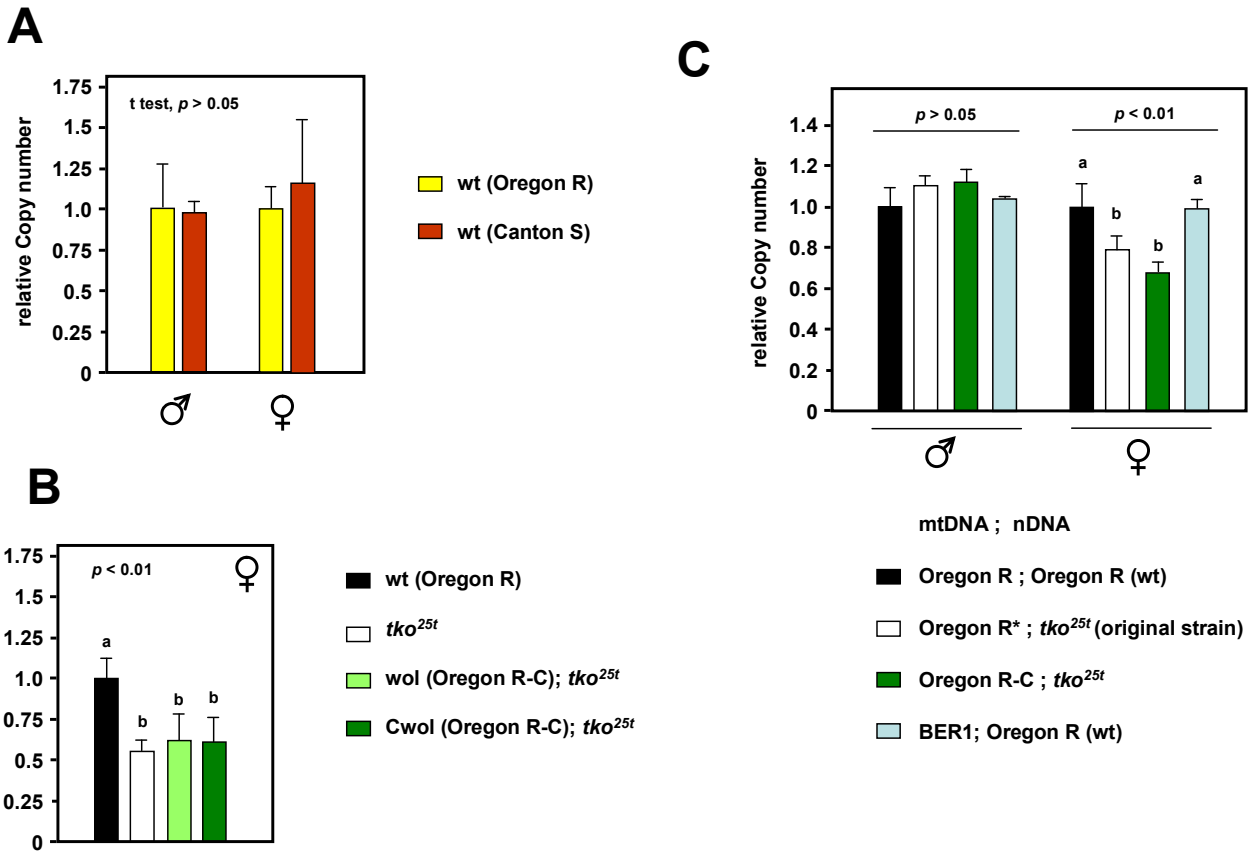
A
t test, p > 0.05
relative Copy number
1.75
1.5
1.25
1.0
0.75
0.5
0.25
0
♂
♀
wt (Oregon R)
wt (Canton S)
B
p < 0.01
♀
relative Copy number
a
b
b
b
wt (Oregon R)
tko25t
wol (Oregon R-C); tko25t
Cwol (Oregon R-C); tko25t
C
p > 0.05
p < 0.01
relative Copy number
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
a
b
b
a
♂
♀
mtDNA ; nDNA
Oregon R ; Oregon R (wt)
Oregon R* ; tko25t (original strain)
Oregon R-C ; tko25t
BER1; Oregon R (wt)

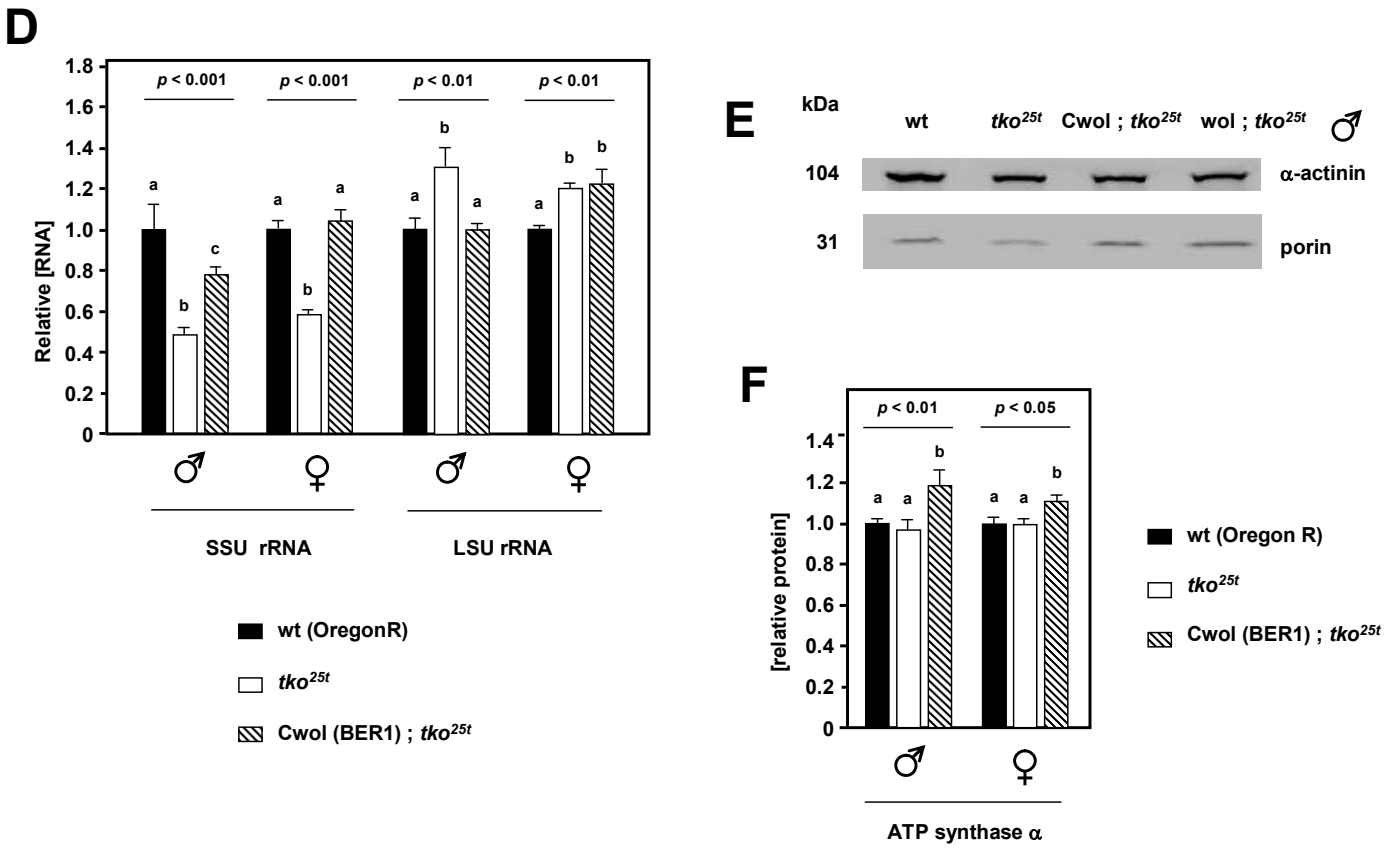

Figure S2 Molecular correlates of partial suppression of *tko*^{25t} by the suppressor mtDNA backgrounds. (A) Supplementary data to Fig. 2D: copy number of mtDNA in two different wild-type strains is similar. Copy number, relative to 18S rDNA, means ± SD, was normalized to that in Oregon R flies of the same sex. The copy number differences seen in *tko*^{25t} flies in different backgrounds (Fig. 2D) are outside the range of variation due to strain background only. (B) Supplementary data to Fig. 2D: the copy number of mtDNA in female *tko*^{25t} flies is significantly lower than in wild-type flies also in a second non-suppressor mtDNA background (Oregon R-C). Data from first two columns reproduced from Fig.2D (experiments were carried out in parallel). (C) Further supplementary data to Fig. 2D: mtDNA copy number is not altered by BER1 mtDNA in a wild-type nuclear background. a, b denote significantly different data classes. Oregon R* denotes the mtDNA of the original *tko*^{25t} strain, whose sequence is very similar (but not identical) to Oregon R or Oregon R-C (Table S1). (D) Supplementary data to Fig. 2E: levels of mitoribosomal SSU and LSU RNA levels in flies of the indicated genotypes relative to the *mRpL32* mRNA standard, means ± SD, normalized to the values in wild-type Oregon R flies of the given sex. The same data were used to compute the SSU/LSU ratios plotted in Fig. 2E. The decreased ratio of SSU to LSU rRNA in *tko*^{25t} flies consists of a decrease in SSU rRNA combined with a small, perhaps compensatory increase in that of LSU rRNA, as reported previously (KEMPPAINEN *et al*. 2009). (E) Representative Western blot of protein extracts from males flies of the indicated genotype, probed for porin (mitochondrial outer membrane marker) and for α-actinin (cytosolic loading control). The global amount of mitochondria, as measured by this assay, is decreased in the presence of the *tko*^{25t} mutation in the original (Oregon R-related) mtDNA background, but restored to wild-type levels in the BER1 background, whether *Wolbachia* are present (wol) or absent (Cwol). The summary data of Fig. 2F are compiled from densitometry of this and equivalent blots. (F) Levels of a representative subunit of complex V (ATP synthase, subunit α), based on densitometry of Western blots, normalized against a cytosolic loading control (α-actinin). In all panels a and b denote significantly different data classes (Newman-Keuls test, $p < 0.05$, based on ANOVA, p values as indicated, each sex and, where appropriate, each gene considered separately).