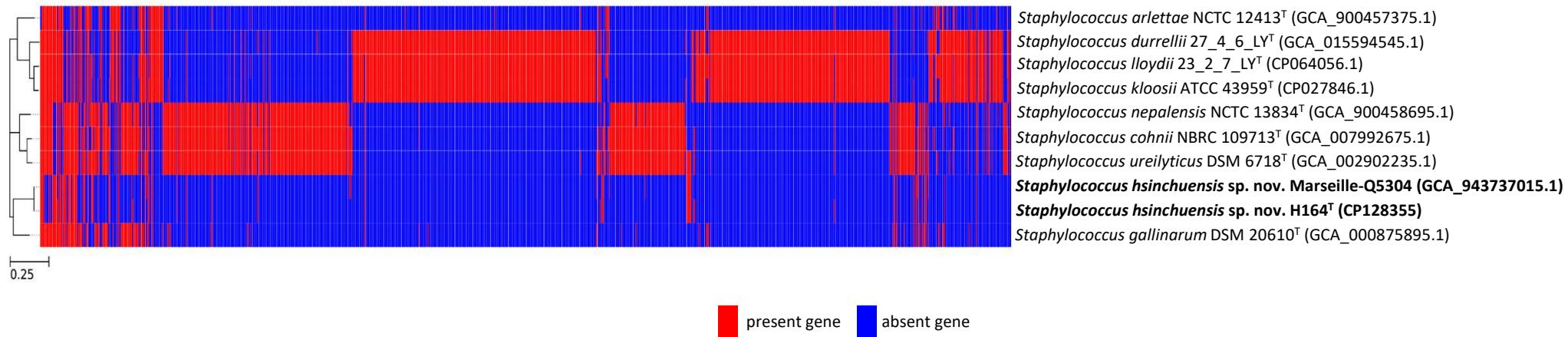
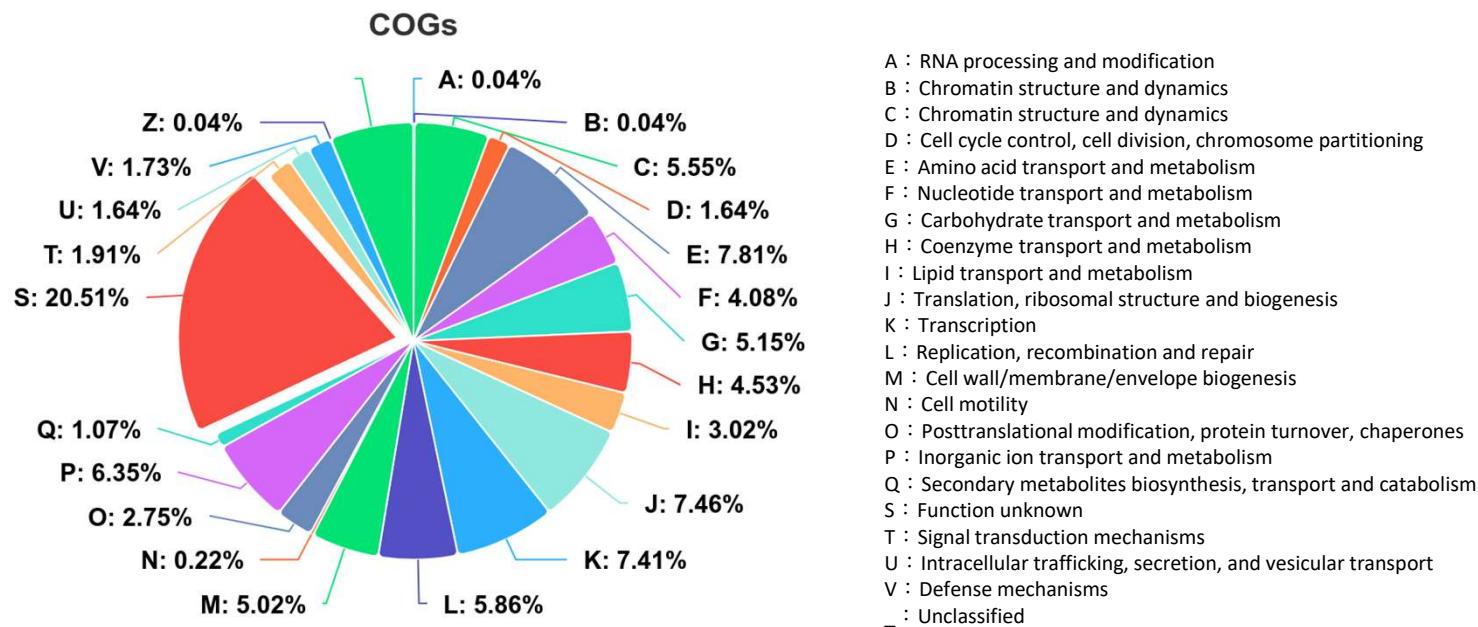


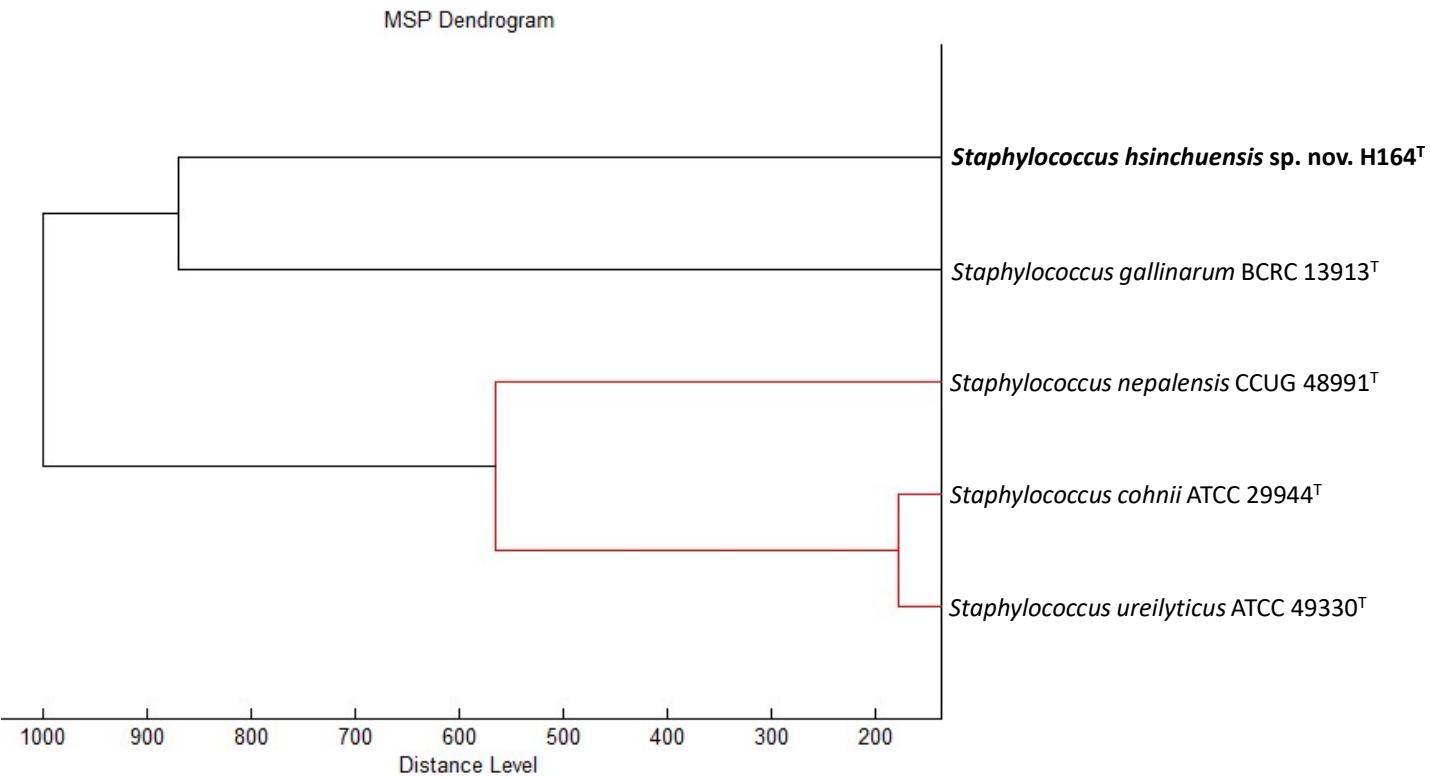
Supplementary Figure. S1. Phylogenomic tree based on TYGS results showing the relationship between *Staphylococcus hsinchuensis* sp. nov. and its phylogenetically related species. The tree was inferred with FastME 2.1.6.1 from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d_5 . The tree was rooted at the midpoint.



Supplementary Figure. S2. Heat map and NJ dendrogram of the analyzed eight *Staphylococcus* strains based on the presence or absence of genes.



Supplementary Figure. S3. Results of an eggNOG functional category analysis of strain H164^T. The major two parts of 2,114 COG categories in strains H164^T, are E (Amino acid transport and metabolism), J (Translation, ribosomal structure and biogenesis) and K (Transcription).



Supplementary Figure S4. Dendrogram showing the clustering of the *Staphylococcus* strains based on MALDI-TOF MS analysis.