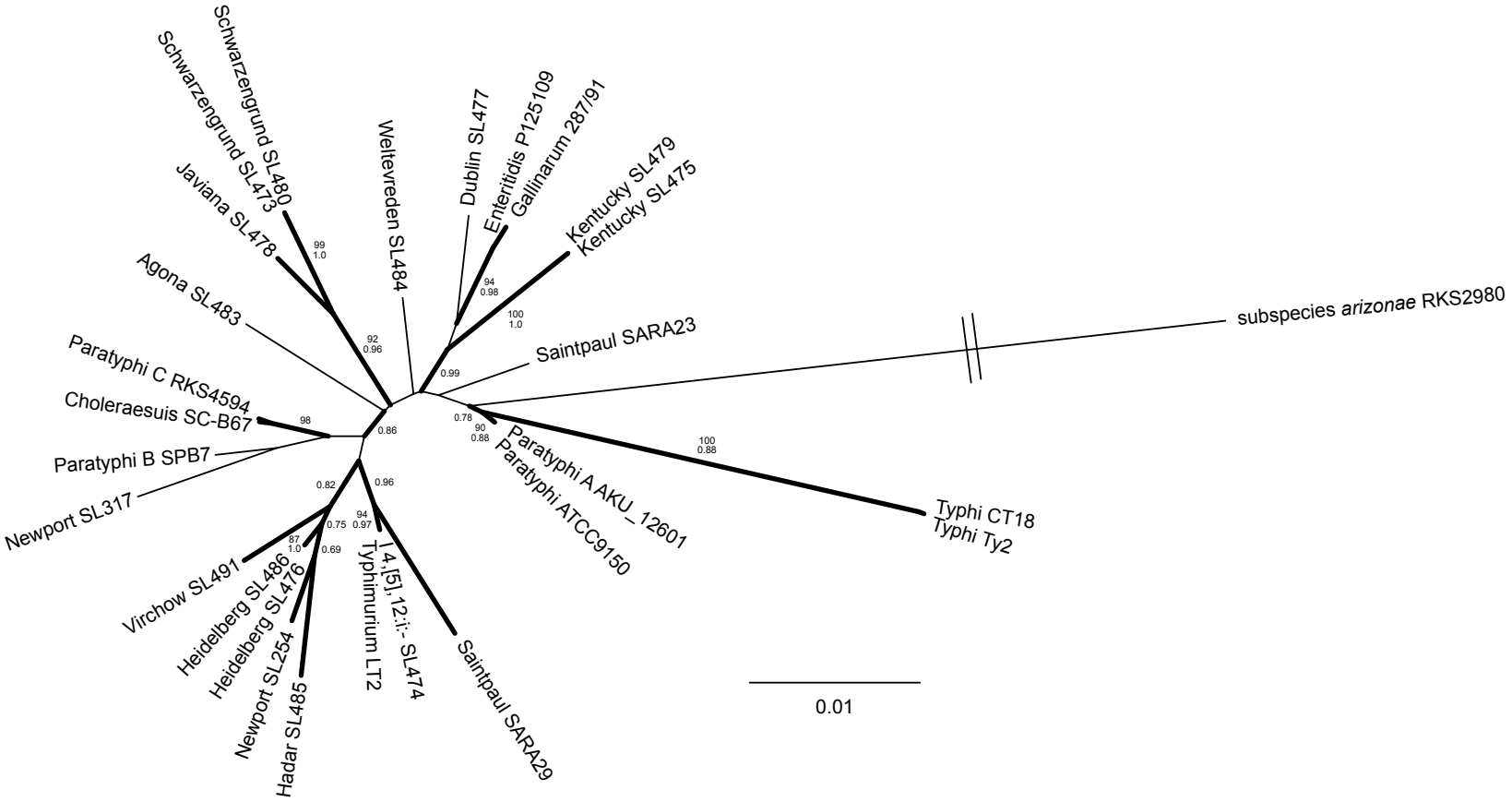
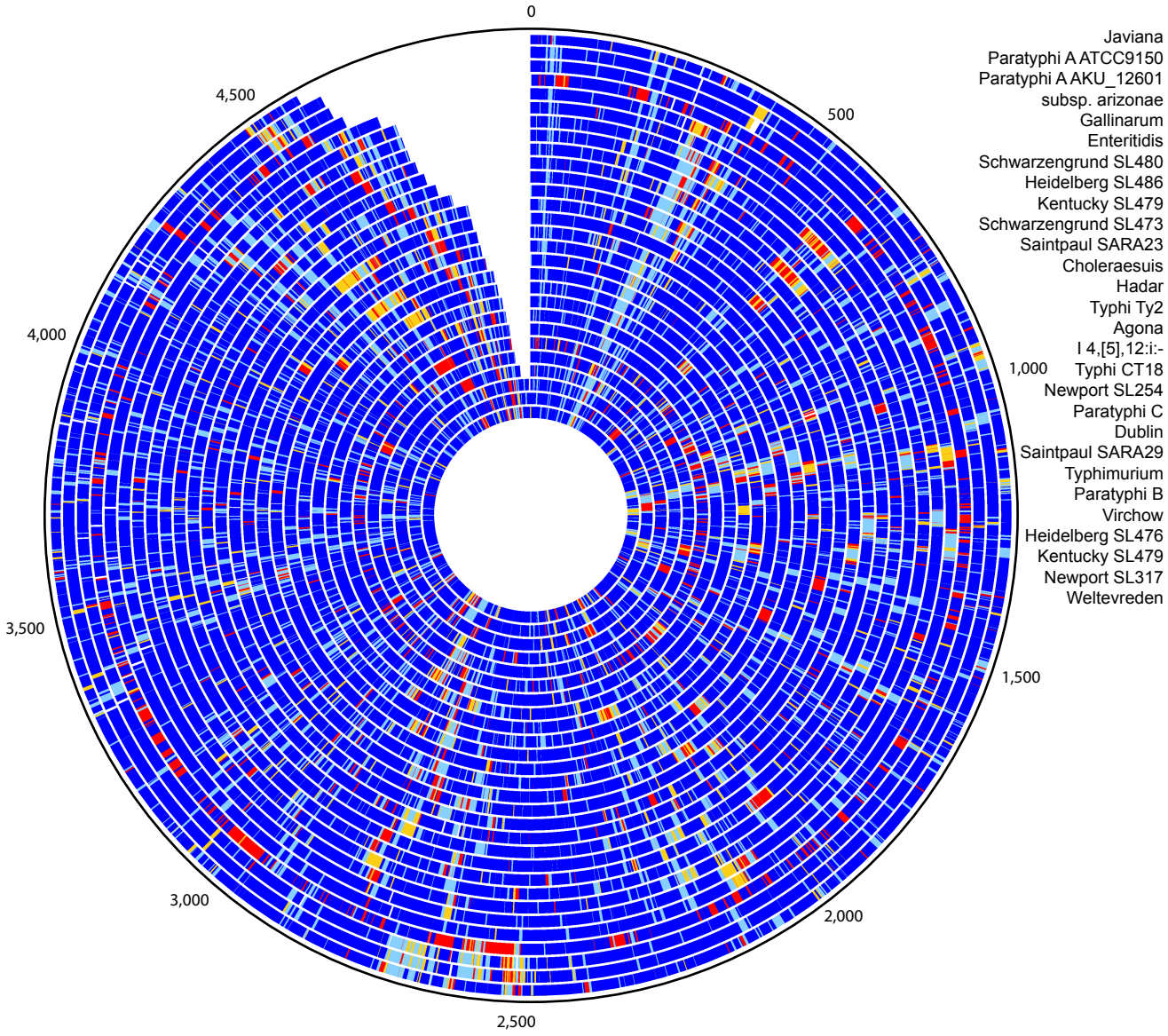
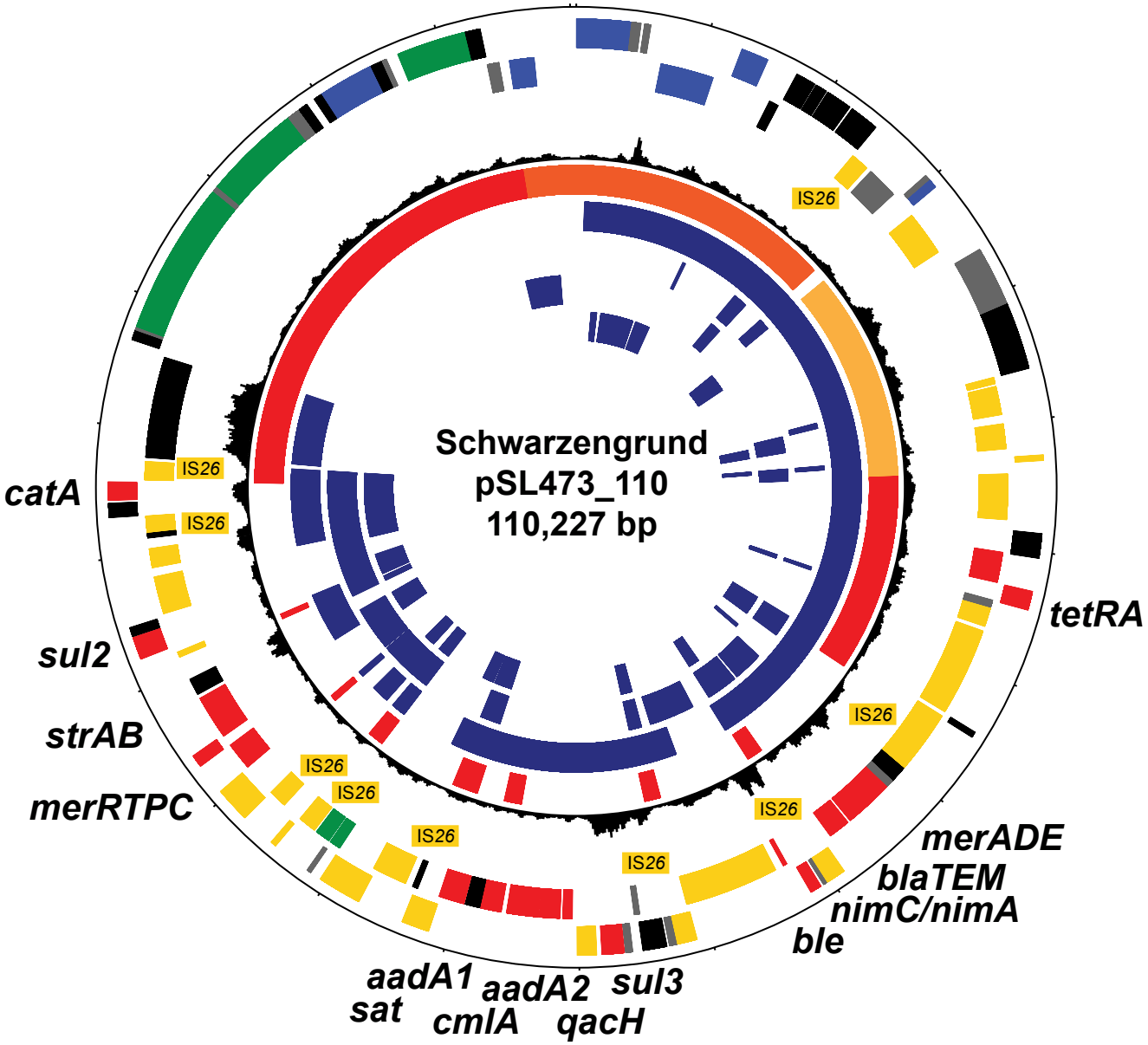


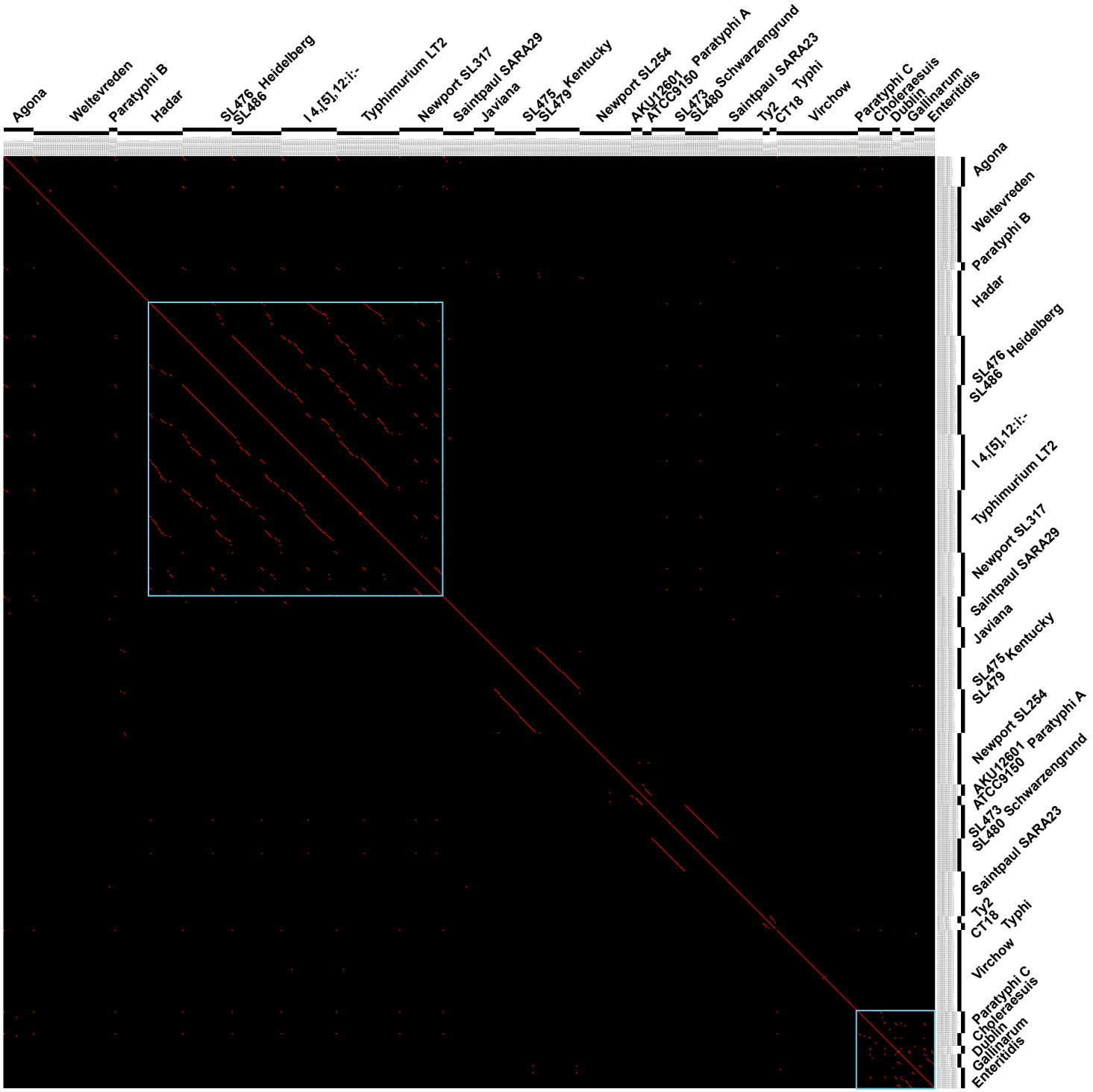
Supplementary Figure S1. Multi-Locus Sequence Typing (MLST) tree of all sequenced *S. enterica* strains. Supporting bootstrap values (>50%, PAUP* [74]) and posterior probabilities (>0.5, MrBayes [75]) are shown as numbers. Branches with bootstrap values >50% are highlighted.



Supplementary Figure S2. Gene-wise BLAST score ratio comparison of all sequenced *S. enterica* chromosomes. Each circle shows all CDS from one *S. enterica* chromosome, color-coded based on the number of orthologous genes that were identified in the other *S. enterica* chromosomes as dark blue (matches in >22 other chromosomes), light blue (5-22 chromosomes), gold (2-4 chromosomes) and red (<2 chromosomes). The chromosomes were ordered by size from the largest chromosome (Weltevreden) on the innermost circle to the smallest genome (Javiana) on the outermost circle.



Supplementary Figure S3. Schwarzengrund SL473 multidrug resistance plasmid pSL473_110. Circles from outside to inside: 1+2, CDS on leading and lagging strand involved in resistance (red), transposition/recombination (gold), conjugative transfer (green), plasmid maintenance (blue), other functions (black) or annotated as hypothetical proteins (gray). 3, trinucleotide sequence composition. 4-7, NUCmer sequence matches to the three plasmid contigs from the Schwarzengrund SL480 draft genome (red, orange, gold; circle 4), pSC138 (AY509004) from Choleraesuis SC-B67 (blue; circle 5), pEC-IMP (EU855787) from *Enterobacter cloacae* (blue; circle 6), and pK245 (DQ449578) from *K. pneumoniae* (blue; circle 7).



Supplementary Figure S4. CRISPR array comparison. CRISPR spacers were identified from all sequenced *S. enterica* genomes and compared by BLASTn. Matches (100% nt identity) are shown as black dots. CRISPR arrays from Heidelberg, Typhimurium, I 4,[5],12:i:-, Newport SL317 and Hadar share large numbers of CRISPR spacer elements as well as Paratyphi C, Choleraesuis, Dublin, Gallinarum and Enteritidis.

Of the 43 CRISPR spacer elements found in the two Heidelberg genomes, 31 (72%) are shared with Typhimurium, 30 (70%) with I 4,[5],12:i:-, 12 (28%) with Newport SL317, and 9 (21%) with Hadar.