

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 22:49:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618637.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_SRR618637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618637_1.fastq.gz SRR618637_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 22:49:31 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,474,022
Mapped reads	18,861,721 / 71.25%
Unmapped reads	7,612,301 / 28.75%
Mapped paired reads	18,861,721 / 71.25%
Mapped reads, first in pair	9,629,050 / 36.37%
Mapped reads, second in pair	9,232,671 / 34.87%
Mapped reads, both in pair	18,052,070 / 68.19%
Mapped reads, singletons	809,651 / 3.06%
Secondary alignments	0
Supplementary alignments	172,340 / 0.65%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	8,308,597 / 31.38%
Duplication rate	32.65%
Clipped reads	5,567,120 / 21.03%

2.2. ACGT Content

Number/percentage of A's	463,483,011 / 26.66%
Number/percentage of C's	386,090,472 / 22.21%
Number/percentage of T's	473,485,241 / 27.23%
Number/percentage of G's	414,430,437 / 23.84%
Number/percentage of N's	1,193,613 / 0.07%

GC Percentage	46.04%
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2.3. Coverage

Mean	0.562
Standard Deviation	2.8009

2.4. Mapping Quality

Mean Mapping Quality	53.08
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2.5. Insert size

Mean	184,581.75
Standard Deviation	4,290,535.24
P25/Median/P75	179 / 211 / 249

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	24,678,253
Insertions	338,722
Mapped reads with at least one insertion	1.77%
Deletions	871,544
Mapped reads with at least one deletion	4.5%
Homopolymer indels	51.7%

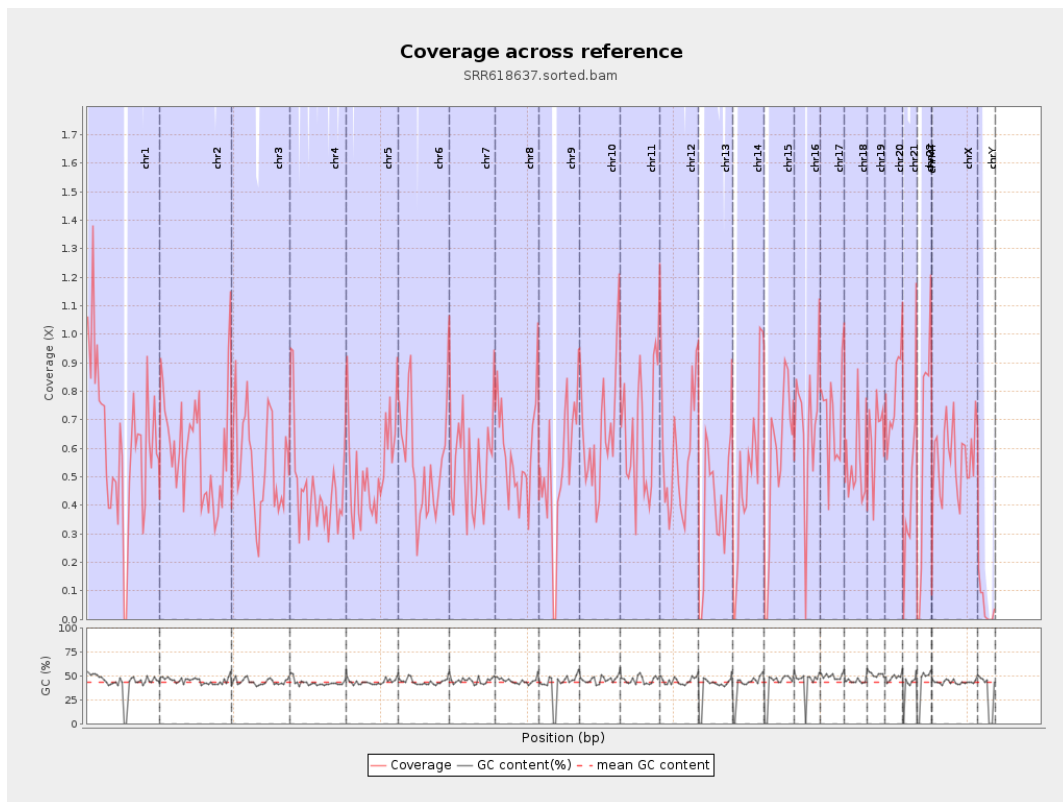
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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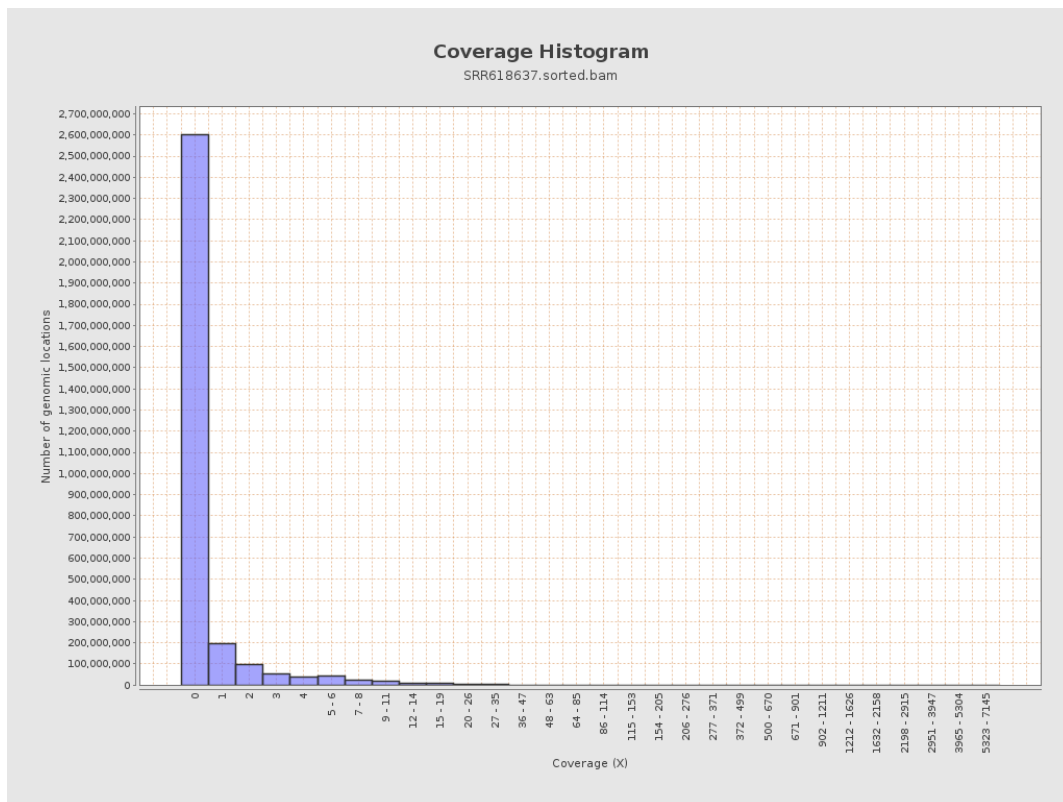
		bases	coverage	deviation
chr1	249250621	153289320	0.615	5.3056
chr2	243199373	144646484	0.5948	2.9329
chr3	198022430	108938099	0.5501	2.1338
chr4	191154276	86788921	0.454	1.9947
chr5	180915260	96024148	0.5308	2.1369
chr6	171115067	93405564	0.5459	2.3982
chr7	159138663	87785063	0.5516	2.4101
chr8	146364022	85841572	0.5865	2.4396
chr9	141213431	74573634	0.5281	2.5542
chr10	135534747	89075877	0.6572	2.4783
chr11	135006516	88893630	0.6584	2.6283
chr12	133851895	77676184	0.5803	2.6069
chr13	115169878	45925143	0.3988	1.8239
chr14	107349540	54622400	0.5088	2.2197
chr15	102531392	56898796	0.5549	2.2263
chr16	90354753	61283618	0.6783	3.8403
chr17	81195210	57958669	0.7138	2.688
chr18	78077248	43060089	0.5515	2.3469
chr19	59128983	38264838	0.6471	2.6779
chr20	63025520	49631268	0.7875	2.7169
chr21	48129895	22520168	0.4679	3.18
chr22	51304566	32039169	0.6245	2.6072
chrMT	16571	1371	0.0827	0.6233
chrX	155270560	87979775	0.5666	2.0948

chrY	59373566	2773562	0.0467	1.3367
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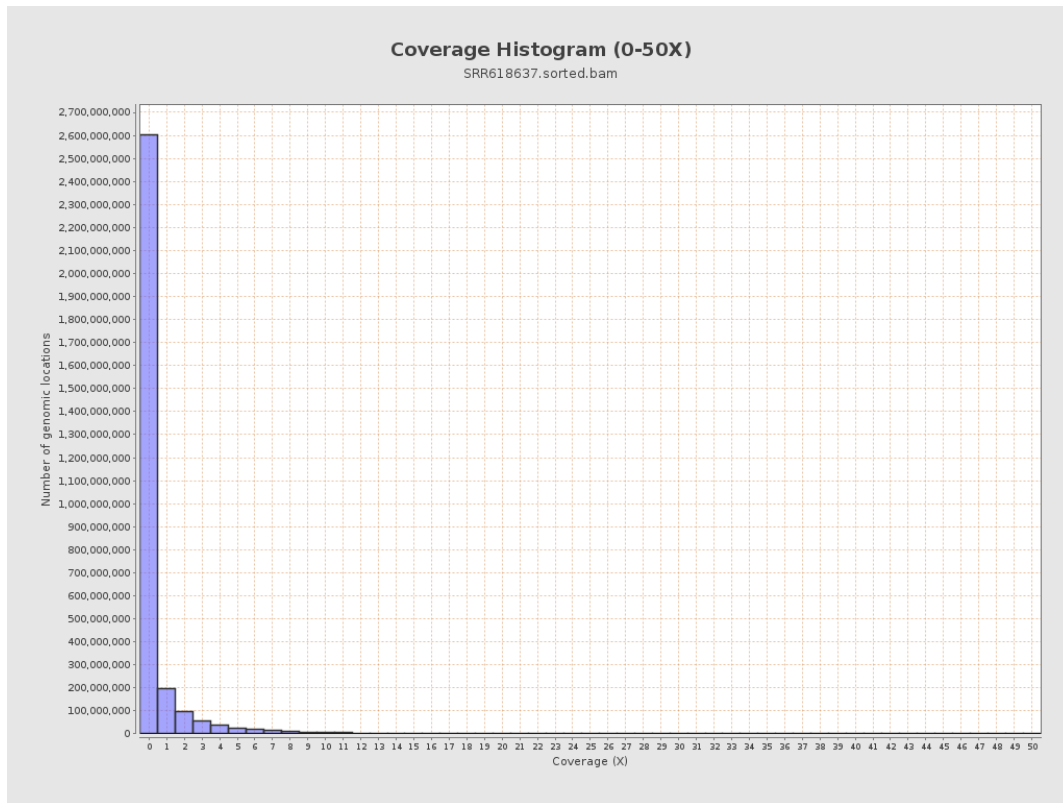
3. Results : Coverage across reference



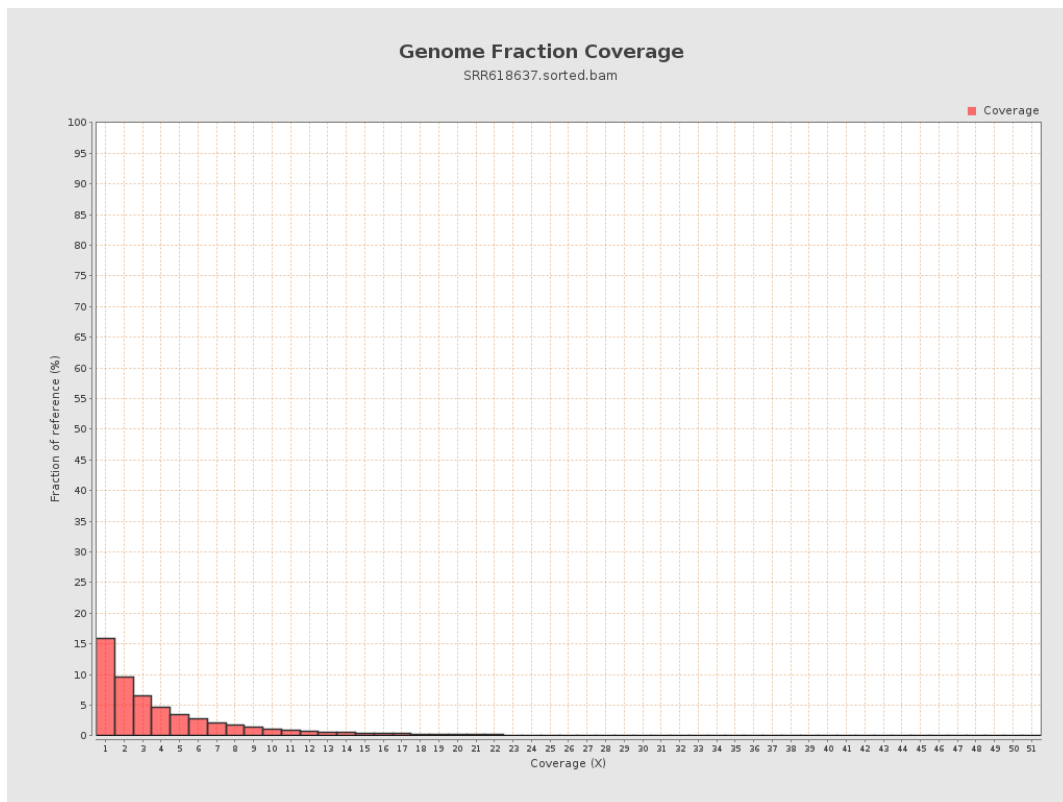
4. Results : Coverage Histogram



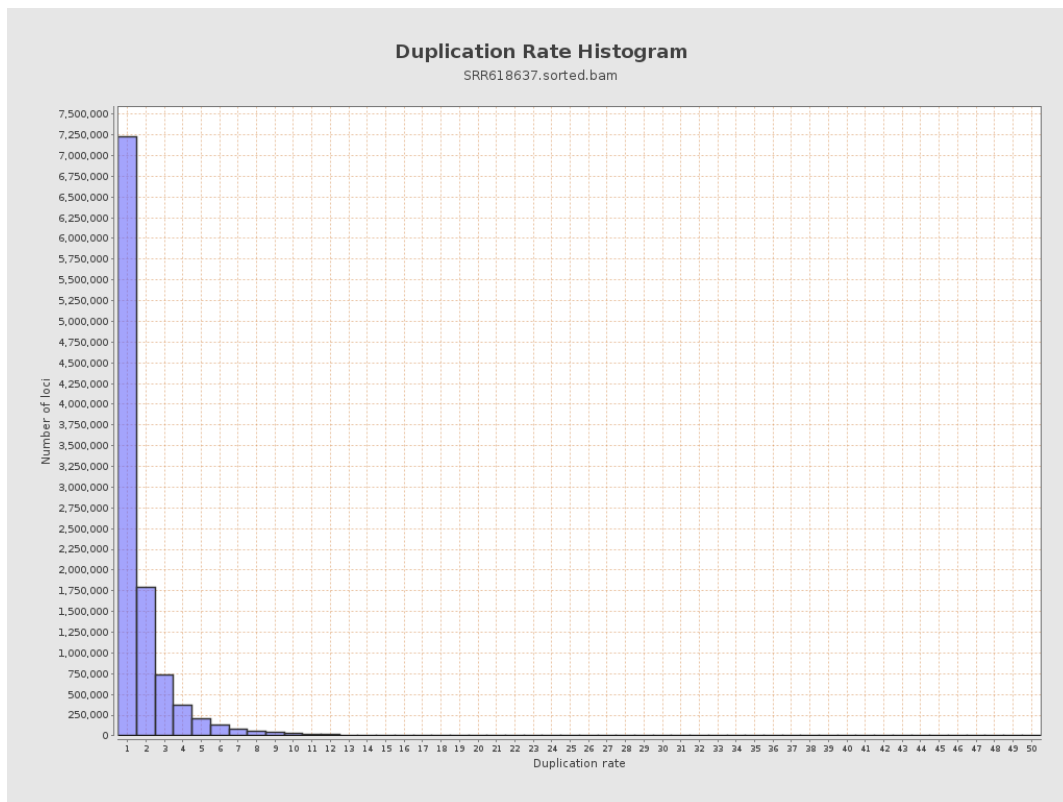
5. Results : Coverage Histogram (0-50X)



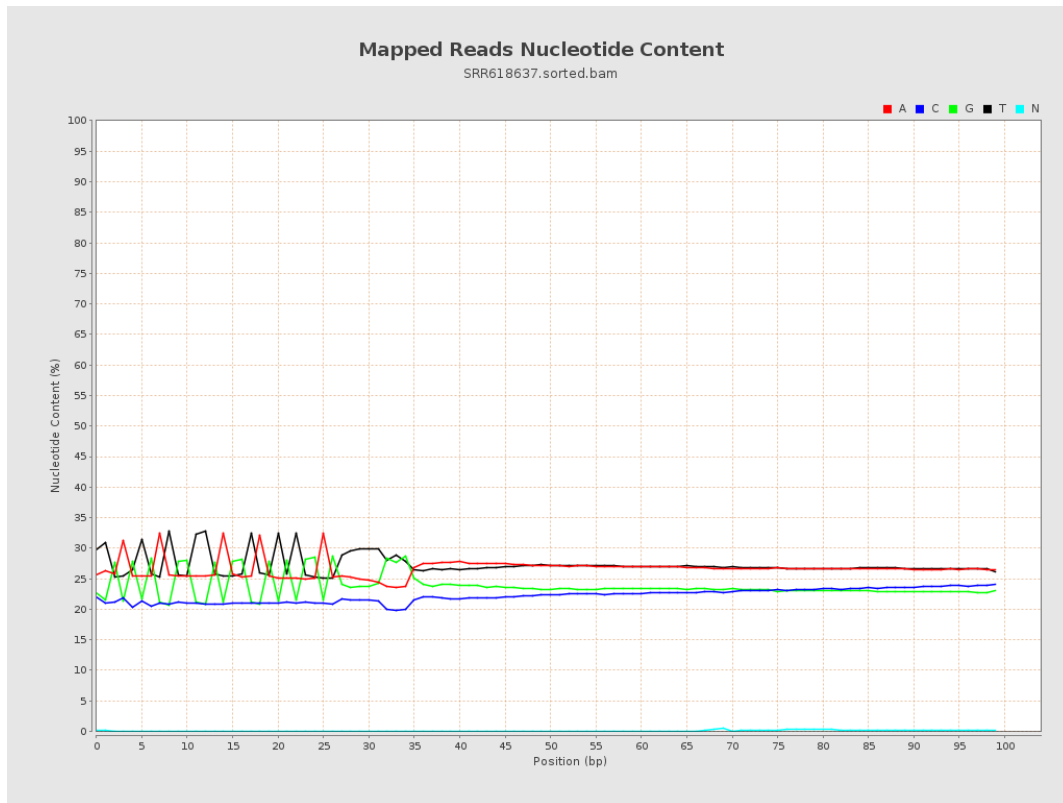
6. Results : Genome Fraction Coverage



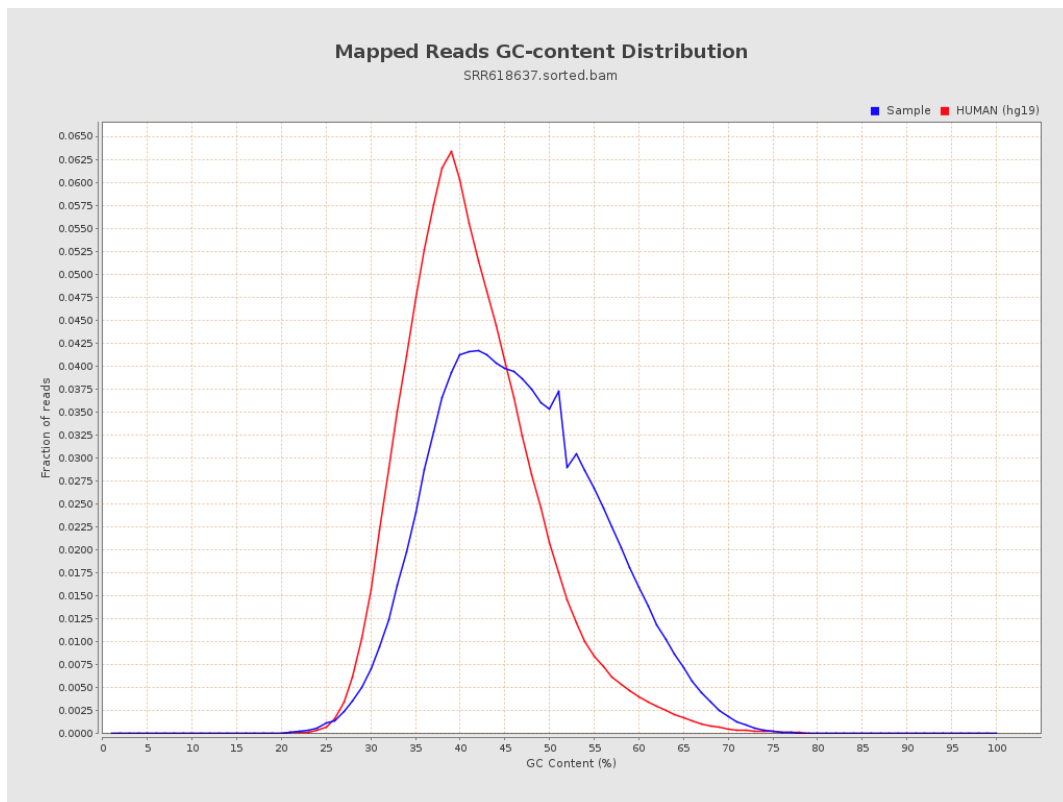
7. Results : Duplication Rate Histogram



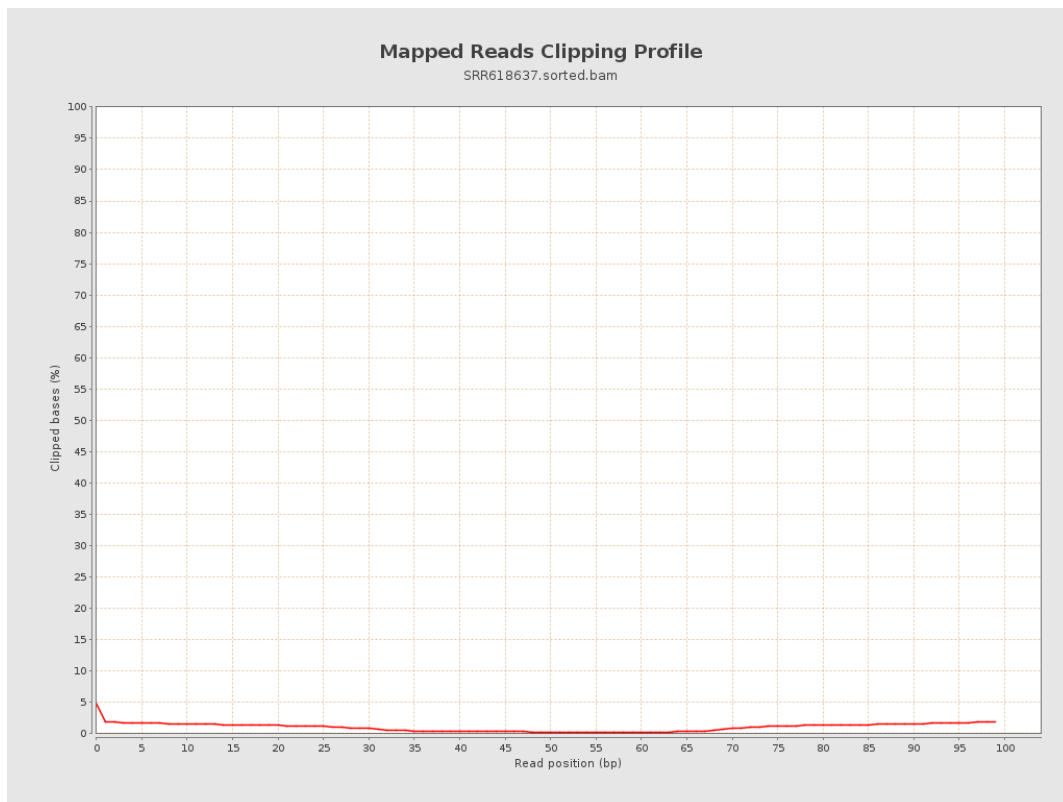
8. Results : Mapped Reads Nucleotide Content



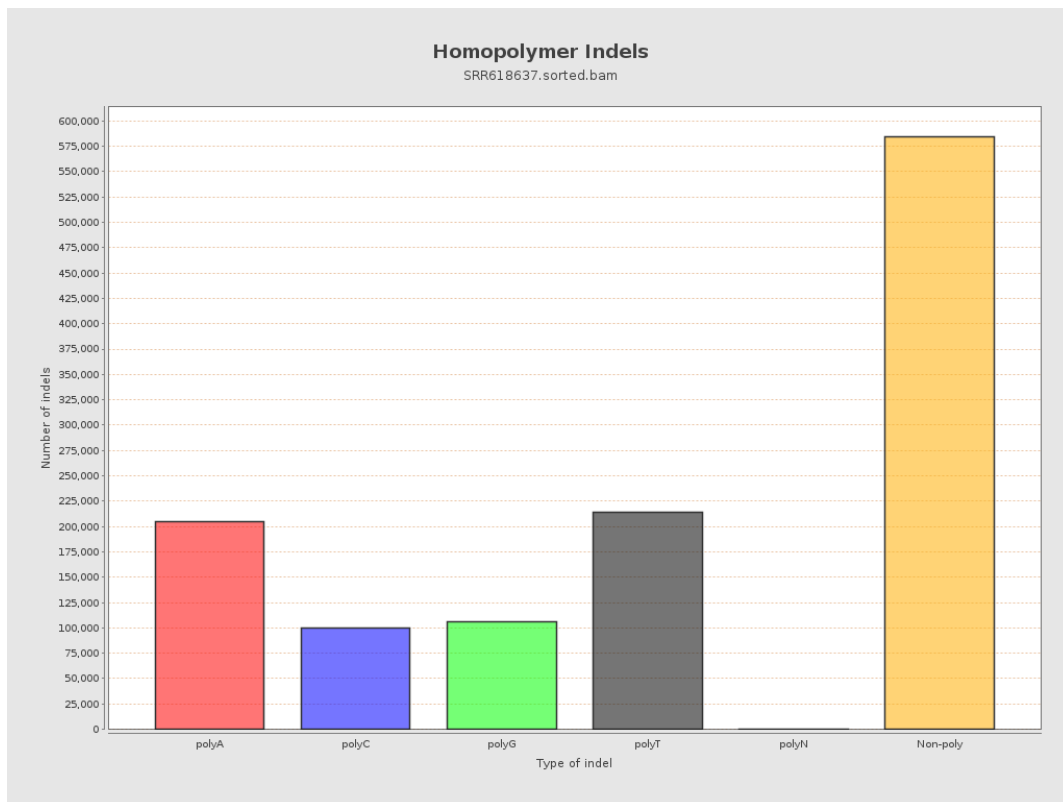
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



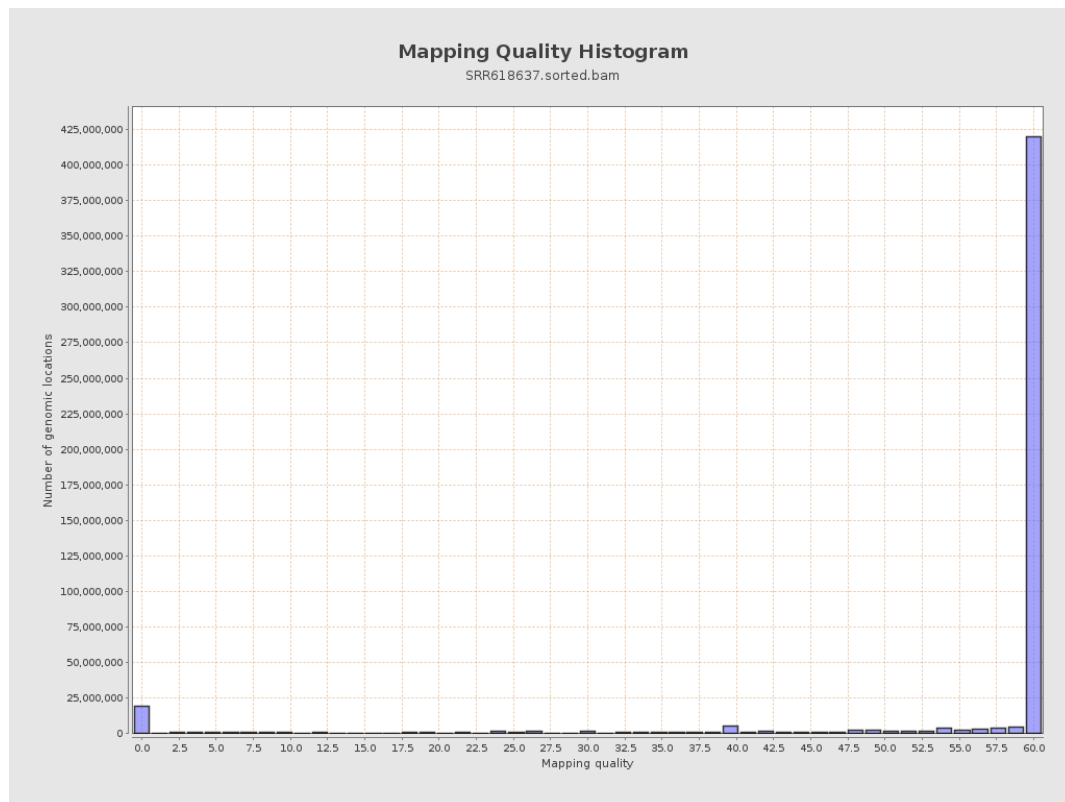
11. Results : Homopolymer Indels



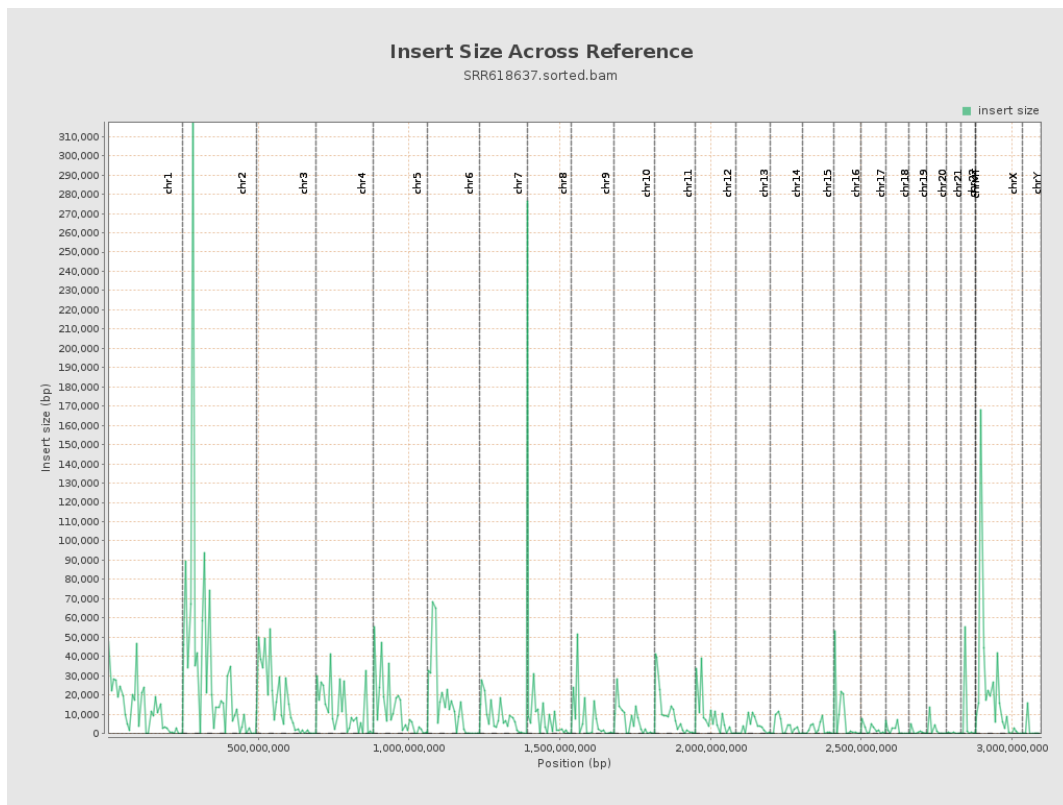
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

