

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/16 19:38:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618565.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_SRR618565 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618565_1.fastq.gz SRR618565_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 16 19:38:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618565.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	268,487,462
Mapped reads	257,388,436 / 95.87%
Unmapped reads	11,099,026 / 4.13%
Mapped paired reads	257,388,436 / 95.87%
Mapped reads, first in pair	129,449,019 / 48.21%
Mapped reads, second in pair	127,939,417 / 47.65%
Mapped reads, both in pair	253,641,308 / 94.47%
Mapped reads, singletons	3,747,128 / 1.4%
Secondary alignments	0
Supplementary alignments	2,930,541 / 1.09%
Read min/max/mean length	30 / 100 / 100.45
Duplicated reads (estimated)	100,734,606 / 37.52%
Duplication rate	31.7%
Clipped reads	65,444,517 / 24.38%

2.2. ACGT Content

Number/percentage of A's	6,444,031,698 / 26.66%
Number/percentage of C's	5,398,181,770 / 22.33%
Number/percentage of T's	6,499,078,322 / 26.89%
Number/percentage of G's	5,829,621,032 / 24.12%
Number/percentage of N's	1,612,006 / 0.01%

GC Percentage	46.45%
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2.3. Coverage

Mean	7.8137
Standard Deviation	28.995

2.4. Mapping Quality

Mean Mapping Quality	52.33
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2.5. Insert size

Mean	141,209.44
Standard Deviation	3,760,694.05
P25/Median/P75	169 / 188 / 212

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	331,110,282
Insertions	4,069,178
Mapped reads with at least one insertion	1.56%
Deletions	11,868,053
Mapped reads with at least one deletion	4.5%
Homopolymer indels	51.97%

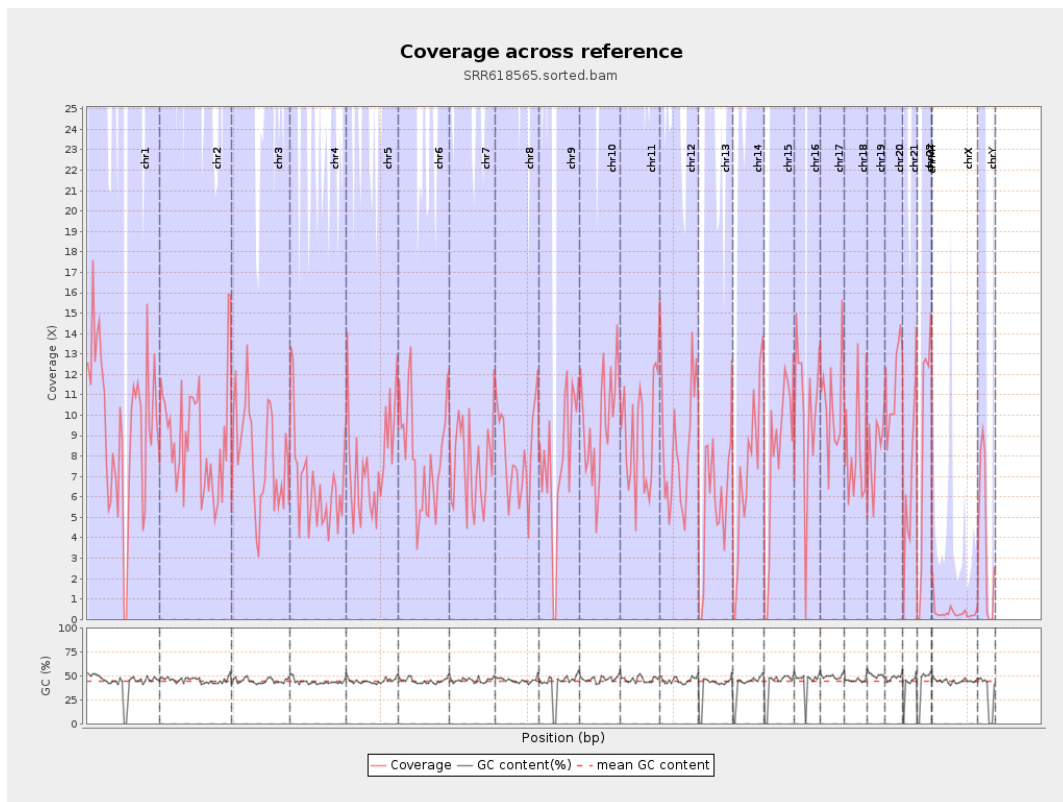
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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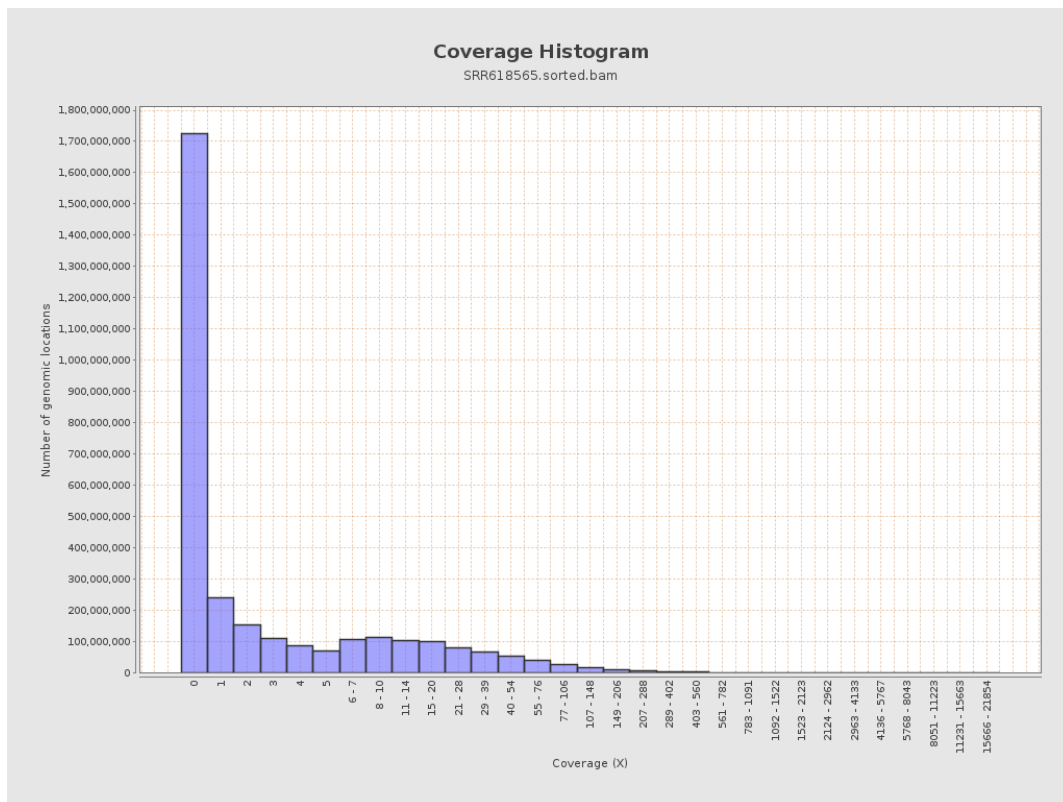
		bases	coverage	deviation
chr1	249250621	2338210978	9.381	37.3209
chr2	243199373	2149176920	8.8371	32.8102
chr3	198022430	1591390465	8.0364	23.7417
chr4	191154276	1250009052	6.5393	25.3227
chr5	180915260	1401634993	7.7475	23.7239
chr6	171115067	1363431026	7.9679	24.6007
chr7	159138663	1212811145	7.6211	23.9742
chr8	146364022	1187399518	8.1126	24.631
chr9	141213431	1101862938	7.8028	31.3364
chr10	135534747	1307311765	9.6456	29.2356
chr11	135006516	1215464529	9.003	32.3478
chr12	133851895	1130077872	8.4427	25.3361
chr13	115169878	650568162	5.6488	18.6561
chr14	107349540	776955317	7.2376	25.8597
chr15	102531392	816989066	7.9682	26.3883
chr16	90354753	907816184	10.0472	45.5956
chr17	81195210	845549452	10.4138	32.8397
chr18	78077248	644829926	8.2589	32.5769
chr19	59128983	488159750	8.2558	30.9202
chr20	63025520	725426446	11.51	34.4403
chr21	48129895	333100738	6.9209	46.5238
chr22	51304566	452611301	8.822	32.6304
chrMT	16571	30159	1.82	6.4422
chrX	155270560	51501813	0.3317	5.7756

chrY	59373566	246613650	4.1536	26.3798
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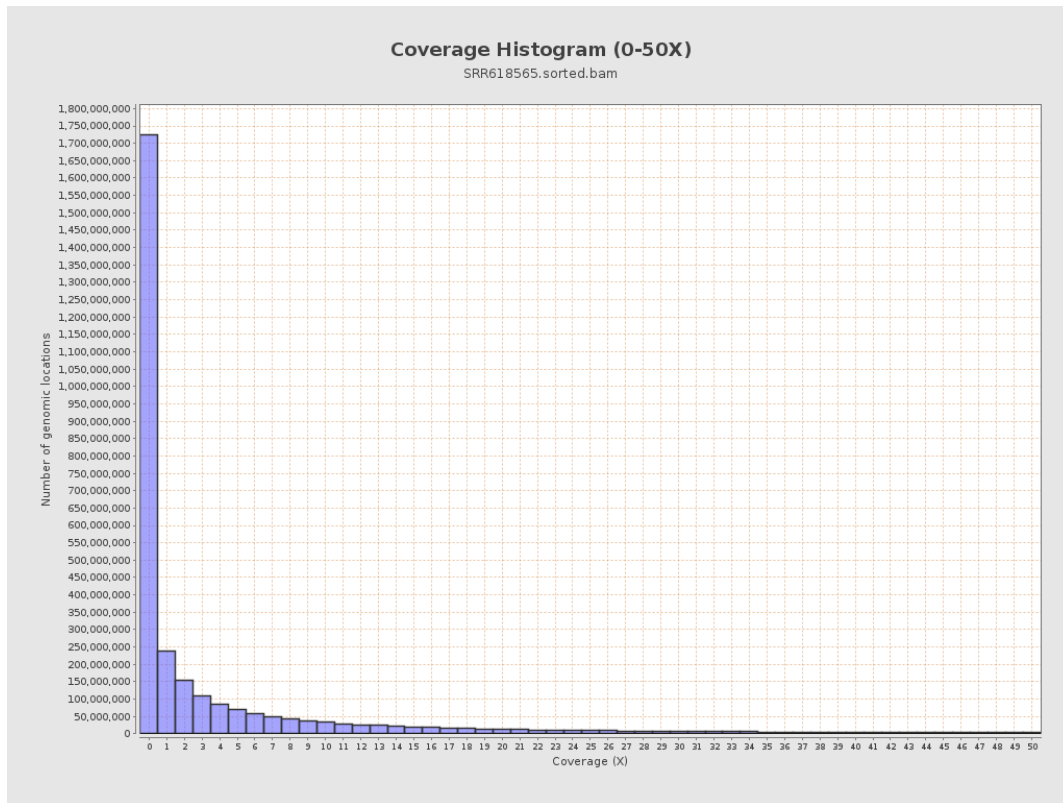
3. Results : Coverage across reference



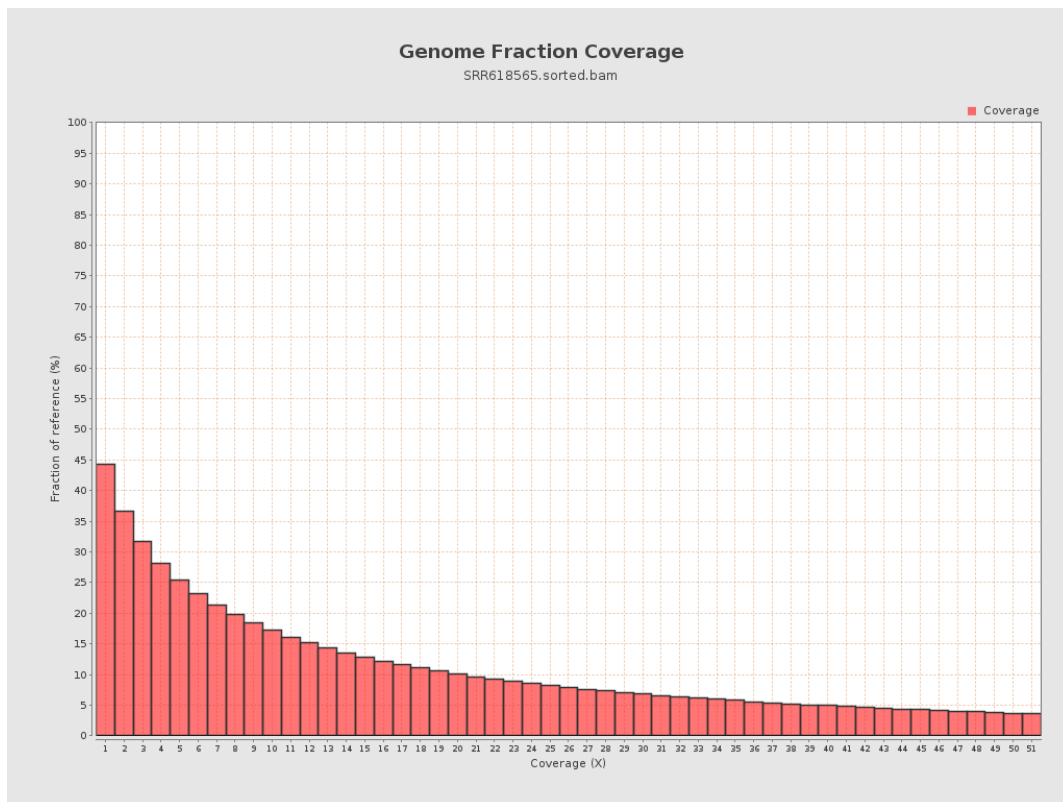
4. Results : Coverage Histogram



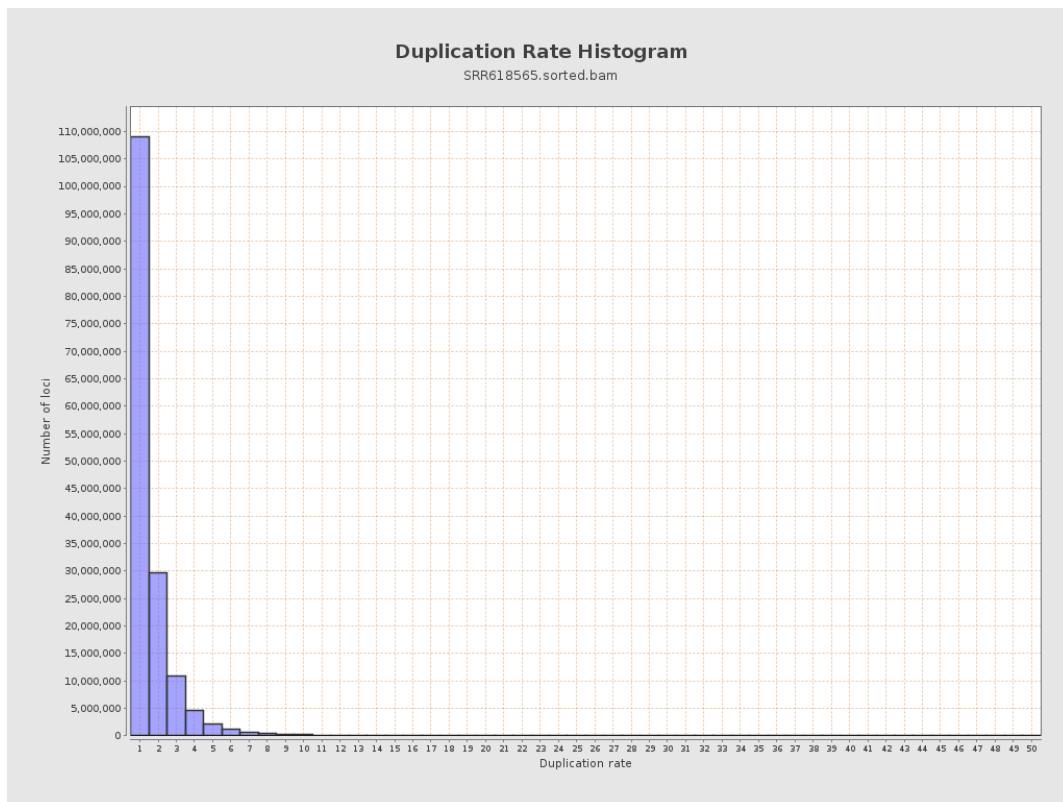
5. Results : Coverage Histogram (0-50X)



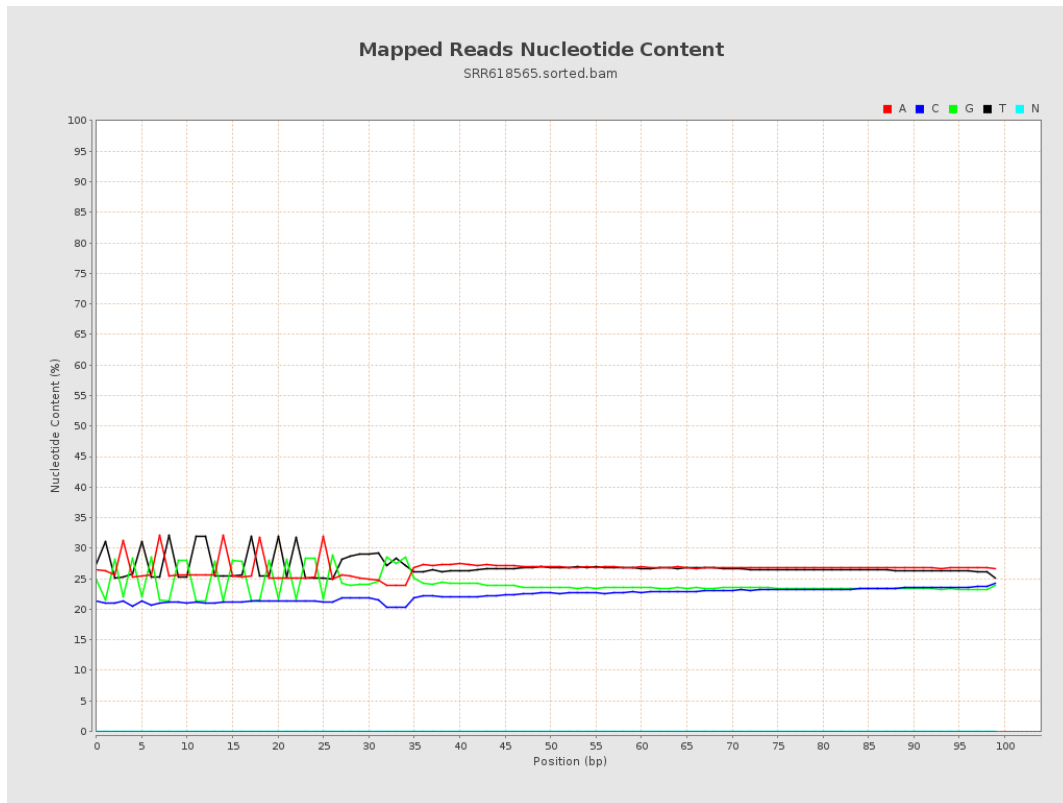
6. Results : Genome Fraction Coverage



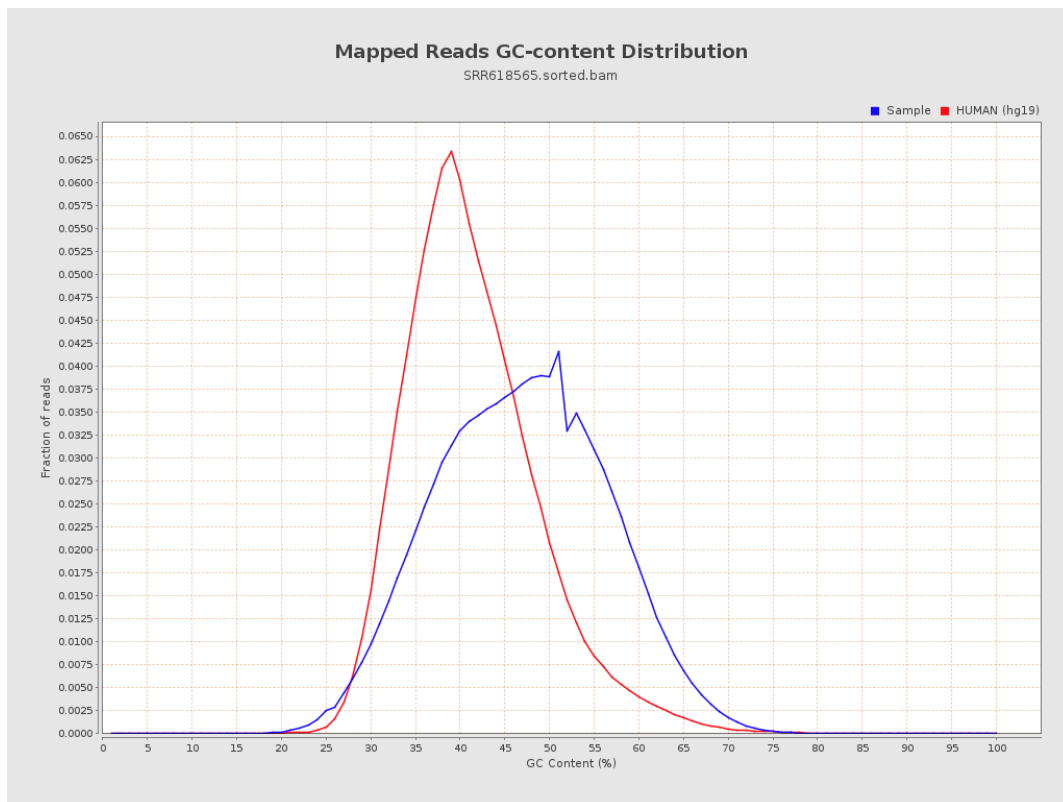
7. Results : Duplication Rate Histogram



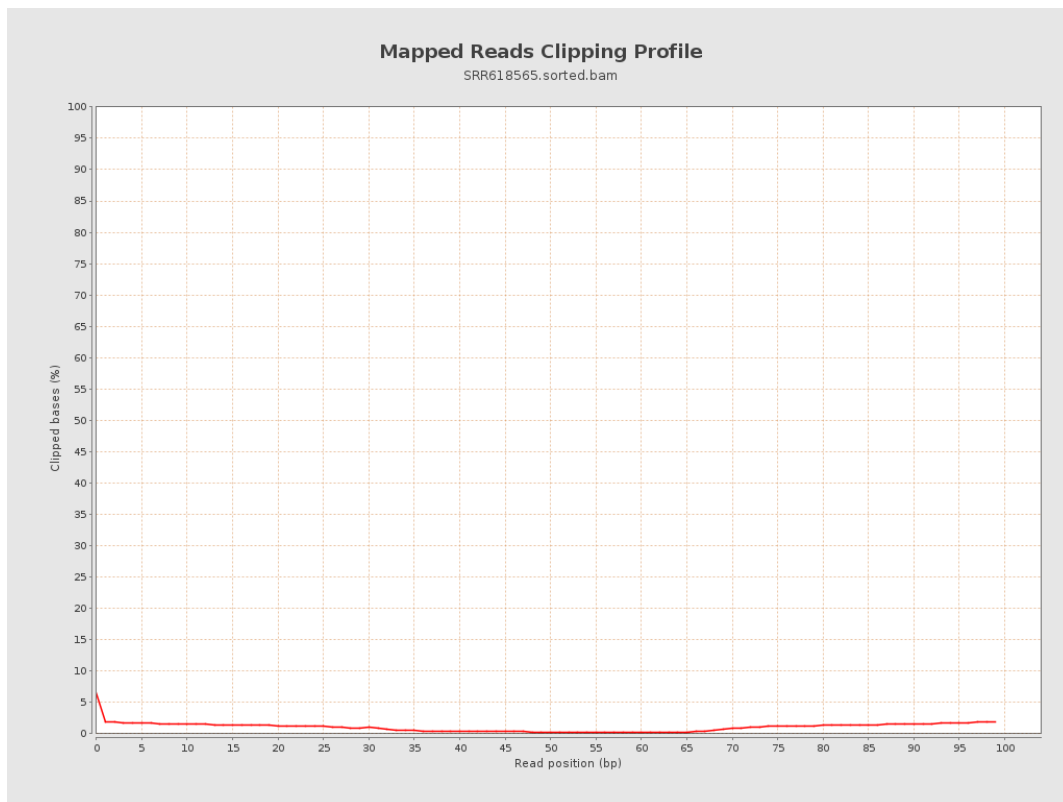
8. Results : Mapped Reads Nucleotide Content



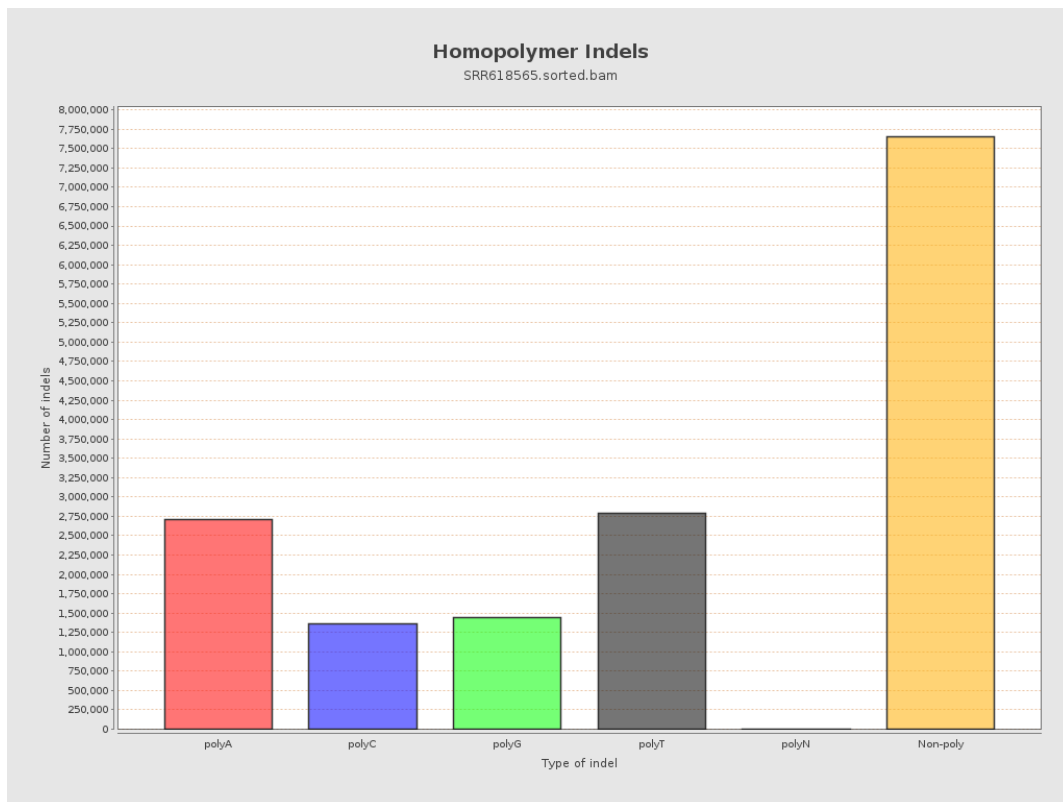
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



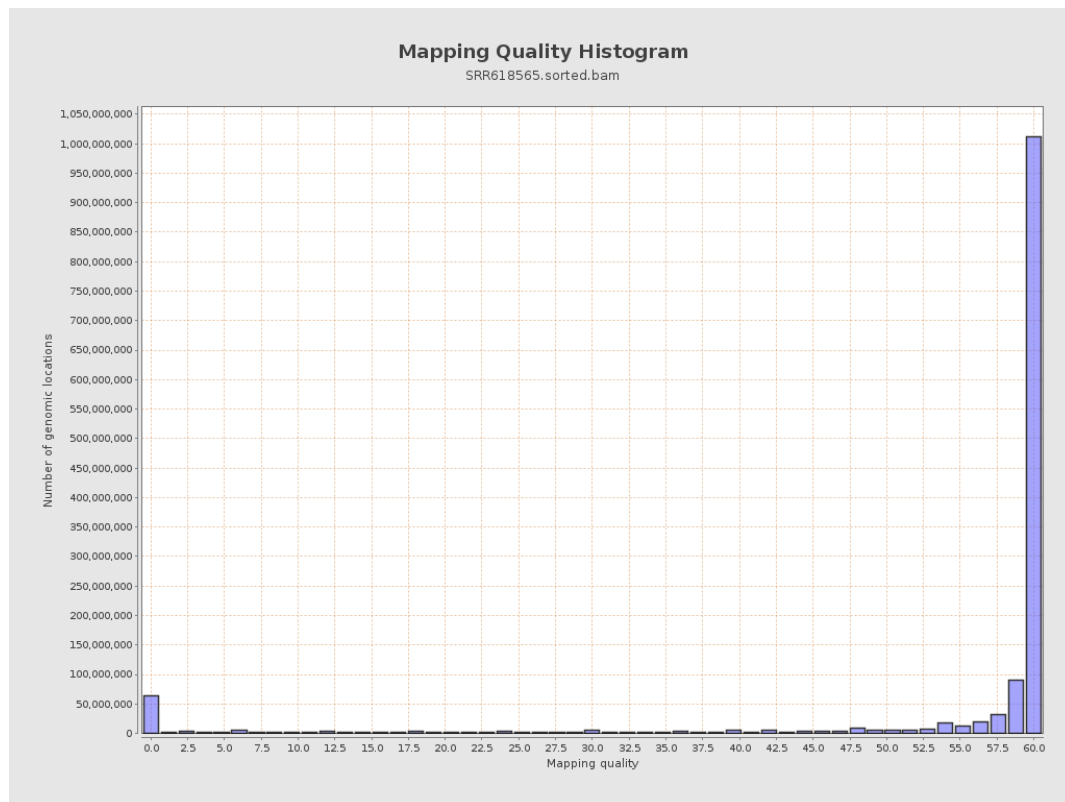
11. Results : Homopolymer Indels



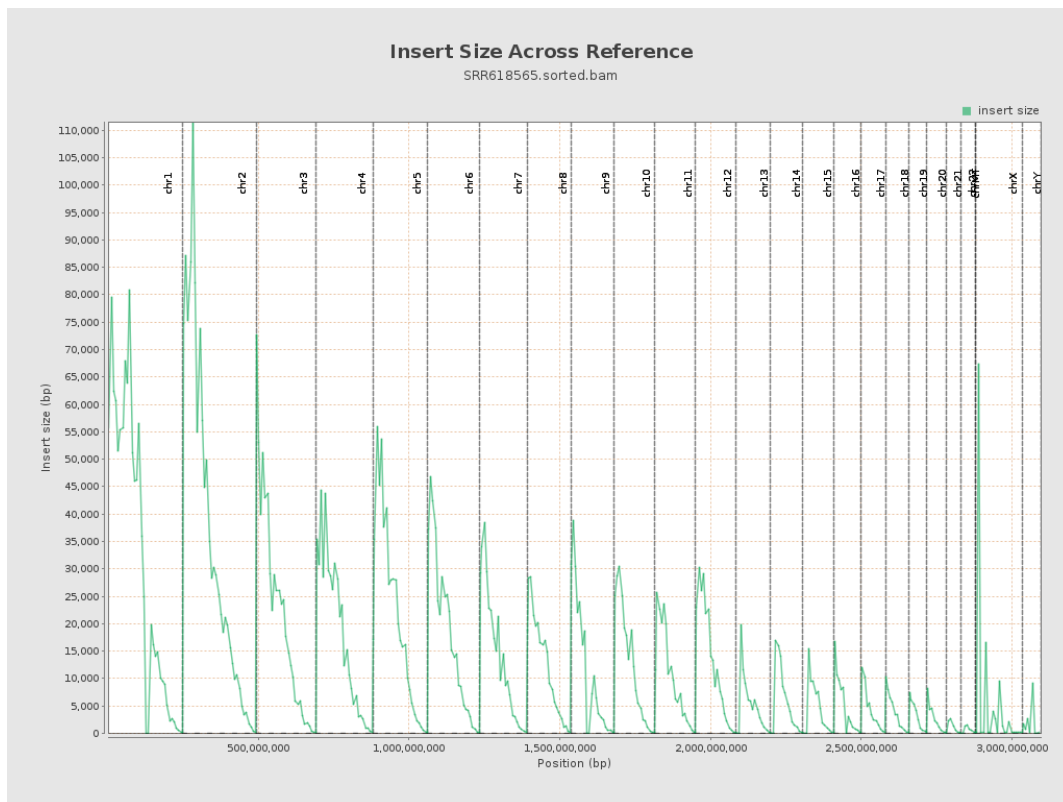
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

