

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 03:19:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104289.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR26104289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104289_1.fastq.gz SRR26104289_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 03:19:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,435,356
Mapped reads	29,378,102 / 96.53%
Unmapped reads	1,057,254 / 3.47%
Mapped paired reads	29,378,102 / 96.53%
Mapped reads, first in pair	14,886,872 / 48.91%
Mapped reads, second in pair	14,491,230 / 47.61%
Mapped reads, both in pair	28,944,214 / 95.1%
Mapped reads, singletons	433,888 / 1.43%
Secondary alignments	0
Supplementary alignments	34,619 / 0.11%
Read min/max/mean length	30 / 97 / 91.04
Duplicated reads (estimated)	16,771,210 / 55.1%
Duplication rate	39.83%
Clipped reads	15,030,450 / 49.38%

2.2. ACGT Content

Number/percentage of A's	553,867,643 / 25.49%
Number/percentage of C's	542,303,808 / 24.95%
Number/percentage of T's	560,745,539 / 25.8%
Number/percentage of G's	515,184,772 / 23.71%
Number/percentage of N's	1,141,215 / 0.05%

GC Percentage	48.66%
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2.3. Coverage

Mean	0.7022
Standard Deviation	31.5864

2.4. Mapping Quality

Mean Mapping Quality	52.84
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2.5. Insert size

Mean	12,024.75
Standard Deviation	1,091,504.56
P25/Median/P75	55 / 91 / 183

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	12,198,165
Insertions	215,899
Mapped reads with at least one insertion	0.73%
Deletions	249,404
Mapped reads with at least one deletion	0.84%
Homopolymer indels	45.26%

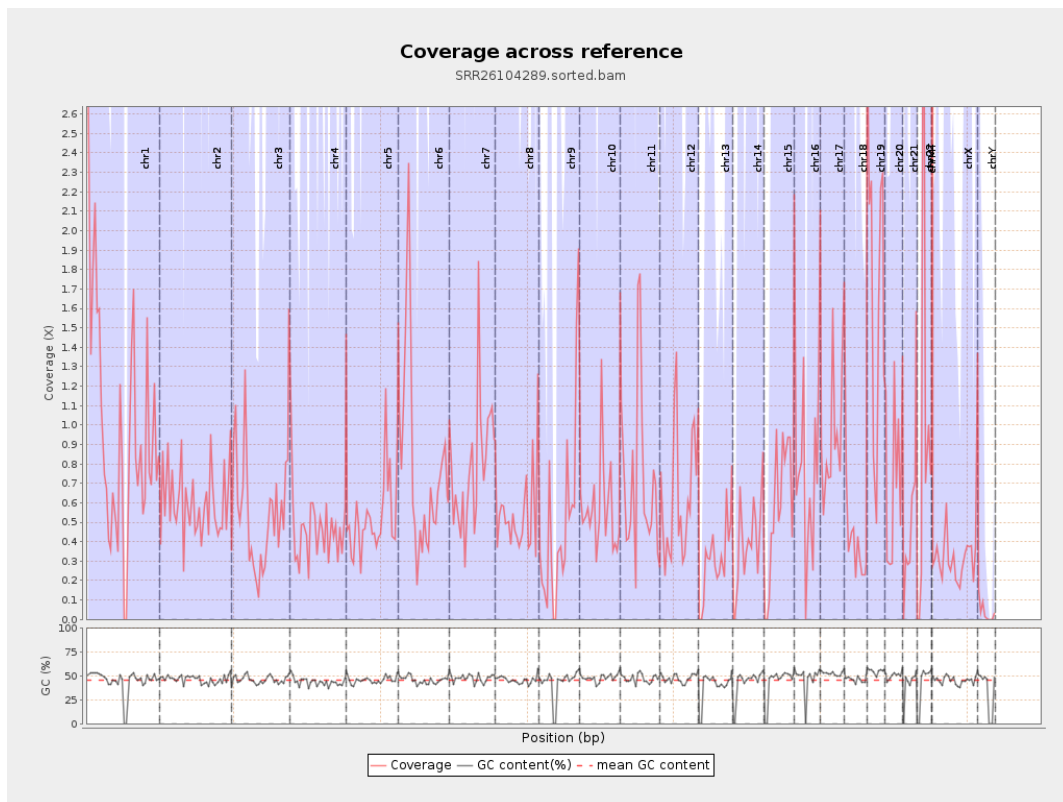
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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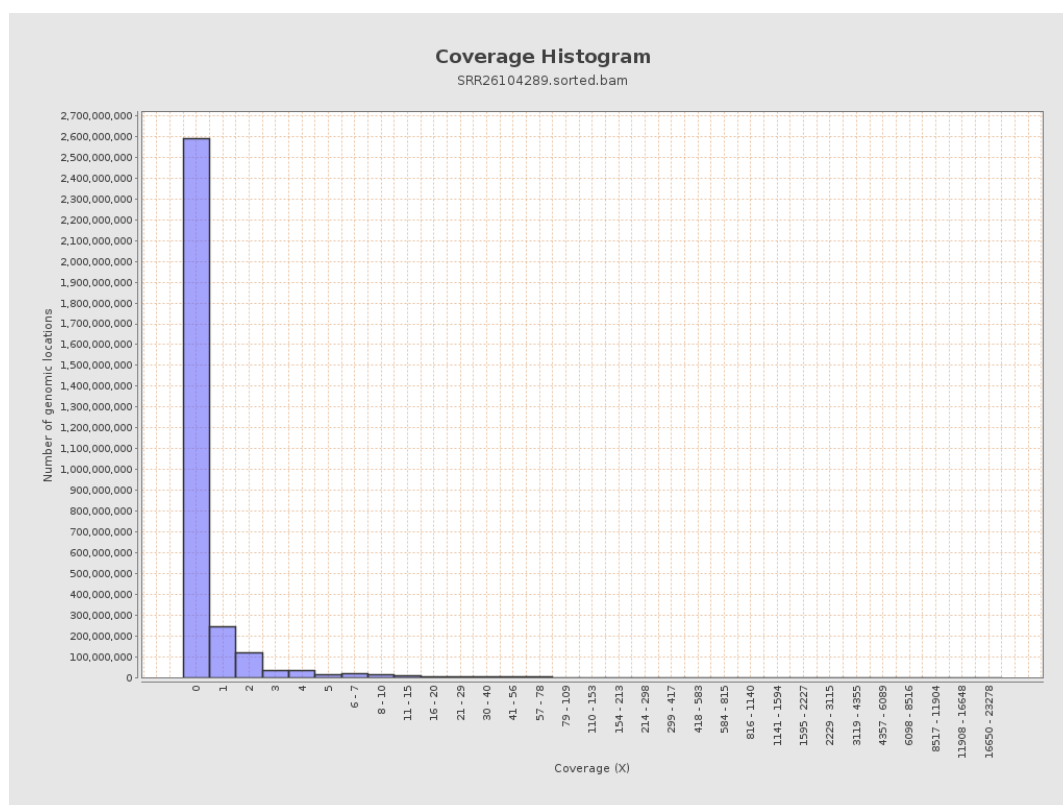
		bases	coverage	deviation
chr1	249250621	245841236	0.9863	15.8372
chr2	243199373	146248329	0.6014	4.7664
chr3	198022430	110250757	0.5568	3.76
chr4	191154276	87244524	0.4564	3.0191
chr5	180915260	97946917	0.5414	5.3919
chr6	171115067	131508762	0.7685	4.9015
chr7	159138663	124791015	0.7842	5.3088
chr8	146364022	78860508	0.5388	5.1802
chr9	141213431	72725684	0.515	4.269
chr10	135534747	77666866	0.573	4.237
chr11	135006516	101430169	0.7513	5.8337
chr12	133851895	84418188	0.6307	4.3013
chr13	115169878	34957886	0.3035	5.8336
chr14	107349540	42088402	0.3921	3.0919
chr15	102531392	57011702	0.556	3.9805
chr16	90354753	73964702	0.8186	5.3995
chr17	81195210	78575915	0.9677	6.3034
chr18	78077248	32080949	0.4109	3.2709
chr19	59128983	103247855	1.7461	9.7634
chr20	63025520	44982046	0.7137	4.5102
chr21	48129895	25132139	0.5222	4.6798
chr22	51304566	53829896	1.0492	9.2001
chrMT	16571	216279085	13,051.6616	2,884.9692
chrX	155270560	50519779	0.3254	2.4219

chrY	59373566	2187757	0.0368	1.5321
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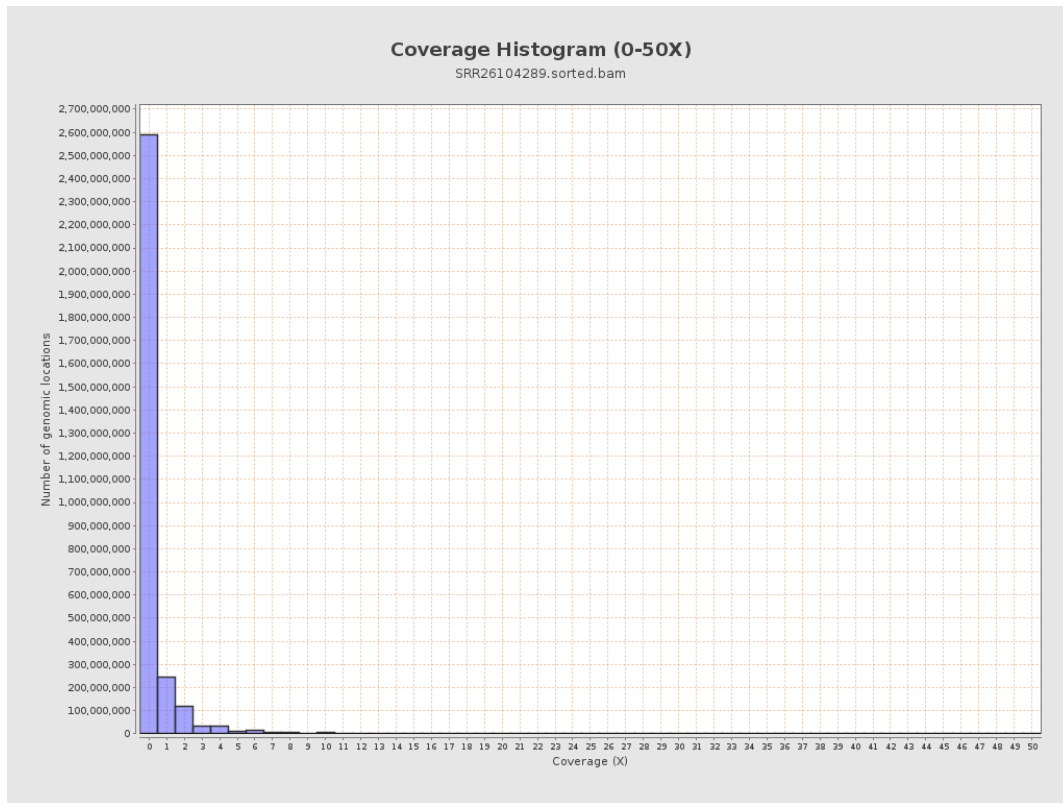
3. Results : Coverage across reference



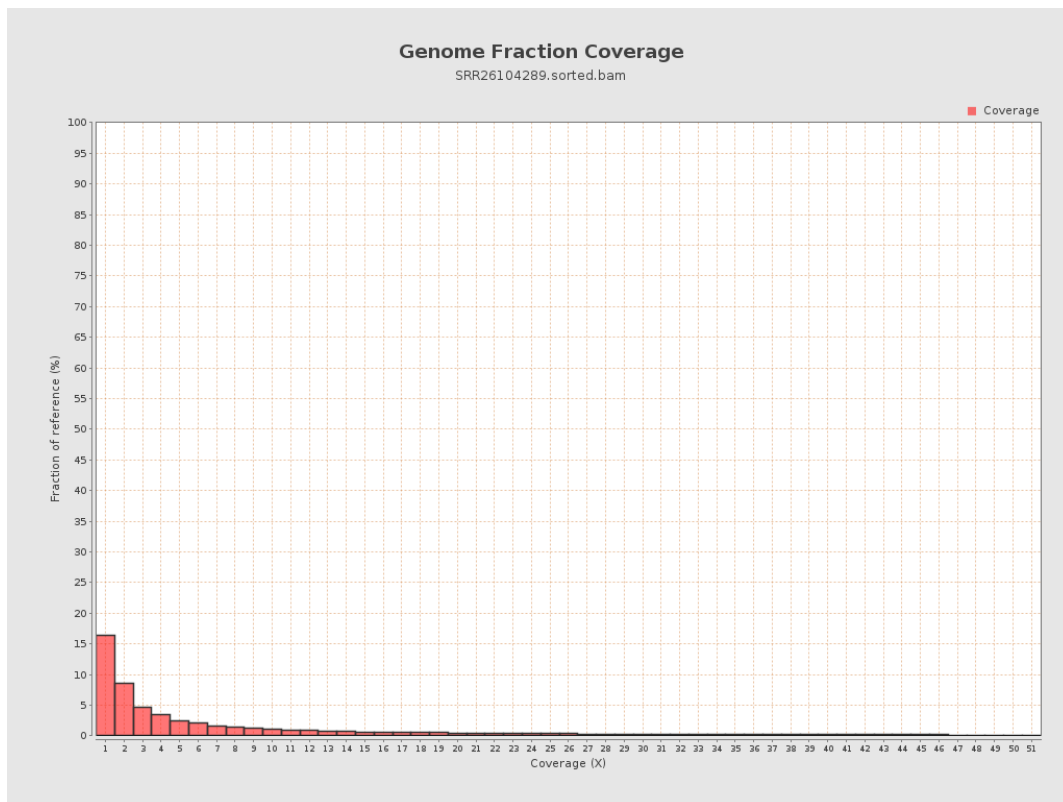
4. Results : Coverage Histogram



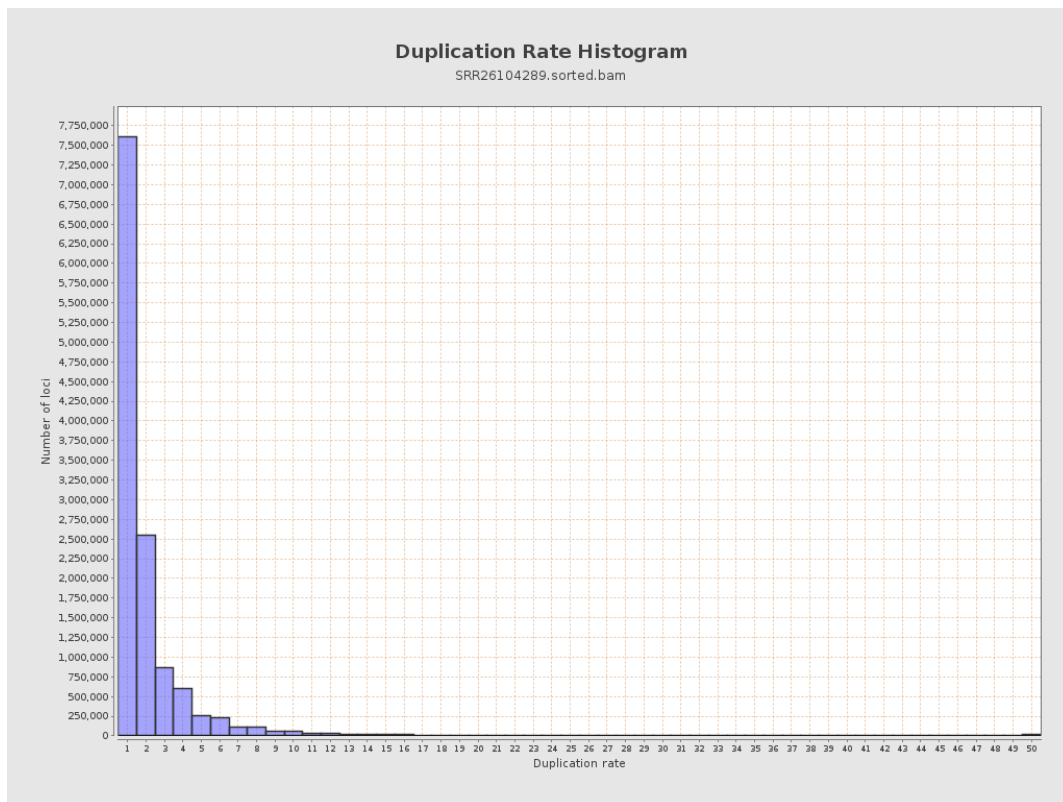
5. Results : Coverage Histogram (0-50X)



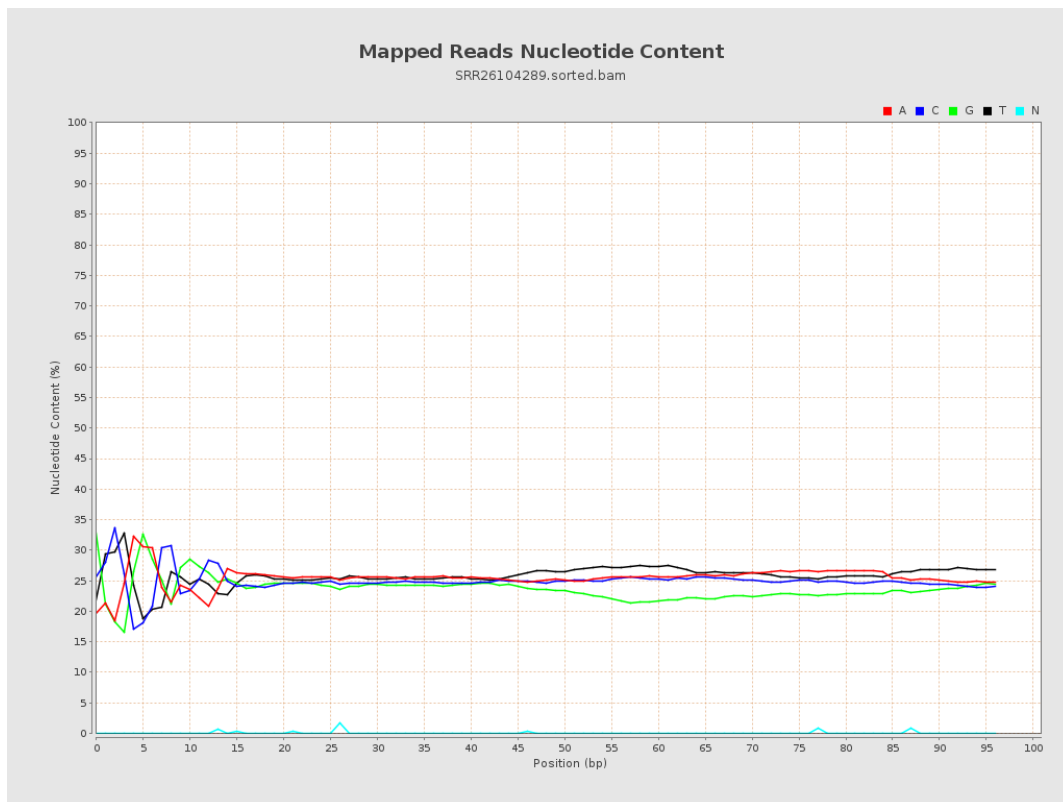
6. Results : Genome Fraction Coverage



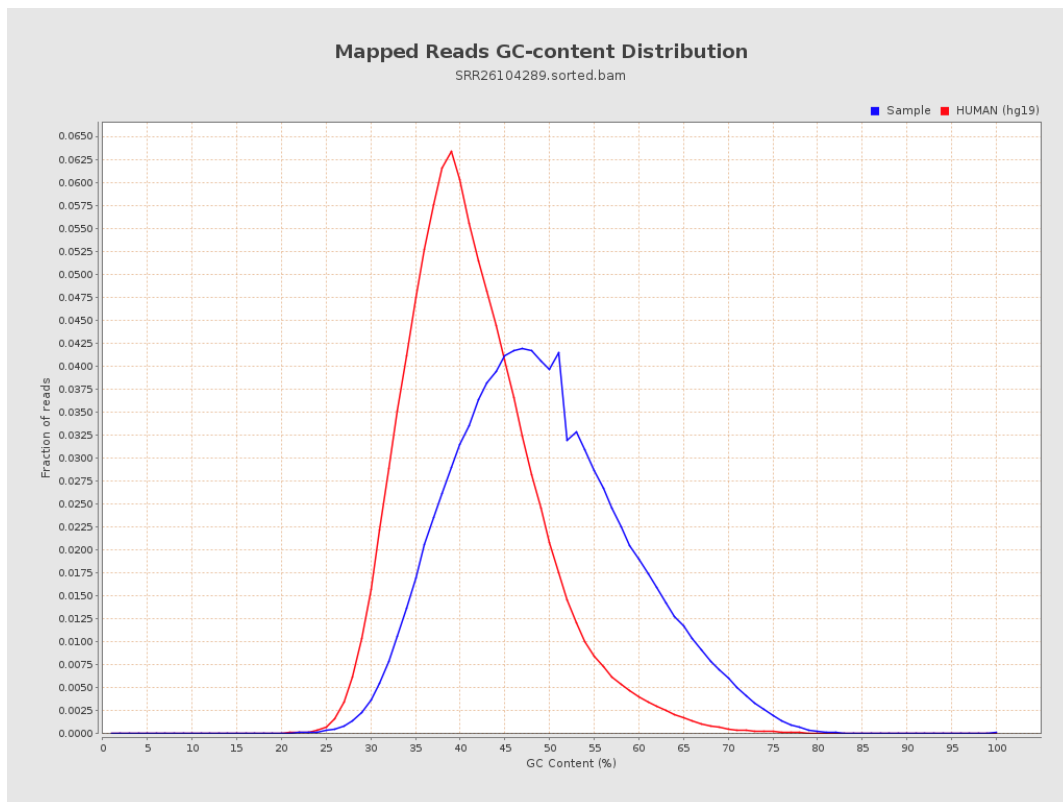
7. Results : Duplication Rate Histogram



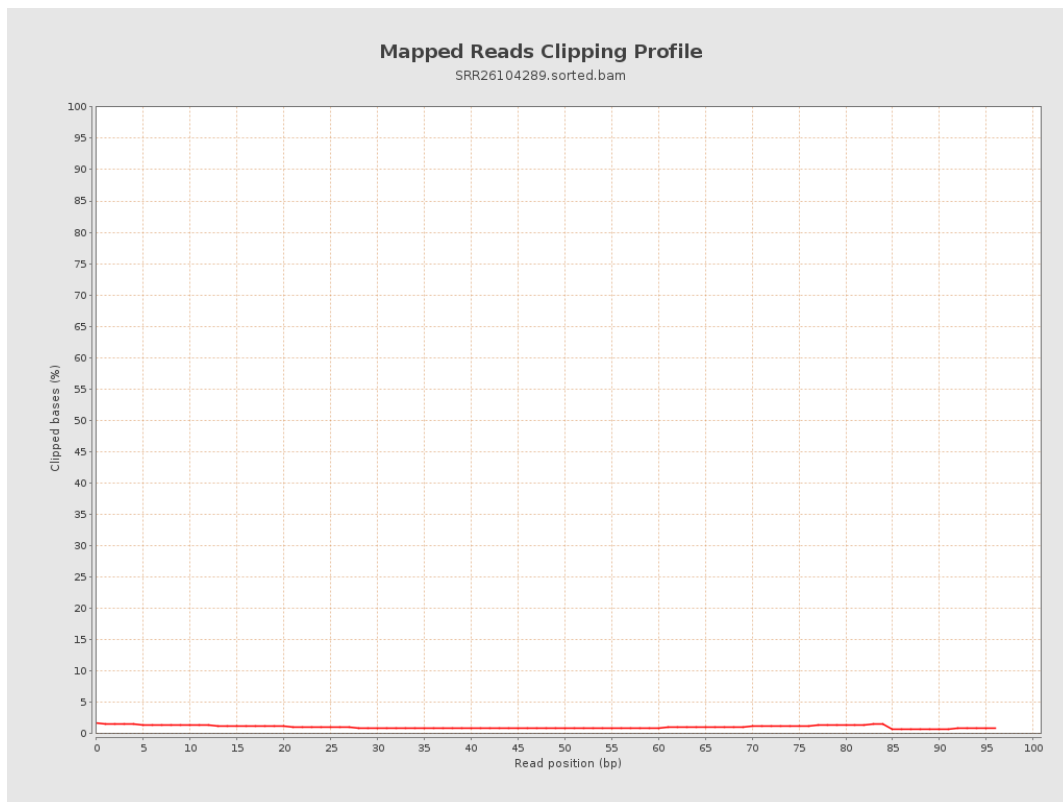
8. Results : Mapped Reads Nucleotide Content



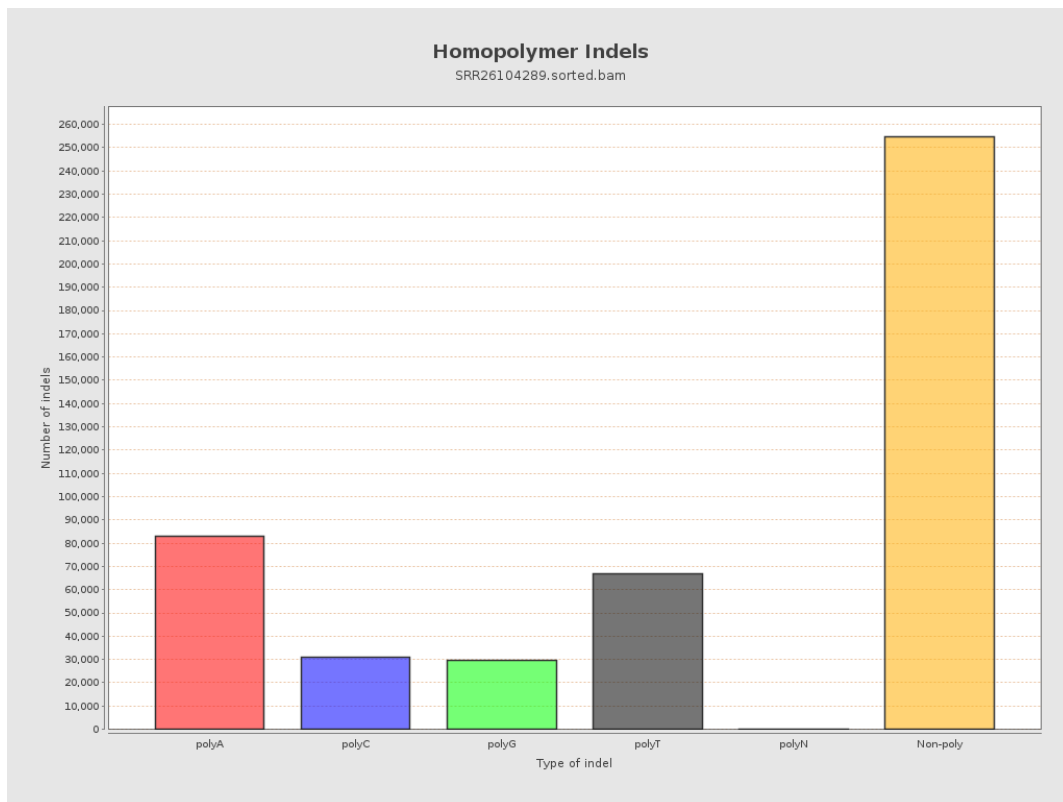
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



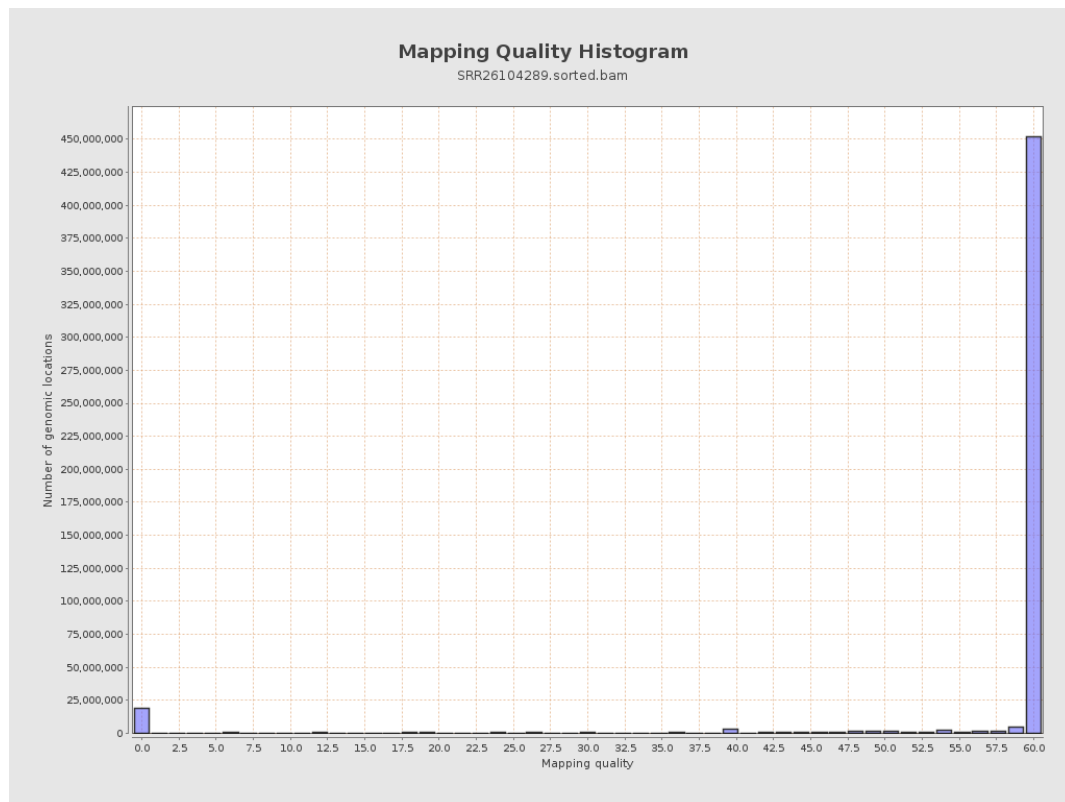
11. Results : Homopolymer Indels



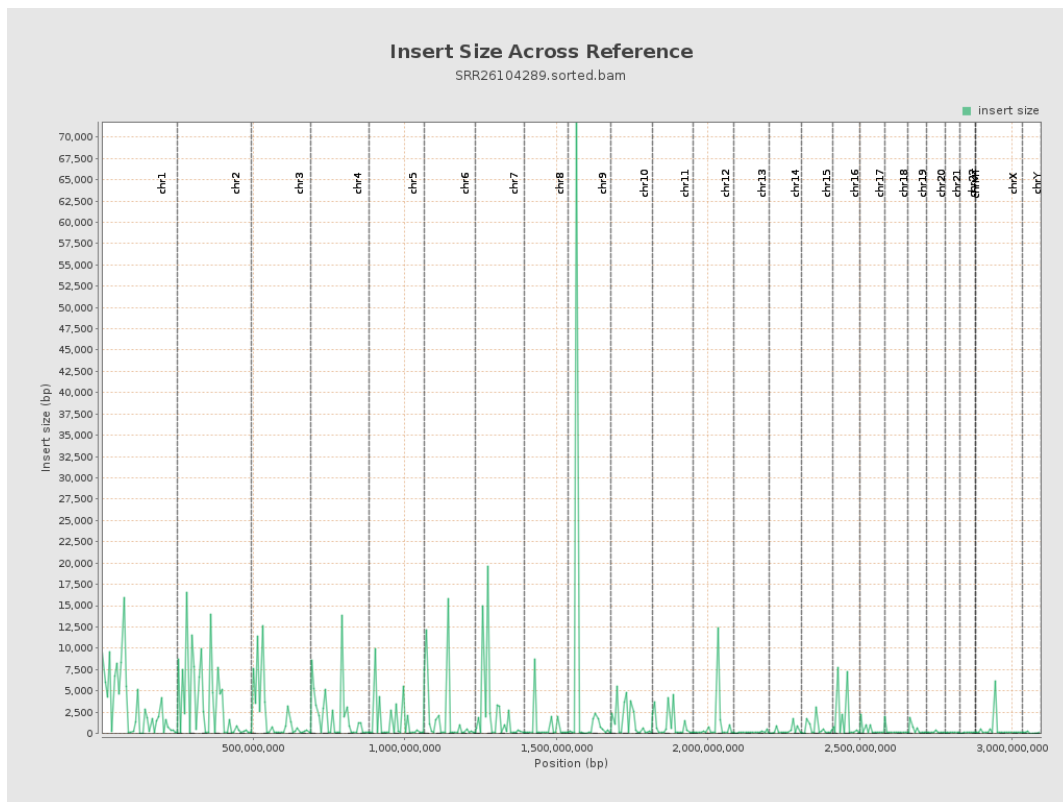
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

