

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	FiaB	<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					