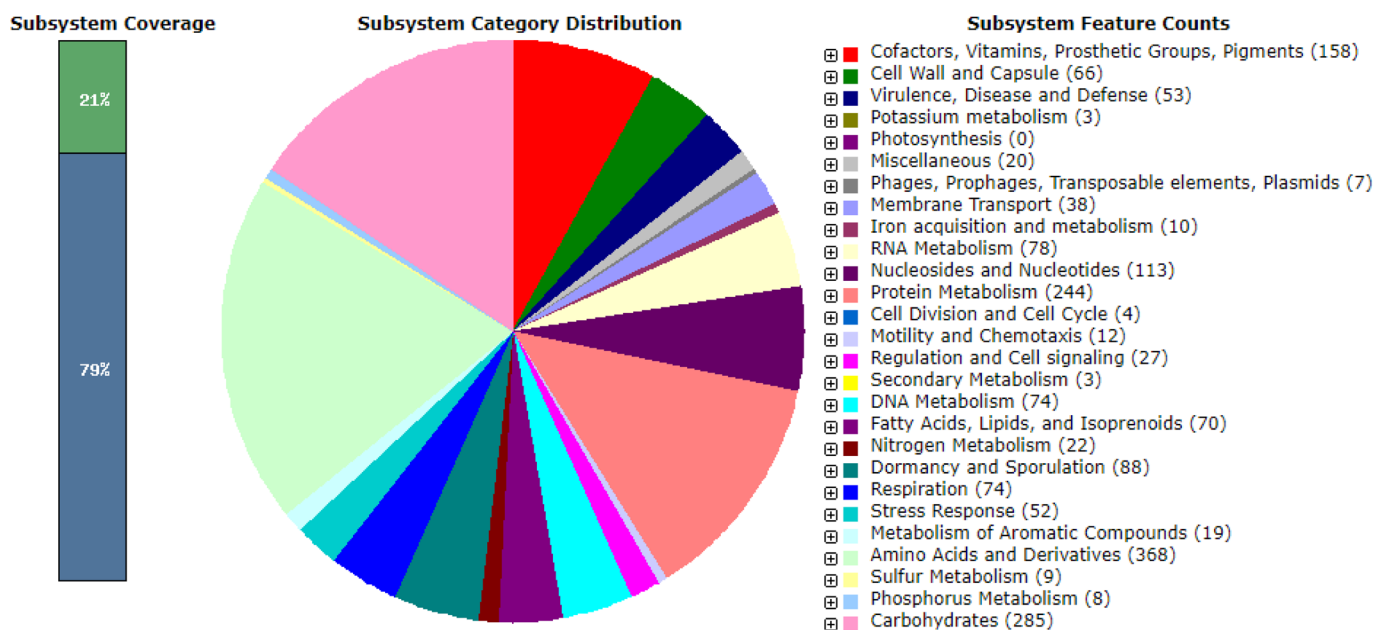


Supplementary Fig. 3. Heatmap of OrthoANI value calculated with Orthologous Average Nucleotide Identity Tool (OAT) software for strain BRMEA1^T and closely related strains of *Neobacillus*. The color-code heatmap displays the closest species in red and the farthest in green. The unweighted pair group method with an arithmetic mean (UPGMA) dendrogram based on the OrthoANI values of eight species is listed on the left.



Supplementary Fig. 4. Count and distribution of the strain BRMEA1^T subsystem categories using RAST annotation.