

Accuracy of allele calling using SRST2 vs assembly and BLAST

MLST analysis of public data from 5 species (N=543 genomes, 3801 loci, details Supplementary Table 1). Tests were grouped by read depth and accuracy rates (left y-axis, correct allele calls as a proportion of tests), calculated at each depth (x-axis, red slashes indicate scale change). Grey bars, number of tests at each depth (right y-axis); Lines, accuracy of allele calling. **(A)** Call rate (total allele calls / 3801). **(B)** True positive rate (correct allele calls / total allele calls).

