

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 06:25:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174081.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_SRR10174081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174081_1.fastq.gz SRR10174081_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 06:25:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,587,848
Mapped reads	2,530,957 / 97.8%
Unmapped reads	56,891 / 2.2%
Mapped paired reads	2,530,957 / 97.8%
Mapped reads, first in pair	1,266,903 / 48.96%
Mapped reads, second in pair	1,264,054 / 48.85%
Mapped reads, both in pair	2,499,978 / 96.6%
Mapped reads, singletons	30,979 / 1.2%
Secondary alignments	0
Supplementary alignments	301,582 / 11.65%
Read min/max/mean length	30 / 133 / 123.02
Duplicated reads (estimated)	1,964,033 / 75.89%
Duplication rate	61.73%
Clipped reads	1,307,816 / 50.54%

2.2. ACGT Content

Number/percentage of A's	84,507,051 / 30.09%
Number/percentage of C's	55,409,539 / 19.73%
Number/percentage of T's	83,533,730 / 29.74%
Number/percentage of G's	57,406,517 / 20.44%
Number/percentage of N's	2,305 / 0%

GC Percentage	40.17%
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2.3. Coverage

Mean	0.0908
Standard Deviation	1.9412

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	654,534.4
Standard Deviation	7,872,498.16
P25/Median/P75	97 / 139 / 207

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	2,515,681
Insertions	40,008
Mapped reads with at least one insertion	1.5%
Deletions	84,943
Mapped reads with at least one deletion	3.26%
Homopolymer indels	40.07%

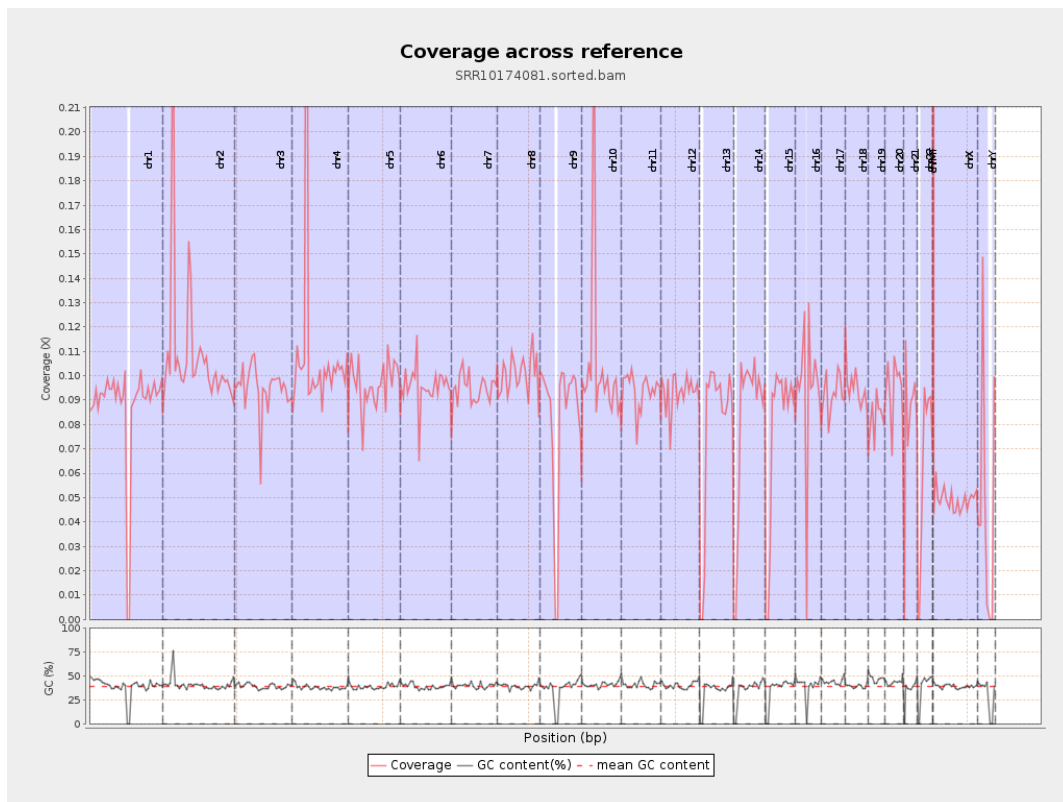
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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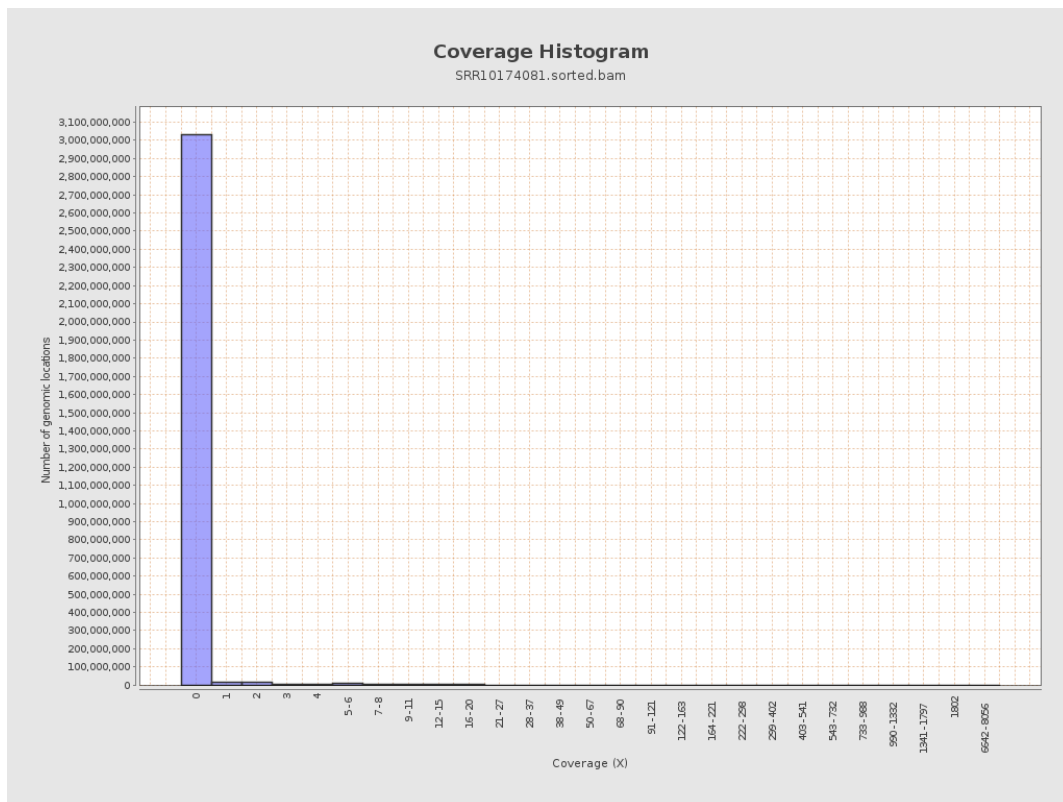
		bases	coverage	deviation
chr1	249250621	21785440	0.0874	1.0162
chr2	243199373	26440927	0.1087	5.7204
chr3	198022430	18782116	0.0948	0.9262
chr4	191154276	21099051	0.1104	1.9479
chr5	180915260	17457997	0.0965	0.9372
chr6	171115067	16364882	0.0956	0.9904
chr7	159138663	15040437	0.0945	1.0659
chr8	146364022	14708440	0.1005	1.3832
chr9	141213431	11672460	0.0827	0.9484
chr10	135534747	14103946	0.1041	1.5579
chr11	135006516	12655607	0.0937	0.9363
chr12	133851895	12493012	0.0933	0.9305
chr13	115169878	9048379	0.0786	0.8539
chr14	107349540	8847867	0.0824	0.8665
chr15	102531392	7769015	0.0758	0.814
chr16	90354753	8402068	0.093	1.0077
chr17	81195210	7546336	0.0929	0.9497
chr18	78077248	7403797	0.0948	1.2173
chr19	59128983	4911522	0.0831	0.9009
chr20	63025520	5973588	0.0948	1.0972
chr21	48129895	3974077	0.0826	1.4476
chr22	51304566	3208227	0.0625	0.8064
chrMT	16571	907327	54.7539	45.3451
chrX	155270560	7608518	0.049	0.6649

chrY	59373566	2870729	0.0484	1.6043
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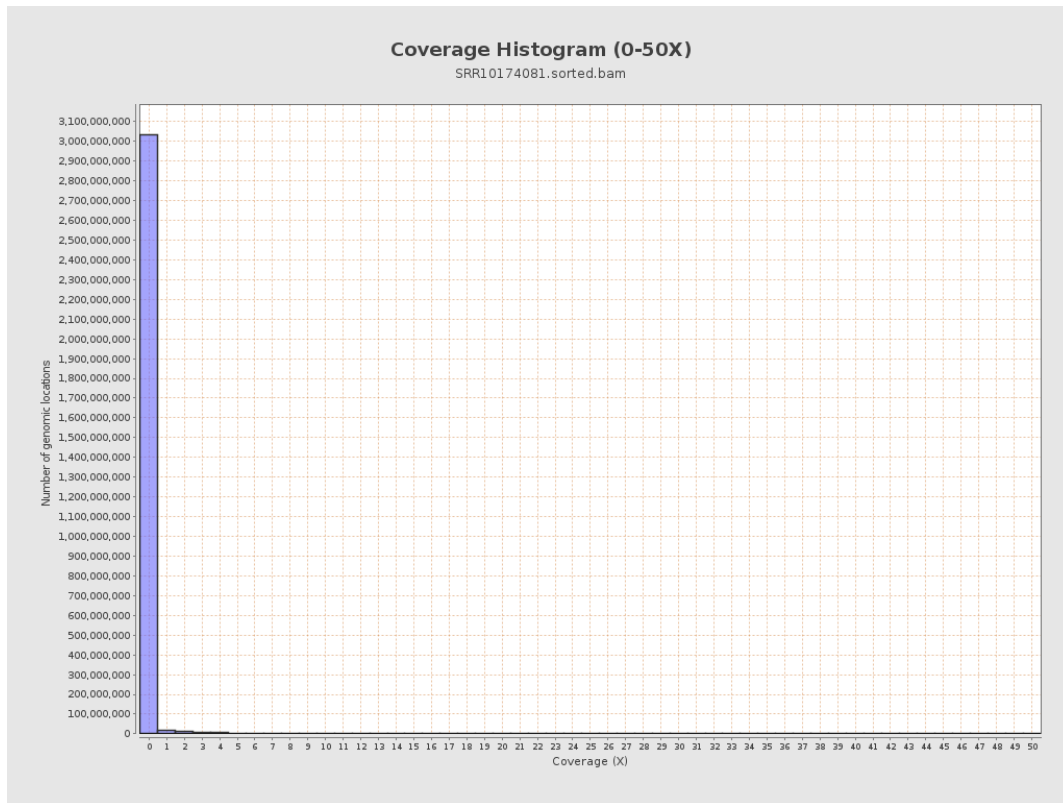
3. Results : Coverage across reference



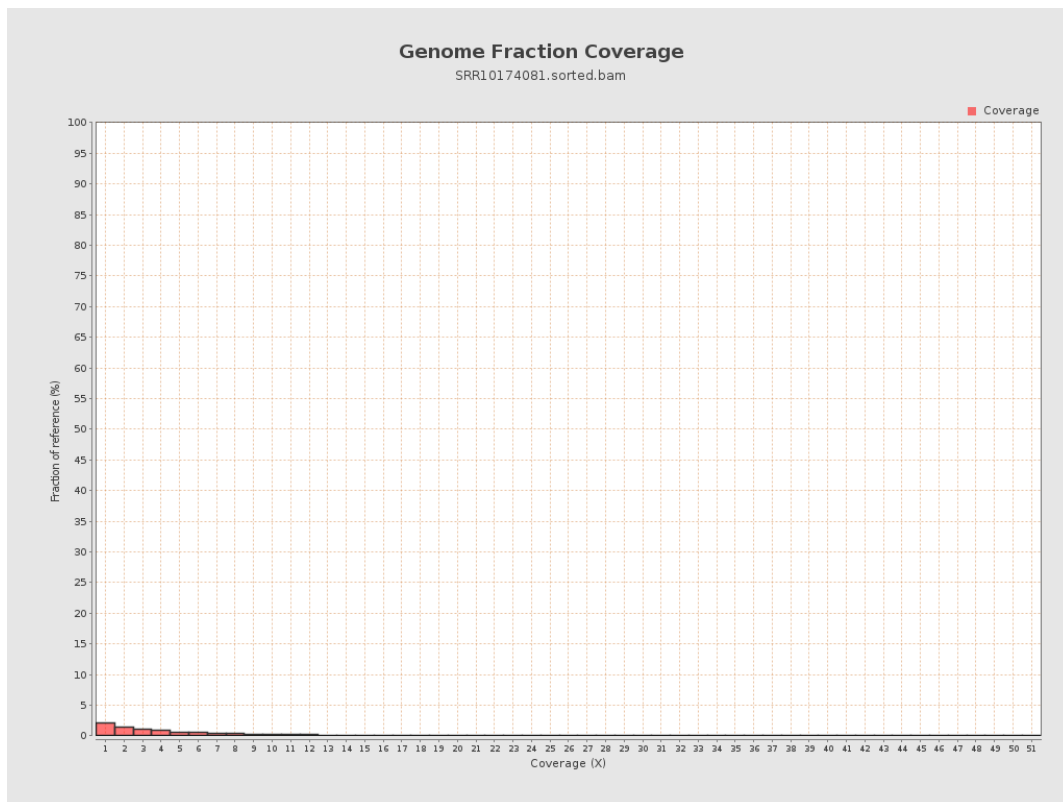
4. Results : Coverage Histogram



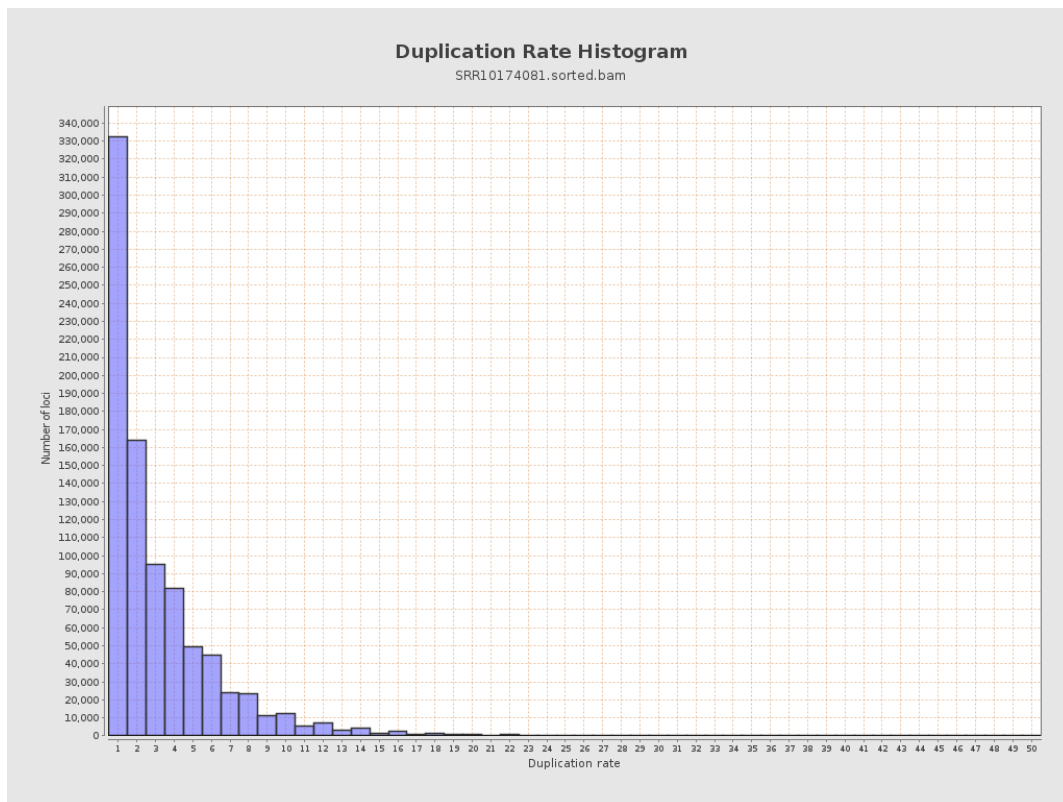
5. Results : Coverage Histogram (0-50X)



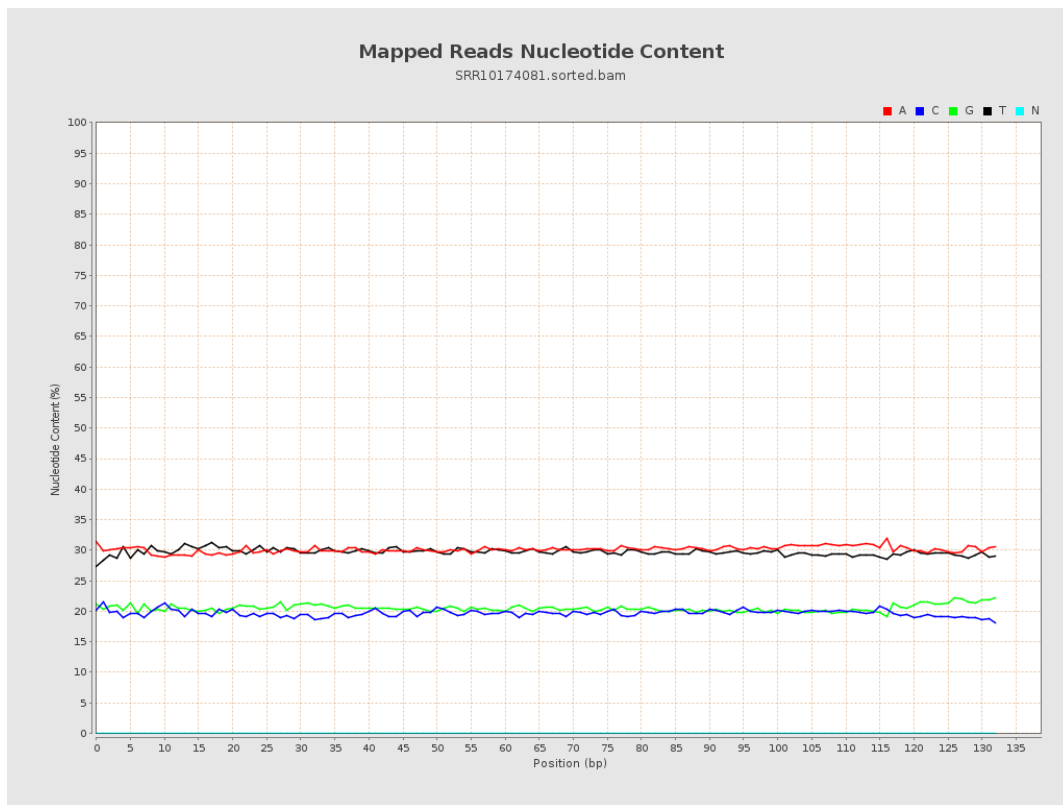
6. Results : Genome Fraction Coverage



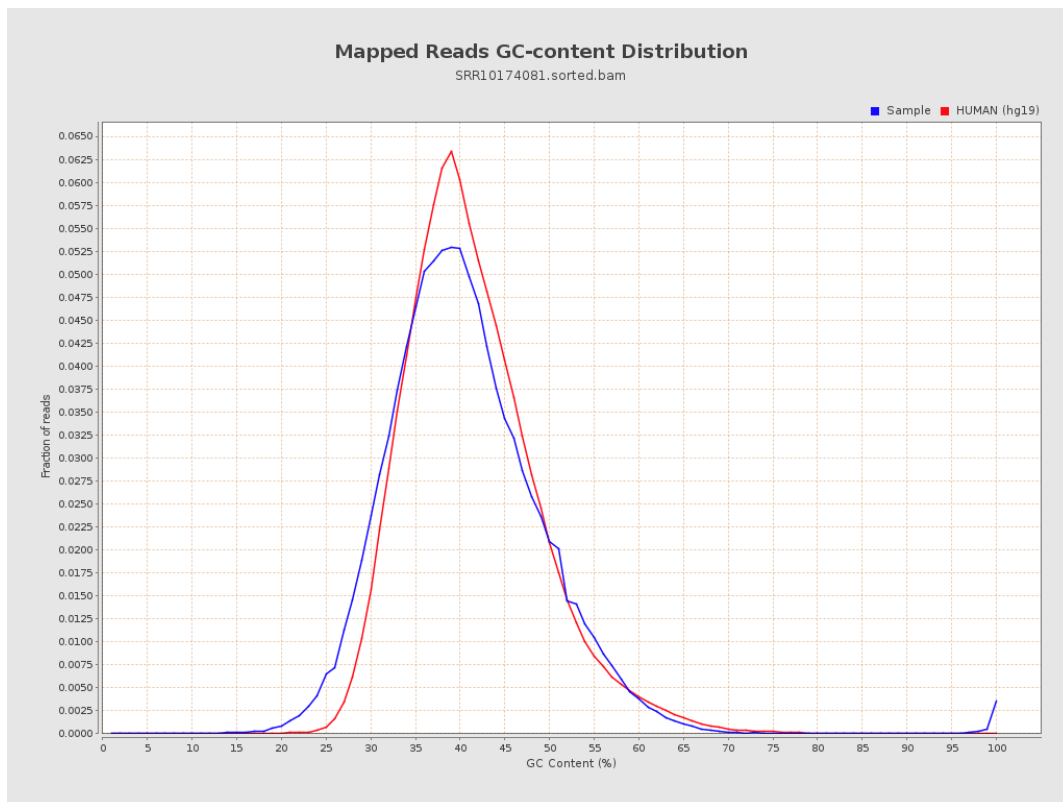
7. Results : Duplication Rate Histogram



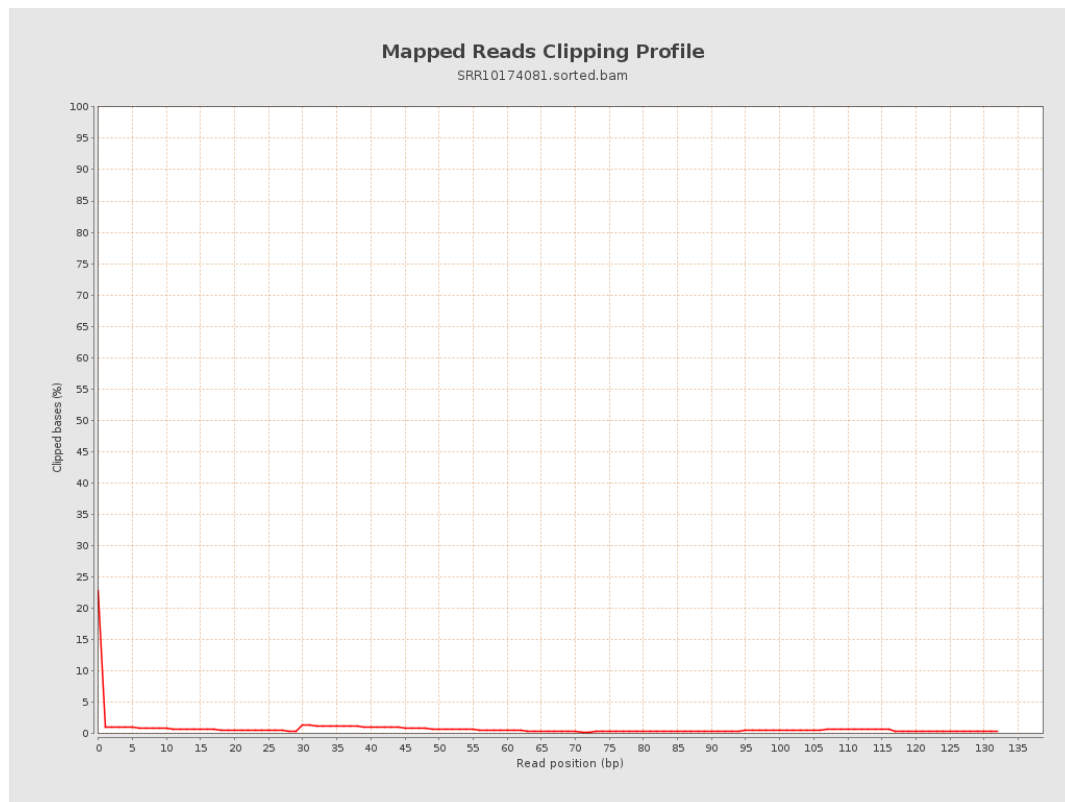
8. Results : Mapped Reads Nucleotide Content



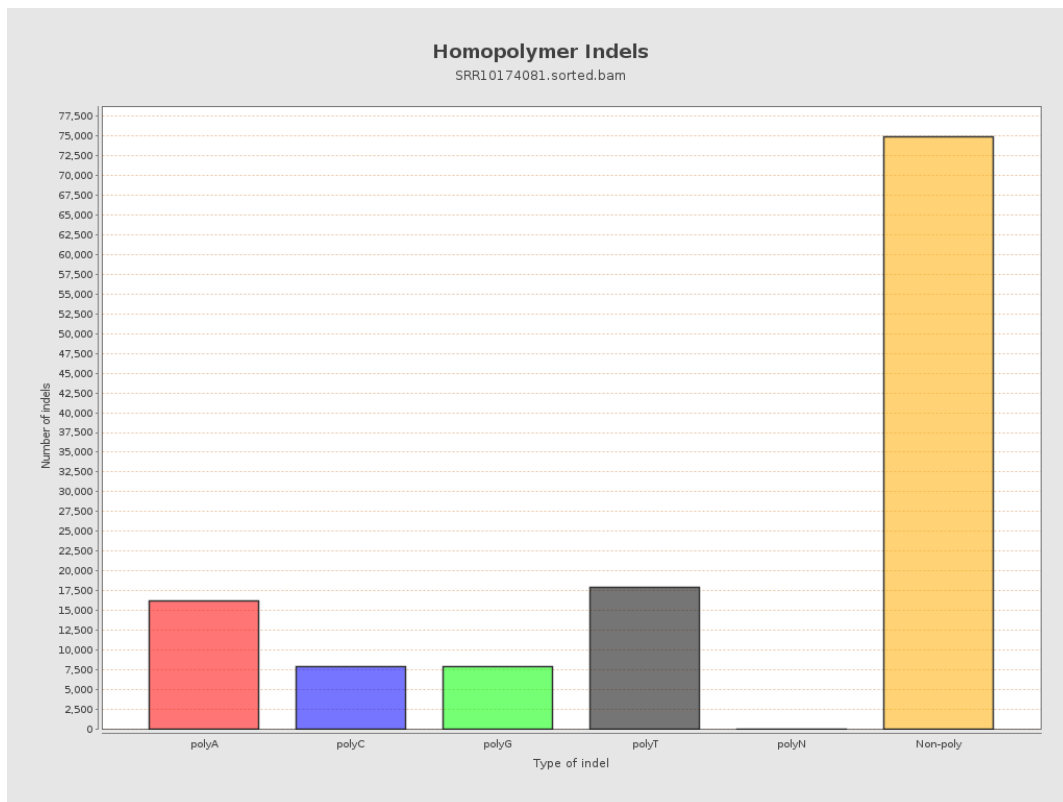
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



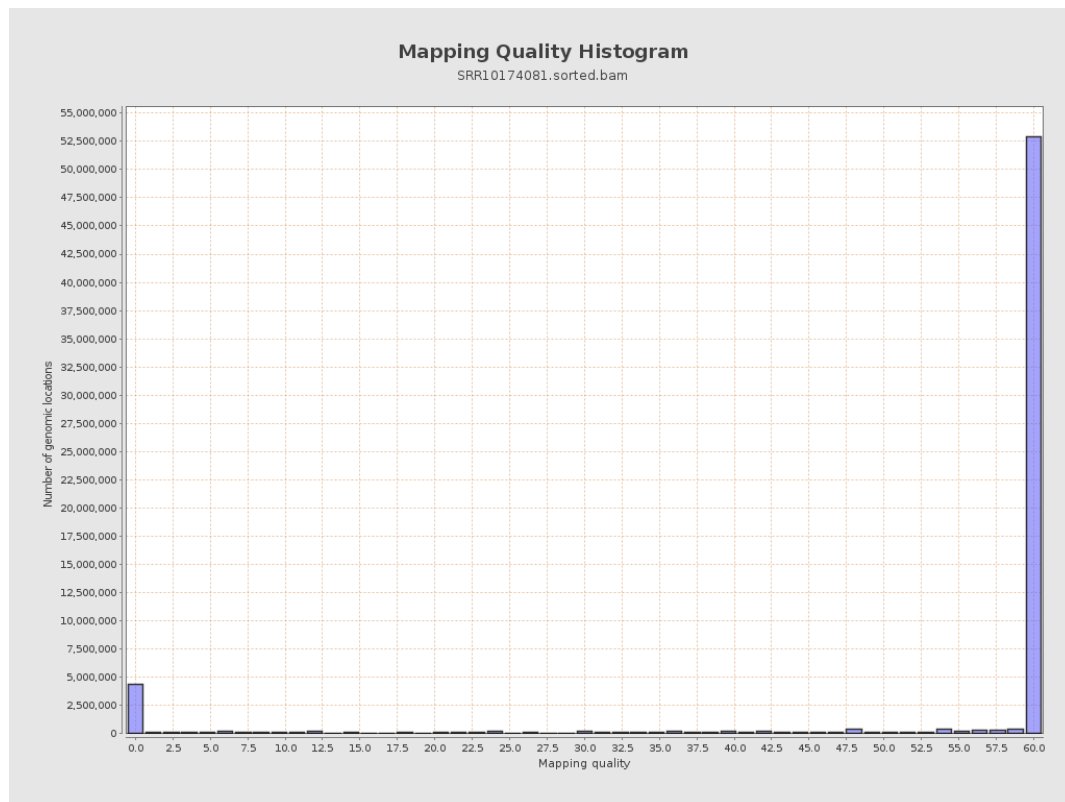
11. Results : Homopolymer Indels



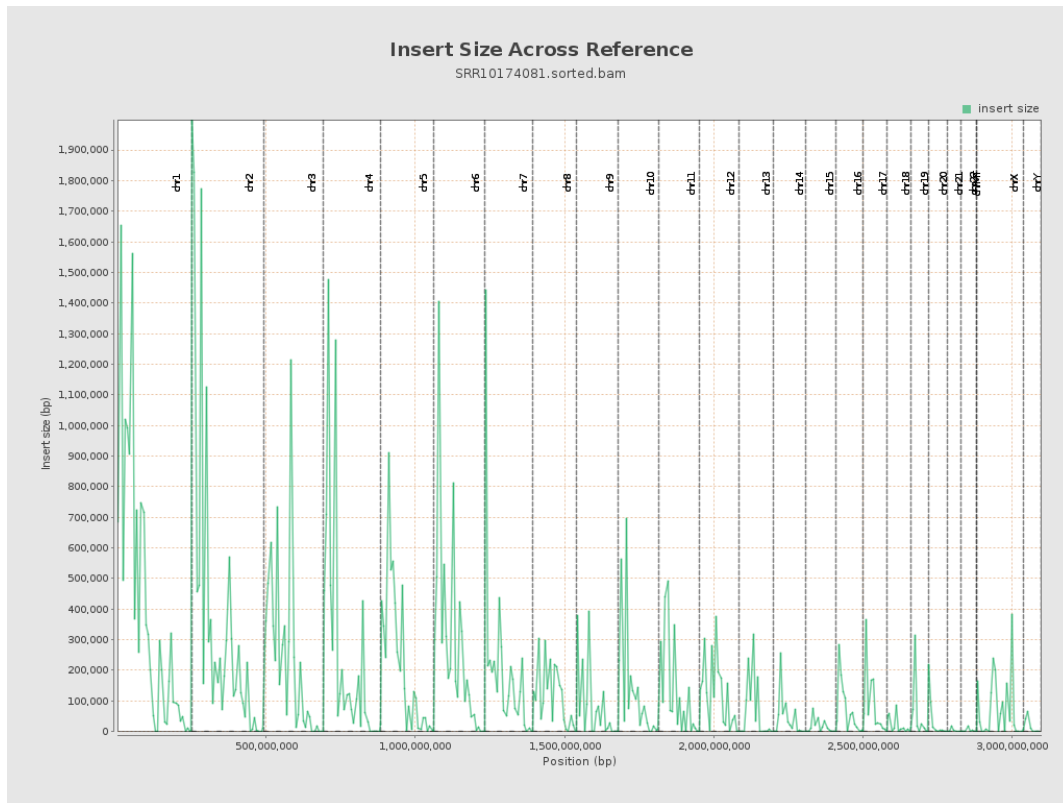
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

