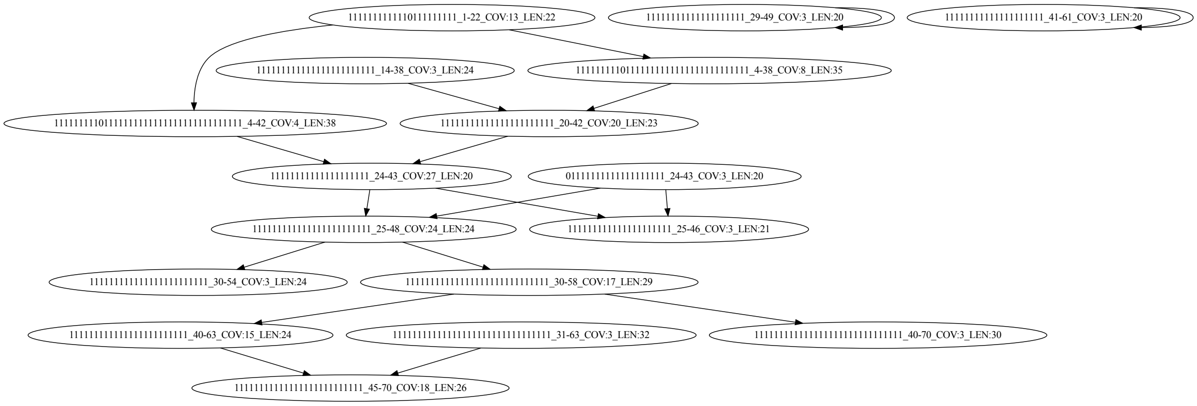
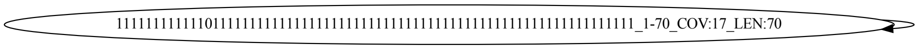
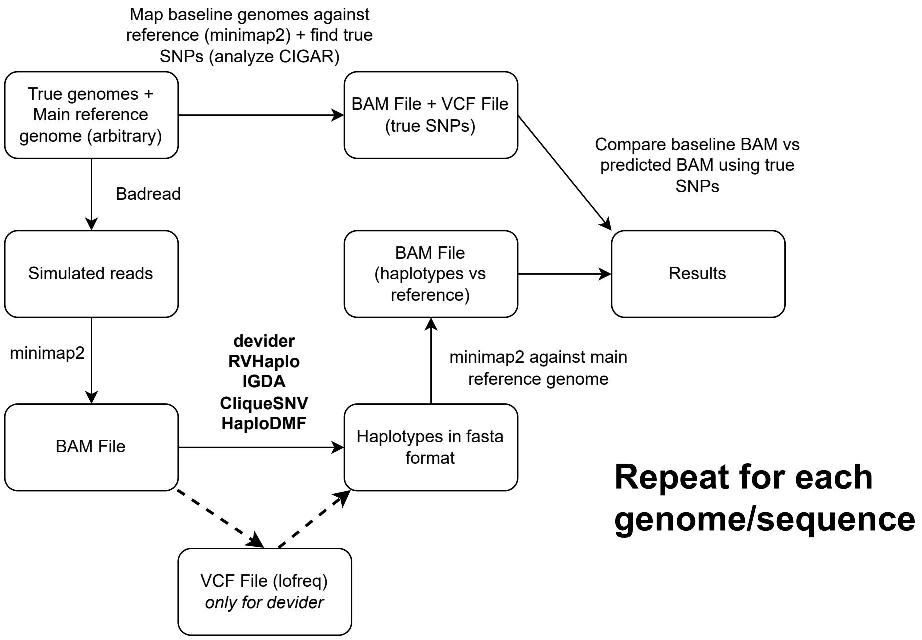


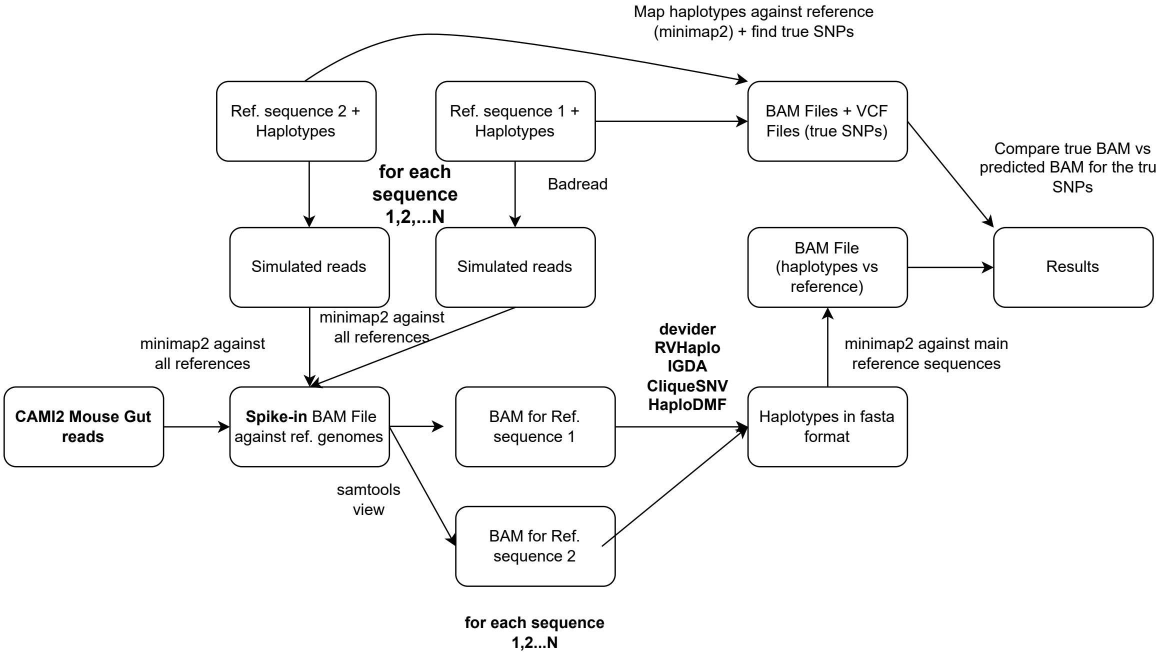
Supplementary Figure 1. Unitig graph for long reads (95% accuracy) for a single HIV-1 genome. The k-mer coverage cutoff was 2. The format is (alleles)_(start-end)_COV:(coverage)_LEN:(number of alleles spanned). Notice that low coverage nodes and nodes with deletions (i.e., end - start + 1 ≠ length) are more likely to be erroneous.



Supplementary Figure 2. Cleaned unitig graph for long reads (95% accuracy) for a single HIV-1 genome. The graph contains one unitig, as expected. The format is (alleles)_(start-end)_COV:(coverage)_LEN:(number of alleles spanned).



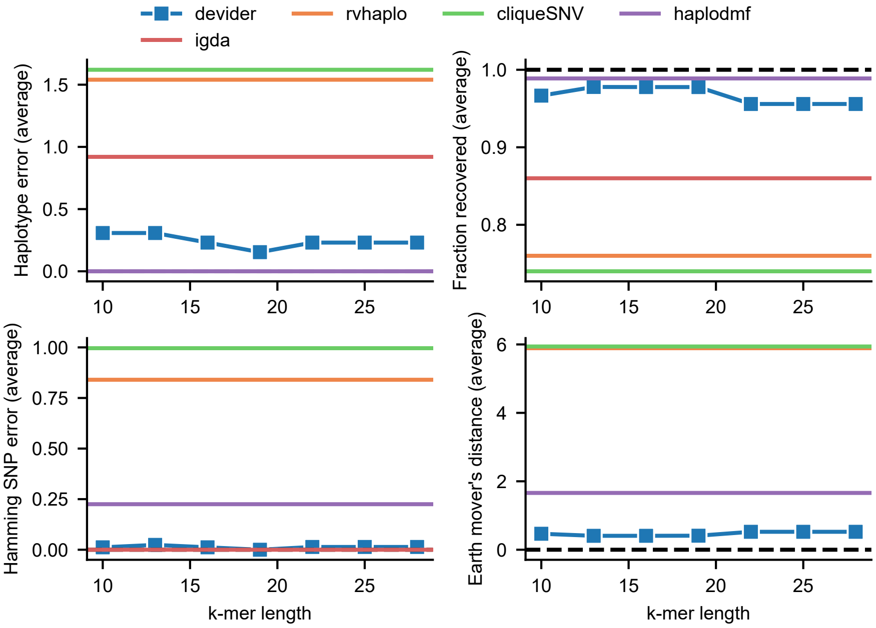
Supplementary Figure 3. Benchmarking flowchart for the HIV-1 and antimicrobial resistance gene synthetic benchmarks.



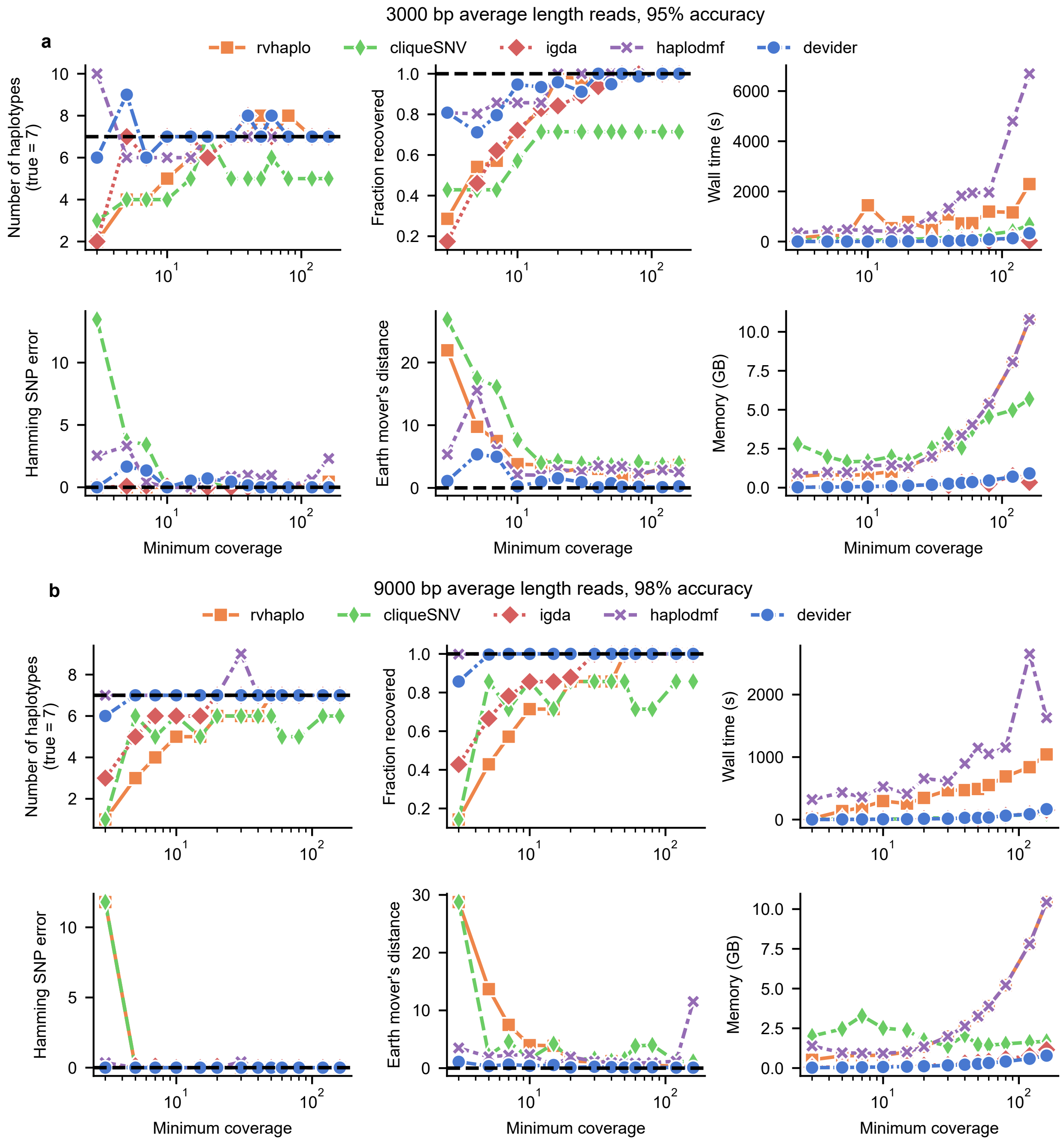
Supplementary Figure 4. Benchmarking flowchart for the antimicrobial resistance gene **spike-in** synthetic benchmarks. The AMR gene reads were spiked into a mouse gut metagenome, and BAM files were generated for each AMR gene of interest with `samtools view` prior to haplotyping.

Genome accessions for HIV communities
- OR483999
- OR483988
- OR483990
- OR483987
- OR484006
- OR484007
- OR484012
- OR484013
- OR484014
- OR484015
- OR484016
- OR483993
- OR483994
- OR483989
- OR483992
- OR483997
- OR484000
- OR484002
- OR483986
- OR484017
- OR484018
- OR484019
- OR484020
- OR484021
- OR484022
- OR484001
- OR483985
- OR484004
- OR484005
- OR483996

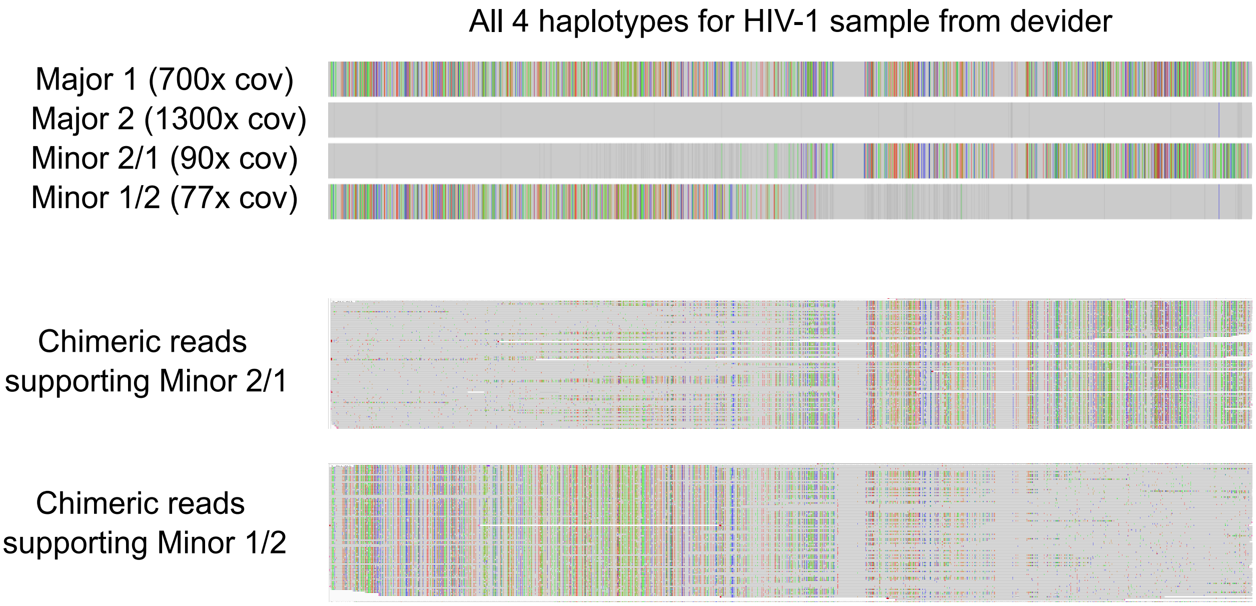
Supplementary Table 1. Genomes used for the HIV community. The first 7 (delimited by an horizontal line) are used for the 7 strain community and all 30 are used when benchmarking communities with 2 - 30 strains.



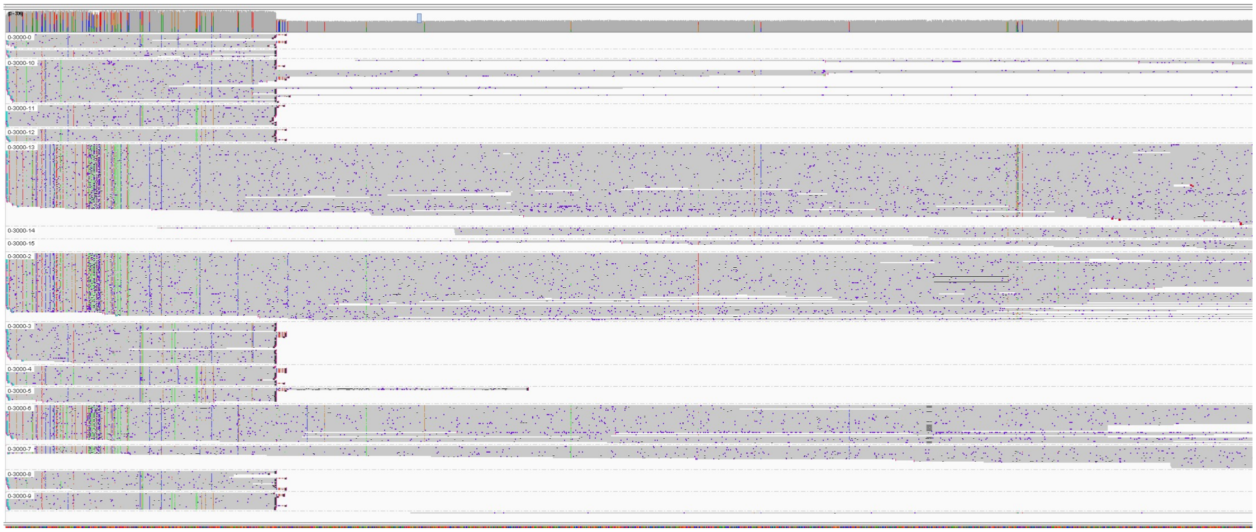
Supplementary Figure 5. devider's results over varying values of k-mer length k on the 7-strain HIV community with 9000 bp length and 95% accuracy simulated reads. devider dynamically selects k based on the data by default; instead, we fixed k from 10 to 30 and show averaged results over all data points. The other three methods are displayed as constant horizontal lines. The dashed black line shows the optimal values.



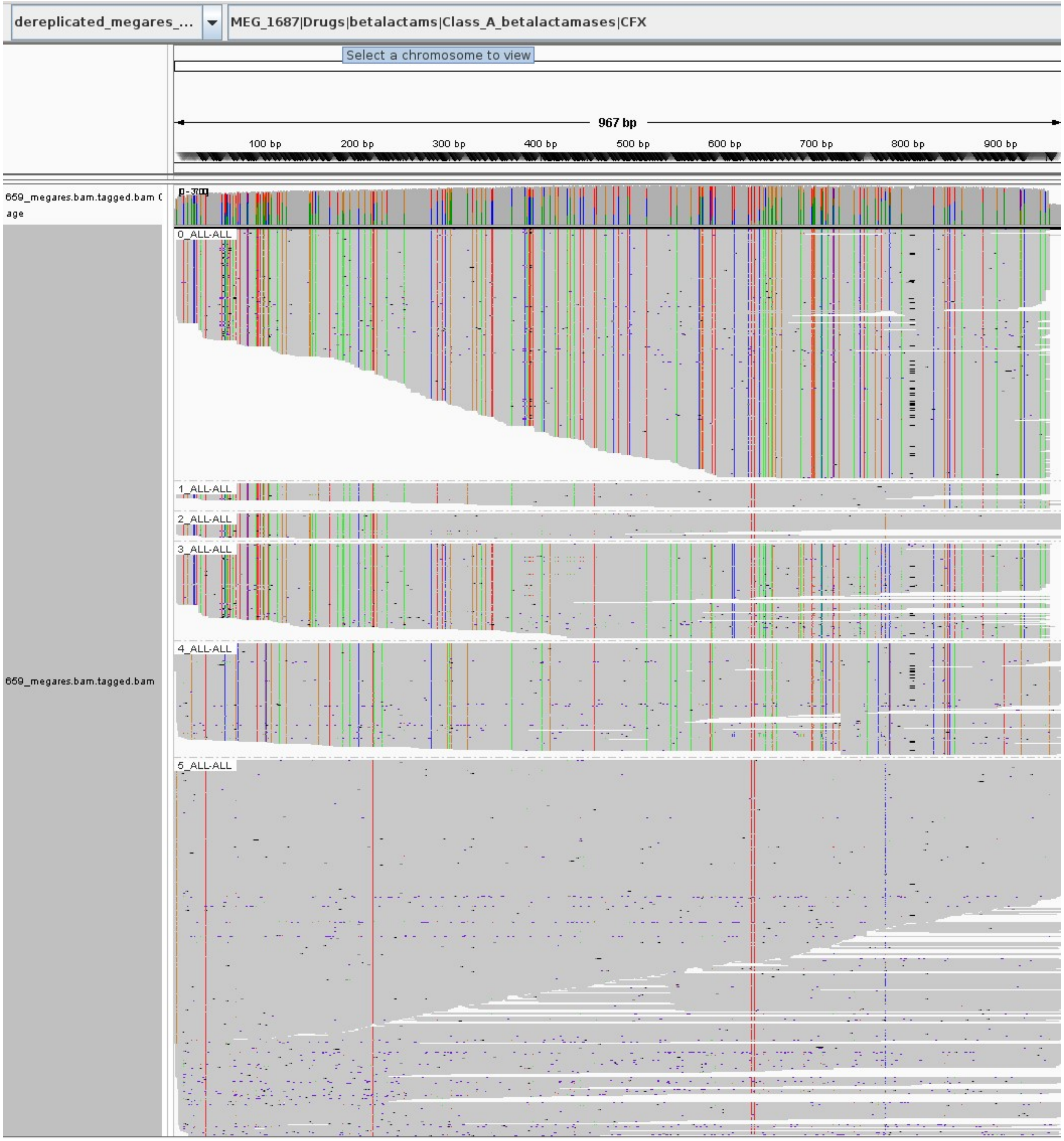
Supplementary Figure 6. The same experiment as Fig. 2a in the main paper on the 7-strain HIV synthetic community with staggered abundances. **a.** simulated reads have 3000bp average length and 95% accuracy. **b.** simulated reads have 9000 bp average length and 98% accuracy.



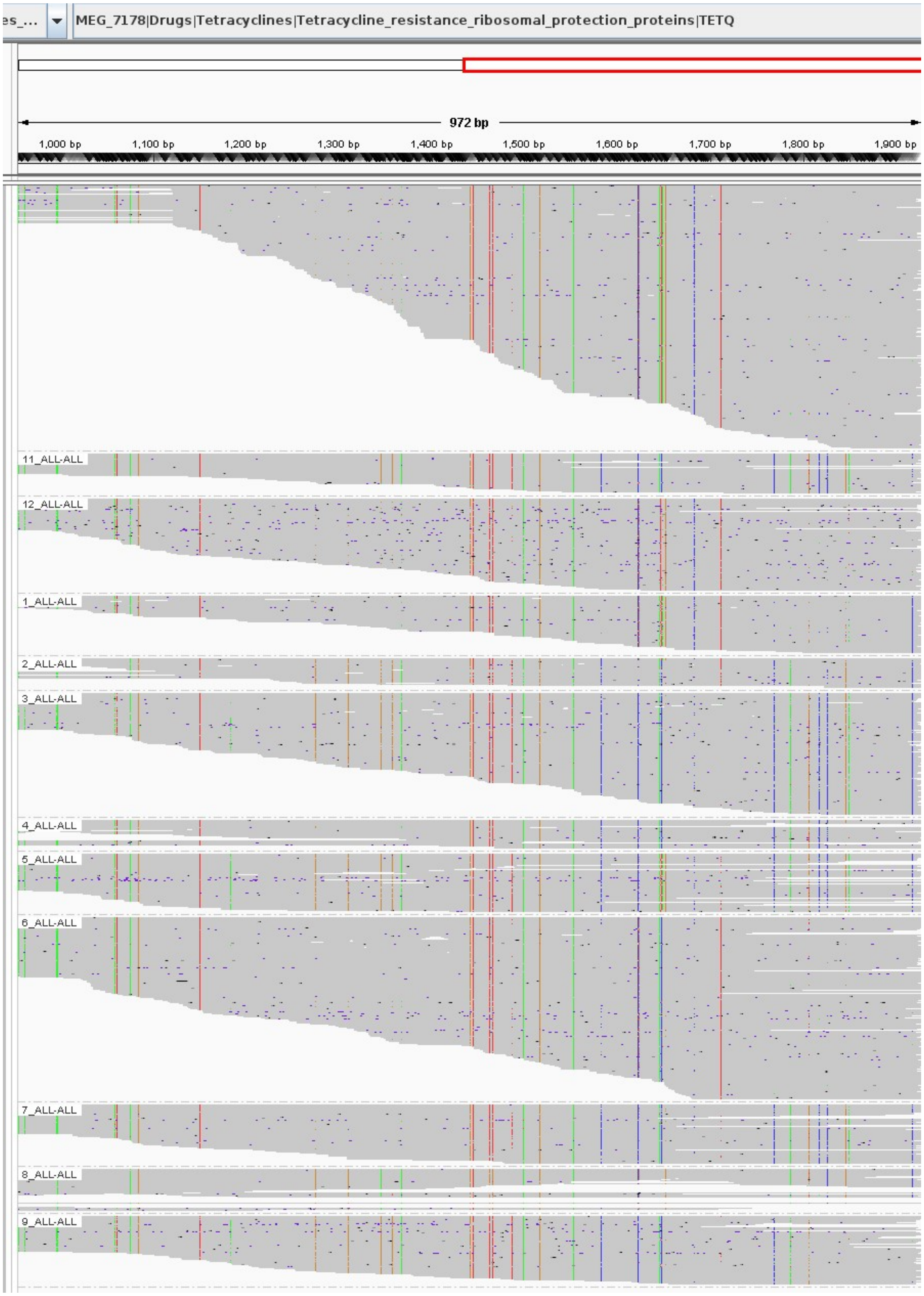
Supplementary Figure 7. All four haplotypes found by devider on the HIV-1 co-infection dataset. Two major haplotypes were found and two minor haplotypes were also found. Gray bars indicate alleles with $< 66\%$ of the reads supporting that allele. For the "chimeric" minor haplotypes, supporting reads assigned by devider are shown. The reference sequence for all alignments is a consensus generated by abPOA [1] from Major Haplotype 2's reads.



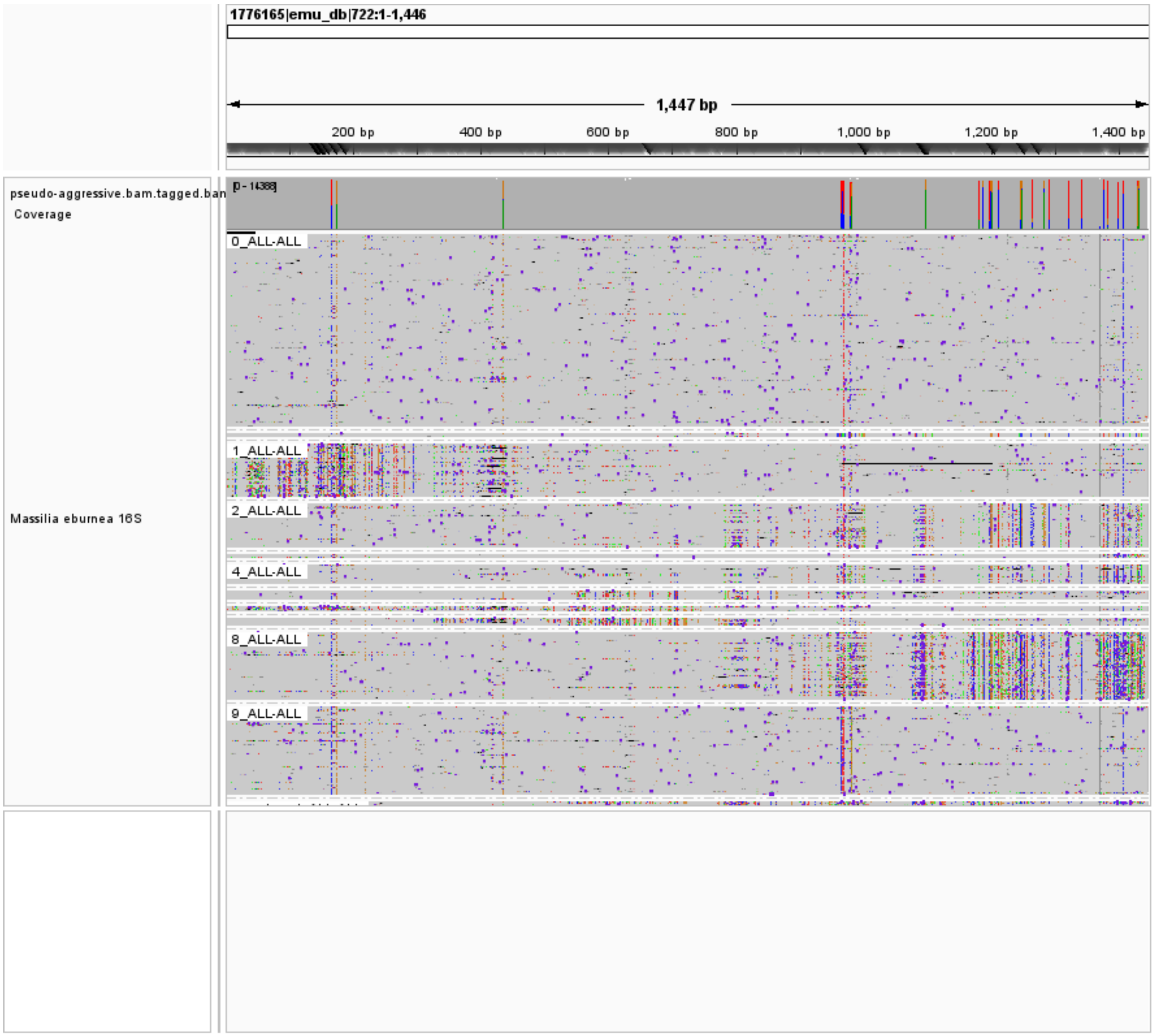
Supplementary Figure 8. A region with 16 estimated haplotypes by devider for the mussel-bacterial symbiont community. An elevated region of high coverage at the start of the contig (mean > 300x coverage vs estimated 220x single-copy coverage) and supplementary mapping reads suggest a duplicated region, which makes the number of haplotypes estimated higher.



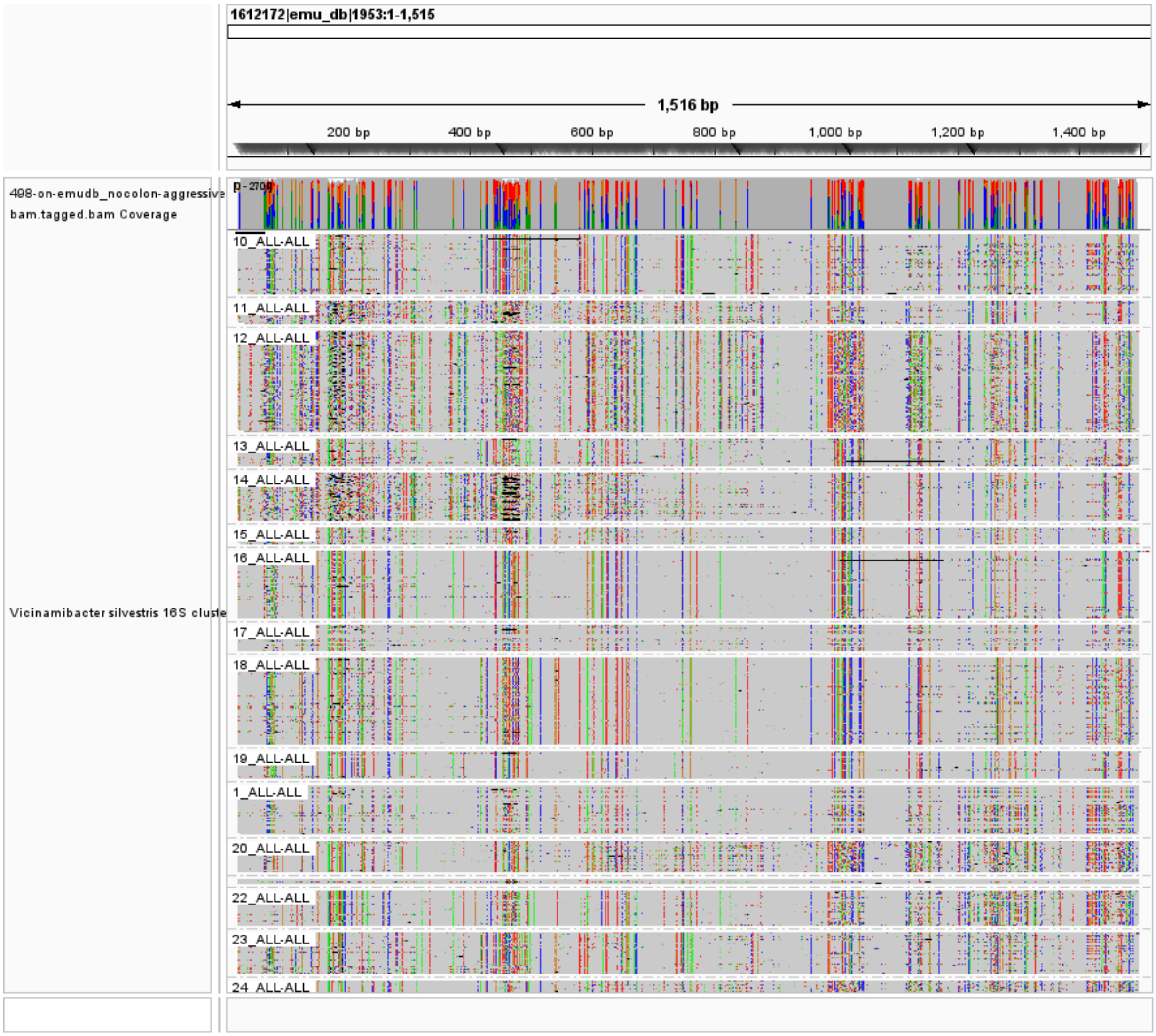
Supplementary Figure 9. Reads supporting the CfxA2 haplotypes shown in Fig. 4 c. Reads were downsampled to 1000x coverage per 1000 bp window for visualization purposes.



Supplementary Figure 10. Reads supporting a subset of the tet(Q) haplotypes shown in Fig. 4 c. Reads were downsampled to 1000x coverage per 1000 bp window for visualization purposes. Only the last 972 bp of the alignments are shown; Fig. 4 c also shows only the last 972 bp.



Supplementary Figure 11. Reads supporting the 16S consensus sequences mapping to *M. eburnea* for the 16S R10.4 ONT sequencing dataset. Reads were downsampled to 500x coverage for visualization purposes.



Supplementary Figure 12. Reads supporting a subset of 16S consensus sequences mapping to *V. silvestris* for the 16S R10.4 ONT sequencing dataset. Reads were downsampled to 500x coverage for visualization purposes.

References

1. Gao, Y. *et al.* abPOA: An SIMD-based C library for fast partial order alignment using adaptive band. *Bioinformatics* **37**, 2209–2211 (2021).