

## 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				