

Table S9. Newly predicted genes with functionally characterized protein products.

Sequence ID and species name	Gene_ID	Fraction of aligned residues		Domain description	Alignment E-value
		in query	in target		
chromosome_AM27098_Aspergillus_niger	gene_7	0.97	1.00	gnl CDD 71315 pfam07876, Dabb, Stress responsive A/B Barrel Domain. The	6.00E-13
chromosome_AM270981_Aspergillus_niger	gene_142	0.22	0.96	gnl CDD 68370 pfam04795, PAPA-1, PAPA-1-like conserved region.	2.00E-07
chromosome_AM270981_Aspergillus_niger	gene_594	0.99	0.93	5' exoribonuclease	2.00E-47
chromosome_AM270981_Aspergillus_niger	gene_607	0.51	0.59	gnl CDD 31007 COG0663, PaaY, Carbonic	2.00E-11
chromosome_AM270981_Aspergillus_niger	gene_903	0.43	0.95	anhydrases/acetyltransferases, gnl CDD 32190 COG2007, RPS8A, Ribosomal protein S8E	3.00E-18
chromosome_AM270981_Aspergillus_niger	gene_1088	0.81	1.00	gnl CDD 72040 pfam08615, RNase_H1_sml, Ribonuclease H1 small subunit.	1.00E-29
chromosome_AM270983_Aspergillus_niger	gene_222	0.33	1.00	gnl CDD 30606 COG0257, RpmJ, Ribosomal protein L36.	3.00E-09
chromosome_AM270983_Aspergillus_niger	gene_725	0.97	1.00	gnl CDD 31565 COG1374, NIP7, Protein involved in ribosomal biogenesis.	4.00E-39
chromosome_AM270987_Aspergillus_niger	gene_241	0.58	0.79	gnl CDD 72409 pfam08991, DUF1903, Domain of unknown function (DUF1903).	1.00E-09
chromosome_AM270987_Aspergillus_niger	gene_297	0.59	0.80	gnl CDD 69301 pfam05768, DUF836, Glutaredoxin-like domain (DUF836).	4.00E-07
chromosome_AM270987_Aspergillus_niger	gene_318	0.87	0.94	gnl CDD 74917 PRK05395, PRK05395, 3-dehydroquinate dehydratase.	7.00E-63

chromosome_AM270987_Aspergillus_niger	gene_476	0.91	1.00	gnl CDD 34019 COG4297, COG4297, Uncharacterized protein	2.00E-21
chromosome_AM270988_Aspergillus_niger	gene_464	0.60	0.94	gnl CDD 71653 pfam08219, TOM13, Outer membrane protein TOM13.	1.00E-16
chromosome_AM270990_Aspergillus_niger	gene_72	1.00	1.00	gnl CDD 47816 smart00512, Skp1, Found in Skp1 protein family;	9.00E-12
chromosome_AM270990_Aspergillus_niger	gene_135	0.70	0.87	gnl CDD 68918 pfam05365, UCR_UQCRX_QCR9, Ubiquinol-cytochrome C reductase,	1.00E-10
chromosome_AM270991_Aspergillus_niger	gene_332	0.95	1.00	gnl CDD 68209 pfam04628, Sedlin_N, Sedlin, N-terminal conserved region.	3.00E-30
chromosome_AM270991_Aspergillus_niger	gene_642	0.41	1.00	gnl CDD 71661 pfam08227, DASH_Hsk3, DASH complex subunit Hsk3 like. The DASH	3.00E-09
chromosome_AM270993_Aspergillus_niger	gene_198	0.85	1.00	gnl CDD 33491 COG3695, COG3695, Predicted methylated DNA-protein cysteine	3.00E-18
chromosome_AM270993_Aspergillus_niger	gene_280	0.83	0.83	gnl CDD 67778 pfam04178, Got1, Got1-like family.	3.00E-15
chromosome_AM270994_Aspergillus_niger	gene_11	0.52	0.92	gnl CDD 71474 pfam08038, Tom7, TOM7 family.	3.00E-09
chromosome_AM270994_Aspergillus_niger	gene_20	0.83	1.00	gnl CDD 72555 pfam09138, Urm1, Urm1 (Ubiquitin related modifier).	2.00E-30
chromosome_AM270996_Aspergillus_niger	gene_175	0.71	0.96	gnl CDD 66614 pfam02953, zf-Tim10_DDP, Tim10/DDP family zinc finger.	2.00E-10
chromosome_AM270996_Aspergillus_niger	gene_180	0.95	0.91	gnl CDD 32119 COG1936, COG1936, Predicted nucleotide kinase	2.00E-35

supercontig_1.1_of_botrytis_cinerea	gene_4	0.95	0.67	gnl CDD 69275 pfam05742, DUF833, Protein of unknown function (DUF833).	3.00E-26
supercontig_1.26_of_botrytis_cinerea	gene_1	0.75	1.00	gnl CDD 58528 cd04413, NDPk_I, Nucleoside diphosphate kinase Group I	2.00E-62
supercontig_1.32_of_botrytis_cinerea	gene_53	0.83	1.00	gnl CDD 31172 COG0830, UreF, Urease accessory protein UreF	3.00E-22
supercontig_1.46_of_botrytis_cinerea	gene_1	0.65	0.75	gnl CDD 29325 cd00250, CAS_like, Clavaminic acid synthetase (CAS) -like.	2.00E-09
supercontig_1.49_of_botrytis_cinerea	gene_12	0.89	1.00	gnl CDD 33440 COG3642, COG3642, Mn2+-dependent serine/threonine protein kinase	6.00E-54
supercontig_1.54_of_botrytis_cinerea	gene_8	1.00	1.00	gnl CDD 79639 pfam00576, Transthyretin, Transthyretin precursor	1.00E-20
supercontig_1.7_of_botrytis_cinerea	gene_144	0.88	0.87	gnl CDD 30229 cd02198, YjgH.	2.00E-19
supercontig_1.70_of_botrytis_cinerea	gene_8	0.29	1.00	gnl CDD 67744 pfam04140, ICMT, Isoprenylcysteine carboxyl methyltransferase	3.00E-19
supercontig_1.73_of_botrytis_cinerea	gene_13	0.39	0.58	gnl CDD 30641 COG0293, FtsJ, 23S rRNA methylase.	3.00E-19
supercontig_1.1_of_botrytis_cinerea	gene_147	0.34	1.00	gnl CDD 71936 pfam08508, DUF1746, Fungal domain of unknown function (DUF1746).	2.00E-28
supercontig_1.100_of_botrytis_cinerea	gene_45	0.31	0.91	gnl CDD 31133 COG0790, COG0790, FOG: TPR repeat, SEL1 subfamily.	2.00E-15
supercontig_1.103_of_botrytis_cinerea	gene_6	0.69	0.79	gnl CDD 29325 cd00250, CAS_like, Clavaminic acid synthetase (CAS) -like.	1.00E-10
supercontig_1.103_of_botrytis_cinerea	gene_11	0.27	0.82	gnl CDD 79643 pfam00583, Acetyltransf_1, Acetyltransferase (GNAT) family.	2.00E-07

supercontig_1.112_of_botrytis_cinerea	gene_36	0.40	0.98	gnl CDD 70208 pfam06728, PIG-U, GPI transamidase subunit PIG-U.	7.00E-41
supercontig_1.115_of_botrytis_cinerea	gene_14	0.43	1.00	gnl CDD 71886 pfam08457, Sfi1, Sfi1 spindle body protein.	1.00E-44
supercontig_1.120_of_botrytis_cinerea	gene_5	0.96	0.82	gnl CDD 70183 pfam06703, SPC25, Microsomal signal peptidase 25 kDa subunit	3.00E-22
supercontig_1.120_of_botrytis_cinerea	gene_28	0.85	1.00	gnl CDD 79991 pfam03155, Alg6_Alg8, ALG6, ALG8 glycosyltransferase family.	e-102
supercontig_1.123_of_botrytis_cinerea	gene_6	0.62	0.36	gnl CDD 48039 cd03444, Thioesterase_II_repeat1.	3.00E-09
supercontig_1.124_of_botrytis_cinerea	gene_3	0.80	1.00	gnl CDD 71474 pfam08038, Tom7, TOM7 family.	5.00E-10
supercontig_1.132_of_botrytis_cinerea	gene_4	1.00	0.62	gnl CDD 72075 pfam08650, DASH_Dad4, DASH complex subunit Dad4.	6.00E-06
supercontig_1.132_of_botrytis_cinerea	gene_6	0.82	0.82	gnl CDD 67778 pfam04178, Got1, Got1-like family.	2.00E-16
supercontig_1.132_of_botrytis_cinerea	gene_17	0.89	0.96	gnl CDD 29067 cd00148, PROF, Profilin binds actin monomers.	3.00E-20
supercontig_1.164_of_botrytis_cinerea	gene_12	0.98	1.00	gnl CDD 79555 pfam00300, PGAM, Phosphoglycerate mutase family.	6.00E-20
supercontig_1.165_of_botrytis_cinerea	gene_2	0.37	0.66	gnl CDD 29021 cd00266, MADS_SRF_like, SRF-like/Type I subfamily of MADS	4.00E-10
supercontig_1.181_of_botrytis_cinerea	gene_10	0.80	0.99	gnl CDD 67743 pfam04139, Rad9, Rad9. Rad9 is required for transient cell-cycle	5.00E-25
supercontig_1.14_of_botrytis_cinerea	gene_15	0.89	0.75	gnl CDD 30892 COG0546, Gph, Predicted phosphatases.	6.00E-15
supercontig_1.14_of_botrytis_cinerea	gene_17	0.90	0.74	gnl CDD 30892 COG0546, Gph, Predicted phosphatases.	6.00E-15

supercontig_1.190_of_botrytis_cinerea	gene_1	0.49	0.75	gnl CDD 47665 smart00338, BRLZ, basic region leucin zipper.	2.00E-08
supercontig_1.16_of_botrytis_cinerea	gene_14	0.92	0.94	gnl CDD 32448 COG2267, PldB, Lysophospholipase [Lipid metabolism].	1.00E-34
supercontig_1.18_of_botrytis_cinerea	gene_3	0.82	1.00	gnl CDD 74982 PRK05498, rplF, 50S ribosomal protein L6.	4.00E-36
supercontig_1.2_of_botrytis_cinerea	gene_32	0.78	1.00	gnl CDD 68096 pfam04511, DER1, Der1-like family. The endoplasmic reticulum (ER)	5.00E-43
supercontig_1.544_of_botrytis_cinerea	gene_1	0.29	0.89	gnl CDD 48003 smart00736, CADG, Dystroglycan-type cadherin-like domains.	4.00E-06
supercontig_Coccidioides_immitis_RS2.1	gene_469	0.70	0.65	gnl CDD 74804 PRK05134, PRK05134, 3-demethylubiquinone-9 3-methyltransferase.	8.00E-22
supercontig_Coccidioides_immitis_RS2.1	gene_488	0.95	1.00	gnl CDD 32448 COG2267, PldB, Lysophospholipase [Lipid metabolism].	1.00E-37
supercontig_Coccidioides_immitis_RS2.1	gene_508	0.60	0.76	gnl CDD 71997 pfam08571, Yos1, Yos1-like.	3.00E-13
supercontig_Coccidioides_immitis_RS2.1	gene_609	0.17	1.00	gnl CDD 47943 smart00668, CTLH, C-terminal to LisH motif. ; Alpha-helical motif	2.00E-06
supercontig_Coccidioides_immitis_RS2.1	gene_1465	0.88	1.00	gnl CDD 30620 COG0271, BoIA, Stress-induced morphogen (activity unknown)	2.00E-12
supercontig_Coccidioides_immitis_RS2.1	gene_1469	0.67	1.00	gnl CDD 67724 pfam04119, HSP9_HSP12, Heat shock protein 9 / 12.	1.00E-06
supercontig_Coccidioides_immitis_RS2.1	gene_1842	0.73	0.77	gnl CDD 69216 pfam05680, ATP-synt_E, ATP synthase E chain.	5.00E-14
supercontig_Coccidioides_immitis_RS2.1	gene_2157	0.79	1.00	gnl CDD 71474 pfam08038, Tom7, TOM7 family.	2.00E-09

supercontig_Coccidioides_immitis_RS2.2	gene_166	0.74	0.38	gnl CDD 76259 PRK07764, PRK07764, DNA polymerase III subunits gamma and tau.	6.00E-07
supercontig_Coccidioides_immitis_RS2.2	gene_585	0.31	1.00	gnl CDD 28942 cd00060, FHA, Forkhead associated domain (FHA);	1.00E-13
supercontig_Coccidioides_immitis_RS2.2	gene_1028	0.68	0.79	gnl CDD 75062 PRK05649, PRK05649, 4-hydroxybenzoate octaprenyltransferase.	2.00E-47
supercontig_Coccidioides_immitis_RS2.2	gene_1568	0.68	1.00	gnl CDD 66614 pfam02953, zf-Tim10_DDP, Tim10/DDP family zinc finger.	4.00E-12
supercontig_Coccidioides_immitis_RS2.2	gene_1731	0.60	0.94	gnl CDD 58650 cd00926, Cyt_c_Oxidase_VIb, Cytochrome c oxidase subunit VIb.	3.00E-26
supercontig_Coccidioides_immitis_RS2.2	gene_1811	0.48	1.00	gnl CDD 72056 pfam08631, SPO22, Sporulation protein SPO22 like.	2.00E-45
supercontig_Coccidioides_immitis_RS2.2	gene_2059	0.85	1.00	gnl CDD 31830 COG1644, RPB10, DNA-directed RNA polymerase, subunit N	3.00E-21
supercontig_Coccidioides_immitis_RS2.3	gene_219	0.21	0.87	gnl CDD 48627 cd03078, GST_N_Metaxin1_like, GST_N family, Metaxin subfamily,	2.00E-11
supercontig_Coccidioides_immitis_RS2.3	gene_274	0.63	0.89	gnl CDD 68638 pfam05071, NDUFA12, NADH ubiquinone oxidoreductase subunit NDUFA12.	1.00E-12
supercontig_Coccidioides_immitis_RS2.3	gene_552	0.81	1.00	gnl CDD 71726 pfam08293, Mit_rib_S27, Mitochondrial ribosomal subunit S27.	7.00E-17
supercontig_Coccidioides_immitis_RS2.3	gene_753	0.44	0.86	gnl CDD 71653 pfam08219, TOM13, Outer membrane protein TOM13. The TOM13 family	5.00E-17

supercontig_Coccidioides_immitis_RS2.3	gene_1041	1.00	0.98	gnl CDD 29166 cd01763, Sumo, Small ubiquitin-related modifier (SUMO) proteins	1.00E-25
supercontig_Coccidioides_immitis_RS2.3	gene_1157	0.85	0.99	gnl CDD 65691 pfam01920, Prefoldin_2, Prefoldin subunit.	3.00E-08
supercontig_Coccidioides_immitis_RS2.3	gene_1351	0.90	0.94	gnl CDD 34731 COG5130, YIP3, Prenylated rab acceptor 1 and related proteins	2.00E-39
supercontig_Coccidioides_immitis_RS2.4	gene_95	0.90	1.00	gnl CDD 29719 cd01732, LSm5, The eukaryotic Sm and Sm-like (LSm) proteins	2.00E-29
supercontig_Coccidioides_immitis_RS2.4	gene_817	0.59	1.00	gnl CDD 71021 pfam07574, SMC_Nse1, Nse1 non-SMC component of SMC5-6 complex.	2.00E-37
supercontig_Coccidioides_immitis_RS2.4	gene_862	0.30	1.00	gnl CDD 47687 smart00360, RRM, RNA recognition motif;	3.00E-12
supercontig_Coccidioides_immitis_RS2.5	gene_648	0.58	1.00	gnl CDD 72775 pfam01900, RNase_P_Rpp14, Rpp14/Pop5 family. tRNA processing enzyme	5.00E-13
supercontig_2.6_of_Fusarium_oxysporum_f._sp._lycopersici	gene_149	0.39	1.00	gnl CDD 71661 pfam08227, DASH_Hsk3, DASH complex subunit Hsk3 like.	1.00E-08
supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_14	0.09	1.00	gnl CDD 79619 pfam00520, lon_trans, lon transport protein.	6.00E-20
supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_130	0.36	1.00	gnl CDD 64629 pfam00773, RNB, RNB domain.	8.00E-55
supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_261	0.65	1.00	gnl CDD 29029 cd00127, DSPc, Dual specificity phosphatases (DSP);	1.00E-23
supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_344	0.33	0.40	gnl CDD 34840 COG5243, HRD1, HRD ubiquitin ligase complex, ER membrane component	8.00E-11
supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_605	0.87	0.66	gnl CDD 29481 cd00687, Terpene_cyclase_nonplant_C1, NonPlant Terpene Cyclases,	1.00E-13

supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_751	0.58	0.44	gnl CDD 76259 PRK07764, PRK07764, DNA polymerase III subunits gamma and tau.	1.00E-06
supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_866	0.95	1.00	gnl CDD 72346 pfam08927, DUF1909, Domain of unknown function (DUF1909).	1.00E-11
supercontig_2.25_of_Fusarium_oxysporum_f._sp._lycopersici	gene_243	0.14	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR.	5.00E-68
supercontig_2.26_of_Fusarium_oxysporum_f._sp._lycopersici	gene_218	0.22	0.92	gnl CDD 67688 pfam04082, Fungal_trans, Fungal specific transcription factor	1.00E-09
supercontig_2.26_of_Fusarium_oxysporum_f._sp._lycopersici	gene_229	0.66	0.77	gnl CDD 32959 COG3145, AlkB, Alkylated DNA repair protein.	5.00E-09
supercontig_2.26_of_Fusarium_oxysporum_f._sp._lycopersici	gene_312	0.40	0.96	gnl CDD 28826 cd02164, PPAT_CoAS.	3.00E-26
supercontig_2.28_of_Fusarium_oxysporum_f._sp._lycopersici	gene_138	1.00	0.44	gnl CDD 48392 cd02146, NfsA_FRP.	1.00E-18
supercontig_2.28_of_Fusarium_oxysporum_f._sp._lycopersici	gene_148	0.45	0.64	gnl CDD 69235 pfam05699, hATC, hAT family dimerisation domain.	6.00E-07
supercontig_2.28_of_Fusarium_oxysporum_f._sp._lycopersici	gene_1	0.33	0.71	Integrase mediates	2.00E-11
supercontig_2.30_of_Fusarium_oxysporum_f._sp._lycopersici	gene_104	1.00	0.44	gnl CDD 48392 cd02146, NfsA_FRP.	1.00E-18
supercontig_2.30_of_Fusarium_oxysporum_f._sp._lycopersici	gene_114	0.45	0.64	gnl CDD 69235 pfam05699, hATC, hAT family dimerisation domain.	6.00E-07
supercontig_2.31_of_Fusarium_oxysporum_f._sp._lycopersici	gene_72	0.14	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR: Reverse transcriptases (RTs)	5.00E-68
supercontig_2.31_of_Fusarium_oxysporum_f._sp._lycopersici	gene_73	0.35	0.75	gnl CDD 64525 pfam00665, rve, Integrase core domain.	4.00E-12
supercontig_2.31_of_Fusarium_oxysporum_f._sp._lycopersici	gene_3	0.74	0.95	gnl CDD 73154 cd01647, RT_LTR, RT_LTR:	3.00E-44
supercontig_2.4_of_Fusarium_oxysporum_f._sp._lycopersici	gene_941	0.15	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR:	1.00E-67

supercontig_2.4_of_Fusarium_oxysporum_f._sp._lycopersici	gene_947	0.86	1.00	gnl CDD 30876 ECM27, Ca2+/Na+ antiporter	COG0530,	3.00E-20
supercontig_2.36_of_Fusarium_oxysporum_f._sp._lycopersici	gene_1	0.18	1.00	gnl CDD 73154 RT_LTR, RT_LTR	cd01647,	1.00E-67
supercontig_2.37_of_Fusarium_oxysporum_f._sp._lycopersici	gene_17	0.14	1.00	gnl CDD 73154 RT_LTR, RT_LTR	cd01647,	5.00E-68
supercontig_2.38_of_Fusarium_oxysporum_f._sp._lycopersici	gene_15	0.14	1.00	gnl CDD 73154 RT_LTR, RT_LTR	cd01647,	5.00E-68
supercontig_2.43_of_Fusarium_oxysporum_f._sp._lycopersici	gene_30	0.10	0.96	gnl CDD 66556 MIZ, MIZ/SP-RING zinc finger.	pfam02891, zf-	3.00E-16
supercontig_2.43_of_Fusarium_oxysporum_f._sp._lycopersici	gene_45	0.34	0.79	gnl CDD 79449 RnaseH, RNase H.	pfam00075,	2.00E-09
supercontig_2.44_of_Fusarium_oxysporum_f._sp._lycopersici	gene_29	0.14	1.00	gnl CDD 73154 RT_LTR, RT_LTR	cd01647,	5.00E-68
supercontig_2.45_of_Fusarium_oxysporum_f._sp._lycopersici	gene_45	0.14	1.00	gnl CDD 73154 RT_LTR, RT_LTR	cd01647,	5.00E-68
supercontig_2.48_of_Fusarium_oxysporum_f._sp._lycopersici	gene_25	0.85	1.00	gnl CDD 48039 Thioesterase_II_repeat1.	cd03444,	1.00E-15
supercontig_2.5_of_Fusarium_oxysporum_f._sp._lycopersici	gene_346	0.65	0.57	gnl CDD 29142 Serine/Threonine protein kinases, catalytic domain.	cd00180, S_TKc,	2.00E-08
supercontig_2.5_of_Fusarium_oxysporum_f._sp._lycopersici	gene_426	0.84	1.00	gnl CDD 69918 PRP1_N, PRP1 splicing factor, N- terminal.	pfam06424,	4.00E-32
supercontig_2.5_of_Fusarium_oxysporum_f._sp._lycopersici	gene_727	0.77	1.00	gnl CDD 31294 RRP4, RNA-binding protein Rrp4 and related proteins	COG1097,	2.00E-40
supercontig_2.54_of_Fusarium_oxysporum_f._sp._lycopersici	gene_2	0.30	0.94	gnl CDD 64525 Integrase core domain.	pfam00665, rve,	5.00E-17
supercontig_2.6_of_Fusarium_oxysporum_f._sp._lycopersici	gene_337	0.55	0.79	gnl CDD 69734 FRG1, FRG1-like family.	pfam06229,	8.00E-06
supercontig_2.74_of_Fusarium_oxysporum_f._sp._lycopersici	gene_5	0.73	1.00	gnl CDD 73154 RT_LTR, RT_LTR:	cd01647,	1.00E-56
supercontig_2.1_of_Fusarium_oxysporum_f._sp._lycopersici	gene_68	0.95	0.96	gnl CDD 34788 Putative transcriptional repressor regulating G2/M	COG5189, SFP1,	1.00E-31

supercontig_2.96_of_Fusarium_oxysporum_f._sp._lycopersici	gene_2	0.66	0.56	gnl CDD 32411 COG2230, Cfa, Cyclopropane fatty acid synthase and related	2.00E-11
supercontig_2.8_of_Fusarium_oxysporum_f._sp._lycopersici	gene_51	0.69	1.00	gnl CDD 65608 pfam01826, TIL, Trypsin Inhibitor like cysteine rich domain.	5.00E-06
supercontig_2.8_of_Fusarium_oxysporum_f._sp._lycopersici	gene_219	0.82	0.95	gnl CDD 79719 pfam00903, Glyoxalase, Glyoxalase/Bleomycin resistance	2.00E-06
supercontig_2.8_of_Fusarium_oxysporum_f._sp._lycopersici	gene_249	0.68	0.92	gnl CDD 34729 COG5128, COG5128, Transport protein particle (TRAPP) complex	2.00E-46
supercontig_2.8_of_Fusarium_oxysporum_f._sp._lycopersici	gene_289	0.47	1.00	gnl CDD 72017 pfam08592, DUF1772, Domain of unknown function (DUF1772).	1.00E-13
supercontig_2.8_of_Fusarium_oxysporum_f._sp._lycopersici	gene_510	0.90	0.87	gnl CDD 67779 pfam04179, Init_tRNA_PT, Initiator tRNA phosphoribosyl transferase.	1.00E-85
supercontig_2.9_of_Fusarium_oxysporum_f._sp._lycopersici	gene_4	0.20	0.98	gnl CDD 64525 pfam00665, rve, Integrase core domain.	2.00E-17
supercontig_2.9_of_Fusarium_oxysporum_f._sp._lycopersici	gene_57	0.31	0.93	gnl CDD 47948 smart00674, CENPB, Putative DNA-binding domain in centromere	7.00E-06
supercontig_2.9_of_Fusarium_oxysporum_f._sp._lycopersici	gene_115	0.14	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR	5.00E-68
supercontig_2.9_of_Fusarium_oxysporum_f._sp._lycopersici	gene_32	0.95	0.65	gnl CDD 73491 PRK00102, rnc, ribonuclease III.	4.00E-07
supercontig_2.2_of_Fusarium_oxysporum_f._sp._lycopersici	gene_57	0.78	1.00	gnl CDD 32694 COG2867, COG2867, Oligoketide cyclase/lipid transport protein	7.00E-26
supercontig_2.2_of_Fusarium_oxysporum_f._sp._lycopersici	gene_163	0.79	1.00	gnl CDD 71474 pfam08038, Tom7, TOM7 family. This family consists of TOM7 family	5.00E-10

supercontig_2.10_of_Fusarium_oxysporum_f._sp._lycopersici	gene_114	0.93	1.00	gnl CDD 31782 COG1594, RPB9, DNA-directed RNA polymerase, subunit M/Transcription	7.00E-14
supercontig_2.10_of_Fusarium_oxysporum_f._sp._lycopersici	gene_554	0.14	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR	5.00E-68
supercontig_2.11_of_Fusarium_oxysporum_f._sp._lycopersici	gene_127	0.96	1.00	gnl CDD 32441 COG2260, COG2260, Predicted Zn-ribbon RNA-binding protein	6.00E-10
supercontig_2.11_of_Fusarium_oxysporum_f._sp._lycopersici	gene_95	1.00	1.00	gnl CDD 71966 pfam08538, DUF1749, Protein of unknown function (DUF1749).	2.00E-71
supercontig_2.11_of_Fusarium_oxysporum_f._sp._lycopersici	gene_190	0.98	1.00	gnl CDD 30426 COG0077, PheA, Prephenate dehydratase	7.00E-71
supercontig_2.12_of_Fusarium_oxysporum_f._sp._lycopersici	gene_283	0.17	0.81	gnl CDD 28964 cd00083, HLH, Helix-loop-helix domain	3.00E-07
supercontig_2.12_of_Fusarium_oxysporum_f._sp._lycopersici	gene_400	0.26	1.00	gnl CDD 48037 cd03442, BFIT_BACH, Brown fat-inducible thioesterase (BFIT).	1.00E-20
supercontig_2.2_of_Fusarium_oxysporum_f._sp._lycopersici	gene_70	0.64	1.00	gnl CDD 72839 pfam08583, UPF0287, Uncharacterised protein family (UPF0287).	1.00E-22
supercontig_2.2_of_Fusarium_oxysporum_f._sp._lycopersici	gene_363	0.91	1.00	gnl CDD 29719 cd01732, LSm5, The eukaryotic Sm and Sm-like (LSm) proteins	3.00E-30
supercontig_2.2_of_Fusarium_oxysporum_f._sp._lycopersici	gene_812	0.94	1.00	gnl CDD 33183 COG3376, HoxN, High-affinity nickel permease	2.00E-78
supercontig_2.2_of_Fusarium_oxysporum_f._sp._lycopersici	gene_890	0.35	0.75	gnl CDD 64525 pfam00665, rve, Integrase core domain.	4.00E-12
supercontig_2.2_of_Fusarium_oxysporum_f._sp._lycopersici	gene_891	0.23	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR	3.00E-67
supercontig_2.14_of_Fusarium_oxysporum_f._sp._lycopersici	gene_44	0.14	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR	5.00E-68
supercontig_2.14_of_Fusarium_oxysporum_f._sp._lycopersici	gene_159	0.70	0.92	gnl CDD 34746 COG5145, RAD14, DNA excision repair protein	5.00E-50

supercontig_2.15_of_Fusarium_oxysporum_f._sp._lycopersici	gene_7	0.78	0.62	gnl CDD 74518 PRK03983, PRK03983, exosome complex exonuclease Rrp41.	3.00E-11
supercontig_2.15_of_Fusarium_oxysporum_f._sp._lycopersici	gene_100	0.62	0.96	gnl CDD 69491 pfam05971, Methyltransf_10, Protein of unknown function (DUF890).	2.00E-53
supercontig_2.15_of_Fusarium_oxysporum_f._sp._lycopersici	gene_198	0.59	0.55	gnl CDD 30614 COG0265, DegQ, Trypsin-like serine proteases,	3.00E-07
supercontig_2.15_of_Fusarium_oxysporum_f._sp._lycopersici	gene_289	0.61	1.00	gnl CDD 47935 smart00659, RPOLCX, RNA polymerase subunit CX;	2.00E-08
supercontig_2.15_of_Fusarium_oxysporum_f._sp._lycopersici	gene_311	0.55	0.49	gnl CDD 66174 pfam02458, Transferase, Transferase family.	3.00E-15
supercontig_2.17_of_Fusarium_oxysporum_f._sp._lycopersici	gene_54	0.97	1.00	gnl CDD 72082 pfam08657, DASH_Spc34, DASH complex subunit Spc34.	5.00E-54
supercontig_2.17_of_Fusarium_oxysporum_f._sp._lycopersici	gene_56	0.12	1.00	gnl CDD 29102 cd00162, RING, RING-finger (Really Interesting New Gene) domain	3.00E-06
supercontig_2.17_of_Fusarium_oxysporum_f._sp._lycopersici	gene_291	0.54	0.62	gnl CDD 29841 cd00632, Prefoldin_beta, Prefoldin beta	6.00E-06
supercontig_2.18_of_Fusarium_oxysporum_f._sp._lycopersici	gene_29	0.49	0.50	gnl CDD 79444 pfam00069, Pkinase, Protein kinase domain.	5.00E-09
supercontig_2.19_of_Fusarium_oxysporum_f._sp._lycopersici	gene_350	0.53	0.73	gnl CDD 69043 pfam05498, RALF, Rapid ALkalinization Factor (RALF).	3.00E-13
supercontig_2.20_of_Fusarium_oxysporum_f._sp._lycopersici	gene_180	0.76	0.55	gnl CDD 69212 pfam05676, NDUF_B7, NADH-ubiquinone oxidoreductase B18 subunit	3.00E-11
supercontig_2.20_of_Fusarium_oxysporum_f._sp._lycopersici	gene_251	0.23	1.00	gnl CDD 48011 smart00744, RINGv, The RING-variant domain is a C4HC3 zinc-finger	8.00E-07
supercontig_2.21_of_Fusarium_oxysporum_f._sp._lycopersici	gene_11	0.49	0.50	gnl CDD 79444 pfam00069, Pkinase, Protein kinase domain.	5.00E-09

supercontig_2.3_of_Fusarium_oxysporum_f._sp._lycopersici	gene_35	0.89	0.93	gnl CDD 66174 pfam02458, Transferase, Transferase family.	4.00E-15
supercontig_2.3_of_Fusarium_oxysporum_f._sp._lycopersici	gene_98	0.92	0.98	gnl CDD 31089 COG0746, MobA, Molybdopterin-guanine dinucleotide biosynthesis	4.00E-14
supercontig_2.3_of_Fusarium_oxysporum_f._sp._lycopersici	gene_422	0.64	0.43	gnl CDD 30669 COG0321, LipB, Lipoate-protein ligase B [Coenzyme metabolism].	2.00E-14
supercontig_2.3_of_Fusarium_oxysporum_f._sp._lycopersici	gene_442	0.97	1.00	gnl CDD 47853 smart00552, ADEAMc, tRNA-specific and double-stranded RNA adenosine	1.00E-47
supercontig_2.3_of_Fusarium_oxysporum_f._sp._lycopersici	gene_455	0.50	1.00	gnl CDD 71661 pfam08227, DASH_Hsk3, DASH complex subunit Hsk3 like.	2.00E-08
supercontig_2.3_of_Fusarium_oxysporum_f._sp._lycopersici	gene_515	0.96	1.00	gnl CDD 69400 pfam05871, ESCRT-II, ESCRT-II complex subunit.	9.00E-50
supercontig_2.3_of_Fusarium_oxysporum_f._sp._lycopersici	gene_654	0.74	1.00	gnl CDD 31778 COG1590, COG1590, Uncharacterized conserved protein.	6.00E-24
supercontig_2.22_of_Fusarium_oxysporum_f._sp._lycopersici	gene_49	0.14	1.00	gnl CDD 73154 cd01647, RT_LTR, RT_LTR	5.00E-68
supercontig_2.23_of_Fusarium_oxysporum_f._sp._lycopersici	gene_241	0.93	0.59	gnl CDD 30949 COG0604, Qor, NADPH:quinone reductase and related Zn-dependent	1.00E-17
supercontig_2.23_of_Fusarium_oxysporum_f._sp._lycopersici	gene_336	0.51	0.93	gnl CDD 29261 cd00204, ANK, ankyrin repeats.	3.00E-08
supercontig_2.24_of_Fusarium_oxysporum_f._sp._lycopersici	gene_60	0.59	1.00	gnl CDD 47626 smart00298, CHROMO, Chromatin organization modifier domain.	6.00E-06
Sclerotinia_sclerotiorum_supercontig_1.1	gene_495	0.70	0.90	gnl CDD 68638 pfam05071, NDUFA12, NADH ubiquinone oxidoreductase subunit NDUFA12.	5.00E-12
Sclerotinia_sclerotiorum_supercontig_1.1	gene_748	0.63	0.94	gnl CDD 47654 smart00326, SH3, Src homology 3 domains; Src homology 3 (SH3)	1.00E-09

Sclerotinia_sclerotiorum_supercontig_1.10	gene_123	0.42	0.80	gnl CDD 30683 COG0335, RpIS, Ribosomal protein L19.	9.00E-10
Sclerotinia_sclerotiorum_supercontig_1.10	gene_132	0.59	1.00	gnl CDD 69040 pfam05495, zf-CHY, CHY zinc finger.	2.00E-09
Sclerotinia_sclerotiorum_supercontig_1.11	gene_143	0.72	1.00	gnl CDD 72881 cd02885, IPP_Isomerase, Isopentenyl diphosphate (IPP).	2.00E-60
Sclerotinia_sclerotiorum_supercontig_1.11	gene_375	0.63	0.87	gnl CDD 75796 PRK06849, PRK06849, hypothetical protein.	2.00E-35
Sclerotinia_sclerotiorum_supercontig_1.11	gene_399	0.96	1.00	gnl CDD 34679 COG5075, COG5075, Uncharacterized conserved protein.	9.00E-62
Sclerotinia_sclerotiorum_supercontig_1.12	gene_320	0.57	0.97	gnl CDD 71474 pfam08038, Tom7, TOM7 family.	2.00E-09
Sclerotinia_sclerotiorum_supercontig_1.14	gene_110	0.62	1.00	gnl CDD 31588 COG1398, OLE1, Fatty-acid desaturase [Lipid metabolism].	3.00E-76
Sclerotinia_sclerotiorum_supercontig_1.18	gene_98	0.65	1.00	gnl CDD 29952 cd00959, DeoC, 2-deoxyribose-5-phosphate aldolase (DERA) of the	1.00E-40
Sclerotinia_sclerotiorum_supercontig_1.2	gene_526	0.34	1.00	gnl CDD 29697 cd00593, RIBOc, RIBOc. Ribonuclease III C terminal domain.	4.00E-21
Sclerotinia_sclerotiorum_supercontig_1.20	gene_57	0.61	0.34	gnl CDD 65423 pfam01624, MutS_I, MutS domain I.	2.00E-08
Sclerotinia_sclerotiorum_supercontig_1.22	gene_154	0.58	0.40	gnl CDD 69613 pfam06101, DUF946, Plant protein of unknown function (DUF946).	6.00E-10
Sclerotinia_sclerotiorum_supercontig_1.26	gene_15	0.29	1.00	gnl CDD 67744 pfam04140, ICMT, Isoprenylcysteine carboxyl methyltransferase	2.00E-19
Sclerotinia_sclerotiorum_supercontig_1.31	gene_24	0.66	1.00	gnl CDD 67469 pfam03856, SUN, Beta-glucosidase (SUN family).	4.00E-53

Sclerotinia_sclerotiorum_supercontig_1.5	gene_309	0.40	0.98	gnl CDD 70208 pfam06728, PIG-U, GPI transamidase subunit PIG-U.	1.00E-40
Sclerotinia_sclerotiorum_supercontig_1.8	gene_263	0.79	1.00	gnl CDD 69301 pfam05768, DUF836, Glutaredoxin-like domain (DUF836).	5.00E-06
Phaeosphaeria_nodorum_supercontig_1.33	gene_13	0.82	1.00	gnl CDD 80120 pfam05721, PhyH, Phytanoyl-CoA dioxygenase (PhyH).	4.00E-28
Phaeosphaeria_nodorum_supercontig_1.10	gene_5	0.74	1.00	gnl CDD 29709 cd01722, Sm_F, The eukaryotic Sm and Sm-like (LSm) proteins	6.00E-25
Phaeosphaeria_nodorum_supercontig_1.6	gene_132	0.64	0.80	gnl CDD 71997 pfam08571, Yos1, Yos1-like. In yeast, Yos1 is a subunit of the	1.00E-16
Phaeosphaeria_nodorum_supercontig_1.7	gene_201	0.63	0.85	gnl CDD 68195 pfam04614, Pex19, Pex19 protein family.	9.00E-20
supercontig_3.1_of_Fusarium_graminearum	gene_131	0.40	1.00	gnl CDD 29261 cd00204, ANK, ankyrin repeats;	7.00E-10
supercontig_3.1_of_Fusarium_graminearum	gene_321	0.35	0.31	gnl CDD 79137 PRK12678, PRK12678, transcription termination factor Rho.	1.00E-07
supercontig_3.4_of_Fusarium_graminearum	gene_334	0.32	0.37	gnl CDD 77212 PRK09510, tolA, cell envelope integrity inner membrane protein	9.00E-06
supercontig_3.4_of_Fusarium_graminearum	gene_698	0.97	1.00	gnl CDD 72839 pfam08583, UPF0287, Uncharacterised protein family (UPF0287).	1.00E-17
supercontig_3.4_of_Fusarium_graminearum	gene_756	0.45	1.00	gnl CDD 65057 pfam01230, HIT, HIT domain.	6.00E-07
supercontig_3.4_of_Fusarium_graminearum	gene_852	0.29	0.98	gnl CDD 65933 pfam02194, PXA, PXA domain. This domain is associated with PX	1.00E-11
supercontig_3.4_of_Fusarium_graminearum	gene_904	0.62	0.92	gnl CDD 79664 pfam00639, Rotamase, PPIC-type PPIASE domain.	5.00E-11

supercontig_3.4_of_Fusarium_graminearum	gene_1192	0.65	0.77	gnl CDD 32959 COG3145, AlkB, Alkylated DNA repair protein [DNA replication,	8.00E-09
supercontig_3.5_of_Fusarium_graminearum	gene_343	0.23	1.00	gnl CDD 70445 pfam06978, POP1, Ribonucleases P/MRP protein subunit POP1.	2.00E-16
supercontig_3.6_of_Fusarium_graminearum	gene_214	0.23	0.95	gnl CDD 79643 pfam00583, Acetyltransf_1, Acetyltransferase (GNAT) family.	4.00E-07
supercontig_3.6_of_Fusarium_graminearum	gene_367	0.22	0.98	gnl CDD 79450 pfam00076, RRM_1, RNA recognition motif. (a.k.a. RRM, RBD, or RNP	3.00E-10
supercontig_3.1_of_Fusarium_graminearum	gene_733	0.82	1.00	gnl CDD 69301 pfam05768, DUF836, Glutaredoxin-like domain (DUF836).	2.00E-09
supercontig_3.1_of_Fusarium_graminearum	gene_1030	0.79	0.56	gnl CDD 34793 COG5194, APC11, Component of SCF ubiquitin ligase	2.00E-08
supercontig_3.6_of_Fusarium_graminearum	gene_347	0.84	1.00	gnl CDD 31782 COG1594, RPB9, DNA-directed RNA polymerase, subunit M/Transcription	1.00E-13
supercontig_3.7_of_Fusarium_graminearum	gene_99	0.79	1.00	gnl CDD 31294 COG1097, RRP4, RNA-binding protein Rrp4 and related proteins	1.00E-40
supercontig_3.1_of_Fusarium_graminearum	gene_37	0.83	0.95	gnl CDD 30036 cd01293, Bact_CD, Bacterial cytosine deaminase	1.00E-48
supercontig_3.1_of_Fusarium_graminearum	gene_85	0.67	0.76	gnl CDD 72809 pfam05493, ATP_synt_H, ATP synthase subunit H.	2.00E-06
supercontig_3.1_of_Fusarium_graminearum	gene_155	0.31	1.00	gnl CDD 29261 cd00204, ANK, ankyrin repeats;	4.00E-12
supercontig_3.2_of_Fusarium_graminearum	gene_379	0.86	1.00	gnl CDD 72162 pfam08738, Gon7, Gon7 family.	1.00E-09

supercontig_3.3_of_Fusarium_graminearum	gene_654	0.70	1.00	gnl CDD 72775 RNase_P_Rpp14, family.	pfam01900, Rpp14/Pop5	3.00E-14
supercontig_3.3_of_Fusarium_graminearum	gene_670	0.59	1.00	gnl CDD 71719 Spc24, Spc24 subunit of Ndc80.	pfam08286,	5.00E-26
supercontig_3.3_of_Fusarium_graminearum	gene_50	0.78	0.93	gnl CDD 28942 Forkhead associated domain (FHA);	cd00060, FHA,	7.00E-10
supercontig_3.3_of_Fusarium_graminearum	gene_239	0.40	1.00	gnl CDD 71675 Methyltransf_11, Methyltransferase domain.	pfam08241,	7.00E-11
Magnaporthe_grisea_70-15_supercontig_5.134	gene_29	0.47	1.00	gnl CDD 71198 DUF1613, Protein of unknown function (DUF1613).	pfam07757,	4.00E-76
Magnaporthe_grisea_70-15_supercontig_5.134	gene_58	0.42	0.97	gnl CDD 79702 PX domain. PX domains bind to phosphoinositides.	pfam00787, PX,	2.00E-17
Magnaporthe_grisea_70-15_supercontig_5.134	gene_167	0.97	0.82	gnl CDD 30800 WcaG, Nucleoside-diphosphate- sugar epimerases	COG0451,	4.00E-07
Magnaporthe_grisea_70-15_supercontig_5.134	gene_168	0.50	0.76	gnl CDD 70740 DUF1446, Protein of unknown function (DUF1446).	pfam07287,	2.00E-52
Magnaporthe_grisea_70-15_supercontig_5.134	gene_186	0.37	0.82	gnl CDD 71939 COQ9, COQ9.	pfam08511,	2.00E-20
Magnaporthe_grisea_70-15_supercontig_5.178	gene_119	0.65	1.00	gnl CDD 72775 RNase_P_Rpp14, family.	pfam01900, Rpp14/Pop5	8.00E-15
Magnaporthe_grisea_70-15_supercontig_5.186	gene_45	0.56	0.36	gnl CDD 76117 PRK07479, 3-ketoacyl-(acyl- carrier-protein)	PRK07479,	1.00E-11
Magnaporthe_grisea_70-15_supercontig_5.187	gene_111	0.87	0.99	gnl CDD 31215 COG1011, Predicted hydrolase (HAD superfamily)	COG1011,	2.00E-11

Magnaporthe_grisea_70-15_supercontig_5.187	gene_85	0.72	0.56	gnl CDD 32715 COG2890, HemK, Methylase of polypeptide chain release factors	2.00E-09
Magnaporthe_grisea_70-15_supercontig_5.190	gene_81	0.90	0.88	gnl CDD 35095 COG5536, BET4, Protein prenyltransferase, alpha subunit	1.00E-28
Magnaporthe_grisea_70-15_supercontig_5.190	gene_266	0.97	0.93	gnl CDD 30426 COG0077, PheA, Prephenate dehydratase	4.00E-58
Magnaporthe_grisea_70-15_supercontig_5.191	gene_38	0.76	1.00	gnl CDD 64803 pfam00955, HCO3_cotransp, HCO3-transporter family.	1.00E-52
Magnaporthe_grisea_70-15_supercontig_5.194	gene_6	0.63	1.00	gnl CDD 31137 COG0794, GutQ, Predicted sugar phosphate isomerase involved in	3.00E-24
Magnaporthe_grisea_70-15_supercontig_5.194	gene_68	0.95	0.75	gnl CDD 48573 cd03024, DsbA_FrnE, DsbA family, FrnE subfamily.	4.00E-18
Magnaporthe_grisea_70-15_supercontig_5.194	gene_68	0.63	0.97	gnl CDD 66296 pfam02594, DUF167, Uncharacterised ACR, YggU family COG1872.	2.00E-09
Magnaporthe_grisea_70-15_supercontig_5.194	gene_616	0.57	0.87	gnl CDD 74772 PRK05014, hscB, co-chaperone HscB.	3.00E-11
Magnaporthe_grisea_70-15_supercontig_5.194	gene_54	0.56	0.97	gnl CDD 29621 cd00520, RRF, Ribosome recycling factor (RRF).	1.00E-08
Magnaporthe_grisea_70-15_supercontig_5.195	gene_12	0.90	1.00	gnl CDD 29648 cd00563, Dtyr_deacylase, D-Tyrosyl-tRNA ^{tyr} deacylases.	6.00E-46
Magnaporthe_grisea_70-15_supercontig_5.195	gene_75	0.83	0.90	gnl CDD 75144 PRK05766, rps14P, 30S ribosomal protein S14P.	3.00E-09
Magnaporthe_grisea_70-15_supercontig_5.195	gene_144	0.59	0.81	gnl CDD 72817 pfam06331, Tbf5, Transcription factor TFIIH complex subunit Tfb5.	6.00E-10

Magnaporthe_grisea_70-15_supercontig_5.196	gene_20	1.00	1.00	gnl CDD 30839 COG0493, GltD, NADPH-dependent glutamate synthase beta chain.	8.00E-32
Magnaporthe_grisea_70-15_supercontig_5.196	gene_85	0.95	1.00	gnl CDD 72839 pfam08583, UPF0287, Uncharacterised protein family (UPF0287).	1.00E-16
Magnaporthe_grisea_70-15_supercontig_5.196	gene_86	0.83	0.85	gnl CDD 35107 COG5548, COG5548, Small integral membrane protein.	9.00E-11
Magnaporthe_grisea_70-15_supercontig_5.196	gene_88	0.57	0.41	gnl CDD 79487 pfam00144, Beta-lactamase, Beta-lactamase.	2.00E-11
Magnaporthe_grisea_70-15_supercontig_5.196	gene_4	0.95	0.87	gnl CDD 68035 pfam04446, Thg1, tRNAHis guanylyltransferase.	3.00E-53
Magnaporthe_grisea_70-15_supercontig_5.196	gene_168	0.56	0.47	gnl CDD 29261 cd00204, ANK, ankyrin repeats; ankyrin repeats mediate	1.00E-06
Magnaporthe_grisea_70-15_supercontig_5.196	gene_188	0.57	1.00	gnl CDD 69428 pfam05903, DUF862, PPPDE putative peptidase domain.	2.00E-33
AACW02000010_ _CONTIG_10__ _Rhizopus_oryzae_supercontig_3.1_ _[2400983-2598834]_ _197852_nt_	gene_22	0.68	1.00	gnl CDD 30376 COG0026, PurK, Phosphoribosylaminoimidazole carboxylase	e-113
AACW02000102_ _CONTIG_102__ _Rhizopus_oryzae_supercontig_3.5_ _[154653-488518]_ _333866_nt_	gene_75	0.73	0.94	gnl CDD 72061 pfam08636, Pkr1, ER protein Pkr1.	2.00E-06
AACW02000011_ _CONTIG_11__ _Rhizopus_oryzae_supercontig_3.1_ _[2598935-3032215]_ _433281_nt_	gene_16	0.90	1.00	gnl CDD 30181 cd01994, Alpha_ANH_like_IV	5.00E-29
AACW02000011_ _CONTIG_11__ _Rhizopus_oryzae_supercontig_3.1_ _[2598935-3032215]_ _433281_nt_	gene_47	0.26	0.95	gnl CDD 47750 smart00443, G_patch, glycine rich nucleic binding domain;	1.00E-06
AACW02000011_ _CONTIG_11__ _Rhizopus_oryzae_supercontig_3.1_ _[2598935-3032215]_ _433281_nt_	gene_111	0.91	1.00	gnl CDD 29719 cd01732, LSm5, The eukaryotic Sm and Sm-like (LSm) proteins	9.00E-30

AACW02000113_ _CONTIG_113_ _Rhizopus_oryzae_supercontig_3.5_ _[1292705-1448586] _155882_nt_	gene_44	0.97	0.96	gnl CDD 34696 COG5093, COG5093, Uncharacterized conserved protein	1.00E-36
AACW02000116_ _CONTIG_116_ _Rhizopus_oryzae_supercontig_3.5_ _[1648264-1804041] _155778_nt_	gene_53	0.55	0.82	gnl CDD 79643 pfam00583, Acetyltransf_1, Acetyltransferase (GNAT) family.	2.00E-07
AACW02000117_ _CONTIG_117_ _Rhizopus_oryzae_supercontig_3.5_ _[1804142-1926323] _122182_nt_	gene_12	0.38	0.98	gnl CDD 68297 pfam04719, TAFII28, hTAFII28-like conserved region.	9.00E-27
AACW02000121_ _CONTIG_121_ _Rhizopus_oryzae_supercontig_3.5_ _[2206362-2288780] _82419_nt_	gene_7	0.97	1.00	gnl CDD 34827 COG5230, COG5230, Uncharacterized conserved protein	9.00E-31
AACW02000121_ _CONTIG_121_ _Rhizopus_oryzae_supercontig_3.5_ _[2206362-2288780] _82419_nt_	gene_21	0.16	0.95	gnl CDD 32274 COG2091, Sfp, Phosphopantetheinyl transferase	2.00E-24
AACW02000143_ _CONTIG_143_ _Rhizopus_oryzae_supercontig_3.6_ _[362262-593047] _230786_nt_	gene_54	0.86	1.00	gnl CDD 79999 pfam03372, Exo_endo_phos, Endonuclease/Exonuclease/phosphatase	5.00E-14
AACW02000143_ _CONTIG_143_ _Rhizopus_oryzae_supercontig_3.6_ _[362262-593047] _230786_nt_	gene_57	0.78	0.99	gnl CDD 71649 pfam08215, DUF1715, Eukaryotic domain of unknown function	8.00E-15
AACW02000144_ _CONTIG_144_ _Rhizopus_oryzae_supercontig_3.6_ _[593148-906311] _313164_nt_	gene_49	0.96	1.00	gnl CDD 33417 COG3618, COG3618, Predicted metal-dependent hydrolase	2.00E-38
AACW02000157_ _CONTIG_157_ _Rhizopus_oryzae_supercontig_3.6_ _[2522494-2859520] _337027_nt_	gene_16	0.29	0.92	gnl CDD 29006 cd02396, PCBP_like_KH, K homology RNA-binding domain, PCBP_like.	2.00E-06
AACW02000166_ _CONTIG_166_ _Rhizopus_oryzae_supercontig_3.7_ _[471419-758678] _287260_nt_	gene_72	0.96	1.00	gnl CDD 72167 pfam08743, Nse4, Nse4. Nse4 is a component of the Smc5/6 DNA repair	2.00E-53
AACW02000173_ _CONTIG_173_ _Rhizopus_oryzae_supercontig_3.7_ _[1109583-1767534] _657952_nt_	gene_238	0.86	0.98	gnl CDD 33461 COG3663, Mug, G:T/U mismatch-specific DNA glycosylase	2.00E-19

AACW02000194_ _CONTIG_194_ _Rhizopus_oryzae_supercontig_3.8_ _[1456944-1811534] _354591_nt_	gene_96	0.87	1.00	gnl CDD 32648 COG2820, Udp, Uridine phosphorylase [Nucleotide transport and	6.00E-19
AACW02000198_ _CONTIG_198_ _Rhizopus_oryzae_supercontig_3.8_ _[2139510-2362744] _223235_nt_	gene_27	0.60	0.34	gnl CDD 79137 PRK12678, PRK12678, transcription termination factor Rho.	3.00E-09
AACW02000210_ _CONTIG_210_ _Rhizopus_oryzae_supercontig_3.9_ _[1865000-2296105] _431106_nt_	gene_22	0.95	0.98	gnl CDD 78584 PRK11587, PRK11587, putative phosphatase.	2.00E-36
AACW02000216_ _CONTIG_216_ _Rhizopus_oryzae_supercontig_3.10_ _[335899-760890] _424992_nt_	gene_23	0.39	0.81	gnl CDD 29705 cd01718, Sm_E, The eukaryotic Sm and Sm-like (LSm) proteins	2.00E-25
AACW02000216_ _CONTIG_216_ _Rhizopus_oryzae_supercontig_3.10_ _[335899-760890] _424992_nt_	gene_151	0.84	0.88	gnl CDD 31007 COG0663, PaaY, Carbonic anhydrases/acetyltransferases, isoleucine	7.00E-16
AACW02000219_ _CONTIG_219_ _Rhizopus_oryzae_supercontig_3.10_ _[1035221-1305776] _270556_nt_	gene_68	0.28	0.92	gnl CDD 67722 pfam04117, Mpv17_PMP22, Mpv17 / PMP22 family.	7.00E-12
AACW02000219_ _CONTIG_219_ _Rhizopus_oryzae_supercontig_3.10_ _[1035221-1305776] _270556_nt_	gene_72	0.72	0.76	gnl CDD 68849 pfam05292, MCD, Malonyl-CoA decarboxylase (MCD).	2.00E-32
AACW02000228_ _CONTIG_228_ _Rhizopus_oryzae_supercontig_3.11_ _[1-736642] _736642_nt_	gene_154	0.53	0.76	gnl CDD 34689 COG5085, COG5085, Predicted membrane protein.	3.00E-19
AACW02000023_ _CONTIG_23_ _Rhizopus_oryzae_supercontig_3.1_ _[3465973-3499457] _33485_nt_	gene_5	0.57	1.00	gnl CDD 69614 pfam06102, DUF947, Domain of unknown function (DUF947).	2.00E-11
AACW02000233_ _CONTIG_233_ _Rhizopus_oryzae_supercontig_3.11_ _[789332-930552] _141221_nt_	gene_33	0.41	0.82	gnl CDD 30935 COG0590, CumB, Cytosine/adenosine deaminases.	1.00E-17
AACW02000235_ _CONTIG_235_ _Rhizopus_oryzae_supercontig_3.11_ _[934731-1439178] _504448_nt_	gene_92	0.98	0.91	gnl CDD 34622 COG5017, COG5017, Uncharacterized conserved protein.	1.00E-13
AACW02000235_ _CONTIG_235_ _Rhizopus_oryzae_supercontig_3.11_ _[934731-1439178] _504448_nt_	gene_118	0.95	1.00	gnl CDD 29161 cd00754, Moad, Moad family.	6.00E-14

AACW02000235_ _CONTIG_235_ _Rhizopus_oryzae_supercontig_3.11_ _[934731-1439178]_ _504448_nt_	gene_147	0.76	0.95	gnl CDD 34813 COG5216, COG5216, Uncharacterized conserved protein.	3.00E-18
AACW02000235_ _CONTIG_235_ _Rhizopus_oryzae_supercontig_3.11_ _[934731-1439178]_ _504448_nt_	gene_171	0.17	1.00	gnl CDD 72053 pfam08628, Nexin_C, Sorting nexin C terminal.	2.00E-07
AACW02000239_ _CONTIG_239_ _Rhizopus_oryzae_supercontig_3.11_ _[1471025-1585522]_ _114498_nt_	gene_25	0.65	1.00	gnl CDD 72882 cd03424, ADPRase_NUDT5, ADP-ribose pyrophosphatase (ADPRase)	5.00E-15
AACW02000250_ _CONTIG_250_ _Rhizopus_oryzae_supercontig_3.12_ _[473879-1120864]_ _646986_nt_	gene_8	0.59	0.40	gnl CDD 68494 pfam04922, DIE2_ALG10, DIE2/ALG10 family.	3.00E-26
AACW02000250_ _CONTIG_250_ _Rhizopus_oryzae_supercontig_3.12_ _[473879-1120864]_ _646986_nt_	gene_80	1.00	1.00	gnl CDD 67275 pfam03647, TMEM14, Transmembrane proteins 14C.	4.00E-11
AACW02000250_ _CONTIG_250_ _Rhizopus_oryzae_supercontig_3.12_ _[473879-1120864]_ _646986_nt_	gene_142	0.77	0.79	gnl CDD 70129 pfam06645, SPC12, Microsomal signal peptidase 12 kDa subunit	1.00E-11
AACW02000250_ _CONTIG_250_ _Rhizopus_oryzae_supercontig_3.12_ _[473879-1120864]_ _646986_nt_	gene_218	0.97	1.00	gnl CDD 68156 pfam04573, SPC22, Signal peptidase subunit.	4.00E-28
AACW02000253_ _CONTIG_253_ _Rhizopus_oryzae_supercontig_3.12_ _[1241831-1398439]_ _156609_nt_	gene_25	0.71	1.00	gnl CDD 47999 smart00731, SprT, SprT homologues.	9.00E-21
AACW02000257_ _CONTIG_257_ _Rhizopus_oryzae_supercontig_3.13_ _[7284-135576]_ _128293_nt_	gene_32	0.88	0.90	gnl CDD 68801 pfam05241, EBP, Emopamil binding protein.	1.00E-26
AACW02000268_ _CONTIG_268_ _Rhizopus_oryzae_supercontig_3.14_ _[586241-956944]_ _370704_nt_	gene_6	0.55	1.00	gnl CDD 79643 pfam00583, Acetyltransf_1, Acetyltransferase (GNAT) family.	1.00E-14
AACW02000268_ _CONTIG_268_ _Rhizopus_oryzae_supercontig_3.14_ _[586241-956944]_ _370704_nt_	gene_130	0.56	0.58	gnl CDD 35095 COG5536, BET4, Protein prenyltransferase, alpha subunit	1.00E-08
AACW02000274_ _CONTIG_274_ _Rhizopus_oryzae_supercontig_3.15_ _[1-410886]_ _410886_nt_	gene_112	0.83	0.82	gnl CDD 70180 pfam06699, PIG-F, Phospho-ethanolamine N-methyltransferase.	1.00E-18

AACW02000275_ _CONTIG_275_ _Rhizopus_oryzae_supercontig_3.15_ _[415307-518953] _103647_nt_	gene_4	0.46	0.56	gnl CDD 30003 cd01393, recA_like, RecA is a bacterial enzyme which has roles in	1.00E-07
AACW02000279_ _CONTIG_279_ _Rhizopus_oryzae_supercontig_3.15_ _[570083-942547] _372465_nt_	gene_3	0.93	0.94	gnl CDD 69821 pfam06320, GCN5L1, GCN5-like protein 1 (GCN5L1).	1.00E-20
AACW02000279_ _CONTIG_279_ _Rhizopus_oryzae_supercontig_3.15_ _[570083-942547] _372465_nt_	gene_41	0.35	0.80	gnl CDD 64946 pfam01111, CKS, Cyclin-dependent kinase regulatory subunit.	2.00E-17
AACW02000288_ _CONTIG_288_ _Rhizopus_oryzae_supercontig_3.16_ _[333133-673130] _339998_nt_	gene_70	0.44	0.36	gnl CDD 34689 COG5085, COG5085, Predicted membrane protein.	2.00E-12
AACW02000293_ _CONTIG_293_ _Rhizopus_oryzae_supercontig_3.17_ _[1-476381] _476381_nt_	gene_49	0.81	0.65	gnl CDD 68305 pfam04727, ELMO_CED12, ELMO/CED-12 family.	2.00E-26
AACW02000293_ _CONTIG_293_ _Rhizopus_oryzae_supercontig_3.17_ _[1-476381] _476381_nt_	gene_62	0.22	0.97	gnl CDD 65389 pfam01585, G-patch, G-patch domain.	1.00E-06
AACW02000293_ _CONTIG_293_ _Rhizopus_oryzae_supercontig_3.17_ _[1-476381] _476381_nt_	gene_168	0.81	1.00	gnl CDD 29769 cd01042, DMQH, Demethoxyubiquinone hydroxylases (DMQH).	5.00E-55
AACW02000003_ _CONTIG_3_ _Rhizopus_oryzae_supercontig_3.1_ _[346323-756733] _410411_nt_	gene_127	0.64	0.62	gnl CDD 71935 pfam08507, COPI_assoc, COPI associated protein.	4.00E-07
AACW02000311_ _CONTIG_311_ _Rhizopus_oryzae_supercontig_3.20_ _[152419-490205] _337787_nt_	gene_38	0.85	0.64	gnl CDD 58647 cd00756, MoeA, MoeA family.	3.00E-21
AACW02000313_ _CONTIG_313_ _Rhizopus_oryzae_supercontig_3.21_ _[1-398826] _398826_nt_	gene_66	0.95	1.00	gnl CDD 66475 pfam02792, Mago_nashi.	4.00E-59
AACW02000327_ _CONTIG_327_ _Rhizopus_oryzae_supercontig_3.25_ _[83094-182798] _99705_nt_	gene_29	1.00	1.00	gnl CDD 30755 COG0406, GpmB, Fructose-2,6-bisphosphatase.	8.00E-19
AACW02000034_ _CONTIG_34_ _Rhizopus_oryzae_supercontig_3.1_ _[4377654-4477405] _99752_nt_	gene_12	0.70	0.91	gnl CDD 30638 COG0290, InfC, Translation initiation factor 3 (IF-3)	3.00E-15
AACW02000004_ _CONTIG_4_ _Rhizopus_oryzae_supercontig_3.1_ _[757263-1437475] _680213_nt_	gene_89	0.85	0.94	gnl CDD 69205 pfam05669, SOH1, SOH1. The family consists of Saccharomyces	6.00E-27

AACW02000041_ _CONTIG_41_ _Rhizopus_oryzae_supercontig_3 .1_ _[5061334-5735491]_ _674158_nt_	gene_181	0.59	0.96	gnl CDD 69362 pfam05832, DUF846, Eukaryotic protein of unknown function (DUF846).	2.00E-42
AACW02000042_ _CONTIG_42_ _Rhizopus_oryzae_supercontig_3 .2_ _[1-107275]_ _107275_nt_	gene_11	0.38	0.92	gnl CDD 68989 pfam05439, JTB, Jumping translocation breakpoint protein (JTB).	2.00E-06
AACW02000056_ _CONTIG_56_ _Rhizopus_oryzae_supercontig_3 .2_ _[1578995-2467034]_ _888040_nt_	gene_317	0.76	0.79	gnl CDD 69216 pfam05680, ATP- synt_E, ATP synthase E chain.	5.00E-10
AACW02000006_ _CONTIG_6_ _Rhizopus_oryzae_supercontig_3. 1_ _[1509808-1953412]_ _443605_nt_	gene_42	0.96	1.00	gnl CDD 68587 pfam05018, DUF667, Protein of unknown function (DUF667).	8.00E-73
AACW02000062_ _CONTIG_62_ _Rhizopus_oryzae_supercontig_3 .2_ _[3248533-3874699]_ _626167_nt_	gene_132	0.98	1.00	gnl CDD 32279 COG2096, COG2096, Uncharacterized conserved protein.	5.00E-44
AACW02000062_ _CONTIG_62_ _Rhizopus_oryzae_supercontig_3 .2_ _[3248533-3874699]_ _626167_nt_	gene_158	0.86	1.00	gnl CDD 72839 pfam08583, UPF0287, Uncharacterised protein family (UPF0287).	3.00E-12
AACW02000073_ _CONTIG_73_ _Rhizopus_oryzae_supercontig_3 .3_ _[601433-1277658]_ _676226_nt_	gene_193	0.96	1.00	gnl CDD 80120 pfam05721, PhyH, Phytanoyl-CoA dioxygenase (PhyH).	1.00E-11
AACW02000074_ _CONTIG_74_ _Rhizopus_oryzae_supercontig_3 .3_ _[1277853-1721144]_ _443292_nt_	gene_59	0.21	1.00	gnl CDD 29102 cd00162, RING, RING-finger (Really Interesting New Gene).	3.00E-07
AACW02000075_ _CONTIG_75_ _Rhizopus_oryzae_supercontig_3 .3_ _[1721245-2450281]_ _729037_nt_	gene_3	0.21	0.94	gnl CDD 71421 pfam07985, SRR1, SRR1.	3.00E-08
AACW02000078_ _CONTIG_78_ _Rhizopus_oryzae_supercontig_3 .3_ _[2477588-2558442]_ _80855_nt_	gene_36	1.00	1.00	gnl CDD 67669 pfam04062, P21- Arc, P21-ARC (ARP2/3 complex 21 kDa subunit).	2.00E-56
AACW02000082_ _CONTIG_82_ _Rhizopus_oryzae_supercontig_3 .3_ _[2888016-2926936]_ _38921_nt_	gene_3	1.00	1.00	gnl CDD 67291 pfam03665, UPF0172, Uncharacterised protein family (UPF0172).	1.00E-37
AACW02000083_ _CONTIG_83_ _Rhizopus_oryzae_supercontig_3 .3_ _[2928881-3133860]_ _204980_nt_	gene_45	0.87	0.61	gnl CDD 34689 COG5085, COG5085, Predicted membrane protein.	6.00E-12

AACW02000009_ _CONTIG_9__ _Rhizopus_oryzae_supercontig_3. 1_ _[2111367-2400882]_ _289516_nt_	gene_99	0.47	0.96	gnl CDD 32314 COG2131, ComEB, Deoxycytidylate deaminase.	1.00E-34
AACW02000091_ _CONTIG_91__ _Rhizopus_oryzae_supercontig_3 .4_ _[1507490-2469713]_ _962224_nt_	gene_143	0.81	0.95	gnl CDD 71948 pfam08520, DUF1748, Fungal protein of unknown function (DUF1748).	5.00E-18
AACW02000091_ _CONTIG_91__ _Rhizopus_oryzae_supercontig_3 .4_ _[1507490-2469713]_ _962224_nt_	gene_191	0.47	0.82	gnl CDD 58521 cd01846, fatty_acyltransferase_like.	2.00E-23