Supplement. Table S1. Putative HP1043 regulon

Gene, description		Position[a]	-10 element[b]	ATG-distance[c]
HP0095	Orf	100505	overlap	35
HP0103	methyl-accepting chemotaxis protein, *tlpB*	110913	+11	165
HP0152	Orf	162929	+32	72
HP0160	Cysteine-rich protein D (cell division)	168772	+34	109
HP0188	Orf	195043	+55	93
HP0189 (divergent)	conserved hypothetical integral membrane protein	195043	overlap	35
HP0226	integral membrane protein	234836	no - 10	47
HP0251	integral membrane protein of the oligopeptide transport system	261423	overlap	18
HP0305	Orf	323004	no - 10	129
HP0330	ketol-acid reductoisomerase	345507	no - 10	30
HP0372	deoxycytidine triphosphate deaminase, *dcd*	380210	overlap	23
HP0383	zinc-metallo protease	393674	+34	86
HP0389	superoxide dismutase, *sodB*	399246	no - 10	145
HP0390 (divergent)	adhesin-thiol peroxidase, *tagD*	399246	no - 10	54
HP0404	protein kinase C inhibitor	416658	overlap	43
HP0427	Orf	444758	no - 10	130
HP0437	IS605 transposase, *tnpA*	454802	no - 10	16
HP0438 (divergent)	IS605 transposase, *tnpB*	454802	overlap	24

HP0536	cag pathogenicity island protein, cag15	568544	overlap	217
HP0537(divergent)	cag pathogenicity island protein, cag16	568544	no -10	158
HP0546	cag pathogenicity island protein, cag25	579174	no -10	60
HP0547	cag pathogenicity island protein, cag26	579769	+ 8	124
HP0588	subunit of the 2-oxoglutarate oxidoreductase, *oorD* (TCA cycle)	620118	no -10	73
HP0596	Orf	630195	no -10	36
HP0637	Orf	684646	no -10	20
HP0638 (divergent)	outer membrane protein, *omp13*	684646	no -10	128
HP0639	Orf	686447	no -10	5
HP0640 (divergent)	poly(A) polymerase, *papS*	686447	overlap	29
HP0685	flagella basal body protein, *fliP*	733967	+19	61
HP0688	Orf	739341	+50	91
HP0687 (divergent)	iron(II) transport protein, *feoB*	739341	no -10	18
HP0698	Orf	750877	+18	51
HP0709	Orf	762618	+80	163
HP0724	anaerobic C4-dicarboxylate transport protein, *dcuA*	777526	no -10	48
HP0723 (divergent)	L-asparaginase II, *ansB*	777526	no -10	54
HP0767	Orf	820461	no -10	61
HP0768	molybdenum cofactor biosynthesis protein A, *moaA*	821491	no -10	21
HP0769 (divergent)	molybdopterin-guanine dinucleotide biosynthesis protein A, *mobA*	821491	no -10	38

HP0781	Orf	835048	overlap	27
HP0834	GTP-binding protein homologue, yphC	886026	overlap	40
HP0833 (divergent)	Orf	886026	no -10	8
HP0836	Orf	888287	+123	150
HP0850	type I restriction enzyme M protein, *hsdM*	902769	overlap	78
HP0851 (divergent)	integral membrane protein	902769	no -10	77
HP0871	CDP-diglyceride hydrolase, cdh	923613	no -10	70
HP0877	Holliday junction endodeoxyribonuclease, *ruvC*	930302	+35	85
HP0877	Holliday junction endodeoxyribonuclease, *ruvC*	930346	overlap	41
HP0988	IS605 transposase, *tnpA*	1051524	no -10	16
HP0989 (divergent)	IS605 transposase, *tnpB*	1051524	overlap	23
HP0992	Orf	1054695	+30	72
HP0998	IS605 transposase, *tnpA*	1061633	no -10	16
HP0989 (divergent)	IS605 transposase, *tnpB*	1061633	overlap	25
HP1000	partitioning protein A	1062609	no -10	52
HP1027	Fur regulatory protein involved in iron homeostasis, *fur*	1090112	+19	72
HP1041	regulator of flagellar biogenesis, *flhA*	1100822	+21	77
HP1043	transcriptional regulator	1105495	+6	51
HP1096	IS605 transposase, *tnpA*	1158033	no -10	16
HP1095 (divergent)	IS605 transposase, *tnpB*	1158033	overlap	25

HP1100	6-phosphogluconate dehydratase	1162168	overlap	5
HP1101 (divergent)	glucose-6-phosphate dehydrogenase	1162168	no -10	5
HP1108	pyruvate: ferredoxin oxidoreductase, gamma subunit, *porG*	1170070	+11	68
HP1167	Orf	1232513	no -10	62
HP1192	secreted protein involved in flagellar motility	1263593	overlap	35
HP1322	Orf	1382590	no -10	102
HP1394	inorganic polyphosphate/ATP-NAD kinase	1455874	no -10	27
HP1394	inorganic polyphosphate/ATP-NAD kinase	1455874	no -10	80
HP1395 (divergent)	outer membrane protein, *horL*	1455874	no -10	56
HP1400	iron(III) dicitrate transport protein, *fecA*	1461279	no -10	125
HP1460	DNA polymerase III alpha-subunit, *dnaE*	1532626	+49	83
HP1461(divergent)	cytochrome c551 peroxidase	1532626	overlap	40
HP1513	selenocysteine synthase, *selA*	1587195	no -10	84
HP1519	Orf	1595701	no -10	13
HP1526	exodeoxyribonuclease, lexA	1605865	+29	61
HP1535	IS605 transposase, *tnpA*	1614310	no -10	16
HP1534 (divergent)	IS605 transposase, *tnpB*	1614310	overlap	25

[a] - position relevant to *H. pylori* 26695 genome

[b] - presence/absence of the – 10 element (TATAAT) and position relevant to – 10 element

[c] – positions relevant to the start of the protein coding sequence