Samtools: stats: Alignment Stats
16 samples Total sequences OM 10M 20M 30M 40M 50M Mapped & paired OM 10M 20M 30M 40M 50M Properly paired OM 10M 20M 30M 40M 50M Duplicated 30M OM 10M 20M 50M 40M QC Failed OM 10M 30M 50M 20M 40M Reads MQ0 10M 20M 50M OM 30M 40M Mapped bases (CIGAR) 0Mb 5000Mb 1000Mb 2000Mb 6000Mb 3000Mb 4000Mb Bases Trimmed 0Mb 1000Mb 2000Mb 3000Mb 4000Mb 5000Mb 6000Mb Duplicated bases • 1000Mb 0Mb 4000Mb 5000Mb 2000Mb 3000Mb 6000Mb Diff chromosomes OM 10M 20M 30M 40M 50M Other orientation OM 10M 20M 30M 50M 40M Inward pairs 10M OM 20M 30M 40M 50M Outward pairs 0M 10M 20M 30M 40M 50M