



Additional Figure 3: Molecular phylogenetic analysis of the *Esi3* genes from *T. aestivum* by Maximum Likelihood method based on the Jukes-Cantor model [42]. The tree with the highest log likelihood (-1283.8239) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.1637)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 29 nucleotide sequences.