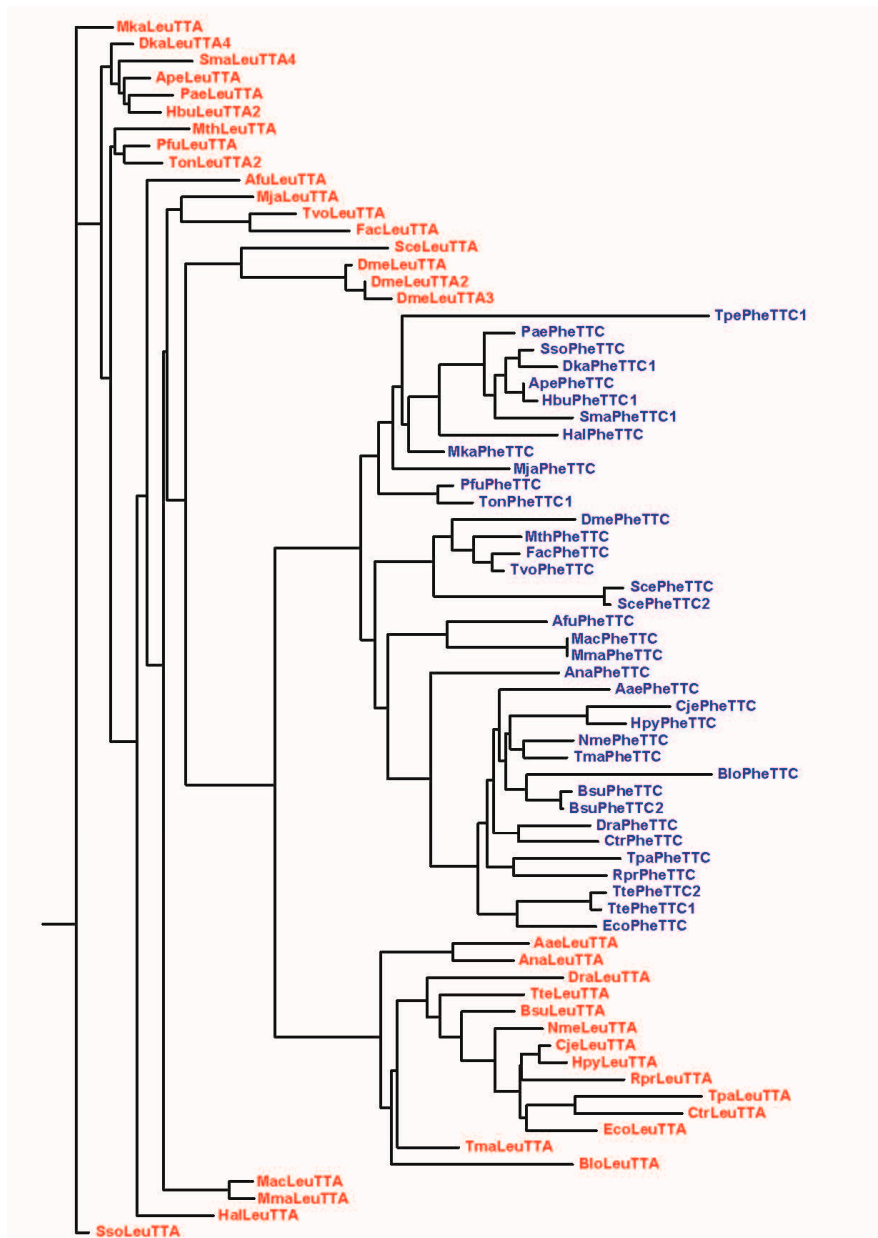


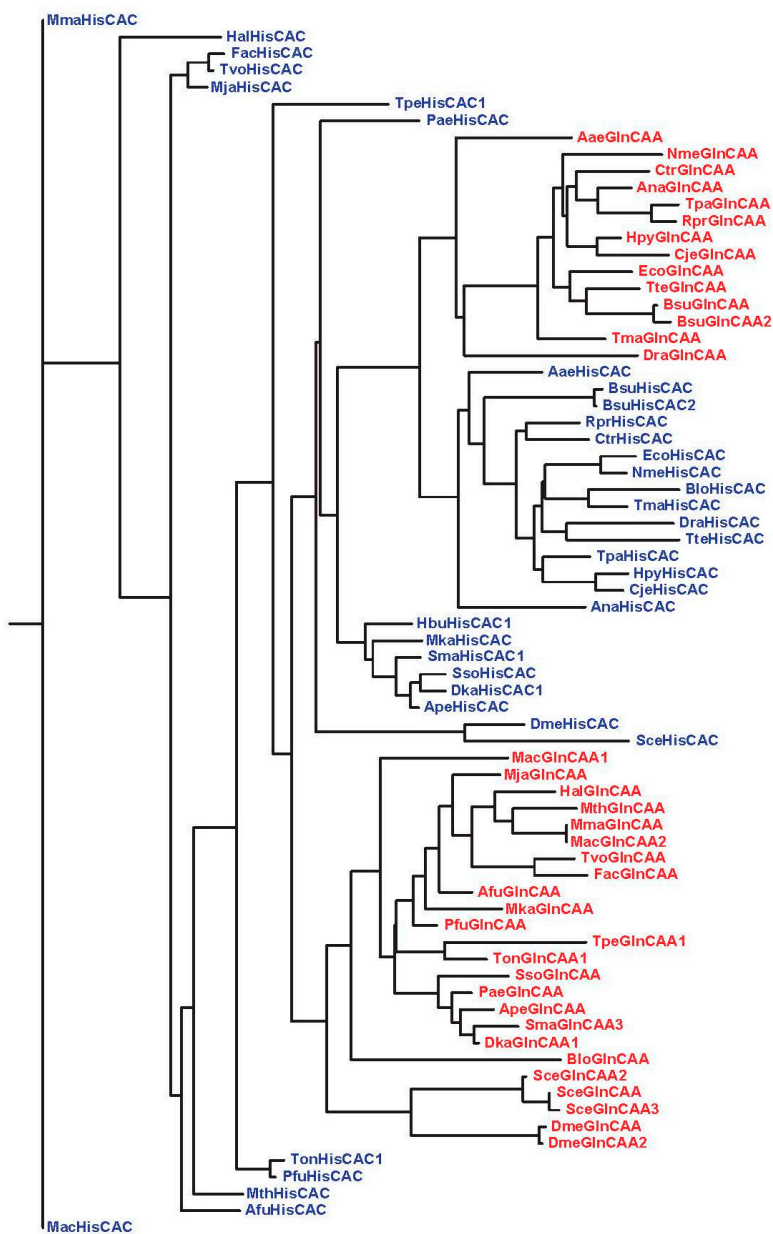
Supplementary Materials: Coevolution Theory of the Genetic Code at Age Forty: Pathway to Translation and Synthetic Life

J. Tze-Fei Wong, Siu-Kin Ng, Wai-Kin Mat, Taobo Hu and Hong Xue



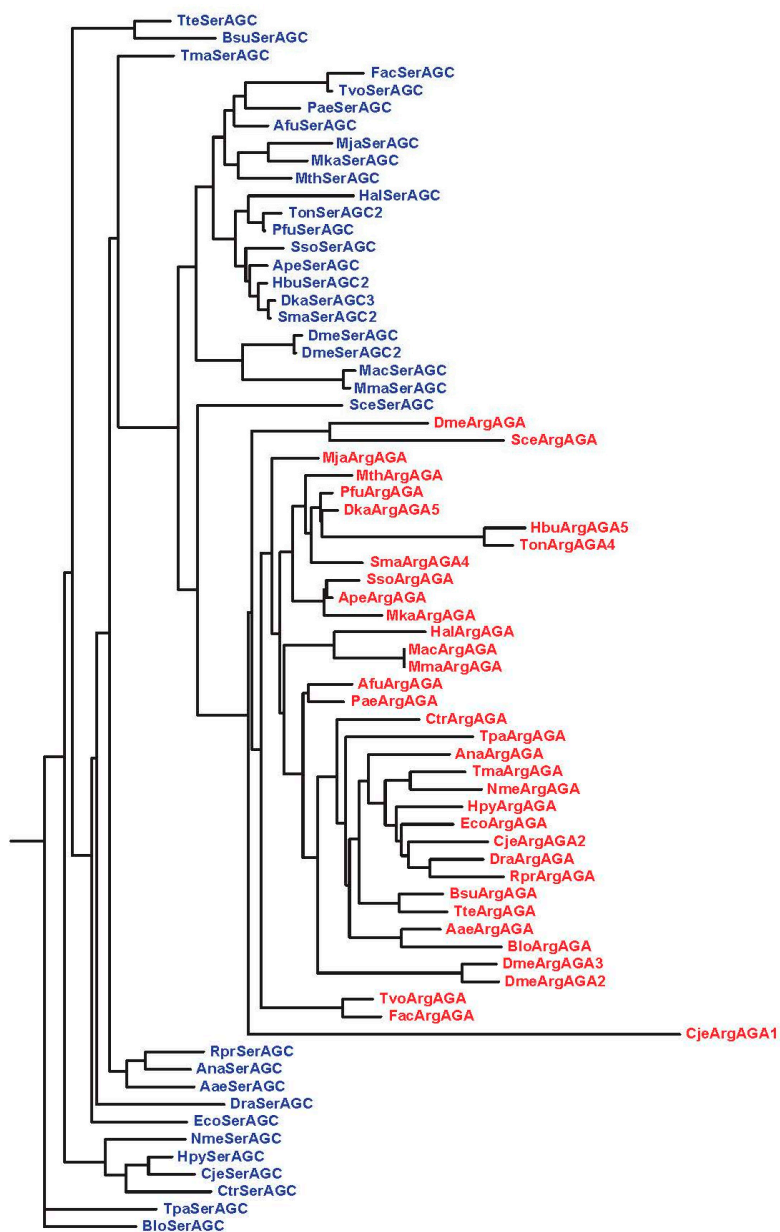
(A)

Figure S1. Cont.



(B)

Figure S1. Cont.



(C)

Figure S1. Gene trees for tRNAs bearing GNN and UNN anticodons. (A) UUN codon box for Phe/Leu; (B) CAN codon box for His/Gln; and (C) AGN codon box for Ser/Arg.

RsoAspGAC	GGAGTGGTAGTTCAGTCCGTTAGAAACCGGCCCTGTCACCGCGGGGGCGCGGGTTCGAGTCCCGTCCACTCCG	73
RsoGluGAA	GTCCCTTCGCTAGAGGCCCTAGGACATCAACCCCTTCAAGGTCAGTACAGGGGTTCGAATCCCCTAGGGGACC	73
Δ=34	1.....10.....20.....30.....40.....50.....60.....70...	
ScoAspGAC	GGTCCCT---GTGGAGCAGTTGGAGTCTCGCCACCCCTGTCAAAGTGGAGCGCGGGTTCAAAATCCCGTACGACCG	74
ScoGluGAA	-GCCCTCATCGTCTAGCGGCCCTAGGA---GCCCGCCCTTCAAGGGGTAGCAAGGGTTCGAATCCCCTAGGGGACC	73
Δ=30	1.....10.....20.....30.....40.....50.....60.....70.....	
SpnAspGAC	GGTCCCGTAGTGTAGCGGTTATCACTGCCCTGTCACGGCGAAGACCGGGTTCGATTCCCGTCCGGACCG	72
SpnGluGAA	GGTCCCTTCGCTAGAGGGGTTAAGACACCCGCTTTTACGGCGGTAAACAGGGTTCGAATCCCGTACGCACTA	72
Δ=21	1.....10.....20.....30.....40.....50.....60.....70..	
StyAspGAC	GGAGCGGTAGTTCAGTTGGTTAGAAACCTGCCCTGTCACCGAGGGGGCGCGGGTTCGAGTCCCGTCCGTTCCG	73
StyGluGAA	GTCCCTTCGCTAGAGGCCCTAGGACACCGCCCTTTCACGGCGGTAAACAGGGTTCGAATCCCCTAGGGGACC	73
Δ=32	1.....10.....20.....30.....40.....50.....60.....70...	
SynAspGAC	GGGTCGTAGTTCAGTTGGTTAGAGCACCGCCCTGTCACGGCGAAGTCCGGGTTCGAGCCCCCTCAGACCCG	73
SynGluGAA	GCCCCATCGCTAGAGGCCCTAGGACACTCCCTTTCACGGAGGCGACAGGGATTCCAATCCCTTCCCTAGGGGACC	73
Δ=36	1.....10.....20.....30.....40.....50.....60.....70...	
TelAspGAC	GGGAGCGTAGTTCAGTTGGTTAGAGCACCGCCCTGTCACGGCGAAGTCCGGGTTCGAGCCCCCTCAGACCCG	73
TelGluGAA	GCCCCATCGCTAGTGGCCCTAGGACACTCCCTTTCACGGAGGCGACAGGGATTCCAATCCCTTCCCTAGGGGACC	73
Δ=35	1.....10.....20.....30.....40.....50.....60.....70...	
TmaAspGAC	GGGAGCGTAGTTCAGTTGGTTAGAGCACCGCCCTGTCACCGCGAAGTCCGGGTTCGAGCCCCCTCAGACCCG	74
TmaGluGAA	GCCCCATCGCTAGGATTAAC--GCCAGTCCCGGATTTCAGTCCGGAGTCCGGGTTCGATTCCCGTCGGGGTCC	72
Δ=34	1.....10.....20.....30.....40.....50.....60.....70...	
TpaAspGAC	GGGGCGTAGTTCAGTTGGTTAGAGCACCGCCCTGTCACCGCGAAGTCCGGGTTCGAGCCCCCTCAGACCCG	73
TpaGluGAA	GGTCCCTTCGCTA--TCGGTTAGAGCAGAGATTCTCAATCTCAAAAGACGGGTTCGAATCCCGTACGGGACC	72
Δ=36	1.....10.....20.....30.....40.....50.....60.....70...	
TteAspGAC	GGCCCGTAGTTCAGTTGGTTAGAGCACCGCCCTGTCACCGGTGGAGGCGAGGGTTCGAATCCCGTCCGGTCCG	73
TteGluGAA	GCCCCATCGCTAGTGGCCCTAGGACACTCCCTTTCACGGCGGTAAACATGGGTTCGAATCCCCTAGGGGACC	72
Δ=24	1.....10.....20.....30.....40.....50.....60.....70...	
VchAspGAC	GGAGCGGTAGTTCAGTTGGTTAGAAACCGGCCCTGTCACCGCGGGGGCGCGGGTTCGAGTCCCGTCCGCTCCG	73
VchGluGAA	GTCCCTTCGCTAGAGGCCCTAGGACACCGCCCTTTCACGGCGGTAAACAGGGTTCGAATCCCGTACGGGATTA	73
Δ=29	1.....10.....20.....30.....40.....50.....60.....70...	
XcaAspGAC	GGAGCGGTAGTTCAGTTGGTTAGAAACCGGCCCTGTCACCGCGGGGGCGCGGGTTCGAGTCCCGTCCGCTCCG	73
XcaGluGAA	GTCCCTTCGCTAGAGGCCCTAGGACACCAACCCCTTTCACGGTGGACAGGGGGTTCGAATCCCGTACGGGACC	73
Δ=33	1.....10.....20.....30.....40.....50.....60.....70...	
XfaAspGAC	GGAGCGGTAGTTCAGTTGGTTAGAAACCGGCCCTGTCACCGCGGGGGCGCGGGTTCGAGTCCCGTCCGCTCCG	73
XfaGluGAA	GTCCCTTCGCTAGAGGCCCTAGGACATCAACCCCTTTCACGGTGGGACAGGGGGTTCGAATCCCGTACGGGACC	73
Δ=34	1.....10.....20.....30.....40.....50.....60.....70...	

Eukarya : Average Δ = 24.3

AthAspGAC	GTCTGTAGTATAGTGGTAAATATCCCGCCCTGTCACCGGGGTGACCCGGGTTCGATCCCGGGGAAAGGGGG	72
AthGluGAA	TCCGATCGTCCAGCGGTTAGGATATCTGGCTTTCACCAAGGAGACCCGGGTTCGATTCGGGCAATGGGAG	72
Δ=20	1.....10.....20.....30.....40.....50.....60.....70..	
CelAspGAC	TCCCTCGTAGTATAGTGGTGGTATCCCGCCTGTCACAGTCCGAGACCCGGGTTCGAATCCCGGGCCGGGAG	72
CelGluGAA	TCCCATGTTGGTCTAGTGGTTAGGATTCGTTTTCACCAAGGCGCCCGGGTTCGATTCGGGCAATGGGAA	72
Δ=21	1.....10.....20.....30.....40.....50.....60.....70..	
DmeAspGAC	TCCCTCGTAGTATAGTGGTGGTATCCCGCCTGTCACAGTCCGAGACCCGGGTTCGAATCCCGGGCCGGGAG	72
DmeGluGAA	TCCCATGTTGGTCTAGTGGTTAGGATTCGTTTTCACCAAGGCGCCCGGGTTCGATTCGGGCAATGGGAA	72
Δ=22	1.....10.....20.....30.....40.....50.....60.....70..	
EcuAspGAC	TCTTCCATAGTCTAGTGGTATATCAATCCCGCCTGTCACCGGGGTGACCCGGGTTCGAATCCCG-GTGGGAGAG	73
EcuGluGAA	TTCCTACTGGTCTAGCGGT-TAGGATGCTCCCTTTCACCAAGGAGGTTGGGGTTCGAATCCCGCGTAGGGAA-	72
Δ=28	1.....10.....20.....30.....40.....50.....60.....70...	
HsaAspGAC	TCCCTCGTAGTATAGTGGTGGTATCCCGCCTGTCACAGTCCGAGACCCGGGTTCGAATCCCGGACGGGAG	72
HsaGluGAA	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTTCACCGGGGACCCGGGTTCGATTCGGGCAATGGGAA	72
Δ=24	1.....10.....20.....30.....40.....50.....60.....70..	
SceAspGAC	TCCGTGATAGTTAATGGTCAGAAAGGGCGCTGTCGCGTCCGAGATCCGGGTTCGAATCCCGGTCGGGAG	72
SceGluGAA	TCCGATATAGTAAACGGCTATCATCATCCCTTTCACCGTGGAGACCCGGGTTCGACTCCCGGTAATGGGAG	72
Δ=23	1.....10.....20.....30.....40.....50.....60.....70...	
SpoAspGAC	TCTCCTTAGTATAGGGG-TAGTACACAAGCCTGTCACCGTTCGAGCCCGGGTTCGAATCCCGGAGGGAGAG	71
SpoGluGAA	TCCGTTGGTCCAAACGGCTAGGATTCGTCGCTTTCACCAAGCGGTTCGGGTTCGACTCCCGGCAACGGAG	72
Δ=32	1.....10.....20.....30.....40.....50.....60.....70..	

(A)

Figure S2. Cont.

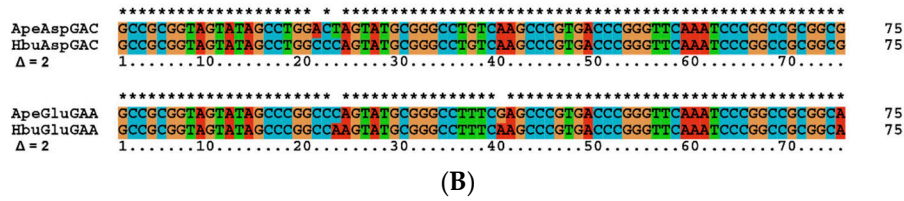


Figure S2. Sequence alignments of AspGAC and GluGAA genes from different species. (A) Sequence alignments from different species. The archaeal, bacterial and eukaryotic species aligned comprise species from Figure 4 and reference [83]. **(B)** Sequence alignments between ApeAspGAC and HbuAspGAC, and between ApeGluGAA and HbuGluGAA. Δ represents number of base differences between a pair of aligned genes. Three-letter names for species additional to those included in Figure 4 are: **ARCHAEA.** Mba *Methanosarcina barkeri*, Pab *Pyrococcus abyssi*, Pho *Pyrococcus horikoshii*, Sto *Sulfolobus tokodaii*, Tac *Thermoplasma acidophilum*. **BACTERIA.** Atu *Agrobacterium tumefaciens*, Bap *Buchnera aphidicola*, Bbu *Borrelia burgdorferi*, Cac *Clostridium acetobutylicum*, Ccr *Caulobacter crescentus*, Hin *Haemophilus influenzae*, Lin *Listeria innocua*, Lla *Lactococcus lactis*, Mpn *Mycoplasma pneumoniae*, Mtu *Mycobacterium tuberculosis*, Psa *Pseudomonas aeruginosa*, Rso *Ralstonia solanacearum*, Sco *Streptomyces coelicolor*, Spn *Streptococcus pneumoniae*, Sty *Salmonella typhi*, Syn *Synechocystis 6803*, Tel *Thermosynechococcus elongatus*, Vch *Vibrio cholerae*, Xca *Xanthomonas campestris*, Xfa *Xylella fastidios*. **EUKARYA.** Ath *Arabidopsis thaliana*, Cel *Caenorhabditis elegans*, Ecu *Encephalitozoon cuniculi*, Hsa *Homo sapiens*, Spo *Schizosaccharomyces pombe*.

Archaea : Average $\Delta = 17.7$

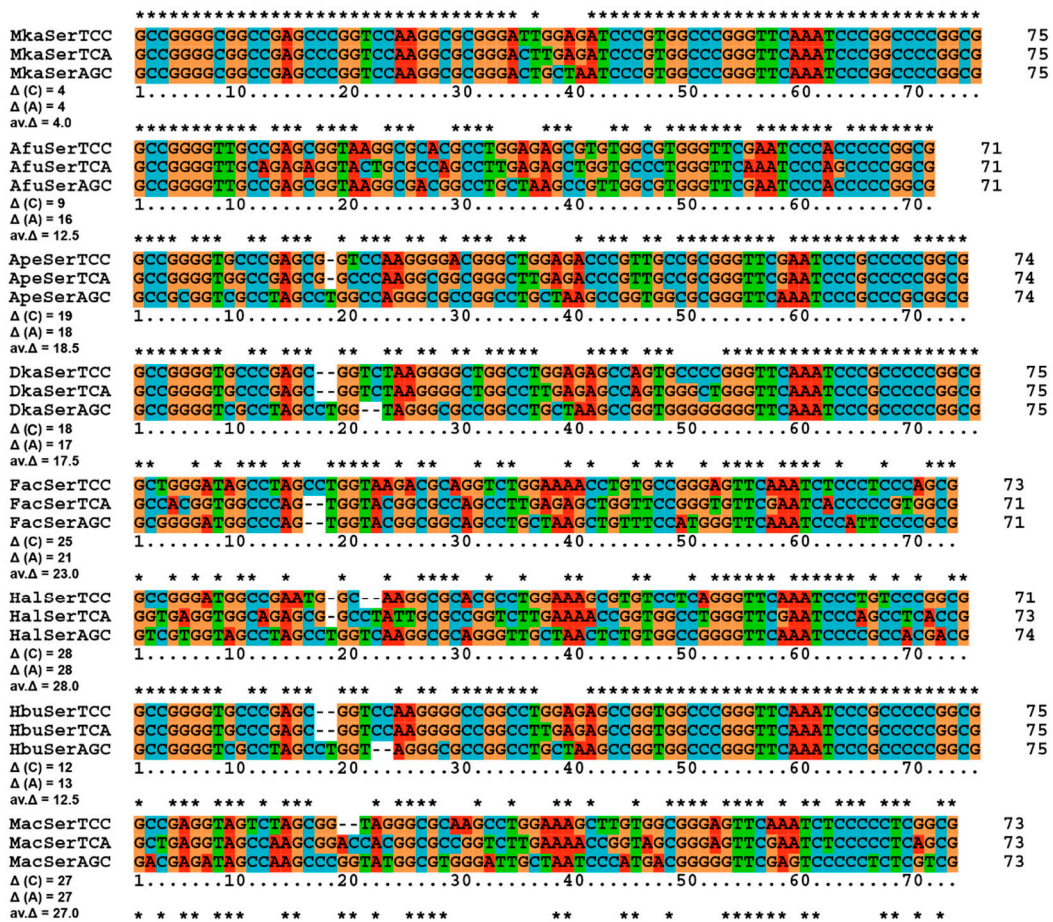


Figure S3. Cont.

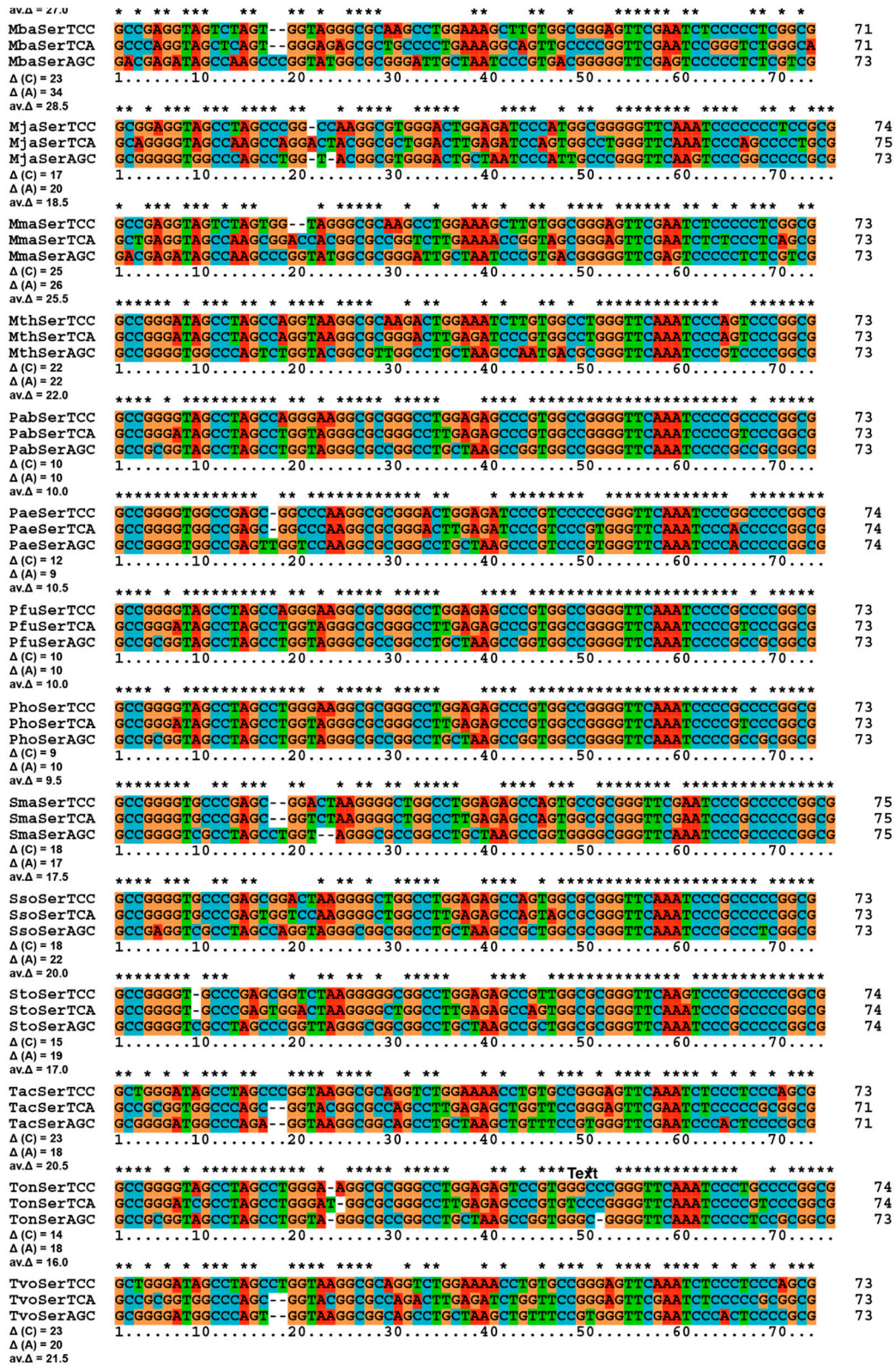


Figure S3. Cont.

Bacteria : Average Δ = 22.3

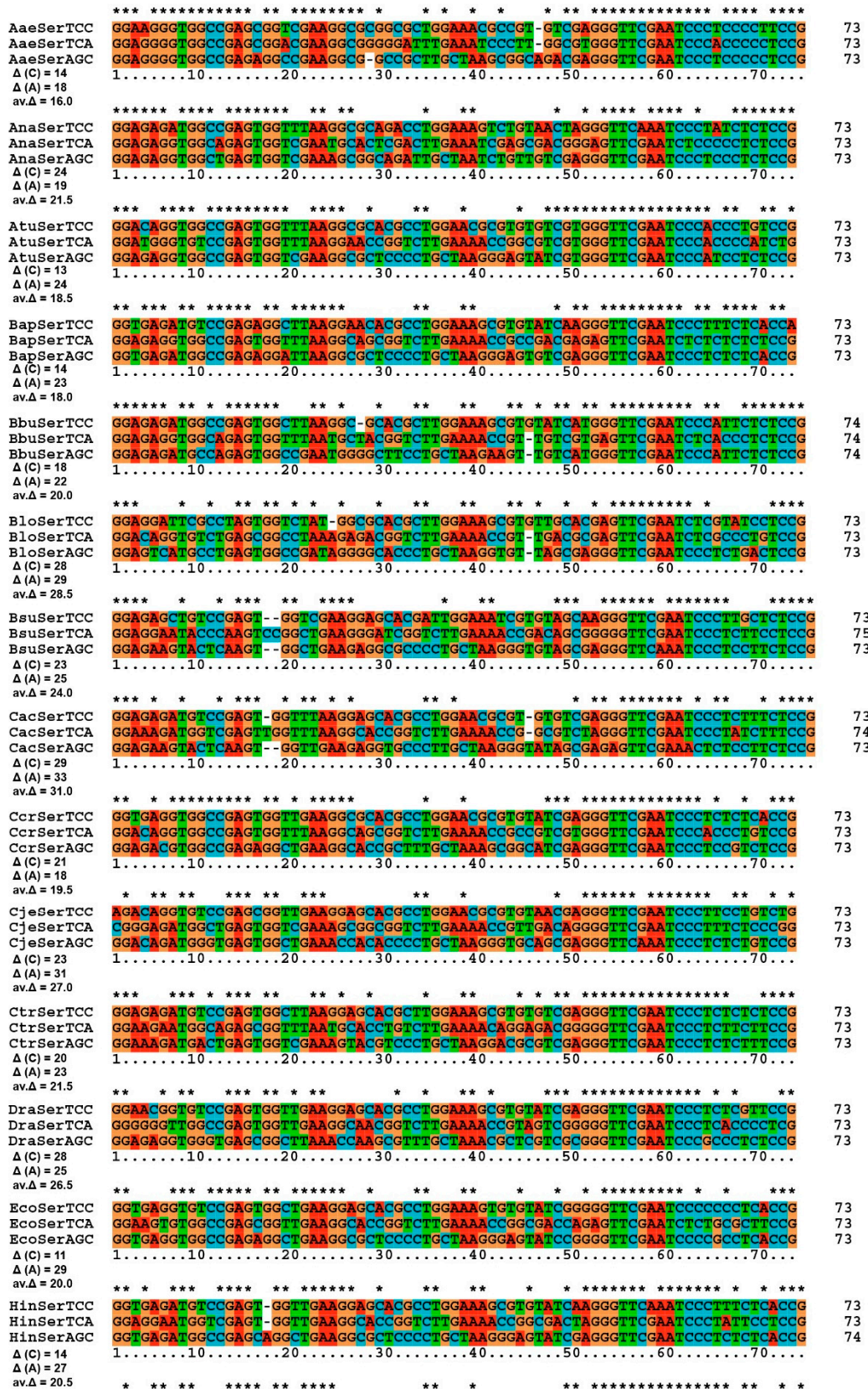


Figure S3. Cont.

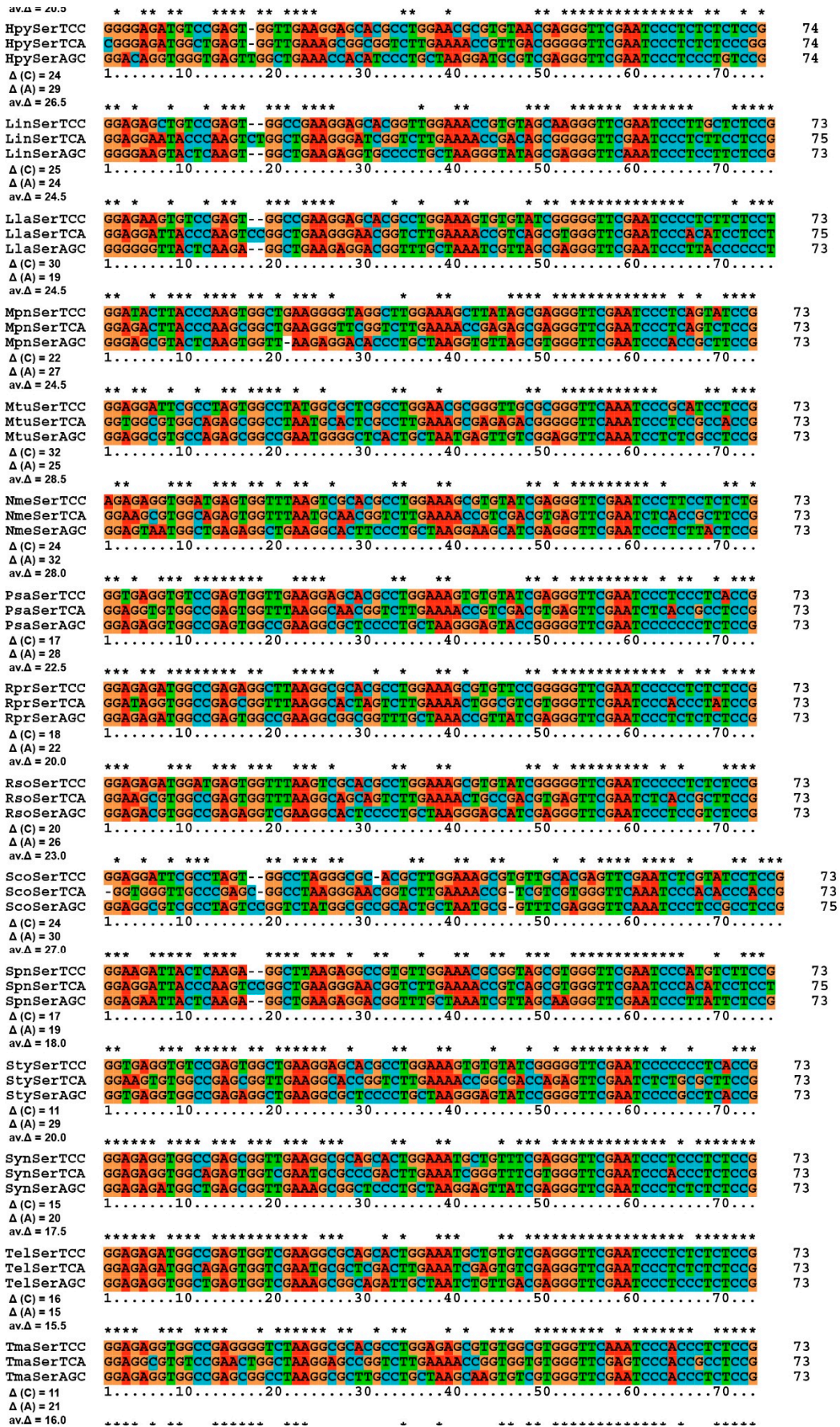


Figure S3. Cont.

