

Table SV. GO and KEGG analysis of the co-expressed PCGs with predicting PCGs and lncRNAs by clusterProfiler.

ONTOLOGY	ID	Description	GeneRatio	P-value	p adjust	q value	Count	SYMBOL_ID
KEGG	hsa03040	Spliceosome	22/336	< 0.001	0.00001	0.00001	22	BCAS2, DDX42, DDX46, DHX15, HNRNPK, LSM5, MAGOH, PLRG1, PPIE, PRPF18, PRPF38A, PRPF8, RBM8A, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6
CC	GO:0098798	Mitochondrial protein complex	36/947	< 0.001	0.00002	0.00002	36	APOO, BCKDHB, GRPEL1, IMMP1L, MRPL27, MRPL30, MRPL35, MRPL49, MRPL50, MRPL57, MRPS14, MRPS21, MRPS31, MRPS33, MTERF4, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, SMDT1, SPG7, TIMM13, TIMM21, TIMM22, UQCC3, UQCRFS1, UQCRH, UQCRHL, COX7C
CC	GO:0031301	Integral component of organelle membrane	28/947	< 0.001	0.00002	0.00002	28	CHST12, LEMD2, TVP23C, APOO, ATP6V1G2, B4GAT1, CASD1, FUNDC2, ITM2B, L2HGDH, MFF, MPC2, PEX10, PEX11B, PEX16, SCO1, SLC22A17, SLC25A4, SLC35B1, SMDT1, SPG7, STEAP2, SV2A, SYP, SYT4, TVP23B, UBIAD1, UQCC3
CC	GO:0005684	U2-type spliceosomal complex	15/947	< 0.001	0.00004	0.00004	15	BCAS2, CWC22, DHX15, GCFC2, LUC7L3, PLRG1, PPIE, PRPF18, PRPF8, SF3A1, SF3B2, SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0005681	Spliceosomal complex	28/947	< 0.001	0.00005	0.00005	28	BCAS2, CWC22, DDX25, DHX15, GCFC2, HNRNPH3, HNRNPK, HNRNPR, IK, LSM5, LUC7L3, MAGOH, PLRG1, PPIE, PRPF18, PRPF38A, PRPF8, RBM8A, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SYNCRIP, WBP4
CC	GO:0031300	Intrinsic component of organelle membrane	28/947	< 0.001	0.00005	0.00005	28	CHST12, LEMD2, TVP23C, APOO, ATP6V1G2, B4GAT1, CASD1, FUNDC2, ITM2B, L2HGDH, MFF, MPC2, PEX10, PEX11B, PEX16, SCO1, SLC22A17, SLC25A4, SLC35B1, SMDT1, SPG7, STEAP2, SV2A, SYP, SYT4, TVP23B, UBIAD1, UQCC3
CC	GO:0098800	Inner mitochondrial membrane protein complex	23/947	< 0.001	0.00005	0.00005	23	APOO, GRPEL1, IMMP1L, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, SMDT1, SPG7, TIMM21, TIMM22, UQCC3, UQCRFS1, UQCRH, UQCRHL, COX7C
CC	GO:0071013	Catalytic step 2 spliceosome	19/947	< 0.001	0.00005	0.00005	19	BCAS2, CWC22, DDX25, HNRNPK, HNRNPR, MAGOH, PLRG1, PPIE, PRPF8, RBM8A, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SYNCRIP
CC	GO:0044455	Mitochondrial membrane part	30/947	< 0.001	0.00006	0.00005	30	APOO, COX7A2, FUNDC2, GRPEL1, IMMP1L, L2HGDH, MFF, MPC2, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, SCO1, SLC25A4, SMDT1, SPG7, TIMM21, TIMM22, UQCC3, UQCRFS1, UQCRH, UQCRHL, COX7C
BP	GO:0060271	Cilium assembly	45/902	< 0.001	0.00009	0.00009	45	ARL3, ATMIN, ATXN10, B9D1, BBS1, BBS2, BBS4, CELSR3, CEP126, CEP63, CEP70, CEP72, CEP97, CFAP20, CYLD, DNAH14, DYNC2H1, FAM161A, IFT43, IFT46, IFT74, IFT88, IQCB1, KIF3A, NME5, NPHP1, PIBF1, PTPN23, RFX2, RFX3, TCTEX1D2, TCTN1, TCTN2, TMEM17, TMEM80, TRIP11, TTBK2, TTC26, TTC30A, TTC30B, UNC119B, WDR34, WDR5B, WRAP73, YWHAE
BP	GO:0006397	mRNA processing	55/902	< 0.001	0.00009	0.00009	55	GEMIN8, ALKBH5, BCAS2, CASC3, CHTOP, CMTR1, CPEB1, CSTF3, CWC22, DDX1, DDX42, DDX46, DDX47, DHX15, DHX9, ELAVL1, GCFC2, HNRNPA0, HNRNPD, HNRNPH3, HNRNPK, HNRNPR, IK, KIN, LSM5, LUC7L3, MAGOH, MBNL2, NOVA1, PHRF1, PLRG1, POLR2K, PPIE, PRPF18, PRPF38A, PRPF8, RBM39, RBM4B, RBM8A, RSR1, SF3A1, SF3B2, SLTM, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, SYNCRIP, TARDBP, WBP4, ZC3H11A, ZRANB2
BP	GO:0000377	RNA splicing, via transesterification reactions with	41/902	< 0.001	0.00009	0.00009	41	GEMIN8, BCAS2, CASC3, CSTF3, CWC22, DDX1, DDX42, DDX46, DHX15, DHX9, ELAVL1, GCFC2, HNRNPA0, HNRNPD, HNRNPH3, HNRNPK, HNRNPR, LSM5, LUC7L3, MAGOH, MBNL2, NOVA1, PLRG1, POLR2K, PPIE, PRPF18, PRPF38A, PRPF8, RBM8A, RSR1, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, SYNCRIP, WBP4

		bulged adenosine as nucleophile						
BP	GO:0000398	mRNA splicing, via spliceosome	41/902	< 0.001	0.00009	0.00009	41	GEMIN8, BCAS2, CASC3, CSTF3, CWC22, DDX1, DDX42, DDX46, DHX15, DHX9, ELAVL1, GCFC2, HNRNPA0, HNRNPD, HNRNPH3, HNRNPK, HNRNPR, LSM5, LUC7L3, MAGOH, MBNL2, NOVA1, PLRG1, POLR2K, PPIE, PRPF18, PRPF38A, PRPF8, RBM8A, RSC1, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, SYNCRIP, WBP4
BP	GO:0044782	Cilium organization	45/902	< 0.001	0.00009	0.00009	45	ARL3, ATMIN, ATXN10, B9D1, BBS1, BBS2, BBS4, CELSR3, CEP126, CEP63, CEP70, CEP72, CEP97, CFAP20, CYLD, DNAH14, DYNC2H1, FAM161A, IFT43, IFT46, IFT74, IFT88, IQCB1, KIF3A, NME5, NPHP1, PIBF1, PTPN23, RFX2, RFX3, TCTEX1D2, TCTN1, TCTN2, TMEM17, TMEM80, TRIP11, TTBK2, TTC26, TTC30A, TTC30B, UNC119B, WDR34, WDR5B, WRAP73, YWHAH
BP	GO:0000375	RNA splicing, via transesterification reactions	41/902	< 0.001	0.00009	0.00009	41	GEMIN8, BCAS2, CASC3, CSTF3, CWC22, DDX1, DDX42, DDX46, DHX15, DHX9, ELAVL1, GCFC2, HNRNPA0, HNRNPD, HNRNPH3, HNRNPK, HNRNPR, LSM5, LUC7L3, MAGOH, MBNL2, NOVA1, PLRG1, POLR2K, PPIE, PRPF18, PRPF38A, PRPF8, RBM8A, RSC1, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, SYNCRIP, WBP4
BP	GO:0008380	RNA splicing	49/902	< 0.001	0.00009	0.00009	49	GEMIN8, BCAS2, CASC3, CSTF3, CWC22, DDX1, DDX25, DDX42, DDX46, DDX47, DHX15, DHX9, ELAVL1, GCFC2, HNRNPA0, HNRNPD, HNRNPH3, HNRNPK, HNRNPR, IK, LSM5, LUC7L3, MAGOH, MBNL2, MTERF4, NOVA1, PLRG1, POLR2K, PPIE, PRPF18, PRPF38A, PRPF8, RBM39, RBM4B, RBM8A, RSC1, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, SYNCRIP, TARDBP, WBP4, ZRANB2
BP	GO:0031503	Protein-containing complex localization	33/902	< 0.001	0.00019	0.00018	33	ALKBH5, ARL3, CASC3, CEP72, CHTOP, DDX25, DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, KIF5A, MAGOH, NSG1, NUP133, NUP153, NUP205, NUP35, POM121C, RBM8A, SNAP25, SNAP47, SRSF1, SRSF6, TCTEX1D2, TERF1, TRIP11, TTC26, TTC30A, TTC30B, WDR34, ZC3H11A
BP	GO:0033108	Mitochondrial respiratory chain complex assembly	19/902	< 0.001	0.00021	0.00021	19	COA5, COX14, COX20, IMM1P, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFAF3, NDUFAF7, NDUFB1, NDUFB6, NDUFC2, PET117, SCO1, TIMM21, UQC3
CC	GO:0005746	Mitochondrial respiratory chain	17/947	< 0.001	0.00022	0.00019	17	COX7A2, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, UQC3, UQCRFS1, UQCRH, UQCRHL, COX7C
CC	GO:0044441	Ciliary part	45/947	< 0.001	0.00022	0.00019	45	ARFGEF2, ARL3, ATP8A2, B9D1, BBS1, BBS2, BBS4, C8orf37, CEP126, CFAP20, CYLD, DYNC2H1, FAM161A, GNAQ, GNB1, GSTM3, IFT43, IFT46, IFT74, IFT88, IQCB1, IQCE, KIF3A, KIF5A, MAATS1, MOK, NAPEPLD, NEK4, NPHP1, PACRG, PIK3R4, PTPN23, SPA17, TCTEX1D2, TCTN1, TCTN2, TMEM17, TMEM80, TTBK2, TTC26, TTC30B, UNC119B, WDR34, WDR5B, WRAP73
CC	GO:0098803	Respiratory chain complex	16/947	< 0.001	0.00026	0.00022	16	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, UQC3, UQCRFS1, UQCRH, UQCRHL, COX7C
BP	GO:0042073	Intraciliary transport	13/902	< 0.001	0.00039	0.00038	13	ARL3, DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, TCTEX1D2, TRIP11, TTC26, TTC30A, TTC30B, WDR34
CC	GO:0071007	U2-type catalytic step 2 spliceosome	9/947	0.00001	0.00042	0.00036	9	BCAS2, CWC22, PLRG1, PPIE, PRPF8, SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0031461	Cullin-RING ubiquitin ligase complex	25/947	0.00001	0.00043	0.00037	25	ANAPC10, ANAPC16, ANAPC5, CUL1, DCAF13, DCAF16, DCAF8, DET1, FBXW11, FBXW4, FZR1, IPP, KBTBD3, KBTBD4, KBTBD6, KBTBD7, KLHL11, KLHL22, KLHL26, KLHL42, KLHL8, PDCD6, PLRG1, USP47, ZSWIM5
CC	GO:0070469	Respiratory chain	17/947	0.00001	0.00043	0.00037	17	COX7A2, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, UQC3, UQCRFS1, UQCRH, UQCRHL, COX7C
CC	GO:0016607	Nuclear speck	40/947	0.00001	0.00043	0.00037	40	CHD5, ACADM, ALKBH5, APBB1, BCAS2, C12orf57, CASC3, CHTOP, CWC22, DDX42, DDX46, DHX15, EP400, FAM76B, GATAD2B, IK, LMNA, LUC7L3, MAGOH, MOCS2, NDUFB1, PLRG1, POLI,

								PPIE, PRKAA2, PRPF18, PRPF8, PUM1, RBM39, RBM8A, RFXAP, RSRC1, SF3A1, SF3B2, SPRTN, SRSF1, SRSF6, TRIP11, VPS72, WBP4
CC	GO:0035869	Ciliary transition zone	13/947	0.00001	0.00049	0.00042	13	ARL3, B9D1, BBS4, FAM161A, IQCB1, NEK4, NPHP1, TCTN1, TCTN2, TMEM17, TMEM80, TTBK2, UNC119B
CC	GO:0000151	Ubiquitin ligase complex	34/947	0.00002	0.00074	0.00063	34	ANAPC10, ANAPC16, ANAPC5, ASB1, BMI1, CBX7, CUL1, DCAF13, DCAF16, DCAF8, DET1, DZIP3, FBXO21, FBXO8, FBXW11, FBXW4, FZR1, IPP, KBTBD3, KBTBD4, KBTBD6, KBTBD7, KLHL11, KLHL22, KLHL26, KLHL42, KLHL8, MED7, MPHOSPH8, PDCD6, PLRG1, USP33, USP47, ZSWIM5
BP	GO:0010970	Transport along microtubule	22/902	0.00000	0.00125	0.00124	22	AP3B2, ARL3, DST, DYNC1H1, DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, KIF5A, PRKCZ, SPG7, SYBU, TCTEX1D2, TERF2, TRIP11, TTC26, TTC30A, TTC30B, WDR34, BICD1
BP	GO:0099111	Microtubule-based transport	22/902	0.00000	0.00125	0.00124	22	AP3B2, ARL3, DST, DYNC1H1, DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, KIF5A, PRKCZ, SPG7, SYBU, TCTEX1D2, TERF2, TRIP11, TTC26, TTC30A, TTC30B, WDR34, BICD1
CC	GO:1990204	Oxidoreductase complex	17/947	0.00005	0.00155	0.00134	17	BCKDHB, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, OGDHL, PARK7, PMPCB, UQC33, UQCRFS1, UQCRH, UQCRHL
CC	GO:0097542	Ciliary tip	10/947	0.00005	0.00170	0.00146	10	CYLD, DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, TTC26, TTC30B, WDR34
CC	GO:0031965	Nuclear membrane	32/947	0.00008	0.00225	0.00194	32	LEMD2, AHCTF1, CASC3, CEP70, CERS5, DNAJB14, DPY19L2, DUX4, FAM169A, FZR1, GNAQ, GTPBP4, HAX1, KLHDC2, LMNA, LPIN1, NUP133, NUP153, NUP205, NUP35, PLRG1, POM121C, PRPF38A, RANBP6, RIF1, SCRNI, SEPHS1, SYNE1, TNKS, TOR1AIP1, TSGA10, SLC30A1
CC	GO:0036064	Ciliary basal body	16/947	0.00013	0.00370	0.00319	16	B9D1, BBS1, BBS2, BBS4, CFAP20, CYLD, FAM161A, IFT46, IFT88, NEK4, PTPN23, TTBK2, TTC26, WDR34, WDR5B, WRAP73
CC	GO:0005813	Centrosome	44/947	0.00017	0.00464	0.00400	44	ARL3, B9D1, BBS1, BBS4, BCAS2, BRSK2, CEP126, CEP350, CEP44, CEP63, CEP70, CEP72, CEP97, CETN3, CRMP1, CYLD, DCAF13, DCTN4, DCTN6, DHX9, ERCC6L2, FAM161A, FBXW11, IFT46, IFT74, IQCB1, KIF3A, KIZ, KLHL22, MPLKIP, PHAX, PIBF1, PPP1R12A, RIC8B, SASS6, SMAD4, TCTEX1D2, TNKS, TTC26, USP33, UVRAG, WRAP73, ZNF12, BICD1
CC	GO:0005747	Mitochondrial respiratory chain complex I	10/947	0.00020	0.00482	0.00415	10	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7
CC	GO:0030964	NADH dehydrogenase complex	10/947	0.00020	0.00482	0.00415	10	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7
CC	GO:0045271	Respiratory chain complex I	10/947	0.00020	0.00482	0.00415	10	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7
CC	GO:0005635	Nuclear envelope	41/947	0.00026	0.00596	0.00513	41	FAM156A, LEMD2, AHCTF1, CASC3, CEP70, CERS5, CSE1L, DNAJB14, DPY19L2, DST, DUX4, FAM169A, FZR1, GNAQ, GNAZ, GTPBP4, HAX1, KLHDC2, LMNA, LPIN1, NUP133, NUP153, NUP205, NUP35, PIK3R4, PLRG1, POM121C, PRKCZ, PRPF38A, RAB40B, RANBP6, RIF1, RNF180, SCRNI, SEPHS1, SYNE1, TERF2IP, TNKS, TOR1AIP1, TSGA10, SLC30A1
CC	GO:0097525	Spliceosomal snRNP complex	11/947	0.00029	0.00596	0.00513	11	LSM5, LUC7L3, PRPF18, PRPF8, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0030173	Integral component of Golgi membrane	9/947	0.00030	0.00596	0.00513	9	CHST12, TVP23C, B4GAT1, CASD1, SLC35B1, STEAP2, SYT4, TVP23B, UBIAD1
CC	GO:0000782	Telomere cap complex	5/947	0.00030	0.00596	0.00513	5	ACD, POT1, TERF1, TERF2, TERF2IP
CC	GO:0000783	Nuclear telomere cap complex	5/947	0.00030	0.00596	0.00513	5	ACD, POT1, TERF1, TERF2, TERF2IP
CC	GO:0030992	Intraciliary transport particle	6/947	0.00035	0.00667	0.00574	6	IFT46, IFT74, IFT88, TTC26, TTC30A, TTC30B

		B						
BP	GO:0042775	Mitochondrial ATP synthesis coupled electron transport	16/902	0.00002	0.00715	0.00708	16	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, UQCC3, UQCRFS1, UQCRH, UQCRHL, COX7C
BP	GO:0035735	Intraciliary transport involved in cilium assembly	10/902	0.00002	0.00715	0.00708	10	DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, TRIP11, TTC26, TTC30B, WDR34
BP	GO:0007018	Microtubule-based movement	34/902	0.00002	0.00715	0.00708	34	AP3B2, ARL3, BBS2, BBS4, CFAP20, DNAH14, DNAL4, DST, DYNC1I1, DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, KIF5A, KLC2, MAATS1, MYH9, MYO9B, NME5, PRKCZ, RFX3, SPA17, SPG7, SYBU, TCTEX1D2, TERF2, TRIP11, TTC26, TTC30A, TTC30B, WDR34, BICD1
BP	GO:0042773	ATP synthesis coupled electron transport	16/902	0.00003	0.00719	0.00711	16	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, UQCC3, UQCRFS1, UQCRH, UQCRHL, COX7C
CC	GO:0005750	Mitochondrial respiratory chain complex III	5/947	0.00045	0.00808	0.00696	5	PMPCB, UQCC3, UQCRFS1, UQCRH, UQCRHL
CC	GO:0045275	respiratory chain complex III	5/947	0.00045	0.00808	0.00696	5	PMPCB, UQCC3, UQCRFS1, UQCRH, UQCRHL
KEGG	hsa05016	Huntington disease	21/336	0.00007	0.00816	0.00804	21	COX7A2, DCTN4, DNAH14, DNAL4, GNAQ, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PLCB4, POLR2K, SLC25A4, UQCRFS1, UQCRH, UQCRHL, COX7C
KEGG	hsa05010	Alzheimer's disease	19/336	0.00012	0.00816	0.00804	19	APBB1, CACNA1D, COX7A2, GNAQ, NAE1, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PLCB4, UQCRFS1, UQCRH, UQCRHL, COX7C
KEGG	hsa04714	Thermogenesis	23/336	0.00012	0.00816	0.00804	23	ACTL6B, COA5, COX14, COX20, COX7A2, LIPE, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFAF3, NDUFAF7, NDUFB1, NDUFB6, NDUFC2, PRKAA2, RPS6KA6, UQCRFS1, UQCRH, UQCRHL, COX7C
KEGG	hsa04723	Retrograde endocannabinoid signaling	17/336	0.00018	0.00925	0.00910	17	CACNA1D, GABRB3, GABRG2, GNAQ, GNB1, GRIA2, NAPEPLD, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PLCB4
BP	GO:0006353	DNA-templated transcription, termination	17/902	0.00004	0.00930	0.00920	17	CASC3, CHTOP, CSTF3, DHX9, MAGOH, MTERF2, POLR1B, POLR1C, POLR2K, RBM8A, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, TTF1, ZC3H11A
BP	GO:0030705	Cytoskeleton-dependent intracellular transport	22/902	0.00004	0.00935	0.00925	22	AP3B2, ARL3, DST, DYNC1I1, DYNC2H1, IFT43, IFT46, IFT74, IFT88, KIF3A, KIF5A, PRKCZ, SPG7, SYBU, TCTEX1D2, TERF2, TRIP11, TTC26, TTC30A, TTC30B, WDR34, BICD1
KEGG	hsa05168	Herpes simplex virus 1 infection	38/336	0.00023	0.01033	0.01017	38	ZNF133, MAP3K7, RBAK, SRSF1, SRSF6, ZFP37, ZNF112, ZNF12, ZNF132, ZNF136, ZNF14, ZNF181, ZNF235, ZNF248, ZNF25, ZNF253, ZNF286A, ZNF304, ZNF334, ZNF33B, ZNF416, ZNF484, ZNF510, ZNF540, ZNF543, ZNF550, ZNF567, ZNF568, ZNF569, ZNF582, ZNF595, ZNF611, ZNF614, ZNF615, ZNF658, ZNF709, ZNF791, ZNF91
CC	GO:0097526	Spliceosomal tri-snRNP complex	7/947	0.00061	0.01043	0.00898	7	LSM5, PRPF18, PRPF8, SNRNP200, SNRPD1, SNRPD3, SNRPE
CC	GO:0005868	Cytoplasmic dynein complex	6/947	0.00062	0.01043	0.00898	6	DCTN4, DYNC1I1, DYNC2H1, SNX4, TCTEX1D2, WDR34

KEGG	hsa03060	Protein export	6/336	0.00031	0.01114	0.01097	6	IMMP1L, SEC61A2, SEC63, SRP68, SRP72, SRP9
KEGG	hsa05012	Parkinson's disease	16/336	0.00034	0.01114	0.01097	16	COX7A2, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, SLC25A4, UQCERS1, UQCRH, UQCRHL, COX7C
CC	GO:0031228	Intrinsic component of Golgi membrane	9/947	0.00070	0.01147	0.00987	9	CHST12, TVP23C, B4GAT1, CASD1, SLC35B1, STEAP2, SYT4, TVP23B, UBIAD1
CC	GO:0030532	Small nuclear ribonucleoprotein complex	11/947	0.00074	0.01147	0.00987	11	LSM5, LUC7L3, PRPF18, PRPF8, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0120114	Sm-like protein family complex	12/947	0.00075	0.01147	0.00987	12	GEMIN8, LSM5, LUC7L3, PRPF18, PRPF8, SF3A1, SF3B2, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0030990	Intraciliary transport particle	7/947	0.00075	0.01147	0.00987	7	IFT43, IFT46, IFT74, IFT88, TTC26, TTC30A, TTC30B
CC	GO:0005682	U5 snRNP	6/947	0.00080	0.01182	0.01018	6	PRPF18, PRPF8, SNRNP200, SNRPD1, SNRPD3, SNRPE
BP	GO:0045333	Cellular respiration	23/902	0.00006	0.01386	0.01371	23	COX20, FASTKD2, MDH1B, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, OGDHL, PARK7, PMPCB, SIRT3, SUCLA2, SUCLG1, UQCC3, UQCERS1, UQCRH, UQCRHL, COX7C
KEGG	hsa00190	Oxidative phosphorylation	15/336	0.00051	0.01495	0.01472	15	ATP6V1G2, COX7A2, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, UQCERS1, UQCRH, UQCRHL, COX7C
BP	GO:0071826	Ribonucleoprotein complex subunit organization	26/902	0.00008	0.01546	0.01530	26	GEMIN8, BRIX1, CIRBP, DDX1, DHX30, DHX9, FASTKD2, GCFC2, HSP90AB1, LUC7L3, MRRF, MTERF4, PRPF18, PRPF8, RPF1, SBDS, SF3A1, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, TAF9, BICD1
BP	GO:0022618	Ribonucleoprotein complex assembly	25/902	0.00008	0.01546	0.01530	25	GEMIN8, BRIX1, CIRBP, DDX1, DHX30, DHX9, FASTKD2, GCFC2, HSP90AB1, LUC7L3, MTERF4, PRPF18, PRPF8, RPF1, SBDS, SF3A1, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, TAF9, BICD1
BP	GO:0010257	NADH dehydrogenase complex assembly	12/902	0.00008	0.01546	0.01530	12	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFAF3, NDUFAF7, NDUFB1, NDUFB6, NDUFC2, TIMM21
BP	GO:0032981	Mitochondrial respiratory chain complex I assembly	12/902	0.00008	0.01546	0.01530	12	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFAF3, NDUFAF7, NDUFB1, NDUFB6, NDUFC2, TIMM21
CC	GO:0071011	Precatalytic spliceosome	7/947	0.00112	0.01589	0.01368	7	BCAS2, PLRG1, PRPF38A, SF3B2, SNRPD1, SNRPD3, SNRPE
CC	GO:0000313	Organellar ribosome	12/947	0.00115	0.01589	0.01368	12	MRPL27, MRPL30, MRPL35, MRPL49, MRPL50, MRPL57, MRPS14, MRPS21, MRPS31, MRPS33, MTERF4, NDUFA7
CC	GO:0005761	Mitochondrial ribosome	12/947	0.00115	0.01589	0.01368	12	MRPL27, MRPL30, MRPL35, MRPL49, MRPL50, MRPL57, MRPS14, MRPS21, MRPS31, MRPS33, MTERF4, NDUFA7
CC	GO:0005666	DNA-directed RNA polymerase III complex	5/947	0.00122	0.01650	0.01421	5	CRCP, POLR1C, POLR2K, POLR3B, POLR3E
CC	GO:0034719	SMN-Sm protein complex	5/947	0.00163	0.02142	0.01844	5	GEMIN8, SNRPD1, SNRPD3, SNRPE, SNRPF

KEGG	hsa00280	Valine, leucine and isoleucine degradation	8/336	0.00085	0.02240	0.02206	8	AACS, ABAT, ACADM, ALDH9A1, AUH, BCKDHB, HMGCLL1, MUT
CC	GO:0005689	U12-type spliceosomal complex	6/947	0.00197	0.02535	0.02183	6	DHX15, SF3B2, SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0005687	U4 snRNP	4/947	0.00233	0.02883	0.02482	4	SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0034709	Methylosome	4/947	0.00233	0.02883	0.02482	4	SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0032592	Integral component of mitochondrial membrane	10/947	0.00265	0.03210	0.02764	10	APOO, FUNDC2, L2HGDH, MFF, MPC2, SCO1, SLC25A4, SMDT1, SPG7, UQCC3
BP	GO:0022904	Respiratory electron transport chain	16/902	0.00020	0.03370	0.03335	16	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7, PMPCB, UQCC3, UQCRFS1, UQCRH, UQCRHL, COX7C
BP	GO:0043966	Histone H3 acetylation	11/902	0.00020	0.03370	0.03335	11	BRPF3, ELP3, KAT6B, MAP3K7, NAP1L2, SMAD4, TADA1, TADA3, TAF9, TAF9B, ZNF451
BP	GO:0022613	Ribonucleoprotein complex biogenesis	43/902	0.00020	0.03370	0.03335	43	GEMIN8, AAMP, BRIX1, CIRBP, DCAF13, DDX1, DDX47, DHX30, DHX9, DIS3L2, EBNA1BP2, EXOSC9, FASTKD2, GCFC2, GNL1, GTPBP4, HSP90AB1, KRR1, LUC7L3, METTL15, MTERF4, NGDN, NOL11, PRPF18, PRPF8, RPF1, RPL34, RPL7A, SBDS, SF3A1, SNRNP200, SNRPD1, SNRPD3, SNRPE, SNRPF, SRSF1, SRSF6, TAF9, TRMT112, UTP14C, YAE1D1, ZNF658, BICD1
CC	GO:0098573	Intrinsic component of mitochondrial membrane	10/947	0.00295	0.03470	0.02987	10	APOO, FUNDC2, L2HGDH, MFF, MPC2, SCO1, SLC25A4, SMDT1, SPG7, UQCC3
CC	GO:0030286	Dynein complex	8/947	0.00298	0.03470	0.02987	8	DCTN4, DNAH14, DNAL4, DYNC1H1, DYNC2H1, SNX4, TCTEX1D2, WDR34
CC	GO:0031304	Intrinsic component of mitochondrial inner membrane	7/947	0.00310	0.03471	0.02988	7	APOO, L2HGDH, MPC2, SCO1, SMDT1, SPG7, UQCC3
CC	GO:0031305	Integral component of mitochondrial inner membrane	7/947	0.00310	0.03471	0.02988	7	APOO, L2HGDH, MPC2, SCO1, SMDT1, SPG7, UQCC3
BP	GO:1905515	Non-motile cilium assembly	10/902	0.00022	0.03473	0.03437	10	ATMIN, BBS1, BBS2, BBS4, CEP126, IFT74, PIBF1, TMEM17, TMEM80, WRAP73
CC	GO:0036038	MKS complex	4/947	0.00324	0.03554	0.03060	4	B9D1, TCTN1, TCTN2, TMEM17
CC	GO:0005685	U1 snRNP	5/947	0.00340	0.03574	0.03077	5	LUC7L3, SNRPD1, SNRPD3, SNRPE, SNRPF
CC	GO:0005686	U2 snRNP	5/947	0.00340	0.03574	0.03077	5	SF3A1, SF3B2, SNRPD1, SNRPD3, SNRPE
CC	GO:0005875	Microtubule associated complex	16/947	0.00344	0.03574	0.03077	16	APPBP2, DCTN4, DCTN6, DNAH14, DNAL4, DYNC1H1, DYNC2H1, KIF3A, KIF5A, KLC2, MAP2, RANBP9, SNX4, TCTEX1D2, WDR34, YWHAE

BP	GO:0006120	Mitochondrial electron transport, NADH to ubiquinone	10/902	0.00026	0.03823	0.03783	10	NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PARK7
BP	GO:0065002	Intracellular protein transmembrane transport	10/902	0.00026	0.03823	0.03783	10	GRPEL1, NDUFA13, PEX10, PEX16, SEC63, SRP72, SRP9, TIMM13, TIMM21, TIMM22
KEGG	hsa04932	Non-alcoholic fatty liver disease (NAFLD)	15/336	0.00166	0.03975	0.03915	15	COX7A2, NDUFA12, NDUFA13, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFB1, NDUFB6, NDUFC2, PRKAA2, UQCRFS1, UQCRH, UQCRHL, COX7C
CC	GO:0005819	Spindle	28/947	0.00422	0.04320	0.03719	28	ARL3, CBX1, CENPV, CEP104, CEP350, CEP44, CEP63, CRMP1, CYLD, DCTN4, DYNC111, FAM161A, IK, IQCB1, KIF3A, KLHL22, KLHL42, LATS1, MAP9, MYH9, RIF1, SBDS, SKA2, TADA3, TCTEX1D2, TERF1, TNKS, MTUS1

PCGs, protein-coding genes; lncRNAs, long non-coding RNAs.