## Samtools: stats: Alignment Stats 14 samples Total sequences OM 20M 40M 50M 60M 70M 10M 30M Mapped & paired OM 10M 20M 30M 40M 50M 70M 60M Properly paired OM 30M 10M 20M 40M 50M 60M 70M Duplicated OM 20M 70M 10M 30M 40M 50M 60M QC Failed OM 10M 20M 30M 40M 50M 60M 70M Reads MQ0 Mapped bases (CIGAR) 4000Mb 0Mb 1000Mb 3000Mb 5000Mb 2000Mb Bases Trimmed 0Mb 1000Mb 4000Mb 5000Mb 2000Mb 3000Mb Duplicated bases 0Mb 1000Mb 2000Mb 4000Mb 5000Mb 3000Mb Diff chromosomes -OM 10M 20M 40M 50M 60M 70M 30M Other orientation OM 10M 20M 30M 40M 50M 60M 70M Inward pairs OM 10M 20M 70M 30M 40M 50M 60M Outward pairs 10M 20M 30M 40M 50M 60M 70M ΟM