



Figure S1. Phylogram generated from maximum likelihood analysis based on combined partial LSU, RPB2, ITS, BTUB and CAM sequences data. Related sequences were obtained from Frisvad et al. (36). 40 strains are included in the combined sequence analyses, which comprise 3271 characters with gaps. *Aspergillus muricatus* (NRRL 35674) is used as the outgroup taxon. The best scoring RAxML

tree with a final likelihood value of -16016.105263 is presented. The matrix had 1036 distinct alignment patterns, with 20.83% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.232666, C = 0.252689, G = 0.268734, T = 0.245911; substitution rates AC = 1.198516, AG = 3.642609, AT = 1.139202, CG = 0.716346, CT = 6.351285, GT = 1.000000; proportion of invariable sites I = 0.430234; gamma distribution shape parameter α = 0.954354. Bootstrap support values for ML equal to or greater than 60% is given above the nodes. Newly generated sequence is in blue color.