

Supp. Table 2. GO Full terms for coevolving genes in the MMM network #5 from Supp. Table 1.

GO Annotation	number of genes ^(a)	q-value ^(b)	#pairs ^(c)	max# pairs ^(d)	#pairs/m ax ^(e)	Genes
chaperonin-containing T-complex	4	1.60E-03	6	6	1.000	CCT2 TCP1 CCT7 CCT5
glycine hydroxymethyltransferase activity	6	1.38E-03	6	15	0.400	SHMT1 ALDH1L2 GARS SHMT2 ATIC GART
COP1 coated vesicle membrane	7	6.29E-04	8	21	0.381	COPB1 COPG2 COPZ1 COPA COPB2 ARCN1 AP4E1
DNA synthesis during DNA repair	6	1.90E-04	5	15	0.333	RFC3 CDC2 POLE POLA1 WRNIP1 POLD1
pseudouridylyl synthase activity	5	6.32E-03	3	10	0.300	PUS7 RPUSD2 PUS1 PUSL1 PUS3
COP1-coated vesicle	8	2.86E-04	8	28	0.286	COPB1 COPG2 COPZ1 COPA COPB2 AP3B2 ARCN1 AP4E1 DARS YARS2 LARS GARS EARS2 AARS NARS2 QARS LARS2 FARSB ZNFX1 NARS DARS2 EPRS RARS RARS2 SARS SARS2 AARSD1 WARS2 HARS
ligase activity, forming aminoacyl-tRNA and related compounds	35	3.39E-21	163	595	0.274	ACO2 SUCLA2 MDH1 MDH2 DLAT SUCLG1 CS ACO1 IDH2 PDHA1 SDHA PDHB SDHB IDH3B NNT SUCLG2 IDH1 IDH3A FH HMGS1 DLST DARS SCYE1 YARS2 LARS GARS EARS2 AARS NARS2 QARS LARS2 FARSB ZNFX1 NARS DARS2 EPRS RARS FARSA FARS2 TARS MARS IARS WARS MARS2 KARS IARS2 PARS2 YARS VARS CARS EIF2AK4 RARS2 SARS SARS2 AARSD1 WARS2 HARS
acetyl-CoA metabolic process	21	3.46E-12	56	210	0.267	ACO2 SUCLA2 MDH1 MDH2 DLAT SUCLG1 CS ACO1 IDH2 PDHA1 SDHA PDHB SDHB IDH3B NNT SUCLG2 IDH1 IDH3A FH HMGS1 DLST DARS SCYE1 YARS2 LARS GARS EARS2 AARS NARS2 QARS LARS2 FARSB ZNFX1 NARS DARS2 EPRS RARS FARSA FARS2 TARS MARS IARS WARS MARS2 KARS IARS2 PARS2 YARS VARS CARS EIF2AK4 RARS2 SARS SARS2 AARSD1 WARS2 HARS
amino acid activation	36	1.70E-22	164	630	0.260	ACO2 SUCLA2 MDH1 MDH2 SUCLG1 CS ACO1 IDH2 SDHA PDHB SDHB IDH3B NNT SUCLG2 IDH1 IDH3A FH DLST DARS SCYE1 YARS2 LARS GARS EARS2 AARS NARS2 QARS LARS2 FARSB ZNFX1 NARS DARS2 EPRS RARS FARSA FARS2 TARS MARS IARS WARS MARS2 KARS IARS2 PARS2 YARS VARS CARS EIF2AK4 RARS2 SARS SARS2 AARSD1 WARS2 HARS
tricarboxylic acid cycle	18	2.72E-11	37	153	0.242	ACO2 SUCLA2 MDH1 MDH2 SUCLG1 CS ACO1 IDH2 SDHA PDHB SDHB IDH3B NNT SUCLG2 IDH1 IDH3A FH DLST
coenzyme catabolic process	19	4.02E-11	37	171	0.216	ACO2 SUCLA2 MDH1 MDH2 SUCLG1 CS ACO1 IDH2 SDHA PDHB SDHB IDH3B NNT SUCLG2 IDH1 ALDH1L2 IDH3A FH DLST
small subunit processome	6	5.82E-04	3	15	0.200	UTP11L TBL3 UTP14A UTP3 WDR36 WDR3
oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor	6	5.82E-04	3	15	0.200	BCKDHB BCKDHA DHTKD1 PDHA1 PDHB OGDH
replisome	7	2.21E-03	4	21	0.190	PRIM1 POLA1 MCM3 RPA2 POLA2 PRIM2 RPA1
isoprenoid biosynthetic process	7	2.21E-03	4	21	0.190	MVK PDSS1 IDI1 FDF1 COQ2 FDP5 MVD
urea cycle intermediate metabolic process	7	3.69E-03	4	21	0.190	FAH OAT ASL ASS1 ARG1 OTC CAD
intra-Golgi vesicle-mediated transport	7	6.00E-03	4	21	0.190	COPB1 COPG2 COPZ1 NAPA COPB2 GOSR1 STX16
cellular respiration	25	1.96E-12	54	300	0.180	MDH1 ACO1 NDUFS1 IDH2 PDHB SDHB NDUFS4 UQCRC2 IDH3A ME3 FH DLST COX15 ACO2 SUCLA2 MDH2 SURF1 SUCLG1 CS SDHA IDH3B NNT SUCLG2 COX10 IDH1
nuclear replication fork	9	2.46E-04	6	36	0.167	PRIM1 POLA1 MCM7 MCM3 RPA2 POLA2 PRIM2 MCM2 RPA1
tRNA methyltransferase activity	9	2.55E-05	6	36	0.167	C14ORF172 TRMT5 METTL1 TRMT1 TRNT1 TRDMT1 RG9MTD2 TRMU NSUN2
aerobic respiration	22	4.21E-12	38	231	0.165	ACO2 SUCLA2 MDH1 SURF1 MDH2 SUCLG1 CS ACO1 IDH2 SDHA PDHB SDHB IDH3B NNT SUCLG2 COX10 IDH1 UQCRC2 IDH3A ME3 FH DLST
tricarboxylic acid cycle intermediate metabolic process	13	4.36E-06	12	78	0.154	ACO2 SUCLA2 MDH1 ME1 MDH2 IDH3B ACLY SUCLG2 OXCT1 IDH1 ME3 FH LDHA PUSL1 DUS3L YARS2 PUS3 AARS QARS LARS2 C14ORF172 ZNFX1 NARS GTPBP3 TRMT1 METTL1 TARS MARS DUS4L THG1L KARS PUS7 POP1 VARS NSUN2 TRIT1 CARS TRMT5 POP4 SARS SARS2 AARSD1 RG9MTD2 WARS2 DARS ELAC2 PUS1 MTO1 SCYE1 LARS GARS EARS2 NARS2 DUS2L FARSB TRMT12 DARS2 EPRS RARS TYW1 TRDMT1 FARSA FARS2 IARS WARS TRMU MARS2 IARS2 QTRT1 PARS2 YARS DUS1L ADAT2 EIF2AK4 RARS2 TRNT1 ADAT1 HARS
tRNA metabolic process	65	2.01E-32	304	2080	0.146	PUSL1 DUS3L YARS2 PUS3 AARS QARS LARS2 C14ORF172 ZNFX1 NARS GTPBP3 TRMT1 METTL1 TARS MARS DUS4L THG1L KARS PUS7 POP1 VARS NSUN2 TRIT1 CARS TRMT5 POP4 SARS SARS2 AARSD1 RG9MTD2 WARS2 DARS ELAC2 PUS1 MTO1 SCYE1 LARS GARS EARS2 NARS2 DUS2L FARSB TRMT12 DARS2 EPRS RARS TYW1 TRDMT1 FARSA FARS2 IARS WARS TRMU MARS2 IARS2 QTRT1 PARS2 YARS DUS1L ADAT2 EIF2AK4 RARS2 TRNT1 ADAT1 HARS
nuclear DNA-directed RNA polymerase complex	11	1.52E-03	8	55	0.145	POLR2E POLR2C POLR3A POLR3H POLR2A POLR1A POLR2B RPA1 POLR3K POLR1C POLR2J
DNA geometric change	8	2.86E-04	4	28	0.143	CCNL1 TOP3A TOP3B MCM4 MCM6 RAD51 MCM2 TOP1
2 iron, 2 sulfur cluster binding	7	6.29E-04	3	21	0.143	XDH NDUFV2 AIFM3 UQCRCF1 NDUFS1 FECH SDHB
proteasome regulatory particle (sensu Eukaryota)	7	2.93E-05	3	21	0.143	PSMD9 PSMD2 PSMD7 PSMD1 PSMD13 PSMD8 PSMD12
replication fork	16	3.19E-07	17	120	0.142	MCM7 MCM3 RFC5 RPA2 RFC2 PCNA RFC1 RFC3 PRIM1 POLA1 PRIM2 POLA2 CHEK1 MCM2 RFC4 RPA1
RNA methyltransferase activity	12	1.82E-05	9	66	0.136	C14ORF172 TRMT5 METTL1 TRMT1 TRNT1 TRDMT1 DITM1L RG9MTD2 TRMU NSUN2 C1ORF66 RNMT
isoprenoid metabolic process	10	1.62E-03	6	45	0.133	MVK NPC2 PDSS1 RDH12 IDI1 ADH5 FDF1 COQ2 FDP5 MVD
tetrapyrrole biosynthetic process	10	1.16E-05	6	45	0.133	CPOX COX10 SUCLA2 HMBS ALAD ALAS2 UROD FECH PPOX COX15
spliceosome assembly	12	9.99E-04	8	66	0.121	USP39 DDX23 SF1 DDX1 SNRPE CRNKL1 PRPF6 ASCC3L1 SFRS5 SF3A2 SF3A1 SLU7
RNA polymerase complex	12	5.01E-04	8	66	0.121	POLR2E POLR2C POLR3A POLR2F POLR3H POLR2A POLR1A POLR2B RPA1 POLR3K POLR1C POLR2J
DNA replication initiation	16	1.65E-07	13	120	0.108	CDC6 ORC2L CDC45L MCM7 CCNL1 MCM3 ORC5L MCM4 ORC1L POLA1 MCM5 WRNIP1 MCM8 MCM6 MCM2 ORC4L
glycine metabolic process	8	5.48E-04	3	28	0.107	GLDC SHMT1 AMT DHFR FPGS SHMT2 C1ORF69 PDPR
nucleobase biosynthetic process	8	1.76E-05	3	28	0.107	GARS PPAT DHODH DPYD CAD UMPS GART PAICS
ubiquinone metabolic process	8	4.46E-06	3	28	0.107	COQ9 COQ5 COQ3 PDSS1 COQ6 COQ4 COQ2 COQ7
glutamine family amino acid biosynthetic process	8	3.88E-03	3	28	0.107	ASL ASS1 ALDH4A1 GLUL OTC PYCR1 CAD ALDH18A1
purine ribonucleoside monophosphate biosynthetic process	8	5.48E-04	3	28	0.107	ADSS PFAS AMPD2 GARS GART PAICS IMPDH2 ADAL
energy derivation by oxidation of organic compounds	37	2.79E-11	71	666	0.107	MDH1 NDUFS1 ACO1 IDH2 PDHB SDHB NDUFS4 UQCRC2 IDH3A ME3 FH DLST COX15 AGL ACO2 BCS1L SUCLA2 GSK3B GFPT2 PYGB SURF1 MDH2 SUCLG1 GK CS SDHA GYS2 IDH3B NNT TREH SUCLG2 COX10 IDH1 GYG1 GBE1 CRAT GAA
tRNA binding	12	4.05E-07	7	66	0.106	KARS CARS XPOT EIF2A SCYE1 TRNT1 AARS RPL35A YARS FARS2 MARS NSUN2
nucleoside monophosphate metabolic process	12	9.81E-06	7	66	0.106	ADSS PFAS ADK AMPD2 GARS DHODH TYMS UMPS GART PAICS IMPDH2 ADAL
pigment biosynthetic process	15	1.14E-05	11	105	0.105	CPOX HMBS IDI1 GARS ALAD AP3D1 PAICS COX10 PPAT ALAS2 UROD FECH COX15 PPOX GART CPOX HMBS IDI1 GARS ALAD AP3D1 PAICS COX10 RDH12 PPAT ADH5 ALAS2 UROD FECH COX15 PPOX GART
secondary metabolic process	17	1.39E-04	14	136	0.103	

^(a) Number genes (n) with that annotation in network^(b) q-value calculated with Bino. is the p-value of the Hvøerdaometric test corrected with the Benjamini & Hochbera False Discoverv Rate (FDR) correction^(c) Number of connections (c) in the network for this GO annotaion^(d) Maximum number of possible connections. M= n(n-1)/2^(e) Connectivity = c/M