Supplementary table 1: List of *Helicobacter* strains used in this study

S. No.	***Helicobacter* species**	**Accession ID**
1	*Helicobacter acinonychis Sheeba*	NC_008229
2	*Helicobacter bizzozeronii CIII-1*	NC_015674
3	*Helicobacter canadensis MIT 98-5491*	NZ_CM000776
4	*Helicobacter bilis ATCC 43879*	ACDN00000000
5	*Helicobacter pylori 26695*	NC_000915
6	*Helicobacter cetorum MIT 00-7128*	NC_017737
7	*Helicobacter canis NCTC 12740*	NZ_AZJJ00000000
8	*Helicobacter fennelliae MRY12-0050*	NZ_BASD00000000
9	*Helicobacter rodentium ATCC 700285*	NZ_JHWC00000000
10	*Helicobacter cinaedi ATCC BAA-847*	NC_020555
11	*Helicobacter felis ATCC 49179*	NC_014810
12	*Helicobacter heilmanii ASB1.4*	HE984298
13	*Helicobacter hepaticus ATCC 51449*	NC_004917
14	*Helicobacter mustelae 12198*	NC_013949
15	*Helicobacter macacae MIT 99-5501*	AZJI01000000
16	*Helicobacter suis HS1*	ADGY00000000
17	*Helicobacter trogontum ATCC 700-114*	JRPL00000000
18	*Helicobacter pullorum MIT 98-5489*	ABQU00000000
19	*Helicobacter pullorum 229254/12*	JNOA00000000
20	*Helicobacter pullorum 229336/12*	JNUR00000000
21	*Helicobacter pullorum 229334/12*	JNOC00000000
22	*Helicobacter pullorum 229313/12*	JNOB00000000
23	*Helicobacter pullorum NAP1W4*	LXWI00000000
24	*Helicobacter pullorum NAP2W5*	MAPE00000000
25	*Helicobacter pullorum NAP3W17*	MAPD00000000
26	*Helicobacter pullorum NAP5W19*	MAPC00000000
27	*Helicobacter pullorum NAP6W24*	MAPB00000000
28	*Helicobacter pullorum NAP8W25*	MAPA00000000
29	*Helicobacter pullorum NAP10B8*	MAOZ00000000
30	*Helicobacter pullorum NAP11B31*	MAJF00000000
31	*Helicobacter pullorum NAP12B32*	MAJG00000000
32	*Helicobacter pullorum NAP13B35*	MANJ00000000
33	*Helicobacter pullorum NAP14B36*	MANK00000000
34	*Wolinella succinogenes DSM 1740*	NC_005090
35	*Campylobacter jejuni NCTC 11168*	NC_002163

Supplementary table 2: In *silico* screening of antimicrobial resistance genes in 11 whole genome sequences of *H. pullorum* isolates from India, as reported in the CARD database (+ presence, - absence).

Strains	antimicrobial resistance genes					
	tufA	Fluoroquinolone resistant DNA *gyrase A*	*cmeB*	*APH(3")-Ib*	*AAC(6')-Ie-APH(2")-Ia*	*APH(3')-IIIa*
NAP1W4	+	+	+	+	−	−
NAP2W5	+	+	+	+	−	−
NAP3W17	+	+	+	+	−	−
NAP5W19	+	+	+	+	−	+
NAP6W24	+	+	+	+	−	+
NAP8W25	+	+	+	−	−	−
NAP10B8	+	+	+	+	−	−
NAP11B31	+	+	+	+	+	−
NAP12B32	+	+	+	+	+	−
NAP13B35	+	+	+	+	+	−
NAP14B36	+	+	+	+	+	−

Supplementary table 3: Status of major virulence factors as reported from the VFDB database of *Campylobacter jejuni* in the sequenced genomes of 11 *H. pullorum* strains from India (+ presence, - absence).

Genes	NAP1W4	NAP2W5	NAP3W17	NAP5W19	NAP6W24	NAP8W25	NAP10B8	NAP11B31	NAP12B32	NAP13B35	NAP14B36
fliM	+	+	+	+	+	+	+	+	+	+	+
fliA	+	+	+	+	+	+	+	+	+	+	+
fliG	+	+	+	+	+	+	+	+	+	+	+
fliN	+	+	+	+	+	+	+	+	+	+	+
fliE	+	+	+	+	+	+	+	+	+	+	+
flgC	+	+	+	+	+	+	+	+	+	+	+
fliS	+	+	+	+	+	+	+	+	+	+	+
flgH	+	+	+	+	+	+	+	+	+	+	+
flgG	+	+	+	+	+	+	+	+	+	+	+
fliP	+	+	+	+	+	+	+	+	+	+	+
flhA	+	+	+	+	+	+	+	+	+	+	+
flgI	+	+	+	+	+	+	+	+	+	+	+
fliQ	+	+	+	+	+	+	+	+	+	+	+
cdtB	+	+	+	+	+	+	+	+	+	+	+
gmhA2	+	+	+	+	+	+	+	+	+	+	+
kpsF	+	+	+	+	+	+	+	+	+	+	+
kpsD	+	+	+	+	+	+	+	+	+	+	+
kpsE	+	+	+	+	+	+	+	+	+	+	+
kpsT	+	+	+	+	+	+	+	+	+	+	+
gmhA	+	+	+	+	+	+	+	+	+	+	+
hldD	+	+	+	+	+	+	+	+	+	+	+
flgR	+	+	+	+	+	+	+	+	+	+	+
pseB	+	+	+	+	+	+	+	+	+	+	+
cheW	+	+	+	+	+	+	+	+	+	+	+
cheA	+	+	+	+	+	+	+	+	+	+	+
cheV	+	+	+	+	+	+	+	+	+	+	+
cheY	+	+	+	+	+	+	+	+	+	+	+
gmhA-2	+	+	+	+	+	+	+	+	+	+	+
kpsF	+	+	+	+	+	+	+	+	+	+	+
kpsD	+	+	+	+	+	+	+	+	+	+	+
kpsE	+	+	+	+	+	+	+	+	+	+	+
kpsT	+	+	+	+	+	+	+	+	+	+	+
kpsF	+	+	+	+	+	+	+	+	+	+	+
kpsD	+	+	+	+	+	+	+	+	+	+	+
gmhA-1	+	+	+	+	+	+	+	+	+	+	+
waaD	+	+	+	+	+	+	+	+	+	+	+
gmhA-1	+	+	+	+	+	+	+	+	+	+	+

waaD	+	+	+	+	+	+	+	+	+	+	+
fliA	+	+	+	+	+	+	+	+	+	+	+
fliE	+	+	+	+	+	+	+	+	+	+	+
flgC	+	+	+	+	+	+	+	+	+	+	+
flgC	+	+	+	+	+	+	+	+	+	+	+
fliS	+	+	+	+	+	+	+	+	+	+	+
flgH	+	+	+	+	+	+	+	+	+	+	+
fliP	+	+	+	+	+	+	+	+	+	+	+
flhA	+	+	+	+	+	+	+	+	+	+	+
flhA	+	+	+	+	+	+	+	+	+	+	+
flgR	+	+	+	+	+	+	+	+	+	+	+
flgR	+	+	+	+	+	+	+	+	+	+	+
flgI	+	+	+	+	+	+	+	+	+	+	+
flgI	+	+	+	+	+	+	+	+	+	+	+
cdtB	+	+	+	+	+	+	+	+	+	+	+
pseB	+	+	+	+	+	+	+	+	+	+	+
pseB	+	+	+	+	+	+	+	+	+	+	+
pglC	+	+	+	+	+	+	+	+	+	+	+
pglC	+	+	+	+	+	+	+	+	+	+	+
pglC	+	+	+	+	+	+	+	+	+	+	+
gmhA	+	+	+	+	+	+	+	+	+	+	+
kpsF	+	+	+	+	+	+	+	+	+	+	+
kpsD	+	+	+	+	+	+	+	+	+	+	+
kpsE	+	+	+	+	+	+	+	+	+	+	+
kpsT	+	+	+	+	+	+	+	+	+	+	+
gmhA-1	+	+	+	+	+	+	+	+	+	+	+
waaD	+	+	+	+	+	+	+	+	+	+	+
fliM	+	+	+	+	+	+	+	+	+	+	+
fliA	+	+	+	+	+	+	+	+	+	+	+
fliG	+	+	+	+	+	+	+	+	+	+	+
fliE	+	+	+	+	+	+	+	+	+	+	+
flgC	+	+	+	+	+	+	+	+	+	+	+
fliS	+	+	+	+	+	+	+	+	+	+	+
flgH	+	+	+	+	+	+	+	+	+	+	+
flgG	+	+	+	+	+	+	+	+	+	+	+
fliP	+	+	+	+	+	+	+	+	+	+	+
flhA	+	+	+	+	+	+	+	+	+	+	+
flgR	+	+	+	+	+	+	+	+	+	+	+
flaA	+	+	+	+	+	+	+	+	+	+	+
flgI	+	+	+	+	+	+	+	+	+	+	+
fliQ	+	+	+	+	+	+	+	+	+	+	+
pseB	+	+	+	+	+	+	+	+	+	+	+
pglC	+	+	+	+	+	+	+	+	+	+	+
kpsF	+	+	+	+	+	+	+	+	+	+	+

gmhA-1	+	+	+	+	+	+	+	+	+	+	+
waaD	+	+	+	+	+	+	+	+	+	+	+
flgC	+	+	+	+	+	+	+	+	+	+	+
fliS	+	+	+	+	+	+	+	+	+	+	+
flhA	+	+	+	+	+	+	+	+	+	+	+
flgR	+	+	+	+	+	+	+	+	+	+	+
cdtB	+	+	+	+	+	+	+	+	+	+	+
pseB	+	+	+	+	+	+	+	+	+	+	+
chuZ	+	+	+	+	+	+	+	+	+	+	+
fliI	+	+	+	+	-	+	+	+	+	+	+
Cj0371	+	+	+	+	+	+	+	-	+	+	+
fliI	+	+	+	+	-	+	+	+	+	+	+
fliI	+	+	+	+	-	+	+	+	+	+	+
pglE	+	+	+	+	-	+	+	+	+	+	+
pglE	+	+	+	+	-	+	+	+	+	+	+
fliI	+	+	+	+	-	+	+	+	+	+	+
pglE	+	+	+	+	-	+	+	+	+	+	+
C8J_1076	-	+	+	+	+	+	+	+	+	+	+
pglE	+	+	+	+	-	+	+	+	+	+	+
kpsS	-	+	+	-	+	+	+	+	+	+	+
kpsS	-	+	+	-	+	+	+	+	+	+	+
kpsS	-	+	+	-	+	+	+	+	+	+	+
flaB	+	+	+	-	+	-	+	+	+	+	+
JJD26997_1746	-	+	+	-	+	+	+	+	+	+	+
kpsS	-	+	+	-	+	+	+	+	+	+	+
flaA	-	+	+	-	-	-	+	+	+	+	+
pseH	-	-	+	+	-	+	-	+	+	+	+
Cj1416c	+	+	+	-	+	+	+	-	-	-	-
Cj1433c	-	+	-	-	-	+	-	+	+	+	+
CJJ81176_1415	+	+	+	-	+	+	+	-	-	-	-
JJD26997_1749	+	+	+	-	+	+	+	-	-	-	-
C8J_1077	-	+	+	+	+	+	+	-	-	-	-
C8J_1084	-	+	+	+	+	+	+	-	-	-	-
Cj1417c	+	+	+	-	+	-	+	-	-	-	-
Cj1419c	-	+	+	+	+	-	+	-	-	-	-
Cj1418c	+	+	+	-	+	-	+	-	-	-	-
CJJ81176_1417	+	+	+	-	+	-	+	-	-	-	-
CJJ81176_1418	-	+	+	+	+	-	+	-	-	-	-
JJD26997_1747	+	+	+	-	+	+	-	-	-	-	-

JJD26997_1751	+	+	+	-	+	-	+	-	-	-	-
JJD26997_1752	-	+	+	+	+	-	+	-	-	-	-
C8J_1331	-	-	-	+	-	-	-	+	+	+	+
C8J_1344	-	-	-	-	-	+	-	+	+	+	+
C8J_1345	-	-	-	-	-	+	-	+	+	+	+
C8J_1346	-	-	-	-	-	+	-	+	+	+	+
C8J_1079	-	+	+	+	+	-	+	-	-	-	-
C8J_1082	-	+	-	+	+	+	+	-	-	-	-
Cj1135	-	+	-	-	+	+	+	-	-	-	-
virB8	-	-	-	-	-	-	-	+	+	+	+
virB10	-	-	-	-	-	-	-	+	+	+	+
virB11	-	-	-	-	-	-	-	+	+	+	+
cysC	-	+	+	-	+	-	+	-	-	-	-
CJJ81176_1414	-	+	+	-	+	-	+	-	-	-	-
CJJ81176_1416	-	+	+	-	+	-	+	-	-	-	-
CJE1277	-	+	-	-	+	+	+	-	-	-	-
CJJ81176_1152	-	+	-	-	+	+	+	-	-	-	-
JJD26997_1748	-	+	+	-	+	-	+	-	-	-	-
JJD26997_0586	-	+	-	-	+	+	+	-	-	-	-
C8J_1340	-	-	-	-	-	-	-	+	+	+	+
C8J_1343	-	-	-	-	-	+	-	+	+	-	+
glf	-	-	+	-	+	-	+	-	-	-	-
virB9	-	-	-	-	-	-	-	-	+	+	+
virD4	-	-	-	-	-	-	-	+	+	+	-
CJE1604	-	-	+	-	+	-	+	-	-	-	-
CJE1605	-	-	+	-	+	-	+	-	-	-	-
CJE1606	-	-	+	-	+	-	+	-	-	-	-
C8J_1348	-	-	-	-	-	-	-	+	+	-	+
flaB	-	-	-	+	-	+	-	-	-	-	-
flaA	+	-	-	+	-	-	-	-	-	-	-
rfbC	+	-	-	+	-	-	-	-	-	-	-
CJJ81176_1430	+	-	-	+	-	-	-	-	-	-	-
C8J_1093	-	-	-	-	+	-	+	-	-	-	-
hddC	+	-	-	-	-	-	-	-	-	-	-
hddA	+	-	-	-	-	-	-	-	-	-	-
fcl	+	-	-	-	-	-	-	-	-	-	-
virB4	-	-	-	-	-	-	-	-	-	+	-
Cj1420c	-	+	-	-	-	-	-	-	-	-	-

Cj1442c	-	-	-	+	-	-	-	-	-	-	-
kpsC	-	-	-	+	-	-	-	-	-	-	-
kpsC	+	-	-	-	-	-	-	-	-	-	-
CJE1607	-	-	+	-	-	-	-	-	-	-	-
CJJ81176_1419	-	+	-	-	-	-	-	-	-	-	-
CJE1608	+	-	-	-	-	-	-	-	-	-	-
CJE1610	+	-	-	-	-	-	-	-	-	-	-
CJJ81176_1422	+	-	-	-	-	-	-	-	-	-	-
wcbK	+	-	-	-	-	-	-	-	-	-	-
fcl	+	-	-	-	-	-	-	-	-	-	-
CJJ81176_1424	+	-	-	-	-	-	-	-	-	-	-
wcbK	+	-	-	-	-	-	-	-	-	-	-
fcl	+	-	-	-	-	-	-	-	-	-	-
CJJ81176_1428	+	-	-	-	-	-	-	-	-	-	-
CJJ81176_1436	-	-	-	+	-	-	-	-	-	-	-
JJD26997_1750	-	-	-	-	-	-	+	-	-	-	-
JJD26997_1753	-	+	-	-	-	-	-	-	-	-	-
JJD26997_1755	+	-	-	-	-	-	-	-	-	-	-
JJD26997_1759	+	-	-	-	-	-	-	-	-	-	-
JJD26997_1763	+	-	-	-	-	-	-	-	-	-	-
JJD26997_1764	+	-	-	-	-	-	-	-	-	-	-
JJD26997_1765	+	-	-	-	-	-	-	-	-	-	-
C8J_1080	-	-	-	-	-	+	-	-	-	-	-
C8J_1081	-	-	+	-	-	-	-	-	-	-	-

Supplementary table 4: List of putative prophage regions identified in broiler and free range chicken isolates of *H. pullorum* with their major functions

Strain	Region	Length (kb)	Status	CDS	Possible Phage	Major Functions
NAP1 W4	1	10.7	Incomplete	6	Cafete_BV_PW1_NC_014637	Putative exodeoxyribonuclease-VII large subunit, hypothetical proteins
	2	9	Incomplete	7	Ostreo_tauri_virus_1_NC_013288	2-methylthioadenine synthetase, ATP-dependent metalloprotease, conserved archaeal viral protein, hypothetical proteins
	3	8	Incomplete	9	Cronob_vB_CsaM_GAP32_NC_019401	Amidophosphoribosyltransfera-se, Isochorismatase hydrolase, hypothetical protein
	4	5.6	Incomplete	7	Caulob_Cr30_NC_025422	GDP-D-mannose dehydratase, D,D-heptose 7-phosphate kinase, hypothetical proteins
NAP2 W5	1	10.7	Incomplete	6	Cafete_BV_PW1_NC_014637,	Ribonucleotide reductase, hypothetical proteins
	2	9.8	Incomplete	12	Aureoc_anophagefferens_virus_MM_2014_NC_024697	putative glycosyltransferase, hypothetical proteins
	3	8.4	Incomplete	6	Cronob_vB_CsaM_GAP32_NC_019401	Peptide deformylase, hypothetical proteins
	4	10	Incomplete	9	Ostreo_tauri_virus_1_NC_013288	2-methylthioadenine synthetase, hypothetical proteins
	5	11.6	Incomplete	13	Cronob_vB_CsaM_GAP32_NC_019401	Isochorismatase hydrolase, putative ELP-3 histone acetyl-transferase, hypothetical proteins
	6	9.5	Incomplete	11	Aureoc_anophagefferens_virus_MM_2014_NC_024697	UDP-N-acetylglucosamine-2-epimerase, hypothetical proteins
	7	10.2	Incomplete	13	Aureoc_anophagefferens_virus_	Capsular polysaccharide-biosynthesis protein, 3,4-

					MM_2014_NC_024697	dihydroxy-2-butanone 4-phosphate synthase
	8	10.4	Incomplete	14	Aureoc_anophagefferens_virus_MM_2014_NC_024697	Hypothetical proteins
	9	6.3	Incomplete	10	Aureoc_anophagefferens_virus_MM_2014_NC_024697	AAA+ family ATPase, hypothetical proteins
NAP3 W17	1	10	Incomplete	9	Acinet_Acj61_NC_014661	Aspartate aminotransferase, 2-methylthioadenine synthetase, ATP-dependent metalloprotease
	2	10.8	Incomplete	7	Cafete_BV_PW1_NC_014637	Putative exodeoxyribonuclease -VII large subunit, hypothetical proteins
	3	8	Incomplete	9	Cronob_vB_CsaM_GAP32_NC_019401	Dihydrodipicolinate reductase, Isochorismatase hydrolase
NAP5 W19	1	10	Incomplete	10	Ostreo_tauri_virus_1_NC_013288	Aspartate aminotransferase,ATP-dependent metalloprotease, hypothetical proteins
	2	10.8	Incomplete	6	Cafete_BV_PW1_NC_014637	Ribonucleotide reductase, putative exodeoxyribonuclease-VII large subunit, hypothetical proteins
	3	12.1	Incomplete	13	Cronob_vB_CsaM_GAP32_NC_019401	Putative minor tail protein, isochorismatase hydrolase, amidophosphoribosyltransferase, hypothetical proteins
	4	8.9	Incomplete	10	Entero_phi92_NC_023693	Lipopolysaccharide- -1,3 galactosyltransferase, ADP-L-glycero-D- mannoheptose-6-epimerase, 2 dehydro-3-deoxyglucarate aldolase, hypothetical proteins

NAP6 W24	1	10	Incomplete	11	Ostreo_tauri_virus_1_NC_013288	ATP-dependent metalloprotease, 2-methylthioadenine synthetase, aspartate aminotransferase, hypothetical proteins
	2	15.8	Incomplete	9	Aeromo_25_NC_008208	Group 1 glycosyl transferase, UDP-galactopyranose mutase, hypothetical proteins
	3	10.8	Incomplete	6	Cafete_BV_PW1_NC_014637	Putative exodeoxyribonuclease VII-large subunit, ribonucleotide reductase, hypothetical proteins
	4	11.5	Incomplete	13	Cronob_vB_CsaM_GAP32_NC_019401	Membrane-bound metallopeptidase, isochorismatase hydrolase, putative ELP-3 histone acetyl – transferase, hypothetical proteins
NAP8 W25	1	10	Incomplete	9	Ostreo_tauri_virus_1_NC_013288	Aspartate aminotransferase, quaternary ammonium transporter-2-methylthioadenine synthetase, ATP-dependent metalloprotease, hypothetical proteins
	2	8	Incomplete	9	Cronob_vB_CsaM_GAP32_NC_019401	Dihydrodipicolinate reductase, putative ELP-3 histone acetyl transferase, isochorismatase hydrolase, hypothetical proteins
	3	10.9	Incomplete	12	Bathyc_BpV1_NC_014765	putative glycosyltransferase hypothetical proteins
NAP10 B8	1	10	Incomplete	10	Ostreo_tauri_virus_1_NC_013288	ATP-dependent metalloprotease, 2-methylthioadenine synthetase, aspartate aminotransferase hypothetical proteins
	2	10.9	Incomplete	7	Cafete_BV_PW1_NC_014637	Putative exodeoxyribonuclease-VII large subunit, hypothetical proteins
	3	6.5	Incomplete	8	Ectoca_siliculosus_virus_1_NC_002687	Putative lysozyme-peptidase ABC transporter, putative lysozyme-peptidase, hypothetical proteins

	4	8	Incomplete	9	Cronob_vB_CsaM_GAP32_NC_019401	Isochorismatase hydrolase, putative ELP-3 histone acetyl transferase, amidophosphoribosyltransferase, hypothetical proteins
NAP11 B31	1	8.7	Intact	18	Stenot_Smp131_NC_023588	Type VI secretion protein, baseplate assembly protein J, TP901 family tail tape measure protein, hypothetical proteins
	2	24.8	Incomplete	11	Entero_P4_NC_001609	Integrase, molybdenum ABC transporter permease, putative methyltransferase endonuclease, hypothetical proteins
NAP12 B32	1	10	Incomplete	10	Ostreo_tauri_virus_1_NC_013288	ATP-dependent metalloprotease, quaternary ammonium transporter, aspartate aminotransferase, hypothetical proteins
	2	10.8	Incomplete	6	Cafete_BV_PW1_NC_014637	Ribonucleotide reductase, putative exodeoxyribonuclease VII large subunit, hypothetical proteins
	3	8	Incomplete	9	Cronob_vB_CsaM_GAP32_NC_019401	Amidophosphoribosyltransferase, putative ELP-3 histone acetyl transferase, isochorismatase hydrolase, hypothetical proteins
	4	15.7	Incomplete	9	Synech_S_SSM7_NC_015287	UDP-glucose dehydrogenase, long tail fiber proximal subunit l, hypothetical proteins
	5	6.4	Intact	12	Escher_ep3_NC_025430	Tail protein X, baseplate assembly protein J, phage tail protein, TP901 family tail tape measure protein, putative cytosine-specific methyltransferase, hypothetical proteins

NAP13 B35	1	8.3	Incomplete	6	Cronob_vB_CsaM_GAP32_NC_019401	Lytic transglycosylase, peptide deformylase, hypothetical proteins
	2	8	Incomplete	9	Cronob_vB_CsaM_GAP32_NC_019401	Isochorismatase hydrolase, putative ELP-3 histone acetyl transferase, hypothetical proteins
	3	10	Incomplete	10	Ostreo_tauri_virus_1_NC_013288	ATP-dependent metalloprotease, aspartate aminotransferase, hypothetical proteins
	4	10.8	Incomplete	6	Cafete_BV_PW1_NC_014637	Putative exodeoxyribonuclease VII large subunit, hypothetical proteins
	5	7.7	Intact	15	Escher_ep3_NC_025430	Tail protein X, baseplate assembly protein J, TP901 family tail tape measure protein, phage tail tape measure protein, hypothetical proteins
NAP14 B36	1	19.8	Intact	24	Escher_ep3_NC_025430	DNA-binding protein, putative DNA topoisomerase, baseplate assembly protein, TP901 family tail tape measure protein, putative thioredoxin hypothetical proteins

Supplementary table 5: Summary of genomic islands identified in 11 whole genome sequences of *H. pullorum* isolates

Strains	Genomic Islands	Start	End	Size (bp)	Important Genes
NAP1W4	1	1,614, 230	1,618,832	4,602	Adenine-specific methyltransferase
	2	1,644, 789	1,672,156	27,367	Major outer membrane protein, Capsular polysaccharide synthesis enzyme CAP51
	3	1,785, 638	1,791,113	5,475	N-acetylneuraminate cytidylyltransferase
	4	2,000, 382	2,006,618	6,236	IncP-type DNA relaxase Tral, Chromosome partitioning protein Par A
NAP5W19	1	1,713, 479	1,756,221	42,742	Haemin uptake system outer membrane receptor, Capsular polysaccharide biosynthesis heptosyltransferase HddD
NAP8W25	1	821,216	835, 141	13,925	Transposase, IcmF-related protein, VgrG protein
NAP11B31	1	1,688,118	1,746,692	58,574	Type IV secretion/ competence protein (VirB10), Type II/IV secretion system ATP hydrolase TadA, VirB11, CpaF, Tad A subfamily

	2	1,876,686	1,940,547	63,861	DNA transformation competency, Abortive infection protein
NAP12B32	1	1,658,189	1,695,288	37,099	Putative regulator of late gene expression, Thermonuclease family protein
	2	1,812, 073	1,858,266	46,193	Type VI secretion lipoprotein/ VasD, Single stranded DNA binding protein, hcp protein
NAP13B35	1	1,753,270	1,763,215	9,945	Type VI secretion lipoprotein / VasD, Uncharacterized protein ImpJ/Vas E,
	2	1,870,419	1,902,747	32, 328	Protein ImpG / VasA, UDP-glucose 4-epimerase
NAP14B36	1	1,628,176	1,695,844	67,668	Protein ImpG / VasA, Plasmid partitioning protein Par A
	2	1,871,624	1,885,705	14,081	Type IV secretion / competence protein (VirB9), Type II/IV secretion system ATP hydrolase, Signal peptidase