Samtools: flagstat: percentage of total 6 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 • 20% 60% 80% 100% 0% 40% Paired in Sequencing 0% 20% 60% 100% 40% 80% Properly Paired 0% 20% 40% 60% 80% Self and mate mapped 0% 20% 60% 100% 40% 80% Singletons 100% 0% 20% 40% 60% 80% Mate mapped to diff chr 0% 20% 60% 100% 40% 80% Diff chr (mapQ >= 5) 0% 100% 20% 40% 60% 80%