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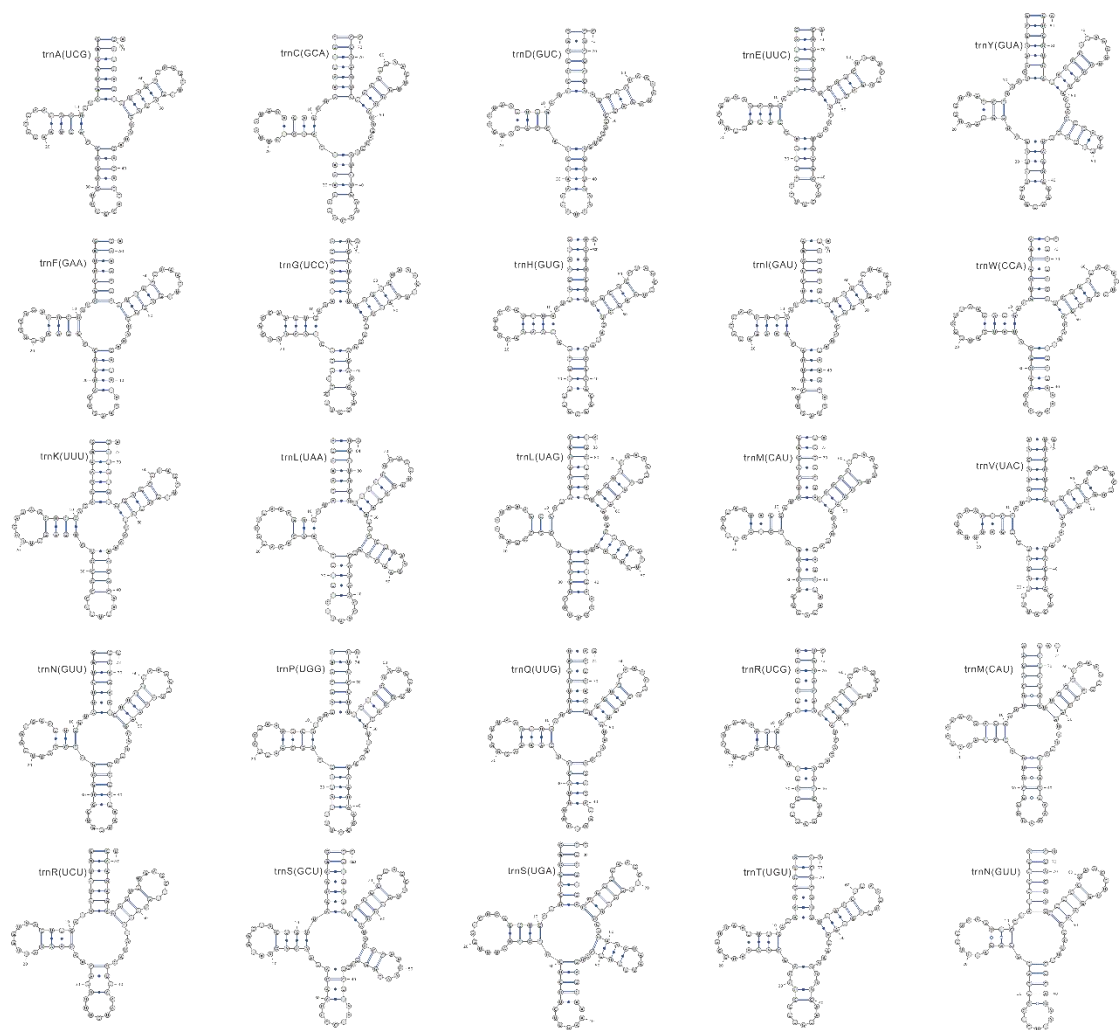


Figure S1. Predicted secondary cloverleaf structures for tRNAs of *Cyathus striatus* 87405.

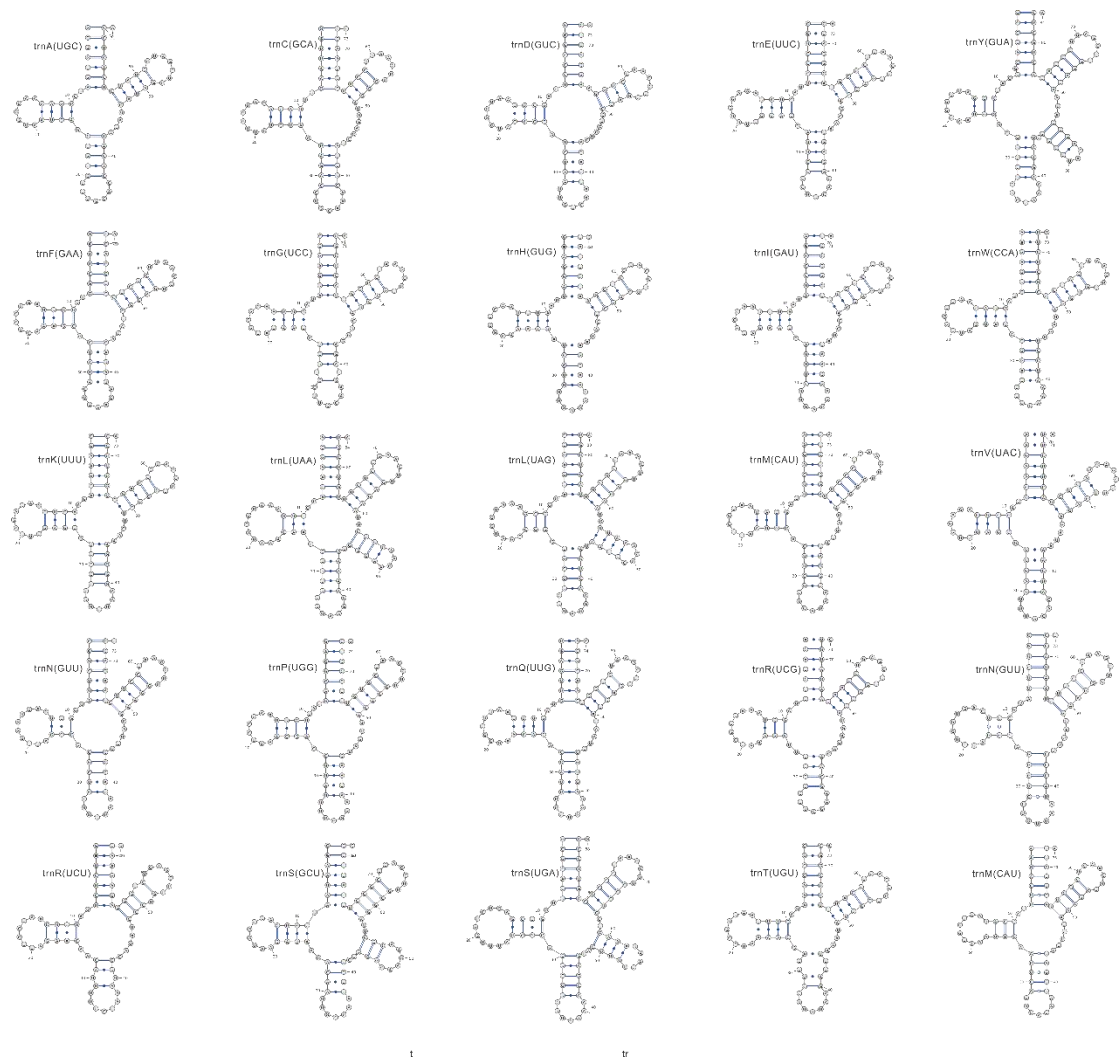


Figure S2. Predicted secondary cloverleaf structures for tRNAs of *Cyathus striatus* AH440044.

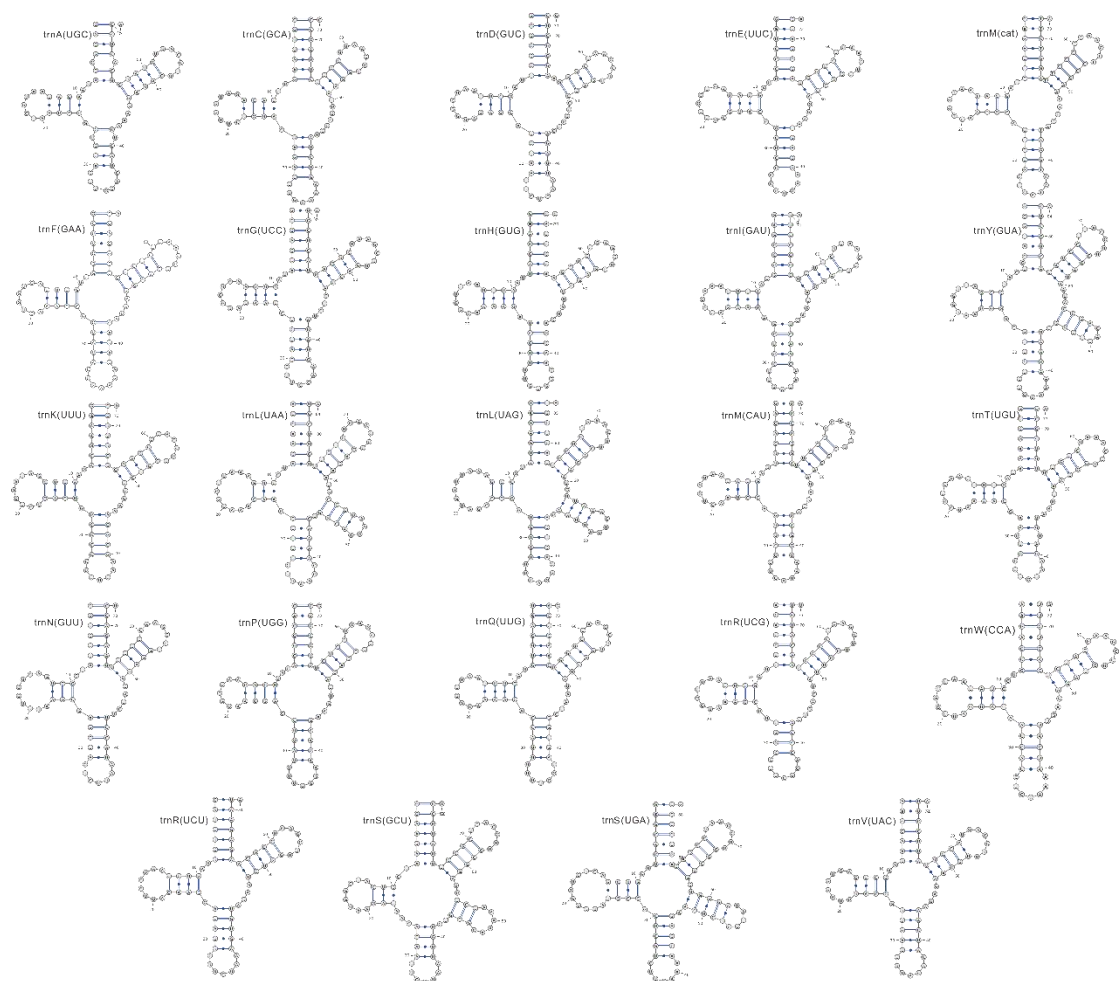


Figure S3. Predicted secondary cloverleaf structures for tRNAs of *Cyathus jaiyuguanensis* 765.

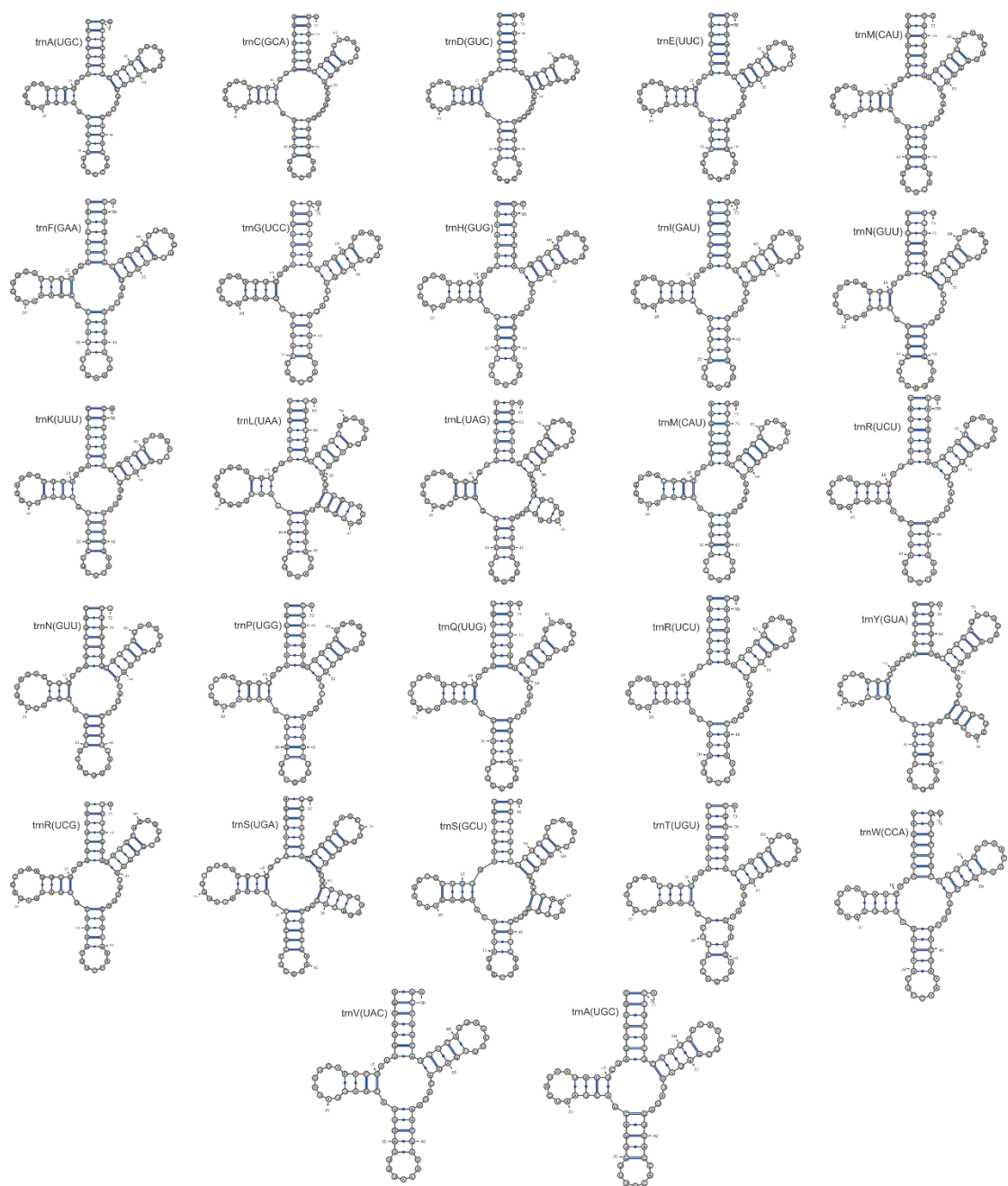


Figure S4. Predicted secondary cloverleaf structures for tRNAs of *Cyathus pallidus* QL1.

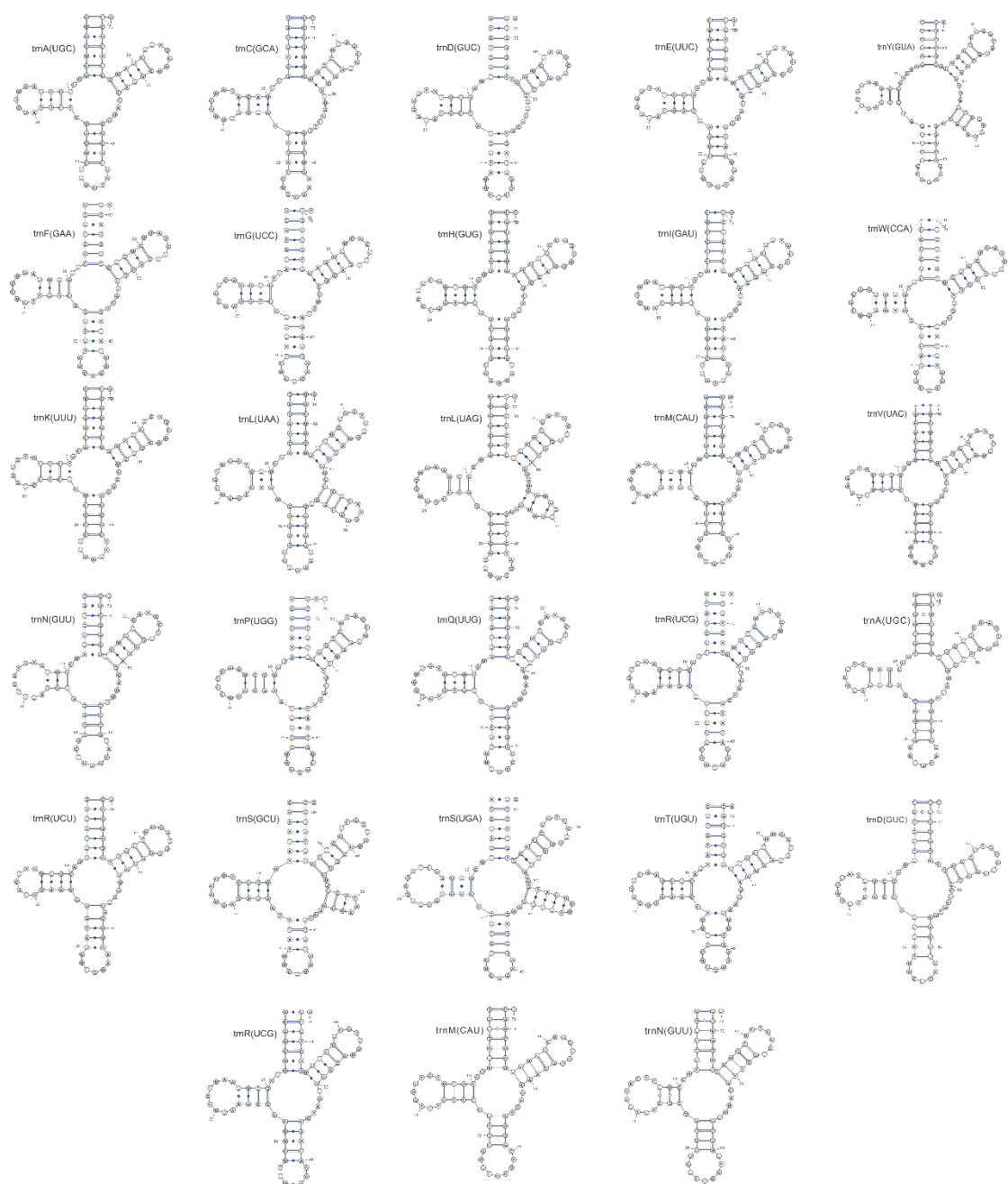


Figure S5. Predicted secondary cloverleaf structures for tRNAs of *Cyathus stercoreus* NPCB004.

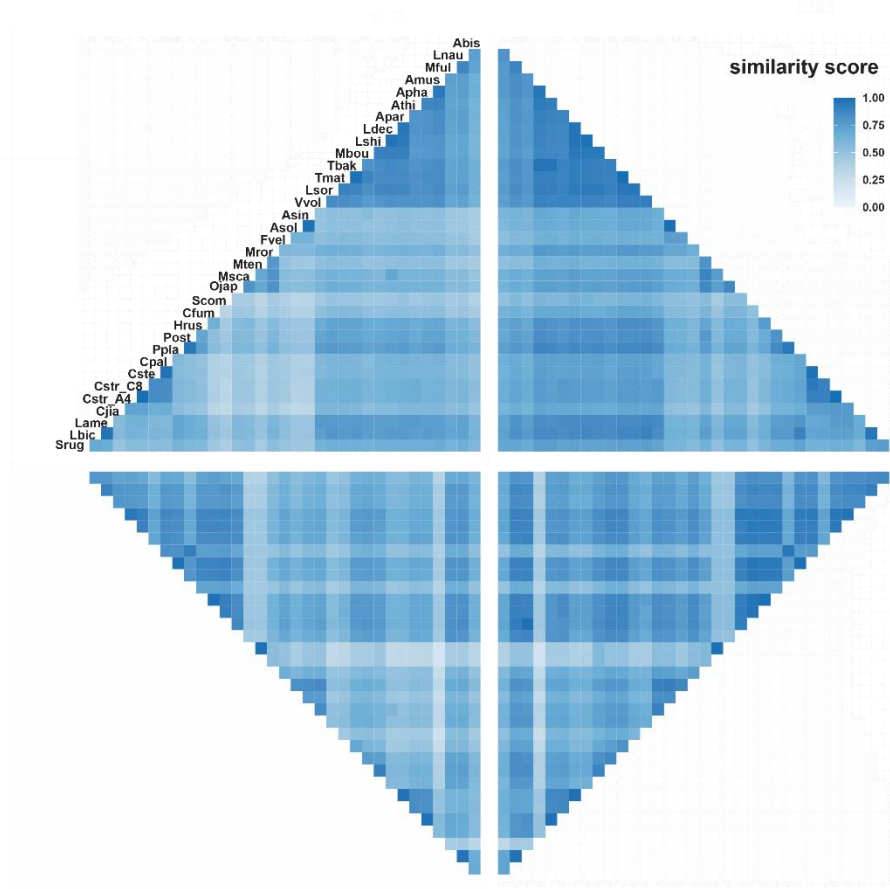


Figure S6. Heterogeneous sequence differentiation of mitochondrial genome based on the four data sets.

The average similarity score between the sequences is represented by a colored block, based on an AliGROOVE2 score from 0 to 1.

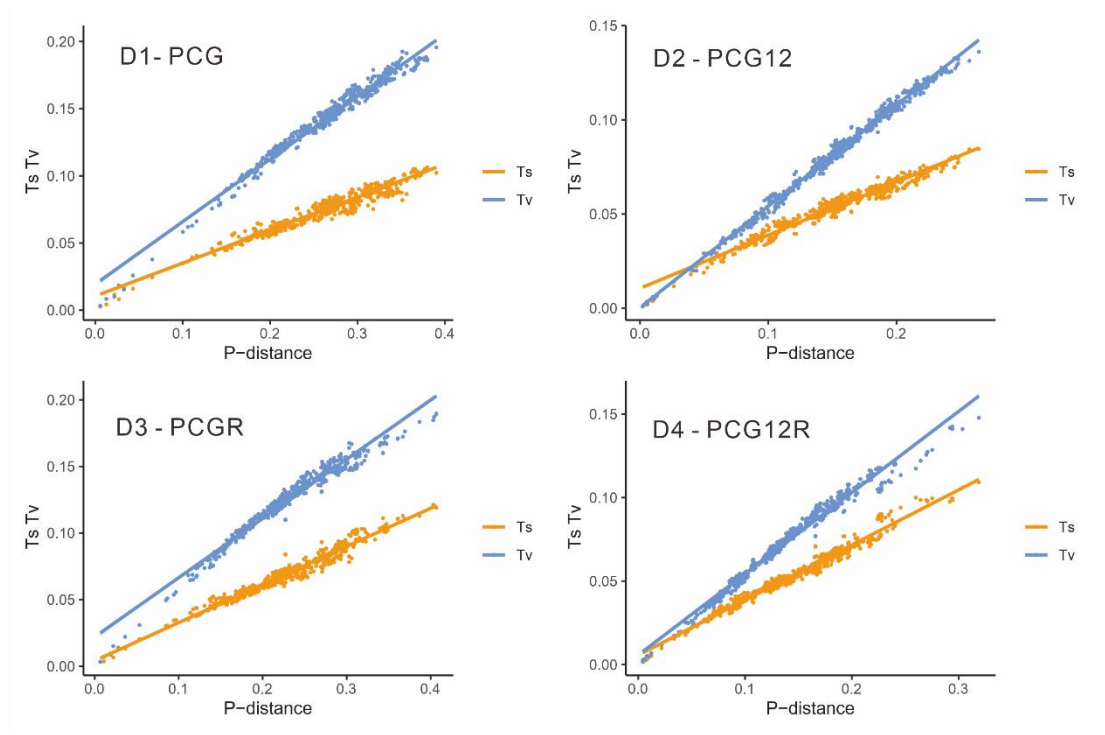


Figure S7. Base substitution saturation analysis based on the four datasets, conducted by DAMBE.