

Supplementary Table 2. 503-gene list differentially expressed between pPCL and MM.

Gene Symbol	Gene Name	Cytoband	Score(d)	Fold Change
FLNA	filamin A, alpha (actin binding protein 280)	Xq28	8.8939	4.3943
TAGLN2	transgelin 2	1q21-q25	6.9247	3.1111
USP36	ubiquitin specific peptidase 36	17q25.3	6.7445	1.5881
ADAM8	ADAM metalloproteinase domain 8	10q26.3	6.7222	2.0512
CORO7	coronin 7	16p13.3	6.4958	2.4215
FAS	Fas (TNF receptor superfamily, member 6)	10q24.1	6.3575	4.2037
FMNL1	formin-like 1	17q21	6.2702	1.8204
TNIP2	TNFAIP3 interacting protein 2	4p16.3	6.2603	2.0729
CD99	CD99 molecule	Xp22.32;Yp11.3	6.2291	6.7692
ANXA11	annexin A11	10q23	6.0995	2.3510
CYB5R3	cytochrome b5 reductase 3	22q13.2-q13.31;22q13.31-qter	6.0525	1.6998
ARHGDI1A	Rho GDP dissociation inhibitor (GDI) alpha	17q25.3	5.9989	1.6278
KIF21B	kinesin family member 21B	1pter-q31.3	5.8725	2.3523
CCR7	chemokine (C-C motif) receptor 7	17q12-q21.2	5.8384	2.7242
SPMD4	sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	2q21.1	5.8162	1.5613
NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	22q13.2	5.8079	1.7231
EMP3	epithelial membrane protein 3	19q13.3	5.8040	2.5566
KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	1p32	5.7410	1.4743
TRAF5	TNF receptor-associated factor 5	1q32	5.7267	2.5907
WDR1	WD repeat domain 1	4p16.1	5.6831	1.8278
LGALS3	lectin, galactoside-binding, soluble, 3	14q22.3	5.6669	2.1458
HABP4	hyaluronan binding protein 4	9q22.3-q31	5.6466	2.2176
C6orf1	chromosome 6 open reading frame 1	6p21.31	5.6343	1.3549
ARF5	ADP-ribosylation factor 5	7q31.3	5.5683	1.4936
MYH9	myosin, heavy chain 9, non-muscle	22q13.1	5.5462	1.9033
ZNF267	zinc finger protein 267	16p11.2	5.5421	2.5590
ESYT2	family with sequence similarity 62 (C2 domain containing), member B	7q36.3	5.5415	1.7251
RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	2q37.3	5.5285	1.6596
ATXN2L	ataxin 2-like	16p11	5.5163	1.4439
MVP	major vault protein	16p13.1-p11.2	5.5103	1.7103
TMOD1	tropomodulin 1	9q22.3	5.4587	2.2916
PLEKHM2	pleckstrin homology domain containing, family M (with RUN domain) member 2	1p36.21	5.4441	1.6418
PSMD6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	3p14.1	5.4116	1.4567
MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	5q35	5.3909	1.4588
GNB2	guanine nucleotide binding protein (G protein), beta polypeptide 2	7q21.3-q22.1;7q22	5.3558	1.5106
SLED1	proteoglycan 3 pseudogene	4q35.1	5.3524	1.4367
NRM	nurim (nuclear envelope membrane protein)	6p21.33	5.3490	1.6215
NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	6p21.1	5.3291	2.0535
BLOC1S2	biogenesis of lysosomal organelles complex-1, subunit 2	10q24.31	5.3240	1.5547
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	12q13.2	5.2949	1.6454
GBP2	guanylate binding protein 2, interferon-inducible	1p22.2	5.2864	3.7843
RHOA	ras homolog gene family, member A	3p21.3	5.2579	1.4642
AXIN1	axin 1	16p13.3	5.2564	1.3254
S100A10	S100 calcium binding protein A10	1q21	5.2525	3.8702
PLXNA1	plexin A1	3q21.3	5.2524	1.6970
C20orf111	chromosome 20 open reading frame 111	20q13.11	5.2504	1.7459
SUN2	unc-84 homolog B (C. elegans)	22q13.1	5.2479	1.7084
MAP4	microtubule-associated protein 4	3p21	5.2384	1.6456
PHF19	PHD finger protein 19	9q33.2	5.2326	1.8400
ZBTB17	zinc finger and BTB domain containing 17	1p36.13	5.2258	1.3539
ZYX	zyxin	7q32	5.1040	1.8313
MIR155	microRNA 155	21q21.3	5.0677	7.9863
FTH1	ferritin, heavy polypeptide 1	11q13	5.0644	1.4734
MIF4G	MIF4G domain containing	17q25.1	5.0599	1.5221
PPDPF	pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)	20q13.33	5.0474	1.7914
STAT6	signal transducer and activator of transcription 6, interleukin-4 induced	12q13	5.0275	1.5646
PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	20q13.33	5.0085	1.5070
MGRN1	mahogunin, ring finger 1	16p13.3	4.9944	1.3314
YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	22q12.3	4.9915	2.1669
LMF2	lipase maturation factor 2	22q13.33	4.9805	1.5761
TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	1q42.13	4.9746	1.5836
MYL12B	myosin, light chain 12B, regulatory	18p11.31	4.9653	1.5625
SMAD3	SMAD family member 3	15q22.33	4.9633	2.1419
DDIT3	DNA-damage-inducible transcript 3	12q13.1-q13.2	4.9521	2.3537
TFE3	transcription factor binding to IGDM enhancer 3	Xp11.22	4.9510	1.5269
FBR5	fibrosin	16p11.2	4.9372	1.3820
KLF11	Kruppel-like factor 11	2p25	4.9305	2.3443
TTC7A	tetratricopeptide repeat domain 7A	2p21	4.8805	1.5406
EMD	emerin	Xq28	4.8784	1.6786
TUBA1A	tubulin, alpha 1a	12q13.12	4.8552	1.9026
CCDC19	coiled-coil domain containing 19	1q22	4.8446	1.5852
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	21q22.3	4.8369	1.5300
UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	16p13.3	4.8317	1.3246
NCAPH2	non-SMC condensin II complex, subunit H2	22q13.33	4.7978	1.3855
TRAF1	TNF receptor-associated factor 1	9q33-q34	4.7921	1.7594
BRI3	brain protein I3	1p21.27q21.3	4.7784	1.4361
CRIP1	cysteine-rich protein 1 (intestinal)	14q32.33	4.7713	2.0091
FOXJ2	forkhead box J2	12p13.31	4.7515	1.3684
RELB	v-rel reticuloendotheliosis viral oncogene homolog B	19q13.32	4.7429	2.0123
CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	Xp11.23	4.7246	1.5962
GPR132	G protein-coupled receptor 132	14q32.3	4.7242	2.0163
EHD1	EH-domain containing 1	11q13	4.7182	2.3607
WEE1	WEE1 homolog (S. pombe)	11p15.3-p15.1	4.7158	2.7162
TRPS1	trichorhinophalangeal syndrome I	8q24.12	4.7142	2.9982
SYNE2	spectrin repeat containing, nuclear envelope 2	14q23.2	4.7105	2.2108
PATL1	protein associated with topoisomerase II homolog 1 (yeast)	11q12.1	4.6874	1.5434
CEBPB	CCAAT/enhancer binding protein (C/EBP), gamma	19q13.11	4.6868	1.5772
UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	4q24	4.6752	1.3390
PRR14	proline rich 14	16p11.2	4.6683	1.2787
HIVP3	human immunodeficiency virus type 1 enhancer binding protein 3	1p34	4.6620	1.4328
IL10RA	interleukin 10 receptor, alpha	11q23	4.6580	3.3342
PPID	peptidylprolyl isomerase D	4q31.3	4.6562	1.6153
FAM53B	family with sequence similarity 53, member B	10q26.13	4.6551	1.9565
KDM5C	lysine (K)-specific demethylase 5C	Xp11.22-p11.21	4.6437	1.3967
TMEM43	transmembrane protein 43	3p25.1	4.6426	1.7413
SNORA70B	small nucleolar RNA, H/ACA box 70B (retrotransposed)	2p15	4.6364	1.5881
ARL8A	ADP-ribosylation factor-like 8A	1q32.1	4.6096	1.7114
RFLL	ring finger and FYVE-like domain containing 1	17q12	4.5979	1.6038
VOPP1	EGFR-coamplified and overexpressed protein	7p11.2	4.5977	1.7962
MED15	mediator complex subunit 15	22q11.2	4.5971	1.4272
SESN2	sestrin 2	1p35.3	4.5859	1.9743

ZMIZ2	zinc finger, MIZ-type containing 2	7p13	4.5816	1.5017
ATG2A	ATG2 autophagy related 2 homolog A (S. cerevisiae)	11q13.1	4.5747	1.4589
PER1	period homolog 1 (Drosophila)	17p13.1-p12	4.5673	2.5143
ELF4	E74-like factor 4 (ets domain transcription factor)	Xq26	4.5669	1.8466
BHLHE40	basic helix-loop-helix family, member e40	3p26	4.5458	2.7385
HNRPD	heterogeneous nuclear ribonucleoprotein D-like	4q21.22	4.5440	1.2689
ABT8	ankyrin repeat and BTB (POZ) domain containing 2	11p13	4.5419	1.4455
CDC42SE1	CDC42 small effector 1	1q21.3	4.5375	1.8843
PFN1	profilin 1	17p13.3	4.5334	1.4035
ARHGAP10	Rho GTPase activating protein 10	4q31.23	4.5213	1.6670
ZNF335	zinc finger protein 335	20q13.12	4.5166	1.3881
PPP4R1	protein phosphatase 4, regulatory subunit 1	18p11.22	4.5130	1.7552
FAM105B	family with sequence similarity 105, member B	5p15.2	4.5110	1.4926
TAB3	mitogen-activated protein kinase kinase kinase 3	Xp21.2	4.5050	1.5686
OPTN	optineurin	10p13	4.5039	1.7418
CRIP2	cysteine-rich protein 2	14q32.3	4.4822	1.6745
TCTA	T-cell leukemia translocation altered gene	3p21	4.4801	1.5531
JOSD1	Josephin domain containing 1	22q13.1	4.4591	1.7045
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	14q13	4.4509	2.5067
DOCK11	dedicator of cytokinesis 11	Xq24	4.4504	2.6152
SH3TC1	SH3 domain and tetra-tricopeptide repeats 1	4p16.1	4.4451	1.5136
EIF2C2	eukaryotic translation initiation factor 2C, 2	8q24	4.4331	1.8624
FMR1	fragile X mental retardation 1	Xq27.3	4.4289	1.5797
PLXNA3	plexin A3	Xq28	4.4288	1.6116
CAMK4	calcium/calmodulin-dependent protein kinase IV	5q21.3	4.4273	2.2058
C16orf42	chromosome 16 open reading frame 42	16p13.3	4.4253	1.4033
PIM3	pim-3 oncogene	22q13	4.4221	1.8120
ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	16p13.3	4.4114	1.4328
SQLE	squalene epoxidase	8q24.1	4.4105	2.1919
UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	Xq24	4.4083	1.4979
HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	5p14-p13	4.4001	1.5655
APH1A	anterior pharynx defective 1 homolog A (C. elegans)	1p36.13-q31.3	4.3982	1.5620
TRAF4	TNF receptor-associated factor 4	17q11-q12	4.3976	1.7879
HPS6	Hermansky-Pudlak syndrome 6	10q24.32	4.3911	1.3196
TSPAN14	tetraspanin 14	10q23.1	4.3899	1.6268
HPRT1	hypoxanthine phosphoribosyltransferase 1	Xq26.1	4.3890	1.7079
MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	1p36	4.3702	1.4875
RUNX3	run-related transcription factor 3	1p36	4.3681	1.4310
HPS1	Hermansky-Pudlak syndrome 1	10q23.1-q23.3	4.3639	1.2578
WHAMM	WAS protein homolog associated with actin, golgi membranes and microtubules	15q25.2	4.3635	1.4149
MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	16q24.2	4.3604	1.8590
CRTC2	CREB regulated transcription coactivator 2	1q21.3	4.3503	1.4372
LYN	v-src-1 Yamaguchi sarcoma viral related oncogene homolog	8q13	4.3406	1.7484
ASXL1	additional sex combs like 1 (Drosophila)	20q11	4.3335	1.4227
ARID5A	AT rich interactive domain 5A (MRF1-like)	2q11.2	4.3269	2.0792
MFS10	major facilitator superfamily domain containing 10	4p16.3	4.3259	1.4246
WDR44	WD repeat domain 44	Xq24	4.3240	1.6325
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	6q23	4.3126	3.1434
TMSB10	thymosin beta 10	2p11.2	4.3042	1.5889
CBLL1	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	7q22.3	4.2915	1.5468
RNF125	ring finger protein 125	18q12.1	4.2879	1.8267
MAP1LC3B2	microtubule-associated protein 1 light chain 3 beta 2	12q24.22	4.2854	1.9335
RAB31	RAB31, member RAS oncogene family	18p11.3	4.2809	2.5438
TUFT1	tuftelin 1	1q21	4.2755	1.8836
RALGDS	ral guanine nucleotide dissociation stimulator	9q34.3	4.2692	1.6011
FYN	FYN oncogene related to SRC, FGR, YES	6q21	4.2648	2.1408
PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	11p13	4.2644	2.0669
CTNNA1	catenin (cadherin-associated protein), alpha-like 1	9q31.2	4.2631	2.1676
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	7q22.1	4.2533	1.7670
BCL7B	B-cell CLL/lymphoma 7B	7q11.23	4.2490	1.4277
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	10q24	4.2490	1.9428
PEA15	phosphoprotein enriched in astrocytes 15	1q21.1	4.2393	1.9862
TOX2	TOX high mobility group box family member 2	20q13.12	4.2368	1.7191
RIOK3	RIO kinase 3 (yeast)	18q11.2	4.2331	1.7210
TNIP1	TNFAIP3 interacting protein 1	5q32-q33.1	4.2320	1.8042
FAM115C	family with sequence similarity 115, member C	7q35	4.2315	1.8643
SGSH	N-sulfoglucosamine sulfohydrolase	17q25.3	4.2314	1.5299
STC2	stanniocalcin 2	5q35.1	4.2270	1.5643
FAM107B	family with sequence similarity 107, member B	10p13	4.2102	2.6033
MIIP	migration and invasion inhibitory protein	1p36.22	4.2073	1.2764
EIF1	eukaryotic translation initiation factor 1	17q21.2	4.2067	1.2504
RAB5C	RAB5C, member RAS oncogene family	17q21.2	4.2032	1.3652
LGALS1	lectin, galactoside-binding, soluble, 1	22q13.1	4.2031	1.9788
CHMP1A	chromatin modifying protein 1A	16q24.3	4.2027	1.3552
RARRES3	retinoic acid receptor responder (tazarotene induced) 3	11q23	4.1798	2.6704
RNF187	ring finger protein 187	1q42.13	4.1791	1.4413
FGF2	fibroblast growth factor 2 (basic)	4q26-q27	4.1743	2.0214
DEDD	death effector domain containing	1q23.3	4.1723	1.3921
C1orf144	chromosome 1 open reading frame 144	1p36.13	4.1631	1.3990
MTCH1	mitochondrial carrier homolog 1 (C. elegans)	6pter-p24.1	4.1600	1.3629
BTG3	BTG family, member 3	21q21.1	4.1539	1.6428
SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	4q28-q32	4.1503	2.9718
NRBP1	nuclear receptor binding protein 1	2p23	4.1493	1.4675
TP53BP2	tumor protein p53 binding protein, 2	1q41	4.1446	1.9490
ZFP36L2	zinc finger protein 36, C3H type-like 2	2p22.3-p21	4.1398	2.2161
CDK16	PCTAIRE protein kinase 1	Xp11	4.1384	1.4564
FLJ35776	hypothetical LOC649446	18p11.31	4.1326	1.8792
PLP2	proteolipid protein 2 (colonic epithelium-enriched)	Xp11.23	4.1322	1.6085
ZC3H12A	zinc finger CCH-type containing 12A	1p34.3	4.1312	1.8973
VANGL1	vang-like 1 (van gogh, Drosophila)	1p13.1	4.1265	1.8244
SYNGR2	synaptogyrin 2	17q25.3	4.1117	1.7764
PIIF	peptidylprolyl isomerase F	10q22-q23	4.1114	1.5648
TBC1D12	TBC1 domain family, member 12	10q23.33	4.1110	1.4311
GET4	chromosome 7 open reading frame 20	7p22.3	4.1066	1.3057
MAP3K3	mitogen-activated protein kinase kinase kinase 3	17q23.3	4.1059	1.4005
HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	17q25	4.1052	1.3092
SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	3p22.1	4.1016	1.4103
PSMC1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	14q32.11	4.0986	1.4113
ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	Xp11.4	4.0974	1.4128
C1orf152	chromosome 1 open reading frame 152	1q21	4.0932	1.5068
TMBIM1	transmembrane BAX inhibitor motif containing 1	2p24.3-p24.1	4.0925	1.7454
ARHGAP21	Rho GTPase activating protein 21	10p12.1;10p12.3	4.0885	1.7276
RNF139	ring finger protein 139	8q24	4.0858	1.4120
FLII	flightless 1 homolog (Drosophila)	17p11.2	4.0752	1.5221

EZH2	enhancer of zeste homolog 2 (Drosophila)	7q35-q36	4.0729	1.7545
RNH1	ribonuclease/angiogenin inhibitor 1	11p15.5	4.0675	1.4544
AHNAK	AHNAK nucleoprotein	11q12.2	4.0672	2.9324
MAP3K14	mitogen-activated protein kinase kinase kinase 14	17q21	4.0655	1.3395
HIVEP1	human immunodeficiency virus type 1 enhancer binding protein 1	6p24-p22.3	4.0632	1.6548
MUSTN1	musculoskeletal, embryonic nuclear protein 1	3p21.1	4.0610	1.3533
ETV6	ets variant 6	12p13	4.0553	1.8262
SGPP2	sphingosine-1-phosphate phosphatase 2	2q36.1	4.0462	2.7168
RGL1	ral guanine nucleotide dissociation stimulator-like 1	1q25.3	4.0451	3.0550
C11orf59	chromosome 11 open reading frame 59	11q13.4	4.0417	1.3909
ANKRD33B	ankyrin repeat domain 33B	5p15.2	4.0391	1.4797
CCDC17	coiled-coil domain containing 17	1p34.1	4.0389	1.2529
WDR45L	WDR45-like	17q25.3	4.0370	1.3467
LOC100131826	TSSP3028	4q21.1	4.0364	1.7911
RAP2C	RAP2C, member of RAS oncogene family	Xq25	4.0357	1.3560
EWSR1	Ewing sarcoma breakpoint region 1	22q12.2	4.0270	1.3597
ACSL1	acyl-CoA synthetase long-chain family member 1	4q35	4.0237	2.1254
FAM127B	family with sequence similarity 127, member B	Xq26.3	4.0234	1.3779
MARCH5	membrane-associated ring finger (C3HC4) 5	10q23.32-q23.33	4.0151	1.4346
GIGYF1	GRB10 interacting GYF protein 1	7q22	4.0145	1.2770
CFL1	cofilin 1 (non-muscle)	11q13	4.0139	1.3518
ILK	integrin-linked kinase	11p15.4	4.0134	1.4297
RNF138	ring finger protein 138	18q12.1	4.0103	1.4875
ESYT1	family with sequence similarity 62 (C2 domain containing), member A	12q13.2	4.0059	1.6092
TSP0	translocator protein (18kDa)	22q13.31	4.0052	1.4155
SOCS1	suppressor of cytokine signaling 1	16p13.13	4.0021	1.5772
SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	10p14	3.9894	1.6310
ADPRH	ADP-ribosylarginine hydrolase	3q13.31-q13.33	3.9843	1.4429
BUD31	BUD31 homolog (S. cerevisiae)	7q22.1	3.9749	1.3898
TWISTNB	TWIST neighbor	7p21.1	3.9706	1.3987
ZNF570	zinc finger protein 570	19q13.12	3.9607	1.8312
SLK	STE20-like kinase (yeast)	10q25.1	3.9580	1.6649
SKI	v-ski sarcoma viral oncogene homolog (avian)	1q22-q24	3.9564	1.3250
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	18q21.32	3.9553	4.0015
LOC642947	hypothetical protein LOC642947	9q21.13	3.9537	1.7082
MKL1	megakaryoblastic leukemia (translocation) 1	22q13	3.9525	1.3402
PIK3IP1	phosphoinositide-3-kinase interacting protein 1	22q12.2	3.9505	2.2192
MAP2K3	mitogen-activated protein kinase kinase 3	17q11.2	3.9486	1.8317
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2q36.1	3.9452	1.3292
C4orf46	chromosome 4 open reading frame 46	4q32.1	3.9404	1.5262
C17orf49	chromosome 17 open reading frame 49	17p13.1	3.9373	1.6089
VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	18p11.22	3.9369	1.3943
MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	16p13.3	3.9360	1.3767
ENO1	enolase 1, (alpha)	1p36.2	3.9356	1.5402
ATP5L2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G2 pseudogene	22q13.33-qter	3.9249	1.3392
MED10	mediator complex subunit 10	5p15.31	3.9194	1.4622
GNA13	guanine nucleotide binding protein (G protein), alpha 13	17q24.3	3.9157	1.5187
RCC2	regulator of chromosome condensation 2	1p36.13	3.9131	1.4287
MFSD5	major facilitator superfamily domain containing 5	12q13.13	3.9110	1.4004
RGPD6	RANBP2-like and GRIP domain containing 6	2q12.32q13	3.9100	1.6173
ADCY5	adenylate cyclase 5	3q13.2-q21	3.9083	1.6627
TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	2q24.2	3.9053	2.3498
SAP30BP	SAP30 binding protein	17q25.1	3.9047	1.4140
RHOG	ras homolog gene family, member G (rho G)	11p15.5-p15.4	3.9043	1.3247
RNF19B	ring finger protein 19B	1p35.1	3.9021	1.7404
NINJ1	ninjurin 1	9q22	3.8965	1.6453
SREBF2	sterol regulatory element binding transcription factor 2	22q13	3.8948	1.4423
FUS	fusion (involved in t(12;16) in malignant liposarcoma)	16p11.2	3.8912	1.3067
C2orf69	chromosome 2 open reading frame 69	2q33.1	3.8880	1.3213
FAM160B1	family with sequence similarity 160, member B1	10q25.3	3.8876	1.6990
RAP1A	RAP1A, member of RAS oncogene family	1p13.3	3.8864	1.5698
PSME4	proteasome (prosome, macropain) activator subunit 4	2p16.2	3.8804	1.4068
PRNP	prion protein	20p13	3.8746	1.7575
RGPD5	RANBP2-like and GRIP domain containing 5	2q12.32q13	3.8680	1.6198
ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	2q23.3	3.8669	1.4757
ZNFX1	zinc finger, NFX1-type containing 1	20q13.13	3.8667	1.5742
C9orf21	chromosome 9 open reading frame 21	9q22.32	3.8656	1.7978
C14orf49	chromosome 14 open reading frame 49	14q32.13	3.8652	1.6977
FAM21A	family with sequence similarity 21, member A	10q11.2210q11.23	3.8642	1.3665
UBR4	ubiquitin protein ligase E3 component n-recognin 4	1p36.13	3.8617	1.4064
INO80D	INO80 complex subunit D	2q33.3	3.8607	1.4776
ZNF777	zinc finger protein 777	7q36.1	3.8571	1.3386
ICOSLG	inducible T-cell co-stimulator ligand	21q22.3	3.8503	1.8306
PPM1L	protein phosphatase 1 (formerly 2C)-like	3q26.1	3.8501	1.6928
SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	11q13	3.8492	1.5423
SRRT	serrate RNA effector molecule homolog (Arabidopsis)	7q21	3.8408	1.2938
FBA1	coagulation factor VIII-associated (intronic transcript) 1	Xq28	3.8362	1.4187
JAZF1	JAZF zinc finger 1	7p15.2-p15.1	3.8326	1.7224
HERPUD2	HERPUD family member 2	7p14.2	3.8269	1.3894
BAT2L2	BAT2 domain containing 1	1q23.3	3.8264	1.3986
HEXIM1	hexamethylene bis-acetamide inducible 1	17q21.31	3.8195	1.4981
PDZD8	PDZ domain containing 8	10q26.12	3.8174	1.3823
EIF1B	eukaryotic translation initiation factor 1B	3p22.1	3.8138	1.4107
GTPBP1	GTP binding protein 1	22q13.1	3.8103	1.3579
PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	14q23.1	3.8099	1.4790
TFEB	transcription factor EB	6p21	3.8073	1.4380
FAM76A	family with sequence similarity 76, member A	1p35.3	3.7999	1.4040
ZNF43	zinc finger protein 43	19p13.1-p12	3.7995	1.7368
CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	1p36.1	3.7976	1.4580
LOC100509022	splicing factor U2AF 35 kDa subunit-like	NA	3.7968	1.3391
EXOSC10	exosome component 10	1p36.22	3.7928	1.3578
GUK1	guanylate kinase 1	1q32-q41	3.7897	1.3889
TTLH	tubulin tyrosine ligase-like family, member 6	17q21.32	3.7890	1.3045
SMAD7	SMAD family member 7	18q21.1	3.7874	1.7533
PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	22q11.21	3.7805	1.4449
COX4I1	cytochrome c oxidase subunit IV isoform 1	16q24.1	3.7803	1.4114
ROCK1	Rho-associated, coiled-coil containing protein kinase 1	18q11.1	3.7792	1.4749
IRF2BP2	interferon regulatory factor 2 binding protein 2	1q42.3	3.7778	1.5663
FAM21B	family with sequence similarity 21, member B	10q11.22	3.7759	1.3687
PDP1	pyruvate dehydrogenase phosphatase catalytic subunit 1	8q22.1	3.7744	1.5387
PXN	paxillin	12q24.31	3.7714	1.2286
MSC	musculin (activated B-cell factor-1)	8q21	3.7705	1.9030
MYO1G	myosin IG	7p13-p11.2	3.7661	1.9818
TRIM8	tripartite motif-containing 8	10q24.3	3.7627	1.4315

CXorf26	chromosome X open reading frame 26	Xq13.3	3.7591	1.3323
HDAC5	histone deacetylase 5	17q21	3.7564	1.2421
SNORA70G	small nucleolar RNA, H/ACA box 70G	12q14	3.7521	1.4915
AGFG1	ArfGAP with FG repeats 1	2q36.3	3.7508	1.3776
KLHL2	kelch-like 2, Mayven (Drosophila)	4q21.2	3.7485	1.3741
FOXP1	forkhead box P1	3p14.1	3.7479	1.7594
C7orf53	chromosome 7 open reading frame 53	7q31.1	3.7451	1.5234
C8orf76	chromosome 8 open reading frame 76	8q24.13	3.7443	1.3074
GMEB2	glucocorticoid modulatory element binding protein 2	20q13.33	3.7415	1.2234
SNORA19	small nucleolar RNA, H/ACA box 19	10q26	3.7393	1.5102
POLDIP3	polymerase (DNA-directed), delta interacting protein 3	22q13.2	3.7379	1.3600
MRPS18A	mitochondrial ribosomal protein S18A	6p21.3	3.7373	1.3831
TADA2B	transcriptional adaptor 2 (ADA2 homolog, yeast)-beta	4p16.1	3.7277	1.4164
CCNY	cyclin Y	10p11.21	3.7275	1.2637
SLC20A1	solute carrier family 20 (phosphate transporter), member 1	2q11-q14	3.7247	1.5707
PELI1	pellino homolog 1 (Drosophila)	2p13.3	3.7242	1.8940
MEX3C	mex-3 homolog C (C. elegans)	18q21.2	3.7228	1.4827
TMEM63B	transmembrane protein 63B	6p21.1	3.7177	1.3986
BRD1	bromodomain containing 1	22q13.33	3.7151	1.3075
AP3S1	adaptor-related protein complex 3, sigma 1 subunit	5q22	3.7101	1.4450
ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	16p11.2	3.7077	2.0587
ZFAND2A	zinc finger, AN1-type domain 2A	7p22.3	3.6991	1.4930
UBE2Z	ubiquitin-conjugating enzyme E2Z	17q21.32	3.6980	1.4398
JMJD6	jumonji domain containing 6	17q25	3.6974	1.4212
SKP1	S-phase kinase-associated protein 1	5q31	3.6962	1.4467
ITGB8	integrin, beta 8	7p21.1	3.6950	2.2909
RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	11q13	3.6939	1.3984
PRDM4	PR domain containing 4	12q23-q24.1	3.6935	1.5079
ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	7q32	3.6927	1.3920
CD44	CD44 molecule (Indian blood group)	11p13	3.6910	3.3677
CAST	calpastatin	5q15	3.6905	1.4704
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	4q24	3.6898	1.6511
STRAP	serine/threonine kinase receptor associated protein	12p12.3	3.6892	1.3101
CCDC109B	coiled-coil domain containing 109B	4q25	3.6888	1.6713
PTP4A2	protein tyrosine phosphatase type IVA, member 2	1p35	3.6809	1.3924
NUDC	nuclear distribution gene C homolog (A. nidulans)	1p35-p34	3.6762	1.2701
TMEM64	transmembrane protein 64	8q21.3	3.6744	1.5337
ANXA2	annexin A2	15q22.2	3.6703	1.7063
TES	testis derived transcript (3 LIM domains)	7q31.2	3.6669	1.5364
LSR	lipolysis stimulated lipoprotein receptor	19q13.12	3.6560	1.4269
SMURF1	SMAD specific E3 ubiquitin protein ligase 1	7q22.1	3.6503	1.5769
SOCS6	suppressor of cytokine signaling 6	18q22.2	3.6456	2.0582
SGPL1	sphingosine-1-phosphate lyase 1	10q21	3.6418	1.4120
ADCK2	aarF domain containing kinase 2	7q34	3.6389	1.3307
GNL1	guanine nucleotide binding protein-like 1	6p21.3	3.6318	1.3289
CORO1A	coronin, actin binding protein, 1A	16p11.2	3.6316	1.8097
BRD9	bromodomain containing 9	5p15.33	3.6266	1.2985
RARA	retinoic acid receptor, alpha	17q21	3.6259	1.3721
PEBP1	phosphatidylethanolamine binding protein 1	12q24.23	3.6256	1.5863
HRASLS2	HRAS-like suppressor 2	11q12.3	3.6222	2.6719
AHR	aryl hydrocarbon receptor	7p15	3.6191	3.1471
SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	1p36.1-p35	3.6153	1.2725
TMPPE	transmembrane protein with metallophosphoesterase domain	3p22.3	3.6118	1.2390
SF3B2	splicing factor 3b, subunit 2, 145kDa	11q13.1	3.6092	1.2930
IL10	interleukin 10	1q31-q32	3.6086	1.7378
HAVCR2	hepatitis A virus cellular receptor 2	5q33.3	3.6060	1.8891
ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	2q37.3	3.6058	1.3620
PDE5A	phosphodiesterase 5A, cGMP-specific	4q27	-3.8861	-1.6424
FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	14q24.3	-3.8875	-2.1946
C13orf15	chromosome 13 open reading frame 15	13q14.11	-3.8929	-2.4426
IFT46	intraflagellar transport 46 homolog (Chlamydomonas)	11q23.3	-3.8968	-1.7132
STAP1	signal transducing adaptor family member 1	4q13.2	-3.9060	-3.4542
SNORD115-33	small nucleolar RNA, C/D box 115-33	15q11.2	-3.9127	-1.9315
SNORD115-32	small nucleolar RNA, C/D box 115-32	15q11.2	-3.9172	-2.5651
SNORD115-12	small nucleolar RNA, C/D box 115-12	15q11.2	-3.9180	-3.4676
NUCB2	nucleobindin 2	11p15.1	-3.9198	-1.8122
LEPROTL1	leptin receptor overlapping transcript-like 1	8p21	-3.9263	-1.4513
PRKD2	protein kinase D2	19q13.3	-3.9310	-1.7162
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	15q26.1	-3.9454	-1.6694
SNORD115-11	mannosyl (beta-1,4)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	22q13.1	-3.9458	-1.4813
SNORD115-26	small nucleolar RNA, C/D box 115-11	15q11.2	-3.9532	-3.5553
SNORD115-26	small nucleolar RNA, C/D box 115-26	15q11.2	-3.9662	-3.5716
WDR27	WD repeat domain 27	6q27	-3.9699	-1.3500
C9orf5	chromosome 9 open reading frame 5	9q31	-3.9730	-1.5783
PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	4q12-q13	-3.9732	-2.5787
ND2	NADH-ubiquinone oxidoreductase chain 2	MT	-3.9763	-1.7681
FSTL1	folliculin-like 1	3q13.33	-3.9769	-1.3602
ERGIC2	ERGIC and golgi 2	12p11.22	-3.9809	-1.5333
UTRN	utrophin	6q24	-3.9815	-1.9810
TSPAN13	tetraspanin 13	7p21.1	-3.9823	-2.0361
TEX2	testis expressed 2	17q23.3	-3.9952	-1.5537
SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	4q34.2	-3.9992	-1.5045
FAM111A	family with sequence similarity 111, member A	11q12.1	-3.9994	-1.6891
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	19q13.32	-4.0066	-2.1697
S100A12	S100 calcium binding protein A12	1q21	-4.0120	-2.6458
TSGA10	testis specific, 10	2q11.2	-4.0217	-1.5139
PTK2B	PTK2B protein tyrosine kinase 2 beta	8p21.1	-4.0387	-1.7095
CPNE5	copine V	6p21.1	-4.0540	-1.4970
SLC31A1	solute carrier family 31 (copper transporters), member 1	9q31-q32	-4.0553	-1.6099
ZNF709	zinc finger protein 709	19p13.2	-4.0629	-1.8901
SAR1B	SAR1 homolog B (S. cerevisiae)	5q31.1	-4.0656	-1.4097
KIAA0040	KIAA0040	1q24-q25	-4.0691	-1.5928
RGS5	regulator of G-protein signaling 5	1q23.1	-4.0724	-1.4647
SNORD115-41	small nucleolar RNA, C/D box 115-41	15q11.2	-4.0759	-1.6223
MMP8	matrix metalloproteinase 8 (neutrophil collagenase)	11q22.3	-4.0788	-3.2993
ZDHHC21	zinc finger, DHHC-type containing 21	9p22.3	-4.0948	-1.7880
BTBD3	BTB (POZ) domain containing 3	20p12.2	-4.1020	-4.3644
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	15q21.1	-4.1049	-2.7331
SNORD115-17	small nucleolar RNA, C/D box 115-17	15q11.2	-4.1112	-1.9078
ZNF215	zinc finger protein 215	11p15.4	-4.1233	-2.2233
C9orf41	chromosome 9 open reading frame 41	9q21.13	-4.1288	-1.5927
MGC29506	hypothetical protein MGC29506	5q23-q31	-4.1289	-1.6106
SEC16B	SEC16 homolog B (S. cerevisiae)	1q25.2	-4.1373	-1.7607
GPD1L	glycerol-3-phosphate dehydrogenase 1-like	3p22.3	-4.1428	-1.7523

CEP57L1	centrosomal protein 57kDa-like 1	6q21	-4.1514	-1.7609
IGHM	immunoglobulin heavy constant mu	14q32.33	-4.1648	-3.2594
SNORD115-20	small nucleolar RNA, C/D box 115-20	15q11.2	-4.1992	-2.9576
ELF2	ELL associated factor 2	3q13.33	-4.2029	-1.9605
C5orf53	chromosome 5 open reading frame 53	5q31	-4.2138	-1.5134
HMG20A	high-mobility group 20A	15q24	-4.2205	-1.6274
COG6	component of oligomeric golgi complex 6	13q14.11	-4.2243	-1.9691
YIPF6	Yip1 domain family, member 6	Xq12	-4.2267	-1.4379
ZNF554	zinc finger protein 554	19p13.3	-4.2343	-1.2602
PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	8p11.23	-4.2391	-1.5214
BTN3A1	butyrophilin, subfamily 3, member A1	6p22.1	-4.2455	-1.7584
SNORD115-44	small nucleolar RNA, C/D box 115-44	15q11.2	-4.2482	-2.9615
BMPR1A	bone morphogenetic protein receptor, type IA	10q22.3	-4.2549	-2.4267
GRN	granulin	17q21.32	-4.2634	-1.9286
CD274	CD274 molecule	9p24	-4.2908	-2.2027
FKTN	fukutin	9q31-q33	-4.2928	-1.7198
PLS1	plastin 1 (I isoform)	3q23	-4.2969	-1.8270
PDCL	phosducin-like	9q12-q13	-4.3105	-1.4689
ATG4C	ATG4 autophagy related 4 homolog C (S. cerevisiae)	1p31.3	-4.3304	-2.1590
SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	2p25.3	-4.3399	-1.5312
ZNF706	zinc finger protein 706	8q22.3	-4.3514	-1.5716
CEP97	centrosomal protein 97kDa	3q12.3	-4.3541	-1.8891
HEY2	hairy/enhancer-of-split related with YRPW motif 2	6q21	-4.3652	-2.7627
RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	14q24-q31	-4.3674	-2.1563
ACSS1	acyl-CoA synthetase short-chain family member 1	20p11.23-p11.21	-4.4086	-1.7037
RTN4IP1	reticulon 4 interacting protein 1	6q21	-4.4230	-1.5469
ND6	NADH-ubiquinone oxidoreductase chain 6	MT	-4.4232	-1.6180
ARMC2	armadillo repeat containing 2	6q21	-4.4241	-2.5414
SNORA60	small nucleolar RNA, H/ACA box 60	20q11.23	-4.4276	-1.4207
ADAM10	ADAM metalloproteinase domain 10	15q21.15q22	-4.4524	-1.6794
DEFA3	defensin, alpha 3, neutrophil-specific	8pter-p23.3	-4.4661	-4.2452
SLAMF7	SLAM family member 7	1q23.1-q24.1	-4.4721	-1.7264
WDR64	WD repeat domain 64	1q43	-4.4870	-2.2375
BTN3A2	butyrophilin, subfamily 3, member A2	6p22.1	-4.4934	-2.0558
CD36	CD36 molecule (thrombospondin receptor)	7q11.2	-4.4938	-2.1434
SULF2	sulfatase 2	20q12-q13.2	-4.5127	-4.8951
NCEH1	arylacetamide deacetylase-like 1	3q26.31	-4.5232	-1.7541
EXTL2	exostosins (multiple)-like 2	1p21	-4.5263	-2.1238
SSPN	sarcospan (Kras oncogene-associated gene)	12p11.2	-4.5505	-1.8540
DTWD2	DTW domain containing 2	5q23.1	-4.5526	-1.9020
MOXD1	monooxygenase, DBH-like 1	6q23.2	-4.5580	-3.7188
NEO1	neogenin homolog 1 (chicken)	15q22.3-q23	-4.5641	-2.0929
ACSM3	acyl-CoA synthetase medium-chain family member 3	16p13.11	-4.5649	-2.0094
RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	14q24-q31	-4.5670	-2.6634
AKD1	adenylate kinase domain containing 1	6q21	-4.5738	-1.4687
TRIM48	tripartite motif-containing 48	11q11	-4.5958	-1.3719
TCF4	transcription factor 4	18q21.1	-4.6545	-3.3407
LAX1	lymphocyte transmembrane adaptor 1	1q32.1	-4.6650	-2.8796
ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	5q12.1	-4.6784	-3.3355
SPICE1	spindle and centriole associated protein 1	3q13.2	-4.6800	-1.9865
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	9q13	-4.6844	-2.5730
IGHA2	immunoglobulin heavy constant alpha 2 (A2m marker)	14q32.33	-4.6859	-1.7368
SEC62	SEC62 homolog (S. cerevisiae)	3q26.2	-4.6959	-1.7201
SLC39A14	solute carrier family 39 (zinc transporter), member 14	8p21.3	-4.7049	-1.7988
AIG1	androgen-induced 1	6q24.2	-4.7085	-1.9496
XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	5q14.2	-4.7102	-2.1240
FAM55D	family with sequence similarity 55, member D	11q23.2	-4.7511	-4.4139
PRG3	proteoglycan 3	11q12	-4.7524	-1.6441
C3orf33	chromosome 3 open reading frame 33	3q25.31	-4.7624	-1.4716
ASB3	ankyrin repeat and SOCS box-containing 3	2p16-p14	-4.8402	-1.6738
KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	1q42-q44	-4.8680	-2.7677
MGC57346	hypothetical LOC401884	17q21.31	-4.8835	-1.8030
DENN5B	DENN/MADD domain containing 5B	12p11.21	-4.8947	-1.7046
POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	12q23.3	-4.8997	-1.7732
ZNF860	zinc finger protein 860	3p23	-4.9278	-3.2257
GLCC11	glucocorticoid induced transcript 1	7p21.3	-4.9515	-2.3651
CRISP3	cysteine-rich secretory protein 3	6p12.3	-5.0177	-3.0145
IGLL5	immunoglobulin lambda-like polypeptide 5	22q11.22	-5.0226	-1.4155
NDFIP2	Nedd4 family interacting protein 2	13q31.1	-5.0557	-1.7901
SPATS2	spermatogenesis associated, serine-rich 2	12q13.12	-5.0564	-1.7880
TMEM45A	transmembrane protein 45A	3q12.2	-5.1127	-3.3929
RIC8B	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	12q23.3	-5.1905	-1.6460
SLFN11	schlafen family member 11	17q12	-5.1928	-2.8414
CCDC125	coiled-coil domain containing 125	5q13.2	-5.1992	-2.1369
SCAMP5	secretory carrier membrane protein 5	15q24.2	-5.2045	-2.2335
ANKRD46	ankyrin repeat domain 46	8q22.2	-5.2786	-2.0372
LTBP1	latent transforming growth factor beta binding protein 1	2p22-p21	-5.3558	-2.8197
TOB2	transducer of ERBB2, 2	22q13.2	-5.3735	-1.9662
ATL1	atlastin GTPase 1	14q22.1	-5.4385	-1.6410
MIR494	microRNA 494	14q32.31	-5.4751	-1.2732
ITGA6	integrin, alpha 6	2q31.1	-5.6489	-3.2315
VCAM1	vascular cell adhesion molecule 1	1p32-p31	-5.6918	-2.8356
FBXO16	F-box protein 16	8p21.1	-5.8506	-2.6132
GLCE	glucuronic acid epimerase	15q23	-5.9121	-2.2870
SDC1	syndecan 1	2p24.1	-5.9640	-1.9721
SLAMF6	SLAM family member 6	1q23.2	-5.9754	-4.8175
CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid hydroxylase) pseudogene	6p21.32	-6.5094	-2.9951
FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	14q24.3	-6.7336	-5.6028
UIMC1	ubiquitin interaction motif containing 1	5q35.2	-6.8527	-2.8772
OSBPL10	oxysterol binding protein-like 10	3p22.3	-7.2605	-4.9258