Samtools flagstat: percentage of total Percentage of total, 10 samples Total Reads 0% 20% 100% 60% 80% 40% Total Passed QC 100% 0% 20% 60% 80% 40% Mapped 40% 0% 20% 60% 80% 100% Secondary Alignments 100% 20% 40% 60% 80% Duplicates 100% 20% 40% 80% Paired in Sequencing Properly Paired 60% 100% 0% 20% 40% 80% Self and mate mapped 100% 0% 20% 40% 60% 80% Singletons -100% 20% 40% 60% 80% Mate mapped to diff chr 👆 100% 0% 20% 40% 60% 80% Diff chr (mapQ >= 5) 0% 20% 40% 60% 80% 100%