Samtools: stats: Alignment Stats 10 samples Total sequences OM 300M 350M 50M 200M 250M 400M 100M 150M Mapped & paired 300M OM 50M 150M 200M 250M 350M 100M 400M Properly paired OM 50M 100M 150M 200M 250M 300M 350M 400M Duplicated OM 50M 100M 150M 200M 250M 300M 350M 400M QC Failed OM 50M 100M 150M 200M 250M 300M 350M 400M Reads MQ0 Mapped bases (CIGAR) 0Mb 5kMb 10kMb 15kMb 20kMb 25kMb 30kMb 35kMb 40kMb Bases Trimmed 0Mb 5kMb 10kMb 15kMb 40kMb 20kMb 25kMb 30kMb 35kMb Duplicated bases 0Mb 5kMb 40kMb 10kMb 15kMb 20kMb 25kMb 30kMb 35kMb Diff chromosomes -ΟM 50M 150M 400M 100M 200M 250M 300M 350M Other orientation OM 50M 100M 150M 200M 250M 300M 400M 350M Inward pairs OM 50M 100M 150M 200M 250M 300M 350M 400M Outward pairs ΟM 50M 150M 400M 100M 200M 250M 300M 350M