

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 13:26:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618569.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_SRR618569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618569_1.fastq.gz SRR618569_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 13:26:46 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	239,646,346
Mapped reads	214,744,217 / 89.61%
Unmapped reads	24,902,129 / 10.39%
Mapped paired reads	214,744,217 / 89.61%
Mapped reads, first in pair	107,980,563 / 45.06%
Mapped reads, second in pair	106,763,654 / 44.55%
Mapped reads, both in pair	209,963,100 / 87.61%
Mapped reads, singletons	4,781,117 / 2%
Secondary alignments	0
Supplementary alignments	1,514,671 / 0.63%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	77,366,664 / 32.28%
Duplication rate	29.2%
Clipped reads	55,162,770 / 23.02%

2.2. ACGT Content

Number/percentage of A's	5,318,410,520 / 26.44%
Number/percentage of C's	4,549,854,397 / 22.62%
Number/percentage of T's	5,352,658,107 / 26.61%
Number/percentage of G's	4,891,984,819 / 24.32%
Number/percentage of N's	3,966,478 / 0.02%

GC Percentage	46.93%
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2.3. Coverage

Mean	6.5027
Standard Deviation	25.683

2.4. Mapping Quality

Mean Mapping Quality	52.57
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2.5. Insert size

Mean	85,585.94
Standard Deviation	2,916,222.93
P25/Median/P75	165 / 185 / 208

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	277,766,558
Insertions	3,264,724
Mapped reads with at least one insertion	1.49%
Deletions	9,631,280
Mapped reads with at least one deletion	4.38%
Homopolymer indels	51.92%

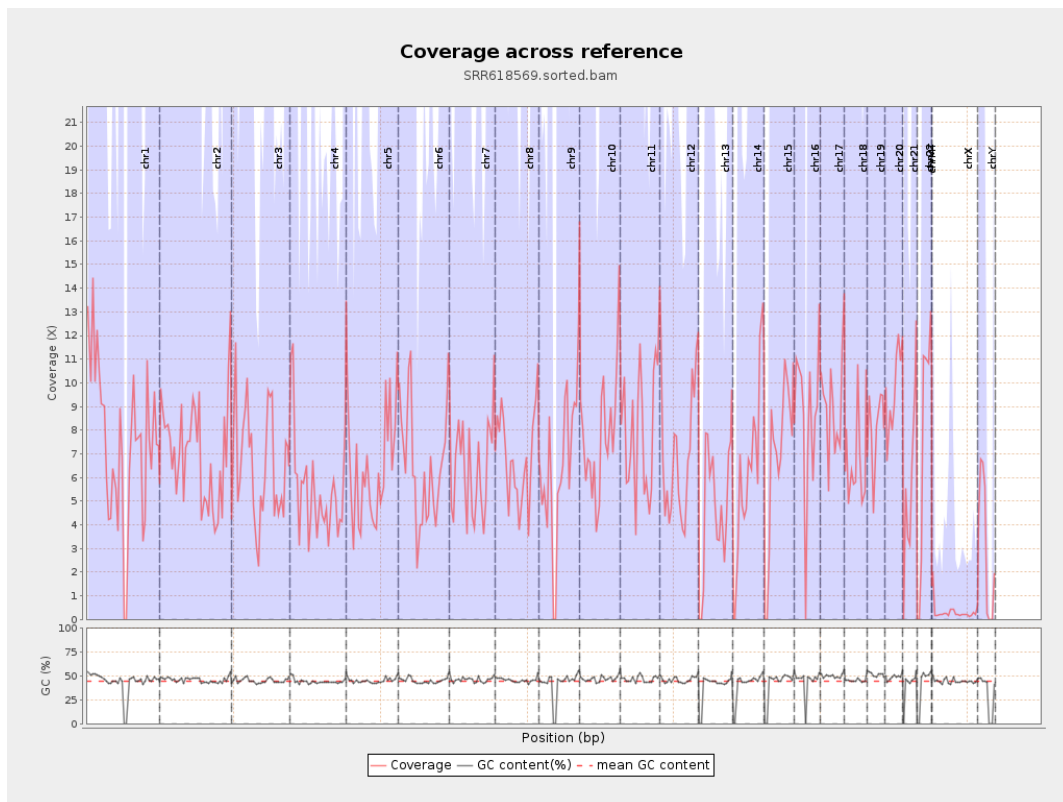
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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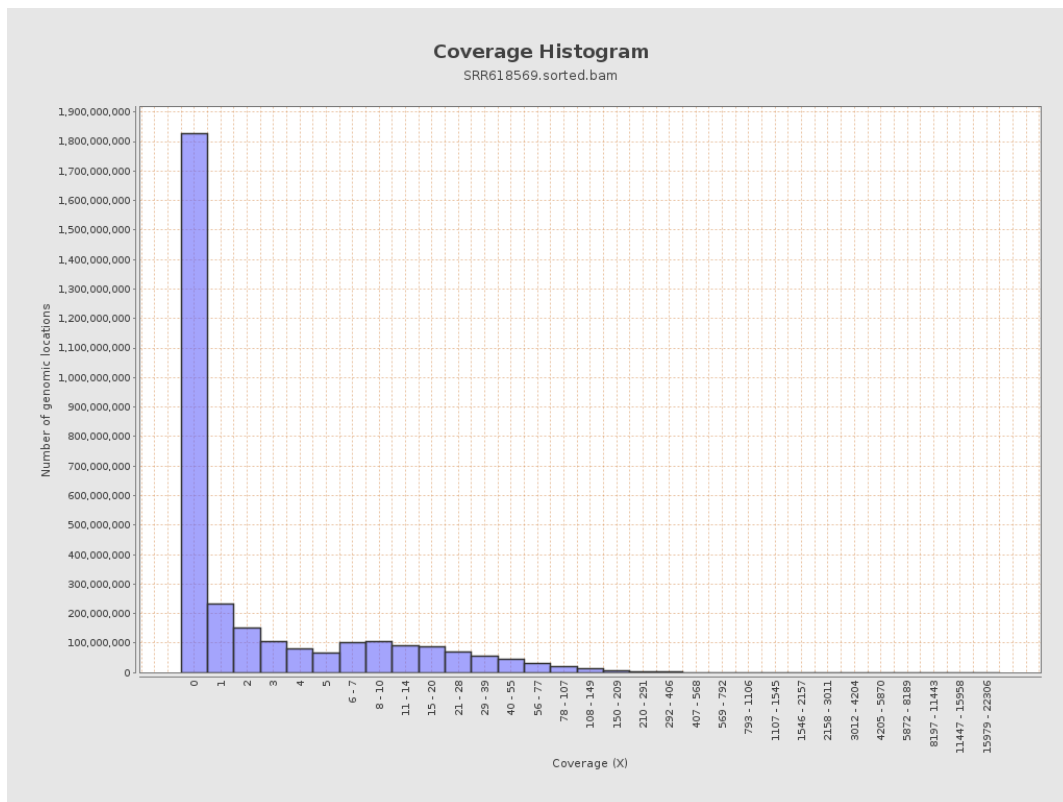
		bases	coverage	deviation
chr1	249250621	1860718004	7.4652	30.3059
chr2	243199373	1704627619	7.0092	30.0279
chr3	198022430	1303350413	6.5818	21.1675
chr4	191154276	1033816300	5.4083	21.5968
chr5	180915260	1164908857	6.439	21.2712
chr6	171115067	1108730392	6.4794	21.0341
chr7	159138663	1030918838	6.4781	21.4236
chr8	146364022	999879950	6.8315	21.5744
chr9	141213431	923034156	6.5364	28.0861
chr10	135534747	1048218510	7.7339	25.3339
chr11	135006516	1076713580	7.9753	29.0361
chr12	133851895	921700800	6.886	21.9751
chr13	115169878	542058159	4.7066	16.4609
chr14	107349540	665347121	6.198	23.3419
chr15	102531392	693888363	6.7676	23.2699
chr16	90354753	778845988	8.6199	43.5433
chr17	81195210	734011290	9.0401	29.7465
chr18	78077248	528555955	6.7697	28.0693
chr19	59128983	485245091	8.2066	29.6115
chr20	63025520	610650321	9.6889	29.8638
chr21	48129895	284230114	5.9055	44.784
chr22	51304566	397243289	7.7428	28.5808
chrMT	16571	23289	1.4054	4.5298
chrX	155270560	46606277	0.3002	5.2901

chrY	59373566	186942318	3.1486	22.3474
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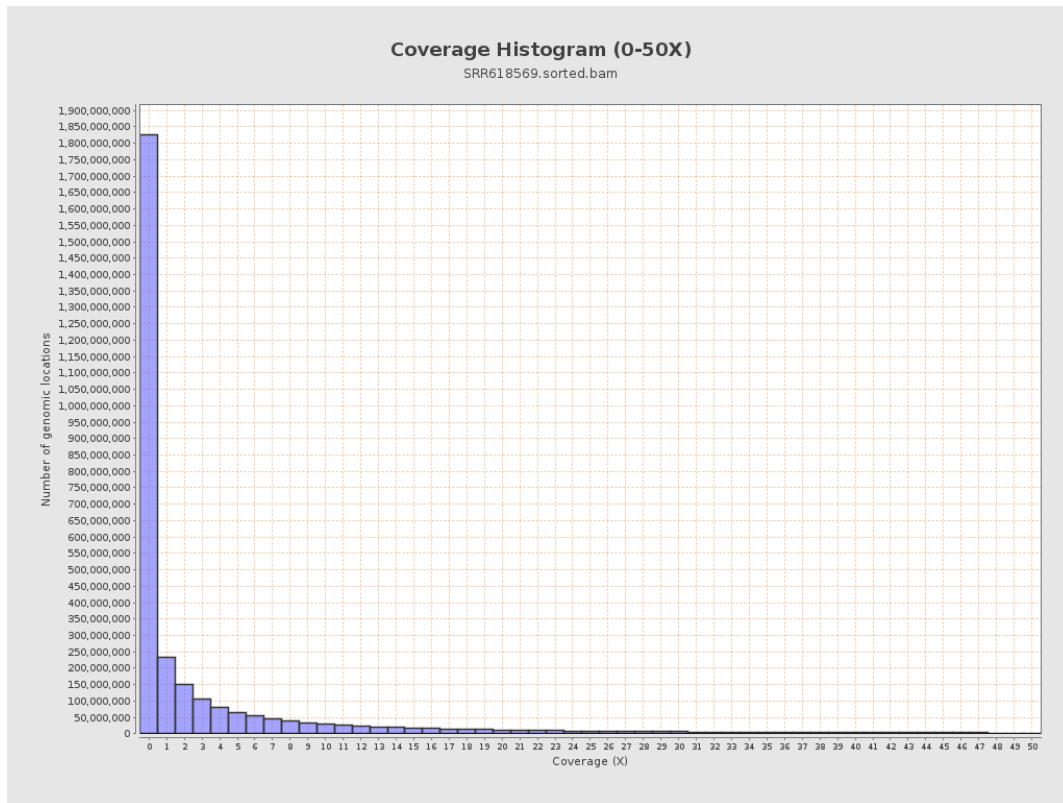
3. Results : Coverage across reference



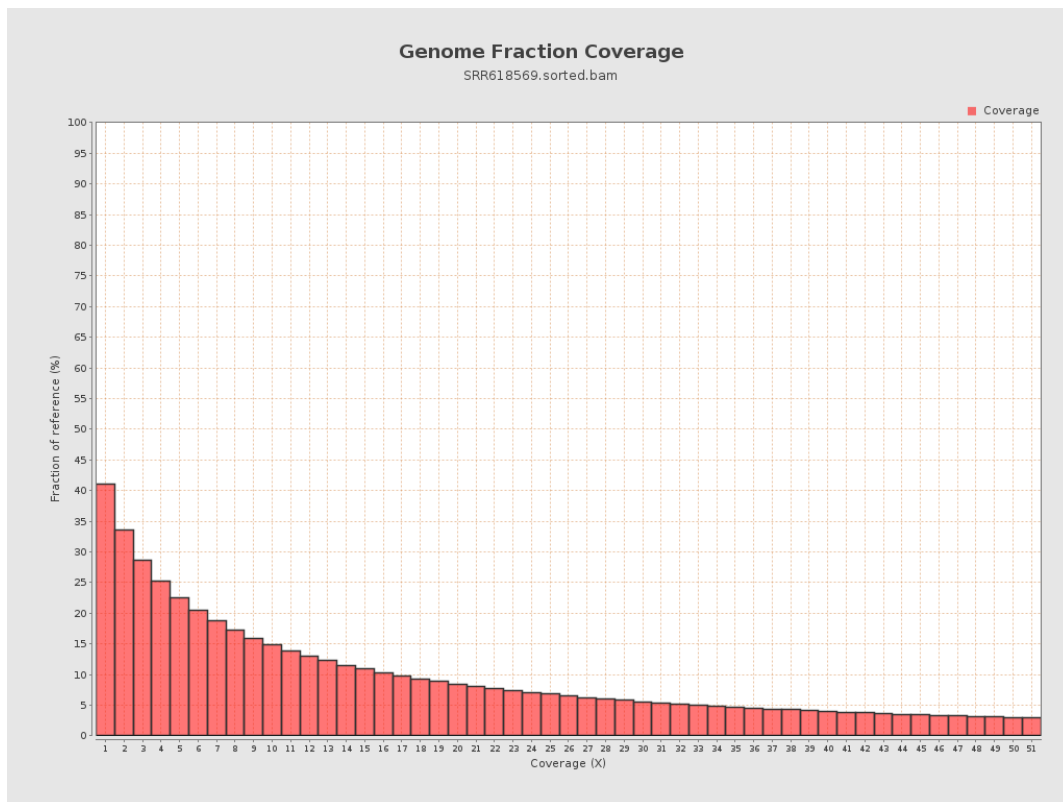
4. Results : Coverage Histogram



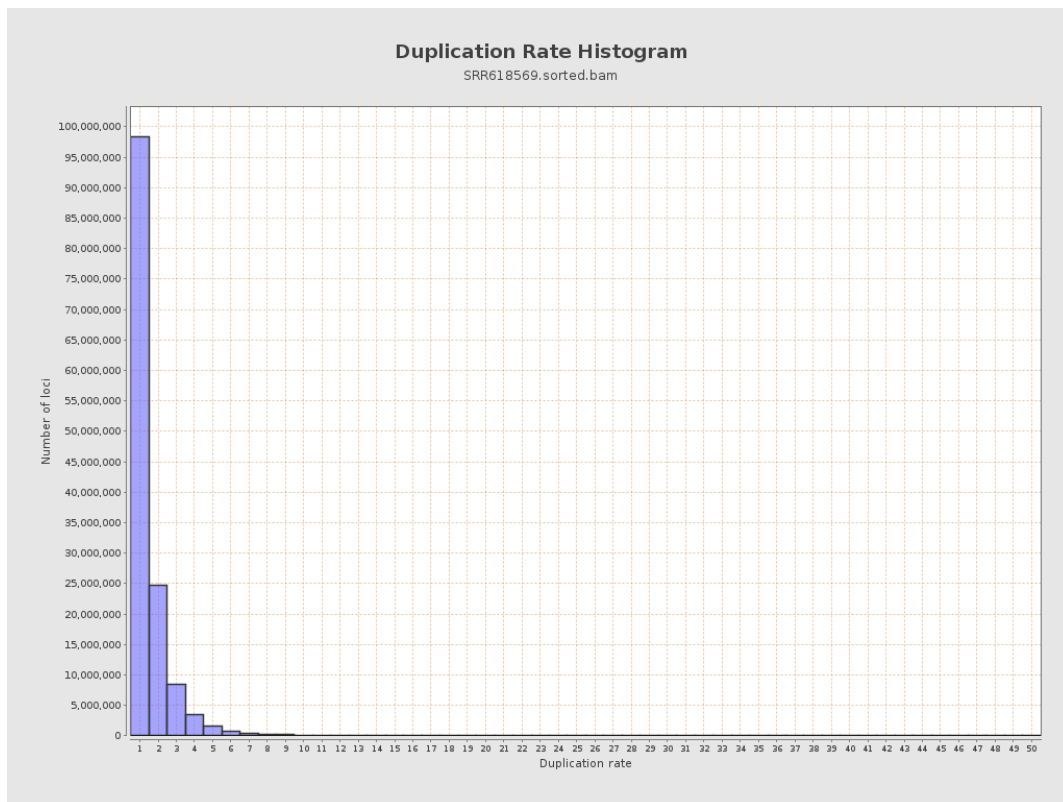
5. Results : Coverage Histogram (0-50X)



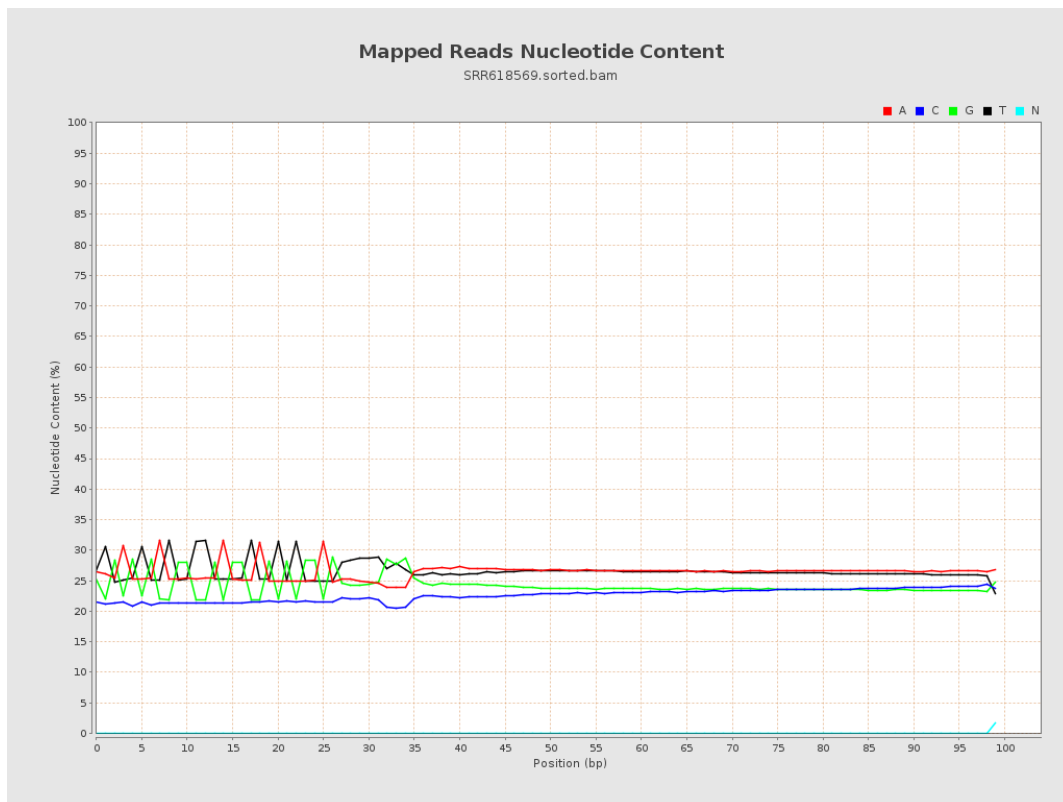
6. Results : Genome Fraction Coverage



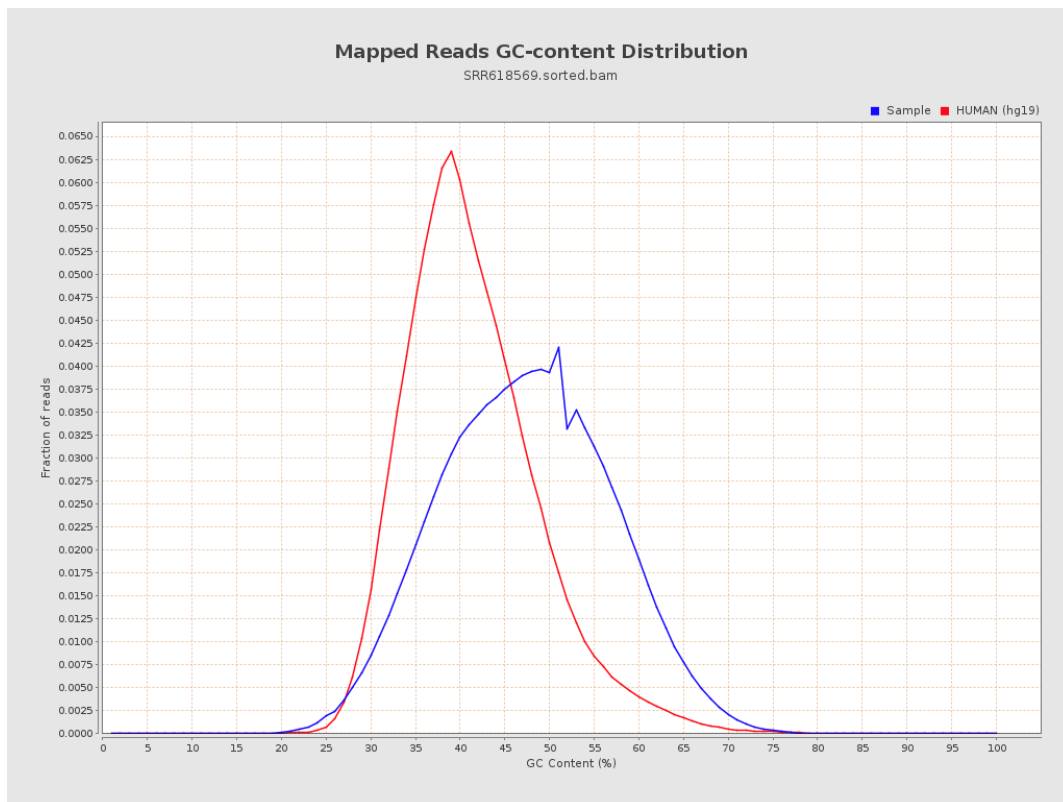
7. Results : Duplication Rate Histogram



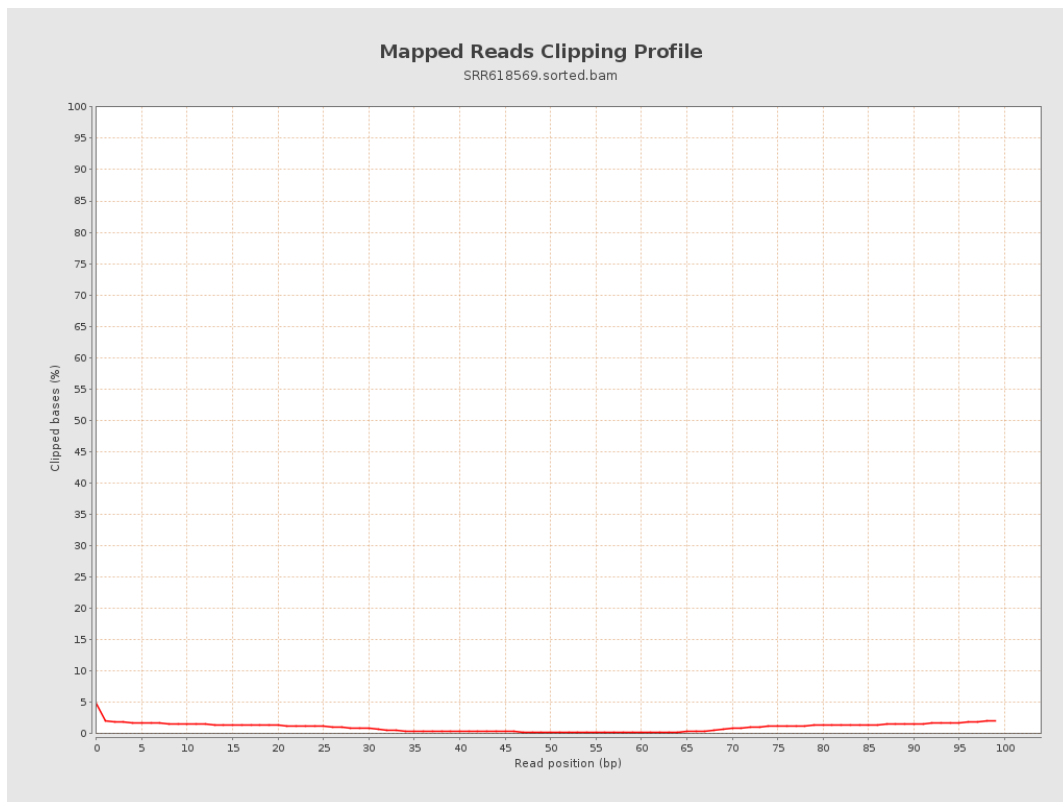
8. Results : Mapped Reads Nucleotide Content



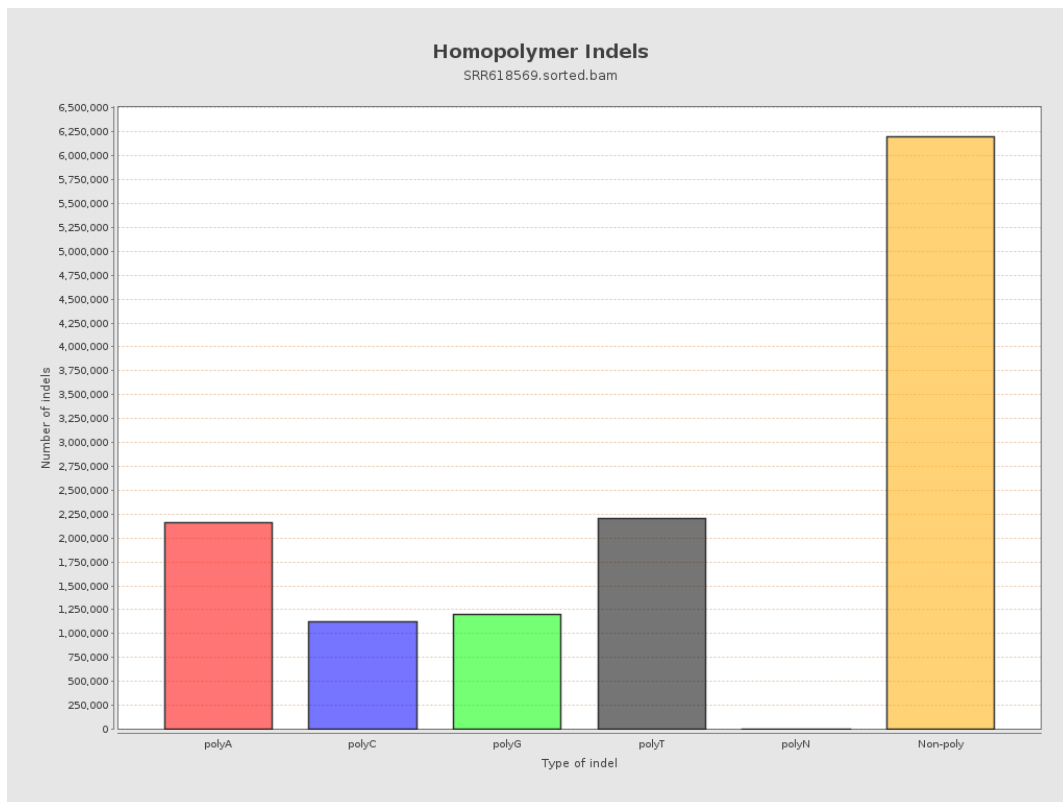
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



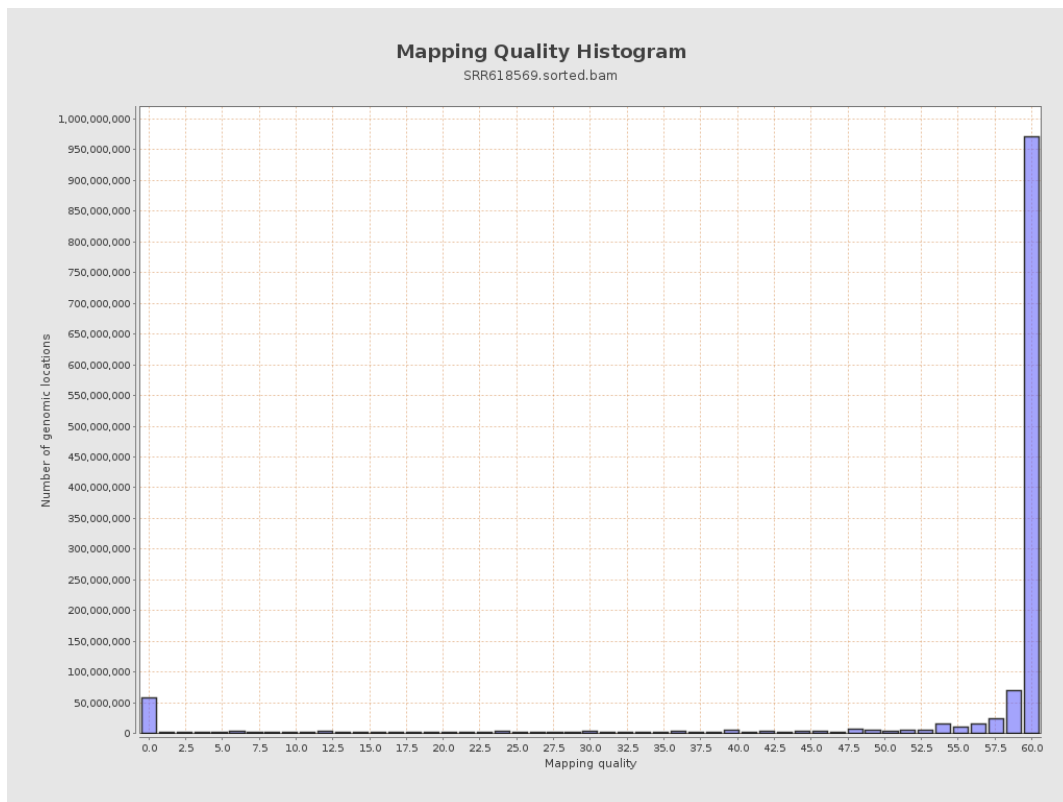
11. Results : Homopolymer Indels



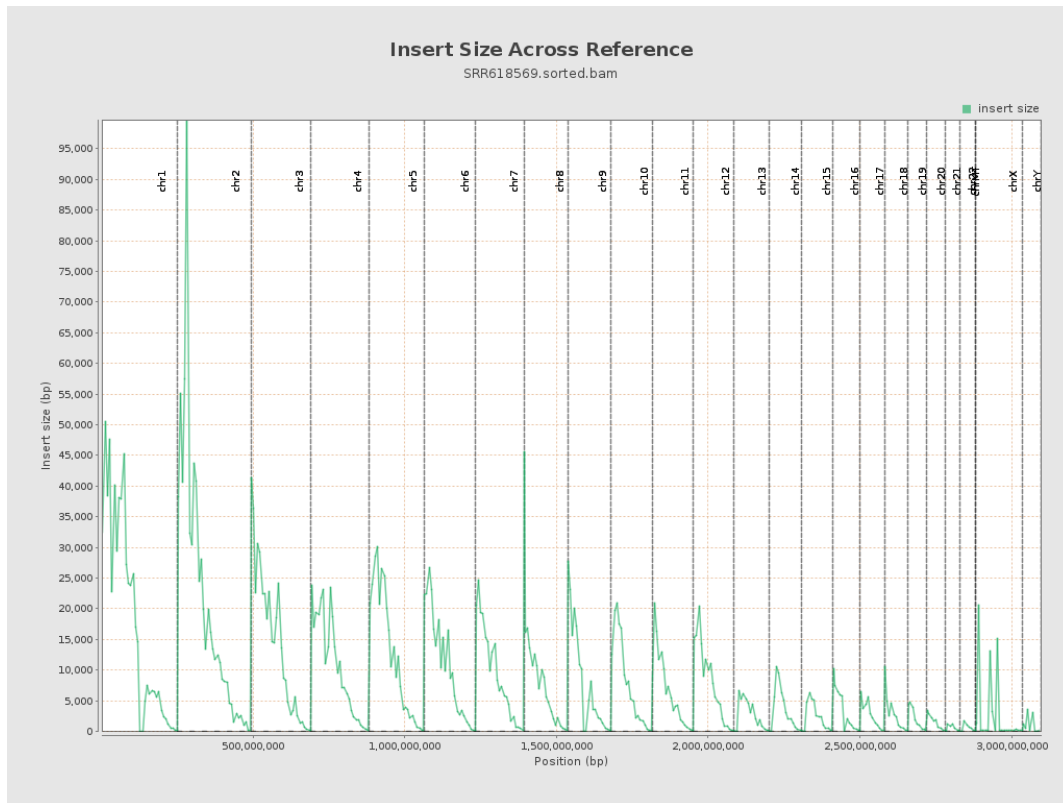
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

