Samtools: flagstat: percentage of total 5 samples Total Reads 0% 20% 40% 60% 80% 100% Total Passed QC 0% 20% 60% 80% 100% 40% Mapped 0% 20% 100% 40% 60% 80% Secondary Alignments 100% 20% 40% 60% 80% 0% Duplicates 100% 0% 20% 40% 60% 80% Paired in Sequencing • 20% 40% 60% 100% 0% 80% Properly Paired • 20% 60% 80% 0% 40% 100% Self and mate mapped • 20% 60% 0% 40% 80% 100% Singletons 100% 0% 20% 40% 60% 80% Mate mapped to diff chr 0% 20% 60% 100% 40% 80% Diff chr (mapQ >= 5)

40%

60%

0%

20%

100%

80%