

# ***In Silico* Safety Assessment of *Bacillus* isolated from Polish Bee Pollen and Bee Bread as Novel Probiotic Candidates**

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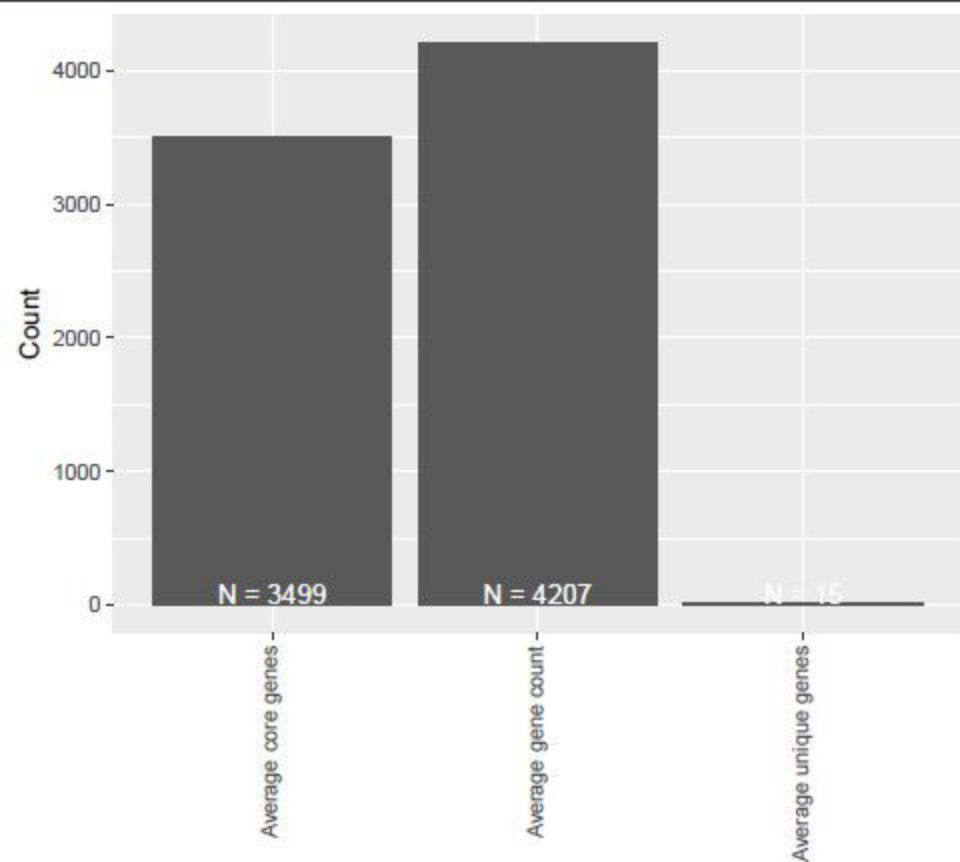
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Total number of genomes:  
180

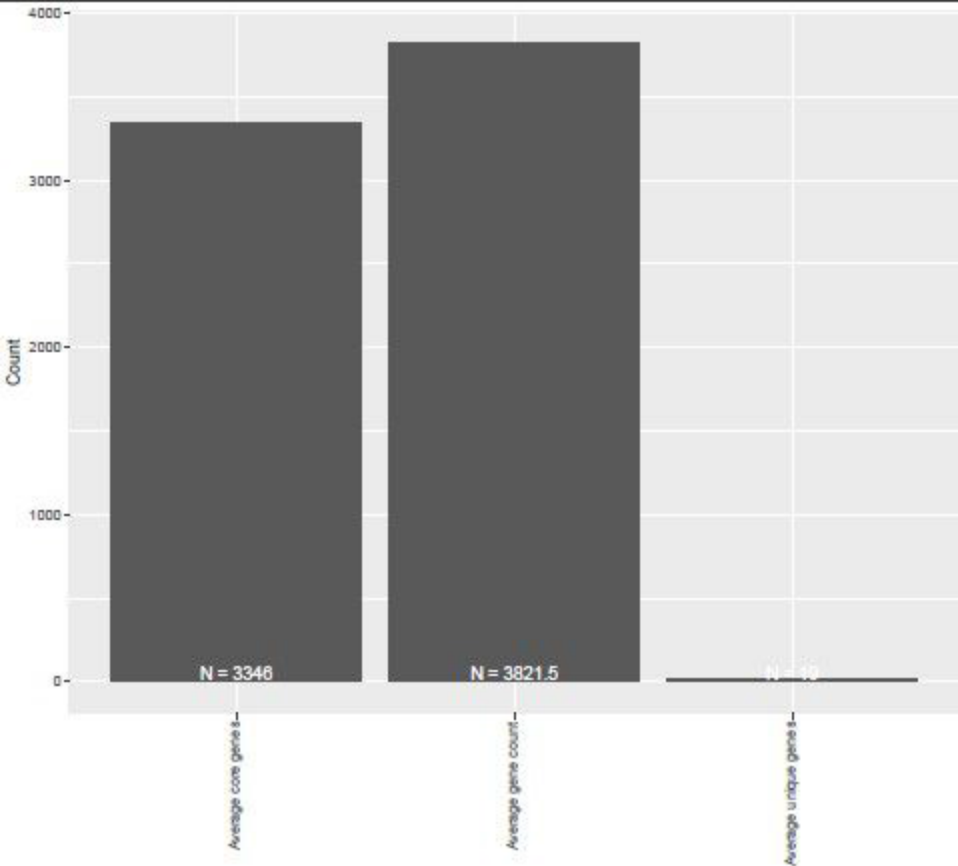
Number of analyzed genes:  
752925

Total orthologous groups  
10810

Total unique genes  
2664

**Figure S1.** Number of Average core genes, average gene count, and average unique genes present in the *B. subtilis* pangenome





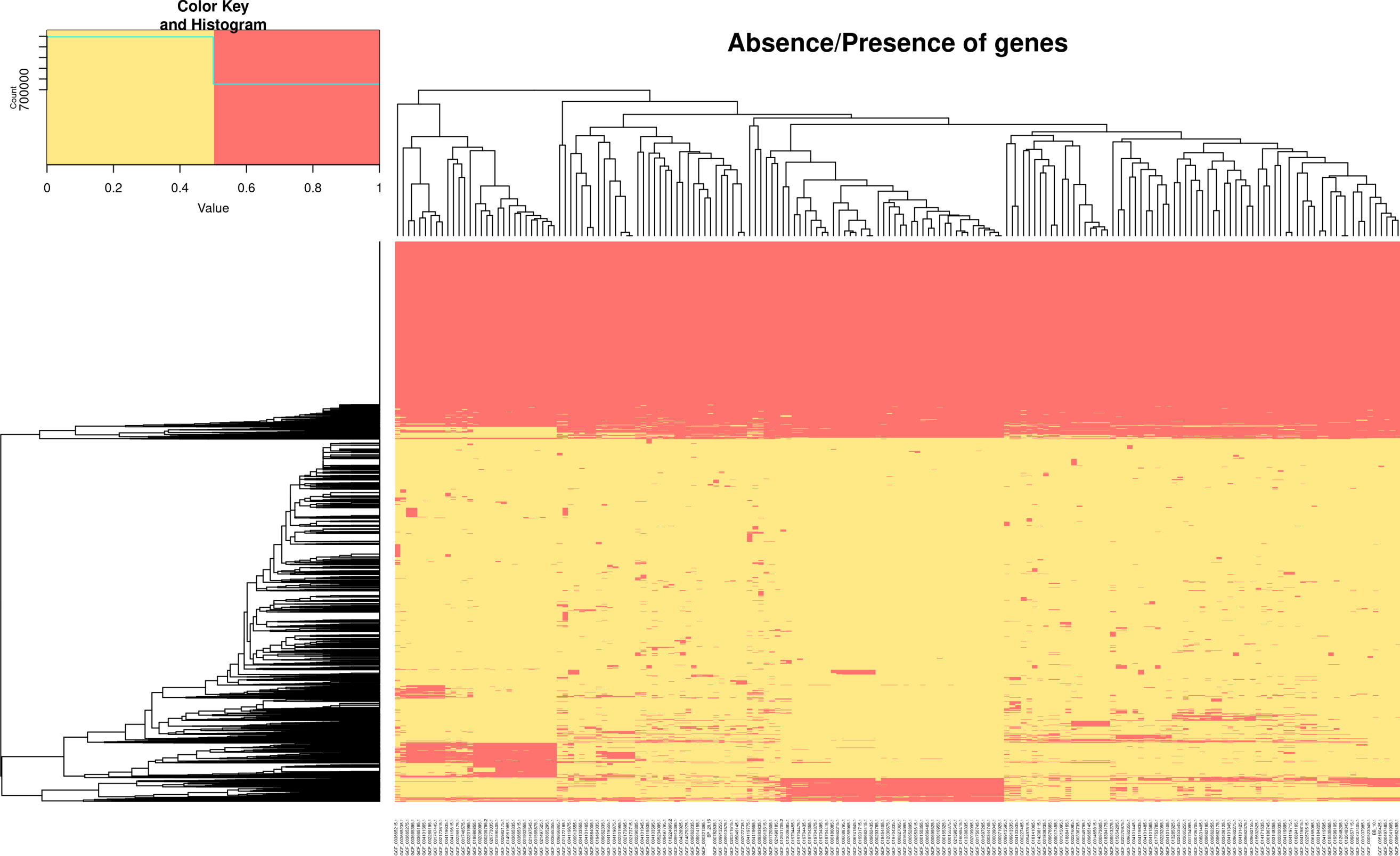
Total number of genomes:  
204

Number of analyzed genes:  
790409

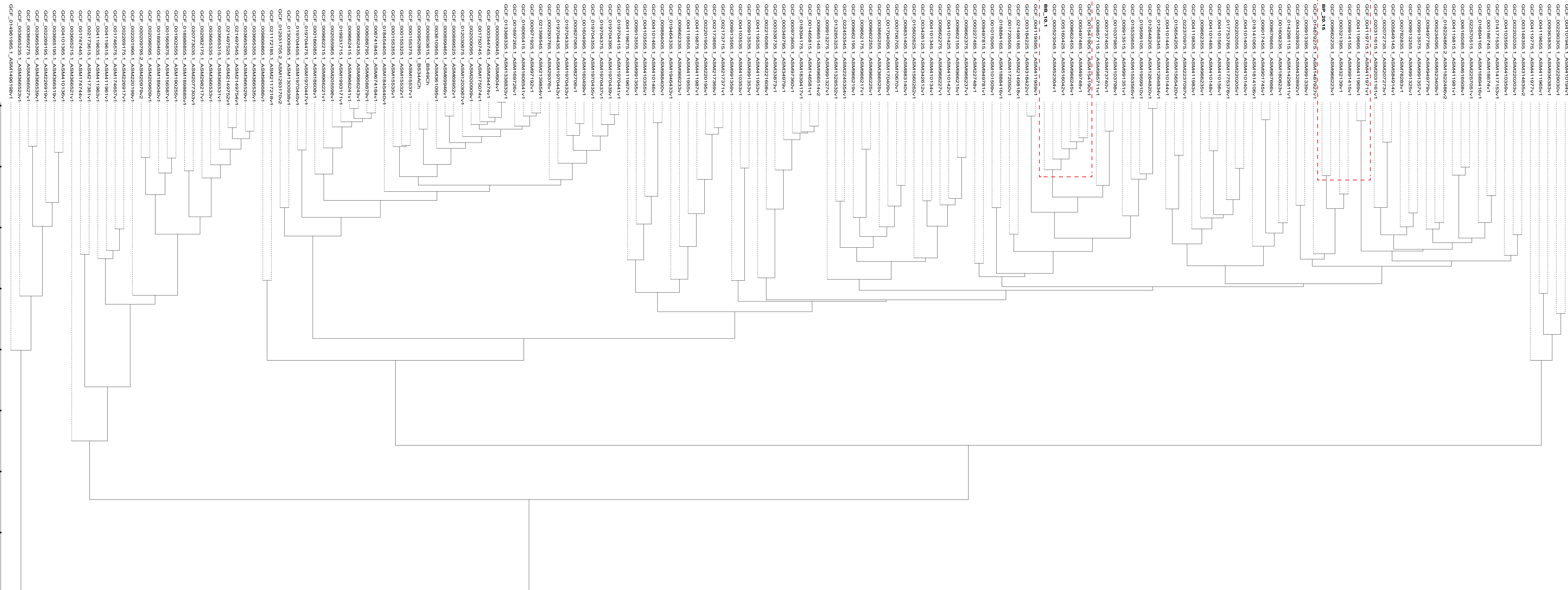
Total orthologous groups  
11759

Total unique genes  
3831

**Figure S2.** Number of Average core genes, average gene count, and average unique genes present in the *B. velezensis* pangenome

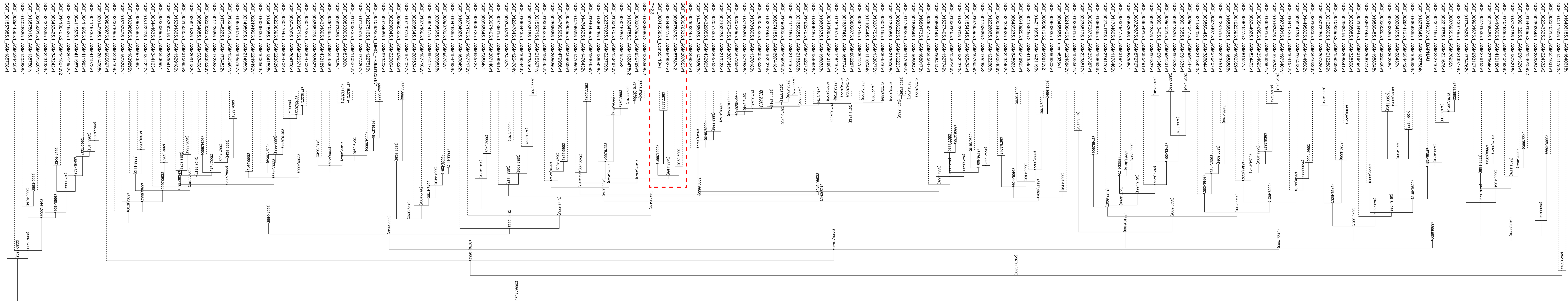


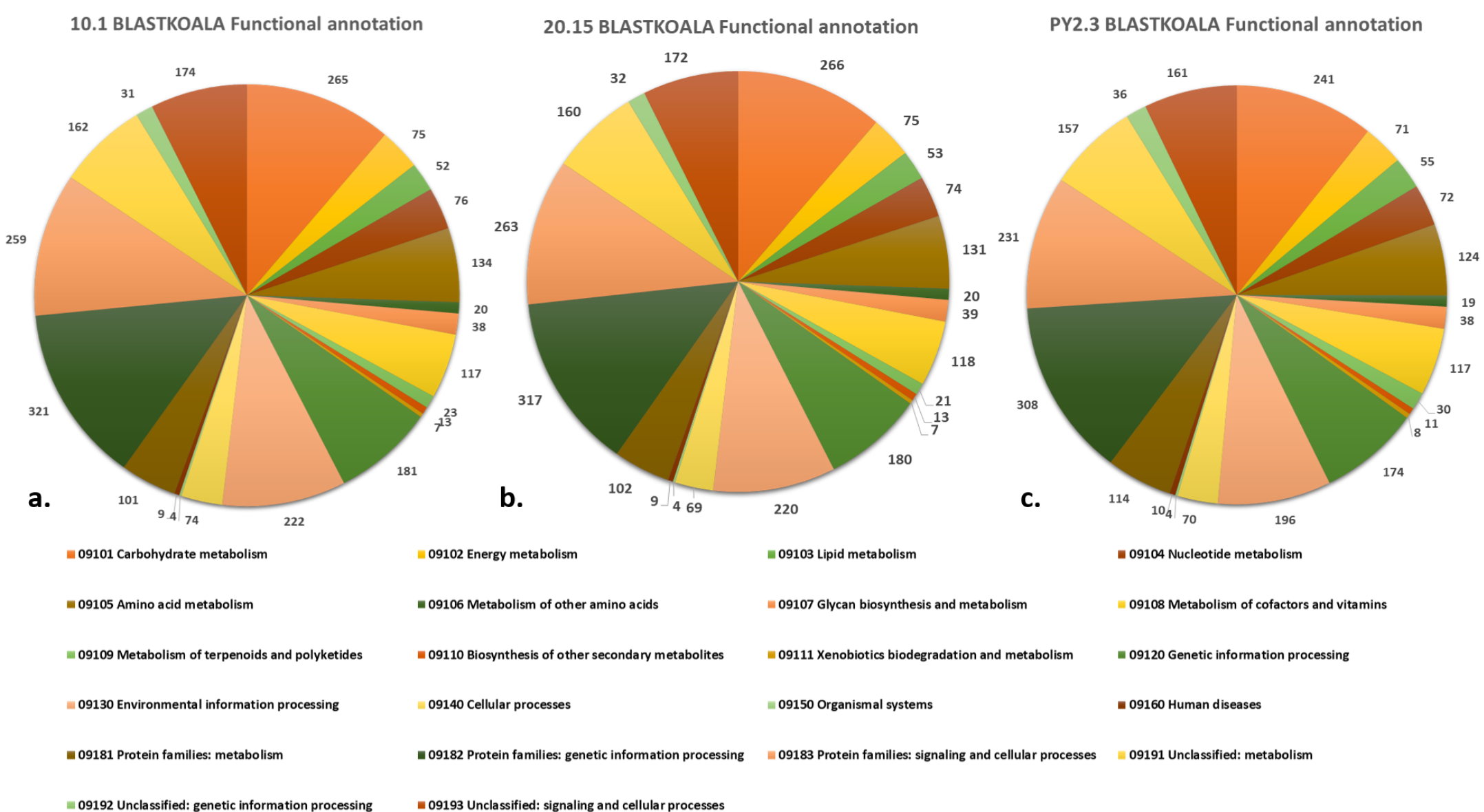




**Figure S4a.** The phylogenetic inference based on the whole genome variation of isolates BB10.1, BP20.15.







**Figure S5 .** The KEGG functional annotation by BLASTKOALA and categorization into 22 different functional categories. a) 60% of the annotated sequences from isolate 10.1 b) 61.2% annotated sequences from isolate 20.15 c) 62.6% annotated sequences from isolate PY2.3. The color scheme and code at the bottom represent the specific functional category of annotated genes.