

Supplemental Data

The Diversity Present in 5140

Human Mitochondrial Genomes

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Figures for polymorphisms with a frequency of at least 0.1%

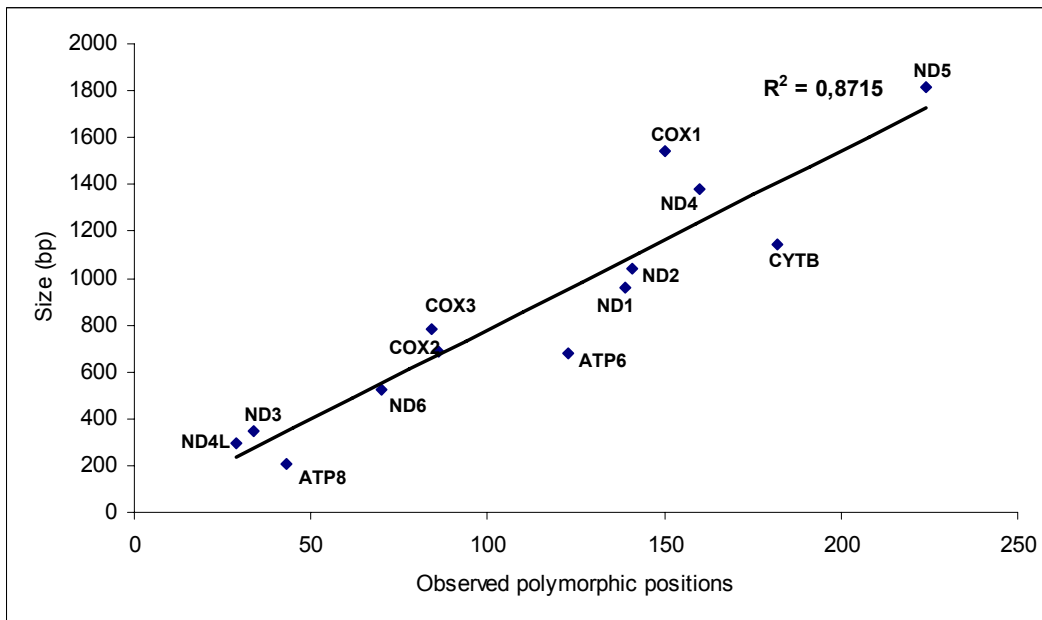


Figure S1. Correlation between the observed polymorphic positions and the size (bp) in the 13 protein-coding genes

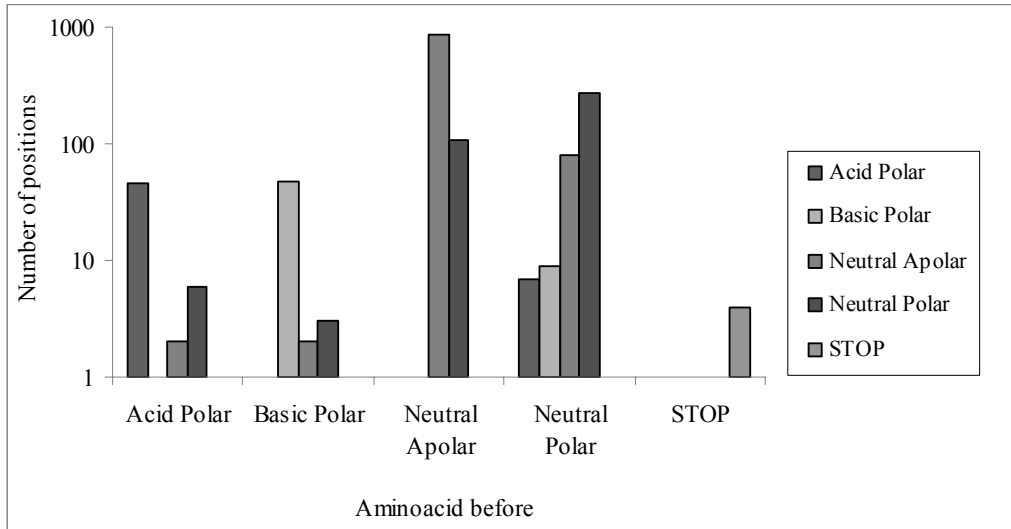


Figure S2. Distributions of types of amino acids before and after the substitution.

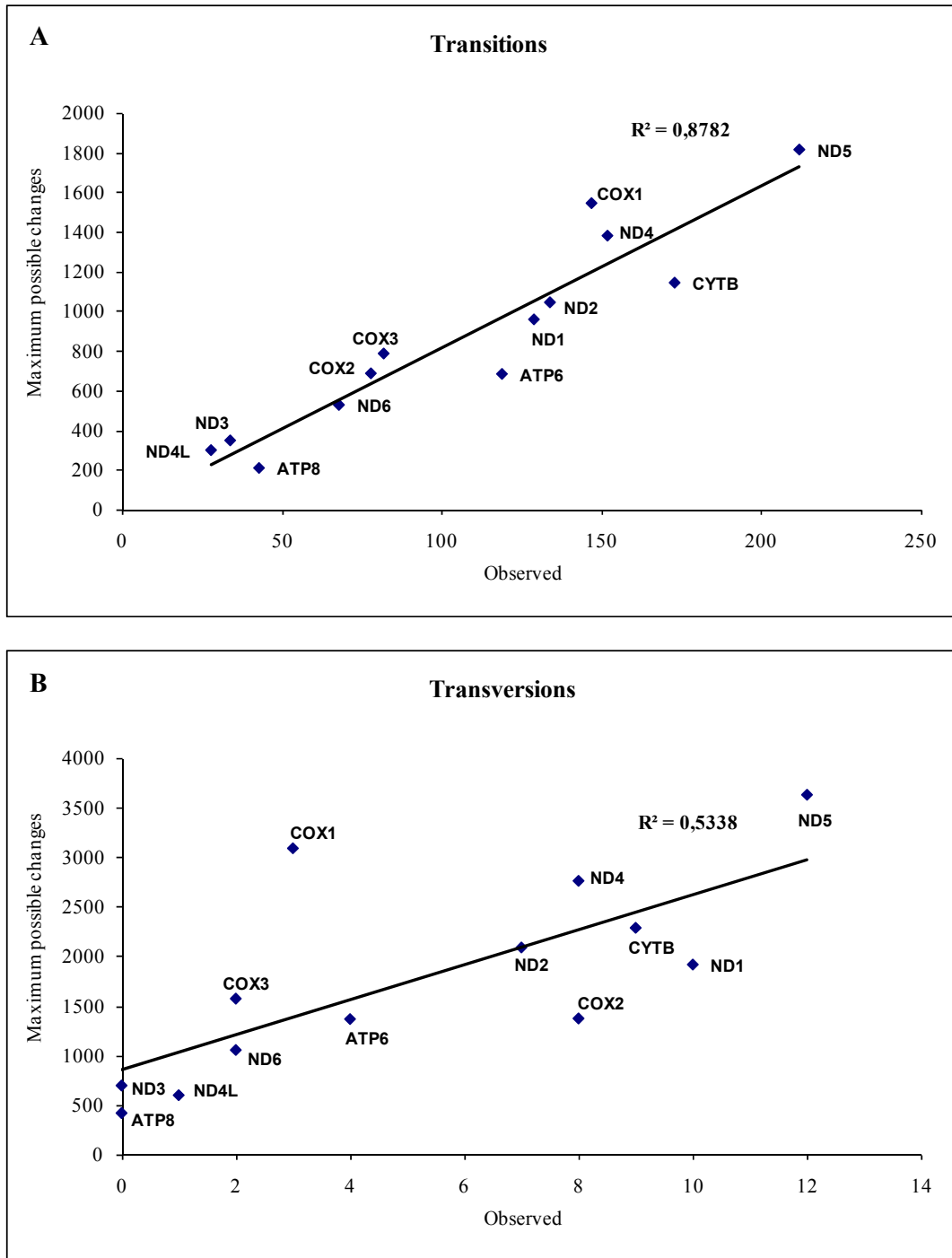


Figure S3. Correlation between the observed and maximum possible variations for transitions (A) and transversions (B) in the 13 protein-coding genes.

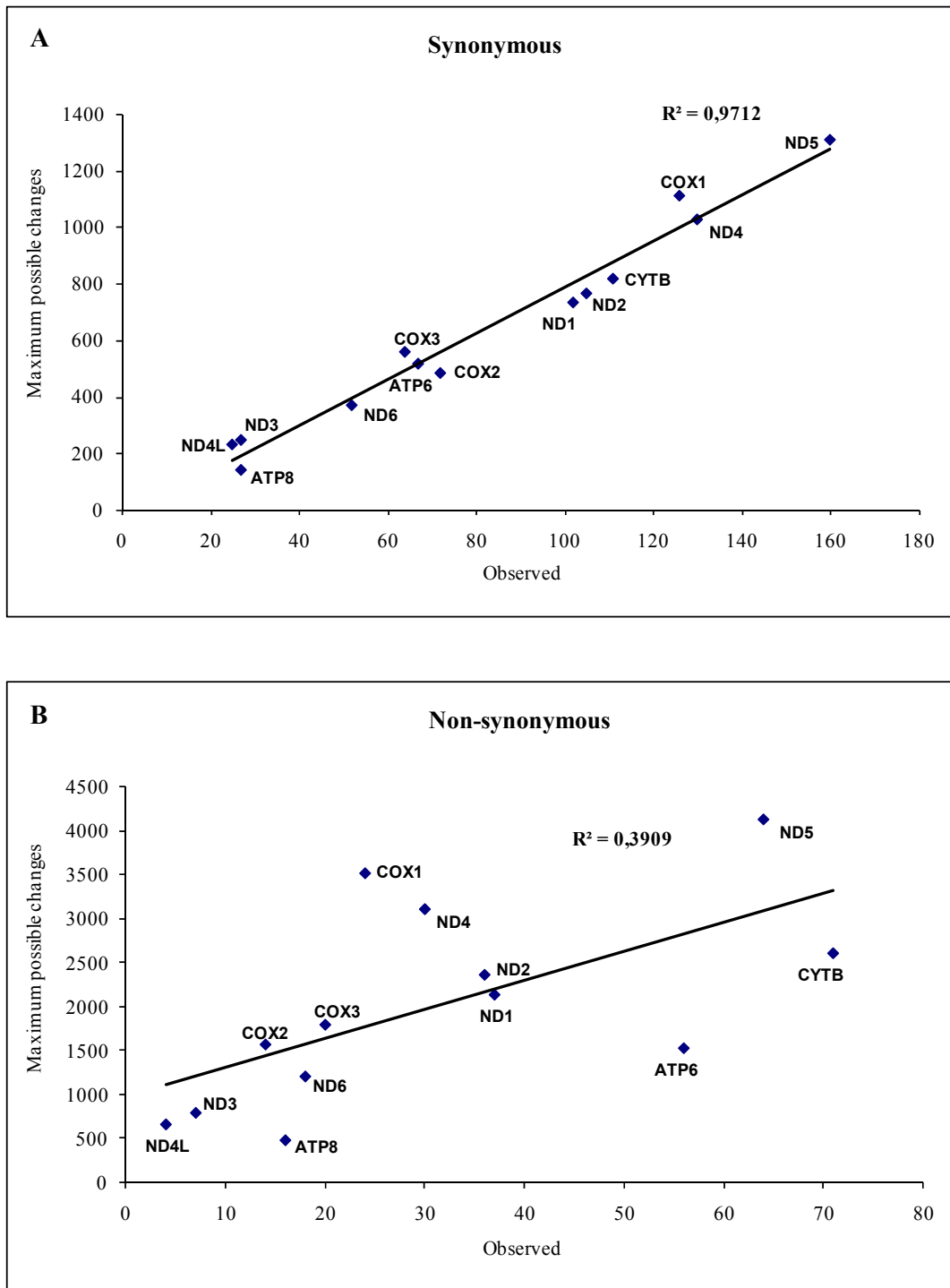


Figure S4. Correlation between observed and maximum possible variations for synonymous (A) and non-synonymous (B) substitutions in the 13 protein-coding genes.

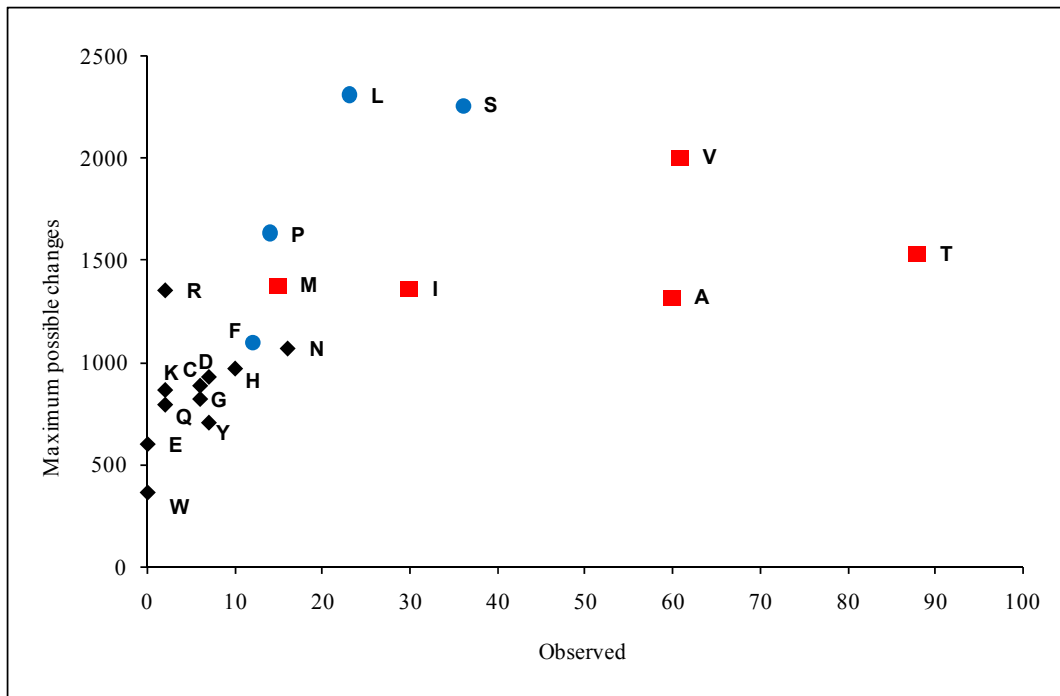


Figure S5. Correlation between observed and maximum possible variations for amino acids originated from non-synonymous mutations.

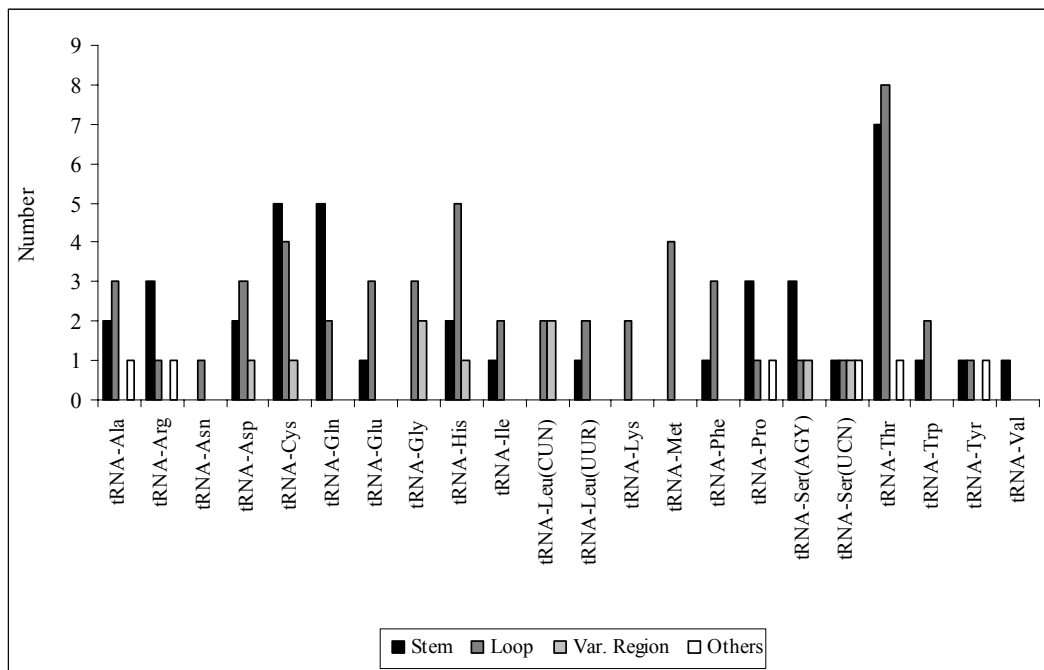
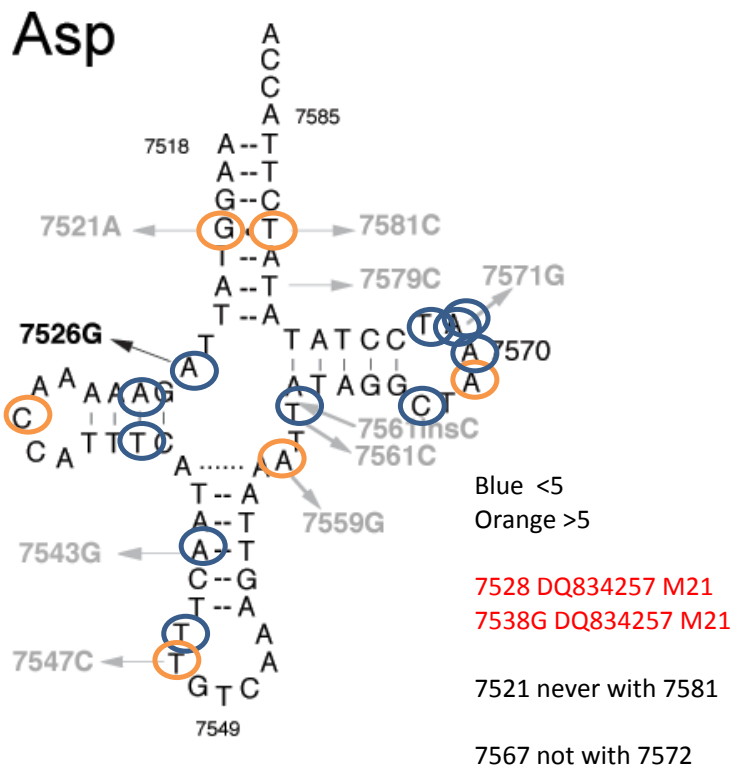
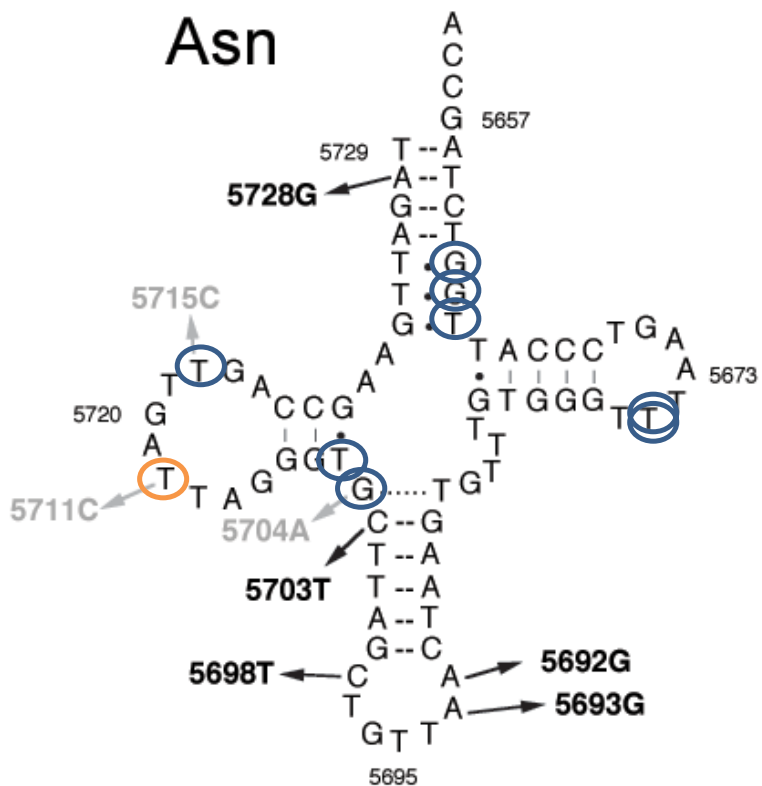
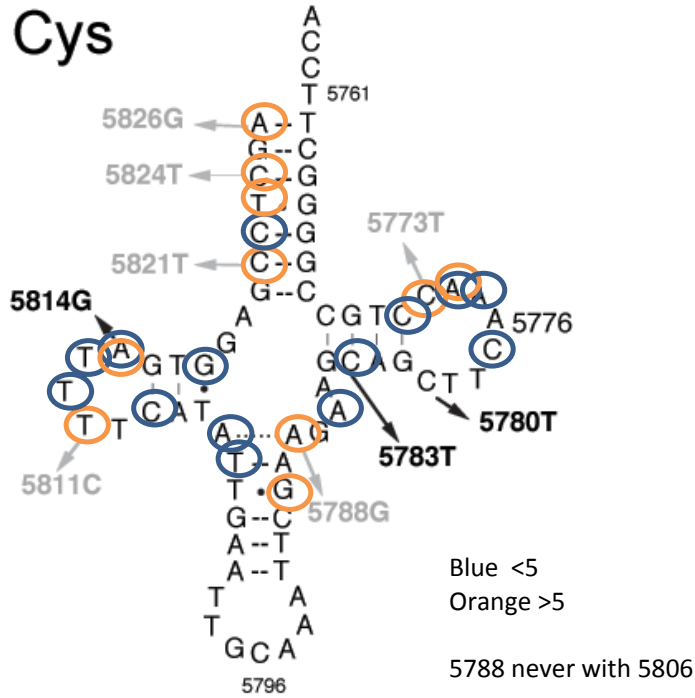


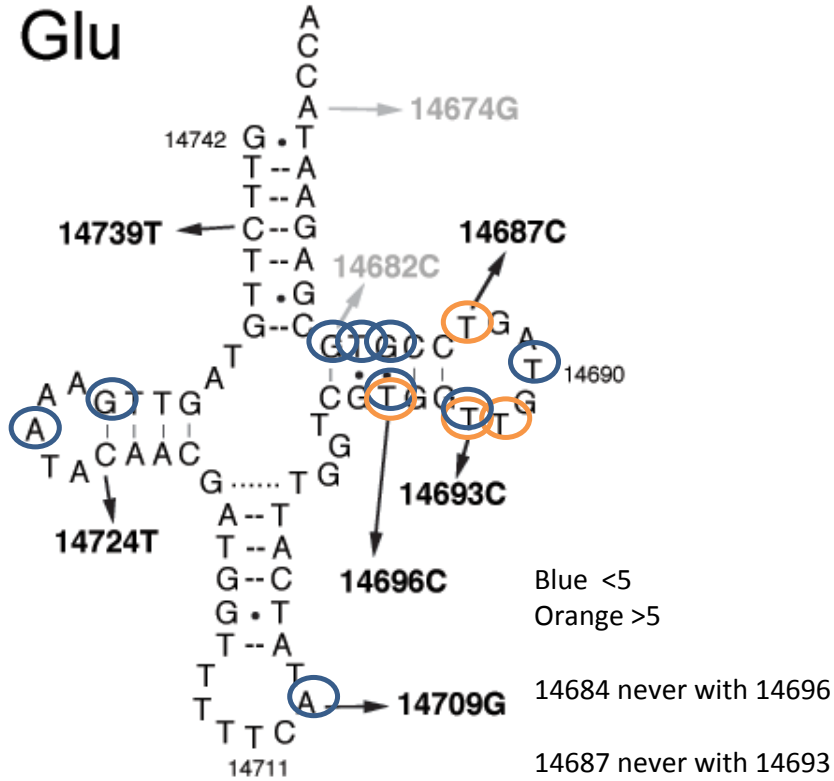
Figure S6. Distribution of polymorphic positions in the various structural regions of tRNAs.



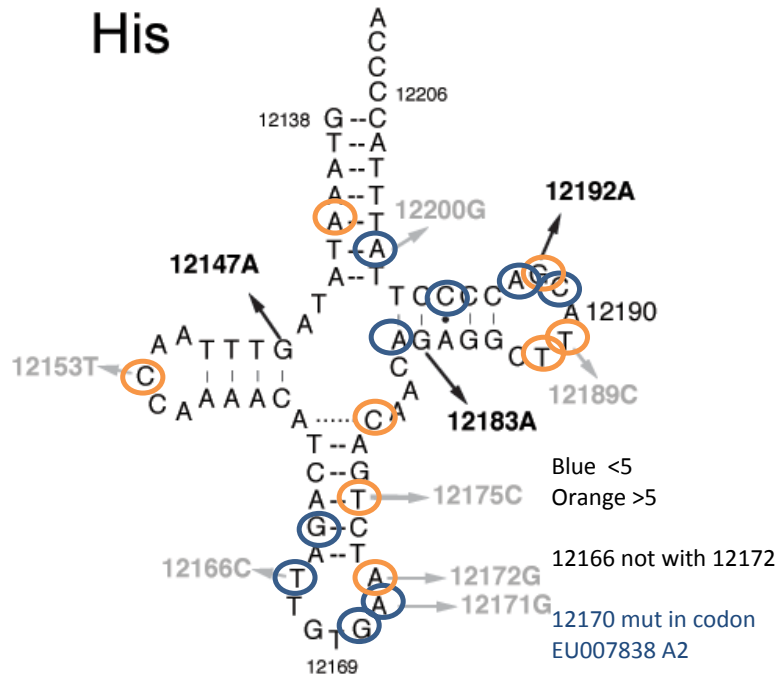
Cys



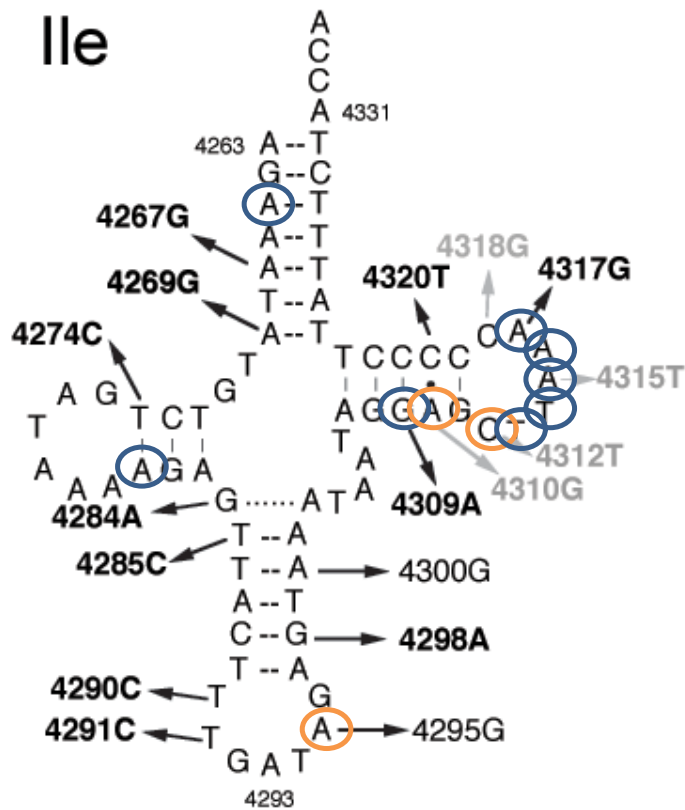
Glu



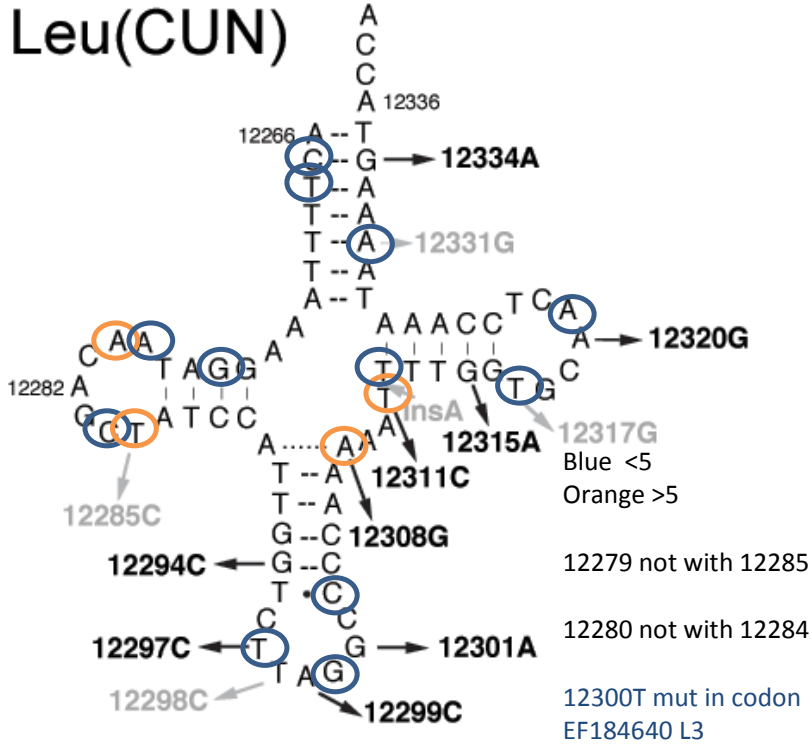
His



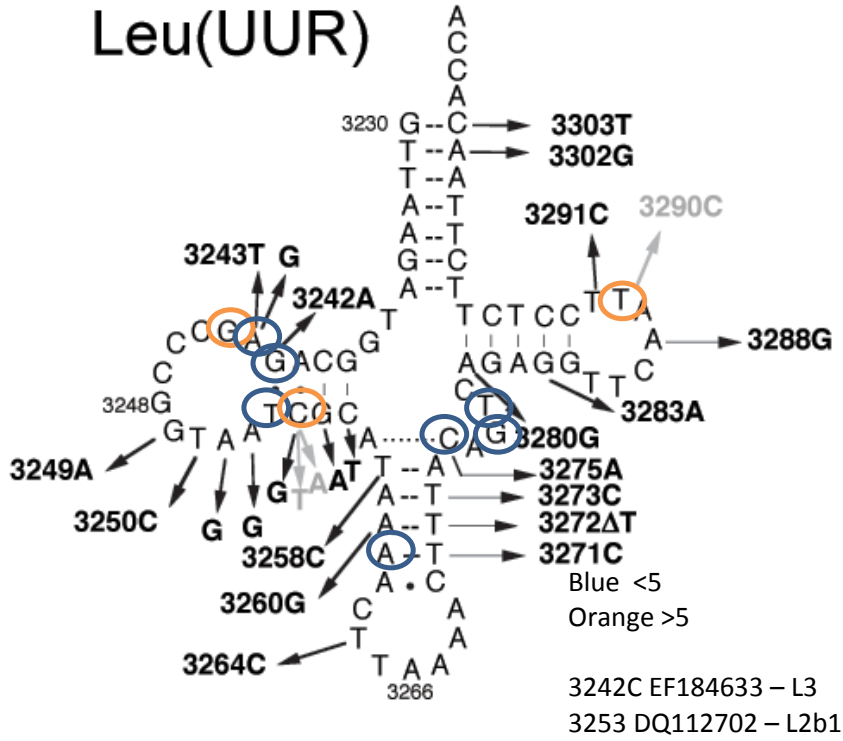
Ile



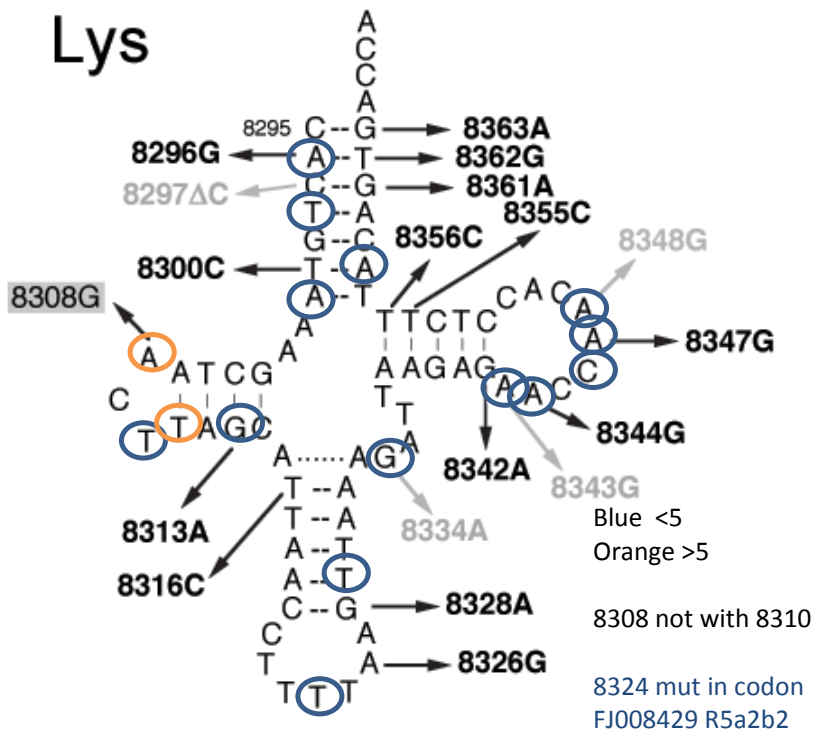
Leu(CUN)



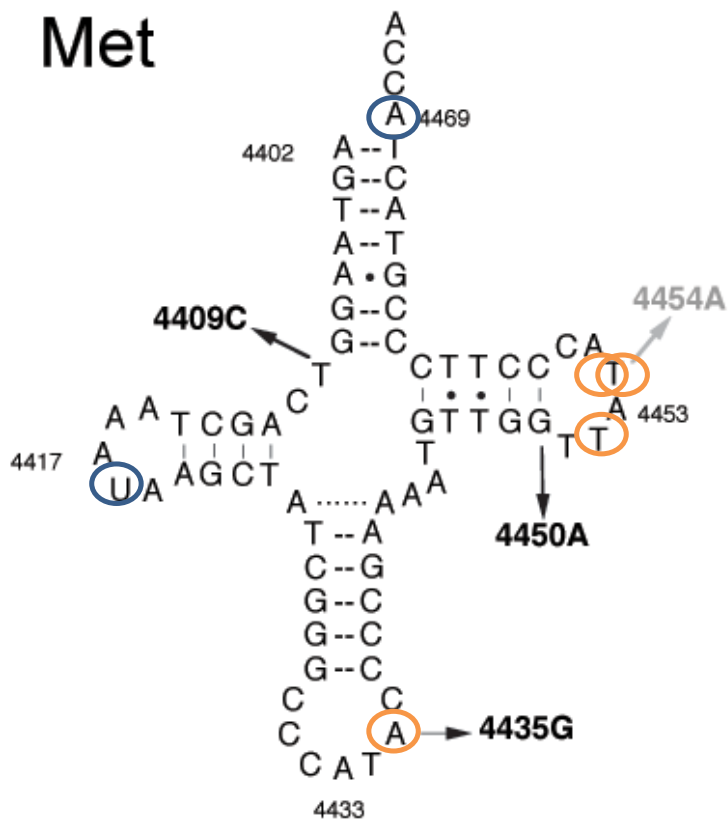
Leu(UUR)



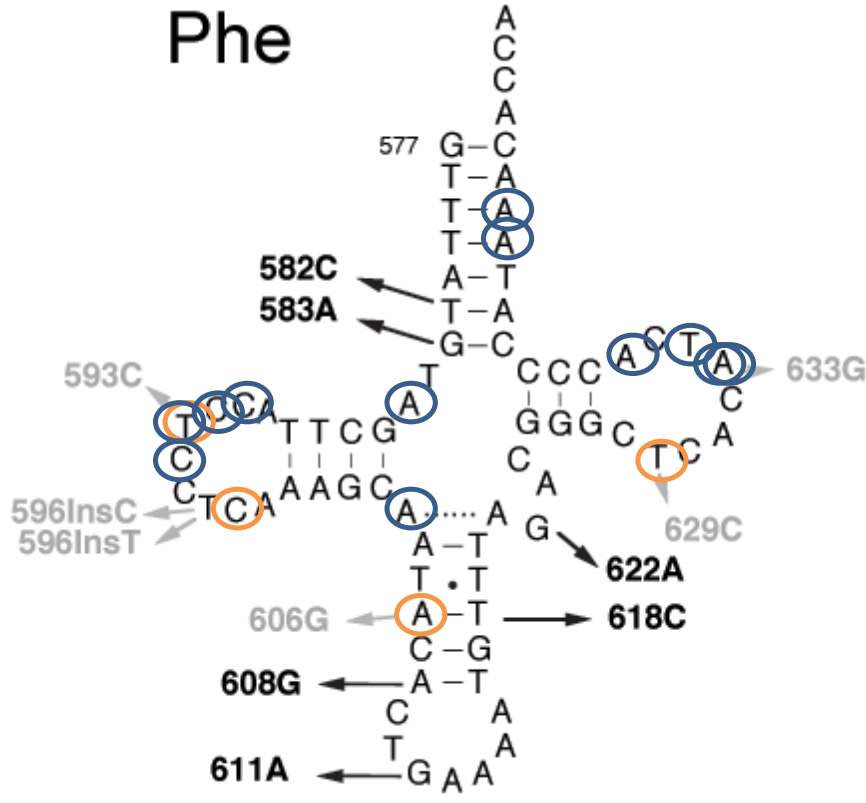
Lys



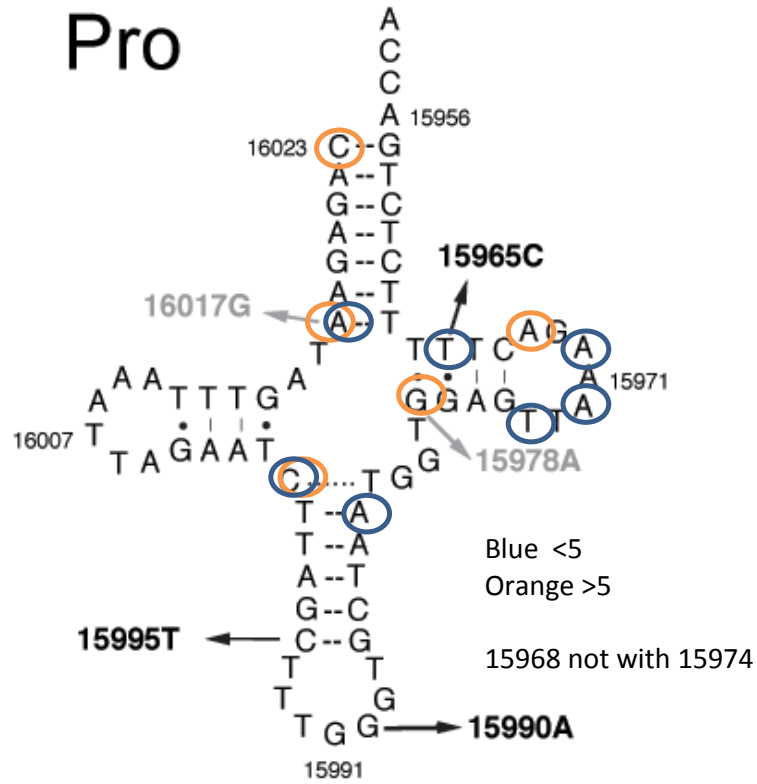
Met



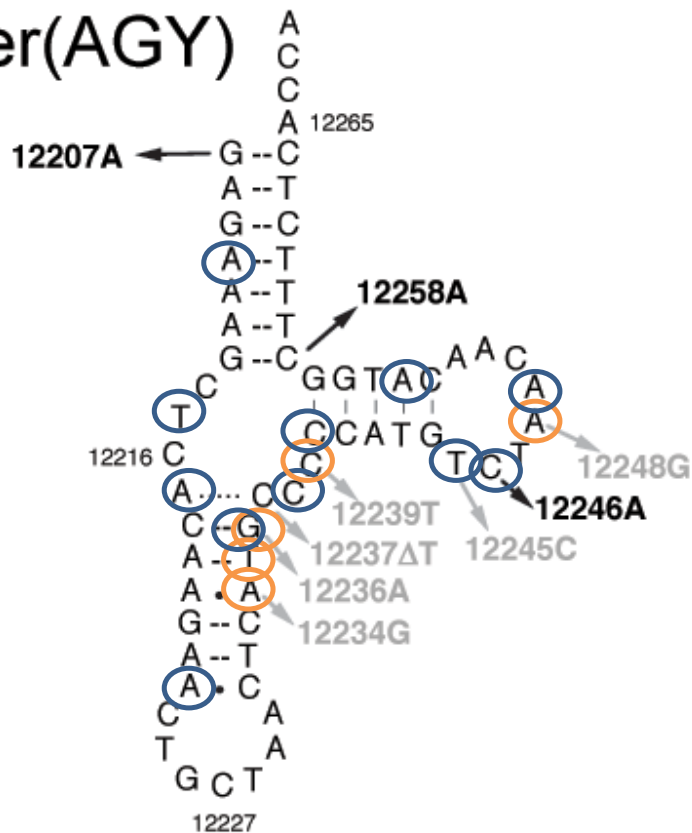
Phe



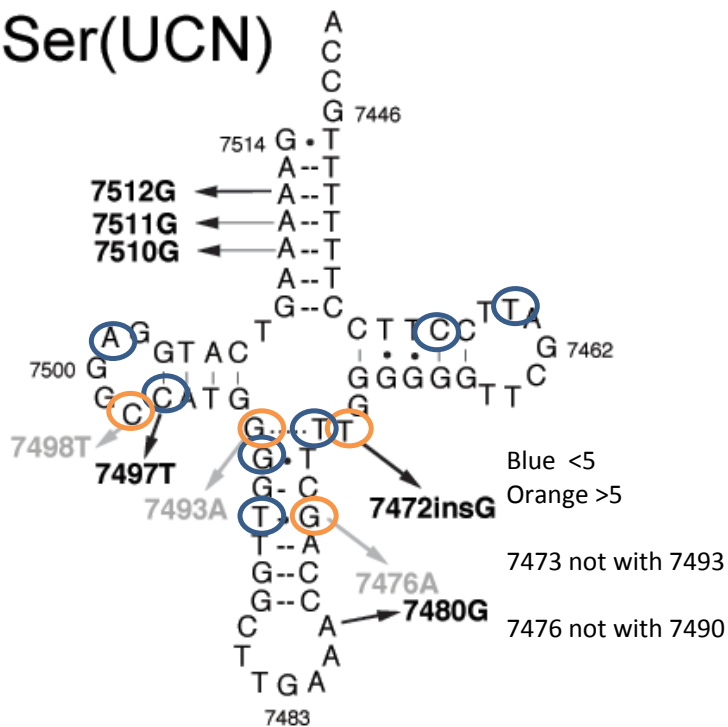
Pro



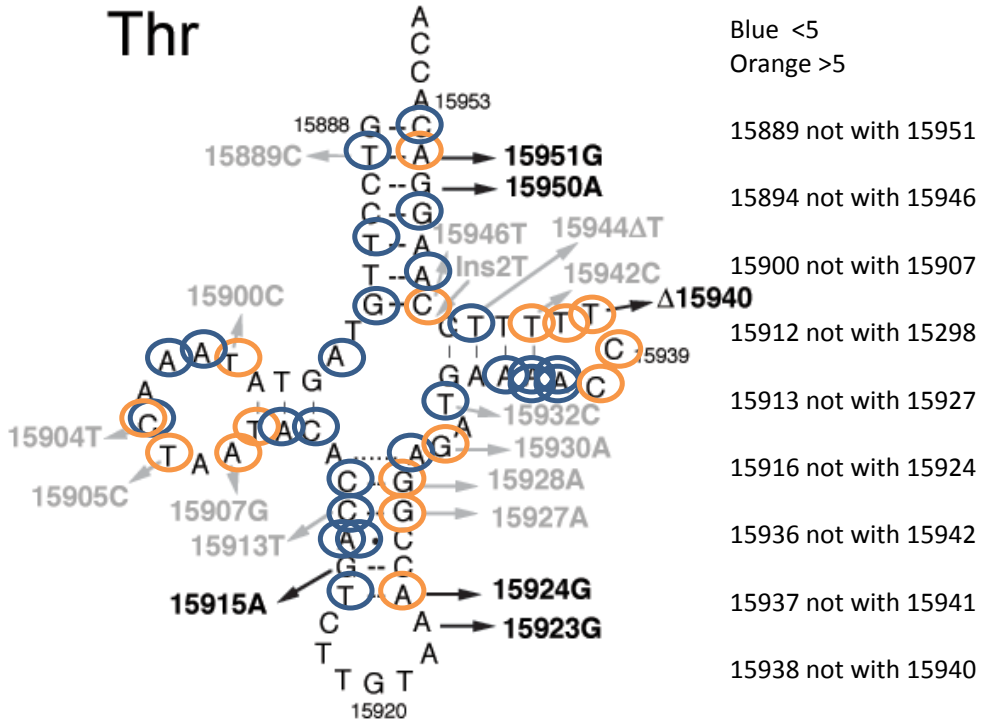
Ser(AGY)



Ser(UCN)



Thr



Trp

