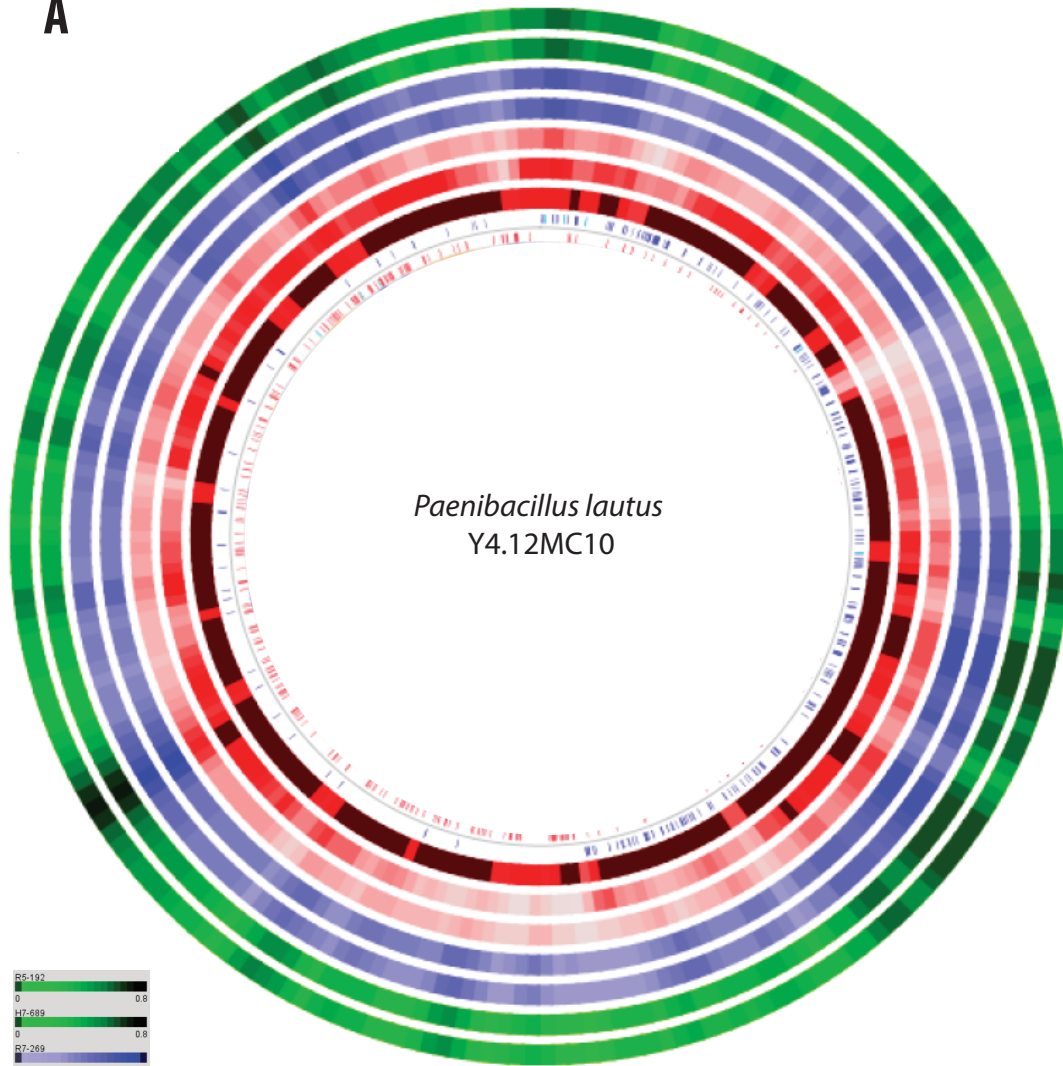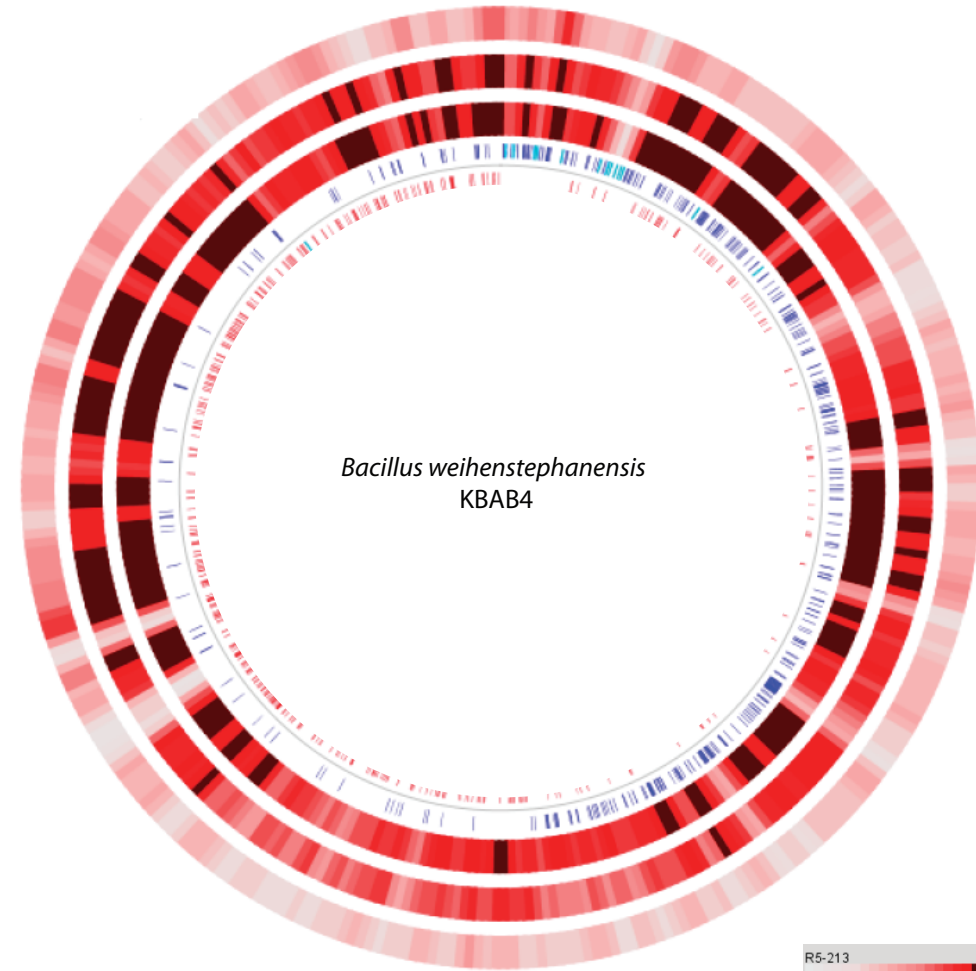# Additional file 2

Circular representation of Blast comparisons for the Paenibacillus and Bacillus genomes. A) BLAST comparison for all *Paenibacillus* using *P. lautus* Y4.12MC10 as reference genome . The inner circles in red and blue represent CDS in leading and lagging strands of *P. lautus* Y4.12MC10. In red from inside to outside are the genomes of FSL H8-457, FSL R5-808, FSL H8-237, in blue are the genomes of FSL R7-277 and FSL R7-269, and in green are the genomes of FSL H7-689 and FSL R5-192. B) BLAST comparison for the *Bacillus* and *Viridibacillus* genomes. The inner circles in red and blue represent CDS in leading and lagging strands of *B. weihenstephanensis* KBAB4. In red from inside to outside are the genomes of FSL H7-687, FSL R5-860, and FSL R5-213. Blast identity percent are represented above for *Paenibacillus* and *Bacillus*. This figure was conducted by mapping proteins homology derived from WGS, determined by BLAST, against a reference genome as it is implemented in GeneWiz browser (http://www.cbs.dtu.dk/services/gwBrowser/).