

**S17 Table. Estimates of Evolutionary Divergence between Sequences (BlastX homology search of M01522:132:000000000-A4LNU:1:1102:17521:21100.1).** The number of amino acid substitutions per site from between sequences are shown. Analyses were conducted using the JTT matrix-based model.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
M01522:132:000000000-A4LNU:1:1102:17521:21100.1_frame+3	1																					
XP_013295164.1_hypothetical_protein_NECAME_18601_partial_Necator_americanus	2	0.75																				
ODM14393.1_hypothetical_protein_SI65_10228_Aspergillus_cristatus	3	0.79	0.81																			
ODM17623.1_hypothetical_protein_SI65_07298_Aspergillus_cristatus	4	0.87	0.77	0.12																		
ODM24136.1_hypothetical_protein_SI65_01726_Aspergillus_cristatus	5	0.87	0.77	0.12	0																	
ODM15244.1_hypothetical_protein_SI65_09185_Aspergillus_cristatus	6	0.87	0.77	0.12	0	0																
KZT62760.1_ribonuclease_H-like_protein_partial_Calocera_cornea_HHB12733	7	1.06	0.93	1.15	1.02	1.02	1.02															
CCG84601.2_protein_of_unknown_function_Taphrina_deformans_PYCC_5710	8	1	0.84	1.12	0.97	0.97	0.97	0.63														
RAN68448.1_hypothetical_protein_B5P42_31445_partial_Bacillus_sp._SRB_331	9	1.17	0.97	1.15	0.98	0.98	0.98	0.47	0.64													
CEP07157.1_hypothetical_protein_Parasitella_parasitica	10	1.09	0.72	0.89	0.76	0.76	0.76	0.6	0.51	0.45												
OJT11278.1_Transposon_Tf2-12_polyprotein_Trametes_pubescens	11	1.24	1.03	1.32	1.25	1.25	1.25	0.56	0.72	0.83	0.75											
CEP09716.1_hypothetical_protein_Parasitella_parasitica	12	1.09	0.72	0.89	0.76	0.76	0.76	0.6	0.51	0.45	0	0.75										
SAL96256.1_hypothetical_protein_Absidia_glauca	13	0.93	0.79	1.07	0.91	0.91	0.91	0.44	0.69	0.61	0.53	0.79	0.53									
XP_002145184.1_retrovirus_polyprotein_putative_Talaromyces_marneffeii_ATCC_182	14	1.18	1.17	0.86	0.81	0.81	0.81	0.79	1.03	0.99	0.85	1.06	0.85	1.01								
SAM05196.1_hypothetical_protein_Absidia_glauca	15	0.97	0.83	1.07	0.9	0.9	0.9	0.38	0.74	0.66	0.52	0.79	0.52	0.11	0.97							
KFX51368.1_Transposon_Tf2-6_polyprotein_Talaromyces_marneffeii_PM1	16	1.18	1.17	0.86	0.81	0.81	0.81	0.79	1.03	0.99	0.85	1.06	0.85	1.01	0	0.97						
KKF92157.1_Retrotransposable_element_protein_type1_Ceratocystis_platani	17	1.17	0.8	0.42	0.38	0.38	0.38	1.05	1.16	1.11	0.98	1.29	0.98	1.11	0.77	1.02	0.77					
pir  T18348_probable_polyprotein_rice_blast_fungus_magnaporthe_gypsy_retrotra	18	1.14	0.9	0.35	0.26	0.26	0.26	0.93	1.09	1.04	0.91	1.32	0.91	0.94	0.79	0.92	0.79	0.31				
OJT06055.1_Transposon_Tf2-12_polyprotein_Trametes_pubescens	19	1.38	1.16	1.35	1.18	1.18	1.18	0.5	0.78	0.82	0.7	0.29	0.7	0.65	1.15	0.65	1.15	1.19	1.24			
GAN03854.1_retrotransposable_element_Tf2_155_kDa_protein_type_1-like_Mucor	20	1.1	0.7	0.93	0.78	0.78	0.78	0.57	0.46	0.58	0.14	0.68	0.14	0.45	0.9	0.44	0.9	0.99	0.92	0.6		
KIM58096.1_hypothetical_protein_SCLCIDRAFT_28376_Scleroderma_citrinum_Foug_A	21	1.34	0.99	1.3	1.32	1.32	1.32	0.89	0.85	1.02	1.15	1.32	1.15	0.97	1.54	1.16	1.54	1.58	1.42	1.19	1.12	