Supplementary Table 2. The UAA/GAN Motifs and Their Structural and Comparative Data[†]

Motif	Dist[‡]	H23S (E23S)	AAA	Receptor	AAA Conservation[¥]	Receptor Conservation[¥]	A-minor
H23S-1096	ABE	UAA/GAG	A1098	G1075:C1084	A(85.8) C(8.4)	G:C(98.2)	Type I
(E23S-999)		(UAA/GAA)	A1097	G1074:C1085	A(94.9)	G:C(55.8) C:G(31.5) A:U(8.2) U:A(3.9)	Type II
			A1259	G1074:C1085	A(98.6)	G:C(55.8) C:G(31.5) A:U(8.2) U:A(3.9)	Type I
H23S-2774	ABE	UAA/GAA	A2776	C2559:G2574	A(98.8)	G:C(91.4) C:G(7.4)	Type I
(E23S-2739)		(UAA/GAA)	A2775	G2558:C2575	A(72.3) U(26.0)	G:C(64.7) U:C(15.8) U:A(8.1) A:U(6.9)	Type II
			A2799	G2558:C2575	A(97.2)	G:C(64.7) U:C(15.8) U:A(8.1) A:U(6.9)	Type I
H23S-1457	ABE	UAA/GAA	A1459	C783:G863	A(98.8)	C:G(87.4) U:G(11.8)	Type I
(E23S-1352)		(UAA/GAU)	A1458	A784:U862	A(94.4)	A:U(52.4) C:G(38.1) U:A(4.6) G:C(3.0)	Type II
			A1485	A1656	A(99.6)	A(99.2)	—
H23S-664	AB	UAA/GGA	A666	C208:G231	A(73.5) U(9.2) C(8.1)	C:G(92.0) U:G(4.7)	Type I
(E23S-607)		(UAA/GGA)	A665	G209:C230	A(71.7) G(11.2) U(10.4)	C:G(73.7) G:C(19.1) U:A(4.7)	Type II
			A682	G209:C230	A(75.4) G(11.1) U(7.3)	C:G(73.7) G:C(19.1) U:A(4.7)	Type I
E23S-1418	B	GAA/UAA	A1580	—	A(43.2)	—	—
			A1579	—	A(88.6)	—	—
			A1419	A1494	A(85.6)	A(90.5)	—
H23S-1579[††]	A(B)	CAA/GAA	A1581	G1540:U1645	A(90.2)	G:U(68.3) C:G(7.3) U:A(7.3)	Type I
(E23S-1475)		(GUA/GAG)	A1580	—	A(95.5)	—	—
			A1615	G1541:C1644	A(95.1)	G:C(100)	Type II
			A1616	G1542:C1643	A(22.0)	G:C(95.1) G:U(2.4) A:U(2.4)	Type I
H23S-1908[††]	B(A)	GAA/GAA	A1910	U2128:A2265	A(100)	G:C(56.1) G:U(43.9)	Type I
(E23S-1852)		(UAA/GAA)	A1909	C2127:G2266	A(100)	U:A(87.8) C:G(9.8)	Type II
			A1930	C2127:G2266	A(98.9)	U:A(87.8) C:G(9.8)	Type II
			A1931	C2126:G2267	A(100)	U:G(75.2) C:G(24.8)	Type I

[†] The UAA/GAN motifs are annotated by the *H. marismortui* 23S rRNA (H23S) and their most 5' nucleotide position with their *E. coli* equivalents (E23S) in parentheses, except for E23S-1418, which is not present in *H. marismortui*.

[‡] Distribution in the three phylognetic domains: A, Archaea; B, Bacteria; E, Eukaryotes. The parenthesis is to indicate the presence of the motif in less than 10% of the sequences in a phylogenetic domain.

[¥] Conservations (%) of the A's and their receptors in the three phylogenetic domains (ABE) for the first four loops and in either the archaeal or bacterial domain for the last three.

[††] Although these positions have UAA/GAN in many 23S rRNAs, related sequences in the *H. marismortui* 23S rRNA adopt an alternative structure including an cross-strand AAAA stack.