Samtools: flagstat: percentage of total 3 samples Total Reads 0% 20% 40% 60% 100% 80% Total Passed QC 0% 20% 40% 60% 80% 100% Mapped 0% 20% 40% 60% 80% 100% Secondary Alignments ••• 0% 20% 40% 100% 60% 80% Supplementary Alignments •• 100% 20% 40% 60% 80% Duplicates 0% 20% 100% 40% 60% 80% Paired in Sequencing 0% 20% 100% 40% 60% 80% Properly Paired 0% 20% 40% 80% 100% 60% Self and mate mapped 80% 100% 20% 40% 60% Singletons • 20% 40% 100% 60% 80% Mate mapped to diff chr 20% 40% 60% 100% 80% Diff chr (mapQ >= 5) 20% 40% 60% 80% 100%