

APPENDIX 1: predicted CDSs and their protein similarities in the *C. jejuni* strain 81-176 plasmid pVir

Locus_id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pVir1	373	Unknown	-	-			
pVir2	292	Unknown	-	-			
pVir3	260	Unknown	TrbM	<i>E. coli</i>	Q03537	5.1e-11	31.84
pVir4	239	Unknown	-	-			
pVir5	417	Unknown	Hypothetical Hp0444	<i>H. pylori</i>	O25192	4.3e-12	32.54
pVir6	142	Unknown	-	-			
pVir7	114	Unknown	-	-			
pVir8	102	Unknown	-	-			
pVir9	73	Unknown	-	-			
pVir10	131	Unknown	-	-			
pVir11	136	Unknown	-	-			
pVir12	143	Unknown	-	-			
pVir13	61	Unknown	-	-			
pVir14	56	Unknown	-	-			
pVir15	42	Unknown	-	-			
pVir16c	66	Unknown	-	-			
pVir17	121	Unknown	-	-			
pVir18	111	Unknown	-	-			
pVir19	120	Unknown	-	-			
pVir20	134	Unknown	-	-			
pVir21	130	Periplasmic protein	Cj1456c	<i>C. jejuni</i>	Q9PMK4	4.6e-31	90.38
pVir22c	523	Unknown	Hypothetical jhp0942	<i>H. pylori</i>	Q9ZKJ3	7.3e-13	28.06
pVir23c	82	Unknown	-	-			
pVir24	101	Unknown	-	-			
pVir25	80	Unknown	Hypothetical Hp0042	<i>H. pylori</i>	O25190	2.6e-03	35.29
pVir26	822	Type IV secretion system protein	VirB4	<i>H. pylori</i>	O25189	1.7e-44	33.87
pVir27	225	Type IV secretion system protein	VirB8/ComB1	<i>C. jejuni</i>	Q9KIS2	3.1e-81	100

Locus_id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pVir28	356	Type IV secretion system protein	ComB2	<i>C. jejuni</i>	Q9KIS1	1.1e-124	100
pVir29	378	Type IV secretion system protein	ComB3	<i>C. jejuni</i>	Q9KIS0	9.2e-122	100
pVir30	66	Unknown	-	-			
pVir31	317	Type IV secretion system protein	VirB11	<i>C. jejuni</i>	Q9KIR9	9.8e-115	100
pVir32	135	Unknown	-	-			
pVir33	628	Type IV secretion system protein	VirD4	<i>E. coli</i>	Q91UW5	4e-20	24.52
pVir34	56	Unknown	-	-			
pVir35	293	Unknown	Hypothetical jhp0926	<i>H. pylori</i>	Q9ZKK9	8e-03	21.56
pVir36	89	Unknown	-	-			
pVir37	382	Conjugal transfer protein	Mlr9255	<i>Rhizobium loti</i>	Q981S2	1.3e-03	22.41
pVir38	655	Topoisomerase	TopA2	<i>H. pylori</i>	Q9ZKL6	7.9e-37	44.89
pVir39	121	Unknown	-	-			
pVir40	152	Single-stranded DNA-binding protein	Ssb-p1	Bacteriophage P1	Q9XJG4	4.3e-12	30.24
pVir41	57	Unknown	-	-			
pVir42	211	Unknown	-	-			
pVir43	155	Unknown	-	-			
pVir44	117	Unknown	-	-			
pVir45	70	Unknown	-	-			
pVir46	156	Unknown	-	-			
pVir47	137	Unknown	-	-			
pVir48	135	Unknown	-	-			
pVir49	107	Unknown	-	-			
pVir50	77	Unknown	-	-			
pVir51c	67	Unknown	-	-			
pVir52	222	Partition protein	ParA	<i>H. pylori</i>	O25646	1.1e-14	38.02
pVir53	209	Unknown	-	-			
pVir54c	278	Replication initiation protein	RepA	<i>Erysipelothrix rhusiopathiae</i>	Q9RHE5	1.1e-13	30.73

APPENDIX 2: predicted CDSs and their protein similarities for the *C. jejuni* strain 81-176 plasmid pTet

Locus id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pTet1	382	Replication initiation protein	replication protein	<i>Selenomonas ruminantium</i> plasmid ps23	Q55007	1.9e-29	36.48
pTet2	126	Unknown	-	-			
pTet3	132	Unknown	Hypothetical cjp38	<i>C. jejuni</i>	Q8GJB7	1.6e-16	40
pTet4	170	Unknown	-	-			
pTet5	185	Unknown	-	-			
pTet6	88	Unknown	Hypothetical rgi82	<i>Oryza sativa</i>	Q944E8	5.2e-03	30.3
pTet7	186	Unknown	-	-			
pTet8	88	Unknown	-	-			
pTet9	1932	DNA methylase	Orf23	<i>Sinorhizobium meliloti</i> phage PBC5	Q8W6K4	3.7e-135	38.19
pTet10c	234	Unknown	-	-			
pTet11c	462	Nickase	MagA2	<i>Actinobacillus actinomycetemcomitans</i>	Q9F276	8.9e-25	32.26
pTet12c	183	unknown	-	-			
pTet13	93	Unknown	-	-			
pTet14	203	Unknown	-	-			
pTet15	217	Unknown	Hypothetical jhp0950	<i>H. pylori</i>	Q9ZK15	1.8e-19	39.63
pTet16	408	DNA primase	TraC	<i>E. coli</i>	P27189	4.1e-15	31.56
pTet17	87	Lipoprotein	MagB5	<i>Actinobacillus actinomycetemcomitans</i>	Q9F247	1.1e-02	37.7
pTet18c	85	Unknown	-	-			
pTet19c	61	Unknown	-	-			
pTet20	72	Unknown	Hypothetical jhp0960	<i>H. pylori</i>	Q9ZKH6	5.6e-10	52.77
pTet21	67	Unknown	Hypothetical jhp0961	<i>H. pylori</i>	Q9ZKH5	4.4e-13	68.42
pTet22	597	Unknown	Hypothetical amv156	<i>Amsacta moorei</i> entomopoxvirus	Q9EMP3	6.1e-04	22.74
pTet23c	204	Site-specific DNA recombinase	Soao172	<i>Shewanella oneidensis</i>	Q8E7Z6	1e-14	33.16

Locus id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pTet24c	125	Virulence-associated protein	Vap2	<i>Riemerella anatipestifer</i> pCFC1	O85171	1.9e-04	36.26
pTet25c	107	Unknown	-	-			
pTet26	87	Type IV secretion system protein	VirB2	<i>E. coli</i>	Q91UX6	1e-06	35.36
pTet27	922	ATPase	MagB3	<i>Actinobacillus actinomycetemcomitans</i>	Q9F245	1e-128	40.67
pTet28	188	Unknown	Hypothetical	<i>C. jejuni</i> pCjA13	Q847A4	1.3e-14	44.8
pTet29	221	Unknown	-	-			
pTet30	141	Single-strand DNA binding protein	Ssb-1	<i>Geobacter sulfurreducens</i>	AAR35527	5.3e-11	33.58
pTet31	86	Unknown	-	-			
pTet32	323	Unknown	MagB4	<i>Actinobacillus actinomycetemcomitans</i>	Q9F246	6e-19	32.66
pTet33	332	Unknown	MagB6	<i>Actinobacillus actinomycetemcomitans</i>	Q9F248	1.4e-15	25.93
pTet34	55	Lipoprotein	Cj1074c	<i>C. jejuni</i>	Q9PNM0	0.24	44.68
pTet35	220	Type IV secretion system protein	VirB8-like protein	<i>C. jejuni</i> pCjA13	Q847A8	1.1e-77	100
pTet36	295	Type IV secretion system protein	VirB9-like protein	<i>C. jejuni</i> pCjA13	Q847A7	3.7e-112	97.28
pTet37	391	Type IV secretion system protein	MagB10	<i>Actinobacillus actinomycetemcomitans</i>	Q9F252	5.7e-39	39.74
pTet38	330	Type IV secretion system protein	VirB11-like protein	<i>C. jejuni</i> pCjA13	Q847A5	4.6e-117	99.69
pTet39	603	Type IV secretion system protein	MagB12	<i>Actinobacillus actinomycetemcomitans</i>	Q9F254	4.9e-89	42.64
pTet40	145	Lipoprotein	MagB13	<i>Actinobacillus actinomycetemcomitans</i>	Q9F255	4.5e-03	26.57

Locus id	length	Putative function	Informative database match	Organism with match	SWALL	E-value	id
pTet41	254	Unknown	TrbM-like protein	<i>Haemophilus aegyptius</i> pF3031	Q8VRC6	4.5e-11	37.17
pTet42	265	Unknown	-	-			
pTet43	206	Unknown	-	-			
pTet44	730	Topoisomerase	TraE	<i>E. coli</i>	Q60215	1.8e-80	41.89
pTet45	473	Unknown	Hypothetical	<i>Plasmodium falciparum</i>	P21421	2.5e-03	25.39
pTet46	59	Unknown	Hypothetical cjp20	<i>C. jejuni</i>	Q8GJD3	3.1e-07	46.42
pTet47	639	Tetracycline resistance	TetO	<i>C. jejuni</i>	AAA23033	0	99.84
pTet48	57	Unknown	Hypothetical Orf6	<i>Enterococcus faecalis</i> transposon tn916	Q56396	4.3e-14	66.66
pTet49	222	Unknown	-	-			
pTet50	140	unknown	-	-			

APPENDIX 3

Predicted CDSs for sequenced pUC library clones of strain 81-176

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
5c06.p	2	753	8P0001	250	Fcl cj1428c	11168	Q9PMM9	56.4	2.70E-51	250
6a02.q	2	730	8P0002c	243	adhesin	<i>Chromobacterium violaceum</i>	Q7NY05	30		
8b03.p	2	815	8P0003	35	GlyA cj0402	11168	P24531	97.14	2.80E-10	35
			8P0004	232	hypothetical cj0403	11168	Q9PIA2	100	1.10E-69	176
6e09.q	2	1055	8P0005	251	hypothetical from LOS cluster	<i>C. jejuni</i> strain 11351 81176	Q9ALY2	100	1.60E-99	251
			8P0006c	73	WaaF	<i>C. jejuni</i> strain 81176	Q6TDC6	100	7.20E-30	73
6h01.q	2	770	8P0007	256	c4-dicarboxylate transporter	<i>Vibrio fulnificus</i>	Q7MJB8	38.93	6.00E-26	244
2a01.p	2	919	8P0008	86	no matches					
			8P0009	60	no matches					
7e10.q	2	532	8P0010c	176	aminotransferase cj1294	11168	Q9PN05	89.2	3.90E-53	176
7e07.q	2	772	8P0011c	189	DsbA cj0872	11168	Q9PP57	48.04	1.20E-28	179
7g05.p	2	1358	8P0012	52	Cj1161	11168	Q9PND4	83.67	2.50E-13	49
			8P0013	173	hydrophobic protein cj1158c	11168	Q9PND7	84.21	6.80E-22	76
			8P0014c	196	DnaX cj1157	11168	Q9PND8	95.91	9.30E-65	196
7d11.q	2	931	8P0015c	310	cj1333 like hypothetical	81-176	Q7X518	100	3.00E-125	309
1b02.p	3	1444	8P0016	165	ribosomal acetyltransferase	<i>Ureaplasma parvum</i>	Q9PQI0	29.1	1.60E-02	134
			8P0017	60	no matches					
			8P0018	136	WbkC	<i>Brucella melitensis</i>	Q9ZHX0	33.96	1.10E-03	106
			8P0019	74	acyl carrier protein cj1308	11168	Q9PMZ1	93.05	1.80E-21	72
5a05.p	3	967	8P0020	61	cj1724c hypothetical	11168	Q9PLV4	100	3.60E-23	60
			8P0021	199	cj1721c outer membrane protein	11168	Q9PLV7	63.77	5.20E-48	196
6a01.p	3	1000	8P0022c	74	hypothetical cj0976	11168	Q9PNW3	94.59	7.70E-26	74
			8P0023c	226	heme-hemopexin HxB	<i>Haemophilus influenzae</i>	AAQ10738	20.5	2.20E-02	239
3a07.q	3	1446	8P0024	70	no matches	match to 1580383-1580533				
			8P0025	261	membrane protein cj1658	11168	Q9PM19	96.52	1.70E-82	259
8b05.p	3	1693	8P0026	187	hypothetical cj1340c	11168	Q9PMV9	34.44	1.20E-16	180
			8P0027	226	FlaA	<i>C. jejuni</i> strain d2677	Q9R953	100	1.80E-74	226
2d02.p	4	1229	8P0028	336	Cst-I	<i>C. jejuni</i> strain oh4384	Q9RGF1	41.14	1.20E-31	367
			8P0029	43	hypothetical cj1431c	11168	Q9PMM6	41.02	6.70E-01	39

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swal	% id (aa)	e-value	no. of aa in match
8h11.p	4	1479	8P0030	59	hypothetical cj0121	11168	Q9PJ06	98.27	7.00E-22	58
			8P0031	402	cj0243c hypothetical	11168	Q9PIQ2	21.51	0.005	344
1a07.p	5	1123	8P0032c	94	no matches					
			8P0033c	279	cj0032	11168	Q9PJ79	64.93	4.90E-54	288
6e04.q	5	1000	8P0034	196	AcnB cj0835c aconitate hydratase	11168	Q9PP88	98.46	5.70E-76	196
			8P0035	116	cj0834c periplasmic protein	11168	Q9PP89	92.24	9.30E-39	116
5a10.q	5	1348	8P0036c	225	cj1442c	11168	Q9PML5	63.34	1.50E-50	221
			8P0037c	224	KpsF	11168	Q9PML4	95.92	5.50E-76	221
2h05.p	5	1445	8P0038c	46	no matches					
			8P0039c	433	hypothetical	<i>Fusobacterium nucleatum</i>	Q8REK3	23.59	2.70E-03	339
3e08.q	6	1267	8P0040c	330	cj1310c hypothetical	11168	Q9PMY9	62.95	1.40E-78	332
			8P0041	61	NeuA2	11168	Q9PMY8	96.72	2.40E-20	61
2e09.q	6	1438	8P0042	451	cj0971	11168	Q9PNW7	83.81	2.30E-22	105
1e08.q	6	1086	8P0043c	340	DrnhA	<i>Yersinia pseudotuberculosis</i>	Q8G8E4	78.2	2.30E-99	335
1c09.q	7	1346	8P0044	218	FlaB	81116	Q9RF25	100	3.60E-66	218
			8P0045c	217	cj1337	81-176	Q7X517	100	7.80E-71	217
3b10.q	8	1985	8P0046c	135	cj0305c	11168	Q9PIJ4	66.66	4.00E-33	135
			8P0047c	380	BioF	11168	Q9PIJ3	75.78	5.40E-112	380
			8P0048	124	BioA	11168	Q9PIJ2	94.35	2.50E-47	124
1b01.p	4	2336	8P0049c	72	type I RM mm2978	<i>Methanosarcina mazei</i>	Q8PSU8	37.03	6.40E-03	54
			8P0050c	636	rm cc0620	<i>Caulobacter crescentus</i>	Q9AAH8	39.62	7.10E-58	641
7b08.q	8	1272	8P0051	130	cj0294 moeb/thif family protein	11168	Q9PIK5	95.38	2.90E-46	130
			8P0052c	126	PanD cj0296c	11168	Q9PIK3	98.41	2.30E-43	126
			8P0053c	137	PanC cj0297c	11168	Q9PIK2	96.35	8.90E-43	137
4a03.p	11	1388	8P0054c	462	FlgE	81-176	Q83WM5	100	1.10E-177	462
6g02.p	11	1765	8P0055c	412	DTPT transporter (disrupted)	<i>Photobacterium luminescens</i>	Q7N5W6	47.99	1.30E-79	398
			8P0056c	117	ABC transporter	<i>Photobacterium luminescens</i>	Q7N5W6	47.66	1.10E-15	107
4e04.p	12	1893	8P0057c	164	ModC	11168	Q9PIJ9	76.22	1.00E-39	164
			8P0058c	222	ModB	11168	Q9PIJ8	85.13	2.40E-70	222
			8P0059c	133	cj0302c	11168	Q9PIJ7	64.61	1.80E-28	130
			8P0060c	109	ModA	11168	Q9PIJ6	81.65	1.40E-30	109
6d08.p	16	2885	8P0061	76	no matches					
			8P0062	879	type I RM mm2976	<i>Methanosarcina mazei</i>	Q8PSV0	44.63	6.10E-131	867

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swal	% id (aa)	e-value	no. of aa in match
2b09.p	14	4502	8P0063	126	Cst-il	81-176	Q9L9Q5	98.4	5.20E-46	125
			8P0064	346	NeuB1	<i>C.jejuni</i> strain atcc 43456	Q93D04	100	6.70E-129	346
			8P0065	374	NeuC1	<i>C.jejuni</i> atcc 43456	Q93D03	100	5.60E-134	374
			8P0066	315	CgtA-II	<i>C.jejuni</i> atcc 43449 and 43456	Q934C5	100	1.20E-126	315
			8P0067	221	NeuA1	<i>C.j</i> strain 43456	Q933W2	100	1.40E-82	221
			8P0068	117	acetyltransferase	<i>C.jejuni</i> strain atcc 43449	Q93CZ2	100	2.30E-46	117
6a11.p	28	2110	8P0069	576	FlaB	<i>C.jejuni</i> 81116	Q9RF25	97.74	3.90E-174	576
7f02.p	31	4287	8P0070	150	TraN	<i>Sphingomonas aromaticivorans</i>	O85935	42	2.60E-17	150
			8P0071	396	TraG	<i>Escherichia coli</i>	P33790	20.44	1.70E-04	357
			8P0072	174	no matches					
			8P0073	294	no matches					
8P0074c	93	no matches								
7f11.p	37	3740	8P0075	49	SecY cj1688	11168	Q9PLZ0	100	1.70E-18	49
			8P0076	398	hypothetical	<i>Clostridium perfringens</i>	Q8XNB6	34.7	8.00E-43	412
			8P0077	670	hypothetical	<i>Rhizobium loti</i>	Q98CJ2	39.13	5.90E-94	672
6g03.q	38	3087	8P0078	740	DmsA	<i>Wolinella succinogenes</i>	Q7MRE1	62.01	5.40E-189	745
			8P0079	218	FdhB	<i>Wolinella succinogenes</i>	Q7M8T2	62.67	2.00E-55	217
			8P0080	70	MraY hypothetical	<i>Wolinella succinogenes</i>	Q7MRE0	47.14	2.40E-07	70
7d05.p	41	4416	8P0081	519	cyt C biogenesis protein	<i>Wolinella succinogenes</i>	Q7M7P8	59.45	3.20E-121	518
			8P0082c	556	GGT jhp1046	<i>H.pylori</i> j99	Q9ZK95	67.2	2.90E-134	558
			8P0083	306	cj0031	11168	Q9PJ80	61.93	9.80E-63	310
4b02.p	47	5554	8P0084	656	cytochrome C	<i>Shewanella oneidensis</i>	Q8EJ16	55.24	1.60E-136	677
			8P0085	689	cytochrome C family protein	<i>Geobacter sulfurreducens</i>	AAR33608	36.31	2.50E-59	614
			8P0086	194	hypothetical	<i>Wolinella succinogenes</i>	Q7MQN4	38.88	3.10E-23	198
			8P0087	234	cyt C biogenesis protein	<i>Helicobacter hepaticus</i>	Q7VHG9	37.97	4.30E-24	237
6d10.q	56	4739	8P0088	273	cj1368	11168	Q9PMT2	89.37	6.70E-97	273
			8P0089	1121	cj1365c serine protease	11168	Q9PMT5	39.66	2.30E-79	1147
			8P0090	147	cj1369 transport	11168	Q9PMT1	81.63	8.20E-45	147
7g11.p	2	1380	8P0091	218	iron uptake ABC transport cj0173c	11168	Q9PIV6	99.08	2.40E-73	218
			8P0092c	158	PurU cj0790	11168	Q9PPC9	100	2.00E-53	146
			8P0093c	61	RNA nucleotidyltransferase cj0789	11168	Q9PPD0	98.21	7.10E-19	56
2h12.p	2	906	8P0094c	286	no matches					
5e04.q	1	396	8P0095c	93	no matches					
3h05.p	1	662	8P0096c	219	cj1342c hypothetical	11168	Q9PMV7	78.53	4.10E-71	219

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
3d09.q	1	176	8P0097c	54	no matches					
1a12.p	1	658	8P0098c	218	LpsA	<i>Vibrio parahaemolyticus</i>	Q87T79	41.36	2.40E-32	220
2c01.q	1	596	8P0099c	162	glycosyltransferase	<i>C.jejuni</i> strain atcc 43456	Q93D08	100	1.40E-60	162
4a04.q	1	634	8P0100c	88	Atpe cj0936	11168	Q9PNZ7	90.9	2.20E-22	88
4c05.q	1	641	8P0101	157	no matches					
8e07.p	1	880	8P0102	119	exonuclease recj cj0028	11168	Q9PJ83	97.36	4.60E-41	114
			8P0103	127	Ansa cj0029	11168	Q9PJ82	83.46	4.40E-33	127
1f07.q	1	595	8P0104	37	WaaV	<i>C.jejuni</i> strain 43456	Q93D01	100	1.50E-12	37
			8P0105c	160	acetyltransferase	<i>C.jejuni</i> strain atcc 43456,	Q93D02	98.75	9.40E-59	161
6a06.p	2	1189	8P0106c	213	hypothetical dsba cj0872	11168	Q9PP57	98.12	9.00E-77	213
			8P0107c	141	arylsulfatase AstA	81-176	Q46098	100	2.80E-54	141
7e09.p	2	901	8P0108c	143	afimbrial adhesin	<i>Escherichia coli</i>	Q93QU8	32.39	0.00034	142
5g02.p	1	197			N/A	11168				
1a08.p	1	357			N/A					
5b12.q	1	666			N/A					
6h03.q	2	742			N/A	11168				
6h12.q	1	274			N/A	11168				

APPENDIX 4

Predicted CDSs for sequenced pUC library clones of strain M1

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
2d02.q	2	512	MP0001	137	serine protease SigA	<i>Shigella flexneri</i> 2a	Q9L8L1	37.4	3.80E-08	139
5d06.p	2	671	MP0002	223	restriction modification protein Cjel	<i>C. jejuni</i> strain p37	Q9JN06	91.55	6.80E-73	225
3a07.p	2	907	MP0003	61	cj1058c	11168	Q9PNN3	77.77	1.50E-10	45
			MP0004	57	cj1057c	11168	Q9PNN4	94.73	9.90E-15	57
			MP0005	184	cj1056c (disrupted)	11168	Q9PNN5	76.34	4.80E-50	186
3a10.q	2	555	MP0006c	163	no matches					
2f03.q	2	664	MP0007c	73	WlaK	<i>C. jejuni</i> strain 81116	O86158	98.63	1.90E-26	73
			MP0008c	115	WlaI	<i>C. jejuni</i> strain 81116	O86157	100	5.30E-43	115
4e10.q	2	457	MP0009c	121	cj1375	11168	Q9PMS5	94.95	1.40E-39	119
5b05.p	2	823	MP0010c	229	DTPT dehydratase	<i>Helicobacter hepaticus</i>	Q7VJZ3	59.29	1.80E-47	226
4e04.p	2	752	MP0011	101	cj0032 RM	11168	Q9PJ79	65.34	1.30E-17	101
			MP0012	148	cj0033 membrane	11168	Q9PJ78	39.37	8.10E-06	160
4e02.q	2	624	MP0013	207	PorA membrane	<i>C. jejuni</i> Strain x7199	Q9F782	88.37	1.30E-67	215
3f12.p	2	812	MP0014c	233	cj0139 endonuclease	11168	Q9PIY8	53.28	3.70E-28	259
3b05.q	3	1437	MP0015c	185	glycosyltransferase	<i>C. jejuni</i> Strain 11828	Q9ALT2	100	8.50E-72	185
			MP0016c	266	glycosyltransferase	<i>C. jejuni</i> Strain 11828	Q9ALT1	100	2.30E-87	228
2h08.p	3	746	MP0017c	195	hypothetical	<i>C. jejuni</i> Strain rm1221	Q8RN32	97.43	3.00E-70	195
4a03.q	3	1095	MP0018c	365	FliA	<i>C. jejuni</i> Strain 81116	FLA2_CAMJ	100	1.20E-116	365
3d02.q	6	1972	MP0019	57	alginate O-acetylation protein	<i>C. jejuni</i> Strain 11828	Q9ALT7	100	5.40E-22	57
			MP0020	371	hypothetical	<i>C. jejuni</i> Strain 11828	Q9ALT8	97.99	6.90E-135	349
			MP0021c	186	cj1149c isomerase	11168	LPC1_CAMJ	96.77	1.40E-65	186
2g06.p	3	887	MP0022	94	ppK cj1359	11168	PPK_CAMJE	98.91	4.00E-29	92
			MP0023c	152	VacA	<i>H. pylori</i> J99	Q9ZME6	26.41	7.70E-03	159
3e04.p	3	1277	MP0024c	425	cj1337 hypothetical	<i>C. jejuni</i> Strain 81-176	Q7X517	99.76	7.90E-159	424
3e08.p	4	1095	MP0025	273	no matches					
2c03.p	4	794	MP0026c	242	no matches					
1g01.q	4	944	MP0027c	314	cj1178c acidic	11168	Q9PNB7	91.42	2.90E-80	315
1f05.p	4	1115	MP0028c	307	RimA transferase	<i>C. jejuni</i> strain 81116	Q9K5D0	98.37	1.40E-110	307
			MP0029c	38	glycosyltransferase wlaNB	<i>C. jejuni</i> strain 81116	Q9K5D1	100	3.40E-17	38
2h03.q	4	718	MP0030	239	cj0262c chemotaxis	11168	Q9PIN3	55.46	3.60E-45	238

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swal	% id (aa)	e-value	no. of aa in match
1b09.q	4	1934	MP0031c	264	phosphodiesterase	<i>Bradyrhizobium japonicum</i>	Q89MQ1	40.9	3.50E-34	264
			MP0032c	202	HAD hydrolase	<i>Caulobacter crescentus</i>	Q9Q7S7	28.19	2.30E-06	188
			MP0033c	156	ABC transporter	<i>Brucella suis</i>	Q8FUP0	36.36	4.50E-09	165
2f12.q	4	1522	MP0034	461	O-acetylation protein	<i>C.jejuni</i> strain 11828	Q9ALT7	100	1.90E-186	459
3e06.q	5	1419	MP0035	469	cj1614 ChuA	11168	Q9PM61	91.19	2.10E-174	477
4f03.q	6	1431	MP0036	317	arylsulfatase	<i>C.jejuni</i> strain 81-176	Q46098	99.68	3.60E-129	317
			MP0037	130	cj0872 DsbA	11168	Q9PP57	96.15	6.30E-48	130
1a12.p	6	1908	MP0038c	496	ABC transporter (disrupted)	<i>Photorhabdus luminescens</i>	CAE14106	47.58	5.60E-80	496
			MP0039c	81	di-tripeptide transporter	<i>Yersinia pseudotuberculosis</i>	Q669J3	44.73	2.20E-09	76
3b03.q	6	1733	MP0040c	552	cj1334 hypothetical	<i>C.jejuni</i> strain 81-176	Q7X519	76.71	1.40E-136	481
5c06.p	6	1714	MP0041	428	WbyH (o-antigen)	<i>Yersinia pseudotuberculosis</i>	Q9RCB8	43.88	1.10E-65	417
			MP0042c	146	AscF reductase	<i>Yersinia pseudotuberculosis</i>	Q57103	32.79	1.10E-07	125
1h04.q	7	2681	MP0043	225	EpsS epimerase	<i>Methylobacillus</i>	Q83VQ2	56.05	2.00E-47	223
			MP0044	384	Glf galactopyranose mutase	<i>Helicobacter hepaticus</i>	Q7VJP0	53.48	7.50E-74	359
			MP0045	291	hypothetical	<i>C.jejuni</i> strain 11828	Q9ALS8	28.04	3.00E-09	296
3d04.q	8	1528	MP0046c	508	adhesin	<i>Chromobacterium violaceum</i>	AAQ59146	24.77	5.00E-03	440
2g01.p	8	1953	MP0047	167	hypothetical	<i>Shewanella oneidensis</i>	Q8E9K9	26.61	3.60E-05	139
			MP0048	169	type I RM	<i>Archaeoglobus fulgidus</i>	O28563	45.94	3.40E-13	111
			MP0049	226	type I RM	<i>Wolinella succinogenes</i>	CAE10680	32.57	1.30E-07	221
1h01.q	8	1192	MP0050	381	cytochrome c	<i>Shewanella oneidensis</i>	Q8EJI6	54	5.70E-71	400
3d07.q	8	1703	MP0051	116	hypothetical (los locus)	<i>C.jejuni</i> strain 11828	Q9ALT0	95.69	7.40E-35	116
			MP0052c	361	aminotransferase	<i>C.jejuni</i> strain 11828	Q9ALS9	98.6	4.40E-139	358
			MP0053c	77	membrane protein	<i>C.jejuni</i> strain tgh9011	Q6EB21	84.5	2.10E-20	71
3e11.p	8	1247	MP0054	375	weak match to hemolysin	<i>Xanthomonas axonopodis</i>	Q8PHP1	23.89	5.30E-02	318
5h04.p	10	1763	MP0055c	69	iron binding protein	11168	Q7AR79	79.7	6.50E-19	69
			MP0056c	220	hypothetical	<i>Helicobacter hepaticus</i>	Q7VK87	34.32	6.70E-16	201
			MP0057c	206	hypothetical	<i>Helicobacter hepaticus</i>	Q7VK87	36.22	3.10E-19	196
5d03.p	8	1526	MP0058	432	UGDH glucose dehydrogenase	<i>Agrobacterium tumefaciens</i>	Q8U8E3	48.84	4.10E-78	434
			MP0059	34	UDP-glucose 4-epimerase	<i>Fusobacterium nucleatum</i>	Q8RGC6	67.64	1.50E-05	34
3c05.q	9	1729	MP0060	183	ribosomal protein	<i>Vibrio vulnificus</i>	Q8DF32	32.96	1.90E-06	179
			MP0061c	115	no matches					
			MP0062c	209	putative phage repressor protein	Bacteriophage phi ETA	Q9G039	28.89	5.20E-05	180
1b10.q	10	1565	MP0063	45	cj1337 hypothetical	<i>C.jejuni</i> strain 81-176	Q7X517	100	2.40E-14	45
			MP0064c	464	FlaB	<i>C.jejuni</i> strain 81116	Q9RF25	100	3.90E-144	462

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swal	% id (aa)	e-value	no. of aa in match
3b09.p	10	1924	MP0065c	81	no matches					
			MP0066c	559	hypothetical	<i>Fusobacterium nucleatum</i>	Q8REK3	23.71	1.50E-04	485
5c01.p	11	1646	MP0067c	85	hypothetical	<i>Wolinella succinogenes</i>	CAE10494	38.09	2.80E-06	84
			MP0068c	288	DmsC type gene (MraY)	<i>Wolinella succinogenes</i>	CAE10493	42.5	8.10E-40	287
			MP0069c	179	oxidoreductase FdhB	<i>Wolinella succinogenes</i>	CAE10492	62.77	1.50E-43	180
2g03.q	11	2942	MP0070c	66	RloA	<i>C.jejuni</i> strain Rm1551 & rm1850	Q8G8E7	100	1.90E-22	66
			MP0071c	769	HsdR	<i>C.jejuni</i> strain 81116	Q8RIX1	100	0	769
			MP0072	71	cj1548c dehydrogenase	11168	Q9PMC1	100	3.40E-30	71
4h06.p	13	1792	MP0073	110	cj0123c	11168	Q9PJ04	90.9	3.70E-36	110
			MP0074c	446	hypothetical	<i>Plasmodium falciparum</i>	Q8IHQ0	19.2	0.012	453
3a05.q	12	1401	MP0075	39	periplasmic protein cj0770c	11168	Q9PPE9	100	1.50E-05	22
			MP0076	149	hypothetical reP	<i>Treponema denticola</i>	Q9AQF2	39.59	8.00E-14	149
			MP0077	60	hypothetical TnpV	<i>Clostridium difficile</i>	O05416	46.42	6.00E-06	56
3e01.p	14	1779	MP0078	146	glucose epimerase	<i>Pyrococcus furiosus</i>	Q8U170	34.09	1.70E-07	132
			MP0079	376	glucose dehydrogenase	<i>Pyrococcus abyssi</i>	Q9UZI8	38.33	1.50E-42	373
4g01.p	15	1955	MP0080c	85	RifA	Bacteriophage P1	Q71TB8	44.57	2.10E-07	85
			MP0081c	552	type I RM	<i>Wolinella succinogenes</i>	CAE10680	70.27	6.60E-149	555
1g05.q	15	2785	MP0082	238	cj0414 oxidoreductase	11168	Q9PI91	44.03	3.20E-34	243
			MP0083	571	cj0415 oxidoreductase (disrupted)	11168	Q9PI90	57.14	7.70E-131	574
2c11.p	15	3856	MP0084	67	hypothetical	<i>C. jejuni</i> strain rm1221	Q8RN32	100	8.20E-22	65
			MP0085	149	hypothetical	<i>C.jejuni</i> strain rm1221	Q8RN33	97.84	2.20E-51	139
			MP0086	251	decarboxylase pcac	<i>Methanosarcina acetivorans</i>	Q8TTM1	42.57	1.30E-37	249
			MP0087c	496	HsdM	<i>C.jejuni</i> strain rm2227	Q8RN18	96.77	2.60E-181	496
			MP0088c	198	HsdS	<i>C.jejuni</i> strain rm1163 & rm1508	Q8G8A9	99.48	6.40E-74	194
4e08.q	16	1909	MP0089	164	cytochrome C	<i>Shewanella oneidensis</i>	Q8EJI6	49.08	1.20E-26	163
			MP0090	457	hpothetical/ possible cyt C	<i>Shewanella oneidensis</i>	Q8EJI5	39.43	1.70E-12	142
3h01.q	16	2537	MP0091c	118	permease protein	<i>Rhodopseudomonas palustris</i>	Q6NDI1	43.75	7.00E-15	112
			MP0092c	285	ABC transporter permease	<i>Rhizobium loti</i>	Q98JZ2	48.54	1.00E-49	274
			MP0093c	372	ABC transporter	<i>Agrobacterium tumefaciens</i>	Q8UIA7	45.43	1.10E-48	372
			MP0094c	41	cj1687	11168	Q9PLZ1	100	1.50E-16	41
3d08.p	18	2768	MP0095	153	Cj1431c hypothetical	11168	Q9PMM6	28.32	2.90E-04	173
			MP0096	264	DdhA (los)	<i>Yersinia enterocolitica</i>	Q56860	59.47	4.80E-60	264
			MP0097	452	glucose dehydratase	<i>Fusobacterium nucleatum</i>	EAA24619	60.67	6.00E-109	445
			MP0098	50	no matches					

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swal	% id (aa)	e-value	no. of aa in match
1d11.p	18	2713	MP0099c	124	no matches					
			MP0100c	57	hypothetical from transposon	<i>Enterococcus faecalis</i>	Q56396	66.66	4.10E-14	57
			MP0101c	582	TetO	<i>C.jejuni</i> plasmid pCjA13	Q84FM6	99.48	1.40E-202	577
1g06.p	21	2261	MP0102c	55	cj1584c periplasmic	11168	Q9PM91	83.33	9.80E-16	54
			MP0103	600	DmsA	<i>Wolinella succinogenes</i>	CAE10491	61.69	6.00E-155	603
4e01.q	35	4308	MP0104c	881	TraG pseudogene	<i>Vibrio vulnificus</i>	BAC97743	21.04	4.10E-11	879
			MP0105	51	cj0937 membrane protein	11168	Q9PNZ6	100	8.40E-20	51
4d08.p	42	4924	MP0106	813	cytochrome C	<i>Wolinella succinogenes</i>	CAE11153	54.26	5.90E-172	820
			MP0107c	556	GGT	<i>H. pylori</i> J99	Q9ZK95	67.74	9.40E-136	558
			MP0108	182	cj0031 RM	11168	Q9PJ80	53.8	3.70E-30	184
1c08.p	2	715	MP0109	197	hypothetical (disrupted)	<i>Helicobacter hepaticus</i>	Q7VK87	39.28	1.40E-19	196
2g10.p	2	1010	MP0110c	202	Ansa cj0029	11168	Q9PJ82	86.13	8.00E-59	202
			MP0111c	87	RecJ cj0028	11168	Q9PJ83	96.55	1.20E-32	87
1f03.p	2	1035	MP0112c	166	HsdS	c.j strain rm1049, rm1861, 81116	Q8RJ16	100	2.70E-64	166
			MP0113c	179	RloB	c.j strain rm1049, rm1861, 81116	Q8RIW9	100	1.70E-66	179
1b04.q	2	760	MP0114c	170	ABC transporter (disrupted)	<i>Rhizobium loti</i>	Q98JZ4	36.25	1.20E-13	160
			MP0115c	60	ABC transporter permease	<i>Rhizobium loti</i>	Q98JZ3	56.66	1.10E-10	60
2d06.q	2	593			no predicted CDSs					
2d03.p	2	762	MP0116c	206	hypothetical	<i>Helicobacter hepaticus</i>	Q7VIF8	51.33	6.50E-33	187
2e03.p	2	824	MP0117c	70	hypothetical	<i>Wolinella succinogenes</i>	Q7MQN4	39.34	2.70E-04	61
			MP0118c	187	formate dehydrogenase	<i>Vibrio cholerae</i>	Q9KRX2	28	9.00E-04	
3a03.p	1	646	MP0119c	151	hypothetical	<i>S. typhimurium</i> phage ST64B	Q8HAA0	30.87	1.30E-06	149
2b12.p	1	591	MP0120c	118	WlanB glycosyltransferase	<i>C.jejuni</i> strain 81116	Q9K5D1	100	1.00E-41	118
			MP0121c	78	WlanA (lipid A synthesis cluster)	<i>C.jejuni</i> strain 81116	Q9K5D2	100	1.00E-32	78
5b01.p	1	585	MP0122	93	cj1305c hypothetical	11168	Q9PMZ4	57.81	8.00E-12	64
2c05.p	1	425	MP0123c	104	no matches					
1e03.q	1	358	MP0124	119	hypothetical	<i>Pasteurella multocida</i>	Q9CKR7	39.02	1.10E-03	82
2a08.q	1	471	MP0125c	99	NADH dehydrogenase	<i>Strongyloides stercoralis</i>	CAD90562	36.45	3.30E-03	96
4d09.p	1	814	MP0126c	49	no matches					
			MP0127c	222	hypothetical	<i>Plasmodium yoelii yoelii</i>	EAA18980	24.27	0.0093	173
2e10.p	1	805	MP0128	20	transferase cj1050c	11168	Q9PNP1	95	6.60E-06	20
			MP0129	199	membrane protein cj1049c	11168	Q9PNP2	87.94	2.90E-65	199
			MP0130	48	Dape or Cj1048c	11168	Q9PNP3	100	1.70E-17	47
2g02.q	2	664	MP0131c	220	pgi cj1535c pseudogene	11168	G6PI_CAMJ	82.27	4.00E-64	220

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
3b01.p	4	1024	MP0132	89	EspC	<i>Escherichia coli</i>	P77070	43.18	4.40E-11	88
			MP0133	225	Argc cj0224	11168 & TGH9011	ARGC_CAM	98.22	6.80E-86	225
3e02.q	1	733	MP0134	238	membrane protein cj0692c	11168	Q9PPL5	85.71	4.00E-54	238
4h07.p	2	932	MP0135	154	cj1295 hypothetical	11168	Q9PN04	88.88	6.40E-53	153
			MP0136	157	cj1296 & cj1297	11168	Q9PN03	79.04	1.30E-31	105
							Q9PN02	56.75	2.10E-03	37
5h05.p	4	1775	MP0137	53	hydrophobic protein	11168	Q9PLV0	97.5	4.40E-13	40
			MP0138	127	cj1724c hypothetical	11168	Q9PLV4	100	8.80E-51	127
			MP0139	214	cj1721c outer membrane protein	11168	Q9PLV7	65.42	2.10E-55	214
			MP0140c	106	cj1720 hypothetical	11168	Q9PLV8	100	8.80E-38	107
4c04.p	3	1057	MP0141	202	Cj0967 periplasmic protein	11168	Q9PNW9	96.42	1.90E-31	112
			MP0142	115	hemagglutinin-related protein/ adhesin	<i>Ralstonia solanacearum</i>	Q8XQ42	36.28	6.00E-05	113
2g07.q	8	1844	MP0143	470	cj0970, cj0971, cj0972, cj0973	11168	Q9PNW7	95.31	4.90E-34	128
							Q9PNW8	85.85	1.20E-21	99
							Q9PNW6	55.78	2.30E-09	95
				MP0144	65	Cj0975	11168	Q9PNW5	93.54	1.60E-03
						Q7AR82	97.29	6.90E-09	37	
4f07.p	2	730	MP0145c	31	hypothetical	11168	Q9PNW8	80	7.50E-05	30
			MP0146c	151	ceub uptake permease cj1352	11168	Q9PMU7	98.01	1.10E-50	151
			MP0147c	35	pidA	11168	Q9PMU8	97.14	7.90E-14	35
2f07.q	4	1193	MP0148	89	haemoglobin protease	<i>Escherichia coli</i>	Q8FKM0	45.97	6.10E-07	87
			MP0149	162	no matches					
			MP0150	89	no matches					
2b05.p	4	1063	MP0151c	255	dicarboxylate transporter	<i>Vibrio vulnificus</i>	BAC95008	35.77	1.00E-20	232
			MP0152	31	hypothetical Cj1523c	11168	Q9PME1	96.77	5.00E-11	31
4d12.p	1	788	MP0153c	97	cj0865 oxidoreductase DsbB	11168	DSBI_CAMJ	95.78	2.40E-39	95
			MP0154c	167	Cj0864 periplasmic protein	11168	Q9PP59	91.76	7.30E-23	85
4e06.p	10	2078	MP0155c	423	BlI0816 hypothetical	<i>Bradyrhizobium japonicum</i>	Q89W77	33.48	1.40E-39	427
			MP0156c	266	cj1394 fumarate lyase	11168	Q9PMR1	95.11	1.70E-95	266

APPENDIX 5

Predicted CDSs for sequenced pUC library clones of strain 40671

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
3e04.q	2	606	4P0001	86	TraH	<i>Comamonas acidovorans</i> pUO1	BAC82023	41.79	1.60E-08	67
			4P0002	110	no matches					
3d01.p	2	1132	4P0003	115	cj0138	11168	Q9PIY9	90.38	2.00E-30	104
			4P0004	95	no matches					
			4P0005	111	no matches					
1d01.p	2	1060	4P0006	345	mcp-type signal transduction	11168	Q9PMF7	40	5.60E-47	345
3f04.p	4	2259	4P0007c	570	cj1440c sugar transferase	11168	Q9PML7	49.64	2.00E-46	423
			4P0008	139	cj1421c sugar transferase	11168	Q9PMN6	84.17	7.10E-43	139
1b09.p	4	988	4P0009c	342	MagB10	<i>Actinobacillus actinomycetemcomitans</i>	Q9F252	40.35	2.20E-34	342
3c10.p	4	1147	4P0010c	333	sialic acid biosynthesis	<i>C. jejuni</i> strain 43446	Q9L9Q4	99.09	4.20E-123	332
3c08.q	4	1341	4P0011	315	no matches					
1c07.p	4	1052	4P0012c	350	FlgE	<i>C. jejuni</i> strain lio7	O86148	99.41	6.90E-122	344
3f07.p	4	1011	4P0013c	336	MagB12	<i>Actinobacillus actinomycetemcomitans</i>	Q9F254	40.95	8.10E-44	337
2d04.p	4	1442	4P0014c	95	no matches					
1d05.p	4	1179	4P0015	101	hypothetical cj1724c	11168	Q9PLV4	100	1.40E-39	101
			4P0016	213	cj1721c membrane protein	11168	Q9PLV7	64.01	5.00E-54	214
1h08.q	4	1079	4P0017	140	hypothetical	<i>Helicobacter hepaticus</i>	Q7VGU0	35.43	4.80E-08	127
			4P0018	97	no matches					
3d10.p	4	1236	4P0019	384	hypothetical cj1341c	11168	Q9PMV8	48.55	3.40E-62	381
1d03.p	4	958	4P0020	143	hypothetical	<i>Wolinella succinogenes</i>	Q7MQT2	32.37	3.80E-09	139
			4P0021	174	hypothetical jhp0950	<i>H. pylori</i> J99	Q9ZKI5	46.7	3.20E-20	167
3g08.p	4	1498	4P0022	494	cj1431c hypothetical	11168	Q9PMM6	28.14	2.20E-22	430
1e07.p	4	1047	4P0023	87	VirB2	<i>Escherichia coli</i>	Q91UX6	35.36	9.90E-07	82
			4P0024	147	TriC	<i>Yersinia enterocolitica</i>	CAD58564	39.16	1.20E-12	143
1f06.p	4	1038	4P0025	309	FlaA	<i>C. jejuni</i> serotype 0:19	Q99QL6	100	2.70E-89	309
1b06.q	6	2049	4P0026	111	hypothetical	<i>Pseudomonas syringae</i>	Q889N9	58.76	6.50E-20	97
			4P0027	241	lipopolysaccharide biosynthesis	<i>Pseudomonas syringae</i>	Q889P3	40.49	2.40E-23	242
			4P0028	132	hypothetical	<i>Actinobacillus suis</i>	Q84CG6	57.93	9.00E-27	126
			4P0029	142	hypothetical	<i>Actinobacillus suis</i>	Q84CG5	40.55	8.60E-16	143
3g02.p	6	1643	4P0030c	521	hypothetical	<i>Actinobacillus suis</i>	Q84CG8	26.03	2.40E-11	338

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swal	% id (aa)	e-value	no. of aa in match
2d09.p	6	1199	4P0031c	338	no matches					
			4P0032c	41	cj0121	11168	Q9PJ06	95.12	1.40E-14	41
3c01.q	7	1537	4P0033	243	hypothetical	<i>Actinobacillus suis</i>	Q84CG7	53.3	4.70E-42	242
			4P0034	265	c-methyltransferase	<i>Bordetella bronchiseptica</i>	Q7WR30	29.16	1.40E-06	216
1b12.q	8	2219	4P0035	633	hypothetical	<i>Chromobacterium violaceum</i>	Q7NTJ9	51.42	7.70E-120	634
			4P0036c	53	cj1161c ATPase	11168	Q9PND4	70.21	3.80E-11	47
1g01.p	8	1564	4P0037c	122	no matches					
			4P0038c	89	no matches					
2b07.p	8	1572	4P0039	446	oxidoreductase	<i>Bacteroides thetaiotaomicron</i>	Q8A7I2	44.61	7.70E-73	455
			4P0040c	82	cj1069	11168	Q9PNM5	83.54	2.60E-22	79
3f05.q	8	2881	4P0041c	295	virB9-like protein	<i>C.jejuni</i> plasmid pCjA13	Q847A7	97.28	3.50E-112	295
			4P0042c	220	virB8-like protein	<i>C.jejuni</i> plasmid pCjA13	Q847A8	100	1.10E-77	220
			4P0043c	333	magb06	<i>Actinobacillus actinomycetemcomitans</i>	Q9F248	26.33	1.60E-15	319
1g12.p	9	2582	4P0044	74	hypothetical	<i>Bacteroides thetaiotaomicron</i>	Q8A5B1	47.22	5.80E-06	72
			4P0045	167	hypothetical	<i>Shewanella oneidensis</i>	Q8E9K9	26.61	2.60E-05	139
			4P0046	480	type I RM	<i>Archaeoglobus fulgidus</i>	O28563	38.63	6.70E-16	176
			4P0047	63	cj1047c	11168	Q9PNP4	88.88	1.00E-18	63
			4P0048	33	cj1046c Moeb	11168	Q9PNP5	93.93	3.10E-14	33
3e05.q	9	1813	4P0049c	276	acetyltransferase	<i>C.jejuni</i> strain 43432	Q9F0M5	98.91	3.90E-106	277
			4P0050c	221	NeuA1	<i>C.jejuni</i> strain 81-176, 43456, 43444	Q933W2	98.64	3.90E-82	221
1e06.p	10	2212	4P0051c	116	hydrolase	<i>Pseudomonas syringae</i>	Q889P1	62.28	8.20E-26	114
			4P0052c	211	hypothetical	<i>Pseudomonas syringae</i>	Q889P2	40.67	6.10E-29	209
			4P0053	295	c-methyltransferase	<i>Leptospira interrogans</i>	Q8F5S5	25	2.00E-09	276
3g05.p	10	3379	4P0054	655	MagB03	<i>Actinobacillus actinomycetemcomitans</i>	Q9F245	44.82	9.20E-103	647
			4P0055	188	hypothetical	<i>C.jejuni</i> plasmid pCjA13	Q847A4	44.8	1.30E-14	183
			4P0056	221	no matches					
			4P0057	45	SSB	<i>C.jejuni</i> plasmid pVir	Q8GJE0	48.88	7.60E-06	45
1d02.q	10	1988	4P0058	402	cj1421c sugar transferase	11168	Q9PMN6	69.38	4.10E-86	343
			4P0059	228	Cst-I (disrupted)	<i>C.jejuni</i> strain 0h4384	Q9RGF1	57.85	7.60E-39	242
3a10.q	10	3859	4P0060c	830	hypothetical jhp1285	<i>H. pylori</i> J99	Q9ZJM1	30.28	5.60E-43	885
			4P0061c	413	no matches					
3f10.p	11	1692	4P0062c	539	Cj1334 hypothetical	<i>C.jejuni</i> strain 81-176	Q7X519	94.83	2.00E-168	465
1a10.p	12	3065	4P0063c	331	DmhA	<i>Yersinia pseudotuberculosis</i>	Q8G8E4	78.46	9.30E-97	325
			4P0064c	351	Fcl cj1428c	11168	Q9PMM9	59.07	2.90E-75	347
			4P0065c	181	cj1430c sugar epimerase	11168	Q9PMM7	80.66	4.40E-59	181
			4P0066c	126	cj1421c sugar transferase	11168	Q9PMN6	37.39	7.60E-05	115

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swal	% id (aa)	e-value	no. of aa in match
3b11.p	15	2239	4P0067c	60	phage hypothetical	Bacteriophage P1	Q9XJP4	46.42	1.10E-03	56
			4P0068c	683	type I RM	<i>Wolinella succinogenes</i>	Q7M8H9	71.04	8.20E-168	632
1g09.q	25	3249	4P0069	501	FlaB	<i>Campylobacter coli</i>	P18245	91.18	9.80E-139	499
			4P0070c	569	cj1337 hypothetical	11168	Q9PMW2	61.13	1.90E-136	566
1h01.p	2	1191	4P0071	382	hypothetical jhp0928	<i>H. pylori</i> J99	Q9ZKK7	42.96	8.80E-50	384
1b02.q	2	725	4P0072c	152	hypothetical ydaa	<i>Wolinella succinogenes</i>	Q7MQX6	39.43	6.30E-14	142
			4P0073c	89	Vap2	<i>Riemerella anatipestifer</i>	O85171	35.59	1.30E-01	59
1d06.p	2	1050	4P0074	246	hypothetical	<i>H. pylori</i> 26695	O25892	45	4.00E-30	220
3f11.p	2	1346	4P0075c	436	putative DNA methylase	<i>Sinorhizobium meliloti</i> phage PBC5	Q8W6K4	44.87	7.20E-39	312
1d10.p	2	1151	4P0076	330	VirB11-like protein (disrupted)	<i>C.jejuni</i> plasmid pCjA13	Q847A5	99.69	4.70E-117	329
2c02.p	2	633	4P0077c	199	TraE (virB8)	<i>Escherichia coli</i>	Q60215	36.54	6.90E-14	197
3e03.p	2	744	4P0078c	247	ABC transporter	<i>Photobacterium luminescens</i>	Q7N5W6	52.67	1.90E-55	243
1c06.p	2	1352	4P0079c	304	no matches					
			4P0080c	97	no matches					
			4P0081c	39	hypothetical	<i>Wolinella succinogenes</i>	Q7MQT0	50	0.00017	36
2b11.p	2	791	4P0082c	262	hypothetical	<i>H. pylori</i> J99	Q9ZKK7	48.47	4.00E-43	262
2c10.p	1	800	4P0083c	201	hypothetical	<i>Clostridium perfringens</i>	Q93M99	26.15	1.20E-02	195
			4P0084c	78	no matches					
1a12.q	1	772	4P0085c	205	ATPase 6	<i>Leishmania tarentolae</i>	Q33561	22.87	1.10E-02	188
3a12.p	1	819	4P0086	32	no matches					32
			4P0087	67	hypothetical	<i>H. pylori</i> J99	Q9ZKH5	66.66	1.40E-12	57
			4P0088	131	no matches					
3a12.q	1	769	4P0089	252	TrbM-like protein	<i>Haemophilus aegyptius</i>	Q8VRC6	37.17	4.50E-11	191
1b05.p	1	696	4P0090c	230	type II RM (cj0032)	11168	Q9PJ79	60.08	2.40E-43	228
1a06.p	1	827	4P0091c	225	CfrA cj0755	11168	Q9PPG3	88	3.80E-78	225
1a05.q	1	695	4P0092	231	sialic acid biosynthesis	<i>C.jejuni</i> strain atcc43432	Q9F0M7	99.56	5.20E-82	231
1g03.p	1	810	4P0093c	87	no matches					
			4P0094c	194	no matches					
2a08.p	1	229	4P0095	70	acetyltransferase	<i>C.jejuni</i> strain 43446	Q9K379	38.57		70
2e08.p	1	728	4P0096c	151	no matches					
			4P0097c	90	no matches					
1g08.p	1	847	4P0098c	281	cj1305c hypothetical protein	11168	Q9PMZ4	75.97	2.10E-80	283
3d03.p	1	770	4P0099c	158	hypothetical cj1337	11168	Q9PMW2	70.77	6.30E-39	154
			4P0100c	45	efflux protein cj1174	11168	Q9PNC1	100	1.40E-15	45
1g10.p	1	151			no predicted CDSs					
2c04.p	1	122			no predicted CDSs					
2b06.p	1	90			no predicted CDSs					

APPENDIX 6

Predicted CDSs for sequenced pUC library clones of strain 52472

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
7h02.q	1	515	5P0001c	88	hypothetical	RM1221	Q5HWU3	98.33	1.10E-19	60
6e05.q	2	726	5P0002	241	di-/tripeptide transporter	RM1221	Q5HVB7_CA	96.9	6.30E-84	226
2f05.p	2	1099	5P0003c	316	type I RM	<i>Staphylococcus aureus</i>	Q6GD64_ST	35.5	2.90E-31	307
6d05.q	2	671	5P0004	223	cj0929 Pepa	11168	AMPA_CAMJ	97.76	5.40E-80	223
2g09.p	2	1098	5P0005	139	cj0807 oxidoreductase	11168	Q9PPB3_CA	98.51	1.10E-47	135
			5P0006c	104	cj0808c hydrophobic hypothetical	11168	Q9PPB2_CA	77.22	3.70E-30	101
			5P0007c	83	cj0809c hydrolase	11168	Q9PPB1_CA	90.36	4.30E-31	83
5b12.p	2	1017	5P0008	144	hypothetical	RM1221	Q5HTG8_CA	71.05	1.20E-04	38
			5P0009	78	hypothetical	RM1221	Q5HTH0_CA	92.3	2.90E-24	78
6c07.q	2	625	5P0010c	197	hypothetical	RM1221	Q5HW50_CA	98.96	1.50E-63	126
6f10.p	2	918	5P0011	300	cj0765c hiss	11168	SYH_CAMJE	87.29	1.30E-102	299
3g06.p	2	799	5P0012c	265	base plate assembly	RM1221	Q5HWS9_CA	98.11	3.70E-88	265
3d03.p	2	1137	5P0013	235	type II RM	RM1221	Q5HXC7_CA	73.39	2.20E-63	233
			5P0014	144	hypothetical	<i>H. pylori</i>	O26049_HEL	56.55	1.20E-21	145
3a04.p	2	763	5P0015	192	TrbM (cpp45)	<i>C. coli</i>	Q69BE2_CA	71.74	1.70E-52	184
			5P0016	60	hypothetical cpp46	<i>C. jejuni</i> pTet	Q69B91_CA	98.3	4.50E-17	
6a09.p	2	906	5P0017c	71	hypothetical	RM1221	Q5HTH6_CA	97.02	7.30E-22	67
			5P0018c	74	hypothetical	RM1221	Q5HTH5_CA	93.24	6.20E-27	74
			5P0019c	134	hypothetical	RM1221	Q5HTH4_CA	98.51	1.20E-50	134
4e02.q	2	543	5P0020c	179	cj1218c Riba	11168	Q9PN77_CA	95.5	2.40E-60	178
5f10.q	2	675	5P0021	224	cj0411 ATP/GTP binding protein	11168	Q9PI94_CAM	97.3	7.90E-68	223
4e01.p	2	764	5P0022	104	cj0578c Tatc sec-independent translocase	11168	TATC_CAMJ	97.08	1.50E-39	103
			5P0023	146	cj0577c QueA	11168	QUEA_CAMJ	97.26	1.40E-53	146
5e08.p	2	889	5P0024	243	HsdM	<i>C.jejuni</i> strain rm 1170	Q8RN38_CA	100	2.90E-90	242
4d12.p	2	974	5P0025	55	hypothetical cpp2	<i>C. jejuni</i> pTet	Q69BD4_CA	97.73	4.90E-17	44
			5P0026	117	hypothetical cpp8	<i>C. jejuni</i> pTet	Q69BC8_CA	99.14	1.00E-42	116
			5P0027	132	hypothetical cpp9	<i>C. jejuni</i> pTet	Q69BC7_CA	100	9.10E-47	132
3a03.q	3	1058	5P0028c	237	cj0812 Thrc	11168	Q9PPA8_CA	78.48	5.70E-70	237
			5P0029c	118	cj0811 Lpxk tetraacyldisaccharide kinase	11168	LPXK_CAMJ	84.21	4.90E-37	114
6c11.p	3	1062	5P0030c	323	hypothetical	RM1221	Q5HXA9_CA	99.69	1.90E-106	323
4d02.q	3	979	5P0031	200	hypothetical cpp46	<i>C. jejuni</i> pTet	Q69B91_CA	99	8.40E-67	200
			5P0032	102	hypothetical cpp47	<i>C. jejuni</i> pTet	Q69B90_CA	98	1.20E-34	102

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
8a03.p	4	815	5P0033c	80	hypothetical	RM1221	Q5HTH3_CA	98.63	1.10E-24	73
			5P0034c	106	hypothetical	RM1221	Q5HTH2_CA	99.06	7.20E-35	106
6a05.p	4	1794	5P0035c	124	MloA	<i>C.jejuni</i> strain rm 1852	Q8RN19_CA	100	1.40E-38	124
			5P0036c	395	HsdS	<i>C.jejuni</i> strain rm 1170	Q8RN40_CA	100	6.00E-152	395
5d07.p	4	1131	5P0037	70	type III RM	<i>H. pylori</i>	O25314_HEL	56.52	1.30E-10	69
			5P0038	304	DNA methyltransferase	<i>H. pylori</i>	O25315_HEL	61.98	8.60E-48	242
5g12.q	4	788	5P0039	74	cj0762c aspb aspartate aminotransferase	11168	Q9PPF7_CA	91.89	2.90E-24	74
			5P0040	185	hypothetical	<i>Nitrosomonas europaea</i>	Q82T36_NIT	33.15	9.90E-10	184
5h07.q	4	1432	5P0041	324	hypothetical	RM1221	Q5HWQ1_CA	99.68	1.90E-116	320
			5P0042	89	hypothetical	RM1221	Q5HWQ2_CA	100	3.20E-37	89
			5P0043	57	hypothetical	RM1221	Q5HWQ3_CA	98.11	1.00E-16	53
8h04.p	4	997	5P0044	331	periplasmic protein cj0737	11168	Q7AR90_CA	38.02	2.90E-22	334
8c09.p	4	1085	5P0045	102	virion morphogenesis protein	RM1221	Q5HWU1_CA	96.94	1.30E-36	98
			5P0046	212	dam DNA adenine methylase	RM1221	Q5HWU2_CA	96.49	8.00E-63	171
7a07.p	4	1280	5P0047c	239	cj0813 KdsB	11168	Q9PPA7_CA	82.85	8.20E-75	239
			5P0048c	157	cj0812 Thrc	11168	Q9PPA8_CA	75.48	1.00E-41	155
4g03.q	4	993	5P0049c	158	phage tail protein	RM1221	Q5HWTo_CA	96.81	3.00E-57	157
			5P0050c	170	base plate assembly	RM1221	Q5HWS9_CA	98.82	3.10E-55	170
5c07.q	6	1056	5P0051c	206	cj0293 Sure	11168	SURE_CAML	93.78	6.60E-67	193
			5P0052	98	transporter	<i>Escherichia coli</i>	Q8FAP1_EC	51.06	1.30E-14	94
6b10.q	5	949	5P0053c	298	transport system permease	<i>Escherichia coli</i>	Q8X8T6_EC	52.03	9.00E-59	296
5f02.p	5	1246	5P0054	65	di-/tripeptide transporter	RM1221	Q5HVB7_CA	60.66	2.40E-11	61
			5P0055	282	di-/tripeptide transporter	RM1221	Q5HVB7_CA	99.65	5.40E-115	282
5f11.q	5	2192	5P0056c	215	hypothetical					
			5P0057c	224	signal peptidase I	RM1221	Q5HTF9_CA	33.18	1.40E-17	223
			5P0058	177	dna transition protein a	RM1221	Q5HWP2_CA	87.82	6.20E-43	156
8b01.p	6	875	5P0059	221	hypothetical					
7e11.p	6	1591	5P0060	287	HsdR	<i>C.jejuni</i> strain rm 1170	Q8RN42_CA	99.29	1.50E-94	283
			5P0061	238	RloF	<i>C.jejuni</i> strain rm 1170	Q8RN41_CA	100	7.10E-89	238
5d04.q	6	1564	5P0062	248	hypothetical	RM1221	Q5HWR6_CA	98.79	1.40E-90	248
			5P0063	152	hypothetical	RM1221	Q5HWR5_CA	98.49	2.80E-45	132
			5P0064	83	hypothetical	RM1221	Q5HWR4_CA	100	3.90E-28	82
8c04.p	6	2259	5P0065	752	type III RM r protein	<i>H. pylori</i>	O25314_HEL	52.78	7.30E-58	773
5h03.q	6	1528	5P0066	470	VacA autotransporter domain	<i>H. pylori</i>	Q9ZHT4_Vac	23.05	9.20E-06	192
8g05.q	6	1619	5P0067c	94	DNA binding protein	RM1221	Q5HWQ7_CA	97.87	5.30E-31	94
			5P0068	223	DNS extracellular deoxyribonuclease	RM1221	Q5HWQ6_CA	99.55	2.80E-91	223
			5P0069c	91	hypothetical	RM1221	Q5HWQ5_CA	100	2.30E-31	91
			5P0070c	84	hypothetical	RM1221	Q5HWQ4_CA	100	2.80E-33	84

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
5h08.p	6	1272	5P0071c	207	hypothetical	<i>Salmonella typhi</i>	Q8Z3Y2_SA	41.44	8.10E-19	152
7g06.p	6	1220	5P0072	382	hypothetical	RM1221	Q5HWR2_CA	99.19	6.80E-134	369
1e12.q	7	1723	5P0073c	493	type I RM	<i>Methanosarcina mazei</i>	Q8PSV0_ME	45.52	1.80E-75	503
6f05.q	7	1270	5P0074	423	cj0629 possible lipoprotein	11168	Q9PHN8_CA	76.21	5.60E-46	269
4e07.q	7	2026	5P0075	77	cj0303c ModA	11168	Q9PIJ6_CAM	81.81	5.60E-22	77
			5P0076	133	cj0302c	11168	Q9PIJ7_CAM	64.61	9.80E-29	130
			5P0077	222	cj0301c ModB	11168	Q9PIJ8_CAM	84.68	3.40E-70	222
			5P0078	240	cj0300c ModC	11168	Q9PIJ9_CAM	78.33	1.80E-59	240
5e04.p	8	1871	5P0079c	73	cj0298c PanB	11168	PANB_CAM	98.59	1.10E-22	71
			5P0080c	236	hypothetical	<i>Helicobacter hepaticus</i>	Q7VI60_HEL	44.29	3.30E-33	228
			5P0081c	104	hypothetical					
8g09.p	8	2154	5P0082	93	DnaK	11168	DNAK_CAM	94.318	1.10E-20	88
			5P0083	579	HsdM (disrupted)	<i>Vibrio cholerae</i>	Q9KR74_VIB	47.03	1.80E-68	608
5a07.q	8	2062	5P0084	122	cj1343c putative periplasmic protein	11168	Q9PMV6_CA	98.36	2.20E-42	122
			5P0085	416	cj1342c hypothetical	11168	Q9PMV7_CA	60.24	7.70E-97	415
			5P0086	144	cj1341c hypothetical	11168	Q9PMV8_CA	94.44	2.10E-49	144
4h09.p	8	1368	5P0087	338	DNA methyltransferase	<i>H. pylori</i>	O25315_HEL	46	3.10E-39	313
			5P0088	112	serine-threonine protein kinase	<i>Debaryomyces hansenii</i>	Q6BHW6_DE	31.13	7.30E-04	106
6c03.q	8	1506	5P0089c	55	Glx2 putative hydrolase	11168	Q9PPB1_CA	78.182	2.90E-15	55
			5P0090	248	cj0810 Nade	11168	NADE_CAM	74.07	1.20E-59	243
			5P0091	164	cj0811 LpxK tetraacyldisaccharide kinas	11168	LPXK_CAMJ	82.31	5.90E-52	164
4g04.p	8	1892	5P0092c	271	Mu-like prophage I protein	RM1221	Q5HWR8_CA	99.26	3.80E-91	271
			5P0093c	144	hypothetical	RM1221	Q5HWR9_CA	100	6.10E-52	144
			5P0094	131	hypothetical	RM1221	Q5HWS1_CA	96.12	7.20E-51	129
6c04.p	8	1547	5P0095	515	Cmgb3/4	<i>C. jejuni</i> pTet	Q69BA6_CA	96.89	9.50E-195	515
2g11.q	8	1062	5P0096c	152	hypothetical	RM1221	Q5HVS2_CA	100	1.80E-58	152
			5P0097c	123	hypothetical	RM1221	Q5HVS4_CA	100	2.10E-49	123
8d12.p	9	2441	5P0098	412	prophage muso1 f protein	RM1221	Q5HWR1_CA	100	1.50E-148	412
			5P0099	124	phage tail protein	RM1221	Q5HWR0_CA	100	9.10E-45	124
			5P0100	140	tail protein D	RM1221	Q5HWRQ8_CA	99.28	2.80E-49	140
2c11.q	10	1275	5P0101c	63	hypothetical	RM1221	Q5HWS7_CA	98.41	8.70E-23	63
			5P0102c	210	base plate assembly protein V	RM1221	Q5HS6_CAM	98.57	4.20E-75	210
			5P0103c	86	hypothetical	no matches				
2e10.p	10	1854	5P0104c	149	hypothetical	<i>C.jejuni</i> strain rm 1221	Q8RN33_CA	97.84	1.10E-50	139
			5P0105c	391	transporter	<i>C.jejuni</i> strain rm 1221	Q5HSN2_CA	98.72	1.20E-139	391
7c10.p	11	1615	5P0106	501	hypothetical phage protein	RM1221	Q5HWR3_CA	100	7.20E-174	442
6a01.q	12	1925	5P0107c	87	cpp23	<i>C. jejuni</i> pTet	Q69BB4_CA	97.7	4.30E-30	87
			5P0108c	409	cpp22 (TraC like)	<i>C. jejuni</i> pTet	Q69BB5_CA	85.92	2.60E-128	412
2f11.q	12	2036	5P0109	298	sialic acid synthase	<i>C.jejuni</i> strain oh4384	Q9LAK2_CA	99.66	2.00E-115	298
			5P0110	374	NeuC1	<i>C.jejuni</i> strain atcc43456	Q93D03_CA	98.66	7.20E-132	374

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
5a06.p	12	3535	5P0111c	238	Cmgb3/4 (virB4)	<i>C. coli</i>	Q69BF6_CA	93.25	7.50E-87	237
			5P0112c	87	Cmgb2 (VirB2)	<i>C. jejuni</i> pTet	Q69BA7_CA	90.8	7.20E-27	87
			5P0113	107	cpp29 hypothetical	<i>C. jejuni</i> pTet	Q69BA8_CA	99.07	2.20E-41	107
			5P0114	125	virulence-associated protein d	<i>C. jejuni</i> pTet	Q69BA9_CA	98.4	1.90E-45	125
			5P0115	204	site-specific recombinase	<i>C. jejuni</i> pTet	Q69BB0_CA	99.02	1.40E-69	204
			5P0116c	286	cpp26 hypothetical	<i>C. jejuni</i> pTet	Q69BB1_CA	94.38	1.70E-97	285
7d08.q	12	2314	5P0117c	269	cj0021c hypothetical	11168	Q9PJ90_CA	85.82	1.20E-90	268
			5P0118c	298	cj0022c ribosomal pseudouridine synthase	11168	Q9PJ89_CA	82.37	2.60E-94	295
			5P0119	130	cj0023 purb	11168	Q9PJ88_CA	93.7	4.60E-41	127
1d01.q	13	2884	5P0120c	844	cpp14 hypothetical	<i>C. jejuni</i> pTet	Q69BC2_CA	99.39	0.00E+00	824
			5P0121c	88	cpp13 hypothetical	<i>C. coli</i>	Q69BH3_CA	100	1.10E-29	88
6g02.q	14	2648	5P0122c	120	cj0304c BioC	11168	Q9PIJ5_CAM	74.16	3.40E-33	120
			5P0123c	203	cj0305c hypothetical	11168	Q9PIJ4_CAM	68.47	1.10E-51	203
			5P0124c	380	cj0306c BioF	11168	Q9PIJ3_CAM	75.78	4.70E-111	380
			5P0125	156	cj0307 BioA	11168	Q9PIJ2_CAM	96.15	1.40E-60	156
2e12.p	14	3074	5P0126	198	site-specific DNA-methyltransferase	RM1221	Q5HVW9_CA	90.91	8.40E-70	198
			5P0127	117	hypothetical	RM1221	Q5HTH9_CA	100	1.17E+02	
			5P0128c	391	site-specific recombinase	RM1221	Q5HTI1_CA	100	1.60E-143	391
			5P0129c	144	hypothetical	no matches				
7h09.p	15	3530	5P0130	309	Cgta-II (disrupted)	<i>C. jejuni</i> strain atcc 43449	Q934C5_CA	99.68	5.90E-125	309
			5P0131	245	NeuA1	<i>C. jejuni</i> strain atcc 43438	Q93MP7_CA	97.28	6.80E-81	221
			5P0132	277	acetyltransferase (disrupted)	<i>C. jejuni</i> strain atcc 43446	Q9L9Q2_CA	97.83	1.10E-103	277
			5P0133c	270	WaaV	<i>C. jejuni</i> lio87	Q6T5A5_CA	95.17	2.70E-102	269
			5P0134	109	WaaF	<i>C. jejuni</i> strain nctc 11828	Q6TDC6_CA	97.96	2.90E-34	98
3e03.p	15	2697	5P0135	315	cj0259 Pycr	11168	Q9PIN6_CA	77.84	2.40E-97	316
			5P0136	576	DNA methyltransferase	RM1221	Q5HWK5_CA	97.24	6.30E-209	579
3e06.p	16	2317	5P0137	211	hypothetical	RM1221	Q5HTE9_CA	99.05	6.30E-67	211
			5P0138	127	hypothetical	RM1221	Q5HTF0_CA	97.64	1.30E-40	127
			5P0139	124	hypothetical	RM1221	Q5HVS5_CA	99.19	5.20E-52	124
			5P0140	294	hypothetical	RM1221	Q5HTF2_CA	99.66	4.50E-96	294
3c11.q	17	3353	5P0141c	51	hypothetical	no matches				
			5P0142c	704	hypothetical	<i>Helicobacter hepaticus</i>	Q7VI58_HEL	40.29	6.20E-81	752
			5P0143c	103	hypothetical	no matches				

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
1c03.q	19	3151	5P0144c	90	hypothetical	RM1221	Q5HWP9_CA	96.66	1.40E-27	90
			5P0145c	161	gam protein (phage)	<i>C. coli</i>	Q9K5D6_CA	98.75	8.90E-53	160
			5P0146c	112	hypothetical	<i>C. coli</i>	Q9K5D7_CA	94.64	5.80E-37	112
			5P0147c	143	hypothetical	no matches				
			5P0148c	242	hypothetical	<i>Helicobacter hepaticus</i>	Q7VI56_HEL	48.73	5.60E-36	236
8g04.q	21	2356	5P0149c	130	phage terminase	RM1221	Q5HTC7_CA	98.46	8.90E-40	130
			5P0150c	113	HNH endonuclease domain protein	RM1221	Q5HTC6_CA	92.04	3.90E-41	113
			5P0151c	96	hypothetical	RM1221	Q5HTC5_CA	100	2.10E-37	96
			5P0152	174	hypothetical	no matches				
5e02.q	23	2304	5P0153	297	Cmgb5 (virB5)	<i>C. jejuni</i> pTet	Q69BA1_CA	98.65	1.90E-98	297
			5P0154	332	Cmgb6 (virB6)	<i>C. coli</i>	Q69BF0_CA	85.46	3.60E-98	330
			5P0155	55	Cmgb7 (virB7)	<i>C. jejuni</i> pTet	Q69B99_CA	100	8.50E-23	55
			5P0156	89	Cmgb8 (virB8)	<i>C. jejuni</i> pTet	Q847A8_CA	100	2.30E-31	89
3g09.q	24	4636	5P0157c	110	hypothetical	RM1221	Q5HWQ0_CA	100	5.30E-43	110
			5P0158c	90	hypothetical	RM1221	Q5HWP9_CA	100	1.90E-28	90
			5P0159c	161	gam protein	RM1221	Q5HWP7_CA	100	3.70E-53	161
			5P0160c	113	hypothetical	<i>C. coli</i> plasmid pBT9810	Q9K5D7_CA	95.57	2.30E-38	113
			5P0161c	307	DNA transposition protein B	RM1221	Q5HWP3_CA	97.07	1.40E-103	307
			5P0162c	419	DNA transposition protein A	RM1221	Q5HWP2_CA	97.85	1.40E-145	419
3b02.p	24	2873	5P0163	730	Cpp49 (VirB8)	<i>C. coli</i>	Q69BD8_CA	98.77	0.00E+00	730
			5P0164	141	Cpp50 hypothetical	<i>C. coli</i>	Q69BD7_CA	100	5.00E-50	141
5d09.p	28	2775	5P0165c	617	TetO	<i>C. jejuni</i> pTet	Q69BD5_CA	99.83	0.00E+00	617
			5P0166c	59	hypothetical Cpp51	<i>C. coli</i>	Q69BD6_CA	100	5.90E+01	
			5P0167c	113	hypothetical Cpp50	<i>C. coli</i>	Q69BD7_CA	100	2.20E-38	112
2f06.p	39	6771	5P0168	198	Cpp18 hypothetical	<i>C. coli</i>	Q69BG8_CA	100	2.40E-54	183
			5P0169	462	(cpp17) nickase MagA2	<i>C. coli</i>	Q69BG9_CA	98.92	2.10E-164	462
			5P0170	234	Cpp16 hypothetical	<i>C. coli</i>	Q69BH0_CA	100	8.00E-93	234
			5P0171c	242	Cpp15 hypothetical	<i>C. coli</i>	Q69BH1_CA	100	1.80E-90	242
			5P0172c	1057	Cpp14 hypothetical	<i>C. coli</i>	Q69BH2_CA	100	0.00E+00	1054
3c07.q	41	5026	5P0173	206	Virb9-like protein	<i>C. jejuni</i> plasmid pCjA13	Q847A7_CA	100	1.90E-76	206
			5P0174	398	Cmgb10 (VirB10)	<i>C. jejuni</i> pTet	Q69B96_CA	100	1.00E-143	398
			5P0175	330	Virb11-like protein	<i>C. jejuni</i> pTet	Q69B95_CA	100	4.40E-119	348
			5P0176	603	MagB12 (virD4)	<i>C. jejuni</i> pTet	Q69B94_CA	100	0.00E+00	603
			5P0177	145	Cpp44 cag island protein	<i>C. jejuni</i> pTet	Q69B93_CA	100	2.70E-54	145

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7c07.p	43	4998	5P0178c	62	hypothetical	RM1221	Q5HTG6_CA	95.16	4.10E-20	62
			5P0179c	95	hypothetical	RM1221	Q5HTG5_CA	100	5.10E-37	95
			5P0180c	244	dna binding protein Roi	RM1221	Q5HTG4_CA	97.54	6.80E-76	244
			5P0181c	94	hypothetical	RM1221	Q5HTG3_CA	95.75	1.10E-26	94
			5P0182	130	hypothetical	no matches				
			5P0183	105	hypothetical	no matches				
			5P0184	326	hypothetical	<i>Lactobacillus johnsonii</i>	Q74HW8_LA	30.2	2.00E-13	308
			5P0185	206	hypothetical	no matches				
			5P0186	71	hypothetical	no matches				
7f04.p	48	6568	5P0187c	740	tail tape measure protein	RM1221	Q5HWU0_CA	98.92	0	738
			5P0188	108	hypothetical	RM1221	Q5HWT9_CA	98.15	1.20E-37	108
			5P0189c	104	hypothetical	RM1221	Q5HWT7_CA	100	4.80E-23	79
			5P0190c	169	major tail tube protein	RM1221	Q5HWt6_CA	100	1.10E-60	169
			5P0191c	397	major tail sheath protein	RM1221	Q5HWT5_CA	98.24	7.30E-147	397
			5P0192c	335	hypothetical protein	RM1221	Q5HWT4_CA	94.93	1.70E-120	335
			5P0193c	128	hypothetical	RM1221	Q5HWT3_CA	90.08	8.70E-47	121
			5P0194c	104	hypothetical	RM1221	Q5HWT2_CA	95.15	5.00E-37	103
7b11.p	55	5186	5P0195	104	hypothetical	RM1221	Q5HWS5_CA	98.08	8.20E-34	104
			5P0196	508	hypothetical	Bacteriophage D3112	Q6TM76_BP	29.48	1.50E-22	502
			5P0197	460	hypothetical	<i>Shewanella oneidensis</i>	Q8EDR3_SH	21.27	1.60E-08	470
			5P0198	377	prophage muso1 F protein	RM1221	Q5HWR1_CA	27.67	8.40E-20	365
			5P0199c	167	phage virion morphogenesis protein	RM1221	Q5HWU1_CA	28.74	1.20E-04	167
5g07.q	51	7892	5P0200	81	hypothetical	no matches				
			5P0201c	160	phage virion morphogenesis protein	RM1221	Q5HWU1_CA	28.57	8.50E-05	168
			5P0202c	142	hypothetical	no matches				
			5P0203c	86	hypothetical	no matches				
			5P0204c	128	hypothetical	RM1221	Q5HWQ0_CA	100	4.00E-50	128
			5P0205c	90	hypothetical	RM1221	Q5HWP9_CA	98.89	5.20E-28	90
			5P0206c	161	host-nuclease inhibitor protein gam	RM1221	Q5HWP7_CA	100	3.70E-53	161
			5P0207c	112	hypothetical	<i>C. coli</i>	Q9K5D7_CA	94.64	5.80E-37	112
			5P0208c	143	hypothetical	no matches				
			5P0209c	285	transposition protein	<i>Helicobacter hepaticus</i>	Q7VI56_HEL	46.02	1.00E-41	289
			5P0210c	705	DNA transposition protein A	RM1221	Q5HWP2_CA	27.14	1.10E-17	689

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2b12.p	82	9176	5P0211c	113	hypothetical	RM1221	Q5HWS2_CA	97.35	1.10E-36	113	
			5P0212c	129	hypothetical	RM1221	Q5HWS1_CA	99.23	3.00E-52	129	
			5P0213c	121	hypothetical		no matches				
			5P0214c	117	hypothetical		no matches				
			5P0215c	89	hypothetical		no matches				
			5P0216c	295	major head subunit		Bacteriophage D3112	Q6TM67_BP	35.59	1.50E-14	295
			5P0217c	346	hypothetical		no matches				
			5P0218	154	hypothetical		no matches				
			5P0219	210	baseplate assembly protein V		RM1221	Q5HWS6_CA	99.52	4.60E-76	210
			5P0220	63	hypothetical		RM1221	Q5HWS7_CA	98.41	8.70E-23	63
			5P0221	96	baseplate assembly protein w		<i>C. coli</i>	Q9K5E0_CA	97.92	7.10E-34	96
			5P0222	388	baseplate assembly protein J		RM1221	Q5HWS9_CA	99.49	1.50E-129	388
			5P0223	206	phage tail protein		RM1221	Q5HWT0_CA	93.69	7.90E-72	206
			5P0224	343	tail fibre protein H		RM1221	Q5HWT1_CA	75.29	8.90E-80	340
			5P0225	168	hypothetical		RM1221	Q5HWT2_CA	95.83	3.20E-56	168
			5P0226	69	hypothetical		RM1221	Q5HWT3_CA	98.55	9.00E-29	69
			4h04.p	102	8165	5P0227c	107	hypothetical	RM1221	Q5HTE8_CA	97.26
5P0228c	521	hypothetical				RM1221	Q5HTE7_CA	99.62	1.30E-167	521	
5P0229c	210	hypothetical				RM1221	Q5HTE6_CA	99.52	6.20E-67	210	
5P0230c	107	phage head-tail adaptor					RM1221	Q5HTE5_CA	100	6.40E-39	105
5P0231c	145	hypothetical					RM1221	Q5HTE4_CA	100	1.60E-37	104
5P0232c	83	hypothetical					RM1221	Q5HTE2_CA	100	7.90E-25	83
5P0233c	388	major capsid protein, hk97 family					RM1221	Q5HTE1_CA	100	4.00E-136	388
5P0234c	185	hypothetical					RM1221	Q5HTE0_CA	100	3.50E-64	185
5P0235c	289	hypothetical					RM1221	Q5HTD9_CA	100	7.20E-119	289
5P0236c	639	hypothetical					RM1221	Q5HTD8_CA	99.53	5.30E-185	639

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7e05.p	124	10407	5P0237	67	phage terminase, small subunit	RM1221	Q5HTC7_CA	83.08	4.30E-17	65
			5P0238	541	phage terminase, large subunit	RM1221	Q5HTC8_CA	100	0.00E+00	541
			5P0239	144	toxin-antitoxin protein	RM1221	Q5HTC9_CA	98.61	1.20E-51	144
			5P0240	390	portal protein, hk97 family	RM1221	Q5HTD0_CA	100	1.20E-143	390
			5P0241	188	phage protein, hk97 gp10 family	RM1221	Q5HTD1_CA	100	7.90E-61	180
			5P0242	116	hypothetical	RM1221	Q5HTD2_CA	99.14	7.50E-39	116
			5P0243	326	hypothetical	RM1221	Q5HTD3_CA	99.39	7.20E-114	326
			5P0244	118	hypothetical	RM1221	Q5HTD4_CA	100	2.10E-37	118
			5P0245	71	hypothetical	RM1221	Q5HTD5_CA	100	1.80E-25	71
			5P0246	124	hypothetical	RM1221	Q5HTD7_CA	97.67	7.30E-13	43
5P0247	1224	hypothetical	RM1221	Q5HTD8_CA	94.2		0	1224		
3b03.q	175	15477	5P0248	222	phage repressor protein	RM1221	Q5HWU7_CA	97.61	8.90E-79	209
			5P0249	106	hypothetical protein	RM1221	Q5HWU6_CA	97.17	1.10E-31	106
			5P0250	95	hypothetical	RM1221	Q5HWU3_CA	96.67	5.80E-18	60
			5P0251c	276	dam DNA adenine methylase	RM1221	Q5HWU2_CA	98.52	1.30E-103	271
			5P0252c	322	tail protein d	RM1221	Q5HWQ8_CA	47.1	2.50E-49	327
			5P0253c	124	phage tail protein	RM1221	Q5HWR0_CA	57.26	2.50E-25	124
			5P0254c	654	tail tape measure protein, tp901 family	RM1221	Q5HWU0_CA	26.06	4.70E-22	765
			5P0255c	78	hypothetical	RM1221	Q5HWT7_CA	31.51	1.30E-02	73
			5P0256c	171	major tail tube protein	RM1221	Q5HWT6_CA	41.92	1.90E-20	167
			5P0257c	396	major tail sheath protein	RM1221	Q5HWT5_CA	96.97	2.10E-144	396
			5P0258c	337	hypothetical	RM1221	Q5HWT4_CA	98.52	2.20E-123	337
			5P0259c	123	hypothetical	RM1221	Q5HWT3_CA	98.37	4.80E-52	123
			5P0260c	168	hypothetical	RM1221	Q5HWT2_CA	95.83	1.20E-55	168
			5P0261c	343	tail fiber protein H	RM1221	Q5HWT1_CA	75.59	1.60E-80	340
			5P0262c	206	tail protein	RM1221	Q5HWT0_CA	91.26	3.30E-70	206
			5P0263c	388	baseplate assembly protein J	RM1221	Q5HWS9_CA	98.2	6.90E-129	388
			5P0264c	96	baseplate assembly protein W	<i>C. coli</i>	Q9K5E0_CA	97.92	5.10E-35	96
5P0265c	63	hypothetical	RM1221	Q5HWS7_CA	100	3.70E-23	63			
5P0266c	210	baseplate assembly protein V	RM1221	Q5HWS6_CA	99.05	3.10E-76	210			
5P0267c	104	hypothetical	RM1221	Q5HWS5_CA	100	2.40E-34	104			
7h10.p	1	717	5P0268	237	Cst-II, alpha-2,3-sialyltransferase	<i>C. jejuni</i> strain 43432	Q9F0M9_CA	95.28	6.20E-91	233
5h05.p	1	781	5P0269	60	cj0168c periplasmic protein	11168	Q9PIW0_CA	90	3.10E-16	60
			5P0270	23	cj0167c integral membrane protein	11168	Y167_CAMJ	95.65	8.50E-10	23
6e09.p	1	510	5P0271	144	cj1624c sdaa L-serine dehydratase	11168	Q9PM51_CA	96.52	7.90E-52	144
7h07.p	1	689	5P0272c	52	hmcd domain protein	RM1221	Q5HXA6_CA	94	1.70E-17	50
			5P0273	126	hypothetical	RM1221	Q5HXA8_CA	96.15	1.60E-14	52
						Q5HXA7_CA	57.38	3.20E-06	61	

contig	no. of reads	length/ bp	systematic_id	length in aa	match	organism with match	swall	% id (aa)	e-value	no. of aa in match
7h08.q	1	438	5P0274c	145	tail protein d	RM1221	Q5HWQ8_CA	97.86	4.70E-49	140
6b02.q	1	678	5P0275c	157	hypothetical cpp32	<i>C. coli</i>	Q69BF5_CA	67.68	6.10E-36	164
			5P0276c	64	cmgb3/4	<i>C. coli</i>	Q69BF6_CA	93.75	2.60E-18	64
5g10.q	1	752	5P0277c	88	Bll0816 protein (propionate catabolism?)	<i>Bradyrhizobium japonicum</i>	Q89W77	40	2.10E-05	85
			5P0278c	158	cj1394 fumarate lyase	11168	Q9PMR1_CA	94.93	7.30E-52	158
7e10.q	1	272	5P0279	50	type I RM fragment	uncultured Archaeon	Q64AS4_9AF	33.8	6.40E-04	71
5d06.q	1	22			no predicted CDSs					
1b11.p	1	107			no predicted CDSs					
6h07.q	1	32			no predicted CDSs					
1d11.p	1	430			no predicted CDSs					
1f11.p	1	206			no predicted CDSs					
5c01.q	1	47			no predicted CDSs					
6b11.p	1	30			no predicted CDSs					
6d11.p	1	326			no predicted CDSs					
4c05.p	1	302			no predicted CDSs					
5f01.p	1	252			no predicted CDSs					