

**Table S1. Comparison of pairing pattern between Archaea and Bacteria in the stem region of the predicted mRNA secondary structures**

Characteristic	Archaea	Bacteria
<b>Natural signal (Nat)</b>		
The most and least frequent pairs in stem regions of mRNA secondary structure	Mesophiles: Phase 1: G1:1C, U3:2G Phase 2: G1:3C, U1:3G Phase 3: G1:2C, U1:2G Thermophiles: Phase 1: G3:2C, G2:3U Phase 2: G1:3C, U1:3G Phase 3: G1:2C, U1:2G	Mesophiles: Phase 1: G1:1C, U3:2G Phase 2: G1:3C, U1:3G Phase 3: G3:3C, U1:2G Thermophiles: Phase 1: G1:1C, U3:2G Phase 2: G1:3C, U1:3G Phase 3: G3:3C, U1:2G
Contributions from the three pairing Phases to the stem pairs	Mesophiles: Phase 3 > Phase 2 > Phase 1 Thermophiles: Phase 3 > Phase 2 > Phase 1	Mesophiles: Phase 3 > Phase 2 > Phase 1 Thermophiles: Phase 2 > Phase 3 > Phase 1
The most and least frequent nucleotide involved in pairing	Mesophiles: C3, U1 Thermophiles: C3, U1	Mesophiles: C3, U1 Thermophiles: C3, U1
Contributions from the three codon sites to the stem pairs	Mesophiles: Site 3 > Site 1 > Site 2 Thermophiles: Site 3 > Site 1 > Site 2	Mesophiles: Site 3 > Site 1 > Site 2 Thermophiles: Site 3 > Site 1 > Site 2
Features in signification correlation with OGT	Phase 1: U2:3G (R = +0.56) Phase 2: U1:3G (R = +0.57) Phase 3: C2:1G (R = -0.50)	None
<b>Purified signal (Nat/dShuffl)</b>		
The most and least frequent pairs in stem regions of mRNA secondary structure	Mesophiles: Phase 1: C2:3G, G2:3U Phase 2: C3:1G, G1:3U Phase 3: A3:3U, U3:3G Thermophiles: Phase 1: G3:2C, G2:3U Phase 2: C2:2G, G1:3U Phase 3: A3:3U, U3:3G	Mesophiles: Phase 1: G3:2U, U3:2G Phase 2: A1:3U, G1:3U Phase 3: G3:3C, U3:3G Thermophiles: Phase 1: C2:3G, G2:3U Phase 2: C3:1G, G1:3U Phase 3: U3:3A, U3:3G
Contributions from the three pairing Phases to the stem pairs	Mesophiles: Phase 3 > Phase 2 > Phase 1 Thermophiles: Phase 3 > Phase 2 > Phase 1	Mesophiles: Phase 3 > Phase 2 > Phase 1 Thermophiles: Phase 3 > Phase 1 > Phase 2
The most and least frequent nucleotide involved in pairing	Mesophiles: C3, A2 Thermophiles: C3, U3	Mesophiles: A1, U3 Thermophiles: A3, U3
Contributions from the three codon sites to the stem pairs	Mesophiles: Site 3 > Site 1 > Site 2 Thermophiles: Site 3 > Site 1 > Site 2	Mesophiles: Site 3 > Site 2 > Site 1 Thermophiles: Site 3 > Site 2 > Site 1
Features in signification correlation with OGT	Phase 1: U3:2G (R = +0.76) Phase 2: U3:1G (R = +0.60) Phase 3: None	None

**Table S2. Purine loading in loop and stem regions of folded mRNA of archaea and bacteria, and its OGT correlation.**

Feature	Loop		Stem		Comparison p-value
	Mean Content	OGT	Mean	OGT	
<b>Archaea</b>					
A+G	0.596	0.46*	0.500	-0.29	4.9E-27
R/Y	1.494	0.44*	1.001	-0.29	4.9E-27
ApG	0.073	0.83**	0.059	0.62**	0.0007
GGR(glycine)	0.032	0.44*	0.052	0.16	1.5E-14
GGY(glycine)	0.015	0.18	0.064	0.16	3.4E-26
AGR(arginine)	0.046	0.68**	0.028	0.55**	9.2E-11
CGR(arginine)	0.016	-0.28	0.032	-0.31	0.0024
CGY(arginine)	0.012	-0.10	0.026	-0.12	0.0010
GAR(glutamate)	0.069	0.60**	0.044	0.48*	4.2E-18
AAR(lysine)	0.096	-0.03	0.018	0.01	2.2E-23
GAY(aspartic)	0.038	-0.27	0.042	-0.63**	0.0158
<b>Bacteria</b>					
A+G	0.539	0.48**	0.501	0.08	4.6E-12
R/Y	1.188	0.51**	1.002	0.08	4.6E-12
ApG	0.054	0.58**	0.046	0.22	0.0020
GGR(glycine)	0.025	0.69**	0.041	0.46**	3.4E-10
GGY(glycine)	0.018	-0.02	0.088	-0.25	6.9E-28
AGR(arginine)	0.028	0.58**	0.019	0.37*	8.5E-08
CGR(arginine)	0.020	-0.07	0.044	-0.08	2.5E-07
CGY(arginine)	0.018	-0.16	0.043	-0.18	9.8E-09
GAR(glutamic)	0.054	0.70**	0.032	0.51**	<2.2E-16
AAR(lysine)	0.081	0.30*	0.017	0.18	<2.2E-16
GAY(aspartic)	0.037	-0.17	0.040	-0.33*	0.0046
<b>Both Archaea and Bacteria</b>					
A+G	0.560	0.59**	0.500	-0.26*	<2.2E-16
R/Y	1.299	0.61**	1.002	-0.26*	<2.2E-16
ApG	0.061	0.79**	0.051	0.50**	0.0002
GGR(glycine)	0.027	0.62**	0.045	0.42**	1.2E-17
GGY(glycine)	0.017	-0.05	0.079	-0.23*	1.0E-42
AGR(arginine)	0.035	0.72**	0.022	0.56**	2.4E-10
CGR(arginine)	0.018	-0.22	0.040	-0.24*	7.1E-09
CGY(arginine)	0.016	-0.25*	0.037	-0.26*	6.2E-10
GAR(glutamic)	0.060	0.71**	0.036	0.59**	<2.2E-16
AAR(lysine)	0.086	0.22	0.017	0.11	<2.2E-16
GAY(aspartic)	0.037	-0.17	0.040	-0.37**	0.0002

'OGT correlation' column shows the correlation coefficient, with '\*' indicating p-value < 0.01 and '\*\*' indicating p-value < 0.0001. Comparison was performed between Loop region and Stem region by Wilcoxon-tests and p-values are shown in the last column.