

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 22:19:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618574.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_SRR618574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618574_1.fastq.gz SRR618574_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 22:19:01 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,468,992
Mapped reads	62,739,404 / 94.39%
Unmapped reads	3,729,588 / 5.61%
Mapped paired reads	62,739,404 / 94.39%
Mapped reads, first in pair	31,688,263 / 47.67%
Mapped reads, second in pair	31,051,141 / 46.72%
Mapped reads, both in pair	61,528,524 / 92.57%
Mapped reads, singletons	1,210,880 / 1.82%
Secondary alignments	0
Supplementary alignments	66,177 / 0.1%
Read min/max/mean length	30 / 100 / 100.04
Duplicated reads (estimated)	11,869,303 / 17.86%
Duplication rate	16.66%
Clipped reads	10,945,882 / 16.47%

2.2. ACGT Content

Number/percentage of A's	1,607,461,619 / 26.8%
Number/percentage of C's	1,365,302,059 / 22.76%
Number/percentage of T's	1,612,546,384 / 26.88%
Number/percentage of G's	1,413,246,622 / 23.56%
Number/percentage of N's	270,106 / 0%

GC Percentage	46.32%
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2.3. Coverage

Mean	1.939
Standard Deviation	8.0718

2.4. Mapping Quality

Mean Mapping Quality	52.64
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2.5. Insert size

Mean	22,326.92
Standard Deviation	1,486,796.8
P25/Median/P75	180 / 209 / 246

2.6. Mismatches and indels

General error rate	1.33%
Mismatches	78,377,825
Insertions	1,048,565
Mapped reads with at least one insertion	1.65%
Deletions	2,751,649
Mapped reads with at least one deletion	4.28%
Homopolymer indels	52.32%

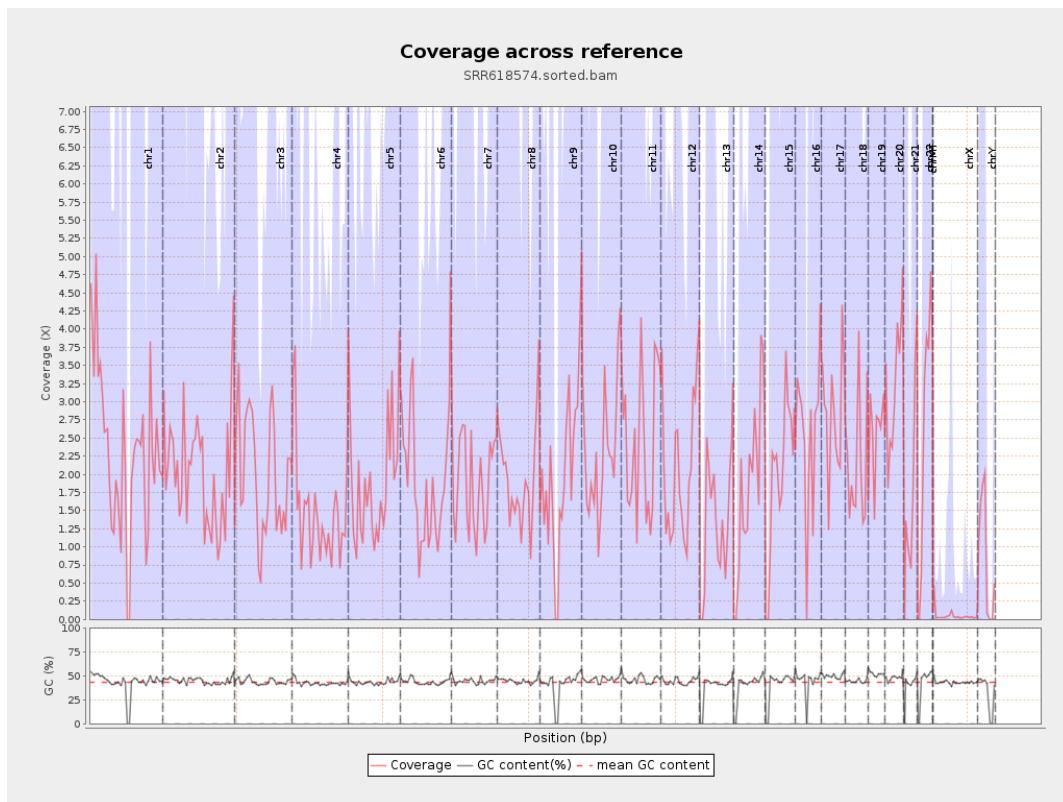
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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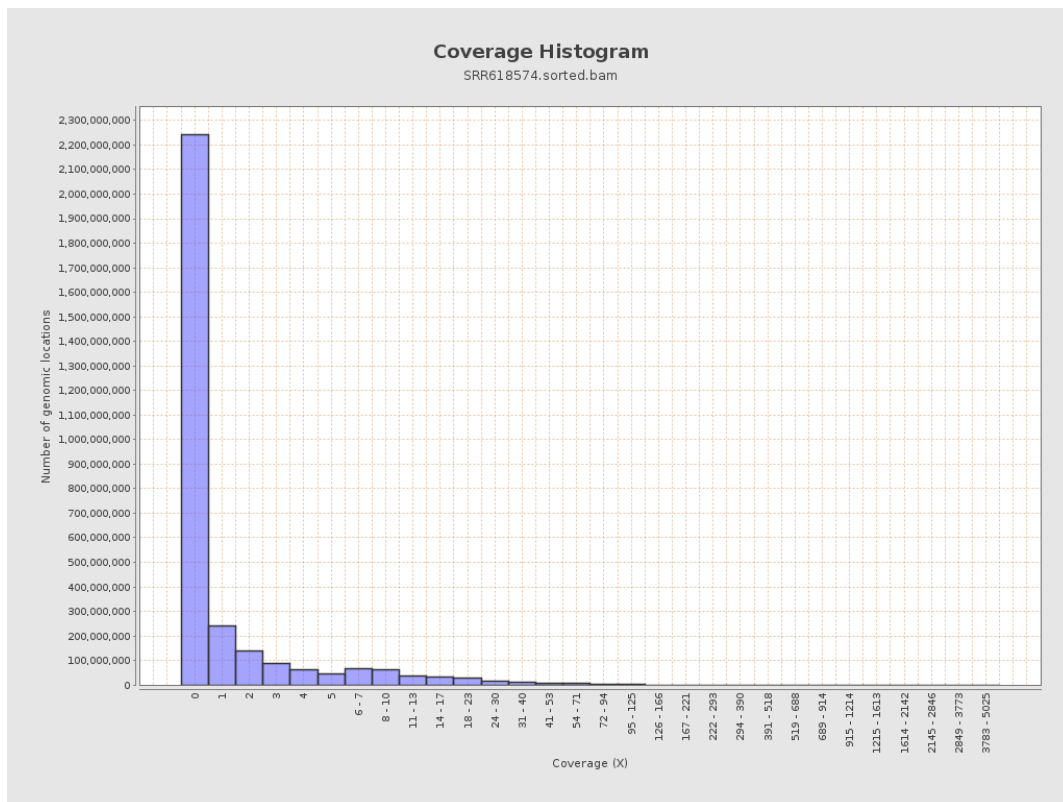
		bases	coverage	deviation
chr1	249250621	570721080	2.2897	9.8422
chr2	243199373	492915724	2.0268	8.3282
chr3	198022430	394557298	1.9925	7.0936
chr4	191154276	279476882	1.462	6.8143
chr5	180915260	345999628	1.9125	6.6961
chr6	171115067	322108664	1.8824	6.9572
chr7	159138663	303478037	1.907	7.1246
chr8	146364022	282608290	1.9309	7.1463
chr9	141213431	278221171	1.9702	8.776
chr10	135534747	310630483	2.2919	8.3253
chr11	135006516	330069302	2.4448	9.2611
chr12	133851895	280697993	2.0971	7.4317
chr13	115169878	154608345	1.3424	5.5455
chr14	107349540	198665572	1.8506	7.4123
chr15	102531392	202311006	1.9732	7.6078
chr16	90354753	230042772	2.546	11.4837
chr17	81195210	228720493	2.8169	9.9298
chr18	78077248	161101156	2.0634	8.6912
chr19	59128983	152678765	2.5821	9.8983
chr20	63025520	201832821	3.2024	10.1167
chr21	48129895	86102127	1.789	13.699
chr22	51304566	133866437	2.6092	9.9043
chrMT	16571	1681	0.1014	0.4697
chrX	155270560	8379732	0.054	1.5287

chrY	59373566	52820407	0.8896	5.4357
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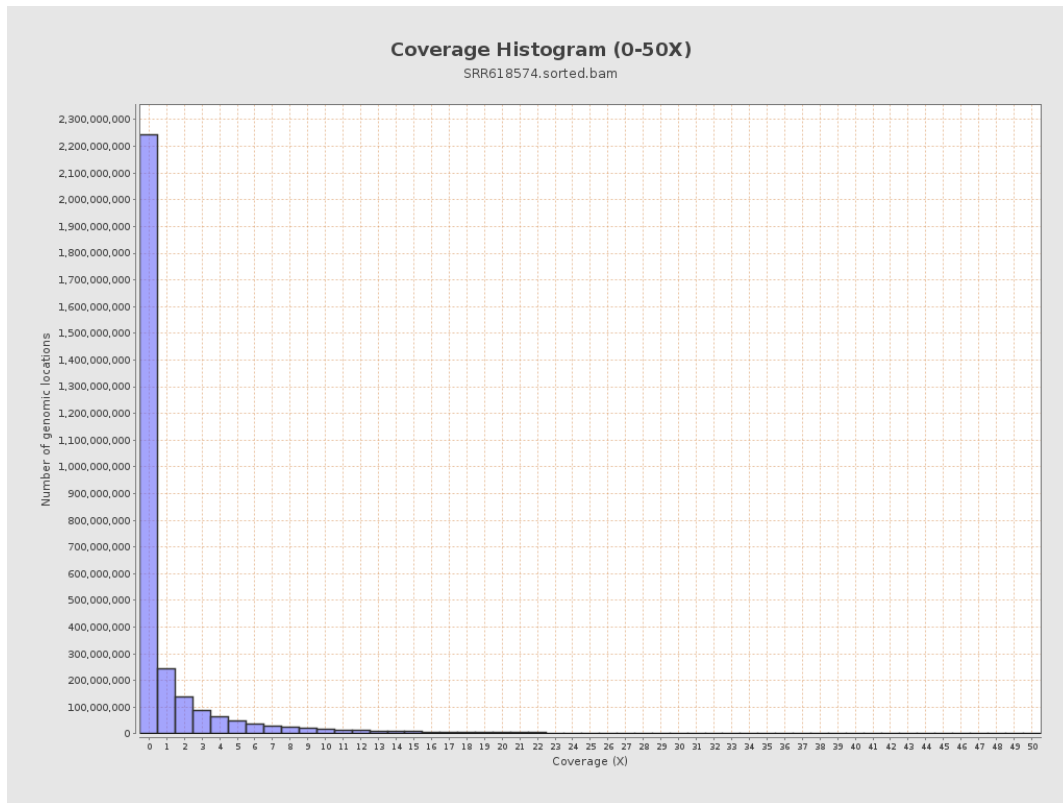
3. Results : Coverage across reference



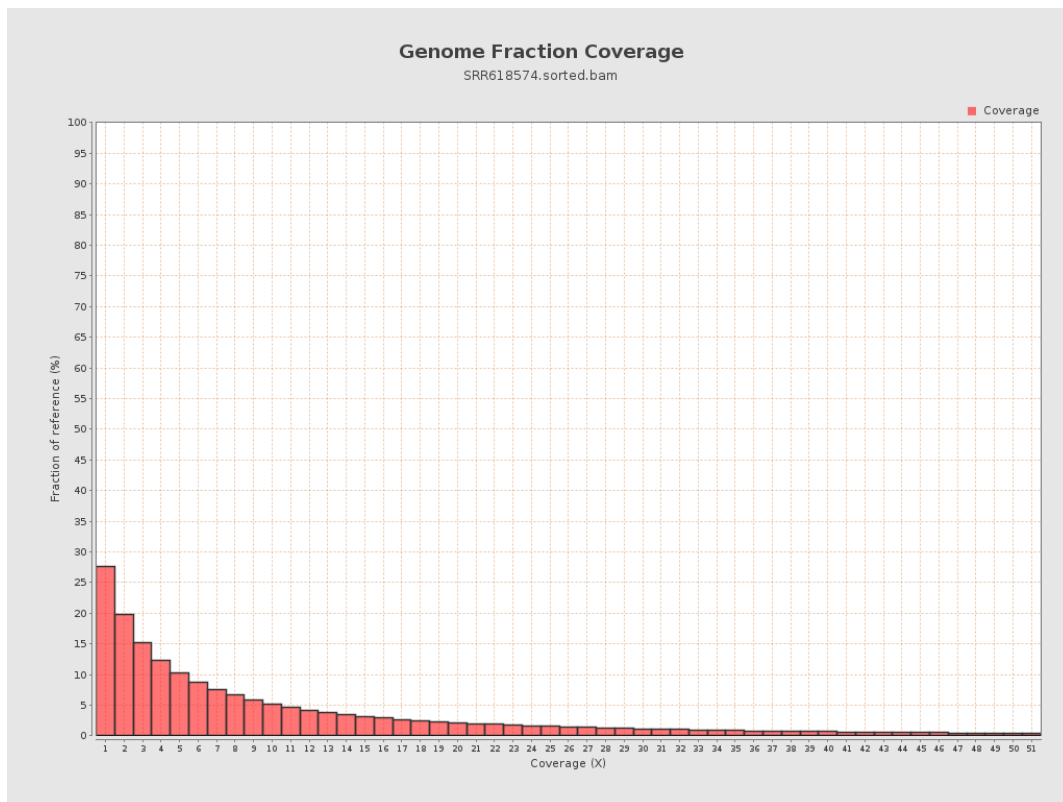
4. Results : Coverage Histogram



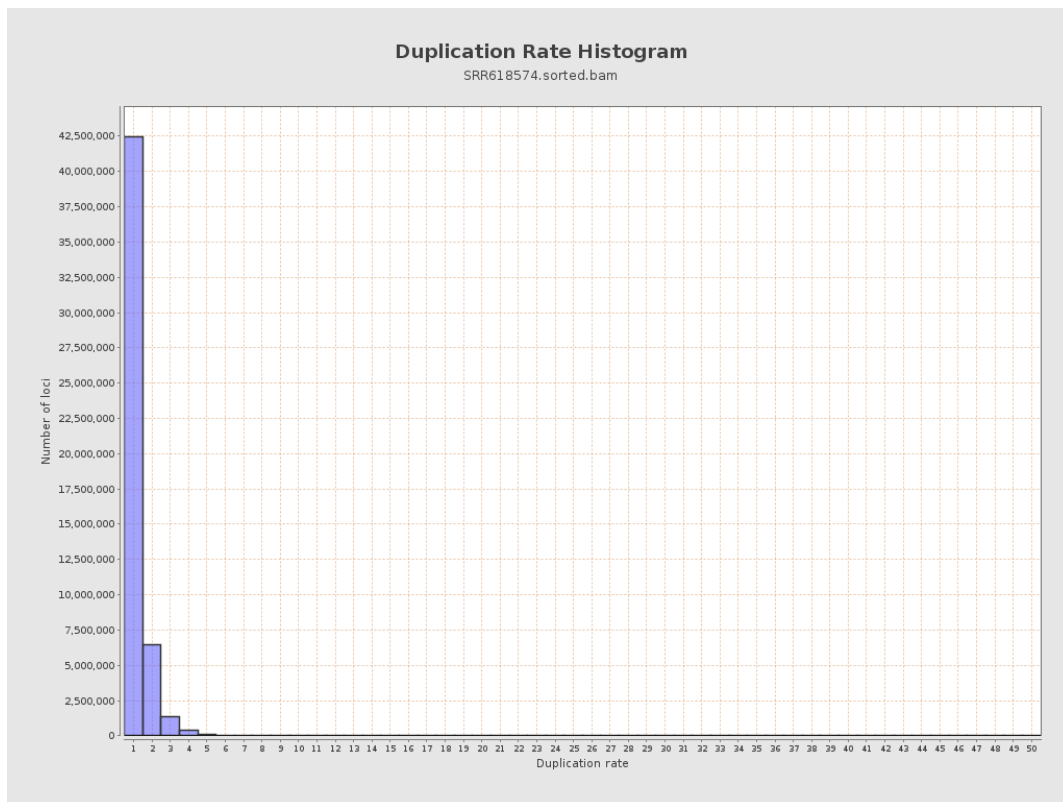
5. Results : Coverage Histogram (0-50X)



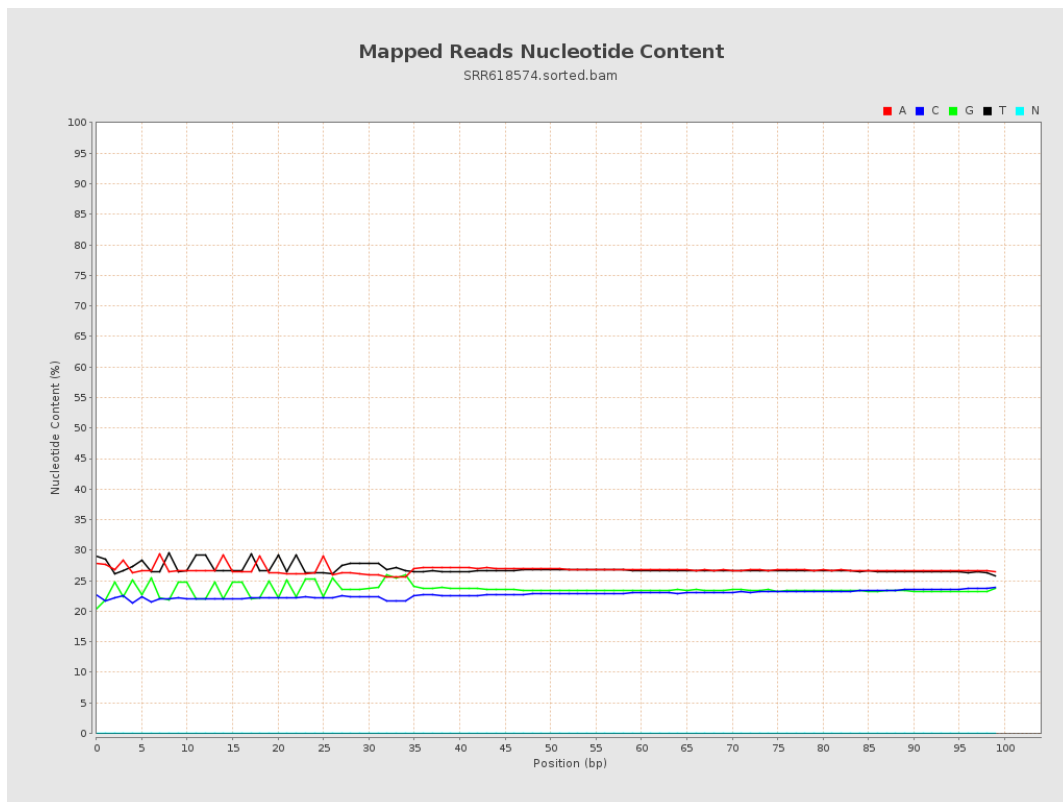
6. Results : Genome Fraction Coverage



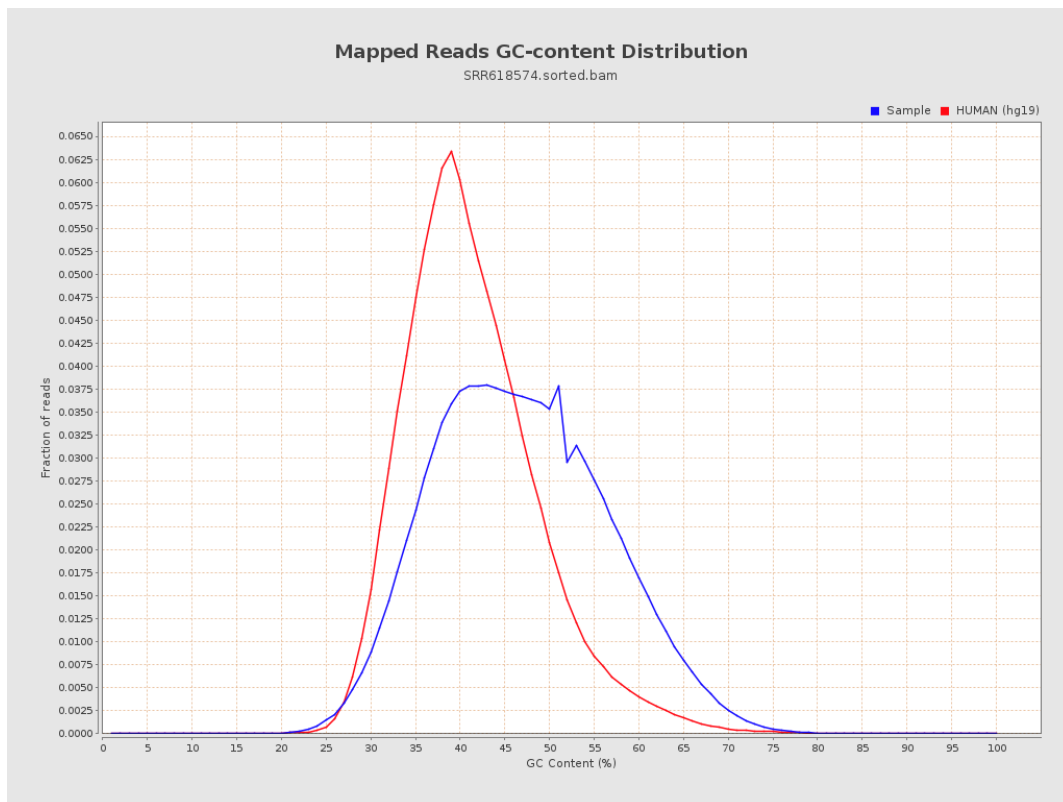
7. Results : Duplication Rate Histogram



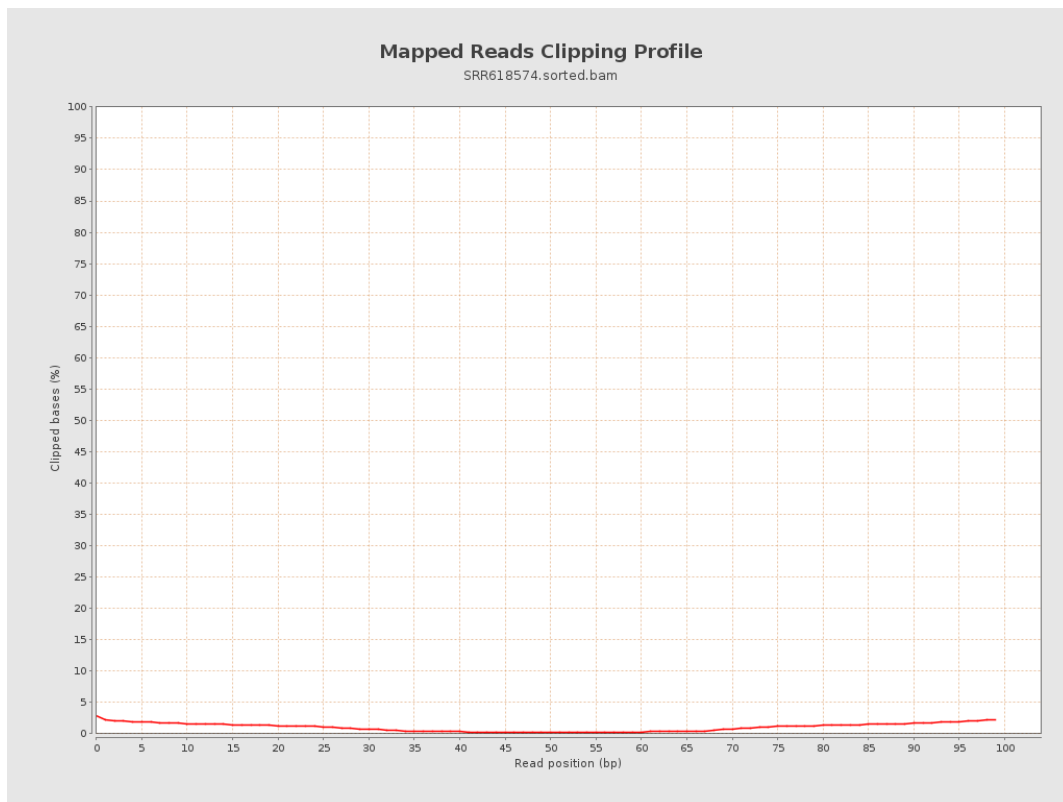
8. Results : Mapped Reads Nucleotide Content



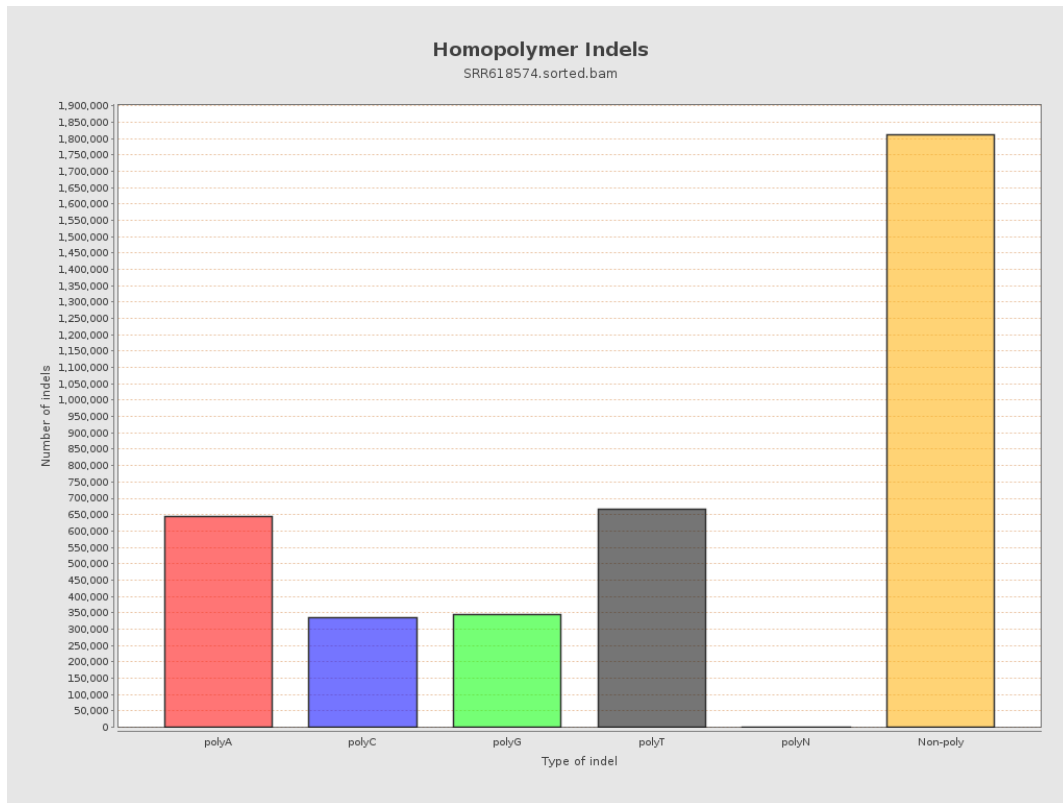
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



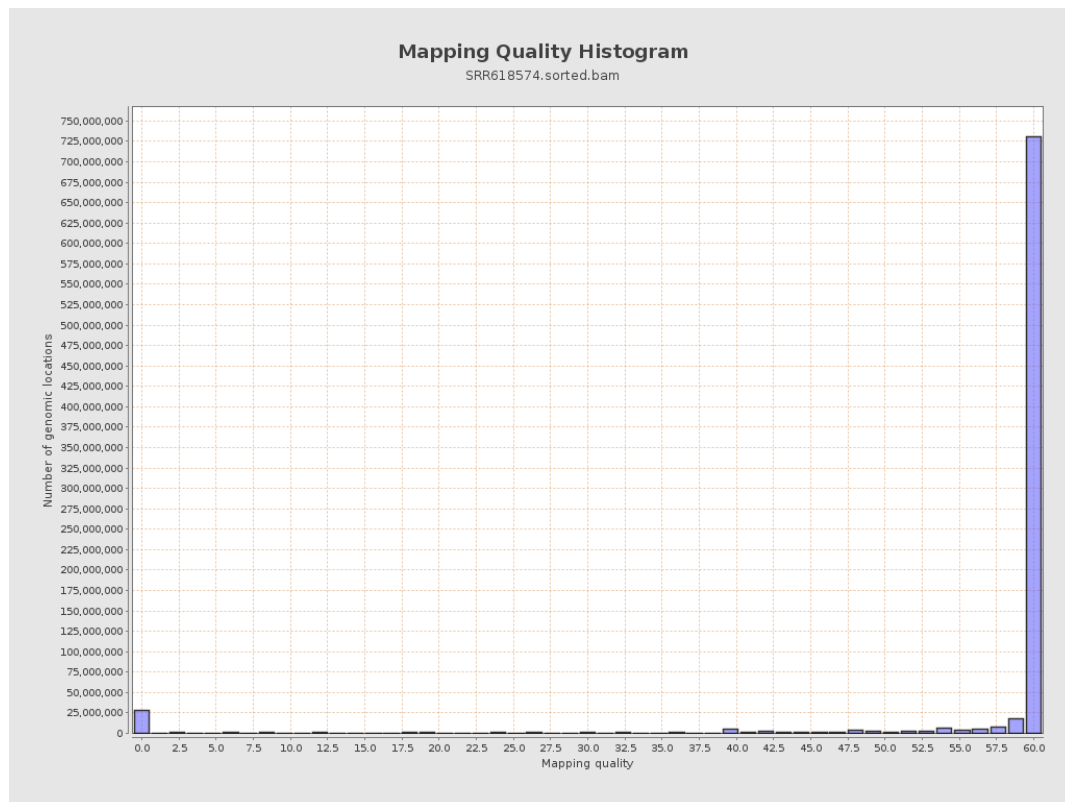
11. Results : Homopolymer Indels



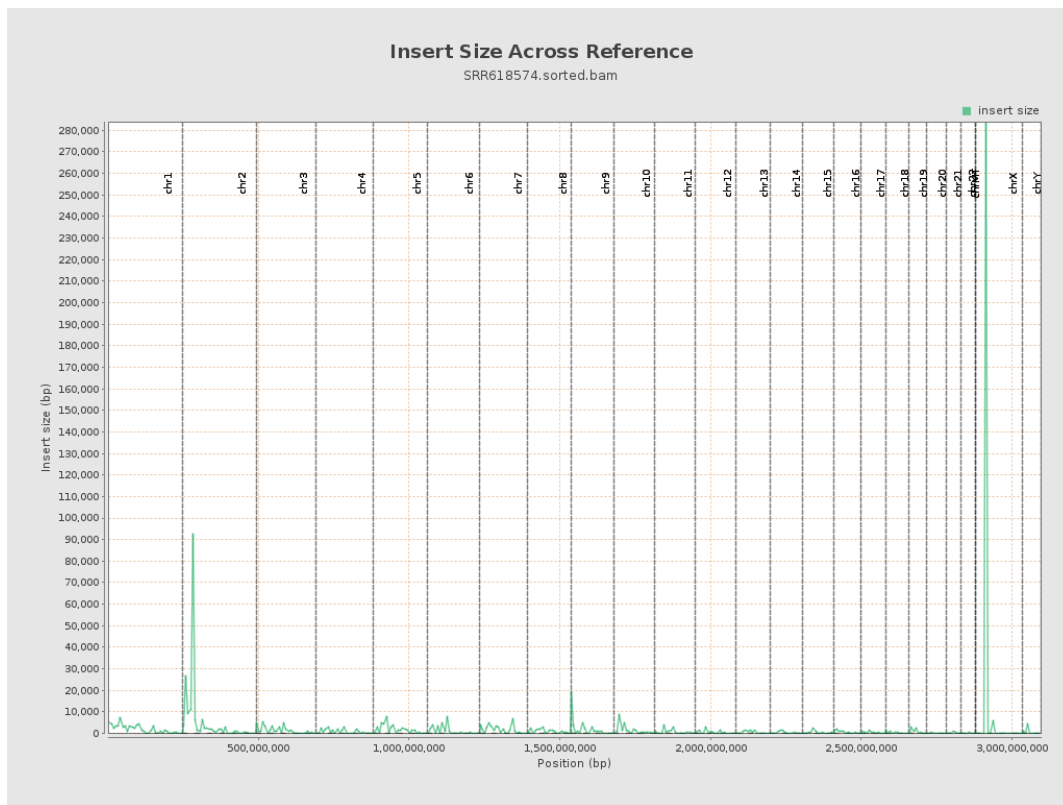
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

