Samtools: stats: Alignment Stats 25 samples Total sequences OM 10M 20M 30M 40M 50M 60M 70M 80M 90M Mapped & paired OM 50M 60M 70M 10M 20M 30M 40M 80M 90M Properly paired 60M 40M 50M 70M ΟM 10M 20M 30M 80M 90M Duplicated • OM 10M 20M 30M 50M 40M 60M 70M 80M 90M QC Failed OM 10M 20M 30M 40M 60M 50M 70M 80M 90M Reads MQ0 Mapped bases (CIGAR) . 8kMb 0Mb 10kMb 2kMb 4kMb 6kMb 12kMb Bases Trimmed 0Mb 2kMb 4kMb 8kMb 10kMb 12kMb 6kMb Duplicated bases • 0Mb 2kMb 4kMb 6kMb 8kMb 10kMb 12kMb Diff chromosomes ΟM 10M 20M 30M 40M 50M 60M 70M 80M 90M Other orientation OM 10M 20M 30M 40M 50M 60M 70M 80M 90M Inward pairs 20M OM 10M 30M 40M 50M 60M 70M 80M 90M Outward pairs

ΟM

10M

20M

30M

40M

60M

50M

70M

80M

90M