

Supplemental Table S1

Pathways Up-Regulated in Maturation: RNA-Seq: MiMaC Vs EV CMs			
pathways	pvals	FDR	
HALLMARK_TNFA_SIGNALING_VIA_NFKB		1.03791E-19	5.18955E-18
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION		5.25223E-16	1.31306E-14
HALLMARK_HYPOXIA		3.12655E-11	5.21092E-10
HALLMARK_APICAL_JUNCTION		9.58324E-09	1.1979E-07
HALLMARK_APOPTOSIS		3.83669E-08	3.83669E-07
HALLMARK_INTERFERON_GAMMA_RESPONSE		4.93238E-08	4.11032E-07
HALLMARK_MYOGENESIS		1.25262E-07	8.94725E-07
HALLMARK_IL2_STAT5_SIGNALING		2.45827E-07	1.53642E-06
HALLMARK_ESTROGEN_RESPONSE_EARLY		8.14596E-07	4.52553E-06
HALLMARK_MTORC1_SIGNALING		1.04319E-06	5.21596E-06
HALLMARK_P53_PATHWAY		4.32939E-06	1.80391E-05
HALLMARK_COAGULATION		4.05167E-06	1.80391E-05
HALLMARK_HEDGEHOG_SIGNALING		5.65155E-06	2.17367E-05
HALLMARK_KRAS_SIGNALING_UP		8.35232E-06	2.98297E-05
HALLMARK_ESTROGEN_RESPONSE_LATE		1.39562E-05	4.65205E-05
HALLMARK_APICAL_SURFACE		0.000331332	0.001035413
HALLMARK_IL6_JAK_STAT3_SIGNALING		0.000517013	0.001520626
HALLMARK_CHOLESTEROL_HOMEOSTASIS		0.000601462	0.001670729
HALLMARK_XENOBIOTIC_METABOLISM		0.000868092	0.002284452
HALLMARK_ANGIOGENESIS		0.001108458	0.002639186
HALLMARK_ALLOGRAFT_REJECTION		0.001077736	0.002639186
HALLMARK_INTERFERON_ALPHA_RESPONSE		0.001530494	0.003478396
HALLMARK_GLYCOLYSIS		0.001942209	0.004222194
HALLMARK_INFLAMMATORY_RESPONSE		0.002208148	0.004600309
HALLMARK_MITOTIC_SPINDLE		0.002311937	0.004623874
HALLMARK_NOTCH_SIGNALING		0.010810557	0.020789532
HALLMARK_PI3K_AKT_MTOR_SIGNALING		0.014356109	0.026585386
HALLMARK_UV_RESPONSE_DN		0.017143679	0.030613713
HALLMARK_UV_RESPONSE_UP		0.022446925	0.038701594
HALLMARK_COMPLEMENT		0.034403115	0.057338526
HALLMARK_TGF_BETA_SIGNALING		0.042950371	0.069274792
HALLMARK_ANDROGEN_RESPONSE		0.050262707	0.078535479
HALLMARK_UNFOLDED_PROTEIN_RESPONSE		0.073072475	0.110715872
HALLMARK_WNT_BETA_CATENIN_SIGNALING		0.108513446	0.159578597
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY		0.137246543	0.19606649
HALLMARK_PEROXISOME		0.168309623	0.228162521
HALLMARK_KRAS_SIGNALING_DN		0.168840266	0.228162521
HALLMARK_ADIPOGENESIS		0.277938071	0.365707988
HALLMARK_G2M_CHECKPOINT		0.313456815	0.401867711
HALLMARK_MYC_TARGETS_V2		0.569863123	0.712328903
HALLMARK_FATTY_ACID_METABOLISM		0.621091747	0.75742896
HALLMARK_HEME_METABOLISM		0.740918005	0.882045244
HALLMARK_BILE_ACID_METABOLISM		0.763420411	0.887698152
HALLMARK_DNA_REPAIR		1	1
HALLMARK_PROTEIN_SECRETION		1	1
HALLMARK_E2F_TARGETS		0.944420888	1
HALLMARK_MYC_TARGETS_V1		1	1
HALLMARK_OXIDATIVE_PHOSPHORYLATION		1	1
HALLMARK_SPERMATOGENESIS		1	1
HALLMARK_PANCREAS_BETA_CELLS		1	1

Pathways Down-Regulated in Maturation: RNA-Seq: MiMaC Vs EV CMs			
pathways	pvals	FDR	
HALLMARK_MITOTIC_SPINDLE	0.000316702	0.015835094	
HALLMARK_G2M_CHECKPOINT	0.003245515	0.05843401	
HALLMARK_E2F_TARGETS	0.003506041	0.05843401	
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.901606965	1	
HALLMARK_HYPOXIA	0.909752348	1	
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0.787478886	1	
HALLMARK_WNT_BETA_CATENIN_SIGNALING	0.567515339	1	
HALLMARK_TGF_BETA_SIGNALING	0.318822358	1	
HALLMARK_IL6_JAK_STAT3_SIGNALING	0.439857677	1	
HALLMARK_DNA_REPAIR	1	1	
HALLMARK_APOPTOSIS	0.395059767	1	
HALLMARK_NOTCH_SIGNALING	1	1	
HALLMARK_ADIPOGENESIS	0.555558131	1	
HALLMARK_ESTROGEN_RESPONSE_EARLY	0.584942236	1	
HALLMARK_ESTROGEN_RESPONSE_LATE	0.094068056	1	
HALLMARK_ANDROGEN_RESPONSE	0.608147322	1	
HALLMARK_MYOGENESIS	0.774695802	1	
HALLMARK_PROTEIN_SECRETION	0.602438002	1	
HALLMARK_INTERFERON_ALPHA_RESPONSE	1	1	
HALLMARK_INTERFERON_GAMMA_RESPONSE	0.732442376	1	
HALLMARK_APICAL_JUNCTION	0.542631473	1	
HALLMARK_APICAL_SURFACE	1	1	
HALLMARK_HEDGEHOG_SIGNALING	0.497240247	1	
HALLMARK_COMPLEMENT	0.145829824	1	
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.676732284	1	
HALLMARK_PI3K_AKT_MTOR_SIGNALING	0.624900736	1	
HALLMARK_MTORC1_SIGNALING	0.789426486	1	
HALLMARK_MYC_TARGETS_V1	0.985430409	1	
HALLMARK_MYC_TARGETS_V2	0.712676608	1	
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.576661301	1	
HALLMARK_INFLAMMATORY_RESPONSE	0.65985536	1	
HALLMARK_XENOBIOTIC_METABOLISM	0.881221283	1	
HALLMARK_FATTY_ACID_METABOLISM	0.95604267	1	
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.986048672	1	
HALLMARK_GLYCOLYSIS	0.386760649	1	
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	1	1	
HALLMARK_P53_PATHWAY	0.915809983	1	
HALLMARK_UV_RESPONSE_UP	0.96139245	1	
HALLMARK_UV_RESPONSE_DN	0.583724384	1	
HALLMARK_ANGIOGENESIS	0.497240247	1	
HALLMARK_HEME_METABOLISM	0.980265868	1	
HALLMARK_COAGULATION	0.904316675	1	
HALLMARK_IL2_STAT5_SIGNALING	0.718250109	1	
HALLMARK_BILE_ACID_METABOLISM	1	1	
HALLMARK_PEROXISOME	0.878679228	1	
HALLMARK_ALLOGRAFT_REJECTION	0.807521966	1	
HALLMARK_SPERMATOGENESIS	0.38051365	1	
HALLMARK_KRAS_SIGNALING_UP	0.976018315	1	
HALLMARK_KRAS_SIGNALING_DN	0.959685577	1	
HALLMARK_PANCREAS_BETA_CELLS	0.452081412	1	

Supplemental Table S2

Categories	Genes
cardiac markers	MYL7
cardiac markers	MYH7
cardiac markers	NKX2-5
cardiac markers	GATA4
up-regulated	ANKRD1
up-regulated	NPPB
up-regulated	ACTA1
up-regulated	SYNPO2L
up-regulated	FLNC
up-regulated	CTGF
up-regulated	MYH7
up-regulated	XIRP1
up-regulated	NES
up-regulated	COL5A2
up-regulated	SYNPO2
up-regulated	GPC1
up-regulated	ACTN1
up-regulated	VCL
up-regulated	ATP2B4
up-regulated	MAP1B
up-regulated	MCAM
up-regulated	RAI14
up-regulated	PDLIM3
up-regulated	PTRF
down-regulated	RPL5
down-regulated	MYH6
down-regulated	RPL35A
down-regulated	ATP5J2
down-regulated	PLN
down-regulated	LINC00881
down-regulated	RPS4X
down-regulated	EIF3E
down-regulated	NDUFS5
down-regulated	RPL31
down-regulated	RPL36AL
down-regulated	RPL6
down-regulated	FHL2
down-regulated	RPL24
down-regulated	FTL
down-regulated	IFITM3
down-regulated	RPL17
down-regulated	EMC10
down-regulated	CCDC80
down-regulated	IGFBP5
OXPPOS	COX7B
OXPPOS	NDUFA6
OXPPOS	ATP5H
OXPPOS	ATP5J2
OXPPOS	NDUFB4

Supplemental Table S3**Human cardiac maturation markers**

TGM2

S100A11

RPL36AL

SH3BGRL3

SLIRP

HSPB1

COX7B

NDUFB4

FTL

GSTP1

S100A10

TAGLN

FLNC

GPC1

RRAS

XRP1

ANKRD1

NPPB

SYNM

SYNPO2

CNN1

ACTA1

TNFRSF12A

PDLIM3

SOD3

AQP1

MYH7

Supplemental Table S4

Pathways Up-Regulated in Maturation-scSeq: Cluster 2 (MiMaC) Vs. Cluster 0 (EV)		
pathways	pvals	FDR
EPITHELIAL_MESENCHYMAL_TRANSITION	1.99072E-15	9.95359E-14
MYOGENESIS	3.06028E-13	7.6507E-12
APICAL_JUNCTION	4.24323E-12	7.07205E-11
HYPOXIA	1.01573E-08	1.26967E-07
TNFA_SIGNALING_VIA_NFKB	1.08449E-06	1.08449E-05
MITOTIC_SPINDLE	5.60548E-06	4.67124E-05
UV_RESPONSE_DN	7.8887E-05	0.000563478
INFLAMMATORY_RESPONSE	0.000139101	0.000869382
APOPTOSIS	0.000300358	0.001668656
COAGULATION	0.000883156	0.004415781
GLYCOLYSIS	0.001232678	0.005192056
KRAS_SIGNALING_DN	0.001246093	0.005192056
MTORC1_SIGNALING	0.006759655	0.025998674
KRAS_SIGNALING_UP	0.01555718	0.055561356
ANDROGEN_RESPONSE	0.024943623	0.083145409
CHOLESTEROL_HOMEOSTASIS	0.029587894	0.092462168
REACTIVE_OXYGEN_SPECIES_PATHWAY	0.033802563	0.099419302
APICAL_SURFACE	0.043343798	0.12039944
ESTROGEN_RESPONSE_LATE	0.05692918	0.149813631
TGF_BETA_SIGNALING	0.064364411	0.160911028
ESTROGEN_RESPONSE_EARLY	0.074249887	0.176785446
ANGIOGENESIS	0.08312261	0.188915022
IL6_JAK_STAT3_SIGNALING	0.109302768	0.229210294
ADIPOGENESIS	0.110020941	0.229210294
COMPLEMENT	0.116845869	0.233691738
ALLOGRAFT_REJECTION	0.13121706	0.252340499
IL2_STAT5_SIGNALING	0.162295082	0.300546448
FATTY_ACID_METABOLISM	0.20865226	0.372593322
P53_PATHWAY	0.319427045	0.550736285
HEDGEHOG_SIGNALING	0.33191622	0.553193701
NOTCH_SIGNALING	0.345964373	0.558007053
PI3K_AKT_MTOR_SIGNALING	0.412188197	0.644044057
G2M_CHECKPOINT	0.468508865	0.709861916
PROTEIN_SECRETION	0.554669517	0.815690466
OXIDATIVE_PHOSPHORYLATION	0.580498891	0.82008414
SPERMATOGENESIS	0.590460581	0.82008414
UNFOLDED_PROTEIN_RESPONSE	0.624501667	0.835902497
XENOBIOTIC_METABOLISM	0.635285897	0.835902497
BILE_ACID_METABOLISM	0.661947939	0.848651204
E2F_TARGETS	0.738352078	0.922940098
PEROXISOME	0.759746666	0.926520324
INTERFERON_GAMMA_RESPONSE	0.814107355	0.969175423
UV_RESPONSE_UP	0.88395345	1
HEME_METABOLISM	0.939076063	1
WNT_BETA_CATENIN_SIGNALING	1	1
DNA_REPAIR	1	1
INTERFERON_ALPHA_RESPONSE	1	1
MYC_TARGETS_V1	1	1
MYC_TARGETS_V2	1	1
PANCREAS_BETA_CELLS	1	1

Pathways Down-Regulated in Maturation-scSeq: Cluster 2 (MiMaC) Vs. Cluster 0 (EV)		
pathways	pvals	FDR
EPITHELIAL_MESENCHYMAL_TRANSITION	0.004001744	0.167856649
MYOGENESIS	0.006714266	0.167856649
WNT_BETA_CATENIN_SIGNALING	0.019994978	0.33324964
UV_RESPONSE_DN	0.055920972	0.699012155
APICAL_JUNCTION	0.072097233	0.701062609
ALLOGRAFT_REJECTION	0.085073512	0.701062609
P53_PATHWAY	0.098148765	0.701062609
INTERFERON_GAMMA_RESPONSE	0.134505279	0.752383447
HEDGEHOG_SIGNALING	0.143514144	0.752383447
NOTCH_SIGNALING	0.150476689	0.752383447
ANGIOGENESIS	0.171030981	0.777413549
MYC_TARGETS_V1	0.187485347	0.781188946
ESTROGEN_RESPONSE_EARLY	0.215342908	0.828241952
INTERFERON_ALPHA_RESPONSE	0.248454068	0.887335959
GLYCOLYSIS	0.26944252	0.898141733
COMPLEMENT	0.517340214	1
ESTROGEN_RESPONSE_LATE	0.555468653	1
IL2_STAT5_SIGNALING	0.562729742	1
APOPTOSIS	0.569873783	1
HYPOXIA	0.65290342	1
HEME_METABOLISM	0.658591567	1
MTORC1_SIGNALING	0.733656106	1
OXIDATIVE_PHOSPHORYLATION	0.795813212	1
TNFA_SIGNALING_VIA_NFKB	1	1
CHOLESTEROL_HOMEOSTASIS	1	1
MITOTIC_SPINDLE	1	1
TGF_BETA_SIGNALING	1	1
IL6_JAK_STAT3_SIGNALING	1	1
DNA_REPAIR	1	1
G2M_CHECKPOINT	1	1
ADIPOGENESIS	1	1
ANDROGEN_RESPONSE	1	1
PROTEIN_SECRETION	1	1
APICAL_SURFACE	1	1
UNFOLDED_PROTEIN_RESPONSE	1	1
PI3K_AKT_MTOR_SIGNALING	1	1
E2F_TARGETS	1	1
MYC_TARGETS_V2	1	1
INFLAMMATORY_RESPONSE	1	1
XENOBIOTIC_METABOLISM	1	1
FATTY_ACID_METABOLISM	1	1
REACTIVE_OXYGEN_SPECIES_PATHWAY	1	1
UV_RESPONSE_UP	1	1
COAGULATION	1	1
BILE_ACID_METABOLISM	1	1
PEROXISOME	1	1
SPERMATOGENESIS	1	1
KRAS_SIGNALING_UP	1	1
KRAS_SIGNALING_DN	1	1
PANCREAS_BETA_CELLS	1	1

Supplemental Table S5

Pathways Up-Regulated in Maturation-scSeq: MiMaC+FA Condition Vs. MiMaC Condition			
pathways	pvals	FDR	
EPITHELIAL_MESENCHYMAL_TRANSITION	5.91207E-05	0.002956035	
HYPOXIA	0.00170467	0.042616748	
UV_RESPONSE_DN	0.014359193	0.239319878	
MYC_TARGETS_V1	0.101182829	0.715921072	
TGF_BETA_SIGNALING	0.117422851	0.715921072	
TNFA_SIGNALING_VIA_NFKB	0.15057313	0.715921072	
INFLAMMATORY_RESPONSE	0.168081386	0.715921072	
FATTY_ACID_METABOLISM	0.190066437	0.715921072	
ALLOGRAFT_REJECTION	0.192189232	0.715921072	
APICAL_JUNCTION	0.21421686	0.715921072	
HEDGEHOG_SIGNALING	0.22649004	0.715921072	
PI3K_AKT_MTOR_SIGNALING	0.226609885	0.715921072	
PEROXISOME	0.226609885	0.715921072	
GLYCOLYSIS	0.235415046	0.715921072	
NOTCH_SIGNALING	0.236886229	0.715921072	
OXIDATIVE_PHOSPHORYLATION	0.259927986	0.715921072	
ANGIOGENESIS	0.267250409	0.715921072	
P53_PATHWAY	0.27513661	0.715921072	
MITOTIC_SPINDLE	0.278787425	0.715921072	
ANDROGEN_RESPONSE	0.286368429	0.715921072	
IL6_JAK_STAT3_SIGNALING	0.305879308	0.717045433	
MYOGENESIS	0.31549999	0.717045433	
COMPLEMENT	0.335890489	0.730196715	
MTORC1_SIGNALING	0.367020398	0.76462583	
ESTROGEN_RESPONSE_LATE	0.384389019	0.76664528	
XENOBIOTIC_METABOLISM	0.398655546	0.76664528	
MYC_TARGETS_V2	0.448738451	0.826894196	
DNA_REPAIR	0.46306075	0.826894196	
G2M_CHECKPOINT	0.485087045	0.830058367	
E2F_TARGETS	0.49803502	0.830058367	
COAGULATION	0.518715681	0.830648797	
CHOLESTEROL_HOMEOSTASIS	0.53161523	0.830648797	
ADIPOGENESIS	0.622709427	0.943499132	
UNFOLDED_PROTEIN_RESPONSE	0.742741503	1	
IL2_STATS_SIGNALING	0.746229754	1	
APOPTOSIS	0.753066116	1	
WNT_BETA_CATENIN_SIGNALING	1	1	
ESTROGEN_RESPONSE_EARLY	1	1	
PROTEIN_SECRETION	1	1	
INTERFERON_ALPHA_RESPONSE	1	1	
INTERFERON_GAMMA_RESPONSE	1	1	
APICAL_SURFACE	1	1	
REACTIVE_OXIGEN_SPECIES_PATHWAY	1	1	
UV_RESPONSE_UP	1	1	
HEME_METABOLISM	1	1	
BILE_ACID_METABOLISM	1	1	
SPERMATOGENESIS	1	1	
KRAS_SIGNALING_UP	1	1	
KRAS_SIGNALING_DN	1	1	
PANCREAS_BETA_CELLS	1	1	

Pathways Down-Regulated in Maturation-scSeq: MiMaC+FA Condition Vs. MiMaC Condition			
pathways	pvals	FDR	
P53_PATHWAY	0.003710748	0.185537422	
MTORC1_SIGNALING	0.00919082	0.190280752	
HYPOXIA	0.011416845	0.190280752	
IL2_STATS_SIGNALING	0.060126498	0.530883303	
OXIDATIVE_PHOSPHORYLATION	0.063268579	0.530883303	
APOPTOSIS	0.063705996	0.530883303	
GLYCOLYSIS	0.110066458	0.786188987	
BILE_ACID_METABOLISM	0.170550364	1	
KRAS_SIGNALING_UP	0.272460574	1	
WNT_BETA_CATENIN_SIGNALING	0.328161875	1	
MYOGENESIS	0.363495866	1	
REACTIVE_OXIGEN_SPECIES_PATHWAY	0.394103832	1	
TNFA_SIGNALING_VIA_NFKB	0.430757953	1	
MYC_TARGETS_V1	0.506066835	1	
DNA_REPAIR	0.507789553	1	
E2F_TARGETS	0.543712263	1	
COAGULATION	0.549163714	1	
INFLAMMATORY_RESPONSE	0.555785724	1	
HEME_METABOLISM	0.573634237	1	
ALLOGRAFT_REJECTION	0.587475089	1	
MITOTIC_SPINDLE	0.598138141	1	
PI3K_AKT_MTOR_SIGNALING	0.628104185	1	
PEROXISOME	0.628104185	1	
INTERFERON_GAMMA_RESPONSE	0.68872205	1	
PROTEIN_SECRETION	0.727650396	1	
COMPLEMENT	0.731665597	1	
ESTROGEN_RESPONSE_LATE	0.768722502	1	
UNFOLDED_PROTEIN_RESPONSE	0.772136285	1	
UV_RESPONSE_UP	0.775500047	1	
ESTROGEN_RESPONSE_EARLY	0.794672182	1	
UV_RESPONSE_DN	0.794672182	1	
FATTY_ACID_METABOLISM	0.809400769	1	
APICAL_JUNCTION	0.828274862	1	
G2M_CHECKPOINT	0.833318183	1	
EPITHELIAL_MESENCHYMAL_TRANSITION	0.854253743	1	
ADIPOGENESIS	0.901173041	1	
CHOLESTEROL_HOMEOSTASIS	1	1	
TGF_BETA_SIGNALING	1	1	
IL6_JAK_STAT3_SIGNALING	1	1	
NOTCH_SIGNALING	1	1	
ANDROGEN_RESPONSE	1	1	
INTERFERON_ALPHA_RESPONSE	1	1	
APICAL_SURFACE	1	1	
HEDGEHOG_SIGNALING	1	1	
MYC_TARGETS_V2	1	1	
XENOBIOTIC_METABOLISM	1	1	
ANGIOGENESIS	1	1	
SPERMATOGENESIS	1	1	
KRAS_SIGNALING_DN	1	1	
PANCREAS_BETA_CELLS	1	1	

Supplemental Table S6

Pathways Up-Regulated in Maturation-scSeq: Cluster 1 (Intermediate) Vs. Cluster 0 (EV)			
pathways	pvals	FDR	
OXIDATIVE_PHOSPHORYLATION	6.15396E-44	3.07698E-42	
MYC_TARGETS_V1	7.26069E-12	1.81517E-10	
REACTIVE_OXIGEN_SPECIES_PATHWAY	2.71479E-08	4.52465E-07	
DNA_REPAIR	0.000126115	0.001576431	
ADIPOGENESIS	0.000478003	0.004780029	
ALLOGRAFT_REJECTION	0.02411717	0.200976417	
APOPTOSIS	0.058887528	0.420625201	
PANCREAS_BETA_CELLS	0.080223842	0.501399014	
GLYCOLYSIS	0.146522111	0.756812295	
MTORC1_SIGNALING	0.151362459	0.756812295	
MYOGENESIS	0.168982202	0.76810092	
P53_PATHWAY	0.206428115	0.780279039	
UV_RESPONSE_UP	0.211292795	0.780279039	
PEROXISOME	0.218478131	0.780279039	
NOTCH_SIGNALING	0.249246046	0.830820154	
HYPOXIA	0.279583005	0.873696892	
UNFOLDED_PROTEIN_RESPONSE	0.348309835	0.985187869	
MYC_TARGETS_V2	0.354667633	0.985187869	
IL6_JAK_STAT3_SIGNALING	0.374701535	0.986056672	
BILE_ACID_METABOLISM	0.446270583	1	
FATTY_ACID_METABOLISM	0.452177657	1	
COAGULATION	0.483993664	1	
APICAL_SURFACE	0.545308354	1	
EZF_TARGETS	0.551931106	1	
EPITHELIAL_MESENCHYMAL_TRANSITION	0.598626694	1	
PROTEIN_SECRETION	0.616061986	1	
PI3K_AKT_MTOR_SIGNALING	0.630906346	1	
ANGIOGENESIS	0.678058588	1	
ESTROGEN_RESPONSE_LATE	0.706922537	1	
ANDROGEN_RESPONSE	0.738505208	1	
CHOLESTEROL_HOMEOSTASIS	0.757896944	1	
COMPLEMENT	0.807849404	1	
INTERFERON_ALPHA_RESPONSE	0.821981556	1	
APICAL_JUNCTION	0.830081706	1	
G2M_CHECKPOINT	0.839633837	1	
KRAS_SIGNALING_DN	0.853910834	1	
IL2_STATS_SIGNALING	0.869977814	1	
TGF_BETA_SIGNALING	0.885907922	1	
ESTROGEN_RESPONSE_EARLY	0.893829395	1	
INTERFERON_GAMMA_RESPONSE	0.898879928	1	
HEME_METABOLISM	0.954672705	1	
XENOBIOTIC_METABOLISM	0.960167363	1	
UV_RESPONSE_DN	0.967653315	1	
KRAS_SIGNALING_UP	0.968522189	1	
TNFA_SIGNALING_VIA_NFKB	0.992909243	1	
MITOTIC_SPINDLE	1	1	
WNT_BETA_CATENIN_SIGNALING	1	1	
HEDGEHOG_SIGNALING	1	1	
INFLAMMATORY_RESPONSE	1	1	
SPERMATOGENESIS	1	1	

Pathways Down-Regulated in Maturation-scSeq: Cluster 1 (Intermediate) Vs. Cluster 0 (EV)			
pathways	pvals	FDR	
EPITHELIAL_MESENCHYMAL_TRANSITION	6.90826E-07	3.298E-05	
MYOGENESIS	1.3192E-06	3.298E-05	
UV_RESPONSE_DN	1.20093E-05	0.000200155	
ANDROGEN_RESPONSE	2.56253E-05	0.000320317	
APICAL_JUNCTION	8.05178E-05	0.000805178	
CHOLESTEROL_HOMEOSTASIS	0.001568361	0.013069676	
MITOTIC_SPINDLE	0.003832946	0.024129492	
ANGIOGENESIS	0.003860719	0.024129492	
IL2_STATS_SIGNALING	0.005261773	0.029232074	
WNT_BETA_CATENIN_SIGNALING	0.010068172	0.050340861	
TGF_BETA_SIGNALING	0.018376972	0.083531692	
HEDGEHOG_SIGNALING	0.026791926	0.104705797	
KRAS_SIGNALING_UP	0.027223507	0.104705797	
PROTEIN_SECRETION	0.032383437	0.115655131	
ESTROGEN_RESPONSE_EARLY	0.038844752	0.129482506	
APICAL_SURFACE	0.0551342	0.172294374	
HEME_METABOLISM	0.060560945	0.178120426	
KRAS_SIGNALING_DN	0.066096782	0.183602172	
GLYCOLYSIS	0.119285255	0.313908565	
ADIPOGENESIS	0.137072934	0.342682334	
HYPOXIA	0.145284416	0.345915277	
G2M_CHECKPOINT	0.155210267	0.352750607	
INTERFERON_GAMMA_RESPONSE	0.198459307	0.419647087	
COMPLEMENT	0.20474089	0.419647087	
ESTROGEN_RESPONSE_LATE	0.209823544	0.419647087	
UV_RESPONSE_UP	0.229832507	0.441985591	
MTORC1_SIGNALING	0.242026039	0.445840036	
INFLAMMATORY_RESPONSE	0.24967042	0.445840036	
UNFOLDED_PROTEIN_RESPONSE	0.32826327	0.565971155	
REACTIVE_OXIGEN_SPECIES_PATHWAY	0.392595228	0.65432538	
PI3K_AKT_MTOR_SIGNALING	0.435264365	0.702039298	
XENOBIOTIC_METABOLISM	0.483071259	0.729135684	
ALLOGRAFT_REJECTION	0.492405117	0.729135684	
APOPTOSIS	0.495812265	0.729135684	
BILE_ACID_METABOLISM	0.522706402	0.746723431	
NOTCH_SIGNALING	0.568654106	0.777015127	
COAGULATION	0.574991194	0.777015127	
PEROXISOME	0.603247362	0.793746528	
PANCREAS_BETA_CELLS	0.624415223	0.800532338	
INTERFERON_ALPHA_RESPONSE	0.646252621	0.807815776	
TNFA_SIGNALING_VIA_NFKB	0.726390091	0.885841575	
OXIDATIVE_PHOSPHORYLATION	0.807128461	0.924149402	
P53_PATHWAY	0.826974404	0.924149402	
EZF_TARGETS	0.828919134	0.924149402	
FATTY_ACID_METABOLISM	0.831734461	0.924149402	
SPERMATOGENESIS	0.913293126	0.971301573	
IL6_JAK_STAT3_SIGNALING	0.929107552	0.971301573	
MYC_TARGETS_V1	0.93244951	0.971301573	
DNA_REPAIR	0.986822991	1	
MYC_TARGETS_V2	1	1	

Supplemental Table S7

Categories	Genes
cardiac markers	MYL7
cardiac markers	MYH7
cardiac markers	NKX2-5
cardiac markers	GATA4
up-regulated	CDKN1A
up-regulated	MTRNR2L1
up-regulated	PLCG2
up-regulated	MYH6
up-regulated	DKK3
up-regulated	RPS27L
up-regulated	AC090498.1
up-regulated	NPPA
up-regulated	ANKRD1
up-regulated	MEG3
up-regulated	MTRNR2L8
up-regulated	ZMAT3
up-regulated	MTRNR2L12
up-regulated	SYNPO2L
up-regulated	NPPB
up-regulated	NES
up-regulated	PAM
up-regulated	CASQ2
up-regulated	SYNPO2
up-regulated	PLD3
down-regulated	RPLP1
down-regulated	RPS12
down-regulated	RPL23A
down-regulated	IFI6
down-regulated	RPL37
down-regulated	HIST1H4C
down-regulated	TUBA1B
down-regulated	ACTB
down-regulated	TMSB4X
down-regulated	RPL39
down-regulated	HMGN2
down-regulated	RPS6
down-regulated	COL1A2
down-regulated	H2AFZ
down-regulated	IFITM3
down-regulated	COL1A1
down-regulated	PTMA
down-regulated	CCDC80
down-regulated	IGFBP5
down-regulated	COL3A1
OXPPOS	ATP5O
OXPPOS	ATP5G3
OXPPOS	COX5B
OXPPOS	COX7B

OXPHOS	COX5A
OXPHOS	COX6B1
OXPHOS	ATP5H
OXPHOS	ATP5J2
OXPHOS	UQCQRQ
OXPHOS	ATP5L
OXPHOS	NDUFB4
OXPHOS	ATP1B1
Cell cycle	BIRC5
Cell cycle	TOP2A
Cell cycle	PRC1
Cell cycle	ANLN
Cell cycle	CENPF
Cell cycle	TPX2
Cell cycle	CDK1
Cell cycle	NUSAP1
Cell cycle	SMC4
non-CM markers	COL1A1
non-CM markers	ENC1
non-CM markers	DCN
non-CM markers	COL5A1
non-CM markers	THY1
non-CM markers	WT1
non-CM markers	TBX18

Supplemental Table S8

Pathways Up-Regulated in HADHA-scSeq: Cluster 0 (HADHA Mutant Non-endoreplicating) Vs. Cluster 3 (WT)			
pathways	pvals	FDR	
MYC_TARGETS_V1	9.33781E-06	0.000466891	
INTERFERON_ALPHA_RESPONSE	0.004026629	0.100665726	
ALLOGRAFT_REJECTION	0.009708816	0.161813598	
HEDGEHOG_SIGNALING	0.023403008	0.292537605	
WNT_BETA_CATENIN_SIGNALING	0.052265093	0.522650926	
P53_PATHWAY	0.089622108	0.746850901	
INTERFERON_GAMMA_RESPONSE	0.126758308	0.839061676	
KRAS_SIGNALING_DN	0.134249868	0.839061676	
PEROXISOME	0.207355918	1	
ANDROGEN_RESPONSE	0.23531219	1	
MYOGENESIS	0.242589031	1	
NOTCH_SIGNALING	0.255338249	1	
APOPTOSIS	0.398042084	1	
IL2_STATS_SIGNALING	0.420773647	1	
HEME_METABOLISM	0.482682484	1	
CHOLESTEROL_HOMEOSTASIS	0.497931667	1	
HYPOXIA	0.503557826	1	
MTORC1_SIGNALING	0.605406177	1	
E2F_TARGETS	0.628291183	1	
UNFOLDED_PROTEIN_RESPONSE	0.69041407	1	
FATTY_ACID_METABOLISM	0.731722546	1	
UV_RESPONSE_UP	0.740450136	1	
ESTROGEN_RESPONSE_LATE	0.751650274	1	
TNFA_SIGNALING_VIA_NFKB	0.76755767	1	
APICAL_JUNCTION	0.772632186	1	
ESTROGEN_RESPONSE_EARLY	0.782453852	1	
EPITHELIAL_MESENCHYMAL_TRANSITION	0.821693309	1	
GLYCOLYSIS	0.821693309	1	
G2M_CHECKPOINT	0.870669284	1	
OXIDATIVE_PHOSPHORYLATION	0.88424864	1	
MITOTIC_SPINDLE	1	1	
TGF_BETA_SIGNALING	1	1	
IL6_JAK_STAT3_SIGNALING	1	1	
DNA_REPAIR	1	1	
ADIPOGENESIS	1	1	
PROTEIN_SECRETION	1	1	
APICAL_SURFACE	1	1	
COMPLEMENT	1	1	
PI3K_AKT_MTOR_SIGNALING	1	1	
MYC_TARGETS_V2	1	1	
INFLAMMATORY_RESPONSE	1	1	
XENOBIOTIC_METABOLISM	1	1	
REACTIVE_OXIGEN_SPECIES_PATHWAY	1	1	
UV_RESPONSE_DN	1	1	
ANGIOGENESIS	1	1	
COAGULATION	1	1	
BILE_ACID_METABOLISM	1	1	
SPERMATOGENESIS	1	1	
KRAS_SIGNALING_UP	1	1	
PANCREAS_BETA_CELLS	1	1	

ays Down-Regulated in HADHA-scSeq: Cluster 0 (HADHA Mutant Non-endoreplicating) Vs. Cluster :			
pathways	pvals	FDR	
MYOGENESIS	6.34362E-16	3.17181E-14	
EPITHELIAL_MESENCHYMAL_TRANSITION	2.48717E-13	6.21794E-12	
CHOLESTEROL_HOMEOSTASIS	1.13518E-12	1.89197E-11	
OXIDATIVE_PHOSPHORYLATION	3.31755E-10	4.14693E-09	
P53_PATHWAY	1.83099E-09	1.83099E-08	
APICAL_JUNCTION	3.50627E-09	2.92189E-08	
COAGULATION	0.000196151	0.001345259	
ANGIOGENESIS	0.000215241	0.001345259	
APOPTOSIS	0.000288361	0.001602003	
TNFA_SIGNALING_VIA_NFKB	0.000488944	0.002304292	
ANDROGEN_RESPONSE	0.000506944	0.002304292	
HYPOXIA	0.000669393	0.002789136	
MTORC1_SIGNALING	0.003952717	0.01520276	
XENOBIOTIC_METABOLISM	0.004422781	0.015508909	
KRAS_SIGNALING_UP	0.004652673	0.015508909	
ESTROGEN_RESPONSE_EARLY	0.006747959	0.021087371	
ESTROGEN_RESPONSE_LATE	0.009906342	0.029136299	
GLYCOLYSIS	0.015955553	0.044320981	
COMPLEMENT	0.036577191	0.096255766	
REACTIVE_OXIGEN_SPECIES_PATHWAY	0.043238166	0.102574953	
INFLAMMATORY_RESPONSE	0.045450574	0.102574953	
PEROXISOME	0.045450574	0.102574953	
FATTY_ACID_METABOLISM	0.047184478	0.102574953	
UV_RESPONSE_UP	0.053170665	0.110772219	
NOTCH_SIGNALING	0.059523153	0.119046306	
IL2_STATS_SIGNALING	0.073955635	0.142222376	
ALLOGRAFT_REJECTION	0.113784023	0.210711154	
BILE_ACID_METABOLISM	0.151586144	0.268828724	
DNA_REPAIR	0.15592066	0.268828724	
HEDGEHOG_SIGNALING	0.165692872	0.276154786	
PROTEIN_SECRETION	0.186814258	0.301313319	
ADIPOGENESIS	0.211570934	0.330579584	
UV_RESPONSE_DN	0.25493384	0.386263395	
PI3K_AKT_MTOR_SIGNALING	0.307027624	0.436147158	
WNT_BETA_CATENIN_SIGNALING	0.313974508	0.436147158	
KRAS_SIGNALING_DN	0.314025954	0.436147158	
MITOTIC_SPINDLE	0.420975128	0.568885308	
TGF_BETA_SIGNALING	0.489565317	0.64416489	
APICAL_SURFACE	0.525960882	0.674308823	
HEME_METABOLISM	0.736760695	0.894644884	
INTERFERON_GAMMA_RESPONSE	0.737412612	0.894644884	
IL6_JAK_STAT3_SIGNALING	0.751501703	0.894644884	
MYC_TARGETS_V1	0.790765434	0.919494691	
MYC_TARGETS_V2	0.845708747	0.961032667	
SPERMATOGENESIS	0.874236285	0.97137365	
G2M_CHECKPOINT	0.95038407	1	
UNFOLDED_PROTEIN_RESPONSE	0.973861807	1	
E2F_TARGETS	0.990030521	1	
INTERFERON_ALPHA_RESPONSE	1	1	
PANCREAS_BETA_CELLS	1	1	

Supplemental Table S9

Pathways Up-Regulated in HADHA-scSeq: Cluster 2 (HADHA Mutant endoreplicating) Vs. Cluster 3 (WT)			
pathways	pvals	FDR	
E2F_TARGETS	2.16664E-96	1.08332E-94	
G2M_CHECKPOINT	1.54661E-75	3.86651E-74	
MYC_TARGETS_V1	2.04081E-33	3.40135E-32	
MITOTIC_SPINDLE	3.05418E-14	3.81773E-13	
SPERMATOGENESIS	5.40019E-08	5.40019E-07	
MTORC1_SIGNALING	0.001076342	0.008969517	
GLYCOLYSIS	0.012837988	0.091699913	
MYC_TARGETS_V2	0.031751059	0.198444119	
DNA_REPAIR	0.066170808	0.367615602	
PEROXISOME	0.107218394	0.530488191	
ESTROGEN_RESPONSE_LATE	0.116707402	0.530488191	
UNFOLDED_PROTEIN_RESPONSE	0.132095491	0.550397878	
UV_RESPONSE_UP	0.206722355	0.795085983	
ALLOGRAFT_REJECTION	0.237116272	0.846843829	
INTERFERON_ALPHA_RESPONSE	0.305856089	1	
PANCREAS_BETA_CELLS	0.347405129	1	
APOPTOSIS	0.384557807	1	
PI3K_AKT_MTOR_SIGNALING	0.512681285	1	
HEDGEHOG_SIGNALING	0.51494318	1	
ANDROGEN_RESPONSE	0.520667363	1	
IL2_STATS_SIGNALING	0.62088764	1	
WNT_BETA_CATENIN_SIGNALING	0.672833968	1	
HEME_METABOLISM	0.713524598	1	
INTERFERON_GAMMA_RESPONSE	0.71729336	1	
FATTY_ACID_METABOLISM	0.749107896	1	
KRAS_SIGNALING_DN	0.856437714	1	
BILE_ACID_METABOLISM	0.869965285	1	
HYPOXIA	0.881438911	1	
APICAL_JUNCTION	0.935497999	1	
ESTROGEN_RESPONSE_EARLY	0.942133356	1	
PROTEIN_SECRETION	0.950113814	1	
P53_PATHWAY	0.963755054	1	
XENOBIOTIC_METABOLISM	0.975922472	1	
OXIDATIVE_PHOSPHORYLATION	0.988349313	1	
EPITHELIAL_MESENCHYMAL_TRANSITION	0.994415362	1	
TNFA_SIGNALING_VIA_NFKB	1	1	
CHOLESTEROL_HOMEOSTASIS	1	1	
TGF_BETA_SIGNALING	1	1	
IL6_JAK_STAT3_SIGNALING	1	1	
NOTCH_SIGNALING	1	1	
ADIPOGENESIS	1	1	
MYOGENESIS	1	1	
APICAL_SURFACE	1	1	
COMPLEMENT	1	1	
INFLAMMATORY_RESPONSE	1	1	
REACTIVE_OXIGEN_SPECIES_PATHWAY	1	1	
UV_RESPONSE_DN	1	1	
ANGIOGENESIS	1	1	
COAGULATION	1	1	
KRAS_SIGNALING_UP	1	1	

Pathways Down-Regulated in HADHA-scSeq: Cluster 2 (HADHA Mutant Non-endoreplicating) Vs. Cluster 3 (WT)			
pathways	pvals	FDR	
MYOGENESIS	1.19544E-25	5.97718E-24	
EPITHELIAL_MESENCHYMAL_TRANSITION	1.29069E-13	3.22672E-12	
P53_PATHWAY	7.64226E-10	1.27371E-08	
CHOLESTEROL_HOMEOSTASIS	6.55372E-08	8.19215E-07	
OXIDATIVE_PHOSPHORYLATION	8.77351E-08	8.77351E-07	
HYPOXIA	3.45689E-07	2.88074E-06	
APICAL_JUNCTION	4.72952E-05	0.000337823	
APOPTOSIS	7.71144E-05	0.000481965	
COAGULATION	9.69166E-05	0.000538425	
TNFA_SIGNALING_VIA_NFKB	0.000484158	0.002420788	
KRAS_SIGNALING_UP	0.000948095	0.004309525	
GLYCOLYSIS	0.002437321	0.010155502	
ANGIOGENESIS	0.003023773	0.011629896	
XENOBIOTIC_METABOLISM	0.010220098	0.036500348	
UV_RESPONSE_DN	0.022796534	0.072462216	
KRAS_SIGNALING_DN	0.023187909	0.072462216	
INFLAMMATORY_RESPONSE	0.02739745	0.078311441	
COMPLEMENT	0.028192119	0.078311441	
MTORC1_SIGNALING	0.050704516	0.133432937	
ADIPOGENESIS	0.058848728	0.147121819	
ALLOGRAFT_REJECTION	0.07000881	0.166687642	
UV_RESPONSE_UP	0.093183579	0.211780861	
ANDROGEN_RESPONSE	0.101220934	0.220045509	
ESTROGEN_RESPONSE_LATE	0.106969859	0.222853874	
IL2_STATS_SIGNALING	0.125692818	0.247484622	
PROTEIN_SECRETION	0.128692003	0.247484622	
FATTY_ACID_METABOLISM	0.167363179	0.309931812	
REACTIVE_OXIGEN_SPECIES_PATHWAY	0.190530927	0.334205267	
APICAL_SURFACE	0.20052316	0.334205267	
HEDGEHOG_SIGNALING	0.20052316	0.334205267	
ESTROGEN_RESPONSE_EARLY	0.27080252	0.423352557	
NOTCH_SIGNALING	0.270945636	0.423352557	
HEME_METABOLISM	0.33094571	0.498793855	
PEROXISOME	0.339179821	0.498793855	
WNT_BETA_CATENIN_SIGNALING	0.368811464	0.526873521	
DNA_REPAIR	0.386620615	0.531637891	
PANCREAS_BETA_CELLS	0.393412039	0.531637891	
TGF_BETA_SIGNALING	0.556413888	0.732123536	
SPERMATOGENESIS	0.675683202	0.866260515	
MITOTIC_SPINDLE	0.703079169	0.878848961	
IL6_JAK_STAT3_SIGNALING	0.793736084	0.963545169	
INTERFERON_GAMMA_RESPONSE	0.809377942	0.963545169	
BILE_ACID_METABOLISM	0.908314803	1	
PI3K_AKT_MTOR_SIGNALING	0.960853276	1	
UNFOLDED_PROTEIN_RESPONSE	0.983948729	1	
G2M_CHECKPOINT	0.999259584	1	
E2F_TARGETS	0.99947921	1	
INTERFERON_ALPHA_RESPONSE	1	1	
MYC_TARGETS_V1	1	1	
MYC_TARGETS_V2	1	1	

Supplemental Table S10

Pathways Up-Regulated in HADHA-scSeq: Cluster 1 (Intermediate) Vs. Cluster 3 (WT)

pathways	pvals	FDR
OXIDATIVE_PHOSPHORYLATION	7.31E-23	3.6565E-21
MYC_TARGETS_V1	1.4E-17	3.50975E-16
ADIPOGENESIS	0.000141	0.002357029
REACTIVE_OXIGEN_SPECIES_PATHWAY	0.007668	0.095856196
ALLOGRAFT_REJECTION	0.017751	0.15800049
UNFOLDED_PROTEIN_RESPONSE	0.01896	0.15800049
P53_PATHWAY	0.08777	0.58642547
MYC_TARGETS_V2	0.093828	0.58642547
PEROXISOME	0.19845	1
PANCREAS_BETA_CELLS	0.227847	1
APOPTOSIS	0.236419	1
MTORC1_SIGNALING	0.307901	1
BILE_ACID_METABOLISM	0.345702	1
APICAL_SURFACE	0.354518	1
HYPOXIA	0.364325	1
GLYCOLYSIS	0.373288	1
FATTY_ACID_METABOLISM	0.421754	1
ESTROGEN_RESPONSE_LATE	0.458099	1
DNA_REPAIR	0.48847	1
PI3K_AKT_MTOR_SIGNALING	0.494947	1
G2M_CHECKPOINT	0.500197	1
MYOGENESIS	0.600709	1
TGF_BETA_SIGNALING	0.62325	1
INTERFERON_GAMMA_RESPONSE	0.660415	1
INTERFERON_ALPHA_RESPONSE	0.697567	1
IL2_STATS_SIGNALING	0.737114	1
E2F_TARGETS	0.742613	1
EPITHELIAL_MESENCHYMAL_TRANSITION	0.818859	1
PROTEIN_SECRETION	0.83737	1
XENOBIOTIC_METABOLISM	0.895397	1
COMPLEMENT	0.897477	1
UV_RESPONSE_UP	0.914434	1
TNFA_SIGNALING_VIA_NFKB	0.930019	1
APICAL_JUNCTION	0.932779	1
CHOLESTEROL_HOMEOSTASIS	1	1
MITOTIC_SPINDLE	1	1
WNT_BETA_CATENIN_SIGNALING	1	1
IL6_JAK_STAT3_SIGNALING	1	1
NOTCH_SIGNALING	1	1
ESTROGEN_RESPONSE_EARLY	1	1
ANDROGEN_RESPONSE	1	1
HEDGEHOG_SIGNALING	1	1
INFLAMMATORY_RESPONSE	1	1
UV_RESPONSE_DN	1	1
ANGIOGENESIS	1	1
HEME_METABOLISM	1	1
COAGULATION	1	1
SPERMATOGENESIS	1	1
KRAS_SIGNALING_UP	1	1
KRAS_SIGNALING_DN	1	1

Pathways Down-Regulated in HADHA-scSeq: Cluster 1 (Intermediate) Vs. Cluster 3 (WT)

pathways	pvals	FDR
EPITHELIAL_MESENCHYMAL_TRANSITION	1.27E-15	6.34457E-14
MYOGENESIS	1.03E-13	2.57744E-12
APICAL_JUNCTION	1.15E-07	1.91385E-06
UV_RESPONSE_DN	2.67E-07	3.34259E-06
ANDROGEN_RESPONSE	8.92E-07	8.92472E-06
HYPOXIA	1.67E-06	1.39511E-05
CHOLESTEROL_HOMEOSTASIS	2.12E-06	1.51647E-05
MITOTIC_SPINDLE	4.14E-06	2.58789E-05
ANGIOGENESIS	7.28E-05	0.000404663
ESTROGEN_RESPONSE_EARLY	0.000104	0.00051915
IL2_STATS_SIGNALING	0.000226	0.001025051
MTORC1_SIGNALING	0.000321	0.001336334
GLYCOLYSIS	0.000462	0.001775053
APOPTOSIS	0.002711	0.009322004
TNFA_SIGNALING_VIA_NFKB	0.002797	0.009322004
TGF_BETA_SIGNALING	0.006183	0.019320612
P53_PATHWAY	0.006866	0.020194743
HEDGEHOG_SIGNALING	0.007753	0.021534955
PROTEIN_SECRETION	0.010333	0.02719335
ESTROGEN_RESPONSE_LATE	0.012094	0.030234608
COAGULATION	0.017006	0.040491081
XENOBIOTIC_METABOLISM	0.023211	0.052752695
WNT_BETA_CATENIN_SIGNALING	0.029527	0.064188096
KRAS_SIGNALING_UP	0.034319	0.071497009
INFLAMMATORY_RESPONSE	0.046711	0.093422984
NOTCH_SIGNALING	0.071434	0.137372874
COMPLEMENT	0.0781	0.144629236
APICAL_SURFACE	0.088933	0.157643228
ADIPOGENESIS	0.091433	0.157643228
HEME_METABOLISM	0.099707	0.166179106
PI3K_AKT_MTOR_SIGNALING	0.135437	0.218446825
UV_RESPONSE_UP	0.202212	0.310210125
UNFOLDED_PROTEIN_RESPONSE	0.204739	0.310210125
FATTY_ACID_METABOLISM	0.255131	0.375192394
KRAS_SIGNALING_DN	0.330131	0.471616319
ALLOGRAFT_REJECTION	0.488109	0.677929258
G2M_CHECKPOINT	0.502093	0.678503918
OXIDATIVE_PHOSPHORYLATION	0.603284	0.793794302
PANCREAS_BETA_CELLS	0.783597	0.986818403
INTERFERON_GAMMA_RESPONSE	0.82713	0.986818403
BILE_ACID_METABOLISM	0.832799	0.986818403
REACTIVE_OXIGEN_SPECIES_PATHWAY	0.836465	0.986818403
IL6_JAK_STAT3_SIGNALING	0.848664	0.986818403
PEROXISOME	0.87762	0.997295154
MYC_TARGETS_V1	0.932712	0.999611692
DNA_REPAIR	0.966527	0.999611692
INTERFERON_ALPHA_RESPONSE	0.992813	0.999611692
SPERMATOGENESIS	0.993521	0.999611692
MYC_TARGETS_V2	0.998479	0.999611692
E2F_TARGETS	0.999612	0.999611692

Supplemental Table S11

genes	names	p_val	avg_logFC	percent.expressed.cluster 3 (WT Mature)	percent.expressed.cluster 1 (Intermediate)	p_val_adj
PLCG2	phospholipase C gamma 2	6.86506E-64	1.483118634	0.876	0.074	2.31311E-59
SORBS2	sorbin and SH3 domain containing 2	1.05873E-62	1.380787006	1	0.807	3.56728E-58
COL5A1	collagen type VI alpha 1	8.32143E-60	0.790887079	0.953	0.178	2.80382E-55
FNBN2	fibrillin 2	1.25959E-59	1.251303459	0.995	0.457	4.2407E-55
ZMAT3	zinc finger matrin-type 3	1.16667E-58	0.965561573	0.974	0.249	3.93099E-54
DKK3	dickkopf WNT signaling pathway inhibitor 3	1.89612E-58	1.226792085	0.99	0.48	6.3888E-54
LAPTM4B	lysosomal protein transmembrane 4 beta	3.68298E-58	1.182648298	1	0.669	1.24094E-53
CADPS	Ca2+ dependent secretion activator	5.09296E-55	0.812099713	0.855	0.123	1.71602E-50
GPC1	glypican 1	1.57504E-54	1.065357653	0.99	0.42	5.30692E-50
TIMP3	TIMP metalloproteinase inhibitor 3	3.90557E-54	1.223174288	0.995	0.372	1.31594E-49
BVES	blood vessel epicardial substance	1.56061E-53	0.971810071	0.99	0.361	5.25831E-49
CDKN1A	cyclin-dependent kinase inhibitor 1A	2.2367E-53	1.349803409	0.995	0.301	7.53635E-49
MXR47	matrix remodeling associated 7	6.70503E-53	0.965505593	0.995	0.502	2.25919E-48
PSAP	prosaposin	7.0916E-53	0.933388635	1	0.576	2.38944E-48
ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2	2.55346E-52	1.285809669	0.99	0.606	8.60362E-48
UNC45B	unc-45 myosin chaperone B	2.85635E-52	0.987212835	1	0.52	9.62419E-48
HTRA1	HtrA serine peptidase 1	1.79612E-51	0.897449046	0.933	0.234	6.05184E-47
MTRNR2L1	MT-RNR2-like 1	2.18885E-51	1.135316175	0.995	0.416	7.37511E-47
PAM	peptidylglycine alpha-amidating monooxygenase	5.56684E-51	1.380783418	0.969	0.572	1.87569E-46
PRP2	prokinectin 2	1.6090E-50	0.972707662	0.99	0.587	5.69631E-46
CHRM2	cholinergic receptor muscarinic 2	1.79524E-50	0.686488818	0.886	0.156	6.04888E-46
MACF1	microtubule-actin crosslinking factor 1	5.47045E-50	0.838995301	0.99	0.476	1.84321E-45
DAG1	dystroglycan 1	5.57453E-50	0.78526861	0.964	0.331	1.87828E-45
SLC8A1	solute carrier family 8 member A1	6.78847E-50	1.029097801	0.995	0.595	2.28731E-45
AEBP1	AE binding protein 1	4.92511E-49	0.869357918	0.953	0.32	1.65947E-44
LAMB2	laminin subunit beta 2	1.53624E-48	0.77289554	0.959	0.301	5.17619E-44
MYADM	myeloid-associated differentiation marker	1.70904E-48	0.903278479	0.964	0.323	5.75843E-44
MGAT5	mannosyl (alpha-1,6)-glycoprotein beta-1,6-N-acetylglucosaminyltransferase	2.59959E-48	0.642110112	0.927	0.219	8.75906E-44
LTPB1	latent transforming growth factor beta binding protein 1	2.61517E-48	0.848318855	0.933	0.286	8.81155E-44
LG2	leucine-rich repeat LGI family member 2	5.99677E-48	0.684349211	0.762	0.078	2.02055E-43
RPL39	ribosomal protein L39	8.11798E-48	-0.902470645	1	0.996	2.73527E-43
RP56	ribosomal protein S6	8.37299E-48	-1.081576483	1	0.996	2.82119E-43
MATN2	matrilin 2	1.05702E-47	0.818983663	0.922	0.283	3.56153E-43
XIRP1	xin actin binding repeat containing 1	1.44956E-47	1.043173021	0.959	0.364	4.88413E-43
PHLD3	pleckstrin homology like domain family A member 3	1.47827E-47	0.679130708	0.876	0.193	4.98089E-43
COL4A1	collagen type IV alpha 1 chain	1.89834E-47	0.882146635	0.979	0.387	6.39627E-43
CACNA1C	calcium voltage-gated channel subunit alpha1 C	2.62275E-47	0.698754311	0.933	0.219	8.83711E-43
ITM2B	integral membrane protein 2B	3.43462E-47	0.838631642	0.974	0.502	1.15726E-42
CD81	CD81 molecule	8.07463E-47	0.852494482	0.99	0.424	2.72067E-42
RPL23A	ribosomal protein L23a	8.16006E-47	-0.916838386	1	0.993	2.74945E-42
LDB3	LIM domain binding 3	1.09794E-46	0.91491087	0.995	0.825	3.6994E-42
GJA1	gap junction protein alpha 1	1.151E-46	1.045409686	0.922	0.29	3.87819E-42
CPE	carboxypeptidase E	1.17836E-46	0.731749097	0.902	0.227	3.97038E-42
MMF15	matrix metalloproteinase 15	1.34768E-46	0.927365352	0.969	0.379	4.54086E-42
EMRP2	epithelial membrane protein 2	1.59126E-46	0.962737872	0.969	0.431	5.3616E-42
RPL38	ribosomal protein L38	1.63928E-46	-0.821662094	0.995	0.996	5.52339E-42
SPTBN1	spectrin beta, non-erythrocytic 1	1.95313E-46	0.814600479	0.995	0.561	6.58088E-42
COL18A1	collagen type XVIII alpha 1 chain	5.27731E-46	0.828926505	0.969	0.379	1.77814E-41
RPL32	ribosomal protein L32	6.09028E-46	-0.905315152	1	1	2.05206E-41
MASP1	mannan binding lectin serine peptidase 1	1.04321E-45	0.796744844	0.865	0.193	3.515E-41
RPL35	ribosomal protein L35	1.14401E-45	-0.778241764	0.995	0.996	3.85461E-41
HEPH	hephaestin	1.23252E-45	0.767218103	0.927	0.253	4.15286E-41
BCAM	basal cell adhesion molecule (Lutheran blood group)	1.31542E-45	0.851768494	0.969	0.394	4.43218E-41
CASQ2	calstaequin 2	1.57111E-45	0.928807409	0.813	0.145	5.29368E-41
RPL37	ribosomal protein L37	1.8081E-45	-0.994729974	1	0.996	6.09221E-41
NPTXR	neuronal pentraxin receptor	1.9241E-45	0.472356949	0.72	0.074	6.48307E-41
HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1	2.12932E-45	1.072500129	0.953	0.424	7.17453E-41
RP527A	ribosomal protein S27a	2.34755E-45	-0.790407939	1	0.996	7.90082E-41
SLIT2	slit guidance ligand 2	2.82727E-45	0.723074938	0.767	0.108	9.52619E-41
ADCY5	adenylate cyclase 5	3.11131E-45	0.790220479	0.959	0.312	1.04832E-40
CTD-2545M3.8	calcium/calmodulin dependent protein kinase II delta	3.7982E-45	0.906992229	0.995	0.859	1.27977E-40
CAMK2D	low density lipoprotein receptor	4.91686E-45	0.818965629	0.995	0.602	1.65659E-40
SPHKAP	SPHK1 interactor, AKAP domain containing	5.23229E-45	0.716577866	0.793	0.145	1.76297E-40
ATP1A1	ATPase Na+/K+ transporting subunit alpha 1	6.32356E-45	0.710966171	0.839	0.16	2.13066E-40
MYLK3	myosin light chain kinase 3	6.42301E-45	0.766559668	0.974	0.353	2.16417E-40
RPL27	ribosomal protein L27	6.77131E-45	0.887357883	0.964	0.387	2.28153E-40
TMEM245	transmembrane protein 245	1.10559E-44	-0.811049962	1	1	3.72519E-40
APP	amyloid beta precursor protein	1.25282E-44	0.750957153	0.959	0.398	4.22125E-40
SEMA5A	semaphorin 5A	1.74822E-44	0.80655011	0.979	0.446	5.89046E-40
RPL26	ribosomal protein L26	2.46743E-44	0.709644869	0.917	0.223	8.31376E-40
RPL24	ribosomal protein L24	2.47298E-44	-0.93455727	1	0.996	8.33244E-40
PLD3	phospholipase D family member 3	2.51E-44	-0.909904729	0.995	0.996	8.45718E-40
RPL19	ribosomal protein L19	3.72569E-44	0.883059964	0.984	0.513	1.25533E-39
RP518	ribosomal protein S18	4.48008E-44	-0.850532888	1	0.993	1.50952E-39
ITGAV	integrin subunit alpha V	5.24777E-44	-0.801386546	1	1	1.76818E-39
APLP2	amyloid beta precursor like protein 2	5.18222E-44	0.794924072	0.959	0.387	1.95837E-39
DCR1D2	discolin, CUB and LCU domain containing 2	7.89948E-44	0.846149681	0.995	0.539	2.66165E-39
TECR1	trans-2,3-enoyl-CoA reductase-like	8.26283E-44	0.835500472	0.979	0.468	2.78408E-39
GADD45A	growth arrest and DNA damage inducible alpha	8.39948E-44	1.021932041	0.995	0.751	2.83021E-39
RP524	ribosomal protein S24	1.04313E-43	0.710930596	0.933	0.271	3.51473E-39
SLC16A12	solute carrier family 16 member 12	1.14369E-43	-0.859937643	1	1	3.85354E-39
MFG8	milk fat globule-EGF factor 8 protein	1.33775E-43	0.508737214	0.746	0.093	4.50743E-39
HSPG2	heparan sulfate proteoglycan 2	2.49691E-43	0.911540254	0.948	0.335	8.41308E-39
PRSS35	protease, serine 35	2.64711E-43	0.684471892	0.917	0.279	8.91917E-39
MEG3	maternally expressed 3 (non-protein coding)	3.03514E-43	0.792525268	0.969	0.364	1.02266E-38
NOST1	N-deacetylase/N-sulfotransferase 1	3.61574E-43	0.944257676	0.751	0.097	1.21829E-38
RPLP2	ribosomal protein lateral stalk subunit P2	6.52061E-43	0.458113112	0.736	0.112	1.19705E-38
VCL	vinculin	7.00374E-43	-0.800001833	1	1	2.35984E-38
NAV1	neuron navigator 1	9.41685E-43	0.88751801	0.974	0.465	3.17291E-38
MTRNR2L8	MT-RNR2-like 8	1.64452E-42	0.938156857	0.979	0.599	5.54106E-38
COL5A2	collagen type V alpha 2 chain	1.90353E-42	0.814513964	0.953	0.312	6.41376E-38
PDLIM5	PDZ and LIM domain 5	2.02249E-42	0.927846534	0.948	0.357	6.81459E-38
RP512	ribosomal protein S12	2.065E-42	0.738398399	0.995	0.844	6.9578E-38
ADPHL1	ADP-ribosylhydrolase like 1	2.08076E-42	-0.870658265	1	0.996	7.01092E-38
NID2	nidogen 2	2.21352E-42	0.708037471	0.912	0.268	7.45825E-38
RPL21	ribosomal protein L21	2.52797E-42	0.493551203	0.731	0.093	8.55144E-38
EPH8	EPH receptor B3	2.86442E-42	-0.76932009	1	1	9.65137E-38
RP516	ribosomal protein S16	3.11607E-42	0.535378967	0.767	0.119	1.04993E-37
LAMC1	laminin subunit gamma 1	6.60368E-42	-0.725719073	1	0.996	2.2504E-37
SYNP02	synaptopodin 2	7.60465E-42	0.692465509	0.922	0.327	2.56231E-37
RPL18A	ribosomal protein L18a	8.3867E-42	1.080496561	0.979	0.375	2.82581E-37
CDH2	cadherin 2	1.27617E-41	-0.8145159914	1	1	4.29994E-37
LWP1	LDL receptor related protein 1	2.42205E-41	0.763792934	0.99	0.498	8.16087E-37
RBMS1	RNA binding motif single stranded interacting protein 1	2.4439E-41	0.433707719	0.767	0.13	2.34447E-37
HSPA5	heat shock protein family A (Hsp70) member 5	2.88408E-41	0.678969698	0.979	0.387	9.71763E-37
ITGB1	integrin subunit beta 1	2.89728E-41	0.752850496	0.969	0.39	9.7621E-37
CHPF	chondroitin polymerizing factor	2.92864E-41	0.775031881	0.99	0.636	9.86776E-37
TTN	titin	3.58445E-41	0.635427833	0.917	0.279	1.20774E-36
MTRNR2L12	MT-RNR2-like 12	3.59268E-41	0.964497579	1	0.922	1.21052E-36
SCUBE3	solute carrier family 12 member 3	4.26772E-41	0.730122621	0.969	0.357	1.43797E-36
RPL11	ribosomal protein L11	4.59687E-41	0.664855386	0.839	0.19	1.54887E-36
RPL36A	ribosomal protein L36a	4.64337E-41	0.844556997	1	0.993	1.56454E-36
FAM134B	family with sequence similarity 134 member B	5.5649E-41	-0.914661564	1	0.989	1.87504E-36
RPL29	ribosomal protein L29	5.60091E-41	0.409425655	0.72	0.093	1.88771E-36
RPLP1	ribosomal protein lateral stalk subunit P1	5.75362E-41	-0.86791005	0.995	0.996	1.93862E-36
ERBB2	erb-b2 receptor tyrosine kinase 2	7.76439E-41	-0.761804021	1	1	2.61613E-36
CTSD	cathepsin D	8.03074E-41	0.664124816	0.917	0.305	2.70588E-36
SLC12A4	solute carrier family 12 member 4	8.87302E-41	0.621878337	0.943	0.294	2.98968E-36
ARMK2	aromatase repeat containing, X-linked 2	8.97894E-41	0.534852876	0.813	0.175	3.32861E-36
EMC10	ER membrane protein complex subunit 10	1.0144E-40	0.727257865	0.933	0.323	3.41791E-36
EPHA4	EPH receptor A4	1.13278E-40	0.699360288	1	0.654	3.81679E-36
NOMO1	NODAL modulator 1	1.4221E-40	0.479436839	0.648	0.056	4.79162E-36
FSTL1	folliculin like 1	1.50103E-40	0.573282311	0.855	0.227	5.05756E-36
HSP90B1	heat shock protein 90kDa beta family member 1	1.68262E-40	0.714923348	0.99	0.454	5.66943E-36
MYBP3	myosin binding protein C, cardiac	2.01857E-40	0.647084855	0.979	0.394	6.80136E-36
C3orf58	chromosome 3 open reading frame 58	2.16912E-40	0.801630616	1	0.777	7.30863E-36
		2.51025E-40	0.619354471	0.819	0.19	8.45805E-36

VCAN	versican	2.61837E-40	0.759782172	0.891	0.238	8.82235E-36
SOD3	superoxide dismutase 3, extracellular	2.99739E-40	0.648679694	0.834	0.186	1.00994E-35
RPL8	ribosomal protein L8	3.91722E-40	0.699457167	1	1	1.31987E-35
GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	0.509008E-40	0.552561778	0.829	0.201	1.71505E-35
RPS25	ribosomal protein S25	5.24475E-40	0.870408964	1	0.993	1.76717E-35
NCAM	melanoma cell adhesion molecule	5.66853E-40	0.641584659	0.803	0.178	1.90995E-35
CASZ1	castor zinc finger 1	5.8359E-40	0.549354702	0.876	0.216	1.96635E-35
RPS17	ribosomal protein S17	5.8713E-40	0.706452546	1	1	1.97828E-35
RPS15A	ribosomal protein S15a	7.08508E-40	0.837202019	1	0.996	2.38725E-35
FAM78A	family with sequence similarity 78 member A	7.1407E-40	0.582426443	0.834	0.186	2.40599E-35
JAG1	jagged 1	8.58478E-40	0.490389224	0.715	0.104	2.89256E-35
STRIP2	striatin interacting protein 2	1.22926E-39	0.560654002	0.881	0.212	4.14188E-35
MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	1.29257E-39	0.511467662	0.87	0.219	4.35518E-35
ANK3	ankyrin 3, node of Ranvier (ankyrin G)	1.4181E-39	0.649363511	0.943	0.323	4.77813E-35
RPS15	ribosomal protein S15	1.72508E-39	0.751493367	1	0.993	5.8125E-35
RPL13	ribosomal protein L13	1.7413E-39	0.746981008	1	1	5.86712E-35
COL4A2	collagen type IV alpha 2	2.10934E-39	0.820861889	0.964	0.454	7.10722E-35
ATP6AP1	ATPase H+ transporting accessory protein 1	2.21826E-39	0.593677665	0.902	0.275	7.47421E-35
MANBA	mannosidase beta	2.99631E-39	0.493097369	0.777	0.156	1.00958E-34
	entropic and polytropic retrovirus receptor 1	3.45819E-39	0.567837433	0.85	0.227	1.1652E-34
APLP1	amyloid beta precursor like protein 1	4.06478E-39	0.383441017	0.632	0.067	1.36959E-34
PPP1R12B	protein phosphatase 1 regulatory subunit 12B	4.62136E-39	0.972463764	0.99	0.58	1.55712E-34
PLXNB2	plexin B2	4.796E-39	0.541257289	0.886	0.245	1.61596E-34
FZD8	frizzled class receptor 8	6.47633E-39	0.470542269	0.715	0.104	2.18214E-34
FRAS1	Fraser extracellular matrix complex subunit 1	7.91273E-39	0.6329787	0.793	0.197	2.66611E-34
RPL35A	ribosomal protein L35a	8.46366E-39	0.775281649	1	0.996	2.85175E-34
NES	nestin	1.07017E-38	0.847378798	0.964	0.401	3.60584E-34
NCAM1	neuronal cell adhesion molecule 1	1.13295E-38	0.618729976	0.912	0.29	3.81736E-34
PTGFRN	prostaglandin F2 receptor inhibitor	1.99951E-38	0.522276313	0.829	0.208	6.73715E-34
IGSF3	immunoglobulin superfamily member 3	2.16023E-38	0.532529736	0.788	0.171	7.27869E-34
KDINS220	kinase D-interacting substrate 220kDa	2.19973E-38	0.565273089	0.891	0.257	7.41177E-34
RPS10	ribosomal protein S10	2.6946E-38	0.790637726	0.995	0.996	9.07919E-34
KLHL21	kelch like family member 21	3.86772E-38	0.53809468	0.824	0.197	1.30319E-33
MYH6	myosin, heavy chain 6, cardiac muscle, alpha	4.18599E-38	1.051169228	0.979	0.435	1.41043E-33
POPCD2	popeye domain containing 2	4.49895E-38	0.74488073	0.995	0.721	1.51588E-33
CNOT11	CCR4-NOT transcription complex subunit 11	7.97704E-38	0.708786801	0.948	0.394	2.68778E-33
CALR	calreticulin	1.00106E-37	0.77039122	0.979	0.539	3.37297E-33
EH03	EH domain containing 3	1.04503E-37	0.657982182	0.865	0.242	5.52111E-33
MDM2	MDM2 proto-oncogene	1.27924E-37	0.534613061	0.824	0.197	4.31026E-33
RPL31	ribosomal protein L31	1.30691E-37	0.88830468	0.995	0.996	4.40351E-33
PLXNA1	plexin A1	1.70556E-37	0.510698809	0.808	0.19	5.74672E-33
TMEM63B	transmembrane protein 63B	1.73911E-37	0.433270534	0.736	0.134	5.85977E-33
ATP2B4	ATPase plasma membrane Ca2+ transporting 4	1.8065E-37	0.772610319	0.912	0.32	6.0868E-33
TNFRSF10B	tumor necrosis factor receptor superfamily member 10b	1.8383E-37	0.414327315	0.689	0.115	6.19395E-33
ACOT11	acyl-CoA thioesterase 11	1.94347E-37	0.569767359	0.845	0.208	6.54832E-33
RPLP0	ribosomal protein lateral stalk subunit P0	2.00436E-37	0.811907149	1	1	6.7355E-33
COL4A6	collagen type IV alpha 6 chain	2.07975E-37	0.473456291	0.705	0.115	7.00751E-33
SPPL3	signal peptide peptidase like 3	2.11997E-37	0.448988764	0.839	0.208	7.14304E-33
CYP51A1	cytochrome P450 family S1 subfamily A member 1	2.46187E-37	0.490817932	0.72	0.13	8.29501E-33
CLTC	clathrin heavy chain	2.97745E-37	0.639588952	0.99	0.487	1.00322E-32
KIFAP3	kinesin associated protein 3	3.03569E-37	0.616348231	0.964	0.323	1.02284E-32
GNAS	GNAS complex locus	3.46301E-37	0.579317477	1	0.892	1.16683E-32
SYNP02L	synaptopodin 2 like	4.16714E-37	0.850853223	0.974	0.535	1.40408E-32
S1PR1	sphingosine-1-phosphate receptor 1	5.03442E-37	0.575474631	0.819	0.201	1.16963E-32
SKBEF2	steroid regulatory element binding transcription factor 2	6.0095E-37	0.608841153	0.927	0.323	2.02484E-32
SRP1	secreted frizzled related protein 1	6.10568E-37	0.61745278	0.886	0.279	2.05725E-32
MTPN	myotrophin	6.42441E-37	0.656266095	0.984	0.472	2.16464E-32
PPM1K	protein phosphatase, Mg2+/Mn2+ dependent 1K	7.06244E-37	0.645119589	0.886	0.301	2.37962E-32
NPNT	nephroretcin	7.13624E-37	0.510101106	0.912	0.264	2.40448E-32
SCD	stearoyl-CoA desaturase	8.44931E-37	0.7079565	0.865	0.264	2.84691E-32
CXADR	coxackievirus and adenovirus receptor	8.70305E-37	0.607908151	0.948	0.335	2.93241E-32
ARL6P5	ADP ribosylation factor like GTPase 6 interacting protein 5	9.0245E-37	0.661772055	0.995	0.58	3.04072E-32
RPS23	ribosomal protein S23	9.16157E-37	0.736483721	0.819	0.996	3.0869E-32
EDAR2	ectodysplasin A2 receptor	1.01046E-36	0.311376028	0.585	0.041	3.40465E-32
VCAM1	vascular cell adhesion molecule 1	1.10323E-36	0.826023089	0.684	0.119	3.71722E-32
RPL27A	ribosomal protein L27a	1.30111E-36	0.8028706	1	1	4.38395E-32
PTPRM	protein tyrosine phosphatase, receptor type M	1.34079E-36	0.424680103	0.71	0.115	4.51765E-32
RPL13A	ribosomal protein L13a	1.65801E-36	0.776291942	0.995	1	5.58649E-32
FLNC	filamin C	1.70459E-36	0.921896993	0.99	0.599	5.74344E-32
PLXNA2	plexin A2	2.01573E-36	0.361344815	0.606	0.059	6.7918E-32
RPS3A	ribosomal protein S3A	2.26895E-36	0.772897432	1	1	7.64499E-32
SOD3	syndecan 3	2.70149E-36	0.483430586	0.72	0.141	9.1024E-32
RPL30	ribosomal protein L30	2.91485E-36	0.722542203	1	0.993	9.82129E-32
RRM2B	ribonucleotide reductase regulatory TP53 inducible subunit M2B	3.41585E-36	0.397353946	0.689	0.108	1.15094E-31
RPS26	ribosomal protein S26	3.59586E-36	0.713287911	0.995	0.996	1.21159E-31
FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	4.14667E-36	0.725179198	0.995	0.978	1.39718E-31
LPP	LM domain containing preferred translocation partner in lipoma	4.17677E-36	0.670395888	0.953	0.416	1.40732E-31
KIRREL	kin of IRRE like (Drosophila)	4.57311E-36	0.347653812	0.653	0.097	1.54086E-31
ACSL3	acyl-CoA synthetase long-chain family member 3	4.92499E-36	0.47555332	0.834	0.216	1.65942E-31
CANX	calnexin	6.99184E-36	0.6596182	0.995	0.561	2.35838E-31
KIF13A	kinesin family member 13A	7.28471E-36	0.646850849	0.943	0.375	2.45451E-31
MAP1B	microtubule associated protein 1B	7.95714E-36	0.709574811	1	0.669	2.68108E-31
RPL37A	ribosomal protein L37a	8.26825E-36	0.558851276	1	1	2.7859E-31
CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	1.46324E-35	0.622743976	0.974	0.513	4.93023E-31
EDNRA	endothelin receptor type A	1.51252E-35	0.55261782	0.834	0.212	5.09629E-31
CTGF	connective tissue growth factor	1.53753E-35	1.377999754	0.953	0.428	5.18055E-31
LGR4	leucine-rich repeat containing G protein-coupled receptor 4	1.75641E-35	0.56954651	0.917	0.294	5.91805E-31
GN5	glucosamine (N-acetyl)-6-sulfatase	1.75882E-35	0.470777953	0.886	0.253	5.92617E-31
FHOD3	formin homology 2 domain containing 3	2.00765E-35	0.604533905	0.922	0.331	6.76456E-31
TNSI	tenascin 1	2.33003E-35	0.524805928	0.881	0.257	7.85079E-31
LRPAP1	LDL receptor related protein associated protein 1	2.3956E-35	0.676439607	0.943	0.39	8.07172E-31
LNPEP	leucyl/cystinyl aminopeptidase	2.42855E-35	0.452842193	0.813	0.201	8.18277E-31
RPL36	ribosomal protein L36	2.52197E-35	0.654567774	1	1	8.49753E-31
NPTN	neuroligin	2.56929E-35	0.651947767	0.959	0.476	8.65697E-31
RASAL2	RAS protein activator like 2	2.71248E-35	0.487343376	0.834	0.23	9.13944E-31
PCYOX1	prenylcysteine oxidase 1	3.58548E-35	0.553369255	0.876	0.294	1.20809E-30
GLG1	golgi glycoprotein 1	3.84235E-35	0.41469349	0.824	0.197	1.29464E-30
CERS6	ceramide synthase 6	4.31823E-35	0.522872045	0.87	0.264	1.45498E-30
FITM2	fat storage inducing transmembrane protein 2	4.49122E-35	0.363309324	0.705	0.119	1.51327E-30
RPL36AL	ribosomal protein L36a like	5.13791E-35	0.958078253	0.917	0.926	1.73117E-30
UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	5.46973E-35	0.694005811	1	0.996	1.84297E-30
ALCAM	activated leukocyte cell adhesion molecule	5.52365E-35	0.584618492	0.85	0.253	1.86114E-30
REEP1	receptor accessory protein 1	5.56163E-35	0.428837005	0.741	0.156	1.87393E-30
PXDN	peroxidasin	6.91938E-35	0.430629305	0.725	0.149	2.33142E-30
SRPX	sushi repeat containing protein, X-linked	7.31377E-35	0.518923128	0.86	0.223	2.4643E-30
PTPRD	protein tyrosine phosphatase, receptor type D	7.80884E-35	0.410652897	0.751	0.164	2.63044E-30
RBM20	RNA binding motif protein 20	1.10868E-34	0.5597784	0.959	0.335	3.7356E-30
FAM189A2	family with sequence similarity 189 member A2	1.16809E-34	0.420269876	0.684	0.115	3.93577E-30
LAMA2	laminin subunit alpha 2	1.33984E-34	0.432550776	0.756	0.145	4.51447E-30
CPEB4	cytoplasmic polyadenylation element binding protein 4	1.35482E-34	0.599946408	0.943	0.357	4.56493E-30
INPP5A	inositol polyphosphate-5-phosphatase A	1.42731E-34	0.465944244	0.86	0.234	4.80917E-30
RPL14	ribosomal protein L14	1.43153E-34	0.873339432	0.995	0.978	4.82339E-30
PGY8	phosphorylase, glycogen; brain	1.9339E-34	0.59167164	0.959	0.413	5.61607E-30
XP24	exportin 4	1.94312E-34	0.575510154	0.86	0.271	6.54716E-30
IER5	immediate early response 5	1.96624E-34	0.369405012	0.596	0.071	6.62505E-30
RPS8	ribosomal protein S8	2.17504E-34	0.822006236	1	1	7.32857E-30
CTS2	cathepsin Z	2.18003E-34	0.428627084	0.767	0.19	7.34539E-30
TIMP2	TIMP metalloproteinase inhibitor 2	2.42935E-34	0.554595545	0.86	0.249	8.18546E-30
RPL12	ribosomal protein L12	2.96089E-34	0.935040449	1	0.996	9.97643E-30
PCDH7	protocadherin 7	3.2207E-34	0.492969171	0.922	0.271	1.08518E-29
RPS27	ribosomal protein S27	3.69387E-34	0.71698641	1	1	1.24461E-29
CAAPA	cytoskeleton-associated protein 4	4.15687E-34	0.571008975	0.886	0.297	1.40062E-29
PEAK1	pseudopodium enriched atypical kinase 1	4.63084E-34	0.478963017	0.819	0.219	1.56031E-29
COLQ	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	5.3808E-34	0.468613049	0.596	0.071	1.81301E-29
GPC6	glypican 6	5.88284E-34	0.399436979	0.71	0.145	1.98216E-29
PRRX1	paired related homeobox 1	6.09989E-34	0.679161589	0.912	0.312	2.0553E-29
TMEM127	transmembrane protein 127	7.27143E-34	0.402232701	0.715	0.138	2.45003E-29
FAT1	FAT atypical cadherin 1	7.45055E-34	0.481364938	0.808	0.212	2.51039E-29
ADAM10	ADAM metalloproteinase domain 10	7.67732E-34	0.441129824	0.834	0.238	2.5868E-29

DDX17	DEAD-box helicase 17	7.85608E-34	0.603968477	0.99	0.52	2.64703E-29
ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	7.9614E-34	0.727004479	0.99	0.494	2.68251E-29
DUSP27	dual specificity phosphatase 27 (putative)	8.14185E-34	0.539188874	0.87	0.249	2.74331E-29
PKRAB2	protein kinase AMP-activated non-catalytic subunit beta 2	9.01865E-34	0.504971841	0.87	0.279	3.03874E-29
PRGMC2	progesterone receptor membrane component 2	9.41608E-34	0.618807434	0.940	0.409	3.17266E-29
IL6ST	interleukin 6 signal transducer	9.46337E-34	0.494863273	0.886	0.26	3.18859E-29
ADGBR2	adhesion G protein-coupled receptor B2	1.06458E-33	0.438109068	0.829	0.208	3.58698E-29
SHROOM3	shroom family member 3	1.28234E-33	0.403522954	0.736	0.16	4.32072E-29
PWAR6		1.32614E-33	0.433649172	0.855	0.264	4.4683E-29
SIPA1L2	signal induced proliferation associated 1 like 2	1.51209E-33	0.603811774	0.969	0.546	5.09484E-29
MSMO1	methylsterol monooxygenase 1	1.52527E-33	0.725671406	0.881	0.357	5.13923E-29
MARVELD1	MARVEL domain containing 1	1.68642E-33	0.411103341	0.756	0.171	5.68221E-29
ITGA7	integrin subunit alpha 7	1.87544E-33	0.597070204	0.834	0.242	6.31912E-29
HRC	histidine rich calcium binding protein	1.90998E-33	0.403524146	0.674	0.104	6.4355E-29
CN3N1	potassium voltage-gated channel subfamily J member 3	1.92442E-33	0.413835069	0.622	0.086	6.48414E-29
GFOO1	glucose-fructose oxidoreductase domain containing 1	2.14295E-33	0.43784142	0.746	0.164	7.22047E-29
SYNM	synemin	2.82143E-33	0.481600113	0.839	0.242	9.50653E-29
PIGT	phosphatidylinositol glycan anchor biosynthesis class T	2.82753E-33	0.460526636	0.865	0.26	9.52707E-29
RP57	ribosomal protein S7	2.90265E-33	-0.819135422	0.995	0.989	9.78018E-29
ANTXR2	anthrax toxin receptor 2	2.95919E-33	0.479745126	0.798	0.208	9.95964E-29
KIAA0319L	KIAA0319 like	3.08208E-33	0.377063193	0.808	0.216	1.03848E-28
CLGN	calmagrin	3.48163E-33	0.364010848	0.617	0.086	1.1731E-28
RPL22	ribosomal protein L22	4.35421E-33	-0.740770507	1	0.989	1.46711E-28
SURP	SRA stem-loop interacting RNA binding protein	4.37949E-33	-0.891510056	0.881	0.922	1.47563E-28
ATG9A	autophagy related 9A	6.08993E-33	0.430621402	0.808	0.227	2.05194E-28
C20orf194	chromosome 20 open reading frame 194	6.54891E-33	0.367211711	0.668	0.123	2.20659E-28
RPL28	ribosomal protein L28	7.07296E-33	-0.731789063	1	1	2.38316E-28
TOM1L2	target of myb1.1 like 2 membrane trafficking protein	7.17164E-33	0.452720001	0.834	0.245	2.41641E-28
BSG	basigin (Ok blood group)	7.18875E-33	0.648937168	0.995	0.684	2.42218E-28
GYS1	glycogen synthase 1	7.65871E-33	0.455300887	0.788	0.204	2.58953E-28
SMYD1	SET and MNND domain containing 1	8.42165E-33	0.6714480933	0.99	0.677	2.83759E-28
RPS13	ribosomal protein S13	1.02743E-32	-0.715954984	1	0.996	3.46183E-28
PVR12		1.04637E-32	0.469762542	0.917	0.309	3.52563E-28
GNA11	G protein subunit alpha 11	1.16244E-32	0.374325407	0.767	0.182	3.91671E-28
SLC16A1	solute carrier family 16 member 1	1.33835E-32	0.554153828	0.881	0.294	4.50945E-28
JUND	JunD proto-oncogene, AP-1 transcription factor subunit	1.50748E-32	0.644547738	0.933	0.424	5.0793E-28
TBC1D4	TBC1 domain family member 4	1.56816E-32	0.427311921	0.824	0.208	5.28375E-28
GC1C	gap junction protein gamma 1	1.60101E-32	0.377650217	0.679	0.119	5.39445E-28
HADHA	hydroxyacyl-CoA dehydrogenase/3-ketocoyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	1.90224E-32	0.514480588	0.907	0.316	5.53337E-28
MIR133A1HG	microRNA 1-2	1.84926E-32	0.462942546	0.653	0.108	6.23088E-28
RPS21	ribosomal protein S21	2.19842E-32	-0.732020602	0.99	0.993	7.40735E-28
ATP1B1	ATPase Na+/K+ transporting subunit beta 1	2.25917E-32	0.61295712	0.984	0.442	7.61204E-28
MSI2	musashi RNA binding protein 2	2.62381E-32	0.44944211	0.845	0.245	8.84067E-28
MYOM1	myomesin 1	2.79042E-32	0.608067791	0.995	0.546	9.40204E-28
RPL6	ribosomal protein L6	2.84206E-32	-0.86260172	0.99	0.985	9.57605E-28
STGALL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1	2.84515E-32	0.399586618	0.782	0.186	9.58444E-28
MAPRE2	microtubule associated protein RP/EB family member 2	2.98457E-32	0.461594961	0.85	0.264	1.00562E-27
CRMP1	collapsin response mediator protein 1	3.26454E-32	0.395978816	0.725	0.152	1.1006E-27
BAGALNT3	beta-1,4-N-acetyl-galactosaminyltransferase 3	3.28733E-32	0.36979194	0.689	0.123	1.10763E-27
EPHA2	EPH receptor A2	3.37066E-32	0.388544905	0.622	0.1	1.13571E-27
BMP7	bone morphogenetic protein 7	3.55113E-32	0.597668215	0.881	0.279	1.19652E-27
BMP5	bone morphogenetic protein 5	3.60279E-32	0.65088369	0.964	0.446	1.21392E-27
LAMP1	lysosomal associated membrane protein 1	3.61304E-32	0.490643992	0.902	0.312	1.21738E-27
KDM4B	lysine demethylase 4B	3.65676E-32	0.358708226	0.653	0.123	1.23211E-27
DHCR24	24-dehydrocholesterol reductase	3.81103E-32	0.480058082	0.788	0.201	1.28409E-27
FAM212B	family with sequence similarity 212 member B	8.44256E-32	0.3810218	0.663	0.115	1.29471E-27
ARHGAP1	Rho GTPase activating protein 1	4.50655E-32	0.580637367	0.907	0.372	1.51844E-27
COL4A5	collagen type IV alpha 5 chain	4.63441E-32	0.408814354	0.803	0.208	1.56152E-27
FGFR1	fibroblast growth factor receptor 1	4.73944E-32	0.381298259	0.741	0.164	1.59691E-27
B4GAT1	beta-1,4-glucuronyltransferase 1	4.82545E-32	0.347205089	0.658	0.119	1.62589E-27
TEX2	testis expressed 2	4.9893E-32	0.385206034	0.71	0.149	1.68109E-27
RASL10B	RAS like family 10 member B	4.99194E-32	0.374386829	0.741	0.164	1.68198E-27
INSR	insulin receptor	5.39747E-32	0.358514316	0.746	0.167	1.81862E-27
ETV1	ETS variant 1	6.50418E-32	0.588317153	0.902	0.323	1.91592E-27
ITGB5	integrin subunit beta 5	6.71849E-32	0.378434115	0.701	0.156	2.26737E-27
RPS20	ribosomal protein S20	6.82988E-32	-0.642259334	1	0.985	2.30126E-27
GATA6	GATA binding protein 6	6.92375E-32	0.511080566	0.865	0.297	2.33289E-27
RTN4	reticulon 4	7.18005E-32	0.589037431	1	0.747	2.41924E-27
FLT1	fms related tyrosine kinase 1	7.24082E-32	0.3749448	0.591	0.067	2.43972E-27
MAP1A	microtubule associated protein 1A	7.75964E-32	0.445784465	0.793	0.208	2.61453E-27
NOTCH2	notch 2	7.76062E-32	0.47087852	0.798	0.223	2.61486E-27
HIPK2	homeodomain interacting protein kinase 2	7.81204E-32	0.490571594	0.922	0.353	2.63219E-27
HIF1A	hypoxia inducible factor 1 alpha subunit	7.83813E-32	0.603481303	0.974	0.621	2.64098E-27
UBE2Q1	ubiquitin conjugating enzyme E2 Q1	8.50207E-32	0.402013307	0.793	0.208	2.86469E-27
PIK3CA	phosphatidylinositol(4,5)-bisphosphate 3-kinase catalytic subunit alpha	8.83041E-32	0.405122319	0.762	0.182	2.97532E-27
PRKAR2A	protein kinase cAMP-dependent type II regulatory subunit alpha	9.63886E-32	0.51297941	0.917	0.342	3.24772E-27
RPS14	ribosomal protein S14	9.86367E-32	-0.648885333	1	1	3.32346E-27
ATP13A3	ATPase 13A3	1.07135E-31	0.56068333	0.927	0.338	3.60981E-27
CDC34	cell division cycle 34	1.07667E-31	0.461665702	0.87	0.29	3.62774E-27
CYIFP2	cytoplasmic FMR1 interacting protein 2	1.12433E-31	0.520408041	0.922	0.331	3.78831E-27
SLC1A3	solute carrier family 1 member 3	1.20997E-31	0.497627975	0.829	0.249	4.07689E-27
GTF2I	general transcription factor III	1.29435E-31	0.605037404	0.984	0.561	4.36117E-27
SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	1.35797E-31	0.519969521	0.601	0.086	4.57554E-27
PRICKLE1	prickle planar cell polarity protein 1	1.3647E-31	0.576553468	0.927	0.401	4.59824E-27
ADHC1	AT-hook DNA binding motif containing 1	1.49868E-31	0.358723653	0.736	0.175	5.04966E-27
ADGRL3	adhesion G protein-coupled receptor L3	1.57807E-31	0.314260262	0.585	0.071	5.31714E-27
TNLN1	talin 1	1.66255E-31	0.547974432	0.912	0.383	5.60181E-27
UBE2H	ubiquitin conjugating enzyme E2 H	2.0581E-31	0.592152576	0.979	0.535	6.93455E-27
MICAL3	microtubule associated monooxygenase, calponin and LIM domain containing 3	2.11308E-31	0.422224115	0.798	0.204	7.11983E-27
SKY12	SKY-box 12	2.21477E-31	0.409242206	0.798	0.257	7.46244E-27
CNND2	cyclin D2	2.85584E-31	0.584263916	0.959	0.532	9.62246E-27
MAGED1	MAGE family member D1	2.9151E-31	0.543361568	0.959	0.405	9.82215E-27
RPL34	ribosomal protein L34	3.32999E-31	-0.672513393	1	0.993	1.12201E-26
ARID1A	AT-rich interaction domain 1A	3.44453E-31	0.535984882	0.922	0.364	1.1606E-26
RPL5	ribosomal protein L5	3.45543E-31	-0.83399975	0.995	0.978	1.16427E-26
AMOTL2	angiomotin like 2	3.57977E-31	0.478294877	0.756	0.19	1.20617E-26
ASPH	aspartate beta-hydroxylase	3.63766E-31	0.534312752	0.938	0.364	1.22567E-26
INVS1ABP	influenza virus NS1A binding protein	3.77491E-31	0.644493306	0.938	0.465	1.27192E-26
RP55	ribosomal protein S5	3.94473E-31	-0.759106388	1	0.993	1.32914E-26
SLC25A23	solute carrier family 25 member 23	3.94993E-31	0.594480876	0.902	0.357	1.33089E-26
NDUFS5	NADH:ubiquinone oxidoreductase subunit S5	4.02227E-31	-0.829129672	0.974	0.974	1.35526E-26
DACT3	dishevelled binding antagonist of beta catenin 3	4.28427E-31	0.391127942	0.715	0.16	1.44354E-26
VSTM2L	V-set and transmembrane domain containing 2 like	4.46469E-31	0.52790059	0.736	0.182	1.50433E-26
NNT	nicotinamide nucleotide transhydrogenase	4.58238E-31	0.487345766	0.933	0.372	1.54399E-26
RPL18	ribosomal protein L18	4.65115E-31	-0.69717047	0.99	0.978	1.56716E-26
LRP10	LDL receptor related protein 10	5.20171E-31	0.4444040348	0.777	0.227	1.75266E-26
ADAMTS15	ADAM metalloproteinase with thrombospondin type 1 motif 15	7.16249E-31	0.305616149	0.518	0.045	2.41333E-26
PERP	PERP, TP53 apoptosis effector	7.8682E-31	0.617120308	0.974	0.506	2.65111E-26
CLSTN1	calsynenin 1	8.70251E-31	0.340989682	0.725	0.178	2.93222E-26
G3BP2	G3BP stress granule assembly factor 2	9.63793E-31	0.580971661	0.984	0.55	3.2474E-26
CTNNA1	catenin alpha 1	1.03816E-30	0.606581447	0.959	0.506	3.49798E-26
SLC38A2	solute carrier family 38 member 2	1.19032E-30	0.537619908	0.896	0.309	4.01065E-26
RPW1	ribophorin 1	1.281E-30	0.415766131	0.881	0.283	4.31621E-26
ABLIM1	actin binding LIM protein 1	1.294E-30	0.583251614	0.963	0.509	4.35999E-26
JPH2	junctophilin 2	1.34777E-30	0.59823531	0.948	0.413	4.54119E-26
PLXNA4	plexin A4	1.61086E-30	0.50472814	0.741	0.175	5.42763E-26
PP6R1	protein phosphatase 6 regulatory subunit 1	1.71341E-30	0.419924902	0.845	0.26	5.77317E-26
ITFG1	integrin alpha FG-GAP repeat containing 1	1.82478E-30	0.465812012	0.834	0.283	6.1484E-26
PIK3R1	phosphoinositide-3-kinase regulatory subunit 1	1.84022E-30	0.46149957	0.756	0.201	6.20045E-26
TUSC3	tumor suppressor candidate 3	2.21702E-30	0.518098933	0.964	0.446	7.47003E-26
RABGAP1	G protein-coupled receptor 21	2.24513E-30	0.410952989	0.767	0.212	7.56475E-26
TMEM447	transmembrane protein 47	2.28328E-30	0.393612396	0.782	0.193	7.69328E-26
CYP2J2	cytochrome P450 family 2 subfamily J member 2	2.37792E-30	0.365372262	0.585	0.082	8.01217E-26
RPL10	ribosomal protein L10	2.37872E-30	-0.834345397	1	0.993	8.01486E-26
FADS1	fatty acid desaturase 1	2.4621E-30	0.494013666	0.907	0.327	8.2958E-26
COL5A1	collagen type V alpha 1	2.47226E-30	0.346494267	0.694	0.138	8.33003E-26
TRIM63	tripartite motif containing 63	2.7161E-30	0.582314131	0.943	0.383	9.15162E-26
EPM2AIP1	EPM2A interacting protein 1	3.31404E-30	0.432504128	0.902	0.316	1.11663E-25
DOR1	discoidin domain receptor tyrosine kinase 1	3.35866E-30	0.40382958	0.741	0.182	1.13167E-25

TGFB2	transforming growth factor beta 2	5.34892E-30	0.592106933	0.71	0.175	1.19577E-25
SPATA18	spermatogenesis associated 18	3.7522E-30	0.301522166	0.518	0.048	1.26427E-25
PLEKHA5	pleckstrin homology domain containing A5	3.98822E-30	0.445639866	0.85	0.264	1.34379E-25
DNAIB9	DnaI heat shock protein family (Hsp40) member B9	4.0147E-30	0.39754508	0.85	0.242	1.35271E-25
STARDA	STAR related lipid transfer domain containing 4	4.23628E-30	0.605484827	0.979	0.494	1.42737E-25
RELN	reelin	4.81137E-30	0.370090307	0.508	0.045	1.62114E-25
MYOCD	myocardin	5.24524E-30	0.446554199	0.943	0.346	1.76733E-25
MTRNR2L6	MT-RNR2-like 6	5.27992E-30	0.299764576	0.518	0.045	1.77902E-25
GRN	granulin	5.29125E-30	0.46980086	0.896	0.297	1.78283E-25
KIAA1324L	KIAA1324-like	5.40796E-30	0.440270585	0.674	0.149	1.82216E-25
NRP1	neuropilin 1	5.99922E-30	0.493130391	0.834	0.245	2.02138E-25
CUX1	cut like homeobox 1	6.26652E-30	0.512702635	0.927	0.39	2.11144E-25
METRN	meteorin, glial cell differentiation regulator	6.2927E-30	0.416793057	0.834	0.245	2.12026E-25
FADS2	fatty acid desaturase 2	7.05085E-30	0.444142026	0.777	0.223	2.37571E-25
ATPI1A	ATPase phospholipid transporting 11A	8.92957E-30	0.374519075	0.756	0.204	3.00873E-25
CEL2F	CUGBP, Elav-like family member 2	9.54896E-30	0.579359819	0.964	0.513	3.21743E-25
TBX5	T-box 5	9.76788E-30	0.466260317	0.767	0.193	3.29119E-25
CD46	CD46 molecule	1.02583E-29	0.405791597	0.777	0.219	3.45642E-25
RPL41	ribosomal protein L41	1.03987E-29	-0.507177387	1	1	3.50375E-25
WSB1	WD repeat and SOCS box containing 1	1.07978E-29	0.514006729	0.938	0.394	3.63821E-25
FOXO1	forkhead box O1	1.09736E-29	0.395991741	0.668	0.138	3.69746E-25
STK39	serine/threonine kinase 39	1.227E-29	0.50612552	0.917	0.357	4.13427E-25
SRRA2	serine/arginine repetitive matrix 2	1.28381E-29	0.538985528	0.948	0.428	4.32566E-25
GPR155	G protein-coupled receptor 155	1.34835E-29	0.323603567	0.617	0.108	4.54312E-25
DNAJC6	DnaJ heat shock protein family (Hsp40) member C6	1.36689E-29	0.366324768	0.627	0.108	4.60588E-25
FASN	fatty acid synthase	1.3797E-29	0.385886821	0.725	0.178	4.64875E-25
KIAA1715	KIAA1715	1.50453E-29	0.362584687	0.782	0.216	5.06937E-25
RHOBTB3	Rho related BTB domain containing 3	1.52693E-29	0.608237794	0.948	0.442	5.14482E-25
NPPA	natriuretic peptide A	1.52798E-29	0.797546496	1	0.851	5.14839E-25
TMEM41B	transmembrane protein 41B	1.60587E-29	0.393407554	0.782	0.212	5.41082E-25
CSD2	CDP-diacylglycerol synthase 2	1.61231E-29	0.349855411	0.705	0.175	5.4325E-25
ATXN1	ataxin 1	1.63592E-29	0.367643771	0.824	0.245	5.51208E-25
NFE2L1	nuclear factor, erythroid 2 like 1	1.7435E-29	0.503778766	0.922	0.372	5.87455E-25
BMP2K	BMP2 inducible kinase	1.8251E-29	0.304564001	0.642	0.123	6.1495E-25
HK1	hexokinase 1	1.86995E-29	0.564592029	0.933	0.472	6.30063E-25
P4HA2	prolyl 4-hydroxylase subunit alpha 2	1.89812E-29	0.338726689	0.617	0.115	6.39552E-25
CNCD1	cyclin D1	2.0035E-29	0.530107836	0.891	0.331	6.7506E-25
DOB1	damage specific DNA binding protein 1	2.03246E-29	0.507341946	0.927	0.368	6.84818E-25
RAB39	RAB39 interacting protein	2.23535E-29	0.600254473	0.943	0.446	7.53178E-25
ROR1	receptor tyrosine kinase-like orphan receptor 1	2.60334E-29	0.423464428	0.777	0.219	8.77716E-25
SLC22A17	solute carrier family 22 member 17	2.83342E-29	0.36733857	0.585	0.097	9.54692E-25
SERINC3	serine incorporator 3	2.84885E-29	0.439015923	0.855	0.275	9.5989E-25
STRN	striatin	2.85923E-29	0.366110039	0.741	0.186	9.63391E-25
DENNDS8	DENN domain containing 5B	3.20743E-29	0.577860984	0.933	0.442	1.08071E-24
DENNDS4	DENN domain containing 5A	3.33238E-29	0.569754218	0.959	0.465	1.22389E-24
CAPN51	calpain small subunit 1	3.67267E-29	0.531185178	0.959	0.513	1.25432E-24
MAPK1	mitogen-activated protein kinase 1	3.7676E-29	0.444587116	0.907	0.346	1.26945E-24
SOBP	sine oculis binding protein homolog	4.34243E-29	0.285593711	0.663	0.123	1.46314E-24
KIAA1456	KIAA1456	4.6316E-29	0.35623673	0.668	0.126	1.56057E-24
ADAM19	ADAM metallopeptidase domain 19	4.90988E-29	0.502673232	0.793	0.242	1.65434E-24
TEAD1	TEA domain transcription factor 1	4.98483E-29	0.393334927	0.813	0.234	1.67959E-24
ALPK2	alpha kinase 2	6.13957E-29	0.470541367	0.896	0.346	2.06867E-24
MAST4	microtubule associated serine/threonine kinase family member 4	6.59424E-29	0.402107707	0.798	0.23	2.22186E-24
CACNB2	calcium voltage-gated channel auxiliary subunit beta 2	6.68521E-29	0.369077766	0.751	0.186	2.25251E-24
LMO7	LMO domain 7	7.3493E-29	0.520221682	0.933	0.416	2.47627E-24
RPS3	ribosomal protein S3	7.41037E-29	0.764023153	1	0.993	2.49685E-24
BGAL72	beta-1,4-galactosyltransferase 2	8.15075E-29	0.370365925	0.793	0.223	2.74631E-24
EZR	ezrin	8.66809E-29	0.551872413	0.979	0.561	2.92063E-24
ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	8.99539E-29	0.477333858	0.85	0.286	3.03091E-24
SLC38A1	solute carrier family 38 member 1	9.30423E-29	0.519921165	0.917	0.387	3.13497E-24
WNT5A	Wnt family member 5A	9.90886E-29	0.399893892	0.71	0.175	3.38869E-24
GAB1	GRB2 associated binding protein 1	1.02807E-28	0.462940483	0.829	0.271	3.46397E-24
RNF150	ring finger protein 150	1.08626E-28	0.400181775	0.85	0.264	3.6605E-24
SLC4A3	solute carrier family 4 member 3	1.10245E-28	0.465749907	0.912	0.349	3.7146E-24
AKAP11	A-kinase anchoring protein 11	1.131E-28	0.340718025	0.694	0.164	3.81079E-24
PSD3	pleckstrin and Sec7 domain containing 3	1.16381E-28	0.489121533	0.907	0.342	3.92133E-24
RAB16	RAB, member RAS oncogene family-like 6	1.18747E-28	0.344537197	0.772	0.204	4.00108E-24
ARMXC3	armadillo repeat containing, X-linked 3	1.44137E-28	0.527751197	0.984	0.543	4.85655E-24
CD151	CD151 molecule (Raph blood group)	1.45306E-28	0.590380552	0.959	0.491	4.89592E-24
TJP2	tight junction protein 2	1.50363E-28	0.361293043	0.668	0.152	5.06635E-24
ASB2	ankyrin repeat and SOCS box containing 2	1.60699E-28	0.540757084	0.808	0.249	5.4146E-24
DKK1	diacylglycerol kinase 1	1.62363E-28	0.555263195	0.71	0.178	5.47066E-24
PTPN21	protein tyrosine phosphatase, non-receptor type 21	1.90311E-28	0.422406093	0.777	0.238	6.41234E-24
CTNND1	catenin delta 1	1.94889E-28	0.450165479	0.845	0.305	6.56658E-24
MTRNR2L10	MT-RNR2-like 10	2.11793E-28	0.264881418	0.528	0.059	7.13616E-24
TRIM55	tripartite motif containing 55	2.16458E-28	0.530860774	0.917	0.357	7.29334E-24
PREPL	prolyl endopeptidase-like	2.17917E-28	0.441533706	0.865	0.297	7.34251E-24
PIOD1	procollagen-lysine-2-oxoglutarate 5-dioxygenase 1	2.21322E-28	0.362878324	0.725	0.186	7.45724E-24
TMEM259	transmembrane protein 259	2.44008E-28	0.372513613	0.772	0.23	8.08924E-24
NEBL	nebulin	2.78883E-28	0.602536042	0.995	0.799	9.36696E-24
UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)	3.04801E-28	0.375938651	0.824	0.238	1.027E-23
ZYG11B	zyg-11 family member B, cell cycle regulator	3.08924E-28	0.385992432	0.855	0.271	1.04089E-23
CEP170	centrosomal protein 170	3.34565E-28	0.420378268	0.803	0.257	1.12728E-23
IRF2BP2	interferon regulatory factor 2 binding protein 2	3.41309E-28	0.445173823	0.839	0.268	1.15001E-23
MEF2C	myocyte enhancer factor 2C	3.48458E-28	0.538073623	0.855	0.297	1.1741E-23
EPDR1	ependymin related 1	3.68952E-28	0.298585578	0.58	0.1	1.24315E-23
CALU	calumenin	4.04067E-28	0.590620247	0.984	0.524	1.36146E-23
HOMER1	homer scaffolding protein 1	4.10361E-28	0.438031919	0.845	0.268	1.38267E-23
OST	O-linked N-acetylglucosamine (GlcNAc) transferase	4.30751E-28	0.483441979	0.741	0.201	1.45137E-23
LRC10	leucine-rich repeat containing 10	4.43684E-28	0.665577707	0.902	0.405	1.49495E-23
DYNLL2	dynein light chain LC8-type 2	4.59267E-28	0.349482986	0.782	0.208	1.54745E-23
TP53NP1	tumor protein p53 inducible nuclear protein 1	4.68577E-28	0.398902801	0.637	0.134	1.57882E-23
TMTC1	transmembrane and tetraatricopeptide repeat containing 1	5.0468E-28	0.359368623	0.699	0.167	1.70047E-23
TNRC18	trinucleotide repeat containing 18	5.08171E-28	0.347098356	0.756	0.201	1.71223E-23
PRRC2B	proline rich coiled-coil 2B	5.17996E-28	0.463466073	0.891	0.349	1.74534E-23
AEN	apoptosis enhancing nuclease	5.7383E-28	0.27964567	0.528	0.071	1.93346E-23
PCNK	very low density lipoprotein receptor	6.65163E-28	0.297281449	0.642	0.13	2.2412E-23
VLDR	vacuole membrane protein 1	7.99418E-28	0.376214807	0.803	0.238	2.69356E-23
VMP1	polymerase I and transcript release factor	8.90298E-28	0.514367274	0.896	0.323	2.99977E-23
PTRF	midnolin	1.0129E-27	0.567777972	0.995	0.665	3.41285E-23
MIDN	CD99 molecule like 2	1.08523E-27	0.426834383	0.86	0.271	3.65658E-23
CD99L2	protein kinase AMP-activated catalytic subunit alpha 2	1.19249E-27	0.287604837	0.627	0.126	4.01796E-23
PRKAA2	MT-RNR2-like 3	1.22071E-27	0.411286829	0.824	0.257	4.11304E-23
MTRNR2L3	thioredoxin related transmembrane protein 4	1.36172E-27	0.252923606	0.523	0.063	4.58816E-23
TM64	solute carrier family 16 member 2	1.39302E-27	0.412324529	0.855	0.279	4.69362E-23
SLC26A2	phosphofurin acidic cluster sorting protein 1	1.46734E-27	0.331385451	0.658	0.149	4.94046E-23
PACS1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	1.50662E-27	0.519455394	0.902	0.364	5.07642E-23
TANC2	Rab interacting lysosomal protein-like 1	1.51182E-27	0.280263026	0.596	0.108	5.09394E-23
RILPL1	cyclin-dependent kinase 2 associated protein 1	1.59979E-27	0.3003406	0.694	0.156	5.39033E-23
CDK2AP1	phosphoglucutase 5	1.61609E-27	0.308968342	0.663	0.141	5.44526E-23
PGMS	signal transducer and activator of transcription 3	1.70429E-27	0.374025439	0.751	0.201	5.74244E-23
STAT3	citrate synthase	1.76958E-27	0.40947182	0.819	0.268	5.96241E-23
CS	mitofusin 2	1.78341E-27	0.467738548	0.922	0.339	6.00903E-23
MFN2	ectonucleoside triphosphate diphosphohydrolase 4	1.986E-27	0.473850762	0.919	0.476	6.69162E-23
ENTPD4	dystonin	2.0247E-27	0.325051875	0.751	0.208	6.78417E-23
DST	sarcoglycan beta	2.16615E-27	0.483353341	0.927	0.379	7.29862E-23
SGCB	ATPase family, AAA domain containing 1	2.21877E-27	0.352398152	0.72	0.193	7.47593E-23
ATAD1	family with sequence similarity 168 member A	2.37415E-27	0.455243615	0.907	0.357	7.99947E-23
FAM168A	ryanodine receptor 2	2.49367E-27	0.298899232	0.642	0.141	8.40218E-23
RYR2	ribosomal protein L23	2.54186E-27	0.381732333	0.933	0.349	8.56454E-23
RPL23	signal regulatory protein alpha	2.64797E-27	0.595432658	0.995	0.993	8.9205E-23
SERP1	prospero homeobox 1	2.68151E-27	0.37728512	0.819	0.253	9.03506E-23
PROX1	junction plakoglobin	2.75719E-27	0.460873444	0.762	0.216	9.29009E-23
JLIP	RNA binding motif protein 24	2.90366E-27	0.395236678	0.891	0.335	9.7836E-23
RBM24	Rho GTPase activating protein 35	3.02663E-27	0.554664436	0.959	0.435	1.01979E-22
ARHGAP35	EH domain containing 4	3.18503E-27	0.372388641	0.793	0.245	1.07317E-22
EH4	ubiquitin specific peptidase 22	3.62189E-27	0.396919952	0.808	0.264	1.22036E-22
USP22	leucine rich repeat (in FLII) interacting protein 1	3.63846E-27	0.486108494	0.959	0.454	1.22594E-22
LRRFIP1		3.7275E-27	0.446364623	0.922	0.357	1.25594E-22

CCNY	cyclin Y	3.78306E-27	0.405144904	0.808	0.271	1.27466E-22
FAM198B	family with sequence similarity 198 member B	4.06016E-27	0.423772089	0.971	0.212	1.36803E-22
AHNAK	AHNAK nucleoprotein	4.09097E-27	0.539084291	0.754	0.494	1.37841E-22
MDI1	midline 1	4.61105E-27	0.323845433	0.637	0.134	1.55365E-22
TAKC1	tetratricopeptide repeat, ankryin repeat and coiled-coil containing 1	4.69671E-27	0.459977733	0.891	0.327	1.58251E-22
IRGQ	immunity-related GTPase Q	4.98513E-27	0.294549291	0.694	0.167	1.67969E-22
KTNI	kinectin 1	5.55347E-27	0.523754242	0.995	0.714	1.87119E-22
SLF2	SMCS-SMC6 complex localization factor 2	5.82705E-27	0.359967327	0.694	0.186	1.96337E-22
TJP1	tight junction protein 1	6.2939E-27	0.469484422	0.943	0.413	2.12067E-22
AC074117.10		6.31432E-27	0.276909788	0.513	0.074	2.12755E-22
PPP1R12A	protein phosphatase 1 regulatory subunit 12A	6.33163E-27	0.43306209	0.896	0.346	2.13388E-22
UBE3C	ubiquitin protein ligase E3C	6.64365E-27	0.317411999	0.777	0.216	2.23851E-22
HIK3	homeodomain interacting protein kinase 3	6.81461E-27	0.448745722	0.927	0.394	2.29611E-22
TRNG5B	truncotide repeat containing 5B	7.50084E-27	0.444227639	0.943	0.47	2.52733E-22
RUNX1T1	RUNX1 translocation partner 1	7.61995E-27	0.511610253	0.886	0.338	2.56747E-22
USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	7.92633E-27	0.369153747	0.746	0.219	2.6707E-22
ZMYM2	zinc finger MYM-type containing 2	8.05645E-27	0.377935708	0.855	0.279	2.71454E-22
IMPAD1	inositol monophosphatase domain containing 1	8.54324E-27	0.358720998	0.741	0.201	2.87856E-22
NUCB1	nucleobindin 1	8.71132E-27	0.422135329	0.824	0.294	2.93519E-22
RICTOR	RPTOR independent companion of MTOR complex 2	8.76911E-27	0.396182171	0.772	0.238	2.95466E-22
PTK7	protein tyrosine kinase 7 (inactive)	9.10096E-27	0.274077242	0.606	0.123	3.06488E-22
B3GALT6	beta-1,3-galactosyltransferase 6	9.88991E-27	0.276302551	0.596	0.119	3.33231E-22
PHF10	PHD finger protein 10	1.01492E-26	0.374504994	0.824	0.264	3.41966E-22
B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	1.03136E-26	0.376071038	0.617	0.138	3.47508E-22
SNTA1	syntrophin alpha 1	1.07501E-26	0.499051789	0.948	0.439	3.62212E-22
ABHD2	abhydrolase domain containing 2	1.12237E-26	0.277295562	0.503	0.071	3.78173E-22
ACTN4	actinin alpha 4	1.20963E-26	0.519316089	0.912	0.349	4.07572E-22
SLCSA1	solute carrier family 5 member 1	1.27291E-26	0.306420286	0.565	0.089	4.28894E-22
SCAMP1	secretory carrier membrane protein 1	1.29469E-26	0.305537198	0.71	0.19	4.36234E-22
TSPAN9	tetraspanin 9	1.31482E-26	0.367478647	0.819	0.245	4.43015E-22
PGS	phosphatidylinositol glycan anchor biosynthesis class 5	1.32305E-26	0.3681783	0.808	0.26	4.45787E-22
AGRN	agrin	1.44799E-26	0.346931813	0.705	0.182	4.87855E-22
MAGT1	magnesium transporter 1	1.468E-26	0.33576544	0.736	0.204	4.94628E-22
SPTAN1	spectrin alpha, non-erythrocytic 1	1.64349E-26	0.517572008	0.948	0.487	5.53756E-22
FAM69B	family with sequence similarity 69 member B	1.84E-26	0.315475124	0.642	0.145	6.19971E-22
USP9X	ubiquitin specific peptidase 9, X-linked	1.87769E-26	0.382840632	0.876	0.32	6.32669E-22
SMG7	SMG7, nonsense mediated mRNA decay factor	2.00122E-26	0.295366464	0.679	0.164	6.74292E-22
PITPNA	phosphatidylinositol transfer protein alpha	2.02213E-26	0.324606422	0.736	0.204	6.81336E-22
C7orf60		2.03536E-26	0.530917405	0.938	0.424	6.85795E-22
PALLD	palladin, cytoskeletal associated protein	2.09293E-26	0.499406435	0.995	0.677	7.05193E-22
YBX3	Y-box binding protein 3	2.0952E-26	0.519034966	0.959	0.491	7.05956E-22
XPO1	exportin 1	2.29729E-26	0.418990716	0.845	0.29	7.74049E-22
EDF1	endothelial differentiation related factor 1	2.46748E-26	-0.689727523	0.891	0.881	8.31392E-22
NUAK1	NUAK family kinase 1	2.65504E-26	0.482004733	0.756	0.227	8.9459E-22
TBC1D9	TBC1 domain family member 9	2.68864E-26	0.352647632	0.601	0.13	9.05909E-22
PDI4A	protein disulfide isomerase family A member 4	2.94948E-26	0.33219271	0.741	0.216	9.93799E-22
ASCC3	activating signal cointegrator 1 complex subunit 3	3.16936E-26	0.369396015	0.915	0.219	1.06789E-21
FST	folistatin	3.32543E-26	0.323457518	0.487	0.056	1.12047E-21
DYRK2	dual specificity tyrosine phosphorylation regulated kinase 2	4.00113E-26	0.360831846	0.777	0.234	1.14598E-21
SLCO3A1	solute carrier organic anion transporter family member 3A1	3.43402E-26	0.36200172	0.699	0.175	1.15706E-21
CNG11	cingulin-like 1	3.59563E-26	0.360636688	0.912	0.349	1.21151E-21
BPTF	bromodomain PHD finger transcription factor	3.60226E-26	0.425631167	0.896	0.357	1.21375E-21
UBQLN1	ubiquilin 1	3.8026E-26	0.409727207	0.87	0.305	1.28125E-21
PNMA11	paraneoplastic Ma antigen family-like 1	3.97084E-26	0.259400762	0.699	0.164	1.33794E-21
VIXORC1L1	vitamin K epoxide reductase complex subunit 1 like 1	4.00645E-26	0.310230297	0.71	0.186	1.34993E-21
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	4.16436E-26	0.334360382	0.648	0.149	1.40314E-21
PICALM	phosphatidylinositol binding clathrin assembly protein	4.23595E-26	0.54606412	0.85	0.349	1.42726E-21
P3H4	prolyl 3-hydroxylase family member 4 (non-enzymatic)	4.58568E-26	0.345655552	0.793	0.23	1.5451E-21
ACTN2	actinin alpha 2	4.68207E-26	0.638110132	0.984	0.625	1.57758E-21
PPP2CB	protein phosphatase 2 catalytic subunit beta	4.69172E-26	0.463202808	0.902	0.372	1.58083E-21
MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	4.83591E-26	0.557107992	1	0.952	1.62941E-21
HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase	4.86408E-26	0.430715413	0.902	0.361	1.6389E-21
MGAT4B	mannosyl (alpha-1,3)-glycosyl protein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	5.01672E-26	0.407907108	0.912	0.327	1.69333E-21
RPJ7	ribosomal protein L7	5.0275E-26	0.646607716	1	0.993	1.69397E-21
DYNC1H1	dynein cytoplasmic 1 heavy chain 1	5.03789E-26	0.456758449	0.896	0.364	1.69747E-21
PPP1R13B	protein phosphatase 1 regulatory subunit 13B	5.12245E-26	0.289201004	0.689	0.164	1.72596E-21
RPL9	ribosomal protein L9	5.22007E-26	-0.543126223	1	0.996	1.75885E-21
GAS6-AS1		5.3926E-26	0.264453093	0.451	0.037	1.81669E-21
NSD1	nuclear receptor binding SET domain protein 1	5.4723E-26	0.342558769	0.762	0.245	1.84384E-21
MESDC1	mesoderm development candidate 1	5.58016E-26	0.344831232	0.658	0.175	1.88018E-21
ACSL4	acyl-CoA synthetase long-chain family member 4	5.69183E-26	0.288857436	0.668	0.156	1.91781E-21
BAG3	BCL2 associated ataxogene 3	5.72478E-26	0.382392733	0.834	0.285	1.92891E-21
RBPMS2	RNA binding protein with multiple splicing 2	5.89106E-26	0.540993924	0.969	0.546	1.98493E-21
SH3PX2A	SH3 and PX domains 2A	5.89603E-26	0.409407347	0.767	0.238	1.98661E-21
RPS11	ribosomal protein S11	6.08934E-26	-0.529768241	0.995	0.996	2.05174E-21
REEP2	receptor accessory protein 2	6.19853E-26	0.390700032	0.865	0.294	2.08853E-21
EVL	Enah/Vasp-like	6.2524E-26	0.357241397	0.788	0.245	2.10668E-21
KCNH2	potassium voltage-gated channel subfamily H member 2	6.30456E-26	0.497867969	0.881	0.346	2.12426E-21
OS9	OS9, endoplasmic reticulum lectin	7.03556E-26	0.295375982	0.798	0.223	2.37056E-21
CLIPA	CAP-Gly domain containing linker protein family member 4	7.07476E-26	0.269739894	0.611	0.119	2.38377E-21
TNIO	tri Rho guanine nucleotide exchange factor	8.16539E-26	0.385109058	0.705	0.208	2.75125E-21
FLRT2	fibronectin leucine rich transmembrane protein 2	8.39216E-26	0.402203513	0.663	0.167	2.82765E-21
KIAA0232	KIAA0232	8.89563E-26	0.336964267	0.751	0.204	2.99729E-21
HIF3A	hypoxia inducible factor 3 alpha subunit	9.70433E-26	0.304182255	0.788	0.223	3.26978E-21
HS2ST1	heparan sulfate 2-O-sulfotransferase 1	1.0215E-25	0.340361494	0.746	0.219	3.44185E-21
SERINC1	serine incorporator 1	1.05047E-25	0.455776838	0.933	0.405	3.53944E-21
MPDZ	multiple PDZ domain crumbs cell polarity complex component	1.17524E-25	0.38452154	0.855	0.309	3.95985E-21
MGEA5	meningioma expressed antigen 5 (hyaluronidase)	1.2746E-25	0.397194082	0.876	0.331	4.29464E-21
NCOA4	nuclear receptor coactivator 4	1.38309E-25	0.470841519	0.927	0.413	4.66018E-21
FAM64A	family with sequence similarity 46 member A	1.39343E-25	0.365974578	0.725	0.193	4.69502E-21
AKAP13	A-kinase anchoring protein 13	1.42664E-25	0.456777342	0.881	0.349	4.80691E-21
LHPF	lipoma HMGIC fusion partner	1.43101E-25	0.288647528	0.767	0.204	4.82165E-21
RBMS	RNA binding motif protein 5	1.53973E-25	0.341418036	0.777	0.234	5.18797E-21
ADAMT51	ADAM metalloproteinase with thrombospondin type 1 motif 1	1.57412E-25	0.353710744	0.518	0.082	5.30384E-21
SURF4	surfeit 4	1.59784E-25	0.319366231	0.839	0.257	5.38375E-21
CDCD8	coiled-coil domain containing 8	1.66482E-25	0.314003058	0.777	0.253	5.60946E-21
LMO2	leiomodin 2	1.70527E-25	0.510563053	0.829	0.309	5.74573E-21
SLC7A6	solute carrier family 7 member 6	1.7058E-25	0.254133699	0.591	0.119	5.74751E-21
TUG1		1.71192E-25	0.405438685	0.886	0.346	5.76814E-21
IQSEC1	IQ motif and Sec7 domain 1	1.75015E-25	0.266288091	0.58	0.115	5.89669E-21
RPSA	ribosomal protein SA	1.81273E-25	-0.671887724	1	0.989	6.10781E-21
TMOD1	tropomodulin 1	1.87946E-25	0.457756979	0.943	0.416	6.33266E-21
SH3BP5	SH3 domain binding protein 5	1.99056E-25	0.372279002	0.694	0.193	6.70699E-21
ZNF219	zinc finger protein 219	2.17356E-25	0.312584936	0.715	0.19	7.3236E-21
ZFYF16	zinc finger FYF-type containing 16	2.31619E-25	0.281153385	0.689	0.167	7.80416E-21
PPP2R3B	protein phosphatase 2 regulatory subunit B''beta	2.33686E-25	0.365077678	0.746	0.216	7.87381E-21
TMTCS	transmembrane and tetratricopeptide repeat containing 3	2.4258E-25	0.257125791	0.778	0.119	8.1735E-21
PIAS1	protein inhibitor of activated STAT 1	2.5416E-25	0.358858599	0.585	0.253	8.56367E-21
COL6A2	collagen type VI alpha 2	2.7296E-25	0.323443302	0.622	0.141	9.17473E-21
EHD1	EH domain containing 1	2.74637E-25	0.346499454	0.751	0.208	9.25363E-21
DBN1	drebirin 1	2.87244E-25	0.33946074	0.793	0.245	9.6784E-21
EXOG	endo/exonuclease (5'-3'), endonuclease G-like	3.11658E-25	0.30108904	0.622	0.149	1.0501E-20
EP300	E1A binding protein p300	3.24017E-25	0.299956669	0.71	0.193	1.09174E-20
YPSL2	ypipes like 2	3.2483E-25	0.33215607	0.71	0.186	1.09448E-20
ITGA3	integrin subunit alpha 3	3.29307E-25	0.289810152	0.658	0.156	1.10957E-20
QKI	QKI, KH domain containing, RNA binding	3.3763E-25	0.502832597	0.959	0.561	1.13761E-20
PANK3	pantothenate kinase 3	3.37702E-25	0.420359948	0.886	0.357	1.13785E-20
ANO6	anoctamin 6	3.70326E-25	0.317842237	0.642	0.152	1.24778E-20
PKD1	pyruvate dehydrogenase kinase 1	3.73252E-25	0.441700409	0.845	0.312	1.25763E-20
RPS27L	ribosomal protein S27 like	4.10037E-25	0.432294602	1	0.836	1.38158E-20
CCP110	centriolar coiled-coil protein 110	4.2045E-25	0.269424365	0.472	0.067	1.41666E-20
IAKS2	isolectin-B4 synthetase 2, mitochondrial	4.23238E-25	0.432944752	0.87	0.346	1.42606E-20
PTH1R	parathyroid hormone 1 receptor	4.27903E-25	0.250002222	0.606	0.112	1.44178E-20
KIF21A	kinesin family member 21A	4.30493E-25	0.313659824	0.798	0.253	1.4505E-20
LAMA5	laminin subunit alpha 5	4.66217E-25	0.295444337	0.694	0.193	1.57087E-20
AC013461.1		5.30891E-25	0.543711863	0.99	0.647	1.78878E-20
RPL15	ribosomal protein L15	5.47925E-25	-0.600007968	1	0.993	1.84618E-20
CASC4	cancer susceptibility candidate 4	5.57018E-25	0.316672811	0.756	0.219	1.87682E-20
FKBP10	FK506 binding protein 10	6.33621E-25	0.3494651	0.756	0.227	2.13492E-20

NEK9	NIMA related kinase 9	6.38633E-25	0.309403015	0.57	0.115	2.15181E-20
ARHGEF17	Rho guanine nucleotide exchange factor 17	6.39586E-25	0.260893979	0.694	0.175	2.15050E-20
MARCH6	membrane associated ring-CH-type finger 6	6.56003E-25	0.383275469	0.839	0.29	2.21033E-20
CTIF	CBP80/20-dependent translation initiation factor	6.61305E-25	0.317042465	0.689	0.178	2.2282E-20
PRKAR2B	protein kinase CAMP-dependent type II regulatory subunit beta	6.63768E-25	0.304342563	0.674	0.167	2.2365E-20
YIP4	Yip1 domain family member 4	6.70037E-25	0.419375008	0.806	0.361	2.25762E-20
PIA2	praja ring finger ubiquitin ligase 2	6.86525E-25	0.441615524	0.943	0.431	2.31318E-20
P3H2	prolyl 3-hydroxylase 2	7.14392E-25	0.299049845	0.549	0.108	2.40707E-20
WLS	wntless Wnt ligand secretion mediator	7.60777E-25	0.398314627	0.798	0.279	2.56334E-20
SCYL2	SCY1 like pseudokinase 2	7.65702E-25	0.348295266	0.813	0.271	2.57996E-20
CAB39	calcium binding protein 39	7.67976E-25	0.297522364	0.725	0.208	2.58762E-20
SPG2	SPEG complex locus	7.92421E-25	0.447358464	0.927	0.387	2.66998E-20
FD06	FYVE, RhoGEF and PH domain containing 6	8.03332E-25	0.287795671	0.684	0.193	2.70675E-20
HNRNP1	heterogeneous nuclear ribonucleoprotein 1	8.10012E-25	0.326840489	0.725	0.216	2.72925E-20
TBIM6	transmembrane BAX inhibitor motif containing 6	8.11503E-25	0.483024341	0.959	0.435	2.73428E-20
DNAJC21	DnaJ heat shock protein family (Hsp40) member C21	8.43542E-25	0.372337626	0.824	0.286	2.84223E-20
ALS2	ALS2, alsin Rho guanine nucleotide exchange factor	8.63842E-25	0.310090196	0.694	0.19	2.91063E-20
EMILIN2	elastin microfibril interfacer 2	9.3329E-25	0.334634693	0.694	0.182	3.14463E-20
PXN	paxillin	9.67314E-25	0.32968035	0.725	0.212	3.25927E-20
DCAF5	DOB1 and CUL4 associated factor 5	9.7905E-25	0.295794023	0.689	0.175	3.29881E-20
RP59	ribosomal protein S9	9.85841E-25	0.579362292	1	0.993	3.32169E-20
POLR2J3	polymerase (RNA) II subunit J3	9.89872E-25	0.399153796	0.829	0.305	3.33528E-20
ZBTB4	zinc finger and BTB domain containing 4	1.00346E-24	0.291330583	0.731	0.219	3.38105E-20
GATA4	GATA binding protein 4	1.02738E-24	0.398618188	0.86	0.342	3.46165E-20
RP529	ribosomal protein S29	1.03011E-24	0.454395366	1	1	3.47086E-20
CTC-44AN24.11		1.05547E-24	0.326150433	0.741	0.219	3.55629E-20
TNKS2	tankyrase 2	1.05561E-24	0.334289585	0.71	0.216	3.55676E-20
FRY	FRY microtubule binding protein	1.08728E-24	0.292358624	0.591	0.126	3.6635E-20
SPPL2A	signal peptide peptidase like 2A	1.12612E-24	0.315146511	0.705	0.201	3.79436E-20
TRIP12	thyroid hormone receptor-interactor 12	1.12949E-24	0.404735514	0.881	0.338	3.80569E-20
IGF1R	insulin like growth factor 1 receptor	1.19139E-24	0.32559885	0.772	0.227	4.01428E-20
USP53	ubiquitin specific peptidase S3	1.23825E-24	0.446461419	0.746	0.253	4.17217E-20
SCAF11	SR-related CTD associated factor 11	1.28163E-24	0.454165051	0.917	0.398	4.31834E-20
NUFIP2	NUFIP2, FMR1 interacting protein 2	1.297E-24	0.314272593	0.829	0.29	4.37012E-20
UBE2Z	ubiquitin conjugating enzyme E2 Z	1.32749E-24	0.34281352	0.803	0.275	4.47285E-20
ZNF462	zinc finger protein 462	1.33835E-24	0.357100212	0.684	0.197	4.50945E-20
ITM2C	integral membrane protein 2C	1.37519E-24	0.477290574	0.953	0.416	4.63357E-20
RYK	receptor-like tyrosine kinase	1.37774E-24	0.335264146	0.813	0.271	4.64425E-20
TMEM56	transmembrane protein S6	1.44898E-24	0.37104449	0.746	0.275	4.88218E-20
TMEM10	transmembrane p24 trafficking protein 10	1.49384E-24	0.472334326	0.938	0.401	5.03335E-20
PTTG1P	pituitary tumor-transforming 1 interacting protein	1.52813E-24	0.436085445	0.969	0.457	5.14888E-20
PTEN	phosphatase and tensin homolog	1.61758E-24	0.362416503	0.855	0.305	5.45027E-20
UBE2M	ubiquitin conjugating enzyme E2 M	1.62253E-24	0.400831306	0.87	0.323	5.46696E-20
TCEB2	transcription elongation factor B subunit 2	1.68007E-24	0.509811677	1	0.978	5.66084E-20
MYEF2	myelin expression factor 2	1.68841E-24	0.293945479	0.71	0.197	5.68891E-20
SLMAP	sarcolemma associated protein	1.75301E-24	0.51506475	0.943	0.476	5.90658E-20
FAM33A	family with sequence similarity 234 member A	1.75621E-24	0.416760548	0.746	0.242	5.91737E-20
ABHD17A	abhydrolase domain containing 17A	2.00778E-24	0.303557512	0.658	0.178	6.765E-20
DOX3X	DEAD-box helicase 3, X-linked	2.09542E-24	0.441861386	0.917	0.398	7.0603E-20
TM9SF2	transmembrane 9 superfamily member 2	2.19592E-24	0.30502999	0.741	0.216	7.39892E-20
BIRC6	baculoviral IAP repeat containing 6	2.3045E-24	0.35720251	0.808	0.283	7.76478E-20
ERC1	ELKS/RAB6-interacting/CAST family member 1	2.35365E-24	0.306716133	0.668	0.178	7.9039E-20
UBR1	ubiquitin protein ligase E3 component n-recognin 1	2.41138E-24	0.32897143	0.622	0.152	8.12492E-20
STRN4	striatin 4	2.4183E-24	0.274916732	0.679	0.175	8.14821E-20
SK3	SK family kinase 3	2.42681E-24	0.270305141	0.658	0.164	8.17688E-20
CDH11	cadherin 11	2.4485E-24	0.335544006	0.648	0.16	8.92385E-20
CORIN	corin, serine peptidase	2.71411E-24	0.557524778	0.813	0.323	9.14493E-20
MEF2A	myocyte enhancer factor 2A	2.76697E-24	0.460938469	0.974	0.58	9.32302E-20
NACA	nascent polypeptide-associated complex alpha subunit	2.89779E-24	0.57850158	1	0.981	9.76381E-20
GOLGB1	golgin B1	2.90677E-24	0.321493574	0.777	0.257	9.79407E-20
WDFY3	WD repeat and FYVE domain containing 3	2.97731E-24	0.25866796	0.674	0.16	1.00317E-19
NAV2	neuron navigator 2	3.11256E-24	0.355899253	0.679	0.193	1.04875E-19
H1FX	H1 histone family member X	3.17615E-24	0.371997286	0.798	0.279	1.07017E-19
RCAN1	regulator of calcineurin 1	3.28636E-24	0.453841927	0.715	0.227	1.10731E-19
DCLK2	doublecortin like kinase 2	3.57805E-24	0.265259027	0.56	0.112	1.20559E-19
HS017B12	hydroxysteroid 17-beta dehydrogenase 12	3.63763E-24	0.327542383	0.756	0.238	1.22566E-19
AAK1	AP2 associated kinase 1	3.74081E-24	0.376218194	0.876	0.338	1.26043E-19
SEC31A	SEC31 homolog A, COPII coat complex component	3.79032E-24	0.406144882	0.891	0.353	1.27711E-19
EXTL3	exostosin like glycosyltransferase 3	3.80459E-24	0.259889909	0.534	0.099	1.28192E-19
MAN1A2	mannosidase alpha class 1A member 2	3.89242E-24	0.339523014	0.731	0.223	1.31151E-19
CTSA	cathepsin A	4.22655E-24	0.357820851	0.756	0.238	1.42409E-19
ADGRB3	adhesion G protein-coupled receptor A3	4.29347E-24	0.267070955	0.648	0.16	1.44646E-19
INSIG1	insulin induced gene 1	4.4578E-24	0.354349368	0.617	0.149	1.50201E-19
STT3B	STT3B, catalytic subunit of the oligosaccharyltransferase complex	4.94511E-24	0.386629422	0.767	0.257	1.6662E-19
BTBD07	BTB domain containing 7	4.97857E-24	0.338830554	0.648	0.171	1.67748E-19
PPDPF	pancreatic progenitor cell differentiation and proliferation factor	5.12665E-24	0.687068662	0.995	0.963	1.72737E-19
PPP4R3A	protein phosphatase 4 regulatory subunit 3A	5.53218E-24	0.306027696	0.653	0.171	1.86401E-19
YTHDF3	YTH N6-methyladenosine RNA binding protein 3	5.56934E-24	0.338449844	0.829	0.283	1.87653E-19
MCCC2	methylcrotonoyl-CoA carboxylase 2	5.96149E-24	0.293556618	0.725	0.227	2.00866E-19
KCTD12	potassium channel tetramerization domain containing 12	5.98859E-24	0.453080079	0.637	0.156	2.01779E-19
CYB5R1	cytochrome b5 reductase 1	6.30059E-24	0.369303768	0.72	0.212	2.12292E-19
SPECCL1	sperm antigen with calponin homology and coiled-coil domains 1-like	6.35409E-24	0.260055319	0.585	0.126	2.14095E-19
RNF217	ring finger protein 217	6.66395E-24	0.311568922	0.585	0.141	2.24535E-19
MYH11	myosin, heavy chain 11, smooth muscle	7.10967E-24	0.412126514	0.756	0.052	2.39535E-19
MYO18B	myosin XVIIIIB	7.13449E-24	0.337043525	0.488	0.26	2.4039E-19
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	7.36585E-24	0.365111666	0.829	0.301	2.48185E-19
GGT7	gamma-glutamyltransferase 7	7.41211E-24	0.367893237	0.56	0.119	2.49744E-19
IGF2R	insulin like growth factor 2 receptor	7.54689E-24	0.324082984	0.674	0.186	2.54285E-19
RPN2	ribophorin II	7.88080E-24	0.388703137	0.845	0.29	2.65781E-19
DCL1	DCL1 Rho GTPase activating protein	8.32691E-24	0.473876046	0.839	0.342	2.80567E-19
ADCY6	adenylate cyclase 6	8.6585E-24	0.301009087	0.803	0.249	2.9174E-19
DNAJC10	DnaJ heat shock protein family (Hsp40) member C10	8.75956E-24	0.337997955	0.777	0.268	2.95145E-19
BAMBI	BMP and activin membrane bound inhibitor	9.10962E-24	0.436030927	0.855	0.338	3.0694E-19
CTSB	cathepsin B	9.56748E-24	0.328754441	0.839	0.286	3.22367E-19
CMYA5	cardiomyopathy associated 5	1.12985E-23	0.504383805	0.907	0.454	3.80692E-19
ITGA9	integrin subunit alpha 9	1.15933E-23	0.291778569	0.528	0.086	3.90624E-19
TAF10	TATA-box binding protein associated factor 10	1.18376E-23	0.328527335	0.803	0.268	3.98856E-19
FOCAD	focadhesin	1.2004E-23	0.263510603	0.648	0.156	4.04463E-19
KIF1C	kinesin family member 1C	1.20133E-23	0.30940289	0.953	0.494	4.04775E-19
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	1.20566E-23	0.573951582	1	1	4.06236E-19
HRK	harakiri, BCL2 interacting protein	1.21345E-23	0.332834362	0.508	0.078	4.08861E-19
RP54X	ribosomal motif S4, X-linked	1.23622E-23	0.670293149	0.87	0.996	4.16532E-19
TRIM24	tripartite motif containing 24	1.29885E-23	0.412125837	1	0.338	4.37635E-19
NC51	neuronal calcium sensor 1	1.32559E-23	0.271600276	0.71	0.201	4.46644E-19
BMPR2	bone morphogenetic protein receptor type 2	1.43344E-23	0.397588235	0.855	0.312	4.82984E-19
TBK2	tau tubulin kinase 2	1.43767E-23	0.296295857	0.642	0.175	4.84407E-19
TRIOBP	TRIO and F-actin binding protein	1.4826E-23	0.423980532	0.912	0.387	4.99548E-19
NPEPPS	aminopeptidase puromycin sensitive	1.50113E-23	0.325577521	0.782	0.268	5.05791E-19
UBE2G2	ubiquitin conjugating enzyme E2 G2	1.54304E-23	0.313948392	0.736	0.234	5.19912E-19
HEG1	heart development protein with EGF like domains 1	1.62818E-23	0.365218112	0.705	0.201	5.48599E-19
FKBP9	FK506 binding protein 9	1.64019E-23	0.271127054	0.653	0.167	5.52647E-19
ERBB4	erb-b2 receptor tyrosine kinase 4	1.72781E-23	0.27244353	0.539	0.093	5.82169E-19
LINC01021	long intergenic non-protein coding RNA 1021	1.76104E-23	0.331821423	0.42	0.041	5.93366E-19
C17orf11	C17orf11-like	1.76965E-23	0.339286979	0.824	0.29	5.96267E-19
MBD3	MeCPG binding domain protein 3	1.84127E-23	0.339326529	0.808	0.283	6.20397E-19
TMED5	transmembrane p24 trafficking protein 5	1.8586E-23	0.308358989	0.762	0.234	6.26236E-19
PIEZO1	piezo type mechanosensitive ion channel component 1	1.88276E-23	0.253517606	0.56	0.119	6.34378E-19
SLC31A1	solute carrier family 31 member 1	1.99262E-23	0.266421657	0.606	0.156	6.71394E-19
EXT1	exostosin glycosyltransferase 1	2.01048E-23	0.347311286	0.627	0.164	6.7741E-19
PPP4R1	protein phosphatase 4 regulatory subunit 1	2.04612E-23	0.29426033	0.699	0.201	6.89418E-19
PPP3R1	protein phosphatase 3 regulatory subunit B, alpha	2.16374E-23	0.313809938	0.694	0.204	7.29049E-19
NOUPA11	NOUPA11-ubiquitinone oxidoreductase subunit A11	2.17876E-23	0.541855867	0.935	0.981	7.34113E-19
PLEKH82	pleckstrin homology domain containing B2	2.27779E-23	0.352916211	0.819	0.283	7.67479E-19
AES	amino-terminal enhancer of split	2.30787E-23	0.423544862	0.995	0.691	7.77614E-19
PRKCI	protein kinase C iota	2.40273E-23	0.257618789	0.746	0.219	8.09576E-19
AGT	angiotensinogen	2.47595E-23	0.294074672	0.539	0.093	8.34247E-19
ARIH1	ariadne RBR E3 ubiquitin protein ligase 1	2.70421E-23	0.282106033	0.762	0.238	9.11156E-19
OLFML2A	olfactomedin like 2A	2.8502E-23	0.284433727	0.482	0.074	9.60347E-19
CLOCK	clock circadian regulator	2.94452E-23	0.326241365	0.756	0.242	9.92127E-19

AAGALT	alpha 1,4-galactosyltransferase	2.97024E-23	0.393002953	0.839	0.29	1.00079E-18
PHTF2	putative homeodomain transcription factor 2	3.02088E-23	0.312347275	0.679	0.19	1.01786E-18
CTBP1	C-terminal binding protein 1	3.02303E-23	0.325340739	0.788	0.249	1.01858E-18
MAP2K4	mitogen-activated protein kinase kinase 4	3.21397E-23	0.261335628	0.622	0.16	1.08292E-18
JMJD1C	jumonj domain containing 1C	3.36164E-23	0.328761611	0.808	0.279	1.13267E-18
TRIM23	tripartite motif containing 23	3.42826E-23	0.2956253144	0.642	0.167	1.15512E-18
NSF	N-ethylmaleimide sensitive factor	3.52782E-23	0.274148639	0.601	0.149	1.18866E-18
ATP6V1H	ATPase H+ transporting V1 subunit H	3.55648E-23	0.297033149	0.736	0.23	1.19832E-18
INPP1L	inositol polyphosphate phosphatase like 1	3.5829E-23	0.346564095	0.891	0.353	1.20722E-18
PHACTR4	phosphatase and actin regulator 4	3.71108E-23	0.290549683	0.689	0.212	1.25041E-18
PBRM1	polybromo 1	3.77822E-23	0.309516365	0.751	0.242	1.27303E-18
C7	complement component 7	3.9405E-23	0.446345264	0.658	0.186	1.32771E-18
MAP2K2	mitogen-activated protein kinase kinase 2	4.02225E-23	0.317159472	0.839	0.271	1.35256E-18
UBE2R2	ubiquitin conjugating enzyme E2 R2	4.15145E-23	0.347192223	0.886	0.32	1.39879E-18
PBX2	PBX homeobox 2	4.19035E-23	0.301502181	0.715	0.204	1.4119E-18
ZN7F04	zinc finger protein 704	4.30369E-23	0.272556932	0.534	0.1	1.45008E-18
AP000769.1		4.36189E-23	0.264839555	0.679	0.182	1.4697E-18
NDN	necdin, MAGE family member	4.61023E-23	0.328465649	0.72	0.219	1.55337E-18
EPB41L3	erythrocyte membrane protein band 4.1 like 3	4.70599E-23	0.378714329	0.87	0.32	1.58564E-18
TLL1	tolloid like 1	4.73277E-23	0.288104847	0.394	0.033	1.59466E-18
ERLIN2	ER lipid raft associated 2	4.83785E-23	0.268281262	0.596	0.134	1.63007E-18
SERPINH1	serpin family H member 1	4.99617E-23	0.471071586	0.917	0.399	1.68341E-18
CHKSR3	CHKSR family member 3	5.08486E-23	0.322940407	0.642	0.178	1.71329E-18
FIGN	figdgetin, microtubule severing factor	5.08784E-23	0.316980393	0.668	0.182	1.7143E-18
EEA1	early endosome antigen 1	5.20437E-23	0.29979925	0.668	0.19	1.75356E-18
RC3H2	ring finger and CCHC-type domains 2	5.34402E-23	0.322771316	0.772	0.264	1.80061E-18
RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	5.35307E-23	0.297294129	0.699	0.201	1.80366E-18
P4H8	prolyl 4-hydroxylase subunit beta	5.35769E-23	0.443701123	0.969	0.468	1.80522E-18
PRKCA	protein kinase cAMP-activated catalytic subunit alpha	6.0782E-23	0.370419575	0.881	0.353	2.04799E-18
HCN4	hyperpolarization activated cyclic nucleotide gated potassium channel 4	6.0864E-23	0.273155966	0.585	0.123	2.05075E-18
CAND2	cullin associated and neddylation dissociated 2 (putative)	6.2565E-23	0.265096966	0.622	0.145	2.10807E-18
DSG2	desmoglein 2	6.37816E-23	0.33805729	0.736	0.219	2.14906E-18
AC090498.1		6.50043E-23	0.42209389	0.995	0.836	2.19026E-18
KMT2C	lysine methyltransferase 2C	6.72316E-23	0.300021132	0.772	0.242	2.2653E-18
DNAJB14	DnaJ heat shock protein family (Hsp40) member B14	6.81853E-23	0.271242898	0.617	0.164	2.29744E-18
SCSD	sterol-C5-desaturase	7.54449E-23	0.302273957	0.736	0.234	2.54204E-18
TSPYL4	TSPY-like 4	7.5928E-23	0.28547401	0.554	0.119	2.55832E-18
PDIA3	protein disulfide isomerase family A member 3	7.74731E-23	0.331925901	0.87	0.297	2.61038E-18
CDS9	CDS9 molecule	8.12558E-23	0.420662252	0.902	0.457	2.73817E-18
ATPAP2	ATPase H+ transporting accessory protein 2	8.4908E-23	0.291225582	0.736	0.212	2.86089E-18
PRRC2A	proline rich coiled-coil 2A	8.51434E-23	0.372140515	0.902	0.387	2.86882E-18
OSTM1	osteopetrosis associated transmembrane protein 1	8.73189E-23	0.317509479	0.736	0.245	2.94212E-18
TTCT8	tetratricopeptide repeat domain 28	8.86503E-23	0.287621396	0.632	0.16	2.98698E-18
AP1B1	adaptor related protein complex 1 beta 1 subunit	9.57584E-23	0.255418572	0.637	0.167	3.22648E-18
STK11	serine/threonine kinase 11	9.90243E-23	0.286899626	0.699	0.201	3.33652E-18
HMBOX1	homeobox containing 1	1.10568E-22	0.306252675	0.725	0.227	3.72547E-18
NPV1C4	NPV1 homolog, ubiquitin recognition factor	1.1183E-22	0.292375116	0.931	0.23	3.768E-18
GA57	growth arrest specific 7	1.12937E-22	0.26723077	0.627	0.149	3.8053E-18
APC	adenomatous polyposis coil	1.13851E-22	0.262836096	0.658	0.186	3.83611E-18
MYH7B	myosin, heavy chain 7B, cardiac muscle, beta	1.18248E-22	0.363225791	0.772	0.245	3.98424E-18
ELL2	elongation factor for RNA polymerase II 2	1.19894E-22	0.263011299	0.606	0.145	4.0397E-18
CYBR3	cytochrome b5 reductase 3	1.28497E-22	0.475124888	0.99	0.628	4.32956E-18
SDFA	stromal cell derived factor 4	1.31234E-22	0.360159473	0.891	0.368	4.42179E-18
KDM3B	lysine demethylase 3B	1.34755E-22	0.279707832	0.71	0.208	4.54042E-18
UBR4	ubiquitin protein ligase E3 component n-recogin 4	1.36483E-22	0.389526736	0.87	0.368	4.59865E-18
ZNFX58	zinc finger protein 358	1.45238E-22	0.294687648	0.803	0.275	4.89365E-18
FERMD3	FERM domain containing 3	1.45275E-22	0.444248749	0.953	0.502	4.8949E-18
RANBP2	RAN binding protein 2	1.47938E-22	0.305583505	0.772	0.271	4.98461E-18
NCKAP1	NCK associated protein 1	1.61505E-22	0.401742301	0.974	0.502	5.44174E-18
TM9SF3	transmembrane 9 superfamily member 3	1.68346E-22	0.332832092	0.85	0.309	5.67226E-18
HERC1	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1	1.76087E-22	0.286767569	0.663	0.19	5.93309E-18
TSR3	TSR3, acp transferase ribosome maturation factor	1.77191E-22	0.320187373	0.777	0.245	5.97028E-18
ADD1	adducin 1	1.77697E-22	0.365251157	0.907	0.361	5.98733E-18
CT3	cystatin C	1.78168E-22	0.433422555	0.979	0.558	6.0032E-18
CS136A7	solute carrier family 16 member 7	1.82056E-22	0.287020496	0.653	0.164	6.13419E-18
DGCR2	DiGeorge syndrome critical region gene 2	1.88797E-22	0.254446596	0.575	0.138	6.36132E-18
SLT3	slit guidance ligand 3	1.92746E-22	0.347686209	0.694	0.204	6.49439E-18
BMPRIA	bone morphogenetic protein receptor type 1A	1.93578E-22	0.276139016	0.627	0.171	6.52243E-18
ANK2	ankyrin 2, neuronal	2.08366E-22	0.340290925	0.741	0.223	7.02067E-18
PIK3R2	phosphoinositide 3-kinase regulatory subunit 2	2.13646E-22	0.27262161	0.622	0.171	7.1986E-18
CAND1	cullin associated and neddylation dissociated 1	2.20199E-22	0.33088415	0.813	0.283	7.41939E-18
CCO42EP3	CCO42 effector protein 3	2.23173E-22	0.487558967	0.984	0.669	7.51961E-18
RSF1	remodeling and spacing factor 1	2.25095E-22	0.339726689	0.922	0.353	7.58436E-18
ASH1L	ASH1 like histone lysine methyltransferase	2.27785E-22	0.289113363	0.788	0.26	7.67499E-18
RAD21	RAD21 cohesin complex component	2.30005E-22	0.366613059	0.896	0.372	7.74979E-18
EEF1B2	eukaryotic translation elongation factor 1 beta 2	2.50284E-22	-0.675996839	0.964	0.937	8.43306E-18
ATP5G2	ATP synthase, H+ transporting, mitochondrial Fo complex subunit C2 (subunit 9)	2.55438E-22	-0.568905973	1	0.974	8.60673E-18
PP2R1A	protein phosphatase 2 scaffold subunit Aalpha	2.62193E-22	0.465800081	0.948	0.539	8.83433E-18
GPATCH2L	G-patch domain containing 2 like	2.70009E-22	0.267760657	0.622	0.164	9.09769E-18
GNAQ	G protein subunit alpha q	2.81306E-22	0.349218667	0.824	0.294	9.47833E-18
POZNR3	POZ domain containing ring finger 3	2.81705E-22	0.308850372	0.715	0.216	9.49177E-18
TMEM30A	transmembrane protein 30A	2.88281E-22	0.344054197	0.803	0.283	9.71334E-18
DOX6	DEAD-box helicase 6	2.89036E-22	0.331151024	0.824	0.309	9.73879E-18
DMD	dystrophin	2.93328E-22	0.388646524	0.865	0.349	9.88341E-18
LEPROT	leptin receptor overlapping transcript	3.03142E-22	0.378646335	0.959	0.424	1.02141E-17
PABPN1	poly(A) binding protein nuclear 1	3.12497E-22	0.416930854	0.907	0.409	1.05293E-17
KIF26B	kinesin family member 26B	3.22223E-22	0.377157799	0.881	0.372	1.0857E-17
PHF20L1	PHD finger protein 20-like 1	3.23228E-22	0.323195918	0.85	0.327	1.08908E-17
CNDORP1	cyclin D1 binding protein 1	3.32861E-22	0.309608155	0.845	0.316	1.12154E-17
NEXN	neslin F-actin binding protein	3.34636E-22	0.548483848	0.989	0.662	1.12752E-17
ANKRD1	ankyrin repeat domain 1	3.56092E-22	1.135357438	1	0.636	1.19892E-17
SH3D19	SH3 domain containing 19	3.56503E-22	0.328046075	0.86	0.312	1.2012E-17
SNRPD2	small nuclear ribonucleoprotein D2 polypeptide	3.59112E-22	-0.706657523	0.933	0.881	1.20999E-17
HMG20A	high mobility group 20A	3.64218E-22	0.255370269	0.585	0.141	1.2272E-17
MAN1C1	mannosidase alpha class 1C member 1	3.77617E-22	0.345243051	0.637	0.178	1.27234E-17
ZFP36L1	ZFP36 ring finger protein-like 1	3.91267E-22	0.638244433	0.922	0.483	1.31834E-17
HSPB7	heat shock protein family B (small) member 7	4.04686E-22	0.504109497	1	0.97	1.36355E-17
CCDC141	coiled-coil domain containing 141	4.08919E-22	0.307087526	0.606	0.141	1.37781E-17
MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2	4.15484E-22	0.370935713	0.746	0.234	1.39993E-17
FND3B	fibronectin type III domain containing 3B	4.29096E-22	0.288187797	0.813	0.279	1.44579E-17
TNFRSF21	tumor necrosis factor receptor superfamily member 21	4.39922E-22	0.260788586	0.58	0.13	1.48227E-17
PVRL1		4.40349E-22	0.297757103	0.492	0.089	1.48371E-17
SEC61A1	Sec61 translocon alpha 1 subunit	4.46637E-22	0.319143079	0.808	0.26	1.5049E-17
DCAF8	DDB1 and CUL4 associated factor 8	4.63166E-22	0.270356178	0.746	0.245	1.56059E-17
ADAM9	ADAM metalloproteinase domain 9	4.67704E-22	0.342407778	0.762	0.26	1.57588E-17
C16orf72	chromosome 16 open reading frame 72	4.69481E-22	0.301859506	0.829	0.301	1.58187E-17
HEXA	hexosaminidase subunit alpha	4.85915E-22	0.290270081	0.668	0.193	1.63724E-17
SESN3	sestrin 3	4.86028E-22	0.280510527	0.725	0.23	1.63762E-17
POG2	pogo transposable element with ZNF domain	4.88493E-22	0.300021661	0.741	0.257	1.64593E-17
NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	5.15479E-22	0.296371957	0.788	0.279	1.73685E-17
ZRANB1	zinc finger RANBP2-type containing 1	5.26261E-22	0.258525656	0.699	0.204	1.77318E-17
RAB58	RAB58, member RAS oncogene family	5.36234E-22	0.395166341	0.881	0.394	1.80679E-17
SATB1	SATB homeobox 1	5.56738E-22	0.256655197	0.663	0.175	1.87587E-17
SOLE	squalene epoxidase	5.65333E-22	0.337232369	0.731	0.23	1.90483E-17
CRY2	cryptochrome circadian clock 2	5.67771E-22	0.265686734	0.611	0.16	1.91305E-17
CAMSAP2	calmodulin regulated spectrin associated protein family member 2	5.84887E-22	0.286478997	0.751	0.257	1.97072E-17
EIF4G1	eukaryotic translation initiation factor 4 gamma 1	5.94307E-22	0.404724259	0.933	0.42	2.00246E-17
SEZ6L2	seizure related 6 homolog like 2	6.03539E-22	0.263645066	0.606	0.141	2.03356E-17
USP46	ubiquitin specific peptidase 46	6.04538E-22	0.302106491	0.741	0.234	2.03693E-17
LOXL2	lysyl oxidase like 2	6.27785E-22	0.282074656	0.585	0.138	2.11526E-17
ACTC1	actin, alpha, cardiac muscle 1	6.50919E-22	0.683599516	1	0.974	2.19321E-17
RPL10A	ribosomal protein L10a	6.59921E-22	-0.659307558	1	0.974	2.22354E-17
AGAP3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	6.64248E-22	0.254895304	0.689	0.19	2.23821E-17
PCDD6P	programmed cell death 6 interacting protein	6.66216E-22	0.334305932	0.829	0.301	2.24475E-17
SIPA1L1	signal induced proliferation associated 1 like 1	6.67583E-22	0.324777251	0.767	0.264	2.24936E-17
SLC35E28	solute carrier family 35 member E28	6.82926E-22	0.26098103	0.679	0.208	2.30105E-17
KNC4	potassium voltage-gated channel subfamily C member 4	6.93809E-22	0.255993592	0.941	0.071	2.33772E-17
LMO4	LIM domain only 4	6.99053E-22	0.525556001	0.467	0.613	2.35539E-17
SLC25A12	solute carrier family 25 member 12	7.54567E-22	0.252137231	0.653	0.175	2.54244E-17

NDUFA13	NADH:ubiquinone oxidoreductase subunit A13	7.9373E-22	-0.600400038	0.984	0.967	2.6744E-17
GYG1	glycogenin 1	8.16591E-22	0.486627991	0.99	0.721	2.75142E-17
TERF2IP	TERF2 interacting protein	8.36187E-22	0.355110348	0.943	0.416	2.81745E-17
GOSR1	golgi SNAP receptor complex member 1	8.48856E-22	0.285165975	0.71	0.219	2.86014E-17
TMED7	transmembrane p24 trafficking protein 7	8.80137E-22	0.29443224	0.756	0.257	2.96553E-17
MTMFR	methylentetrahydrofolate reductase (NAD(P)H)	9.13874E-22	0.282438779	0.71	0.216	3.07321E-17
TRIM33	tripartite motif containing 33	9.35239E-22	0.294716591	0.642	0.193	3.15119E-17
PBXIP1	PBX homeobox interacting protein 1	9.44485E-22	0.271571661	0.617	0.167	3.18235E-17
ROBO1	roundabout guidance receptor 1	9.52719E-22	0.284113259	0.513	0.1	3.21009E-17
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	1.00528E-21	0.380595474	0.865	0.387	3.38719E-17
REST	RE1 silencing transcription factor	1.03975E-21	0.285943656	0.772	0.257	3.50335E-17
SPCS3	signal peptidase complex subunit 3	1.05107E-21	0.300130594	0.731	0.242	3.54147E-17
TCF7L2	transcription factor 7 like 2	1.06373E-21	0.271907685	0.689	0.204	3.58413E-17
UBQLN2	ubiquitin 2	1.08051E-21	0.291695121	0.705	0.219	3.64067E-17
HYOU1	hyposia up-regulated 1	1.12631E-21	0.253758751	0.539	0.126	3.795E-17
REP1N1	replication initiator 1	1.17143E-21	0.341343097	0.793	0.294	3.94702E-17
SPARC	secreted protein acidic and cysteine rich	1.19273E-21	0.350213746	0.979	0.572	4.01879E-17
LINC00657		1.22706E-21	0.440237361	0.964	0.513	4.13447E-17
PLPFR2	phospholipid phosphatase related 2	1.27138E-21	0.302010789	0.663	0.197	4.28378E-17
PRKARI	protein kinase cAMP-dependent type I regulatory subunit alpha	1.28544E-21	0.417440391	1	0.825	4.33116E-17
POMGNT1	protein O-linked mannosidase N-acetylglucosaminyltransferase 1 (beta 1,2-)	1.29198E-21	0.290474153	0.86	0.323	4.3352E-17
IFTM3	interferon induced transmembrane protein 3	1.36729E-21	0.1031310959	0.908	0.888	4.60696E-17
HHP	hedgehog interacting protein	1.37953E-21	0.44715619	0.394	0.041	4.64817E-17
STK38L	serine/threonine kinase 38 like	1.42143E-21	0.372734006	0.751	0.249	4.78936E-17
PP2R4		1.4296E-21	0.389492737	0.902	0.42	4.81688E-17
GALNT1	polypeptide N-acetylgalactosaminyltransferase 1	1.43781E-21	0.292317012	0.689	0.223	4.84456E-17
RAPGEF1	Rap guanine nucleotide exchange factor 1	1.4398E-21	0.270082452	0.762	0.249	4.85126E-17
NFIC	nuclear factor I C	1.44131E-21	0.348369095	0.87	0.346	4.85636E-17
EXOC68	exocyst complex component 68	1.50753E-21	0.315639737	0.746	0.257	5.07948E-17
RPS28	ribosomal protein S28	1.5202E-21	0.381260079	1	0.996	5.12216E-17
FAM217B	family with sequence similarity 217 member B	1.53111E-21	0.29191512	0.674	0.216	5.15892E-17
LARP4	La ribonucleoprotein domain family member 4	1.53142E-21	0.302608689	0.751	0.234	5.15988E-17
YY1	YY1 transcription factor	1.55243E-21	0.366635673	0.938	0.401	5.23077E-17
NRXN1	neurexin 1	1.59057E-21	0.30957824	0.399	0.045	5.35928E-17
JADE1	jade family PHD finger 1	1.60218E-21	0.341729635	0.632	0.171	5.39837E-17
KCTD10	potassium channel tetramerization domain containing 10	1.67986E-21	0.26615713	0.684	0.204	5.66013E-17
LINC00969		1.71296E-21	0.267334843	0.663	0.193	5.77164E-17
MAT2A	methionine adenosyltransferase 2A	1.71541E-21	0.309685568	0.839	0.309	5.77991E-17
NSC4	nicotinic	1.83438E-21	0.276372689	0.674	0.201	6.18075E-17
OSBP1L	oxysterol binding protein like 8	1.88917E-21	0.392014044	0.808	0.216	6.36536E-17
ATF6	activating transcription factor 6	1.91365E-21	0.282111043	0.58	0.156	6.44784E-17
IBTK	inhibitor of Bruton tyrosine kinase	2.01769E-21	0.261414505	0.767	0.249	6.79841E-17
MT-CO3	cytochrome c oxidase III	2.07822E-21	0.506478116	1	1	7.00236E-17
KPN1A	karyopherin subunit alpha 1	2.11509E-21	0.313958638	0.741	0.245	7.12657E-17
ZNF277	zinc finger protein 277	2.15491E-21	0.647522618	0.601	0.16	7.26077E-17
RLP4	ribosomal protein L4	2.21643E-21	-0.6053102	0.99	0.989	7.46804E-17
APBB1	amyloid beta precursor protein binding family B member 1	2.21755E-21	0.296296787	0.819	0.29	7.4718E-17
AFG3L2	AFG3 like matrix AAA peptidase subunit 2	2.22188E-21	0.390750458	0.865	0.349	7.48641E-17
UBP1	upstream binding protein 1 (LBP-1a)	2.28823E-21	0.283212973	0.637	0.178	7.70995E-17
DIP2C	disco interacting protein 2 homolog C	2.29566E-21	0.250380561	0.554	0.13	7.73501E-17
RIOK3	RIO kinase 3	2.31049E-21	0.368327421	0.813	0.312	7.78498E-17
CTDNBP1	CTD nuclear envelope phosphatase 1	2.445E-21	0.336810016	0.819	0.305	8.23817E-17
TEAD3	TEA domain transcription factor 3	2.71913E-21	0.332173455	0.788	0.297	9.16183E-17
SLC20A2	solute carrier family 20 member 2	2.77511E-21	0.379433599	0.793	0.301	9.35046E-17
FAM65B	family with sequence similarity 63 member B	2.79232E-21	0.358097227	0.715	0.242	9.40844E-17
GAPD1	GTPase activating protein and VP59 domains 1	2.82723E-21	0.267778063	0.642	0.182	9.86302E-17
WDR82	WD repeat domain 82	2.93998E-21	0.304654567	0.772	0.275	9.90598E-17
ARHGAP24	Rho GTPase activating protein 24	3.04843E-21	0.250925116	0.492	0.097	1.02714E-16
PBX3	PBX homeobox 3	3.17689E-21	0.281658562	0.731	0.238	1.07042E-16
G3BP1	G3BP stress granule assembly factor 1	3.22286E-21	0.33439241	0.896	0.361	1.08591E-16
LGMN	legumain	3.26959E-21	0.321937381	0.653	0.193	1.10165E-16
FAM65B	family with sequence similarity 65 member B	3.26996E-21	0.294292646	0.425	0.056	1.10178E-16
DVL3	dishevelled segment polarity protein 3	3.30787E-21	0.29609186	0.86	0.342	1.11456E-16
SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	3.38125E-21	0.314291214	0.804	0.316	1.13328E-16
POI4E	protein disulfide isomerase family A member 6	3.42182E-21	0.368180995	0.927	0.409	1.15295E-16
RAB3GAP1	RAB3 GTPase activating protein catalytic subunit 1	3.47673E-21	0.252758534	0.756	0.257	1.17145E-16
PLCL1	phospholipase C like 1	3.69736E-21	0.257563942	0.591	0.141	1.24579E-16
EFR3A	EFR3 homolog A	4.01612E-21	0.317595744	0.782	0.29	1.35319E-16
ACTN1	actinin alpha 1	4.2065E-21	0.691557705	0.927	0.498	1.41734E-16
FAM84B	family with sequence similarity 84 member B	4.21437E-21	0.512270805	0.917	0.476	1.41999E-16
RLP3	ribosomal protein L3	4.28341E-21	0.621114989	1	0.989	1.44325E-16
IMMT	inner membrane mitochondrial protein	4.28977E-21	0.352297393	0.876	0.383	1.44539E-16
ROCK2	Rho associated coiled-coil containing protein kinase 2	4.41127E-21	0.276889973	0.705	0.216	1.48633E-16
EPS15	epidermal growth factor receptor pathway substrate 15	4.57157E-21	0.400032549	0.912	0.435	1.54035E-16
EFNB3	ephrin B3	4.72118E-21	0.287487239	0.549	0.126	1.59075E-16
HACD2	3-hydroxyacyl-CoA dehydratase 2	4.84669E-21	0.294039628	0.611	0.178	1.63304E-16
CUL3	cullin 3	4.98581E-21	0.331743285	0.798	0.297	1.67992E-16
AKAP6	A-kinase anchoring protein 6	5.40846E-21	0.367065596	0.798	0.286	1.82233E-16
LRRFP2	leucine rich repeat (in FLN) interacting protein 2	5.4143E-21	0.325509116	0.881	0.368	1.82429E-16
COR6G	coronin 6	5.95244E-21	0.307011263	0.762	0.26	2.00561E-16
IREB2	iron responsive element binding protein 2	6.5032E-21	0.316314425	0.819	0.301	2.19119E-16
NCSTN	nicastatin	7.1615E-21	0.251525208	0.575	0.149	2.413E-16
AF4	AFA/FMR2 family member 4	7.69025E-21	0.356298561	0.808	0.312	2.59115E-16
CELF1	CUGBP, Elav-like family member 1	7.83792E-21	0.373014186	0.922	0.401	2.64091E-16
PGRMC1	progesterone receptor membrane component 1	9.43385E-21	0.335718423	0.85	0.335	3.17864E-16
ARHGAP23	Rho GTPase activating protein 23	1.0086E-20	0.256408823	0.591	0.141	3.39837E-16
SH3GL3	SH3 domain containing GRB2 like endophilin A3	1.01547E-20	0.338233262	0.824	0.32	3.42152E-16
RAB12	RAB12, member RAS oncogene family	1.06767E-20	0.340393337	0.601	0.156	3.5974E-16
COPB2	coatamer protein complex subunit beta 2	1.07407E-20	0.307473186	0.865	0.338	3.61896E-16
CNK1E	casein kinase 1 epsilon	1.09666E-20	0.28639172	0.777	0.283	3.69508E-16
TTCL1	tetratricopeptide repeat domain 17	1.15954E-20	0.254952534	0.591	0.16	3.90696E-16
HECTD1	HECT domain E3 ubiquitin protein ligase 1	1.17342E-20	0.296745777	0.808	0.29	3.95371E-16
SRF	serum response factor	1.17721E-20	0.381029736	0.819	0.323	3.96651E-16
FEM1A	fem-1 homolog A	1.17784E-20	0.268896851	0.684	0.216	3.96863E-16
PROS1	protein S (alpha)	1.23272E-20	0.327891764	0.71	0.253	4.15335E-16
TAOK1	TAO kinase 1	1.30123E-20	0.314687827	0.829	0.29	4.38437E-16
WAC	WW domain containing adaptor with coiled-coil	1.3013E-20	0.381850388	0.87	0.383	4.3946E-16
HERC2	HECT and RLD domain containing E3 ubiquitin protein ligase 2	1.31857E-20	0.3158839	0.751	0.275	4.4428E-16
FBXO18	F-box protein, helicase, 18	1.36554E-20	0.274608982	0.751	0.26	4.60104E-16
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	1.39607E-20	0.286477676	0.653	0.197	4.70392E-16
MEGF8	multiple EGF like domains 8	1.41631E-20	0.260158397	0.674	0.201	4.77211E-16
TMEM106B	transmembrane protein 106B	1.51331E-20	0.30086888	0.741	0.26	5.09895E-16
PUM1	pumilio RNA binding family member 1	1.59254E-20	0.294176863	0.86	0.327	5.3659E-16
ARRDC3	arrestin domain containing 3	1.63252E-20	0.334484557	0.648	0.197	5.50062E-16
SAP9D	sphingomyelin phosphodiesterase 1	1.71445E-20	0.265097686	0.57	0.149	5.7666E-16
NPRB	natruietic peptide B	1.72082E-20	0.816977551	0.948	0.494	5.79813E-16
LTPB3	latent transforming growth factor beta binding protein 3	1.7344E-20	0.291605909	0.715	0.242	5.84254E-16
CTNNB1	catenin beta 1	1.82827E-20	0.398275355	1	0.662	6.16016E-16
SVIL	supervillin	1.83116E-20	0.350410384	0.99	0.651	6.16991E-16
FAM120A	family with sequence similarity 120A	1.8838E-20	0.352632308	0.813	0.323	6.34729E-16
SEC23A	Sec23 homolog A, coat complex II component	1.96363E-20	0.383958924	0.938	0.468	6.61627E-16
PCNXL4		2.12458E-20	0.315199724	0.622	0.201	7.15857E-16
ETS2	ETS proto-oncogene 2, transcription factor	2.14356E-20	0.289984843	0.689	0.212	7.2225E-16
MYH9	myosin, heavy chain 9, non-muscle	2.16732E-20	0.50930554	0.959	0.491	7.30256E-16
BLCAP	bladder cancer associated protein	2.44322E-20	0.324215008	0.834	0.331	8.2327E-16
DLST	dihydrolipoamide S-succinyltransferase	2.50606E-20	0.274850444	0.772	0.271	8.44393E-16
HBEGF	heparin binding EGF like growth factor	2.67886E-20	0.341165349	0.503	0.112	9.02614E-16
SSPN	sarcomspan	2.68683E-20	0.268239879	0.596	0.156	9.05299E-16
MAP4	microtubule associated protein 4	2.69078E-20	0.439186907	0.984	0.68	9.0663E-16
PRKAG2	protein kinase AMP-activated non-catalytic subunit gamma 2	2.7359E-20	0.4400281	0.953	0.491	9.21833E-16
CDC88A	coiled-coil domain containing 88A	2.8307E-20	0.253746557	0.705	0.219	9.53777E-16
PAWR	pro-apoptotic WTI regulator	2.91604E-20	0.308459172	0.762	0.253	9.82529E-16
CNK	cyclin K	3.10398E-20	0.25589104	0.632	0.193	1.04586E-15
RAPGEF2	Rap guanine nucleotide exchange factor 2	3.18713E-20	0.268110097	0.705	0.223	1.07387E-15
RASSF4	Ras associated family member 4	3.35044E-20	0.264204576	0.637	0.178	1.12888E-15
SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	3.66505E-20	0.28799415	0.881	0.372	1.2349E-15
TBC1D1	TBC1 domain family member 1	3.81428E-20	0.291402012	0.751	0.264	1.28518E-15
AQP1	aquaporin 1 (Colton blood group)	4.01136E-20	0.306357403	0.57	0.138	1.35159E-15
MLLT3	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 3	4.08392E-20	0.255411447	0.606	0.167	1.37604E-15

RNF115	ring finger protein 115	4.18354E-20	0.355752205	0.876	0.398	1.4096E-15
MGRN1	mahogunin ring finger 1	4.24952E-20	0.262139523	0.653	0.208	1.43183E-15
STX16	syntaxin 16	4.26434E-20	0.251159267	0.705	0.245	1.43683E-15
NACC2	NACC family member 2	4.27898E-20	0.261417942	0.554	0.141	1.44176E-15
SLC39A10	solute carrier family 39 member 10	4.42908E-20	0.251192021	0.549	0.138	1.49233E-15
FARP1	FERM, ARN/RbuGEF and pleckstrin domain protein 1	4.43566E-20	0.409037655	0.855	0.39	1.49455E-15
ATP5J2	ATP synthase, H+ transporting, mitochondrial Fo complex subunit F2	4.4708E-20	0.703407836	0.995	0.963	1.50639E-15
MTU52	microtubule associated tumor suppressor candidate 2	4.54069E-20	0.385837027	0.933	0.45	1.52994E-15
NDFIP2	Nedd4 family interacting protein 2	4.73025E-20	0.313725123	0.808	0.305	1.59381E-15
IL11RA	interleukin 11 receptor subunit alpha	4.81773E-20	0.291753473	0.658	0.201	1.62329E-15
CDV3	CDV3 homolog	5.11249E-20	0.445831855	0.943	0.517	1.7226E-15
TRIB1	tribbles pseudokinase 1	5.19924E-20	0.309015457	0.637	0.204	1.75183E-15
CRY2	crystallin zeta	5.30131E-20	0.251600935	0.617	0.178	1.78622E-15
TRIM28	tripartite motif containing 28	5.30279E-20	0.293784873	0.876	0.353	1.81705E-15
RP56KA2	ribosomal protein S6 kinase A2	5.57631E-20	0.298875254	0.601	0.171	1.87888E-15
MLLT4	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 4	5.59734E-20	0.337524798	0.808	0.32	1.88597E-15
YAP1	Yes associated protein 1	5.62177E-20	0.363077258	0.907	0.413	1.8942E-15
ATXN2	ataxin 2	5.67241E-20	0.278151158	0.679	0.219	1.91126E-15
SERPINE1	serpin family E member 1	5.7189E-20	0.466623953	0.482	0.093	1.92693E-15
ZNF451	zinc finger protein 451	5.79634E-20	0.255995429	0.591	0.171	1.95302E-15
GBA2	glucosylceramidase beta 2	6.19238E-20	0.294519862	0.663	0.208	2.08646E-15
INHBA	inhibin beta A subunit	6.24738E-20	0.334282078	0.58	0.145	2.10499E-15
SNHG23	maternally expressed 8 (non-protein coding)	6.26218E-20	0.297282887	0.347	0.033	2.10998E-15
NR2F6	nuclear receptor subfamily 2 group F member 6	6.28539E-20	0.290194524	0.756	0.275	2.1178E-15
LATS2	large tumor suppressor kinase 2	6.40762E-20	0.26633166	0.648	0.197	2.15898E-15
UBFD1	ubiquitin family domain containing 1	6.4644E-20	0.282163499	0.741	0.26	2.17811E-15
MPP5	membrane palmitoylated protein 5	6.57106E-20	0.258513052	0.627	0.186	2.21405E-15
SORT1	soritin 1	6.6641E-20	0.290128237	0.756	0.26	2.2454E-15
ALDH3A2	aldehyde dehydrogenase 3 family member A2	6.85373E-20	0.376870821	0.767	0.286	2.3093E-15
BCCL1	BCCL1 like 1	6.87167E-20	0.291356734	0.699	0.253	2.31534E-15
IGF2BP2	insulin like growth factor 2 mRNA binding protein 2	7.29902E-20	0.358023667	0.829	0.335	2.45934E-15
REEP3	receptor accessory protein 3	7.40911E-20	0.374658337	0.953	0.45	2.49642E-15
GBE1	glucan (1,4-alpha-), branching enzyme 1	7.46138E-20	0.359372676	0.715	0.253	2.51404E-15
SSR1	signal sequence receptor subunit 1	7.50367E-20	0.275700986	0.845	0.29	2.52829E-15
UBE2S	ubiquitin conjugating enzyme E2 S	7.80503E-20	0.262800171	0.694	0.227	2.62983E-15
KIAA0100	KIAA0100	7.83576E-20	0.256592403	0.658	0.204	2.64018E-15
OGDH	oxoglutarate dehydrogenase	7.93327E-20	0.307527226	0.751	0.275	2.67304E-15
KCCL1	kinesin light chain 1	8.97847E-20	0.284554747	0.813	0.312	3.02521E-15
PON2	peroxanase 2	1.0103E-19	0.304136288	0.813	0.297	3.4041E-15
EFCA814	EF-hand calcium binding domain 14	1.02561E-19	0.26066618	0.98	0.238	3.45659E-15
GANAB	glucosidase II alpha subunit	1.05233E-19	0.280887227	0.736	0.249	3.54571E-15
TMEM248	transmembrane protein 248	1.06137E-19	0.285997989	0.699	0.227	3.57619E-15
T0B1	transducer of ERBB2, 1	1.13962E-19	0.25555933	0.642	0.201	3.8982E-15
LENG8	leukocyte receptor cluster member 8	1.28754E-19	0.280752817	0.72	0.253	4.33824E-15
DHCR7	7-dehydrocholesterol reductase	1.35103E-19	0.283056728	0.57	0.16	4.55216E-15
GPRIN3	GPRIN family member 3	1.36232E-19	0.308591136	0.72	0.245	4.5902E-15
TARS12	threonyl-tRNA synthetase-like 2	1.40023E-19	0.260048061	0.813	0.305	4.71795E-15
TIA1	TIA1 cytosolic granule-associated RNA binding protein	1.49095E-19	0.257913471	0.653	0.197	5.0236E-15
PPARGC1A	PPARG coactivator 1 alpha	1.54436E-19	0.264686475	0.601	0.152	5.20357E-15
GABRB2	gamma-aminobutyric acid type A receptor beta2 subunit	1.60397E-19	0.280931466	0.321	0.019	5.40442E-15
KPNAB	karyopherin subunit alpha 6	1.7093E-19	0.313743152	0.813	0.323	5.75932E-15
NCOR2	nuclear receptor corepressor 2	1.72205E-19	0.281495435	0.767	0.286	5.80227E-15
USP28	ubiquitin specific peptidase 28	1.76166E-19	0.350397492	0.855	0.346	5.93574E-15
ATP2C1	ATPase secretory pathway Ca2+ transporting 1	1.84043E-19	0.3289352	0.72	0.268	6.20113E-15
SAMD0A	sterile alpha motif domain containing 4A	1.88684E-19	0.294553682	0.772	0.286	6.35753E-15
COPA	costomer protein complex subunit alpha	1.96194E-19	0.32257561	0.813	0.309	6.61055E-15
RRAD	RRAD, Ras related glycylcysis inhibitor and calcium channel regulator	2.02107E-19	0.293850198	0.611	0.164	6.80978E-15
YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein gamma	2.13173E-19	0.382220121	0.964	0.55	7.18265E-15
CIB2	calcium and integrin binding family member 2	2.21812E-19	0.303574409	0.71	0.238	7.47372E-15
RBPMS	RNA binding protein with multiple splicing	2.27853E-19	0.398235719	0.933	0.599	7.67728E-15
NID1	nidogen 1	2.39724E-19	0.298826935	0.57	0.149	8.07728E-15
PDSSA	PDSS cohesin associated factor A	2.44518E-19	0.255931092	0.668	0.227	8.2388E-15
DYRK1A	dual specificity tyrosine phosphorylation regulated kinase 1A	2.67057E-19	0.266445343	0.72	0.249	8.98823E-15
SBF2	SBF binding factor 2	2.73248E-19	0.284135516	0.539	0.152	9.20681E-15
KIF18	kinesin family member 18	2.73331E-19	0.350640333	0.876	0.364	9.20961E-15
VEZT	vezatin, adherens junctions transmembrane protein	2.87098E-19	0.29648908	0.731	0.268	9.67348E-15
ABR	active BCR-related	2.91548E-19	0.250137894	0.534	0.145	9.82342E-15
RMND5A	required for meiotic nuclear division 5 homolog A	3.02313E-19	0.330831125	0.881	0.368	1.01861E-14
GNB2L1	1	3.129E-19	-0.659913258	1	0.97	1.05429E-14
SIAH2	siah E3 ubiquitin protein ligase 2	3.33164E-19	0.259128458	0.627	0.193	1.12256E-14
USP34	ubiquitin specific peptidase 34	3.3808E-19	0.265099041	0.85	0.331	1.13913E-14
LPXCA14	lysophosphatidylcholine acyltransferase 4	3.57707E-19	0.256882976	0.679	0.223	1.20526E-14
SUN1	Sad1 and UNC8A domain containing 1	3.85296E-19	0.271861075	0.85	0.316	1.29822E-14
AKAP9	A-kinase anchoring protein 9	3.91576E-19	0.296981618	0.803	0.316	1.31938E-14
KLF6	Kruppel like factor 6	4.16928E-19	0.329735227	0.731	0.257	1.4048E-14
TACC2	transforming acidic coiled-coil containing protein 2	4.25977E-19	0.340680166	0.865	0.364	1.43529E-14
MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	4.49265E-19	0.258812081	0.953	0.465	1.51375E-14
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	4.52501E-19	0.359404448	0.865	0.387	1.52466E-14
PPFBP1	PPFIA binding protein 1	4.53108E-19	0.29951135	0.793	0.305	1.5267E-14
FAM134A	family with sequence similarity 134 member A	4.98053E-19	0.270293994	0.653	0.212	1.67814E-14
DENN1D1B	DENN domain containing 1B	5.12542E-19	0.294706188	0.658	0.208	1.72729E-14
MLEC	malectin	5.23804E-19	0.301771783	0.798	0.309	1.76491E-14
SCARB2	scavenger receptor class B member 2	5.33961E-19	0.282806078	0.725	0.26	1.79913E-14
ADIPOR2	adiponectin receptor 2	5.41975E-19	0.255760232	0.72	0.26	1.82613E-14
ZNF207	zinc finger protein 207	5.61746E-19	0.293735449	0.881	0.372	1.89275E-14
MYH7	myosin, heavy chain 7, cardiac muscle, beta	5.62657E-19	0.473741775	1	0.948	1.89582E-14
F0FT1	farnesyl-diphosphate farnesyltransferase 1	5.66578E-19	0.416059738	0.912	0.4	1.90903E-14
C047	C047 molecule	5.98056E-19	0.267025006	0.71	0.242	2.01509E-14
SBP3	single stranded DNA binding protein 3	6.02591E-19	0.284916018	0.845	0.327	2.03037E-14
C0X7A2	cytochrome c oxidase subunit 7A2	6.03937E-19	0.512964968	0.756	0.967	2.03491E-14
KCNQ10T1	KCNQ1 opposite strand/antisense transcript 1 (non-protein coding)	6.19503E-19	0.271827258	0.637	0.193	2.08735E-14
USP25	ubiquitin specific peptidase 25	6.4632E-19	0.253298183	0.58	0.171	2.17771E-14
FOXP1	forkhead box P1	6.89201E-19	0.343787744	0.933	0.428	2.32219E-14
RYBP	RING1 and YY1 binding protein	6.89244E-19	0.274289613	0.736	0.264	2.32234E-14
LMOD1	leiomodin 1	7.07815E-19	0.332874569	0.622	0.178	2.38491E-14
CAPN2	calpain 2	7.43644E-19	0.368918401	0.876	0.394	2.50564E-14
SAMD04B	sterile alpha motif domain containing 4B	7.45311E-19	0.280273906	0.767	0.283	2.51125E-14
G0T2	glutamic-oxaloacetic transaminase 2	7.57815E-19	0.346561133	0.881	0.401	2.55338E-14
ARCN1	archain 1	7.92499E-19	0.306242191	0.808	0.316	2.67025E-14
WEE1	WEE1 G2 checkpoint kinase	8.46679E-19	0.384675535	0.87	0.383	2.8528E-14
NF1	neurofibromin 1	8.78422E-19	0.274501819	0.782	0.286	2.95976E-14
CBX6	chromobox 6	8.92194E-19	0.384848135	0.943	0.48	3.00616E-14
RAB31	RAB31, member RAS oncogene family	9.02296E-19	0.2568423	0.622	0.178	3.0402E-14
ATXN2L	ataxin 2 like	9.05197E-19	0.272325246	0.596	0.186	3.04997E-14
WDR26	WD repeat domain 26	9.26652E-19	0.255008658	0.819	0.312	3.12226E-14
MSN	meslin	1.04669E-18	0.355705412	0.756	0.301	3.51326E-14
GLS	glutaminase	1.07142E-18	0.327626803	0.834	0.316	3.61003E-14
PPP1R14C	protein phosphatase 1 regulatory inhibitor subunit 14C	1.0938E-18	0.410995404	0.969	0.524	3.68546E-14
MCC	mutated in colorectal cancers	1.0983E-18	0.27003402	0.622	0.186	3.70062E-14
AGL	amlyo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	1.12295E-18	0.365558328	0.845	0.383	3.78366E-14
SCNSA	sodium voltage-gated channel alpha subunit 5	1.14952E-18	0.294759217	0.788	0.238	3.8732E-14
WDR6	WD repeat domain 6	1.16436E-18	0.326544681	0.715	0.316	3.92318E-14
ICMT	isoprenylcysteine carboxyl methyltransferase	1.19767E-18	0.256117614	0.679	0.223	4.03543E-14
ITRNA1	inositol-3-phosphate synthase 1	1.16039E-18	0.364446257	0.886	0.446	4.5935E-14
CERK	ceramide kinase	1.38168E-18	0.255087691	0.606	0.182	4.65542E-14
RBM26	RNA binding motif protein 26	1.38207E-18	0.290624488	0.699	0.249	4.65675E-14
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	1.38432E-18	0.294570945	0.627	0.204	4.66434E-14
REEP5	receptor accessory protein 5	1.47838E-18	0.327536243	0.933	0.431	4.98127E-14
THBS1	thrombospondin 1	1.51071E-18	0.441579941	0.513	0.13	5.0902E-14
USP2	USP and G-patch domain containing 2	1.53184E-18	0.269299638	0.756	0.275	5.16137E-14
PSCK7	proprotein convertase subtilisin/kexin type 7	1.53503E-18	0.276791642	0.839	0.349	5.17214E-14
RPI7A	ribosomal protein L7a	1.66039E-18	0.600653051	1	0.97	5.59453E-14
SPINT2	serine peptidase inhibitor, Kunitz type, 2	1.66713E-18	0.347627097	0.896	0.428	5.61724E-14
C14orf2	chromosome 14 open reading frame 2	1.6817E-18	-0.509600094	1	0.989	5.66632E-14
AP3D1	adaptor related protein complex 3 delta 1 subunit	1.69095E-18	0.258859351	0.839	0.335	5.69748E-14
MT-ND1	NADH dehydrogenase, subunit 1 (complex I)	1.72441E-18	0.43751242	1	0.981	5.81022E-14
ARHGAP29	Rho GTPase activating protein 29	1.77617E-18	0.311620262	0.731	0.279	5.98461E-14
SLC27A6	solute carrier family 27 member 6	1.79536E-18	0.257863173	0.42	0.071	6.04929E-14
PPIC	peptidylprolyl isomerase C	1.993E-18	0.37836215	0.984	0.602	6.71521E-14

TSC22D2	TSC22 domain family member 2	2.036E-18	0.303222047	0.793	0.316	6.86009E-14
TGM2	transglutaminase 2	2.09197E-18	0.622720563	0.948	0.625	7.04869E-14
NOP10	NOP10 ribonucleoprotein	2.10926E-18	-0.620374351	0.974	0.914	7.10694E-14
FILIP1	filamin A interacting protein 1	2.123937E-18	0.38730768	0.999	0.68	7.17471E-14
REK5	arginine-glutamic acid dipeptide repeats	2.15988E-18	0.319651365	0.824	0.331	7.40892E-14
BT3F	basic transcription factor 3	2.22623E-18	-0.58115664	0.974	0.959	7.50102E-14
RAD23B	RAD23 homolog B, nucleotide excision repair protein	2.24807E-18	0.336334379	0.933	0.45	7.57466E-14
MT-CO1	cytochrome c oxidase subunit I	2.2863E-18	0.445502431	1	1	7.70347E-14
DLD	dihydrodipicolinate dehydrogenase	2.36244E-18	0.359032718	0.933	0.472	7.96001E-14
NTS2C	5'-nucleotidase, cytosolic II	2.463E-18	0.259375992	0.705	0.257	8.29882E-14
CUL4A	cullin 4A	2.69901E-18	0.292996013	0.746	0.294	9.09405E-14
SDHA	succinate dehydrogenase complex flavoprotein subunit A	3.0549E-18	0.389377445	0.886	0.424	1.02932E-13
SP1	splicing factor 1	3.38087E-18	0.337359888	0.912	0.424	1.133915E-13
MAGEF1	MAGE family member F1	3.60032E-18	0.338453685	0.813	0.364	1.21309E-13
PKDC	protein kinase domain containing, cytoplasmic	3.74431E-18	0.262108268	0.565	0.167	1.26161E-13
GADD45GIP1	GADD45G interacting protein 1	3.86263E-18	-0.572151887	0.943	0.862	1.30148E-13
DNAJB2	DnaJ heat shock protein family (Hsp40) member B2	3.9491E-18	0.255241343	0.782	0.305	1.33061E-13
COX6C	cytochrome c oxidase subunit 6C	3.98177E-18	-0.588430417	1	0.989	1.34162E-13
XRCC4	X-ray repair cross complementing 4	4.28657E-18	0.355710724	0.964	0.554	1.44432E-13
TAPBP	TAP binding protein (tapasin)	4.44473E-18	0.268739809	0.782	0.297	1.49828E-13
ADD3	adducin 3	4.82106E-18	0.3938257	0.896	0.465	1.62441E-13
AC02	aconitase 2	4.9248E-18	0.393694404	0.959	0.617	1.65936E-13
TMEM178A	transmembrane protein 178A	5.04511E-18	0.300317878	0.544	0.16	1.6999E-13
SMAD2	SMAD family member 2	5.26108E-18	0.297255949	0.855	0.338	1.77267E-13
ZCCHC24	zinc finger CCHC-type containing 24	5.46108E-18	0.275753482	0.788	0.301	1.84006E-13
UBE3A	ubiquitin protein ligase E3A	5.56239E-18	0.298229116	0.876	0.387	1.87419E-13
NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	5.65094E-18	0.357477468	0.808	0.338	1.90403E-13
SVPL1	synaptophysin like 1	6.34424E-18	0.263464596	0.803	0.301	2.13763E-13
FDZ1	frizzled class receptor 1	6.41441E-18	0.350734388	0.668	0.242	2.16127E-13
TMEM97	transmembrane protein 97	6.85344E-18	0.31961252	0.565	0.171	2.3092E-13
TNRG5A	trinucleotide repeat containing 6A	7.14161E-18	0.29930143	0.791	0.283	2.40629E-13
IKR3	iroquois homeobox 3	7.19351E-18	0.289340312	0.663	0.201	2.42378E-13
PFDN5	prefoldin subunit 5	7.38745E-18	-0.469428749	0.99	0.963	2.48913E-13
HNRNPJ	heterogeneous nuclear ribonucleoprotein U	7.39613E-18	0.36486006	0.948	0.546	2.49205E-13
PFKP	phosphofructokinase, platelet	7.5855E-18	0.395351114	0.943	0.506	2.55586E-13
PUM2	pumilio RNA binding family member 2	7.64009E-18	0.256301109	0.705	0.257	2.57425E-13
PNISR	PNN-interacting serine/arginine-rich protein	7.97251E-18	0.353926789	0.891	0.39	2.68626E-13
ZNF106	zinc finger protein 106	8.43442E-18	0.366704778	0.922	0.506	2.84189E-13
CD34	CD34 molecule	8.50787E-18	0.343273677	0.679	0.227	2.86646E-13
PTP4A2	protein tyrosine phosphatase type IVA, member 2	9.30729E-18	0.354291084	0.953	0.55	3.136E-13
CD164	CD164 molecule	9.7255E-18	0.346207799	0.948	0.461	3.27691E-13
RAB21	RAB21, member RAS oncogene family	1.05999E-17	0.377495291	0.902	0.454	3.69283E-13
CXCC5	CXCC finger protein 5	1.14808E-17	0.26865863	0.793	0.32	3.86833E-13
HAND2	heart and neural crest derivatives expressed 2	1.21024E-17	0.406764223	0.933	0.476	4.07777E-13
TRIM8	tripartite motif containing 8	1.24694E-17	0.259127403	0.705	0.242	4.20145E-13
RHOB	ras homolog family member B	1.30872E-17	0.256237329	0.658	0.216	4.40959E-13
TMEM18A	transmembrane protein 18A	1.31122E-17	0.261382395	0.857	0.286	4.41801E-13
RHOQ	ras homolog family member Q	1.34988E-17	0.384434653	0.953	0.572	4.54829E-13
GPI	glucose-6-phosphate isomerase	1.44228E-17	0.338960754	0.953	0.487	4.85963E-13
ARHGAP5	Rho GTPase activating protein 5	1.45314E-17	0.353413628	0.953	0.509	4.8962E-13
RRAS	related RAS viral (r-ras) oncogene homolog	1.46494E-17	0.360903687	0.731	0.283	4.93597E-13
LIMS2	LIM zinc finger domain containing 2	1.4884E-17	0.378978152	0.938	0.532	5.01501E-13
KIAA1191	KIAA1191	1.52078E-17	0.30198379	0.933	0.428	5.12413E-13
RBMS8	RNA binding motif protein 38	1.56537E-17	0.289654269	0.798	0.312	5.27437E-13
KHLH31	kelch like family member 31	1.70846E-17	0.280872147	0.803	0.309	5.75647E-13
NUD3	nudix hydrolase 3	1.71525E-17	0.28912201	0.829	0.368	5.77326E-13
METAP1	methionyl aminopeptidase 1	1.79097E-17	0.295820004	0.762	0.312	6.03448E-13
CYR61	cysteine rich angiogenic inducer 61	1.85479E-17	0.300039789	0.777	0.312	6.24954E-13
PRNP	prion protein	1.85635E-17	0.287072816	0.772	0.301	6.25479E-13
SYNGR2	syngaptin 2	1.92646E-17	0.343031327	0.86	0.416	6.49101E-13
PRKDC	protein kinase, DNA-activated, catalytic polypeptide	1.92818E-17	0.309722999	0.793	0.312	6.49681E-13
GOLIM4	golgi integral membrane protein 4	1.93366E-17	0.286432767	0.705	0.257	6.51528E-13
CD99	CD99 molecule	2.08003E-17	0.359959164	0.964	0.625	7.00844E-13
MTF	melanogenesis associated transcription factor	2.11445E-17	0.262498973	0.782	0.294	7.12444E-13
SMAD5	SMAD family member 5	2.20162E-17	0.258039655	0.725	0.268	7.41815E-13
FBXO32	F-box protein 32	2.22154E-17	0.293485661	0.679	0.219	7.48526E-13
WWC2	WW and C2 domain containing 2	2.22319E-17	0.257705644	0.648	0.223	7.4908E-13
KLHL24	kelch like family member 24	2.24295E-17	0.264334592	0.741	0.268	7.55739E-13
SSH1	slingshot protein phosphatase 1	2.29133E-17	0.251507822	0.591	0.186	7.7204E-13
FAM168B	family with sequence similarity 168 member B	2.30493E-17	0.251010884	0.634	0.361	7.76624E-13
FLNA	filamin A	2.41669E-17	0.40853437	0.907	0.39	8.14281E-13
MRAS	mouse RAS oncogene homolog	2.62983E-17	0.361287668	0.902	0.487	8.86094E-13
UBA1	ubiquitin like modifier activating enzyme 1	2.66193E-17	0.253033048	0.772	0.297	8.96912E-13
GA56	growth arrest specific 6	2.76485E-17	0.303345582	0.845	0.361	9.31589E-13
MCL1	myeloid cell leukemia 1	2.82601E-17	0.321063968	0.829	0.349	9.52196E-13
KCTD20	potassium channel tetramerization domain containing 20	2.9413E-17	0.250922998	0.793	0.323	9.91043E-13
GJA5	gap junction protein alpha 5	3.06346E-17	0.466368004	0.394	0.074	1.0322E-12
CKD6	cyclin-dependent kinase 6	3.18908E-17	0.33220111	0.922	0.513	1.07453E-12
BCAP29	B-cell receptor-associated protein 29	3.42534E-17	0.270419292	0.808	0.335	1.15413E-12
FGF1	fibroblast growth factor 1	3.66149E-17	0.263927645	0.663	0.212	1.2337E-12
OLFM3	olfactomedin like 3	3.81601E-17	0.300359587	0.451	0.104	1.28577E-12
DHX15	DEAH-box helicase 15	3.93604E-17	0.279337395	0.788	0.323	1.32621E-12
SUMO1	small ubiquitin-like modifier 1	3.93891E-17	-0.561484447	0.891	0.825	1.32718E-12
ARHGEF12	Rho guanine nucleotide exchange factor 12	4.0846E-17	0.293471451	0.808	0.342	1.37627E-12
UBA3	ubiquitin like modifier activating enzyme 3	4.13145E-17	0.281856576	0.813	0.346	1.39205E-12
ACB03	acyl-CoA binding domain containing 3	4.61919E-17	0.28337073	0.782	0.305	1.55639E-12
MAPRE1	microtubule associated protein RP/EB family member 1	4.7148E-17	0.345210466	0.953	0.532	1.5886E-12
GDI1	GDP dissociation inhibitor 1	4.89757E-17	0.272099623	0.642	0.223	1.65019E-12
SARAF	store-operated calcium entry associated regulatory factor	5.07323E-17	0.350121207	0.953	0.55	1.70938E-12
MT-ATP8	ATP synthase F0 subunit 8	5.52461E-17	0.304707073	0.948	0.468	1.86146E-12
ZFAND5	zinc finger AN1-type containing 5	5.56432E-17	0.311828683	0.922	0.483	1.87484E-12
COX7B	cytochrome c oxidase subunit 7B	6.12535E-17	-0.755198971	0.984	0.985	2.06388E-12
EC1	enoyl-CoA delta isomerase 1	6.44992E-17	0.304672498	0.829	0.357	2.17323E-12
SFQ	splicing factor proline/glutamine-rich	7.43619E-17	0.28755897	0.876	0.398	2.50555E-12
COX6B1	cytochrome c oxidase subunit 6B1	7.66646E-17	-0.582397512	0.995	0.989	2.58314E-12
ANKRD9	ankyrin repeat domain 9	7.87437E-17	0.267677905	0.689	0.253	2.65319E-12
PMP22	peripheral myelin protein 22	8.0378E-17	0.33034689	0.663	0.242	2.70826E-12
POMP	proteasome maturation protein	8.18913E-17	-0.639089241	0.99	0.9	2.75924E-12
ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	9.17153E-17	-0.664151972	0.959	0.922	3.09026E-12
IST1	IST1, ESCRT-III associated factor	9.8881E-17	0.254822159	0.788	0.327	3.3317E-12
MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	1.11504E-16	0.310655451	0.896	0.45	3.75703E-12
EEF1D	eukaryotic translation elongation factor 1 delta	1.24042E-16	-0.549285957	0.984	0.911	4.17947E-12
ATXN10	ataxin 10	1.31282E-16	0.308799133	0.912	0.472	4.42341E-12
SRGAP2C	SLIT-ROBO Rho GTPase activating protein 2C	1.32557E-16	0.254650508	0.694	0.271	4.46638E-12
GSN	gelosin	1.39114E-16	0.290226025	0.782	0.323	4.68973E-12
EEF1A2	eukaryotic translation elongation factor 1 alpha 2	1.53064E-16	0.34680668	0.824	0.368	5.15735E-12
AMFR	autocrine motility factor receptor	1.54012E-16	0.267940282	0.71	0.268	5.18927E-12
ZFAS1	ZNFX1 antisense RNA 1	1.62284E-16	-0.719670163	0.969	0.874	5.46799E-12
DCAF7	DOB1 and CUL4 associated factor 7	1.68781E-16	0.275929867	0.808	0.335	5.68689E-12
LARP1	La ribonucleoprotein domain family member 1	1.72876E-16	0.291944533	0.86	0.413	5.82487E-12
UGP2	UDP-glucose pyrophosphorylase 2	1.74663E-16	0.38338616	0.984	0.822	5.88511E-12
HSPB8	heat shock protein family B (small) member 8	2.02403E-16	0.371025459	0.922	0.457	6.81978E-12
MT-CO2	cytochrome c oxidase subunit II	2.17034E-16	0.405563825	1	1	7.31273E-12
KPNA3	karyopherin subunit alpha 3	2.57658E-16	0.259936758	0.793	0.331	8.68153E-12
PCBP1	poly(C) binding protein 1	2.59153E-16	0.349483506	0.99	0.725	8.73191E-12
CHMP4B	charged multivesicular body protein 4B	2.59715E-16	0.357498199	0.917	0.491	8.75084E-12
APOE	apolipoprotein E	2.6507E-16	0.304060692	0.933	0.52	8.93127E-12
C15orf52	chromosome 15 open reading frame 52	2.8118E-16	0.262504983	0.725	0.271	9.47407E-12
PFKM	phosphofructokinase, muscle	3.64826E-16	0.261198274	0.886	0.394	1.22924E-11
RPL17	ribosomal protein L17	3.80579E-16	-0.552761591	0.979	0.959	1.28232E-11
HNRNP9	heterogeneous nuclear ribonucleoprotein D	4.20524E-16	0.262353327	0.87	0.383	1.41691E-11
ATN1	atrophin 1	4.88877E-16	0.262745651	0.679	0.253	1.64722E-11
TRDN	trisadin	6.27885E-16	0.278566289	0.715	0.257	2.1156E-11
KPNA4	karyopherin subunit alpha 4	8.43383E-16	0.287188971	0.87	0.398	2.8417E-11
FXYD1	FXYD domain containing ion transport regulator 1	8.57863E-16	0.302355882	0.736	0.275	2.89048E-11
CDC6	coiled-coil domain containing 6	9.3401E-16	0.278309799	0.782	0.331	3.14705E-11
COL12A1	collagen type XII alpha 1 chain	1.0525E-15	0.267378358	0.477	0.134	3.55555E-11
GOT1	glutamic-oxaloacetic transaminase 1	1.23013E-15	0.304345327	0.902	0.431	4.14482E-11
BANF1	barrier to autointegration factor 1	1.28656E-15	-0.580451093	0.865	0.81	4.33494E-11

TXNL4A	thioredoxin like 4A	1.34297E-15	0.292178424	0.845	0.379	4.52499E-11
COL2A1	collagen type II alpha 1 chain	1.38755E-15	0.250607069	0.446	0.108	4.6752E-11
CAPRN1	cell cycle associated protein 1	1.40754E-15	0.292046011	0.907	0.439	4.74258E-11
COX7C	cytochrome c oxidase subunit 7C	1.4571E-15	-0.461608156	1	0.996	4.90954E-11
NDFP1	Nesdof family interacting protein 7C	1.5448E-15	0.267804408	0.87	0.394	5.20398E-11
ACLY	AT citrate lyase	1.59877E-15	0.296592611	0.725	0.312	5.3869E-11
HACD1	3-hydroxyacyl-CoA dehydrogenase 1	1.59903E-15	0.371964741	0.938	0.572	5.38779E-11
NDUFS1	NADH:ubiquinone oxidoreductase core subunit 51	1.64652E-15	0.268109746	0.865	0.39	5.54778E-11
FTH1	ferritin heavy chain 1	1.74959E-15	-0.587937191	1	1	5.89508E-11
MBNL1	muscleblind like splicing regulator 1	1.76105E-15	0.250299721	0.736	0.294	5.93369E-11
NUDT4	nudix hydrolase 4	1.76269E-15	0.528658663	0.974	0.71	5.93922E-11
DUSP1	dual specificity phosphatase 1	1.82855E-15	0.255768097	0.56	0.175	6.16113E-11
ARIH2	ariadne RBR E3 ubiquitin protein ligase 2	1.94755E-15	0.272279355	0.782	0.335	6.56207E-11
FBXO9	F-box protein 9	1.98518E-15	0.265147066	0.813	0.379	6.68887E-11
ZNF64	zinc finger protein 664	1.99641E-15	0.282559612	0.876	0.409	6.72671E-11
KOM5B	lysine demethylase 5B	2.06703E-15	0.255886543	0.715	0.279	6.96464E-11
PHLDB2	pleckstrin homology like domain family 8 member 2	2.16851E-15	0.281028676	0.689	0.29	7.30658E-11
BCAP31	B-cell receptor-associated protein 31	2.17453E-15	0.283251207	0.845	0.372	7.32686E-11
PBX1	PBX homeobox 1	3.06532E-15	0.422053622	0.865	0.457	1.03283E-10
UQCRC	ubiquinol-cytochrome c reductase binding protein	3.17701E-15	-0.45879457	1	0.97	1.07046E-10
BCYRN1	brain cytoplasmic RNA 1	3.28185E-15	0.749253453	0.409	0.093	1.10579E-10
TMEM113	transmembrane protein 123	4.13214E-15	0.295631747	0.803	0.349	1.39228E-10
BRD4	bromodomain containing 4	4.42666E-15	0.25055415	0.829	0.346	1.49152E-10
KPNB1	karyopherin subunit beta 1	4.8479E-15	0.343337731	0.948	0.509	1.63345E-10
NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	5.52376E-15	0.312472708	0.984	0.71	1.86118E-10
EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	7.01831E-15	0.275498548	0.876	0.413	2.36475E-10
EIF3E	eukaryotic translation initiation factor 3 subunit E	7.21868E-15	-0.629061133	0.85	0.818	2.43226E-10
ROCK1	Rho associated coiled-coil containing protein kinase 1	7.76444E-15	0.25597899	0.839	0.383	2.61615E-10
CITED2	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2	7.79783E-15	0.348882421	0.959	0.546	2.6274E-10
Clorf19B	chromosome 1 open reading frame 19B	7.92871E-15	0.318462396	0.87	0.446	2.6715E-10
GNB1	G protein subunit beta 1	8.60958E-15	0.305148204	0.905	0.981	6.07269E-10
DUSP3	dual specificity phosphatase 3	8.74209E-15	0.311409269	0.902	0.502	2.94556E-10
DPYSL3	dihydropyrimidinease like 3	9.67056E-15	0.373118144	0.917	0.539	3.2584E-10
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta	1.14361E-14	0.312957966	0.99	0.743	3.85329E-10
COX4I1	cytochrome c oxidase subunit 4I1	1.19776E-14	-0.426397251	1	0.985	4.03573E-10
GUCY1A3	guanylate cyclase 1, soluble, alpha 3	1.24362E-14	0.443823831	0.896	0.528	4.19026E-10
BR13	brain protein 13	1.28427E-14	0.268786365	0.855	0.413	4.32723E-10
IARS	isoleucyl-tRNA synthetase	1.62205E-14	0.253915198	0.803	0.349	4.56434E-10
PNN1	profilin 1	1.80231E-14	-0.62367109	0.905	0.981	6.07269E-10
VCP	valosin containing protein	2.037E-14	0.271356346	0.891	0.42	6.86345E-10
IER3	immediate early response 3	2.10361E-14	0.309444466	0.756	0.32	7.08791E-10
FERMT2	fermitin family member 2	2.14469E-14	0.250453188	0.808	0.357	7.22633E-10
HSPA4	heat shock protein family A (Hsp70) member 4	2.27289E-14	0.255441398	0.813	0.361	7.65827E-10
PPP1R14B	protein phosphatase 1 regulatory inhibitor subunit 14B	2.47024E-14	0.315881165	0.907	0.442	8.32324E-10
NDUFB7	NADH:ubiquinone oxidoreductase subunit 17	2.90353E-14	-0.489041572	0.938	0.888	9.78315E-10
DLGAF4	DLG associated protein 4	3.02958E-14	0.254020824	0.632	0.249	1.02079E-09
RPS2	ribosomal protein S2	3.11774E-14	-0.430013357	0.97	1	1.05049E-09
RBBP4	RB binding protein 4, chromatin remodeling factor	3.13694E-14	0.283662226	0.927	0.472	1.05696E-09
TNP01	transportin 1	3.37648E-14	0.253991873	0.85	0.383	1.13767E-09
ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha	3.5625E-14	0.262459986	0.86	0.42	1.20035E-09
TRAK1	trafficking kinesis protein 1	3.68974E-14	0.257944414	0.803	0.364	1.24322E-09
LMCH1	LIM and calponin homology domains 1	3.8635E-14	0.322759532	0.913	0.171	1.30177E-09
SNRPG	small nuclear ribonucleoprotein polypeptide G	4.01635E-14	-0.505617147	0.553	0.892	1.35327E-09
DMPK	dystrophin myotonia protein kinase	4.05355E-14	0.25302631	0.87	0.428	1.3658E-09
ILF3	interleukin enhancer binding factor 3	4.29991E-14	0.255101962	0.845	0.39	1.62739E-09
CAV2	caveolin 2	4.95606E-14	0.313144194	0.927	0.502	1.6699E-09
EIF4G2	eukaryotic translation initiation factor 4 gamma 2	4.95737E-14	0.262005689	0.995	0.918	1.67034E-09
OClAD1	OClA domain containing 1	5.24573E-14	0.289364189	0.922	0.487	1.7675E-09
FAM213A	family with sequence similarity 213 member A	6.91447E-14	0.326798516	0.927	0.565	2.32976E-09
SUB1	SUB1 homolog, transcriptional regulator	7.47218E-14	-0.512853076	0.964	0.911	2.51768E-09
SEC61G	Sec61 translocon gamma subunit	1.06524E-13	-0.566697657	0.984	0.914	3.58922E-09
NREP	neuronal regeneration related protein	1.3705E-13	0.412419745	1	0.944	4.61775E-09
CTSV	cathepsin V	1.37231E-13	0.261018768	0.477	0.149	4.62386E-09
EFI1	eukaryotic translation initiation factor 1	1.393E-13	-0.555648937	0.97	0.952	4.69358E-09
SEPT9	septin 9	1.41983E-13	0.270255669	0.855	0.431	4.78396E-09
PGAM1	phosphoglycerate mutase 1	1.51091E-13	0.288755005	0.995	0.836	5.09086E-09
H3F3A	H3 histone, family 3A	1.59169E-13	-0.412668382	1	0.974	5.36303E-09
TSPYL1	TSPY-like 1	1.63986E-13	0.266221128	0.933	0.468	5.52535E-09
DUSP5	dual specificity phosphatase 5	1.64569E-13	0.358441368	0.627	0.268	5.545E-09
UQCRC1	ubiquinol-cytochrome c reductase, complex III subunit X	1.90603E-13	-0.465315395	0.91	0.993	6.42217E-09
PSMB6	proteasome subunit beta 6	1.98814E-13	0.622723874	0.793	0.743	6.69884E-09
SAP1B	Sin3A associated protein 1B	2.49434E-13	-0.51790484	0.86	0.822	8.40444E-09
NONO	non-POU domain containing, octamer-binding	2.74972E-13	0.295483526	0.912	0.483	9.2649E-09
HSPB1	heat shock protein family B (small) member 1	3.1766E-13	-0.753959301	1	1	1.07033E-08
ANKA6	annexin A6	3.20155E-13	0.283370394	0.938	0.561	1.07873E-08
DDX5	DEAD-box helicase 5	3.31285E-13	0.278718859	0.99	0.658	1.11623E-08
BTG1	B-cell translocation gene 1, anti-proliferative	3.65917E-13	0.414248115	0.922	0.546	1.23292E-08
KIF5B	kinesin family member 5B	3.72186E-13	0.330980583	0.959	0.625	1.25404E-08
TRH	thyrotropin releasing hormone	5.62445E-13	0.269694537	0.383	0.089	1.96249E-08
ATP9VB08	ATPase H+ transporting VO subunit b	5.88473E-13	0.254782574	0.969	0.606	2.04964E-08
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	6.1736E-13	-0.67534025	0.839	0.765	2.08013E-08
PGK1	phosphoglycerate kinase 1	6.50888E-13	0.291854628	0.969	0.595	2.1931E-08
CYCS	cytochrome c, somatic	1.09046E-12	-0.522816124	0.995	0.963	3.67418E-08
SERF2	small EDRK-rich factor 2	1.10773E-12	-0.382851497	1	1	3.73239E-08
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.18827E-12	0.270588544	0.896	0.45	4.00375E-08
PDE4DIP	phosphodiesterase 4D interacting protein	1.26142E-12	0.347484943	0.974	0.721	4.25024E-08
GPX4	glutathione peroxidase 4	1.53423E-12	-0.454384682	0.969	0.914	5.16944E-08
MRPL51	mitochondrial ribosomal protein L51	1.56847E-12	0.647484732	0.803	0.736	5.28482E-08
CNMD	uncharacterized LOC101927480	2.01741E-12	0.276793802	0.845	0.442	6.79747E-08
SEI	SET and MYND domain containing 2	2.02679E-12	0.273732263	0.902	0.502	6.82906E-08
BZW2	basic leucine zipper and W2 domains 2	2.13266E-12	0.272869695	0.969	0.554	7.18578E-08
TSC2D1	TSC22 domain family member 1	2.33513E-12	0.278030911	0.917	0.569	7.868E-08
SHFM1	split hand/foot malformation (ectrodactyly) type 1	2.51579E-12	-0.448881801	0.948	0.848	8.47669E-08
PTMA	prothymosin, alpha	2.52779E-12	-0.746715797	0.948	0.881	8.51715E-08
MT-ND4	NADH dehydrogenase, subunit 4 (complex I)	2.95082E-12	0.25196359	1	1	9.9425E-08
HINT1	histidine triad nucleotide binding protein 1	3.05635E-12	0.384440292	0.995	0.981	1.02981E-07
AK3	adenylate kinase 3	3.7643E-12	0.286419916	0.922	0.52	1.26834E-07
C5orf24	chromosome 5 open reading frame 24	3.87814E-12	0.264460426	0.948	0.558	1.3067E-07
ERH	enhancer of rudimentary homolog (Drosophila)	5.40419E-12	-0.481351275	0.938	0.866	1.82089E-07
YBK1	Y-box binding protein 1	5.45739E-12	-0.440500982	1	0.993	1.83881E-07
MEIS2	Meis homeobox 2	5.76123E-12	0.271358539	0.922	0.55	1.94119E-07
NDUF56	NADH:ubiquinone oxidoreductase subunit S6	6.28527E-12	-0.526134869	0.995	0.97	2.11776E-07
PARK7	Parkinsonism associated deglycase	6.63437E-12	-0.470779403	0.922	0.836	2.23538E-07
NDUFAG	NADH:ubiquinone oxidoreductase subunit A6	9.18036E-12	-0.593342702	0.938	0.848	3.09323E-07
EIZ4	EIZ4, autophagy associated transmembrane protein	9.2213E-12	0.278796639	0.912	0.491	3.10703E-07
PDX5	peroxiredoxin 5	1.01606E-11	-0.421077773	0.99	0.955	3.42352E-07
AZIN1	antizyme inhibitor 1	1.1204E-11	0.306433419	0.839	0.472	3.77508E-07
RAI14	retinoic acid induced 14	1.78246E-11	0.275657488	0.829	0.439	6.00583E-07
TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	2.2449E-11	0.26527594	0.881	0.465	7.56398E-07
ATP5F	ATP synthase, H+ transporting, mitochondrial Fo complex subunit D	2.34352E-11	-0.606541297	0.933	0.833	7.89626E-07
DES	desmin	3.57173E-11	0.284719953	0.409	0.126	1.20346E-06
PCGF5	polycomb group ring finger 5	4.71015E-11	0.28598096	0.86	0.517	1.58704E-06
SPATS2L	spermatogenesis associated serine rich 2 like	6.34799E-11	0.268426378	0.855	0.468	2.13889E-06
NDUF4B	NADH:ubiquinone oxidoreductase subunit B4	7.05284E-11	-0.521746961	0.912	0.81	2.37639E-06
ZYX	zyxin	7.80020E-11	0.279476657	0.854	0.454	2.62881E-06
SNRPE	small nuclear ribonucleoprotein polypeptide E	8.23606E-11	-0.537674734	0.881	0.781	2.77506E-06
NDUF4A	NDUF4A, mitochondrial complex associated	8.66155E-11	-0.413015921	1	0.996	2.91842E-06
TRMT112	tRNA methyltransferase 11-2 homolog (S. cerevisiae)	9.98557E-11	-0.463232197	0.912	0.799	3.0276E-06
OAZ1	ornithine decarboxylase antizyme 1	9.37912E-11	-0.353081491	1	0.978	3.1602E-06
OSBP19	oxysterol binding protein like 9	9.65795E-11	0.287165925	0.917	0.58	3.25415E-06
SFB85	splicing factor 3b subunit 5	1.00194E-10	-0.417548566	0.886	0.799	3.37594E-06
POU2L1	polymrase (RNA) II subunit L1	1.06411E-10	-0.377916817	0.995	0.993	3.5854E-06
ATP5G1	ATP synthase, H+ transporting, mitochondrial Fo complex subunit C1 (subunit 9)	1.14188E-10	-0.551896462	0.964	0.911	3.84744E-06
NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	1.27478E-10	-0.609167683	1	0.907	4.29525E-06
HSP90AA1	heat shock protein 90kDa alpha family class A member 1	1.31224E-10	0.269245987	1	0.829	4.42147E-06
MRPS21	mitochondrial ribosomal protein S21	1.48082E-10	-0.425794659	0.917	0.836	4.98946E-06
COX5B	cytochrome c oxidase subunit 5B	1.4975E-10	-0.446975254	1	0.974	5.04568E-06
NDUFB11	NADH:ubiquinone oxidoreductase subunit B11	1.68161E-10	-0.409156829	0.953	0.84	5.66602E-06
PABPC1	poly(A) binding protein cytoplasmic 1	1.958E-10	-0.505297246	0.979	0.844	6.5973E-06

SF3B6	splicing factor 3b subunit 6	2.26013E-10	-0.468966736	0.891	0.777	7.61529E-06
RAB6A	RAB6A, member RAS oncogene family	2.38309E-10	0.253197194	0.896	0.535	8.02959E-06
ATP5L	ATP synthase, H+ transporting, mitochondrial Fo complex subunit G	2.91622E-10	-0.3790417	1	0.996	9.82593E-06
MMP23B	matrix metalloproteinase 23B	3.2988E-10	0.259287985	0.876	0.476	1.1115E-05
PEAL5	phosphoprotein enriched in astrocytes 15	3.57674E-10	0.394086912	0.902	0.524	1.20515E-05
HSPE1	heat shock protein family E (Hsp10) member 1	4.17304E-10	0.533590538	0.974	0.885	1.40606E-05
SNRPC	small nuclear ribonucleoprotein polypeptide C	4.40469E-10	0.542432787	0.689	0.695	1.48412E-05
ROMO1	reactive oxygen species modulator 1	4.98127E-10	-0.362544363	0.974	0.944	1.67839E-05
COX6A1	cytochrome c oxidase subunit 6A1	5.04311E-10	-0.473341071	0.979	0.926	1.69923E-05
NDUFA2	NADH:ubiquinone oxidoreductase subunit A2	5.25259E-10	-0.420995468	0.938	0.892	1.76981E-05
GSTP1	glutathione S-transferase pi 1	5.88369E-10	-0.646461329	0.943	0.833	1.98245E-05
SRP9	signal recognition particle 9kDa	8.30258E-10	-0.494803872	0.959	0.836	2.79747E-05
COX8A	cytochrome c oxidase subunit 8A	9.00151E-10	-0.36207589	0.995	0.989	3.03297E-05
CDC80	coiled-coil domain containing 80	1.01836E-09	-0.275900146	0.555	0.216	3.43127E-05
DOT	D-dopachrome tautomerase	1.1983E-09	-0.480074342	0.855	0.773	4.03755E-05
HMG2	high mobility group nucleosomal binding domain 2	1.28313E-09	-0.681188991	0.964	0.836	4.32338E-05
LSM4	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated	1.46959E-09	-0.445854425	0.902	0.833	4.95165E-05
STMN1	stathmin 1	1.84127E-09	-0.580737325	0.917	0.799	6.20398E-05
USMG5	up-regulated during skeletal muscle growth 5 homolog (mouse)	2.02017E-09	-0.328055985	0.995	0.981	6.80677E-05
EIF3K	eukaryotic translation initiation factor 3 subunit K	2.30243E-09	-0.437854354	0.943	0.844	7.75781E-05
TM5B10	thymosin beta 10	2.42924E-09	-0.623246512	1	0.981	8.18508E-05
CAV1	caveolin 1	2.8085E-09	0.301430016	0.694	0.364	9.46297E-05
NDUFAF3	NADH:ubiquinone oxidoreductase complex assembly factor 3	3.34343E-09	-0.469864293	0.881	0.792	0.00019284
H2AF2	H2A histone family member 2	4.51743E-09	-0.630432898	0.886	0.792	0.00015221
SOD1	superoxide dismutase 1, soluble	4.94675E-09	-0.473526767	0.953	0.855	0.000166676
PSMB3	proteasome subunit beta 3	4.95383E-09	-0.545202769	0.642	0.651	0.000166914
TNNI1	tropoin I1, slow skeletal type	6.30046E-09	-0.724616213	1	0.989	0.00021288
PSMA7	proteasome subunit alpha 7	6.60588E-09	-0.562649223	0.907	0.777	0.00022578
SUMO2	small ubiquitin-like modifier 2	6.63283E-09	-0.366742254	0.979	0.855	0.000223486
FKBP1A	FK506 binding protein 1A	7.81565E-09	-0.439997999	0.979	0.885	0.00026334
SNX3	sorting nexin 3	9.15728E-09	-0.384179164	0.979	0.881	0.000308545
TMEM256	transmembrane protein 256	1.01154E-08	-0.445059882	0.876	0.762	0.000340827
AURKAIP1	aurora kinase A interacting protein 1	1.22805E-08	-0.37171359	0.881	0.833	0.000413779
PHB	prohibitin	1.24865E-08	-0.472076353	0.881	0.747	0.00042072
PSMA2	proteasome subunit alpha 2	1.60605E-08	-0.474068731	0.845	0.714	0.000541142
TNNC1	tropoin C1, slow skeletal and cardiac type	1.70312E-08	-0.591363473	1	0.967	0.000573851
COX5A	cytochrome c oxidase subunit 5A	1.75175E-08	-0.502547038	0.979	0.955	0.000590236
TOMM22	translocase of outer mitochondrial membrane 22	2.11677E-08	-0.384296627	0.912	0.777	0.000713225
ACTA2	actin, alpha 2, smooth muscle, aorta	2.5978E-08	-0.301063449	0.751	0.361	0.000875303
NDUFB3	NADH:ubiquinone oxidoreductase subunit B3	2.66589E-08	-0.464003141	0.938	0.851	0.000898244
MRPL20	mitochondrial ribosomal protein L20	2.9333E-08	-0.374471495	0.943	0.792	0.000988347
NUTF2	nuclear transport factor 2	3.00698E-08	-0.434355466	0.896	0.755	0.001013172
MRPL52	mitochondrial ribosomal protein L52	3.95427E-08	-0.46200125	0.845	0.747	0.001332353
C12orf57	chromosome 12 open reading frame 57	5.09348E-08	-0.411174196	0.855	0.777	0.001716196
ALDOA	aldolase, fructose-bisphosphate A	5.55034E-08	-0.340088454	0.995	0.97	0.001870132
SSBP1	single stranded DNA binding protein 1	6.53853E-08	-0.514237034	0.689	0.639	0.002203091
CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	9.21325E-08	-0.492163719	1	0.955	0.003104314
CARHSP1	calcium regulated heat stable protein 1	9.91887E-08	-0.484053481	0.56	0.587	0.003342063
MINO51	mitochondrial inner membrane organizing system 1	1.17622E-07	-0.354358652	0.974	0.922	0.003963154
SLC25A6	solute carrier family 25 member 6	1.34191E-07	-0.407794903	0.99	0.918	0.004521433
NDUFA81	NADH:ubiquinone oxidoreductase subunit A81	1.40377E-07	-0.462400544	0.938	0.851	0.004729856
UQCRRH	ubiquinol-cytochrome c reductase hinge protein	2.59407E-07	-0.276695986	1	0.993	0.008740466
PLN	phospholamban	2.95877E-07	-0.729269306	1	0.978	0.00969284
TP1	triosephosphate isomerase 1	2.98423E-07	-0.378171245	0.984	0.911	0.010050507
BRK1	BRICK1, SCAR/WAVE actin nucleating complex subunit	3.00847E-07	-0.399565076	0.964	0.848	0.010136738
MRPL36	mitochondrial ribosomal protein L36	3.22028E-07	-0.4650440154	0.554	0.599	0.010850421
C19orf53	chromosome 19 open reading frame 53	3.27559E-07	-0.338957883	0.953	0.866	0.011036777
PET100	PET100 homolog	3.42433E-07	-0.35607513	0.86	0.792	0.011537945
PFND2	prefoldin subunit 2	3.47087E-07	-0.446910358	0.808	0.71	0.011694752
MEST	mesoderm specific transcript	4.16636E-07	-0.315549848	0.632	0.279	0.014038136
HIGD2A	HIG1 hypoxia inducible domain family member 2A	4.75806E-07	-0.372775823	0.995	0.881	0.016031804
LSM7	LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated	5.58946E-07	-0.496109379	0.829	0.669	0.018833123
MFAP4	microfibrillar associated protein 4	5.83587E-07	0.268577316	0.658	0.372	0.019663396
CFL1	cofilin 1	6.3066E-07	-0.355521305	0.995	0.967	0.021249459
RNF181	ring finger protein 181	6.78108E-07	-0.500068501	0.746	0.658	0.022848173
NDUFA12	NADH:ubiquinone oxidoreductase subunit A12	7.78432E-07	-0.459977671	0.959	0.781	0.026228484
SNRPF	small nuclear ribonucleoprotein polypeptide F	8.99405E-07	-0.487215728	0.575	0.576	0.030304543
TCEB1	transcription elongation factor B subunit 1	1.08253E-06	-0.381813275	0.927	0.81	0.036474859
PTTG1	pituitary tumor-transforming 1	1.14171E-06	-0.516960553	1.009	0.279	0.038468725
NDUFS8	NADH:ubiquinone oxidoreductase core subunit 58	1.37915E-06	-0.370254635	0.953	0.836	0.046468926
MYL6	myosin light chain 6	1.38974E-06	-0.334207416	1	0.046825953	
NHP2	NHP2 ribonucleoprotein	1.40625E-06	-0.434203039	0.808	0.703	0.047382134
HSO17B10	hydroxysteroid 17-beta dehydrogenase 10	1.45815E-06	-0.448001004	0.575	0.576	0.049130758
SEC6B	Sec61 translocon beta subunit	1.95916E-06	-0.436766313	0.876	0.743	0.066011959
NDUFA1	NADH:ubiquinone oxidoreductase subunit A1	2.06822E-06	-0.300206013	1	0.97	0.069686534
NME4	NME/NM23 nucleoside diphosphate kinase 4	2.14178E-06	-0.3509361601	0.917	0.877	0.07216503
MYL2	myosin light chain 2	2.37929E-06	-0.33631814	0.86	0.494	0.080167839

Supplemental Table S12: gRNA for LentiCRISPRV2

Name	Forward Primer	Reverse Primer
205-5p	CACCGCCGGAGTCTGTCTCATAC CC	AAACGGGTATGAGACAGACTCCG GC
200a-3p	CACCGAGCTTGACTCTAACACTGT C	AAACGACAGTGTTAGAGTCAAGC TC
122-5p	CACCGAGTTTCCTTAGCAGAGCT G	AAACCAGCTCTGCTAAGGAAACT C
HADH A Ex1 gRNA 1	CACCGGGCAGGCCTCACCTCGG GAG	AAACCTCCCGAGGTGAGGCCTG CCC
HADH A Ex1 gRNA 2	CACCGGGAAGGCAGAAAAGCGG CTG	AAACCAGCCGCTTTTCTGCCTTC CC

Supplemental Table S13: Primers for off-target analysis

Name	Forward Primer	Reverse Primer
HADHA_OFFT_1	CGTACGTGTTCTGCACAGCC	CAGCAATGTTCTGAAGGCCC
HADHA_OFFT_2	CCTGCCCCCTTCAAGGTAAG	CTGGTCTGATAGGTGGGGGA
HADHA_OFFT_3	GAGAGCTAGGCTTTGTGCCA	CTTATGTGGCCCCGTGTTCT

Supplemental Table S14: Quantitative RT-qPCR primers for human genes

Gene Name	Forward Primer	Reverse Primer
MYL2	TGTCCCTACCTTGTCTGTTAGCCA	ATTGGAACATGGCCTCTGGATG GA
TNNC1	TGGTTCGGTGCATGAAGGAC	GTCGATGTAGCCATCAGCATT
GAPDH	CTGGGCTACACTGAGCACC	AAGTGGTCGTTGAGGGCAATG
NPPA	CAACGCAGACCTGATGGATTT	AGCCCCCGCTTCTTCATTC

Supplemental Table S15: Primers for genomic amplification of microRNA region

Name	Forward Primer	Reverse Primer
miR-208b	CCGGTGAGTTCTGAGCAGCC TGACTT	ATCCTCTGCCTGATGTTCTCGAATT C
miR-452	AAAAAACCAGGTCTCACACGA GCTCCATTCCC	AAAAAGAATTCCAACCCCAGTTGGT AAGCGT
miR-378e	ACTAGGACGAGCTAGTGGG G	ACCCAAAGTGTACAATCATTGACT