

Supplementary Table 2. Comparison of spike-in WGS and G_3C reads that map to spike-in genomes

Spike-in	<i>E. coli</i> E3090		<i>E. faecium</i> E745	
	G_3C	WGS	G_3C	WGS
Total reads	14,497,782	1,284,538	8,170,430	3,333,334
Reads mapped to G_3C assembly (MAPQ>20)	14,237,338	1,256,272	7,764,542	3,175,581
%mapped to G_3C assembly	98.20%	97.80%	95.03%	95.27%
Intercontig reads	141,473	10,080	81,191	78,106
%intercontig reads	0.98%	0.78%	0.99%	2.34%

WGS = whole genome sequencing; MAPQ = mapping quality; nt = nucleotides