

Table S1. Gene list using BLAST. The similarity search was performed using the stand-alone blast program against the NCBI NR database (Altschul *et al.*, 1997; Camacho *et al.*, 2009; O'Leary *et al.*, 2016; Sayers *et al.*, 2020).

Query ^a	Species	Database (NCBI database)	The number of hits (e-value < 3.63E-71 ^b)
XP_750931.1	<i>Aspergillus fumigatus</i> Af293	1	proteome
XP_001258169.1	<i>Aspergillus fischeri</i> NRRL 181	1	proteome
XP_659456.1	<i>Aspergillus nidulans</i> FGSC A4	2	proteome
XP_023090511.1	<i>Aspergillus oryzae</i> RIB40	1	proteome
XP_001560867.1	<i>Botrytis cinerea</i> B05.10	3	proteome
XP_024551837.1	<i>Botrytis cinerea</i> B05.10	3	proteome
XP_001554986.1	<i>Botrytis cinerea</i> B05.10	2	proteome
AAK84438.1	<i>Blumeria graminis</i> f.sp.	1	genome
XP_018995941.1	<i>Cryptococcus amyloletus</i> CBS 6039	2	proteome
XP_003193766.1	<i>Cryptococcus gatti</i> WM276	1	proteome
XP_003194854.1	<i>Cryptococcus gatti</i> WM276	1	proteome
XP_003193716.1	<i>Cryptococcus gatti</i> WM276	1	proteome
XP_003197451.1	<i>Cryptococcus gatti</i> WM276	1	proteome
AAT68493.1	<i>Colletotrichum lindemuthianum</i>	1	genome
XP_012049402.1	<i>Cryptococcus neoformans</i> var grubii H99	1	proteome
XP_012049409.1	<i>Cryptococcus neoformans</i> var grubii H99	1	proteome
XP_012053383.1	<i>Cryptococcus neoformans</i> var grubii H99	1	proteome
XP_012050538.1	<i>Cryptococcus neoformans</i> var grubii H99	1	proteome
XP_571516.1	<i>Cryptococcus neoformans</i> var. neoformans JEC21	1	proteome
XP_570200.1	<i>Cryptococcus neoformans</i> var. neoformans JEC21	1	proteome
XP_570561.1	<i>Cryptococcus neoformans</i> var. neoformans JEC21	1	proteome
NP_586357.1	<i>Encephalitozoon cuniculi</i> GB-M1	1	proteome
XP_009265516.1	<i>Encephalitozoon romaleae</i> SJ-2008	1	proteome
KLO89559.1	<i>Fusarium fujikuroi</i>	2	proteome
XP_011326160.1	<i>Fusarium graminearum</i> PH-1	3	proteome
XP_011321484.1	<i>Fusarium graminearum</i> PH-1	3	proteome
XP_011324448.1	<i>Fusarium graminearum</i> PH-1	3	proteome
KPA45975.1	<i>Fusarium langsethiae</i>	3	proteome
XP_019049621.1	<i>Kwoniella bestiolae</i> CBS 10118	1	proteome
XP_018259205.1	<i>Kwoniella dejecticola</i> CBS 10117	1	proteome
XP_019009862.1	<i>Kwoniella pini</i> CBS 10737	1	proteome
XP_003712529.1	<i>Pyricularia oryzae</i> 70-15	3	proteome
XP_016845950.1	<i>Pyricularia oryzae</i> 70-15	4	proteome
XP_003712634.1	<i>Pyricularia oryzae</i> 70-15	2	proteome
XP_001799819.1	<i>Parastagonospora nodorum</i> SN15	4	proteome
XP_001798667.1	<i>Parastagonospora nodorum</i> SN15	4	proteome
XP_001797954.1	<i>Parastagonospora nodorum</i> SN15	4	proteome
XP_001802089.1	<i>Parastagonospora nodorum</i> SN15	4	proteome
XP_001805210.1	<i>Parastagonospora nodorum</i> SN15	4	proteome
XP_007836581.1	<i>Pestalotiopsis fici</i> W106-1	1	proteome
KY024221.1	<i>Pestalotiopsis</i> sp. Isolate	1	genome
XP_003323413.1	<i>Puccinia graminis</i> f. sp. tritici	3	proteome
NP_013411.1	<i>Saccharomyces cerevisiae</i> S288C	2	proteome

NP_013410.1	<i>Saccharomyces cerevisiae</i> S288C	2	proteome
XP_013024037.1	<i>Schizosaccharomyces cryophilus</i> OY26	1	proteome
XP_002174182.1	<i>Schizosaccharomyces japonicus</i> yFS275	1	proteome
XP_013016981.1	<i>Schizosaccharomyces octosporus</i> yFS286	1	proteome
NP_001342829.1	<i>Schizosaccharomyces pombe</i>	1	proteome
XP_001598553.1	<i>Sclerotinia sclerotiorum</i> 1980 UF-70	3	proteome
XP_001598179.1	<i>Sclerotinia sclerotiorum</i> 1980 UF-70	3	proteome
XP_003016479.1	<i>Trichophyton benhamiae</i> CBS 112371	2	proteome
XP_014180455.1	<i>Trichosporon asahii</i> var. <i>asahii</i> CBS 2479	1	proteome

^aGenbank accession numbers.

^bThis e-value was chosen as this is the lowest threshold for the query to pass through in the stand-alone blast (blastp and tblastn) analysis.