

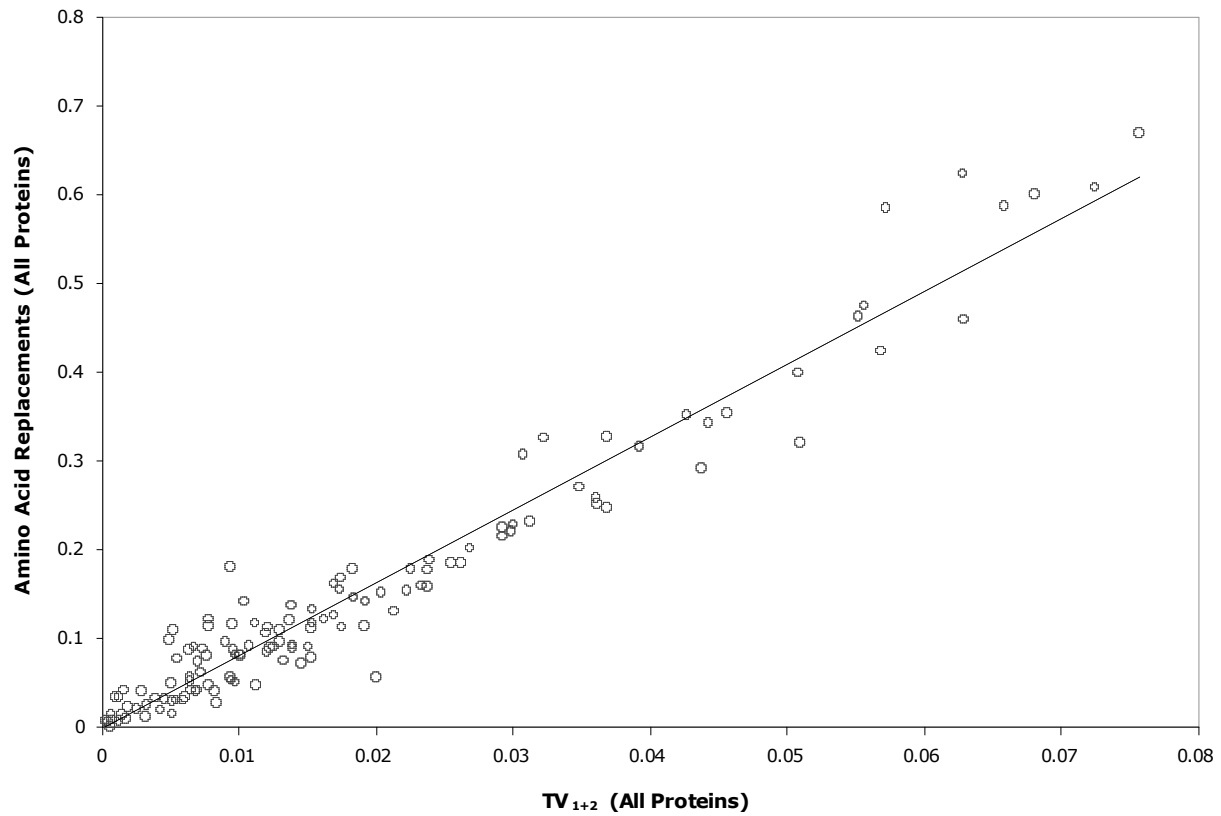


Figure S10. Estimated amino acid replacements (proportion of replacements per sequence) versus transversion substitutions at 1st and 2nd codon positions (dN_{TV12}). Values are given per site for all mitochondrial protein-coding genes. The number of amino acid replacements were estimated using PAML (see Methods). Best-fit line: $y = 8.1932x$, $r^2 = 0.9456$, $p < 0.001$.