

Supplementary Data 37

Supporting results of the assessment of the impact of applying a different assembly pipeline and updating the allele caller

----- CLUSTER CONGRUENCE AT ALL LEVELS -----

Table 37.1. Number maximum threshold levels obtained with the original pipeline (AQUAMIS assemblies and chewBBACA v2.8.5) and with each of the alternative workflows (INNUca assemblies with chewBBACA v2.8.5 or AQUAMIS assemblies with chewBBACA v3.3.5).

	<i>L. monocytogenes</i>		<i>S. enterica</i>		<i>E. coli</i>		<i>C. jejuni</i>	
	HC	GT	HC	GT	HC	GT	HC	GT
Original (assemblies)	1643	1731	2937	3054	2191	2288	641	671
Alternative (assemblies)	1646	1731	2913	3066	2178	2287	641	671
Original (allele calling)	1657	1731	2937	3054	2191	2288	641	671
Alternative (allele calling)	1653	1724	2925	3051	2186	2282	641	671

Table 37.2. Slope of the linear tendency line that fits the corresponding points of each pairwise comparison. All comparisons yielded an $r^2 > 0.99$.

	HC		GT	
	Alternative (assemblies)	Alternative (allele calling)	Alternative (assemblies)	Alternative (allele calling)
<i>L. monocytogenes</i>	0.999	1.001	0.999	1.001
<i>S. enterica</i>	0.999	1.002	0.997	1.003
<i>E. coli</i>	0.999	1.001	0.987	1.008
<i>C. jejuni</i>	0.984	1.001	0.995	1.003

----- CLUSTER CONGRUENCE AT OUTBREAK LEVEL -----

Table 37.3. Percentage of the clusters detected by the original pipeline that are also detected with the exact same composition at the exact same outbreak threshold per species.

	Threshold (ADs)	HC			GT		
		Original	Alternative (assemblies)	Alternative (allele calling)	Original	Alternative (assemblies)	Alternative (allele calling)
<i>L. monocytogenes</i>	7	100%	96%	99%	100%	92%	96%
<i>S. enterica</i>	14	100%	91%	98%	100%	85%	91%
<i>E. coli</i>	9	100%	96%	100%	100%	93%	98%
<i>C. jejuni</i>	4	100%	95%	100%	100%	93%	100%