

Supplemental Table 1. ORF identification of FCL-2 genes.

ORF	Start	End	Length	Putative function	Best hit	Number of hits (max 100)	E-value, Score, Bitscore, Identities
orf00001	18	725	708	Hypothetical protein	hypothetical protein [Muricauda sp. MAR_2010_75]	3	E-value = 4.04e-26, Score = 279, Bitscore = 112.079, Identities = 71/222 (31%)
orf00002	805	1,008	204	NO RESULTS			
orf00003	1,015	1,275	261	NO RESULTS			
orf00004	1,288	3,327	2,040	Terminase	phage terminase [Cellulophaga phage phiSM] >gi 451988688 gb AGF91164.1 terminase [Cellulophaga phage phi3:1] >gi 451989197 gb AGF91668.1 terminase large subunit [Cellulophaga phage phi47:1] >gi 460109484 gb AGH07751.1 phage terminase [Cellulophaga phage phiSM] >gi 514341476 gb AGO47735.1 phage terminase large subunit [Cellulophaga phage phi3ST:2] >gi 514341946 gb AGO48199.1 phage terminase large subunit [Cellulophaga phage phiSM] >gi 514343005 gb AGO49243.1 phage terminase large subunit [Cellulophaga phage phi38:2] >gi 514343086 gb AGO49323.1 phage terminase large subunit [Cellulophaga phage phi3:1] >gi 514343509 gb AGO49741.1 phage terminase large subunit [Cellulophaga phage phi47:1]	100	E-value = 0, Score = 1501, Bitscore = 582.793, Identities = 294/680 (43%)
orf00005	3,424	3,828	405	NO RESULTS			
orf00006	3,825	4,148	324	Hypothetical protein	hypothetical protein [Flavobacterium columnare] >gi 365960115 ref YP_004941682.1 hypothetical protein FCOL_05320 [Flavobacterium columnare ATCC 49512] >gi 365736796 gb AEW85889.1 hypothetical protein FCOL_05320 [Flavobacterium columnare ATCC 49512]	8	E-value = 3.61e-59, Score = 479, Bitscore = 189.119, Identities = 92/107 (85%)
orf00007	4,145	5,356	1,212	Hypothetical protein	hypothetical protein [Flavobacterium columnare] >gi 365960113 ref YP_004941680.1 hypothetical protein FCOL_05310 [Flavobacterium columnare ATCC 49512] >gi 365736794 gb AEW85887.1 hypothetical protein FCOL_05310 [Flavobacterium columnare ATCC 49512]	100	E-value = 6.89e-165, Score = 1238, Bitscore = 481.485, Identities = 241/391 (61%)
orf00008	5,340	5,894	555	Hypothetical protein (IbrB)	nuclease [Flavobacterium psychrophilum] >gi 150024891 ref YP_001295717.1 Protein of unknown function IbrB [Flavobacterium psychrophilum JIP02/86] >gi 526120163 ref YP_008320442.1 hypothetical protein [Flavobacterium phase 6H] >gi 149771432 emb CAL42901.1 Protein of unknown function IbrB [Flavobacterium psychrophilum JIP02/86] >gi 511624410 gb AGN89411.1 hypothetical protein [Flavobacterium phase 6H] >gi 697783246 gb AIT65708.1 chromosome partitioning protein ParB [Flavobacterium psychrophilum]	100	E-value = 1.05e-111, Score = 841, Bitscore = 328.561, Identities = 158/179 (88%)
orf00009	5,876	7,009	1,134	Hypothetical protein (IbrA)	hypothetical protein [Flavobacterium psychrophilum] >gi 150024890 ref YP_001295716.1 Protein of unknown function IbrA [Flavobacterium psychrophilum JIP02/86] >gi 149771431 emb CAL42900.1 Protein of unknown function IbrA [Flavobacterium psychrophilum JIP02/86] >gi 697783245 gb AIT65707.1 hypothetical protein IB65_07475 [Flavobacterium psychrophilum]	100	E-value = 0, Score = 1601, Bitscore = 621.313, Identities = 296/380 (77%)
orf00010	7,161	7,454	294	Hypothetical protein	hypothetical protein [Muricauda sp. MAR_2010_75]	2	E-value = 4.63e-12, Score = 162, Bitscore = 67.0106, Identities = 35/91 (38%)
orf00011	7,472	9,085	1,614	Phage portal protein	phage portal protein [Cellulophaga phage phiSM] >gi 460109486 gb AGH07753.1 phage portal protein [Cellulophaga phage phiSM] >gi 514341478 gb AGO47737.1 phage portal protein [Cellulophaga phage phi3ST:2] >gi 514341948 gb AGO48201.1 phage portal protein [Cellulophaga phage phiSM] >gi 514343007 gb AGO49245.1 phage portal protein [Cellulophaga phage phi38:2] >gi 514343088 gb AGO49325.1 phage portal protein [Cellulophaga phage phi3:1] >gi 514343511 gb AGO49743.1 phage portal protein [Cellulophaga phage phi47:1]	100	E-value = 1.53e-133, Score = 1056, Bitscore = 411.379, Identities = 210/494 (42%)
orf00012	9,099	9,332	234	NO RESULTS			
orf00013	9,439	9,564	126	NO RESULTS			
orf00014	9,566	9,865	300	Hypothetical protein	hypothetical protein P2559Y_0020 [Croceibacter phage P2559Y] >gi 505838236 gb AGM14083.1 hypothetical protein P2559Y_0020 [Croceibacter phage P2559Y]	1	E-value = 6.82e-03, Score = 97, Bitscore = 41.9726, Identities = 30/84 (35%)
orf00015	9,849	10,190	342	Hypothetical protein	hypothetical protein P2559Y_0021 [Croceibacter phage P2559Y] >gi 505838237 gb AGM14084.1 hypothetical protein P2559Y_0021 [Croceibacter phage P2559Y]	1	E-value = 1.99e-10, Score = 151, Bitscore = 62.7734, Identities = 29/62 (46%)
orf00016	10,195	10,659	465	Hypothetical protein	hypothetical protein [Sediminibacter sp. Hel_I_10]	100	E-value = 2.96e-75, Score = 594, Bitscore = 233.417, Identities = 104/151 (68%)

orf00017	10,662	11,006	345	Hypothetical protein	hypothetical protein PHG11b_30 [Flavobacterium phage 11b] >gi 53748196 emb CAH56657.1 hypothetical protein PHG11b_30 [Flavobacterium phage 11b]	2	E-value = 1.07e-11, Score = 162, Bitscore = 67.0106, Identities = 41/111 (36%)
orf00018	11,171	11,413	243	NO RESULTS			
orf00019	11,415	11,798	384	Hypothetical protein	hypothetical protein Phi18:1_gp65 [Cellulophaga phage phi18:1] >gi 514342263 gb AGO48512.1 hypothetical protein Phi18:1_gp65 [Cellulophaga phage phi18:1] >gi 514342986 gb AGO49226.1 hypothetical protein Phi18:2_gp63 [Cellulophaga phage phi18:2]	3	E-value = 1.46e-02, Score = 98, Bitscore = 42.3578, Identities = 31/77 (40%)
orf00020	12,063	13,325	1,263	Protease	hypothetical protein CEPG_00014 [Cellulophaga phage phiSM] >gi 451989184 gb AGF91655.1 hypothetical protein CDPG_00051 [Cellulophaga phage phi47:1] >gi 460109495 gb AGH07762.1 hypothetical protein CEPG_00014 [Cellulophaga phage phiSM] >gi 514341487 gb AGO47746.1 Clp protease [Cellulophaga phage phi3ST:2] >gi 514341957 gb AGO48210.1 Clp protease [Cellulophaga phage phiSM] >gi 514343016 gb AGO49254.1 Clp protease [Cellulophaga phage phi38:2] >gi 514343097 gb AGO49334.1 Clp protease [Cellulophaga phage phi3:1] >gi 514343520 gb AGO49752.1 Clp protease [Cellulophaga phage phi47:1]	100	E-value = 1.05e-135, Score = 1048, Bitscore = 408.297, Identities = 217/424 (51%)
orf00021	13,338	13,793	456	Hypothetical protein	hypothetical protein CEPG_00015 [Cellulophaga phage phiSM] >gi 451989183 gb AGF91654.1 hypothetical protein CDPG_00050 [Cellulophaga phage phi47:1] >gi 460109496 gb AGH07763.1 hypothetical protein CEPG_00015 [Cellulophaga phage phiSM] >gi 514341488 gb AGO47747.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514341958 gb AGO48211.1 structural protein [Cellulophaga phage phiSM] >gi 514343017 gb AGO49255.1 structural protein [Cellulophaga phage phi38:2] >gi 514343098 gb AGO49335.1 structural protein [Cellulophaga phage phi3:1] >gi 514343521 gb AGO49753.1 structural protein [Cellulophaga phage phi47:1]	2	E-value = 2.91e-23, Score = 247, Bitscore = 99.7525, Identities = 53/141 (37%)
orf00022	13,796	14,878	1,083	Hypothetical protein	hypothetical protein CEPG_00016 [Cellulophaga phage phiSM] >gi 460109497 gb AGH07764.1 hypothetical protein CEPG_00016 [Cellulophaga phage phiSM]	58	E-value = 5.90e-143, Score = 1084, Bitscore = 422.165, Identities = 199/354 (56%)
orf00023	14,878	15,042	165	NO RESULTS			
orf00024	15,057	15,440	384	Structural protein	hypothetical protein CEPG_00018 [Cellulophaga phage phiSM] >gi 451988698 gb AGF91174.1 hypothetical protein CHPG_00022 [Cellulophaga phage phi3:1] >gi 451989180 gb AGF91651.1 hypothetical protein CDPG_00047 [Cellulophaga phage phi47:1] >gi 460109499 gb AGH07766.1 hypothetical protein CEPG_00018 [Cellulophaga phage phiSM] >gi 514341491 gb AGO47750.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514341961 gb AGO48214.1 structural protein [Cellulophaga phage phiSM] >gi 514343020 gb AGO49258.1 structural protein [Cellulophaga phage phi38:2] >gi 514343101 gb AGO49338.1 structural protein [Cellulophaga phage phi3:1] >gi 514343524 gb AGO49756.1 structural protein [Cellulophaga phage phi47:1]	2	E-value = 1.57e-34, Score = 319, Bitscore = 127.487, Identities = 58/126 (46%),
orf00025	15,437	16,042	606	Hypothetical protein	hypothetical protein [Muricauda sp. MAR_2010_75]	5	E-value = 3.72e-39, Score = 363, Bitscore = 144.436, Identities = 78/199 (39%)
orf00026	16,048	17,568	1,521	Tail sheath protein	tail protein [Cellulophaga phage phiSM] >gi 451989178 gb AGF91649.1 tail protein [Cellulophaga phage phi47:1] >gi 460109501 gb AGH07768.1 tail protein [Cellulophaga phage phiSM] >gi 514341493 gb AGO47752.1 tail sheat protein [Cellulophaga phage phi3ST:2] >gi 514341963 gb AGO48216.1 tail sheat protein [Cellulophaga phage phiSM] >gi 514343022 gb AGO49260.1 tail sheat protein [Cellulophaga phage phi38:2] >gi 514343103 gb AGO49340.1 tail sheat protein [Cellulophaga phage phi3:1] >gi 514343526 gb AGO49758.1 tail sheat protein [Cellulophaga phage phi47:1]	100	E-value = 0, Score = 1638, Bitscore = 635.565, Identities = 312/508 (61%)
orf00027	17,589	17,999	411	Structural protein	hypothetical protein CEPG_00021 [Cellulophaga phage phiSM] >gi 451988704 gb AGF91180.1 hypothetical protein CHPG_00028 [Cellulophaga phage phi3:1] >gi 451989177 gb AGF91648.1 hypothetical protein CDPG_00044 [Cellulophaga phage phi47:1] >gi 460109502 gb AGH07769.1 hypothetical protein CEPG_00021 [Cellulophaga phage phiSM] >gi 514341494 gb AGO47753.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514343023 gb AGO49261.1 structural protein [Cellulophaga phage phi38:2] >gi 514343104 gb AGO49341.1 structural protein [Cellulophaga phage phi3:1] >gi 514343527 gb AGO49759.1 structural protein [Cellulophaga phage phi47:1]	4	E-value = 1.36e-44, Score = 388, Bitscore = 154.066, Identities = 70/136 (51%)
orf00028	18,055	18,471	417	Hypothetical protein	hypothetical protein [Muricauda sp. MAR_2010_75]	1	E-value = 8.94e-06, Score = 121, Bitscore = 51.2174, Identities = 41/140 (29%)
orf00029	18,719	20,548	1,83	Hypothetical protein	hypothetical protein [Riemerella anatipestifer] >gi 407452085 ref YP_006723810.1 hypothetical protein B739_1312 [Riemerella anatipestifer RA-CH-1] >gi 403313069 gb AFR35910.1 hypothetical protein B739_1312 [Riemerella anatipestifer RA-CH-1]	100	E-value = 1.11e-44, Score = 462, Bitscore = 182.57, Identities = 118/348 (33%)

orf00030	20,564	21,043	480	Hypothetical protein	hypothetical protein CEPG_00025 [Cellulophaga phage phiSM] >gi 451989173 gb AGF91644.1 hypothetical protein CDPG_00040 [Cellulophaga phage phi47:1] >gi 460109506 gb AGH07773.1 hypothetical protein CEPG_00025 [Cellulophaga phage phiSM] >gi 514341498 gb AGO47757.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514341968 gb AGO48221.1 structural protein [Cellulophaga phage phiSM] >gi 514343027 gb AGO49265.1 structural protein [Cellulophaga phage phi38:2] >gi 514343108 gb AGO49345.1 structural protein [Cellulophaga phage phi3:1] >gi 514343531 gb AGO49763.1 structural protein [Cellulophaga phage phi47:1]	3	E-value = 3.86e-48, Score = 416, Bitscore = 164.851, Identities = 82/158 (51%)
orf00031	21,049	22,224	1,176	Baseplate J-like protein	hypothetical protein CEPG_00026 [Cellulophaga phage phiSM] >gi 451989172 gb AGF91643.1 hypothetical protein CDPG_00039 [Cellulophaga phage phi47:1] >gi 460109507 gb AGH07774.1 hypothetical protein CEPG_00026 [Cellulophaga phage phiSM] >gi 514341499 gb AGO47758.1 baseplate J-like protein [Cellulophaga phage phi3ST:2] >gi 514341969 gb AGO48222.1 baseplate J-like protein [Cellulophaga phage phiSM] >gi 514343028 gb AGO49266.1 baseplate J-like protein [Cellulophaga phage phi38:2] >gi 514343109 gb AGO49346.1 baseplate J-like protein [Cellulophaga phage phi3:1] >gi 514343532 gb AGO49764.1 baseplate J-like protein [Cellulophaga phage phi47:1]	100	E-value = 1.61e-140, Score = 1074, Bitscore = 418.313, Identities = 215/390 (55%)
orf00032	22,229	23,008	780	Tail protein	hypothetical protein CEPG_00027 [Cellulophaga phage phiSM] >gi 451989171 gb AGF91642.1 hypothetical protein CDPG_00038 [Cellulophaga phage phi47:1] >gi 460109508 gb AGH07775.1 hypothetical protein CEPG_00027 [Cellulophaga phage phiSM] >gi 514341500 gb AGO47759.1 putative tail protein [Cellulophaga phage phi3ST:2] >gi 514341970 gb AGO48223.1 putative tail protein [Cellulophaga phage phiSM] >gi 514343029 gb AGO49267.1 putative tail protein [Cellulophaga phage phi38:2] >gi 514343110 gb AGO49347.1 putative tail protein [Cellulophaga phage phi3:1] >gi 514343533 gb AGO49765.1 putative tail protein [Cellulophaga phage phi47:1]	29	E-value = 4.73e-79, Score = 640, Bitscore = 251.136, Identities = 121/253 (47%)
orf00033	23,031	24,077	1,047	Structural protein	hypothetical protein CEPG_00028 [Cellulophaga phage phiSM] >gi 451988684 gb AGF91160.1 hypothetical protein CHPG_00008 [Cellulophaga phage phi3:1] >gi 451989170 gb AGF91641.1 hypothetical protein CDPG_00037 [Cellulophaga phage phi47:1] >gi 460109509 gb AGH07776.1 hypothetical protein CEPG_00028 [Cellulophaga phage phiSM] >gi 514341501 gb AGO47760.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514341971 gb AGO48224.1 structural protein [Cellulophaga phage phiSM] >gi 514343030 gb AGO49268.1 structural protein [Cellulophaga phage phi38:2] >gi 514343111 gb AGO49348.1 structural protein [Cellulophaga phage phi3:1] >gi 514343534 gb AGO49766.1 structural protein [Cellulophaga phage phi47:1]	6	E-value = 5.66e-58, Score = 515, Bitscore = 202.986, Identities = 108/241 (44%)
orf00034	24,081	25,250	1,17	Hypothetical protein	hypothetical protein [Muricauda sp. MAR_2010_75]	5	E-value = 2.84e-66, Score = 578, Bitscore = 227.254, Identities = 138/395 (34%)
orf00035	25,247	25,906	660	Structural protein	hypothetical protein CDPG_00035 [Cellulophaga phage phi47:1] >gi 514341503 gb AGO47762.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514341973 gb AGO48226.1 structural protein [Cellulophaga phage phiSM] >gi 514343032 gb AGO49270.1 structural protein [Cellulophaga phage phi38:2] >gi 514343113 gb AGO49350.1 structural protein [Cellulophaga phage phi3:1] >gi 514343536 gb AGO49768.1 structural protein [Cellulophaga phage phi47:1]	5	E-value = 2.76e-36, Score = 349, Bitscore = 139.043, Identities = 94/249 (37%)
orf00036	25,903	27,117	1,215	Structural protein	hypothetical protein CEPG_00032 [Cellulophaga phage phiSM] >gi 451989167 gb AGF91638.1 hypothetical protein CDPG_00034 [Cellulophaga phage phi47:1] >gi 460109513 gb AGH07780.1 hypothetical protein CEPG_00032 [Cellulophaga phage phiSM] >gi 514341504 gb AGO47763.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514341974 gb AGO48227.1 structural protein [Cellulophaga phage phiSM] >gi 514343033 gb AGO49271.1 structural protein [Cellulophaga phage phi38:2] >gi 514343114 gb AGO49351.1 structural protein [Cellulophaga phage phi3:1] >gi 514343537 gb AGO49769.1 structural protein [Cellulophaga phage phi47:1]	7	E-value = 6.66e-87, Score = 720, Bitscore = 281.952, Identities = 160/409 (39%)
orf00037	27,120	28,166	1,047	Tail protein	hypothetical protein CEPG_00033 [Cellulophaga phage phiSM] >gi 451989166 gb AGF91637.1 tail protein [Cellulophaga phage phi47:1] >gi 460109514 gb AGH07781.1 hypothetical protein CEPG_00033 [Cellulophaga phage phiSM] >gi 514341505 gb AGO47764.1 putative tail protein [Cellulophaga phage phi3ST:2] >gi 514341975 gb AGO48228.1 putative tail protein [Cellulophaga phage phiSM] >gi 514343034 gb AGO49272.1 putative tail protein [Cellulophaga phage phi38:2] >gi 514343115 gb AGO49352.1 putative tail protein [Cellulophaga phage phi3:1] >gi 514343538 gb AGO49770.1 putative tail protein [Cellulophaga phage phi47:1]	100	E-value = 6.05e-83, Score = 682, Bitscore = 267.314, Identities = 142/336 (42%)
orf00038	28,169	28,657	489	Hypothetical protein	hypothetical protein CHPG_00033 [Cellulophaga phage phi3:1] >gi 451989165 gb AGF91636.1 hypothetical protein CDPG_00032 [Cellulophaga phage phi47:1] >gi 514341506 gb AGO47765.1 structural protein [Cellulophaga phage phi3ST:2] >gi 514341976 gb AGO48229.1 structural protein [Cellulophaga phage phiSM] >gi 514343035 gb AGO49273.1 structural protein [Cellulophaga phage phi38:2] >gi 514343116 gb AGO49353.1 structural protein [Cellulophaga phage phi3:1] >gi 514343539 gb AGO49771.1 structural protein [Cellulophaga phage phi47:1]	10	E-value = 9.54e-20, Score = 225, Bitscore = 91.2781, Identities = 47/124 (37%)

orf00039	28,817	29,059	243	Hypothetical protein	PREDICTED: kinesin-like protein KIF21B isoform X6 [Esox lucius]	18	E-value = 3.91e-02, Score = 97, Bitscore = 41.9726, Identities = 20/47 (42%)
orf00040	29,203	29,499	297	Hypothetical protein	hypothetical protein Phi19:3_gp062 [Cellulophaga phage phi19:3] >gi 514341204 gb AGO47466.1 hypothetical protein Phi19:3_gp062 [Cellulophaga phage phi19:3]	3	E-value = 2.29e-08, Score = 139, Bitscore = 58.151, Identities = 33/94 (35%)
orf00041	29,663	29,959	297	Hypothetical protein	hypothetical protein [Hassallia byssoides] >gi 746975558 gb KIF32209.1 hypothetical protein P195_39980 [Hassallia byssoides VB512170]	1	E-value = 1.31e-02, Score = 100, Bitscore = 43.1282, Identities = 28/97 (28%)
orf00042	30,066	30,302	237	NO RESULTS			
orf00043	30,305	30,565	261	NO RESULTS			
orf00044	30,568	30,753	186	NO RESULTS			
orf00045	30,773	31,933	1,161	Hypothetical protein	hypothetical protein [Leeuwenhoekiella sp. Hel_1_48]	3	E-value = 2.19e-33, Score = 350, Bitscore = 139.428, Identities = 110/320 (34%)
orf00046	31,936	32,304	369	NO RESULTS			
orf00047	32,318	33,073	756	Hypothetical protein	hypothetical protein, partial [Clostridium sp. K25]	100	E-value = 6.52e-63, Score = 530, Bitscore = 208.764, Identities = 108/218 (49%)
orf00048	33,060	33,413	354	Hypothetical protein	nucleoside triphosphate pyrophosphohydrolase, MazG [Cellulophaga phage phi19:3] >gi 514341214 gb AGO47476.1 nucleoside triphosphate pyrophosphohydrolase, MazG [Cellulophaga phage phi19:3]	100	E-value = 1.43e-22, Score = 237, Bitscore = 95.9005, Identities = 50/115 (43%)
orf00049	33,478	33,615	138	NO RESULTS			
orf00050	33,615	34,358	744	Hypothetical protein	hypothetical protein, partial [Chryseobacterium daeguense]	1	E-value = 1.71e-03, Score = 113, Bitscore = 48.1358, Identities = 48/173 (27%)
orf00051	34,351	36,876	2,526	DNA methylase	DNA methylase N-4 [Treponema sp. OM2 838]	100	E-value = 0, Score = 2092, Bitscore = 810.446, Identities = 397/835 (47%)
orf00052	36,857	37,225	369	NO RESULTS			
orf00053	37,218	37,469	252	NO RESULTS			
orf00054	37,596	38,312	717	Hypothetical protein	hypothetical protein [Pseudomonas putida] >gi 428763530 gb EKX85699.1 hypothetical protein CSV86_08191 [Pseudomonas putida CSV86]	100	E-value = 1.55e-23, Score = 265, Bitscore = 106.686, Identities = 55/113 (48%)
orf00055	38,411	39,364	954	Hypothetical protein	TOPRIM domain-containing protein [Phaeosporillum fulvum MGU-K5]	100	E-value = 1.04e-22, Score = 270, Bitscore = 108.612, Identities = 77/277 (27%)
orf00056	39,376	39,819	444	NO RESULTS			
orf00057	39,824	40,009	186	NO RESULTS			
orf00058	40,013	40,534	522	NO RESULTS			
orf00059	40,629	41,153	525	Hypothetical protein	hypothetical protein [Flavobacterium phage FCV-1]	1	E-value = 1.29e-119, Score = 891, Bitscore = 347.821, Identities = 171/174 (98%)
orf00060	41,210	41,437	228	Hypothetical protein	hypothetical protein [Chitinophaga pinensis] >gi 256422896 ref YP_003123549.1 hypothetical protein Cpin_3886 [Chitinophaga pinensis DSM 2588] >gi 256037804 gb ACU61348.1 hypothetical protein Cpin_3886 [Chitinophaga pinensis DSM 2588]	17	E-value = 4.55e-16, Score = 186, Bitscore = 76.2554, Identities = 37/69 (53%)
orf00061	41,453	41,887	435	Hypothetical protein	MULTISPECIES: hypothetical protein [Myroides] >gi 373909951 gb EHQ41500.1 hypothetical protein Myrod_0664 [Myroides odoratus DSM 2801] >gi 404603027 gb EK802707.1 hypothetical protein HMPREF9716_03736 [Myroides [odoratimimus] CIP 103059]	3	E-value = 2.27e-25, Score = 258, Bitscore = 103.99, Identities = 53/93 (56%)
orf00062	41,884	42,027	144	NO RESULTS			
orf00063	42,032	42,478	447	Hypothetical protein	single-stranded DNA-binding protein [Sediminibacterium sp. C3]	100	E-value = 4.61e-14, Score = 183, Bitscore = 75.0998, Identities = 43/148 (29%)
orf00064	42,600	42,998	399	NO RESULTS			

orf00065	43,049	43,348	300	Hypothetical protein	hypothetical protein [Flavobacterium columnare] >gi 365960114 ref YP_004941681.1 hypothetical protein FCOL_05315 [Flavobacterium columnare ATCC 49512] >gi 365736795 gb AEW85888.1 hypothetical protein FCOL_05315 [Flavobacterium columnare ATCC 49512]	1	E-value = 7.74e-44, Score = 386, Bitscore = 153.295, Identities = 79/99 (79%)
orf00066	43,599	43,736	138	NO RESULTS			
orf00067	43,767	44,015	249	NO RESULTS			
orf00068	44,050	44,262	213	Hypothetical protein	hypothetical protein P2559S_07 [Croceibacter phage P2559S] >gi 392284355 gb AFM54785.1 hypothetical protein P2559S_07 [Croceibacter phage P2559S]	1	E-value = 7.82e-03, Score = 96, Bitscore = 41.5874, Identities = 19/46 (41%)
orf00069	44,277	44,546	270	NO RESULTS			
orf00070	44,709	45,056	348	NO RESULTS			
orf00071	45,363	45,806	444	Hypothetical protein	hypothetical protein [Flavobacterium indicum] >gi 383451233 ref YP_005357954.1 hypothetical protein KQS_09835 [Flavobacterium indicum GPTSA100-9 = DSM 17447] >gi 380502855 emb CCG53897.1 Protein of unknown function precursor [Flavobacterium indicum GPTSA100-9 = DSM 17447]	51	E-value = 1.25e-05, Score = 124, Bitscore = 52.373, Identities = 28/57 (49%)
orf00072	45,809	46,195	387	Hypothetical protein	phage_TIGR01671: phage conserved hypothetical protein TIGR01671 [Desulfitobacterium hafniense]	100	E-value = 6.39e-15, Score = 188, Bitscore = 77.0258, Identities = 50/146 (34%)
orf00073	46,330	46,671	342	NO RESULTS			
orf00074	46,674	46,985	312	Hypothetical protein	hypothetical protein Phi19:1_gp075 [Cellulophaga phage phi19:1] >gi 514341102 gb AGO47365.1 hypothetical protein Phi19:1_gp075 [Cellulophaga phage phi19:1]	2	E-value = 1.22e-30, Score = 288, Bitscore = 115.546, Identities = 52/76 (68%)