

Table S6. MTase genes in strain BCS 100 and reisolates, and their cognate REase and S subunits genes.

Number of R-M systems	Position within H1 genome		Type of enzyme	Specificity ^a	Modified base	Type of R-M system	Assignment	<i>H. pylori</i> ortholog enzymes	Comment	
1	6944	8898	M	CCA A K	m6A	Type III	M.HpyH1I	-	Novel phase variable MTase gene. Motif not found before. Methylated in 12A3, 12C8, 81A1, 81C9	
	8901	11816	R				HpyH1IP			
2	11940	15812	RM	GCR C A	m6A	Type IIG	HpyH1II	-	Novel MTase gene. Motif not found before	
3	62571	64610	RM	CYANNNNNN <u>I</u> RG	m6A	Type IIB	HpyH1III	HpyUM032XIII	Phase variable. Methylation absent in 12A3, 12C8, 48C8, 81A1, 81C9, 87C7	
	64661	65229	S1				S1.HpyH1III			
	65236	65836	S2				S2.HpyH1III			
4	219029	217884	M	G <u>I</u> NNAC	m6A	Type IIP	M.HpyH1IV	M.Hpy30IX		
	219633	218998	R				HpyH1IVP			
5	264412	265401	M	CA <u>I</u> G	m6A	Type IIP	M.HpyH1V	M.Hpy57I		
6	302568	302056	R	<u>I</u> CNGA	m6A	Type IIP	HpyH1VIP	M.HpyUM032V		
	303826	302528	M				M.HpyH1VI			
7	361489	362430	M	G <u>C</u> GC	m5C	Type IIP	M.HpyH1VII	M.Hpy99III		
8	399176	398628	R	<u>I</u> CNNGA	m6A	Type IIP	HpyH1VIII	HpyGI		
	400138	399176	M				M.HpyH1VIII			M.Hpy32VIII
9	475250	476887	M	A <u>I</u> TAAT	m6A	Type IIP	M.HpyH1IX	M.HpyFVII		
	476853	477698	R				HpyH1IXP			Hpy66VII
10	481204	482259	M	AC <u>G</u> T	m5C	Type IIP	M.HpyH1X	M.Hpy99XI		
	482252	483005	R				HpyH1XP			Hpy66ORF5135P
11	506456	507484	M	GT <u>A</u> C	m6A	Type IIP	M.HpyH1XI	M.HpyFXII		
	507471	508226	R				HpyH1XIP			Hpy50I
12	844213	845196	M	GGCC	m5C	Type IIP	M.HpyH1XII	M.Hpy35ORF20746P		
	845193	846048	R				HpyH1XIIP			Hpy35ORF20746P
13	1143316	1144425	M	CTNA <u>G</u>	m6A	Type IIP	M.HpyH1XIII	M.Hpy30X		
	1144436	1145128	R				HpyH1XIIIP			HpyHI
14	1200899	1200141	M	CC <u>G</u> G	m4C	Type IIP	M.HpyH1XIV	M.Hpy66IX		
	1201591	1200896	R				HpyH1XIV			Hpy299IX
15	1202393	1203547	M	<u>I</u> CGA	m6A	Type IIP	M.HpyH1XV	M.HpyFII		
16	1370586	1369753	M	GA <u>I</u> C	m6A	Type IIP	M.HpyH1XVI	M.HpyFIII		
	1371413	1370580	R				HpyH1XVIP			HpyAIII
17	1411490	1412335	M	GAGG/CCTC	m6A / m5C	Type IIS	M1.HpyH1XVII	M2.HpyAVI		
	1412332	1413030	M				M2.HpyH1XVII			M1.HpyAVI
18	1423592	1422513	M	GAN <u>I</u> C	m6A	Type IIP	M.HpyH1XVIII	M.HpyAIV		
19	1439225	1437954	R	GAAGA/TCTTC	m6A / m4C	Type IIS	HpyH1XIX	HpyAII		
	1440017	1439241	M1				M1.HpyH1XIX			M1.HpyAII
	1440873	1440010	M2				M2.HpyH1XIX			M2.HpyAII
20	1441122	1443374	M	GGCAA	m6A	Type III	M.HpyH1XX	-	Novel MTase	
	1443384	1446275	R				HpyH1XXP			
21	1532818	1532087	R	<u>I</u> GCA	m6A	Type IIP	HpyH1XXIP	HpyCH4V		
	1533707	1532811	M				M.HpyH1XXI			M.HpyFVI
22	?	?	?	VCGRAG	m6A	?	?	-	MTase was not identified	

^a Modified base is represented in bold, and methylated base on the complementary strand is underlined.

Novel motifs and MTase genes described in this study are highlighted in grey.