Illumina vs. AVITI

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We performed sequencing experiments on identical samples from the same donor (Baby 2, B002). In one experiment, Illumina was used; in the other, AVITI.

1 Sequencing quality

2 Variant calling

3 Sequence typing

We used software `srst2` to perform sequence typing for E. coli (MLST database name `Escherichia coli#1`) with CLI pseudocode:

```
$ module load srst2/0.2.0
$ srst2 --input_pe {trimmed reads} --mlst_* '{Escherichia_coli#1}'
```

We found that:

- (ST)73 is the dominant sequence type (figure 1)

- AVITI (⋄) has higher seq. depth at core genes used for sequence typing than Illumina (●) (figure 1)

- $\frac{250}{256} \approx 98\%$ agreement between AVITI and Illumina (table 1)
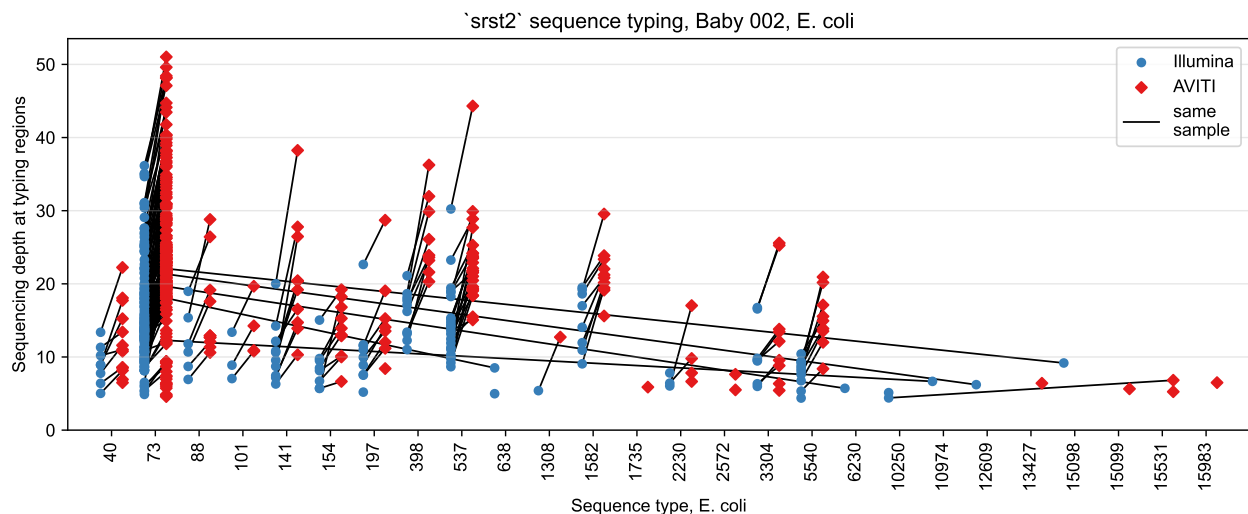
- Results are nearly identical between technologies

Figure 1: **Sequence typing results** for successful `srst2` sequence typing of identical samples (−) prepared using AVITI (⋄) or Illumina (●).

	Count
AVITI & Illumina (total)	317
AVITI, typed (total)	309
Illumina, typed (total)	264
AVITI & Illumina, typed (total)	256
AVITI & Illumina, typed (agree)	250

Table 1: **Summary of sequence typing results**, tallying the number of samples for different criteria. The top row provides the total number of samples; the bottom row provides the number of samples *successfully* sequence typed for *both* AVITI *and* Illumina *and agree* in the designated sequence type.

4   Reconstructing phylogenies of dominant STs

5   Appendix

Code to reproduce is available on GitHub at t-silvers/sequencing-comparison-aviti-illumina.