

Table S2. SNPs identified in *H. pylori* strains used in the study.

<i>H. pylori</i> B128 ΔfapH pflA* (lab strain H54) – SNPs not present in wild-type <i>H. pylori</i> B128					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	^a Impact	^b Frequency
CV725_RS00010	HP1527	<i>comH</i> , competence protein	Δ 1 bp (708/1440 nt)	Val236fs	98.8%
CV725_RS00395	HP1451	Cag VirB11 inhibitory protein	+T (689/798 nt)	Tyr230fs	98.1%
CV725_RS00960	HP1274	<i>pflA</i> , paralyzed flagella protein	+G (1428/2406 nt) Δ 1 bp (1391/2406 nt)	offsetting fs mutations	98.4% 98.5%
<i>maf</i> CV725_RS01150	HP1239 HP1240	^c DS of <i>maf</i> , ^c US of <i>hp1239</i> (hypothetical protein)	(A) _{13→14} intergenic (+61/+394)	unknown	80.5%
<i>mreC</i>	HP1372	<i>mreC</i> , rod shape-determining protein	codon-220 (TAC→CAC)	Tyr220His	98.8%
CV725_RS02745	HP0098	<i>thrC</i> , threonine synthase	codon-417 (GAA→AAA)	Glu417Lys	98.9%
<i>tlpB</i>	HP0103	<i>tlpB</i> , methyl-accepting chemotaxis protein	codon-26 (GGG→GAG)	Gly26Glu	98.6%
CV725_RS03745	HP0298	<i>dppA</i> , dipeptide ABC transporter, periplasmic dipeptide-binding protein	(T) _{10→9} (30/1644 nt)	Phe10fs	96.4%
CV725_RS04335	HP1028	hypothetical protein	codon-16 (GCT→GTT)	Ala16Val	98.5%
CV725_RS04505	HP0475	<i>modD</i> , molybdenum ABC transport protein	codon-155 (TTA→TTG)	Leu155Leu	99.1%
CV725_RS04600 CV725_RS04605	HP0875 HP0876	US of <i>kata</i> , US of <i>frpB</i>	(A) _{5→6} intergenic (-34/-290)	unknown	83.4%
CV725_RS04785	HP0838	<i>fapH</i> , flagellum-associated protein H	codon-18 (GTC→GCC) Δ 490 bp	Val18Ala gene deletion	99.1%
CV725_RS06350	HP0527	cag pathogenicity island protein Cag7	codon-752 (ACC→ACG) codon-742 (GCT→GCC)	Thr752Thr Ala742Ala	96.2% 99.3%
<i>babA</i> CV725_RS06645	HP1243 tRNA_fMet	US of <i>babA</i> , DS of tRNA_fMet	(T) _{13→12} intergenic (-131/+149)	unknown	86.2%
CV725_RS08550 <i>queF</i>	HP1412 HP1413	DS of <i>hp1412</i> (hypothetical protein), DS of <i>queF</i>	(C) _{11→10} intergenic (+11/+121)	unknown	94.6%
bacitracin-resistant isolate of ΔfapH pflA* strain (H150) – SNPs not present in ΔfapH pflA* parental strain					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→12} (1452/2053 nt)	no effect	94.8%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.2%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	93.4%
CV725_RS03925	HP0337	hypothetical protein	(A) _{7→8} (62/339 nt)	Asn19-fs	98%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	97.4%
CV725_RS05120	HP0771	hypothetical protein.	(T) _{8→9} (59/738 nt)	Phe19-fs	96.5%
bacitracin-resistant isolate of ΔfapH pflA* strain (H151) – SNPs not present in ΔfapH pflA* parental strain					

NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	91.4%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	100%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	88.6%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	97.1%
CV725_RS05120	HP0771	hypothetical protein.	(T) _{8→9} (59/738 nt)	Phe19-fs	97.2%
bacitracin-resistant isolate of $\Delta fapH pflA^*$ strain (H152) – SNPs not present in $\Delta fapH pflA^*$ parental strain					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	90.3%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.6%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	91.9%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	96.7%
CV725_RS05120	HP0771	hypothetical protein.	(T) _{8→9} (59/738 nt)	Phe19-fs	96%
<i>hefC</i>	HP0607	efflux RND transporter permease subunit HefC.	codon-808 (GCT→GTT)	Ala808Val	99.5%
bacitracin-resistant isolate of $\Delta fapH pflA^*$ strain (H153) – SNPs not present in $\Delta fapH pflA^*$ parental strain					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	91.6%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.3%
CV725_RS01830		HP1117 family Sel1-like repeat protein	Δ 108 bp (231-338/771 nt)	truncation	99.8%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	92.4%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	100%
CV725_RS05120	HP0771	hypothetical protein	Δ 27 bp (68-94/738 nt)	in-frame deletion	100%
CV725_RS05665	HP0659	SurA N-terminal domain protein; predicted periplasmic peptidyl-prolyl cis-trans isomerase.	codon-398 (CGC→TGC)	Arg398Cys	100%

bacitracin-resistant isolate of Δ <i>fapH pflA</i> * strain (H154) – SNPs not present in Δ <i>fapH pflA</i> * parental strain					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→12} (1452/2053 nt)	no effect	94.5%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	90.1%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	C→T (GAC→AAC)	Asp135Asn	99.7%
CV725_RS05120	HP0771	hypothetical protein.	Δ27 bp (68-94/738 nt)	truncation	100%
<i>hefC</i>	HP0607	efflux RND transporter permease subunit HefC.	codon-808 (GCT→GTT)	Ala808Val	99.7%
bacitracin-resistant isolate of Δ <i>fapH pflA</i> * strain (H155) – SNPs not present in Δ <i>fapH pflA</i> * parental strain					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	92.2%
CV725_RS00385 <i>mnme</i>	HP1453	outer membrane beta-barrel protein/tRNA uridine-5-carboxymethylaminomethyl (34) synthesis GTPase MnME	(T) _{17→16} intergenic (-105/+113)	unknown	80.5%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.5%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	91.4%
CV725_RS03700	HP0289	vacuolating cytotoxin domain-containing protein.	Codon-670 (GGG→AGG)	Gly670Arg	100%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	94.9%
CV725_RS05120	HP0771	hypothetical protein.	(T) _{8→9} (59/738 nt)	Phe19-fs	94.7%
CV725_RS07860	HP1581	<i>llm</i> , methicillin resistance protein	codon-43 (CCA→ACA)	Pro43Thr	100%
bacitracin-resistant isolate of Δ <i>fapH pflA</i> * strain (H156) – SNPs not present in Δ <i>fapH pflA</i> * parental strain					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	90.4%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.7%
<i>rpsR</i> <i>babA</i>	HP1244 HP1243	DS of HP1244 rpsR 30S ribosomal protein S18 and US of HP1243 outer membrane protein <i>babA</i>	(A) _{13→14} intergenic (+195/-132)	unknown	80.3%

CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	89.8%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	C→T (<u>G</u> AC→ <u>A</u> AC)	Asp135Asn	100%
CV725_RS05120	HP0771	hypothetical protein.	Δ27 bp (68-94/738 nt)	truncation	100%
<i>hefC</i>	HP0607	efflux RND transporter permease subunit HefC.	codon-71 (<u>G</u> GG→ <u>A</u> GG)	Gly71Arg	100%

bacitracin-resistant isolate of *ΔfapH pflA strain (H157) – SNPs not present in *ΔfapH pflA** parental strain**

NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	93.5%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	98.8%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	88.1%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	94.8%
CV725_RS05120	HP0771	hypothetical protein.	(T) _{8→9} (59/738 nt)	Phe19-fs	93.3%
CV725_RS06910	HP0947	hypothetical protein	+T coding (173/363 nt)	Lys58-fs	100%

bacitracin-resistant isolate of *ΔfapH pflA strain (H158) – SNPs not present in *ΔfapH pflA** parental strain**

NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	96.5%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	100%
CV725_RS02330 CV725_RS02335	HP1370 NA	biotin synthase/type III restriction enzyme.	(C) _{13→14} intergenic (-243/-51)	unknown	85%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	99.5%
CV725_RS05120	HP0771	hypothetical protein.	Δ27 bp (68-94/738 nt)	in-frame deletion	100%
<i>hefC</i>	HP0607	efflux RND transporter permease subunit HefC.	codon-642 (<u>A</u> AT→ <u>G</u> AT)	Asn64Asp	100%

bacitracin-resistant isolate of *ΔfapH pflA strain (H159) – SNPs not present in *ΔfapH pflA** parental strain**

NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	95.9%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.1%

CV725_RS02330 CV725_RS02335	HP1370 NA	biotin synthase/type III restriction enzyme.	(C) _{13→14} intergenic (-243/-51)	unknown	88.3%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	89.4%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	98.1%
CV725_RS05120	HP0771	hypothetical protein.	(T) _{8→9} (59/738 nt)	Phe19-fs	94.8%

bacitracin-resistant isolate of <i>ΔfapH pflA</i> * strain (H160) – SNPs not present in <i>ΔfapH pflA</i> * parental strain					
NCBI designation	26695 locus tag	Gene/description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	94.2%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99%
CV725_RS02330 CV725_RS02335	HP1370 NA	biotin synthase/type III restriction enzyme.	(C) _{13→14} intergenic (-243/-51)	unknown	81.7%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→11} pseudogene (3222-3224/3372 nt)	no effect	81.9%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	C→T (<u>G</u> AC→ <u>A</u> AC)	Asp135Asn	100%
CV725_RS05120	HP0771	hypothetical protein	Δ27 bp coding (68-94/738 nt)	truncation	100%
CV725_RS06720 <i>alpA</i>	HP0911 HP0912	DS of ATP-dependent helicase/US of Hop family adhesin AlpA (HopC).	(T) _{14→15} intergenic (+380/-206)	unknown	85%
CV725_RS06910	HP0947	hypothetical protein (No hits for HP designation)	codon-114 (<u>G</u> CC→ <u>A</u> CC)	Ala114Thr	100%

bacitracin-resistant isolate of <i>ΔfapH pflA</i> * strain (H161) – SNPs not present in <i>ΔfapH pflA</i> * parental strain					
NCBI designation	26695 locus tag	Gene/ description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	85.9%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.7%
CV725_RS00915	HP1284	glycosyltransferase family 9 protein ADP-heptose:LPS heptosyltransferase	codon-236 (<u>G</u> GC→ <u>G</u> TC)	Gly236Val	98.9%
CV725_RS02330 CV725_RS02335	HP1370 NA	biotin synthase/type III restriction enzyme.	(C) _{13→14} intergenic (-243/-51)	unknown	84.6%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	91.8%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	(A) _{8→9} (55/453 nt)	Ile18-fs	96.8%
CV725_RS05120	HP0771	hypothetical protein	(T) _{8→9} (59/738 nt)	Phe19-fs	93.1%

<i>H. pylori</i> B128 <i>Δfur-7</i> – SNPs not present in wild-type <i>H. pylori</i> B128					
NCBI designation	26695 locus tag	Gene/ description	Mutation/annotation	Impact	Frequency

CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	100%
CV725_RS02305 CV725_RS02315	HP0427 23S rRNA	US of <i>hp0427</i> (hypothetical protein), US of 23S rRNA gene	A→G intergenic (-235/-735)	unknown	89.7%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	Δ436 bp	gene deletion	100%
CV725_RS04600 CV725_RS04605	HP0875 HP0876	US of <i>katA</i> , US of <i>frpB</i>	(A) _{5→6} intergenic (-34/-290)	unknown	93.9%
<i>motA</i>	HP0815	<i>motA</i>	codon-201 (G <u>G</u> C→G <u>A</u> C)	Gly201Asp	99.3%
CV725_RS06350	HP0527	<i>cag</i> pathogenicity island protein (<i>cag7</i>)	codon-1226 (<u>T</u> TA→ <u>C</u> TA) codon-752 (A <u>C</u> C→A <u>C</u> G) codon-742 (G <u>C</u> T→G <u>C</u> C)	Leu1226Leu Thr752Thr Ala742Ala	99.5% 89.5% 80.8%
CV725_RS06500	HP0499	<i>pldA</i> , phospholipase A pseudogene	(G) _{10→8} (683/1070 nt)	phase 'off' to phase 'on'	98.2%
CV725_RS07515 <i>queF</i>	HP1412 HP1413	DS of HP1412 hypothetical protein and DS of <i>queF</i>	(C) _{11→10} intergenic (+11/+121)	unknown	96.1%

***H. pylori* B128 Δ*fur*-10 – SNPs not present in wild-type *H. pylori* B128**

NCBI designation	26695 locus tag	Gene/ description	Mutation/annotation	Impact	Frequency
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.6%
<i>rpsS</i> <i>rplV</i>		30S ribosomal protein S19/50S ribosomal protein L22	(G) _{5→4} intergenic (+5/-5)	unknown	99.6%
CV725_RS00895	HP1288	pantothenate kinase	-T (81/351 nt)	Phe27-fs	99.3%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	Δ436 bp	gene deletion	100%
CV725_RS04600 CV725_RS04605	HP0875 HP0876	US of <i>katA</i> , US of <i>frpB</i>	(A) _{5→6} intergenic (-34/-290)	unknown	91.9%
<i>motA</i>	HP0815	<i>motA</i>	codon-201 (G <u>G</u> C→G <u>A</u> C)	Gly201Asp	100%
CV725_RS06350	HP0527	<i>cag</i> pathogenicity island protein (<i>cag7</i>)	codon-1226 (<u>T</u> TA→ <u>C</u> TA) codon-936 (A <u>C</u> G→A <u>C</u> C) codon-752 (A <u>C</u> C→A <u>C</u> G) codon-742 (G <u>C</u> T→G <u>C</u> C)	Leu1226Leu Thr936Thr Thr752Thr Ala742Ala	99.6% 97.1% 95.4% 96.3%
CV725_RS06500	HP0499	<i>pldA</i> , phospholipase A pseudogene	(G) _{10→7} (683/1070 nt)	remains phase 'off'	85.1%
CV725_RS07515 <i>queF</i>	HP1412 HP1413	DS of HP1412 hypothetical protein and DS of <i>queF</i>	(C) _{11→10} intergenic (+11/+121)	unknown	96.1%

<i>H. pylori</i> B128 $\Delta fapH$ <i>pflA</i>* Δfur-5 – SNPs not present in $\Delta fapH$ <i>pflA</i>* parental strain					
NCBI designation	26695 locus tag	Gene/ description	Mutation/annotation	Impact	Frequency
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	89.5%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.5%
<i>maf</i> CV725_RS01150	HP1239 HP1240	DS of <i>maf</i> , US of <i>hp1239</i> (hypothetical protein)	(A) _{13→16} intergenic (+74/+381)	unknown	83.9%
CV725_RS02330 CV725_RS02335	HP1370 NA	biotin synthase/type III restriction enzyme.	(C) _{13→14} intergenic (-243/-51)	unknown	88.4%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	89.3%
CV725_RS03080	HP0164	<i>arsS</i> , histidine kinase	(C) _{11→12} coding (1261/1281 nt)	Pro424-fs	86.7%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	Δ 436 bp	gene deletion	100%
CV725_RS04785	HP0838	<i>fapH</i> , flagellar-associate protein H	Δ 490 bp	gene deletion	100%
CV725_RS05175 <i>my</i>	HP0761	5-formyltetrahydrofolate cyclo-ligase ribonuclease Y	codon-208 (TAC→TAT)	Tyr208Tyr	99.2%
CV725_RS07655 <i>labA</i>	HP0026 HP0025	citrate synthase/Hop family adhesin LabA	(T) _{17→16} intergenic (+379/-149)	unknown	83.3%
<i>H. pylori</i> B128 $\Delta fapH$ <i>pflA</i>* Δfur-9 – SNPs not present in $\Delta fapH$ <i>pflA</i>* parental strain					
CV725_RS00040	NA	site-specific DNA-methyltransferase, pseudogene	(G) _{14→13} (1453/2053 nt)	phase 'off' to phase 'on'	89.7%
CV725_RS00720 CV725_RS00725	HP1321 HP1322	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.6%
CV725_RS08420	HP1353	Type ISP C-terminal specificity domain, pseudogene	(C) _{14→13} (3223/3372 nt)	no effect	89.4%
CV725_RS03080	HP0164	<i>arsS</i> , histidine kinase	(C) _{11→12} coding (1261/1281 nt)	Pro424-fs	80.3%
<i>fur</i>	HP1027	<i>fur</i> , ferric uptake regulator	Δ 436 bp	gene deletion	100%
CV725_RS04785	HP0838	<i>fapH</i> , flagellar-associated protein H	Δ 490 bp	gene deletion	100%
CV725_RS05175 <i>my</i>	HP0761	5-formyltetrahydrofolate cyclo-ligase ribonuclease Y	codon-208 (TAC→TAT)	Tyr208Tyr	100%
CV725_RS05825	HP0628	sel1 repeat family protein	(C) _{7→6} coding (505/1059 nt)	Gly169-fs	95.6%
CV725_RS06350	HP0527	cag pathogenicity island protein (Cag7)	codon-936 (ACG→ACC)	Thr936Thr	96.9%
CV725_RS07655 <i>labA</i>	HP0026 HP0025	citrate synthase/Hop family adhesin LabA	(T) _{17→16} intergenic (+379/-149)	unknown	83.1%

<i>ΔfapH-2</i> – SNPs not present in wild-type <i>H. pylori</i> B128					
CV725_RS00720 CV725_RS00725	HP1322 HP1321	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.0%
CV725_RS02305 CV725_RS02315	HP0427 23S rRNA	US of <i>hp0427</i> (hypothetical protein), US of 23S rRNA gene	C→T intergenic (-235/-735)	unknown	81.6%
CV725_RS02465	HP1375	N-6 DNA methylase	(C) _{14→13} pseudogene (3224/3372 nt)	restore full-length ORF	91.8%
CV725_RS03080	HP0164	<i>arsS</i> , histidine kinase	(C) _{11→12} coding (1261/1281 nt)	Pro424-fs	85.7%
CV725_RS04600 CV725_RS04605	HP0875 HP0876	US of HP0875 <i>katA</i> , US of HP0876 <i>frpB</i>	(A) _{5→6} intergenic (-34/-290)	unknown	93.0%
CV725_RS04785	HP0838	<i>fapH</i> , flagellar-associated protein H	Δ490 bp	gene deletion	100%
CV725_RS06500	HP0499	<i>pldA</i> , phospholipase A pseudogene	(G) _{10→9} (683/1070 nt)	remains phase 'off'	94.8%
CV725_RS07515 <i>queF</i>	HP1412 HP1413	DS of HP1412 hypothetical protein and DS of <i>queF</i>	(C) _{11→10} intergenic (+11/+121)	unknown	96.4%
<i>lpxF</i>	HP1580	membrane-associated phospholipid phosphatase	G→A (TGG→TGA)	W14stop	100%
<i>ΔfapH-11</i> – SNPs not present in wild-type <i>H. pylori</i> B128					
<i>serS</i>	HP1480	serine-tRNA ligase	C→G (TCC→TCG)	Ser352Ser	99.6%
CV725_RS00720 CV725_RS00725	HP1322 HP1321	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	98.2%
CV725_RS02305 CV725_RS02315	HP0427 23S rRNA	US of <i>hp0427</i> (hypothetical protein), US of 23S rRNA gene	+32 bp intergenic (-234/-736)	unknown	92.3%
CV725_RS02465	HP1375	N-6 DNA methylase	(C) _{14→13} pseudogene (3224/3372 nt)	restore full-length ORF	90.5%
CV725_RS04600 CV725_RS04605	HP0875 HP0876	US of HP0875 <i>katA</i> , US of HP0876 <i>frpB</i>	(A) _{5→6} intergenic (-34/-290)	unknown	95.6%
CV725_RS04785	HP0838	<i>fapH</i> , flagellar-associated protein H	Δ490 bp	gene deletion	100%
CV725_RS06350	HP0527	cag pathogenicity island protein (Cag7)	codon-752 (ACC→ACG) codon-742 (GCT→GCC)	Thr752Thr Ala742Ala	91.2% 95.5%
CV725_RS06500	HP0499	<i>pldA</i> , phospholipase A pseudogene	(G) _{10→9} (683/1070 nt)	remains phase 'off'	95.1%
CV725_RS07515 <i>queF</i>	HP1412 HP1413	DS of HP1412 hypothetical protein and DS of <i>queF</i>	(C) _{11→10} intergenic (+11/+121)	unknown	94.5%
<i>lpxF</i>	HP1580	membrane-associated phospholipid phosphatase	G→A (TGG→TGA)	W14stop	99.3%
<i>ΔfapH-4</i> – SNPs not present in wild-type <i>H. pylori</i> B128					

CV725_RS00720 CV725_RS00725	HP1322 HP1321	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	99.6%
CV725_RS02305 CV725_RS02315	HP0427 23S rRNA	US of <i>hp0427</i> (hypothetical protein), US of 23S rRNA gene	A→G intergenic (-235/-735)	unknown	86.2%
CV725_RS02465	HP1375	N-6 DNA methylase	(C) _{14→13} pseudogene (3224/3372 nt)	restore full-length ORF	92.3%
CV725_RS03080	HP0164	<i>arsS</i> , histidine kinase	(C) _{11→12} coding (1261/1281 nt)	Pro424-fs	80.8%
CV725_RS04600 CV725_RS04605	HP0875 HP0876	US of HP0875 <i>katA</i> , US of HP0876 <i>frpB</i>	(A) _{5→6} intergenic (-34/-290)	unknown	92.8%
CV725_RS04785	HP0838	<i>fapH</i> , flagellar-associated protein H	Δ490 bp	gene deletion	100%
CV725_RS06350	HP0527	cag pathogenicity island protein (cag7)	codon-742 (GCT→GCC)	Ala742Ala	82.3%
CV725_RS06500	HP0499	<i>pldA</i> , phospholipase A pseudogene	(G) _{10→9} (683/1070 nt)	remains phase 'off'	93.3%
CV725_RS07515 <i>queF</i>	HP1412 HP1413	DS of HP1412 hypothetical protein and DS of <i>queF</i>	(C) _{11→10} intergenic (+11/+121)	unknown	98.0%
Δ<i>fapH</i>-9 – SNPs not present in wild-type <i>H. pylori</i> B128					
CV725_RS00720 CV725_RS00725	HP1322 HP1321	DS of HP1321 conserved hypothetical ATP-binding protein and US of HP1322 hypothetical protein.	(ATACATAA) _{10→5} intergenic (-194/+7)	unknown	100%
CV725_RS02305 CV725_RS02315	HP0427 23S rRNA	US of <i>hp0427</i> (hypothetical protein), US of 23S rRNA gene	+32 bp intergenic (-234/-736)	unknown	89.3%
CV725_RS02465	HP1375	N-6 DNA methylase	(C) _{14→13} pseudogene (3224/3372 nt)	restore full-length ORF	84.3%
CV725_RS04600 CV725_RS04605	HP0875 HP0876	US of HP0875 <i>katA</i> , US of HP0876 <i>frpB</i>	(A) _{5→6} intergenic (-34/-290)	unknown	97.1%
CV725_RS04780	HP0839	outer membrane protein P1 (ompP1)	altered 30 bp sequence coding (494-523/1764 nt)	Asn-165 through Thr-175 altered	100%
CV725_RS04785	HP0838	<i>fapH</i> , flagellar-associated protein H	Δ490 bp	gene deletion	100%
CV725_RS06350	HP0527	cag pathogenicity island protein (Cag7)	codon-752 (ACC→ACG)	Thr752Thr	82.6%
CV725_RS06500	HP0499	<i>pldA</i> , phospholipase A pseudogene	(G) _{10→9} (683/1070 nt)	remains phase 'off'	95.2%
CV725_RS07515 <i>queF</i>	HP1412 HP1413	DS of HP1412 hypothetical protein and DS of <i>queF</i>	(C) _{11→10} intergenic (+11/+121)	unknown	98%
CV725_RS07950	HP1562	iron(III) ABC transporter, periplasmic iron-binding protein (<i>ceuE</i>)	codon-180 (GAG→GAT)	Glu180Asp	100%

^a"fs" indicates frameshift

^bFrequency is the number of times the SNP was identified relative to the total number of reads for that sequence. Only SNPs that had a frequency $\geq 80\%$ are shown.

^c'DS' and 'US' are abbreviations for sequences that are 'downstream' and 'upstream' of the gene, respectively.