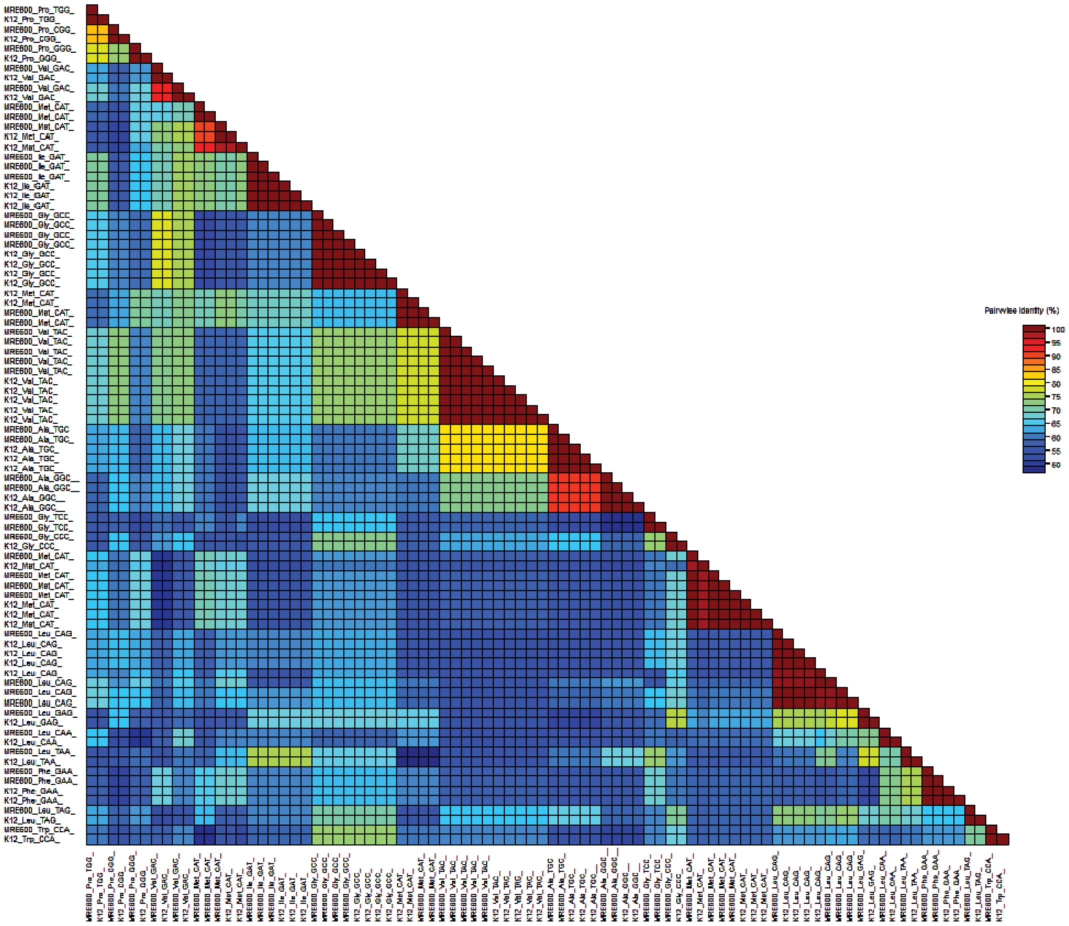
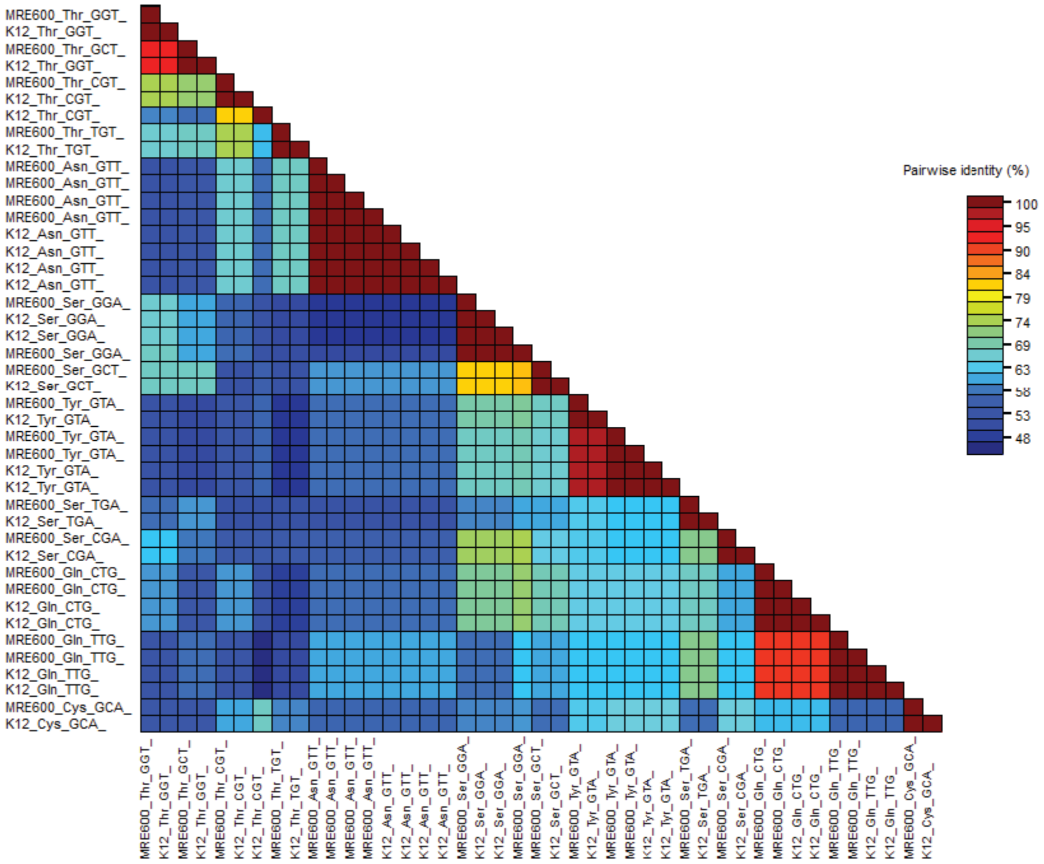
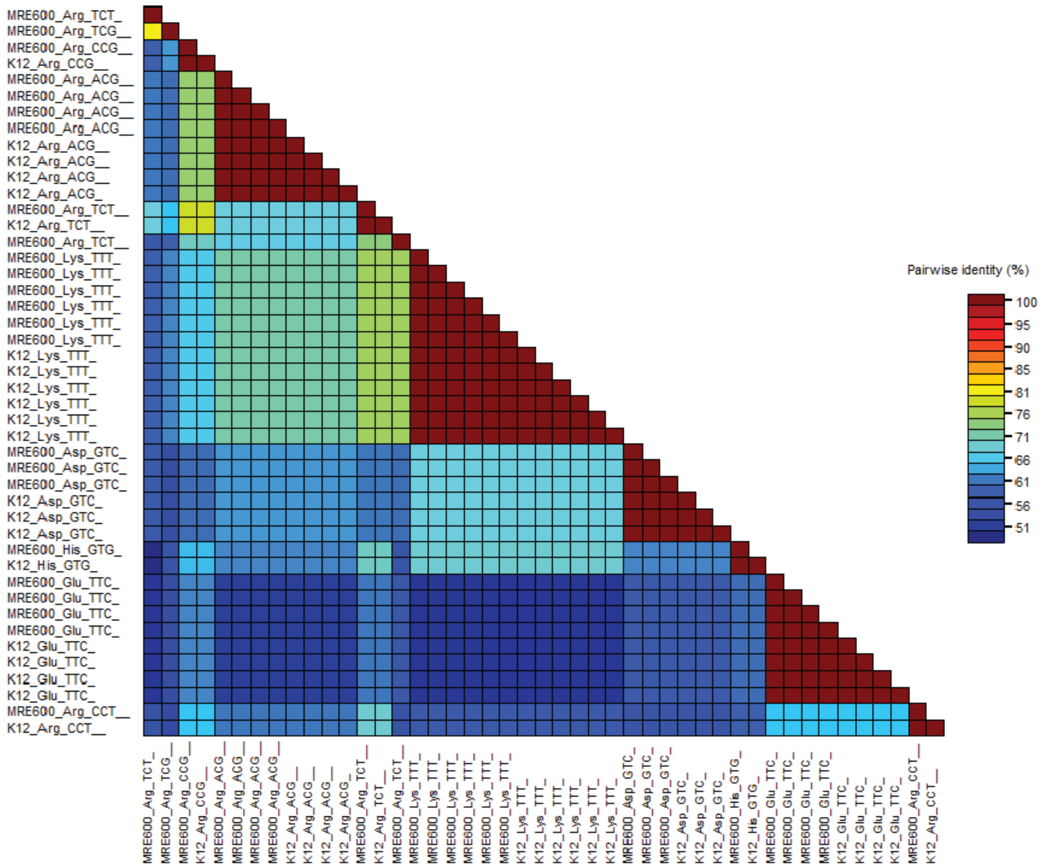
SUPPLEMENTARY FIGURES:



SUPPLEMENTARY FIGURE S1. A sequence comparison of MRE600 and K12[1] tRNAs that carry nonpolar amino acids. Pairwise sequence alignments were performed using the MUSCLE algorithm (Edgar 2004) and visualized using the Sequence Demarcation Tool Version 1.2 (Muhire, et al. 2014). tRNAs are labelled using the format: "organism_amino acid_anticodon." [1]From GOLD Analysis Project ID: Ga0021515.



SUPPLEMENTARY FIGURE S2. A sequence comparison of MRE600 and K12[1] tRNAs that carry polar amino acids. Pairwise sequence alignments were performed using the MUSCLE algorithm (Edgar 2004) and visualized using the Sequence Demarcation Tool Version 1.2 (Muhire, et al. 2014). tRNAs are labelled using the format: "organism_amino acid_anticodon." [1]From GOLD Analysis Project ID: Ga0021515.



SUPPLEMENTARY FIGURE S3. A sequence comparison of MRE600 and K12[1] tRNAs that carry charged amino acids. Pairwise sequence alignments were performed using the MUSCLE algorithm (Edgar 2004) and visualized using the Sequence Demarcation Tool Version 1.2 (Muhire, et al. 2014). tRNAs are labelled using the format: "organism_amino acid_anticodon." [1]From GOLD Analysis Project ID: Ga0021515.

SUPPLEMENTARY TABLES:

SUPPLEMENTARY TABLE S1. Comparing the ribosomal protein gene content of MRE600 to K12[1]. All annotated ribosomal protein genes in K12 were identified in MRE600 with 100% amino acid sequence identity, with the exception of S2 and L15. S2 has a D127E substitution, while L15 has a V77I substitution.

Ribosomal Protein	Gene Name	% Identity to K12 Homolog	Identities
S1	*rpsA*	100	557/557
S2	*rpsB*	99	240/241
S3	*rpsC*	100	233/233
S4	*rpsD*	100	206/206
S5	*rpsE*	100	167/167
S6	*rpsF*	100	120/120
S7	*rpsG*	100	156/156
S8	*rpsH*	100	130/130
S9	*rpsI*	100	130/130
S10	*rpsJ*	100	103/103
S11	*rpsK*	100	129/129
S12	*rpsL*	100	124/124
S13	*rpsM*	100	118/118
S14	*rpsN*	100	101/101
S15	*rpsO*	100	89/89
S16	*rpsP*	100	82/82
S17	*rpsQ*	100	84/84
S18	*rpsR*	100	75/75
S19	*rpsS*	100	83/83
S20	*rpsT*	100	87/87
S21	*rpsU*	100	71/71
L1	*rplA*	100	234/234
L2	*rplB*	100	273/273
L3	*rplC*	100	209/209
L4	*rplD*	100	201/201
L5	*rplE*	100	179/179
L6	*rplF*	100	159/159
L9	*rplI*	100	149/149
L10	*rplJ*	100	165/165
L11	*rplK*	100	142/142
L7/L12	*rplL*	100	100/100
L13	*rplM*	100	142/142
L14	*rplN*	100	123/123
L15	*rplO*	99	127/128
L16	*rplP*	100	136/136
L17	*rplQ*	100	127/127
L18	*rplR*	100	117/117
L19	*rplS*	100	115/115

L20	*rplT*	100	107/107
L21	*rplU*	100	103/103
L22	*rplV*	100	110/110
L23	*rplW*	100	100/100
L24	*rplX*	100	94/94
L25	*rplY*	100	94/94
L27	*rpmA*	100	85/85
L28	*rpmB*	100	78/78
L29	*rpmC*	100	63/63
L30	*rpmD*	100	59/59
L31	*rpmE*	100	70/70
L32	*rpmF*	100	57/57
L33	*rpmG*	100	55/55
L34	*rpmH*	100	46/46
L35	*rpmI*	100	65/65
L36	rpmJ	100	37/37

[1] From accession #U00096.3

REFERENCES:

Edgar RC 2004. MUSCLE: a multiple sequence alignment method with reduced time and space complexity. BMC Bioinformatics 5: 113. doi: 10.1186/1471-2105-5-113

Muhire BM, Varsani A, Martin DP 2014. SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9: e108277. doi: 10.1371/journal.pone.0108277