

Supplementary Table 1. Summary of Positive related gene correlated to PLODs in PAAD from TCGA database

PLOD Protein Genes	Correlated Genes	Correlation Coefficient	P-Value
PLOD1	SERPINH1	0.756853328	2.46E-34
PLOD1	LGALS1	0.740135424	3.77E-32
PLOD1	LOXL2	0.731454472	4.43E-31
PLOD1	CD276	0.730869588	5.21E-31
PLOD1	ENO1	0.710445436	1.18E-28
PLOD1	FKBP10	0.70693988	2.85E-28
PLOD1	MMP14	0.703519295	6.65E-28
PLOD1	LEPRE1	0.698456168	2.29E-27
PLOD1	ITGA5	0.686631895	3.71E-26
PLOD1	BMP1	0.680869623	1.38E-25
PLOD1	RCN3	0.67532425	4.73E-25
PLOD1	ARSI	0.674491169	5.67E-25
PLOD1	GLT25D1	0.673553718	6.97E-25
PLOD1	TMEM158	0.669286315	1.76E-24
PLOD1	FN1	0.660522771	1.12E-23
PLOD1	ITGB5	0.659831959	1.29E-23
PLOD1	COL5A1	0.658248797	1.79E-23
PLOD1	CALU	0.654831465	3.60E-23
PLOD1	MXRA8	0.653915087	4.34E-23
PLOD1	C1QTNF6	0.653118199	5.09E-23
PLOD1	LOXL3	0.65246642	5.81E-23
PLOD1	MRC2	0.643744645	3.27E-22
PLOD1	COL1A2	0.642063864	4.54E-22
PLOD1	P4HA1	0.6412932	5.27E-22
PLOD1	COL1A1	0.641123442	5.44E-22
PLOD1	PTK7	0.640562137	6.06E-22
PLOD1	MFAP2	0.639988758	6.77E-22
PLOD1	COL5A3	0.638125552	9.68E-22
PLOD1	PPAPDC1A	0.637827692	1.02E-21
PLOD1	PLOD2	0.636779824	1.25E-21
PLOD1	TUBB	0.636204092	1.40E-21
PLOD1	EFEMP2	0.635563682	1.58E-21
PLOD1	PLAU	0.633554361	2.30E-21
PLOD1	ANGPTL2	0.630613853	3.98E-21
PLOD1	TWIST1	0.630072836	4.41E-21
PLOD1	COL6A1	0.628630535	5.75E-21

PLOD1	P4HA3	0.628030652	6.42E-21
PLOD1	SRPX2	0.622808475	1.66E-20
PLOD1	C3orf21	0.620789702	2.39E-20
PLOD1	AEBP1	0.617264501	4.49E-20
PLOD1	TMEM45A	0.615751252	5.86E-20
PLOD1	GUCA1A	0.615141027	6.53E-20
PLOD1	EMP3	0.614939923	6.76E-20
PLOD1	COL3A1	0.613224794	9.13E-20
PLOD1	PCOLCE	0.610729925	1.41E-19
PLOD1	PXDN	0.609263773	1.81E-19
PLOD1	CERCAM	0.608067713	2.23E-19
PLOD1	CMTM3	0.607794773	2.33E-19
PLOD1	PODNL1	0.606459968	2.93E-19
PLOD1	FAP	0.604847033	3.86E-19
PLOD1	RPSAP52	0.602410657	5.82E-19
PLOD1	ADAMTS7	0.602046641	6.19E-19
PLOD1	SNAI2	0.601621259	6.64E-19
PLOD1	COL5A2	0.601475762	6.81E-19
PLOD1	C9orf109	0.600946281	7.44E-19
PLOD1	COL6A3	0.600672134	7.79E-19
PLOD2	LOX	0.812909546	1.00E-43
PLOD2	FN1	0.785621013	3.51E-43
PLOD2	FNDC3B	0.771030419	1.53E-38
PLOD2	FRMD6	0.765718601	2.48E-36
PLOD2	COL6A3	0.761418758	1.44E-35
PLOD2	COL5A2	0.757242953	5.80E-35
PLOD2	ADAMTS12	0.753676899	2.18E-34
PLOD2	PXDN	0.753222399	6.60E-34
PLOD2	RAI14	0.749922606	7.59E-34
PLOD2	COL3A1	0.747023584	2.08E-33
PLOD2	ZNF532	0.744135199	4.97E-33
PLOD2	COL5A1	0.739446712	1.17E-32
PLOD2	COL1A2	0.739162309	4.60E-32
PLOD2	VCAN	0.738486898	4.99E-32
PLOD2	NID2	0.737638569	6.06E-32
PLOD2	EDNRA	0.732217892	7.73E-32
PLOD2	SPARC	0.731888515	3.58E-31
PLOD2	LOXL2	0.731082908	3.92E-31
PLOD2	VGLL3	0.730900316	4.91E-31
PLOD2	ADAM12	0.730123101	5.16E-31
PLOD2	ITGA5	0.729133326	6.40E-31
PLOD2	ANTXR1	0.728440228	8.41E-31
PLOD2	FSTL1	0.727890481	1.02E-30
PLOD2	TNFAIP6	0.723684927	1.18E-30

PLOD2	SPOCK1	0.722818031	3.70E-30
PLOD2	LOXL3	0.722490822	4.67E-30
PLOD2	COL4A1	0.722224163	5.10E-30
PLOD2	COL8A1	0.720340106	5.48E-30
PLOD2	WISP1	0.719063375	9.04E-30
PLOD2	CLIC4	0.71562536	1.27E-29
PLOD2	SULF1	0.712796265	3.11E-29
PLOD2	MTMR2	0.711658101	6.46E-29
PLOD2	FAP	0.709099234	8.64E-29
PLOD2	INHBA	0.708946068	1.65E-28
PLOD2	CHSY1	0.708859625	1.72E-28
PLOD2	COL12A1	0.708838121	1.76E-28
PLOD2	CALU	0.707124102	1.77E-28
PLOD2	SNAI2	0.706734877	2.72E-28
PLOD2	IKBIP	0.706187235	3.00E-28
PLOD2	ITGB1	0.705894434	3.43E-28
PLOD2	PRRX1	0.704193953	3.69E-28
PLOD2	POSTN	0.702960135	5.63E-28
PLOD2	PRSS23	0.701088396	7.64E-28
PLOD2	FBN1	0.699336123	1.21E-27
PLOD2	PDGFRB	0.69872116	1.85E-27
PLOD2	COL1A1	0.69724188	2.15E-27
PLOD2	MAP4K5	0.695619277	3.07E-27
PLOD2	GPR176	0.695140503	4.52E-27
PLOD2	RAB31	0.695139669	5.07E-27
PLOD2	NTM	0.690687649	5.07E-27
PLOD2	LAMA4	0.68984184	1.45E-26
PLOD2	HMCN1	0.689452787	1.77E-26
PLOD2	PDGFC	0.688910029	1.93E-26
PLOD2	TMEFF1	0.688844437	2.19E-26
PLOD2	PLS3	0.68818469	2.23E-26
PLOD2	FKBP14	0.686705646	2.59E-26
PLOD2	SEC23A	0.685448691	3.65E-26
PLOD2	GPX8	0.684833316	4.87E-26
PLOD2	OSMR	0.684295577	5.61E-26
PLOD2	THBS2	0.682245253	6.34E-26
PLOD2	CDH11	0.682186544	1.01E-25
PLOD2	TMEM45A	0.681929392	1.02E-25
PLOD2	TNFSF4	0.681843668	1.08E-25
PLOD2	LTBP1	0.681794258	1.11E-25
PLOD2	CHSY3	0.680158534	1.12E-25
PLOD2	ATXN1	0.679982816	1.62E-25
PLOD2	CSGALNACT2	0.678891806	1.68E-25
PLOD2	GBE1	0.678382593	2.14E-25

PLOD2	MRC2	0.676880249	2.40E-25
PLOD2	COL4A2	0.674625435	3.35E-25
PLOD2	ADAMTS2	0.674590566	5.51E-25
PLOD2	ITGA11	0.672993786	5.55E-25
PLOD2	NID1	0.672678493	7.87E-25
PLOD2	BNC2	0.671979726	8.43E-25
PLOD2	PRR16	0.67136531	9.81E-25
PLOD2	GJA1	0.669975567	1.12E-24
PLOD2	KIRREL	0.668934671	1.51E-24
PLOD2	RBMS1	0.6683976	1.89E-24
PLOD2	ITGAV	0.666131373	2.12E-24
PLOD2	PCDH7	0.664861191	3.44E-24
PLOD2	PABPC4L	0.664548554	4.51E-24
PLOD2	PANX1	0.663973072	4.81E-24
PLOD2	P4HA3	0.663426887	5.43E-24
PLOD2	ADAM19	0.663238946	6.10E-24
PLOD2	LUM	0.662574982	6.34E-24
PLOD2	CEP170	0.662470904	7.29E-24
PLOD2	ARL4C	0.662173369	7.45E-24
PLOD2	GXYLT2	0.662102311	7.93E-24
PLOD2	SSH1	0.661207299	8.05E-24
PLOD2	CALD1	0.659525378	9.70E-24
PLOD2	MMP14	0.659384946	1.37E-23
PLOD2	KCND2	0.658929914	1.42E-23
PLOD2	CNN3	0.658924978	1.55E-23
PLOD2	PICALM	0.65738596	1.56E-23
PLOD2	CERCAM	0.656366989	2.14E-23
PLOD2	SERPINH1	0.655296362	2.63E-23
PLOD2	RASSF8	0.654878557	3.28E-23
PLOD2	SRPX2	0.654865027	3.57E-23
PLOD2	ENPEP	0.6537821	3.58E-23
PLOD2	TWIST1	0.653548752	4.45E-23
PLOD2	FNDC1	0.65323195	4.67E-23
PLOD2	RECQL	0.6531575	4.98E-23
PLOD2	PPFIBP1	0.653152431	5.05E-23
PLOD2	KDELC1	0.65301018	5.06E-23
PLOD2	CD109	0.652791838	5.21E-23
PLOD2	LTBP2	0.652681869	5.44E-23
PLOD2	EFEMP2	0.651832507	5.56E-23
PLOD2	THBS1	0.65107682	6.60E-23
PLOD2	PLXDC2	0.650463706	7.68E-23
PLOD2	SH3GLB1	0.650054818	8.68E-23
PLOD2	AXL	0.649948752	9.42E-23
PLOD2	TIMP3	0.649381813	9.62E-23

PLOD2	MAF	0.648221079	1.08E-22
PLOD2	LIMS1	0.648065856	1.36E-22
PLOD2	PLAU	0.646974538	1.40E-22
PLOD2	GLI3	0.646936235	1.74E-22
PLOD2	ASAM	0.646455353	1.75E-22
PLOD2	P4HA1	0.646446833	1.92E-22
PLOD2	CTSK	0.646404902	1.93E-22
PLOD2	NOX4	0.646303709	1.94E-22
PLOD2	GFPT2	0.646282212	1.98E-22
PLOD2	IL1RAP	0.646144718	1.99E-22
PLOD2	QKI	0.645993127	2.05E-22
PLOD2	SLC2A3	0.645284023	2.11E-22
PLOD2	LAMC1	0.644602701	2.42E-22
PLOD2	ADAMTS5	0.644283242	2.77E-22
PLOD2	CTHRC1	0.643367714	2.95E-22
PLOD2	BASP1	0.642260241	3.52E-22
PLOD2	PDLIM3	0.641988755	4.37E-22
PLOD2	KANK4	0.641028979	4.60E-22
PLOD2	SEPT11	0.64051633	5.54E-22
PLOD2	WWTR1	0.639616665	6.12E-22
PLOD2	HIF1A	0.638384111	7.27E-22
PLOD2	GAS1	0.637455069	9.21E-22
PLOD2	SLC2A14	0.637227846	1.10E-21
PLOD2	FAM26E	0.636952816	1.15E-21
PLOD2	PLOD1	0.636779824	1.21E-21
PLOD2	MSN	0.636564529	1.25E-21
PLOD2	COMMD2	0.635690246	1.30E-21
PLOD2	UNC5B	0.635648025	1.54E-21
PLOD2	C5orf13	0.635516093	1.55E-21
PLOD2	BICC1	0.635432171	1.59E-21
PLOD2	DDR2	0.634449852	1.61E-21
PLOD2	CXCR7	0.634154842	1.94E-21
PLOD2	MEX3B	0.634122512	2.05E-21
PLOD2	PTRF	0.633438851	2.07E-21
PLOD2	ELK3	0.632584996	2.35E-21
PLOD2	DNAJB4	0.6322255	2.76E-21
PLOD2	ODZ3	0.632206703	2.95E-21
PLOD2	AEBP1	0.631547867	2.96E-21
PLOD2	COL11A1	0.630990632	3.35E-21
PLOD2	ITPRIP	0.630101488	3.71E-21
PLOD2	FUT11	0.629894841	4.38E-21
PLOD2	FERMT2	0.629223813	4.55E-21
PLOD2	PAPPA	0.628844485	5.16E-21
PLOD2	ANGPTL2	0.628232144	5.53E-21

PLOD2	SSPN	0.627471181	6.19E-21
PLOD2	INSIG2	0.62730785	7.12E-21
PLOD2	ADAM17	0.62691188	7.34E-21
PLOD2	SERPINE1	0.626760463	7.89E-21
PLOD2	LRP12	0.626623324	8.11E-21
PLOD2	PDLIM5	0.626599565	8.32E-21
PLOD2	KAL1	0.625731076	8.36E-21
PLOD2	PIK3CA	0.624974889	9.79E-21
PLOD2	MMP2	0.624774903	1.12E-20
PLOD2	KDELC2	0.624478019	1.17E-20
PLOD2	PALLD	0.624471903	1.23E-20
PLOD2	C9orf110	0.624366583	1.23E-20
PLOD2	COL8A2	0.624276192	1.26E-20
PLOD2	STC1	0.62408813	1.28E-20
PLOD2	ST6GAL2	0.623099088	1.32E-20
PLOD2	THY1	0.621148273	1.58E-20
PLOD2	CMTM3	0.620909588	2.25E-20
PLOD2	SEMA3C	0.619332721	2.34E-20
PLOD2	SOCS5	0.619156486	3.11E-20
PLOD2	WWC2	0.618539957	3.21E-20
PLOD2	LPAR4	0.618204008	3.58E-20
PLOD2	F2R	0.617798888	3.80E-20
PLOD2	PTK7	0.617632796	4.08E-20
PLOD2	KLHL5	0.61762843	4.20E-20
PLOD2	TSHZ3	0.616340332	4.21E-20
PLOD2	COL10A1	0.616137514	5.28E-20
PLOD2	DCBLD2	0.615035697	5.48E-20
PLOD2	COL6A1	0.614990114	6.65E-20
PLOD2	MXRA5	0.614758774	6.70E-20
PLOD2	UBE2E2	0.614609342	6.98E-20
PLOD2	HIVEP2	0.61454882	7.17E-20
PLOD2	UNC5C	0.614253201	7.24E-20
PLOD2	GDF6	0.613796054	7.63E-20
PLOD2	FZD1	0.613395645	8.26E-20
PLOD2	TMEM43	0.613267209	8.86E-20
PLOD2	SAV1	0.612967785	9.06E-20
PLOD2	C10orf72	0.612602752	9.55E-20
PLOD2	CD248	0.612146992	1.02E-19
PLOD2	NOTCH3	0.61179149	1.10E-19
PLOD2	MSRB3	0.611762364	1.17E-19
PLOD2	PRDM1	0.611206626	1.18E-19
PLOD2	B3GALTL	0.610053408	1.30E-19
PLOD2	PPAPDC1A	0.609738865	1.58E-19
PLOD2	GNAI3	0.609209085	1.67E-19

PLOD2	FLNA	0.608913146	1.83E-19
PLOD2	DIO2	0.608844738	1.93E-19
PLOD2	KLF7	0.608807343	1.95E-19
PLOD2	CLDND1	0.608794461	1.96E-19
PLOD2	GLT8D2	0.608776709	1.97E-19
PLOD2	DPYD	0.6085664	1.97E-19
PLOD2	FKBP7	0.607669103	2.05E-19
PLOD2	FIBIN	0.607091953	2.39E-19
PLOD2	DPYSL3	0.607089752	2.63E-19
PLOD2	BGN	0.606813617	2.63E-19
PLOD2	ITGA1	0.606701371	2.76E-19
PLOD2	ITGB3	0.606348457	2.81E-19
PLOD2	RAB23	0.606285363	2.99E-19
PLOD2	HTRA1	0.6061651	3.02E-19
PLOD2	SFRP2	0.606022293	3.08E-19
PLOD2	PARD6G	0.605388829	3.16E-19
PLOD2	FAM198B	0.605064775	3.52E-19
PLOD2	ZEB2	0.604895471	3.72E-19
PLOD2	SH3PXD2B	0.604701091	3.83E-19
PLOD2	TMEM200A	0.60468671	3.95E-19
PLOD2	BNIP3L	0.604587315	3.96E-19
PLOD2	CDK14	0.604564786	4.03E-19
PLOD2	ASAP1	0.60418857	4.05E-19
PLOD2	RASAL2	0.60388313	4.31E-19
PLOD2	YEATS2	0.603778387	4.54E-19
PLOD2	RRAGC	0.603612608	4.62E-19
PLOD2	NUAK1	0.602923605	4.75E-19
PLOD2	STON1	0.602886024	5.34E-19
PLOD2	ZFHX4	0.602820424	5.37E-19
PLOD2	TSC22D2	0.601478834	5.43E-19
PLOD2	LATS2	0.601392076	6.80E-19
PLOD2	NRP1	0.600888746	6.90E-19
PLOD2	SPSB1	0.600832786	7.51E-19
PLOD2	ZFPM2	0.600038716	7.58E-19
PLOD3	GNB2	0.603216559	5.08E-19
PLOD3	CTSA	0.598607357	1.10E-18
PLOD3	CALR	0.586921361	7.33E-18
PLOD3	PDIA4	0.584484132	1.08E-17
PLOD3	TAF6	0.576300419	3.86E-17
PLOD3	AP1S1	0.575507318	4.36E-17
PLOD3	C20orf20	0.55985537	4.50E-16
PLOD3	CHPF2	0.558159567	5.75E-16
PLOD3	PIGT	0.558154447	5.76E-16
PLOD3	POP7	0.554151062	1.02E-15

PLOD3	ARF1	0.55296286	1.21E-15
PLOD3	KDELR1	0.551074107	1.58E-15
PLOD3	ZNHIT1	0.539190997	8.18E-15
PLOD3	TMED9	0.538480296	9.00E-15
PLOD3	KDELR2	0.529510367	2.98E-14
PLOD3	CARM1	0.528794296	3.27E-14
PLOD3	TBRG4	0.528731921	3.30E-14
PLOD3	SLC35A2	0.523329107	6.65E-14
PLOD3	MOSPD3	0.520759619	9.24E-14
PLOD3	ERGIC3	0.519163644	1.13E-13
PLOD3	DPP9	0.517291973	1.43E-13
PLOD3	DLGAP4	0.516642043	1.56E-13
PLOD3	FAM189B	0.513953512	2.18E-13
PLOD3	C19orf10	0.513188344	2.40E-13
PLOD3	MOGS	0.511733081	2.87E-13
PLOD3	PTCD1	0.510492534	3.35E-13
PLOD3	GPR172A	0.509800746	3.65E-13
PLOD3	TMEM189	0.509546559	3.77E-13
PLOD3	REEP4	0.508879084	4.09E-13
PLOD3	LGALS3BP	0.508071043	4.51E-13
PLOD3	YKT6	0.506340306	5.57E-13
PLOD3	UBE2S	0.504375891	7.07E-13
PLOD3	MDH2	0.503323662	8.03E-13
PLOD3	PDAP1	0.501884065	9.55E-13
PLOD3	EIF6	0.501771089	9.68E-13

*Only genes with correlation coefficient > 0.5 are listed.

Supplementary Table 2. Summary of Negative related gene correlated to PLODs in PAAD from TCGA database

PLOD Protein	Correlated	Correlation	P-Value
Genes	Genes	Coefficient	
PLOD1	RALGPS1	-0.685981573	4.31E-26
PLOD1	ATP8A1	-0.631276127	3.52E-21
PLOD1	ZNF620	-0.623646089	1.43E-20
PLOD1	ATP2A3	-0.605410221	3.51E-19
PLOD1	C2orf15	-0.602259817	5.97E-19
PLOD1	C12orf27	-0.59910186	1.01E-18
PLOD1	PHOSPHO2	-0.581964452	1.60E-17
PLOD1	LRRC16B	-0.56833432	1.29E-16
PLOD1	TTLL6	-0.565080405	2.09E-16
PLOD1	BTNL9	-0.563438865	2.67E-16

PLOD1	PTPRN2	-0.562849369	2.91E-16
PLOD1	ZNF33A	-0.56168864	3.44E-16
PLOD1	VIPR1	-0.561433865	3.58E-16
PLOD1	LOC400027	-0.556415535	7.39E-16
PLOD1	PIP5K1B	-0.552666048	1.26E-15
PLOD1	CNNM3	-0.544590117	3.91E-15
PLOD1	SEPSECS	-0.541940276	5.62E-15
PLOD1	ZNF44	-0.541370368	6.08E-15
PLOD1	TPD52	-0.54127754	6.16E-15
PLOD1	C11orf92	-0.540370443	6.97E-15
PLOD1	PNPLA7	-0.538814517	8.61E-15
PLOD1	ANKRD43	-0.538702711	8.74E-15
PLOD1	RALGAPA1	-0.537418615	1.04E-14
PLOD1	SLAIN1	-0.536376621	1.20E-14
PLOD1	ZNF708	-0.534433261	1.55E-14
PLOD1	PPP1R9A	-0.532675826	1.96E-14
PLOD1	TSPAN12	-0.53250738	2.00E-14
PLOD1	EPHA10	-0.530165079	2.73E-14
PLOD1	EXOC6	-0.530007055	2.79E-14
PLOD1	ZNF564	-0.527900764	3.67E-14
PLOD1	RUNDC1	-0.527853992	3.70E-14
PLOD1	ZNF91	-0.527072687	4.09E-14
PLOD1	CCDC125	-0.526596833	4.36E-14
PLOD1	DDC	-0.526092619	4.65E-14
PLOD1	MTMR10	-0.525764633	4.85E-14
PLOD1	C10orf108	-0.525661928	4.92E-14
PLOD1	BEND7	-0.525655379	4.92E-14
PLOD1	DGKE	-0.52424809	5.90E-14
PLOD1	CA8	-0.524104855	6.01E-14
PLOD1	RALGPS1	-0.685981573	4.31E-26
PLOD1	ATP8A1	-0.631276127	3.52E-21
PLOD1	ZNF620	-0.623646089	1.43E-20
PLOD1	ATP2A3	-0.605410221	3.51E-19
PLOD1	C2orf15	-0.602259817	5.97E-19
PLOD1	C12orf27	-0.59910186	1.01E-18
PLOD1	PHOSPHO2	-0.581964452	1.60E-17
PLOD1	LRRC16B	-0.56833432	1.29E-16
PLOD1	TTL6	-0.565080405	2.09E-16
PLOD1	BTNL9	-0.563438865	2.67E-16
PLOD1	PTPRN2	-0.562849369	2.91E-16
PLOD1	ZNF33A	-0.56168864	3.44E-16
PLOD1	VIPR1	-0.561433865	3.58E-16
PLOD1	LOC400027	-0.556415535	7.39E-16
PLOD1	PIP5K1B	-0.552666048	1.26E-15

PLOD1	CNNM3	-0.544590117	3.91E-15
PLOD1	SEPSECS	-0.541940276	5.62E-15
PLOD1	ZNF44	-0.541370368	6.08E-15
PLOD1	TPD52	-0.54127754	6.16E-15
PLOD1	C11orf92	-0.540370443	6.97E-15
PLOD1	PNPLA7	-0.538814517	8.61E-15
PLOD1	ANKRD43	-0.538702711	8.74E-15
PLOD1	RALGAPA1	-0.537418615	1.04E-14
PLOD1	SLAIN1	-0.536376621	1.20E-14
PLOD1	ZNF708	-0.534433261	1.55E-14
PLOD1	PPP1R9A	-0.532675826	1.96E-14
PLOD1	TSPAN12	-0.53250738	2.00E-14
PLOD1	EPHA10	-0.530165079	2.73E-14
PLOD1	EXOC6	-0.530007055	2.79E-14
PLOD1	ZNF564	-0.527900764	3.67E-14
PLOD1	RUNDC1	-0.527853992	3.70E-14
PLOD1	ZNF91	-0.527072687	4.09E-14
PLOD1	CCDC125	-0.526596833	4.36E-14
PLOD1	DDC	-0.526092619	4.65E-14
PLOD1	MTMR10	-0.525764633	4.85E-14
PLOD1	C10orf108	-0.525661928	4.92E-14
PLOD1	BEND7	-0.525655379	4.92E-14
PLOD1	DGKE	-0.52424809	5.90E-14
PLOD1	CA8	-0.524104855	6.01E-14
PLOD1	ACACB	-0.523600677	6.42E-14
PLOD1	CCDC64	-0.522573071	7.33E-14
PLOD1	HIP1R	-0.517110176	1.47E-13
PLOD1	EPHX2	-0.516912039	1.50E-13
PLOD1	C2orf72	-0.516289971	1.63E-13
PLOD1	ZSWIM5	-0.5157223	1.75E-13
PLOD1	ZNF782	-0.515396607	1.82E-13
PLOD1	NR3C2	-0.51519868	1.87E-13
PLOD1	ANUBL1	-0.51439753	2.06E-13
PLOD1	SECISBP2	-0.514358643	2.07E-13
PLOD1	ZNF443	-0.51375928	2.23E-13
PLOD1	LOC389332	-0.511905009	2.81E-13
PLOD1	SLC25A20	-0.511213608	3.07E-13
PLOD1	MOAP1	-0.510613199	3.30E-13
PLOD1	ZNF33B	-0.508490044	4.29E-13
PLOD1	EML5	-0.506054699	5.77E-13
PLOD1	HNF1A	-0.505993421	5.81E-13
PLOD1	ABCA5	-0.50550761	6.17E-13
PLOD1	SUGT1L1	-0.50395252	7.45E-13
PLOD1	KIAA1147	-0.503144279	8.21E-13

PLOD1	RAVER2	-0.502322747	9.06E-13
PLOD1	KIAA0528	-0.501946571	9.48E-13
PLOD1	ZFYVE28	-0.501406206	1.01E-12
PLOD1	C9orf103	-0.500004262	1.20E-12
PLOD2	REPIN1	-0.641537908	5.02E-22
PLOD2	FBXW4	-0.626225081	8.95E-21
PLOD2	C19orf73	-0.612787124	9.85E-20
PLOD2	TYSND1	-0.610235835	1.53E-19
PLOD2	PLEKHJ1	-0.603226917	5.07E-19
PLOD2	AES	-0.602856645	5.40E-19
PLOD2	SAFB	-0.600903346	7.49E-19
PLOD2	ZFYVE27	-0.593070125	2.73E-18
PLOD2	SLC48A1	-0.591568953	3.48E-18
PLOD2	C19orf39	-0.590004008	4.48E-18
PLOD2	TOR2A	-0.589727883	4.68E-18
PLOD2	FUK	-0.586252821	8.15E-18
PLOD2	SDHAF1	-0.585040444	9.88E-18
PLOD2	ZFAND2B	-0.583138986	1.33E-17
PLOD2	SURF6	-0.580683464	1.96E-17
PLOD2	SF4	-0.577709229	3.11E-17
PLOD2	ATG4D	-0.573955632	5.52E-17
PLOD2	SMPD2	-0.572798042	6.59E-17
PLOD2	CCDC94	-0.572694834	6.69E-17
PLOD2	ALKBH7	-0.572087185	7.34E-17
PLOD2	ASPSCR1	-0.571905794	7.54E
PLOD2	PNPLA7	-0.570133802	9.85E-17
PLOD2	CABC1	-0.569781358	1.04E-16
PLOD2	SPRN	-0.568822196	1.20E-16
PLOD2	SFXN4	-0.568016581	1.35E-16
PLOD2	NSMCE4A	-0.566650344	1.66E-16
PLOD2	C1orf56	-0.566338324	1.74E-16
PLOD2	MRPS26	-0.56451827	2.27E-16
PLOD2	GLYCTK	-0.564351567	2.33E-16
PLOD2	MTG1	-0.561153649	3.72E-16
PLOD2	JTB	-0.56062552	4.02E-16
PLOD2	TIMM13	-0.559761774	4.56E-16
PLOD2	ATP2A3	-0.55951129	4.73E-16
PLOD2	PICK1	-0.559104679	5.02E-16
PLOD2	COQ4	-0.558700516	5.32E-16
PLOD2	MMAB	-0.55782503	6.04E-16
PLOD2	HIP1R	-0.557819447	6.04E-16
PLOD2	C22orf32	-0.557509932	6.32E-16
PLOD2	CISD3	-0.557471881	6.35E-16
PLOD2	RNF167	-0.557220704	6.59E-16

PLOD2	PTPN18	-0.557173423	6.63E-16
PLOD2	NDUFA7	-0.557064978	6.73E-16
PLOD2	SNHG11	-0.555775143	8.10E-16
PLOD2	C21orf2	-0.555273687	8.71E-16
PLOD2	MRM1	-0.554369852	9.91E-16
PLOD2	C19orf45	-0.553682939	1.09E-15
PLOD2	MPND	-0.553681597	1.09E-15
PLOD2	DDRKG1	-0.55363773	1.10E-15
PLOD2	PTGES2	-0.553352886	1.15E-15
PLOD2	NPDC1	-0.553018158	1.20E-15
PLOD2	POLRMT	-0.552147157	1.36E-15
PLOD2	TSEN54	-0.551090553	1.58E-15
PLOD2	C20orf134	-0.550832325	1.64E-15
PLOD2	BLOC1S1	-0.549421033	1.99E-15
PLOD2	SNHG8	-0.548591484	2.24E-15
PLOD2	FBXL15	-0.548156117	2.38E-15
PLOD2	C7orf55	-0.547301487	2.68E-15
PLOD2	CCDC22	-0.546725051	2.91E-15
PLOD2	ZNF653	-0.545615355	3.39E-15
PLOD2	LOC729991	-0.545049137	3.67E-15
PLOD2	IRF2BP1	-0.544429447	3.99E-15
PLOD2	MED16	-0.544420708	4.00E-15
PLOD2	C7orf26	-0.544029915	4.22E-15
PLOD2	FAM195A	-0.544024819	4.22E-15
PLOD2	COG2	-0.543419884	4.59E-15
PLOD2	UQCR11	-0.542065091	5.53E-15
PLOD2	AIFM1	-0.541752185	5.77E-15
PLOD2	NUDT16L1	-0.541466432	6.00E-15
PLOD2	EPHX2	-0.54132508	6.12E-15
PLOD2	LOC100128822	-0.54112152	6.29E-15
PLOD2	SURF2	-0.540477366	6.87E-15
PLOD2	PSTK	-0.539741332	7.59E-15
PLOD2	C9orf7	-0.537463211	1.03E-14
PLOD2	SURF1	-0.537187807	1.07E-14
PLOD2	SLC2A8	-0.536263847	1.21E-14
PLOD2	PRMT7	-0.536108002	1.24E-14
PLOD2	ANKRD16	-0.534985525	1.44E-14
PLOD2	MRPL4	-0.534701064	1.50E-14
PLOD2	NECAB3	-0.534527265	1.53E-14
PLOD2	GTPBP5	-0.534477251	1.54E-14
PLOD2	CSRP2BP	-0.534109306	1.62E-14
PLOD2	DUS3L	-0.534096343	1.62E-14
PLOD2	DCI	-0.533118264	1.85E-14
PLOD2	ERP29	-0.532768658	1.94E-14

PLOD2	POLL	-0.531992775	2.15E-14
PLOD2	ATP5D	-0.53130922	2.35E-14
PLOD2	MRP63	-0.531252012	2.37E-14
PLOD2	SLC35D2	-0.53124522	2.37E-14
PLOD2	LSM7	-0.531062677	2.43E-14
PLOD2	CNNM3	-0.530238918	2.70E-14
PLOD2	FLJ39653	-0.53019744	2.72E-14
PLOD2	C19orf25	-0.530183966	2.72E-14
PLOD2	C6orf136	-0.529881613	2.83E-14
PLOD2	SPPL2B	-0.529657411	2.92E-14
PLOD2	COMTD1	-0.528803486	3.27E-14
PLOD2	TMEM205	-0.528450643	3.42E-14
PLOD2	LRWD1	-0.528095843	3.58E-14
PLOD2	ZNF296	-0.527712265	3.77E-14
PLOD2	NDUFS7	-0.527262676	3.99E-14
PLOD2	RANBP3	-0.526187933	4.59E-14
PLOD2	FOXP4	-0.524923077	5.41E-14
PLOD2	VIPR1	-0.524832206	5.48E-14
PLOD2	LRRC16B	-0.52341475	6.57E-14
PLOD2	ZNF564	-0.522627255	7.27E-14
PLOD2	ALKBH4	-0.522592664	7.31E-14
PLOD2	SNAPC4	-0.521857257	8.03E-14
PLOD2	MON1A	-0.521701406	8.19E-14
PLOD2	SNHG7	-0.521372979	8.54E-14
PLOD2	PWWP2B	-0.521323353	8.60E-14
PLOD2	TTC15	-0.519590539	1.07E-13
PLOD2	PMPCA	-0.519532324	1.08E-13
PLOD2	ECSIT	-0.51884953	1.18E-13
PLOD2	ILKAP	-0.518795745	1.19E-13
PLOD2	IDI2	-0.51874496	1.19E-13
PLOD2	LOC113230	-0.51858239	1.22E-13
PLOD2	QTRT1	-0.517996951	1.31E-13
PLOD2	KIAA0664	-0.517538965	1.39E-13
PLOD2	XAB2	-0.517449063	1.41E-13
PLOD2	C17orf59	-0.516281099	1.63E-13
PLOD2	ENTPD6	-0.515664548	1.76E-13
PLOD2	THAP7	-0.514410074	2.06E-13
PLOD2	C9orf142	-0.51423121	2.11E-13
PLOD2	FGFBP3	-0.514170636	2.12E-13
PLOD2	LIAS	-0.514168505	2.12E-13
PLOD2	SAPS2	-0.514112029	2.14E-13
PLOD2	RPS10P7	-0.514071987	2.15E-13
PLOD2	PEX11G	-0.514039004	2.16E-13
PLOD2	VMAC	-0.513313805	2.36E-13

PLOD2	TPRN	-0.512762732	2.53E-13
PLOD2	C14orf93	-0.512320447	2.67E-13
PLOD2	PEX16	-0.511619034	2.92E-13
PLOD2	LRSAM1	-0.511588092	2.93E-13
PLOD2	MTIF3	-0.511577147	2.93E-13
PLOD2	EIF3G	-0.511447418	2.98E-13
PLOD2	NDOR1	-0.510956279	3.16E-13
PLOD2	PELP1	-0.510631224	3.29E-13
PLOD2	PCBD1	-0.5102527	3.45E-13
PLOD2	NRL	-0.510246372	3.45E-13
PLOD2	GLTSCR2	-0.510031402	3.55E-13
PLOD2	C9orf86	-0.510008968	3.56E-13
PLOD2	C21orf57	-0.50892254	4.07E-13
PLOD2	NDUFB11	-0.508616687	4.22E-13
PLOD2	OVCA2	-0.507435409	4.88E-13
PLOD2	RASA4P	-0.507101662	5.08E-13
PLOD2	ANAPC2	-0.506621598	5.39E-13
PLOD2	TRMU	-0.505885256	5.89E-13
PLOD2	PMVK	-0.505679387	6.04E-13
PLOD2	HDHD3	-0.505621677	6.08E-13
PLOD2	DOHH	-0.504999577	6.56E-13
PLOD2	TACC2	-0.504830287	6.70E-13
PLOD2	PHLDB3	-0.504608296	6.88E-13
PLOD2	HNF1A	-0.504519308	6.95E-13
PLOD2	ICA1	-0.504288039	7.15E-13
PLOD2	C2orf79	-0.503794828	7.59E-13
PLOD2	KIAA1543	-0.503737026	7.64E-13
PLOD2	SLC25A38	-0.503646638	7.73E-13
PLOD2	CLPP	-0.503459664	7.90E-13
PLOD2	ILVBL	-0.503148729	8.20E-13
PLOD2	ATP13A1	-0.502867943	8.49E-13
PLOD2	MRPL54	-0.502636931	8.73E-13
PLOD2	C9orf114	-0.502587397	8.78E-13
PLOD2	DUS1L	-0.502395096	8.98E-13
PLOD2	TSTD1	-0.502283214	9.10E-13
PLOD2	PGPEP1	-0.502076425	9.33E-13
PLOD2	ZNF672	-0.501901565	9.53E-13
PLOD2	C1orf66	-0.501865685	9.57E-13
PLOD2	ZNF688	-0.501522437	9.97E-13
PLOD2	ZNF444	-0.501469257	1.00E-12
PLOD2	APOA1BP	-0.501293201	1.03E-12
PLOD2	DPM3	-0.501168165	1.04E-12
PLOD2	NOL12	-0.500573722	1.12E-12
PLOD2	ENDOG	-0.500499933	1.13E-12

PLOD2	NDUFS6	-0.500142643	1.18E-12
PLOD3	ZNF543	-0.500070869	1.19E-12
PLOD3	ABCC9	-0.500865188	1.08E-12
PLOD3	REV1	-0.501410539	1.01E-12
PLOD3	LONRF2	-0.501545416	9.95E-13
PLOD3	ZNF570	-0.501662373	9.81E-13
PLOD3	SCN4B	-0.501695149	9.77E-13
PLOD3	GCNT4	-0.502229285	9.16E-13
PLOD3	PRKRIR	-0.502890859	8.46E-13
PLOD3	FAM13B	-0.503353875	8.00E-13
PLOD3	KRT222	-0.506017488	5.80E-13
PLOD3	ARHGEF6	-0.506168861	5.69E-13
PLOD3	BCL2	-0.506265453	5.63E-13
PLOD3	ZBTB44	-0.509174193	3.94E-13
PLOD3	RORA	-0.511552716	2.94E-13
PLOD3	NCOA1	-0.511968408	2.79E-13
PLOD3	KIAA1370	-0.513578386	2.29E-13
PLOD3	ZNF626	-0.515023264	1.91E-13
PLOD3	ZNF671	-0.515271208	1.85E-13
PLOD3	ZIK1	-0.516359941	1.61E-13
PLOD3	ZNF383	-0.518350291	1.25E-13
PLOD3	SASH1	-0.519238413	1.12E-13
PLOD3	EPM2AIP1	-0.520026294	1.01E-13
PLOD3	ZNF649	-0.520375676	9.70E-14
PLOD3	LIFR	-0.520799766	9.19E-14
PLOD3	LRRK2	-0.526187069	4.59E-14
PLOD3	CYSLTR1	-0.526437354	4.45E-14
PLOD3	ZNF551	-0.532708136	1.95E-14
PLOD3	CENPC1	-0.53358562	1.74E-14
PLOD3	LMO3	-0.535506216	1.34E-14
PLOD3	TEK	-0.53648312	1.18E-14
PLOD3	DNAJC27	-0.536623547	1.16E-14
PLOD3	RRG	-0.539213614	8.15E-15
PLOD3	ARHGEF3	-0.539999259	7.33E-15
PLOD3	ASPA	-0.546803781	2.88E-15
PLOD3	ZNF677	-0.547774256	2.51E-15
PLOD3	ZNF615	-0.551672478	1.45E-15
PLOD3	CRBN	-0.555100488	8.93E-16
PLOD3	ATM	-0.555866658	8.00E-16
PLOD3	ABCA8	-0.560064298	4.36E-16
PLOD3	ZNF154	-0.570550199	9.25E-17
PLOD3	ZNF167	-0.582809534	1.40E-17
PLOD3	CEP68	-0.595276047	1.90E-18

*Only genes with correlation coefficient < - 0.5 are listed.

Supplementary Table 3. significantly rich summary of GO annotation for PLADS positively related genes

Description	Gene Count	pValue	Enriched Genes
<i>Biological Process</i>			
mitotic cell cycle process	24	7.05E-11	RHOC;ECT2;RCC1;E2F7;ANLN;KIF23;GPSM2;HMMR;KIF20A;NDC80;CENPF;MELK;CDC6;PRC1;EIF4G1;KIF18A;CENPE;CEP55;PLK4;NCAPH;BUB1;CCNJL;KIF14;PML
cell division	20	4.49E-10	RHOC;RALA;ECT2;RCC1;E2F7;ANLN;KIF23;GPSM2;KIF20A;NDC80;CENPF;CDC6;PRC1;NCAPG2;CENPE;CEP55;NCAPH;BUB1;FAM83D;KIF14
chromosome segregation	15	9.27E-10	ECT2;RCC1;KIF23;NDC80;CENPF;CDC6;HJURP;PRC1;KIF18A;CENPE;CEP55;NCAPH;BUB1;FAM83D;KIF14
mitotic cell cycle	24	1.88E-09	RHOC;ECT2;RCC1;E2F7;ANLN;KIF23;GPSM2;HMMR;KIF20A;NDC80;CENPF;MELK;CDC6;PRC1;EIF4G1;KIF18A;CENPE;CEP55;PLK4;NCAPH;BUB1;CCNJL;KIF14;PML
mitotic nuclear division	14	2.33E-09	RCC1;ANLN;KIF23;NDC80;CENPF;CDC6;PRC1;KIF18A;CENPE;CEP55;NCAPH;BUB1;CCNJL;KIF14
mitotic sister chromatid segregation	11	3.35E-09	KIF23;NDC80;CENPF;CDC6;PRC1;KIF18A;CENPE;CEP55;NCAPH;BUB1;KIF14
nuclear chromosome segregation	13	7.60E-09	ECT2;KIF23;NDC80;CENPF;CDC6;PRC1;KIF18A;CENPE;CEP55;NCAPH;BUB1;FAM83D;KIF14
regulation of cell cycle process	20	7.90E-09	ECT2;RCC1;E2F7;ANLN;KIF23;GPSM2;HMMR;KIF20A;NDC80;CENPF;CDC6;PRC1;EIF4G1;CENPE;PLK4;BUB1;CCNJL;FAM83D;KIF14;PML
protein hydroxylation	6	1.36E-08	PLOD1;PLOD2;PLOD3;P4HA1;P4HA2;EGLN3
sister chromatid segregation	11	2.13E-08	KIF23;NDC80;CENPF;CDC6;PRC1;KIF18A;CENPE;CEP55;NCAPH;BUB1;KIF14

**Cellular
Component**

midbody	13	6.64E-12	RALA;ECT2;SLC2A1;ANLN;KIF23;HSP90B1;KIF20A;CENPF;PRC1;CENPE;CEP55;HSPA5;KIF14
cell division site part	7	4.80E-08	RHOC;RALA;ECT2;ANLN;KIF20A;CEP55;PLK4
cell division site	7	8.16E-08	RHOC;RALA;ECT2;ANLN;KIF20A;CEP55;PLK4
endoplasmic reticulum lumen	12	8.27E-08	PLOD3;RCN3;P4HA1;COL7A1;PLAUR;TMEM132A;P4HA2;CKAP4;HSP90B1;PDIA6;HSPA5;RCN1
spindle	12	1.75E-07	ECT2;KIF23;GPSM2;KIF20A;CKAP2L;CENPF;CDC6;PRC1;KIF18A;CENPE;FAM83D;KIF14
cleavage furrow	6	4.65E-07	RHOC;RALA;ECT2;KIF20A;CEP55;PLK4
cytoskeletal part	25	8.26E-07	FSCN1;ZYX;ECT2;SLC2A1;ANLN;KIF23;TFAP2A;GPSM2;HMMR;TNNT1;C4orf47;KIF20A;CKAP2L;LASP1;NDC80;CENPF;ACTN4;CDC6;PRC1;KIF18A;CENPE;CEP55;PLK4;FAM83D;KIF14
mitotic spindle	7	9.89E-07	ECT2;KIF23;GPSM2;CKAP2L;KIF18A;CENPE;FAM83D
endoplasmic reticulum part	22	1.47E-06	PLOD3;PLOD2;PLOD1;RCN3;P4HA1;AGTRAP;COL7A1;PLAUR;TMEM132A;OSTC;DDOST;P4HA2;SLC39A1;TFG;CKAP4;HSP90B1;PDIA6;STT3A;HSPA5;RCN1;FATE1;PML
endoplasmic reticulum	26	3.06E-06	PLOD3;PLOD2;PLOD1;RCN3;P4HA1;AGTRAP;COL7A1;PLAUR;TMEM132A;FKBP9;ULBP2;OSTC;DDOST;SLC39A13;P4HA2;SLC39A1;TFG;CKAP4;HSP90B1;ULBP1;PDIA6;STT3A;HSPA5;RCN1;FATE1;PML

**Molecular
Function**

L-ascorbic acid binding	6	1.84E-09	PLOD3;PLOD2;PLOD1;P4HA1;P4HA2;EGLN3
oxidoreductase activity	6	4.45E-07	PLOD3;PLOD2;PLOD1;P4HA1;P4HA2;EGLN3
carboxylic acid binding	9	4.61E-06	PLOD3;PLOD2;PLOD1;P4HA1;AGRN;P4HA2;EGLN3;HMMR;HAPLN1
monosaccharide binding	6	6.70E-06	PLOD3;PLOD2;PLOD1;P4HA1;P4HA2;EGLN3

organic acid binding	9	7.11E-06	PLOD3;PLOD2;PLOD1;P4HA1;AGRN;P4HA2;EGLN3;HMMR;HAPLN1
dolichyl-diphosphooligosaccharide-protein glycosyltransferase activity	3	1.93E-05	OSTC;DDOST;STT3A
dioxygenase activity	6	2.36E-05	PLOD3;PLOD2;PLOD1;P4HA1;P4HA2;EGLN3
oligosaccharyl transferase activity	3	2.74E-05	OSTC;DDOST;STT3A
peptidyl-proline 4-dioxygenase activity	3	3.75E-05	P4HA1;P4HA2;EGLN3
cell adhesion molecule binding	12	4.26E-05	ENO1;ITGB5;FSCN1;ARHGAP1;TBC1D2;DIAPH3;ANLN;ITGA3;PLIN3;LASP1;ACTN4;HSPA5
KEGG			
Pathway			
ECM-receptor interaction	5	2.30E-04	ITGB5;AGRN;LAMB3;HMMR;ITGA3
Protein processing in endoplasmic reticulum	6	8.67E-04	DDOST;CKAP4;HSP90B1;PDIA6;STT3A;HSPA5
Focal adhesion	6	0.002271064	ITGB5;ZYX;ACTB;LAMB3;ITGA3;ACTN4
HIF-1 signaling pathway	4	0.004778962	ENO1;PGK1;EGLN3;SLC2A1
Lysine degradation	3	0.007590955	PLOD3;PLOD2;PLOD1

Arrhythmogenic right ventricular cardiomyopathy (ARVC)	3	0.013085 039	ITGB5;ACTB;ITGA3
Regulation of actin cytoskeleton	5	0.014959 261	ITGB5;ACTB;DIAPH3;ITGA3;ACTN4
Hypertrophic cardiomyopathy (HCM)	3	0.019126 69	ITGB5;ACTB;ITGA3
Dilated cardiomyopathy (DCM)	3	0.023653 108	ITGB5;ACTB;ITGA3
Pathways in cancer	8	0.025233 077	RALA;EGLN3;TFG;SLC2A1;LAMB3;HSP90B1;ITGA3;PML

Supplementary Table 4. significantly rich summary of GO annotation for PLADS negatively related gene related networks

Description	Gene Count	Adjusted P-Value	Enriched Genes
Biological Process			
cellular amino acid catabolic process	9	1.37242E-06	AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8 /GLS2/ASRGL1
alpha-amino acid metabolic process	11	3.66603E-06	AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8 /GLS2/SEPSECS/ASRGL1/MTHFD2L
alpha-amino acid catabolic process	8	3.78617E-06	AMT/AUH/IVD/OTC/PAH/ACAD8/GLS2/ASR GL1
organic acid catabolic process	12	4.87553E-06	ACACB/AMT/AUH/IVD/OTC/PAH/ALDH5A1 /ACAD8/GLS2/ASRGL1/MCEE/NUDT7
carboxylic acid catabolic process	12	4.87553E-06	ACACB/AMT/AUH/IVD/OTC/PAH/ALDH5A1 /ACAD8/GLS2/ASRGL1/MCEE/NUDT7

cellular amino acid metabolic process	12	8.17026E-05	AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/SEPSECS/QRSL1/ASRGL1/MTHFD2L
fatty acid metabolic process	12	0.000125275	ACACB/AUH/CYP2C8/EPHX2/IVD/ACSM3/ALDH5A1/ACSL6/MCEE/NUDT7/ZADH2/CYP4V2
small molecule catabolic process	13	0.000131344	ACACB/AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/ASRGL1/CDADC1/MCEE/NUDT7
positive regulation of ion transport	10	0.000140654	ATP1B2/CACNB2/CAPN3/CHRN2/KCNJ11/MLLT6/NPPA/RAMP3/ATP8A1/AMIGO1
monocarboxylic acid catabolic process	7	0.000148807	ACACB/AUH/IVD/ALDH5A1/ASRGL1/MCEE/NUDT7
positive regulation of cation transmembrane transport	7	0.000254518	ATP1B2/CACNB2/CAPN3/KCNJ11/NPPA/RAMP3/AMIGO1
regulation of skeletal muscle adaptation	3	0.000391621	CAMK2B/GTF2IRD2/GTF2IRD2B
positive regulation of ion transmembrane transport	7	0.000413753	ATP1B2/CACNB2/CAPN3/KCNJ11/NPPA/RAMP3/AMIGO1
branched-chain amino acid metabolic process	3	0.000746814	AUH/IVD/ACAD8
branched-chain amino acid catabolic process	3	0.000746814	AUH/IVD/ACAD8

Cellular Component

Rough endoplasmic reticulum membrane	3	0.002471542	PLOD3, PLOD2, PLOD1
mitochondrial matrix	10	0.00439838	ACAD8, MCEE, ALDH5A1, AUH, ACSM3, GLS2, IVD, MTHFD2L, AMT, OTC
neuronal cell body membrane	3	0.012680811	SLC4A8, AMIGO1, FLRT1
intracellular	22	0.016969865	ZNF540, ZNF782, RAMP3, ZNF44, MYRIP, CLU, ZNF33B, ZNF33A, RDH12, RAB37, ZNF506, SEC14L5, ZNF30, DCX, TRIM68, CAPN3, RHOU, ZNF557, ZNF589, ZNF763, ZNF620, ZNF596
myofibril	3	0.029431117	TMOD1, ANKRD23, CAPN3
Molecular Function			
alkali metal ion binding	3	0.000429708	ATP1A2/CAPN3/KCNJ11
ATPase activity, coupled to transmembrane movement of substances	6	0.000802459	ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P
ATPase activity, coupled to movement of substances	6	0.000802459	ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P
P-P-bond-hydrolysis-driven transmembrane transporter activity	6	0.001138934	ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P

hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	6	0.001138934	ADARB2/GLS2/QRSL1/ASRGL1/CDADC1/MTHFD2L
primary active transmembrane transporter activity	6	0.001237839	ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P
KEGG Pathway			
Herpes simplex virus 1 infection	13	0.00067523	ZNF33A/ZNF33B/ZNF589/ZNF44/ZNF557/ZNF30/ZNF799/ZNF782/ZNF540/ZNF596/ZNF620/ZNF763/ZNF506
Valine, leucine and isoleucine degradation	4	0.001029969	AUH/IVD/ACAD8/MCEE
Proximal tubule bicarbonate reclamation	3	0.00123878	ATP1A2/ATP1B2/GLS2
Aldosterone synthesis and secretion	5	0.002221761	ATP1A2/ATP1B2/CAMK2B/KCNK3/NPPA