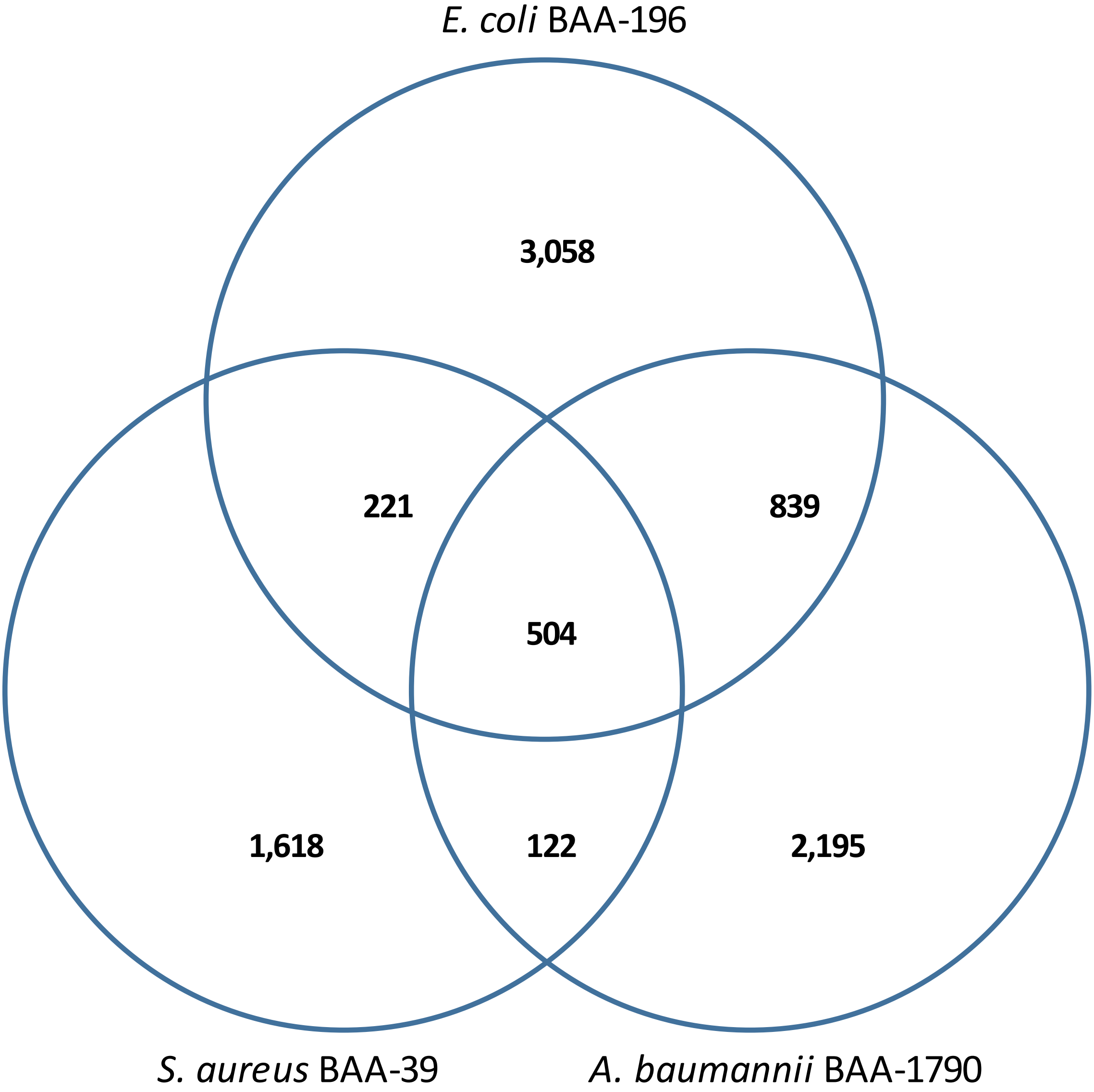

Supplementary Fig. S2. Venn diagram of distribution of strain-specific and homologous genes between shared by *E. coli* ATCC BAA-196, *S. aureus* ATCC BAA-39 and *A. baumannii* ATCC BAA-1790 as predicted by the program GET_HOMOLOGUES. Large admixed clusters of homologous phage-related integrases and transposases were considered as strain-specific genes.