## Samtools: stats: Alignment Stats 4 samples Total sequences OM 0.015M 0.02M 0.005M 0.01M Mapped & paired 0.02M OM 0.005M 0.01M 0.015M Properly paired 0.02M ΟM 0.005M 0.01M 0.015M Duplicated 0.02M OM 0.005M 0.01M 0.015M QC Failed 0.02M OM 0.005M 0.01M 0.015M Reads MQ0 Mapped bases (CIGAR) 0Mb 0.1Mb 0.05Mb 0.15Mb 0.2Mb 0.25Mb 0.3Mb Bases Trimmed 0Mb 0.3Mb 0.05Mb 0.1Mb 0.15Mb 0.2Mb 0.25Mb Duplicated bases 0Mb 0.05Mb 0.1Mb 0.15Mb 0.2Mb 0.25Mb 0.3Mb Diff chromosomes • • 0.02M OM 0.005M 0.01M 0.015M Other orientation OM 0.005M 0.01M 0.015M 0.02M Inward pairs • 0.02M 0.005M 0.01M 0.015M Outward pairs • • 0.02M 0.005M 0.01M 0.015M Created with MultiQC