## Samtools flagstat: read count Read counts, 10 samples Total Reads 0 M 300 M 350 M 50 M 250 M 400 M 100 M 150 M 200 M Total Passed QC 150 M 0 M 50 M 100 M 200 M 250 M 300 M 350 M 400 M Mapped 0 M 50 M 100 M 150 M 200 M 250 M 300 M 350 M 400 M Secondary Alignments 0 M 50 M 100 M 150 M 200 M 250 M 300 M 350 M 400 M Duplicates 0 M 50 M 100 M 150 M 200 M 250 M 300 M 350 M 400 M Paired in Sequencing 150 M Properly Paired 100 M 0 M 50 M 150 M 200 M 250 M 300 M 350 M 400 M Self and mate mapped 0 M 50 M 100 M 150 M 200 M 250 M 300 M 350 M 400 M Singletons -0 M 50 M 100 M 150 M 200 M 250 M 300 M 350 M 400 M Mate mapped to diff chr 50 M 150 M 200 M 300 M 400 M 0 M 100 M 250 M 350 M Diff chr (mapQ >= 5) 0 M 50 M 400 M 100 M 150 M 200 M 250 M 300 M 350 M