Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 11:19:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472768.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_SRR3472768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472768_1.fastq.gz SRR3472768_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 11:19:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472768.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,054,514
Mapped reads	15,887,652 / 98.96%
Unmapped reads	166,862 / 1.04%
Mapped paired reads	15,887,652 / 98.96%
Mapped reads, first in pair	7,974,014 / 49.67%
Mapped reads, second in pair	7,913,638 / 49.29%
Mapped reads, both in pair	15,790,222 / 98.35%
Mapped reads, singletons	97,430 / 0.61%
Secondary alignments	0
Supplementary alignments	52,220 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	9,933,161 / 61.87%
Duplication rate	47.35%
Clipped reads	1,201,446 / 7.48%

2.2. ACGT Content

Number/percentage of A's	432,097,187 / 27.6%
Number/percentage of C's	352,723,948 / 22.53%
Number/percentage of T's	429,636,953 / 27.44%
Number/percentage of G's	351,039,363 / 22.42%
Number/percentage of N's	301,920 / 0.02%

GC Percentage	44.95%

2.3. Coverage

Mean	0.5059
Standard Deviation	16.9497

2.4. Mapping Quality

Mean Mapping Quality	55.02

2.5. Insert size

Mean	21,979.39
Standard Deviation	1,484,465.62
P25/Median/P75	182 / 257 / 346

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	10,057,532
Insertions	90,186
Mapped reads with at least one insertion	0.56%
Deletions	91,085
Mapped reads with at least one deletion	0.57%
Homopolymer indels	45.7%

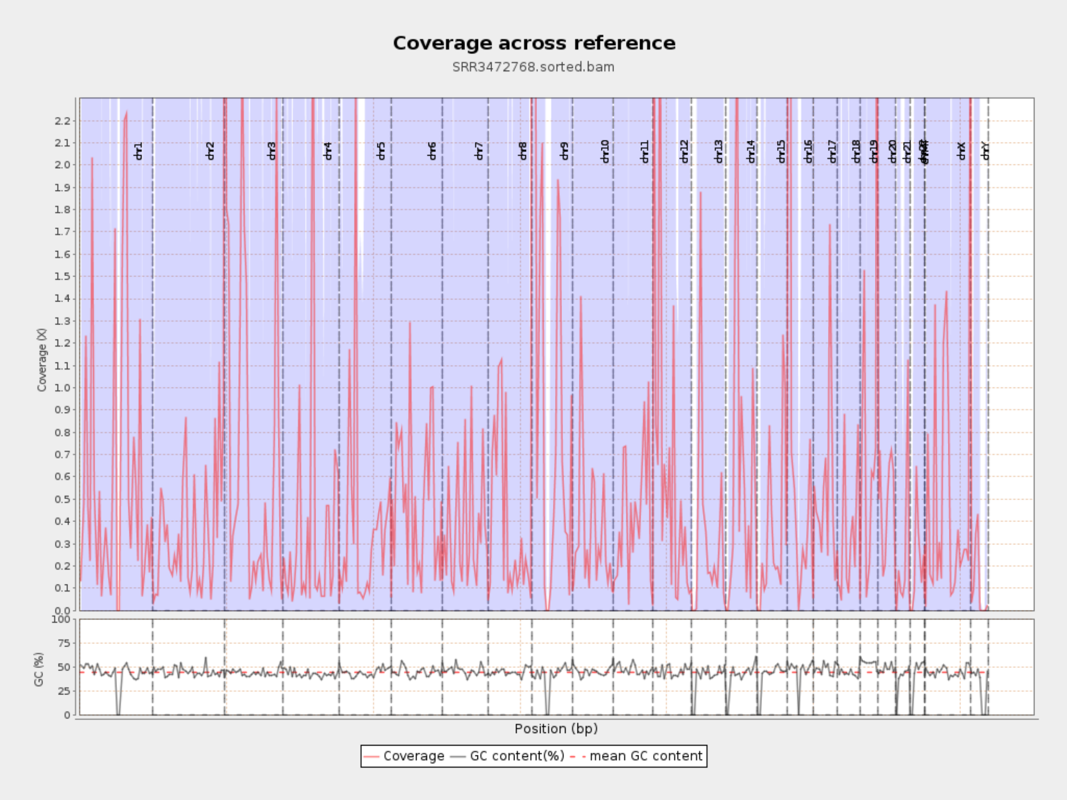
2.7. Chromosome stats

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

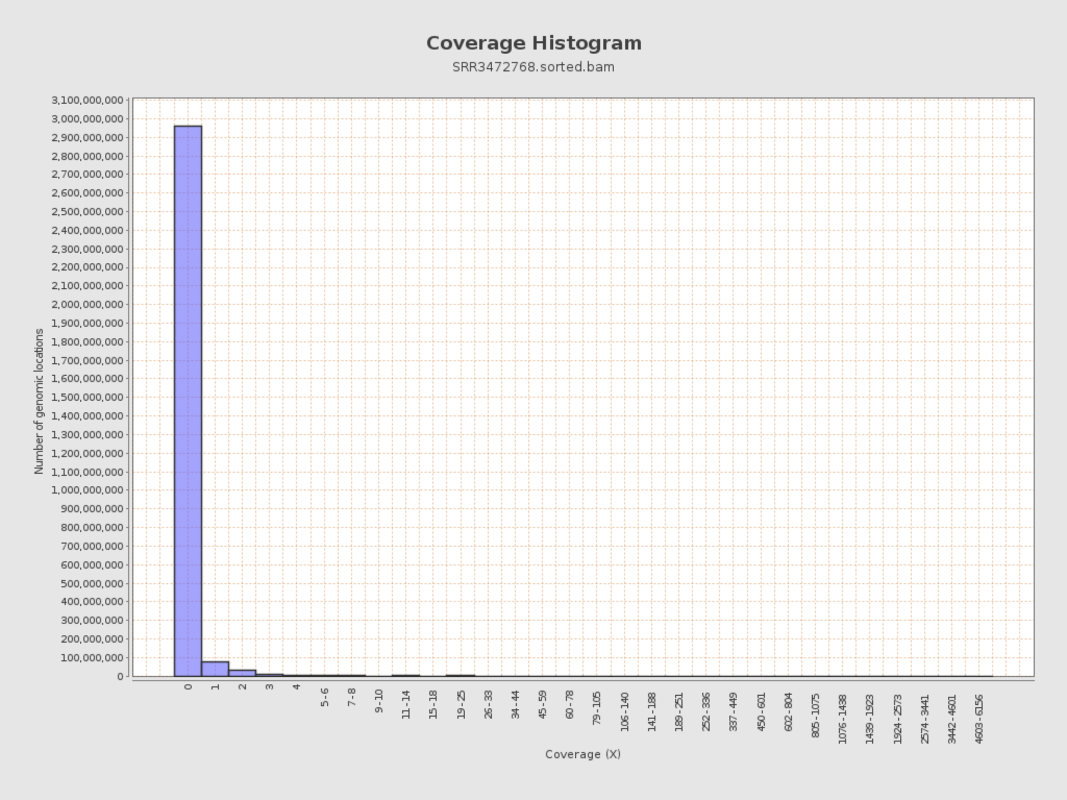
		bases	coverage	deviation
chr1	249250621	154780642	0.621	20.7644
chr2	243199373	83715283	0.3442	11.4672
chr3	198022430	156672121	0.7912	18.7951
chr4	191154276	67941167	0.3554	16.1079
chr5	180915260	71409402	0.3947	12.1038
chr6	171115067	85458053	0.4994	15.7082
chr7	159138663	59936576	0.3766	10.5985
chr8	146364022	56995479	0.3894	12.2517
chr9	141213431	142752621	1.0109	25.8366
chr10	135534747	50174570	0.3702	17.4079
chr11	135006516	58907127	0.4363	14.2376
chr12	133851895	97278601	0.7268	23.1933
chr13	115169878	40710919	0.3535	15.8636
chr14	107349540	67974521	0.6332	21.6289
chr15	102531392	36907827	0.36	11.0121
chr16	90354753	86997898	0.9628	31.3038
chr17	81195210	42912299	0.5285	12.057
chr18	78077248	26725346	0.3423	15.359
chr19	59128983	42798783	0.7238	17.4177
chr20	63025520	30752272	0.4879	15.3938
chr21	48129895	12703093	0.2639	12.229
chr22	51304566	11464331	0.2235	8.0794
chrMT	16571	4833	0.2917	0.8238
chrX	155270560	72916908	0.4696	14.3382

chrY	59373566	7138061	0.1202	4.5502

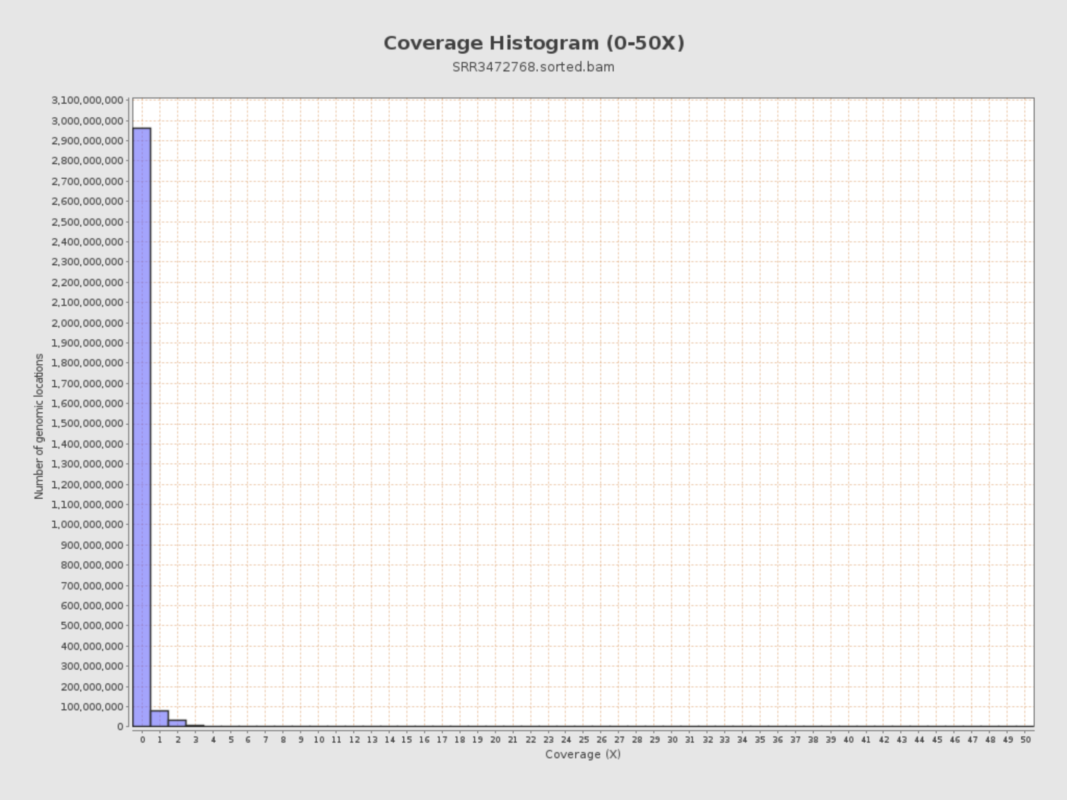
3. Results : Coverage across reference



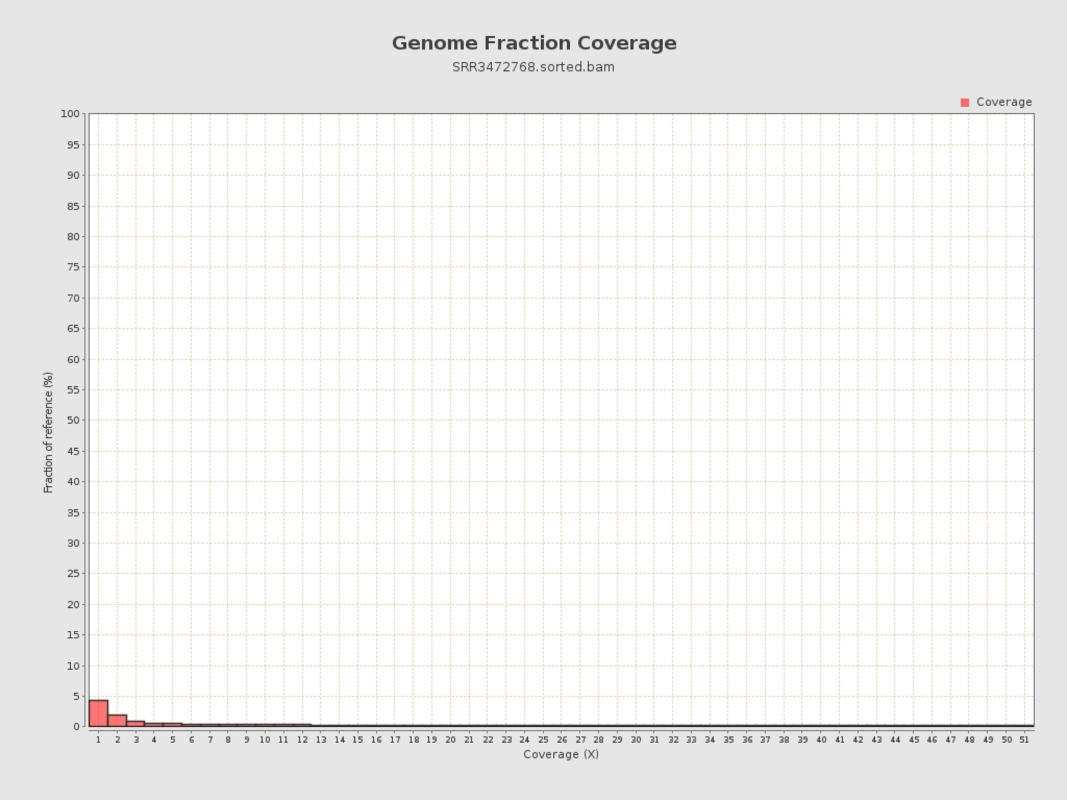
4. Results : Coverage Histogram



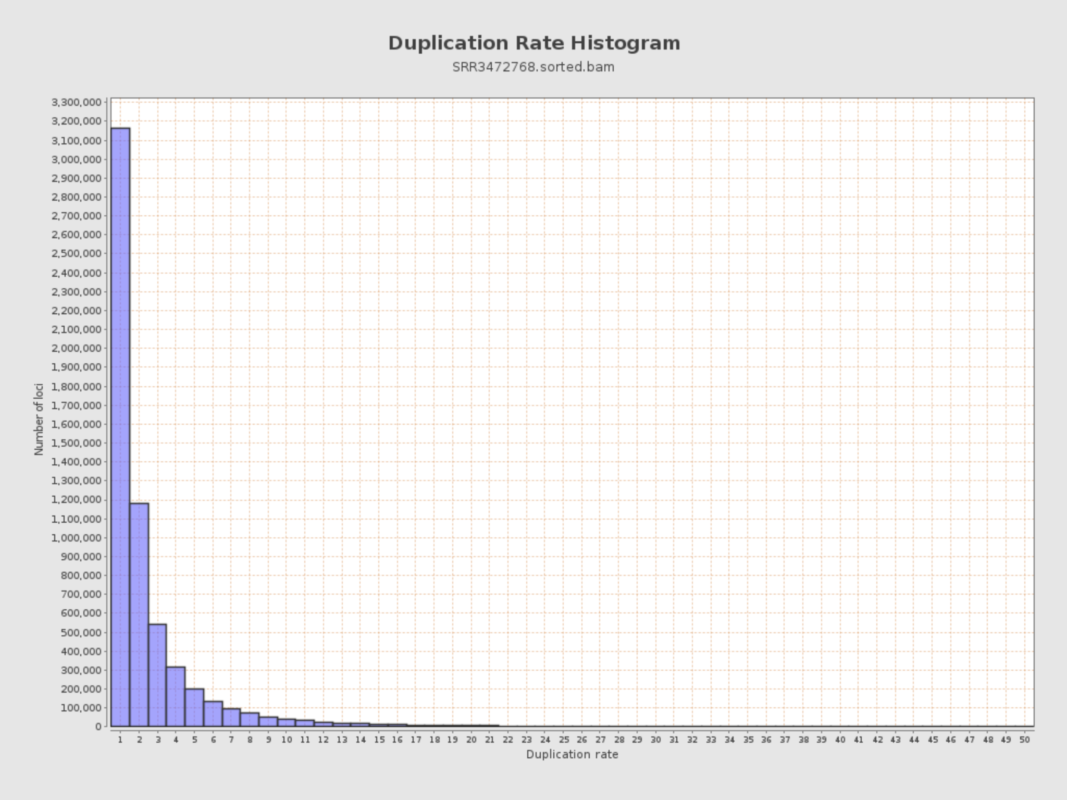
5. Results : Coverage Histogram (0-50X)



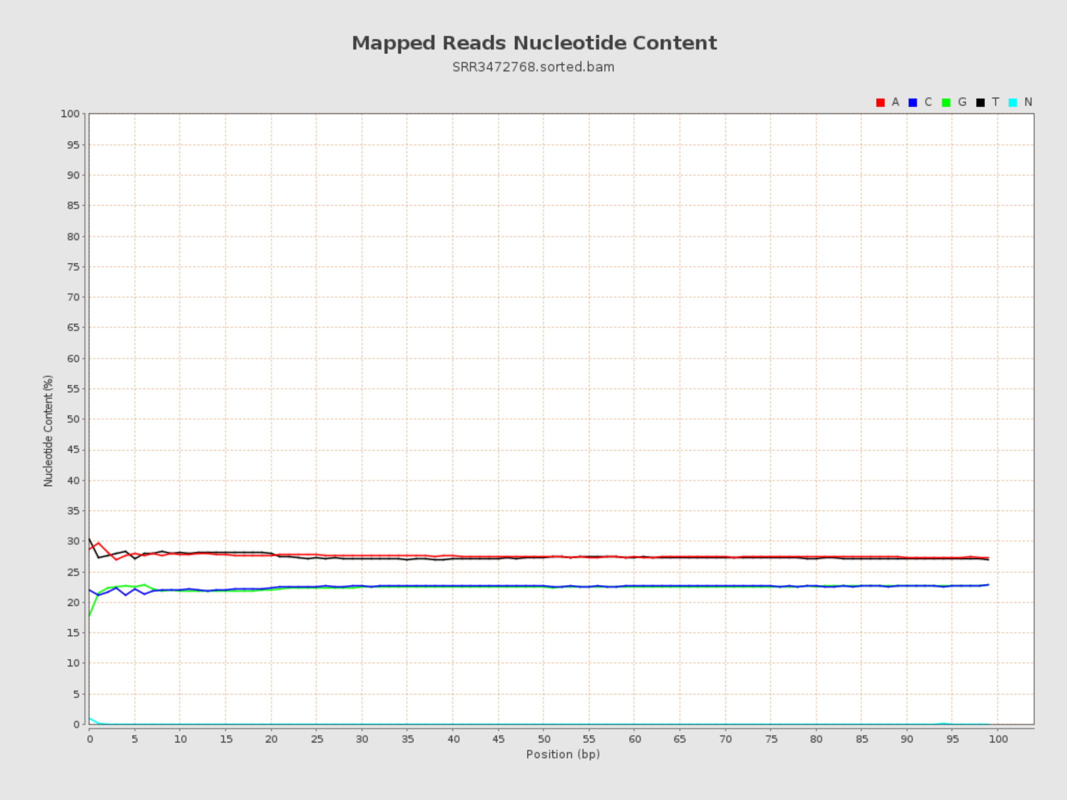
6. Results : Genome Fraction Coverage



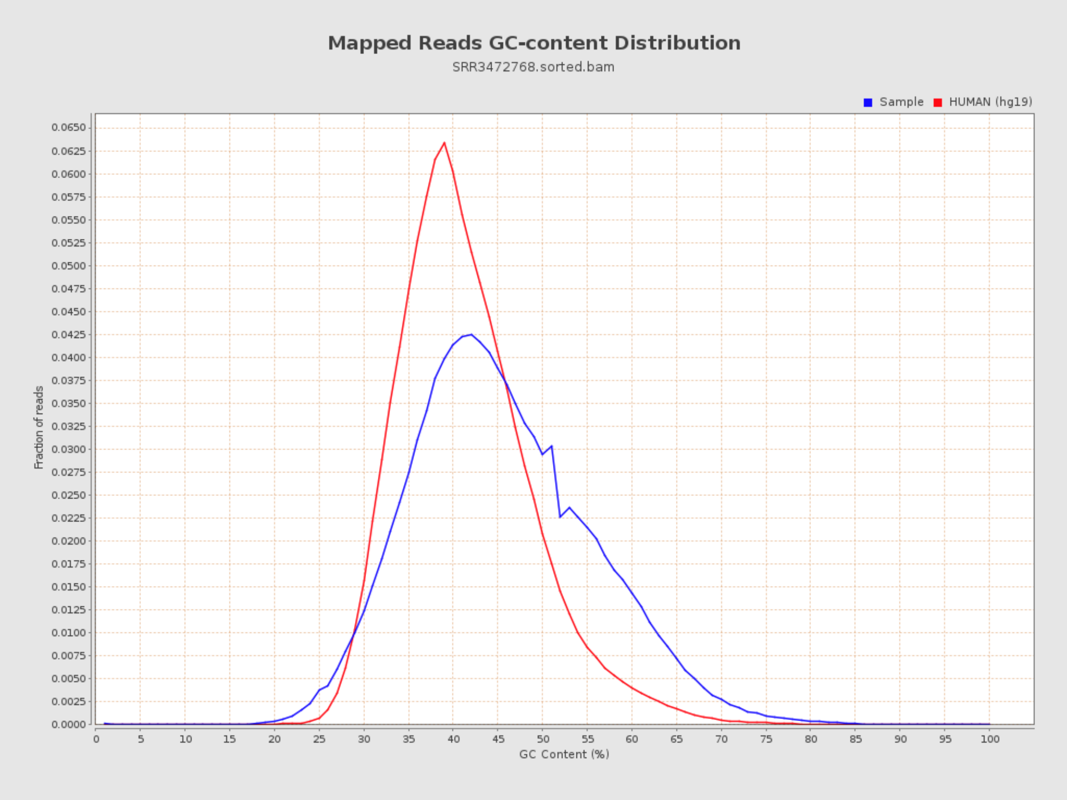
7. Results : Duplication Rate Histogram



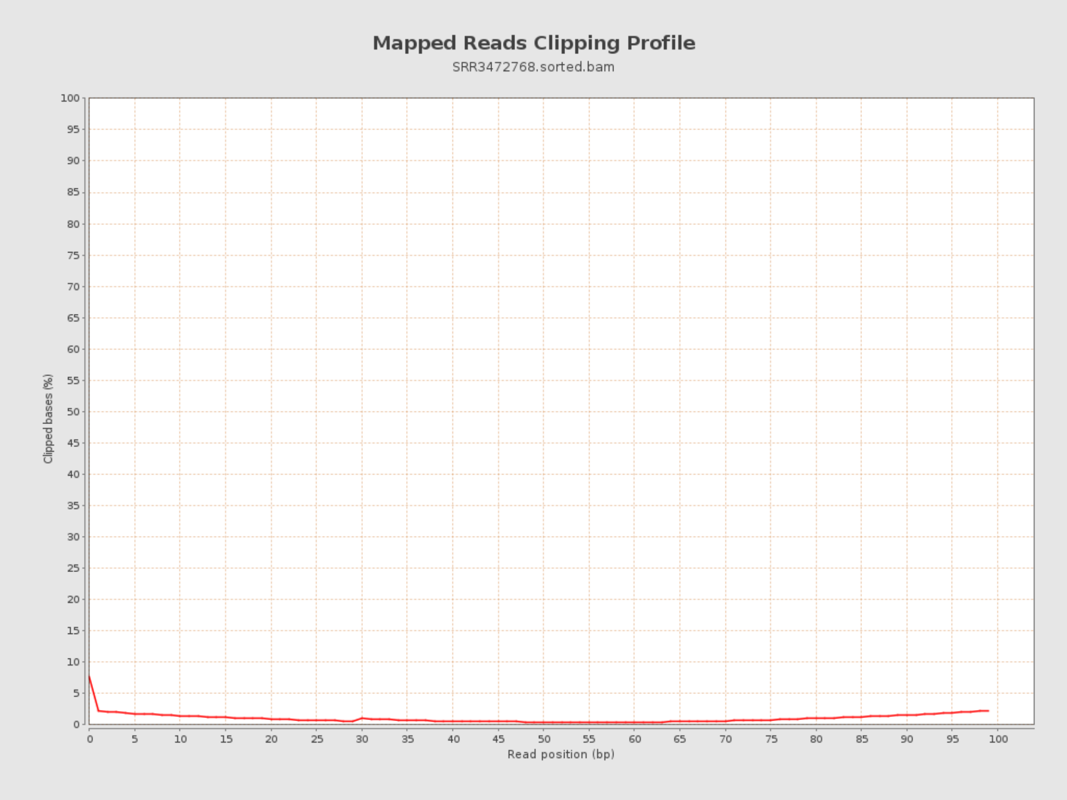
8. Results : Mapped Reads Nucleotide Content



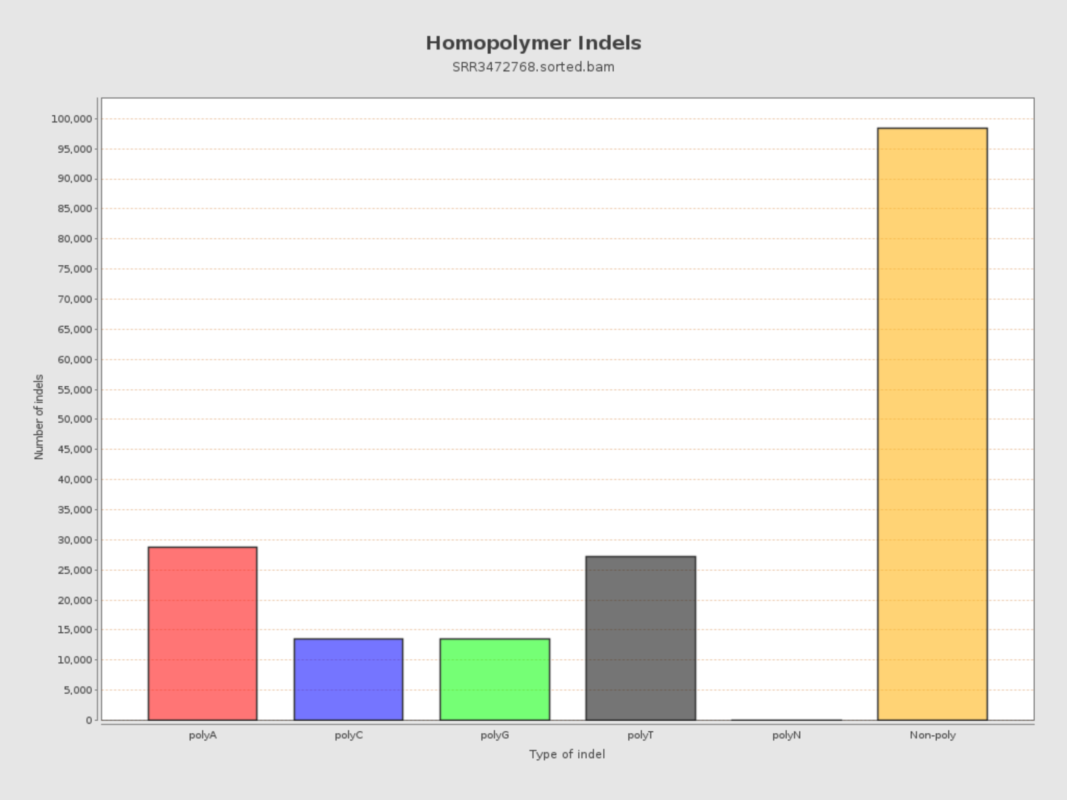
9. Results : Mapped Reads GC-content Distribution



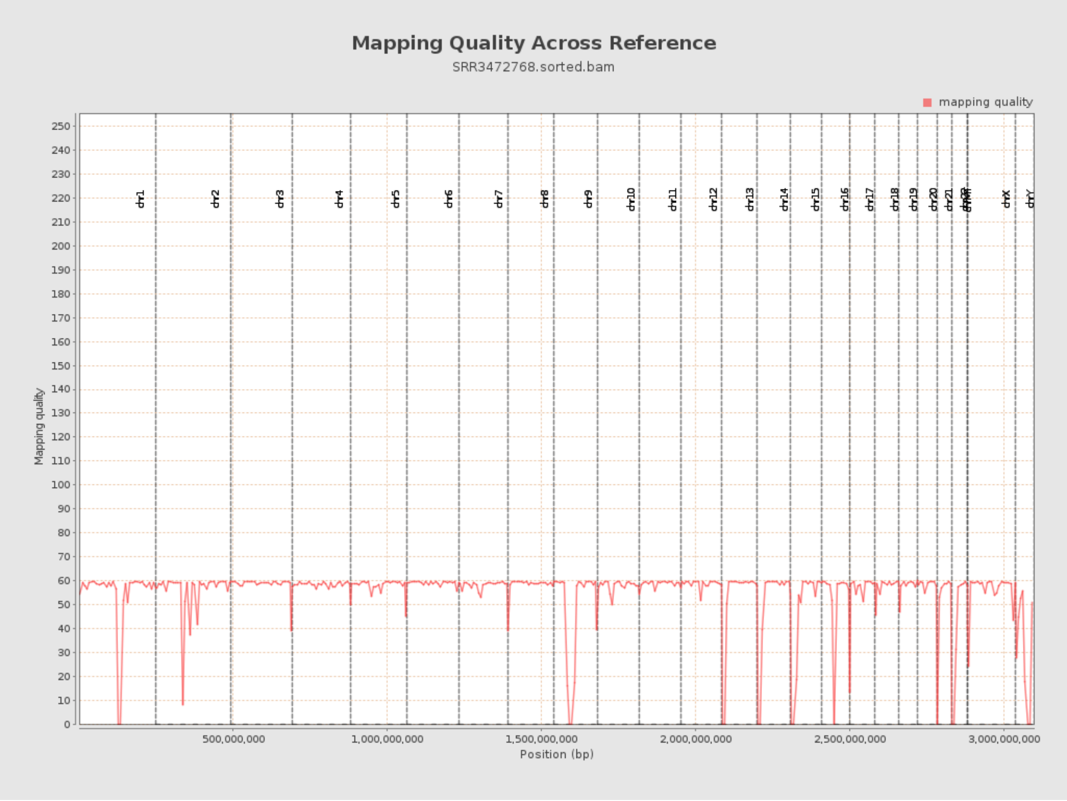
10. Results : Mapped Reads Clipping Profile



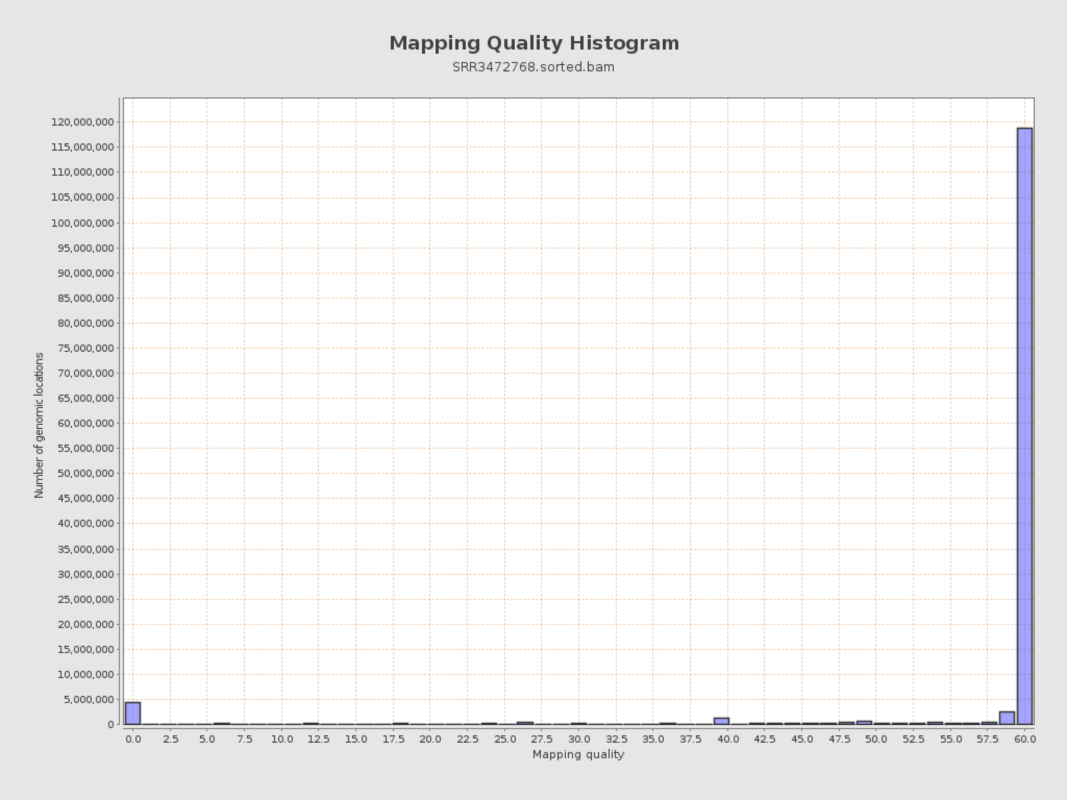
11. Results : Homopolymer Indels



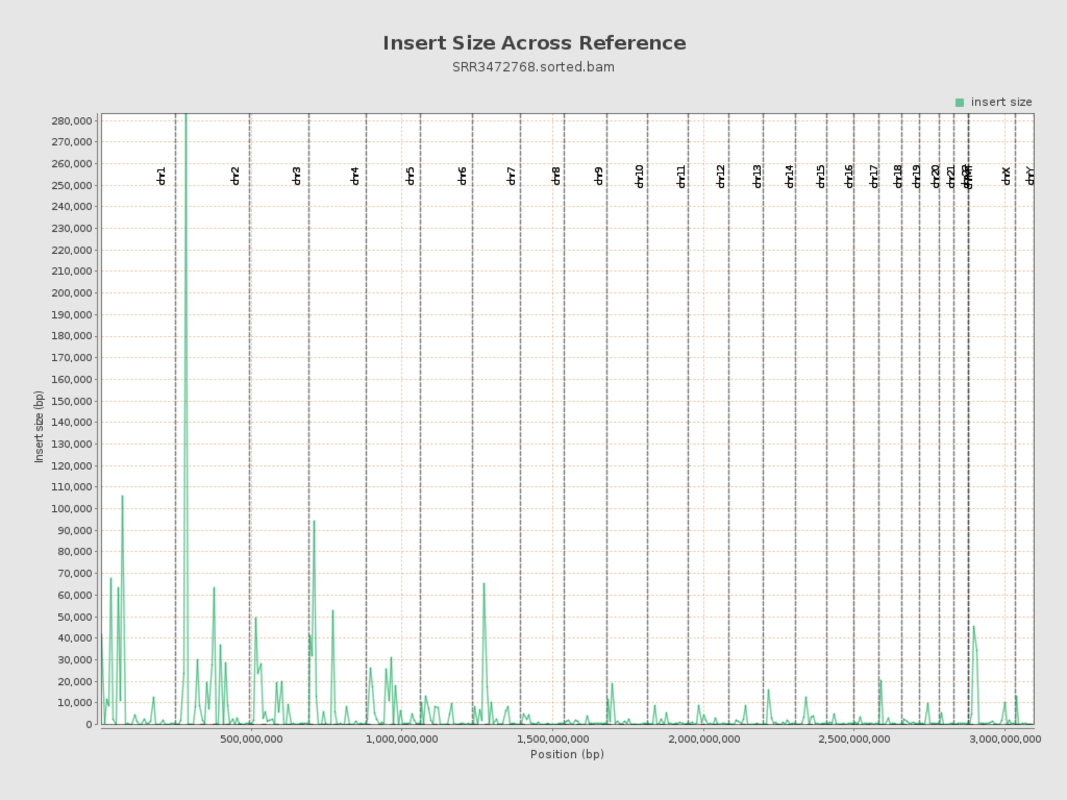
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram