

**Table 3. Observed and predicted phase variable genes in *Helicobacter hepaticus*****Length variation observed in shotgun sequencing**

Gene(s) affected	Polymorphism	No. of clones @repeat length	Length of ORF for different repeat lengths	Putative function
HH66/HH67	G(10-11)	3@10, 1@11	G(10):157, G(11):410	Conserved hypothetical protein, similar to sugar transferase
HH69/HH70	G(11-12)	2@11, 1@12	G(11):146, G(12):150, G(13):299	$\alpha$ -1,2-fucosyltransferase
HH90	G(9-11)	1@9, 9@11	G(9):454, G(11):452,	Conserved hypothetical protein, similar to <i>Haemophilus influenzae</i> O-succinylbenzoate-CoA ligase
HH96	G(9-10)	1@9, 9@10	G(9):134, G(10):136	Conserved hypothetical protein
HH205	G(12-14)	2@12, 3@13, 2@14	G(12):374, G(13):376, G(14):403	Conserved hypothetical glycosyl transferase
HH329/ HH330	G(12-13)	1@12, 1@13	G(12):103, G(13):282	Hypothetical protein
HH456	C(13-15)	1@13, 2@15	C(13):232, C(15):237	Chemotaxis protein methylesterase CheB
HH540	G(10-11)	1@10, 3@11	G(10):110, G(11):256,	Hypothetical protein
HH584	G(10-11)	2@10, 6@11	G(10):167, G(11):157	Hypothetical protein
HH763	C(8-9)	13@8, 4@9	C(8):269, C(9):521	Hypothetical protein
HH1165	C(13-16)	2@13, 4@16	C(16):823, C(15):332, C(13):822	Conserved hypothetical protein, similar to <i>Helicobacter pylori</i> HP0022

HH1300	C(11-12)	3@11, 3@12	C(11):40, C(12):37	Hypothetical protein
HH1425	C(10-11)	1@10, 5@11	C(10):233, C(11):526	Hypothetical protein
HH1426	G(10-13)	10@10, 2@13	G(13):281, G(12):162, G(10):280	Conserved hypothetical protein, possible methyltransferase
HH1428	C(10-12)	2@10, 3@11, 1@12	C(12):110, C(11):530, C(10):115	Hypothetical protein
HH1499	G(10-11)	3@10, 3@11	G(10):145, G(11):730	Conserved hypothetical protein, similar to <i>Campylobacter jejuni</i> putative integral membrane protein CJ1055c
HH1676/ HH1677	G(16-20)	1@16, 3@19, 1@20	G(16):43, G(18):270, G(19):44, G(20):57	Conserved hypothetical protein, similar to <i>H. pylori</i> putative outer membrane protein HP0117

### Phase variation predicted

Gene(s) affected	Length in all shotgun clones	Effect	Putative function
HH72	C(10)	C(10):320, C(9):319	Conserved hypothetical protein, predicted fucosyltransferase
HH73	G(9)	G(9):362, G(10):197	Conserved hypothetical protein, predicted glycosyltransferase
HH75	G(10)	G(10):241, G(9):205	Aspartate racemase
HH76	G(11)	G(11):271, G(10):198	Conserved hypothetical protein, similar to <i>Salmonella typhi</i> putative methyltransferase
HH79	G(9)	G(9):489, G(10):350	Hypothetical protein
HH83	G(12)	G(12):244, G(11):139	Conserved hypothetical protein
HH85/HH86	G(13)	G(13):104, G(12):137	Conserved hypothetical protein fragment, similar to <i>C. jejuni</i> CJ1301
HH89	G(13)	G(13):320, G(14):275	Conserved hypothetical protein
HH91	G(10)	G(10):503, G(9):442	Hypothetical protein
HH95	G(10)	G(10):187, G(9):151	Conserved hypothetical protein, similar to <i>C. jejuni</i> putative acetyl transferase
HH99	G(12)	G(12):343, G(11):370	dTDP-D-glucose 4,6-dehydratase
HH181/ HH182	G(11)	G(11):78, G(10):265	Hypothetical protein
HH192	G(10)	G(10):41, G(11):14	Hypothetical protein
HH207	G(12)	G(12):272, G(13):9	Conserved hypothetical protein, similar to <i>Klebsiella pneumoniae</i> RFBC protein
HH323	G(10)	G(10):239, G(11):245	Conserved hypothetical protein, similar to <i>H. pylori</i> putative lipopolysaccharide biosynthesis protein HP0805

HH379	G(9)	G(9):524, G(10):319	Anaerobic C4-dicarboxylate transporter DcuA
HH503/ HH504	G(12)	G(12):41, G(13):142	Hypothetical protein
HH648	G(10)	G(10):337, G(11):134	Conserved hypothetical protein, similar to <i>Dichelobacter nodosus</i> lipopolysaccharide biosynthesis protein LpsA
HH811	G(9)	G(9):465, G(10):73	Conserved hypothetical protein, similar to <i>H. pylori</i> HP0497, putative sodium-dependent transporter
HH957	C(13)	C(13):129, C(12):142	Conserved hypothetical protein, similar to <i>H. pylori</i> replication protein A
HH967	G(10)	G(10):573, G(11):13	Hypothetical protein
HH980	C(10)	C(10):252, C(9):99	Conserved hypothetical protein, predicted glycosyl transferase
HH981	C(9)	C(9):354, C(8):194	Conserved hypothetical protein, glucosyl transferase
HH1047	C(12)	C(12):44, C(11):37	Hypothetical protein
HH1058	T(14)	T(14):41, T(15):25	Hypothetical protein, predicted membrane-associated
HH1089	A(14)	A(14):35, A(15):18	Hypothetical protein
HH1129/ HH1130	G(11)	G(11):101, G(10):580	Alginate O- acetylation protein
HH1188	G(9)	G(9):415, G(10):68	Hypothetical protein
HH1631	G(9)	G(9):416, G(10):69	Predicted amino-acid transport protein
HH1672	C(11)	C(11):430, C(10):58	Conserved hypothetical protein, similar to <i>H. pylori</i> HP0580, predicted membrane-associated
HH1794	G(9)	G(9):100, G(10):194	Hypothetical protein

HH1776	G(10)	G(10):459, G(9):324	$\alpha$ -1,3-fucosyltransferase
HH1822/ HH1823	C(11)	C(11):107, C(10):313	Conserved hypothetical protein, similar to <i>C. jejuni</i> CJ1429c