

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 05:38:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618609.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_SRR618609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618609_1.fastq.gz SRR618609_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 05:38:10 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,431,120
Mapped reads	32,564,207 / 97.41%
Unmapped reads	866,913 / 2.59%
Mapped paired reads	32,564,207 / 97.41%
Mapped reads, first in pair	16,421,967 / 49.12%
Mapped reads, second in pair	16,142,240 / 48.29%
Mapped reads, both in pair	32,126,686 / 96.1%
Mapped reads, singletons	437,521 / 1.31%
Secondary alignments	0
Supplementary alignments	39,088 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	4,523,214 / 13.53%
Duplication rate	12.65%
Clipped reads	4,873,259 / 14.58%

2.2. ACGT Content

Number/percentage of A's	840,754,912 / 26.8%
Number/percentage of C's	710,069,134 / 22.64%
Number/percentage of T's	843,735,694 / 26.9%
Number/percentage of G's	741,874,389 / 23.65%
Number/percentage of N's	248,614 / 0.01%

GC Percentage	46.29%
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2.3. Coverage

Mean	1.0139
Standard Deviation	4.2016

2.4. Mapping Quality

Mean Mapping Quality	54.07
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2.5. Insert size

Mean	24,815.74
Standard Deviation	1,573,958.71
P25/Median/P75	177 / 207 / 247

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	35,884,684
Insertions	529,065
Mapped reads with at least one insertion	1.6%
Deletions	1,429,781
Mapped reads with at least one deletion	4.29%
Homopolymer indels	52.78%

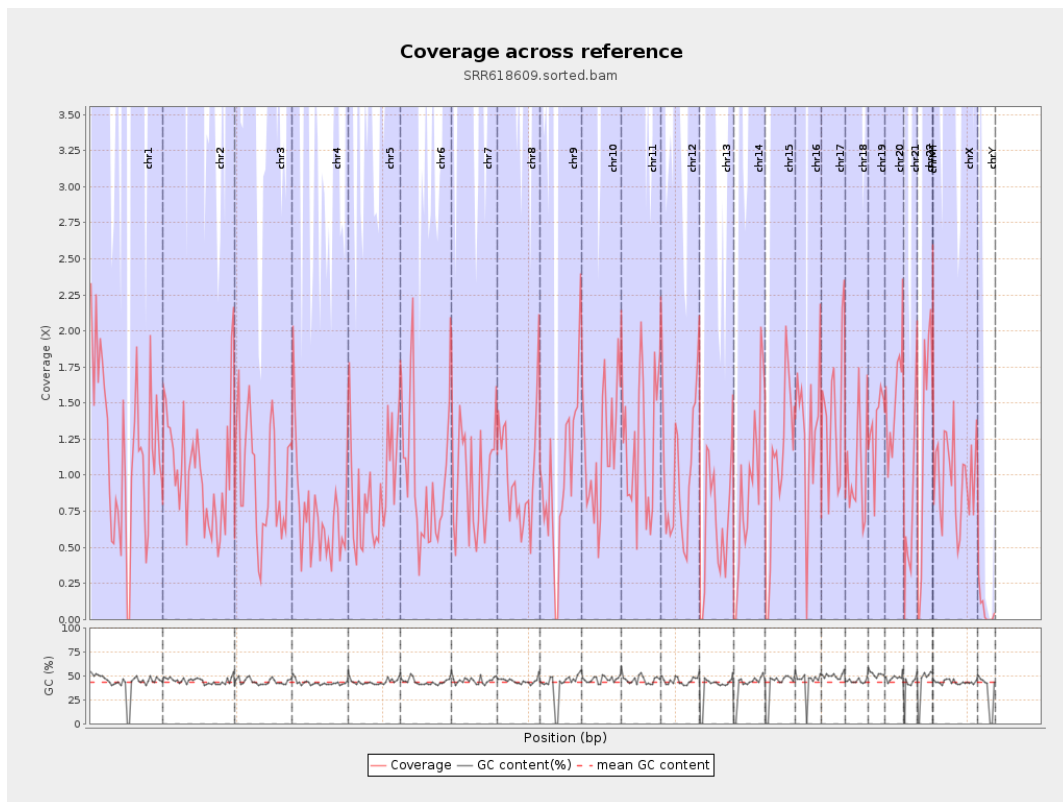
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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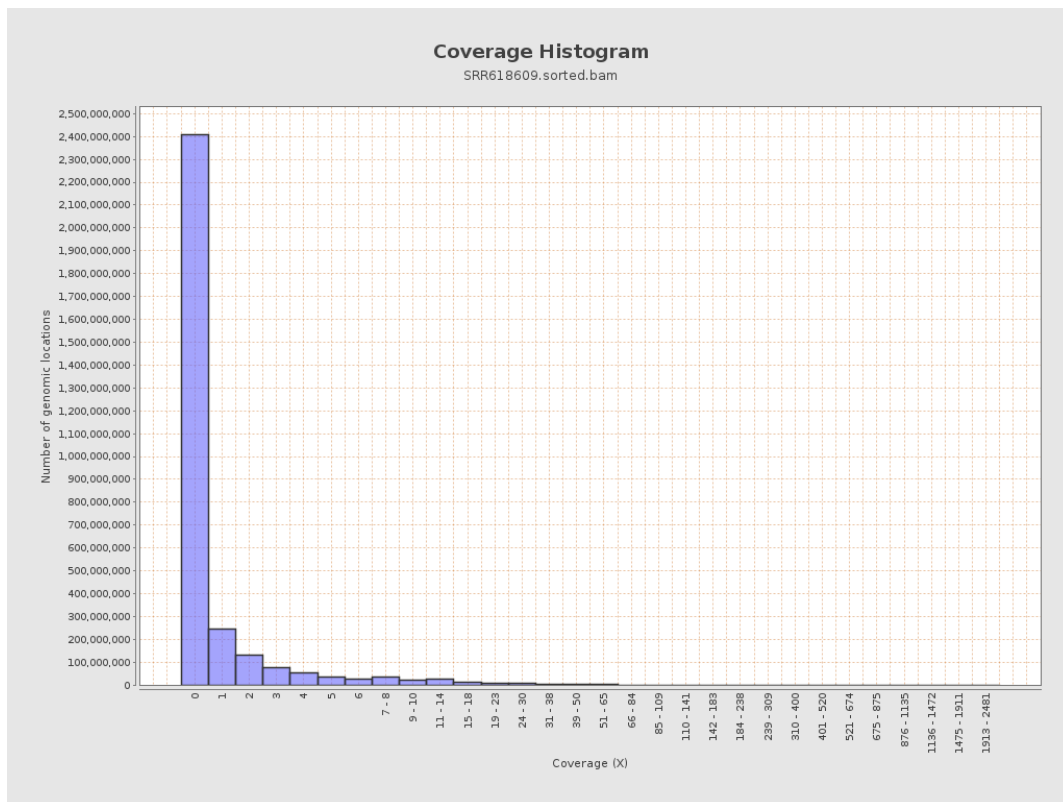
		bases	coverage	deviation
chr1	249250621	290759445	1.1665	5.1245
chr2	243199373	249706903	1.0268	4.2921
chr3	198022430	191429916	0.9667	3.5607
chr4	191154276	138835122	0.7263	3.3071
chr5	180915260	165283588	0.9136	3.4938
chr6	171115067	164092728	0.959	3.7606
chr7	159138663	156217771	0.9816	3.7
chr8	146364022	148010855	1.0113	3.7354
chr9	141213431	139456181	0.9876	4.5154
chr10	135534747	158866885	1.1721	4.2991
chr11	135006516	165303782	1.2244	4.7593
chr12	133851895	138562186	1.0352	3.8857
chr13	115169878	76320327	0.6627	2.7954
chr14	107349540	99295697	0.925	3.8547
chr15	102531392	108056992	1.0539	4.0822
chr16	90354753	119482638	1.3224	5.9324
chr17	81195210	116719287	1.4375	5.232
chr18	78077248	78528980	1.0058	4.4544
chr19	59128983	79382045	1.3425	5.3092
chr20	63025520	94921473	1.5061	5.0999
chr21	48129895	39467912	0.82	5.932
chr22	51304566	64332444	1.2539	5.096
chrMT	16571	43070	2.5991	3.1318
chrX	155270560	151646990	0.9767	3.4903

chrY	59373566	3919234	0.066	1.7332
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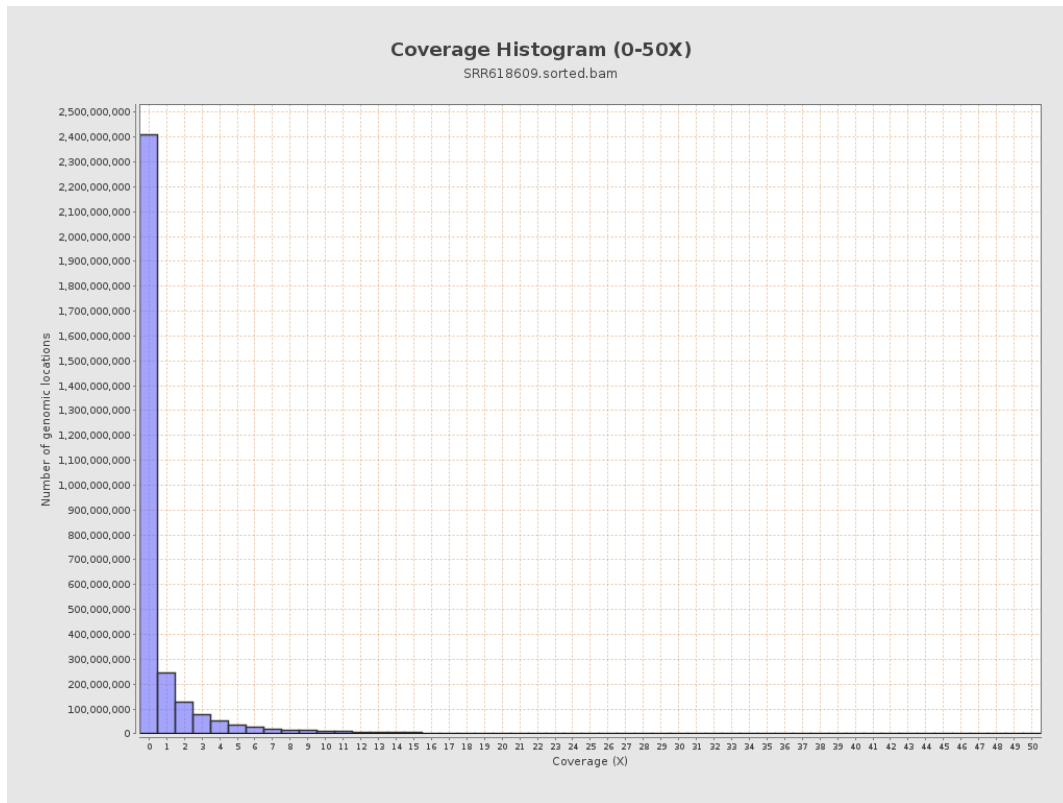
3. Results : Coverage across reference



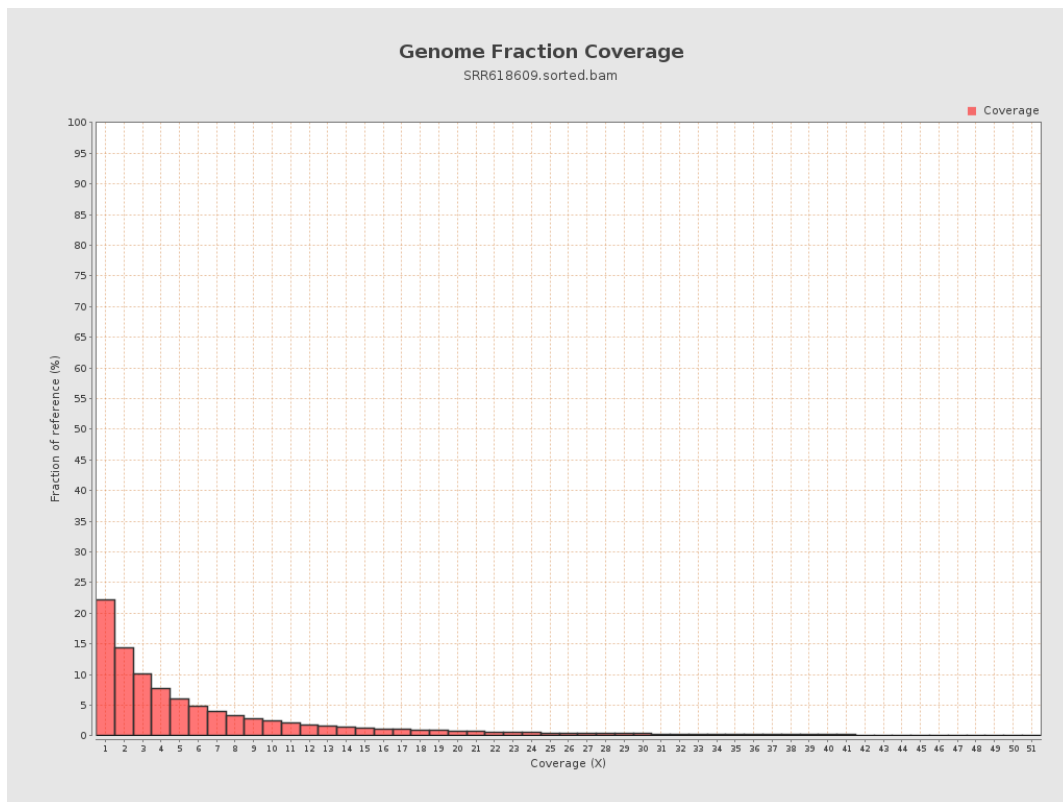
4. Results : Coverage Histogram



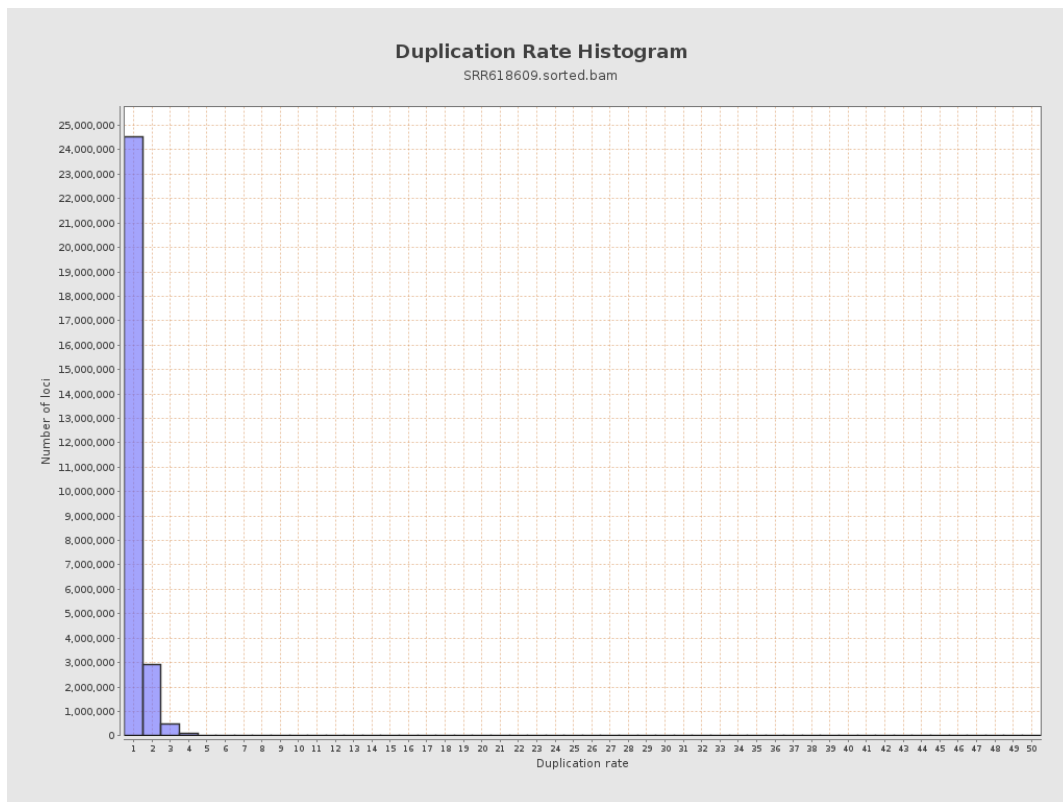
5. Results : Coverage Histogram (0-50X)



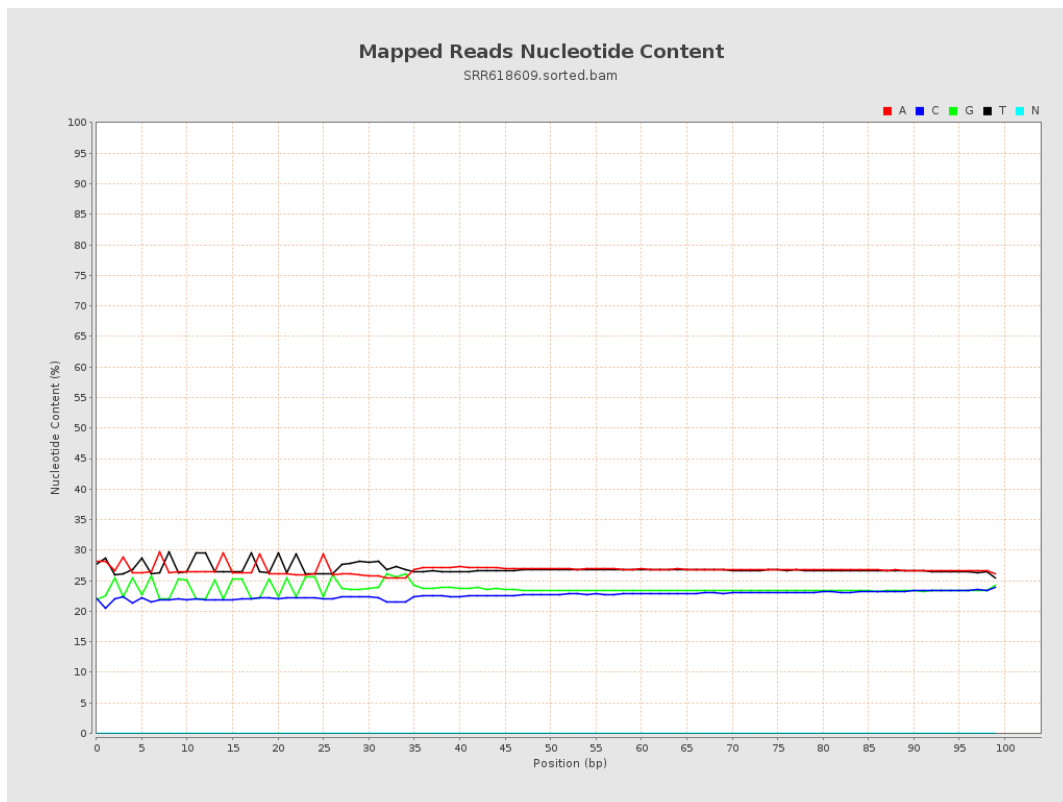
6. Results : Genome Fraction Coverage



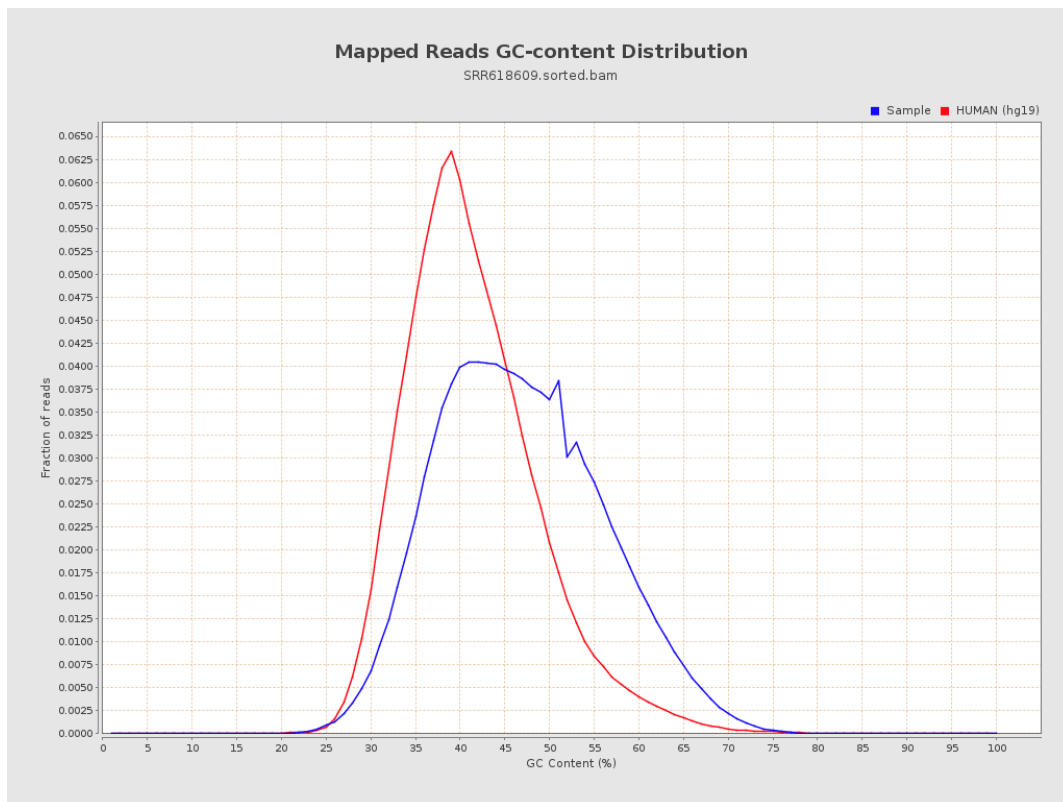
7. Results : Duplication Rate Histogram



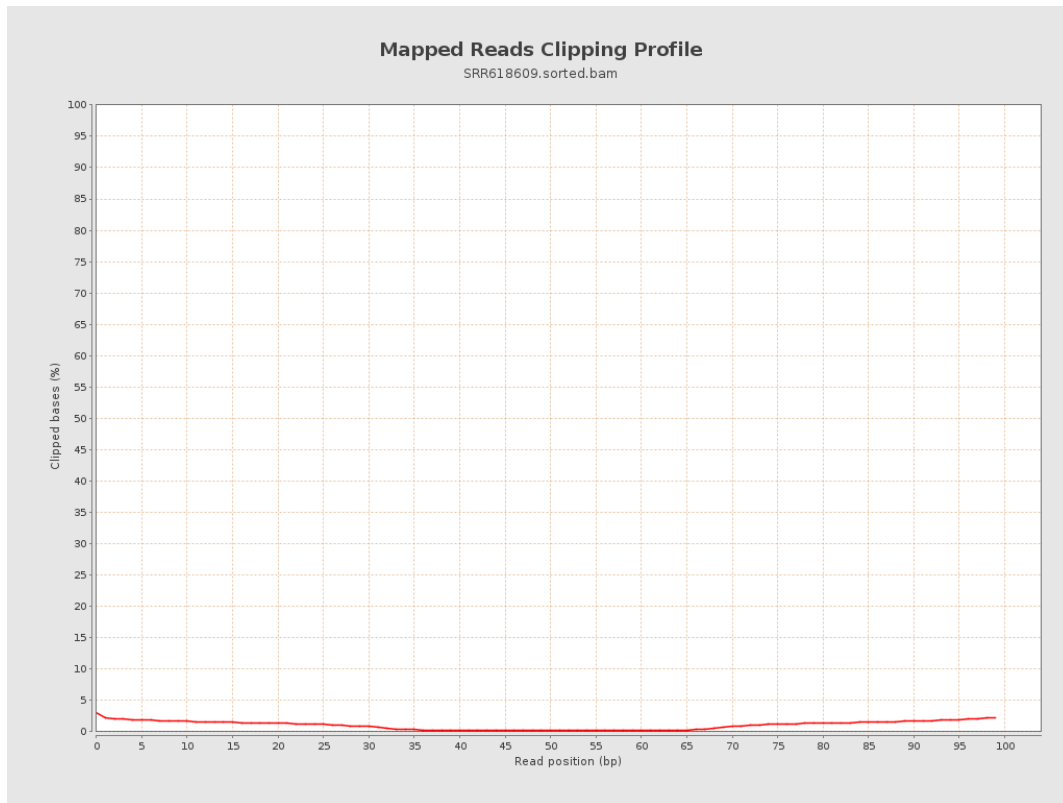
8. Results : Mapped Reads Nucleotide Content



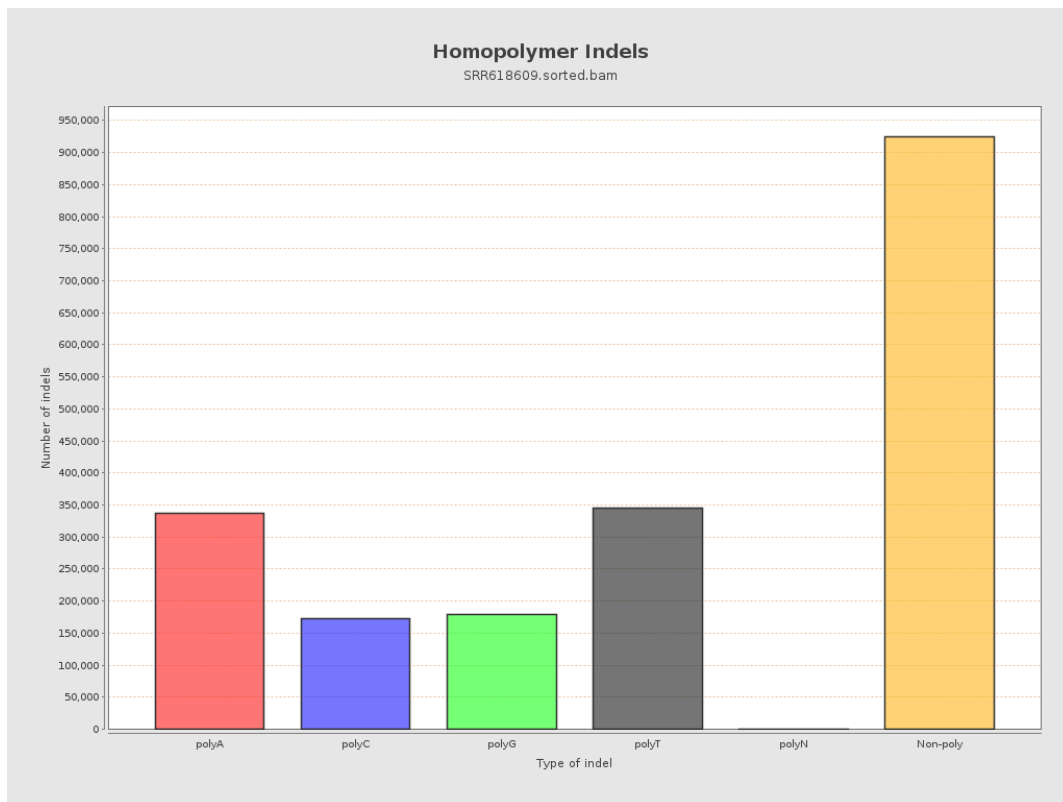
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



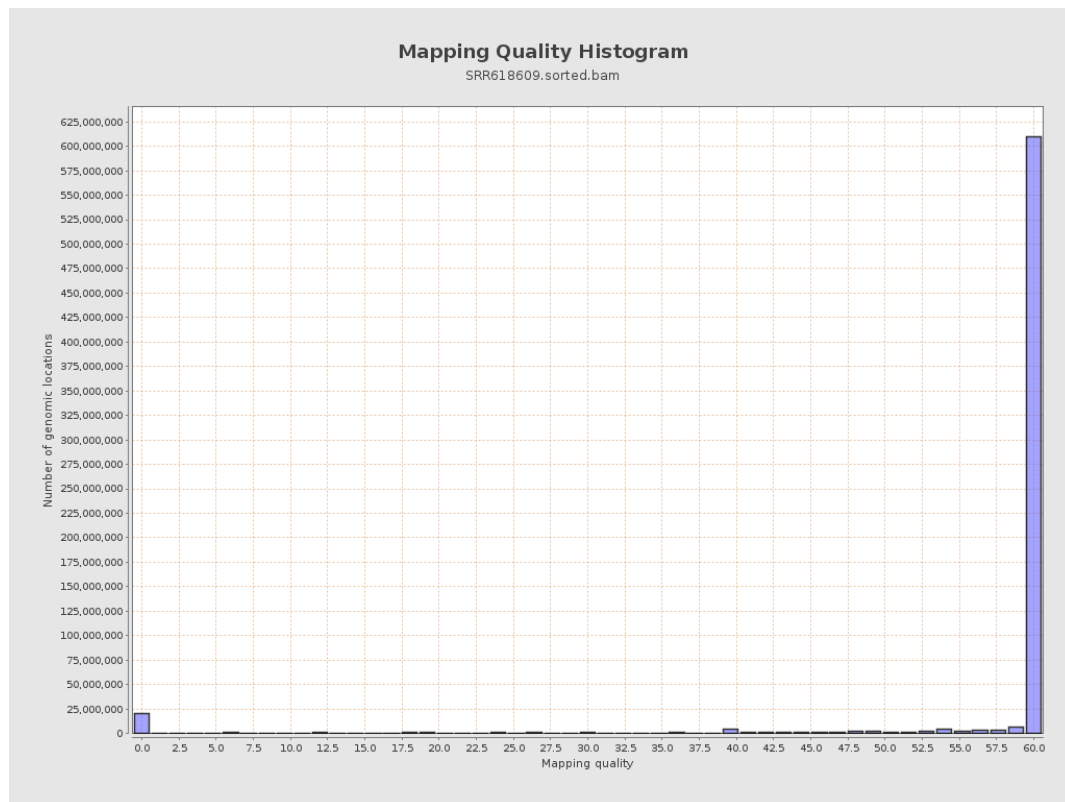
11. Results : Homopolymer Indels



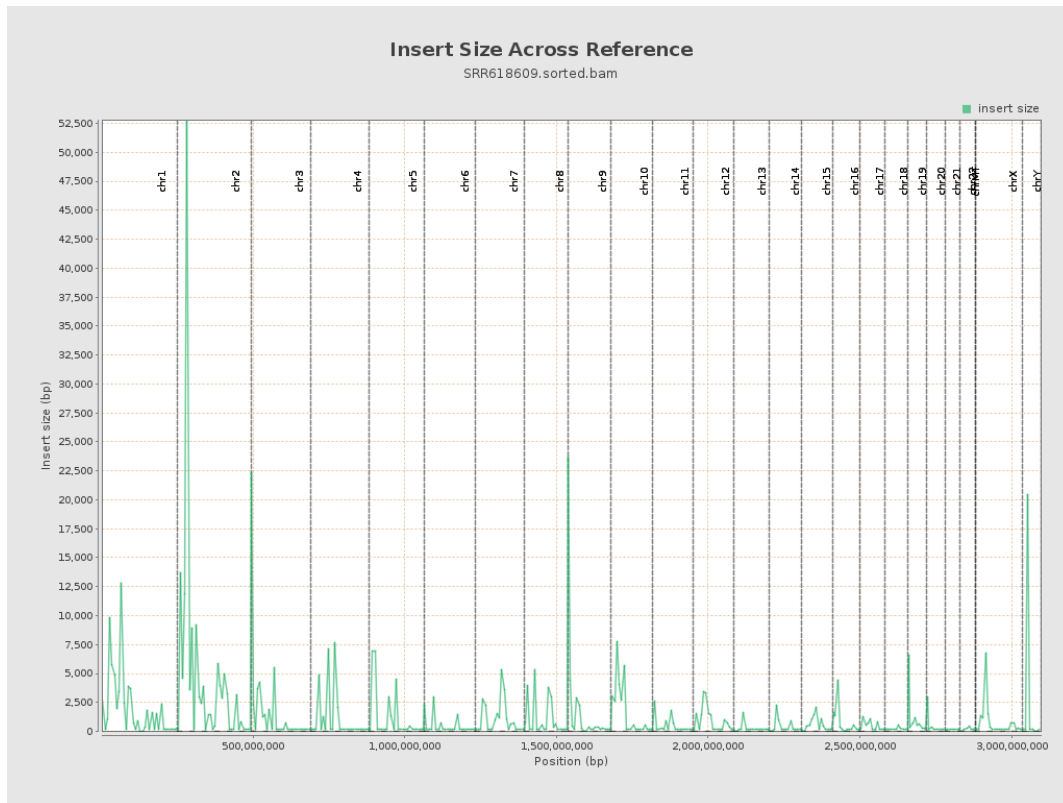
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

