Supplementary Table 1. Sequence Variations for UAA/GAN Motifs in 23S rRNA

Motif[†]	A[‡]		B[‡]		E[‡]		ABE[‡]	
H23S-1096	**UAA/GAG**	27(73%)	**UAA/GAA**	234(97%)	**UAA/GAU**	26(13%)	**UAA/GAA**	241(51%)
(E23S-999)	**UAA/GAU**	8(22%)	**UAA/GAC**	6(2%)	**UAA/GAC**	16(8%)	**UAA/GAU**	34(7%)
	UGA/GAU	1(3%)	others	2	**UAA/GAA**	7(4%)	**UAA/GAG**	31(6%)
	others	1	gap	0	**UAA/GAG**	4(2%)	**UAA/GAC**	22(5%)
	gap	0			others	141	UGA/GAU	1
					gap	2	others	144(30%)
							gap	2
	Total	37(100%)	Total	242(100%)	Total	196(100%)	Total	475(100%)
H23S-2774	**UAA/GAA**	37(90%)	**UAA/GAA**	210(90%)	UUA/GAA	88(70%)	**UAA/GAA**	266(67%)
(E23S-2739)	**UAA/GAG**	3(7%)	others	20	**UAA/GAA**	19(15%)	UUA/GAA	88(22%)
	others	0	gap	3	UGA/GAA	2(2%)	**UAA/GAG**	3
	gap	1			others	16	UGA/GAA	2
					gap	1	others	36(9%)
							gap	5(1%)
	Total	41(100%)	Total	233(100%)	Total	126(100%)	Total	400(100%)
H23S-1457	**UAA/GAA**	38(93%)	**UAA/GAU**	256(96%)	**UAA/GAA**	141(78%)	**UAA/GAU**	258(53%)
(E23S-1352)	UCA/GAA	1(2%)	**UAA/GAC**	3(1%)	UGA/GAA	12(7%)	**UAA/GAA**	181(37%)
	others	2	**UAA/GAA**	2(1%)	**UAA/GAU**	2(1%)	UGA/GAA	12(2%)
	gap	0	others	5	**UAA/GAC**	2(1%)	**UAA/GAC**	5(1%)
			gap	0	others	22	UCA/GAA	1
					gap	1	others	29(6%)
							gap	1
	Total	41(100%)	Total	266(100%)	Total	180(100%)	Total	487(100%)
H23S-664	**UAA/GAA**	18(49%)	UAA/GGA	191(67%)	others	154	UAA/GGA	197(38%)
(E23S-607)	UAA/GGA	6(16%)	**UAA/GAA**	44(16%)	gap	48	**UAA/GAA**	62(12%)
	others	11	others	48			others	213(41%)
	gap	2	gap	0			gap	50(10%)
	Total	37(100%)	Total	283(100%)	Total	202(100%)	Total	522(100%)
E23S-1418	Absent		**UAA/GAU**	87(33%)	Absent			
			UAA/GAA	20(7%)				
			UAA/GAC	1				
			others	12				
			gap	147				
			Total	267				
H23S-1579	**UAA/GAA**	10(23%)	GUA/GAG	94(36%)	Misc[$]	180(100%)		
(E23S-1475)	others	33(77%)	UUA/GAG	35(13%)				
			UGA/GAG	18(7%)				
			UAA/AAG	12(5%)				
			GUA/GAA	10(4%)				
			UAA/GAG	5(2%)				
			others	50(19%)				
			gap	40(15%)				
	Total	43(100%)	Total	264(100%)	Total	180(100%)		
H23S-1908	GAA/GAA	36(90)	**UAA/GAA**	205(79%)	CAA/CAA	112(72%)		
(E23S-1852)	**UAA/GAA**	3(8%)	UAA/UAA	40(15%)	CAA/GAA	17(11%)		
	others	1	GAA/GAA	2	UAA/UAA	7(5%)		
			CAA/GAA	2	CAA/GAC	5(3%)		
			others	8(3%)	**UAA/GAA**	1		
			gap	3	others	12(8%)		
					gap	1		
	Total	40(100%)	Total	260(100%)	Total	155 (100%)		

[†] Each motif is named with the combination of the *H. marismortui* 23S rRNA (H23S) and its most 5' nucleotide numbering with their *E. coli* equivalents in parentheses, except for E23S-1418, which is not present in *H. marismortui*.

[‡] Only complete sequences in the alignments for the three major phylogenetic domains (A, Archaea; B, Bacteria; E, Eukaryotes) available at http://www.rna.icmb.utexas.edu/ are included in the analysis. Sequences are shown for the UAA/GAN and related motifs, whereas loops that have more diverged sequences are included as "others". Loops in which one or two positions of the six are absent are represented as "gap". Total numbers of analyzed sequences are not the same for each loop position, even within the same phylogenetic domain, because some sequences do not have internal loops at a given position and were not included.

[$] The equivalent internal loop is present in the majority of the eukaryotic sequences with variance in size and without the consensus UAA/GAN sequence.