Samtools: stats: Alignment Stats 6 samples Total sequences OM 5M 25M 30M 35M 10M 15M 20M 40M Mapped & paired OM 20M 5M 10M 15M 25M 30M 35M 40M Properly paired OM 20M 25M 5M 10M 15M 30M 35M 40M Duplicated OM 5M 20M 10M 15M 25M 30M 35M 40M QC Failed 0M 5M 10M 15M 20M 25M 30M 35M 40M Reads MQ0 OM 5M 10M 15M 20M 25M 30M 35M 40M Mapped bases (CIGAR) 3500Mb 4000Mb 0Mb 500Mb 1000Mb 1500Mb 2000Mb 2500Mb 3000Mb Bases Trimmed 0Mb 500Mb 1000Mb 1500Mb 2000Mb 2500Mb 3000Mb 3500Mb 4000Mb Duplicated bases • 0Mb 500Mb 1000Mb 1500Mb 2000Mb 2500Mb 3000Mb 3500Mb 4000Mb Diff chromosomes 0M 5M 10M 15M 20M 25M 30M 35M 40M Other orientation 5M OM 10M 15M 20M 25M 30M 35M 40M Inward pairs 10M OM 5M 15M 20M 25M 30M 35M 40M Outward pairs 5M 10M 15M 20M 25M 30M 35M 40M