Samtools: flagstat: read count 6 samples Total Reads 0 M 5 M 10 M 15 M 20 M 25 M 30 M 35 M 40 M Total Passed QC 5 M 10 M 15 M 35 M 40 M 0 M 20 M 25 M 30 M Mapped 0 M 10 M 15 M 35 M 40 M 5 M 20 M 25 M 30 M Secondary Alignments 0 M 5 M 10 M 15 M 20 M 25 M 30 M 35 M 40 M Duplicates 5 M 10 M 15 M 20 M 25 M 0 M 30 M 35 M 40 M Paired in Sequencing 15 M 35 M 40 M 0 M 5 M 10 M 20 M 25 M 30 M Properly Paired 5 M 10 M 15 M 25 M 40 M 0 M 20 M 35 M 30 M Self and mate mapped 10 M 15 M 20 M 35 M 40 M 0 M 5 M 25 M 30 M Singletons -0 M 5 M 10 M 15 M 25 M 30 M 35 M 40 M 20 M Mate mapped to diff chr 0 M 5 M 10 M 15 M 20 M 25 M 30 M 35 M 40 M

20 M

25 M

30 M

35 M

40 M

Diff chr (mapQ >= 5)

0 M

5 M

10 M

15 M