Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 18:23:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960902.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_SRR960902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960902_1.fastq.gz SRR960902_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 18:23:38 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	118,460,170
Mapped reads	116,770,635 / 98.57%
Unmapped reads	1,689,535 / 1.43%
Mapped paired reads	116,770,635 / 98.57%
Mapped reads, first in pair	58,469,489 / 49.36%
Mapped reads, second in pair	58,301,146 / 49.22%
Mapped reads, both in pair	116,314,252 / 98.19%
Mapped reads, singletons	456,383 / 0.39%
Secondary alignments	0
Supplementary alignments	278,972 / 0.24%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	10,061,378 / 8.49%
Duplication rate	4.46%
Clipped reads	12,252,568 / 10.34%

2.2. ACGT Content

Number/percentage of A's	3,408,920,441 / 29.58%
Number/percentage of C's	2,347,854,382 / 20.37%
Number/percentage of T's	3,393,558,701 / 29.45%
Number/percentage of G's	2,373,984,439 / 20.6%
Number/percentage of N's	300,072 / 0%

GC Percentage	40.97%

2.3. Coverage

Mean	3.7239
Standard Deviation	41.0894

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	22,628.78
Standard Deviation	1,407,159.43
P25/Median/P75	137 / 148 / 159

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	76,427,526
Insertions	1,281,403
Mapped reads with at least one insertion	1.06%
Deletions	1,400,711
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.42%

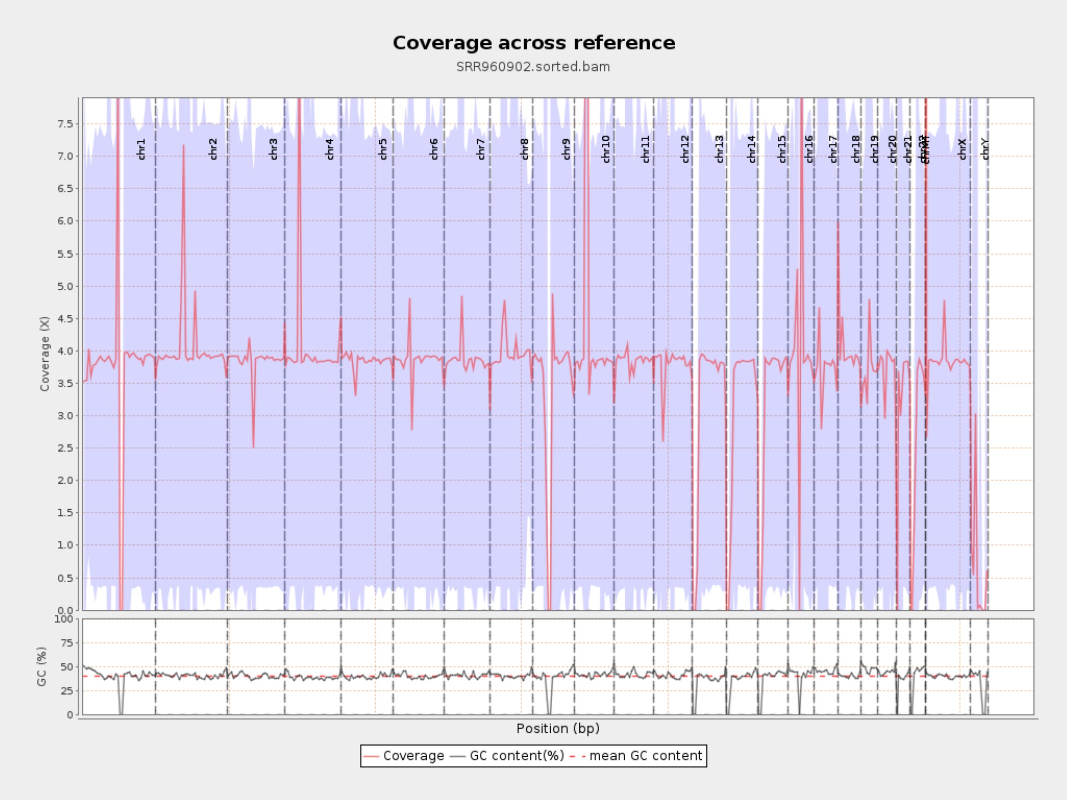
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

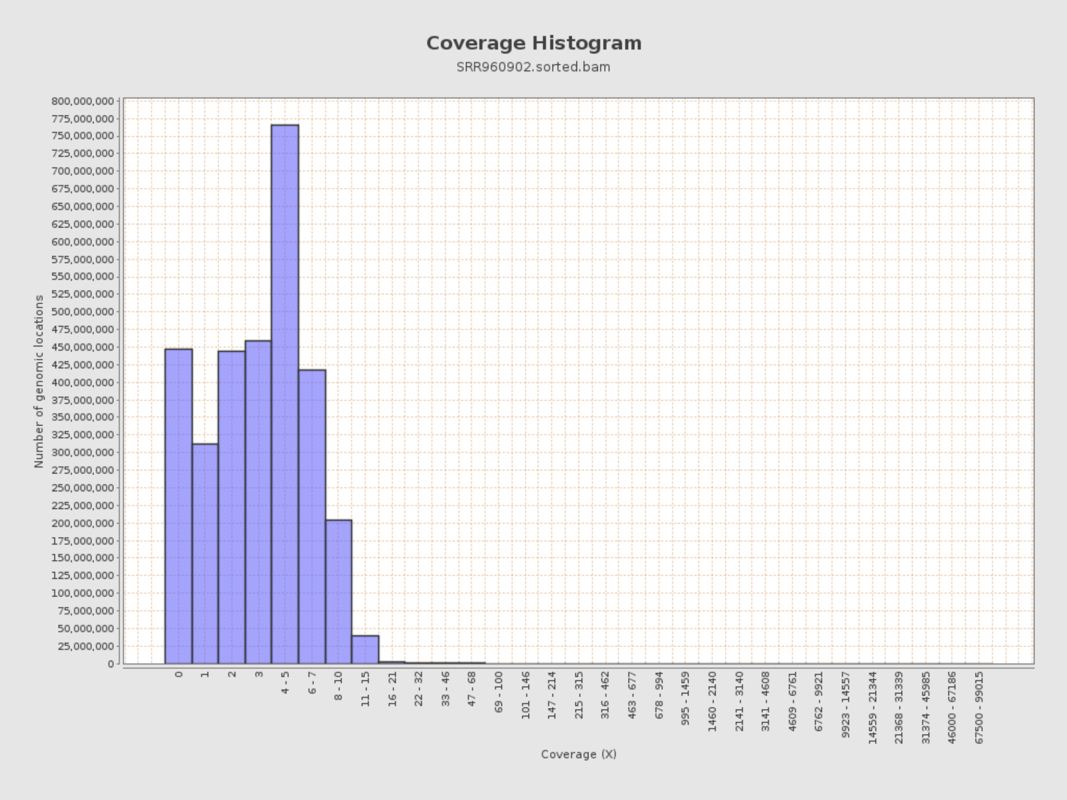
		bases	**coverage**	**deviation**
chr1	249250621	936799333	3.7585	98.8013
chr2	243199373	989660027	4.0693	25.8188
chr3	198022430	761759401	3.8468	8.1388
chr4	191154276	779669464	4.0787	35.3448
chr5	180915260	694469212	3.8386	4.3209
chr6	171115067	662190164	3.8699	12.1296
chr7	159138663	615689209	3.8689	25.1556
chr8	146364022	580553956	3.9665	42.0403
chr9	141213431	480691299	3.404	35.3733
chr10	135534747	600899958	4.4335	94.1758
chr11	135006516	518641055	3.8416	16.2736
chr12	133851895	508460779	3.7987	4.6475
chr13	115169878	367832541	3.1938	2.8698
chr14	107349540	339705486	3.1645	3.9505
chr15	102531392	319108297	3.1123	2.8996
chr16	90354753	365497206	4.0451	38.3085
chr17	81195210	304261995	3.7473	15.4165
chr18	78077248	314791988	4.0318	42.5818
chr19	59128983	219886280	3.7188	47.589
chr20	63025520	235514314	3.7368	13.6582
chr21	48129895	158176715	3.2865	17.8077
chr22	51304566	132494839	2.5825	3.4931
chrMT	16571	8932557	539.0476	79.701
chrX	155270560	594061397	3.826	12.7216

chrY	59373566	38416996	0.647	37.7661

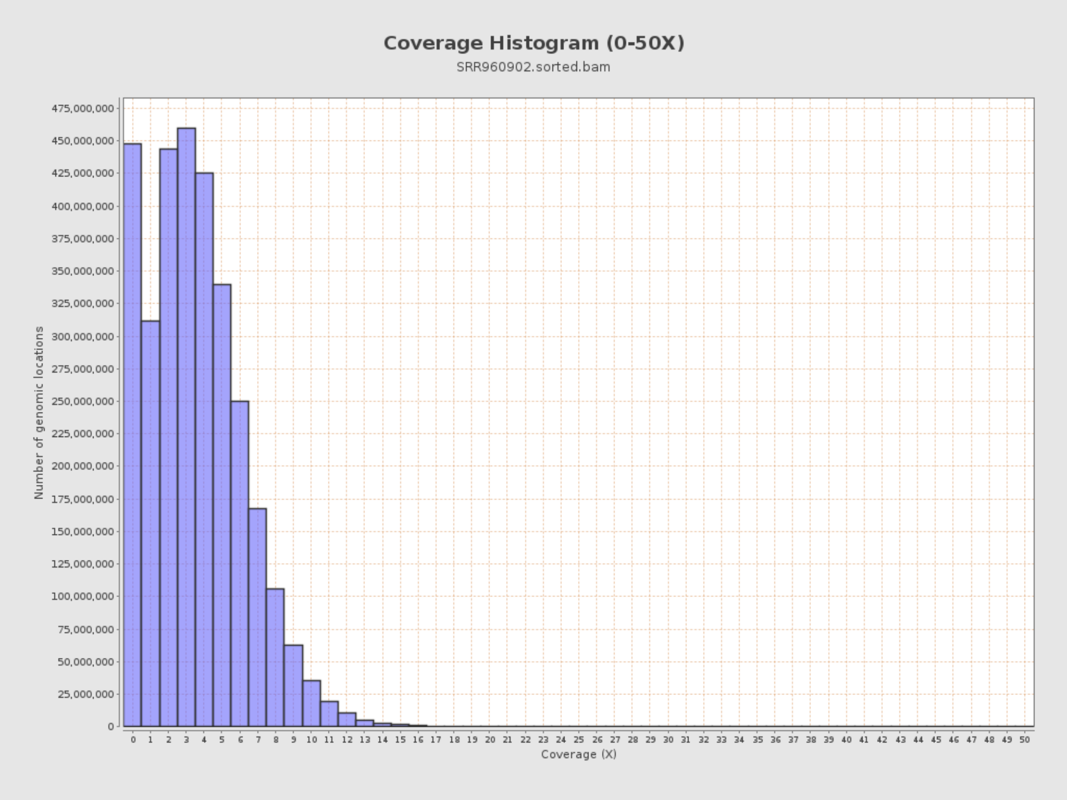
3. Results : Coverage across reference



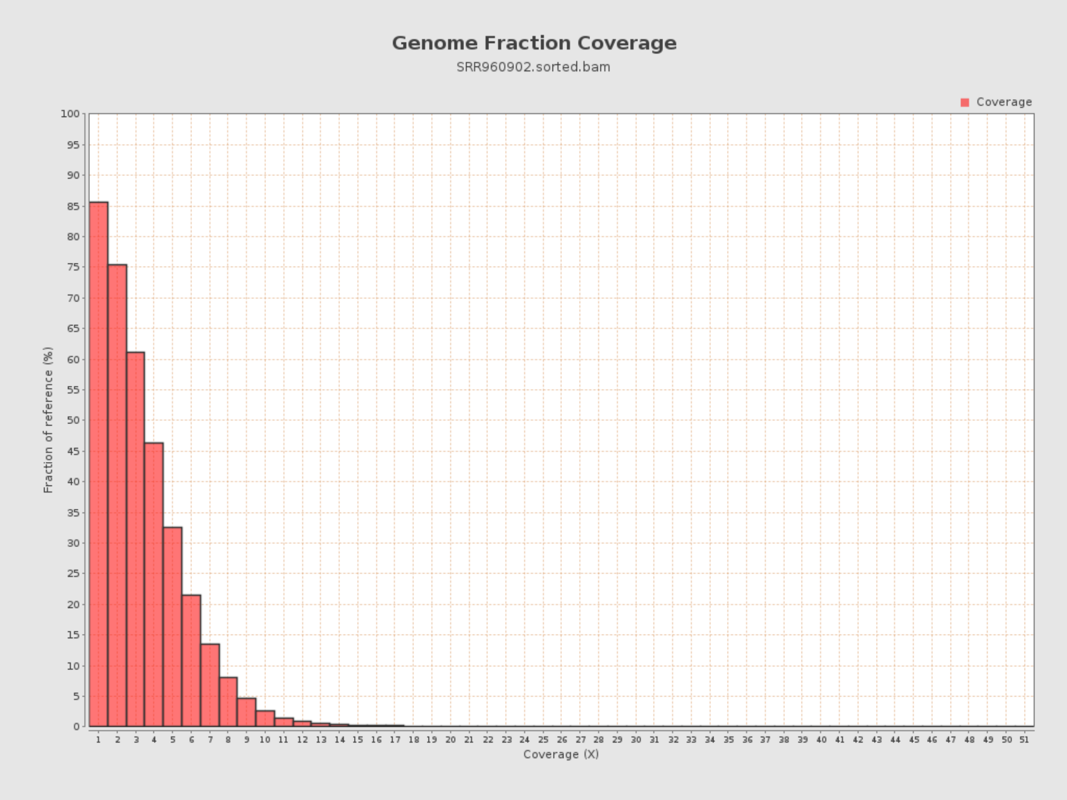
4. Results : Coverage Histogram



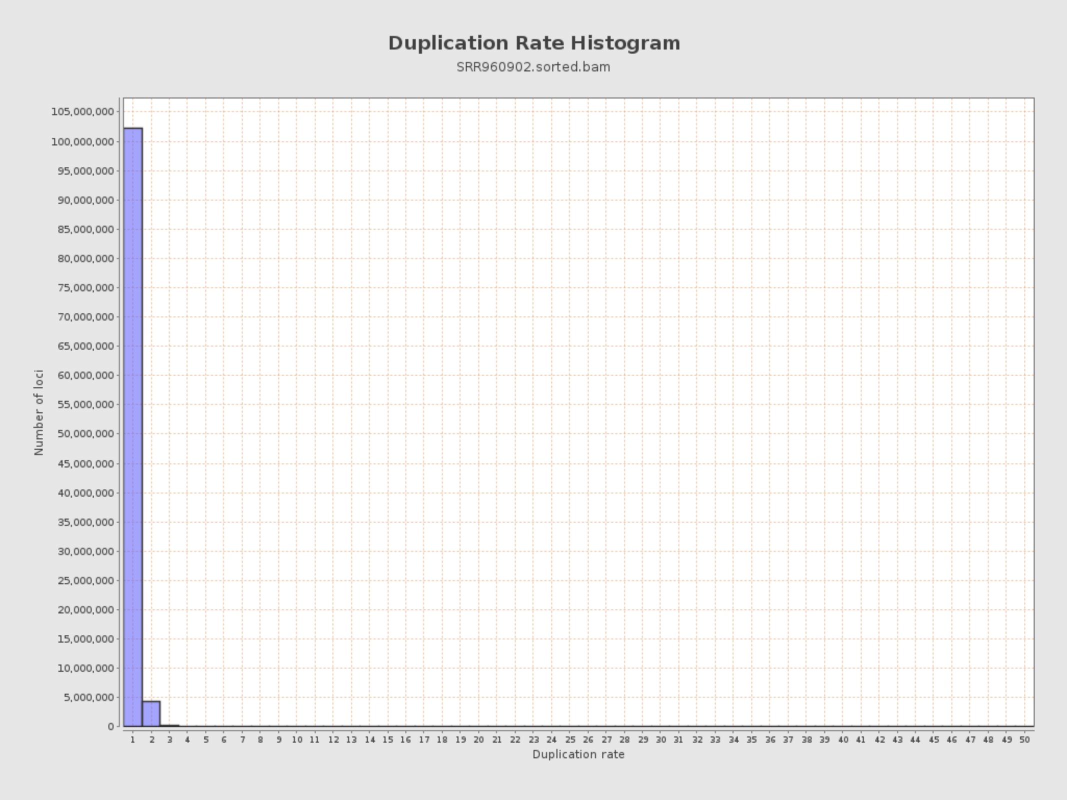
5. Results : Coverage Histogram (0-50X)



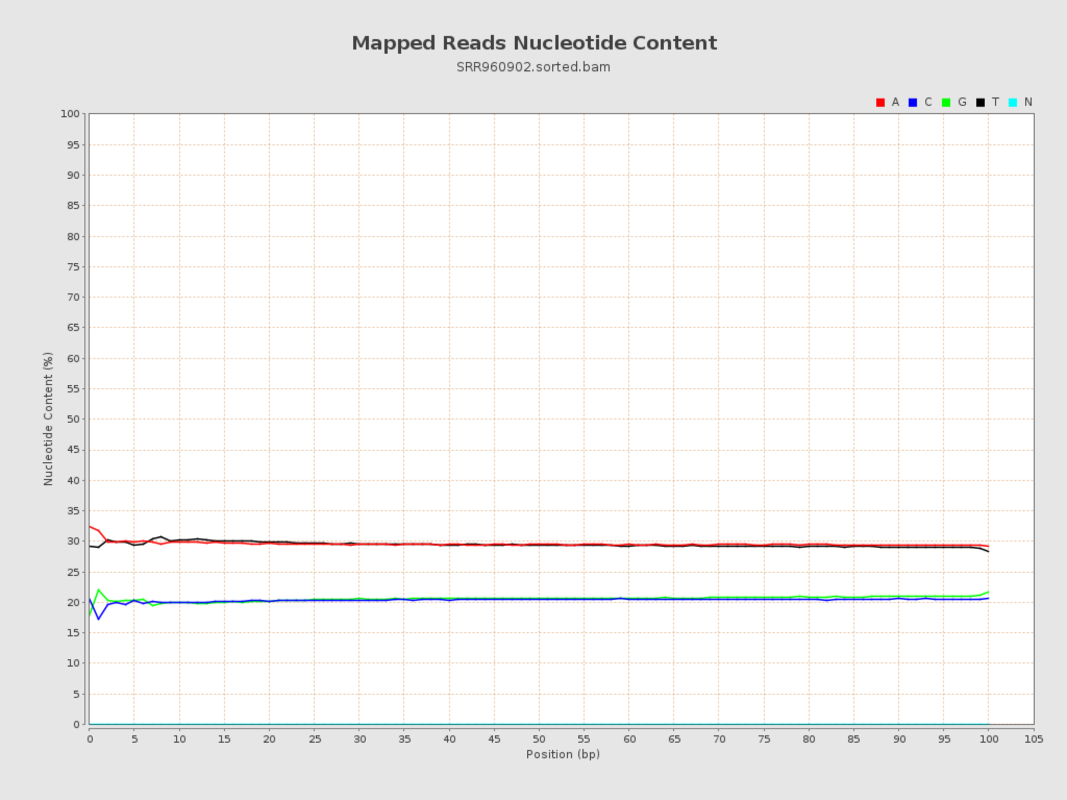
6. Results : Genome Fraction Coverage



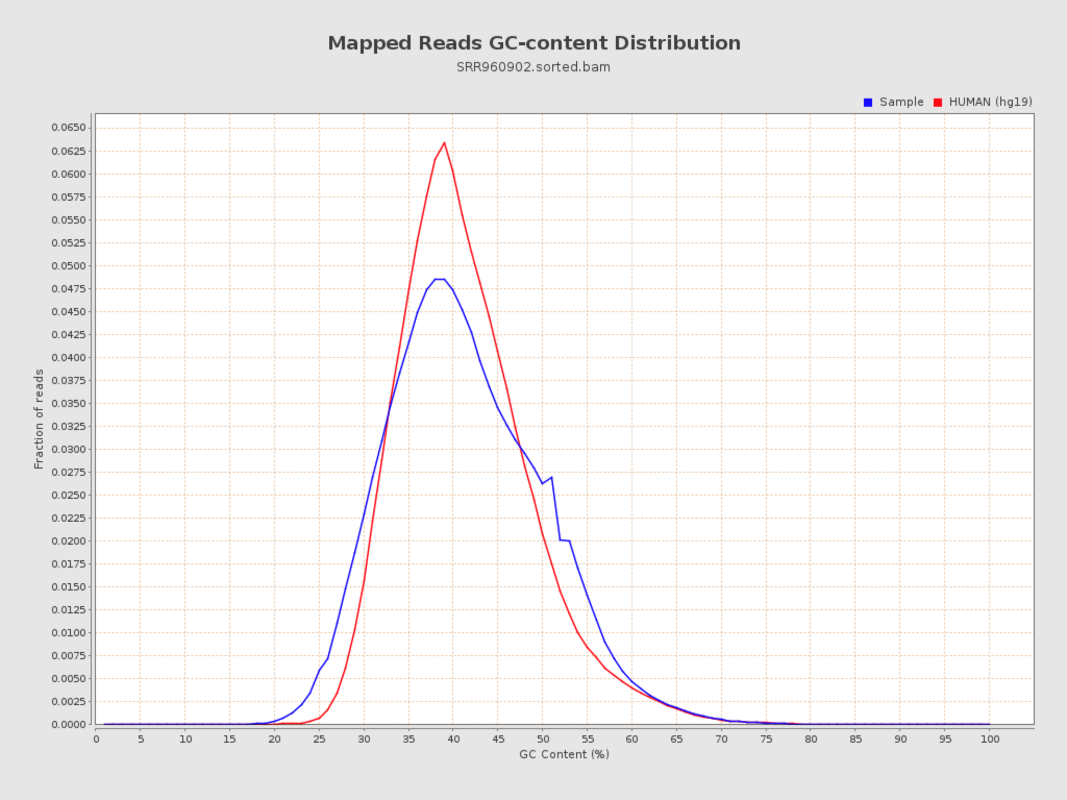
7. Results : Duplication Rate Histogram



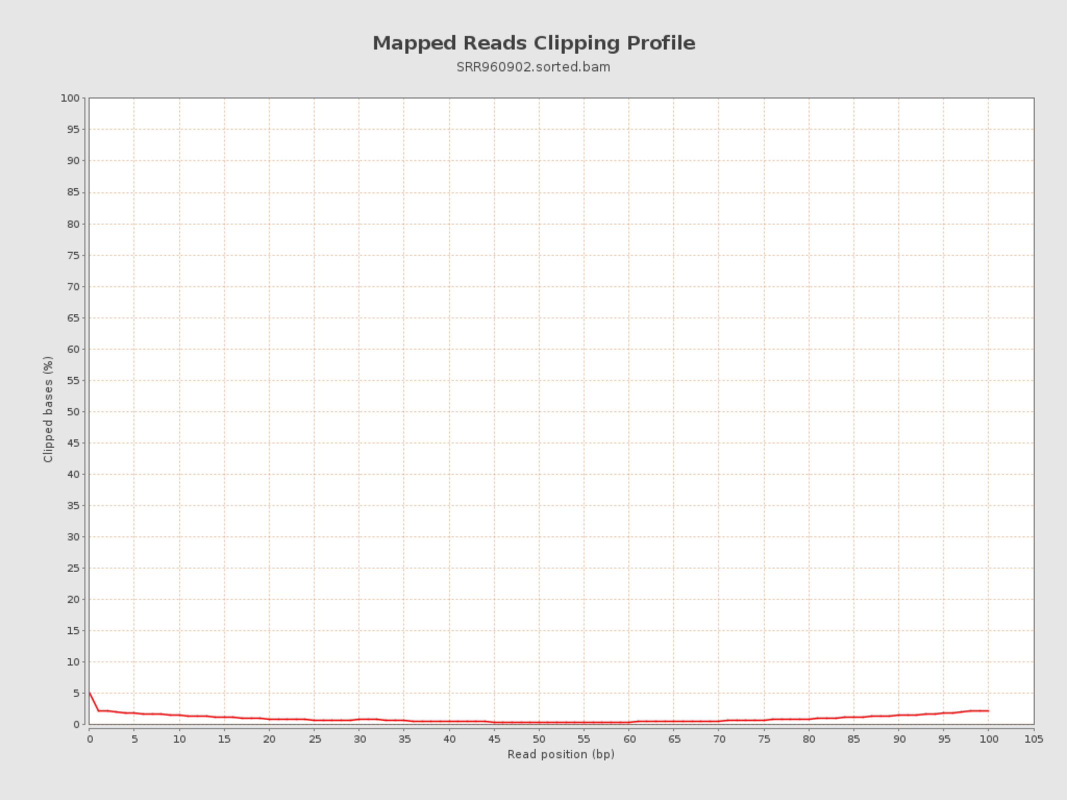
8. Results : Mapped Reads Nucleotide Content



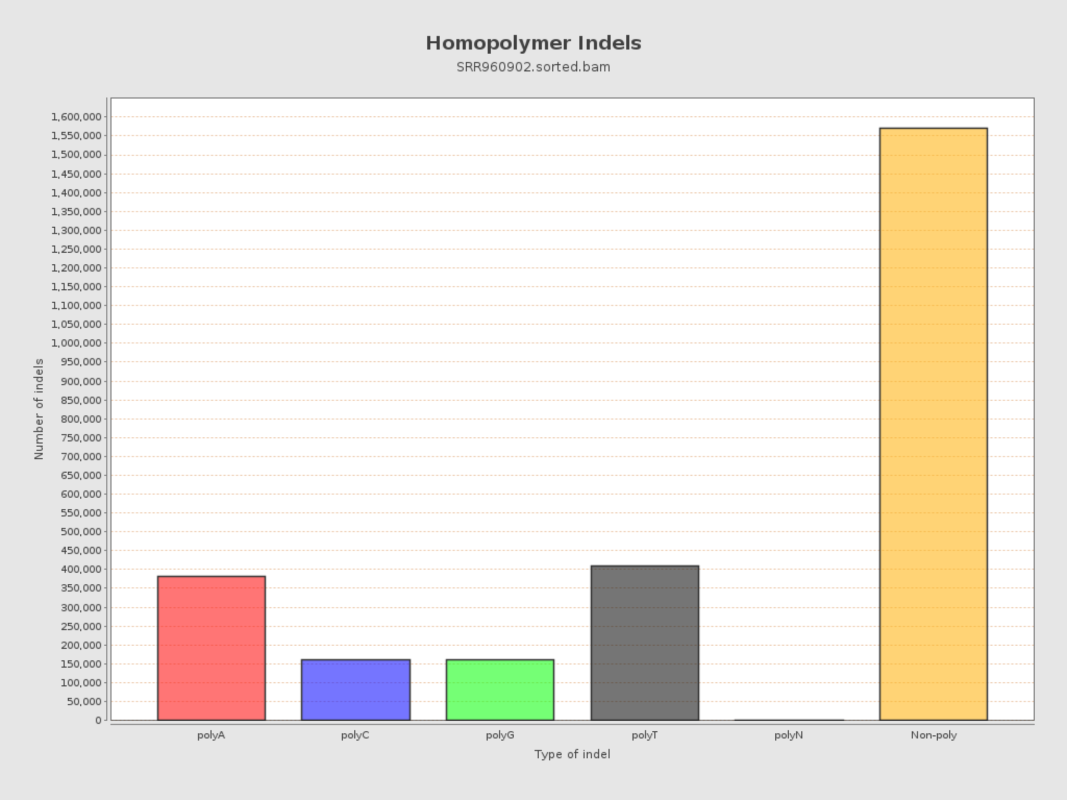
9. Results : Mapped Reads GC-content Distribution



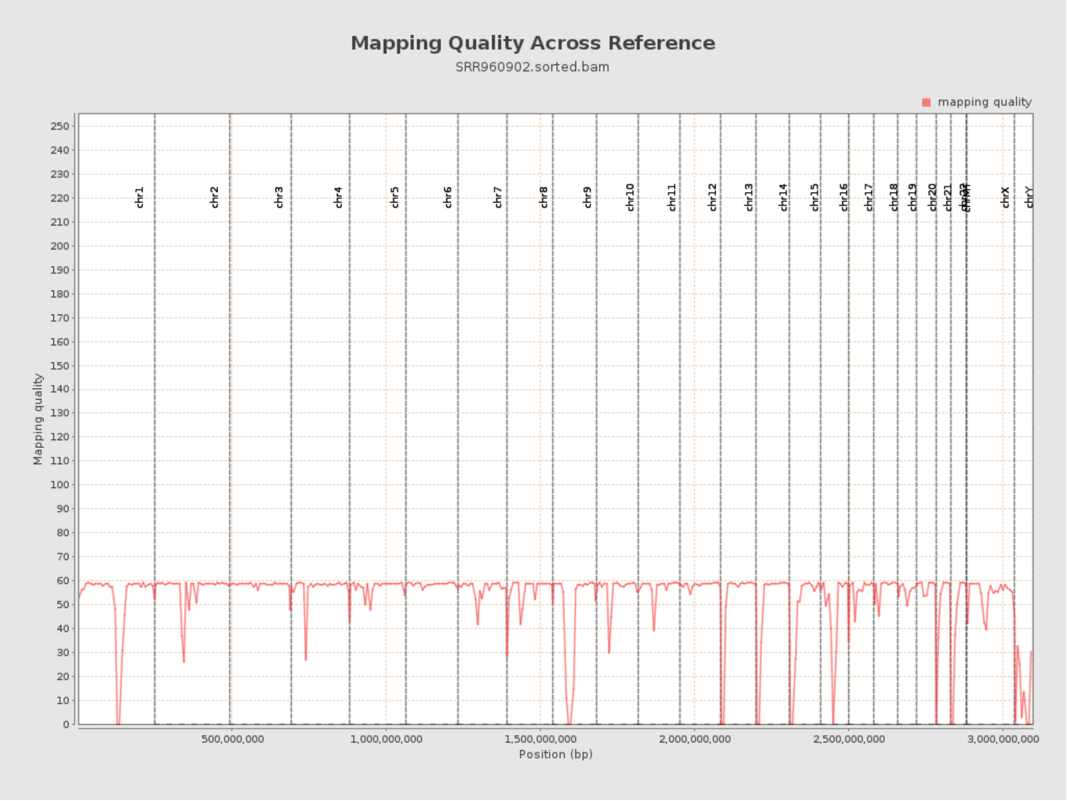
10. Results : Mapped Reads Clipping Profile



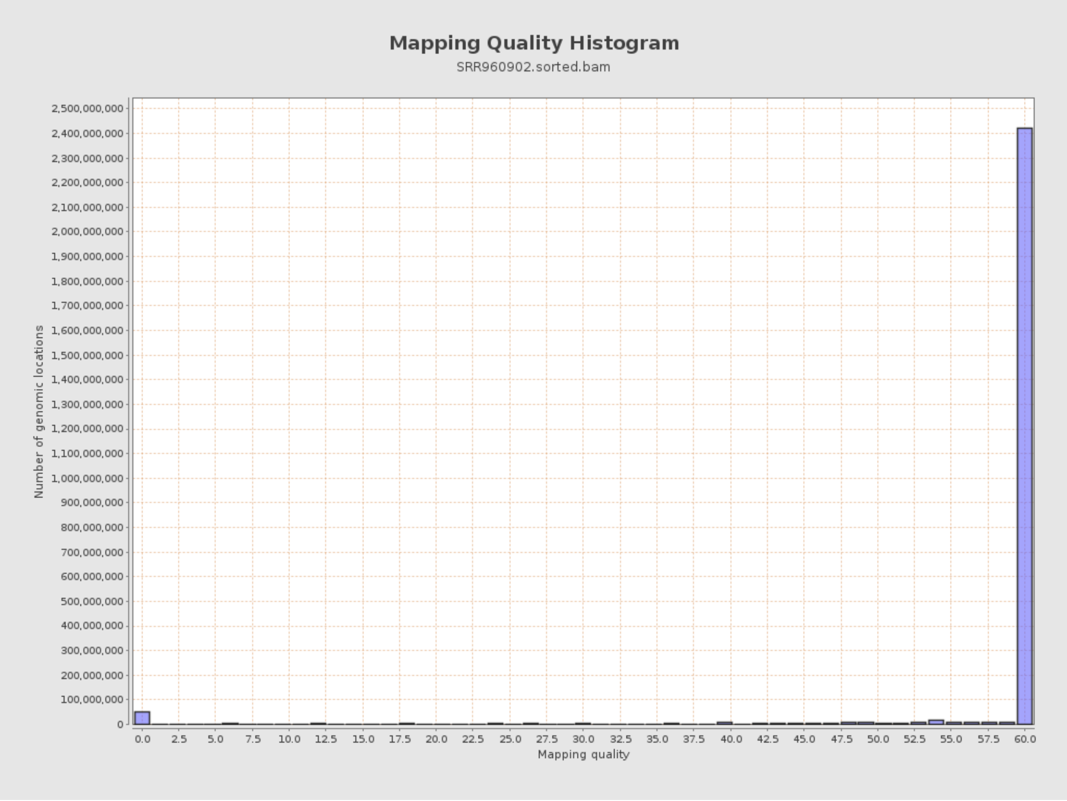
11. Results : Homopolymer Indels



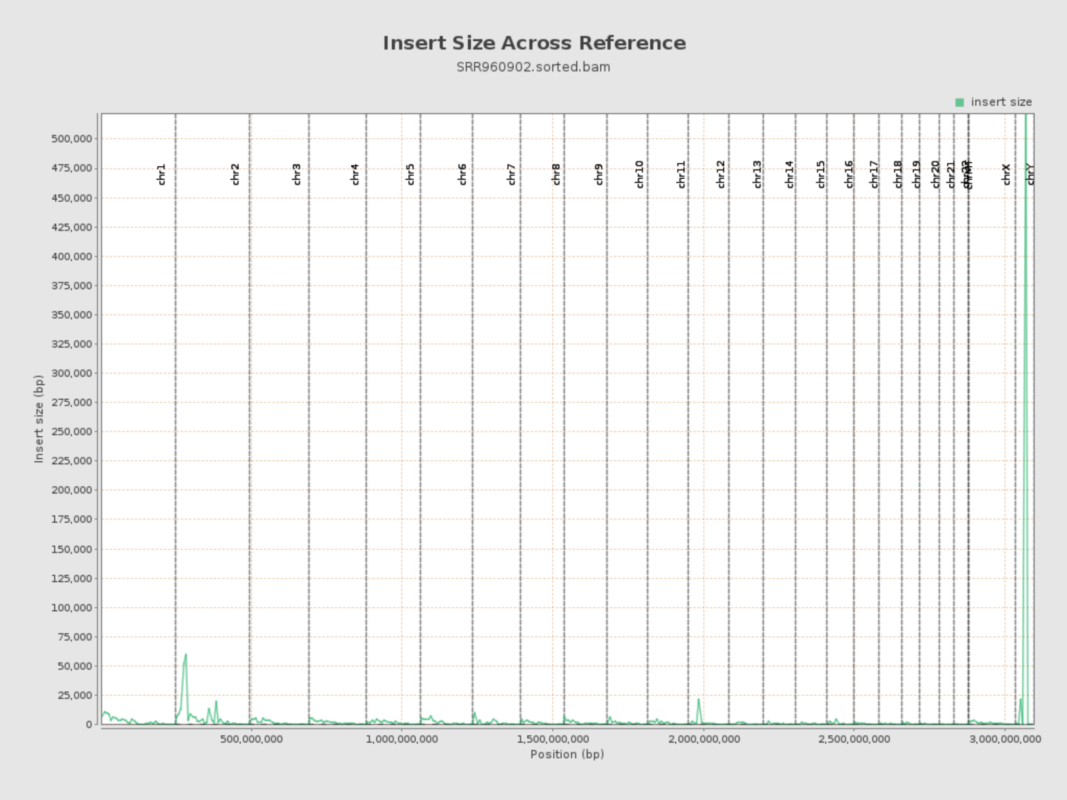
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram