



Figure S1. Homologous alignment result of GAPDH between *Cordyceps farinosa* and other fungi. The sequence with dark background is 100% homologous, the sequence with green background is ≥ 75 homologous, and the sequence with pink background is ≥ 50 homologous. The blue and red regions below the sequence represent the conservative N-terminal and C-terminal domains of GAPDH, respectively.