

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 CjeI	<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	swall	% 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	swall	% 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	31
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	Bll0816 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