

Supplementary Tables

Table S1. Assembly and mapping statistics for RNA-seq datasets used to estimate transcript abundance for mt- and nuclear-encoded genes. For most datasets only a subset (~15 million) of the available numbers of reads were used.

Species	SRA Accession #	# Reads Used	# Contigs Assembled	Source
<i>Homo sapiens</i>	SRR1163061	15 M	NA	Goodwin et al. 2014. Cancer Cell 26:851-62
<i>Macaca mulatta</i>	SRR1104954	15 M	NA	XO et al. 2014. BMC Genomics 15:287.
<i>Humulus lupulus</i>	DRR024457	30 M	81,492	Natsume et al. 2015. Plant Cell Physiol. 56:428-41.
<i>Silene conica</i>	SRX1085373	13.4 M	79,242	Rockenbach et al. In revision.
<i>Silene macrodonta</i>	SRR2093712	~15 M	63,956	Rockenbach et al. In revision.
<i>Silene noctiflora</i>	SRX1153129	44.6 M	131,103	Wu et al. 2015. BMC Genomics 16:938.
<i>Arabidopsis thaliana</i>	SRR1030235	15.7 M	NA	NA
<i>Vitis vinifera</i>	SRX245255	15 M	30,561	Poojari et al. 2013. PLoS ONE 8(6): e64194.
<i>Saccharomyces cerevisiae</i>	SRR2046321	15 M	NA	NA

Table S2. Data sources and taxonomic group for the 84 different species used to estimate d_N , d_S , and ω for mt- and nuclear-encoded OXPHOS and glycolysis genes.

Group	Species	Data Source
Primates	Homo sapiens (human)	KEGG
Primates	Pan troglodytes (chimpanzee)	KEGG
Primates	Pan paniscus (bonobo)	KEGG
Primates	Pongo abelii (Sumatran orangutan)	KEGG
Primates	Nomascus leucogenys (northern white-cheeked gibbon)	KEGG
Primates	Macaca mulatta (rhesus monkey)	KEGG
Primates	Macaca fascicularis (crab-eating macaque)	KEGG
Primates	Rhinopithecus roxellana (golden snub-nosed monkey)	KEGG
Primates	Callithrix jacchus (white-tufted-ear marmoset)	KEGG
Rodents	Heterocephalus glaber (naked mole rat)	KEGG
Rodents	Nannospalax galili (Upper Galilee mountains blind mole rat)	KEGG
Rodents	Cricetulus griseus (Chinese hamster)	KEGG
Rodents	Mus musculus (mouse)	KEGG
Rodents	Rattus norvegicus (rat)	KEGG
Cetartiodactyls	Equus caballus (horse)	KEGG
Cetartiodactyls	Camelus ferus (Wild Bactrian camel)	KEGG
Cetartiodactyls	Lipotes vexillifer (Yangtze River dolphin)	KEGG
Cetartiodactyls	Sus scrofa (pig)	KEGG
Cetartiodactyls	Bos mutus (wild yak)	KEGG
Cetartiodactyls	Bos taurus (cow)	KEGG
Cetartiodactyls	Pantholops hodgsonii (chiru)	KEGG
Cetartiodactyls	Ovis aries (sheep)	KEGG
Cetartiodactyls	Capra hircus (goat)	KEGG
Carnivores	Felis catus (domestic cat)	KEGG
Carnivores	Canis familiaris (dog)	KEGG
Carnivores	Ursus maritimus (polar bear)	KEGG
Carnivores	Ailuropoda melanoleuca (giant panda)	KEGG
Bats	Myotis brandtii (Brandt's bat)	KEGG
Bats	Myotis davidii	KEGG

Bats	<i>Pteropus alecto</i> (black flying fox)	KEGG
Birds	<i>Gallus gallus</i> (chicken)	KEGG
Birds	<i>Meleagris gallopavo</i> (turkey)	KEGG
Birds	<i>Anas platyrhynchos</i> (mallard)	KEGG
Birds	<i>Columba livia</i> (rock pigeon)	KEGG
Birds	<i>Ficedula albicollis</i> (collared flycatcher)	KEGG
Birds	<i>Taeniopygia guttata</i> (zebra finch)	KEGG
Birds	<i>Pseudopodoces humilis</i> (Tibetan ground-tit)	KEGG
Birds	<i>Falco peregrinus</i> (peregrine falcon)	KEGG
Birds	<i>Falco cherrug</i> (Saker falcon)	KEGG
Birds	<i>Corvus cornix</i> (hooded crow)	KEGG
Reptiles	<i>Anolis carolinensis</i> (green anole)	KEGG
Reptiles	<i>Alligator sinensis</i> (Chinese alligator)	KEGG
Reptiles	<i>Alligator mississippiensis</i> (American alligator)	KEGG
Reptiles	<i>Pelodiscus sinensis</i> (Chinese soft-shelled turtle)	KEGG
Reptiles	<i>Chelonia mydas</i> (green sea turtle)	KEGG
Amphibians	<i>Xenopus tropicalis</i> (western clawed frog)	KEGG
Amphibians	<i>Xenopus laevis</i> (African clawed frog)	KEGG
Teleosts	<i>Xiphophorus maculatus</i> (southern platyfish)	KEGG
Teleosts	<i>Oryzias latipes</i> (Japanese medaka)	KEGG
Teleosts	<i>Takifugu rubripes</i> (torafugu)	KEGG
Teleosts	<i>Danio rerio</i> (zebrafish)	KEGG
Dipterans	<i>Drosophila sechellia</i>	KEGG
Dipterans	<i>Drosophila simulans</i>	KEGG
Dipterans	<i>Drosophila melanogaster</i> (fruit fly)	KEGG
Dipterans	<i>Drosophila yakuba</i>	KEGG
Dipterans	<i>Aedes aegypti</i> (yellow fever mosquito)	KEGG
Dipterans	<i>Anopheles gambiae</i> (mosquito)	KEGG
Dipterans	<i>Musca domestica</i> (house fly)	KEGG
Corals	<i>Acropora tenuis</i>	Transcriptomes (http://www.bio.utexas.edu/research/matz_lab/matzlab/Data.html) / NC_003522.1
Corals	<i>Acropora hyacinthus</i>	Transcriptomes (http://www.bio.utexas.edu/research/matz_lab/matzlab/Data.html) / NC_022826.1

Corals	<i>Porites porites</i> (mt)/ <i>P. asteroides</i> (nuc)	Transcriptomes (http://www.bio.utexas.edu/research/matz_lab/matzlab/Data.html) / NC_008166.1
Corals	<i>Montastrea faveolata</i> (mt)/ <i>M. cavernosa</i> (nuc)	Transcriptomes (http://people.oregonstate.edu/~meyere/data.html) / NC_007226.1
Corals	<i>Seriatopora hystrix</i>	Transcriptomes (http://people.oregonstate.edu/~meyere/data.html) / NC_010244.2
Corals	<i>Madracis myriaster</i> (mt)/ <i>M. auretenra</i> (nuc)	Transcriptomes (http://people.oregonstate.edu/~meyere/data.html) / NC_011160.1
Corals	<i>Platygyra carnosus</i> (mt)/ <i>P. daedalea</i> (nuc)	Transcriptomes (http://people.oregonstate.edu/~meyere/data.html) / NC_020049.1
Silene	<i>S. conica</i>	Transcriptomes (see Table S1)
Silene	<i>S. macrodonta</i>	Transcriptomes (see Table S1)
Silene	<i>S. noctiflora</i>	Transcriptomes (see Table S1)
Eudicots	<i>Vitis vinifera</i> (wine grape)	KEGG
Eudicots	<i>Arabidopsis thaliana</i> (thale cress)	KEGG
Eudicots	<i>Ricinus communis</i> (castor bean)	KEGG
Eudicots	<i>Glycine max</i> (soybean)	KEGG
Eudicots	<i>Cucumis sativus</i> (cucumber)	KEGG
Eudicots	<i>Nicotiana tabacum</i> (tobacco)	Transcriptomes (see Table S1)
Eudicots	<i>Humulus lupulus</i> (hop)	Transcriptomes (see Table S1)
Eudicots	<i>Lupinus albus</i> (white lupine)	Transcriptomes (see Table S1)
Eudicots	<i>Vigna radiata</i> (mung bean)	KEGG
Monocots	<i>Musa acuminata</i> (wild Malaysian banana)	KEGG
Monocots	<i>Zea mays</i> (maize)	KEGG
Monocots	<i>Oryza sativa japonica</i> (Japanese rice) (RefSeq)	KEGG
Monocots	<i>Sorghum bicolor</i> (sorghum)	KEGG
Monocots	<i>Phoenix dactylifera</i> (date palm)	KEGG
Fungi (Aspergillus)	<i>Aspergillus nidulans</i>	KEGG
Fungi (Aspergillus)	<i>Aspergillus niger</i>	KEGG

Table S3. Sources of phylogenetic data used to estimate d_N , d_S , and ω for mt- and nuclear-encoded oxidative phosphorylation and glycolysis genes. Note that some groups did not require reference trees due to a limited number of taxa.

Taxonomic group	Source
Primates	Perelman et al. 2011. PLoS Genet 7(3): e1001342.
Rodents	Blanga-Kanfi et al. 2009. BMC Evol Biol 9:71.
Cetartiodactyls	Agnarsson et al. 2008. Mol Phylogenet Evol 48: 964-85.
Carnivores	Nyakatura et al. 2012. BMC Biology 10:12.
Birds	Prum et al. 2015. Nature 526:569-73.
Reptiles	Crawford et al. 2012. Biol Lett 8: 783–786.
Teleosts	Near et al. 2012. PNAS 109: 13698–13703.
Dipterans	Seetharam et al. 2013. PeerJ 1:e226
Silene	Rautenberg et al. 2012. Syst Bot 37:226-237.
Corals	Kitchen et al. 2015. G3 5:2441-52.
Eudicots	Adams et al. 2002. PNAS 99: 9905–9912.
Monocots	Adams et al. 2002. PNAS 99: 9905–9912.

Supplementary figures and captions

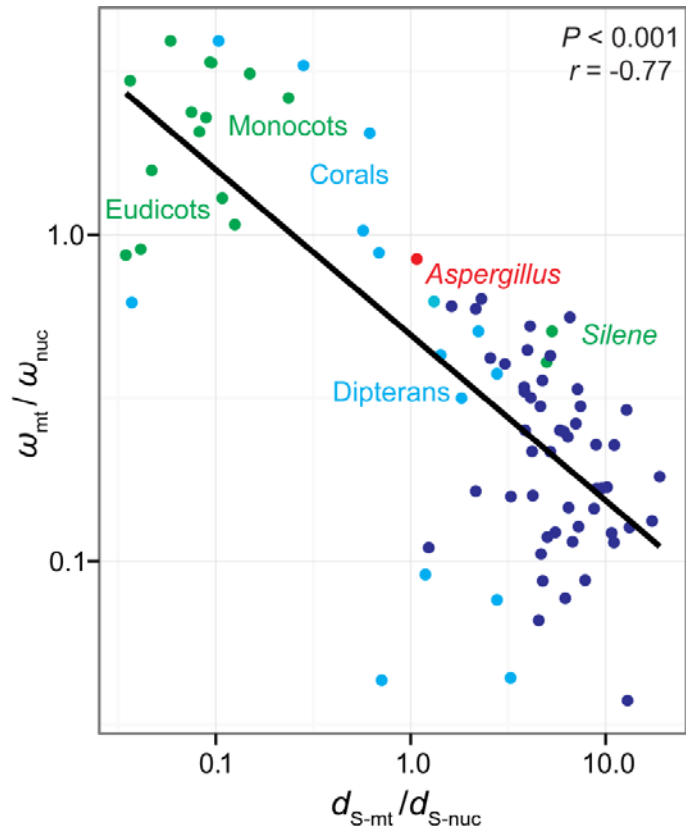


Fig. S1. Signatures of selection on mt and N-mt OXPHOS subunits across eukaryotic lineages when considering individual taxa (using model = 1 in PAML, which estimates separate ω values for each branch in a tree, instead of model = 0, which estimates a single ω value for the entire tree). Color schemes and labeling are as in Fig. 1.

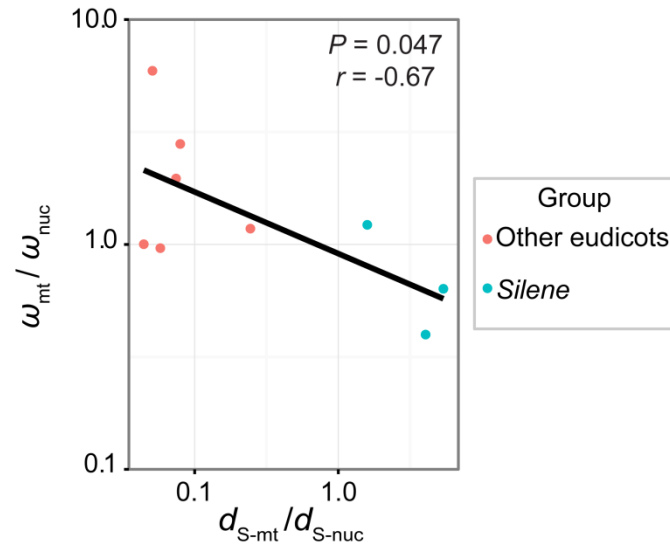


Fig. S2. Signatures of selection on mt and N-mt OXPHOS genes in eudicots with slow- and fast-evolving mt genomes after removal of predicted N-terminal signal peptides from N-mt genes.

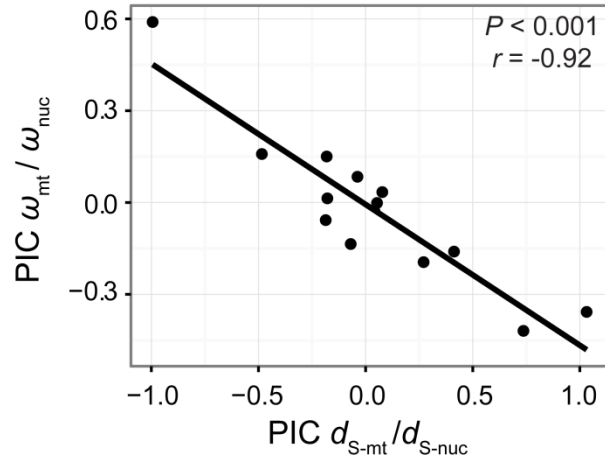


Fig. S3. Signatures of selection on mt and N-mt OXPHOS genes across eukaryotic lineages after accounting for phylogeny with phylogenetic independent contrasts (PIC).

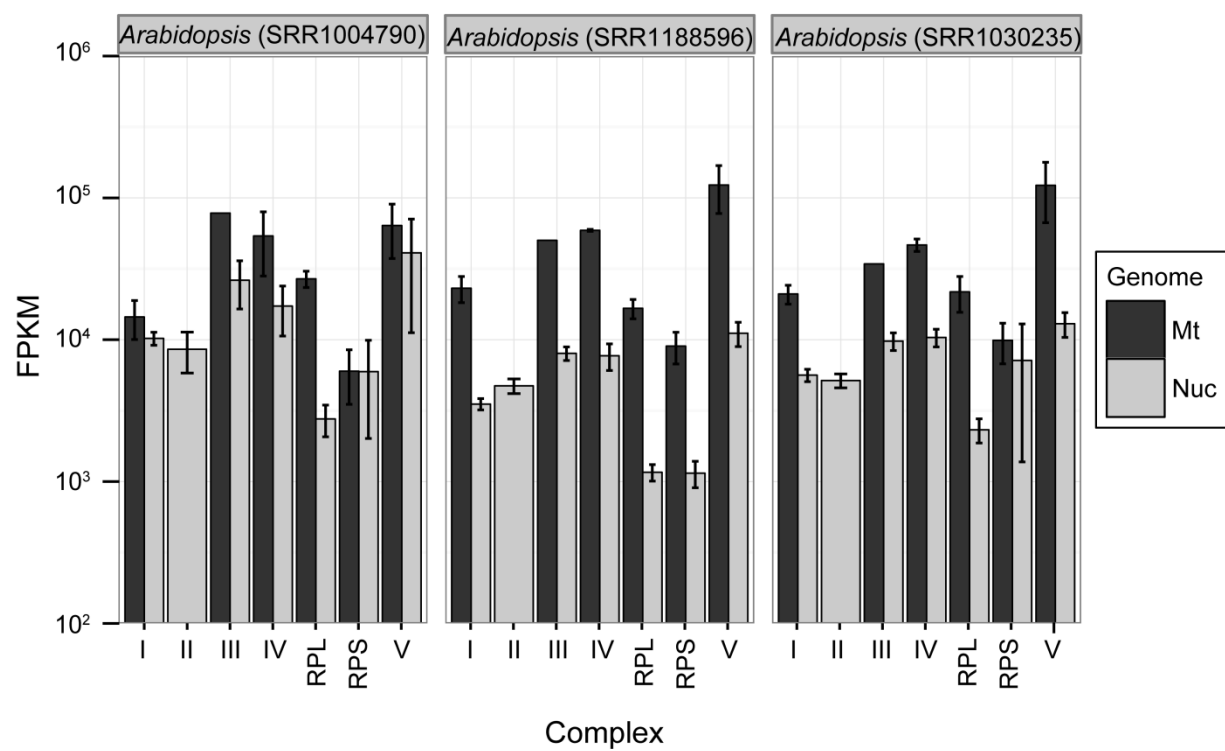


Fig. S4. Differences in transcript abundance between mt and N-mt OXPHOS and ribosomal subunits in three different *Arabidopsis thaliana* datasets. Error bars show \pm SEM.

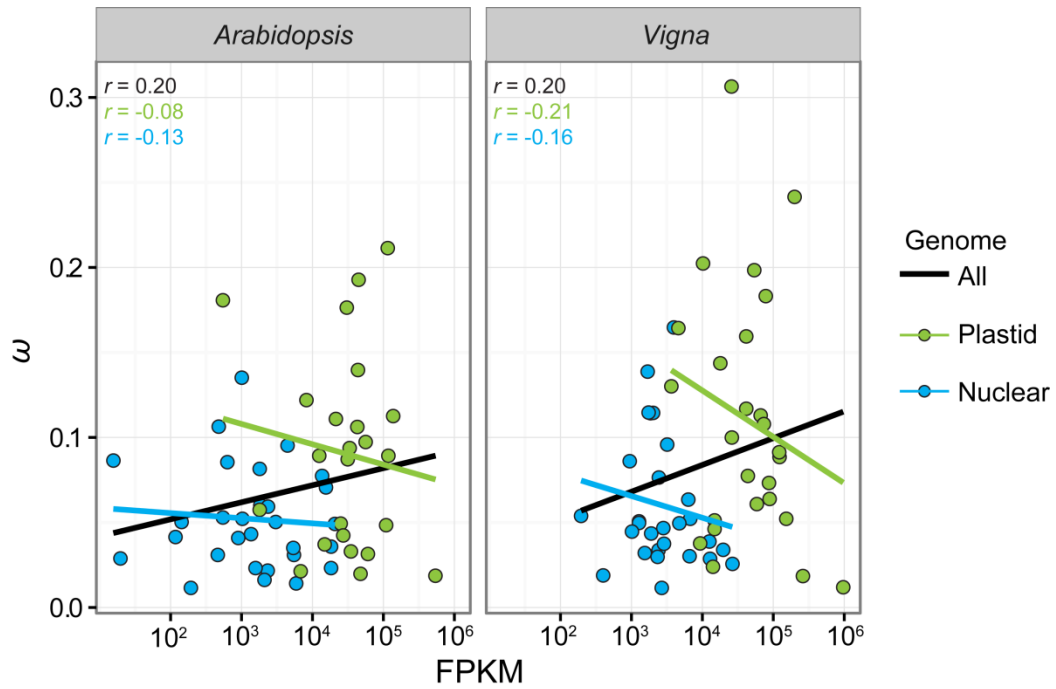


Fig. S5. Relationship between transcript abundance and ω for plastid- and nuclear-encoded genes that produce subunits in the plastid ATP synthase, NADH-plastoquinone oxidoreductase, and photosystems I and II. Best-fit lines in black are for the total dataset, including both plastid and nuclear genes, while those in green and blue are when using either set, respectively.

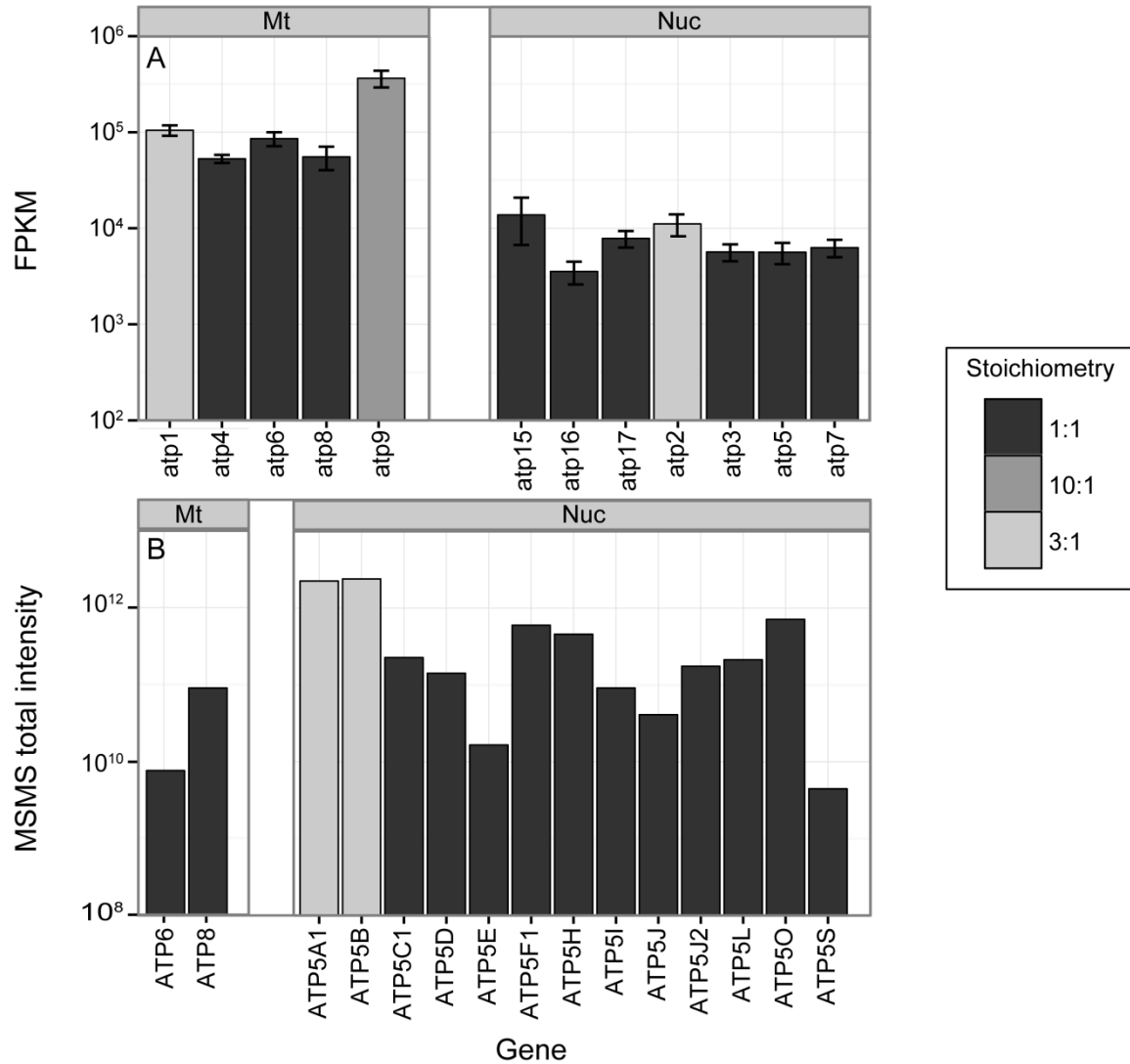


Fig. S6. Differences in (A) transcript abundance and (B) protein abundance among complex V (ATP synthase) genes incorporated into the multisubunit complex at different stoichiometries. Transcript abundance was quantified for angiosperms shown in Fig. 3 (Error bars show \pm SEM). Protein abundance was quantified via MitoCarta (19) as “MSMS total intensity” from pooling spectra from 14 different mouse tissues. Stoichiometric ratios were taken from: Stock et al. 1999. *Science* 286, 1700-1705.

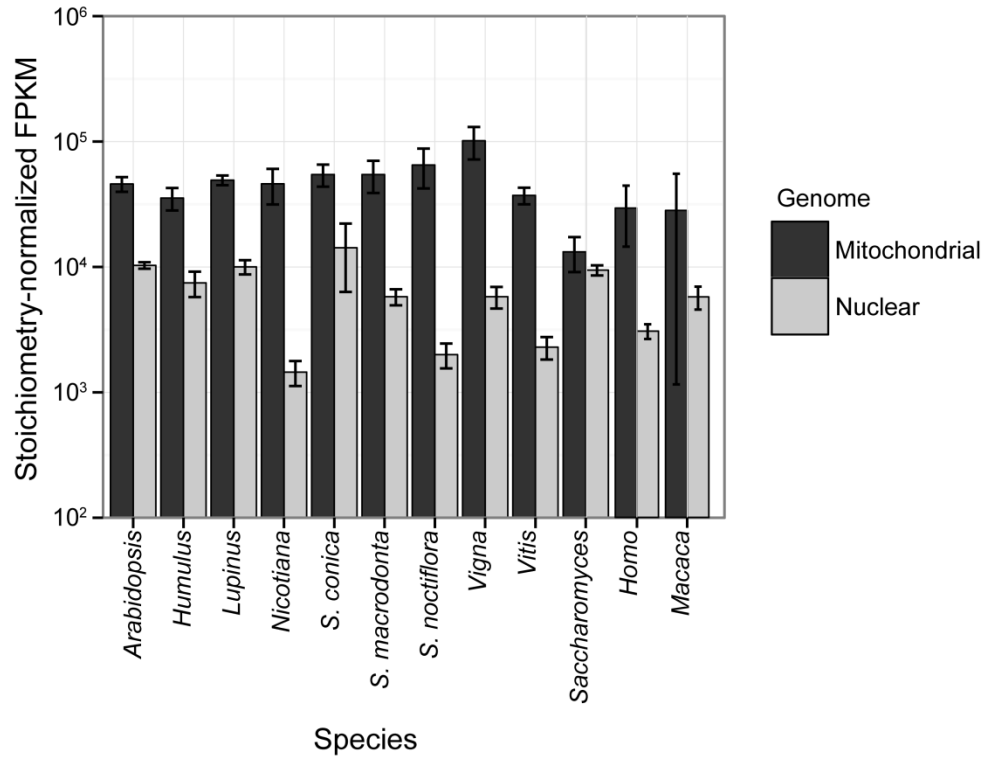


Fig. S7. Differences in transcript abundance between mt and N-mt complex V (ATP synthase) genes after accounting for stoichiometry. FPKM values were normalized by dividing by the number of subunit copies incorporated into the final ATP synthase multisubunit complex. Error bars show \pm SEM.

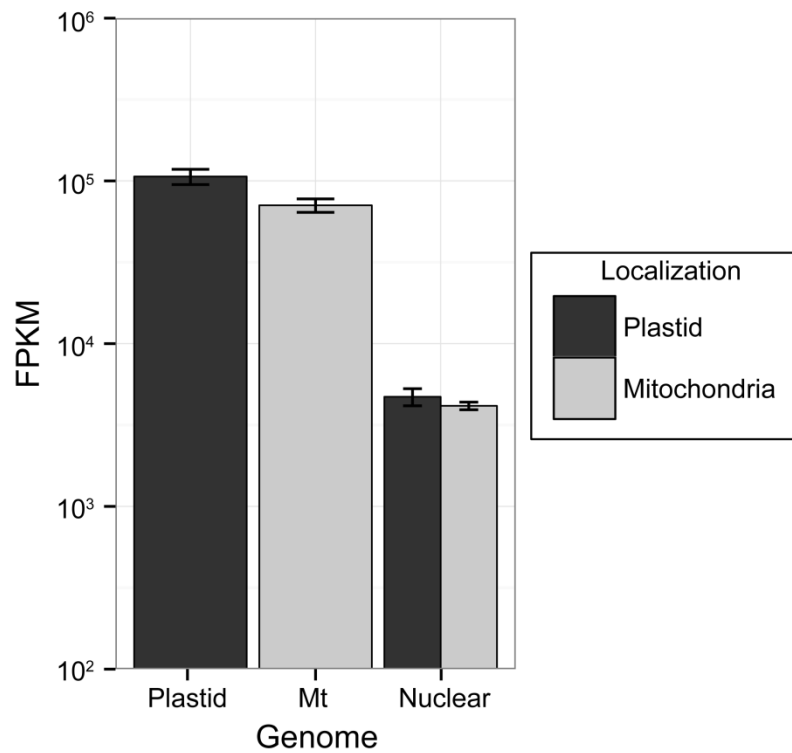


Fig. S8. Differences in transcript abundance between organelle and nuclear-encoded genes targeted to mitochondria vs. plastids in the nine angiosperm taxa studied for expression (i.e., in Fig. 3). For the mt genome, only OXPHOS subunits were used (no ribosomal proteins, because these were only measured in *Arabidopsis*). For the plastid genome, only the plastid ATP synthase and NADH-plastoquinone oxidoreductase were used (no photosystem genes, because these were only measured in *Arabidopsis* and *Vigna*). Individual genes (not averages of species) were used to calculate averages for each category as well as error bars (\pm SEM).

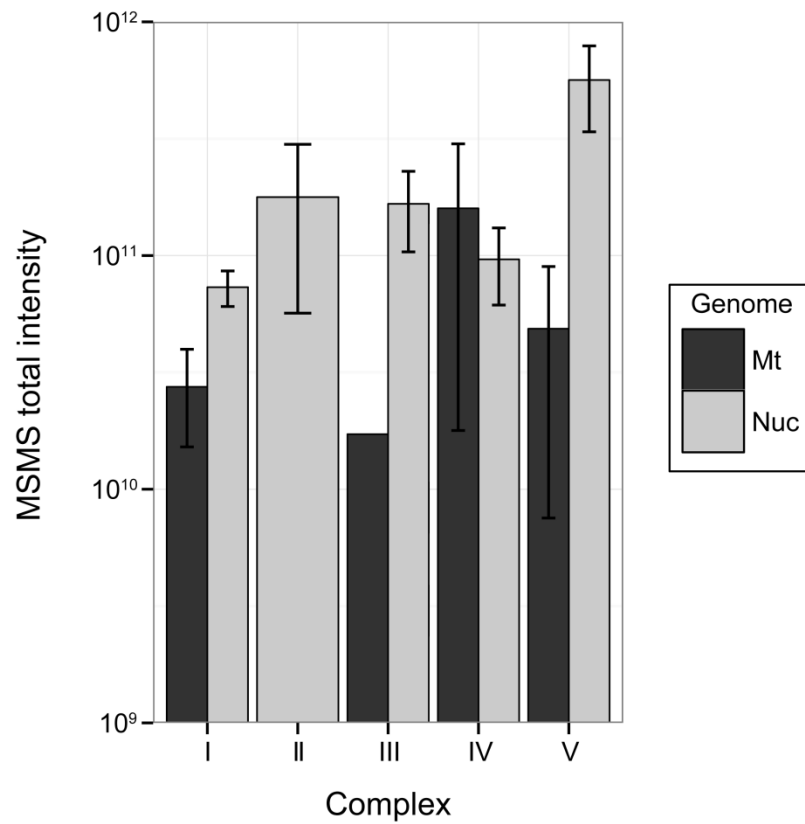


Fig. S9. Differences in protein abundance between mt and N-mt OXPHOS genes. Protein abundance was quantified via MitoCarta (19) as “MSMS total intensity” from pooling spectra from 14 different mouse tissues. Error bars show \pm SEM.

Supplementary Data Files

Supplementary Data File 1. Estimates of transcript abundance for mt- and nuclear-encoded genes examined in this study.

Supplementary Data File 2. d_N , d_S , and ω values estimated in this study.

Supplementary Data File 3. Transcript abundances and ω values estimated for angiosperms and primates.