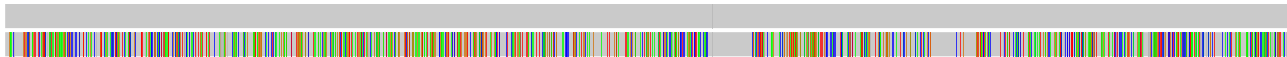
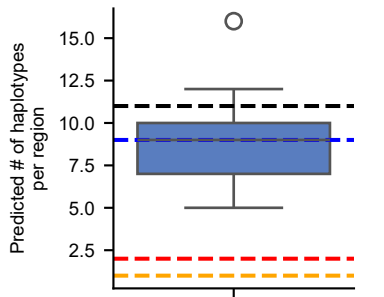


a

HIV-1 co-infection (2 major strains, 33.4% + 59.6% abundance)

**b**

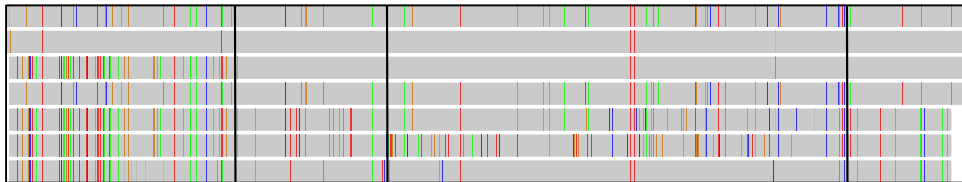
dbghaplo on bacteria-mussel symbiont community (n = 25 candidate regions)



- Published estimate (11 haplotypes)
- dbghaplo median (9 haplotypes)
- igda median (2 haplotypes)
- rvhaplo (1 haplotypes)

c Haplotypes from ARG-enriched metagenome (with recombination blocks)

CfxA2 (beta lactamase) - 7 haplotypes



tet(Q) (tetracycline resistance) - 14 haplotypes

