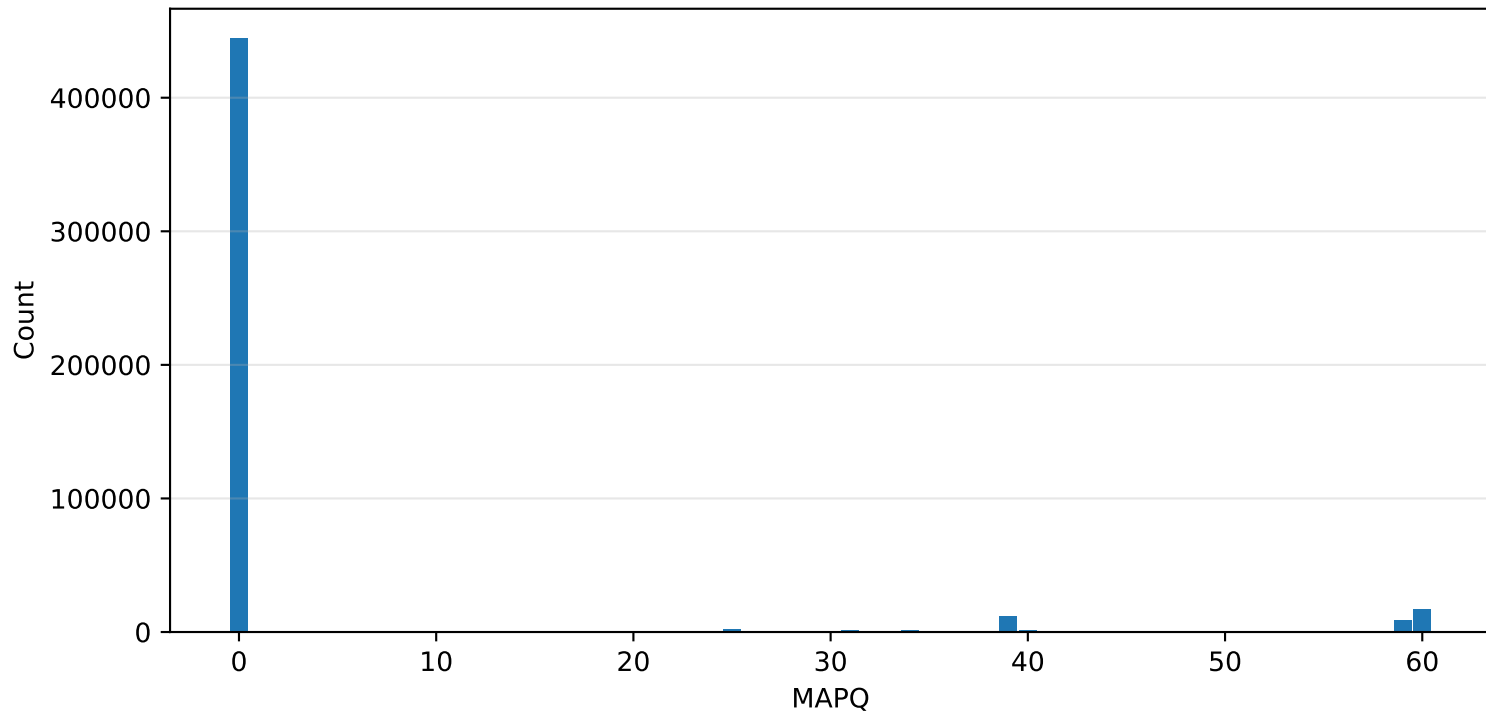
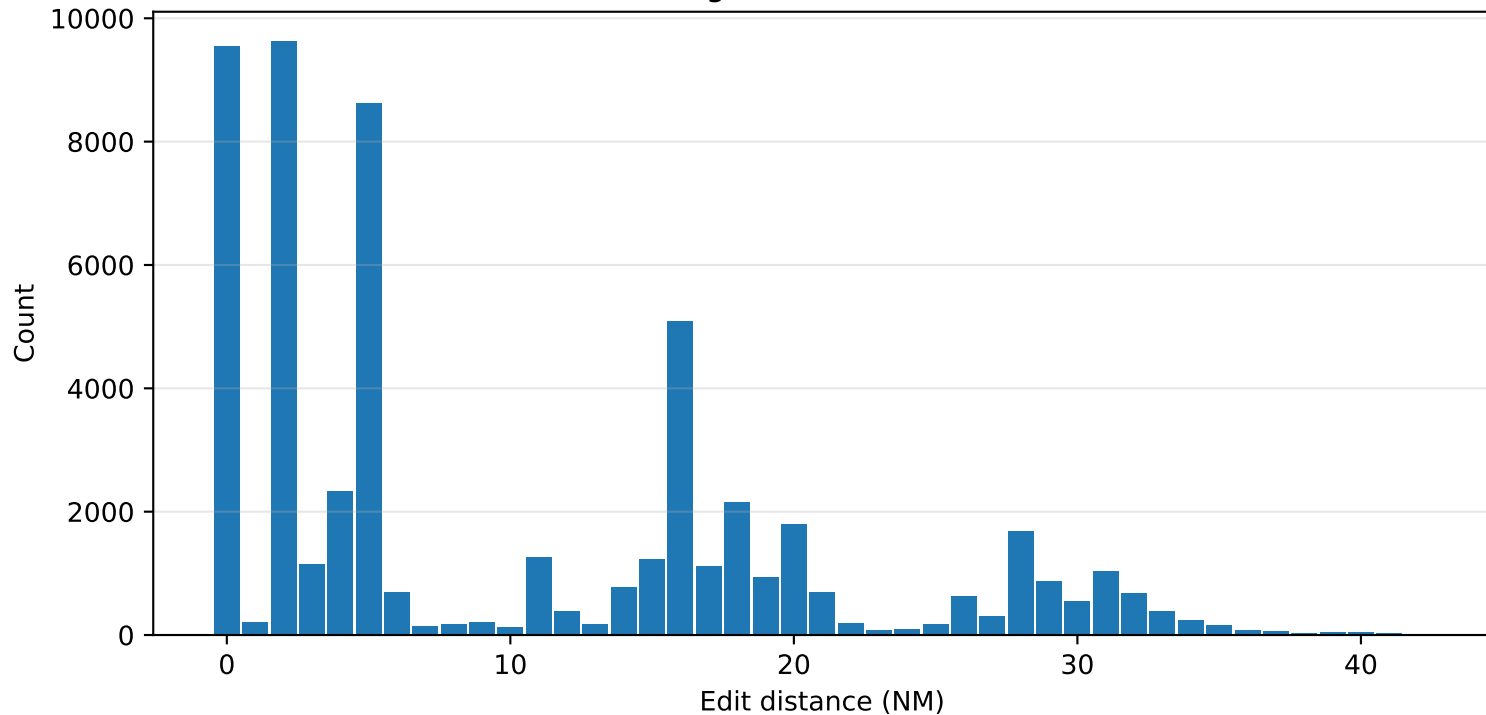


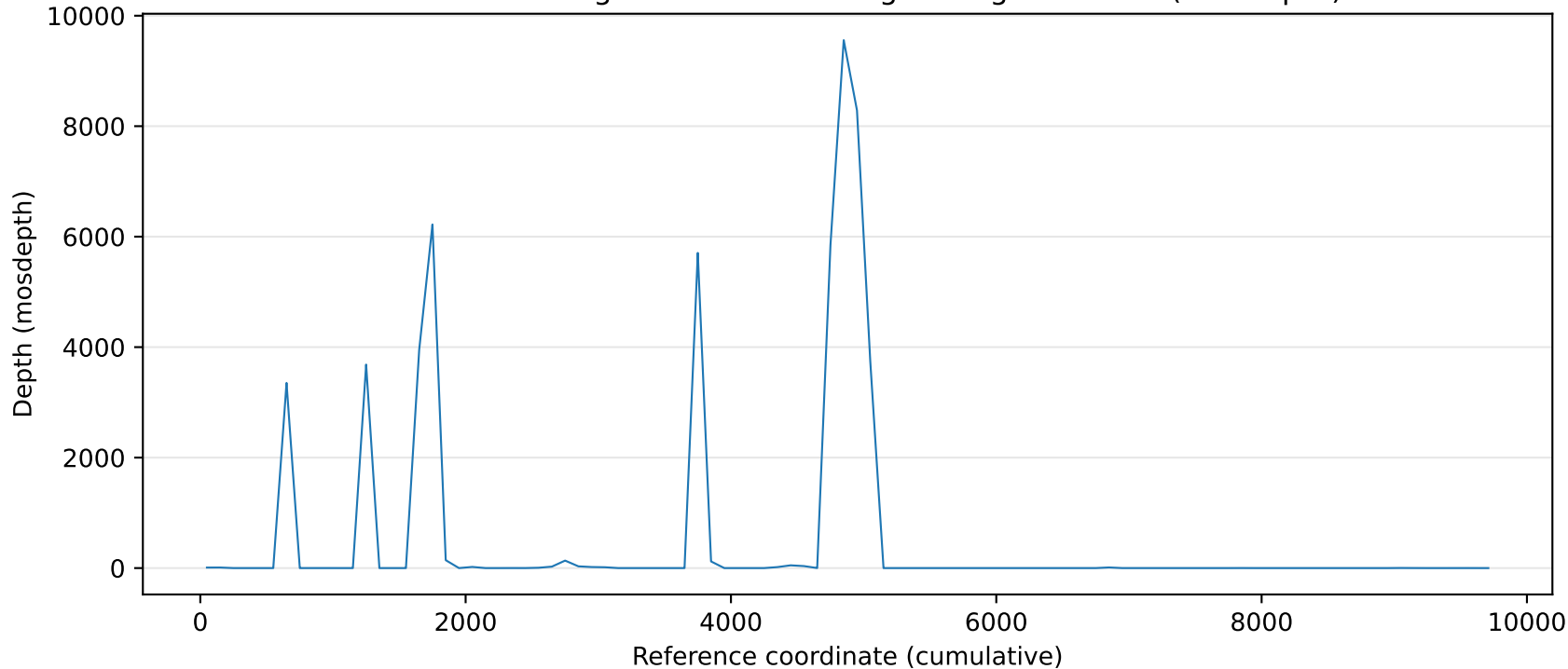
BWA MEM SE Alignments — Mapping Quality (MAPQ)



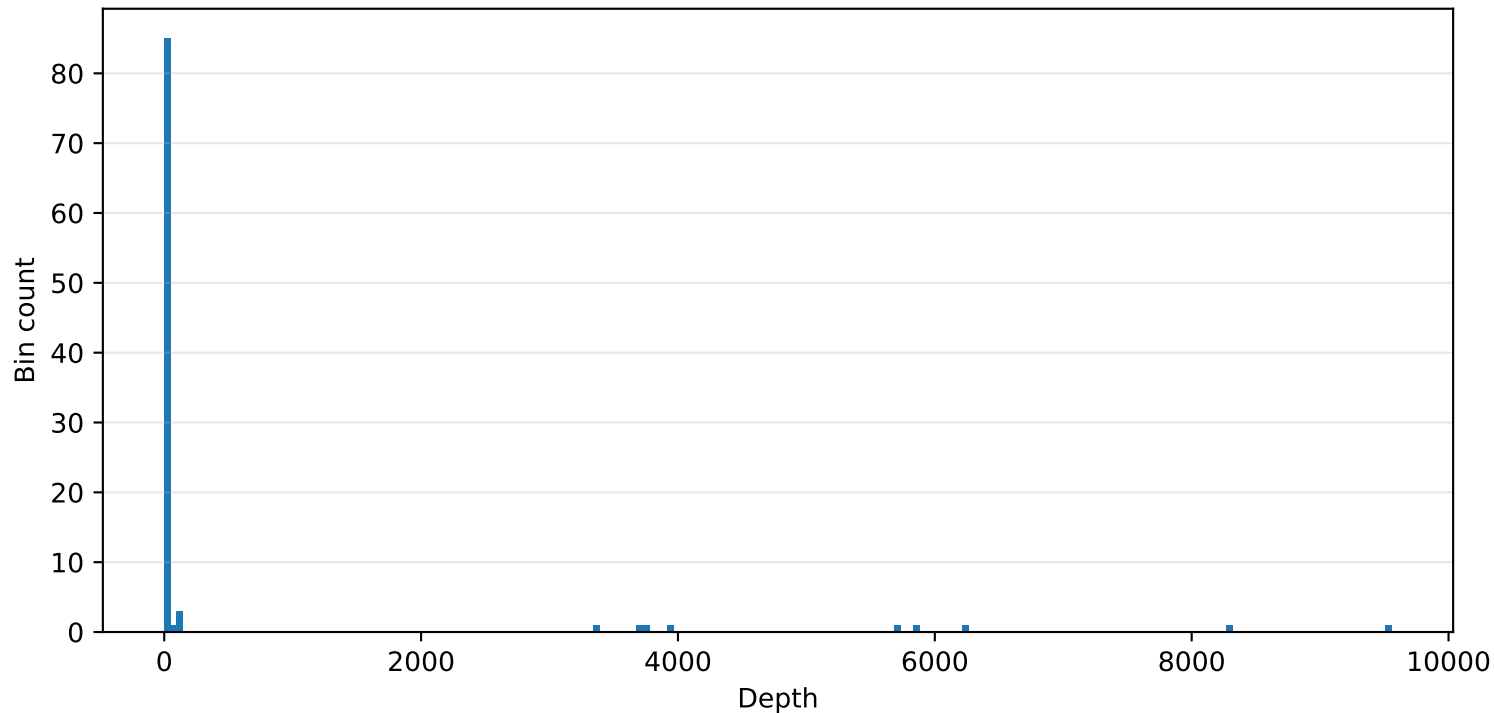
BWA MEM SE Alignments — Edit Distance (NM)



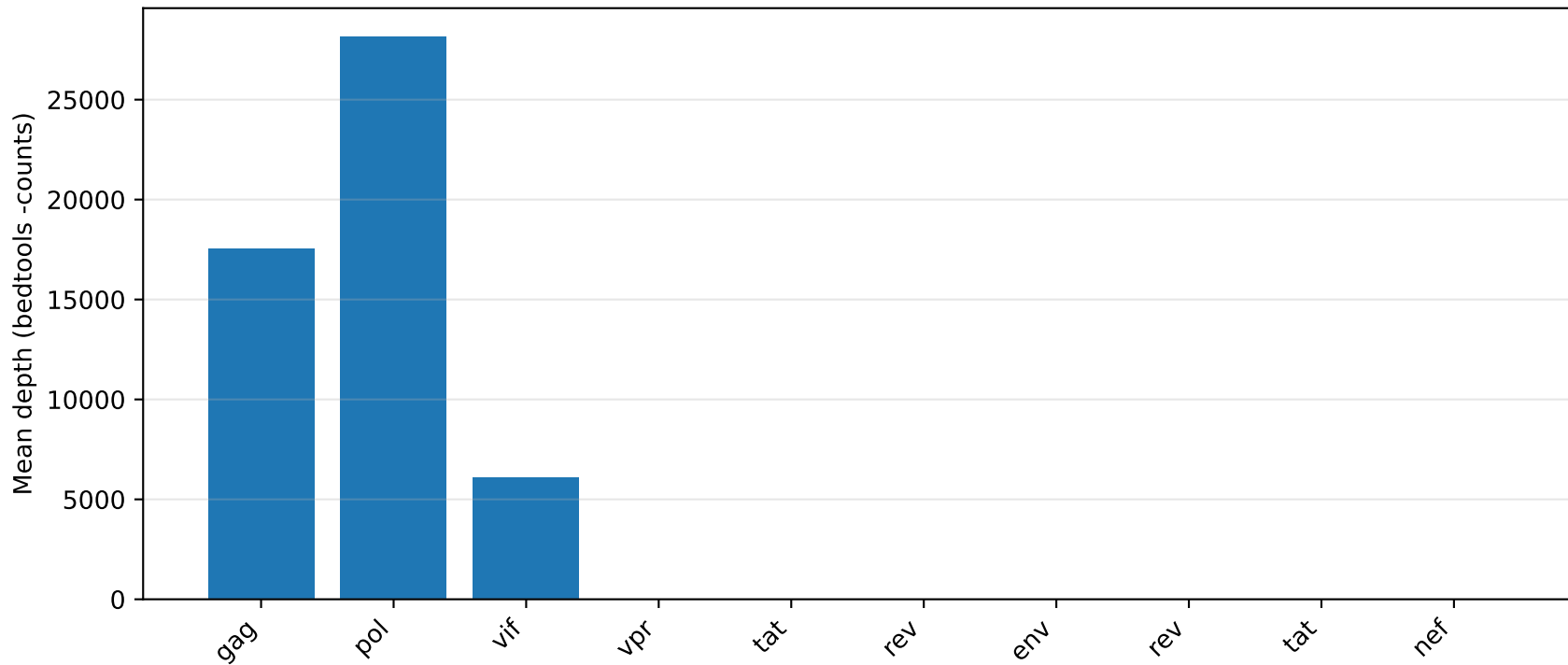
BWA MEM SE Alignments — Coverage along reference (mosdepth)



BWA MEM SE Alignments — Coverage distribution (mosdepth)



BWA MEM SE Alignments — Per-gene counts



plot_align_stats.py – summary

Title: BWA MEM SE Alignments

MAPQ hist: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_bwa_mem_defaults.sorted.m

NM hist: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_bwa_mem_defaults.sorted.nm

mosdepth regions: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_bwa_mem_defaults.s

mosdepth per-base: (none)

gene coverage: art_illumina_msv3_0.FR.2005.LA49RBF189.KU168292_l250_c500000_bwa_mem_defaults.sort

Max MAPQ: 60

Max NM: 50

Max depth (hist clip): (none)