Samtools flagstat: read count Read counts, 6 samples Total Reads 250k 300k 350k 400k 50k 100k 150k 200k 450k Total Passed QC 250k 300k 350k 50k 100k 150k 200k 400k 450k Mapped 350k 50k 100k 150k 200k 250k 300k 400k 450k Secondary Alignments 50k 150k 100k 200k 250k 300k 350k 400k 450k Duplicates 50k 100k 150k 200k 250k 300k 350k 400k 450k Paired in Sequencing 250k 300k 350k 200k Properly Paired 150k 250k 300k 350k 400k 50k 100k 200k 450k Self and mate mapped 50k 150k 250k 300k 350k 400k 100k 200k 450k Singletons 50k 100k 150k 250k 350k 400k 450k 200k 300k Mate mapped to diff chr 50k 100k 150k 250k 300k 350k 400k 450k 200k Diff chr (mapQ >= 5)

200k

250k

300k

350k

400k

50k

100k

150k

450k