

**Figure S1** **The structure validation of the R. oryzae RdRp model built in silico.** The scatter plot of Ψ (y-axis) versus Φ (x-axis) for each amino acid is represented by red circles (Ramachandran plot). The dark-green region represents the most favorable region, while green, faint-green, and white regions represent the allowed, strictly allowed, and forbidden regions.