

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 04:45:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174071.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_SRR10174071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174071_1.fastq.gz SRR10174071_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 04:45:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,785,026
Mapped reads	3,699,411 / 97.74%
Unmapped reads	85,615 / 2.26%
Mapped paired reads	3,699,411 / 97.74%
Mapped reads, first in pair	1,850,897 / 48.9%
Mapped reads, second in pair	1,848,514 / 48.84%
Mapped reads, both in pair	3,642,178 / 96.23%
Mapped reads, singletons	57,233 / 1.51%
Secondary alignments	0
Supplementary alignments	519,211 / 13.72%
Read min/max/mean length	30 / 133 / 126.3
Duplicated reads (estimated)	2,979,521 / 78.72%
Duplication rate	64.94%
Clipped reads	1,950,862 / 51.54%

2.2. ACGT Content

Number/percentage of A's	125,055,083 / 29.7%
Number/percentage of C's	84,062,478 / 19.96%
Number/percentage of T's	124,111,486 / 29.48%
Number/percentage of G's	87,823,021 / 20.86%
Number/percentage of N's	3,329 / 0%

GC Percentage	40.82%
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2.3. Coverage

Mean	0.1361
Standard Deviation	2.704

2.4. Mapping Quality

Mean Mapping Quality	52.51
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2.5. Insert size

Mean	1,241,854.09
Standard Deviation	10,587,126.07
P25/Median/P75	107 / 157 / 239

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,644,953
Insertions	47,332
Mapped reads with at least one insertion	1.23%
Deletions	145,023
Mapped reads with at least one deletion	3.82%
Homopolymer indels	40.63%

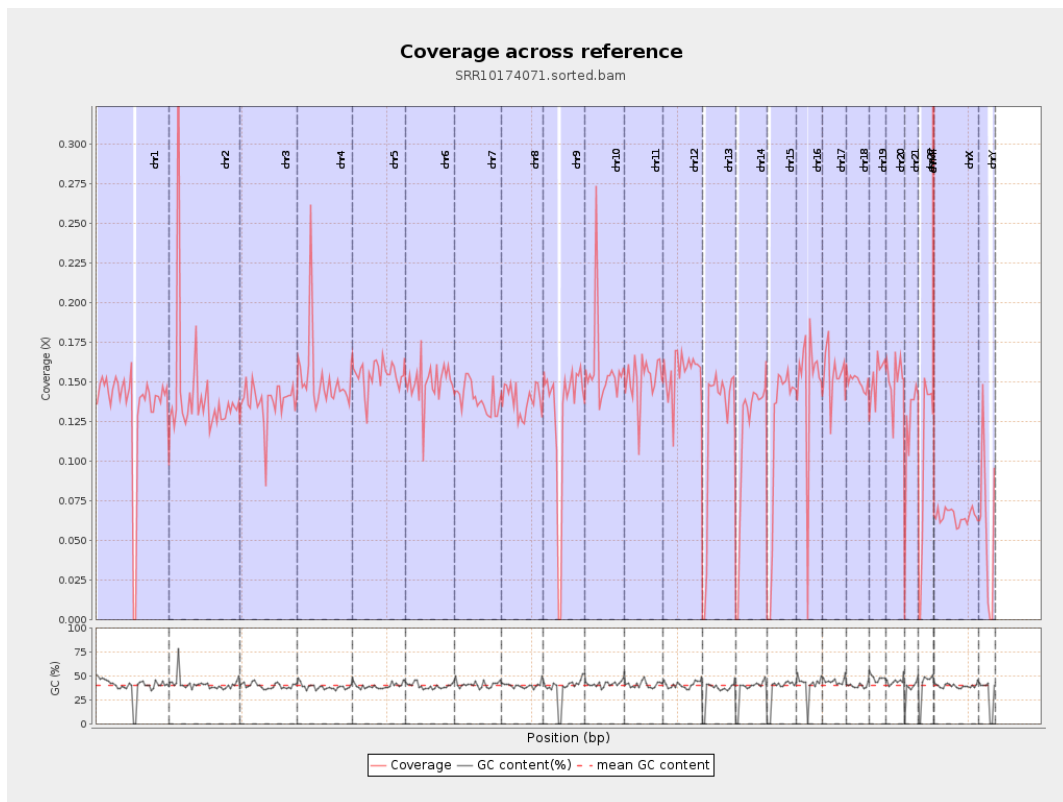
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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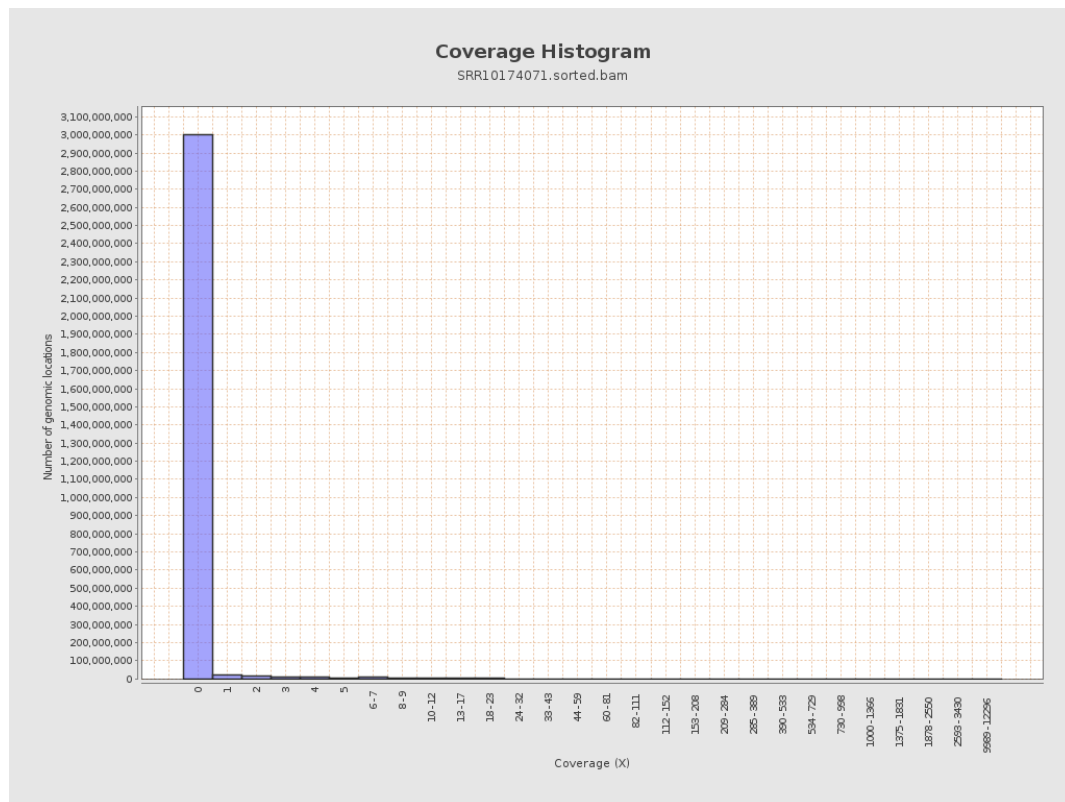
		bases	coverage	deviation
chr1	249250621	33485472	0.1343	1.3402
chr2	243199373	34683358	0.1426	8.6484
chr3	198022430	27218382	0.1375	1.1023
chr4	191154276	28967768	0.1515	1.4346
chr5	180915260	27964193	0.1546	1.1757
chr6	171115067	25543537	0.1493	1.2478
chr7	159138663	22210141	0.1396	1.2198
chr8	146364022	20257914	0.1384	1.4155
chr9	141213431	18260838	0.1293	1.2254
chr10	135534747	21330129	0.1574	1.6846
chr11	135006516	20529352	0.1521	1.1836
chr12	133851895	20933045	0.1564	1.1892
chr13	115169878	14028629	0.1218	1.0532
chr14	107349540	12413653	0.1156	1.0126
chr15	102531392	12156815	0.1186	1.0281
chr16	90354753	13421682	0.1485	1.2707
chr17	81195210	12533530	0.1544	1.2307
chr18	78077248	11715246	0.15	1.6536
chr19	59128983	9067212	0.1533	1.2543
chr20	63025520	9517787	0.151	1.1909
chr21	48129895	5793285	0.1204	1.1501
chr22	51304566	5145302	0.1003	1.0241
chrMT	16571	762723	46.0276	38.4523
chrX	155270560	10150946	0.0654	0.7511

chrY	59373566	3298945	0.0556	1.0369
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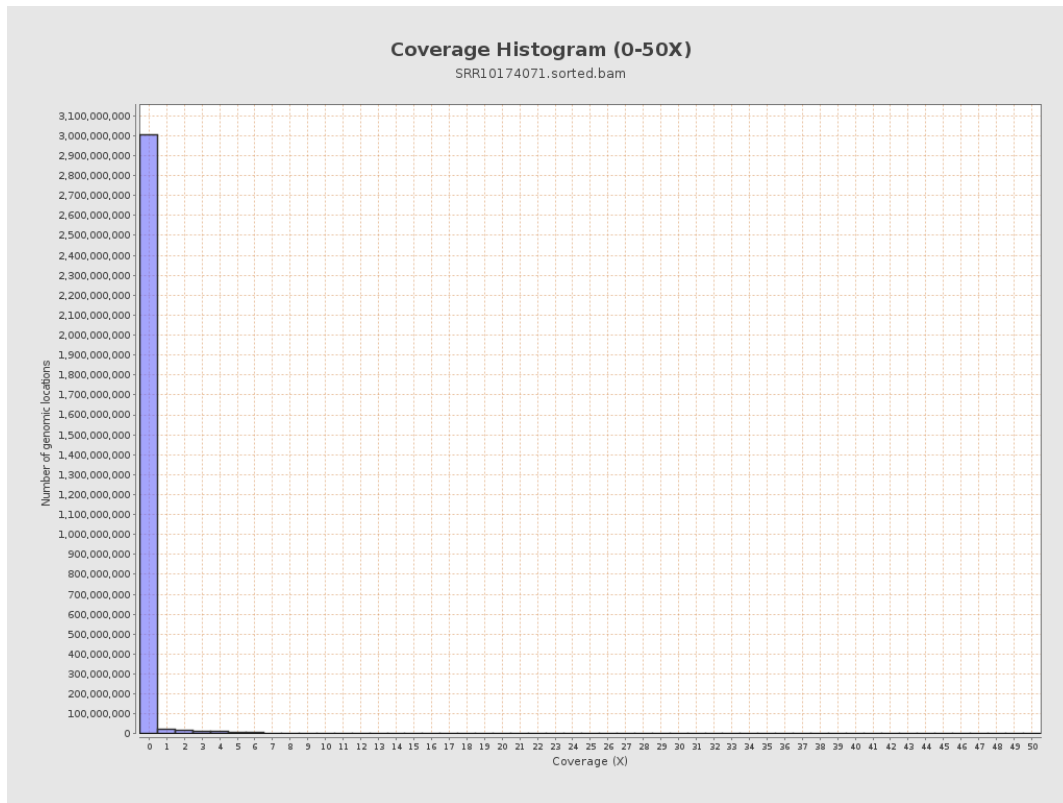
3. Results : Coverage across reference



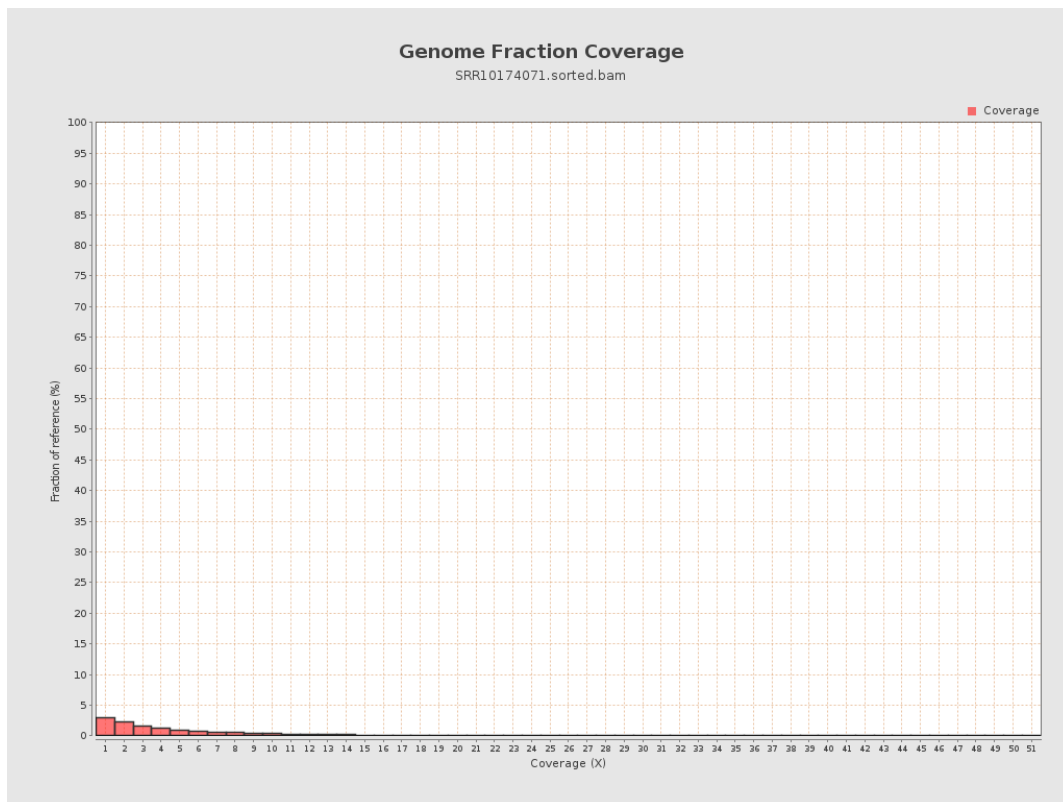
4. Results : Coverage Histogram



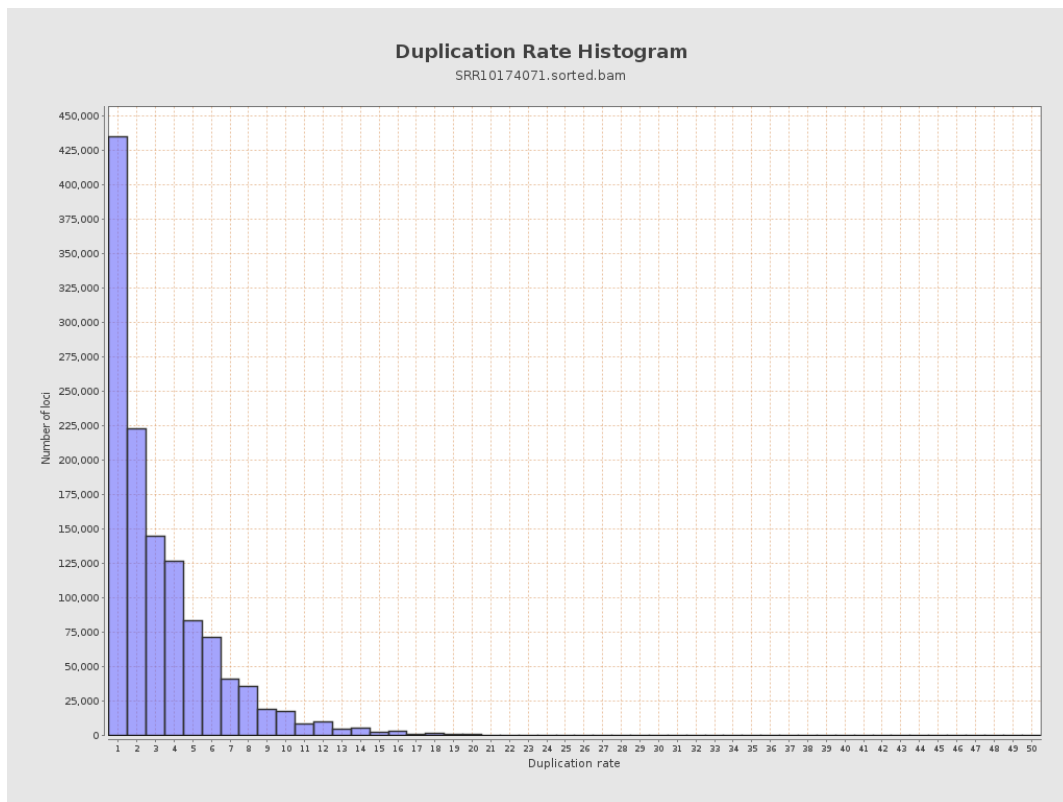
5. Results : Coverage Histogram (0-50X)



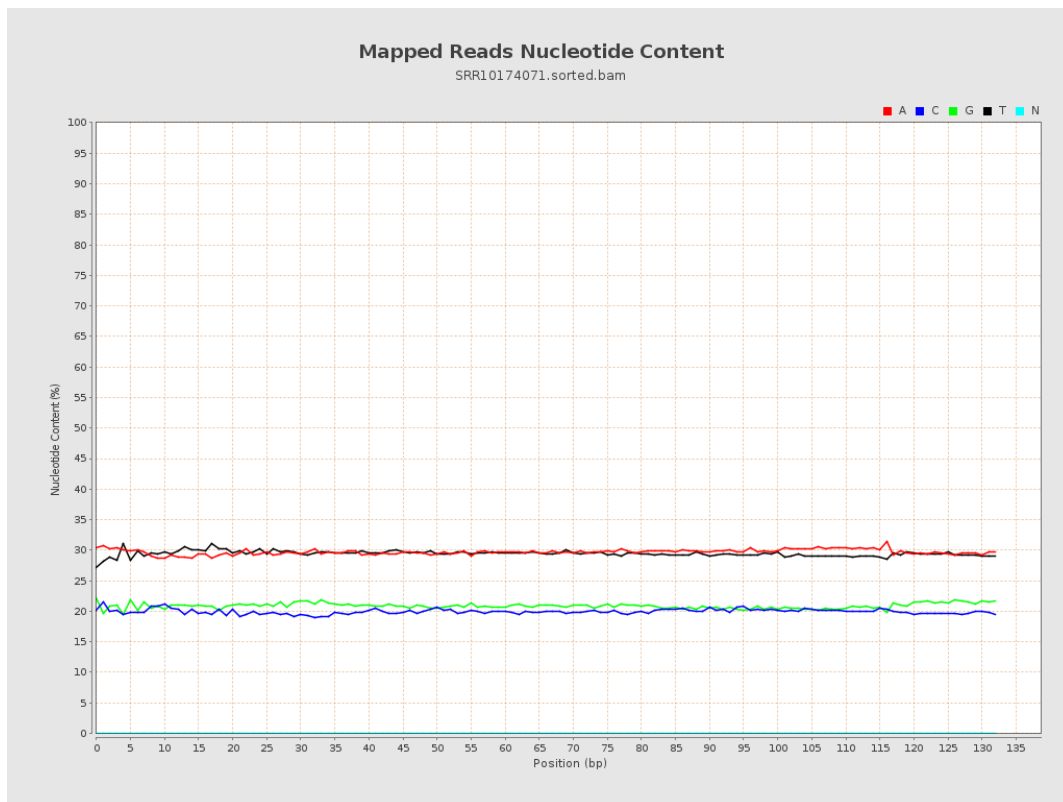
6. Results : Genome Fraction Coverage



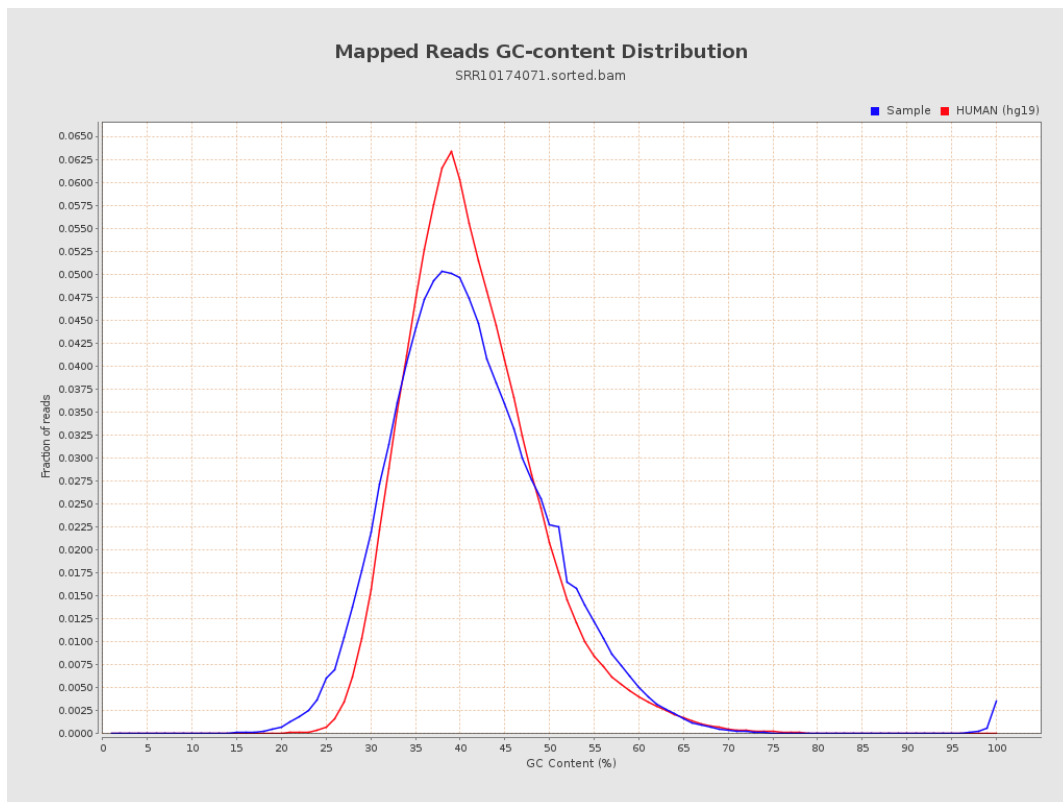
7. Results : Duplication Rate Histogram



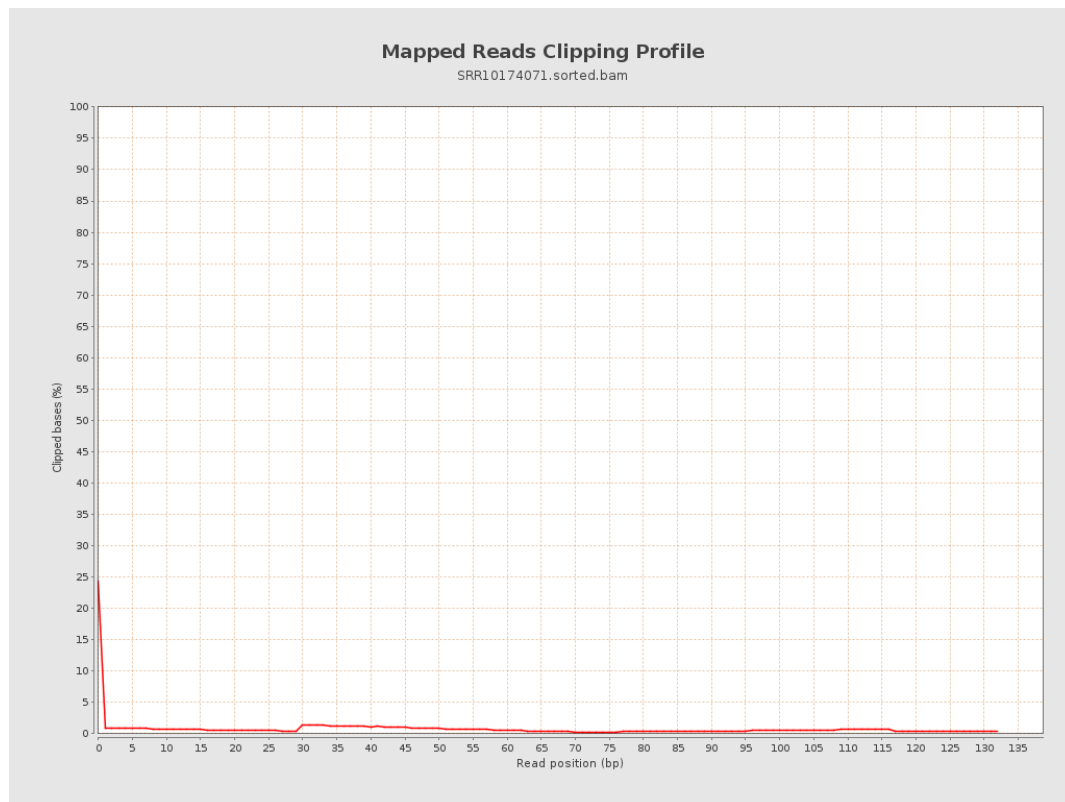
8. Results : Mapped Reads Nucleotide Content



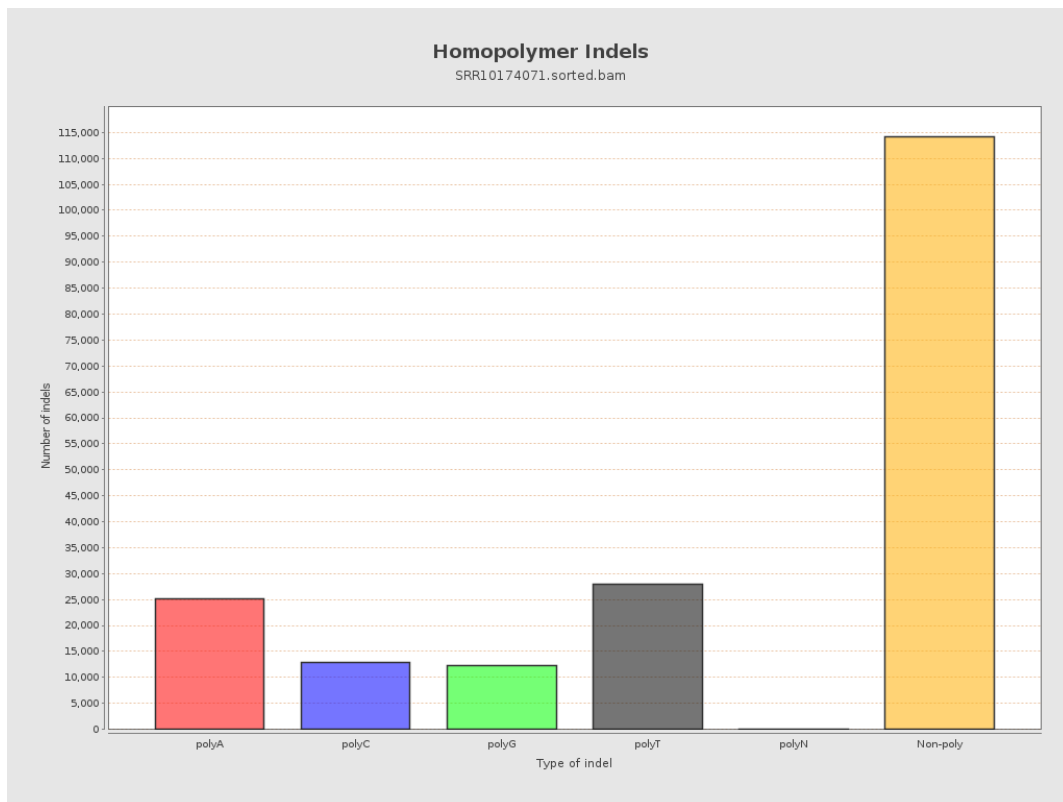
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



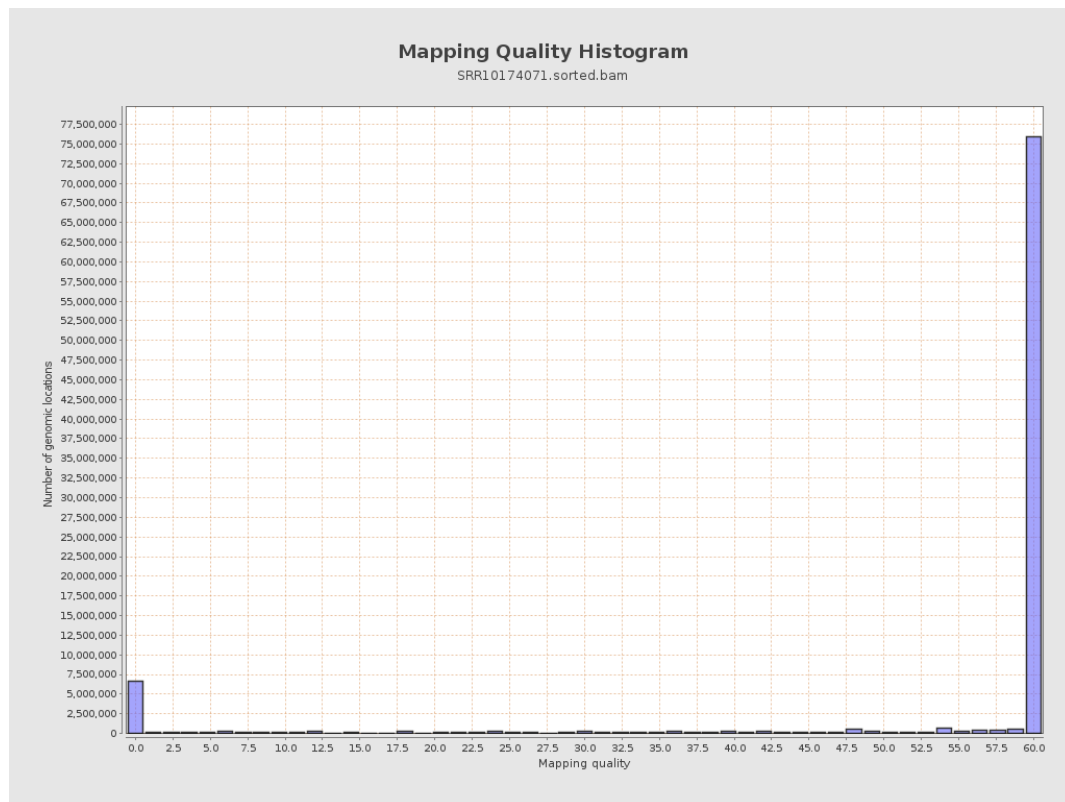
11. Results : Homopolymer Indels



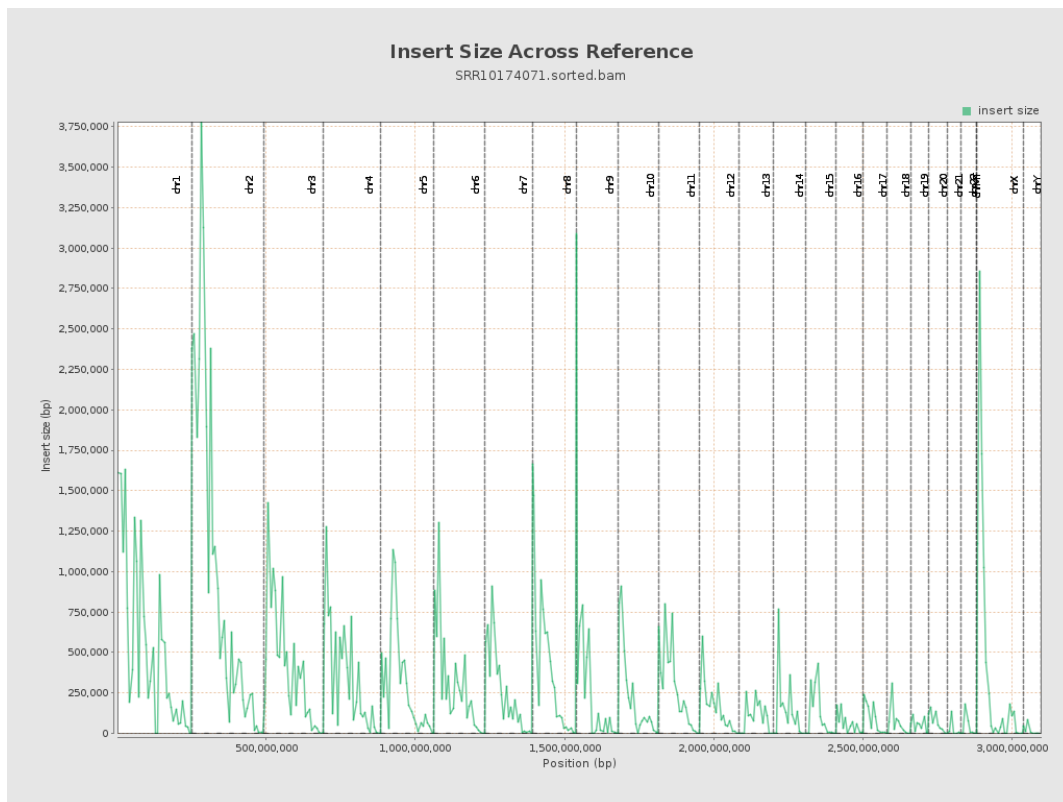
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

