

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 kinase	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	Q5HWR8_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

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
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

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	
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

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
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					