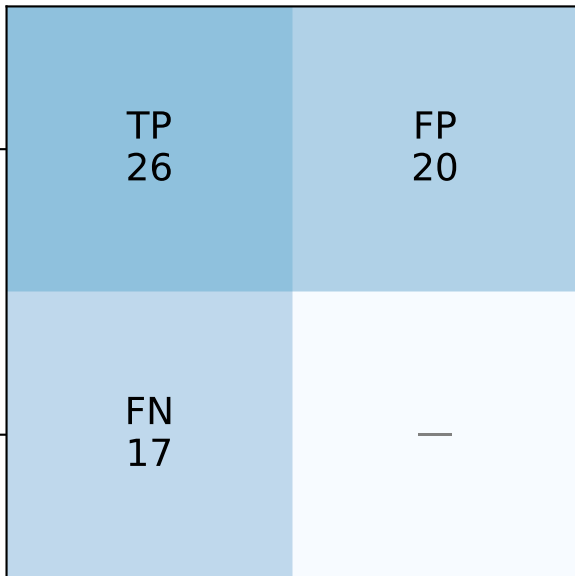


Confusion Matrices - G60
(SNPs only, GT=1/1; ploidy=2, min-alt=5)

ParaDISM



Base Aligner

