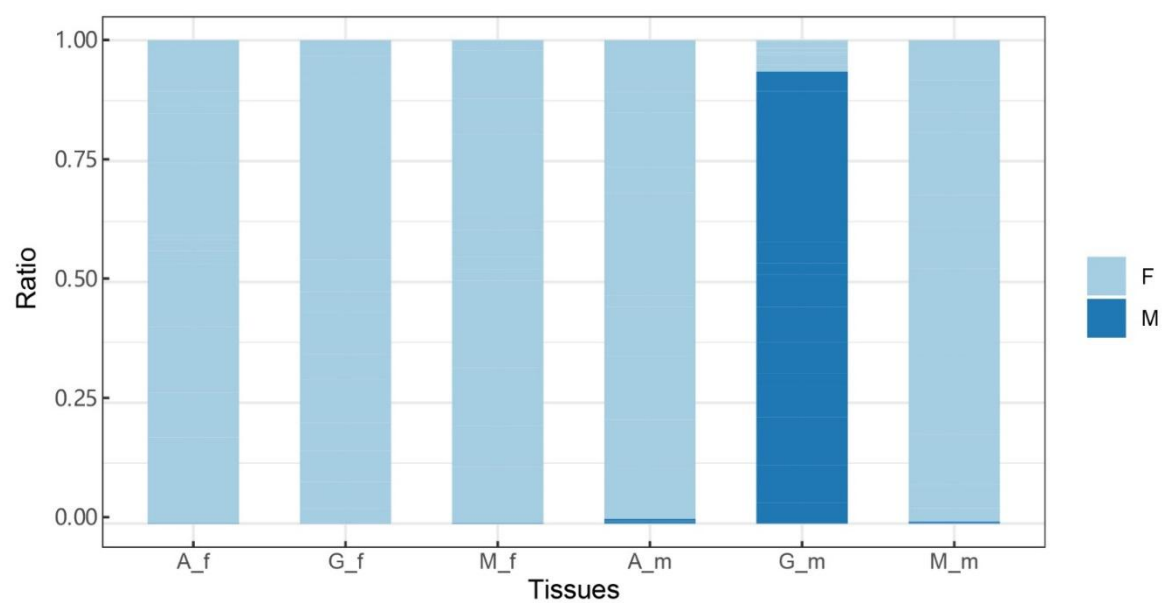
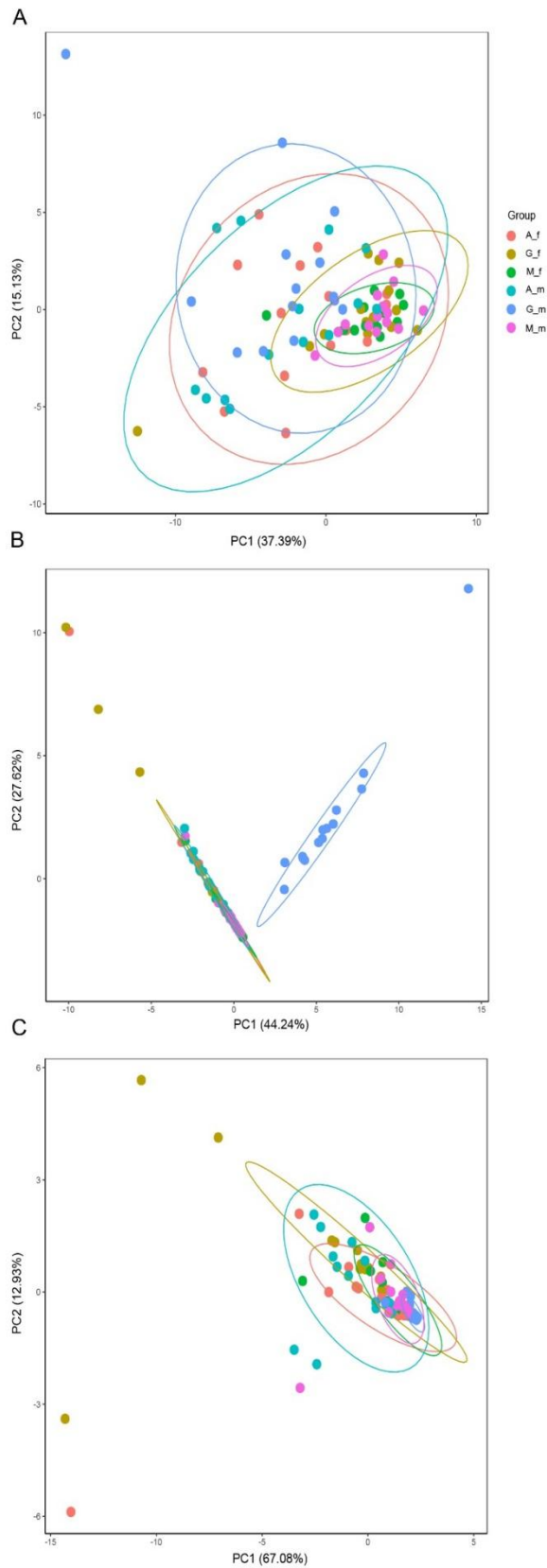


Supplementary Material



Supplementary Figure S1 The ratio of reads mapped to the F- and M-type genomes in each tissue.

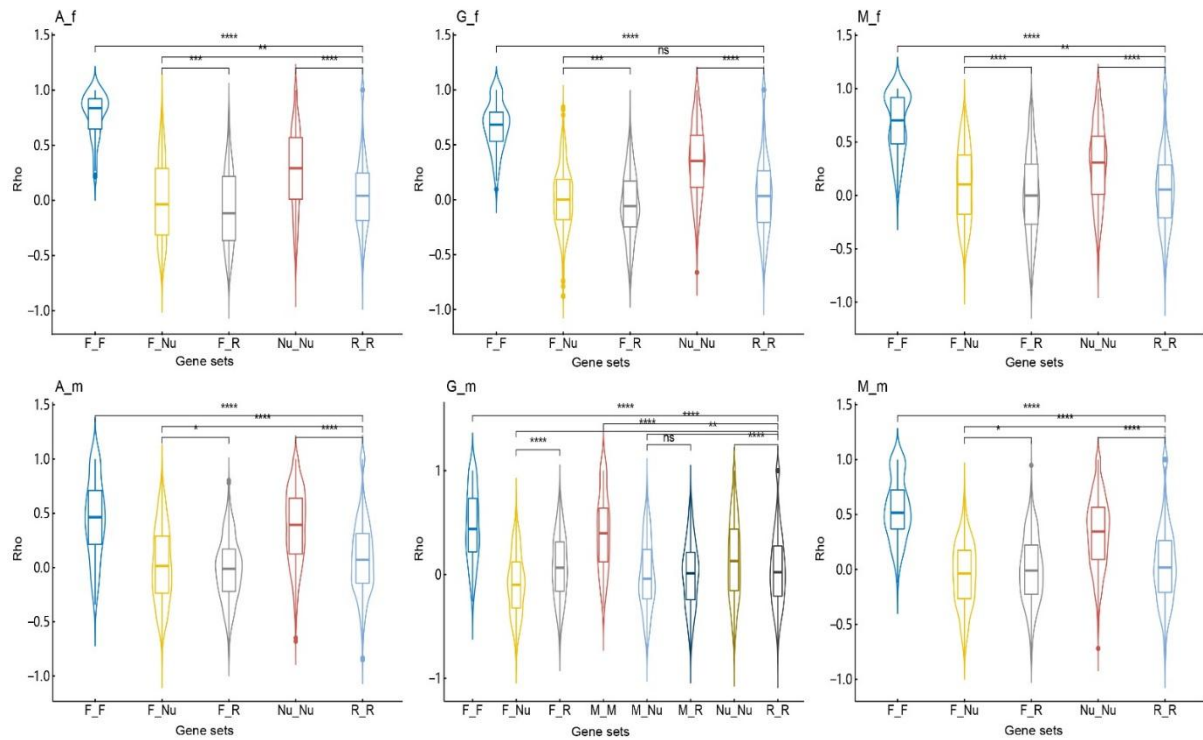


Supplementary Figure S2 The PCA plot based on the transcriptional levels of OXPHOS genes.

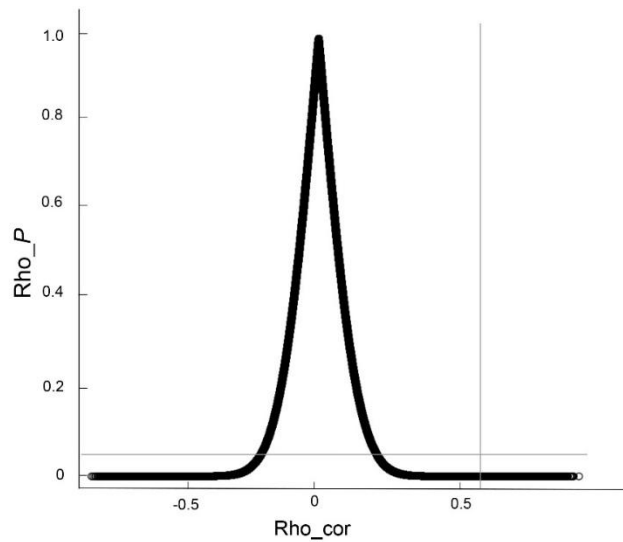
A: PCA plot based on nuclear OXPHOS genes. B: PCA plot based on all the mitochondrial genes; C: PCA plot based on F-type mitochondrial genes.



Supplementary Figure S3 The transcriptional levels of mitochondrial genes (A) and nuclear OXPHOS genes (B) in each tissue.

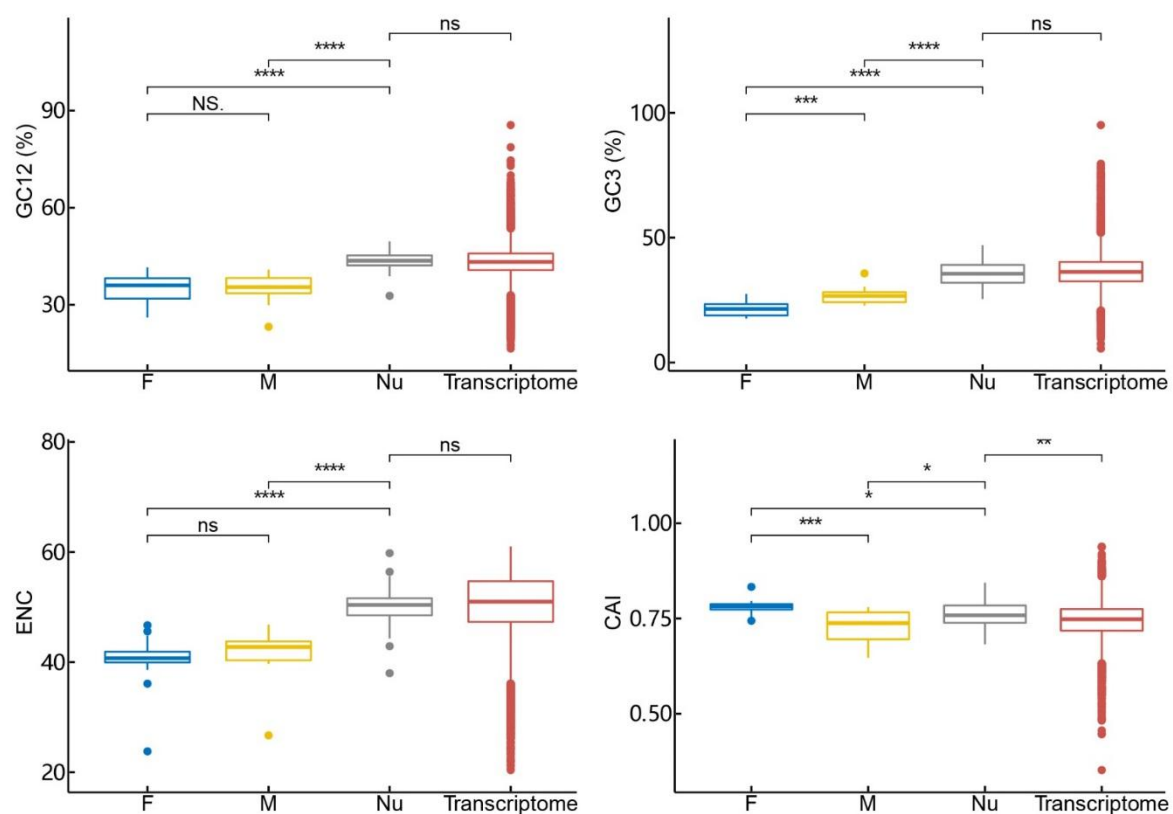


Supplementary Figure S4 The co-transcription between and within OXPHOS genes in each tissue. Statistical significance was performed using Wilcoxon rank-sum test with Bonferroni correction. *: $-P < 0.05$, **: $-P < 0.001$, ***: $-P < 1 \times 10^{-5}$, ns—not significant.



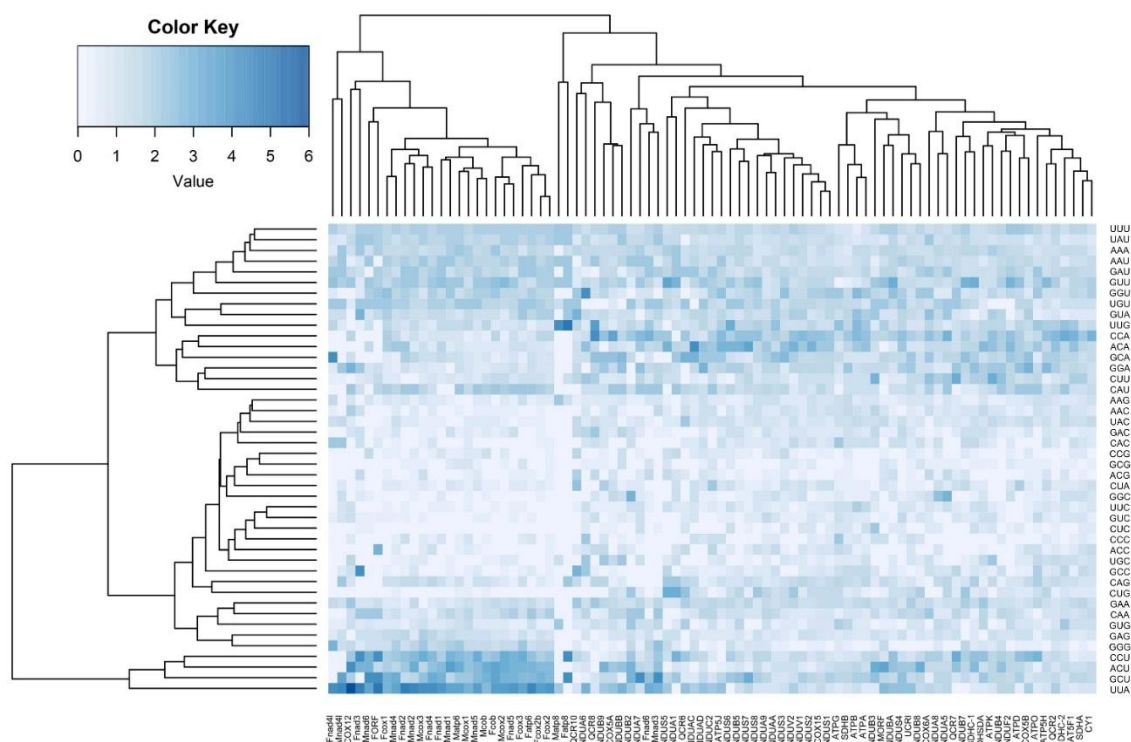
Supplementary Figure S5 The distribution of P -values (y-axis) and corresponding correlation coefficients (x-axis) for nuclear genes co-transcribed with OXPHOS genes.

The horizontal line represents $P = 0.05$, and the vertical line represents correlation coefficients of 0.6.



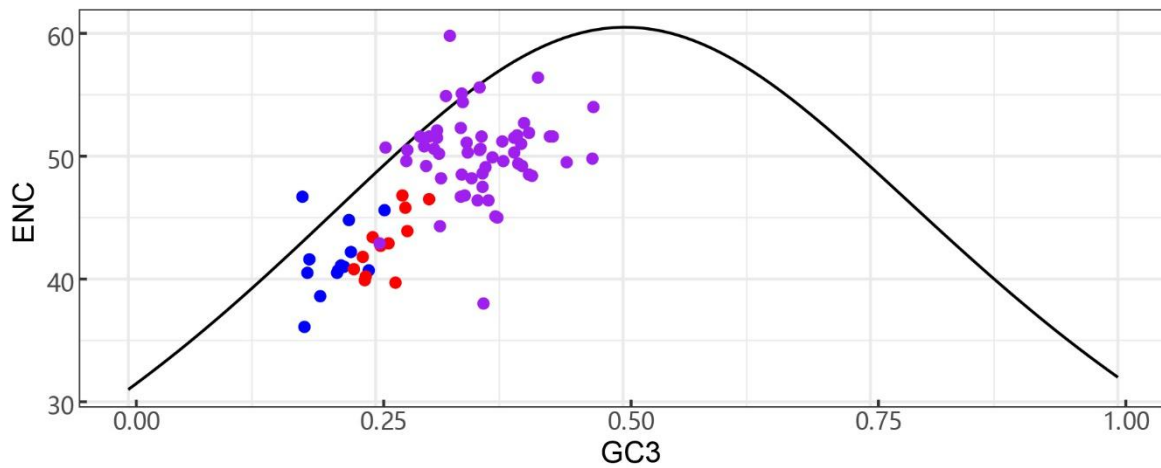
Supplementary Figure S7 The distribution of ENC, CAI, GC3 and GC12 for mitochondrial and nuclear OXPHOS genes.

Statistical significance was performed using Wilcoxon rank-sum test with Bonferroni correction.



Supplementary Figure S8 The heatmap based on the RSCU values for four-fold degenerate families.

Considering the Met, Trp, Ser, Arg and Ile were different between mt and nuOXPHOS, they were not included here.



Supplementary Figure S9 ENC and GC3 relation plot (Nc-plot) for mitochondrial genes and nuclear OXPHOS.

The blue, red, purple points represented F-type, M-type and nuOXPHOS genes, respectively. The black curve represented the expected relation between GC3 and ENC.

Supplementary Table S1 The number of reads mapped to the mitochondrial genomes and de novo transcriptome.

Sample	Transcriptome	Mitochondria	F-type	M-type
f_42_A	2894639	56208	56206	2
f_42_G	2206483	40960	40960	0
f_42_M	2210169	35600	35598	2
f_44_A	1645260	29528	29496	32
f_44_G	2786702	69372	69364	8
f_44_M	1653967	25438	25428	10
f_45_A	2257626	42954	42954	0
f_45_G	2967846	82284	82278	6
f_45_M	2456851	36866	36750	116
f_47_A	2558833	40852	40846	6
f_47_G	2224394	74568	74566	2
f_47_M	2617141	54824	54822	2
f_54_A	2289943	8506	8486	20
f_54_G	2409236	113736	113734	2
f_54_M	3131851	7090	7082	8
f_56_A	2474876	7248	7246	2
f_56_G	3037805	68392	68390	2
f_56_M	2571151	7952	7946	6
f_57_A	1119542	3100	3098	2
f_57_G	2816784	113348	113348	0
f_57_M	2124616	16604	16602	2
f_59_A	3134698	23596	23590	6
f_59_G	3399806	52452	52452	0
f_59_M	2509865	10954	10948	6
f_60_A	1690192	13846	13844	2
f_60_G	2105336	84212	84160	52
f_60_M	1972654	49494	49492	2
f_61_A	2982253	10132	10130	2
f_61_G	4487987	309132	309118	14
f_61_M	3239555	22348	22316	32
f_63_A	2518974	32310	32292	18
f_63_G	3378726	87292	87170	122
f_63_M	3419645	19474	19424	50
f_64_A	2285222	4962	4962	0
f_64_G	4248176	82450	82438	12
f_67_A	3195087	9428	9412	16
f_67_G	11502	416	416	0
f_67_M	47076	490	490	0
f_71_A	1532479	15250	15202	48
f_71_G	3282704	60784	60784	0

f_71_M	1971730	10914	10906	8
f_73_A	2387404	18304	18272	32
f_73_G	3663750	42694	42692	2
f_73_M	2392651	6302	6284	18
m_48_A	2649635	35616	35534	82
m_48_G	1611185	73690	3472	70218
m_48_M	510868	7478	7434	44
m_49_A	2971154	35406	35382	24
m_49_G	2621208	136546	6992	129554
m_49_M	2114899	13254	13220	34
m_50_A	2436208	47034	45816	1218
m_50_G	2896472	174112	12124	161988
m_50_M	1527749	28320	28300	20
m_51_A	2770680	15276	15164	112
m_51_G	4092860	136192	30970	105222
m_51_M	2777476	42916	42866	50
m_52_A	2888568	19966	19932	34
m_52_G	2057982	46890	1486	45404
m_52_M	2994454	50234	50134	100
m_53_A	2209858	8042	8022	20
m_53_G	1941134	110870	5950	104920
m_53_M	4183516	23714	23684	30
m_55_A	4120008	38268	38262	6
m_55_G	3219729	127388	5594	121794
m_55_M	3430301	17906	17882	24
m_58_A	2129826	35686	35312	374
m_58_G	2801871	119852	9216	110636
m_58_M	3146362	23878	23858	20
m_62_A	2142204	7726	7722	4
m_62_G	2699748	42196	2408	39788
m_62_M	1943205	11786	11784	2
m_65_A	2350512	10620	10522	98
m_65_G	3397753	71648	2810	68838
m_65_M	2025220	10790	10738	52
m_66_A	6278717	23596	23554	42
m_66_G	3806270	114438	4916	109522
m_66_M	2031938	9774	9756	18
m_68_A	1586352	15452	15366	86
m_68_G	3103656	226678	15076	211602
m_68_M	2483422	8350	8340	10
m_69_A	1579951	15712	14998	714
m_69_G	3583137	199078	3952	195126
m_69_M	1845055	15826	15096	730
m_70_A	1566008	6714	6684	30

m_70_G	2409439	31192	30488	704		
m_70_M	1264732	4110	4100	10		
	GO.ID	Term	Annotated	Significant	Expected	Fisher
F_BP	GO:0019725	cellular homeostasis	15	3	0.14	0.00029
	GO:0042592	homeostatic process	22	3	0.2	0.00093
	GO:0045454	cell redox homeostasis	6	2	0.06	0.00119
	GO:0033108	mitochondrial respiratory chain complex assembly	9	2	0.08	0.0028
	GO:0065008	regulation of biological quality	43	3	0.4	0.0066
M_BP	GO:0022414	reproductive process	27	13	1.76	2.20E-09
m_72_A	2966941	37570	37010	560		
m_72_G	1448649	68880	2068	66812		
m_72_M	1537146	7486	7406	80		

Supplementary Table S2 The median depth of the OXPHOS genes. Samples with the transcription of M-type mt genes were marked blue.

Supplementary Table S3 The normalized counts for all the OXPHOS genes.

Supplementary Table S4 Statistical test for the transcriptional differences across tissues.

		A_f	G_f	M_f	A_m	G_m
Across tissue comparison for Nu-OXPHOS	G_f	**				
	M_f	**	ns			
	A_m	ns	**	**		
	G_m	ns	**	**	ns	
	M_m	**	ns	ns	**	**
		A_f	G_f	M_f	A_m	G_m
Across tissue comparison for mt-OXPHOS	G_f	*				
	M_f	*	**			
	A_m	*	ns	**		
	G_m	**	**	**	**	
	M_m	*	**	ns	**	**

Kruskal-Wallis test indicates the significant differences ($p < 0.001$) for both mt and nuOXPHOS across tissues. Dunn test with Bonferroni correction was used for the pairwise comparisons.

Supplementary Table S5 The list of genes co-transcribed with the OXPHOS.

Supplementary Table S6 The enriched GO terms for the genes co-transcribed with the F-type, M-type and nuOXPHOS genes.

GO:0000003	reproduction	31	13	2.02	1.80E-08
GO:0051704	multi-organism process	43	13	2.8	1.60E-06
GO:0007276	gamete generation	16	7	1.04	3.10E-05
GO:0007283	spermatogenesis	16	7	1.04	3.10E-05
GO:0019953	sexual reproduction	16	7	1.04	3.10E-05
GO:0044703	multi-organism reproductive process	16	7	1.04	3.10E-05
GO:0048232	male gamete generation	16	7	1.04	3.10E-05
GO:0048609	multicellular organismal reproductive process	16	7	1.04	3.10E-05
GO:0051321	meiotic cell cycle	9	5	0.59	0.00011
GO:0007017	microtubule-based process	98	17	6.39	0.00013
GO:0032504	multicellular organism reproduction	20	7	1.3	0.00017
GO:0016310	phosphorylation	110	18	7.17	0.00018
GO:0044419	biological process involved in interspecies interaction between organisms	17	6	1.11	0.00047
GO:0007127	meiosis I	7	4	0.46	0.00052
GO:0061982	meiosis I cell cycle process	7	4	0.46	0.00052
GO:0140013	meiotic nuclear division	7	4	0.46	0.00052
GO:0007018	microtubule-based movement	31	8	2.02	0.00059
GO:0006928	movement of cell or subcellular component	48	10	3.13	0.00079
GO:0046939	nucleotide phosphorylation	19	6	1.24	0.00093
GO:1903046	meiotic cell cycle process	8	4	0.52	0.00099
GO:0016032	viral process	9	4	0.59	0.00169
GO:0006793	phosphorus metabolic process	213	25	13.88	0.00212
GO:0006796	phosphate-containing compound metabolic process	213	25	13.88	0.00212
GO:0000280	nuclear division	22	6	1.43	0.00217
GO:0044403	symbiont process	10	4	0.65	0.00268
GO:0051716	cellular response to stimulus	229	26	14.92	0.00278
GO:0006310	DNA recombination	23	6	1.5	0.00278
GO:0048285	organelle fission	23	6	1.5	0.00278
GO:0072527	pyrimidine-containing compound metabolic process	13	4	0.85	0.00781
GO:0003006	developmental process involved in reproduction	7	3	0.46	0.00783
GO:0022402	cell cycle process	55	9	3.58	0.00802
GO:0007049	cell cycle	75	11	4.89	0.00815
GO:0006281	DNA repair	66	10	4.3	0.00917
GO:0034404	nucleobase-containing small molecule biosynthetic process	21	5	1.37	0.00957
GO:0050896	response to stimulus	302	30	19.68	0.00987

Nu_BP	GO:0006412	translation	196	90	36.36	3.00E-20
	GO:0043043	peptide biosynthetic process	198	90	36.73	7.20E-20
	GO:0043604	amide biosynthetic process	200	90	37.11	1.70E-19
	GO:0006518	peptide metabolic process	202	90	37.48	3.90E-19
	GO:0043603	cellular amide metabolic process	213	92	39.52	1.90E-18
	GO:1901566	organonitrogen compound biosynthetic process	309	111	57.33	5.30E-15
	GO:0044267	cellular protein metabolic process	414	130	76.81	2.30E-12
	GO:0019538	protein metabolic process	510	143	94.62	2.00E-09
	GO:0044271	cellular nitrogen compound biosynthetic process	508	132	94.25	1.90E-06
	GO:1901564	organonitrogen compound metabolic process	690	169	128.01	2.50E-06
	GO:0005977	glycogen metabolic process	7	7	1.3	7.30E-06
	GO:0006112	energy reserve metabolic process	7	7	1.3	7.30E-06
	GO:0007005	mitochondrion organization	51	23	9.46	1.00E-05
	GO:0034645	cellular macromolecule biosynthetic process	485	124	89.98	1.10E-05
	GO:0009059	macromolecule biosynthetic process	488	124	90.54	1.60E-05
	GO:1901576	organic substance biosynthetic process	613	149	113.73	2.30E-05
	GO:0009058	biosynthetic process	629	152	116.7	2.60E-05
	GO:0044249	cellular biosynthetic process	609	147	112.99	4.20E-05
	GO:0044262	cellular carbohydrate metabolic process	11	8	2.04	0.00013
	GO:0044260	cellular macromolecule metabolic process	776	177	143.97	0.00018
	GO:0006073	cellular glucan metabolic process	9	7	1.67	0.00019
	GO:0044042	glucan metabolic process	9	7	1.67	0.00019
	GO:0044264	cellular polysaccharide metabolic process	9	7	1.67	0.00019
	GO:0071806	protein transmembrane transport	11	7	2.04	0.0012
	GO:0031032	actomyosin structure organization	9	6	1.67	0.002
	GO:0005976	polysaccharide metabolic process	12	7	2.23	0.00242
	GO:0010467	gene expression	598	135	110.94	0.00256
F_CC	GO:0005737	cytoplasm	1171	18	9.02	0.0004
	GO:0044444	cytoplasmic part	670	11	5.16	0.0075
M_CC	GO:0044430	cytoskeletal part	214	36	13.85	4.20E-08
	GO:0015630	microtubule cytoskeleton	167	29	10.81	5.10E-07
	GO:0005856	cytoskeleton	262	38	16.96	9.60E-07
	GO:0042995	cell projection	74	16	4.79	1.30E-05
	GO:0031514	motile cilium	32	10	2.07	1.90E-05
	GO:0005929	cilium	62	14	4.01	2.70E-05
	GO:0019012	virion	8	5	0.52	5.20E-05
	GO:0120025	plasma membrane bounded cell	68	14	4.4	8.10E-05

		projection				
	GO:0005815	microtubule organizing center	56	12	3.62	0.00018
	GO:0018995	host	3	3	0.19	0.00027
	GO:0033643	host cell part	3	3	0.19	0.00027
	GO:0033646	host intracellular part	3	3	0.19	0.00027
	GO:0033647	host intracellular organelle	3	3	0.19	0.00027
	GO:0033648	host intracellular membrane-bounded organelle	3	3	0.19	0.00027
	GO:0042025	host cell nucleus	3	3	0.19	0.00027
	GO:0043656	intracellular region of host	3	3	0.19	0.00027
	GO:0043657	host cell	3	3	0.19	0.00027
	GO:0044215	other organism	3	3	0.19	0.00027
	GO:0044216	other organism cell	3	3	0.19	0.00027
	GO:0044217	other organism part	3	3	0.19	0.00027
	GO:0000794	condensed nuclear chromosome	7	4	0.45	0.00051
	GO:0044423	virion part	7	4	0.45	0.00051
	GO:0005930	axoneme	9	4	0.58	0.00166
	GO:0097014	ciliary plasm	9	4	0.58	0.00166
	GO:0032838	plasma membrane bounded cell projection cytoplasm	10	4	0.65	0.00263
	GO:1990716	axonemal central apparatus	2	2	0.13	0.00417
	GO:0019028	viral capsid	6	3	0.39	0.00462
	GO:0005875	microtubule associated complex	45	8	2.91	0.00727
Nu_CC	GO:0005840	ribosome	133	78	24.2	2.00E-26
	GO:0005737	cytoplasm	1171	296	213.03	2.90E-14
	GO:1990904	ribonucleoprotein complex	242	90	44.03	2.90E-13
	GO:0044444	cytoplasmic part	670	188	121.89	1.20E-12
	GO:0044391	ribosomal subunit	38	22	6.91	4.50E-08
	GO:0005739	mitochondrion	134	50	24.38	7.50E-08
	GO:0005759	mitochondrial matrix	20	13	3.64	4.70E-06
	GO:0032991	protein-containing complex	871	202	158.45	9.50E-06
	GO:0098798	mitochondrial protein complex	39	19	7.09	1.20E-05
	GO:0015934	large ribosomal subunit	22	13	4	2.10E-05
	GO:0044429	mitochondrial part	85	31	15.46	4.10E-05
	GO:0000313	organellar ribosome	14	9	2.55	0.00017
	GO:0005761	mitochondrial ribosome	14	9	2.55	0.00017
	GO:0005838	proteasome regulatory particle	10	7	1.82	0.00046
	GO:0000502	proteasome complex	38	16	6.91	0.0005
	GO:1905369	endopeptidase complex	38	16	6.91	0.0005
	GO:0043232	intracellular non-membrane-bounded organelle	603	139	109.7	0.00054
F_MF	GO:0016782	transferase activity, transferring sulfur-containing groups	17	2	0.14	0.0081

M_MF	GO:0016301	kinase activity	250	40	15.12	5.10E-09
	GO:0016773	phosphotransferase activity, alcohol group as acceptor	208	33	12.58	1.60E-07
	GO:0016772	transferase activity, transferring phosphorus-containing groups	304	40	18.38	1.30E-06
	GO:0016849	phosphorus-oxygen lyase activity	6	5	0.36	4.40E-06
	GO:0004672	protein kinase activity	186	28	11.25	4.50E-06
	GO:0017076	purine nucleotide binding	661	61	39.97	0.00026
	GO:0032555	purine ribonucleotide binding	661	61	39.97	0.00026
	GO:0032553	ribonucleotide binding	666	61	40.27	0.00032
	GO:0030554	adenyl nucleotide binding	529	51	31.99	0.00033
	GO:0032559	adenyl ribonucleotide binding	529	51	31.99	0.00033
	GO:0042578	phosphoric ester hydrolase activity	83	14	5.02	0.00037
	GO:0004112	cyclic-nucleotide phosphodiesterase activity	7	4	0.42	0.0004
	GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	7	4	0.42	0.0004
	GO:0097367	carbohydrate derivative binding	704	63	42.57	0.00048
	GO:0035639	purine ribonucleoside triphosphate binding	652	59	39.43	0.00057
	GO:0043168	anion binding	800	69	48.37	0.0007
	GO:0005524	ATP binding	520	49	31.44	0.00075
	GO:0008144	drug binding	576	53	34.83	0.00078
	GO:0000166	nucleotide binding	819	70	49.52	0.00082
	GO:1901265	nucleoside phosphate binding	819	70	49.52	0.00082
	GO:0036094	small molecule binding	882	74	53.33	0.00096
	GO:0000287	magnesium ion binding	29	7	1.75	0.00134
	GO:0016740	transferase activity	628	55	37.97	0.00201
	GO:0140096	catalytic activity, acting on a protein	577	50	34.89	0.00416
	GO:0008081	phosphoric diester hydrolase activity	19	5	1.15	0.00448
	GO:0003774	motor activity	76	11	4.6	0.00544
	GO:0043167	ion binding	1683	121	101.77	0.0069
	GO:0097159	organic cyclic compound binding	1564	113	94.57	0.00857
	GO:1901363	heterocyclic compound binding	1564	113	94.57	0.00857
u_MF	GO:0003735	structural constituent of ribosome	121	72	21.26	9.00E-26
	GO:0005198	structural molecule activity	236	94	41.46	6.70E-17
	GO:0019843	rRNA binding	63	34	11.07	4.60E-11
	GO:0005267	potassium channel activity	21	15	3.69	7.80E-08
	GO:0015079	potassium ion transmembrane transporter activity	25	15	4.39	2.30E-06
	GO:0005261	cation channel activity	42	20	7.38	6.50E-06
	GO:0022838	substrate-specific channel activity	77	29	13.53	1.90E-05
	GO:0005216	ion channel activity	74	28	13	2.40E-05

GO:0015267	channel activity	80	29	14.05	4.40E-05
GO:0022803	passive transmembrane transporter activity	80	29	14.05	4.40E-05
GO:0003723	RNA binding	304	79	53.4	8.60E-05
GO:0005516	calmodulin binding	22	12	3.86	9.10E-05
GO:0008135	translation factor activity, RNA binding	80	28	14.05	0.00012
GO:0003779	actin binding	123	38	21.61	0.00018
GO:0022839	ion gated channel activity	59	22	10.36	0.00023
GO:0022836	gated channel activity	60	22	10.54	0.0003
GO:0046873	metal ion transmembrane transporter activity	79	26	13.88	0.00063
GO:0005244	voltage-gated ion channel activity	26	12	4.57	0.00069
GO:0022832	voltage-gated channel activity	26	12	4.57	0.00069
GO:0004339	glucan 1,4-alpha-glucosidase activity	4	4	0.7	0.00095
GO:0022843	voltage-gated cation channel activity	14	8	2.46	0.00097
GO:0003743	translation initiation factor activity	57	20	10.01	0.00108
GO:0005249	voltage-gated potassium channel activity	12	7	2.11	0.00175
GO:0015926	glucosidase activity	7	5	1.23	0.00254
GO:0019200	carbohydrate kinase activity	7	5	1.23	0.00254
GO:0015077	inorganic cation transmembrane transporter activity	74	23	13	0.003
GO:0004396	hexokinase activity	3	3	0.53	0.0054
GO:0005231	excitatory extracellular ligand-gated ion channel activity	3	3	0.53	0.0054
GO:0005234	extracellularly glutamate-gated ion channel activity	3	3	0.53	0.0054
GO:0005536	glucose binding	3	3	0.53	0.0054
GO:0030943	mitochondrion targeting sequence binding	3	3	0.53	0.0054
GO:0071933	Arp2/3 complex binding	3	3	0.53	0.0054
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	8	5	1.41	0.00579
GO:0043022	ribosome binding	8	5	1.41	0.00579
GO:0044877	protein-containing complex binding	70	21	12.3	0.00705
GO:0022890	inorganic cation transmembrane transporter activity	115	31	20.2	0.00722
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	42	14	7.38	0.00978

F: F-type OXPHOS genes; M: M-type OXPHOS genes; Nu: nuclear OXPHOS; BP: biological process; MF: molecular function; CC: cellular component.

Supplementary Table S7 The candidate genes that might be involved in the co-transcriptional regulation.

OXPHOS	Locus	No. of gene	Annotation in NR db
F-type	Locus1895123	1	Zinc finger protein 558
	Locus226176	3	DNA-directed RNA polymerase II subunit RPB9
M-type	Locus8350352	2	Zinc finger protein 341
	Locus7670362	1	Dynein light chain 1
	Locus572990	4	APOBEC1 complementation factor
	Locus382505	3	Eukaryotic translation initiation factor 3 subunit G
M-type & Nu	Locus1618449	1	Transcriptional activator protein Pur-beta
Nu	Locus4607497	4	Pentatricopeptide repeat domain-containing protein 3
	Locus2398964	3	DNA-directed RNA polymerase III subunit RPC3
	Locus1549169	3	Muscle blind-like protein 3
	Locus1065041	4	BRCA1-A complex subunit BRE
	Locus4177360	4	Transcription factor RFX3
	Locus7072300	3	Transcriptional coactivator YAP1
	Locus7055868	3	Y-box factor homolog
	Locus1872614	2	Cyclic AMP-dependent transcription factor ATF-4

Supplementary Table S8: Statistics for the percentage of synonymous and nonsynonymous SNPs in OXPHOS genes.

Polymorphism	OXPHOS genes	F-all	F-no	M
Nonsynonymous	F-no	**		
	M	**	ns	
	Nu	**	**	**
Synonymous	F-no	**		
	M	**	ns	
	Nu	**	**	**

** : $-P < 0.05$, ns: not significant.

Supplementary Table S9 The McDonald-Kreitman test and neutrality test in OXPHOS genes and randomly selected genes.

Supplementary Table S10 Codon Usage for eight four-fold degenerate codon families in F-type, M-type and nuclear OXPHOS genes.

F-type			M-type			Nu-OXPHOS		
Codon	Amino acids	Number	Codon	amino acids	Number	Codon	amino acids	Number
<u>GCA</u>	A	38	<u>GCA</u>	A	35	GCA	A	287
GCC	A	11	GCC	A	14	GCC	A	177
GCG	A	10	GCG	A	19	GCG	A	70
GCU	A	117	GCU	A	98	GCU	A	219

<u>GGA</u>	G	86	<u>GGA</u>	G	54	GGA	G	252
GGC	G	14	GGC	G	16	GGC	G	182
GGG	G	126	GGG	G	120	GGG	G	117
GGU	G	166	GGU	G	121	GGU	G	218
<u>CUA</u>	L	46	<u>CUA</u>	L	53	CUA	L	189
CUC	L	4	CUC	L	7	CUC	L	205
CUG	L	10	CUG	L	20	CUG	L	313
CUU	L	93	CUU	L	71	CUU	L	341
<u>CCA</u>	P	45	<u>CCA</u>	P	24	CCA	P	292
CCC	P	11	CCC	P	12	CCC	P	155
CCG	P	9	CCG	P	19	CCG	P	92
CCU	P	81	CCU	P	81	CCU	P	207
<u>CGA</u>	R	30	<u>CGA</u>	R	27	CGA	R	111
CGC	R	0	CGC	R	2	CGC	R	68
CGG	R	13	CGG	R	13	CGG	R	87
CGU	R	32	CGU	R	22	CGU	R	107
<u>UCA</u>	S	47	<u>UCA</u>	S	48	UCA	S	367
UCC	S	11	UCC	S	14	UCC	S	259
UCG	S	12	UCG	S	16	UCG	S	104
UCU	S	132	UCU	S	111	UCU	S	421
<u>ACA</u>	T	40	<u>ACA</u>	T	27	ACA	T	409
ACC	T	8	ACC	T	10	ACC	T	233
ACG	T	11	ACG	T	11	ACG	T	120
ACU	T	93	ACU	T	92	ACU	T	262
<u>GUA</u>	V	187	<u>GUA</u>	V	109	GUA	V	273
GUC	V	26	GUC	V	26	GUC	V	218
GUG	V	60	GUG	V	91	GUG	V	263
GUU	V	224	GUU	V	210	GUU	V	365

The codons complemently match to the anticodon of tRNA in mitochondrial genome is underlined.

Supplementary Tables 2, 3, 5 and 9 are listed as a separate excel file due to their large size.

Supplementary File 1 The annotation of mitochondrial genes.

Supplementary File 2 Codon usage table for codon adaptation index inference.

Supplementary File 3 The OXPHOS gene list.

Supplementary files 1–3 are listed as a separate package file due to their special file format.

