SUPPLEMENTAL INFORMATION

SUPPLEMENTAL TABLES

Supplemental Table S1. Description of the gene complement of the Faustovirus E12 isolate genome.

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_001	complement(513..1478)	322	Yes	738376820	Hypothetical protein, partial (putative Hef-like homing endonuclease)	Mollicutes bacterium HR2	1,00E-04	34
Faustovirus_002	complement(1594..2130)	179	Yes					
Faustovirus_003	complement(2171..2539)	123						
Faustovirus_004	complement(2587..3159)	191		421960576	Putative exported 24-amino acid repeat protein	Campylobacter showae CSUNSWCD	8,00E-09	28
Faustovirus_005	complement(3181..3783)	201		652357991	Hypothetical protein (MORN repeat-containing protein)	Sediminibacter sp. Hel_I_10	4,00E-14	32
Faustovirus_006	complement(3846..4247)	134						
Faustovirus_007	complement(4435..5091)	219						
Faustovirus_008	complement(5148..5726)	193						
Faustovirus_009	complement(5814..6347)	178	Yes *					
Faustovirus_010	complement(6464..7081)	206	Yes					
Faustovirus_011	complement(7355..7810)	152						
Faustovirus_012	complement(7897..8340)	148						
Faustovirus_013	complement(8361..8999)	213						
Faustovirus_014	complement(9069..9725)	219		518484612	Hypothetical protein (MORN repeat-containing protein)	Variovorax paradoxus	6,00E-08	30
Faustovirus_015	complement(9783..10265)	161						
Faustovirus_016	10662..11174	171						
Faustovirus_017	complement(11314..15477)	1388		363539884	mg675 gene product (DNA repair exonuclease)	Megavirus chiliensis	2,00E-39	25
Faustovirus_018	15594..16271	226						
Faustovirus_019	16580..16990	137						
Faustovirus_020	complement(17000..18220)	407		299472065	EsV-1-7 (Partial) (Zn-finger-containing protein)	Ectocarpus siliculosus	6,00E-04	31
Faustovirus_021	18591..20690	700	Yes	593791112	PHAVU_002G165800g (AAA family ATPase)	Phaseolus vulgaris	2,00E-26	39
Faustovirus_022	20814..22421	536		300122679	Unnamed protein product (Hypothetical protein)	Blastocystis hominis	7,00E-04	54

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_023	complement(22448..23155)	236						
Faustovirus_024	23486..24037	184						
Faustovirus_025	complement(24053..25720)	556						
Faustovirus_026	complement(25783..26445)	221						
Faustovirus_027	26559..28115	519		218199724	Hypothetical protein OsI_26209 (AAA family ATPase)	Oryza sativa Indica Group	1,00E-16	34
Faustovirus_028	28196..29869	558		218199723	Hypothetical protein OsI_26207 (AAA family ATPase)	Oryza sativa Indica Group	2,00E-15	26
Faustovirus_029	complement(29862..30260)	133	Yes	131579	Puff II/9-1 protein; Flags: Precursor	Bradysia coprophila	3,00E-03	37
Faustovirus_030	complement(30344..33787)	1148		321444493	Hypothetical protein DAPPUDRAFT_124236	Daphnia pulex	5,00E-41	33
Faustovirus_031	complement(33972..34886)	305		493608916	Hypothetical protein	Oscillochloris trichoides	5,00E-04	47
Faustovirus_032	34994..35665	224	Yes					
Faustovirus_033	complement(35662..36462)	267		593778002	gp559 (putative Tryptophan repeat gene family protein)	Bacillus phage G	6,00E-15	25
Faustovirus_034	complement(36497..37093)	199						
Faustovirus_035	37193..37612	140	Yes					
Faustovirus_036	37640..39076	479	Yes *	322510730	Putative deoxyribodipyrimidine photo-lyase	Organic Lake phycodnavirus 1	3,00E-69	32
Faustovirus_037	39156..39656	167						
Faustovirus_038	39689..40330	214	Yes *	495395246	Deoxyuridine 5'-triphosphate nucleotidohydrolase	Bacteroides pectinophilus CAG:437	5,00E-26	45
Faustovirus_039	40551..41585	349						
Faustovirus_040	complement(41597..43564)	656	Yes *	353238251	Related to ankyrin repeat-containing protein-Dictyostelium discoideum	Piriformospora indica DSM 11827	4,00E-05	32
Faustovirus_041	complement(43960..44334)	125						
Faustovirus_042	44491..48216	1242	Yes *	218547416	DNA-directed RNA polymerase subunit 2	African swine fever virus pig/Kenya/KEN-50/1950	0,00E+00	41
Faustovirus_043	48974..50614	547						
Faustovirus_044	50649..50912	88	Yes *	470291948	Glutaredoxin-C3	Capsaspora owczarzaki ATCC 30864	3,00E-21	48
Faustovirus_045	complement(51064..51921)	286						
Faustovirus_046	complement(52015..55140)	1042	Yes *	291335991	Possible T4-like proximal tail fiber	uncultured phage MedDCM-OCT-S09-C5	9,00E-95	42
Faustovirus_047	complement(55247..56002)	252						
Faustovirus_048	complement(56103..57017)	305	Yes *	547865682	Phosphatidylglycerophosphate synthase	Eubacterium siraeum CAG:80	8,00E-04	31

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_049	complement(57141..57521)	127	Yes					
Faustovirus_050	complement(57557..58021)	155						
Faustovirus_051	complement(58087..58848)	254						
Faustovirus_052	complement(58897..59382)	162						
Faustovirus_053	59476..62331	952	Yes	685073826	Glycosyl hydrolase family 81	Chlamydia sp. 'Rubis'	3,00E-153	36
Faustovirus_054	62766..63797	344						
Faustovirus_055	63891..64241	117	Yes *					
Faustovirus_056	64548..65009	154						
Faustovirus_057	complement(65045..65353)	103						
Faustovirus_058	65470..65997	176	Yes					
Faustovirus_059	66153..66863	237		628347862	Ubiquitin-conjugating enzyme E2 J1	Cladophialophora psammophila CBS 110553	2,00E-13	25
Faustovirus_060	complement(66888..68294)	469	Yes *	162849262	pK421R	African swine fever virus Benin 97/1	4,00E-15	23
Faustovirus_061	complement(68388..68975)	196	Yes *					
Faustovirus_062	69391..72882	1164	Yes *	652629697	Ribonucleoside-diphosphate reductase	Flexibacter elegans	6,00E-173	47
Faustovirus_063	73070..74098	343	Yes	397531943	Ribonucleotide reductase small subunit p53R2ii	Carassius carassius	1,00E-90	47
Faustovirus_064	74439..74813	125						
Faustovirus_065	complement(74846..75352)	169						
Faustovirus_066	complement(75533..76135)	201	Yes					
Faustovirus_067	complement(76157..76672)	172						
Faustovirus_068	complement(76748..78262)	505		358338692	BTB/POZ domain-containing protein 9	Clonorchis sinensis	1,00E-04	26
Faustovirus_069	78367..79353	329						
Faustovirus_070	79451..80383	311		145344561	Predicted protein (ankyrin repeat-containing protein)	Ostreococcus lucimarinus CCE9901	3,00E-13	31
Faustovirus_071	80496..83777	1094		162849430	Helicase	African swine fever virus OURT 88/3	1,00E-111	31
Faustovirus_072	84093..84983	297						
Faustovirus_073	complement(85041..85733)	231	Yes					
Faustovirus_074	complement(86015..86506)	164	Yes *					
Faustovirus_075	86630..87223	198	Yes *	640350001	Hypothetical protein	Tolumonas sp. BRL6-1	3,00E-10	59
Faustovirus_076	87604..88215	204						
Faustovirus_077	complement(88225..89814)	530						

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_078	89776..90324	183						
Faustovirus_079	90376..90900	175						
Faustovirus_080	91205..91705	167						
Faustovirus_081	91797..92945	383	Yes *	351737862	Putative UV damage endonuclease	Acanthamoeba castellanii mamavirus	1,00E-80	36
Faustovirus_082	93033..93647	205						
Faustovirus_083	93747..94079	111						
Faustovirus_084	94143..94643	167						
Faustovirus_085	94694..95227	178						
Faustovirus_086	95307..97205	633		340025889	Hypothetical protein	Paramecium bursaria Chlorella virus 1	9,00E-04	28
Faustovirus_087	97232..97684	151						
Faustovirus_088	complement(97697..97912)	72	Yes *					
Faustovirus_089	97989..98567	193	Yes					
Faustovirus_090	complement(99339..100607)	423		157952317	Hypothetical protein NY2A_B013L	Paramecium bursaria Chlorella virus NY2A	2,00E-07	22
Faustovirus_091	complement(100676..102358)	561		495050881	Hypothetical protein	Rhizobium sp. CF080	8,00E-05	29
Faustovirus_092	102764..103150	129						
Faustovirus_093	103552..105045	498						
Faustovirus_094	105187..106830	548		298711929	EsV-1-7	Ectocarpus siliculosus	1,00E-24	29
Faustovirus_095	complement(106862..107281)	140	Yes *	524885705	Protein disulfide-isomerase A4-like isoform X2	Aplysia californica	2,00E-09	34
Faustovirus_096	complement(107361..108323)	321	Yes *	268564494	C. briggsae CBR-CRN-1 protein (5'-3' exonuclease (including N-terminal domain of PolI))	Caenorhabditis briggsae	2,00E-37	34
Faustovirus_097	complement(108383..110740)	786	Yes *	229890278	Putative RNA Helicase B962L	African swine fever virus warthog/Namibia/Wart80/1980	2,00E-99	32
Faustovirus_098	complement(110812..111228)	139	Yes					
Faustovirus_099	111315..112661	449						
Faustovirus_100	112760..114193	478						
Faustovirus_101	complement(114247..115017)	257	Yes *					
Faustovirus_102	complement(115082..116116)	345	Yes	229891468	Putative helicase/primase complex protein; Short=pF1055L	African swine fever virus Malawi LIL 20/1	6,00E-14	28
Faustovirus_103	complement(116180..117706)	509	Yes *	229891413	Putative poly(A) polymerase catalytic subunit	African swine fever virus Malawi LIL 20/1	1,00E-39	38

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_104	complement(117790..118971)	394		229891973	Uncharacterized protein C315R	African swine fever virus pig/Kenya/KEN-50/1950	3,00E-04	23
Faustovirus_105	119154..119603	150	Yes *					
Faustovirus_106	119624..120811	396	Yes *	657394360	Kinase AFC1	Medicago truncatula	1,00E-23	30
Faustovirus_107	complement(120851..121528)	226	Yes *					
Faustovirus_108	complement(121651..124698)	1016		229890280	Putative helicase C962R	African swine fever virus tick/South Africa/Pretoriuskop Pr4/1996	4,00E-92	29
Faustovirus_109	complement(124822..125382)	187						
Faustovirus_110	125481..125933	151	Yes *	562972599	Subunit common to RNA polymerases I, II, and III	Ogataea parapolymorpha DL-1	4,00E-10	33
Faustovirus_111	complement(125970..126305)	112						
Faustovirus_112	complement(126346..127134)	263	Yes *	441432025	Hypothetical protein Moumou_00085	Acanthamoeba polyphaga moumouvirus	2,00E-27	36
Faustovirus_113	complement(127211..127525)	105	Yes *	723456165	pC105R	African swine fever virus	3,00E-12	32
Faustovirus_114	127889..128956	356						
Faustovirus_115	129026..130048	341						
Faustovirus_116	complement(130085..130597)	171	Yes *					
Faustovirus_117	complement(130690..132954)	755	Yes *	229891938	Uncharacterized protein C717R	African swine fever virus Malawi LIL 20/1	4,00E-50	24
Faustovirus_118	133057..133668	204	Yes *	229891826	Uncharacterized protein C129R	African swine fever virus Malawi LIL 20/1	4,00E-06	32
Faustovirus_119	complement(133711..134262)	184						
Faustovirus_120	complement(134338..135699)	454						
Faustovirus_121	135949..136857	303	Yes					
Faustovirus_122	137167..137982	272						
Faustovirus_123	138080..138922	281						
Faustovirus_124	139065..139949	295		538448057	Hypothetical protein (immunoglobulin G-binding protein G)	Streptococcus constellatus	7,00E-08	78
Faustovirus_125	140246..141142	299		7474118	Albumin-binding protein precursor - Streptococcus sp. (fragment)	0	3,00E-11	80
Faustovirus_126	complement(141223..141468)	82	Yes *					
Faustovirus_127	complement(141767..143803)	679	Yes	229892017	Uncharacterized protein M448R	African swine fever virus tick/South Africa/Pretoriuskop Pr4/1996	7,00E-19	25

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_128	144065..148183	1373	Yes *	229891898	Uncharacterized protein M1249L	African swine fever virus pig/Kenya/KEN-50/1950	8,00E-39	23
Faustovirus_129	148486..149010	175						
Faustovirus_130	complement(149020..150312)	431		9628167	pEP364R (ERCC4 domain-containing protein)	African swine fever virus	5,00E-28	26
Faustovirus_131	150422..151495	358						
Faustovirus_132	complement(151457..152050)	198						
Faustovirus_133	152315..152752	146						
Faustovirus_134	152812..153219	136						
Faustovirus_135	complement(153265..154941)	559	Yes *					
Faustovirus_136	complement(155016..155828)	271						
Faustovirus_137	complement(155905..156666)	254						
Faustovirus_138	complement(156751..157701)	317						
Faustovirus_139	158010..158807	266						
Faustovirus_140	complement(159159..159956)	266						
Faustovirus_141	complement(160034..160888)	285						
Faustovirus_142	complement(161188..161655)	156	Yes *					
Faustovirus_143	161782..163119	446	Yes					
Faustovirus_144	163219..164340	374						
Faustovirus_145	164380..165663	428		229892019	Uncharacterized protein B475L	African swine fever virus pig/Kenya/KEN-50/1950	1,00E-10	23
Faustovirus_146	165725..166087	121	Yes *					
Faustovirus_147	166189..167259	357	Yes	229891991	Uncharacterized protein B354L	African swine fever virus pig/Kenya/KEN-50/1950	3,00E-21	26
Faustovirus_148	complement(167256..168956)	567	Yes *	290984181	Predicted protein (Poly A polymerase regulatory subunit)	Naegleria gruberi	4,00E-11	27
Faustovirus_149	complement(169014..169247)	78	Yes					
Faustovirus_150	complement(169333..170952)	540	Yes *	229891919	Protein B602L	African swine fever virus pig/Kenya/KEN-50/1950	8,00E-37	26
Faustovirus_151	171006..172292	429		229892000	Zinc finger protein B385R	African swine fever virus warthog/Namibia/Wart80/1980	2,00E-15	29
Faustovirus_152	complement(172349..172759)	137						
Faustovirus_153	complement(172764..173255)	164						
Faustovirus_154	173367..174347	327						

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_155	174732..176264	511						
Faustovirus_156	complement(176357..177013)	219	Yes *					
Faustovirus_157	177744..178079	112	Yes					
Faustovirus_158	178163..181069	969	Yes *	493681319	Hypothetical protein	Microcoleus vaginatus	2,00E-15	26
Faustovirus_159	181157..182875	573						
Faustovirus_160	complement(182925..183164)	80	Yes *					
Faustovirus_161	complement(183246..183719)	158						
Faustovirus_162	183816..184895	360						
Faustovirus_163	184992..185186	65	Yes *					
Faustovirus_164	complement(185391..186032)	214		652353374	Dihydrofolate reductase	Leptotrichia trevisanii	1,00E-10	30
Faustovirus_165	186405..187700	432						
Faustovirus_166	187852..188877	342						
Faustovirus_167	188959..189576	206						
Faustovirus_168	189735..190409	225	Yes	672551201	Putative RNA methylase	Aureococcus anophagefferens virus	1,00E-26	36
Faustovirus_169	complement(190735..191751)	339						
Faustovirus_170	191867..192865	333		503153938	MORN repeat-containing protein	Ilyobacter polytropus	6,00E-17	29
Faustovirus_171	192946..193686	247						
Faustovirus_172	193802..194794	331		492611264	Hypothetical protein (MORN repeat-containing protein)	Fusobacterium nucleatum	2,00E-15	32
Faustovirus_173	194875..195621	249						
Faustovirus_174	196192..196347	52	Yes *	283765127	B646L, partial (major capsid protein, partial)	African swine fever virus	1,00E-09	57
Faustovirus_175	complement(196684..197682)	333						
					Intron_gpI			
Faustovirus_177	complement(198144..198641)	166						
Faustovirus_178	complement(198689..198886)	66	Yes					
Faustovirus_179	complement(199014..199376)	121						
Faustovirus_180	199950..200699	250	Yes	448929966	GIY-YIG catalytic domain-containing endonuclease	Acanthocystis turfacea Chlorella virus GM0701.1	1,00E-11	37
					Intron_gpI			
					Intron_gpI			

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_183	complement(201200..201469)	90	Yes					
Faustovirus_184	complement(201977..202285)	103						
					Intron_gpI			
Faustovirus_186	complement(203193..204050)	286						
Faustovirus_187	complement(204338..204706)	123						
					Intron_gpI			
Faustovirus_189	204992..205258	89	Yes *					
					Intron_gpI			
Faustovirus_191	206117..206521	135	Yes *	566016778	Protein F443_14731 (major capsid protein, partial)	Phytophthora parasitica P1569	1,00E-17	40
Faustovirus_192	206887..207987	367		738879757	Hypothetical protein, partial (GIY-YIG-like endonuclease)	Peptostreptococcaceae bacterium VA2	2,00E-11	40
Faustovirus_193	complement(210875..211264)	130						
Faustovirus_194	212187..212552	122	Yes *	570944290	Hypothetical protein F441_14586, partial (major capsid protein, partial)	Phytophthora parasitica CJ01A1	1,00E-07	35
Faustovirus_195	212788..213525	246		66219837	p72 (capsid protein)	African swine fever virus	4,00E-04	43
Faustovirus_196	complement(213482..214210)	243						
Faustovirus_197	complement(214249..215511)	421		356980056	Hypothetical protein MPWG_00045 (DUF4379 domain-containing protein)	Micromonas pusilla virus PL1	9,00E-09	30
Faustovirus_198	215555..216097	181						
Faustovirus_199	216124..216921	266	Yes					
Faustovirus_200	216951..217190	80						
Faustovirus_201	217299..218654	452		441432831	T5orf172 domain-containing protein	Acanthamoeba polyphaga moumouvirus	7,00E-08	34
Faustovirus_202	218736..219164	143						
Faustovirus_203	complement(219214..220047)	278		310831525	Hypothetical protein crov535	Cafeteria roenbergensis virus BV-PW1	2,00E-16	29
Faustovirus_204	220116..220508	131						
Faustovirus_205	220609..221826	406						
Faustovirus_206	221904..222365	154						
Faustovirus_207	222445..222981	179						
Faustovirus_208	223402..227412	1337	Yes	322510888	Putative site-specific DNA-methyltransferase	Organic Lake phycodnavirus 2	3,00E-170	31
Faustovirus_209	complement(227441..227953)	171	Yes					

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_210	228058..228558	167	Yes					
Faustovirus_211	complement(228579..228986)	136		547892309	UvrB/UvrC protein	Clostridium sp. CAG:465	8,00E-04	33
Faustovirus_212	229086..229904	273						
Faustovirus_213	229997..230578	194						
Faustovirus_214	complement(230616..231185)	190						
Faustovirus_215	231317..231763	149						
Faustovirus_216	231816..232646	277						
Faustovirus_217	232709..233341	211						
Faustovirus_218	complement(233367..233852)	162	Yes *	648484013	Hypothetical protein	Methylobacterium sp. 88A	4,00E-25	53
Faustovirus_219	complement(233891..234100)	70	Yes	356980016	Hypothetical protein MPWG_00005	Micromonas pusilla virus PL1	7,00E-04	35
Faustovirus_220	complement(234149..234835)	229						
Faustovirus_221	235180..235767	196						
Faustovirus_222	complement(235811..236092)	94						
Faustovirus_223	236173..237027	285						
Faustovirus_224	237081..237572	164						
Faustovirus_225	complement(237585..238484)	300						
Faustovirus_226	238856..240004	383						
Faustovirus_227	240432..241232	267						
Faustovirus_228	241537..242082	182						
Faustovirus_229	complement(242123..242683)	187						
Faustovirus_230	complement(242806..243312)	169	Yes *	470376935	TM2 domain containing protein	Acanthamoeba castellanii str. Neff	2,00E-03	36
Faustovirus_231	complement(243560..244630)	357						
Faustovirus_232	245286..246041	252						
Faustovirus_233	complement(246063..246539)	159	Yes *					
Faustovirus_234	246616..248019	468		737995869	Histidinol phosphate aminotransferase	Bryobacter aggregatus	5,00E-33	28
Faustovirus_235	248420..248986	189	Yes					
Faustovirus_236	249037..249564	176						
Faustovirus_237	249640..250185	182		497473819	DNA polymerase I	Lyngbya sp. PCC 8106	2,00E-06	31
Faustovirus_238	complement(250234..250692)	153		497723327	Hypothetical protein, partial (Swarming motility protein YbiA)	Gemmata obscuriglobus	3,00E-53	57

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_239	complement(250755..251360)	202						
Faustovirus_240	251460..252377	306						
Faustovirus_241	252447..253202	252						
Faustovirus_242	complement(253191..253868)	226						
Faustovirus_243	complement(253940..254476)	179	Yes					
Faustovirus_244	254586..255107	174						
Faustovirus_245	255138..255665	176						
Faustovirus_246	complement(255677..256576)	300	Yes *	11931733	Iridoviral protein homologue	Diadromus pulchellus ascovirus 4a	7,00E-06	26
Faustovirus_247	256643..256984	114	Yes *					
Faustovirus_248	257051..257734	228						
Faustovirus_249	257813..258751	313						
Faustovirus_250	258904..259440	179						
Faustovirus_251	complement(259492..259815)	108						
Faustovirus_252	complement(259829..260284)	152						
Faustovirus_253	complement(260565..261296)	244						
Faustovirus_254	261661..262146	162	Yes					
Faustovirus_255	262227..263333	369						
Faustovirus_256	complement(263566..265050)	495		302836439	Hypothetical protein VOLCADRAFT_90158 (ankyrin repeat-containing protein)	Volvox carteri f. nagariensis	9,00E-05	34
Faustovirus_257	complement(265256..266065)	270		470516696	Ubiquitin domain containing protein	Acanthamoeba castellanii str. Neff	9,00E-33	32
Faustovirus_258	266130..266828	233						
Faustovirus_259	266874..267365	164						
Faustovirus_260	complement(267412..267996)	195	Yes *					
Faustovirus_261	268647..269222	192						
Faustovirus_262	269285..270109	275						
Faustovirus_263	270206..271075	290						
Faustovirus_264	271123..271476	118						
Faustovirus_265	271530..272291	254						
Faustovirus_266	complement(272355..273554)	400	Yes *	448932251	Amino oxidase	Acanthocystis turfacea Chlorella virus MN0810.1	1,00E-39	29

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics		GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_267	273858..274658	267							
Faustovirus_268	274755..275126	124	Yes						
Faustovirus_269	complement(275355..275945)	197	Yes	*					
Faustovirus_270	276025..276609	195	Yes		229891867	Uncharacterized protein B175L (A1L transcription factor/late transcription factor VLTF-2)	African swine fever virus tick/South Africa/Pretoriuskop Pr4/1996	5,00E-10	29
Faustovirus_271	complement(276628..277404)	259							
Faustovirus_272	277506..278621	372	Yes	*	162849294	pB407L	African swine fever virus Benin 97/1	2,00E-22	26
Faustovirus_273	278946..280325	460			229891906	Uncharacterized protein B263R	African swine fever virus pig/Kenya/KEN-50/1950	4,00E-03	37
Faustovirus_274	complement(280368..280646)	93	Yes						
Faustovirus_275	complement(280709..284827)	1373	Yes	*	229891832	Uncharacterized protein G1340L (putative early transcription factor large subunit VETF-L)	African swine fever virus warthog/Namibia/Wart80/1980	3,00E-97	25
Faustovirus_276	284934..285602	223	Yes	*	508182059	Metal-dependent hydrolase	Phaeocystis globosa virus	8,00E-26	40
Faustovirus_277	285653..286111	153							
Faustovirus_278	complement(286208..286729)	174	Yes	*					
Faustovirus_279	286810..287385	192			657695079	Hypothetical protein (MORN repeat-containing protein)	Fusobacterium hwasookii	1,00E-16	32
Faustovirus_280	287459..287965	169	Yes						
Faustovirus_281	288029..288694	222							
Faustovirus_282	288768..289232	155							
Faustovirus_283	289659..294128	1490			552912589	Protein GLOINDRAFT_10982 (DNA polymerase elongation subunit family B)	Rhizophagus irregularis DAOM 181602	5,00E-62	34
Faustovirus_284	294240..294800	187	Yes	*					
Faustovirus_285	complement(294866..295522)	219							
Faustovirus_286	complement(295573..296454)	294							
Faustovirus_287	complement(296600..296749)	50	Yes	*	735019541	Hypothetical protein QT04_C0005G0003/aspartic peptidase	archaeon GW2011_AR11	2,00E-08	67
Faustovirus_288	complement(296845..297402)	186			518991882	Hypothetical protein (MORN repeat-containing protein)	Verrucomicrobia bacterium SCGC AAA164-E04	4,00E-07	27
Faustovirus_289	297454..298071	206							
Faustovirus_290	complement(298093..299175)	361	Yes		145532086	Hypothetical protein (Ubiquitin carboxyl-terminal hydrolase)	Paramecium tetraurelia strain d4-2	4,00E-07	33

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics		GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_291	299351..300547	399	Yes	*					
Faustovirus_292	complement(300651..309590)	2980			229891460	220 kDa polyprotein	African swine fever virus Malawi LIL 20/1	1,00E-141	27
Faustovirus_293	309773..311482	570	Yes	*	723633433	60 kDa polyprotein	African swine fever virus	1,00E-14	22
Faustovirus_294	complement(311623..312087)	155							
Faustovirus_295	312561..312169	131							
Faustovirus_296	312680..312898	73	Yes	*					
Faustovirus_297	complement(312921..314066)	382	Yes	*	527060079	Fibrillarin-like rRNA methylase	Cyclobacterium qasimii	2,00E-05	27
Faustovirus_298	314486..315406	307	Yes						
Faustovirus_299	complement(315456..315905)	150			503793157	N-acetyltransferase (ribosomal-protein-alanine acetyltransferase)	Pyrolobus fumarii	3,00E-30	45
Faustovirus_300	316181..316492	104	Yes	*					
Faustovirus_301	complement(316489..318111)	541							
Faustovirus_302	complement(318433..318714)	94	Yes	*					
Faustovirus_303	complement(318815..319165)	117	Yes	*	673042869	Hypothetical protein H310_10725 (MORN repeat-containing protein)	Aphanomyces invadans	4,00E-06	30
Faustovirus_304	319269..320246	326							
Faustovirus_305	320305..321390	362			496966979	Phophatidylinositol-4-phosphate 5-kinase	Fusobacterium sp. oral taxon 370	4,00E-06	25
Faustovirus_306	complement(321447..325772)	1442	Yes	*	229891560	Probable DNA-directed RNA polymerase subunit 1 homolog	African swine fever virus tick/South Africa/Pretoriuskop Pr4/1996	0,00E+00	36
Faustovirus_307	326004..326333	110							
Faustovirus_308	326404..326985	194	Yes	*					
Faustovirus_309	complement(327007..327849)	281							
Faustovirus_310	328182..328685	168							
Faustovirus_311	328797..329648	284	Yes	*					
Faustovirus_312	330003..332366	788							
Faustovirus_313	complement(332363..333865)	501			568035652	Hypothetical protein L914_19448	Phytophthora parasitica	2,00E-28	29
Faustovirus_314	334256..335644	463	Yes	*	229485343	DNA ligase	African swine fever virus pig/Kenya/KEN-50/1950	5,00E-61	34
Faustovirus_315	336010..336387	126							

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_316	336494..336940	149	Yes *	472342598	Hypothetical protein MPVG_00037	Micromonas pusilla virus 12T	1,00E-03	27
Faustovirus_317	complement(337321..338631)	437						
Faustovirus_318	complement(338744..339505)	254		327409766	Putative deoxynucleotide monophosphate kinase	Lausannevirus	4,00E-08	29
Faustovirus_319	339946..340968	341						
Faustovirus_320	complement(341120..343792)	891	Yes *	229890400	Probable mRNA-capping enzyme (mRNA guanylyltransferase)	African swine fever virus pig/Kenya/KEN-50/1950	2,00E-104	31
Faustovirus_321	343902..344282	127						
Faustovirus_322	344326..344625	100						
Faustovirus_323	344669..345067	133						
Faustovirus_324	345197..345871	225						
Faustovirus_325	345964..346338	125	Yes					
Faustovirus_326	346402..346776	125						
Faustovirus_327	346891..347385	165						
Faustovirus_328	347452..347799	116						
Faustovirus_329	347858..348232	125						
Faustovirus_330	348338..348772	145						
Faustovirus_331	349122..349682	187						
Faustovirus_332	349747..350190	148						
Faustovirus_333	350243..350692	150	Yes					
Faustovirus_334	350776..351195	140						
Faustovirus_335	351299..351751	151						
Faustovirus_336	351814..352230	139						
Faustovirus_337	complement(352289..353710)	474	Yes *					
Faustovirus_338	complement(353800..354540)	247						
Faustovirus_339	complement(354527..355189)	221	Yes					
Faustovirus_340	complement(355261..356115)	285						
Faustovirus_341	356222..357184	321	Yes *	516676352	Hypothetical protein (DNA polymerase family X)	Marine Group II euryarchaeote SCGC AB-629-J06	5,00E-41	35
Faustovirus_342	complement(357192..358499)	436						

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics		GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_343	358587..359762	392	Yes	*	157953925	Hypothetical protein AR158_C735R (F10-like kinase)	Paramecium bursaria Chlorella virus AR158	1,00E-07	36
Faustovirus_344	359769..360095	109	Yes	*					
Faustovirus_345	360496..361686	397							
Faustovirus_346	complement(361740..362330)	197			663506229	Transcription elongation factor TFIIS/Cofactor of enhancer-binding protein Sp1	uncultured marine group II/III euryarchaeote AD1000_88_G11	4,00E-18	31
Faustovirus_347	complement(362445..363662)	406	Yes						
Faustovirus_348	complement(363813..364706)	298	Yes	*	303398818	EP296R (AP (apurinic) endonuclease family 2)	African swine fever virus Georgia 2007/1	2,00E-27	31
Faustovirus_349	complement(364723..365283)	187							
Faustovirus_350	complement(365710..367161)	484	Yes		303398807	QP509L (DNA or RNA helicases of superfamily II)	African swine fever virus Georgia 2007/1	1,00E-33	27
Faustovirus_351	367234..367725	164							
Faustovirus_352	367898..369259	454							
Faustovirus_353	complement(369853..369993)	47	Yes	*					
Faustovirus_354	complement(370074..370232)	53	Yes	*					
Faustovirus_355	complement(370327..371271)	315	Yes	*	229892042	Cysteine protease S273R	African swine fever virus pig/Kenya/KEN-50/1950	4,00E-41	33
Faustovirus_356	371361..372116	252	Yes	*					
Faustovirus_357	372146..372304	53	Yes	*					
Faustovirus_358	372480..372845	122	Yes	*					
Faustovirus_359	complement(373112..374095)	328			9628234	Proliferating cell nuclear antigen-like protein	African swine fever virus	4,00E-27	26
Faustovirus_360	complement(374434..376137)	568	Yes	*					
Faustovirus_361	376311..377024	238	Yes	*					
Faustovirus_362	377364..378638	425	Yes	*					
Faustovirus_363	complement(378714..379103)	130							
Faustovirus_364	complement(379180..380523)	448	Yes	*	740198580	Cysteine desulfurase	Thermomicrobiales bacterium KI4	6,00E-52	32
Faustovirus_365	complement(380629..382782)	718	Yes	*	284504412	Zinc finger protein	Marseillevirus marseillevirus	2,00E-16	21
Faustovirus_366	complement(382974..384323)	450			655382372	Uracil-DNA glycosylase	Terrimonas ferruginea	1,00E-35	39
Faustovirus_367	384413..384649	79	Yes	*					
Faustovirus_368	complement(384653..385360)	236							

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics		GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_369	complement(385412..386536)	375	Yes	*	751748632	OIDMADRAFT_44370 (thymidylate synthase)	Oidiodendron maius Zn	3,00E-77	45
Faustovirus_370	complement(386624..387454)	277							
Faustovirus_371	complement(387744..388970)	409	Yes	*					
Faustovirus_372	complement(389061..389870)	270	Yes		550986136	Hypothetical protein	Thalassospira lucentensis	3,00E-04	31
Faustovirus_373	389945..390862	306			447031585	Patatin (Patatin phospholipase)	Bacillus thuringiensis	3,00E-48	33
Faustovirus_374	complement(390882..392312)	477	Yes	*	303398740	EP424R (FtsJ-like methyltransferase)	African swine fever virus Georgia 2007/1	1,00E-40	33
Faustovirus_375	392369..392770	134	Yes						
Faustovirus_376	392846..393907	354	Yes	*	552924301	Hypothetical protein GLOINDRAFT_84836	Rhizophagus irregularis DAOM 181602	2,00E-33	29
Faustovirus_377	complement(394257..394718)	154	Yes						
Faustovirus_378	394835..395611	259	Yes	*					
Faustovirus_379	395887..396429	181							
Faustovirus_380	396486..397025	180							
Faustovirus_381	397081..397746	222							
Faustovirus_382	398085..399329	415			493386218	Hypothetical protein (MORN repeat-containing protein)	Parachlamydia acanthamoebae	4,00E-19	27
Faustovirus_383	399411..400427	339	Yes	*					
Faustovirus_384	400474..401193	240			696306976	Membrane-binding protein, partial	Fusobacterium nucleatum	3,00E-05	26
Faustovirus_385	401193..401900	236			505294699	Hypothetical protein (MORN repeat-containing protein)	Polaribacter sp. MED152	8,00E-06	34
Faustovirus_386	401962..402687	242			493694477	Hypothetical protein (MORN repeat-containing protein)	Photobacterium sp. SKA34	6,00E-08	36
Faustovirus_387	complement(402698..405304)	869	Yes	*	82059328	Putative ATP-dependent RNA helicase Q706L	African swine fever virus Malawi LIL 20/1	2,00E-48	32
Faustovirus_388	405678..407015	446			534481265	Hypothetical protein HRAG_00328 (MORN repeat-containing protein)	Helicobacter bilis ATCC 43879	2,00E-29	28
Faustovirus_389	complement(407084..407956)	291	Yes	*					
Faustovirus_390	complement(408307..409422)	372	Yes	*	589910733	DNA-directed RNA polymerase subunit D	Thermococcus nautili	7,00E-04	33
Faustovirus_391	complement(409753..411099)	449	Yes	*					
Faustovirus_392	complement(411197..414901)	1235	Yes		303398797	P1192R (DNA topoisomerase II)	African swine fever virus Georgia 2007/1	9,00E-131	29
Faustovirus_393	complement(415386..415604)	73	Yes	*					

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_394	complement(415776..416156)	127	Yes *					
Faustovirus_395	416346..417014	223	Yes *	159118208	RNA polymerase II subunit Rpb5b	Giardia lamblia ATCC 50803	1,00E-12	29
Faustovirus_396	complement(417044..418033)	330		9628216	pD345L (YqaJ viral recombinase)	African swine fever virus	2,00E-20	28
Faustovirus_397	complement(418136..418378)	81	Yes *					
Faustovirus_398	418522..419520	333	Yes *	229485368	mRNA-decapping protein (Diphosphoinositol polyphosphate phosphohydrolase)	African swine fever virus pig/Kenya/KEN-50/1950	3,00E-34	35
Faustovirus_399	complement(419564..420271)	236						
Faustovirus_400	420339..424886	1516	Yes *	291289549	BA71V-D1133L (g10L) (unclassified DEAD/SNF2-like helicase)	African swine fever virus E75	9,00E-115	29
Faustovirus_401	425216..426265	350	Yes *					
Faustovirus_402	426344..426682	113						
Faustovirus_403	426752..427399	216	Yes *					
Faustovirus_404	427474..428301	276						
Faustovirus_405	428404..429852	483	Yes *	442771778	Rhs family protein	uncultured bacterium A1Q1_fos_493	1,00E-08	37
Faustovirus_406	429925..430773	283						
Faustovirus_407	430860..431204	115	Yes					
Faustovirus_408	complement(431272..431880)	203						
Faustovirus_409	complement(431984..432802)	273						
Faustovirus_410	433196..433561	122						
Faustovirus_411	complement(433536..433919)	128						
Faustovirus_412	complement(433951..434328)	126						
Faustovirus_413	434846..435547	234						
Faustovirus_414	complement(435619..436344)	242						
Faustovirus_415	436595..437509	305						
Faustovirus_416	complement(437797..438219)	141						
Faustovirus_417	438567..439025	153						
Faustovirus_418	complement(439177..439920)	248						
Faustovirus_419	440300..441211	304	Yes					
Faustovirus_420	complement(441251..442012)	254						
Faustovirus_421	complement(442147..442539)	131		516663344	Hypothetical protein (MORN repeat-containing protein)	Porphyromonas somerae	1,00E-06	38

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_422	442640..443572	311						
Faustovirus_423	443615..444220	202						
Faustovirus_424	444553..445275	241						
Faustovirus_425	445316..445852	179						
Faustovirus_426	complement(445853..446278)	142		676379365	Protein AURANDRAFT_20639 (Translation initiation factor SUI1)	Aureococcus anophagefferens	9,00E-28	57
Faustovirus_427	446350..446940	197	Yes *	491358983	Phophatidylinositol-4-phosphate 5-kinase	Helicobacter bilis	1,00E-06	32
Faustovirus_428	446993..447556	188						
Faustovirus_429	447642..448109	156						
Faustovirus_430	448196..448762	189						
Faustovirus_431	complement(448805..449044)	80	Yes *					
Faustovirus_432	449121..449591	157						
Faustovirus_433	449687..450190	168						
Faustovirus_434	450263..450802	180						
Faustovirus_435	450853..451266	138						
Faustovirus_436	451302..451901	200						
Faustovirus_437	451940..452569	210						
Faustovirus_438	452670..453308	213	Yes					
Faustovirus_439	453312..454025	238		492752400	Hypothetical protein (MORN repeat-containing protein)	Fusobacterium varium	1,00E-06	24
Faustovirus_440	454072..454755	228		739520856	Hypothetical protein, partial (MORN repeat-containing protein)	Smithella	2,00E-08	29
Faustovirus_441	454848..455357	170		492752400	Hypothetical protein (MORN repeat-containing protein)	Fusobacterium varium	3,00E-07	35
Faustovirus_442	455411..456019	203						
Faustovirus_443	456085..456792	236						
Faustovirus_444	456841..457569	243						
Faustovirus_445	457631..458482	284						
Faustovirus_446	458548..458889	114						
Faustovirus_447	458968..459291	108						
Faustovirus_448	459391..459990	200						

Supplemental Table S1. *(continued)*

ORF number	ORF coordinates	Predicted protein length (amino acids)	Detection by proteomics	GenBank identifier of the first BLAST hit	Identity of the first BLAST hit in GenBank_nr (completed annotation)	Organism corresponding to the first BLAST hit in GenBank_nr	e-value	Pourcentage of identity (%)
Faustovirus_449	459987..460334	116						
Faustovirus_450	460447..461376	310						
Faustovirus_451	461467..462033	189						
Faustovirus_452	462088..462630	181						
Faustovirus_453	462709..463233	175						
Faustovirus_454	463275..463712	146						
Faustovirus_455	463757..464218	154						
Faustovirus_456	464400..465116	239						
Faustovirus_457	465126..465659	178						

* indicates that proteins were identified in at least two first dimension LC fractions.