E-14	1.11 E-12
694	BTG1	B-cell translocation gene 1, anti-proliferative	10.69	12.57	1.86	8.26 E-17	3.41 E-15
81618	ITM2C	integral membrane protein 2C	9.27	11.12	1.86	7.08 E-17	2.97 E-15
5064	PALM	paralemmin	7.31	9.40	1.86	1.45 E-16	5.71 E-15
8128	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	8.20	10.15	1.86	1.02 E-16	4.17 E-15
1512	CTSH	cathepsin H	7.23	9.33	1.85	1.16 E-15	3.73 E-14
9750	FAM65B	family with sequence similarity 65, member B	6.59	8.94	1.85	2.11 E-15	6.39 E-14
57556	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	6.61	8.94	1.84	6.77 E-15	1.82 E-13
2817	GPC1	glypican 1	8.43	10.33	1.84	2.74 E-16	1.02 E-14
8611	PPAP2A	phosphatidic acid phosphatase type 2A	8.38	10.28	1.83	1.04 E-15	3.40 E-14
84075	FSCB	fibrous sheath CABYR binding protein	6.53	8.86	1.82	2.40 E-15	7.15 E-14
338773	TMEM119	transmembrane protein 119	6.49	8.83	1.82	1.96 E-17	9.54 E-16
9499	MYOT	myotilin	6.59	8.90	1.82	2.35 E-15	7.01 E-14
23588	KLHDC2	kelch domain containing 2	9.44	11.23	1.81	3.10 E-16	1.14 E-14
1831	TSC22D3	TSC22 domain family,	8.99	10.82	1.80	2.33	1.11

		member 3				E-17	E-15
54800	KLHL24	kelch-like 24 (Drosophila)	7.60	9.57	1.80	4.28 E-16	1.54 E-14
23710	GABARAPL1	GABA(A) receptor-associated protein like 1	8.27	10.15	1.80	6.62 E-16	2.28 E-14
57722	IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	6.92	9.06	1.80	5.53 E-16	1.94 E-14
23048	FNBP1	formin binding protein 1	8.32	10.19	1.79	4.80 E-16	1.72 E-14
8780	RIOK3	RIO kinase 3 (yeast)	9.67	11.45	1.79	1.09 E-17	5.73 E-16
5814	PURB	purine-rich element binding protein B	10.28	12.09	1.78	1.01 E-13	2.11 E-12
1649	DDIT3	DNA-damage-inducible transcript 3	7.79	9.71	1.78	5.29 E-11	6.01 E-10
22882	ZHX2	zinc fingers and homeoboxes 2	7.47	9.45	1.78	1.01 E-15	3.33 E-14
10184	LHFPL2	lipoma HMGIC fusion partner-like 2	8.41	10.25	1.78	7.04 E-16	2.42 E-14
79605	PGBD5	piggyBac transposable element derived 5	6.73	8.93	1.78	7.13 E-18	3.91 E-16
1605	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	8.95	10.74	1.77	3.59 E-17	1.60 E-15
130827	TMEM182	transmembrane protein 182	6.45	8.76	1.77	6.03 E-17	2.58 E-15
57571	CARNS1	carnosine synthase 1	6.47	8.77	1.77	1.16 E-16	4.69 E-15
165904	XIRP1	xin actin-binding repeat containing 1	6.74	8.93	1.77	1.87 E-14	4.60 E-13
57158	JPH2	junctophilin 2	7.39	9.38	1.77	2.80 E-17	1.31 E-15
8878	SQSTM1	sequestosome 1	11.75	13.65	1.76	5.36 E-16	1.89 E-14
84706	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	8.65	10.45	1.76	7.50 E-12	1.01 E-10
140825	NEURL2	neuralized homolog 2 (Drosophila)	6.93	9.02	1.75	1.14 E-15	3.70 E-14
7078	TIMP3	TIMP metallopeptidase inhibitor 3	8.47	10.27	1.74	2.75 E-10	2.70 E-09
4303	FOXO4	forkhead box O4	7.48	9.41	1.74	1.76 E-15	5.42 E-14
56999	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	6.42	8.70	1.73	1.84 E-15	5.66 E-14
5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	6.66	8.84	1.73	1.33	5.33

						E-16	E-15
5308	PITX2	paired-like homeodomain 2	8.84	10.59	1.72	3.42 E-16	1.25 E-14
23175	LPIN1	lipin 1	8.44	10.23	1.72	2.13 E-13	4.08 E-12
5361	PLXNA1	plexin A1	8.08	9.90	1.72	9.53 E-16	3.17 E-14
715	C1R	complement component 1, r subcomponent	6.60	8.79	1.72	1.08 E-12	1.75 E-11
139818	DOCK11	dedicator of cytokinesis 11	7.50	9.41	1.71	7.52 E-15	2.00 E-13
22843	PPM1E	protein phosphatase, Mg2+/Mn2+ dependent, 1E	6.84	8.93	1.71	7.80 E-16	2.65 E-14
4779	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	9.42	11.11	1.70	1.91 E-16	7.32 E-15
5412	UBL3	ubiquitin-like 3	8.79	10.51	1.70	1.45 E-17	7.42 E-16
6310	ATXN1	ataxin 1	7.64	9.49	1.70	1.32 E-14	3.38 E-13
4854	NOTCH3	notch 3	7.35	9.26	1.69	1.58 E-16	6.12 E-15
7136	TNNI2	troponin I type 2 (skeletal, fast)	6.65	8.79	1.69	4.94 E-16	1.76 E-14
12	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	6.67	8.80	1.69	1.04 E-15	3.41 E-14
22846	VASH1	vasohibin 1	6.91	8.94	1.68	3.43 E-17	1.54 E-15
10124	ARL4A	ADP-ribosylation factor-like 4A	8.80	10.51	1.68	3.39 E-14	7.99 E-13
5414	4-Sep	septin 4	6.74	8.84	1.68	7.08 E-17	2.97 E-15
56937	PMEPA1	prostate transmembrane protein, androgen induced 1	9.12	10.82	1.68	2.43 E-16	9.12 E-15
29968	PSAT1	phosphoserine aminotransferase 1	9.52	11.18	1.68	7.49 E-10	6.82 E-09
400818	NBPF9	neuroblastoma breakpoint family, member 9	11.14	12.88	1.68	7.22 E-09	5.45 E-08
7351	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	8.17	9.95	1.68	3.51 E-16	1.28 E-14
547	KIF1A	kinesin family member 1A	6.48	8.68	1.68	8.47 E-14	1.82 E-12
7164	TPD52L1	tumor protein D52-like 1	6.72	8.80	1.67	3.12 E-17	1.43 E-15

8408	ULK1	unc-51-like kinase 1 (C. elegans)	9.42	11.06	1.67	4.17E-15	1.18E-13
3418	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	9.61	11.26	1.66	3.11E-14	7.36E-13
10231	RCAN2	regulator of calcineurin 2	7.49	9.35	1.66	1.11E-14	2.89E-13
836	CASP3	caspase 3, apoptosis-related cysteine peptidase	10.07	11.73	1.65	8.20E-16	2.77E-14
5997	RGS2	regulator of G-protein signaling 2, 24kDa	8.99	10.67	1.65	6.49E-16	2.24E-14
4060	LUM	lumican	8.21	9.96	1.65	5.08E-13	8.87E-12
167227	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	8.16	9.91	1.65	6.55E-15	1.76E-13
83445	GSG1	germ cell associated 1	6.57	8.70	1.65	2.21E-16	8.41E-15
10456	HAX1	HCLS1 associated protein X-1	9.01	10.68	1.65	1.40E-12	2.22E-11
219771	CCNY	cyclin Y	8.82	10.49	1.64	5.56E-17	2.39E-15
9770	RASSF2	Ras association (RalGDS/AF-6) domain family member 2	6.69	8.76	1.64	2.00E-15	6.08E-14
8648	NCOA1	nuclear receptor coactivator 1	8.05	9.79	1.64	1.41E-16	5.58E-15
5176	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	8.73	10.40	1.63	1.11E-13	2.29E-12
861	RUNX1	runt-related transcription factor 1	8.85	10.51	1.63	1.93E-15	5.91E-14
100132406	NBPF10	neuroblastoma breakpoint family, member 10	11.21	12.89	1.63	2.80E-08	1.90E-07
868	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	8.34	10.05	1.63	5.74E-14	1.28E-12
6450	SH3BGR	SH3 domain binding glutamic acid-rich protein	6.92	8.88	1.63	1.15E-12	1.85E-11
81544	GDPD5	glycerophosphodiester phosphodiesterase domain containing 5	7.16	9.04	1.63	4.94E-16	1.76E-14
2308	FOXO1	forkhead box O1	7.82	9.58	1.62	4.83E-16	1.73E-14
490	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	6.76	8.78	1.62	3.96E-15	1.13E-13
6444	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	8.21	9.92	1.61	1.17E-15	3.75E-14

100008589	RN28S1	RNA, 28S ribosomal 1	11.45	13.14	1.61	1.23 E-13	2.50 E-12
9686	VGLL4	vestigial like 4 (Drosophila)	8.84	10.48	1.61	5.13 E-15	1.43 E-13
1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	6.48	8.61	1.61	5.85 E-16	2.04 E-14
51400	PPME1	protein phosphatase methylesterase 1	10.30	11.91	1.61	6.80 E-15	1.83 E-13
23066	CAND2	cullin-associated and neddylation-dissociated 2 (putative)	7.35	9.17	1.60	1.17 E-15	3.75 E-14
779	CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S subunit	7.06	8.94	1.60	3.83 E-14	8.92 E-13
56995	TULP4	tubby like protein 4	8.38	10.05	1.60	5.53 E-11	6.25 E-10
1545	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	6.46	8.58	1.59	8.63 E-12	1.14 E-10
83643	CCDC3	coiled-coil domain containing 3	7.61	9.37	1.59	2.21 E-15	6.66 E-14
1301	COL11A1	collagen, type XI, alpha 1	8.93	10.55	1.59	5.76 E-16	2.01 E-14
51339	DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	7.45	9.23	1.59	7.13 E-16	2.44 E-14
255743	NPNT	nephronectin	6.60	8.65	1.57	1.05 E-14	2.75 E-13
23612	PHLDA3	pleckstrin homology-like domain, family A, member 3	8.81	10.41	1.57	1.93 E-15	5.91 E-14
54843	SYTL2	synaptotagmin-like 2	9.47	11.02	1.57	1.58 E-15	4.90 E-14
124152	IQCK	IQ motif containing K	8.38	10.02	1.57	5.66 E-16	1.97 E-14
54715	RBFOX1	RNA binding protein, fox-1 homolog (C. elegans) 1	6.59	8.63	1.57	2.45 E-16	9.19 E-15
203	AK1	adenylate kinase 1	8.28	9.92	1.57	5.76 E-15	1.58 E-13
221937	FOXK1	forkhead box K1	8.16	9.81	1.56	3.88 E-13	6.97 E-12
57664	PLEKHA4	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	7.69	9.41	1.56	5.90 E-16	2.05 E-14
5269	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	11.51	13.16	1.56	1.31 E-16	5.25 E-15
6520	SLC3A2	solute carrier family 3 (activators of dibasic and	8.34	9.98	1.56	2.09	2.54

		neutral amino acid transport), member 2				E-11	E-10
56940	DUSP22	dual specificity phosphatase 22	8.30	9.94	1.56	1.81E-14	4.48E-13
255488	RNF144B	ring finger protein 144B	6.44	8.52	1.56	2.59E-15	7.66E-14
25878	MXRA5	matrix-remodelling associated 5	8.39	10.01	1.56	8.84E-12	1.17E-10
29995	LMCD1	LIM and cysteine-rich domains 1	8.49	10.10	1.55	1.49E-15	4.67E-14
728734	LOC728734	nuclear pore complex-interacting protein-like 3-like	9.10	10.67	1.55	3.48E-13	6.32E-12
6286	S100P	S100 calcium binding protein P	6.26	8.39	1.55	5.62E-09	4.32E-08
81603	TRIM8	tripartite motif containing 8	10.66	12.24	1.55	1.01E-15	3.33E-14
9644	SH3PXD2A	SH3 and PX domains 2A	9.80	11.33	1.54	2.15E-12	3.28E-11
3799	KIF5B	kinesin family member 5B	8.93	10.49	1.54	1.27E-13	2.58E-12
64112	MOAP1	modulator of apoptosis 1	7.94	9.58	1.54	2.53E-15	7.51E-14
9220	TIAF1	TGFB1-induced anti-apoptotic factor 1	8.57	10.14	1.53	7.62E-14	1.66E-12
26512	INTS6	integrator complex subunit 6	6.84	8.73	1.52	2.79E-13	5.18E-12
8019	BRD3	bromodomain containing 3	8.94	10.49	1.52	5.02E-13	8.77E-12
340348	TSPAN33	tetraspanin 33	6.53	8.54	1.52	2.28E-15	6.82E-14
55640	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	7.90	9.54	1.52	1.54E-16	6.02E-15
5664	PSEN2	presenilin 2 (Alzheimer disease 4)	7.67	9.35	1.52	6.29E-15	1.70E-13
6307	SC4MOL	sterol-C4-methyl oxidase-like	9.27	10.80	1.52	1.25E-10	1.31E-09
3006	HIST1H1C	histone cluster 1, H1c	8.13	9.75	1.52	1.44E-13	2.89E-12
8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	7.61	9.29	1.52	1.71E-14	4.26E-13
285193	DUSP28	dual specificity phosphatase 28	7.97	9.59	1.51	3.35E-15	9.65E-14
6920	TCEA3	transcription elongation factor A (SII), 3	9.41	10.92	1.51	5.16E-13	9.00E-12
716	C1S	complement component 1,	6.85	8.71	1.51	2.95	7.02

		s subcomponent				E-14	E-13
5660	PSAP	prosaposin	11.57	13.18	1.51	3.02 E-16	1.11 E-14
3638	INSIG1	insulin induced gene 1	9.66	11.15	1.51	8.26 E-11	9.03 E-10
6709	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	8.89	10.41	1.51	1.05 E-11	1.36 E-10
6638	SNRPN	small nuclear ribonucleoprotein polypeptide N	9.78	11.27	1.51	5.66 E-15	1.55 E-13
26010	SPATS2L	spermatogenesis associated, serine-rich 2-like	11.01	12.54	1.50	1.04 E-14	2.71 E-13
256281	NUDT14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	8.53	10.08	1.50	6.15 E-12	8.41 E-11
7325	UBE2E2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	9.62	11.10	1.50	1.19 E-14	3.07 E-13
7273	TTN	titin	6.32	8.36	1.50	3.94 E-13	7.06 E-12
8926	SNURF	SNRPN upstream reading frame	9.93	11.40	1.49	3.24 E-15	9.39 E-14
10500	SEMA6C	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	6.50	8.49	1.49	1.52 E-14	3.84 E-13
54536	EXOC6	exocyst complex component 6	7.52	9.19	1.49	2.74 E-15	8.06 E-14
6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	9.02	10.53	1.49	1.61 E-13	3.19 E-12
53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	6.46	8.46	1.49	4.96 E-16	1.76 E-14
166336	PRICKLE2	prickle homolog 2 (Drosophila)	8.51	10.05	1.48	2.70 E-14	6.47 E-13
7158	TP53BP1	tumor protein p53 binding protein 1	8.33	9.89	1.48	9.62 E-14	2.03 E-12
9361	LONP1	lon peptidase 1, mitochondrial	8.93	10.43	1.47	2.14 E-13	4.08 E-12
11149	BVES	blood vessel epicardial substance	6.39	8.39	1.47	1.40 E-14	3.55 E-13
3655	ITGA6	integrin, alpha 6	7.26	8.96	1.47	1.82 E-14	4.51 E-13
84940	CORO6	coronin 6	7.69	9.31	1.47	9.11 E-13	1.52 E-11
10079	ATP9A	ATPase, class II, type 9A	8.45	9.98	1.46	8.52 E-14	1.82 E-12

10493	VAT1	vesicle amine transport protein 1 homolog (T. californica)	9.37	10.83	1.46	2.58 E-13	4.82 E-12
28992	MACROD1	MACRO domain containing 1	7.78	9.37	1.45	6.98 E-15	1.87 E-13
55228	PNMAL1	PNMA-like 1	8.32	9.84	1.45	1.37 E-14	3.49 E-13
352954	GATS	GATS, stromal antigen 3 opposite strand	6.76	8.60	1.45	2.00 E-15	6.09 E-14
152926	PPM1K	protein phosphatase, Mg2+/Mn2+ dependent, 1K	6.84	8.65	1.45	1.64 E-15	5.07 E-14
3908	LAMA2	laminin, alpha 2	7.47	9.10	1.44	5.61 E-14	1.25 E-12
81606	LBH	limb bud and heart development homolog (mouse)	9.16	10.61	1.44	1.14 E-15	3.69 E-14
8076	MFAP5	microfibrillar associated protein 5	9.70	11.13	1.44	1.02 E-14	2.67 E-13
23462	HEY1	hairy/enhancer-of-split related with YRPW motif 1	6.90	8.68	1.44	1.65 E-14	4.13 E-13
60370	AVPI1	arginine vasopressin-induced 1	9.50	10.94	1.44	9.25 E-14	1.97 E-12
144165	PRICKLE1	prickle homolog 1 (Drosophila)	7.79	9.37	1.44	3.83 E-15	1.09 E-13
84676	TRIM63	tripartite motif containing 63	6.66	8.53	1.44	1.14 E-13	2.33 E-12
8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	8.21	9.72	1.43	1.44 E-12	2.28 E-11
23558	WBP2	WW domain binding protein 2	10.65	12.11	1.43	4.15 E-14	9.54 E-13
8605	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	6.76	8.58	1.43	6.99 E-14	1.53 E-12
54813	KLHL28	kelch-like 28 (Drosophila)	7.25	8.89	1.43	1.38 E-15	4.37 E-14
25903	OLFML2B	olfactomedin-like 2B	6.75	8.57	1.42	2.58 E-13	4.81 E-12
79156	PLEKHF1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	7.60	9.17	1.41	3.76 E-12	5.38 E-11
5920	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	6.63	8.48	1.41	7.12 E-11	7.88 E-10
23452	ANGPTL2	angiopoietin-like 2	8.29	9.77	1.41	4.93 E-12	6.88 E-11
5348	FXYD1	FXYD domain containing ion transport regulator 1	6.66	8.50	1.41	1.31 E-12	2.10 E-11

81619	TSPAN14	tetraspanin 14	7.23	8.86	1.41	1.05 E-13	2.18 E-12
54749	EPDR1	ependymin related protein 1 (zebrafish)	10.34	11.76	1.41	5.97 E-15	1.63 E-13
79090	TRAPPC6A	trafficking protein particle complex 6A	7.59	9.15	1.41	3.92 E-13	7.03 E-12
6016	RIT1	Ras-like without CAAX 1	8.59	10.04	1.41	2.58 E-14	6.19 E-13
801	CALM1	calmodulin 1 (phosphorylase kinase, delta)	11.28	12.75	1.41	7.94 E-15	2.11 E-13
59	ACTA2	actin, alpha 2, smooth muscle, aorta	11.99	13.48	1.40	3.38 E-15	9.72 E-14
144363	LYRM5	LYR motif containing 5	9.03	10.45	1.40	5.80 E-13	1.00 E-11
57214	KIAA1199	KIAA1199	9.00	10.43	1.40	1.15 E-11	1.48 E-10
9181	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	11.56	13.04	1.40	5.19 E-15	1.44 E-13
84561	SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	6.88	8.62	1.40	3.24 E-13	5.92 E-12
9846	GAB2	GRB2-associated binding protein 2	7.84	9.37	1.40	2.03 E-14	4.97 E-13
6272	SORT1	sortilin 1	9.69	11.07	1.40	4.57 E-14	1.04 E-12
81493	SYNC	syncoilin, intermediate filament protein	8.33	9.79	1.39	4.75 E-13	8.35 E-12
9873	FCHSD2	FCH and double SH3 domains 2	7.68	9.21	1.39	1.42 E-13	2.86 E-12
8334	HIST1H2AC	histone cluster 1, H2ac	6.67	8.49	1.39	1.40 E-13	2.83 E-12
51313	FAM198B	family with sequence similarity 198, member B	7.48	9.05	1.39	8.38 E-13	1.40 E-11
51155	HN1	hematological and neurological expressed 1	9.96	11.34	1.39	7.90 E-13	1.33 E-11
26508	HEYL	hairy/enhancer-of-split related with YRPW motif-like	9.31	10.70	1.39	1.63 E-11	2.04 E-10
4199	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	8.11	9.59	1.39	5.03 E-14	1.14 E-12
10468	FST	follistatin	9.35	10.73	1.39	2.54 E-15	7.53 E-14
3949	LDLR	low density lipoprotein receptor	10.58	12.00	1.39	7.73 E-11	8.49 E-10
55294	FBXW7	F-box and WD repeat domain containing 7	7.38	8.96	1.39	2.11 E-14	5.14 E-13

3727	JUND	jun D proto-oncogene	10.96	12.39	1.39	4.84 E-15	1.35 E-13
56704	JPH1	junctophilin 1	6.21	8.15	1.38	9.85 E-15	2.58 E-13
30011	SH3KBP1	SH3-domain kinase binding protein 1	6.74	8.51	1.38	3.51 E-14	8.26 E-13
2181	ACSL3	acyl-CoA synthetase long-chain family member 3	9.67	11.03	1.37	8.18 E-13	1.37 E-11
56907	SPIRE1	spire homolog 1 (Drosophila)	9.59	10.96	1.37	1.84 E-14	4.54 E-13
151126	ZNF385B	zinc finger protein 385B	6.55	8.40	1.37	1.83 E-13	3.58 E-12
29948	OSGIN1	oxidative stress induced growth inhibitor 1	8.68	10.10	1.37	8.89 E-10	7.97 E-09
79443	FYCO1	FYVE and coiled-coil domain containing 1	8.05	9.52	1.37	1.72 E-13	3.38 E-12
8209	C21orf33	chromosome 21 open reading frame 33	10.20	11.56	1.37	1.17 E-14	3.04 E-13
22906	TRAK1	trafficking protein, kinesin binding 1	8.22	9.66	1.37	9.52 E-14	2.01 E-12
400916	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	9.64	10.99	1.36	1.13 E-14	2.93 E-13
54897	CASZ1	castor zinc finger 1	6.46	8.32	1.36	1.31 E-15	4.17 E-14
1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	8.46	9.88	1.36	1.01 E-12	1.66 E-11
10147	SUGP2	SURP and G patch domain containing 2	8.76	10.15	1.36	2.39 E-15	7.13 E-14
6868	ADAM17	ADAM metallopeptidase domain 17	8.38	9.80	1.36	2.58 E-12	3.83 E-11
388403	YPEL2	yippee-like 2 (Drosophila)	6.71	8.47	1.35	8.20 E-14	1.77 E-12
734	OSGIN2	oxidative stress induced growth inhibitor family member 2	7.65	9.14	1.35	2.52 E-13	4.72 E-12
2887	GRB10	growth factor receptor-bound protein 10	7.95	9.41	1.35	4.01 E-13	7.18 E-12
59338	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	7.96	9.42	1.35	1.69 E-14	4.22 E-13
2009	EML1	echinoderm microtubule associated protein like 1	8.32	9.74	1.35	1.69 E-14	4.22 E-13
4155	MBP	myelin basic protein	6.30	8.18	1.35	6.11 E-11	6.85 E-10
3005	H1F0	H1 histone family, member 0	9.57	10.90	1.35	3.02	8.83

						E-15	E-14
150864	FAM117B	family with sequence similarity 117, member B	7.32	8.87	1.34	7.14 E-15	1.91 E-13
22796	COG2	component of oligomeric golgi complex 2	8.29	9.69	1.34	1.08 E-14	2.82 E-13
8531	CSDA	cold shock domain protein A	12.44	13.91	1.34	4.83 E-13	8.45 E-12
6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	8.63	10.02	1.34	1.07 E-08	7.83 E-08
64333	ARHGAP9	Rho GTPase activating protein 9	6.72	8.46	1.34	1.38 E-12	2.20 E-11
224	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	8.70	10.09	1.34	1.44 E-13	2.88 E-12
79720	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	9.07	10.42	1.34	5.59 E-14	1.25 E-12
8644	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	10.20	11.51	1.34	2.77 E-13	5.15 E-12
2222	FDFT1	farnesyl-diphosphate farnesyltransferase 1	8.97	10.34	1.34	1.09 E-11	1.41 E-10
1109	AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	8.75	10.13	1.33	6.16 E-14	1.37 E-12
9066	SYT7	synaptotagmin VII	6.80	8.49	1.33	4.51 E-08	2.95 E-07
7328	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	8.50	9.88	1.33	3.19 E-13	5.85 E-12
1573	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	6.54	8.34	1.33	7.51 E-15	2.00 E-13
23099	ZBTB43	zinc finger and BTB domain containing 43	7.87	9.31	1.32	4.64 E-13	8.17 E-12
8777	MPDZ	multiple PDZ domain protein	8.10	9.51	1.32	4.56 E-13	8.06 E-12
114915	NCRNA00219	non-protein coding RNA 219	9.36	10.68	1.31	3.87 E-13	6.97 E-12
10659	CELF2	CUGBP, Elav-like family member 2	7.57	9.04	1.31	2.15 E-12	3.28 E-11
8087	FXR1	fragile X mental retardation, autosomal homolog 1	10.92	12.27	1.31	2.82 E-12	4.15 E-11
10311	DSCR3	Down syndrome critical region gene 3	8.89	10.24	1.31	2.05 E-13	3.94 E-12

98	ACYP2	acylphosphatase 2, muscle type	8.45	9.81	1.31	2.25E-13	4.28E-12
9236	CCPG1	cell cycle progression 1	8.28	9.65	1.30	3.50E-12	5.05E-11
51465	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	8.98	10.32	1.30	1.51E-13	3.01E-12
9209	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	6.24	8.09	1.30	1.01E-12	1.66E-11
287	ANK2	ankyrin 2, neuronal	6.75	8.43	1.30	4.42E-14	1.01E-12
4908	NTF3	neurotrophin 3	6.69	8.40	1.30	9.36E-13	1.55E-11
11345	GABARAPL2	GABA(A) receptor-associated protein-like 2	10.98	12.32	1.30	8.58E-14	1.84E-12
3714	JAG2	jagged 2	7.03	8.60	1.30	9.79E-14	2.06E-12
7750	ZMYM2	zinc finger, MYM-type 2	7.83	9.25	1.30	1.01E-13	2.12E-12
55034	MOCOS	molybdenum cofactor sulfurase	8.28	9.64	1.30	1.48E-09	1.27E-08
1717	DHCR7	7-dehydrocholesterol reductase	8.21	9.58	1.29	1.61E-08	1.14E-07
23596	OPN3	opsin 3	8.02	9.41	1.29	2.07E-13	3.97E-12
7043	TGFB3	transforming growth factor, beta 3	6.45	8.24	1.29	1.80E-13	3.54E-12
1629	DBT	dihydrolipoamide branched chain transacylase E2	8.87	10.20	1.29	4.08E-14	9.41E-13
677800	SNORA12	small nucleolar RNA, H/ACA box 12	7.91	9.31	1.29	1.54E-13	3.06E-12
440270	GOLGA8B	golgin A8 family, member B	8.54	9.88	1.29	5.76E-13	9.95E-12
178	AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	7.47	8.93	1.29	3.75E-13	6.77E-12
7145	TNS1	tensin 1	8.17	9.54	1.28	5.87E-12	8.06E-11
85461	TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	7.41	8.88	1.28	6.65E-12	9.04E-11
2194	FASN	fatty acid synthase	10.39	11.68	1.28	1.55E-08	1.10E-07
4205	MEF2A	myocyte enhancer factor 2A	7.66	9.09	1.28	9.35E-13	1.55E-11
10628	TXNIP	thioredoxin interacting protein	10.79	12.11	1.28	3.65E-13	6.62E-12
4076	CAPRIN1	cell cycle associated	8.91	10.23	1.28	1.52	3.84

		protein 1				E-14	E-13
55719	FAM178A	family with sequence similarity 178, member A	8.81	10.13	1.28	1.05 E-12	1.71 E-11
6309	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	9.07	10.37	1.28	8.07 E-10	7.28 E-09
51660	BRP44L	brain protein 44-like	8.95	10.26	1.27	1.04 E-13	2.16 E-12
8495	PPFIBP2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	6.44	8.21	1.27	1.36 E-12	2.16 E-11
441951	NCRNA00275	non-protein coding RNA 275	11.58	12.91	1.27	3.05 E-14	7.23 E-13
10570	DPYSL4	dihydropyrimidinase-like 4	9.04	10.34	1.27	2.46 E-13	4.63 E-12
1281	COL3A1	collagen, type III, alpha 1	10.37	11.66	1.27	1.11 E-12	1.80 E-11
10765	KDM5B	lysine (K)-specific demethylase 5B	8.48	9.80	1.27	1.14 E-13	2.34 E-12
10443	N4BP2L2	NEDD4 binding protein 2-like 2	8.25	9.59	1.27	1.49 E-13	2.97 E-12
65249	ZSWIM4	zinc finger, SWIM-type containing 4	7.93	9.32	1.27	4.88 E-13	8.55 E-12
8522	GAS7	growth arrest-specific 7	6.29	8.09	1.27	1.20 E-13	2.45 E-12
6773	STAT2	signal transducer and activator of transcription 2, 113kDa	9.40	10.67	1.27	8.40 E-13	1.41 E-11
387914	SHISA2	shisa homolog 2 (Xenopus laevis)	10.12	11.36	1.27	3.20 E-12	4.66 E-11
1612	DAPK1	death-associated protein kinase 1	7.03	8.57	1.27	1.77 E-12	2.75 E-11
57161	PELI2	pellino homolog 2 (Drosophila)	6.37	8.15	1.27	7.80 E-15	2.07 E-13
3759	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	6.48	8.23	1.27	8.94 E-14	1.91 E-12
66000	TMEM108	transmembrane protein 108	8.22	9.56	1.27	8.11 E-13	1.36 E-11
6301	SARS	seryl-tRNA synthetase	9.51	10.78	1.27	2.68 E-12	3.97 E-11
5723	PSPH	phosphoserine phosphatase	8.36	9.68	1.27	4.69 E-08	3.06 E-07
31	ACACA	acetyl-CoA carboxylase alpha	8.23	9.57	1.26	9.24 E-12	1.21 E-10
8527	DGKD	diacylglycerol kinase, delta 130kDa	7.13	8.64	1.26	4.47 E-14	1.02 E-12

1778	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	9.23	10.49	1.26	2.22 E-09	1.85 E-08
53346	TM6SF1	transmembrane 6 superfamily member 1	6.62	8.31	1.26	3.44 E-09	2.75 E-08
9056	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	7.07	8.58	1.26	6.15 E-11	6.89 E-10
10577	NPC2	Niemann-Pick disease, type C2	11.20	12.48	1.25	5.53 E-12	7.62 E-11
10600	USP16	ubiquitin specific peptidase 16	6.70	8.36	1.25	6.27 E-14	1.39 E-12
55924	C1orf183	chromosome 1 open reading frame 183	6.56	8.27	1.25	1.01 E-13	2.11 E-12
2766	GMPR	guanosine monophosphate reductase	7.00	8.52	1.25	2.29 E-13	4.33 E-12
80790	CMIP	c-Maf-inducing protein	10.00	11.21	1.25	7.40 E-14	1.61 E-12
8975	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	8.38	9.68	1.25	1.76 E-13	3.45 E-12
23645	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	10.19	11.40	1.25	2.39 E-13	4.51 E-12
51646	YPEL5	yippee-like 5 (Drosophila)	9.56	10.81	1.25	1.08 E-13	2.23 E-12
147906	DACT3	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	6.69	8.34	1.25	3.59 E-13	6.50 E-12
389125	MUSTN1	musculoskeletal, embryonic nuclear protein 1	6.69	8.33	1.24	8.25 E-14	1.78 E-12
5226	PGD	phosphogluconate dehydrogenase	10.96	12.24	1.24	6.20 E-13	1.06 E-11
162394	SLFN5	schlafen family member 5	7.76	9.13	1.24	1.83 E-09	1.54 E-08
4921	DDR2	discoidin domain receptor tyrosine kinase 2	8.51	9.79	1.23	1.07 E-10	1.15 E-09
54873	PALMD	palmdelphin	7.80	9.16	1.23	1.43 E-13	2.87 E-12
55084	SOBP	sine oculis binding protein homolog (Drosophila)	6.56	8.25	1.23	7.83 E-10	7.10 E-09
1495	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	10.90	12.16	1.23	5.55 E-14	1.24 E-12
2634	GBP2	guanylate binding protein 2, interferon-inducible	8.25	9.55	1.23	2.23 E-12	3.38 E-11
204	AK2	adenylate kinase 2	10.69	11.94	1.23	7.84 E-13	1.32 E-11
51438	MAGEC2	melanoma antigen family	6.50	8.20	1.23	6.10	5.62

		C, 2				E-10	E-09
10580	SORBS1	sorbin and SH3 domain containing 1	6.65	8.30	1.23	1.69 E-13	3.33 E-12
84216	TMEM117	transmembrane protein 117	7.41	8.82	1.23	6.27 E-14	1.39 E-12
8544	PIR	pirin (iron-binding nuclear protein)	7.77	9.12	1.23	3.90 E-12	5.57 E-11
341	APOC1	apolipoprotein C-I	7.04	8.52	1.22	8.30 E-09	6.20 E-08
84814	PPAPDC3	phosphatidic acid phosphatase type 2 domain containing 3	8.17	9.48	1.22	4.02 E-14	9.32 E-13
63908	NAPB	N-ethylmaleimide-sensitive factor attachment protein, beta	7.98	9.31	1.22	1.45 E-13	2.90 E-12
3831	KLC1	kinesin light chain 1	9.43	10.65	1.22	1.01 E-12	1.67 E-11
55852	TEX2	testis expressed 2	8.90	10.15	1.22	6.07 E-14	1.35 E-12
7707	ZNF148	zinc finger protein 148	8.95	10.20	1.22	7.67 E-12	1.03 E-10
66008	TRAK2	trafficking protein, kinesin binding 2	10.26	11.48	1.22	1.42 E-10	1.48 E-09
10253	SPRY2	sprouty homolog 2 (Drosophila)	9.42	10.64	1.22	1.51 E-13	3.00 E-12
116987	AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	8.30	9.58	1.22	4.23 E-14	9.70 E-13
58497	PRUNE	prune homolog (Drosophila)	7.51	8.89	1.22	2.41 E-14	5.78 E-13
23077	MYCBP2	MYC binding protein 2	7.45	8.83	1.21	3.92 E-10	3.74 E-09
401237	FLJ22536	hypothetical locus LOC401237	6.80	8.37	1.21	1.02 E-13	2.13 E-12
55915	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	8.12	9.42	1.21	1.98 E-13	3.82 E-12
2254	FGF9	fibroblast growth factor 9 (glia-activating factor)	6.82	8.38	1.21	1.80 E-12	2.79 E-11
89801	PPP1R3F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	6.96	8.46	1.21	3.69 E-13	6.67 E-12
55151	TMEM38B	transmembrane protein 38B	7.63	8.98	1.21	3.29 E-12	4.78 E-11
1601	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	10.02	11.19	1.21	2.40 E-11	2.88 E-10
10043	TOM1	target of myb1 (chicken)	9.13	10.35	1.21	1.50	2.36

						E-12	E-11
10763	NES	nestin	12.20	13.49	1.21	9.66 E-12	1.26 E-10
3422	IDI1	isopentenyl-diphosphate delta isomerase 1	8.09	9.39	1.21	3.41 E-10	3.30 E-09
7296	TXNRD1	thioredoxin reductase 1	10.71	11.94	1.21	3.53 E-11	4.11 E-10
160518	DENND5B	DENN/MADD domain containing 5B	7.29	8.69	1.20	1.51 E-13	3.01 E-12
22933	SIRT2	sirtuin 2	7.77	9.10	1.20	2.03 E-13	3.92 E-12
4097	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	7.48	8.85	1.20	1.21 E-13	2.48 E-12
55227	LRRC1	leucine rich repeat containing 1	7.73	9.07	1.20	3.05 E-12	4.45 E-11
3376	IARS	isoleucyl-tRNA synthetase	10.08	11.26	1.20	1.05 E-11	1.36 E-10
125050	RN7SK	RNA, 7SK small nuclear	6.99	8.46	1.20	8.93 E-13	1.49 E-11
1634	DCN	decorin	7.93	9.23	1.20	2.98 E-11	3.53 E-10
25937	WWTR1	WW domain containing transcription regulator 1	6.95	8.44	1.20	1.07 E-13	2.20 E-12
6913	TBX15	T-box 15	7.49	8.85	1.20	1.13 E-11	1.46 E-10
1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	8.45	9.69	1.20	9.02 E-13	1.50 E-11
9200	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	10.23	11.40	1.20	9.90 E-13	1.64 E-11
6472	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	11.29	12.51	1.19	1.87 E-13	3.64 E-12
90203	SNX21	sorting nexin family member 21	7.78	9.10	1.19	6.39 E-13	1.09 E-11
90	ACVR1	activin A receptor, type I	9.47	10.67	1.19	2.54 E-12	3.78 E-11
183	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	6.35	8.04	1.19	4.90 E-14	1.11 E-12
51621	KLF13	Kruppel-like factor 13	8.69	9.93	1.19	4.43 E-13	7.85 E-12
8555	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	7.85	9.16	1.19	7.25 E-13	1.23 E-11
7324	UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5	10.84	12.05	1.19	9.53	1.58

		homolog, yeast)				E-13	E-11
401152	C4orf3	chromosome 4 open reading frame 3	9.71	10.89	1.19	2.99 E-13	5.53 E-12
2273	FHL1	four and a half LIM domains 1	9.49	10.68	1.19	1.08 E-12	1.75 E-11
23630	KCNE1L	KCNE1-like	6.78	8.33	1.19	5.64 E-13	9.75 E-12
25798	BRI3	brain protein I3	11.03	12.27	1.19	4.91 E-12	6.87 E-11
3125	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	8.05	9.34	1.19	1.03 E-12	1.70 E-11
6774	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	8.43	9.67	1.19	3.97 E-12	5.65 E-11
51523	CXXC5	CXXC finger protein 5	11.38	12.60	1.19	4.64 E-13	8.17 E-12
2180	ACSL1	acyl-CoA synthetase long-chain family member 1	7.59	8.91	1.18	5.63 E-13	9.74 E-12
6445	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	6.36	8.04	1.18	1.84 E-13	3.59 E-12
1842	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	6.34	8.02	1.18	7.61 E-11	8.37 E-10
84557	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	10.20	11.35	1.18	4.58 E-13	8.09 E-12
122809	SOCS4	suppressor of cytokine signaling 4	7.17	8.58	1.18	1.73 E-12	2.69 E-11
63876	PKNOX2	PBX/knotted 1 homeobox 2	7.96	9.24	1.18	7.66 E-14	1.66 E-12
1013	CDH15	cadherin 15, type 1, M-cadherin (myotubule)	11.96	13.20	1.17	1.36 E-11	1.73 E-10
3017	HIST1H2BD	histone cluster 1, H2bd	6.42	8.07	1.17	7.40 E-14	1.61 E-12
6167	RPL37	ribosomal protein L37	7.68	8.99	1.17	2.53 E-11	3.02 E-10
818	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	8.35	9.58	1.17	7.45 E-13	1.26 E-11
1959	EGR2	early growth response 2	6.62	8.22	1.17	6.07 E-11	6.81 E-10
27190	IL17B	interleukin 17B	6.27	7.95	1.17	1.46 E-11	1.84 E-10
115	ADCY9	adenylate cyclase 9	7.19	8.58	1.17	4.05 E-14	9.37 E-13
115207	KCTD12	potassium channel tetramerisation domain	8.61	9.83	1.17	5.11	5.82

		containing 12				E-11	E-10
100129885	SCXA	scleraxis homolog A (mouse)	6.68	8.25	1.17	2.00E-12	3.08E-11
3689	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	7.95	9.22	1.17	1.54E-13	3.06E-12
114902	C1QTNF5	C1q and tumor necrosis factor related protein 5	8.02	9.28	1.16	1.20E-11	1.54E-10
10513	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	8.77	9.97	1.16	1.86E-13	3.62E-12
291	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	9.94	11.08	1.16	3.38E-11	3.95E-10
27231	ITGB1BP3	integrin beta 1 binding protein 3	6.58	8.17	1.16	3.09E-13	5.70E-12
351	APP	amyloid beta (A4) precursor protein	9.37	10.53	1.15	2.38E-10	2.36E-09
2805	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	9.96	11.09	1.15	7.26E-11	8.03E-10
23062	GGA2	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	7.53	8.83	1.15	1.86E-13	3.62E-12
119032	C10orf32	chromosome 10 open reading frame 32	7.97	9.22	1.15	2.14E-13	4.08E-12
1051	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	11.03	12.22	1.15	7.11E-11	7.88E-10
119710	C11orf74	chromosome 11 open reading frame 74	9.51	10.66	1.15	3.21E-12	4.67E-11
1054	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	8.68	9.87	1.15	4.76E-09	3.71E-08
80232	WDR26	WD repeat domain 26	8.18	9.41	1.15	4.00E-12	5.69E-11
23332	CLASP1	cytoplasmic linker associated protein 1	8.35	9.55	1.14	4.75E-12	6.66E-11
9127	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	7.88	9.13	1.14	1.81E-10	1.84E-09
112752	C14orf179	chromosome 14 open reading frame 179	8.73	9.92	1.14	1.42E-12	2.26E-11
10464	PIBF1	progesterone immunomodulatory binding factor 1	7.47	8.77	1.14	8.42E-12	1.12E-10
9581	PREPL	prolyl endopeptidase-like	7.45	8.75	1.14	7.26E-11	8.03E-10
55298	RNF121	ring finger protein 121	9.25	10.40	1.14	1.26E-11	1.61E-10

126969	SLC44A3	solute carrier family 44, member 3	7.01	8.41	1.14	1.27E-11	1.62E-10
114876	OSBPL1A	oxysterol binding protein-like 1A	8.55	9.73	1.14	2.45E-12	3.67E-11
57609	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	8.00	9.23	1.14	8.19E-11	8.97E-10
54507	ADAMTSL4	ADAMTS-like 4	7.57	8.84	1.13	6.99E-13	1.19E-11
7108	TM7SF2	transmembrane 7 superfamily member 2	6.50	8.09	1.13	3.48E-10	3.36E-09
9788	MTSS1	metastasis suppressor 1	7.72	8.98	1.13	3.92E-13	7.03E-12
57493	HEG1	HEG homolog 1 (zebrafish)	8.54	9.71	1.13	7.77E-10	7.05E-09
196483	FAM86A	family with sequence similarity 86, member A	6.61	8.16	1.13	3.57E-11	4.16E-10
10087	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	6.96	8.37	1.13	9.01E-11	9.79E-10
9215	LARGE	like-glycosyltransferase	7.92	9.15	1.13	4.35E-13	7.72E-12
91461	PKDCC	protein kinase domain containing, cytoplasmic homolog (mouse)	6.85	8.31	1.13	2.37E-11	2.85E-10
2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	9.20	10.33	1.13	1.30E-12	2.07E-11
50854	C6orf48	chromosome 6 open reading frame 48	11.73	12.89	1.12	2.06E-12	3.16E-11
55573	CDV3	CDV3 homolog (mouse)	10.50	11.62	1.12	3.05E-13	5.63E-12
143458	LDLRAD3	low density lipoprotein receptor class A domain containing 3	7.25	8.58	1.12	3.69E-12	5.29E-11
7188	TRAF5	TNF receptor-associated factor 5	7.19	8.52	1.12	6.88E-13	1.17E-11
100133941	CD24	CD24 molecule	7.41	8.70	1.12	3.01E-12	4.40E-11
10133	OPTN	optineurin	8.49	9.65	1.11	1.00E-11	1.30E-10
166614	DCLK2	doublecortin-like kinase 2	6.93	8.34	1.11	4.64E-11	5.32E-10
3913	LAMB2	laminin, beta 2 (laminin S)	8.13	9.33	1.11	7.73E-13	1.30E-11
3992	FADS1	fatty acid desaturase 1	9.70	10.81	1.11	2.02E-09	1.69E-08

26018	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	6.78	8.24	1.11	1.64 E-12	2.56 E-11
23513	SCRIB	scribbled homolog (Drosophila)	9.22	10.34	1.11	2.94 E-13	5.44 E-12
79929	MAP6D1	MAP6 domain containing 1	8.21	9.39	1.10	2.85 E-12	4.19 E-11
80024	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	7.94	9.13	1.10	2.26 E-13	4.29 E-12
135112	NCOA7	nuclear receptor coactivator 7	7.81	9.03	1.10	1.01 E-13	2.12 E-12
1523	CUX1	cut-like homeobox 1	7.52	8.78	1.10	5.44 E-10	5.07 E-09
56985	C17orf48	chromosome 17 open reading frame 48	7.94	9.14	1.10	1.71 E-12	2.66 E-11
25831	HECTD1	HECT domain containing 1	9.37	10.47	1.10	3.77 E-10	3.61 E-09
4192	MDK	midkine (neurite growth-promoting factor 2)	10.17	11.24	1.10	1.79 E-10	1.83 E-09
201164	PLD6	phospholipase D family, member 6	7.74	8.96	1.10	2.26 E-11	2.73 E-10
54993	ZSCAN2	zinc finger and SCAN domain containing 2	7.66	8.89	1.10	2.52 E-12	3.76 E-11
23162	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	7.86	9.07	1.10	5.28 E-12	7.31 E-11
79901	CYBRD1	cytochrome b reductase 1	10.29	11.37	1.10	5.62 E-13	9.73 E-12
55323	LARP6	La ribonucleoprotein domain family, member 6	8.81	9.94	1.10	2.79 E-07	1.56 E-06
8671	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	6.71	8.18	1.09	9.52 E-11	1.03 E-09
1756	DMD	dystrophin	6.70	8.17	1.09	2.30 E-13	4.35 E-12
8874	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	9.05	10.17	1.09	1.22 E-11	1.56 E-10
10742	RAI2	retinoic acid induced 2	6.63	8.13	1.09	1.63 E-11	2.04 E-10
3720	JARID2	jumonji, AT rich interactive domain 2	7.93	9.13	1.09	2.25 E-12	3.40 E-11
84268	RPAIN	RPA interacting protein	10.03	11.10	1.09	1.03 E-11	1.34 E-10
9931	HELZ	helicase with zinc finger	7.40	8.67	1.08	1.17 E-10	1.24 E-09
51207	DUSP13	dual specificity phosphatase 13	7.65	8.86	1.08	7.19 E-11	7.95 E-10

259217	HSPA12A	heat shock 70kDa protein 12A	8.15	9.31	1.08	6.12 E-13	1.05 E-11
3029	HAGH	hydroxyacylglutathione hydrolase	9.49	10.58	1.08	1.40 E-12	2.22 E-11
78999	LRFN4	leucine rich repeat and fibronectin type III domain containing 4	7.41	8.67	1.08	2.18 E-12	3.32 E-11
115294	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	7.98	9.16	1.08	9.54 E-12	1.25 E-10
8707	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	7.88	9.07	1.08	2.38 E-11	2.86 E-10
23387	SIK3	SIK family kinase 3	8.26	9.40	1.07	1.68 E-11	2.08 E-10
114789	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	8.83	9.94	1.07	7.32 E-13	1.24 E-11
9915	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	8.15	9.30	1.07	6.28 E-10	5.78 E-09
113146	AHNAK2	AHNAK nucleoprotein 2	7.97	9.14	1.07	4.76 E-07	2.56 E-06
55508	SLC35E3	solute carrier family 35, member E3	8.86	9.97	1.07	3.47 E-13	6.31 E-12
29903	CCDC106	coiled-coil domain containing 106	8.32	9.45	1.07	2.56 E-12	3.81 E-11
83707	TRPT1	tRNA phosphotransferase 1	9.72	10.80	1.07	2.09 E-12	3.19 E-11
90161	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	6.99	8.33	1.07	4.28 E-10	4.06 E-09
4239	MFAP4	microfibrillar-associated protein 4	6.80	8.21	1.07	8.87 E-12	1.17 E-10
1153	CIRBP	cold inducible RNA binding protein	11.92	13.03	1.07	2.87 E-11	3.40 E-10
9240	PNMA1	paraneoplastic antigen MA1	8.58	9.68	1.07	1.79 E-12	2.77 E-11
445	ASS1	argininosuccinate synthase 1	10.35	11.41	1.07	4.00 E-12	5.69 E-11
5495	PPM1B	protein phosphatase, Mg2+/Mn2+ dependent, 1B	8.53	9.63	1.07	7.08 E-11	7.85 E-10
9771	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	6.62	8.09	1.06	8.53 E-11	9.30 E-10
84939	MUM1	melanoma associated antigen (mutated) 1	9.04	10.14	1.06	9.84 E-12	1.28 E-10
23352	UBR4	ubiquitin protein ligase E3 component n-recognin 4	7.95	9.12	1.06	4.99 E-10	4.68 E-09

23270	TSPYL4	TSPY-like 4	7.39	8.63	1.06	8.60E-13	1.44E-11
91694	LONRF1	LON peptidase N-terminal domain and ring finger 1	6.94	8.29	1.06	6.88E-13	1.17E-11
79573	TTC13	tetratricopeptide repeat domain 13	8.21	9.35	1.06	4.71E-12	6.62E-11
79745	CLIP4	CAP-GLY domain containing linker protein family, member 4	7.75	8.93	1.06	1.65E-11	2.05E-10
11096	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	6.58	8.06	1.06	2.23E-12	3.38E-11
10801	9-Sep	septin 9	12.66	13.84	1.06	1.09E-12	1.77E-11
389538	MGC72080	MGC72080 pseudogene	8.00	9.15	1.06	3.08E-12	4.49E-11
1185	CLCN6	chloride channel 6	7.28	8.52	1.06	1.72E-12	2.67E-11
3475	IFRD1	interferon-related developmental regulator 1	8.22	9.36	1.06	2.90E-08	1.96E-07
9903	KLHL21	kelch-like 21 (Drosophila)	7.62	8.80	1.06	3.32E-12	4.81E-11
1993	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	6.79	8.18	1.05	3.00E-11	3.54E-10
2934	GSN	gelsolin	8.96	10.05	1.05	3.28E-11	3.84E-10
6249	CLIP1	CAP-GLY domain containing linker protein 1	6.80	8.19	1.05	3.46E-12	5.00E-11
57633	LRRN1	leucine rich repeat neuronal 1	6.89	8.24	1.05	1.94E-11	2.37E-10
6509	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	6.55	8.03	1.05	3.78E-10	3.62E-09
3814	KISS1	KiSS-1 metastasis-suppressor	6.91	8.26	1.05	8.92E-12	1.18E-10
1134	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	9.29	10.34	1.05	1.27E-09	1.11E-08
157922	CAMSAP1	calmodulin regulated spectrin-associated protein 1	8.28	9.39	1.05	1.02E-11	1.33E-10
9821	RB1CC1	RB1-inducible coiled-coil 1	8.79	9.86	1.05	6.33E-12	8.63E-11
10904	BLCAP	bladder cancer associated protein	9.62	10.67	1.04	5.94E-11	6.68E-10
80728	ARHGAP39	Rho GTPase activating protein 39	7.46	8.66	1.04	1.30E-12	2.08E-11

100132247	LOC100132247	nuclear pore complex interacting protein related gene	8.65	9.75	1.04	2.15E-11	2.60E-10
23564	DDAH2	dimethylarginine dimethylaminohydrolase 2	9.39	10.43	1.04	3.69E-12	5.29E-11
10277	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	8.55	9.63	1.04	1.71E-10	1.75E-09
604	BCL6	B-cell CLL/lymphoma 6	8.73	9.81	1.04	4.45E-13	7.87E-12
79085	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	7.92	9.06	1.04	6.68E-11	7.44E-10
23380	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	7.04	8.32	1.04	1.20E-11	1.54E-10
2	A2M	alpha-2-macroglobulin	6.21	7.75	1.04	6.68E-13	1.14E-11
9284	NPIP	nuclear pore complex interacting protein	8.48	9.57	1.04	2.92E-12	4.28E-11
6235	RPS29	ribosomal protein S29	8.48	9.57	1.04	1.35E-09	1.17E-08
815	CAMK2A	calcium/calmodulin-dependent protein kinase II alpha	6.38	7.88	1.04	1.13E-11	1.45E-10
5108	PCM1	pericentriolar material 1	8.93	10.00	1.04	7.77E-12	1.04E-10
7844	RNF103	ring finger protein 103	8.75	9.83	1.03	2.10E-10	2.10E-09
337867	UBAC2	UBA domain containing 2	8.96	10.04	1.03	9.79E-12	1.28E-10
26053	AUTS2	autism susceptibility candidate 2	9.08	10.14	1.03	3.31E-12	4.80E-11
11278	KLF12	Kruppel-like factor 12	7.81	8.96	1.03	1.20E-10	1.27E-09
11075	STMN2	stathmin-like 2	6.49	7.96	1.03	1.50E-11	1.89E-10
253782	LASS6	LAG1 homolog, ceramide synthase 6	9.53	10.56	1.03	4.63E-09	3.62E-08
8543	LMO4	LIM domain only 4	9.16	10.21	1.03	3.21E-08	2.16E-07
23112	TNRC6B	trinucleotide repeat containing 6B	7.97	9.10	1.03	1.40E-07	8.29E-07
57184	C15orf17	chromosome 15 open reading frame 17	8.18	9.29	1.03	5.78E-12	7.95E-11
55527	FEM1A	fem-1 homolog a (C. elegans)	9.37	10.40	1.03	3.00E-12	4.40E-11
376267	RAB15	RAB15, member RAS onocogene family	7.42	8.61	1.03	7.83E-12	1.05E-10

127495	LRRC39	leucine rich repeat containing 39	6.60	8.03	1.03	1.27 E-11	1.62 E-10
84617	TUBB6	tubulin, beta 6	11.13	12.21	1.03	3.07 E-09	2.48 E-08
1108	CHD4	chromodomain helicase DNA binding protein 4	9.84	10.86	1.02	3.95 E-11	4.57 E-10
7058	THBS2	thrombospondin 2	7.23	8.44	1.02	2.10 E-11	2.55 E-10
23644	EDC4	enhancer of mRNA decapping 4	9.15	10.19	1.02	1.60 E-10	1.64 E-09
80205	CHD9	chromodomain helicase DNA binding protein 9	9.09	10.14	1.02	2.13 E-07	1.21 E-06
2617	GARS	glycyl-tRNA synthetase	12.16	13.24	1.02	7.14 E-09	5.40 E-08
353116	RILPL1	Rab interacting lysosomal protein-like 1	8.95	10.00	1.02	2.66 E-11	3.17 E-10
96459	FNIP1	folliculin interacting protein 1	8.03	9.14	1.02	8.82 E-12	1.17 E-10
79924	ADM2	adrenomedullin 2	6.88	8.20	1.02	2.67 E-08	1.81 E-07
5364	PLXNB1	plexin B1	6.98	8.27	1.02	6.22 E-13	1.06 E-11
85457	KIAA1737	KIAA1737	7.70	8.84	1.02	8.51 E-13	1.42 E-11
100113407	TMEM170B	transmembrane protein 170B	6.83	8.16	1.01	1.94 E-12	2.99 E-11
6938	TCF12	transcription factor 12	8.61	9.66	1.01	1.85 E-11	2.27 E-10
51118	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	10.50	11.50	1.01	2.73 E-12	4.03 E-11
91947	ARRDC4	arrestin domain containing 4	7.05	8.31	1.01	9.49 E-12	1.24 E-10
51466	EVL	Enah/Vasp-like	10.56	11.57	1.01	8.88 E-12	1.17 E-10
84085	FBXO30	F-box protein 30	8.09	9.18	1.01	2.49 E-11	2.99 E-10
64121	RRAGC	Ras-related GTP binding C	8.78	9.82	1.01	6.26 E-11	7.01 E-10
5336	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	6.77	8.12	1.01	8.56 E-12	1.14 E-10
374882	TMEM205	transmembrane protein 205	9.96	10.95	1.01	9.08 E-11	9.85 E-10
94134	ARHGAP12	Rho GTPase activating protein 12	8.42	9.48	1.01	2.66 E-11	3.16 E-10
4780	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	9.22	10.24	1.01	4.66	4.38

						E-10	E-09
57679	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	8.89	9.93	1.01	4.21E-12	5.96E-11
84033	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	6.45	7.89	1.01	1.79E-11	2.20E-10
51804	SIX4	SIX homeobox 4	8.74	9.78	1.01	2.31E-12	3.47E-11
476	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	9.46	10.47	1.00	1.12E-11	1.44E-10
63941	NECAB3	N-terminal EF-hand calcium binding protein 3	6.96	8.24	1.00	1.52E-10	1.57E-09
6442	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	9.83	10.83	1.00	1.62E-11	2.02E-10
114991	ZNF618	zinc finger protein 618	7.69	8.80	1.00	1.49E-11	1.88E-10
5613	PRKX	protein kinase, X-linked	7.54	8.55	0.88	2.81E-11	3.33E-10
613037	LOC613037	nuclear pore complex interacting protein pseudogene	8.32	9.23	0.86	1.79E-09	1.51E-08
991	CDC20	cell division cycle 20 homolog (S. cerevisiae)	12.45	6.62	-5.31	2.59E-27	6.23E-24
3397	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	12.56	6.88	-5.29	1.16E-26	1.79E-23
9768	KIAA0101	KIAA0101	11.93	6.46	-4.88	2.27E-27	6.15E-24
22943	DKK1	dickkopf homolog 1 (Xenopus laevis)	12.67	7.73	-4.75	2.01E-25	1.74E-22
4885	NPTX2	neuronal pentraxin II	13.59	8.97	-4.45	6.37E-26	6.89E-23
11065	UBE2C	ubiquitin-conjugating enzyme E2C	11.57	6.75	-4.40	2.30E-26	3.11E-23
7153	TOP2A	topoisomerase (DNA) II alpha 170kDa	11.38	6.47	-4.36	1.85E-24	9.74E-22
51129	ANGPTL4	angiopoietin-like 4	11.35	6.50	-4.31	1.85E-25	1.67E-22
4071	TM4SF1	transmembrane 4 L six family member 1	11.65	7.10	-4.26	3.47E-24	1.53E-21
3887	KRT81	keratin 81	11.32	6.74	-4.16	1.11E-24	6.49E-22
9133	CCNB2	cyclin B2	11.17	6.62	-4.07	2.34E-24	1.18E-21

3399	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	13.13	9.04	-4.02	7.62E-24	2.94E-21
5054	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	13.79	9.83	-3.83	1.38E-18	9.15E-17
9055	PRC1	protein regulator of cytokinesis 1	11.33	7.29	-3.82	2.26E-24	1.17E-21
4617	MYF5	myogenic factor 5	11.98	8.08	-3.79	6.22E-23	1.67E-20
4907	NT5E	5'-nucleotidase, ecto (CD73)	11.60	7.70	-3.76	2.98E-24	1.43E-21
51203	NUSAP1	nucleolar and spindle associated protein 1	10.82	6.57	-3.73	6.27E-23	1.67E-20
55165	CEP55	centrosomal protein 55kDa	10.82	6.70	-3.66	1.30E-24	7.39E-22
4493	MT1E	metallothionein 1E	14.17	10.37	-3.66	7.34E-20	7.34E-18
26255	PTTG3P	pituitary tumor-transforming 3 (pseudogene)	11.30	7.48	-3.64	5.46E-22	1.05E-19
1164	CKS2	CDC28 protein kinase regulatory subunit 2	11.74	8.00	-3.63	8.21E-24	3.01E-21
55872	PBK	PDZ binding kinase	10.53	6.31	-3.62	8.18E-24	3.01E-21
5021	OXTR	oxytocin receptor	12.11	8.52	-3.52	1.07E-22	2.56E-20
1033	CDKN3	cyclin-dependent kinase inhibitor 3	10.68	6.85	-3.44	2.53E-21	3.75E-19
7083	TK1	thymidine kinase 1, soluble	10.65	6.80	-3.44	9.91E-22	1.73E-19
196792	FAM24B	family with sequence similarity 24, member B	11.08	7.47	-3.43	5.71E-23	1.62E-20
11010	GLIPR1	GLI pathogenesis-related 1	11.31	7.77	-3.42	3.81E-20	4.18E-18
332	BIRC5	baculoviral IAP repeat containing 5	10.60	6.77	-3.41	2.96E-23	9.13E-21
8436	SDPR	serum deprivation response	11.46	8.00	-3.36	4.09E-22	8.03E-20
890	CCNA2	cyclin A2	10.78	7.13	-3.36	1.43E-22	3.19E-20
10112	KIF20A	kinesin family	10.45	6.66	-3.29	4.14	8.07

		member 20A				E-22	E-20
7298	TYMS	thymidylate synthetase	11.44	8.07	-3.28	1.07E-20	1.34E-18
9232	PTTG1	pituitary tumor-transforming 1	11.37	8.03	-3.25	9.06E-23	2.33E-20
4499	MT1M	metallothionein 1M	10.93	7.53	-3.23	1.62E-20	1.95E-18
6790	AURKA	aurora kinase A	10.93	7.52	-3.23	1.28E-22	2.91E-20
1906	EDN1	endothelin 1	10.32	6.61	-3.20	3.50E-23	1.05E-20
64151	NCAPG	non-SMC condensin I complex, subunit G	10.16	6.37	-3.20	1.56E-21	2.47E-19
3833	KIFC1	kinesin family member C1	10.22	6.44	-3.20	2.70E-23	8.46E-21
9787	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	10.27	6.54	-3.19	7.50E-22	1.39E-19
5552	SRGN	serglycin	12.48	9.26	-3.19	9.24E-19	6.44E-17
113130	CDCA5	cell division cycle associated 5	10.51	6.96	-3.19	2.32E-22	4.86E-20
4495	MT1G	metallothionein 1G	10.61	7.15	-3.18	4.37E-19	3.36E-17
79019	CENPM	centromere protein M	10.20	6.45	-3.16	2.02E-22	4.32E-20
9404	LPXN	leupaxin	11.12	7.85	-3.16	5.17E-20	5.48E-18
9833	MELK	maternal embryonic leucine zipper kinase	10.57	7.16	-3.14	7.09E-23	1.87E-20
857	CAV1	caveolin 1, caveolae protein, 22kDa	12.44	9.28	-3.13	2.56E-22	5.33E-20
55355	HJURP	Holliday junction recognition protein	10.14	6.51	-3.07	1.76E-21	2.72E-19
11013	TMSB15A	thymosin beta 15a	10.76	7.50	-3.07	8.28E-21	1.09E-18
8318	CDC45	cell division cycle 45 homolog (S. cerevisiae)	10.07	6.43	-3.06	2.36E-21	3.54E-19
9212	AURKB	aurora kinase B	10.03	6.40	-3.05	7.45E-22	1.39E-19
9319	TRIP13	thyroid hormone receptor interactor 13	10.51	7.21	-3.03	2.55E-21	3.75E-19
51659	GINS2	GINS complex subunit 2 (Psf2 homolog)	10.78	7.60	-3.02	1.22E-22	2.88E-20

7424	VEGFC	vascular endothelial growth factor C	10.99	7.86	-3.02	8.20E-23	2.14E-20
983	CDK1	cyclin-dependent kinase 1	10.12	6.62	-2.99	6.25E-20	6.40E-18
150468	CKAP2L	cytoskeleton associated protein 2-like	9.91	6.32	-2.99	9.17E-23	2.33E-20
23671	TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2	10.59	7.41	-2.98	1.07E-21	1.84E-19
54908	CCDC99	coiled-coil domain containing 99	10.54	7.42	-2.91	4.87E-20	5.19E-18
83879	CDCA7	cell division cycle associated 7	10.43	7.28	-2.90	6.92E-21	9.12E-19
29127	RACGAP1	Rac GTPase activating protein 1	10.27	7.06	-2.89	9.30E-22	1.65E-19
55143	CDCA8	cell division cycle associated 8	10.04	6.72	-2.85	5.88E-22	1.12E-19
56944	OLFML3	olfactomedin-like 3	11.54	8.67	-2.85	1.08E-18	7.46E-17
72	ACTG2	actin, gamma 2, smooth muscle, enteric	10.03	6.73	-2.85	5.81E-20	6.00E-18
5167	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	10.09	6.84	-2.84	2.44E-21	3.64E-19
3491	CYR61	cysteine-rich, angiogenic inducer, 61	12.47	9.62	-2.84	1.99E-17	9.62E-16
4489	MT1A	metallothionein 1A	14.39	11.47	-2.82	2.98E-18	1.80E-16
54478	FAM64A	family with sequence similarity 64, member A	10.01	6.76	-2.80	6.09E-20	6.27E-18
147841	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	10.08	6.94	-2.78	1.53E-21	2.44E-19
54443	ANLN	anillin, actin binding protein	9.78	6.50	-2.72	2.72E-21	3.97E-19
131566	DCBLD2	discoidin, CUB and LCCL domain containing 2	12.09	9.39	-2.69	6.58E-19	4.81E-17
4501	MT1X	metallothionein 1X	12.60	9.91	-2.69	1.95E-18	1.24E-16
84913	ATOH8	atonal homolog 8	9.88	6.78	-2.66	8.76	1.58

		(Drosophila)				E-22	E-19
23204	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	12.29	9.62	-2.65	1.08 E-19	1.01 E-17
2171	FABP5	fatty acid binding protein 5 (psoriasis-associated)	10.45	7.65	-2.63	1.35 E-19	1.24 E-17
397	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	9.70	6.53	-2.63	1.52 E-21	2.44 E-19
22974	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	9.85	6.79	-2.63	1.67 E-20	1.99 E-18
55723	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	9.79	6.76	-2.60	1.91 E-20	2.25 E-18
4085	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	9.90	6.94	-2.59	1.24 E-20	1.54 E-18
10974	C10orf116	chromosome 10 open reading frame 116	10.86	8.21	-2.58	1.40 E-15	4.41 E-14
3159	HMGA1	high mobility group AT-hook 1	11.21	8.59	-2.58	1.12 E-18	7.65 E-17
4502	MT2A	metallothionein 2A	14.64	12.00	-2.58	1.78 E-21	2.73 E-19
57552	NCEH1	neutral cholesterol ester hydrolase 1	10.31	7.55	-2.57	2.89 E-21	4.19 E-19
5328	PLAU	plasminogen activator, urokinase	13.17	10.57	-2.56	1.38 E-16	5.50 E-15
25923	ATL3	atlastin GTPase 3	9.92	7.03	-2.56	1.56 E-20	1.88 E-18
3161	HMMR	hyaluronan-mediated motility receptor (RHAMM)	9.47	6.34	-2.53	1.31 E-19	1.20 E-17
10234	LRRC17	leucine rich repeat containing 17	13.04	10.47	-2.52	9.54 E-21	1.22 E-18
595	CCND1	cyclin D1	13.94	11.26	-2.51	2.66 E-20	3.04 E-18
5999	RGS4	regulator of G-protein signaling 4	11.15	8.63	-2.49	3.70 E-19	2.93 E-17
3037	HAS2	hyaluronan synthase 2	9.92	7.15	-2.48	3.89 E-19	3.04 E-17
8515	ITGA10	integrin, alpha 10	9.90	7.12	-2.47	7.21 E-20	7.25 E-18
1163	CKS1B	CDC28 protein kinase regulatory subunit 1B	11.63	9.16	-2.47	7.39 E-20	7.36 E-18
53827	FXYD5	FXYD domain containing ion	11.26	8.79	-2.45	1.99 E-18	1.25 E-16

		transport regulator 5					
5228	PGF	placental growth factor	10.83	8.32	-2.45	2.44E-19	2.05E-17
3575	IL7R	interleukin 7 receptor	9.33	6.26	-2.45	1.65E-17	8.28E-16
8407	TAGLN2	transgelin 2	12.29	9.83	-2.45	4.03E-20	4.36E-18
1058	CENPA	centromere protein A	9.47	6.46	-2.45	4.02E-20	4.36E-18
10383	TUBB2C	tubulin, beta 2C	12.68	10.21	-2.43	5.44E-19	4.05E-17
26271	FBXO5	F-box protein 5	10.15	7.53	-2.43	6.42E-19	4.71E-17
11004	KIF2C	kinesin family member 2C	9.60	6.71	-2.43	9.95E-20	9.51E-18
84823	LMNB2	lamin B2	11.21	8.77	-2.41	1.20E-19	1.11E-17
84141	FAM176A	family with sequence similarity 176, member A	10.10	7.51	-2.40	1.04E-19	9.91E-18
58504	ARHGAP22	Rho GTPase activating protein 22	11.14	8.72	-2.40	1.71E-18	1.10E-16
81610	FAM83D	family with sequence similarity 83, member D	9.34	6.36	-2.39	2.94E-20	3.30E-18
57559	STAMBPL1	STAM binding protein-like 1	10.14	7.57	-2.39	2.08E-19	1.80E-17
79974	C7orf58	chromosome 7 open reading frame 58	10.17	7.60	-2.39	4.30E-18	2.47E-16
558	AXL	AXL receptor tyrosine kinase	11.11	8.71	-2.39	2.51E-18	1.54E-16
83461	CDCA3	cell division cycle associated 3	9.35	6.38	-2.38	5.43E-20	5.67E-18
55859	BEX1	brain expressed, X-linked 1	9.60	6.80	-2.38	6.95E-20	7.05E-18
5214	PFKP	phosphofructokinase, platelet	11.30	8.93	-2.36	3.97E-19	3.08E-17
387103	CENPW	centromere protein W	10.29	7.80	-2.35	3.65E-18	2.17E-16
5420	PODXL	podocalyxin-like	11.16	8.79	-2.35	7.19E-20	7.25E-18
1017	CDK2	cyclin-dependent kinase 2	10.48	8.03	-2.35	1.05E-19	9.95E-18
11130	ZWINT	ZW10 interactor	9.53	6.77	-2.33	2.06E-20	2.41E-18
290	ANPEP	alanyl (membrane)	9.89	7.32	-2.32	2.96	2.45

		aminopeptidase				E-19	E-17
10460	TACC3	transforming, acidic coiled-coil containing protein 3	9.37	6.50	-2.32	7.26 E-19	5.25 E-17
699	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	9.21	6.30	-2.31	2.04 E-19	1.78 E-17
55839	CENPN	centromere protein N	10.06	7.56	-2.31	7.67 E-19	5.53 E-17
3832	KIF11	kinesin family member 11	9.31	6.47	-2.28	7.76 E-20	7.66 E-18
6241	RRM2	ribonucleotide reductase M2	9.23	6.37	-2.28	2.22 E-20	2.59 E-18
7272	TTK	TTK protein kinase	9.45	6.72	-2.27	9.58 E-20	9.29 E-18
3927	LASP1	LIM and SH3 protein 1	13.23	10.89	-2.27	1.53 E-17	7.75 E-16
81620	CDT1	chromatin licensing and DNA replication factor 1	9.23	6.38	-2.26	1.83 E-19	1.62 E-17
10733	PLK4	polo-like kinase 4	9.35	6.55	-2.26	1.32 E-18	8.82 E-17
1075	CTSC	cathepsin C	10.06	7.64	-2.25	2.68 E-19	2.24 E-17
50861	STMN3	stathmin-like 3	10.89	8.61	-2.24	3.17 E-19	2.60 E-17
9582	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	9.17	6.34	-2.24	5.43 E-20	5.67 E-18
302	ANXA2	annexin A2	10.63	8.34	-2.24	7.02 E-19	5.09 E-17
58538	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	9.22	6.42	-2.23	6.90 E-19	5.03 E-17
203068	TUBB	tubulin, beta	13.48	11.11	-2.23	4.96 E-18	2.79 E-16
249	ALPL	alkaline phosphatase, liver/bone/kidney	12.91	10.62	-2.22	1.12 E-15	3.64 E-14
2192	FBLN1	fibulin 1	11.26	9.03	-2.22	9.05 E-19	6.35 E-17
7025	NR2F1	nuclear receptor subfamily 2, group F, member 1	9.87	7.48	-2.19	2.56 E-18	1.56 E-16
10487	CAP1	CAP, adenylate	13.40	11.10	-2.19	5.92	3.29

		cyclase-associated protein 1 (yeast)				E-18	E-16
6591	SNAI2	snail homolog 2 (Drosophila)	11.26	9.07	-2.18	4.47E-18	2.56E-16
25886	POC1A	POC1 centriolar protein homolog A (Chlamydomonas)	9.99	7.64	-2.18	1.38E-19	1.26E-17
55771	PRR11	proline rich 11	9.17	6.42	-2.18	1.17E-17	6.16E-16
960	CD44	CD44 molecule (Indian blood group)	10.36	8.10	-2.18	8.62E-19	6.11E-17
4173	MCM4	minichromosome maintenance complex component 4	10.43	8.17	-2.17	2.34E-18	1.44E-16
5010	CLDN11	claudin 11	9.71	7.30	-2.17	4.50E-17	1.97E-15
57574	4-Mar	membrane-associated ring finger (C3HC4) 4	9.58	7.13	-2.16	1.21E-18	8.18E-17
1295	COL8A1	collagen, type VIII, alpha 1	11.26	9.10	-2.16	9.29E-18	4.98E-16
7035	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	11.11	8.95	-2.16	3.84E-18	2.25E-16
23234	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	11.46	9.31	-2.16	4.76E-18	2.69E-16
259266	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	9.38	6.81	-2.16	6.74E-17	2.84E-15
79783	C7orf10	chromosome 7 open reading frame 10	10.52	8.30	-2.16	3.30E-19	2.69E-17
6611	SMS	spermine synthase	12.01	9.85	-2.15	3.34E-19	2.70E-17
899	CCNF	cyclin F	9.83	7.47	-2.15	3.72E-18	2.21E-16
214	ALCAM	activated leukocyte cell adhesion molecule	10.84	8.67	-2.15	1.25E-18	8.44E-17
11339	OIP5	Opa interacting protein 5	9.23	6.57	-2.14	5.05E-18	2.83E-16
8771	TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy	9.53	7.09	-2.14	6.73E-17	2.84E-15
1535	CYBA	cytochrome b-245,	9.91	7.62	-2.12	9.51	3.17

		alpha polypeptide				E-16	E-14
122769	LRR1	leucine rich repeat protein 1	9.98	7.70	-2.12	1.25 E-18	8.42 E-17
51200	CPA4	carboxypeptidase A4	9.24	6.67	-2.10	1.28 E-17	6.68 E-16
10051	SMC4	structural maintenance of chromosomes 4	10.21	8.00	-2.09	5.39 E-19	4.03 E-17
23576	DDAH1	dimethylarginine dimethylaminohydrolase 1	10.81	8.71	-2.07	2.98 E-14	7.08 E-13
9590	AKAP12	A kinase (PRKA) anchor protein 12	9.97	7.75	-2.07	2.70 E-18	1.64 E-16
9585	KIF20B	kinesin family member 20B	9.59	7.28	-2.06	3.77 E-18	2.22 E-16
57228	SMAGP	small cell adhesion glycoprotein	10.20	8.01	-2.06	4.27 E-18	2.46 E-16
10535	RNASEH2A	ribonuclease H2, subunit A	9.62	7.34	-2.05	3.32 E-19	2.69 E-17
23762	OSBP2	oxysterol binding protein 2	9.75	7.51	-2.04	1.50 E-18	9.87 E-17
84058	WDR54	WD repeat domain 54	10.81	8.75	-2.04	3.06 E-17	1.41 E-15
3487	IGFBP4	insulin-like growth factor binding protein 4	10.50	8.40	-2.04	2.57 E-17	1.22 E-15
63901	FAM111A	family with sequence similarity 111, member A	10.09	7.96	-2.02	4.50 E-18	2.57 E-16
3489	IGFBP6	insulin-like growth factor binding protein 6	10.28	8.19	-2.01	8.36 E-16	2.81 E-14
2791	GNG11	guanine nucleotide binding protein (G protein), gamma 11	12.00	9.98	-2.01	1.17 E-17	6.16 E-16
25927	CNRIP1	cannabinoid receptor interacting protein 1	10.56	8.51	-2.01	1.83 E-18	1.16 E-16
5891	RAGE	renal tumor antigen	10.06	7.93	-2.00	4.68 E-18	2.66 E-16
116832	RPL39L	ribosomal protein L39-like	9.86	7.71	-1.99	7.08 E-18	3.90 E-16
4176	MCM7	minichromosome maintenance complex component 7	12.00	10.00	-1.99	2.32 E-17	1.11 E-15
7070	THY1	Thy-1 cell surface antigen	11.62	9.65	-1.98	1.18 E-14	3.06 E-13
84650	EBPL	emopamil binding	10.00	7.89	-1.97	8.08	4.38

		protein-like				E-18	E-16
9493	KIF23	kinesin family member 23	9.45	7.22	-1.97	7.71E-17	3.21E-15
6675	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	10.21	8.14	-1.97	8.51E-14	1.82E-12
23589	CARHSP1	calcium regulated heat stable protein 1, 24kDa	11.91	9.93	-1.97	1.75E-17	8.64E-16
55055	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	10.32	8.30	-1.96	4.00E-18	2.34E-16
23446	SLC44A1	solute carrier family 44, member 1	10.99	9.03	-1.96	1.06E-17	5.62E-16
1062	CENPE	centromere protein E, 312kDa	9.27	6.96	-1.96	7.83E-18	4.25E-16
993	CDC25A	cell division cycle 25 homolog A (S. pombe)	8.92	6.41	-1.96	3.45E-17	1.55E-15
22936	ELL2	elongation factor, RNA polymerase II, 2	9.76	7.65	-1.95	1.29E-15	4.13E-14
3885	KRT34	keratin 34	9.12	6.75	-1.95	5.44E-17	2.35E-15
6001	RGS10	regulator of G-protein signaling 10	9.83	7.76	-1.93	3.51E-17	1.56E-15
8061	FOSL1	FOS-like antigen 1	9.26	7.01	-1.92	2.03E-17	9.82E-16
2202	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	11.16	9.25	-1.92	5.18E-17	2.24E-15
2274	FHL2	four and a half LIM domains 2	12.41	10.46	-1.92	2.18E-13	4.16E-12
4172	MCM3	minichromosome maintenance complex component 3	11.53	9.62	-1.92	1.49E-18	9.80E-17
55159	RFWD3	ring finger and WD repeat domain 3	9.94	7.90	-1.91	8.82E-17	3.63E-15
26147	PHF19	PHD finger protein 19	9.14	6.86	-1.90	7.55E-18	4.12E-16
2189	FANCG	Fanconi anemia, complementation group G	9.38	7.21	-1.90	3.94E-17	1.74E-15
805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	13.79	11.76	-1.90	1.03E-15	3.39E-14
9156	EXO1	exonuclease 1	8.89	6.46	-1.89	1.66	8.32

						E-17	E-16
11015	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	10.07	8.08	-1.89	1.34E-17	6.96E-16
81831	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	9.65	7.57	-1.89	6.00E-15	1.63E-13
1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	8.96	6.59	-1.89	1.06E-17	5.63E-16
891	CCNB1	cyclin B1	9.03	6.70	-1.88	2.84E-16	1.05E-14
8914	TIMELESS	timeless homolog (Drosophila)	9.97	7.96	-1.88	2.60E-17	1.23E-15
2305	FOXM1	forkhead box M1	8.90	6.50	-1.87	1.48E-15	4.64E-14
157313	CDCA2	cell division cycle associated 2	8.82	6.39	-1.87	2.00E-18	1.26E-16
6574	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	12.62	10.73	-1.87	1.45E-15	4.54E-14
6119	RPA3	replication protein A3, 14kDa	11.19	9.33	-1.87	2.68E-17	1.26E-15
4174	MCM5	minichromosome maintenance complex component 5	9.59	7.53	-1.86	1.13E-16	4.59E-15
10635	RAD51AP1	RAD51 associated protein 1	9.14	6.93	-1.86	3.46E-17	1.55E-15
130576	LYPD6B	LY6/PLAUR domain containing 6B	10.37	8.46	-1.86	7.50E-16	2.56E-14
197259	MLKL	mixed lineage kinase domain-like	9.04	6.78	-1.86	1.37E-16	5.47E-15
6446	SGK1	serum/glucocorticoid regulated kinase 1	10.24	8.32	-1.86	2.50E-13	4.68E-12
2237	FEN1	flap structure-specific endonuclease 1	11.11	9.27	-1.85	1.01E-15	3.33E-14
2289	FKBP5	FK506 binding protein 5	11.04	9.20	-1.85	2.94E-17	1.37E-15
3148	HMGB2	high-mobility group box 2	10.41	8.52	-1.84	7.14E-15	1.91E-13
6624	FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	13.14	11.22	-1.84	2.40E-16	9.07E-15
1515	CTSL2	cathepsin L2	9.23	7.09	-1.84	3.60E-18	2.15E-16
4751	NEK2	NIMA (never in	8.75	6.36	-1.84	1.70	6.57

		mitosis gene a)-related kinase 2				E-16	E-15
51303	FKBP11	FK506 binding protein 11, 19 kDa	10.01	8.06	-1.83	1.42 E-16	5.63 E-15
55320	MIS18BP1	MIS18 binding protein 1	9.22	7.09	-1.83	1.03 E-16	4.20 E-15
9123	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	12.59	10.74	-1.83	1.86 E-13	3.62 E-12
2201	FBN2	fibrillin 2	9.93	7.98	-1.83	2.24 E-13	4.26 E-12
83442	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3	12.03	10.20	-1.83	6.07 E-17	2.59 E-15
8412	BCAR3	breast cancer anti-estrogen resistance 3	10.75	8.91	-1.82	9.47 E-17	3.88 E-15
6240	RRM1	ribonucleotide reductase M1	11.82	10.00	-1.82	2.28 E-17	1.09 E-15
7057	THBS1	thrombospondin 1	12.72	10.86	-1.82	5.37 E-15	1.48 E-13
7106	TSPAN4	tetraspanin 4	10.11	8.21	-1.82	1.11 E-15	3.61 E-14
1305	COL13A1	collagen, type XIII, alpha 1	9.03	6.84	-1.81	6.43 E-17	2.73 E-15
3939	LDHA	lactate dehydrogenase A	14.02	12.06	-1.81	1.98 E-17	9.60 E-16
5427	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	9.06	6.89	-1.81	7.73 E-18	4.21 E-16
2297	FOXD1	forkhead box D1	10.90	9.09	-1.81	3.13 E-14	7.41 E-13
24137	KIF4A	kinesin family member 4A	8.68	6.31	-1.81	3.05 E-17	1.41 E-15
29108	PYCARD	PYD and CARD domain containing	9.60	7.63	-1.80	3.33 E-16	1.22 E-14
316	AOX1	aldehyde oxidase 1	8.92	6.68	-1.80	7.01 E-16	2.41 E-14
3838	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	10.03	8.14	-1.79	2.13 E-16	8.13 E-15
3835	KIF22	kinesin family member 22	9.93	8.03	-1.79	2.72 E-17	1.28 E-15
4001	LMNB1	lamin B1	8.99	6.82	-1.79	1.71 E-16	6.60 E-15
51512	GTSE1	G-2 and S-phase	8.86	6.57	-1.79	1.80	8.84

		expressed 1				E-17	E-16
54733	SLC35F2	solute carrier family 35, member F2	8.97	6.78	-1.79	2.97 E-17	1.38 E-15
1948	EFNB2	ephrin-B2	10.25	8.41	-1.79	6.51 E-17	2.76 E-15
2022	ENG	endoglin	10.12	8.26	-1.78	2.07 E-15	6.27 E-14
303	ANXA2P1	annexin A2 pseudogene 1	9.92	8.03	-1.78	4.59 E-14	1.04 E-12
5880	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	8.74	6.43	-1.77	1.71 E-17	8.53 E-16
55038	CDCA4	cell division cycle associated 4	9.41	7.43	-1.77	4.67 E-18	2.66 E-16
147372	CCBE1	collagen and calcium binding EGF domains 1	9.21	7.16	-1.77	1.86 E-16	7.12 E-15
6491	STIL	SCL/TAL1 interrupting locus	8.84	6.57	-1.77	9.03 E-18	4.87 E-16
6839	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	9.33	7.34	-1.77	9.09 E-18	4.89 E-16
1063	CENPF	centromere protein F, 350/400kDa (mitosin)	9.04	6.92	-1.77	1.31 E-13	2.65 E-12
148741	ANKRD35	ankyrin repeat domain 35	9.65	7.73	-1.76	1.28 E-15	4.09 E-14
653888	LOC653888	actin-related protein 2/3 complex subunit 1B-like	9.63	7.71	-1.76	3.01 E-17	1.39 E-15
7052	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	9.69	7.79	-1.76	1.18 E-14	3.06 E-13
55388	MCM10	minichromosome maintenance complex component 10	8.78	6.50	-1.76	2.41 E-16	9.12 E-15
133	ADM	adrenomedullin	11.64	9.91	-1.76	2.31 E-16	8.79 E-15
353142	LCE3A	late cornified envelope 3A	8.75	6.47	-1.76	2.54 E-15	7.53 E-14
5557	PRIM1	primase, DNA, polypeptide 1 (49kDa)	9.20	7.19	-1.75	2.76 E-17	1.29 E-15
7171	TPM4	tropomyosin 4	11.09	9.36	-1.75	9.94	2.09

						E-14	E-12
29089	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	10.33	8.53	-1.75	1.84E-15	5.66E-14
11098	PRSS23	protease, serine, 23	11.02	9.28	-1.74	7.38E-17	3.09E-15
23603	CORO1C	coronin, actin binding protein, 1C	10.57	8.80	-1.74	5.54E-16	1.94E-14
7048	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	12.40	10.62	-1.74	8.14E-16	2.75E-14
25976	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	10.67	8.91	-1.73	3.07E-15	8.96E-14
2014	EMP3	epithelial membrane protein 3	13.56	11.70	-1.73	2.31E-13	4.36E-12
8710	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	8.80	6.57	-1.73	4.54E-15	1.28E-13
79622	SNRNP25	small nuclear ribonucleoprotein 25kDa (U11/U12)	10.89	9.16	-1.73	2.61E-16	9.71E-15
4175	MCM6	minichromosome maintenance complex component 6	10.96	9.24	-1.73	2.08E-13	3.99E-12
6627	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	11.32	9.62	-1.72	2.25E-15	6.74E-14
81848	SPRY4	sprouty homolog 4 (Drosophila)	9.59	7.72	-1.72	4.68E-17	2.05E-15
64859	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	9.93	8.12	-1.71	1.60E-17	8.06E-16
143888	KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	9.76	7.93	-1.71	9.92E-16	3.29E-14
8836	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	10.40	8.66	-1.70	1.65E-16	6.36E-15
9928	KIF14	kinesin family member 14	8.84	6.71	-1.70	2.18E-16	8.31E-15
1192	CLIC1	chloride intracellular channel 1	13.17	11.42	-1.70	4.81E-17	2.10E-15
130497	OSR1	odd-skipped related 1 (Drosophila)	9.07	7.10	-1.69	1.00E-16	4.11E-15
4860	PNP	purine nucleoside	8.96	6.93	-1.69	1.15	3.70

		phosphorylase				E-15	E-14
4521	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	10.16	8.40	-1.69	1.32E-15	4.18E-14
3065	HDAC1	histone deacetylase 1	11.40	9.72	-1.69	3.39E-17	1.53E-15
10024	TROAP	trophinin associated protein (tastin)	8.77	6.62	-1.68	3.17E-17	1.44E-15
220042	C11orf82	chromosome 11 open reading frame 82	8.99	7.00	-1.68	3.17E-17	1.44E-15
8673	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	9.96	8.19	-1.68	1.90E-13	3.68E-12
7291	TWIST1	twist homolog 1 (Drosophila)	9.71	7.91	-1.67	2.24E-13	4.26E-12
388610	TRNP1	TMF1-regulated nuclear protein 1	9.55	7.73	-1.67	1.05E-16	4.27E-15
65062	ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	10.42	8.71	-1.67	4.97E-16	1.77E-14
5111	PCNA	proliferating cell nuclear antigen	10.57	8.89	-1.66	1.82E-14	4.50E-13
388121	TNFAIP8L3	tumor necrosis factor, alpha-induced protein 8-like 3	9.82	8.05	-1.66	1.17E-16	4.72E-15
220134	SKA1	spindle and kinetochore associated complex subunit 1	8.63	6.43	-1.66	8.78E-16	2.95E-14
1894	ECT2	epithelial cell transforming sequence 2 oncogene	9.36	7.51	-1.66	7.35E-14	1.61E-12
811	CALR	calreticulin	11.34	9.69	-1.65	2.22E-12	3.36E-11
10403	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	8.62	6.44	-1.65	2.58E-16	9.63E-15
54892	NCAPG2	non-SMC condensin II complex, subunit G2	9.20	7.34	-1.65	5.02E-16	1.78E-14
8683	SRSF9	serine/arginine-rich splicing factor 9	12.34	10.68	-1.64	7.90E-17	3.27E-15
8613	PPAP2B	phosphatidic acid phosphatase type 2B	10.10	8.41	-1.63	5.88E-16	2.04E-14
123	PLIN2	perilipin 2	11.39	9.77	-1.62	8.58	3.54

						E-17	E-15
8614	STC2	stanniocalcin 2	12.43	10.80	-1.61	9.60E-11	1.04E-09
23729	SHPK	sedoheptulokinase	9.14	7.31	-1.61	4.50E-16	1.62E-14
1465	CSRP1	cysteine and glycine-rich protein 1	11.64	10.06	-1.61	1.78E-12	2.76E-11
5050	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	10.17	8.50	-1.61	1.10E-15	3.60E-14
1847	DUSP5	dual specificity phosphatase 5	10.20	8.54	-1.61	5.58E-15	1.53E-13
8364	HIST1H4C	histone cluster 1, H4c	14.40	12.72	-1.60	2.11E-14	5.14E-13
10903	MTMR11	myotubularin related protein 11	8.95	7.07	-1.60	1.41E-16	5.60E-15
84675	TRIM55	tripartite motif containing 55	10.77	9.18	-1.59	1.37E-15	4.33E-14
5984	RFC4	replication factor C (activator 1) 4, 37kDa	10.01	8.35	-1.59	1.61E-15	4.99E-14
5905	RANGAP1	Ran GTPase activating protein 1	11.28	9.70	-1.59	4.60E-14	1.04E-12
3014	H2AFX	H2A histone family, member X	9.19	7.41	-1.58	1.69E-15	5.21E-14
54206	ERRFI1	ERBB receptor feedback inhibitor 1	12.01	10.41	-1.58	1.57E-09	1.35E-08
89958	C9orf140	chromosome 9 open reading frame 140	8.64	6.60	-1.57	2.17E-14	5.26E-13
51435	SCARA3	scavenger receptor class A, member 3	8.61	6.54	-1.57	6.13E-15	1.66E-13
276	AMY1A	amylase, alpha 1A (salivary)	9.35	7.62	-1.57	2.81E-15	8.25E-14
9446	GSTO1	glutathione S-transferase omega 1	12.22	10.64	-1.56	1.32E-15	4.19E-14
51393	TRPV2	transient receptor potential cation channel, subfamily V, member 2	9.38	7.66	-1.56	1.44E-14	3.66E-13
5393	EXOSC9	exosome component 9	10.38	8.79	-1.56	2.25E-15	6.74E-14
5351	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	12.60	11.01	-1.56	5.64E-16	1.97E-14
5902	RANBP1	RAN binding protein 1	11.03	9.50	-1.55	5.96E-15	1.63E-13

55707	NECAP2	NECAP endocytosis associated 2	9.93	8.31	-1.55	2.46E-16	9.19E-15
1490	CTGF	connective tissue growth factor	13.23	11.64	-1.54	5.04E-10	4.71E-09
9955	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	9.78	8.14	-1.54	6.75E-16	2.33E-14
71	ACTG1	actin, gamma 1	14.20	12.54	-1.54	1.23E-12	1.98E-11
64105	CENPK	centromere protein K	8.67	6.72	-1.54	4.85E-15	1.36E-13
64943	NT5DC2	5'-nucleotidase domain containing 2	9.73	8.10	-1.53	3.84E-15	1.10E-13
9918	NCAPD2	non-SMC condensin I complex, subunit D2	10.18	8.59	-1.53	9.28E-14	1.97E-12
5725	PTBP1	polypyrimidine tract binding protein 1	13.02	11.43	-1.53	1.52E-15	4.73E-14
1174	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	9.98	8.38	-1.53	2.00E-14	4.90E-13
6385	SDC4	syndecan 4	9.64	8.00	-1.53	7.73E-13	1.30E-11
3329	HSPD1	heat shock 60kDa protein 1 (chaperonin)	12.34	10.79	-1.53	6.42E-15	1.73E-13
85012	TCEAL3	transcription elongation factor A (SII)-like 3	11.43	9.92	-1.52	2.10E-13	4.02E-12
3398	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	10.32	8.77	-1.52	2.89E-15	8.48E-14
90853	SPOCD1	SPOC domain containing 1	9.48	7.83	-1.52	6.30E-15	1.70E-13
55635	DEPDC1	DEP domain containing 1	8.62	6.67	-1.52	2.16E-14	5.25E-13
11164	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	10.86	9.37	-1.51	5.14E-16	1.82E-14
5985	RFC5	replication factor C (activator 1) 5, 36.5kDa	9.48	7.84	-1.51	4.17E-15	1.18E-13
5329	PLAUR	plasminogen activator, urokinase receptor	9.46	7.82	-1.50	4.23E-15	1.20E-13
8208	CHAF1B	chromatin assembly factor 1, subunit B	8.53	6.54	-1.49	3.39E-16	1.24E-14

		(p60)					
51192	CKLF	chemokine-like factor	11.38	9.90	-1.49	5.36E-15	1.48E-13
93659	CGB5	chorionic gonadotropin, beta polypeptide 5	8.47	6.48	-1.49	1.30E-14	3.31E-13
26578	OSTF1	osteoclast stimulating factor 1	10.05	8.51	-1.49	2.42E-16	9.12E-15
114800	CCDC85A	coiled-coil domain containing 85A	8.36	6.35	-1.49	1.18E-15	3.79E-14
55732	C1orf112	chromosome 1 open reading frame 112	8.75	6.94	-1.49	2.82E-16	1.04E-14
5223	PGAM1	phosphoglycerate mutase 1 (brain)	10.54	9.04	-1.49	2.85E-13	5.28E-12
619571	SNORD96A	small nucleolar RNA, C/D box 96A	8.79	7.00	-1.48	3.47E-14	8.17E-13
154	ADRB2	adrenergic, beta-2-, receptor, surface	9.03	7.35	-1.48	6.99E-15	1.87E-13
858	CAV2	caveolin 2	10.96	9.50	-1.48	4.39E-15	1.24E-13
55010	C12orf48	chromosome 12 open reading frame 48	8.60	6.70	-1.47	1.16E-14	3.00E-13
5352	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	9.36	7.74	-1.47	2.46E-12	3.67E-11
2040	STOM	stomatin	10.05	8.53	-1.47	5.55E-14	1.24E-12
353376	TICAM2	toll-like receptor adaptor molecule 2	9.14	7.49	-1.47	4.77E-15	1.34E-13
286527	TMSB15B	thymosin beta 15B	10.72	9.25	-1.47	3.72E-16	1.35E-14
29028	ATAD2	ATPase family, AAA domain containing 2	8.60	6.71	-1.47	1.67E-14	4.19E-13
88455	ANKRD13A	ankyrin repeat domain 13A	11.21	9.76	-1.47	2.11E-14	5.13E-13
4015	LOX	lysyl oxidase	9.56	7.97	-1.47	3.26E-13	5.95E-12
10095	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	9.53	7.95	-1.47	1.41E-14	3.57E-13
6320	CLEC11A	C-type lectin domain family 11, member A	9.52	7.93	-1.47	2.04E-15	6.21E-14
26872	STEAP1	six transmembrane epithelial antigen of the prostate 1	8.77	7.01	-1.46	2.22E-12	3.37E-11
57415	C3orf14	chromosome 3 open	10.44	8.95	-1.46	1.48	3.76

		reading frame 14				E-14	E-13
329	BIRC2	baculoviral IAP repeat containing 2	10.80	9.35	-1.46	1.11 E-13	2.28 E-12
51668	HSPB11	heat shock protein family B (small), member 11	10.90	9.44	-1.46	1.00 E-13	2.11 E-12
26002	MOXD1	monooxygenase, DBH-like 1	8.57	6.68	-1.46	2.23 E-15	6.69 E-14
966	CD59	CD59 molecule, complement regulatory protein	9.82	8.31	-1.45	9.55 E-15	2.51 E-13
10370	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	10.42	8.95	-1.45	2.19 E-12	3.32 E-11
29956	LASS2	LAG1 homolog, ceramide synthase 2	9.96	8.44	-1.45	4.40 E-14	1.01 E-12
6542	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	8.83	7.11	-1.45	5.80 E-14	1.29 E-12
726	CAPN5	calpain 5	9.03	7.40	-1.44	2.79 E-14	6.66 E-13
4982	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	9.33	7.73	-1.44	1.82 E-13	3.56 E-12
56604	TUBB4Q	tubulin, beta polypeptide 4, member Q	9.39	7.82	-1.44	1.31 E-13	2.65 E-12
25941	C18orf10	chromosome 18 open reading frame 10	9.53	7.98	-1.44	1.10 E-14	2.85 E-13
132299	OCIAD2	OCIA domain containing 2	8.57	6.71	-1.44	1.27 E-13	2.58 E-12
8829	NRP1	neuropilin 1	10.49	9.03	-1.43	2.27 E-12	3.42 E-11
84790	TUBA1C	tubulin, alpha 1c	13.93	12.37	-1.43	1.40 E-14	3.55 E-13
29128	UHRF1	ubiquitin-like with PHD and ring finger domains 1	11.36	9.95	-1.43	1.78 E-14	4.42 E-13
6781	STC1	stanniocalcin 1	8.78	7.06	-1.43	1.69 E-15	5.21 E-14
2650	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2	8.82	7.13	-1.43	2.78 E-14	6.65 E-13
1854	DUT	deoxyuridine	9.26	7.69	-1.42	7.46	1.99

		triphosphatase				E-15	E-13
2177	FANCD2	Fanconi anemia, complementation group D2	8.68	6.93	-1.42	1.41 E-15	4.44 E-14
5355	PLP2	proteolipid protein 2 (colonic epithelium-enriched)	9.30	7.72	-1.42	1.20 E-14	3.09 E-13
134285	TMEM171	transmembrane protein 171	8.52	6.67	-1.42	2.68 E-15	7.90 E-14
24147	FJX1	four jointed box 1 (Drosophila)	10.01	8.53	-1.42	1.74 E-14	4.33 E-13
9697	TRAM2	translocation associated membrane protein 2	10.58	9.16	-1.42	3.78 E-14	8.80 E-13
131076	CCDC58	coiled-coil domain containing 58	8.65	6.91	-1.42	1.22 E-14	3.14 E-13
995	CDC25C	cell division cycle 25 homolog C (S. pombe)	8.31	6.37	-1.41	8.18 E-15	2.16 E-13
7431	VIM	vimentin	14.37	12.85	-1.41	1.25 E-14	3.21 E-13
161742	SPRED1	sprouty-related, EVH1 domain containing 1	10.49	9.06	-1.41	9.38 E-16	3.13 E-14
53340	SPA17	sperm autoantigenic protein 17	9.71	8.22	-1.41	2.46 E-14	5.91 E-13
8601	RGS20	regulator of G-protein signaling 20	8.51	6.68	-1.40	7.17 E-15	1.92 E-13
7295	TXN	thioredoxin	13.43	11.94	-1.40	3.81 E-15	1.09 E-13
57333	RCN3	reticulocalbin 3, EF-hand calcium binding domain	10.27	8.84	-1.40	2.28 E-14	5.51 E-13
164284	APCDD1L	adenomatosis polyposis coli down-regulated 1-like	10.58	9.18	-1.40	2.44 E-11	2.92 E-10
81624	DIAPH3	diaphanous homolog 3 (Drosophila)	8.41	6.53	-1.40	1.22 E-15	3.89 E-14
51495	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	11.24	9.86	-1.40	3.16 E-15	9.17 E-14
5058	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	9.41	7.89	-1.39	7.13 E-16	2.44 E-14
29015	SLC43A3	solute carrier family 43, member 3	8.47	6.63	-1.39	3.69 E-14	8.65 E-13
9060	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate	9.08	7.52	-1.39	1.93 E-14	4.74 E-13

		synthase 2					
2091	FBL	fibrillarin	11.11	9.75	-1.38	1.05E-12	1.71E-11
6470	SHMT1	serine hydroxymethyltransferase 1 (soluble)	8.62	6.91	-1.38	1.55E-14	3.89E-13
728378	POTEF	POTE ankyrin domain family, member F	14.17	12.68	-1.38	7.56E-15	2.01E-13
78995	C17orf53	chromosome 17 open reading frame 53	8.71	7.04	-1.38	3.04E-14	7.23E-13
5327	PLAT	plasminogen activator, tissue	11.64	10.29	-1.37	1.61E-13	3.18E-12
57407	NMRAL1	NmrA-like family domain containing 1	9.85	8.41	-1.37	1.84E-13	3.59E-12
7283	TUBG1	tubulin, gamma 1	11.03	9.67	-1.37	1.03E-13	2.14E-12
79001	VKORC1	vitamin K epoxide reductase complex, subunit 1	12.76	11.35	-1.36	7.30E-14	1.60E-12
23594	ORC6	origin recognition complex, subunit 6	8.47	6.68	-1.36	9.45E-15	2.48E-13
144455	E2F7	E2F transcription factor 7	8.85	7.27	-1.36	1.31E-14	3.34E-13
113174	SAAL1	serum amyloid A-like 1	9.47	8.00	-1.36	5.42E-15	1.50E-13
874	CBR3	carbonyl reductase 3	8.68	7.03	-1.36	3.09E-13	5.70E-12
6626	SNRPA	small nuclear ribonucleoprotein polypeptide A	9.72	8.30	-1.35	2.27E-14	5.48E-13
5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	9.02	7.49	-1.35	2.19E-13	4.17E-12
10376	TUBA1B	tubulin, alpha 1b	14.24	12.80	-1.35	1.04E-12	1.70E-11
10970	CKAP4	cytoskeleton-associated protein 4	12.12	10.76	-1.35	3.78E-12	5.41E-11
6502	SKP2	S-phase kinase-associated protein 2 (p45)	10.85	9.51	-1.35	2.83E-13	5.25E-12
3486	IGFBP3	insulin-like growth factor binding protein 3	12.12	10.76	-1.35	5.00E-09	3.88E-08
3015	H2AFZ	H2A histone family, member Z	13.85	12.39	-1.35	6.02E-12	8.26E-11
8438	RAD54	RAD54-like (S.	8.31	6.46	-1.35	2.98	8.72

	L	cerevisiae)				E-15	E-14
1611	DAP	death-associated protein	9.64	8.21	-1.34	1.59E-14	4.00E-13
9735	KNTC1	kinetochore associated 1	8.73	7.13	-1.34	5.35E-13	9.30E-12
896	CCND3	cyclin D3	11.56	10.24	-1.34	3.76E-14	8.78E-13
7884	SLBP	stem-loop binding protein	10.24	8.86	-1.34	2.83E-14	6.74E-13
10953	TOMM34	translocase of outer mitochondrial membrane 34	10.65	9.32	-1.34	2.81E-12	4.14E-11
10606	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	11.47	10.15	-1.34	4.08E-14	9.41E-13
6274	S100A3	S100 calcium binding protein A3	8.59	6.92	-1.34	1.87E-13	3.63E-12
4833	NME4	non-metastatic cells 4, protein expressed in	10.95	9.63	-1.34	6.63E-13	1.13E-11
284996	RNF149	ring finger protein 149	10.79	9.46	-1.33	8.40E-15	2.22E-13
9510	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	9.80	8.41	-1.33	1.02E-13	2.13E-12
4016	LOXL1	lysyl oxidase-like 1	9.88	8.49	-1.33	2.38E-11	2.86E-10
2303	FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	8.79	7.24	-1.33	2.13E-15	6.45E-14
8801	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	10.00	8.63	-1.32	3.12E-13	5.75E-12
262	AMD1	adenosylmethionine decarboxylase 1	10.23	8.87	-1.32	5.46E-15	1.50E-13
6238	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	11.70	10.39	-1.32	1.46E-13	2.92E-12
54935	DUSP23	dual specificity phosphatase 23	10.72	9.41	-1.32	5.90E-13	1.01E-11
221150	SKA3	spindle and kinetochore associated complex subunit 3	8.24	6.43	-1.32	1.20E-14	3.08E-13

278	AMY1C	amylase, alpha 1C (salivary)	12.50	11.16	-1.32	1.26E-12	2.02E-11
377	ARF3	ADP-ribosylation factor 3	9.43	8.01	-1.32	5.13E-15	1.43E-13
10098	TSPAN5	tetraspanin 5	10.45	9.12	-1.31	1.50E-12	2.37E-11
353139	LCE2A	late cornified envelope 2A	8.28	6.48	-1.31	1.05E-14	2.75E-13
3212	HOXB2	homeobox B2	10.39	9.06	-1.31	9.09E-14	1.93E-12
10785	WDR4	WD repeat domain 4	9.81	8.44	-1.31	3.74E-14	8.74E-13
7184	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	12.97	11.60	-1.31	3.39E-12	4.91E-11
9088	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	8.28	6.49	-1.31	8.03E-14	1.73E-12
4616	GADD45B	growth arrest and DNA-damage-inducible, beta	9.75	8.39	-1.30	1.36E-13	2.75E-12
23531	MMD	monocyte to macrophage differentiation-associated	9.10	7.66	-1.30	3.71E-14	8.69E-13
64855	FAM129B	family with sequence similarity 129, member B	10.84	9.55	-1.30	3.22E-12	4.68E-11
728643	LOC728643	heterogeneous nuclear ribonucleoprotein A1 pseudogene	10.07	8.74	-1.30	1.54E-10	1.58E-09
6628	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	12.01	10.70	-1.30	5.32E-14	1.20E-12
84844	PHF5A	PHD finger protein 5A	10.61	9.31	-1.29	4.24E-14	9.73E-13
4218	RAB8A	RAB8A, member RAS oncogene family	10.88	9.59	-1.29	2.08E-14	5.09E-13
60	ACTB	actin, beta	14.75	13.48	-1.29	3.92E-13	7.03E-12
143903	LAYN	layilin	8.87	7.40	-1.29	2.27E-13	4.30E-12
8482	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	8.52	6.90	-1.28	8.38E-14	1.80E-12

2963	GTF2F2	general transcription factor IIF, polypeptide 2, 30kDa	10.99	9.73	-1.28	6.88 E-14	1.51 E-12
205	AK4	adenylate kinase 4	8.99	7.55	-1.28	8.03 E-12	1.07 E-10
29109	FHOD1	formin homology 2 domain containing 1	8.67	7.14	-1.28	1.26 E-13	2.56 E-12
55198	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	9.96	8.64	-1.28	1.00 E-13	2.10 E-12
286016	TPI1P2	triosephosphate isomerase 1 pseudogene 2	10.12	8.80	-1.27	8.83 E-13	1.47 E-11
1843	DUSP1	dual specificity phosphatase 1	11.12	9.87	-1.27	7.76 E-14	1.68 E-12
83982	IFI27L2	interferon, alpha-inducible protein 27-like 2	10.81	9.54	-1.27	2.42 E-13	4.55 E-12
5935	RBM3	RNA binding motif (RNP1, RRM) protein 3	10.65	9.39	-1.27	5.86 E-13	1.01 E-11
50615	IL21R	interleukin 21 receptor	8.46	6.86	-1.27	9.76 E-14	2.06 E-12
55240	STEAP3	STEAP family member 3	9.45	8.09	-1.27	8.10 E-13	1.36 E-11
6275	S100A4	S100 calcium binding protein A4	14.05	12.63	-1.27	3.55 E-13	6.44 E-12
10721	POLQ	polymerase (DNA directed), theta	8.37	6.70	-1.26	9.28 E-12	1.22 E-10
7851	MALL	mal, T-cell differentiation protein-like	8.60	7.07	-1.26	7.98 E-14	1.72 E-12
10491	CRTAP	cartilage associated protein	9.63	8.31	-1.26	1.64 E-11	2.04 E-10
7045	TGFBI	transforming growth factor, beta-induced, 68kDa	14.46	13.18	-1.25	3.95 E-14	9.18 E-13
1479	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	9.98	8.69	-1.25	2.77 E-13	5.15 E-12
151246	SGOL2	shugoshin-like 2 (S. pombe)	8.54	6.99	-1.25	3.91 E-13	7.03 E-12
3150	HMGN1	high-mobility group nucleosome binding	11.52	10.28	-1.25	9.03 E-14	1.93 E-12

		domain 1					
5547	PRCP	prolylcarboxypeptidase (angiotensinase C)	10.50	9.23	-1.25	6.92E-14	1.52E-12
5983	RFC3	replication factor C (activator 1) 3, 38kDa	8.59	7.07	-1.25	4.21E-13	7.48E-12
56776	FMN2	formin 2	8.31	6.64	-1.24	1.14E-12	1.84E-11
84321	THOC3	THO complex 3	9.22	7.85	-1.24	1.20E-12	1.92E-11
808	CALM3	calmodulin 3 (phosphorylase kinase, delta)	13.12	11.85	-1.24	2.74E-14	6.55E-13
2023	ENO1	enolase 1, (alpha)	14.38	13.11	-1.24	2.38E-12	3.56E-11
10019	SH2B3	SH2B adaptor protein 3	10.90	9.66	-1.24	4.26E-12	6.01E-11
28988	DBNL	drebrin-like	11.14	9.93	-1.24	1.84E-12	2.85E-11
3710	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	10.02	8.74	-1.24	1.35E-12	2.14E-11
4804	NGFR	nerve growth factor receptor	8.98	7.59	-1.24	1.96E-12	3.01E-11
11343	MGLL	monoglyceride lipase	9.74	8.45	-1.23	1.69E-12	2.64E-11
8793	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	8.78	7.36	-1.23	5.11E-14	1.15E-12
51388	NIP7	nuclear import 7 homolog (S. cerevisiae)	10.39	9.14	-1.23	7.66E-14	1.66E-12
23165	NUP205	nucleoporin 205kDa	9.78	8.50	-1.23	1.34E-13	2.71E-12
93081	C13orf27	chromosome 13 open reading frame 27	9.29	7.93	-1.23	1.70E-11	2.10E-10
79077	DCTPP1	dCTP pyrophosphatase 1	10.61	9.39	-1.23	2.56E-12	3.81E-11
440093	H3F3C	H3 histone, family 3C	11.27	10.07	-1.23	1.92E-12	2.96E-11
90411	MCFD2	multiple coagulation factor deficiency 2	9.83	8.55	-1.23	1.85E-13	3.61E-12
64399	HHIP	hedgehog interacting protein	8.28	6.61	-1.23	1.03E-13	2.13E-12
152189	CMTM8	CKLF-like MARVEL	9.09	7.72	-1.23	2.18	5.28

		transmembrane domain containing 8				E-14	E-13
10589	DRAP1	DR1-associated protein 1 (negative cofactor 2 alpha)	11.91	10.67	-1.23	1.59 E-12	2.50 E-11
23623	RUSC1	RUN and SH3 domain containing 1	10.29	9.05	-1.23	3.50 E-12	5.05 E-11
116028	C16orf75	chromosome 16 open reading frame 75	8.47	6.94	-1.23	9.04 E-14	1.93 E-12
92667	C20orf72	chromosome 20 open reading frame 72	9.88	8.61	-1.23	9.46 E-14	2.00 E-12
8853	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	10.46	9.22	-1.23	2.46 E-12	3.67 E-11
54780	NSMCE4A	non-SMC element 4 homolog A (S. cerevisiae)	9.93	8.66	-1.23	6.72 E-14	1.48 E-12
6281	S100A10	S100 calcium binding protein A10	13.41	12.11	-1.23	5.61 E-13	9.73 E-12
10952	SEC61B	Sec61 beta subunit	12.31	11.05	-1.22	1.52 E-10	1.57 E-09
10312	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	8.40	6.84	-1.22	3.86 E-12	5.51 E-11
51053	GMNN	geminin, DNA replication inhibitor	8.67	7.23	-1.22	1.00 E-12	1.65 E-11
305	ANXA2P3	annexin A2 pseudogene 3	8.83	7.42	-1.22	2.26 E-14	5.46 E-13
11137	PWP1	PWP1 homolog (S. cerevisiae)	11.03	9.82	-1.22	1.12 E-13	2.29 E-12
55276	PGM2	phosphoglucomutase 2	8.56	7.06	-1.22	8.03 E-15	2.13 E-13
1969	EPHA2	EPH receptor A2	8.63	7.17	-1.22	2.59 E-12	3.84 E-11
55215	FANCI	Fanconi anemia, complementation group I	8.14	6.43	-1.22	9.45 E-14	2.00 E-12
3251	HPRT1	hypoxanthine phosphoribosyltransferase 1	10.73	9.51	-1.22	6.51 E-14	1.44 E-12
6576	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate	9.49	8.19	-1.22	7.60 E-11	8.37 E-10

		transporter), member 1					
7167	TPI1	triosephosphate isomerase 1	13.58	12.26	-1.22	3.89 E-12	5.55 E-11
65003	MRPL11	mitochondrial ribosomal protein L11	9.94	8.68	-1.22	2.15 E-12	3.28 E-11
4154	MBNL1	muscleblind-like (Drosophila)	9.92	8.67	-1.21	2.18 E-12	3.31 E-11
51228	GLTP	glycolipid transfer protein	11.88	10.66	-1.21	1.57 E-13	3.11 E-12
27341	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	10.85	9.64	-1.21	1.68 E-13	3.32 E-12
574042	SNORA10	small nucleolar RNA, H/ACA box 10	8.70	7.29	-1.21	1.44 E-12	2.28 E-11
5604	MAP2K1	mitogen-activated protein kinase kinase 1	11.02	9.82	-1.21	1.06 E-12	1.72 E-11
5358	PLS3	plastin 3	9.90	8.64	-1.21	2.19 E-12	3.32 E-11
26035	GLCE	glucuronic acid epimerase	9.29	7.96	-1.21	8.50 E-14	1.82 E-12
10552	ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	11.86	10.65	-1.21	7.28 E-13	1.24 E-11
493	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	8.74	7.34	-1.21	1.24 E-11	1.59 E-10
10276	NET1	neuroepithelial cell transforming 1	9.86	8.61	-1.21	5.34 E-11	6.06 E-10
29980	DONSON	downstream neighbor of SON	8.85	7.48	-1.21	1.02 E-12	1.68 E-11
84168	ANTXR1	anthrax toxin receptor 1	9.96	8.72	-1.20	1.12 E-12	1.82 E-11
84057	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	8.10	6.42	-1.20	9.36 E-14	1.99 E-12
5634	PRPS2	phosphoribosyl pyrophosphate synthetase 2	8.88	7.51	-1.20	1.03 E-13	2.13 E-12
1002	CDH4	cadherin 4, type 1, R-cadherin (retinal)	8.12	6.44	-1.20	9.07 E-14	1.93 E-12
388962	BOLA3	bolA homolog 3 (E. coli)	11.18	10.00	-1.20	1.17 E-12	1.89 E-11
10092	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	11.82	10.61	-1.20	3.64 E-11	4.23 E-10
30851	TAX1B	Tax1 (human T-cell	11.93	10.71	-1.20	1.54	3.88

	P3	leukemia virus type I) binding protein 3				E-14	E-13
9397	NMT2	N-myristoyltransferase 2	9.28	7.96	-1.20	1.14 E-12	1.85 E-11
7360	UGP2	UDP-glucose pyrophosphorylase 2	9.31	8.00	-1.20	2.93 E-12	4.29 E-11
4171	MCM2	minichromosome maintenance complex component 2	9.22	7.90	-1.20	6.24 E-14	1.38 E-12
2771	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	11.48	10.29	-1.20	3.35 E-13	6.10 E-12
56005	C19orf10	chromosome 19 open reading frame 10	11.55	10.37	-1.20	7.91 E-12	1.06 E-10
109	ADCY3	adenylate cyclase 3	9.58	8.32	-1.20	1.49 E-12	2.35 E-11
7280	TUBB2A	tubulin, beta 2A	9.99	8.75	-1.19	4.49 E-14	1.02 E-12
79866	C13orf34	chromosome 13 open reading frame 34	8.60	7.16	-1.19	1.93 E-11	2.37 E-10
51232	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	9.35	8.06	-1.19	7.68 E-11	8.44 E-10
8826	IQGAP1	IQ motif containing GTPase activating protein 1	9.11	7.80	-1.19	1.80 E-11	2.21 E-10
79980	DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	8.54	7.10	-1.19	4.04 E-13	7.21 E-12
151648	SGOL1	shugoshin-like 1 (S. pombe)	8.15	6.50	-1.18	4.06 E-14	9.39 E-13
3178	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	8.68	7.29	-1.18	4.20 E-13	7.47 E-12
5347	PLK1	polo-like kinase 1	8.16	6.52	-1.18	4.11 E-14	9.48 E-13
83463	MXD3	MAX dimerization protein 3	8.01	6.34	-1.18	1.93 E-13	3.73 E-12
115106	HAUS1	HAUS augmin-like complex, subunit 1	9.49	8.24	-1.18	2.23 E-12	3.38 E-11
1211	CLTA	clathrin, light chain A	10.86	9.69	-1.18	3.51 E-13	6.38 E-12
29950	SERTA	SERTA domain	10.66	9.49	-1.18	4.02	7.18

	D1	containing 1				E-13	E-12
441531	PGAM4	phosphoglycerate mutase family member 4	9.84	8.62	-1.18	2.88E-12	4.23E-11
7533	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	12.53	11.34	-1.18	5.53E-14	1.24E-12
4201	MEA1	male-enhanced antigen 1	9.65	8.42	-1.17	9.87E-12	1.28E-10
114908	TMEM123	transmembrane protein 123	11.11	9.97	-1.17	1.81E-13	3.55E-12
10549	PRDX4	peroxiredoxin 4	11.71	10.55	-1.17	8.94E-12	1.18E-10
824	CAPN2	calpain 2, (m/II) large subunit	9.05	7.75	-1.17	1.68E-13	3.32E-12
56913	C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	8.96	7.67	-1.17	2.65E-12	3.92E-11
10544	PROCR	protein C receptor, endothelial	8.33	6.83	-1.16	1.74E-13	3.43E-12
6434	TRA2B	transformer 2 beta homolog (Drosophila)	10.58	9.42	-1.16	4.36E-10	4.12E-09
1453	CSNK1D	casein kinase 1, delta	10.23	9.05	-1.16	2.78E-13	5.17E-12
151188	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	9.96	8.75	-1.16	1.76E-11	2.17E-10
9948	WDR1	WD repeat domain 1	12.88	11.68	-1.16	4.02E-13	7.19E-12
391	RHOG	ras homolog gene family, member G (rho G)	10.60	9.45	-1.16	1.27E-13	2.58E-12
3776	KCNK2	potassium channel, subfamily K, member 2	8.18	6.58	-1.16	2.35E-13	4.43E-12
201254	STRA13	stimulated by retinoic acid 13 homolog (mouse)	10.72	9.56	-1.16	3.02E-12	4.41E-11
10536	LEPREL2	leprecan-like 2	8.75	7.42	-1.16	8.42E-13	1.41E-11

1903	S1PR3	sphingosine-1-phosphate receptor 3	8.39	6.93	-1.16	3.77E-13	6.80E-12
10592	SMC2	structural maintenance of chromosomes 2	8.55	7.15	-1.16	3.18E-13	5.84E-12
56675	NRIP3	nuclear receptor interacting protein 3	9.36	8.11	-1.15	4.33E-12	6.11E-11
389	RHOC	ras homolog gene family, member C	13.12	11.93	-1.15	4.02E-14	9.32E-13
57045	TWSG1	twisted gastrulation homolog 1 (Drosophila)	10.65	9.50	-1.15	6.39E-12	8.71E-11
10212	DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A	11.34	10.21	-1.15	1.46E-13	2.92E-12
55967	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	12.36	11.17	-1.15	3.28E-13	5.99E-12
152503	SH3D19	SH3 domain containing 19	8.68	7.35	-1.15	7.43E-13	1.26E-11
6427	SRSF2	serine/arginine-rich splicing factor 2	12.31	11.14	-1.15	3.19E-13	5.85E-12
4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in	9.30	8.06	-1.15	2.45E-13	4.61E-12
114335	CGB1	chorionic gonadotropin, beta polypeptide 1	8.29	6.79	-1.15	2.90E-13	5.36E-12
1786	DNMT1	DNA (cytosine-5-)-methyltransferase 1	11.42	10.29	-1.15	9.31E-12	1.22E-10
60559	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	9.01	7.73	-1.14	7.05E-11	7.82E-10
5441	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	9.25	8.01	-1.14	1.26E-12	2.02E-11
2542	SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	9.48	8.26	-1.14	2.42E-13	4.56E-12
1774	DNASE1L1	deoxyribonuclease I-like 1	9.41	8.18	-1.14	2.78E-11	3.30E-10
1434	CSE1L	CSE1 chromosome segregation 1-like (yeast)	11.22	10.10	-1.14	1.53E-12	2.40E-11
3336	HSPE1	heat shock 10kDa	11.98	10.83	-1.14	2.68	3.97

		protein 1 (chaperonin 10)				E-12	E-11
7117	TMSL3	thymosin-like 3	10.94	9.82	-1.14	1.40 E-09	1.22 E-08
93109	TMEM44	transmembrane protein 44	8.91	7.63	-1.14	2.04 E-13	3.93 E-12
378	ARF4	ADP-ribosylation factor 4	10.91	9.78	-1.14	5.11 E-11	5.82 E-10
6746	SSR2	signal sequence receptor, beta (translocon-associated protein beta)	11.78	10.63	-1.14	2.03 E-12	3.10 E-11
7443	VRK1	vaccinia related kinase 1	8.50	7.12	-1.14	3.38 E-12	4.89 E-11
396	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	11.50	10.38	-1.13	5.51 E-11	6.23 E-10
57570	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	12.96	11.77	-1.13	1.71 E-12	2.66 E-11
79083	MLPH	melanophilin	11.15	10.05	-1.13	1.90 E-11	2.33 E-10
729086	LOC729086	vesicular, overexpressed in cancer, prosurvival protein 1-like	9.03	7.78	-1.13	2.51 E-10	2.48 E-09
5768	QSOX1	quiescin Q6 sulfhydryl oxidase 1	11.04	9.94	-1.13	9.24 E-08	5.66 E-07
5757	PTMA	prothymosin, alpha	8.62	7.29	-1.13	1.62 E-07	9.46 E-07
835	CASP2	caspase 2, apoptosis-related cysteine peptidase	10.50	9.37	-1.13	1.56 E-12	2.46 E-11
79668	PARP8	poly (ADP-ribose) polymerase family, member 8	10.21	9.06	-1.12	1.18 E-10	1.25 E-09
83540	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	8.00	6.41	-1.12	1.77 E-13	3.48 E-12
140576	S100A16	S100 calcium binding protein A16	12.06	10.93	-1.12	4.21 E-12	5.96 E-11
27292	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	10.69	9.58	-1.12	3.28 E-13	5.99 E-12

113457	TUBA3D	tubulin, alpha 3d	8.67	7.38	-1.12	3.81E-10	3.65E-09
10465	PPIH	peptidylprolyl isomerase H (cyclophilin H)	10.01	8.85	-1.12	1.20E-10	1.27E-09
8507	ENC1	ectodermal-neural cortex 1 (with BTB-like domain)	8.86	7.61	-1.12	1.18E-12	1.89E-11
55002	TMCO3	transmembrane and coiled-coil domains 3	10.13	8.99	-1.11	1.95E-12	3.00E-11
91614	DEPDC7	DEP domain containing 7	8.41	7.03	-1.11	6.04E-10	5.58E-09
11332	ACOT7	acyl-CoA thioesterase 7	11.43	10.33	-1.11	1.08E-11	1.40E-10
159	ADSS	adenylosuccinate synthase	9.83	8.69	-1.11	5.40E-12	7.46E-11
79850	FAM57A	family with sequence similarity 57, member A	9.26	8.06	-1.11	1.65E-13	3.26E-12
9204	ZMYM6	zinc finger, MYM-type 6	9.72	8.57	-1.10	7.25E-12	9.80E-11
9847	KIAA0528	KIAA0528	9.19	7.99	-1.10	2.69E-11	3.20E-10
3619	INCENP	inner centromere protein antigens 135/155kDa	8.22	6.77	-1.10	1.68E-12	2.62E-11
2621	GAS6	growth arrest-specific 6	11.49	10.40	-1.10	5.98E-13	1.03E-11
664709	HNRNPA1P10	heterogeneous nuclear ribonucleoprotein A1 pseudogene 10	10.12	8.99	-1.10	6.66E-11	7.42E-10
1870	E2F2	E2F transcription factor 2	8.20	6.74	-1.10	7.36E-13	1.25E-11
5337	PLD1	phospholipase D1, phosphatidylcholine-specific	8.24	6.80	-1.10	3.01E-12	4.40E-11
4942	OAT	ornithine aminotransferase	9.47	8.31	-1.10	1.30E-12	2.08E-11
5932	RBBP8	retinoblastoma binding protein 8	9.59	8.44	-1.10	2.53E-11	3.02E-10
2012	EMP1	epithelial membrane protein 1	12.37	11.22	-1.09	1.86E-12	2.87E-11
1716	DGUOK	deoxyguanosine kinase	11.62	10.55	-1.09	7.78E-12	1.04E-10
64847	SPATA20	spermatogenesis associated 20	9.37	8.20	-1.09	9.55E-12	1.25E-10

26499	PLEK2	pleckstrin 2	8.14	6.64	-1.09	7.09E-12	9.60E-11
54069	MIS18A	MIS18 kinetochore protein homolog A (S. pombe)	9.08	7.88	-1.09	2.28E-12	3.44E-11
5732	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	8.70	7.44	-1.09	2.08E-09	1.74E-08
81930	KIF18A	kinesin family member 18A	7.91	6.35	-1.09	3.11E-11	3.67E-10
9637	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	11.95	10.84	-1.09	2.70E-13	5.04E-12
5362	PLXNA2	plexin A2	8.35	6.97	-1.09	7.36E-10	6.70E-09
91039	DPP9	dipeptidyl-peptidase 9	9.46	8.31	-1.09	4.63E-12	6.52E-11
5872	RAB13	RAB13, member RAS oncogene family	9.88	8.75	-1.09	1.19E-12	1.92E-11
6428	SRSF3	serine/arginine-rich splicing factor 3	9.63	8.48	-1.09	5.33E-11	6.05E-10
256364	EML3	echinoderm microtubule associated protein like 3	9.36	8.20	-1.09	1.53E-11	1.93E-10
64420	SUSD1	sushi domain containing 1	8.28	6.89	-1.08	1.15E-13	2.35E-12
81029	WNT5B	wingless-type MMTV integration site family, member 5B	10.34	9.25	-1.08	1.72E-09	1.46E-08
735301	SNHG9	small nucleolar RNA host gene 9 (non-protein coding)	10.51	9.42	-1.08	1.95E-10	1.96E-09
64785	GINS3	GINS complex subunit 3 (Psf3 homolog)	8.89	7.68	-1.08	6.99E-12	9.47E-11
6432	SRSF7	serine/arginine-rich splicing factor 7	9.64	8.50	-1.08	3.85E-12	5.51E-11
7534	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	12.82	11.70	-1.08	5.25E-11	5.96E-10
203427	SLC25A43	solute carrier family 25, member 43	9.04	7.85	-1.08	6.88E-11	7.65E-10
200150	PLD5	phospholipase D family, member 5	8.35	7.00	-1.08	9.56E-13	1.58E-11

81691	LOC81691	exonuclease NEF-sp	8.19	6.75	-1.08	6.24 E-12	8.52 E-11
100216001	LOC100216001	hypothetical LOC100216001	8.10	6.62	-1.08	2.10 E-13	4.02 E-12
93323	HAUS8	HAUS augmin-like complex, subunit 8	8.32	6.96	-1.07	6.26 E-13	1.07 E-11
1000	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	12.27	11.17	-1.07	1.16 E-06	5.78 E-06
80178	C16orf59	chromosome 16 open reading frame 59	8.45	7.14	-1.07	1.56 E-12	2.46 E-11
30844	EHD4	EH-domain containing 4	9.86	8.75	-1.07	1.39 E-12	2.20 E-11
9274	BCL7C	B-cell CLL/lymphoma 7C	9.96	8.84	-1.07	5.08 E-12	7.06 E-11
201161	CENPV	centromere protein V	10.11	9.02	-1.07	2.13 E-11	2.58 E-10
5538	PPT1	palmitoyl-protein thioesterase 1	10.13	9.04	-1.07	6.58 E-11	7.34 E-10
8660	IRS2	insulin receptor substrate 2	10.08	8.99	-1.07	3.62 E-12	5.21 E-11
3725	JUN	jun proto-oncogene	10.51	9.44	-1.07	4.72 E-12	6.63 E-11
5734	PTGER4	prostaglandin E receptor 4 (subtype EP4)	9.29	8.14	-1.07	2.08 E-12	3.18 E-11
677838	SNORA61	small nucleolar RNA, H/ACA box 61	8.83	7.62	-1.07	2.25 E-10	2.24 E-09
650157	LOC650157	peptidyl-prolyl cis-trans isomerase A-like	10.88	9.83	-1.07	1.87 E-12	2.88 E-11
121457	IKBIP	IKBKB interacting protein	8.73	7.51	-1.07	6.39 E-12	8.71 E-11
8301	PICALM	phosphatidylinositol binding clathrin assembly protein	11.09	10.05	-1.07	5.83 E-13	1.00 E-11
10613	ERLIN1	ER lipid raft associated 1	8.56	7.30	-1.07	1.09 E-12	1.77 E-11
7205	TRIP6	thyroid hormone receptor interactor 6	11.23	10.18	-1.07	2.09 E-12	3.19 E-11
728026	LOC728026	hypothetical protein LOC728026	8.53	7.26	-1.06	4.95 E-08	3.21 E-07
29097	CNIH4	cornichon homolog 4 (Drosophila)	10.99	9.95	-1.06	6.12 E-10	5.64 E-09
51318	MRPL35	mitochondrial ribosomal protein L35	10.20	9.11	-1.06	3.52 E-12	5.07 E-11
7867	MAPKAPK3	mitogen-activated protein kinase-	10.89	9.84	-1.06	1.08 E-11	1.40 E-10

		activated protein kinase 3					
5230	PGK1	phosphoglycerate kinase 1	10.56	9.50	-1.06	1.63 E-11	2.04 E-10
3892	KRT86	keratin 86	8.07	6.59	-1.06	1.82 E-12	2.82 E-11
7381	UQCRB	ubiquinol-cytochrome c reductase binding protein	9.63	8.51	-1.06	5.01 E-12	6.97 E-11
4277	MICB	MHC class I polypeptide-related sequence B	8.32	6.99	-1.06	1.01 E-12	1.66 E-11
771	CA12	carbonic anhydrase XII	8.49	7.22	-1.06	9.65 E-13	1.60 E-11
54918	CMTM6	CKLF-like MARVEL transmembrane domain containing 6	9.87	8.77	-1.05	4.24 E-12	5.99 E-11
83596	BCL2L12	BCL2-like 12 (proline rich)	10.10	9.02	-1.05	4.47 E-12	6.29 E-11
4603	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	7.98	6.47	-1.05	2.01 E-12	3.08 E-11
51514	DTL	denticleless homolog (Drosophila)	7.94	6.43	-1.05	2.54 E-12	3.78 E-11
80071	CCDC15	coiled-coil domain containing 15	8.46	7.20	-1.05	1.27 E-12	2.04 E-11
2118	ETV4	ets variant 4	8.52	7.27	-1.05	4.47 E-11	5.14 E-10
51278	IER5	immediate early response 5	9.82	8.74	-1.05	1.02 E-12	1.67 E-11
91289	LMF2	lipase maturation factor 2	9.11	7.96	-1.05	1.06 E-12	1.72 E-11
115908	CTHRC1	collagen triple helix repeat containing 1	10.52	9.47	-1.05	6.14 E-12	8.41 E-11
91057	CCDC34	coiled-coil domain containing 34	8.80	7.61	-1.05	2.45 E-12	3.67 E-11
7538	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	9.27	8.14	-1.05	6.64 E-12	9.03 E-11
8818	DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit	8.85	7.67	-1.05	4.07 E-12	5.78 E-11
728255	KRTAP1-4	keratin associated protein 1-4	7.91	6.41	-1.04	1.05 E-12	1.71 E-11
7041	TGFB1I	transforming growth	10.35	9.31	-1.04	1.39	1.76

	1	factor beta 1 induced transcript 1				E-11	E-10
2717	GLA	galactosidase, alpha	9.76	8.68	-1.04	3.22 E-13	5.90 E-12
5580	PRKCD	protein kinase C, delta	9.34	8.22	-1.04	1.65 E-12	2.59 E-11
51099	ABHD5	abhydrolase domain containing 5	8.88	7.72	-1.04	4.96 E-12	6.92 E-11
51490	C9orf114	chromosome 9 open reading frame 114	9.13	7.99	-1.04	2.36 E-12	3.54 E-11
64834	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	9.29	8.17	-1.04	9.98 E-13	1.65 E-11
23421	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	8.03	6.57	-1.04	1.52 E-11	1.91 E-10
1503	CTPS	CTP synthase	9.85	8.77	-1.04	1.52 E-09	1.30 E-08
83895	KRTAP1-5	keratin associated protein 1-5	8.13	6.74	-1.04	7.00 E-11	7.77 E-10
440145	MZT1	mitotic spindle organizing protein 1	9.36	8.26	-1.03	1.17 E-12	1.88 E-11
4580	MTX1	metaxin 1	8.83	7.66	-1.03	3.67 E-12	5.27 E-11
26289	AK5	adenylate kinase 5	9.39	8.30	-1.03	1.95 E-11	2.38 E-10
2146	EZH2	enhancer of zeste homolog 2 (Drosophila)	8.54	7.32	-1.03	2.36 E-12	3.54 E-11
1318	SLC31A2	solute carrier family 31 (copper transporters), member 2	9.63	8.55	-1.03	1.57 E-11	1.97 E-10
8624	PSMG1	proteasome (prosome, macropain) assembly chaperone 1	10.27	9.24	-1.02	1.05 E-12	1.71 E-11
54793	KCTD9	potassium channel tetramerisation domain containing 9	8.66	7.49	-1.02	1.44 E-11	1.81 E-10
51010	EXOSC3	exosome component 3	9.68	8.61	-1.02	2.87 E-12	4.22 E-11
9117	SEC22C	SEC22 vesicle trafficking protein homolog C (S.	9.79	8.73	-1.02	1.10 E-12	1.78 E-11

		cerevisiae)					
54587	MXRA8	matrix-remodelling associated 8	8.72	7.55	-1.02	7.67E-12	1.03E-10
644936	LOC644936	actin, beta pseudogene	8.41	7.16	-1.02	1.85E-11	2.27E-10
83468	GLT8D2	glycosyltransferase 8 domain containing 2	8.78	7.62	-1.02	5.58E-12	7.68E-11
6132	RPL8	ribosomal protein L8	8.96	7.83	-1.02	6.49E-12	8.83E-11
64744	SMAP2	small ArfGAP2	10.26	9.23	-1.02	3.29E-12	4.77E-11
1902	LPAR1	lysophosphatidic acid receptor 1	10.23	9.20	-1.02	1.69E-11	2.10E-10
10954	PDIA5	protein disulfide isomerase family A, member 5	8.79	7.63	-1.01	2.71E-12	4.00E-11
64866	CDCP1	CUB domain containing protein 1	8.06	6.65	-1.01	9.71E-12	1.27E-10
2956	MSH6	mutS homolog 6 (E. coli)	9.79	8.74	-1.01	1.66E-11	2.06E-10
27131	SNX5	sorting nexin 5	9.27	8.18	-1.01	8.98E-12	1.18E-10
84131	CEP78	centrosomal protein 78kDa	8.64	7.47	-1.01	1.44E-12	2.28E-11
2697	GJA1	gap junction protein, alpha 1, 43kDa	8.92	7.80	-1.01	4.29E-09	3.37E-08
6237	RRAS	related RAS viral (r-ras) oncogene homolog	11.31	10.33	-1.01	1.43E-11	1.80E-10
27235	COQ2	coenzyme Q2 homolog, prenyltransferase (yeast)	10.07	9.04	-1.01	3.40E-11	3.97E-10
89822	KCNK17	potassium channel, subfamily K, member 17	7.85	6.39	-1.01	1.42E-11	1.79E-10
23333	DPY19L1	dpy-19-like 1 (C. elegans)	10.44	9.42	-1.01	1.30E-11	1.65E-10
113115	FAM54A	family with sequence similarity 54, member A	8.05	6.66	-1.01	1.69E-10	1.73E-09
64332	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	8.84	7.71	-1.01	2.75E-11	3.27E-10

6117	RPA1	replication protein A1, 70kDa	10.66	9.66	-1.00	9.58 E-12	1.25 E-10
51293	CD320	CD320 molecule	8.87	7.74	-1.00	4.42 E-11	5.09 E-10
56992	KIF15	kinesin family member 15	8.02	6.62	-1.00	7.50 E-13	1.27 E-11
54962	TIPIN	TIMELESS interacting protein	8.21	6.92	-1.00	5.65 E-13	9.77 E-12
10026	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	9.27	8.19	-1.00	2.96 E-10	2.90 E-09
3151	HMGN2	high-mobility group nucleosomal binding domain 2	13.04	12.01	-0.99	5.15 E-12	7.15 E-11
140885	SIRPA	signal-regulatory protein alpha	8.39	7.20	-0.98	7.91 E-11	8.68 E-10
7398	USP1	ubiquitin specific peptidase 1	8.71	7.60	-0.98	6.19 E-12	8.46 E-11
5315	PKM2	pyruvate kinase, muscle	11.82	10.85	-0.96	6.90 E-11	7.67 E-10
8751	ADAM15	ADAM metallopeptidase domain 15	8.30	7.13	-0.94	1.20 E-10	1.27 E-09
706	TSPO	translocator protein (18kDa)	11.67	10.75	-0.93	5.87 E-11	6.62 E-10
2113	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	9.07	8.07	-0.92	1.15 E-10	1.22 E-09
730101	LOC730101	hypothetical LOC730101	7.96	6.76	-0.88	3.55 E-10	3.42 E-09

[a] Myoblast Mean lists the mean value from three biologically independent primary human myoblast RNA samples collected under proliferative conditions while at low confluency.
[b] Myotube Mean lists the mean value from three biologically independent primary human myotube RNA samples grown to confluency and placed in differentiation media for 72 h.
[c] Fold change represents the difference between the myotube and myoblast values and is a log2 value.

Supplemental Table S2. Upregulated myogenic genes that are expressed at reduced levels in RD cells.

Entrez ID	Symbol	Gene Name	RD value[a]	Myotube value[b]	Fold change[c]	p-value	FDR
59	ACTA2	actin, alpha 2, smooth muscle, aorta	6.48	13.48	7.01	8.67E-38	1.53E-34
845	CASQ2	calsequestrin 2 (cardiac muscle)	6.84	13.80	6.95	6.28E-38	1.23E-34
7134	TNNC1	troponin C type 1 (slow)	7.66	14.56	6.90	3.10E-33	1.61E-30
1410	CRYAB	crystallin, alpha B	6.95	13.32	6.38	1.34E-34	1.03E-31
4626	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	6.48	12.73	6.24	2.51E-32	1.08E-29
58	ACTA1	actin, alpha 1, skeletal muscle	6.65	12.88	6.23	7.86E-34	4.84E-31
1346	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	6.47	12.46	5.99	3.88E-35	3.42E-32
8988	HSPB3	heat shock 27kDa protein 3	7.71	13.58	5.86	1.20E-33	7.07E-31
3316	HSPB2	heat shock 27kDa protein 2	6.47	12.13	5.65	9.92E-32	3.46E-29
5919	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	6.49	12.12	5.62	1.42E-30	3.74E-28
7139	TNNT2	troponin T type 2 (cardiac)	8.74	14.24	5.51	4.07E-32	1.71E-29
8470	SORBS2	sorbin and SH3 domain containing 2	6.47	11.49	5.02	3.43E-33	1.73E-30
25890	ABI3BP	ABI family, member 3 (NESH) binding protein	6.50	11.41	4.91	7.77E-32	2.80E-29
4635	MYL4	myosin, light chain 4, alkali; atrial, embryonic	9.11	13.99	4.91	1.12E-29	2.41E-27
9200	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	6.52	11.40	4.89	9.87E-33	4.84E-30
4208	MEF2C	myocyte enhancer factor 2C	6.96	11.80	4.84	3.05E-33	1.61E-30
9891	NUAK1	NUAK family, SNF1-	8.01	12.77	4.74	6.15E-	2.31

		like kinase, 1				32	E-29
80206	FHOD3	formin homology 2 domain containing 3	6.21	10.90	4.69	2.82E-31	8.90E-29
8076	MFAP5	microfibrillar associated protein 5	6.49	11.13	4.64	6.03E-32	2.31E-29
786	CACNG1	calcium channel, voltage-dependent, gamma subunit 1	6.95	11.56	4.61	1.25E-29	2.62E-27
2162	F13A1	coagulation factor XIII, A1 polypeptide	6.44	11.02	4.59	5.38E-29	9.69E-27
7140	TNNT3	troponin T type 3 (skeletal, fast)	6.70	11.23	4.54	5.83E-32	2.29E-29
2034	EPAS1	endothelial PAS domain protein 1	6.90	11.36	4.48	2.98E-27	3.36E-25
4625	MYH7	myosin, heavy chain 7, cardiac muscle, beta	6.54	11.01	4.47	1.88E-29	3.82E-27
9235	IL32	interleukin 32	7.89	12.35	4.47	8.61E-29	1.46E-26
347273	MURC	muscle-related coiled-coil protein	7.26	11.73	4.46	3.60E-30	8.83E-28
6588	SLN	sarcolipin	7.19	11.65	4.45	3.38E-28	4.81E-26
10468	FST	follistatin	6.30	10.73	4.43	1.04E-31	3.53E-29
10457	GPNMB	glycoprotein (transmembrane) nmb	6.93	11.27	4.35	4.98E-26	3.90E-24
4633	MYL2	myosin, light chain 2, regulatory, cardiac, slow	6.39	10.66	4.26	1.26E-27	1.53E-25
8537	BCAS1	breast carcinoma amplified sequence 1	6.44	10.59	4.15	2.51E-30	6.33E-28
5239	PGM5	phosphoglucomutase 5	6.76	10.83	4.05	3.78E-31	1.11E-28
1396	CRIP1	cysteine-rich protein 1 (intestinal)	6.90	10.95	4.04	1.09E-26	1.03E-24
134265	AFAP1L1	actin filament associated protein 1-like 1	6.79	10.72	3.93	6.10E-26	4.64E-24
22885	ABLIM3	actin binding LIM protein family, member 3	6.65	10.55	3.90	9.73E-30	2.15E-27
4619	MYH1	myosin, heavy chain 1, skeletal muscle, adult	6.37	10.26	3.89	1.86E-28	2.91E-26
4621	MYH3	myosin, heavy chain 3, skeletal muscle,	10.72	14.54	3.82	2.34E-27	2.68E-25

		embryonic					
116496	FAM129A	family with sequence similarity 129, member A	6.55	10.35	3.80	4.42E-21	1.25E-19
859	CAV3	caveolin 3	7.13	10.93	3.80	2.22E-26	1.94E-24
4620	MYH2	myosin, heavy chain 2, skeletal muscle, adult	6.53	10.30	3.77	1.46E-26	1.35E-24
57214	KIAA1199	KIAA1199	6.71	10.43	3.72	6.46E-25	4.00E-23
10777	ARPP21	cAMP-regulated phosphoprotein, 21kDa	7.36	11.08	3.72	3.00E-28	4.37E-26
158471	PRUNE2	prune homolog 2 (Drosophila)	7.70	11.37	3.68	6.04E-23	2.47E-21
1158	CKM	creatine kinase, muscle	8.14	11.83	3.68	2.06E-26	1.84E-24
7169	TPM2	tropomyosin 2 (beta)	9.84	13.52	3.68	7.26E-28	9.31E-26
7130	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	6.75	10.43	3.68	2.24E-25	1.51E-23
26471	NUPR1	nuclear protein, transcriptional regulator, 1	7.47	11.15	3.68	1.58E-26	1.45E-24
64084	CLSTN2	calsyntenin 2	6.64	10.26	3.62	1.05E-26	1.01E-24
9289	GPR56	G protein-coupled receptor 56	6.40	10.00	3.60	1.46E-26	1.35E-24
8082	SSPN	sarcospan (Kras oncogene-associated gene)	6.29	9.83	3.53	1.74E-24	9.80E-23
6711	SPTBN1	spectrin, beta, non-erythrocytic 1	7.00	10.53	3.53	4.30E-27	4.60E-25
8128	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	6.63	10.15	3.52	5.83E-26	4.47E-24
89795	NAV3	neuron navigator 3	6.33	9.85	3.51	1.06E-26	1.01E-24
8736	MYOM1	myomesin 1, 185kDa	7.21	10.71	3.50	1.50E-26	1.39E-24
1339	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	7.05	10.56	3.50	1.95E-23	8.83E-22
4632	MYL1	myosin, light chain 1,	10.41	13.89	3.48	2.29E-	1.27

		alkali; skeletal, fast				24	E-22
25878	MXRA5	matrix-remodelling associated 5	6.61	10.01	3.41	3.64E-24	1.93E-22
22808	MRAS	muscle RAS oncogene homolog	6.82	10.19	3.36	2.51E-23	1.10E-21
7412	VCAM1	vascular cell adhesion molecule 1	6.24	9.60	3.36	8.68E-21	2.32E-19
58494	JAM2	junctional adhesion molecule 2	8.90	12.27	3.36	1.36E-25	9.43E-24
23439	ATP1B4	ATPase, Na+/K+ transporting, beta 4 polypeptide	6.39	9.72	3.33	8.42E-25	5.09E-23
26353	HSPB8	heat shock 22kDa protein 8	6.82	10.14	3.32	2.64E-26	2.24E-24
4608	MYBPH	myosin binding protein H	10.33	13.67	3.31	3.43E-24	1.83E-22
348	APOE	apolipoprotein E	8.77	12.09	3.30	1.54E-24	8.80E-23
7296	TXNRD1	thioredoxin reductase 1	8.63	11.94	3.29	4.37E-24	2.28E-22
7857	SCG2	secretogranin II	6.63	9.92	3.29	7.33E-25	4.49E-23
22809	ATF5	activating transcription factor 5	8.39	11.68	3.28	9.22E-20	2.03E-18
6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	7.24	10.53	3.28	7.49E-26	5.58E-24
477	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	6.30	9.53	3.23	9.79E-28	1.22E-25
22924	MAPRE3	microtubule-associated protein, RP/EB family, member 3	6.95	10.18	3.23	1.46E-23	6.72E-22
157285	SGK223	homolog of rat pragma of Rnd2	7.50	10.68	3.18	3.06E-26	2.57E-24
64115	C10orf54	chromosome 10 open reading frame 54	6.43	9.60	3.17	3.56E-22	1.27E-20
1601	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	8.06	11.19	3.15	9.58E-26	7.02E-24
389827	TMEM8C	transmembrane protein 8C	7.95	11.09	3.14	1.30E-25	9.13E-24
80144	FRAS1	Fraser syndrome 1	6.64	9.75	3.11	5.40E-21	1.50E-19

3270	HRC	histidine rich calcium binding protein	8.99	12.10	3.11	3.17E-26	2.62E-24
88	ACTN2	actinin, alpha 2	7.08	10.18	3.10	1.25E-23	5.90E-22
81493	SYNC	syncoilin, intermediate filament protein	6.76	9.79	3.03	1.92E-23	8.67E-22
55034	MOCOS	molybdenum cofactor sulfurase	6.62	9.64	3.03	1.90E-21	5.78E-20
29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	7.09	10.09	3.00	1.16E-25	8.23E-24
10079	ATP9A	ATPase, class II, type 9A	6.98	9.98	2.99	1.22E-25	8.59E-24
83937	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	7.53	10.50	2.98	4.48E-25	2.84E-23
256691	MAMDC2	MAM domain containing 2	9.50	12.46	2.95	8.79E-22	2.92E-20
782	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	6.49	9.42	2.94	7.45E-25	4.55E-23
2634	GBP2	guanylate binding protein 2, interferon-inducible	6.63	9.55	2.93	7.54E-25	4.59E-23
54937	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	6.68	9.61	2.93	2.16E-22	7.99E-21
166336	PRICKLE2	prickle homolog 2 (Drosophila)	7.12	10.05	2.92	1.78E-25	1.22E-23
84617	TUBB6	tubulin, beta 6	9.27	12.21	2.92	7.18E-23	2.89E-21
94241	TP53INP1	tumor protein p53 inducible nuclear protein 1	8.02	10.93	2.91	3.60E-22	1.28E-20
861	RUNX1	runt-related transcription factor 1	7.62	10.51	2.89	8.31E-26	6.14E-24
5730	PTGDS	prostaglandin D2 synthase 21kDa (brain)	7.72	10.61	2.89	8.76E-25	5.26E-23
7111	TMOD1	tropomodulin 1	7.45	10.32	2.87	3.11E-26	2.58E-24
57571	CARNS1	carnosine synthase 1	6.44	9.29	2.84	3.35E-22	1.20E-20
30061	SLC40	solute carrier family	7.20	10.03	2.83	1.14E-	6.69

	A1	40 (iron-regulated transporter), member 1				24	E-23
9915	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	6.48	9.30	2.82	6.13E-22	2.09E-20
414325	DEFB103A	defensin, beta 103A	6.60	9.41	2.81	6.25E-19	1.15E-17
2348	FOLR1	folate receptor 1 (adult)	7.48	10.29	2.81	7.52E-26	5.58E-24
22882	ZHX2	zinc fingers and homeoboxes 2	6.64	9.45	2.81	2.79E-24	1.51E-22
79933	SYNPO2L	synaptopodin 2-like	7.79	10.59	2.80	5.29E-23	2.19E-21
10611	PDLIM5	PDZ and LIM domain 5	7.41	10.21	2.79	1.84E-24	1.03E-22
5997	RGS2	regulator of G-protein signaling 2, 24kDa	7.88	10.67	2.79	2.65E-24	1.44E-22
22801	ITGA11	integrin, alpha 11	7.06	9.85	2.78	3.60E-21	1.04E-19
28227	PPP2R3B	protein phosphatase 2, regulatory subunit B", beta	7.08	9.84	2.76	4.24E-23	1.79E-21
55608	ANKRD10	ankyrin repeat domain 10	7.48	10.23	2.75	7.00E-23	2.84E-21
26137	ZBTB20	zinc finger and BTB domain containing 20	6.79	9.53	2.73	9.50E-18	1.46E-16
8611	PPAP2A	phosphatidic acid phosphatase type 2A	7.58	10.28	2.71	8.86E-23	3.47E-21
4656	MYOG	myogenin (myogenic factor 4)	9.36	12.06	2.69	1.22E-22	4.70E-21
90441	ZNF622	zinc finger protein 622	9.69	12.38	2.68	1.05E-23	5.01E-22
1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	12.04	14.72	2.68	5.67E-25	3.53E-23
10630	PDPN	podoplanin	6.65	9.33	2.68	2.98E-22	1.08E-20
57159	TRIM54	tripartite motif containing 54	6.50	9.15	2.65	9.12E-24	4.39E-22
9201	DCLK1	doublecortin-like kinase 1	6.86	9.51	2.65	1.44E-23	6.66E-22
5412	UBL3	ubiquitin-like 3	7.87	10.51	2.65	3.49E-25	2.28E-23
400818	NBPF9	neuroblastoma breakpoint family, member 9	10.25	12.88	2.63	3.00E-15	2.96E-14

5269	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	10.52	13.16	2.63	7.48E-24	3.69E-22
8140	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	10.15	12.76	2.60	3.09E-22	1.12E-20
389136	VGLL3	vestigial like 3 (Drosophila)	7.15	9.74	2.59	1.40E-21	4.45E-20
9499	MYOT	myotilin	6.30	8.90	2.59	4.07E-22	1.43E-20
114299	PALM2	paralemmin 2	7.71	10.27	2.57	6.43E-23	2.62E-21
84886	C1orf198	chromosome 1 open reading frame 198	8.84	11.42	2.57	2.46E-23	1.09E-21
100132406	NBPF10	neuroblastoma breakpoint family, member 10	10.32	12.89	2.57	1.46E-14	1.30E-13
7102	TSPAN7	tetraspanin 7	7.27	9.84	2.56	1.64E-22	6.17E-21
7421	VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor	6.55	9.11	2.56	8.86E-24	4.28E-22
11341	SCRG1	stimulator of chondrogenesis 1	6.42	8.98	2.56	9.18E-22	3.05E-20
160622	GRASP	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	6.99	9.55	2.56	3.69E-22	1.31E-20
165904	XIRP1	xin actin-binding repeat containing 1	6.37	8.93	2.56	8.60E-21	2.30E-19
131377	KBTBD5	kelch repeat and BTB (POZ) domain containing 5	7.24	9.80	2.56	4.00E-20	9.41E-19
144165	PRICKLE1	prickle homolog 1 (Drosophila)	6.81	9.37	2.55	1.24E-23	5.83E-22
11155	LDB3	LIM domain binding 3	6.71	9.25	2.54	4.04E-19	7.80E-18
677800	SNORA12	small nucleolar RNA, H/ACA box 12	6.77	9.31	2.53	6.35E-23	2.59E-21
4320	MMP11	matrix metallopeptidase 11 (stromelysin 3)	9.36	11.90	2.52	4.34E-22	1.51E-20
6345	SRL	sarcalumenin	9.08	11.61	2.52	7.92E-	3.88

						24	E-22
8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	7.94	10.45	2.51	3.36E-21	9.76E-20
23095	KIF1B	kinesin family member 1B	8.22	10.71	2.50	2.91E-20	7.00E-19
127294	MYOM3	myomesin family, member 3	7.25	9.76	2.50	8.63E-23	3.39E-21
9260	PDLIM7	PDZ and LIM domain 7 (enigma)	10.46	12.96	2.50	3.34E-24	1.80E-22
51339	DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	6.55	9.04	2.49	3.37E-21	9.76E-20
4199	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	7.11	9.59	2.48	3.85E-22	1.36E-20
10443	N4BP2L2	NEDD4 binding protein 2-like 2	7.12	9.59	2.47	1.06E-23	5.04E-22
2889	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	9.91	12.38	2.47	1.79E-22	6.70E-21
59285	CACNG6	calcium channel, voltage-dependent, gamma subunit 6	7.19	9.64	2.45	5.86E-21	1.61E-19
8365	HIST1H4H	histone cluster 1, H4h	6.93	9.38	2.44	1.21E-21	3.90E-20
7164	TPD52L1	tumor protein D52-like 1	6.75	9.18	2.43	5.05E-21	1.41E-19
25798	BRI3	brain protein I3	9.83	12.27	2.43	9.09E-23	3.55E-21
7125	TNNC2	troponin C type 2 (fast)	9.99	12.43	2.42	8.20E-22	2.75E-20
1028	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	7.40	9.82	2.41	1.73E-19	3.59E-18
10930	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	8.37	10.80	2.41	2.23E-20	5.57E-19
4130	MAP1A	microtubule-associated protein 1A	8.66	11.07	2.41	1.46E-21	4.61E-20
207107	SFTA1P	surfactant associated 1 (pseudogene)	9.31	11.72	2.40	1.77E-21	5.46E-20
4861	NPAS1	neuronal PAS domain protein 1	6.80	9.20	2.40	1.06E-21	3.46E-20

5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	8.03	10.42	2.39	6.82E-19	1.25E-17
10966	RAB40B	RAB40B, member RAS oncogene family	8.61	10.99	2.39	4.79E-21	1.34E-19
84075	FSCB	fibrous sheath CABYR binding protein	6.49	8.86	2.37	1.63E-19	3.41E-18
51706	CYB5R1	cytochrome b5 reductase 1	9.99	12.35	2.36	5.52E-22	1.89E-20
100133941	CD24	CD24 molecule	6.34	8.70	2.35	2.47E-21	7.34E-20
56999	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	6.35	8.70	2.35	1.24E-20	3.22E-19
377007	KLHL30	kelch-like 30 (Drosophila)	7.64	9.97	2.34	1.94E-20	4.89E-19
83445	GSG1	germ cell associated 1	6.37	8.70	2.34	1.72E-21	5.32E-20
2273	FHL1	four and a half LIM domains 1	8.37	10.68	2.31	8.33E-22	2.78E-20
5308	PITX2	paired-like homeodomain 2	8.28	10.59	2.31	3.99E-22	1.40E-20
51155	HN1	hematological and neurological expressed 1	9.04	11.34	2.30	1.20E-19	2.57E-18
148738	HFE2	hemochromatosis type 2 (juvenile)	7.72	10.01	2.29	1.07E-20	2.83E-19
23676	SMPX	small muscle protein, X-linked	8.19	10.47	2.28	5.86E-19	1.09E-17
604	BCL6	B-cell CLL/lymphoma 6	7.54	9.81	2.28	2.72E-23	1.18E-21
23612	PHLDA3	pleckstrin homology-like domain, family A, member 3	8.14	10.41	2.27	1.26E-21	4.04E-20
9839	ZEB2	zinc finger E-box binding homeobox 2	7.61	9.88	2.27	3.34E-18	5.50E-17
6520	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	9.28	11.54	2.27	1.35E-17	2.00E-16
4134	MAP4	microtubule-associated protein 4	7.38	9.64	2.26	1.48E-18	2.58E-17
162394	SLFN5	schlafen family member 5	6.87	9.13	2.25	1.45E-17	2.14E-16

23066	CAND2	cullin-associated and neddylation-dissociated 2 (putative)	6.92	9.17	2.25	2.51E-20	6.18E-19
6664	SOX11	SRY (sex determining region Y)-box 11	9.88	12.14	2.25	2.34E-20	5.80E-19
12	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	6.57	8.80	2.23	3.09E-19	6.14E-18
1837	DTNA	dystrobrevin, alpha	8.29	10.49	2.22	5.86E-20	1.32E-18
6249	CLIP1	CAP-GLY domain containing linker protein 1	7.41	9.62	2.22	8.99E-18	1.39E-16
23596	OPN3	opsin 3	7.20	9.41	2.21	2.47E-21	7.34E-20
224	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	7.88	10.09	2.21	8.50E-21	2.28E-19
10231	RCAN2	regulator of calcineurin 2	7.14	9.35	2.20	5.87E-21	1.61E-19
8821	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	8.53	10.72	2.19	3.46E-18	5.68E-17
22982	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	7.26	9.45	2.18	1.93E-19	3.99E-18
255488	RNF144B	ring finger protein 144B	6.34	8.52	2.18	7.08E-22	2.39E-20
222166	C7orf41	chromosome 7 open reading frame 41	10.36	12.52	2.17	5.31E-20	1.21E-18
10133	OPTN	optineurin	7.50	9.65	2.17	3.69E-21	1.06E-19
113146	AHNAK2	AHNAK nucleoprotein 2	6.99	9.14	2.15	4.14E-15	4.00E-14
53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	6.32	8.46	2.14	1.50E-21	4.73E-20
115207	KCTD12	potassium channel tetramerisation domain containing 12	7.70	9.83	2.13	6.22E-20	1.39E-18
51313	FAM198B	family with sequence similarity 198,	6.93	9.05	2.12	2.29E-20	5.69E-19

		member B					
113451	ADC	arginine decarboxylase	8.06	10.18	2.12	5.69E-22	1.94E-20
1109	AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	8.01	10.13	2.12	2.32E-21	6.96E-20
23645	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	9.29	11.40	2.12	2.02E-20	5.04E-19
716	C1S	complement component 1, s subcomponent	6.60	8.71	2.11	2.21E-19	4.52E-18
3799	KIF5B	kinesin family member 5B	8.38	10.49	2.11	9.18E-20	2.02E-18
388551	CEACAM16	carcinoembryonic antigen-related cell adhesion molecule 16	6.82	8.93	2.11	1.19E-20	3.11E-19
29895	MYLPF	myosin light chain, phosphorylatable, fast skeletal muscle	12.45	14.56	2.11	2.44E-22	9.03E-21
84814	PPAPDC3	phosphatidic acid phosphatase type 2 domain containing 3	7.37	9.48	2.10	2.98E-22	1.08E-20
23564	DDAH2	dimethylarginine dimethylaminohydrolase 2	8.34	10.43	2.09	8.05E-21	2.17E-19
8326	FZD9	frizzled homolog 9 (Drosophila)	7.44	9.53	2.08	6.08E-21	1.67E-19
9236	CCPG1	cell cycle progression 1	7.58	9.65	2.08	4.40E-20	1.02E-18
66008	TRAK2	trafficking protein, kinesin binding 2	9.38	11.48	2.08	1.66E-18	2.87E-17
1917	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	8.19	10.27	2.07	1.34E-15	1.41E-14
734	OSGIN2	oxidative stress induced growth inhibitor family member 2	7.08	9.14	2.07	4.82E-20	1.11E-18
10217	CTDSPL	CTD (carboxy-terminal domain, RNA	9.05	11.10	2.06	7.12E-21	1.94E-19

		polymerase II, polypeptide A) small phosphatase-like					
440	ASNS	asparagine synthetase (glutamine-hydrolyzing)	11.11	13.17	2.06	7.85E-17	1.01E-15
11149	BVES	blood vessel epicardial substance	6.33	8.39	2.05	3.34E-19	6.58E-18
10124	ARL4A	ADP-ribosylation factor-like 4A	8.47	10.51	2.05	4.94E-20	1.14E-18
1545	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	6.53	8.58	2.04	2.69E-17	3.81E-16
1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	6.58	8.61	2.03	2.75E-20	6.70E-19
130827	TMEM182	transmembrane protein 182	6.73	8.76	2.03	5.05E-19	9.56E-18
6444	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	7.95	9.98	2.03	3.74E-15	3.65E-14
79156	PLEKHF1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	7.14	9.17	2.03	1.46E-18	2.55E-17
7273	TTN	titin	6.33	8.36	2.02	5.49E-17	7.27E-16
3418	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	9.25	11.26	2.02	4.30E-20	1.00E-18
4088	SMAD3	SMAD family member 3	8.92	10.92	2.00	3.77E-19	7.31E-18
6450	SH3BGR	SH3 domain binding glutamic acid-rich protein	6.89	8.88	1.99	4.53E-17	6.08E-16
114907	FBXO32	F-box protein 32	8.28	10.27	1.99	1.18E-16	1.46E-15
57761	TRIB3	tribbles homolog 3 (Drosophila)	8.79	10.79	1.99	1.75E-09	7.10E-09
715	C1R	complement component 1, r subcomponent	6.80	8.79	1.99	2.59E-16	3.04E-15
8707	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-	7.08	9.07	1.99	9.81E-19	1.76E-17

		galactosyltransferase, polypeptide 2					
779	CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S subunit	6.96	8.94	1.98	4.78E-17	6.37E-16
84940	CORO6	coronin 6	7.33	9.31	1.97	2.76E-17	3.89E-16
7707	ZNF148	zinc finger protein 148	8.24	10.20	1.97	1.17E-19	2.51E-18
4205	MEF2A	myocyte enhancer factor 2A	7.12	9.09	1.96	9.47E-20	2.08E-18
8975	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	7.73	9.68	1.96	1.43E-18	2.51E-17
55573	CDV3	CDV3 homolog (mouse)	9.65	11.62	1.96	1.86E-20	4.70E-19
7145	TNS1	tensin 1	7.59	9.54	1.96	1.63E-18	2.83E-17
3655	ITGA6	integrin, alpha 6	7.00	8.96	1.95	5.04E-19	9.56E-18
144363	LYRM5	LYR motif containing 5	8.51	10.45	1.94	7.74E-19	1.41E-17
9770	RASSF2	Ras association (RalGDS/AF-6) domain family member 2	6.82	8.76	1.94	1.56E-17	2.30E-16
1674	DES	desmin	10.17	12.12	1.94	2.61E-20	6.39E-19
26512	INTS6	integrator complex subunit 6	6.79	8.73	1.93	1.19E-16	1.47E-15
84216	TMEM117	transmembrane protein 117	6.89	8.82	1.93	1.87E-19	3.87E-18
8908	GYG2	glycogenin 2	7.97	9.90	1.93	6.06E-20	1.36E-18
8878	SQSTM1	sequestosome 1	11.72	13.65	1.92	4.16E-19	8.01E-18
9518	GDF15	growth differentiation factor 15	8.85	10.78	1.92	1.16E-15	1.23E-14
1400	CRMP1	collapsin response mediator protein 1	9.19	11.11	1.92	2.00E-19	4.12E-18
166614	DCLK2	doublecortin-like kinase 2	6.18	8.09	1.92	3.60E-19	6.99E-18
140465	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle	12.47	14.38	1.91	2.27E-21	6.85E-20

1301	COL11A1	collagen, type XI, alpha 1	8.65	10.55	1.90	3.98E-17	5.43E-16
10962	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	11.02	12.92	1.89	4.54E-21	1.27E-19
122809	SOCS4	suppressor of cytokine signaling 4	6.68	8.58	1.89	3.73E-20	8.82E-19
23499	MACF1	microtubule-actin crosslinking factor 1	9.25	11.14	1.89	2.81E-12	1.72E-11
23630	KCNE1L	KCNE1-like	6.45	8.33	1.88	9.58E-18	1.47E-16
1512	CTSH	cathepsin H	7.45	9.33	1.87	6.78E-18	1.07E-16
1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	7.83	9.69	1.87	1.52E-19	3.19E-18
5106	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	8.75	10.62	1.87	9.70E-14	7.49E-13
6286	S100P	S100 calcium binding protein P	6.51	8.39	1.86	3.86E-12	2.31E-11
140825	NEURL2	neuralized homolog 2 (Drosophila)	7.16	9.02	1.86	1.32E-17	1.97E-16
6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	8.16	10.02	1.85	2.35E-13	1.71E-12
8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	7.87	9.72	1.85	2.17E-16	2.59E-15
151126	ZNF385B	zinc finger protein 385B	6.54	8.40	1.85	5.35E-18	8.56E-17
5361	PLXNA1	plexin A1	8.05	9.90	1.85	1.01E-19	2.21E-18
23294	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	9.61	11.47	1.85	1.39E-19	2.95E-18
94134	ARHGAP12	Rho GTPase activating protein 12	7.66	9.48	1.83	1.36E-18	2.39E-17
54507	ADAMTSL4	ADAMTS-like 4	7.02	8.84	1.83	1.70E-19	3.55E-18
56997	ADCK3	aarF domain containing kinase 3	8.17	10.00	1.83	7.29E-19	1.33E-17
54843	SYTL2	synaptotagmin-like 2	7.99	9.81	1.82	5.46E-18	8.73E-17

3759	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	6.42	8.23	1.81	1.29E-17	1.93 E-16
836	CASP3	caspase 3, apoptosis-related cysteine peptidase	9.92	11.73	1.81	2.08E-19	4.27 E-18
55615	PRR5	proline rich 5 (renal)	9.18	10.99	1.81	7.78E-18	1.21 E-16
5348	FXYD1	FXYD domain containing ion transport regulator 1	6.69	8.50	1.81	1.13E-17	1.70 E-16
26576	SRPK3	SRSF protein kinase 3	7.92	9.73	1.80	2.39E-18	4.03 E-17
1573	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	6.54	8.34	1.80	6.83E-20	1.52 E-18
9209	LRRFIP 2	leucine rich repeat (in FLII) interacting protein 2	6.28	8.09	1.80	1.61E-17	2.36 E-16
8522	GAS7	growth arrest-specific 7	6.29	8.09	1.79	6.16E-18	9.80 E-17
27231	ITGB1B P3	integrin beta 1 binding protein 3	6.37	8.17	1.79	8.88E-17	1.13 E-15
4779	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	9.33	11.11	1.78	2.86E-19	5.75 E-18
23077	MYCBP 2	MYC binding protein 2	7.05	8.83	1.78	4.47E-15	4.30 E-14
56937	PMEPA 1	prostate transmembrane protein, androgen induced 1	9.04	10.82	1.78	1.75E-19	3.64 E-18
51400	PPME1	protein phosphatase methylesterase 1	10.14	11.91	1.77	2.62E-17	3.72 E-16
10464	PIBF1	progesterone immunomodulatory binding factor 1	7.00	8.77	1.77	7.55E-18	1.18 E-16
29948	OSGIN 1	oxidative stress induced growth inhibitor 1	8.34	10.10	1.75	1.31E-13	9.92 E-13
81603	TRIM8	tripartite motif containing 8	10.48	12.24	1.75	1.20E-20	3.13 E-19
60370	AVPI1	arginine vasopressin-induced 1	9.19	10.94	1.75	3.62E-18	5.93 E-17
3898	LAD1	ladinin 1	7.34	9.09	1.74	1.52E-17	2.23 E-16

98	ACYP2	acylphosphatase 2, muscle type	8.07	9.81	1.74	1.54E-18	2.68E-17
10193	RNF41	ring finger protein 41	8.26	9.99	1.74	5.03E-19	9.56E-18
6261	RYR1	ryanodine receptor 1 (skeletal)	8.69	10.42	1.74	3.76E-17	5.16E-16
2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	8.60	10.33	1.74	4.42E-18	7.13E-17
4060	LUM	lumican	8.23	9.96	1.73	1.04E-16	1.31E-15
11278	KLF12	Kruppel-like factor 12	7.23	8.96	1.72	4.74E-17	6.33E-16
221914	GPC2	glypican 2	9.01	10.72	1.72	1.42E-16	1.75E-15
8780	RIOK3	RIO kinase 3 (yeast)	9.73	11.45	1.71	2.36E-19	4.81E-18
1842	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	6.31	8.02	1.71	2.42E-15	2.43E-14
10184	LHFPL2	lipoma HMGIC fusion partner-like 2	8.55	10.25	1.70	1.18E-17	1.77E-16
6445	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	6.34	8.04	1.70	3.86E-17	5.28E-16
84676	TRIM63	tripartite motif containing 63	6.83	8.53	1.70	6.21E-14	4.97E-13
55508	SLC35E3	solute carrier family 35, member E3	8.28	9.97	1.69	1.42E-19	2.99E-18
56940	DUSP22	dual specificity phosphatase 22	8.25	9.94	1.69	7.31E-16	8.00E-15
63908	NAPB	N-ethylmaleimide-sensitive factor attachment protein, beta	7.62	9.31	1.69	1.96E-17	2.83E-16
23588	KLHDC2	kelch domain containing 2	9.55	11.23	1.69	1.41E-16	1.73E-15
84561	SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	6.93	8.62	1.68	9.70E-17	1.22E-15

1993	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	6.50	8.18	1.68	1.25E-17	1.86E-16
10600	USP16	ubiquitin specific peptidase 16	6.68	8.36	1.68	5.81E-17	7.67E-16
64397	ZFP106	zinc finger protein 106 homolog (mouse)	11.35	13.04	1.68	7.99E-14	6.26E-13
219771	CCNY	cyclin Y	8.82	10.49	1.67	9.79E-18	1.50E-16
53346	TM6SF1	transmembrane 6 superfamily member 1	6.64	8.31	1.66	1.64E-12	1.04E-11
81544	GDPD5	glycerophosphodiester phosphodiesterase domain containing 5	7.37	9.04	1.66	4.21E-18	6.80E-17
80232	WDR26	WD repeat domain 26	7.75	9.41	1.66	8.86E-18	1.37E-16
9873	FCHSD2	FCH and double SH3 domains 2	7.56	9.21	1.66	1.68E-15	1.73E-14
56961	SHD	Src homology 2 domain containing transforming protein D	9.67	11.32	1.65	1.03E-18	1.83E-17
1756	DMD	dystrophin	6.52	8.17	1.65	3.45E-17	4.79E-16
9127	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	7.49	9.13	1.65	1.00E-15	1.07E-14
10580	SORBS1	sorbin and SH3 domain containing 1	6.66	8.30	1.64	5.16E-18	8.28E-17
57158	JPH2	junctophilin 2	7.76	9.38	1.61	3.90E-15	3.79E-14
127495	LRRC39	leucine rich repeat containing 39	6.43	8.03	1.61	1.42E-15	1.49E-14
2318	FLNC	filamin C, gamma	11.90	13.50	1.60	4.97E-14	4.02E-13
388403	YPEL2	yippee-like 2 (Drosophila)	6.87	8.47	1.60	2.63E-16	3.07E-15
54749	EPDR1	ependymin related protein 1 (zebrafish)	10.17	11.76	1.59	3.79E-18	6.20E-17
274	BIN1	bridging integrator 1	11.98	13.35	1.37	4.15E-15	4.01E-14

[a] RD Mean lists the mean value from three biologically independent RD RNA samples from RD cells infected with a GFP-expressing lentivirus and placed in differentiation media for 72 h.

[b] Myotube Mean lists the mean value from three biologically independent primary human myotube RNA samples grown to confluency and placed in differentiation media for 72 h.

[c] Fold change represents the difference between the myotube and RD values and is a log2 value.

Supplemental Table S3. Upregulated myogenic genes expressed at comparable levels in RD cells.

Entrez ID	Symbol	Gene Name	RD value[a]	Myotube value[b]	Fold change[c]	p-value	FDR
3983	ABLIM1	actin binding LIM protein 1	8.63	8.35	-0.29	0.0123	0.0189
31	ACACA	acetyl-CoA carboxylase alpha	9.51	9.28	-0.24	0.0283	0.0409
116987	AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	9.70	9.58	-0.12	0.2123	0.2585
204	AK2	adenylate kinase 2	11.46	11.94	0.47	1.57E-05	3.66E-05
57679	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	9.69	9.93	0.23	0.0140	0.0212
351	APP	amyloid beta (A4) precursor protein	11.76	10.99	-0.77	8.31E-08	2.66E-07
10513	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	9.45	9.97	0.52	2.75E-07	8.15E-07
80728	ARHGAP39	Rho GTPase activating protein 39	8.57	8.66	0.10	0.2463	0.2958
55616	ASAP3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	9.67	10.19	0.52	7.13E-06	1.74E-05
26053	AUTS2	autism susceptibility candidate 2	9.62	10.14	0.52	3.20E-06	8.21E-06
10904	BLCAP	bladder cancer associated protein	11.10	10.67	-0.43	5.68E-05	0.0001
8019	BRD3	bromodomain containing 3	10.43	10.49	0.06	0.6285	0.6782
119032	C10orf32	chromosome 10 open reading frame 32	8.94	9.22	0.28	0.0019	0.0033
119710	C11orf74	chromosome 11 open reading frame 74	10.37	10.66	0.28	0.0033	0.0056
112752	C14orf179	chromosome 14 open reading frame 179	9.54	9.92	0.37	0.0005	0.0009
56911	C21orf7	chromosome 21 open reading frame 7	12.63	12.60	-0.02	0.7984	0.8298
50854	C6orf48	chromosome 6 open reading frame 48	7.26	6.97	-0.31	0.0064	0.0102
157922	CAMSAP1	calmodulin regulated spectrin-associated protein 1	8.86	9.39	0.53	9.25E-07	2.56E-06

54897	CASZ1	castor zinc finger 1	6.91	7.46	0.56	7.10E-07	1.99E-06
868	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	9.90	10.05	0.14	0.2172	0.2639
875	CBS	cystathionine-beta-synthase	9.97	10.32	0.36	0.0038	0.0062
29903	CCDC106	coiled-coil domain containing 106	9.11	9.45	0.34	0.0018	0.0031
83643	CCDC3	coiled-coil domain containing 3	9.76	9.37	-0.39	0.0005	0.0010
8555	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	8.82	9.16	0.33	0.0016	0.0028
400916	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	10.59	10.99	0.39	8.76E-05	0.0002
1108	CHD4	chromodomain helicase DNA binding protein 4	10.11	9.93	-0.18	0.0678	0.0914
80205	CHD9	chromodomain helicase DNA binding protein 9	10.38	10.14	-0.24	0.0794	0.1057
1134	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	13.16	12.67	-0.48	1.92E-05	4.44E-05
23332	CLASP1	cytoplasmic linker associated protein 1	9.42	9.55	0.13	0.1733	0.2152
1185	CLCN6	chloride channel 6	8.42	8.66	0.22	0.0612	0.0833
80790	CMIP	c-Maf-inducing protein	11.05	11.21	0.17	0.0584	0.0797
1307	COL16A1	collagen, type XVI, alpha 1	9.82	9.84	0.02	0.8152	0.8436
404217	CTXN1	cortexin 1	10.08	10.61	0.53	2.75E-06	7.10E-06
1523	CUX1	cut-like homeobox 1	8.48	8.78	0.30	0.0162	0.0245
51523	CXXC5	CXXC finger protein 5	12.43	13.21	0.77	2.48E-09	9.86E-09
147906	DACT3	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	8.68	8.34	-0.35	0.0025	0.0043
1605	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	11.09	10.74	-0.34	0.0006	0.0010
1612	DAPK1	death-associated protein kinase 1	9.04	8.57	-0.47	3.02E-05	6.80E-05

79007	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	10.83	10.36	-0.48	7.80E-06	1.89E-05
1629	DBT	dihydrolipoamide branched chain transacylase E2	9.72	10.20	0.48	4.77E-06	1.20E-05
167227	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	9.76	9.91	0.15	0.1720	0.2138
160518	DENND5B	DENN/MADD domain containing 5B	8.36	8.69	0.33	0.0024	0.0041
8527	DGKD	diacylglycerol kinase, delta 130kDa	8.85	8.64	-0.22	0.0263	0.0382
57609	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	9.12	9.23	0.11	0.3241	0.3783
28514	DLL1	delta-like 1 (Drosophila)	9.00	9.56	0.56	9.42E-06	2.26E-05
285193	DUSP28	dual specificity phosphatase 28	9.30	9.59	0.29	0.0034	0.0057
23644	EDC4	enhancer of mRNA decapping 4	9.85	10.19	0.35	0.0015	0.0027
2065	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	6.98	7.57	0.59	1.54E-07	4.75E-07
51466	EVL	Enah/Vasp-like	11.67	11.57	-0.10	0.2122	0.2584
3992	FADS1	fatty acid desaturase 1	10.36	10.81	0.45	0.0008	0.0014
9750	FAM65B	family with sequence similarity 65, member B	8.46	8.94	0.48	0.0002	0.0003
2222	FDFT1	farnesyl-diphosphate farnesyltransferase 1	10.07	10.34	0.26	0.0221	0.0325
23048	FNBP1	formin binding protein 1	10.08	10.19	0.10	0.3056	0.3586
252995	FNDC5	fibronectin type III domain containing 5	12.44	11.99	-0.47	0.0005	0.0009
96459	FNIP1	folliculin interacting protein 1	8.58	9.14	0.57	2.45E-06	6.39E-06
221937	FOXK1	forkhead box K1	9.49	9.81	0.32	0.0114	0.0175
4303	FOXO4	forkhead box O4	9.31	9.41	0.10	0.3171	0.3708
8087	FXR1	fragile X mental retardation, autosomal homolog 1	10.74	12.27	1.51	5.41E-16	6.06E-15
10912	GADD45	growth arrest and	9.37	9.56	0.19	0.0927	0.1216

	G	DNA-damage-inducible, gamma					
352954	GATS	GATS, stromal antigen 3 opposite strand	9.03	8.60	-0.43	2.18E-05	5.02E-05
23062	GGA2	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	9.08	8.83	-0.24	0.0098	0.0153
2805	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	10.56	11.09	0.54	7.16E-06	1.75E-05
84706	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	10.23	10.45	0.21	0.1100	0.1422
3017	HIST1H2BD	histone cluster 1, H2bd	8.13	7.50	-0.63	1.67E-06	4.46E-06
3125	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	9.70	9.34	-0.36	0.0012	0.0021
3157	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	10.96	11.47	0.51	0.0094	0.0146
3376	IARS	isoleucyl-tRNA synthetase	10.99	11.26	0.27	0.0187	0.0279
57722	IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	8.18	7.99	-0.18	0.0841	0.1113
27190	IL17B	interleukin 17B	7.63	7.95	0.32	0.0072	0.0114
3636	INPPL1	inositol polyphosphate phosphatase-like 1	10.71	11.12	0.40	0.0004	0.0007
3689	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	9.52	9.22	-0.30	0.0199	0.0295
3720	JARID2	jumonji, AT rich interactive domain 2	8.86	9.13	0.26	0.0043	0.0071
56704	JPH1	junctophilin 1	8.43	8.15	-0.28	0.0059	0.0095
10324	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	10.99	12.22	1.23	4.24E-14	3.48E-13
10765	KDM5B	lysine (K)-specific demethylase 5B	9.83	9.80	-0.03	0.7966	0.8283
23095	KIF1B	kinesin family	8.22	10.71	2.50	2.91E-	7.00E-

		member 1B				20	19
51621	KLF13	Kruppel-like factor 13	9.58	9.93	0.34	0.0043	0.0071
116138	KLHDC3	kelch domain containing 3	11.66	12.05	0.40	6.48E-05	0.0001
79412	KREMEN2	kringle containing transmembrane protein 2	8.99	9.18	0.19	0.0921	0.1209
3908	LAMA2	laminin, alpha 2	8.35	9.10	0.75	3.65E-08	1.23E-07
3911	LAMA5	laminin, alpha 5	11.42	11.19	-0.22	0.0449	0.0627
9215	LARGE	like-glycosyltransferase	8.91	8.20	-0.72	8.04E-06	1.95E-05
253782	LASS6	LAG1 homolog, ceramide synthase 6	10.83	10.56	-0.28	0.0171	0.0257
29995	LMCD1	LIM and cysteine-rich domains 1	10.23	10.10	-0.13	0.2141	0.2605
9361	LONP1	lon peptidase 1, mitochondrial	10.44	10.43	-0.01	0.9353	0.9467
26018	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	8.85	7.95	-0.89	2.35E-11	1.25E-10
55227	LRRC1	leucine rich repeat containing 1	8.90	9.07	0.17	0.0919	0.1207
28992	MACROD1	MACRO domain containing 1	9.15	9.37	0.22	0.0216	0.0318
84557	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	11.66	11.35	-0.30	0.0017	0.0030
4155	MBP	myelin basic protein	6.93	7.19	0.27	0.0235	0.0344
389538	MGC72080	MGC72080 pseudogene	8.80	9.15	0.35	0.0013	0.0024
64112	MOAP1	modulator of apoptosis 1	9.28	9.58	0.31	0.0010	0.0019
9242	MSC	musculin	9.74	9.79	0.07	0.5400	0.5950
84939	MUM1	melanoma associated antigen (mutated) 1	10.38	10.14	-0.25	0.0126	0.0192
4684	NCAM1	neural cell adhesion molecule 1	7.24	8.70	1.46	4.01E-14	3.30E-13
8648	NCOA1	nuclear receptor coactivator 1	9.68	9.79	0.12	0.1937	0.2378
114915	NCRNA00219	non-protein coding RNA 219	10.90	10.68	-0.22	0.0201	0.0298
441951	NCRNA00275	non-protein coding RNA 275	13.05	12.91	-0.14	0.0927	0.1217
63941	NECAB3	N-terminal EF-hand calcium binding	8.12	8.24	0.11	0.3892	0.4458

		protein 3					
4854	NOTCH3	notch 3	9.46	9.26	-0.20	0.0332	0.0475
10577	NPC2	Niemann-Pick disease, type C2	12.46	12.48	0.03	0.7746	0.8085
55714	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)	10.91	10.74	-0.17	0.1366	0.1734
114876	OSBPL1A	oxysterol binding protein-like 1A	9.22	9.73	0.51	2.42E-06	6.31E-06
54510	PCDH18	protocadherin 18	8.34	8.86	0.52	9.95E-05	0.0002
5108	PCM1	pericentriolar material 1	9.57	10.15	0.58	1.96E-06	5.16E-06
79605	PGBD5	piggyBac transposable element derived 5	8.55	8.93	0.38	0.0013	0.0023
26227	PHGDH	phosphoglycerate dehydrogenase	13.12	12.95	-0.17	0.0848	0.1121
8544	PIR	pirin (iron-binding nuclear protein)	8.42	9.12	0.70	7.48E-08	2.41E-07
91461	PKDCC	protein kinase domain containing, cytoplasmic homolog (mouse)	8.44	7.63	-0.81	2.03E-09	8.19E-09
63876	PKNOX2	PBX/knotted 1 homeobox 2	9.63	9.24	-0.39	0.0002	0.0004
11145	PLA2G16	phospholipase A2, group XVI	7.14	7.71	0.57	5.34E-05	0.0001
59338	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	8.70	9.42	0.72	2.62E-09	1.04E-08
55228	PNMAL1	PNMA-like 1	9.48	9.84	0.36	0.0010	0.0019
9581	PREPL	prolyl endopeptidase-like	8.05	8.73	0.67	1.82E-05	4.21E-05
29968	PSAT1	phosphoserine aminotransferase 1	10.99	11.18	0.21	0.1722	0.2141
9771	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	7.93	8.09	0.16	0.1870	0.2304
768211	RELL1	RELT-like 1	9.87	10.42	0.56	3.04E-05	6.84E-05
100008589	RN28S1	RNA, 28S ribosomal 1	11.51	10.89	-0.62	2.58E-05	5.87E-05

125050	RN7SK	RNA, 7SK small nuclear	6.65	7.38	0.72	1.02E-07	3.21E-07
7844	RNF103	ring finger protein 103	9.58	9.83	0.24	0.0255	0.0371
84268	RPAIN	RPA interacting protein	10.59	11.10	0.51	4.94E-06	1.23E-05
6167	RPL37	ribosomal protein L37	7.16	6.87	-0.30	0.0032	0.0053
58528	RRAGD	Ras-related GTP binding D	9.89	9.78	-0.11	0.3111	0.3645
23513	SCRIB	scribbled homolog (Drosophila)	9.79	10.34	0.55	5.58E-07	1.59E-06
10500	SEMA6C	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	8.59	8.49	-0.10	0.3651	0.4208
5413	SEPT5	septin 5	11.34	11.39	0.05	0.6564	0.7034
6442	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	10.62	10.83	0.20	0.0511	0.0706
6444	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	7.95	9.98	2.03	3.74E-15	3.65E-14
9644	SH3PXD2A	SH3 and PX domains 2A	11.34	11.33	-0.02	0.8446	0.8688
22933	SIRT2	sirtuin 2	8.37	8.63	0.25	0.0411	0.0577
51804	SIX4	SIX homeobox 4	10.29	9.78	-0.50	1.60E-06	4.27E-06
291	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	10.63	11.08	0.45	8.34E-05	0.0002
150572	SMYD1	SET and MYND domain containing 1	10.31	10.60	0.29	0.0163	0.0245
26010	SPATS2L	spermatogenesis associated, serine-rich 2-like	12.37	12.54	0.18	0.0711	0.0954
10253	SPRY2	sprouty homolog 2 (Drosophila)	10.82	10.64	-0.18	0.0997	0.1300
23380	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	8.32	8.06	-0.25	0.0194	0.0289
6774	STAT3	signal transducer and	9.62	9.67	0.06	0.5753	0.6289

		activator of transcription 3 (acute-phase response factor)					
10147	SUGP2	SURP and G patch domain containing 2	9.94	10.15	0.22	0.0179	0.0268
85461	TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	8.96	8.88	-0.07	0.4673	0.5245
6913	TBX15	T-box 15	9.25	8.85	-0.40	0.0008	0.0014
6938	TCF12	transcription factor 12	9.34	9.66	0.32	0.0030	0.0050
7043	TGFB3	transforming growth factor, beta 3	8.34	8.24	-0.11	0.2356	0.2841
7058	THBS2	thrombospondin 2	8.16	8.44	0.28	0.0040	0.0066
7078	TIMP3	TIMP metallopeptidase inhibitor 3	10.03	10.27	0.22	0.1623	0.2028
54972	TMEM132A	transmembrane protein 132A	9.71	9.70	0.01	0.9502	0.9596
374882	TMEM205	transmembrane protein 205	11.41	10.95	-0.46	2.07E-05	4.75E-05
55151	TMEM38B	transmembrane protein 38B	8.98	8.98	0.00	0.9790	0.9830
27242	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	10.57	10.30	-0.27	0.0055	0.0089
10188	TNK2	tyrosine kinase, non-receptor, 2	10.46	11.01	0.56	1.23E-06	3.35E-06
7136	TNNI2	troponin I type 2 (skeletal, fast)	8.41	8.79	0.38	0.0015	0.0027
23112	TNRC6B	trinucleotide repeat containing 6B	9.01	9.10	0.09	0.5619	0.6161
10043	TOM1	target of myb1 (chicken)	9.85	10.35	0.51	6.37E-06	1.57E-05
7158	TP53BP1	tumor protein p53 binding protein 1	9.42	9.89	0.47	3.38E-05	7.56E-05
79090	TRAPPC6A	trafficking protein particle complex 6A	8.59	9.15	0.57	7.02E-06	1.72E-05
83707	TRPT1	tRNA phosphotransferase 1	10.83	10.80	-0.05	0.5442	0.5990
56995	TULP4	tubby like protein 4	9.72	10.05	0.33	0.0170	0.0255
10628	TXNIP	thioredoxin interacting protein	12.25	12.11	-0.16	0.1428	0.1805
23352	UBR4	ubiquitin protein ligase E3 component n-recognin 4	8.96	9.12	0.16	0.2148	0.2614

245806	VGLL2	vestigial like 2 (Drosophila)	10.34	10.20	-0.14	0.3010	0.3537
65249	ZSWIM4	zinc finger, SWIM-type containing 4	9.63	9.32	-0.31	0.0047	0.0077

[a] RD value lists the mean value from three biologically independent RD RNA samples from RD cells infected with a GFP-expressing lentivirus and placed in differentiation media for 72 h.

[b] Myotube value lists the mean value from three biologically independent primary human myotube RNA samples grown to confluency and placed in differentiation media for 72 h.

[c] Fold change represents the difference between the myotube and RD values and is a log2 value.

Supplemental Table S4. Downregulated myogenic genes that are expressed at higher levels in RD cells.

Entrez ID	Symbol	Gene Name	RD value[a]	Myotube value[b]	Fold change[c]	p-value	FDR
11065	UBE2C	ubiquitin-conjugating enzyme E2C	12.45	6.58	-5.86	4.71 E-34	3.33 E-31
9768	KIAA0101	KIAA0101	12.07	6.46	-5.61	3.20 E-36	3.53 E-33
991	CDC20	cell division cycle 20 homolog (S. cerevisiae)	12.04	6.62	-5.41	7.24 E-34	4.74 E-31
26002	MOXD1	monooxygenase, DBH-like 1	11.43	6.68	-4.75	3.45 E-31	1.03 E-28
7153	TOP2A	topoisomerase (DNA) II alpha 170kDa	11.12	6.47	-4.64	1.50 E-31	5.01 E-29
9212	AURKB	aurora kinase B	10.52	6.40	-4.13	4.76 E-30	1.12 E-27
51203	NUSAP1	nucleolar and spindle associated protein 1	10.60	6.57	-4.02	2.20 E-29	4.36 E-27
51659	GINS2	GINS complex subunit 2 (Psf2 homolog)	11.60	7.60	-4.01	2.14 E-31	6.86 E-29
11013	TMSB15A	thymosin beta 15a	11.50	7.50	-3.99	9.27 E-28	1.18 E-25
81848	SPRY4	sprouty homolog 4 (Drosophila)	11.65	7.72	-3.93	6.35 E-30	1.42 E-27
1164	CKS2	CDC28 protein kinase regulatory subunit 2	11.88	8.00	-3.89	7.03 E-31	1.94 E-28
3833	KIFC1	kinesin family member C1	10.27	6.44	-3.82	5.10 E-29	9.29 E-27
113130	CDCA5	cell division cycle associated 5	10.66	6.96	-3.70	1.35 E-28	2.23 E-26
29028	ATAD2	ATPase family, AAA domain containing 2	10.33	6.71	-3.62	4.50 E-28	6.14 E-26
9232	PTTG1	pituitary tumor-transforming 1	11.98	8.37	-3.60	1.76 E-27	2.06 E-25
22974	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	10.36	6.79	-3.57	6.94 E-28	9.01 E-26
10112	KIF20A	kinesin family member 20A	10.20	6.66	-3.54	7.76 E-27	7.78 E-25
1870	E2F2	E2F transcription factor 2	10.26	6.74	-3.51	1.33 E-28	2.22 E-26
9133	CCNB2	cyclin B2	10.14	6.62	-3.51	2.37 E-28	3.55 E-26
81620	CDT1	chromatin licensing and DNA replication factor 1	9.88	6.38	-3.50	4.91 E-27	5.16 E-25

332	BIRC5	baculoviral IAP repeat containing 5	10.23	6.77	-3.47	3.96E-28	5.59E-26
55355	HJURP	Holliday junction recognition protein	9.98	6.51	-3.46	5.68E-27	5.93E-25
55143	CDCA8	cell division cycle associated 8	10.07	6.72	-3.36	5.19E-24	2.66E-22
50861	STMN3	stathmin-like 3	11.89	8.61	-3.29	3.98E-26	3.18E-24
6001	RGS10	regulator of G-protein signaling 10	11.04	7.76	-3.28	2.21E-26	1.94E-24
6502	SKP2	S-phase kinase-associated protein 2 (p45)	9.96	6.69	-3.26	2.39E-26	2.06E-24
89958	C9orf140	chromosome 9 open reading frame 140	9.87	6.60	-3.26	5.71E-23	2.35E-21
83879	CDCA7	cell division cycle associated 7	10.50	7.28	-3.23	1.62E-26	1.49E-24
84058	WDR54	WD repeat domain 54	11.94	8.75	-3.20	1.59E-24	8.99E-23
6790	AURKA	aurora kinase A	10.68	7.52	-3.17	9.41E-27	9.23E-25
147841	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	10.08	6.94	-3.15	1.41E-26	1.33E-24
150468	CKAP2L	cytoskeleton associated protein 2-like	9.45	6.32	-3.14	4.43E-28	6.12E-26
54478	FAM64A	family with sequence similarity 64, member A	9.89	6.76	-3.12	3.58E-25	2.31E-23
79019	CENPM	centromere protein M	9.56	6.45	-3.11	2.22E-26	1.94E-24
11004	KIF2C	kinesin family member 2C	9.76	6.71	-3.04	2.22E-25	1.49E-23
64151	NCAPG	non-SMC condensin I complex, subunit G	9.40	6.37	-3.04	2.64E-26	2.24E-24
7298	TYMS	thymidylate synthetase	11.09	8.07	-3.01	8.31E-24	4.05E-22
8318	CDC45	cell division cycle 45 homolog (S. cerevisiae)	9.44	6.43	-3.00	2.38E-25	1.59E-23
5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	10.47	7.49	-2.98	9.96E-26	7.24E-24
116028	C16orf75	chromosome 16 open reading frame 75	9.91	6.94	-2.98	1.48E-25	1.02E-23
9055	PRC1	protein regulator of cytokinesis 1	10.27	7.29	-2.98	3.23E-26	2.64E-24

9787	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	9.48	6.54	-2.93	5.08 E-26	3.97 E-24
81610	FAM83D	family with sequence similarity 83, member D	9.27	6.36	-2.92	1.20 E-24	6.97 E-23
26255	PTTG3P	pituitary tumor-transforming 3 (pseudogene)	10.40	7.48	-2.91	2.95 E-24	1.59 E-22
84823	LMNB2	lamin B2	11.68	8.77	-2.91	1.08 E-25	7.79 E-24
896	CCND3	cyclin D3	13.11	10.24	-2.87	1.97 E-26	1.77 E-24
4521	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	11.22	8.40	-2.82	1.16 E-24	6.80 E-23
993	CDC25A	cell division cycle 25 homolog A (S. pombe)	9.17	6.41	-2.76	6.09 E-23	2.49 E-21
899	CCNF	cyclin F	10.23	7.47	-2.76	2.13 E-24	1.19 E-22
4885	NPTX2	neuronal pentraxin II	11.72	8.97	-2.74	2.82 E-23	1.21 E-21
699	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	9.02	6.30	-2.73	2.23 E-24	1.24 E-22
1163	CKS1B	CDC28 protein kinase regulatory subunit 1B	11.87	9.16	-2.72	4.77 E-25	2.99 E-23
1535	CYBA	cytochrome b-245, alpha polypeptide	10.33	7.62	-2.72	7.03 E-23	2.84 E-21
11339	OIP5	Opa interacting protein 5	9.29	6.57	-2.71	9.81 E-25	5.85 E-23
3065	HDAC1	histone deacetylase 1	12.37	9.72	-2.66	8.78 E-25	5.26 E-23
890	CCNA2	cyclin A2	9.77	7.13	-2.63	1.51 E-24	8.60 E-23
9319	TRIP13	thyroid hormone receptor interactor 13	9.83	7.21	-2.62	1.30 E-23	6.07 E-22
4085	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	9.54	6.94	-2.61	1.44 E-23	6.66 E-22
3832	KIF11	kinesin family member 11	9.08	6.47	-2.60	6.97 E-24	3.49 E-22
55872	PBK	PDZ binding kinase	8.89	6.31	-2.59	8.21 E-23	3.25 E-21
9833	MELK	maternal embryonic leucine zipper kinase	9.75	7.16	-2.59	4.85 E-23	2.02 E-21
55723	ASF1B	ASF1 anti-silencing function 1 homolog B (S.	9.33	6.76	-2.58	2.45 E-23	1.08 E-21

		cerevisiae)					
10733	PLK4	polo-like kinase 4	9.12	6.55	-2.56	5.15E-23	2.13E-21
259266	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	9.36	6.81	-2.56	4.44E-22	1.54E-20
6624	FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	13.80	11.22	-2.56	4.88E-24	2.54E-22
4001	LMNB1	lamin B1	9.34	6.82	-2.54	3.95E-22	1.39E-20
1058	CENPA	centromere protein A	9.01	6.46	-2.54	6.08E-24	3.08E-22
29128	UHRF1	ubiquitin-like with PHD and ring finger domains 1	12.49	9.95	-2.53	3.42E-24	1.83E-22
25886	POC1A	POC1 centriolar protein homolog A (Chlamydomonas)	10.12	7.64	-2.49	1.32E-24	7.61E-23
983	CDK1	cyclin-dependent kinase 1	9.06	6.62	-2.43	8.32E-20	1.84E-18
29127	RACGAP1	Rac GTPase activating protein 1	9.45	7.06	-2.40	1.59E-23	7.27E-22
10535	RNASEH2A	ribonuclease H2, subunit A	9.73	7.34	-2.39	8.89E-24	4.29E-22
10592	SMC2	structural maintenance of chromosomes 2	9.54	7.15	-2.39	1.70E-23	7.76E-22
728643	LOC728643	heterogeneous nuclear ribonucleoprotein A1 pseudogene	11.11	8.74	-2.37	7.25E-18	1.14E-16
6119	RPA3	replication protein A3, 14kDa	11.69	9.33	-2.36	2.48E-23	1.09E-21
55839	CENPN	centromere protein N	9.92	7.56	-2.35	1.08E-21	3.54E-20
4176	MCM7	minichromosome maintenance complex component 7	12.35	10.00	-2.34	1.35E-23	6.30E-22
84057	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	8.76	6.42	-2.34	9.30E-23	3.63E-21
7083	TK1	thymidine kinase 1, soluble	9.11	6.80	-2.32	4.25E-20	9.92E-19
4173	MCM4	minichromosome maintenance complex component 4	10.43	8.17	-2.25	3.38E-22	1.21E-20
2189	FANCG	Fanconi anemia, complementation group	9.46	7.21	-2.25	1.23E-19	2.62E-18

		G					
9582	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	8.58	6.34	-2.25	1.75E-20	4.45E-19
3835	KIF22	kinesin family member 22	10.28	8.03	-2.24	4.05E-20	9.50E-19
10544	PROCR	protein C receptor, endothelial	9.06	6.83	-2.24	1.34E-20	3.43E-19
2091	FBL	fibrillarin	11.98	9.75	-2.23	3.34E-20	7.97E-19
4171	MCM2	minichromosome maintenance complex component 2	10.13	7.90	-2.22	5.80E-21	1.60E-19
1063	CENPF	centromere protein F, 350/400kDa (mitosin)	9.12	6.92	-2.20	2.16E-18	3.67E-17
3489	IGFBP6	insulin-like growth factor binding protein 6	10.37	8.19	-2.19	1.45E-18	2.53E-17
157313	CDCA2	cell division cycle associated 2	8.57	6.39	-2.19	2.11E-23	9.45E-22
55165	CEP55	centrosomal protein 55kDa	8.88	6.70	-2.18	7.82E-24	3.85E-22
10383	TUBB2C	tubulin, beta 2C	12.38	10.21	-2.18	8.55E-22	2.85E-20
55038	CDCA4	cell division cycle associated 4	9.59	7.43	-2.17	5.49E-24	2.80E-22
1515	CTSL2	cathepsin L2	9.25	7.09	-2.16	3.52E-22	1.26E-20
9585	KIF20B	kinesin family member 20B	9.44	7.28	-2.16	5.24E-22	1.80E-20
891	CCNB1	cyclin B1	8.84	6.70	-2.14	5.66E-19	1.06E-17
64943	NT5DC2	5'-nucleotidase domain containing 2	10.23	8.10	-2.13	2.37E-18	4.01E-17
10460	TACC3	transforming, acidic coiled-coil containing protein 3	8.64	6.50	-2.13	5.28E-21	1.47E-19
78995	C17orf53	chromosome 17 open reading frame 53	9.15	7.04	-2.12	4.45E-21	1.26E-19
3329	HSPD1	heat shock 60kDa protein 1 (chaperonin)	12.90	10.79	-2.11	2.86E-22	1.04E-20
4175	MCM6	minichromosome maintenance complex component 6	11.36	9.24	-2.11	3.36E-19	6.60E-18
2305	FOXM1	forkhead box M1	8.63	6.50	-2.11	3.51E-19	6.84E-18
10024	TROAP	trophinin associated	8.73	6.62	-2.11	6.44	2.18

		protein (tastin)				E-22	E-20
24137	KIF4A	kinesin family member 4A	8.40	6.31	-2.11	9.38E-20	2.06E-18
10635	RAD51AP1	RAD51 associated protein 1	9.02	6.93	-2.10	1.02E-21	3.35E-20
3161	HMMR	hyaluronan-mediated motility receptor (RHAMM)	8.41	6.34	-2.08	5.61E-21	1.55E-19
1033	CDKN3	cyclin-dependent kinase inhibitor 3	8.92	6.85	-2.08	2.96E-19	5.92E-18
7272	TTK	TTK protein kinase	8.79	6.72	-2.08	2.36E-21	7.07E-20
286527	TMSB15B	thymosin beta 15B	11.25	9.18	-2.07	2.49E-22	9.19E-21
1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	8.67	6.59	-2.06	1.62E-20	4.15E-19
54443	ANLN	anillin, actin binding protein	8.57	6.50	-2.06	9.02E-20	1.99E-18
995	CDC25C	cell division cycle 25 homolog C (S. pombe)	8.41	6.37	-2.05	1.27E-21	4.06E-20
4172	MCM3	minichromosome maintenance complex component 3	11.67	9.62	-2.05	6.87E-22	2.33E-20
84141	FAM176A	family with sequence similarity 176, member A	9.55	7.51	-2.04	5.53E-22	1.89E-20
51293	CD320	CD320 molecule	9.79	7.74	-2.04	3.20E-20	7.65E-19
51512	GTSE1	G-2 and S-phase expressed 1	8.61	6.57	-2.04	3.59E-21	1.03E-19
6491	STIL	SCL/TAL1 interrupting locus	8.61	6.57	-2.03	1.87E-20	4.72E-19
5604	MAP2K1	mitogen-activated protein kinase kinase 1	11.82	9.82	-2.01	1.03E-20	2.73E-19
23446	SLC44A1	solute carrier family 44, member 1	11.04	9.03	-2.01	1.67E-18	2.89E-17
2177	FANCD2	Fanconi anemia, complementation group D2	8.93	6.93	-2.01	8.22E-19	1.48E-17
65062	ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	10.70	8.71	-1.99	1.82E-21	5.58E-20
2192	FBLN1	fibulin 1	10.48	8.49	-1.98	1.29E-19	2.75E-18
5557	PRIM1	primase, DNA, polypeptide 1 (49kDa)	9.17	7.19	-1.98	1.32E-20	3.40E-19

55732	C1orf112	chromosome 1 open reading frame 112	8.91	6.94	-1.98	5.15E-21	1.44E-19
2118	ETV4	ets variant 4	9.22	7.27	-1.97	5.66E-16	6.32E-15
664709	HNRNPA1P10	heterogeneous nuclear ribonucleoprotein A1 pseudogene 10	10.96	8.99	-1.96	3.67E-17	5.06E-16
3336	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	12.80	10.83	-1.95	1.22E-19	2.61E-18
26271	FBXO5	F-box protein 5	9.48	7.53	-1.95	2.47E-19	5.03E-18
53827	FXYD5	FXYD domain containing ion transport regulator 5	10.74	8.79	-1.95	9.83E-19	1.76E-17
10051	SMC4	structural maintenance of chromosomes 4	9.96	8.00	-1.95	9.57E-21	2.54E-19
4174	MCM5	minichromosome maintenance complex component 5	9.47	7.53	-1.94	4.80E-19	9.15E-18
4833	NME4	non-metastatic cells 4, protein expressed in	11.56	9.63	-1.94	8.64E-18	1.34E-16
23421	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	8.49	6.57	-1.92	1.27E-18	2.24E-17
83461	CDCA3	cell division cycle associated 3	8.29	6.38	-1.91	6.12E-19	1.13E-17
8914	TIMELESS	timeless homolog (Drosophila)	9.88	7.96	-1.91	2.02E-20	5.04E-19
1062	CENPE	centromere protein E, 312kDa	8.83	6.96	-1.88	1.07E-20	2.83E-19
5050	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	10.38	8.50	-1.88	3.46E-19	6.76E-18
109	ADCY3	adenylate cyclase 3	10.17	8.32	-1.85	6.16E-20	1.38E-18
5880	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	8.28	6.43	-1.85	8.84E-21	2.36E-19
55771	PRR11	proline rich 11	8.27	6.42	-1.84	3.16E-18	5.23E-17
6839	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	9.17	7.34	-1.84	1.81E-20	4.58E-19
493	ATP2B4	ATPase, Ca++	8.74	6.93	-1.83	1.33	1.64

		transporting, plasma membrane 4				E-16	E-15
113457	TUBA3D	tubulin, alpha 3d	9.19	7.38	-1.83	4.73 E-16	5.35 E-15
6241	RRM2	ribonucleotide reductase M2	8.19	6.37	-1.82	2.28 E-19	4.64 E-18
9918	NCAPD2	non-SMC condensin I complex, subunit D2	10.40	8.59	-1.80	7.70 E-17	9.93 E-16
83468	GLT8D2	glycosyltransferase 8 domain containing 2	9.40	7.62	-1.79	6.84 E-18	1.08 E-16
8407	TAGLN2	transgelin 2	9.60	7.81	-1.79	8.67 E-18	1.34 E-16
2956	MSH6	mutS homolog 6 (E. coli)	10.52	8.74	-1.79	3.42 E-19	6.70 E-18
54733	SLC35F2	solute carrier family 35, member F2	8.69	6.92	-1.78	7.62 E-19	1.39 E-17
1786	DNMT1	DNA (cytosine-5-)-methyltransferase 1	12.06	10.29	-1.77	5.77 E-19	1.07 E-17
84321	THOC3	THO complex 3	10.01	8.26	-1.76	4.10 E-17	5.57 E-16
201161	CENPV	centromere protein V	10.76	9.02	-1.74	2.81 E-17	3.96 E-16
91057	CCDC34	coiled-coil domain containing 34	10.86	9.15	-1.73	2.61 E-17	3.70 E-16
4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2	8.07	6.36	-1.72	1.23 E-15	1.30 E-14
54780	NSMCE4A	non-SMC element 4 homolog A (S. cerevisiae)	10.38	8.66	-1.72	3.96 E-18	6.45 E-17
5538	PPT1	palmitoyl-protein thioesterase 1	10.74	9.04	-1.71	5.42 E-16	6.07 E-15
286016	TPI1P2	triosephosphate isomerase 1 pseudogene 2	10.50	8.80	-1.70	5.84 E-18	9.30 E-17
9928	KIF14	kinesin family member 14	8.40	6.71	-1.69	3.54 E-18	5.80 E-17
8438	RAD54L	RAD54-like (S. cerevisiae)	8.14	6.46	-1.68	1.37 E-18	2.40 E-17
29089	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	10.20	8.53	-1.67	1.48 E-17	2.19 E-16
9204	ZMYM6	zinc finger, MYM-type 6	10.22	8.57	-1.65	7.83 E-17	1.01 E-15
26147	PHF19	PHD finger protein 19	7.98	6.34	-1.65	4.19 E-18	6.78 E-17
7035	TFPI	tissue factor pathway inhibitor (lipoprotein-	10.59	8.95	-1.65	1.32 E-18	2.33 E-17

		associated coagulation inhibitor)					
51278	IER5	immediate early response 5	10.38	8.74	-1.65	8.56E-17	1.09E-15
8208	CHAF1B	chromatin assembly factor 1, subunit B (p60)	8.19	6.54	-1.64	6.18E-19	1.14E-17
23165	NUP205	nucleoporin 205kDa	10.13	8.50	-1.63	1.04E-17	1.58E-16
23204	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	11.26	9.62	-1.63	7.04E-16	7.75E-15
9735	KNTC1	kinetochore associated 1	8.75	7.13	-1.62	8.09E-15	7.46E-14
196792	FAM24B	family with sequence similarity 24, member B	9.09	7.47	-1.62	3.35E-17	4.66E-16
5725	PTBP1	polypyrimidine tract binding protein 1	13.04	11.43	-1.61	5.36E-19	1.01E-17
5351	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	12.61	11.01	-1.61	6.96E-15	6.46E-14
25923	ATL3	atlastin GTPase 3	8.63	7.03	-1.60	1.01E-17	1.54E-16
93323	HAUS8	HAUS augmin-like complex, subunit 8	8.59	6.99	-1.60	4.03E-17	5.49E-16
51129	ANGPTL4	angiopoietin-like 4	8.10	6.50	-1.59	1.47E-16	1.79E-15
65003	MRPL11	mitochondrial ribosomal protein L11	10.28	8.68	-1.59	3.41E-15	3.34E-14
79001	VKORC1	vitamin K epoxide reductase complex, subunit 1	12.93	11.35	-1.59	1.11E-16	1.39E-15
10276	NET1	neuroepithelial cell transforming 1	10.19	8.61	-1.59	4.32E-16	4.92E-15

[a] RD Mean lists the mean value from three biologically independent RD RNA samples from RD cells infected with a GFP-expressing lentivirus and placed in differentiation media for 72 h.

[b] Myotube Mean lists the mean value from three biologically independent primary human myotube RNA samples grown to confluency and placed in differentiation media for 72 h.

[c] Fold change represents the difference between the myotube and RD values and is a log2 value.

Supplemental Table S5. Downregulated myogenic genes expressed at comparable levels in RD cells.

Entrez ID	Symbol	Gene Name	RD value[a]	Myotube value[b]	Fold change[c]	p-value	FDR
60	ACTB	actin, beta	13.92	14.13	0.18	0.0396	0.0557
71	ACTG1	actin, gamma 1	14.09	14.31	0.24	0.0114	0.0176
72	ACTG2	actin, gamma 2, smooth muscle, enteric	6.20	6.73	0.53	6.23E-05	0.0001
8751	ADAM15	ADAM metallopeptidase domain 15	7.69	7.13	-0.55	1.10E-06	3.00E-06
159	ADSS	adenylosuccinate synthase	8.97	8.69	-0.28	0.0075	0.0119
262	AMD1	adenosylmethionine decarboxylase 1	8.24	8.01	-0.22	0.0315	0.0452
276	AMY1A	amylase, alpha 1A (salivary)	7.40	7.62	0.21	0.0394	0.0555
84168	ANTXR1	anthrax toxin receptor 1	10.40	11.37	0.99	2.90E-11	1.53E-10
316	AOX1	aldehyde oxidase 1	6.34	6.68	0.34	0.0012	0.0021
396	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	9.87	10.38	0.51	0.0001	0.0002
397	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	6.37	6.53	0.17	0.1006	0.1310
151188	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	9.09	8.75	-0.34	0.0023	0.0040
10552	ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	10.87	10.65	-0.24	0.0126	0.0193
10095	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	8.38	7.95	-0.42	0.0002	0.0005
10092	ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	10.05	10.61	0.55	2.73E-05	6.17E-05
8853	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	10.09	9.36	-0.73	1.01E-07	3.18E-07
558	AXL	AXL receptor tyrosine kinase	9.10	8.71	-0.39	0.0004	0.0007
9274	BCL7C	B-cell CLL/lymphoma 7C	8.56	8.84	0.29	0.0057	0.0092

55859	BEX1	brain expressed, X-linked 1	6.38	6.80	0.41	0.0002	0.0003
329	BIRC2	baculoviral IAP repeat containing 2	8.59	9.35	0.76	3.46E-08	1.17E-07
79866	C13orf34	chromosome 13 open reading frame 34	7.46	7.16	-0.32	0.0116	0.0179
56005	C19orf10	chromosome 19 open reading frame 10	10.70	10.37	-0.33	0.0045	0.0075
57415	C3orf14	chromosome 3 open reading frame 14	8.58	8.95	0.36	0.0004	0.0008
805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	12.12	11.76	-0.37	0.0008	0.0014
835	CASP2	caspase 2, apoptosis-related cysteine peptidase	9.68	9.37	-0.32	0.0017	0.0030
874	CBR3	carbonyl reductase 3	6.87	7.03	0.16	0.1216	0.1557
147372	CCBE1	collagen and calcium binding EGF domains 1	8.16	9.02	0.86	7.10E-08	2.30E-07
80071	CCDC15	coiled-coil domain containing 15	7.66	7.20	-0.46	6.74E-06	1.65E-05
114800	CCDC85A	coiled-coil domain containing 85A	6.24	6.35	0.09	0.3355	0.3902
960	CD44	CD44 molecule (Indian blood group)	9.53	10.74	1.21	3.07E-13	2.21E-12
966	CD59	CD59 molecule, complement regulatory protein	8.67	8.31	-0.37	0.0007	0.0013
64866	CDCP1	CUB domain containing protein 1	6.40	6.59	0.20	0.0667	0.0900
1000	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	11.39	11.17	-0.19	0.2099	0.2558
1002	CDH4	cadherin 4, type 1, R-cadherin (retinal)	6.92	6.44	-0.48	5.83E-06	1.44E-05
84131	CEP78	centrosomal protein 78kDa	7.96	7.47	-0.49	2.72E-06	7.05E-06
114335	CGB1	chorionic gonadotropin, beta polypeptide 1	6.66	6.79	0.12	0.2280	0.2758
93659	CGB5	chorionic gonadotropin, beta polypeptide 5	6.45	6.48	0.03	0.7648	0.8002
10370	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-	8.68	8.95	0.26	0.0297	0.0428

		terminal domain, 2					
10970	CKAP4	cytoskeleton-associated protein 4	11.31	10.76	-0.56	6.44E-06	1.58E-05
1192	CLIC1	chloride intracellular channel 1	11.75	11.42	-0.33	0.0005	0.0009
54918	CMTM6	CKLF-like MARVEL transmembrane domain containing 6	8.89	8.77	-0.11	0.2783	0.3298
29097	CNIH4	cornichon homolog 4 (Drosophila)	9.74	9.95	0.21	0.0499	0.0691
25927	CNRIP1	cannabinoid receptor interacting protein 1	7.58	8.51	0.94	1.27E-11	7.06E-11
1305	COL13A1	collagen, type XIII, alpha 1	7.05	6.84	-0.23	0.0481	0.0668
23603	CORO1C	coronin, actin binding protein, 1C	8.38	8.80	0.44	5.23E-05	0.0001
51200	CPA4	carboxypeptidase A4	6.83	6.67	-0.16	0.1199	0.1538
1453	CSNK1D	casein kinase 1, delta	7.53	8.00	0.48	1.45E-05	3.40E-05
1465	CSRP1	cysteine and glycine-rich protein 1	10.54	10.06	-0.49	0.0002	0.0003
1479	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	9.36	8.69	-0.68	1.09E-07	3.44E-07
1503	CTPS	CTP synthase	9.22	8.77	-0.44	0.0003	0.0006
79077	DCTPP1	dCTP pyrophosphatase 1	9.90	9.39	-0.51	1.37E-05	3.22E-05
23576	DDAH1	dimethylarginine dimethylaminohydrolase 1	8.83	8.71	-0.13	0.2862	0.3381
91614	DEPDC7	DEP domain containing 7	7.32	7.81	0.49	3.21E-05	7.20E-05
81624	DIAPH3	diaphanous homolog 3 (Drosophila)	6.97	6.63	-0.34	0.0006	0.0011
22943	DKK1	dickkopf homolog 1 (Xenopus laevis)	7.59	7.73	0.15	0.1212	0.1553
23234	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	9.88	9.31	-0.57	2.99E-06	7.68E-06
91039	DPP9	dipeptidyl-peptidase 9	8.68	8.31	-0.38	0.0005	0.0009
10589	DRAP1	DR1-associated protein 1 (negative cofactor 2 alpha)	10.24	10.67	0.41	0.0001	0.0003
1847	DUSP5	dual specificity phosphatase 5	8.44	8.54	0.10	0.3189	0.3728
1854	DUT	deoxyuridine	8.03	7.39	-0.65	5.35E-	1.76E-

		triphosphatase				08	07
144455	E2F7	E2F transcription factor 7	7.28	7.27	-0.02	0.8450	0.8692
1906	EDN1	endothelin 1	6.52	6.61	0.09	0.2852	0.3371
64834	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	8.01	8.17	0.15	0.1377	0.1747
2012	EMP1	epithelial membrane protein 1	10.84	11.22	0.38	0.0007	0.0014
2014	EMP3	epithelial membrane protein 3	11.59	11.70	0.10	0.3969	0.4539
2022	ENG	endoglin	8.74	8.26	-0.48	1.93E-05	4.46E-05
5167	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	6.67	6.84	0.16	0.1040	0.1350
1969	EPHA2	EPH receptor A2	7.55	7.17	-0.38	0.0024	0.0042
5393	EXOSC9	exosome component 9	8.69	8.65	-0.04	0.7000	0.7431
2146	EZH2	enhancer of zeste homolog 2 (Drosophila)	7.83	7.32	-0.52	5.17E-06	1.29E-05
64855	FAM129B	family with sequence similarity 129, member B	9.36	9.55	0.19	0.0910	0.1196
2289	FKBP5	FK506 binding protein 5	9.69	9.20	-0.48	5.07E-05	0.0001
56776	FMN2	formin 2	6.34	6.64	0.30	0.0096	0.0149
8061	FOSL1	FOS-like antigen 1	6.75	7.01	0.25	0.0139	0.0212
2297	FOXD1	forkhead box D1	9.20	9.09	-0.11	0.3632	0.4189
2697	GJA1	gap junction protein, alpha 1, 43kDa	7.24	7.80	0.55	5.36E-05	0.0001
51228	GLTP	glycolipid transfer protein	10.71	10.66	-0.05	0.5945	0.6470
51053	GMNN	geminin, DNA replication inhibitor	7.78	7.23	-0.55	8.11E-05	0.0002
3015	H2AFZ	H2A histone family, member Z	12.89	12.39	-0.50	3.22E-05	7.23E-05
64399	HHIP	hedgehog interacting protein	6.59	6.61	0.03	0.7547	0.7912
3150	HMGN1	high-mobility group nucleosome binding domain 1	11.10	10.28	-0.82	9.32E-10	3.95E-09
3151	HMGN	high-mobility group	8.03	7.57	-0.46	0.0004	0.0007

	2	nucleosomal binding domain 2					
3212	HOXB2	homeobox B2	9.21	9.06	-0.14	0.1193	0.1531
9955	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	8.32	8.14	-0.18	0.0849	0.1123
3397	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	7.55	6.88	-0.68	1.34E-07	4.15E-07
3399	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	9.61	9.04	-0.57	1.86E-06	4.91E-06
83982	IFI27L2	interferon, alpha-inducible protein 27-like 2	8.13	8.38	0.24	0.0558	0.0764
121457	IKBIP	IKBKB interacting protein	8.17	7.95	-0.21	0.0842	0.1114
50615	IL21R	interleukin 21 receptor	7.00	6.86	-0.15	0.1330	0.1691
8826	IQGAP1	IQ motif containing GTPase activating protein 1	7.84	7.80	-0.04	0.7344	0.7738
8515	ITGA10	integrin, alpha 10	7.11	7.12	0.01	0.8975	0.9155
3725	JUN	jun proto-oncogene	9.16	9.44	0.28	0.0107	0.0166
89822	KCNK17	potassium channel, subfamily K, member 17	6.50	6.39	-0.12	0.2650	0.3157
3776	KCNK2	potassium channel, subfamily K, member 2	6.42	6.61	0.20	0.0724	0.0970
54793	KCTD9	potassium channel tetramerisation domain containing 9	7.38	7.49	0.10	0.2934	0.3457
3885	KRT34	keratin 34	6.49	6.75	0.25	0.0133	0.0203
3887	KRT81	keratin 81	6.43	6.74	0.30	0.0025	0.0043
3892	KRT86	keratin 86	6.52	6.59	0.09	0.3977	0.4546
728255	KRTAP1-4	keratin associated protein 1-4	6.47	6.41	-0.06	0.5422	0.5972
83895	KRTAP1-5	keratin associated protein 1-5	6.50	6.74	0.23	0.0466	0.0649
3927	LASP1	LIM and SH3 protein 1	11.21	10.89	-0.31	0.0070	0.0111
353139	LCE2A	late cornified envelope	6.51	6.48	-0.02	0.8665	0.8885

		2A					
353142	LCE3A	late cornified envelope 3A	6.40	6.47	0.07	0.4770	0.5341
91289	LMF2	lipase maturation factor 2	8.09	7.96	-0.12	0.1384	0.1754
100216001	LOC100216001	hypothetical LOC100216001	6.55	6.62	0.07	0.4559	0.5135
644936	LOC644936	actin, beta pseudogene	7.29	7.16	-0.14	0.2534	0.3033
653888	LOC653888	actin-related protein 2/3 complex subunit 1B-like	8.21	7.71	-0.49	2.01E-05	4.63E-05
728026	LOC728026	hypothetical protein LOC728026	7.55	7.26	-0.30	0.0505	0.0699
729086	LOC729086	vesicular, overexpressed in cancer, prosurvival protein 1-like	7.33	6.80	-0.54	2.61E-06	6.76E-06
4016	LOXL1	lysyl oxidase-like 1	8.04	8.49	0.45	0.0014	0.0024
9404	LPXN	leupaxin	7.53	7.85	0.32	0.0090	0.0142
130576	LYPD6B	LY6/PLAUR domain containing 6B	7.55	7.77	0.22	0.0653	0.0884
4154	MBNL1	muscleblind-like (Drosophila)	8.16	8.67	0.50	8.04E-05	0.0002
90411	MCFD2	multiple coagulation factor deficiency 2	8.77	8.55	-0.23	0.0394	0.0555
4201	MEA1	male-enhanced antigen 1	8.91	8.42	-0.50	0.0002	0.000340001
11343	MGLL	monoglyceride lipase	8.09	8.45	0.35	0.0016	0.0027
197259	MLKL	mixed lineage kinase domain-like	7.09	6.78	-0.32	0.0034	0.0057
58538	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	6.65	6.42	-0.23	0.0422	0.0591
51318	MRPL35	mitochondrial ribosomal protein L35	9.52	9.11	-0.42	7.63E-05	0.0002
4489	MT1A	metallothionein 1A	10.88	11.47	0.57	1.98E-05	4.57E-05
4501	MT1X	metallothionein 1X	10.36	9.91	-0.45	0.0002	0.0003
10903	MTMR11	myotubularin related protein 11	7.29	7.07	-0.23	0.0165	0.0249
4603	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	6.63	6.47	-0.15	0.2118	0.2579

4617	MYF5	myogenic factor 5	6.69	8.08	1.39	1.71E-14	1.50E-13
440145	MZT1	mitotic spindle organizing protein 1	6.73	7.65	0.92	3.22E-10	1.46E-09
54892	NCAPG2	non-SMC condensin II complex, subunit G2	7.77	7.34	-0.44	7.01E-05	0.0001
57552	NCEH1	neutral cholesterol ester hydrolase 1	6.80	7.55	0.75	1.84E-10	8.62E-10
55967	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	11.70	11.17	-0.53	4.28E-07	1.24E-06
64332	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	7.81	7.71	-0.11	0.2712	0.3223
51388	NIP7	nuclear import 7 homolog (S. cerevisiae)	9.49	9.14	-0.36	0.0002	0.0004
4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in	7.67	7.96	0.30	0.0037	0.0062
57407	NMRAL1	NmrA-like family domain containing 1	8.39	8.41	0.02	0.8137	0.8425
9397	NMT2	N-myristoyltransferase 2	6.56	6.94	0.37	0.0008	0.0015
7025	NR2F1	nuclear receptor subfamily 2, group F, member 1	7.94	7.48	-0.46	8.89E-05	0.0002
56675	NRIP3	nuclear receptor interacting protein 3	7.99	8.11	0.12	0.3164	0.3702
11164	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	9.89	9.37	-0.53	1.52E-06	4.06E-06
4942	OAT	ornithine aminotransferase	9.89	9.19	-0.70	5.49E-06	1.36E-05
64859	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	7.65	8.12	0.48	4.88E-06	1.22E-05
132299	OCIAD2	OCIA domain containing 2	6.55	7.98	1.44	1.52E-14	1.35E-13
56944	OLFML3	olfactomedin-like 3	8.74	8.67	-0.08	0.5365	0.5918
23762	OSBP2	oxysterol binding protein 2	7.07	7.51	0.45	6.47E-05	0.0001

130497	OSR1	odd-skipped related 1 (Drosophila)	6.97	7.10	0.12	0.2701	0.3211
9060	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	7.49	7.52	0.04	0.6960	0.7397
79668	PARP8	poly (ADP-ribose) polymerase family, member 8	9.39	9.06	-0.34	0.0056	0.0090
5111	PCNA	proliferating cell nuclear antigen	9.43	8.89	-0.54	1.33E-05	3.13E-05
5315	PKM2	pyruvate kinase, muscle	9.01	8.68	-0.33	0.0056	0.0090
5327	PLAT	plasminogen activator, tissue	10.34	10.29	-0.05	0.6865	0.7312
5329	PLAUR	plasminogen activator, urokinase receptor	6.78	7.24	0.46	3.74E-05	8.30E-05
5337	PLD1	phospholipase D1, phosphatidylcholine-specific	7.31	6.80	-0.53	3.73E-06	9.48E-06
200150	PLD5	phospholipase D family, member 5	6.58	7.00	0.41	0.0003	0.0006
26499	PLEK2	pleckstrin 2	6.46	6.64	0.18	0.0857	0.1132
123	PLIN2	perilipin 2	10.01	9.77	-0.24	0.0158	0.0239
5352	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	7.27	7.74	0.46	0.0003	0.0006
5420	PODXL	podocalyxin-like	7.83	8.79	0.97	1.49E-12	9.49E-12
5441	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	7.75	8.01	0.26	0.0104	0.0162
728378	POTEF	POTE ankyrin domain family, member F	13.10	12.68	-0.41	0.0003	0.0005
10549	PRDX4	peroxiredoxin 4	10.89	10.55	-0.34	0.0022	0.0038
5580	PRKCD	protein kinase C, delta	8.19	8.22	0.03	0.7402	0.7790
8624	PSMG1	proteasome (prosome, macropain) assembly chaperone 1	8.60	8.55	-0.05	0.6597	0.7066
5757	PTMA	prothymosin, alpha	7.62	7.29	-0.37	0.0745	0.0996
51495	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	10.84	9.86	-0.99	4.05E-12	2.42E-11
11137	PWP1	PWP1 homolog (S. cerevisiae)	10.31	9.82	-0.48	2.87E-06	7.41E-06
5768	QSOX1	quiescin Q6 sulfhydryl	10.00	9.94	-0.08	0.5873	0.6404

		oxidase 1					
5891	RAGE	renal tumor antigen	8.25	7.93	-0.31	0.0041	0.0068
5932	RBBP8	retinoblastoma binding protein 8	8.65	8.44	-0.21	0.0323	0.0462
57333	RCN3	reticulocalbin 3, EF-hand calcium binding domain	8.63	8.84	0.21	0.0337	0.0481
8601	RGS20	regulator of G-protein signaling 20	7.25	6.68	-0.57	9.54E-07	2.63E-06
389	RHOC	ras homolog gene family, member C	11.34	10.59	-0.75	1.90E-08	6.66E-08
391	RHOG	ras homolog gene family, member G (rho G)	9.63	9.45	-0.19	0.0432	0.0604
284996	RNF149	ring finger protein 149	9.92	9.46	-0.46	1.35E-05	3.19E-05
6237	RRAS	related RAS viral (r-ras) oncogene homolog	10.23	10.33	0.09	0.3889	0.4455
6238	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	11.01	10.39	-0.62	1.81E-06	4.80E-06
27341	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	9.56	9.64	0.08	0.3680	0.4238
1903	S1PR3	sphingosine-1-phosphate receptor 3	7.45	6.93	-0.53	1.02E-06	2.80E-06
51435	SCARA3	scavenger receptor class A, member 3	6.89	6.54	-0.34	0.0021	0.0037
9117	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	8.58	8.73	0.16	0.0735	0.0984
8482	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	6.92	6.90	-0.03	0.7627	0.7981
8710	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	6.57	6.44	-0.13	0.1757	0.2180
29950	SERTAD1	SERTA domain containing 1	9.09	9.49	0.40	6.53E-05	0.0001
6446	SGK1	serum/glucocorticoid regulated kinase 1	7.76	8.10	0.33	0.0068	0.0109
10019	SH2B3	SH2B adaptor protein	9.92	9.66	-0.25	0.0258	0.0376

		3					
83442	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3	10.32	10.20	-0.12	0.1914	0.2352
152503	SH3D19	SH3 domain containing 19	7.65	7.35	-0.31	0.0013	0.0023
7884	SLBP	stem-loop binding protein	9.45	8.86	-0.58	1.82E-06	4.83E-06
6574	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	10.69	10.73	0.04	0.6769	0.7227
29015	SLC43A3	solute carrier family 43, member 3	6.58	6.93	0.35	0.0016	0.0028
57228	SMAGP	small cell adhesion glycoprotein	7.24	7.32	0.08	0.4759	0.5330
574042	SNORA10	small nucleolar RNA, H/ACA box 10	7.55	7.29	-0.27	0.0244	0.0357
677838	SNORA61	small nucleolar RNA, H/ACA box 61	7.45	7.62	0.17	0.1369	0.1738
619571	SNORD96A	small nucleolar RNA, C/D box 96A	7.11	7.00	-0.13	0.2485	0.2981
27131	SNX5	sorting nexin 5	8.60	8.36	-0.24	0.0155	0.0235
60559	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	8.37	7.24	-1.13	1.13E-12	7.37E-12
6427	SRSF2	serine/arginine-rich splicing factor 2	11.45	11.14	-0.30	0.0008	0.0014
6428	SRSF3	serine/arginine-rich splicing factor 3	8.98	8.48	-0.49	2.53E-05	5.77E-05
8614	STC2	stanniocalcin 2	11.27	10.80	-0.49	0.0018	0.0031
55240	STEAP3	STEAP family member 3	8.34	8.09	-0.25	0.0167	0.0250
8801	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	8.79	8.63	-0.17	0.0864	0.1140
85012	TCEAL3	transcription elongation factor A (SII)-like 3	9.45	9.92	0.47	5.71E-05	0.0001
7041	TGFB1I1	transforming growth factor beta 1 induced transcript 1	9.23	9.31	0.08	0.4091	0.4662
7052	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	6.45	7.79	1.34	3.47E-14	2.89E-13

134285	TMEM 171	transmembrane protein 171	6.29	6.67	0.38	0.0003	0.0005
93109	TMEM 44	transmembrane protein 44	8.13	7.63	-0.50	1.68E-06	4.47E-06
7117	TMSL3	thymosin-like 3	9.82	9.82	0.00	0.9805	0.9843
8771	TNFRS F6B	tumor necrosis factor receptor superfamily, member 6b, decoy	6.60	6.85	0.24	0.0531	0.0731
7169	TPM2	tropomyosin 2 (beta)	9.84	13.52	3.68	7.26E-28	9.31E-26
6434	TRA2B	transformer 2 beta homolog (Drosophila)	9.90	9.42	-0.48	0.0002	0.0003
9697	TRAM 2	translocation associated membrane protein 2	8.75	9.16	0.41	0.0001	0.0003
84675	TRIM5 5	tripartite motif containing 55	6.41	7.09	0.67	2.66E-07	7.91E-07
57570	TRMT 5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	12.06	11.77	-0.28	0.0090	0.0141
388610	TRNP1	TMF1-regulated nuclear protein 1	8.13	7.73	-0.40	7.08E-05	0.0002
7106	TSPAN 4	tetraspanin 4	9.95	9.37	-0.58	6.25E-06	1.54E-05
706	TSPO	translocator protein (18kDa)	9.93	10.40	0.47	0.0003	0.0006
84790	TUBA1 C	tubulin, alpha 1c	13.67	13.19	-0.50	1.28E-05	3.02E-05
7280	TUBB2 A	tubulin, beta 2A	8.24	8.75	0.51	9.44E-07	2.60E-06
57045	TWSG 1	twisted gastrulation homolog 1 (Drosophila)	7.95	7.77	-0.18	0.1148	0.1478
7295	TXN	thioredoxin	13.31	12.64	-0.66	1.16E-08	4.19E-08
7360	UGP2	UDP-glucose pyrophosphorylase 2	9.93	10.73	0.80	3.93E-10	1.76E-09
7381	UQCR B	ubiquinol-cytochrome c reductase binding protein	8.80	8.51	-0.29	0.0023	0.0039
8673	VAMP 8	vesicle-associated membrane protein 8 (endobrevin)	8.10	8.19	0.08	0.4952	0.5515
7424	VEGF C	vascular endothelial growth factor C	7.58	7.86	0.29	0.0100	0.0156

7431	VIM	vimentin	13.69	13.30	-0.40	7.50E-05	0.0002
7533	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	11.38	11.34	-0.05	0.5544	0.6090
7534	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	11.82	11.70	-0.12	0.2023	0.2475
7538	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	8.36	8.14	-0.22	0.0593	0.0808

[a] RD Mean lists the mean value from three biologically independent RD RNA samples from RD cells infected with a GFP-expressing lentivirus and placed in differentiation media for 72 h.

[b] Myotube Mean lists the mean value from three biologically independent primary human myotube RNA samples grown to confluency and placed in differentiation media for 72 h.

[c] Fold change represents the difference between the myotube and RD values and is a log2 value.

Supplemental Table S6. Locations and scores of regional differences in MyoD binding between RD and primary cells.

Chromosome[a]	Start position[b]	End position[c]	Width[d]	Difference[e]
chr1	80014899	84293968	4279070	109.25
chr8	49930842	52438946	2508105	77.72
chr20	57626569	58519308	892740	56.83
chr2	129138573	130467481	1328909	54.82
chr20	46471676	47133160	661485	52.16
chr14	105965574	107252545	1286972	47.76
chr2	136823055	137135587	312533	46.86
chr5	134968512	135166582	198071	44.98
chr2	167023541	168732445	1708905	44.31
chr19	34058818	34732757	673940	44.24
chr8	2511430	6322072	3810643	42.18
chr2	3715754	5662045	1946292	40.77
chr19	57386639	57651476	264838	40.25
chr16	78964512	79614766	650255	38.02
chr3	89411319	94025601	4614283	37.55
chr11	15521224	16473403	952180	37.37
chr7	42145191	42999648	854458	37.30
chr21	32746619	33286557	539939	36.12
chr2	75780939	78305135	2524197	36.05
chr7	37328882	37983984	655103	35.44
chr1	245306233	245751394	445162	34.92
chr8	13086189	17022848	3936660	34.66
chr18	58113869	58731031	617163	33.63
chr5	116095643	116498060	402418	33.40
chr17	10802560	11827796	1025237	33.26
chr14	43273392	45553911	2280520	32.87
chr7	8383272	10469041	2085770	32.76
chr8	23772283	23904625	132343	31.74
chr20	18820069	19400520	580452	30.88
chr14	69966437	70448267	481831	30.49
chr10	56168174	59783236	3615063	30.39
chr22	46709872	47164882	455011	-30.10
chr15	81136255	81605992	469738	-30.21
chr1	161101915	161692661	590747	-30.30
chr20	6056064	8064221	2008158	-30.85
chr15	75901954	77080035	1178082	-30.97
chr3	10231204	11237389	1006186	-31.04
chr7	131305379	133113705	1808327	-31.12

chr2	18284403	20001544	1717142	-31.17
chr16	88037122	88264888	227767	-31.17
chr16	86551307	87367104	815798	-31.61
chr9	129747250	129958181	210932	-31.74
chr18	7608523	8744382	1135860	-31.80
chr12	4942557	5478822	536266	-31.97
chr21	42513900	43528632	1014733	-32.00
chr11	61583397	62212488	629092	-32.40
chr20	14546905	16289848	1742944	-32.44
chr2	133081609	134898174	1816566	-32.52
chr14	25254211	25591332	337122	-32.56
chr10	105594236	106070523	476288	-32.62
chr20	48816911	49068197	251287	-33.26
chr3	139809844	140618582	808739	-33.71
chr4	152641023	153231947	590925	-33.78
chr3	64126214	65734423	1608210	-33.93
chr7	16768248	20394972	3626725	-34.06
chr2	218669154	218786460	117307	-34.14
chr3	16355369	18337076	1981708	-34.24
chr15	91849405	92727767	878363	-34.25
chr10	71256049	71676454	420406	-34.83
chr17	68651346	70731104	2079759	-34.93
chr2	220543732	222840241	2296510	-35.29
chr11	69259134	70364994	1105861	-35.31
chr2	16735506	17826729	1091224	-35.34
chr15	78944376	79922572	978197	-35.39
chr16	67575333	68102392	527060	-35.47
chr5	150027381	150554744	527364	-35.66
chr10	124047100	124423429	376330	-35.77
chr16	56970868	57668607	697740	-36.01
chr20	23615018	25021495	1406478	-36.26
chr6	164444508	166298113	1853606	-36.45
chr22	26849184	27635577	786394	-37.37
chr11	131787533	132592644	805112	-37.43
chr10	13937838	14651116	713279	-37.54
chr5	52463531	54060865	1597335	-37.65
chr12	3347229	3838556	491328	-37.76
chr4	13990496	15978707	1988212	-37.94
chr5	88009635	89432331	1422697	-38.23
chr20	38287285	39806889	1519605	-38.37
chr6	105811215	107397633	1586419	-38.65
chr5	148208019	148661992	453974	-38.72
chr5	162835563	167831807	4996245	-38.97

chr9	70971163	72626682	1655520	-39.71
chr3	52486420	53835049	1348630	-39.79
chr13	101202242	107185843	5983602	-40.37
chr1	115610050	116742800	1132751	-40.49
chr1	110257298	110663189	405892	-40.60
chr15	70154300	70620853	466554	-40.63
chr5	8974441	10331133	1356693	-40.88
chr3	127472578	127998772	526195	-41.61
chr3	107429745	111480632	4050888	-42.46
chr3	44155540	45261003	1105464	-43.26
chr2	99528446	101359637	1831192	-44.04
chr5	1765162	7828979	6063818	-44.14
chr16	15905440	17577543	1672104	-44.19
chr1	176035845	178506994	2471150	-44.33
chr10	3012368	3823274	810907	-45.05
chr1	101088100	109842619	8754520	-45.73
chr9	18405088	20386786	1981699	-46.25
chr17	66755473	68401878	1646406	-46.89
chr20	20868934	22786337	1917404	-49.15
chr1	231727147	233181808	1454662	-49.44
chr14	72195072	74211522	2016451	-52.11
chr10	43800111	45375359	1575249	-54.22
chr8	131526451	134369056	2842606	-55.15
chr12	105351352	106961002	1609651	-63.68
chr1	55520673	57013577	1492905	-68.70
chr18	32171837	37333828	5161992	-74.09

[a] Chromosome (hg19) on which a regional difference was identified.
[b] Chromosomal coordinates for the start of the observed regional difference.
[c] Chromosomal coordinates for the end of the observed regional difference.
[d] The total size (in basepairs) of the indicated region.
[e] The corrected log2 fold change in MyoD peak heights between the primary and RD cells (for details, see Methods). Positive values represent higher RD peaks, and negative values higher primary cell peaks.

Supplemental Table S7. Differentially expressed genes located in regions with regional MyoD ChIP-seq peak differences.

Entrez ID	Gene Symbol	Myoblast value[a]	Myotube value[b]	RD value[c]	Prox Promoter Analysis[d]
Higher MyoD region in primary cells					
845	CASQ2	6.49	13.80	6.84	MT > RD
8988	HSPB3	8.40	13.58	7.71	MT > RD
9891	NUAK1	10.16	12.77	8.01	MT > RD
5654	HTRA1	13.14	12.20	6.78	
4208	MEF2C	7.56	11.80	6.96	MT > RD
2108	ETFA	11.05	11.49	10.44	
25907	TMEM158	11.79	11.39	9.95	
50863	NTM	10.84	11.05	6.55	
80206	FHOD3	7.82	10.90	6.21	MT > RD
5239	PGM5	6.53	10.83	6.76	MT > RD
1316	KLF6	11.81	10.82	9.51	
10468	FST	9.35	10.73	6.30	MT > RD
134265	AFAP1L1	7.52	10.72	6.79	MT > RD
8459	TPST2	10.43	10.59	8.68	
22885	ABLIM3	8.61	10.55	6.65	MT > RD
1837	DTNA	6.72	10.49	8.29	MT > RD
23180	RFTN1	11.03	10.45	8.45	
57214	KIAA1199	9.00	10.43	6.71	MT > RD
2495	FTH1	9.41	10.35	7.97	
64084	CLSTN2	6.40	10.26	6.64	MT > RD
92912	UBE2Q2	9.78	10.06	8.30	
166336	PRICKLE2	8.51	10.05	7.12	MT > RD
25945	PVRL3	10.26	10.01	7.75	
9289	GPR56	6.90	10.00	6.40	MT > RD
55034	MOCOS	8.28	9.64	6.62	MT > RD
125476	INO80C	9.31	9.56	8.50	
7145	TNS1	8.17	9.54	7.59	MT > RD
51105	PHF20L1	9.21	9.44	7.92	
29091	STXBP6	9.23	9.35	6.50	
641371	ACOT1	8.20	9.20	7.87	
2073	ERCC5	8.76	9.12	7.72	
54841	BIVM	8.71	9.09	7.64	
57568	SIPA1L2	6.47	9.05	8.46	
83641	FAM107B	8.20	8.90	7.86	
56999	ADAMTS9	6.42	8.70	6.35	MT > RD
6560	SLC12A4	7.96	8.69	7.38	
10531	PITRM1	9.40	8.58	7.36	

5797	PTPRM	7.84	8.56	6.70
25825	BACE2	9.10	8.50	6.50
8613	PPAP2B	10.10	8.41	6.47
1948	EFNB2	10.25	8.41	6.38
28232	SLCO3A1	7.42	8.36	6.55
389125	MUSTN1	6.69	8.33	6.98
84899	TMTC4	7.41	8.24	6.99
113802	HENMT1	8.11	8.20	6.62
6387	CXCL12	8.24	7.94	6.43
9935	MAFB	6.38	7.59	6.40
10351	ABCA8	7.26	7.48	6.46
1755	DMBT1	8.35	7.46	6.24
Higher MyoD region in RD cells				
1908	EDN3	6.30	6.28	10.65
23266	LPHN2	6.28	6.52	10.39
7852	CXCR4	6.33	7.14	10.95
7991	TUSC3	7.50	7.01	10.57
6335	SCN9A	6.83	7.18	9.94
84141	FAM176A	10.10	7.51	9.55
63939	C20orf177	7.99	8.66	10.70
64093	SMOC1	6.49	6.46	8.21
57419	SLC24A3	6.43	6.42	7.94
5509	PPP1R3D	7.15	6.83	8.22
2737	GLI3	6.91	6.83	8.21
116154	PHACTR3	6.32	6.25	7.59
9844	ELMO1	6.59	6.47	7.80

[a] Myoblast value lists the mean value from three biologically independent myoblast RNA samples.

[b] Myotube value lists the mean value from three primary human myotube RNA samples.

[c] RD value represents the mean value from three RD RNA samples.

[d] The designation of MT>RD indicates those members of this table that were also identified in the proximal promoter analysis as having higher MyoD peaks and gene expression in myotubes compared to RD cells.

Supplemental Table S8. Clinical information for the primary rhabdomyosarcoma patient samples and Reduced Representation Bisulfite Sequencing at the CpG shore in the promoter of *JDP2*.

Sample		RRBS Reads[a]						
		Region 1[b,c]		Region 2				
Primary Tumors	Diagnosis	A	B	A	B	C	D	E
1	ARMS	1/1	1/1	0/1	1/1	0/1	1/1	0/1
2	ARMS	1/1	1/1	1/1	1/1	1/1	1/1	1/1
3	ERMS (lung)	2/4	4/4	0/4	0/4	2/4	0/4	4/4
4	ERMS	15/23; 9/9	19/21; 5/8	1/9; 3/21	4/21; 4/9	6/9; 8/21	10/21; 3/9	21/23; 7/15
5	ERMS	13/25; 5/5	15/23; 4/5	2/5; 9/23	4/5; 8/23	2/5; 7/23	4/5; 9/23	23/29; 7/10
6	ARMS	19/23; 5/6	18/23; 4/4	17/23; 5/5	17/23; 5/5	18/23; 5/5	18/23; 5/5	21/26; 7/10
7	ERMS (botryoid)	18/24; 4/4	17/23; 3/4	1/4; 10/24	1/4; 8/24	2/4; 9/24	15/24; 2/4	2/6; 24/27
8	ARMS	1/6	3/6	2/6	1/6	0/6	5/6	5/6
9	ARMS	1/1; 5/5	1/1; 5/5	0/1; 4/5	1/1; 3/5	1/1; 4/5	1/1; 5/5	0/1; 5/7
10	ARMS	1/5	2/4	1/4	0/4	2/4	1/4	4/4
11	ARMS	1/1; 2/6	0/1; 2/4	0/4; 0/4	0/4; 0/4	0/4; 0/4	0/3; 0/4	0/3; 4/4
12	ERMS	48/66; 7/7	4/6; 56/65	1/7; 25/65	35/65; 5/7	36/65; 6/7	31/65; 5/7	10/16; 61/80
13	ERMS	21/34; 8/8	10/10; 27/33	6/11; 9/32	5/11; 7/33	10/33; 3/11	10/33; 6/11	30/37; 5/15
Cultured Cells								
RDs	N/A	3/3; 3/3	3/3; 3/3	3/3; 3/3	3/3; 3/3	3/3; 3/3	3/3; 3/3	4/4; 4/4
Primary myotubes	N/A	5/5; 8/41	1/6; 7/40	0/6; 3/40	0/6; 2/40	0/6; 3/40	0/5; 3/40	37/41; 4/8
Adult Muscle								
Sample 1	N/A	3/4; 6/28	1/4; 10/27	0/4; 2/27	1/27; 1/4	1/27; 1/4	0/27; 1/4	0/4; 24/27
Sample 2	N/A	3/3; 6/19	0/2; 8/19	0/3; 3/19	0/3; 3/19	0/3; 3/19	0/3; 4/19	19/21; 3/6

[a] The number of reads positive for methylation are represented as # methylated CpG reads/total # of reads for the indicated CpG.

[b] Fields with two fractions separated by a semicolon represent data from the positive (first value) and negative (second value) strands.

[c] The indicated regions and positions within the regions are as depicted in Figure 6.