Samtools: flagstat: percentage of total 9 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 0% 100% 20% 60% 80% 40% Duplicates 100% 20% 40% 60% 80% 0% 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

