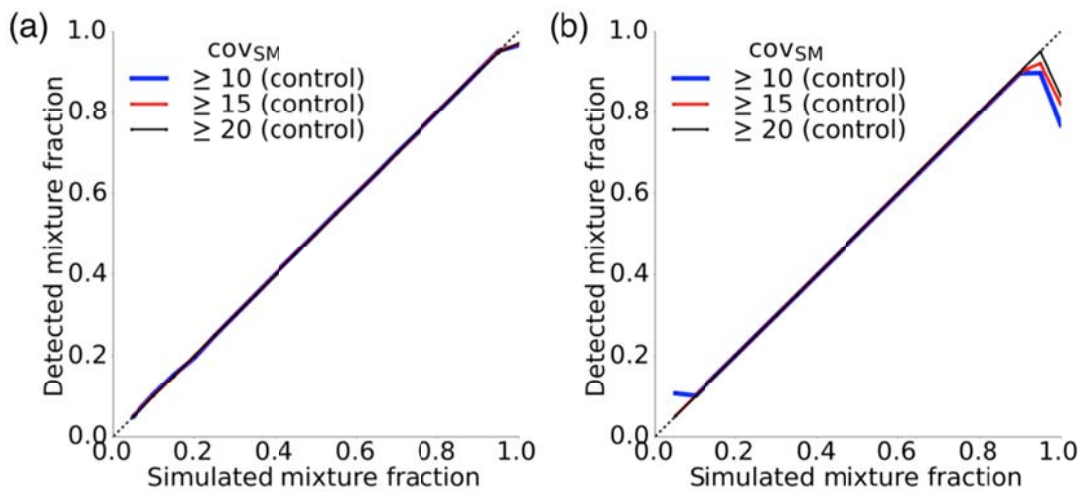
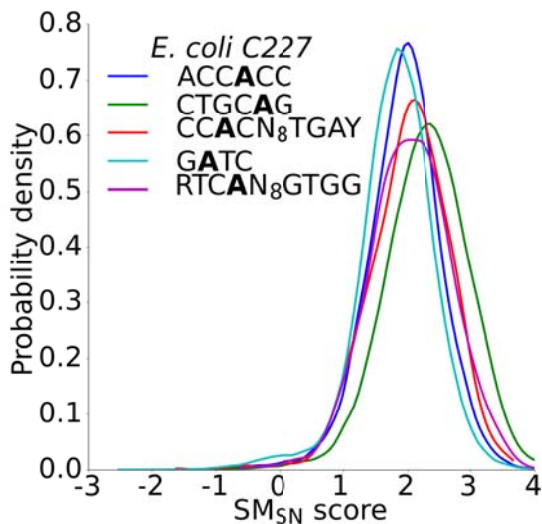


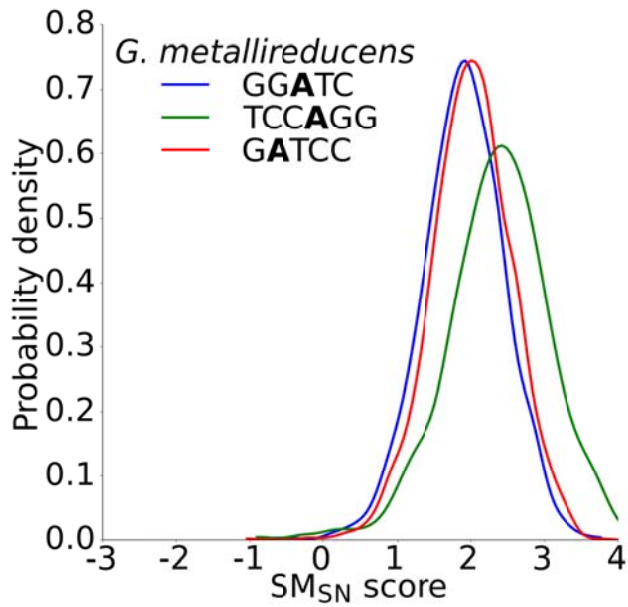
**Supplementary Figure 1:** Sensitivity and specificity of the  $SM_{SN}$  method for detecting DNA modifications using three thresholds for minimum single-molecule coverage ( $cov_{SM}$ ): **(a)** 6mA modifications in the 5'-ACCACC motif in *E. coli* C227, **(b)** 6mA modifications in the 5'-GATC motif in *E. coli* C227, and **(c)** 4mC modifications in the 5'-CGWCG motif in *H. pylori* J99.



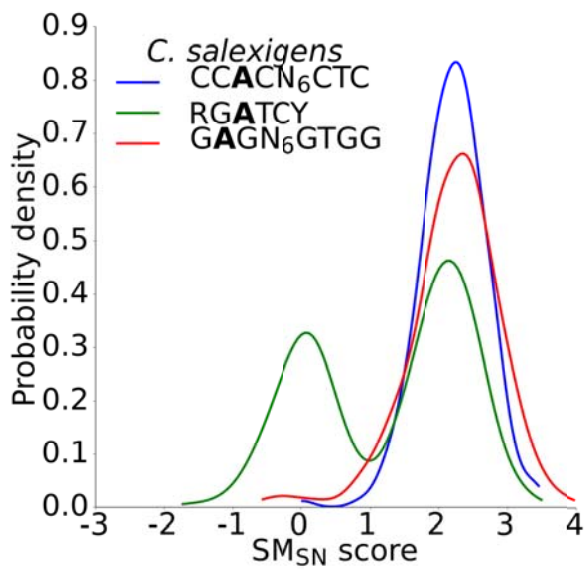
**Supplementary Figure 2:** Two alternative approaches for generating simulated modified and non-modified distributions used to test the ability of the  $SM_{SN}$  scores to estimate the size of the modified fraction. Instead of mixing varying proportions of WGA and native molecules, we instead **(a)** simulated two normal distributions centered around the mean  $SM_{SN}$  scores for modified ( $SM_{SN} = 2$ ) and non-modified ( $SM_{SN} = 0$ ) adenine residues and varied their relative proportions, and **(b)** exclusively used WGA molecules, but simulated the presence of a modification by adding 2 to the WGA  $SM_{SN}$  scores in a varying number of WGA molecules.



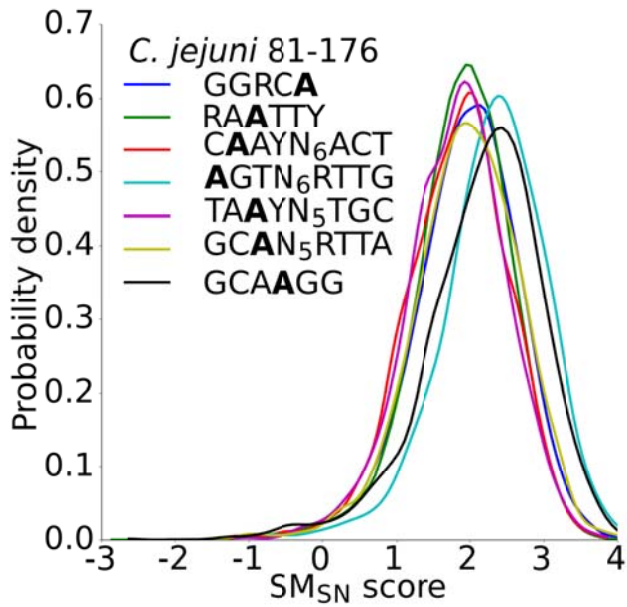
**Supplementary Figure 3:**  $SM_{SN}$  score distributions ( $cov_{SM} \geq 10$ ) for all five 6mA motifs in *E. coli* C227.



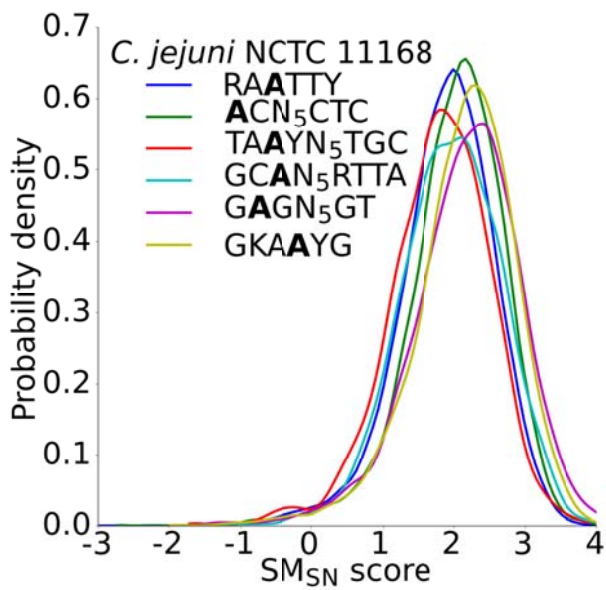
**Supplementary Figure 4:** SM<sub>SN</sub> score distributions ( $\text{cov}_{\text{SM}} \geq 10$ ) for all three 6mA motifs in *G. metallireducens*.



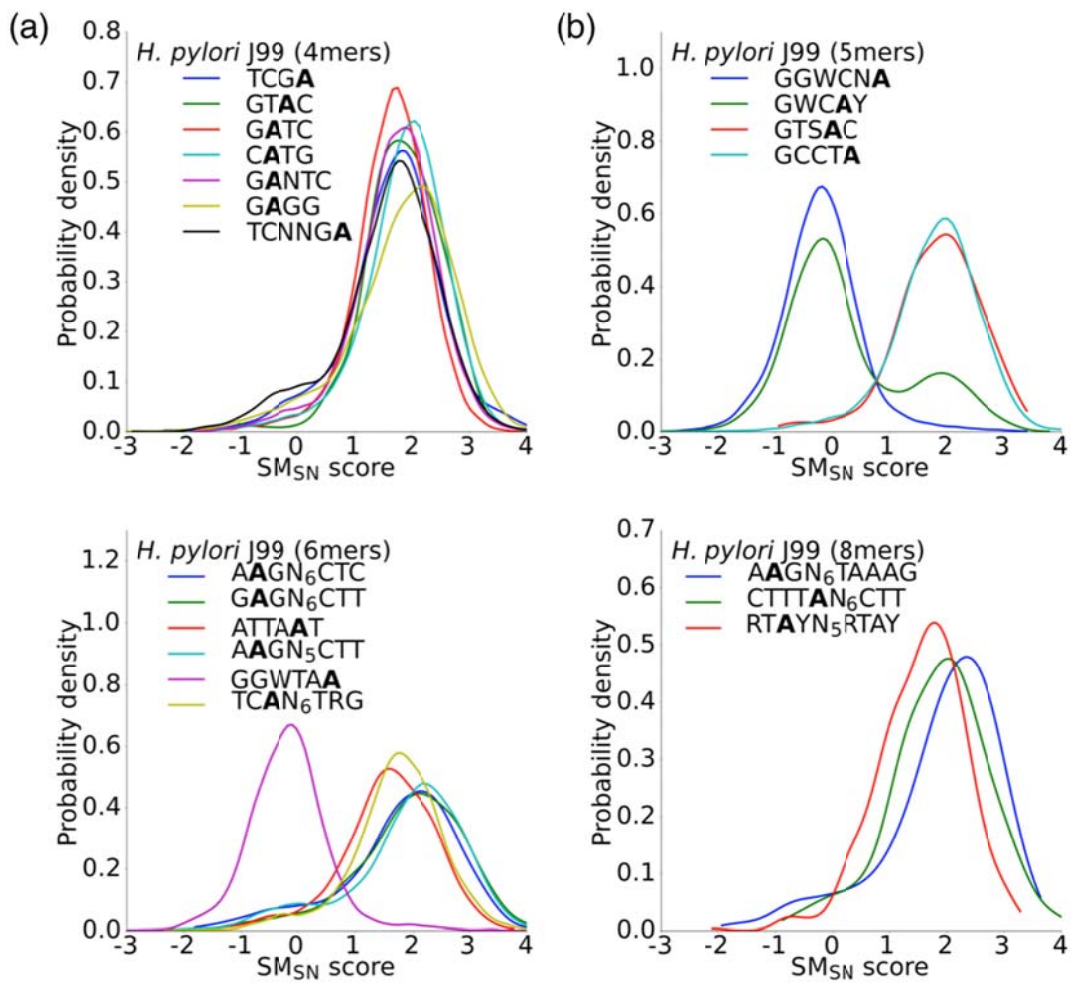
**Supplementary Figure 5:** SM<sub>SN</sub> score distributions ( $\text{cov}_{\text{SM}} \geq 10$ ) for all three 6mA motifs in *C. salexigens*.



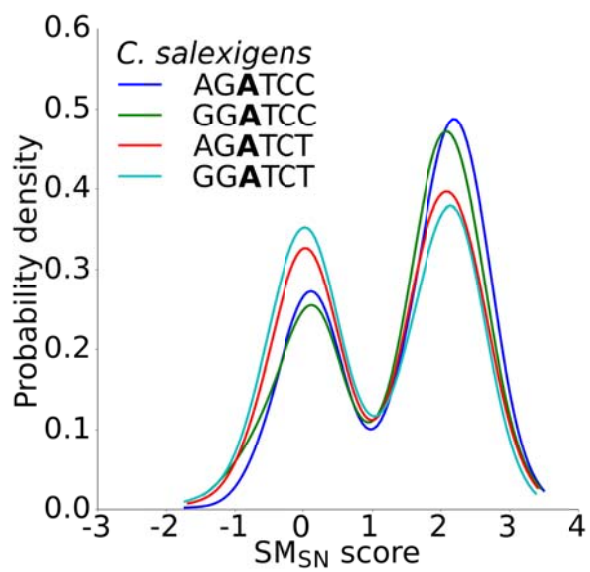
**Supplementary Figure 6:** SM<sub>SN</sub> score distributions ( $\text{cov}_{\text{SM}} \geq 5$ ) for all seven 6mA motifs in *C. jejuni* 81-176.



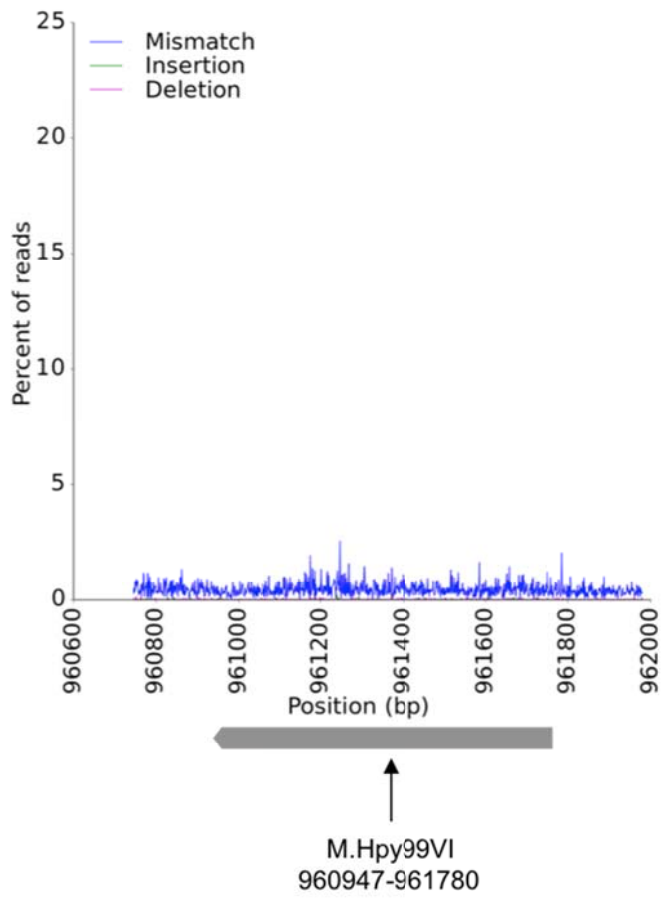
**Supplementary Figure 7:** SM<sub>SN</sub> score distributions ( $\text{cov}_{\text{SM}} \geq 5$ ) for all six 6mA motifs in *C. jejuni* NCTC 11168.



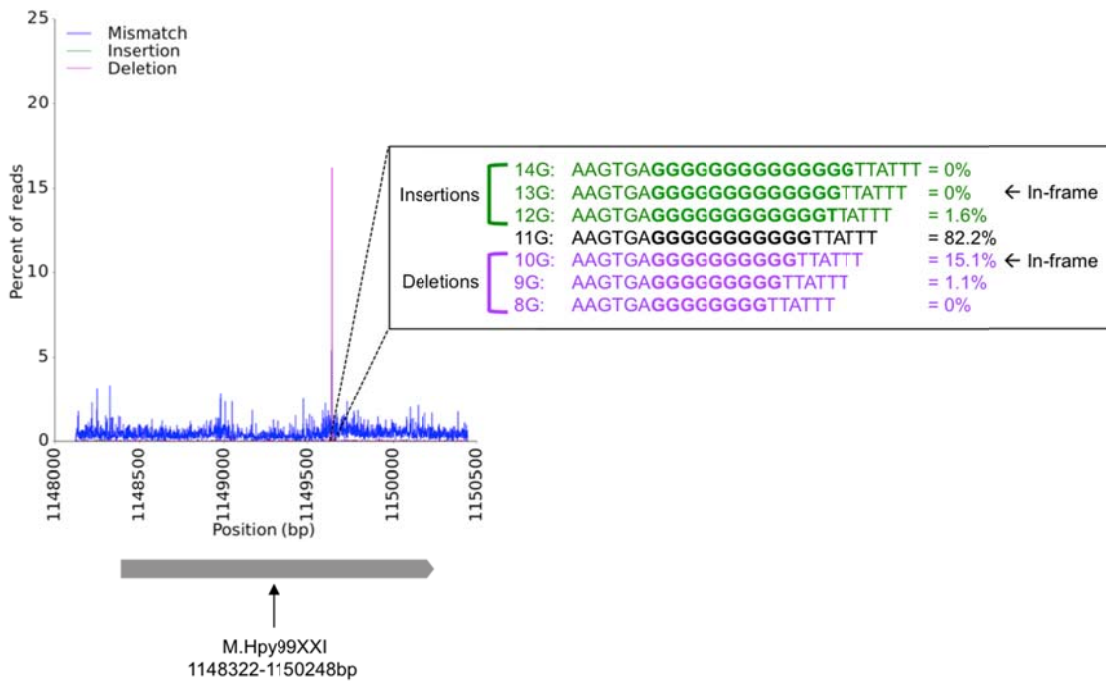
**Supplementary Figure 8:** SM<sub>SN</sub> score distributions ( $\text{cov}_{\text{SM}} \geq 5$ ) in *H. pylori* J99 for (a) all 4mer 6mA motifs, (b) all 5mer 6mA motifs, (c) all 6mer 6mA motifs, and (d) all 8mer 6mA motifs.



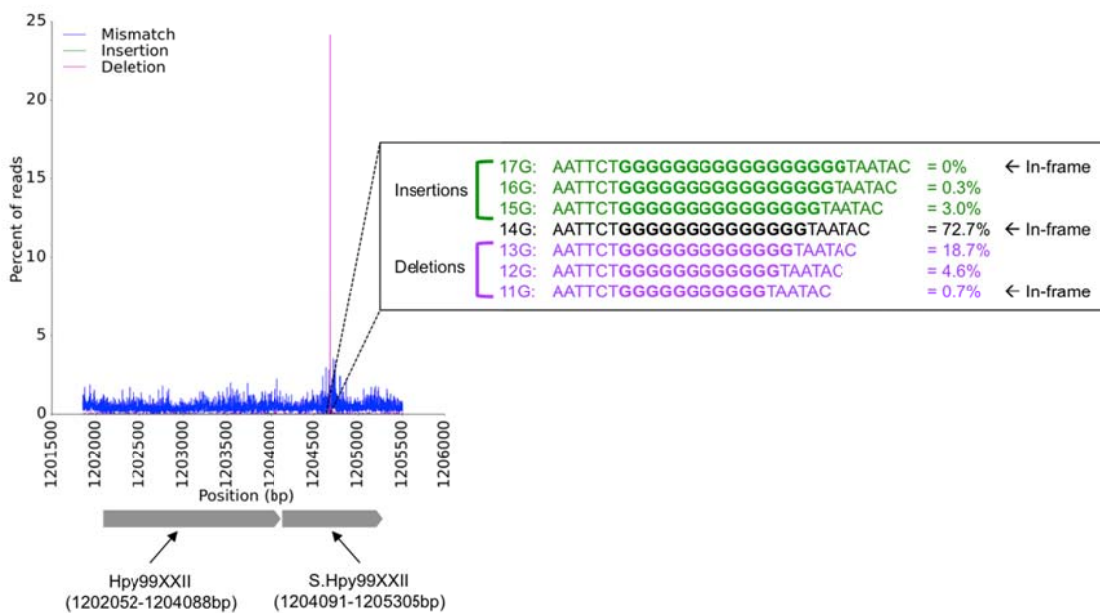
**Supplementary Figure 9:** The SM<sub>SN</sub> score distributions ( $\text{cov}_{\text{SM}} \geq 10$ ) for each specification of the degenerate 5'-RGATCY 6mA motif show similar levels of global heterogeneity.



**Supplementary Figure 10:** Read-level MiSeq mismatch and insertion/deletion calls in the coding region ( $\pm 200$ bp) of the 5'-GATC-targeting *M.Hpy99VI* gene in *H. pylori* J99.

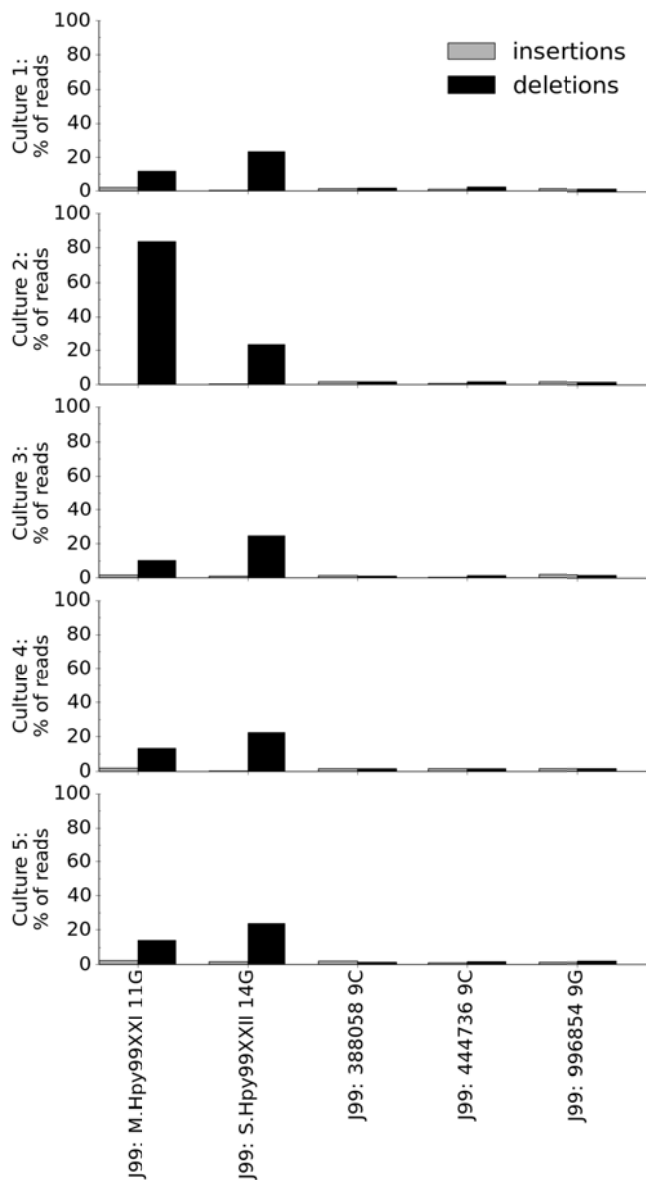


**Supplementary Figure 11:** Read-level MiSeq mismatch and insertion/deletion calls in the coding region (+/-200bp) of the 5'-GWCAY-targeting *M.Hpy99XXI* gene in *H. pylori* J99.

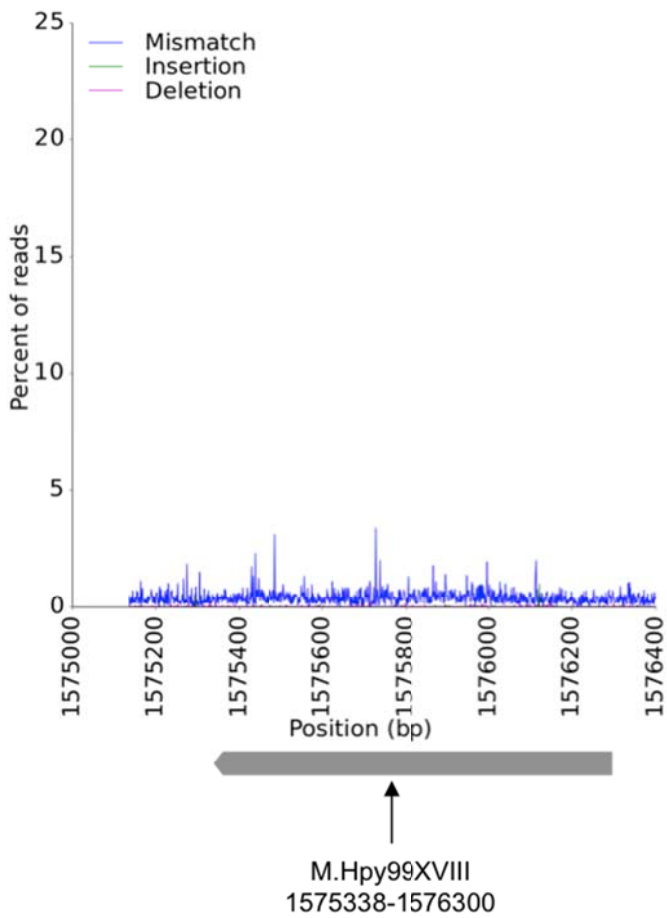


**Supplementary Figure 12:** Read-level MiSeq mismatch and insertion/deletion calls in the coding region (+/-200bp) of the 5'-TCAN<sub>6</sub>TRG/5'-CYAN<sub>6</sub>TGA-targeting *Hpy99XXII* and *S.Hpy99XXII* genes in *H. pylori* J99.

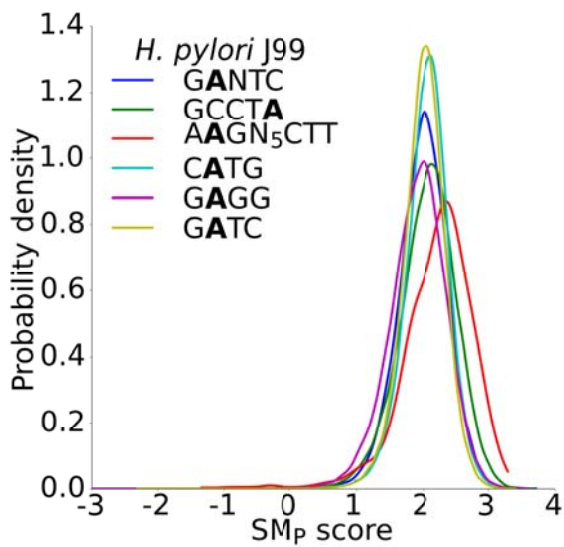




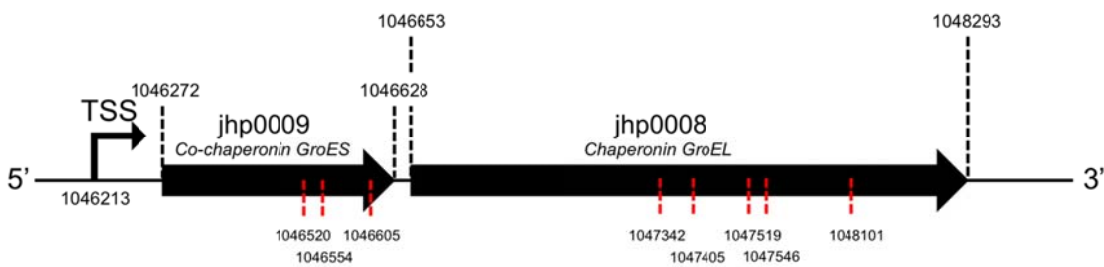
**Supplementary Figure 13:** Percentage of reads with insertion/deletion calls at multiple C/G homopolymer loci in five clonal cultures isolated from the original *H. pylori* J99 lab strain. The significant percentage of deletions in two specific poly-G regions within the coding sequences of *M.Hpy99XXI* and *S.Hpy99XXII* stand apart from the minimal length variation observed at three other 9C/G homopolymer loci in *H. pylori* J99. This suggests that the homopolymer length variation in *M.Hpy99XXI* and *S.Hpy99XXII* occurs even in clonal samples rapidly within 144 hours and is not the result of diverging, stable subpopulations within the original cell culture. One of the five colonies has a large percentage of deletions in *M.Hpy99XXI* (i.e. mostly 10G homopolymer rather than 11G), which suggests that this single colony is likely derived from a parent cell with a 10G homopolymer



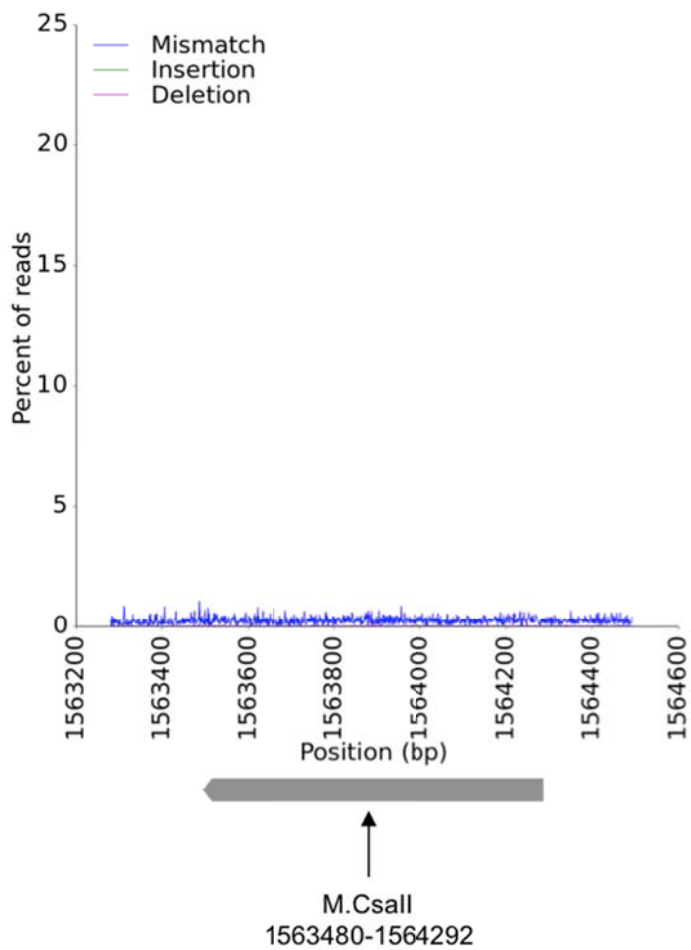
**Supplementary Figure 14:** Read-level MiSeq mismatch and insertion/deletion calls in the coding region ( $\pm 200$ bp) of the 5'-TCNNGA-targeting *M.Hpy99XVIII* gene in *H. pylori* J99.



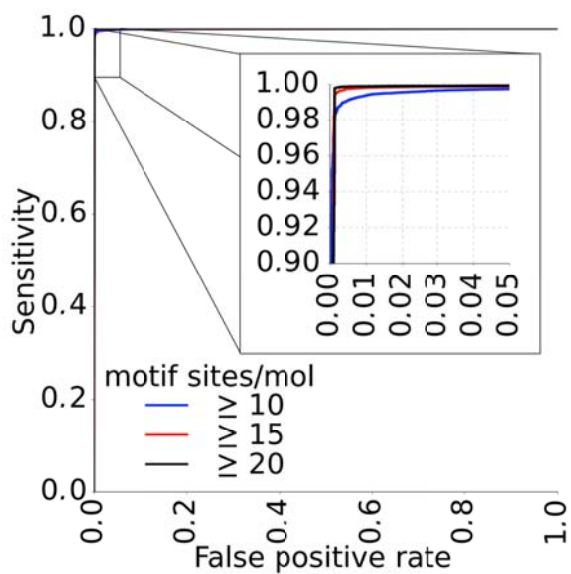
**Supplementary Figure 15:** SM<sub>P</sub> score distributions (at least 10 motif sites per molecule) for all 6mA motifs in *H. pylori* J99 (excluding 5'-GWCAY, 5'-TCAN<sub>6</sub>TRG, and 5'-TCNNGA) that contained at least ten distinct motif sites on at least 500 molecules.



**Supplementary Figure 16:** Distribution of 5'-GWCAY motif sites in the two-gene operon encoding GroES and GroEL that are significantly up-regulated in HPXZ1401, from the left to the right (5' → 3').



**Supplementary Figure 17:** Read-level MiSeq mismatch and insertion/deletion calls in the coding region ( $\pm 200$ bp) of the 5'-RGATCY-targeting *M.Csall* gene in *C. salexigens*.



**Supplementary Figure 18:** Sensitivity and specificity of the SM<sub>P</sub> method for detecting molecules that are methylated at the 5'-GATC motif in *H. pylori* J99.

**Supplementary Table 1:** SMRT sequencing statistics.

Organism	Sample type	Library	Reference GenBank accession	Mean insert length	Coverage	Mean read length	Mean subread length
<i>Escherichia coli</i> O104:H4 C227							
	Native	Short	CP011331	202	402.46	5609	172
	WGA	Short	CP011331	197	97.33	6091	167
<i>Chromohalobacter salexigens</i>							
	Native	Short	NC_007963.1	183	78.57	8119	183
		Long	NC_007963.1	3357	49.13	5233	3357
	WGA	Short	NC_007963.1	180	184.76	9023	180
<i>Helicobacter pylori</i> J99							
	Native	Short	NC_000921.1	171	71.31	4735	168
		Long	CP011330	7304	1093.73	7965	6871
	WGA	Short	NC_000921.1	195	215.19	6873	167
		Long	CP011330	3978	390.35	4957	3978

**Supplementary Table 2:** Genome-wide motif counts.

Organism (reference GenBank accession)	Motif	Count
<i>Escherichia coli</i> O104:H4 C227 (CP011331)		
	ACCACC	4321
	CTGCAG	2528
	CCACNNNNNNNTGAY	478
	GATC	42186
	RTCANNNNNNNGTGG	478
<i>Chromohalobacter salexigens</i> (NC_007963.1)		
	CCACNNNNNNCTC	784
	RGATCY	5084
	GAGNNNNNNGTGG	784
<i>Geobacter metallireducens</i> (NC_007517.1)		
	GGATC	11347
	TCCAGG	5821
	GATCC	11347
<i>Campylobacter jejuni</i> 81-176 (NC_008787.1)		
	GGRCA	1849
	RAATTY	26876
	CAAYNNNNNNACT	309
	AGTNNNNNRRTTG	309
	TAAYNNNNNTGC	460

	GCANNNNNRRTTA	460
	GCAAGG	699
<i>Campylobacter jejuni</i> NCTC 11168 (NC_018521.1)		
	RAATTY	27280
	ACNNNNNCTC	1062
	TAAYNNTGC	588
	GCANNNNNRRTTA	469
	GAGNNNNNGT	1062
	GKAAYG	1255
<i>Helicobacter pylori</i> J99 (NC_000921.1)		
	TCGA	674
	GTAC	368
	GATC	10958
	CATG	15120
	GANTC	5516
	GAGG	5001
	TCNNGA	3906
	GGWCNA	1635
	GWCA Y	5101
	GTSAC	210
	GCCTA	3106
	AAGNNNNNCTC	611
	GAGNNNNNCTT	611
	ATTAAT	854
	AAGNNNNNCTT	1582
	GGWTAA	2676
	AAANNNNNNTGG	2211
	CCANNNNNNTTT	2211
	TCANNNNNNTRG	1978
	CYANNNNNNTGA	1978
	AAGNNNNNNTAAAG	286
	CTTTANNNNNNCTT	286
	RTAYNNNNNRRTAY	362
<i>Helicobacter pylori</i> J99 (CP011330)		
	TCGA	690
	GTAC	368
	GATC	11140
	CATG	15336
	GANTC	5588
	GAGG	5120
	TCNNGA	4056
	GGWCNA	1688
	GWCA Y	5263
	GTSAC	208

	GCCTA	3214
	AAGNNNNNNCTC	639
	GAGNNNNNNCTT	639
	ATTAAT	862
	AAGNNNNNNCTT	1626
	GGWTAA	2765
	AAANNNNNNNTGG	2256
	CCANNNNNNNTTT	2256
	TCANNNNNNNTRG	2041
	CYANNNNNNNTGA	2041
	AAGNNNNNNNTAAAG	303
	CTTTANNNNNNCTT	303
	RTAYNNNNNNRTAY	372

**Supplementary Table 3:** Oligonucleotides used in this study.

Oligonucleotide	Primer sequence (5'=>3')*
SC-F-XbaI	GCTCTAGATATAAGCCATTTTCATGCTCC
SC-R-XbaI	GCTCTAGACTCGAGGCGTGATATAGATTGAAAAGTG
JHP1365LF-SacII	TCCCCGCGGCGCATGAATTGTCCCGCATAACCATG
JHP1365LR-SpeI	GGACTAGTCCAAACGCCCCCAAAGTGATTGGCC
JHP1365RF-SpeI	GGACTAGTGGCTCAATAGATTGAACTTTATTC
JHP1365RR-PstI	AAACTGCAGGAATGCGTTGTTTAACTGTTTGAAG
JHP1411LF-SacII	TCCCCGCGGGTAATTGATCGTGGCTTCATTTTG
JHP1411LR-SpeI	GGACTAGTGGGGGTAGAGGTGAAAATCAAATTC
JHP1411RF-SpeI	GGACTAGTCTTTATTTTGCATCTCTATCCTTT
JHP1411RR-PstI	AAACTGCAGGATGGAGAAAATTAGCGAAGAAATCG
Catup	TGGATGAATTACAAGACT
PGEMTe-seqF	GCTGGCGAAAGGGGGATGTGCTGCAAG
PGEMTe-seqR	CGCTCGCCGCAGCCGAACGA
	* Restriction sites underlined; <i>XbaI</i> (TCTAGA), <i>SacII</i> (CCGCGG), <i>SpeI</i> (ACTAGT), <i>PstI</i> (CTGCAG).

**Supplementary Table 4:** Plasmids and bacterial strains used.

Plasmid or strain	Relevant characteristics*	Source or reference
pGEM-T easy	Vector to construct gene mutations, Ap <sup>R</sup>	Promega
pXZ032	pGEM-T easy, carrying <i>sacB-cat</i> cassette, Ap <sup>R</sup> , Cm <sup>R</sup>	REF 64
pXZ577	pGEM-T easy, <i>jhp1365</i> upstream flanking region directly fused with <i>jhp1365</i> downstream flanking region, Ap <sup>R</sup>	This work
pXZ578	pXZ577, <i>sacB-cat</i> cassette inserted between <i>jhp1365</i> upstream and downstream flanking region to construct $\Delta$ <i>jhp1365::sacB-cat</i> mutation, Ap <sup>R</sup> , Cm <sup>R</sup>	This work
pXZ579	pGEM-T easy, <i>jhp1411</i> upstream flanking region directly fused with <i>jhp1411</i> downstream flanking region, Ap <sup>R</sup>	This work
pXZ580	pXZ579, <i>sacB-cat</i> cassette inserted between <i>jhp1411</i> upstream and downstream flanking region to construct $\Delta$ <i>jhp1411::sacB-cat</i> mutation, Ap <sup>R</sup> , Cm <sup>R</sup>	This work
<i>E. coli</i>		

XL1-blue	Host for cloning plasmid	Stratagene
<i>H. pylori</i>		
J99	USA-origin isolate	REF 53
HPXZ1398	J99 $\Delta$ <i>jhp1365::sacB-cat</i>	This work
HPXZ1401	J99 $\Delta$ <i>jhp1411::sacB-cat</i>	This work
	*Ap <sup>R</sup> and Cm <sup>R</sup> represent ampicillin-resistant and chloramphenicol-resistant, respectively.	

**Supplementary Table 5:** Differentially expressed genes (FDR < 0.05) in HPXZ1401 vs. HPXZ1383-1387. Start/End positions listed for the *H. pylori* J99 HGAP reference assembly.

Induced gene list											
ORF	Gene	Start	End	Strand	Description	log2 fold change (KO vs. WT)	p value	FDR	Distance to 5 nearest upstream GWCA Y sites	GWCA Y positions in coding region	Distance to 5 nearest downstream GWCA Y sites
<i>Flagellum related</i>											
jhp0688	<i>flaG</i>	768725	769084	+	flagellar protein FlaG	3.44	7.58E-04	4.10E-02	-760,-1222,-1300,-2697,-3106,-3673		+856,+1282,+1531,+1549,+1840,+2088
jhp0804	<i>flgE</i>	881778	883934	-	flagellar hook protein FlgE	4.12	1.50E-10	2.19E-07	-283,-381,-652,-2028,-2958,-2973	883237,883141,82916,882643	+252,+357,+462,+684,+1326,+1544
jhp1467	<i>flgB</i>	1617081	1617503	-	flagellar basal-body rod protein FlgB	2.81	1.51E-05	2.01E-03	-205,-623,-1704,-1767,-2154,-2919	1617193	+819,+1295,+2588,+3637,+4282,+4331
<i>chaperone</i>											
jhp0008	<i>groEL</i>	7758	9398	-	molecular chaperone GroEL	2.32	4.20E-04	2.83E-02	-43,-94,-128,-955,-2114,-3797	8704,8641,8527,8500,7945	+461,+665,+738,+1393,+3215,+3302
jhp0009	<i>groES</i>	9423	9779	-	co-chaperonin GroES	3.58	7.99E-09	2.34E-06	-574,-1733,-3416,-3911,-4080,-5505	9526,9492,9441	+719,+782,+896,+923,+1478,+2126
jhp0102	<i>grpE</i>	114404	114979	-	heat shock protein GrpE	3.20	9.98E-04	4.55E-02	-175,-430,-1244,-1457,-1715,-1779		+2312,+3723,+4146,+4347,+5116,+5655
jhp0103	<i>hrcA</i>	114979	115779	-	heat-inducible transcription repressor	3.11	1.04E-06	1.69E-04	-444,-657,-915,-979,-1786,-2410	115409,115154	+2887,+4298,+4721,+4922,+5691,+6230
<i>DNA processing</i>											
jhp1266	<i>ung</i>	1383952	1384653	-	uracil-DNA glycosylase	2.61	1.08E-03	4.55E-02	-103,-472,-517,-1058,-1352,-1745		+327,+441,+648,+1056,+1226,+1934
<i>Metabolism, transporter, and other</i>											
jhp0099	<i>cysK</i>	110644	111561	-	cysteine synthase	2.37	1.08E-03	4.55E-02	-531,-3593,-3848,-4662,-4875,-5133	110681	+386,+587,+1356,+1895,+2114,+2414
jhp0126		140867	142312	-	predicted iron-sulfur protein	2.35	9.36E-04	4.55E-02	-155,-168,-637,-998,-1744,-2677	142215,140916	+567,+618,+1908,+3093,+3509,+4000
jhp0545	<i>bioF</i>	593501	594622	-	8-amino-7-oxononanoate synthase	3.82	4.25E-09	1.55E-06	-162,-324,-744,-828,-3459,-3473	594315,593901,593838,593565	+262,+304,+1372,+2089,+2227,+5699
jhp0560	<i>aspS</i>	621872	623611	+	aspartyl-tRNA synthetase	2.23	9.97E-04	4.55E-02	-248,-965,-3689,-4280,-6431,-10466	621881,622168,623242	+1163,+1672,+2082,+2829,+4577,+4841
jhp0627	<i>feoB</i>	697655	699583	-	ferrous iron transport protein B	2.55	1.24E-03	4.73E-02	-661,-1320,-1374,-1574,-2572,-3274	699264	+147,+294,+1202,+1250,+2150,+2201
jhp0640	<i>dggA</i>	714369	714755	+	diacylglycerol kinase	2.25	5.07E-04	3.16E-02	-1047,-1517,-1721,-1775,-2643,-4883	714491,714671	+13,+273,+450,+480,+2136,+2241
jhp0653		731774	732496	-	ABC transporter ATP-binding protein	2.88	1.11E-04	1.19E-02	-269,-562,-2204,-3273,-3813,-3970	731973	+4,+658,+2289,+3086,+4094,+4266
jhp0935		1037343	1037885	-	Predicted partitioning protein A	2.48	5.20E-04	3.16E-02	-358,-1548,-1560,-1745,-2081,-2402	1037671,1037593,1037437	+287,+456,+858,+960,+2009,+2513
jhp1093	<i>pgi</i>	1211430	1213067	+	glucose-6-phosphate isomerase	2.44	1.69E-04	1.64E-02	-550,-4094,-4303,-4746,-4864,-5609	1212530,1212911	+189,+683,+1233,+1284,+2965,+3649
jhp1324	<i>kpsF</i>	1453242	1454231	+	Predicted polysialic acid capsule expression protein	3.34	6.54E-08	1.59E-05	-1,-299,-671,-860,-1580,-6136		+116,+2023,+2377,+2780,+4027,+5490



Unknown function											
jhp0143		158730	159005	+	hypothetical protein	3.45	3.50E-04	2.64E-02	-1477,-1540,-2436,-2880,-3099,-5118		+439,+1142,+1652,+1757,+2140,+2225
jhp0153		168125	168598	-	hypothetical protein	4.10	1.09E-03	4.55E-02	-455,-844,-1253,-1717,-1753,-2285		+301,+1212,+2564,+3560,+4873,+5098
jhp0619		687381	688148	-	hypothetical protein, predicted integral membrane protein	3.21	7.49E-05	9.12E-03	-495,-606,-669,-1735,-1963,-3289	687769	+80,+383,+1085,+1671,+3068,+3616
jhp0654		732509	732910	-	hypothetical protein	3.78	1.14E-04	1.19E-02	-148,-1790,-2859,-3399,-3556,-3568	732765	+536,+739,+1393,+3024,+3821,+4829
jhp0986		1096410	1097078	+	hypothetical protein	4.15	1.77E-09	1.29E-06	-125,-317,-368,-662,-746,-1525		+1043,+1283,+2074,+3631,+4488,+6066
jhp0987		1097080	1097838	+	hypothetical protein	4.01	3.77E-09	1.55E-06	-795,-987,-1038,-1332,-1416,-2195		+283,+523,+1314,+2871,+3728,+5306
jhp1163		1295719	1295949	+	hypothetical protein	2.71	1.49E-05	2.01E-03	-201,-345,-1278,-3697,-3816,-4813	1295814	+9,+1955,+2801,+3108,+3817,+8756
jhp1319		1448519	1449139	+	hypothetical protein	3.68	6.59E-07	1.20E-04	-1413,-2232,-2296,-2434,-4834,-5522		+2523,+3243,+3432,+3804,+4102,+5208

**Repressed gene list**

ORF	Gene	Start	End	Strand	Description	log2 fold change (KO vs. WT)	p value	FDR	Distance to 5 nearest upstream GWCA Y sites	GWCA Y positions in coding region	Distance to 5 nearest downstream GWCA Y sites
<i>DNA processing</i>											
jhp0811	<i>ruvC</i>	891084	891557	-	Holliday junction resolvase	-3.29	6.46E-04	3.63E-02	-1343,-1516,-1810,-2115,-3739,-4861	891443	+98,+1016,+1534,+1629,+2914,+3184
jhp0826	<i>tmpB</i>	908966	910294	-	IS606 transposase	-3.62	1.20E-03	4.73E-02	-575,-1442,-1774,-3148,-3295,-3688	909750,909627,909585,909401,909060	+403,+1497,+1918,+3654,+3735,+4531
jhp0931	<i>topA_3</i>	1032846	1034906	+	topoisomerase I	-4.33	4.25E-04	2.83E-02	-503,-935,-2639,-3263,-3578,-3905	1032860	+590,+675,+758,+1445,+1583,+1607
<i>Metabolism</i>											
jhp0006	<i>panC</i>	3235	4065	+	pantoate--beta-alanine ligase	-5.29	1.80E-04	1.65E-02	-438,-444	3735	+89,+306,+631,+1733,+2587,+2717
jhp0709	<i>amiA</i>	786502	787911	-	N-acetylmuramoyl-L-alanine amidase	-4.14	1.26E-03	4.73E-02	-410,-3136,-3394,-4384,-4735,-5095	787533,787097,787016	+1020,+1141,+1149,+1276,+1617,+2204
jhp0968	<i>cfa</i>	1072958	1074127	+	cyclopropane fatty acid synthase	-3.45	1.17E-03	4.73E-02	-211,-3983,-4061,-4442,-7279,-7375	1073107,1073119,1073377,1073926	+1038,+1359,+2211,+3337,+3515,+4177
jhp1023		1134753	1135505	+	short chain alcohol dehydrogenase	-3.78	8.19E-04	4.28E-02	-102,-249,-906,-1281,-3269,-4847	1135058,1135067,1135388	+745,+785,+1071,+3399,+4852,+4868
<i>Unknown function</i>											
jhp0869		961971	962456	+	hypothetical protein	-3.49	5.73E-04	3.35E-02	-2593,-2908,-5249,-5567,-5588,-7961		+18,+352,+402,+2685,+5238,+5282
jhp0927		1023777	1025174	+	hypothetical protein	-4.97	3.61E-04	2.64E-02	-2612,-2774,-4635,-7078,-8448,-8651	1024973	+451,+1361,+1937,+2258,+2357,+2489
jhp0933		1035401	1036204	+	hypothetical protein	-5.22	2.91E-04	2.36E-02	-2541,-3058,-3490,-5194,-5818,-6133	1035496,1035581,1035664	+147,+285,+309,+1926,+2043,+2214
jhp0934		1036277	1037296	-	hypothetical protein	-5.23	2.37E-04	2.04E-02	-141,-297,-375,-947,-2137,-2149	1037056,1036887,1036485,1036383	+943,+1447,+2074,+2272,+3283,+5291
jhp1397		1528923	1529639	-	hypothetical protein	-4.19	8.57E-04	4.32E-02	-379,-552,-1642,-1657,-2224,-2372	1529518,1529158	+1394,+1892,+3425,+3611,+3638,+3821

**Supplementary Table 6:** Differentially expressed genes (FDR<0.05) in HPXZ1398 vs. HPXZ1383-1387. Start/End positions listed for the *H. pylori* J99 HGAP reference assembly.

Induced gene list											
ORF	Gene	Start	End	Strand	Description	log2 fold change (KO vs. WT)	p value	FDR	Distance to 5 nearest upstream	TCANNNNNT RG positions in coding region	Distance to 5 nearest downstream

						WT)			TCANNNNN NTRG sites		TCANNNNN TRG sites
<i>Flagellum related</i>											
jhp0804	<i>flgE</i>	881778	883934	-	flagellar hook protein FlgE	3.58	1.60E-08	3.58E-06	-716,-4949,-5395,-5582,-7217,-7442	883641	+5645,+6839,+8596,+12802,+15209,+16300
<i>DNA processing</i>											
jhp0785	<i>hsdS_2</i>	864828	865451	-	type I restriction enzyme S genes	2.29	7.13E-04	3.24E-02	-27,-1118,-3525,-7731,-9488,-10682		+219,+2264,+2678,+4138,+4882,+5035
jhp1438	<i>dnaQ</i>	1585662	1586633	-	DNA polymerase III subunit epsilon	2.05	9.45E-04	3.73E-02	-3035,-5289,-6320,-6641,-9129,-10817		+1409,+2225,+3402,+5547,+5672,+7655
<i>Metabolism, transporter, and other</i>											
jhp0099	<i>cysK</i>	110644	111561	-	cysteine synthase	2.46	5.38E-04	2.77E-02	-4253,-5073,-7195,-7494,-7934,-8655		+476,+524,+7472,+9656,+10355,+14846
jhp0180	<i>tpiA</i>	197063	197767	+	triosephosphate isomerase	2.47	3.57E-04	2.39E-02	-314,-1676,-5803,-6909,-9529,-12558		+5093,+7708,+8011,+8479,+10368,+11124
jhp0200		218958	220604	+	solute carrier family 13, sodium-dependent transporter	1.98	1.42E-03	4.75E-02	-542,-1145,-3057,-6644,-9385,-10067	219252,220110,220277	+264,+6024,+7786,+13763,+14906,+16129
jhp0342	<i>hofB</i>	373015	374454	+	Predicted outer membrane transport protein HofB	2.05	6.78E-04	3.24E-02	-1463,-3134,-4367,-5359,-7869,-9957		+588,+2912,+3117,+4547,+5789,+6052
jhp0384	<i>rpsO</i>	413760	414032	+	30S ribosomal protein S15	2.20	9.23E-04	3.73E-02	-432,-468,-8669,-14040,-14292,-16763		+742,+1883,+776,+12049,+12264,+14570
jhp0423	<i>kefB</i>	455743	456993	-	glutathione-regulated potassium-efflux system protein	2.19	1.51E-03	4.83E-02	-65,-566,-1896,-2307,-3479,-4655	456167	+1201,+4679,+9634,+12305,+14494,+16389
jhp0545	<i>bioF</i>	593501	594622	-	8-amino-7-oxononanoate synthase	4.19	7.70E-11	1.03E-07	-5066,-5270,-5417,-6375,-6673,-9424	594156	+589,+3799,+7199,+8273,+8461,+10730
jhp0724	<i>lolC</i>	804721	805953	+	Predicted lipoprotein release system transmembrane protein	2.48	6.71E-05	7.64E-03	-2504,-2630,-4877,-5359,-13684,-13951	805233,805707,805854	+2196,+2641,+13328,+13798,+15155,+15573
jhp0769	<i>gatA</i>	846840	848201	-	aspartyl/glutamyl-tRNA amidotransferase subunit A	2.13	9.21E-04	3.73E-02	-1480,-2409,-3571,-3983,-5046,-5386	847084	+4851,+6863,+7028,+9870,+12971,+16468
jhp0781	<i>thiE</i>	859321	859974	-	thiamine-phosphate pyrophosphorylase	3.09	5.92E-05	7.64E-03	-716,-2176,-2590,-4635,-5504,-6595	859946,859793,859610	+4640,+5262,+5734,+6074,+7137,+7549
jhp0841	<i>pta</i>	920263	921822	-	phosphotransacetylase	2.00	1.15E-03	4.16E-02	-761,-2049,-3333,-4700,-5891,-7363	921536	+1609,+1835,+8654,+9097,+12275,+14594
jhp0980	<i>aroA</i>	1088513	1089802	+	3-phosphoshikimate 1-carboxyvinyltransferase	2.29	3.91E-04	2.39E-02	-4494,-5359,-6435,-8215,-8874,-8955	1089535	+112,+400,+1427,+2358,+2441,+3054
jhp1324	<i>kpsF</i>	1453242	1454231	+	Predicted polysialic acid capsule expression protein	3.61	3.78E-09	1.61E-06	-1625,-2791,-7288,-7657,-8766,-9353		+7193,+7902,+10051,+11292,+12286,+12705
<i>Unknown function</i>											
jhp0355		386564	386824	-	hypothetical protein	3.58	1.60E-08	3.58E-06	-967,-2530,-4358,-5278,-14608,-15431		+1103,+1210,+2246,+2420,+9227,+10399
jhp0440		475860	478598	+	hypothetical protein	2.50	1.67E-04	1.31E-02	-1305,-2752,-4237,-7338,-8832,-9195	477137	+944,+1541,+4108,+4988,+7793,+13259
jhp0555		607216	607785	+	hypothetical protein	2.45	4.01E-04	2.39E-02	-336,-920,-1950,-2186,-2589,-6885		+1705,+1906,+7473,+8500,+19576,+20337
jhp0619		687381	688148	-	hypothetical protein, predicted integral membrane protein	3.04	3.53E-04	2.39E-02	-1936,-3088,-7106,-8451,-9595,-10750		+3713,+4129,+6139,+6225,+8131,+8552

jhp0687		767426	768628	+	hypothetical protein	2.79	4.57E-06	7.66E-04	-767,-3485,-7607,-7961,-12266,-14704	768196	+112,+3641,+5859,+6186,+8033,+9336	
jhp0986		1096410	1097078	+	hypothetical protein	4.12	2.02E-09	1.36E-06	-317,-368,-1409,-1658,-1973,-3335	1096445,1096493	+3565,+3581,+3634,+3895,+4519,+6294	
jhp0987		1097080	1097838	+	hypothetical protein	4.00	4.79E-09	1.61E-06	-587,-635,-987,-1038,-2079,-2328		+2805,+2821,+2874,+3135,+3759,+5534	
jhp1044		1157436	1160900	-	hypothetical protein	2.65	7.98E-05	7.64E-03	-762,-1554,-2466,-4624,-8164,-12590	1159381,1157580	+2079,+2700,+4012,+5812,+6840,+7792	
jhp1319		1448519	1449139	+	hypothetical protein	3.67	7.46E-07	1.43E-04	-2565,-2934,-4043,-4630,-5517,-7955		+1312,+2478,+12285,+12994,+15143,+16384	
<b>Repressed gene list</b>												
ORF	Gene	Start	End	Strand	Description	log2 fold change (KO vs. WT)	p value	FDR	Distance to 5 nearest upstream TCANNNNN NTRG sites	TCANNNNNNT RG positions in coding region	Distance to 5 nearest downstream TCANNNNNN TRG sites	
<i>DNA processing</i>												
jhp0629	<i>hpy991 VM</i>	700587	701801	+	type II DNA modification enzyme	-3.76	6.92E-04	3.24E-02	-1603,-4178,-4573,-6132,-7322,-10700		+1724,+3952,+6651,+7152,+8997,+9063	
jhp0931	<i>topA_3</i>	1032846	1034906	+	topoisomerase I	-4.37	4.27E-04	2.39E-02	-786,-2443,-2477,-2918,-4814,-5333	1033118,1034267	+273,+686,+4793,+5491,+7331,+7675	
jhp1166	<i>ssb</i>	1299583	1300128	-	single-stranded DNA-binding protein	-3.45	7.24E-04	3.24E-02	-1496,-3340,-5076,-13422,-14199,-23258		+1244,+3776,+6511,+7429,+9805,+10132	
<i>Metabolism and other</i>												
jhp0135	<i>fixP</i>	151681	152559	+	cytochrome oxidase (CBB3-type)	-5.94	5.30E-04	2.77E-02	-1215,-1452,-2531,-14240,-15086,-15664		+222,+2197,+2668,+3484,+5398,+5494	
jhp0709	<i>amiA</i>	786502	787911	-	N-acetylmuramoyl-L-alanine amidase	-4.13	1.26E-03	4.44E-02	-2265,-3121,-3217,-3575,-5281,-5530		+2915,+3260,+4221,+5725,+7702,+7780	
jhp0909	<i>gatC</i>	1005692	1005973	+	aspartylglutamyl-tRNA amidotransferase subunit C	-5.90	2.31E-05	3.44E-03	-1709,-3568,-5496,-6403,-8742,-9127		+1927,+2881,+4107,+7179,+9308,+10211	
jhp0968	<i>cfa</i>	1072958	1074127	+	cyclopropanoic fatty acid synthase	-4.44	8.58E-05	7.68E-03	-831,-5025,-5375,-5970,-9402,-12694		+1243,+1651,+3224,+4108,+5280,+5431	
jhp1039	<i>purB</i>	1151605	1152927	+	adenylosuccinate lyase	-5.59	1.26E-04	1.06E-02	-516,-1833,-9063,-10604,-10928,-11430		+2842,+3478,+4189,+5361,+10450,+12079	
jhp1437	<i>hcpG</i>	1584853	1585623	+	Cysteine-rich protein G, related to amoxicillin resistance	-5.93	4.23E-04	2.39E-02	-1417,-2106,-2856,-4834,-5409,-5476		+141,+1185,+1657,+3199,+5793,+6378	
<i>Unknown function</i>												
jhp0093		103627	104388	+	hypothetical protein	-4.19	1.47E-03	4.80E-02	-2421,-2985,-4215,-4909,-13452,-14022		+848,+1124,+1930,+3141,+6601,+8226	
jhp0360		391140	391547	-	hypothetical protein	-4.33	1.03E-03	3.85E-02	-555,-9885,-10708,-12948,-15620,-17594	391182	+1786,+3349,+5679,+5786,+6822,+6996	
jhp0816		894929	896773	-	hypothetical protein	-5.23	2.37E-04	1.77E-02	-2272,-2625,-3799,-3895,-6010,-6049	895374,895125	+259,+3553,+3778,+5413,+5600,+6046	
jhp0928		1025324	1032019	+	hypothetical protein	-4.13	1.31E-03	4.52E-02	-2870,-8112,-8769,-9140,-10043,-12172	1025645,1026292,1027513,1028032,1029928,1030369,1030403	+41,+1099,+2248,+3160,+3573,+7680	
jhp0934		1036277	1037296	-	hypothetical protein	-4.55	9.83E-04	3.77E-02	-1609,-2816,-4140,-5659,-7214,-8098		+2386,+6192,+7488,+7973,+8444,+8492	
jhp1070		1183290	1185569	-	hypothetical protein	-5.12	7.92E-05	7.64E-03	-1161,-1950,-2188,-3085,-3729,-6379		+1337,+1595,+5254,+6642,+8389,+9800	
jhp1113		1237715	1238866	-	hypothetical protein	-4.39	9.10E-04	3.73E-02	-775,-2692,-4531,-4882,-4979,-6467		+599,+2655,+3012,+3823,+4366,+4510	