

Table S30. 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. 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 results are categorized as described in the column headers.

Ratio of [Coverage genome A]/[Coverage Genome B]	Fully concordant basecalls between tools	Discordant basecalls between BioHansel and Snippy	No basecall from either tool	BioHansel Call: Snippy No Call	BioHansel No Call: Snippy Call
0/120	1078	0	1	0	0
2/118	1078	0	1	0	0
6/114	1068	0	4	4	3
12/108	996	0	49	22	12
16/104	955	0	96	19	9
20/100	939	0	124	12	4
40/80	934	0	144	1	0
60/60	934	0	145	0	0
80/40	935	0	144	0	0
100/20	937	0	132	6	4
104/16	954	0	101	15	9
108/12	991	0	48	17	23
114/6	1070	0	6	1	2
118/2	1079	0	0	0	0
120/0	1079	0	0	0	0
Total	15027	0	995	97	66
Percentage (n=16,185)	92.85%	0.00%	6.15%	0.60%	0.41%