Samtools: flagstat: percentage of total 16 samples Total Reads 0% 20% 40% 60% 80% 100% Total Passed QC 0% 20% 40% 60% 80% 100% Mapped 0% 20% 40% 60% 80% 100% Secondary Alignments 100% 0% 20% 40% 60% 80% Duplicates • 100% 0% 20% 40% 60% 80% Paired in Sequencing 100% 0% 20% 60% 40% 80% Properly Paired 100% 0% 20% 40% 60% 80% Self and mate mapped 0% 20% 60% 80% 100% 40% 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%