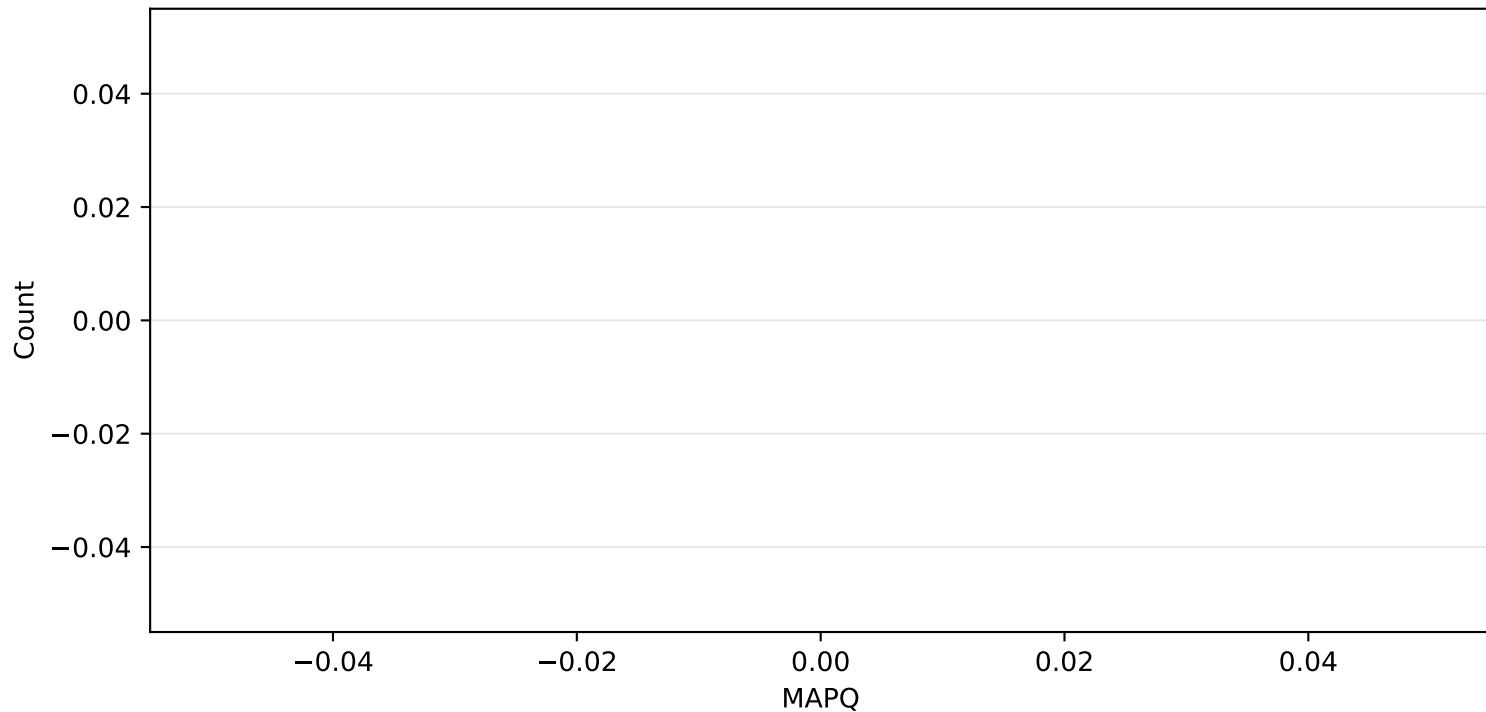
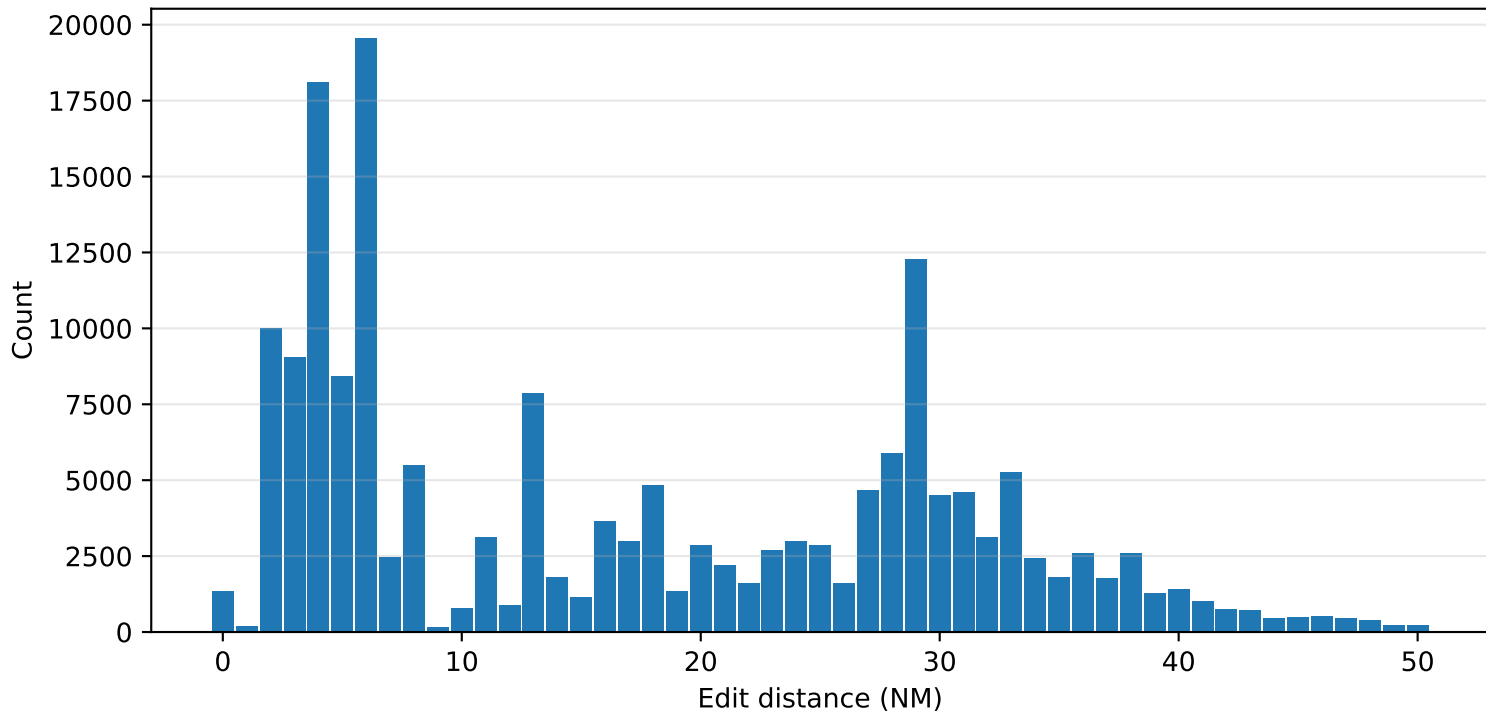


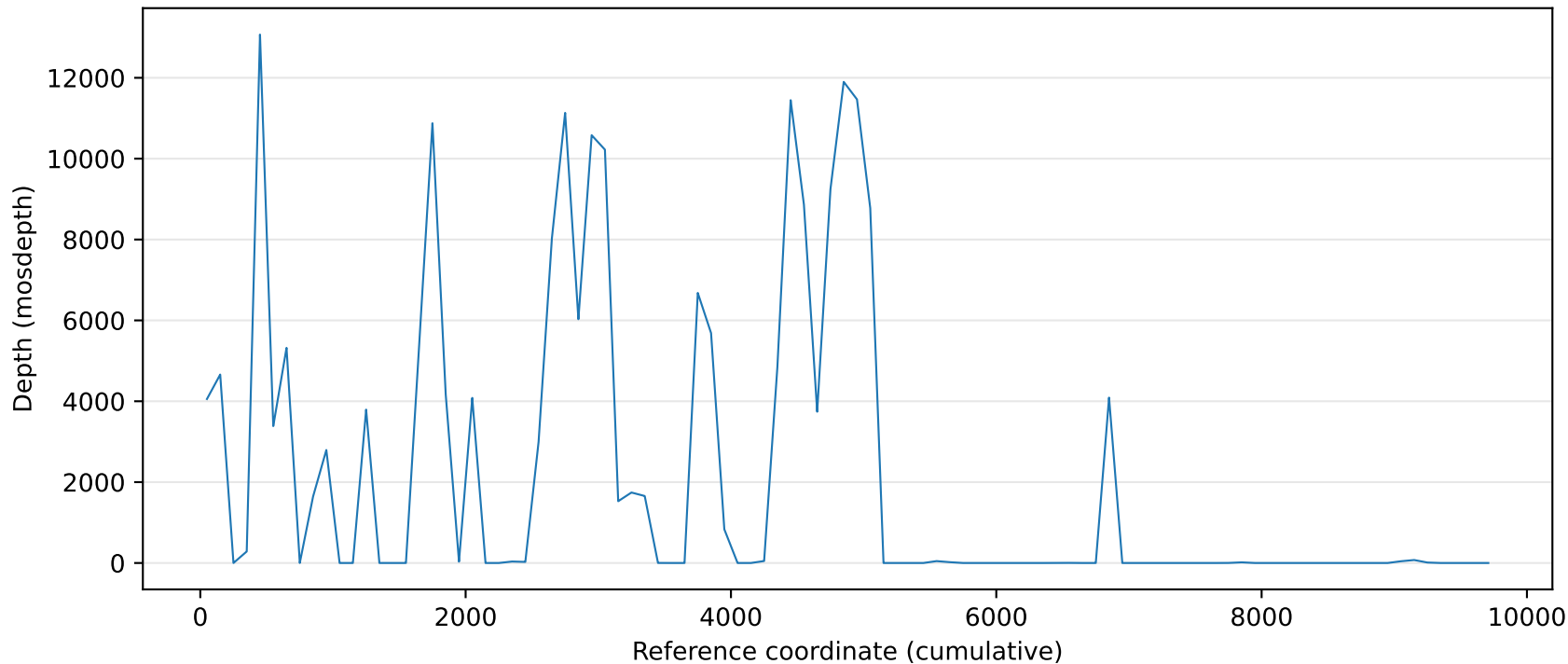
Accelgpu SE Alignments — Mapping Quality (MAPQ)



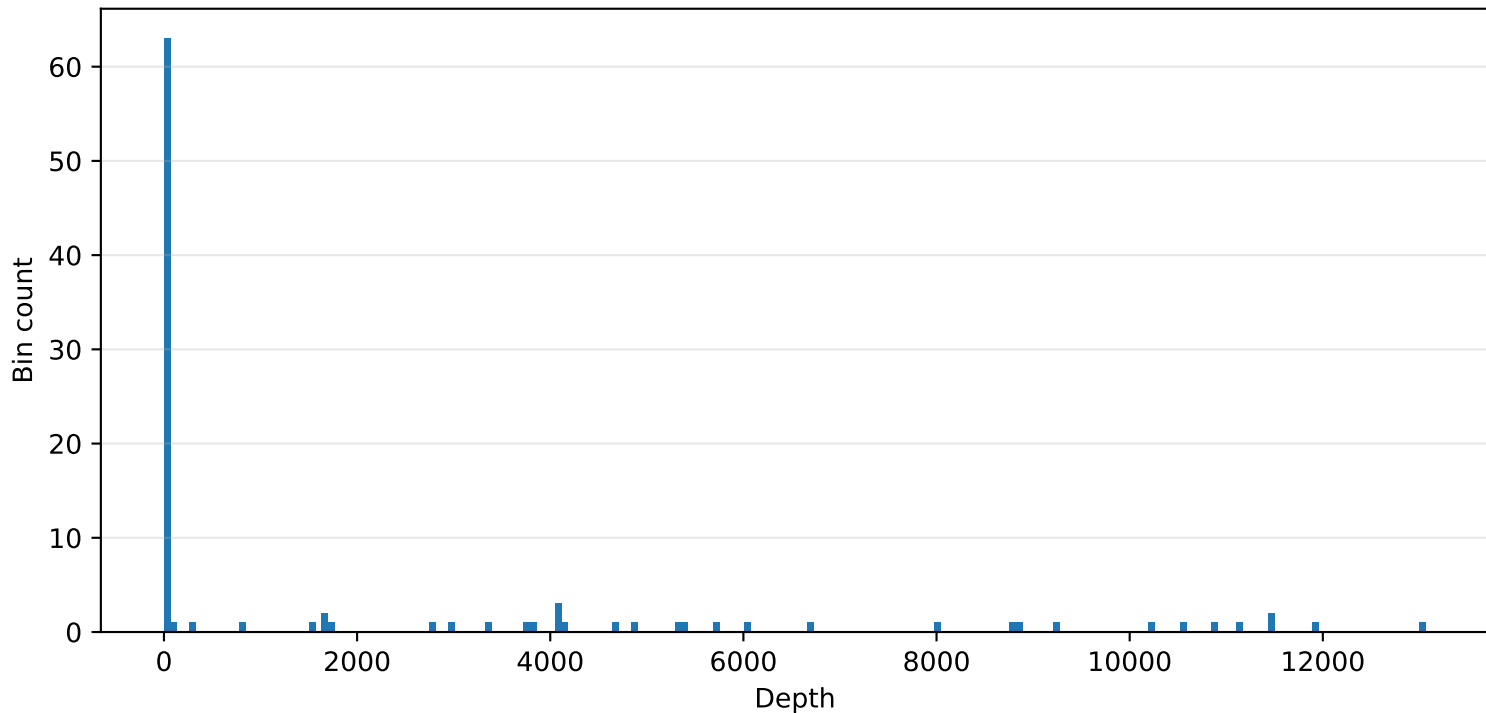
Accelgpu SE Alignments — Edit Distance (NM)



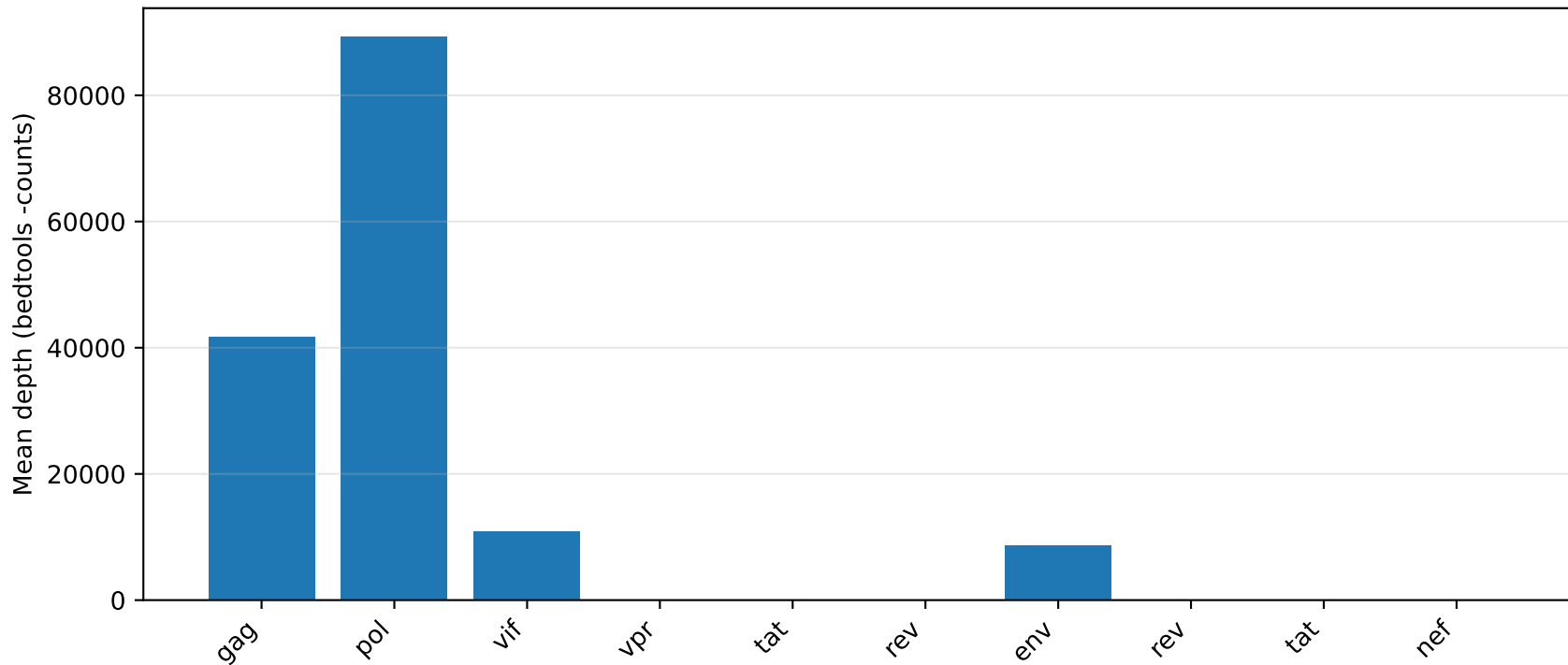
Accelgpu SE Alignments — Coverage along reference (mosdepth)



Accelgpu SE Alignments — Coverage distribution (mosdepth)



Accelgpu SE Alignments — Per-gene counts



plot_align_stats.py – summary

Title: Accelgpu SE Alignments

MAPQ hist: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_minscore30.sorted.mapq_hist

NM hist: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_minscore30.sorted.nm_hist

mosdepth regions: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_minscore30.sorted

mosdepth per-base: (none)

gene coverage: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_minscore30.sorted.gen

Max MAPQ: 60

Max NM: 50

Max depth (hist clip): (none)