chr20 strawman benchmark

A summary of truvari's assessment of TRGT VCF

	truvari bench	truvari refine	region summary
Precision	0.013	0.91	0.91
Recall	0.020	0.99	0.98
F1	0.016	0.95	0.94

# Assessment of 100 pileups corresponding to FPs and FNs

- A subset of regions appears to be correctly genotyped by TRGT; these may correspond to assembly errors

- The remaining regions are likely TRGT errors due to
  - Polymorphic flanks
  - Consensus algorithm errors
  - Alignments supporting more than two alleles

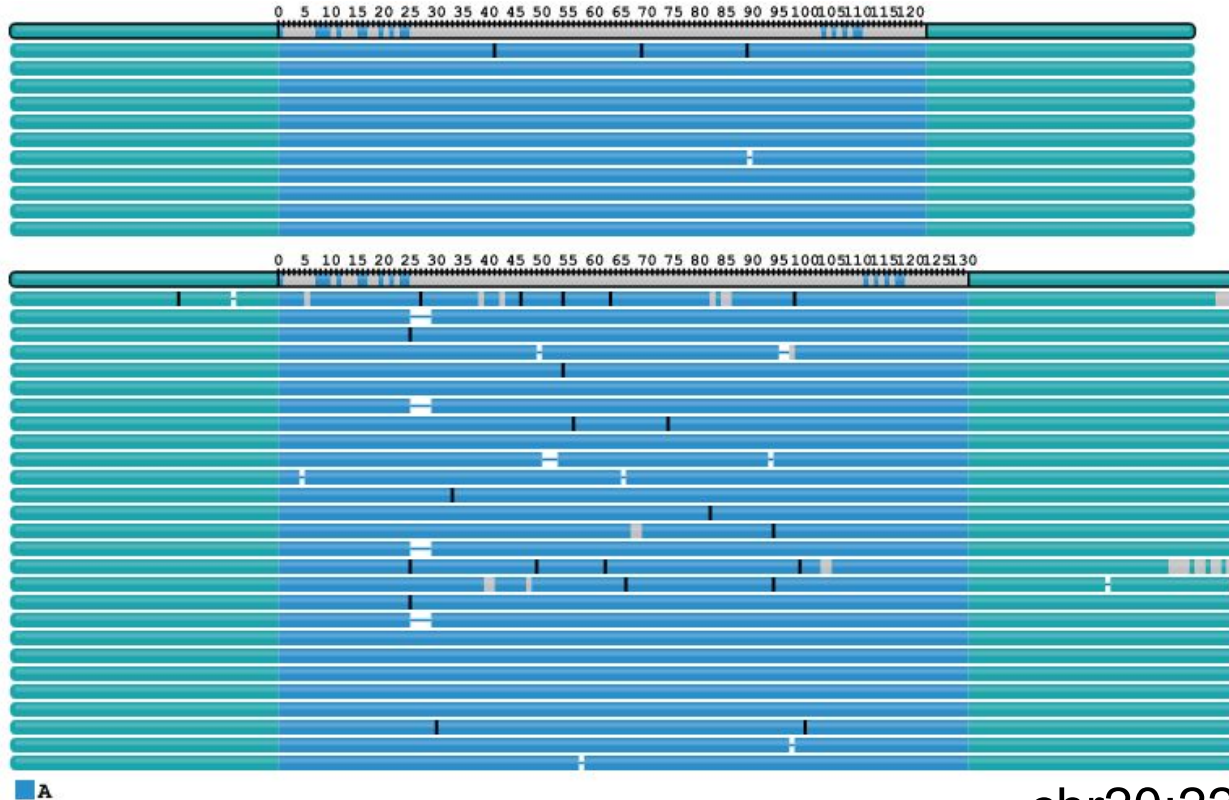# A confident TRGT call
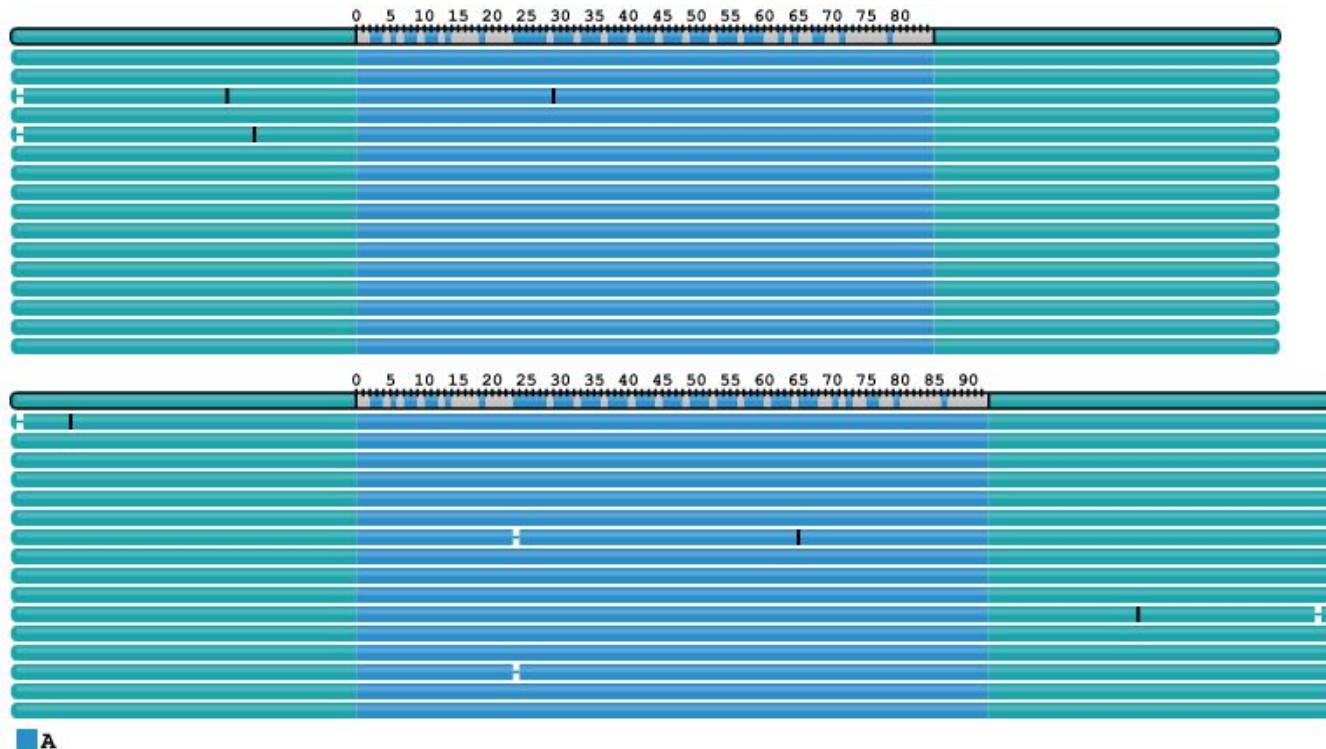
chr20:3814328-3814425

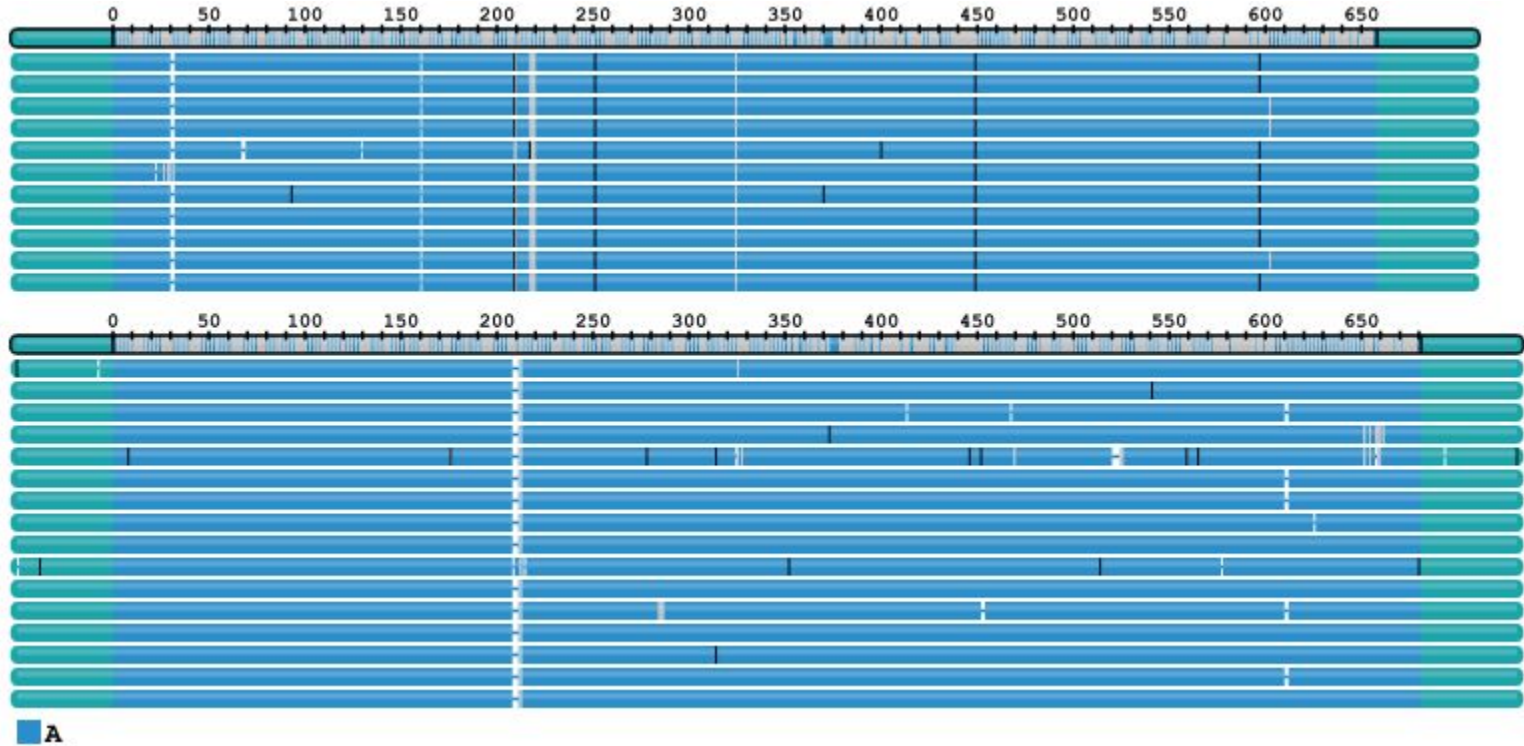# A slightly less confident call
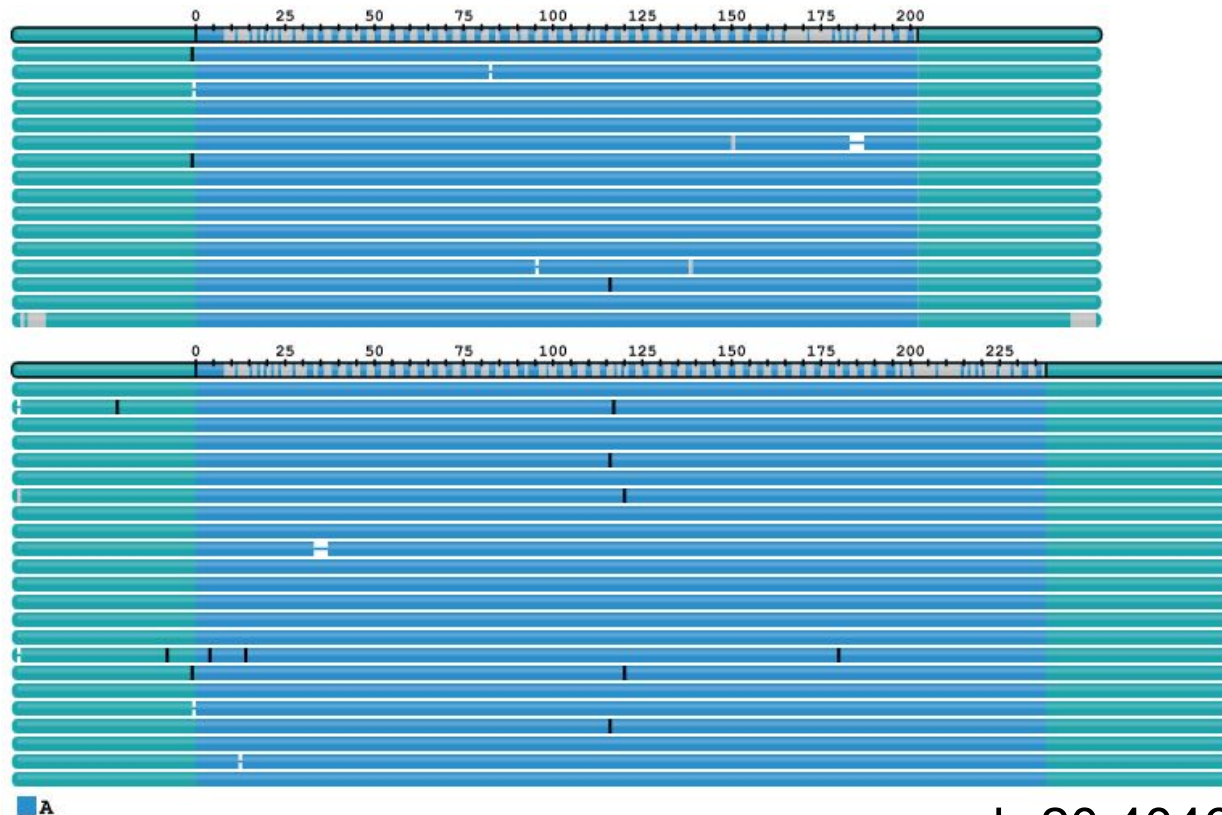
chr20:40460114-40460364
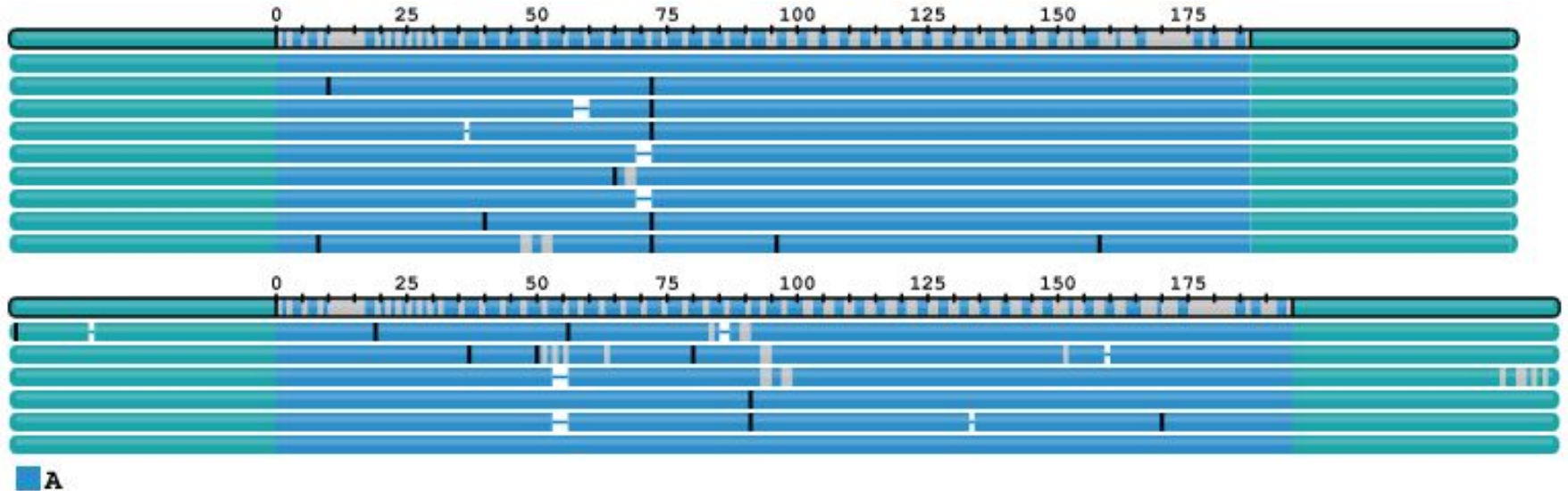
The longer allele may be incorrectly called

chr20:2281292-2281427

Consensus sequences of both alleles are incorrect

chr20:6327068-6327756

Consensus sequences of both alleles are incorrect

chr20:5011162-5011342