Figure S1. Comparison of base detection results in synthetically contaminated datasets between BioHansel and Snippy using defined genotyping bases from five schemes: SE, SH, ST, Typhi, and MTB. The two most divergent genotypes for each scheme were artificially mixed at different fold coverage to make up a total of 120X coverage for each read set, as shown in the X axis. The comparison was restricted to the BioHansel genotyping bases for each scheme (SH=202 bases; SE=317 bases; ST=430 bases; Typhi=68 bases; MTB=62 bases), resulting in 1079 bases compared for each of the 15 coverage ratios, with a total of 16,185 basecalling comparisons. The two tools gave a fully concordant basecall for 15,027 (92.85%) of the target genotyping bases (Table S22). This graph is only showing the 1,158 results (equivalent to 7.15% of the comparisons) where there was not a fully concordant and unambiguous basecall between the 2 tools. Results are categorized as shown in the figure legend on the right.