Table S5. Enzymes involved the mitochondrial metabolic pathway.

Pathway	Pathway ID	KO	Enzyme	Gene
Purine metabolism	ko00230	K00856	adenosine kinase [EC:2.7.1.20]	ADK
Purine metabolism	ko00230	K19836	hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]	HPRT1
Purine metabolism	ko00230	K20881	GMP/IMP 5'-nucleotidase [EC:3.1.3.-]	yrfG
Purine metabolism	ko00230	K00892	inosine kinase [EC:2.7.1.73]	GSK
Purine metabolism	ko00230	K00769	xanthine phosphoribosyltransferase [EC:2.4.2.22]	GPT
Purine metabolism	ko00230	K01488	adenosine deaminase [EC:3.5.4.4]	ADA
Purine metabolism	ko00230	K05810	purine-nucleoside/S-methyl-5'-thioadenosine phosphorylase / adenosine deaminase [EC:2.4.2.1 2.4.2.28 3.5.4.4]	LACC1
Purine metabolism	ko00230	K03783	purine-nucleoside phosphorylase [EC:2.4.2.1]	Pnp
Purine metabolism	ko00230	K09913	purine/pyrimidine-nucleoside phosphorylase [EC:2.4.2.1 2.4.2.2]	PPnp
Purine metabolism	ko00230	K01119	2',3'-cyclic-nucleotide 2'-phosphodiesterase / 3'-nucleotidase [EC:3.1.4.16 3.1.3.6]	cpdB
Purine metabolism	ko00230	K01487	guanine deaminase [EC:3.5.4.3]	GDA
Purine metabolism	ko00230	K00106	xanthine dehydrogenase/oxidase [EC:1.17.1.4 1.17.3.2]	Xdh
Purine metabolism	ko00230	K13480	xanthine dehydrogenase iron-sulfur-binding subunit	xdhC
Purine metabolism	ko00230	K13479	xanthine dehydrogenase FAD-binding subunit [EC:1.17.1.4]	xdhB
Purine metabolism	ko00230	K13483	xanthine dehydrogenase YagT iron-sulfur-binding subunit	yagT
Purine metabolism	ko00230	K25589	inosine/uridine nucleosidase [EC:3.2.2.2 3.2.2.3]	URH2
Purine metabolism	ko00230	K19970	5'-nucleotidase [EC:3.1.3.5]	NT5E
Glutathione metabolism	ko00480	K00383	glutathione reductase (NADPH) [EC:1.8.1.7]	Gsr
Glutathione metabolism	ko00480	K00031	isocitrate dehydrogenase [EC:1.1.1.42]	IDH2
Glutathione metabolism	ko00480	K00432	glutathione peroxidase [EC:1.11.1.9]	Gpx7
Glutathione metabolism	ko00480	K00033	6-phosphogluconate dehydrogenase [EC:1.1.1.44 1.1.1.343]	KIF1B
Glutathione metabolism	ko00480	K00032	phosphogluconate 2-dehydrogenase [EC:1.1.1.43]	kguD
Glutathione metabolism	ko00480	K00036	glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49 1.1.1.363]	G6PD
Glutathione metabolism	ko00480	K05360	protein-disulfide reductase (glutathione) [EC:1.8.4.2]	TXNDC12
Glutathione metabolism	ko00480	K05361	phospholipid-hydroperoxide glutathione peroxidase [EC:1.11.1.12]	GPX4
Glutathione metabolism	ko00480	K00310	pyrimidodiazepine synthase [EC:1.5.4.1]	GstO2
Glutathione metabolism	ko00480	K24137	glutaredoxin/glutathione-dependent peroxiredoxin [EC:1.11.1.25 1.11.1.27]	PRDX3
Glutathione metabolism	ko00480	K24136	glutathione-dependent peroxiredoxin [EC:1.11.1.27]	PRDX6
Nicotinate and nicotinamide metabolism	ko00760	K00858	NAD kinase [EC:2.7.1.23]	Nadk
Nicotinate and nicotinamide metabolism	ko00760	K00323	proton-translocating NAD(P)+ transhydrogenase [EC:7.1.1.1]	NNT
Nicotinate and nicotinamide metabolism	ko00760	K00322	NAD(P) transhydrogenase [EC:1.6.1.1]	udhA
Nicotinate and nicotinamide metabolism	ko00760	K01242	ADP-ribosyl cyclase 1 [EC:3.2.2.6 2.4.99.20]	CD38
Nicotinate and nicotinamide metabolism	ko00760	K00541	nicotinamide N-methyltransferase [EC:2.1.1.1]	NNMT

Nicotinate and nicotinamide metabolism	ko00760	K00157	aldehyde oxidase [EC:1.2.3.1]	AOX1
Nicotinate and nicotinamide metabolism	ko00760	K18152	ADP-ribosyl cyclase 2 [EC:3.2.2.6 2.4.99.20]	BST1
Aminoacyl-tRNA biosynthesis	ko00970	K04567	lysyl-tRNA synthetase, class II [EC:6.1.1.6]	KARS1
Aminoacyl-tRNA biosynthesis	ko00970	K01889	phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]	FARS2
Aminoacyl-tRNA biosynthesis	ko00970	K01890	phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]	FARSB
Biosynthesis of various other secondary metabolites	ko00997	K03897	lysine N6-hydroxylase [EC:1.14.13.59]	iucD
Biosynthesis of various other secondary metabolites	ko00997	K23669	L-lysine 4-chlorinase [EC:1.14.20.-]	arpA