

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 15:02:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618624.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_SRR618624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618624_1.fastq.gz SRR618624_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 15:02:06 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	46,316,672
Mapped reads	42,433,788 / 91.62%
Unmapped reads	3,882,884 / 8.38%
Mapped paired reads	42,433,788 / 91.62%
Mapped reads, first in pair	22,103,159 / 47.72%
Mapped reads, second in pair	20,330,629 / 43.89%
Mapped reads, both in pair	39,791,770 / 85.91%
Mapped reads, singletons	2,642,018 / 5.7%
Secondary alignments	0
Supplementary alignments	226,854 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	24,408,085 / 52.7%
Duplication rate	39.75%
Clipped reads	10,564,023 / 22.81%

2.2. ACGT Content

Number/percentage of A's	1,116,058,425 / 28.18%
Number/percentage of C's	828,311,791 / 20.91%
Number/percentage of T's	1,145,454,394 / 28.92%
Number/percentage of G's	868,657,192 / 21.93%
Number/percentage of N's	2,210,766 / 0.06%

GC Percentage	42.85%
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2.3. Coverage

Mean	1.2804
Standard Deviation	6.6342

2.4. Mapping Quality

Mean Mapping Quality	53.5
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2.5. Insert size

Mean	153,943.23
Standard Deviation	3,899,872.44
P25/Median/P75	180 / 211 / 251

2.6. Mismatches and indels

General error rate	1.47%
Mismatches	57,150,826
Insertions	777,569
Mapped reads with at least one insertion	1.8%
Deletions	2,124,131
Mapped reads with at least one deletion	4.87%
Homopolymer indels	52.5%

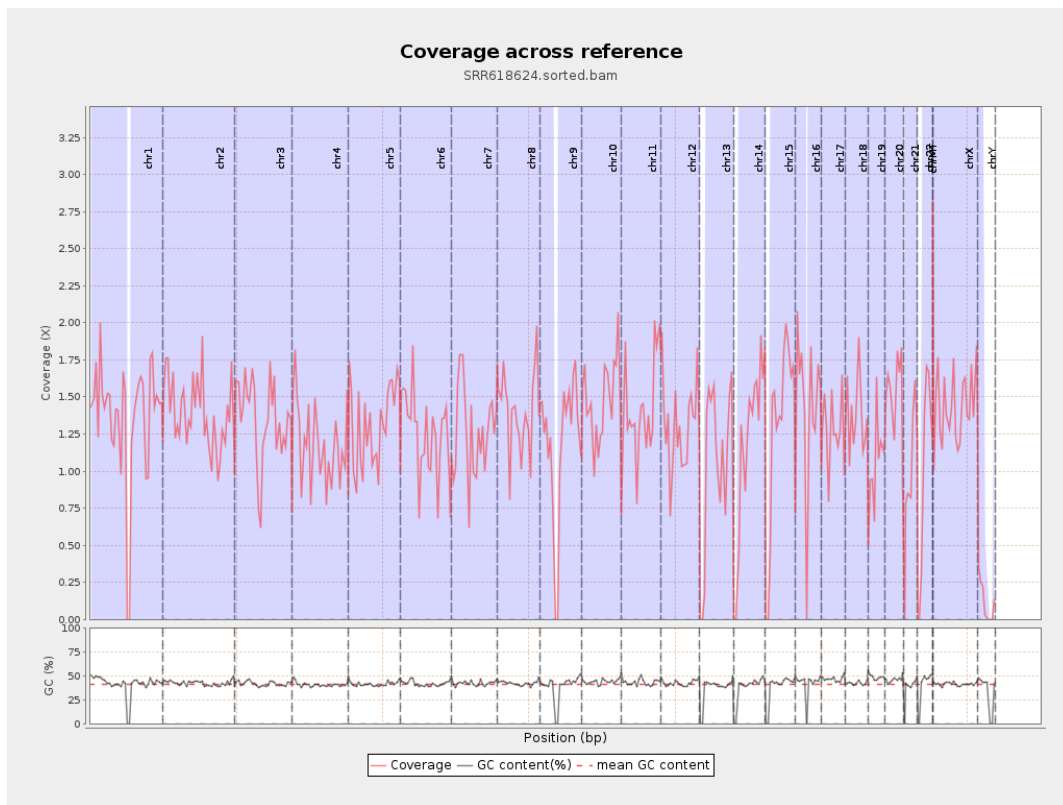
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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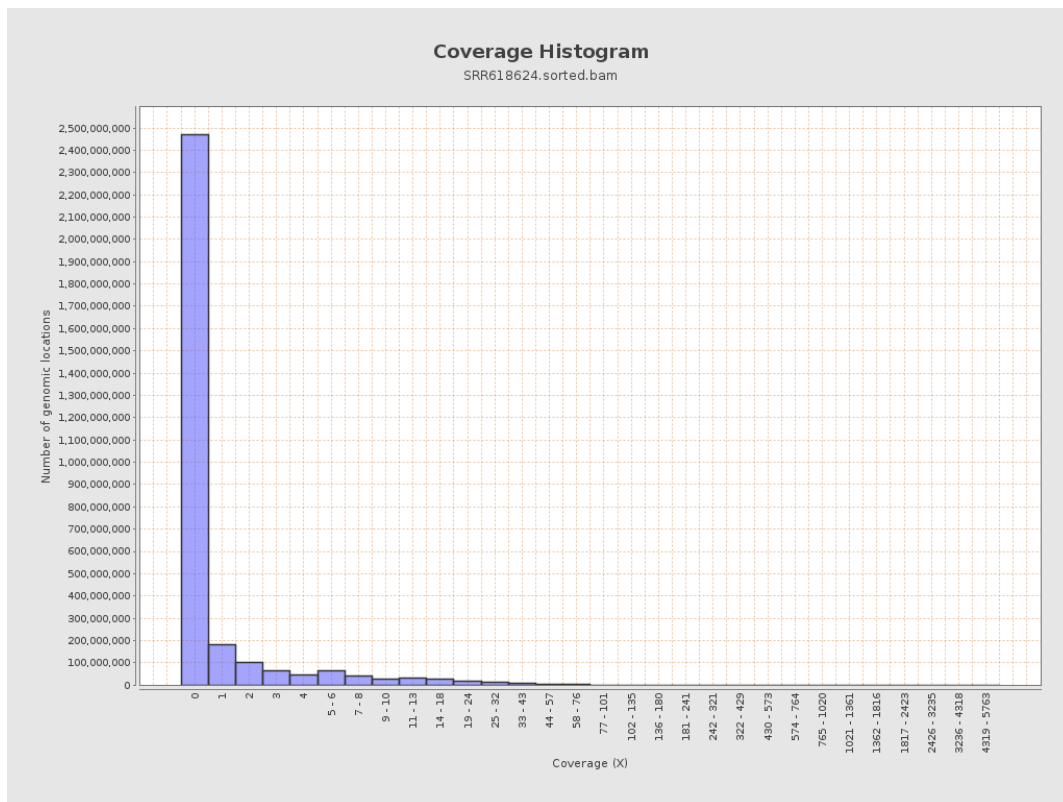
		bases	coverage	deviation
chr1	249250621	338808026	1.3593	7.2035
chr2	243199373	338045350	1.39	7.5207
chr3	198022430	264570119	1.3361	5.8878
chr4	191154276	225971277	1.1821	6.0085
chr5	180915260	237383007	1.3121	6.0778
chr6	171115067	213444248	1.2474	5.5703
chr7	159138663	199895749	1.2561	6.2393
chr8	146364022	204473846	1.397	6.9863
chr9	141213431	166118684	1.1764	6.8632
chr10	135534747	200267054	1.4776	7.8077
chr11	135006516	190335952	1.4098	6.9325
chr12	133851895	175745808	1.313	8.42
chr13	115169878	121100407	1.0515	4.9804
chr14	107349540	125096992	1.1653	5.5381
chr15	102531392	132622093	1.2935	5.6863
chr16	90354753	126733754	1.4026	10.7367
chr17	81195210	104494291	1.287	6.0193
chr18	78077248	107051531	1.3711	6.6077
chr19	59128983	62808089	1.0622	5.3668
chr20	63025520	97614258	1.5488	5.8944
chr21	48129895	48454768	1.0067	5.6791
chr22	51304566	52509461	1.0235	6.2059
chrMT	16571	46998	2.8362	17.0998
chrX	155270560	223165460	1.4373	5.6146

chrY	59373566	6815491	0.1148	3.8769
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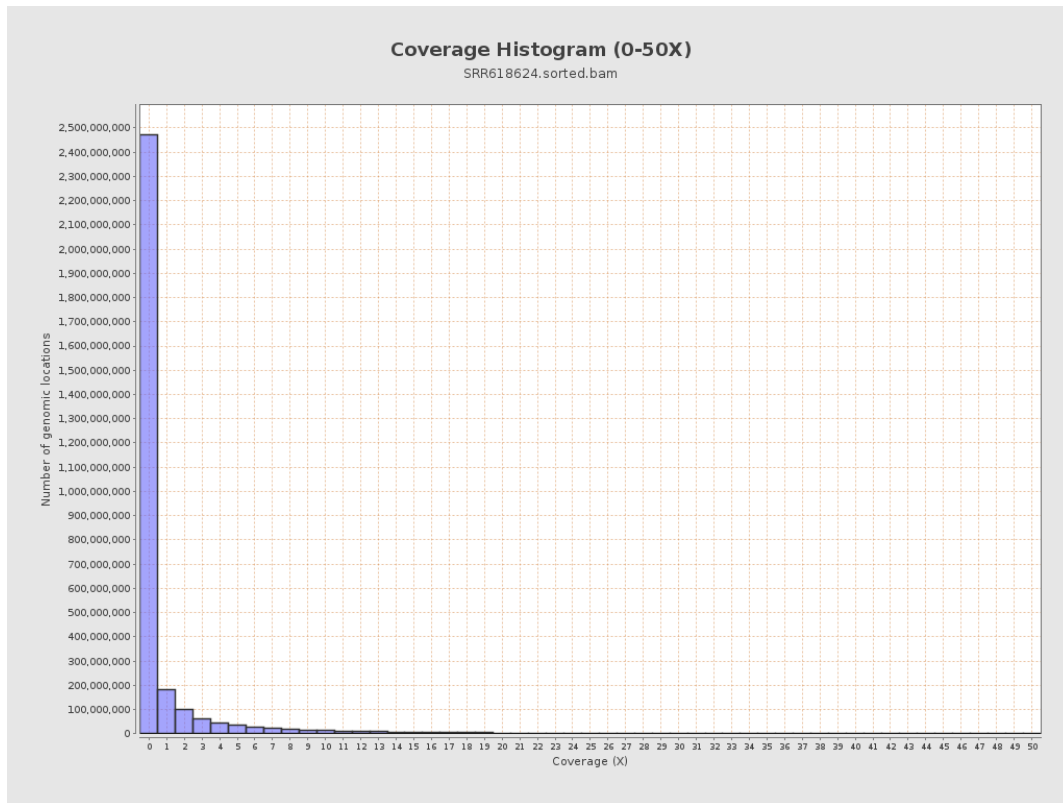
3. Results : Coverage across reference



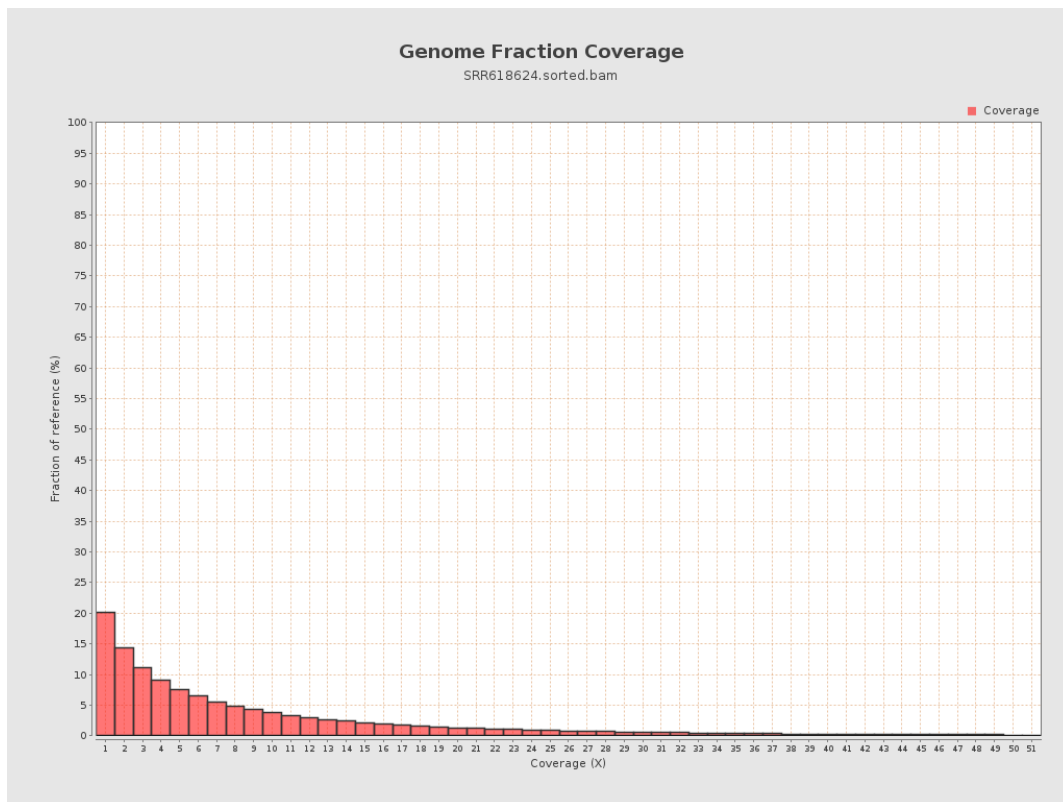
4. Results : Coverage Histogram



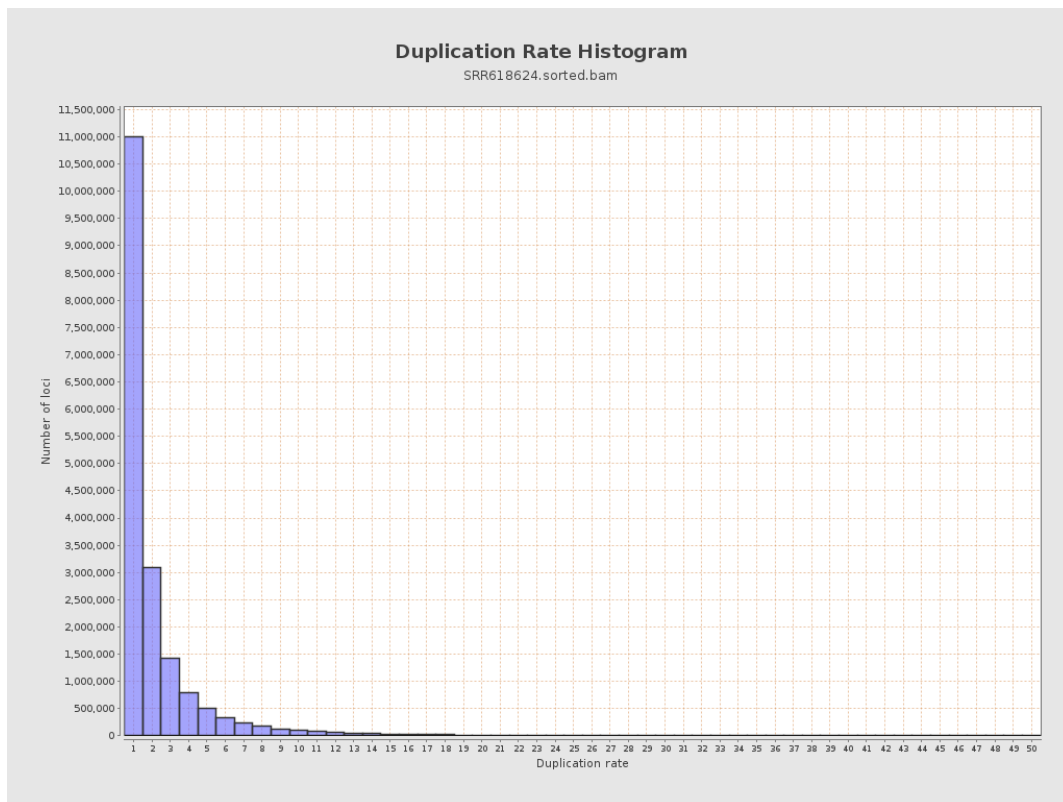
5. Results : Coverage Histogram (0-50X)



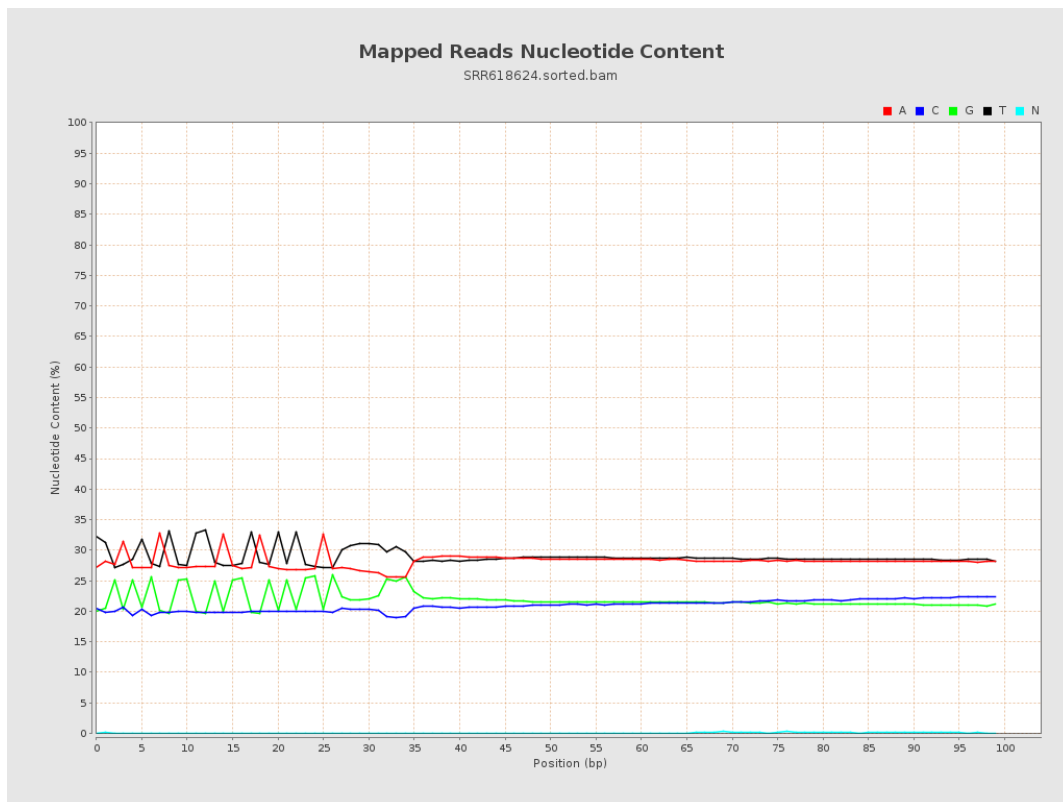
6. Results : Genome Fraction Coverage



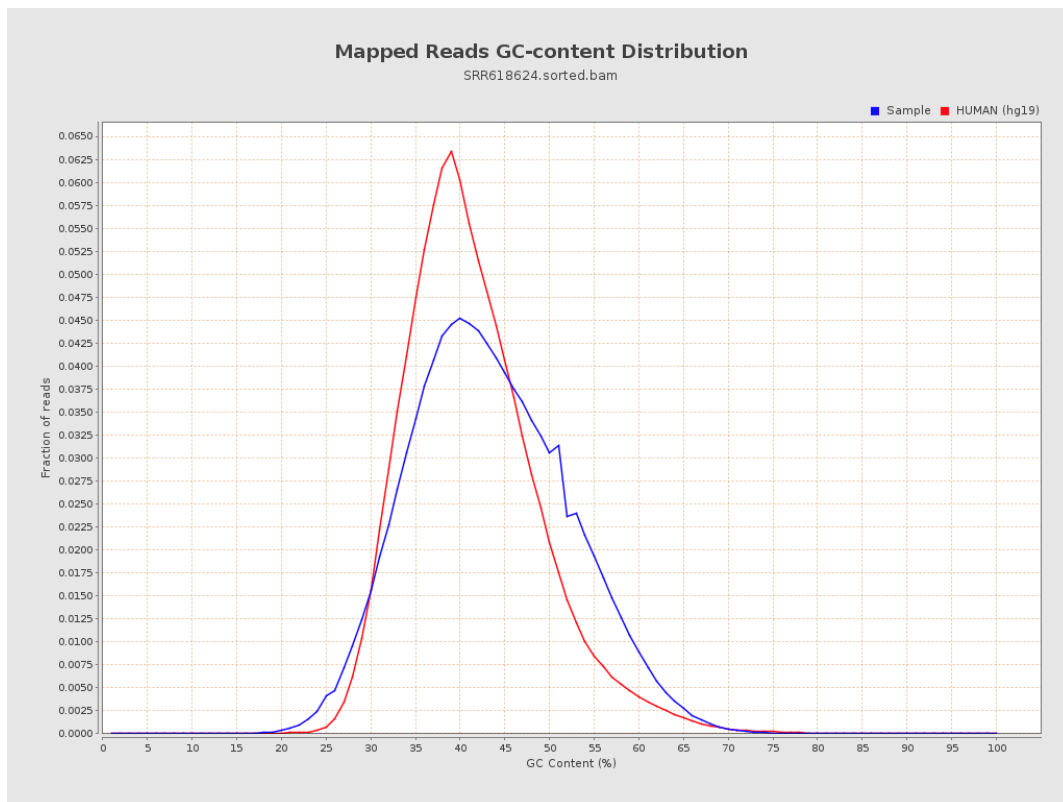
7. Results : Duplication Rate Histogram



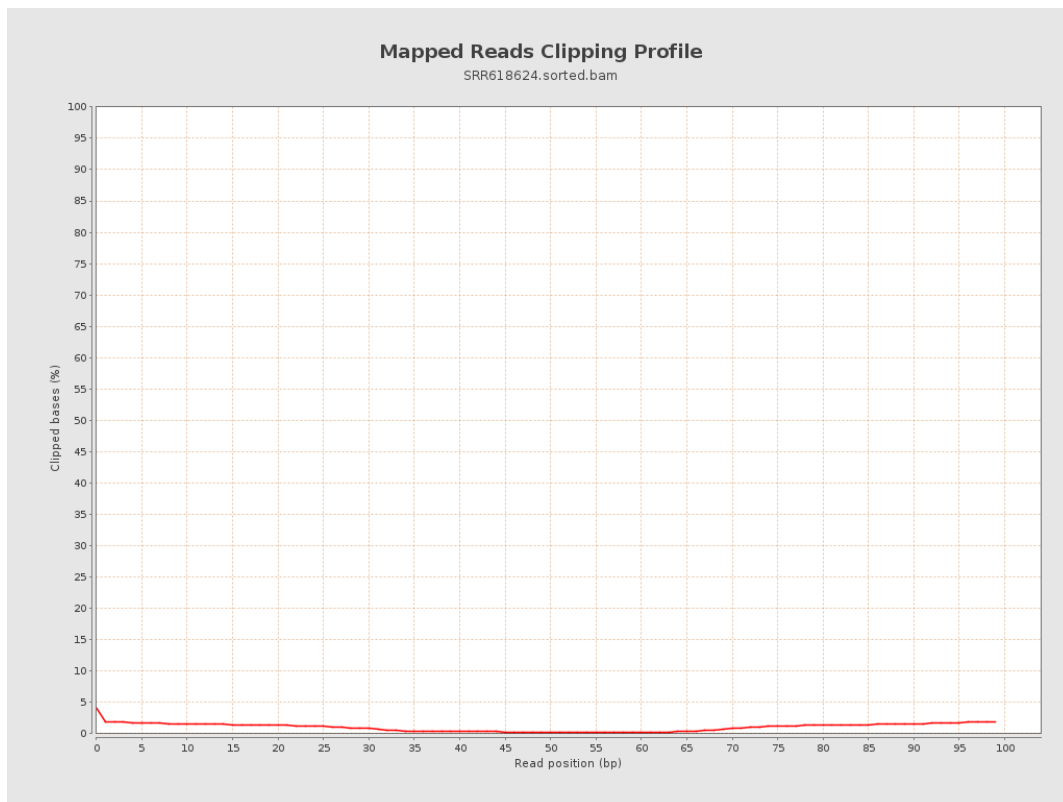
8. Results : Mapped Reads Nucleotide Content



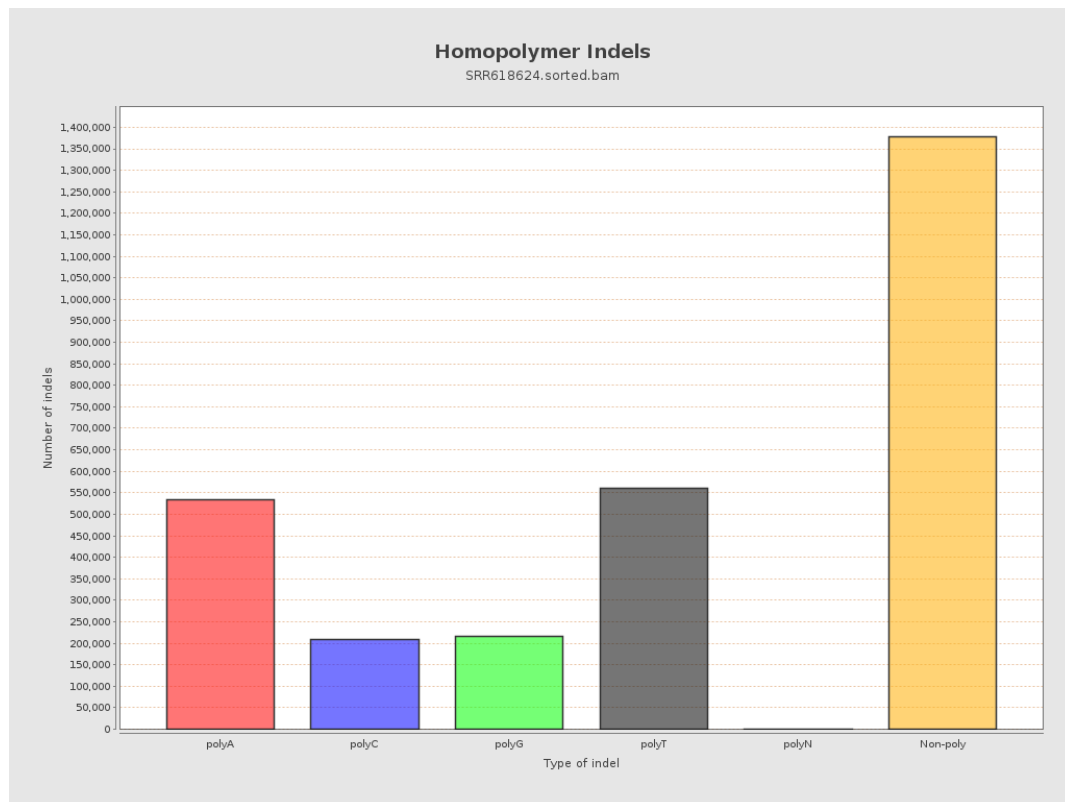
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



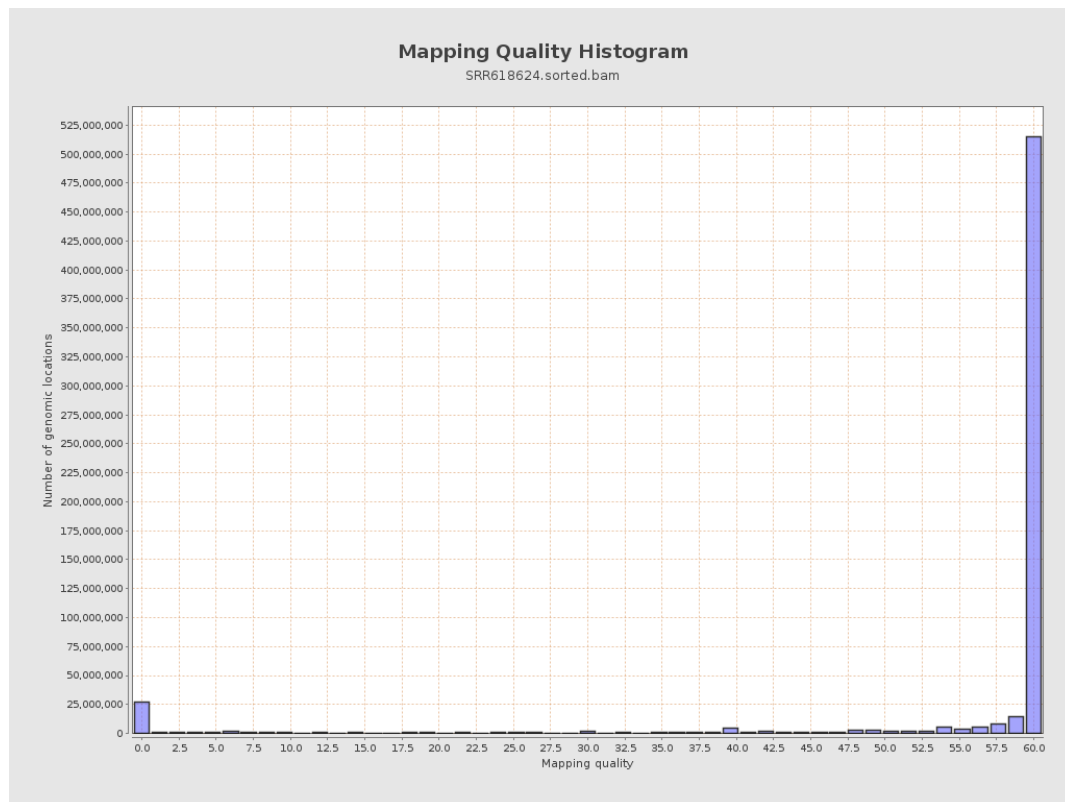
11. Results : Homopolymer Indels



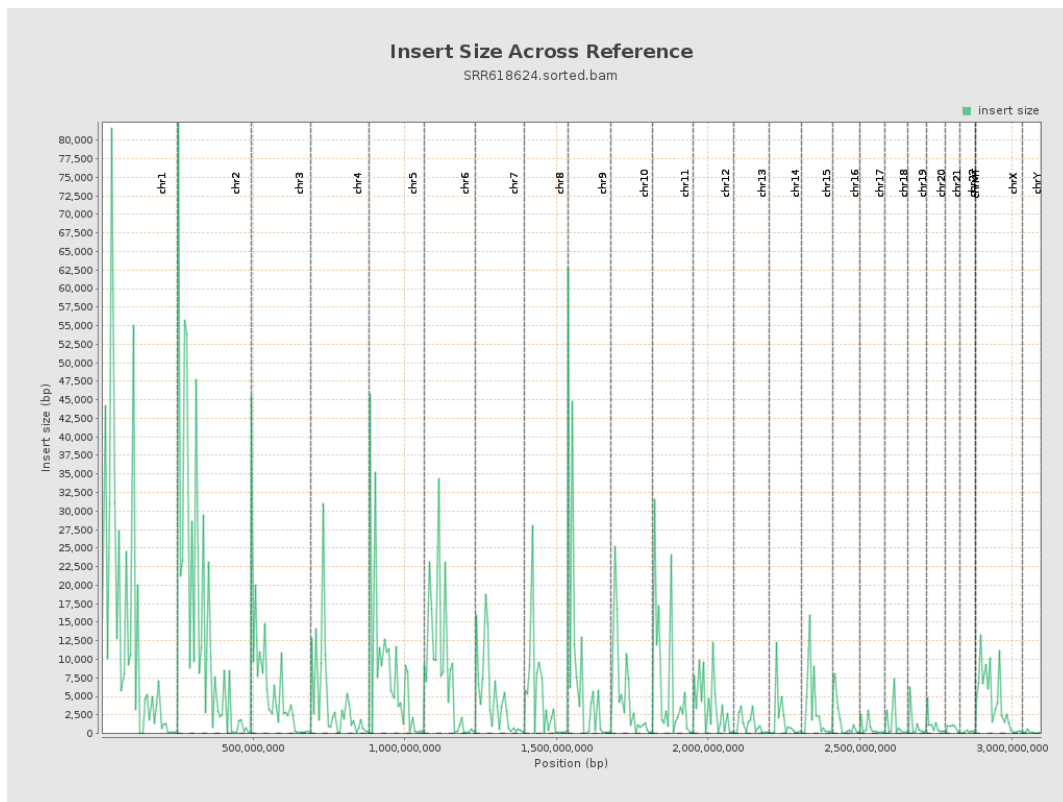
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

