Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 13:06:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472698.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_SRR3472698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472698_1.fastq.gz SRR3472698_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 13:06:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,260,590
Mapped reads	16,145,288 / 99.29%
Unmapped reads	115,302 / 0.71%
Mapped paired reads	16,145,288 / 99.29%
Mapped reads, first in pair	8,107,851 / 49.86%
Mapped reads, second in pair	8,037,437 / 49.43%
Mapped reads, both in pair	16,068,352 / 98.82%
Mapped reads, singletons	76,936 / 0.47%
Secondary alignments	0
Supplementary alignments	118,593 / 0.73%
Read min/max/mean length	30 / 101 / 99.69
Duplicated reads (estimated)	12,001,436 / 73.81%
Duplication rate	48.28%
Clipped reads	1,165,917 / 7.17%

2.2. ACGT Content

Number/percentage of A's	426,276,881 / 26.85%
Number/percentage of C's	367,428,085 / 23.15%
Number/percentage of T's	431,511,039 / 27.18%
Number/percentage of G's	361,835,412 / 22.79%
Number/percentage of N's	365,111 / 0.02%

GC Percentage	45.94%

2.3. Coverage

Mean	0.5129
Standard Deviation	31.1534

2.4. Mapping Quality

Mean Mapping Quality	54.5

2.5. Insert size

Mean	27,404.57
Standard Deviation	1,605,910.84
P25/Median/P75	155 / 212 / 281

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	6,589,705
Insertions	103,545
Mapped reads with at least one insertion	0.64%
Deletions	84,680
Mapped reads with at least one deletion	0.52%
Homopolymer indels	47.85%

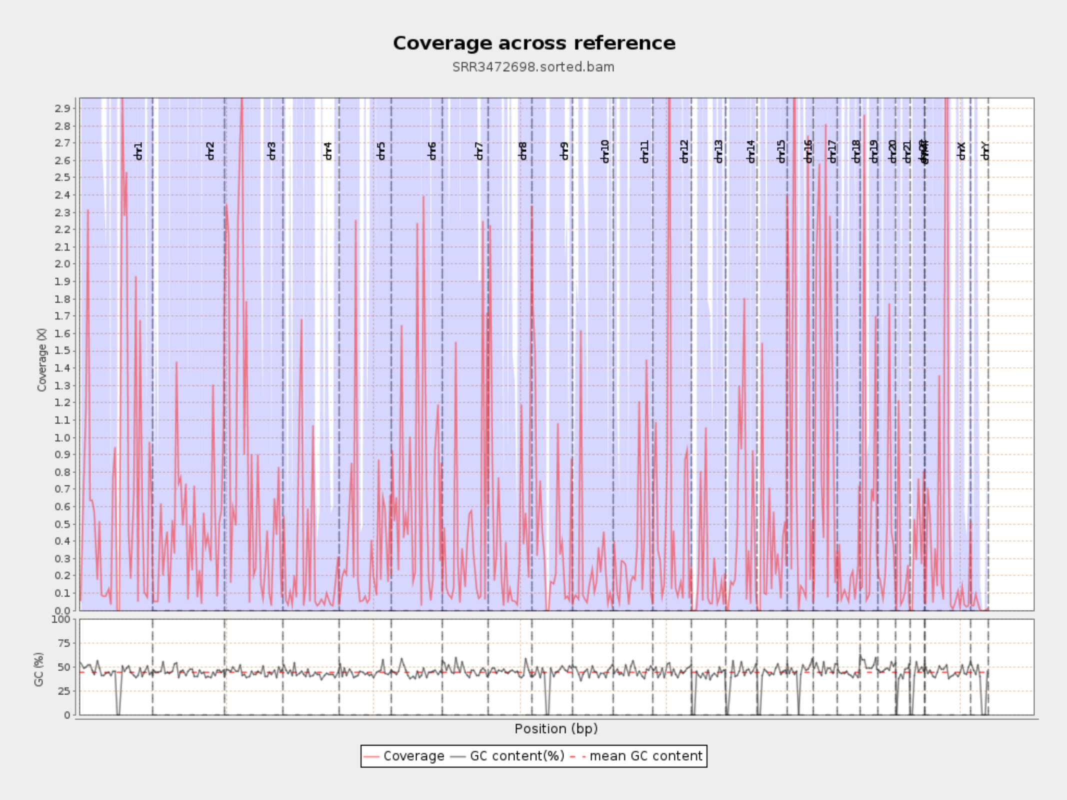
2.7. Chromosome stats

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

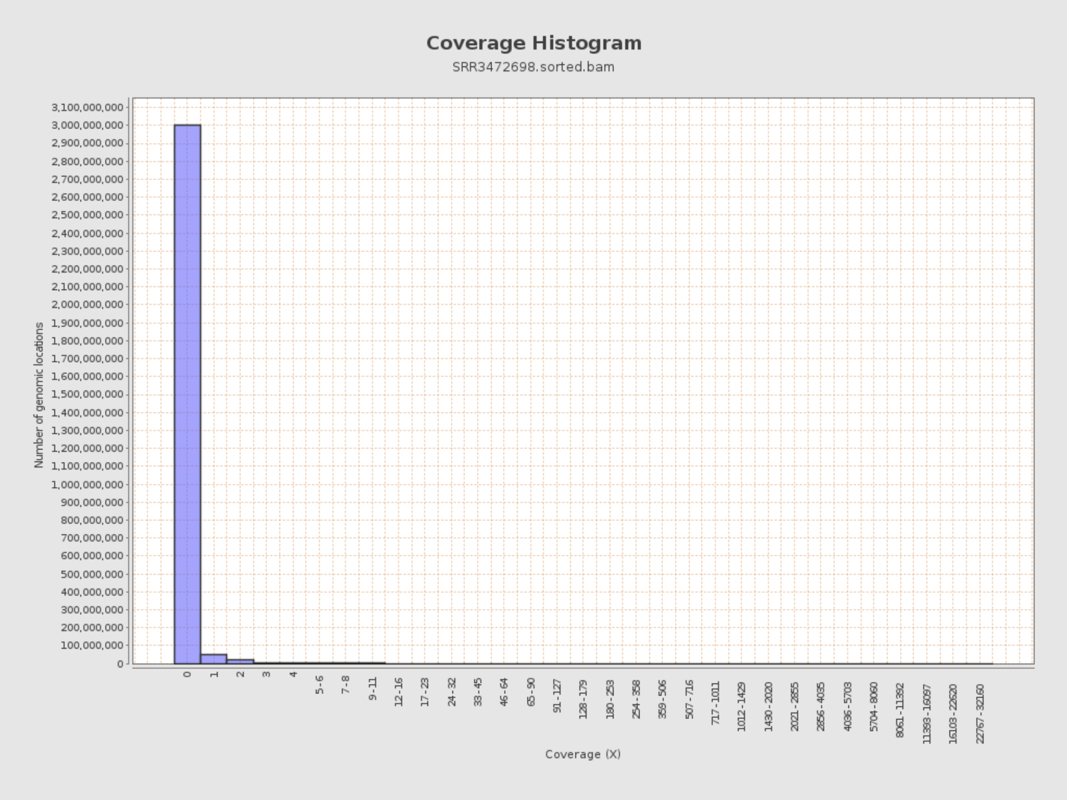
		bases	coverage	deviation
chr1	249250621	187315752	0.7515	32.5153
chr2	243199373	108807618	0.4474	22.6999
chr3	198022430	175149346	0.8845	41.0034
chr4	191154276	50706334	0.2653	37.6009
chr5	180915260	69559855	0.3845	16.974
chr6	171115067	121529924	0.7102	30.5231
chr7	159138663	73207875	0.46	33.1927
chr8	146364022	72339591	0.4942	38.4092
chr9	141213431	68088440	0.4822	29.4512
chr10	135534747	31668137	0.2337	21.7607
chr11	135006516	49991146	0.3703	23.0644
chr12	133851895	79216714	0.5918	31.5033
chr13	115169878	22963234	0.1994	11.7095
chr14	107349540	49782776	0.4637	25.6696
chr15	102531392	37082528	0.3617	19.205
chr16	90354753	90476365	1.0013	53.7898
chr17	81195210	97707009	1.2034	60.3959
chr18	78077248	14927422	0.1912	8.7223
chr19	59128983	48940310	0.8277	34.3732
chr20	63025520	28911692	0.4587	23.357
chr21	48129895	13189177	0.274	21.6153
chr22	51304566	20683622	0.4032	18.428
chrMT	16571	5526	0.3335	0.8131
chrX	155270560	73943477	0.4762	34.5867

chrY	59373566	1539924	0.0259	2.4216

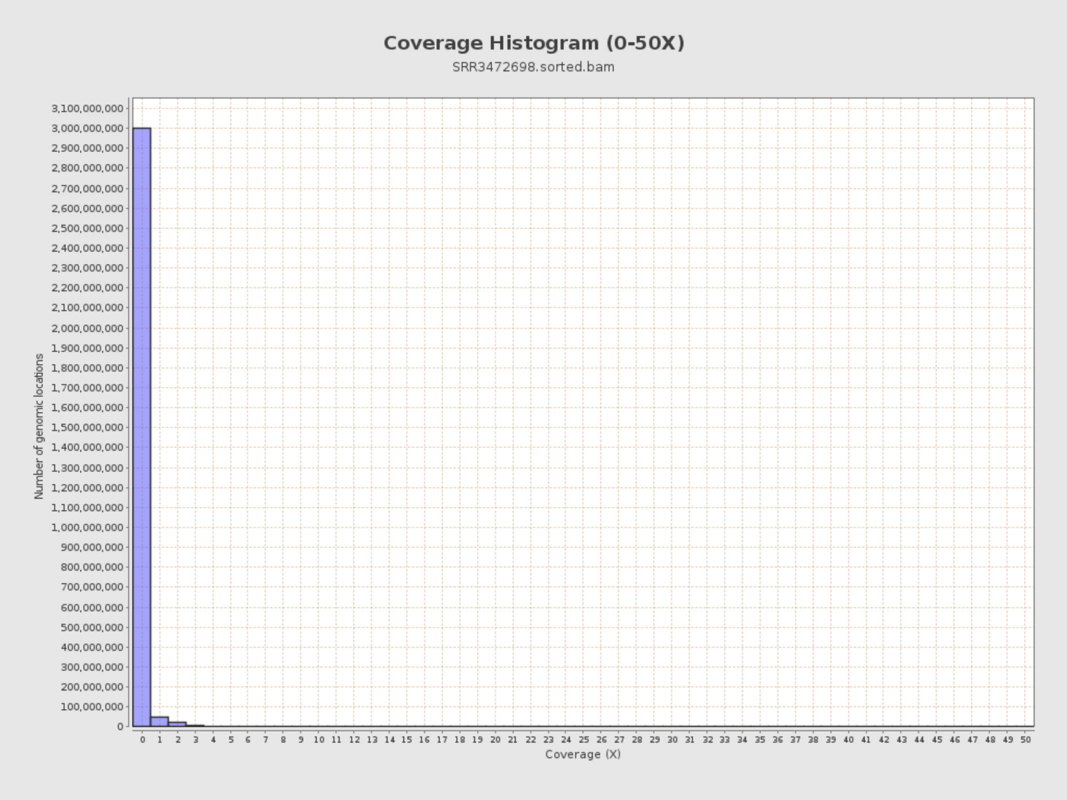
3. Results : Coverage across reference



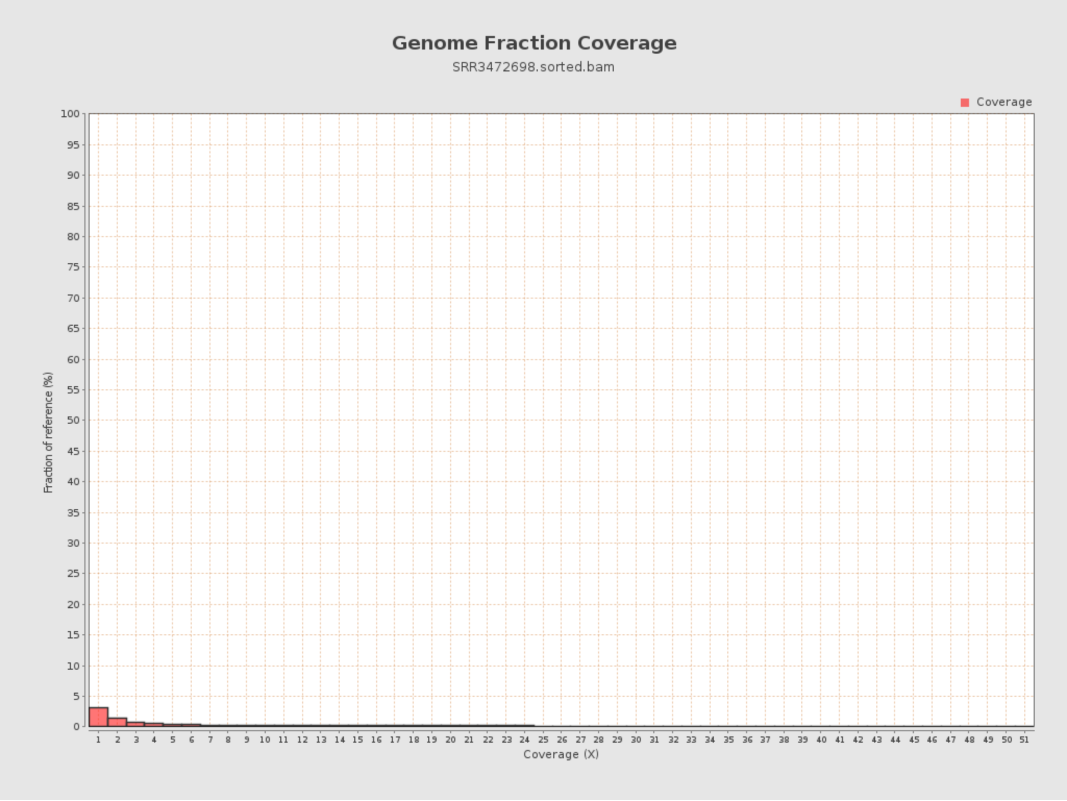
4. Results : Coverage Histogram



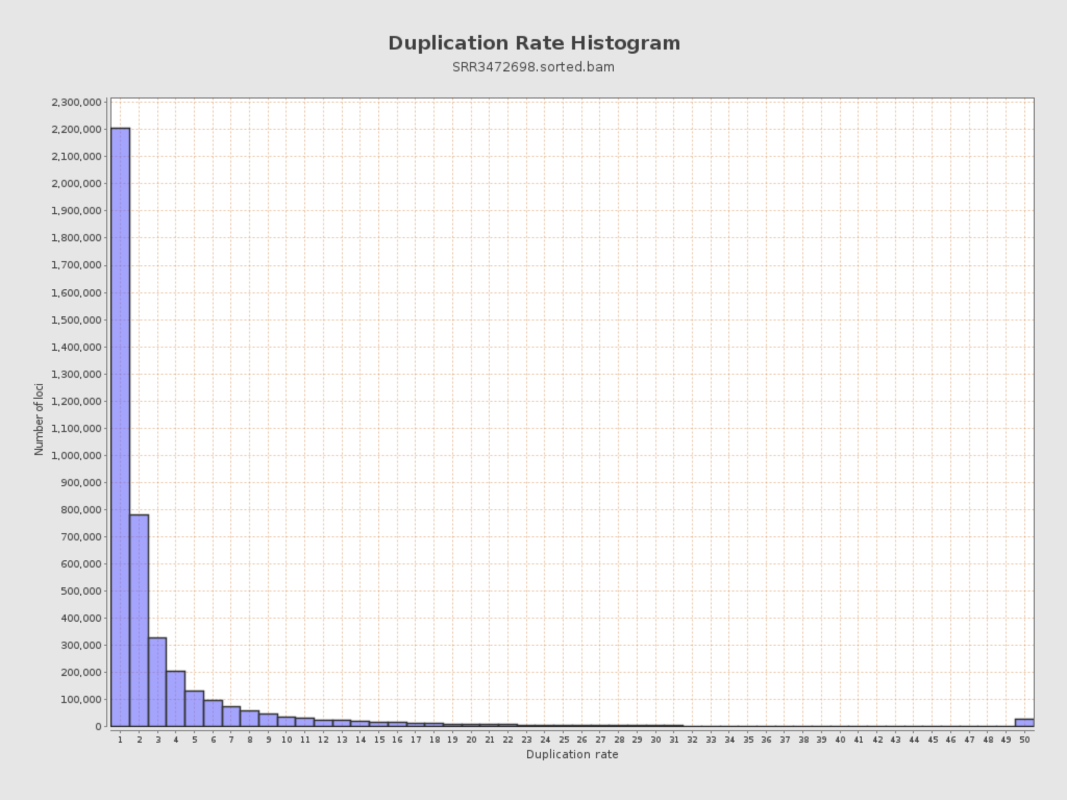
5. Results : Coverage Histogram (0-50X)



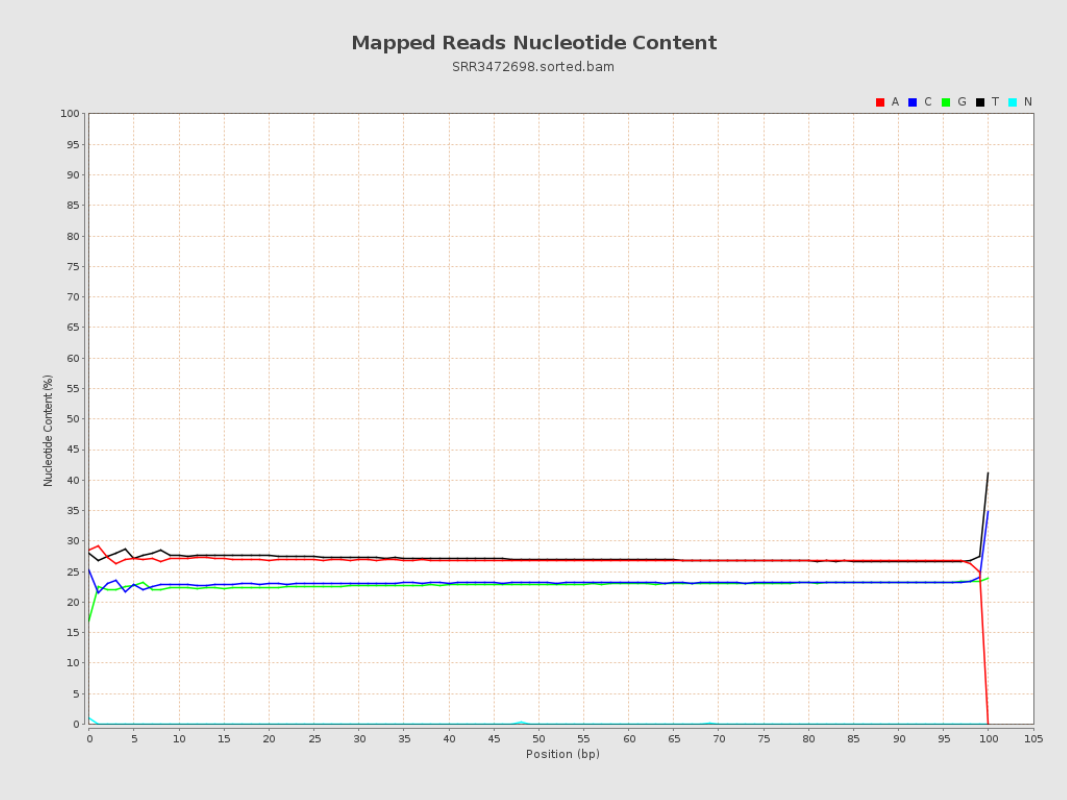
6. Results : Genome Fraction Coverage



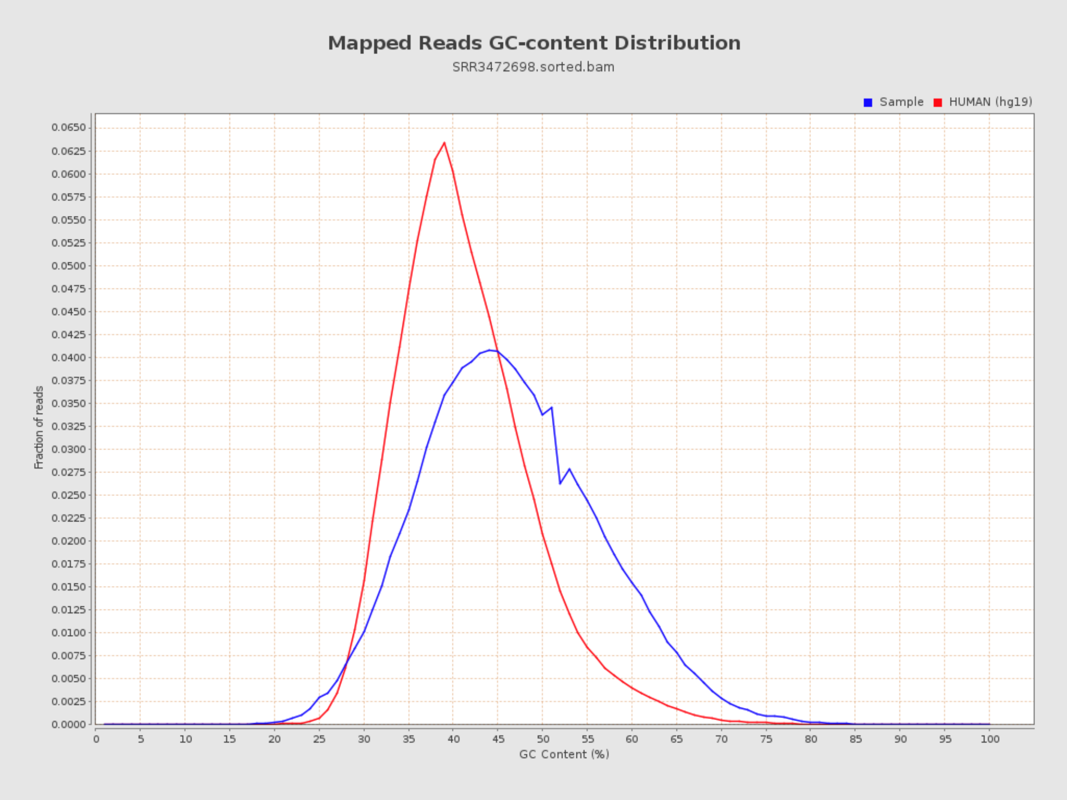
7. Results : Duplication Rate Histogram



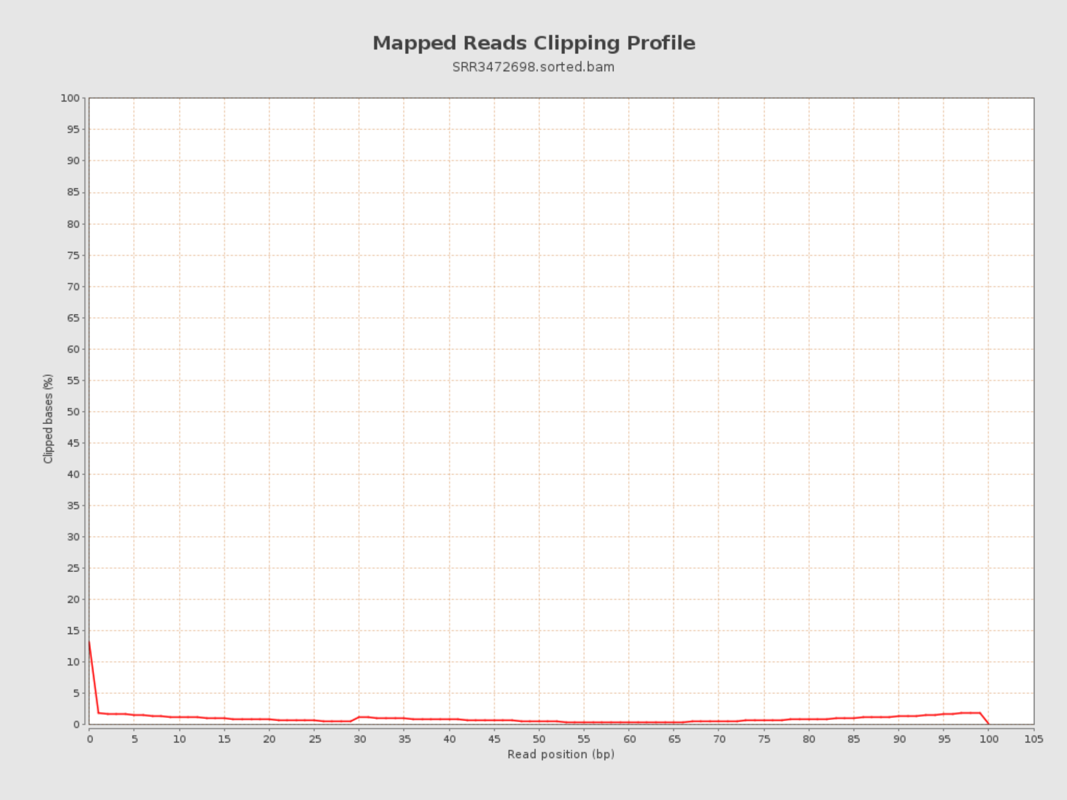
8. Results : Mapped Reads Nucleotide Content



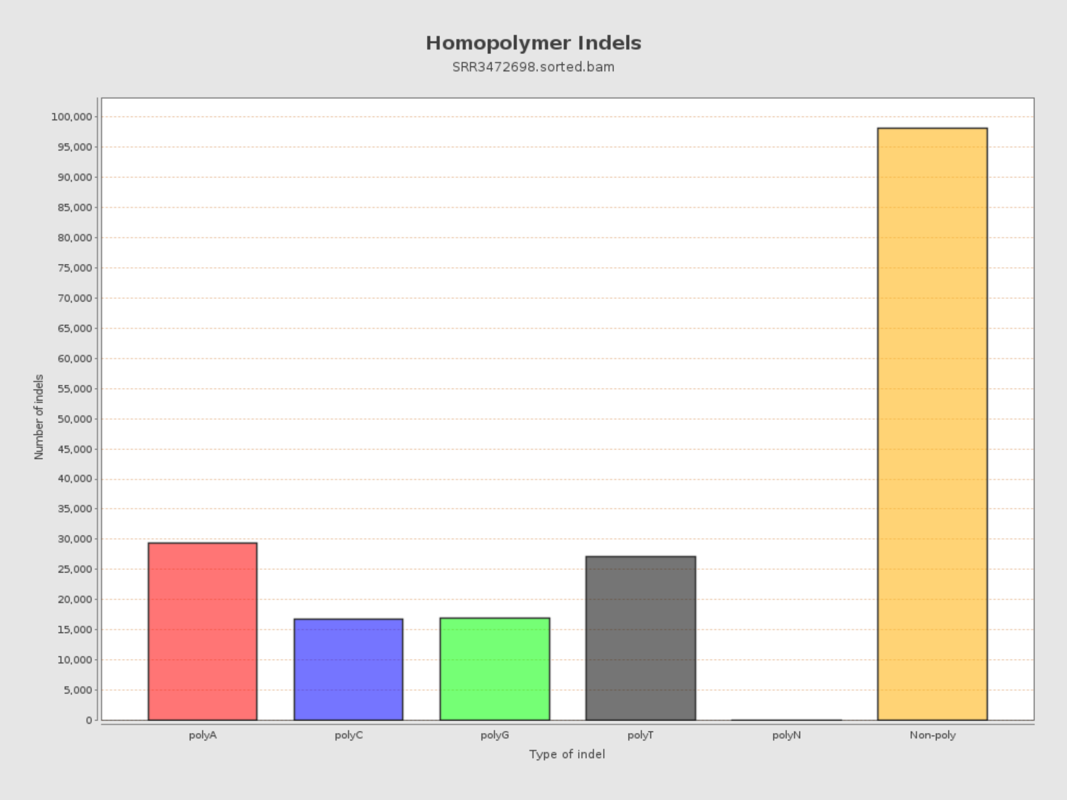
9. Results : Mapped Reads GC-content Distribution



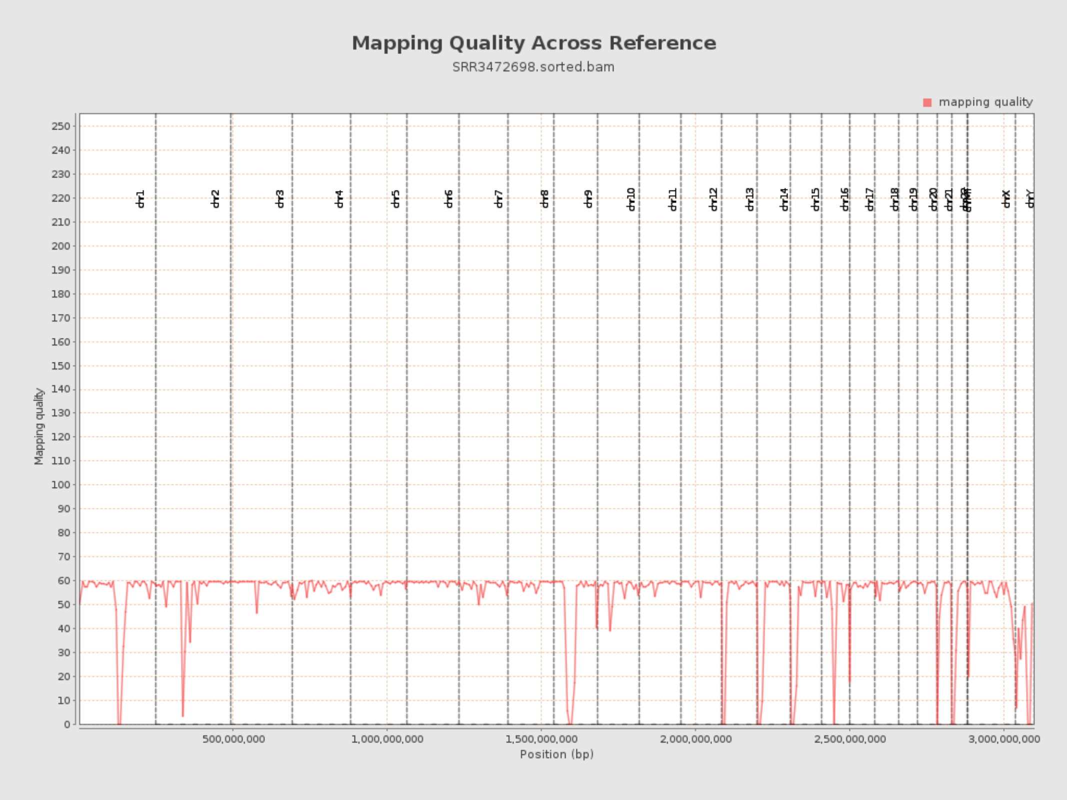
10. Results : Mapped Reads Clipping Profile



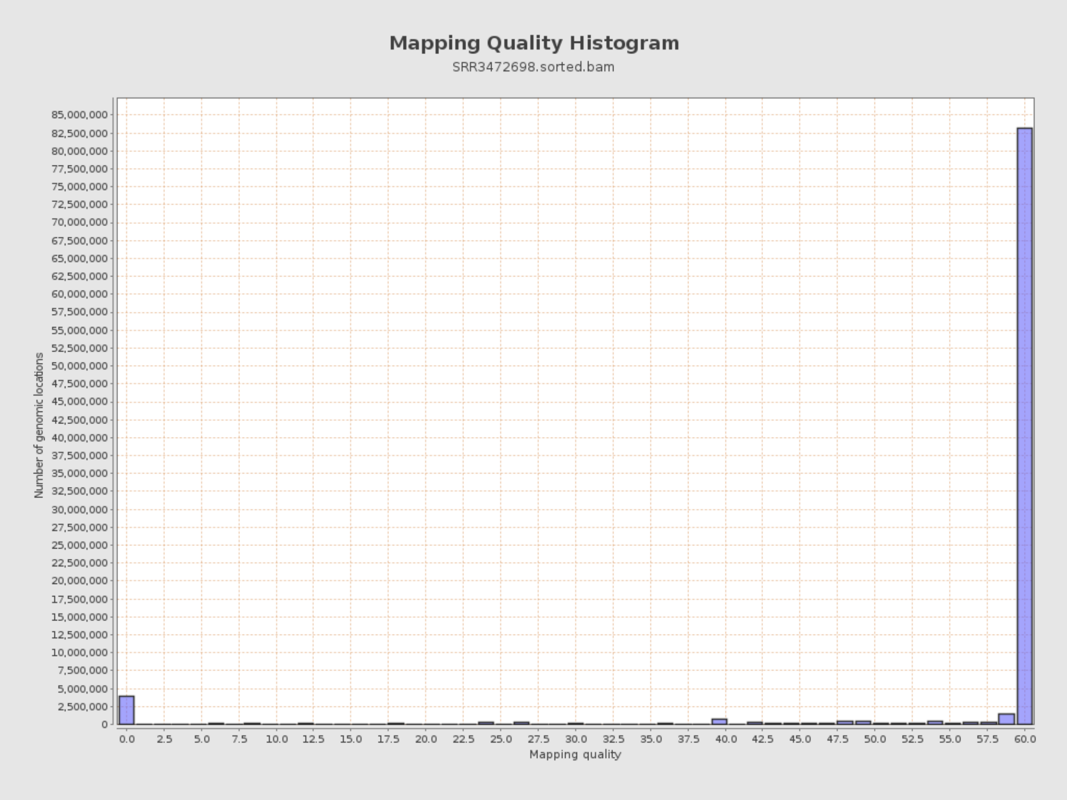
11. Results : Homopolymer Indels



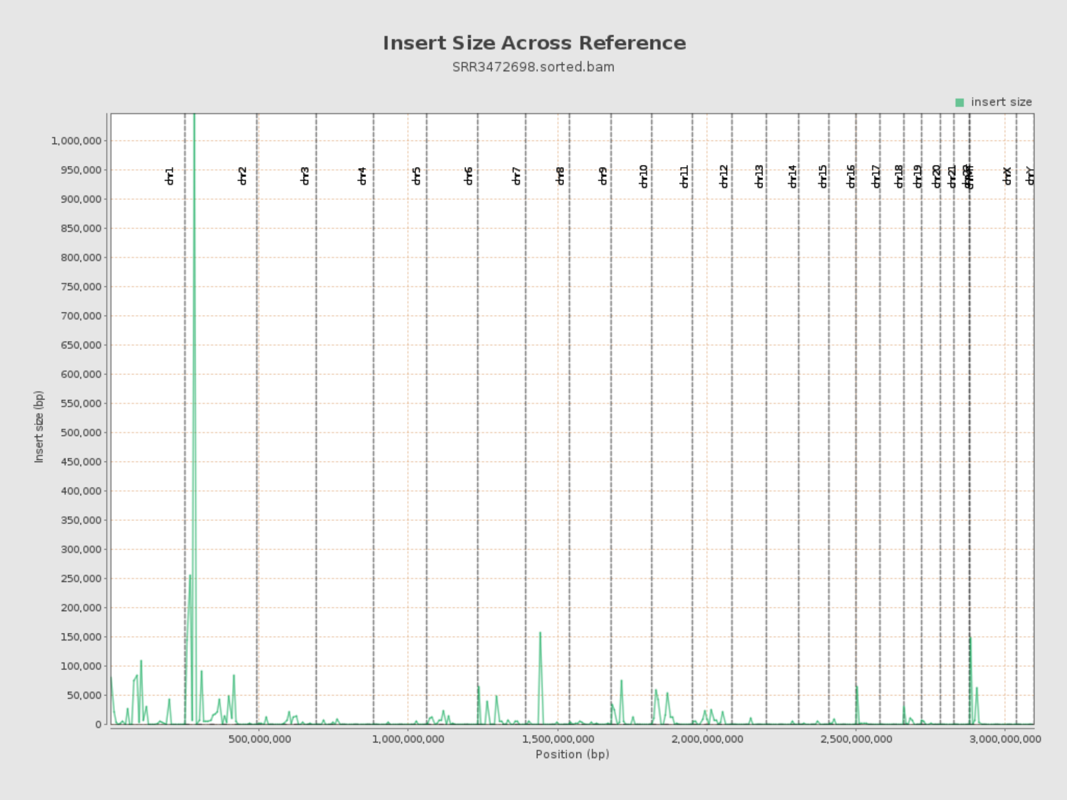
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram