Samtools: flagstat: read count 16 samples Total Reads 40 M 0 M 10 M 20 M 30 M 50 M Total Passed QC 0 M 10 M 20 M 30 M 40 M 50 M Mapped 0 M 10 M 40 M 50 M 20 M 30 M Secondary Alignments 0 M 10 M 20 M 30 M 40 M 50 M Duplicates • 0 M 10 M 20 M 30 M 40 M 50 M Paired in Sequencing 40 M 10 M 0 M 20 M 30 M 50 M Properly Paired 40 M 10 M 30 M 50 M 0 M 20 M Self and mate mapped 40 M 0 M 10 M 30 M 50 M 20 M Singletons -0 M 10 M 20 M 30 M 40 M 50 M Mate mapped to diff chr 0 M 10 M 30 M 50 M 20 M 40 M Diff chr (mapQ >= 5)

30 M

40 M

50 M

0 M

10 M

20 M