Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 03:23:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472585.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_SRR3472585 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472585_1.fastq.gz SRR3472585_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 03:23:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472585.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,858,632
Mapped reads	8,009,113 / 90.41%
Unmapped reads	849,519 / 9.59%
Mapped paired reads	8,009,113 / 90.41%
Mapped reads, first in pair	4,041,888 / 45.63%
Mapped reads, second in pair	3,967,225 / 44.78%
Mapped reads, both in pair	7,818,342 / 88.26%
Mapped reads, singletons	190,771 / 2.15%
Secondary alignments	0
Supplementary alignments	201,498 / 2.27%
Read min/max/mean length	30 / 100 / 100.88
Duplicated reads (estimated)	1,339,017 / 15.12%
Duplication rate	14.38%
Clipped reads	6,115,233 / 69.03%

2.2. ACGT Content

Number/percentage of A's	169,822,348 / 26.25%
Number/percentage of C's	126,313,315 / 19.53%
Number/percentage of T's	195,486,909 / 30.22%
Number/percentage of G's	154,826,091 / 23.93%
Number/percentage of N's	430,659 / 0.07%

GC Percentage	43.46%

2.3. Coverage

Mean	0.2091
Standard Deviation	2.2744

2.4. Mapping Quality

Mean Mapping Quality	50.68

2.5. Insert size

Mean	163,932.63
Standard Deviation	3,860,462.86
P25/Median/P75	90 / 130 / 183

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	7,764,589
Insertions	60,813
Mapped reads with at least one insertion	0.75%
Deletions	148,016
Mapped reads with at least one deletion	1.81%
Homopolymer indels	43.37%

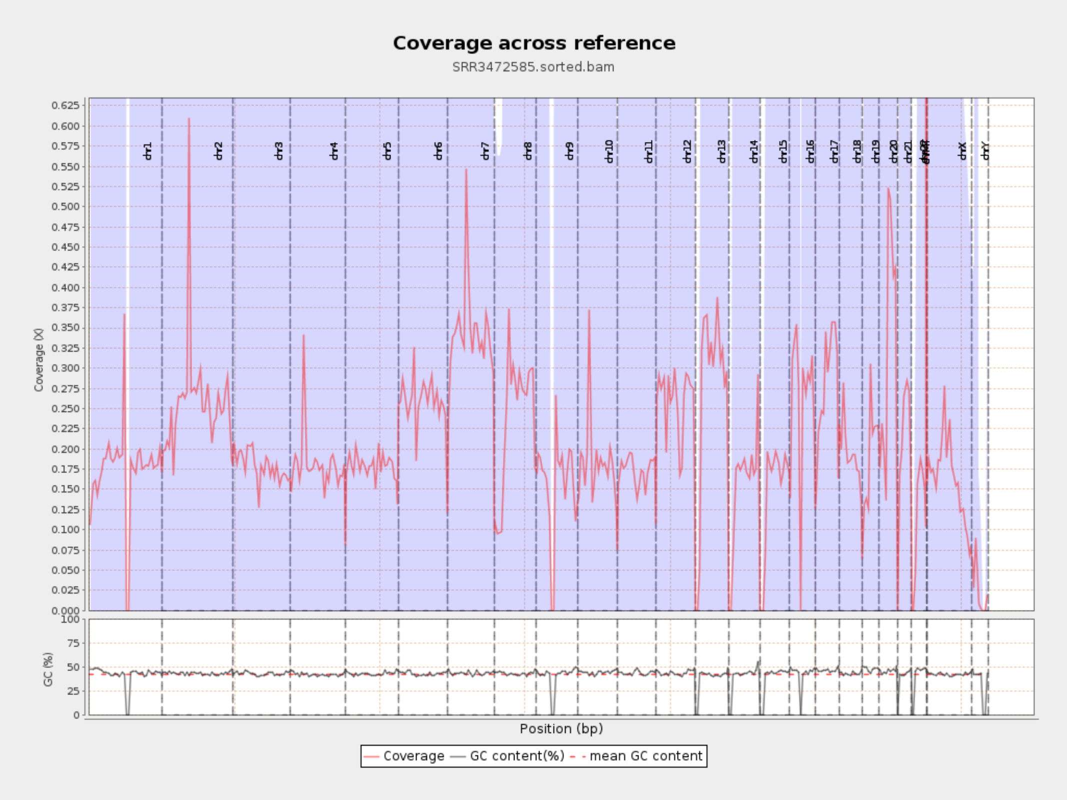
2.7. Chromosome stats

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

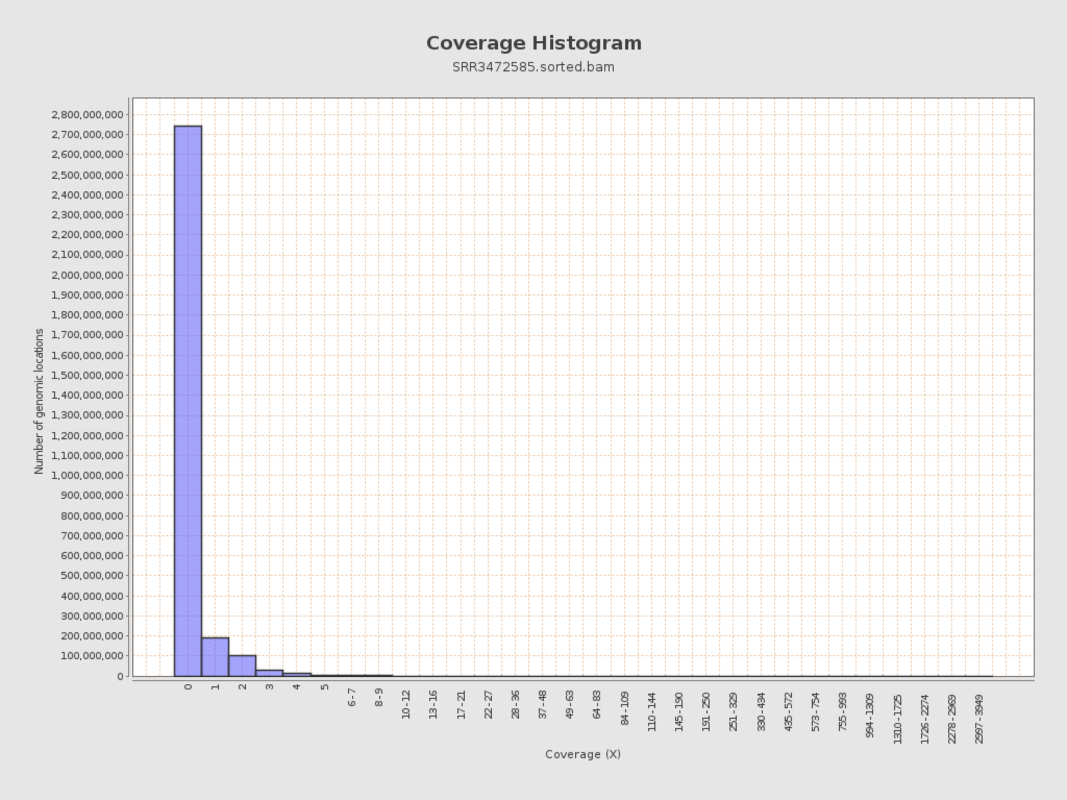
		bases	coverage	deviation
chr1	249250621	43354085	0.1739	3.4021
chr2	243199373	62956361	0.2589	2.9698
chr3	198022430	35397721	0.1788	0.6442
chr4	191154276	34515955	0.1806	1.1377
chr5	180915260	32405723	0.1791	0.6779
chr6	171115067	44399923	0.2595	1.1749
chr7	159138663	55531085	0.3489	3.9022
chr8	146364022	34785291	0.2377	1.8395
chr9	141213431	21971168	0.1556	2.0534
chr10	135534747	25065514	0.1849	2.072
chr11	135006516	23072132	0.1709	1.2219
chr12	133851895	34528404	0.258	0.8062
chr13	115169878	31055972	0.2697	0.8232
chr14	107349540	16632327	0.1549	6.1277
chr15	102531392	15088697	0.1472	0.5921
chr16	90354753	23621537	0.2614	1.223
chr17	81195210	22739010	0.2801	1.7056
chr18	78077248	15416203	0.1974	3.2044
chr19	59128983	11302790	0.1912	2.1249
chr20	63025520	20488082	0.3251	1.3608
chr21	48129895	9917182	0.2061	0.8709
chr22	51304566	5728451	0.1117	0.5172
chrMT	16571	238826	14.4123	9.0085
chrX	155270560	25484594	0.1641	0.9066

chrY	59373566	1458285	0.0246	0.9556

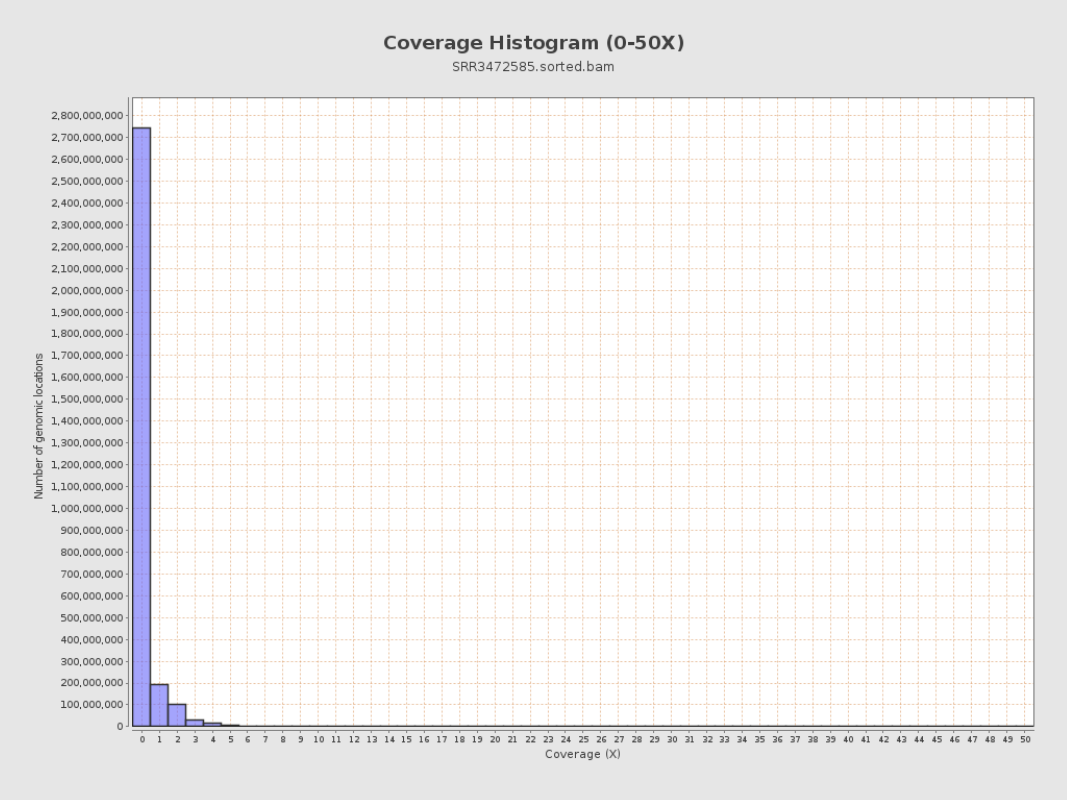
3. Results : Coverage across reference



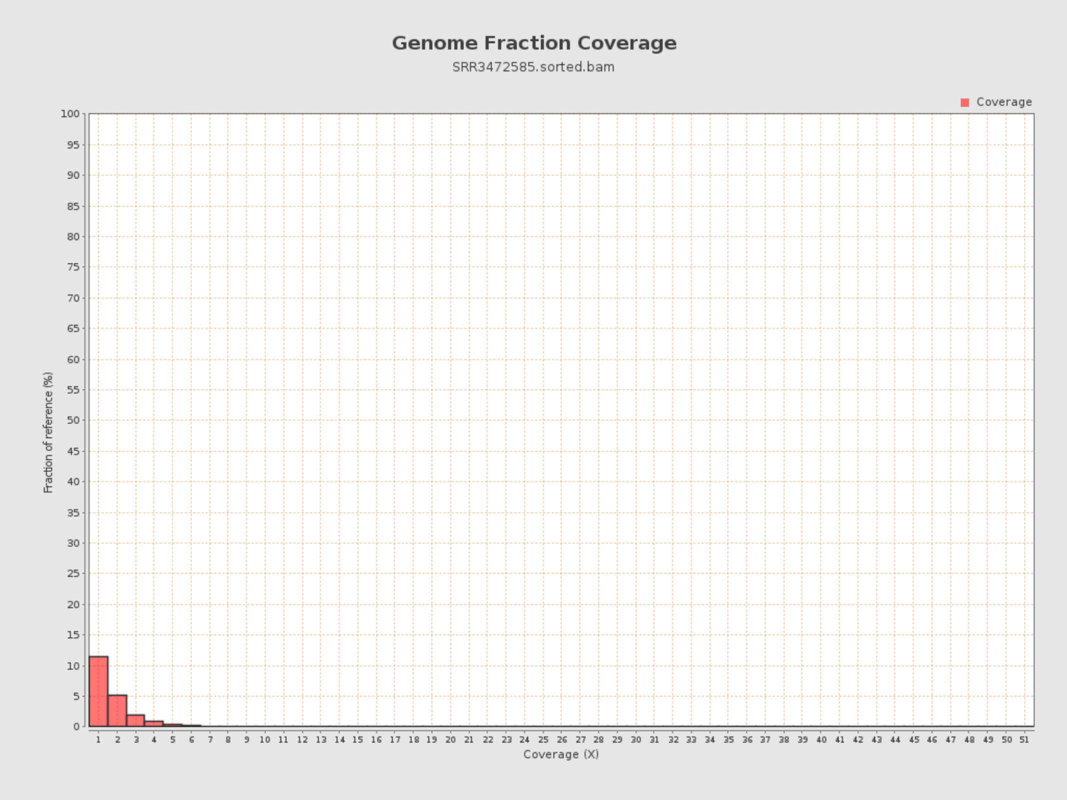
4. Results : Coverage Histogram



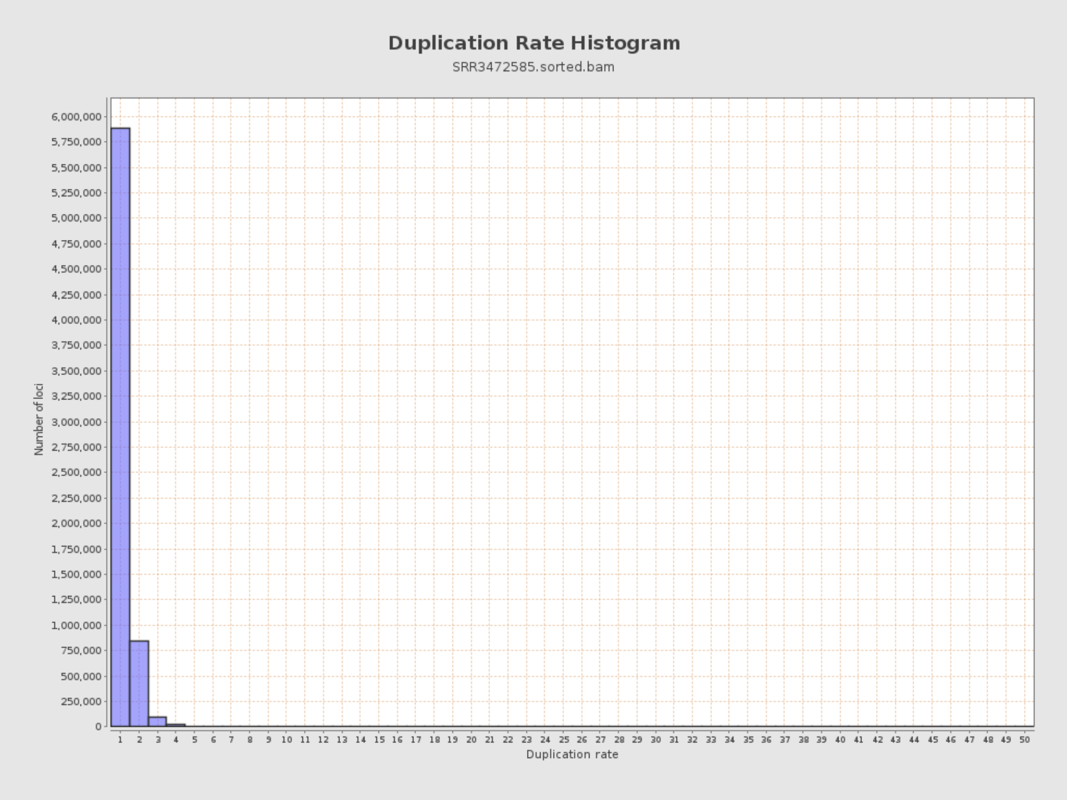
5. Results : Coverage Histogram (0-50X)



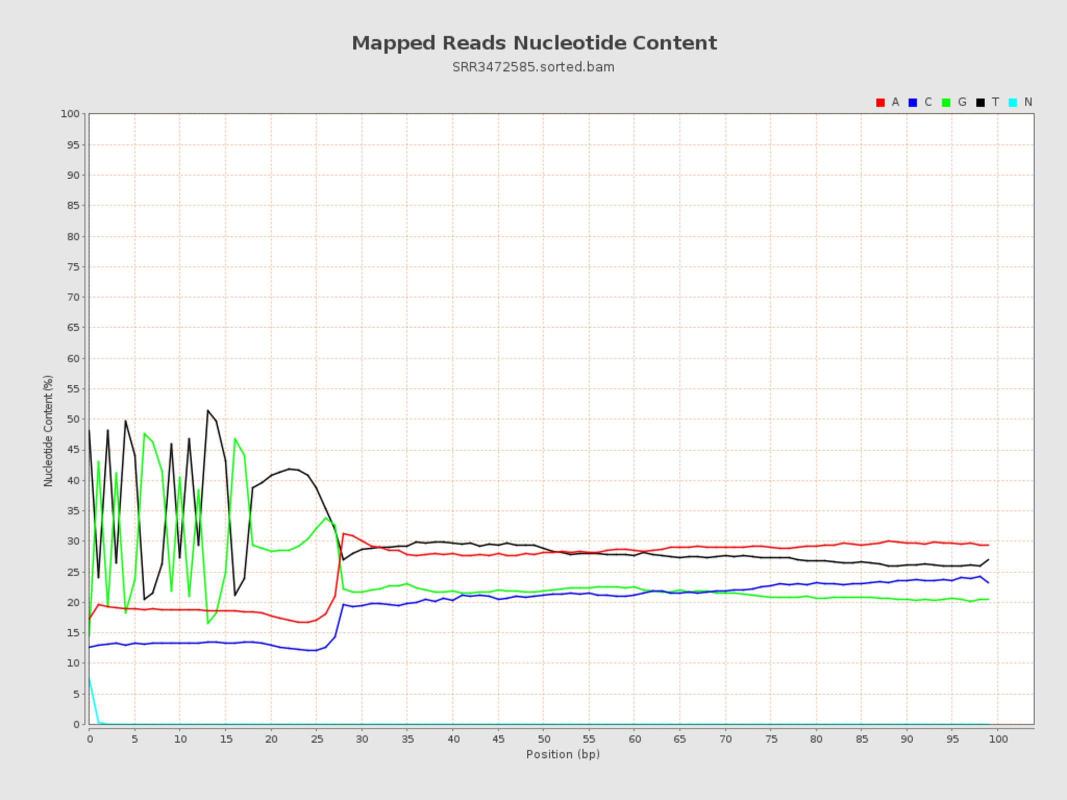
6. Results : Genome Fraction Coverage



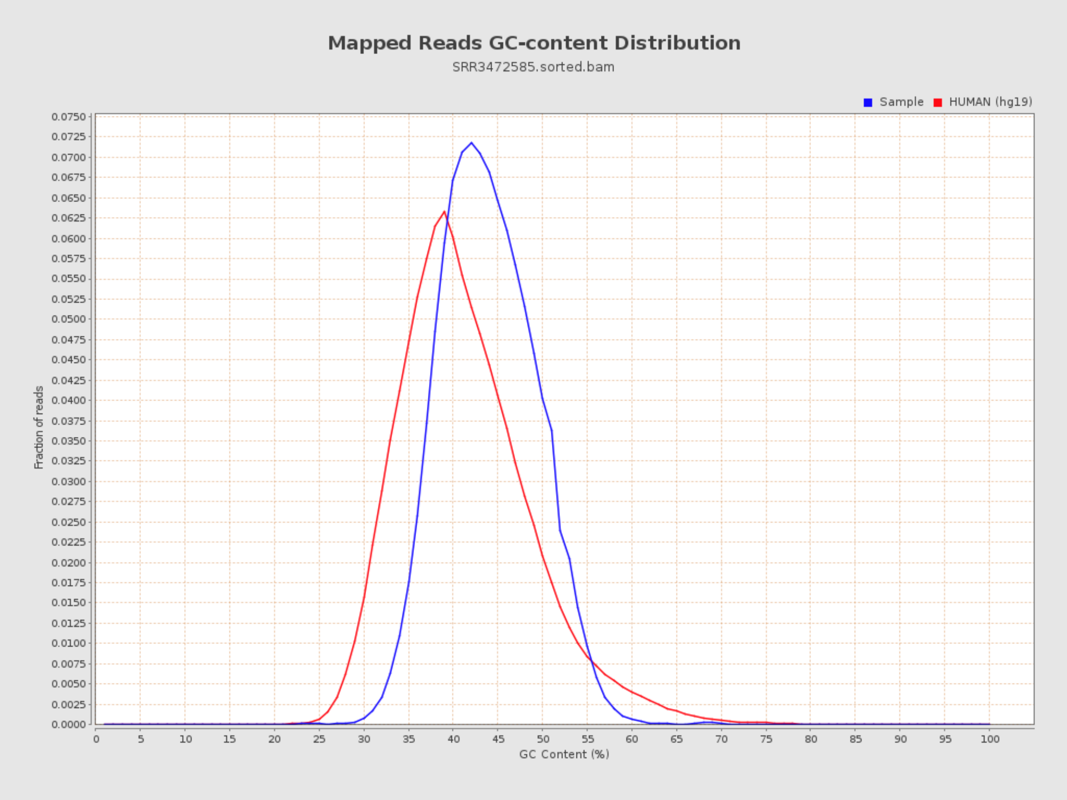
7. Results : Duplication Rate Histogram



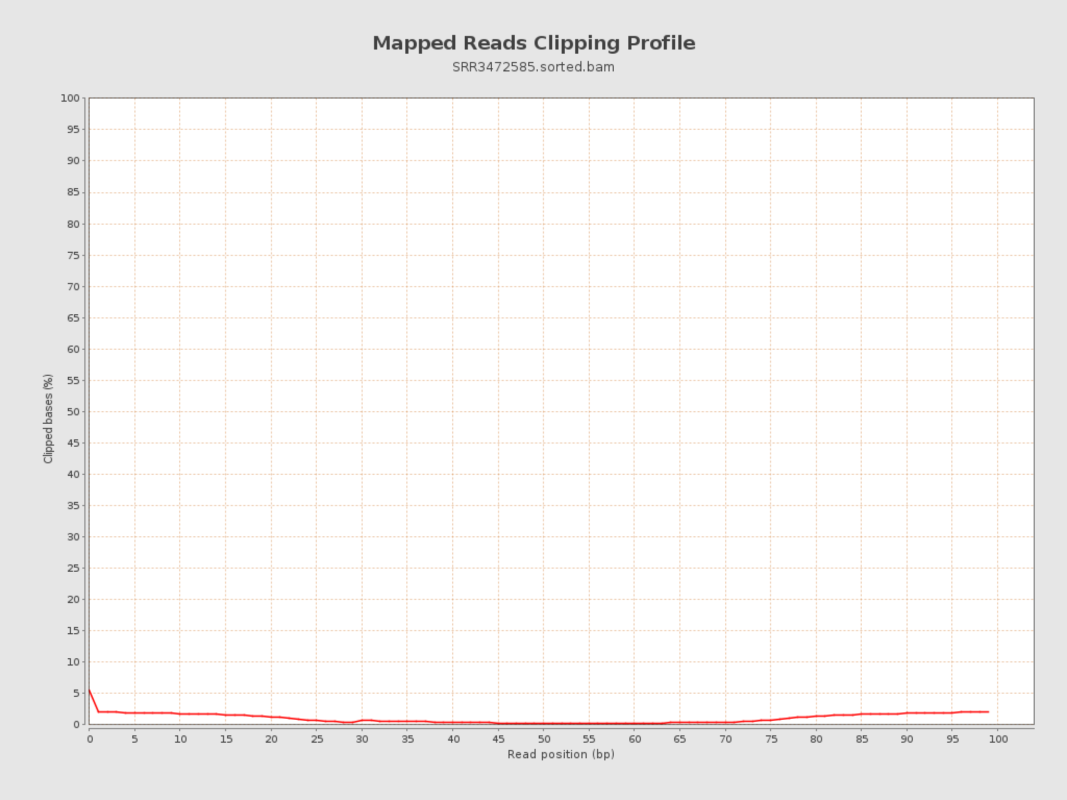
8. Results : Mapped Reads Nucleotide Content



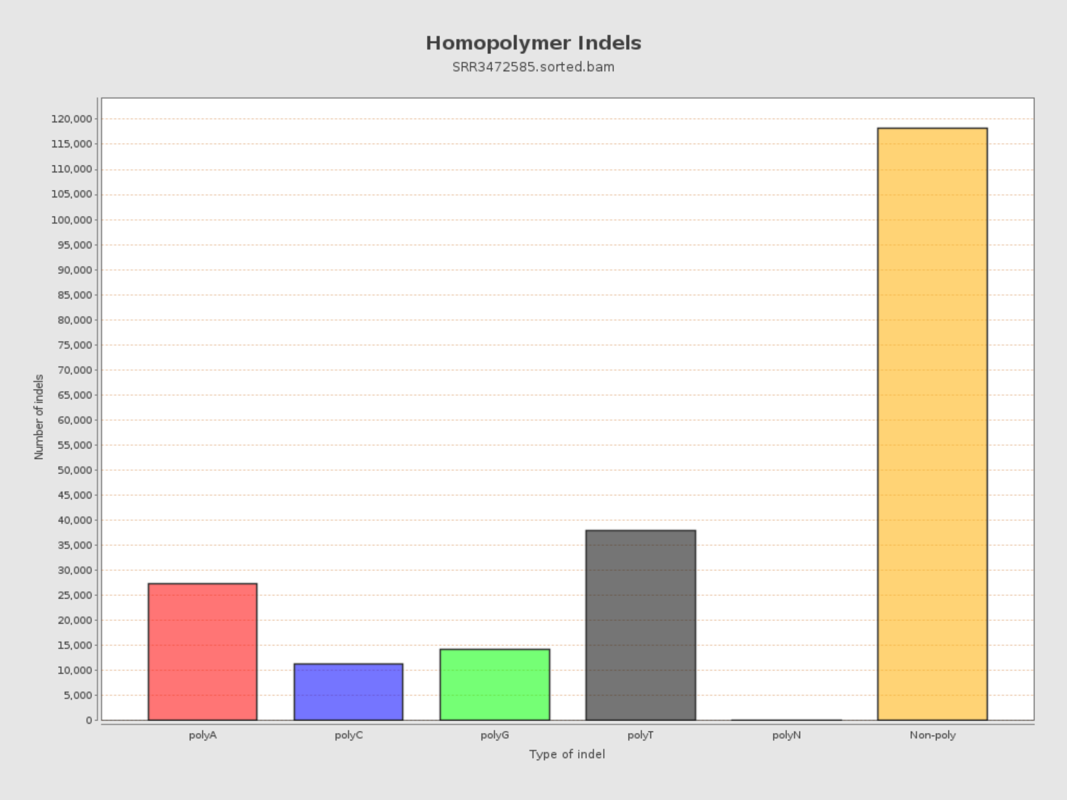
9. Results : Mapped Reads GC-content Distribution



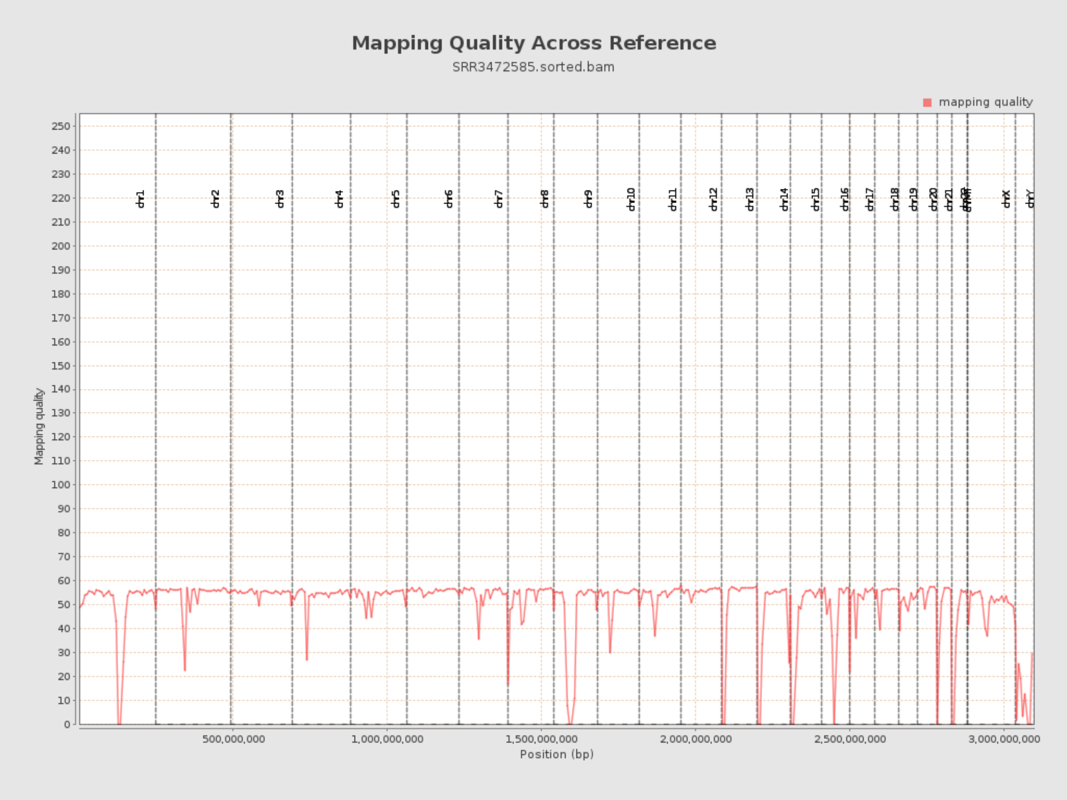
10. Results : Mapped Reads Clipping Profile



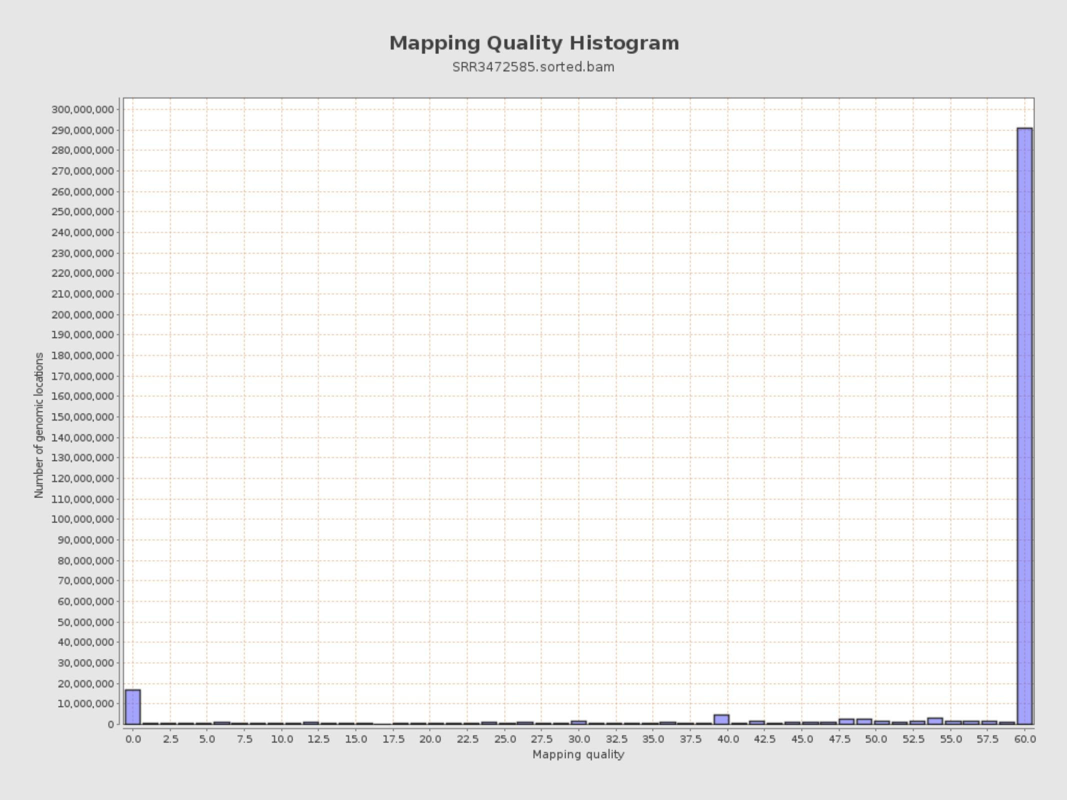
11. Results : Homopolymer Indels



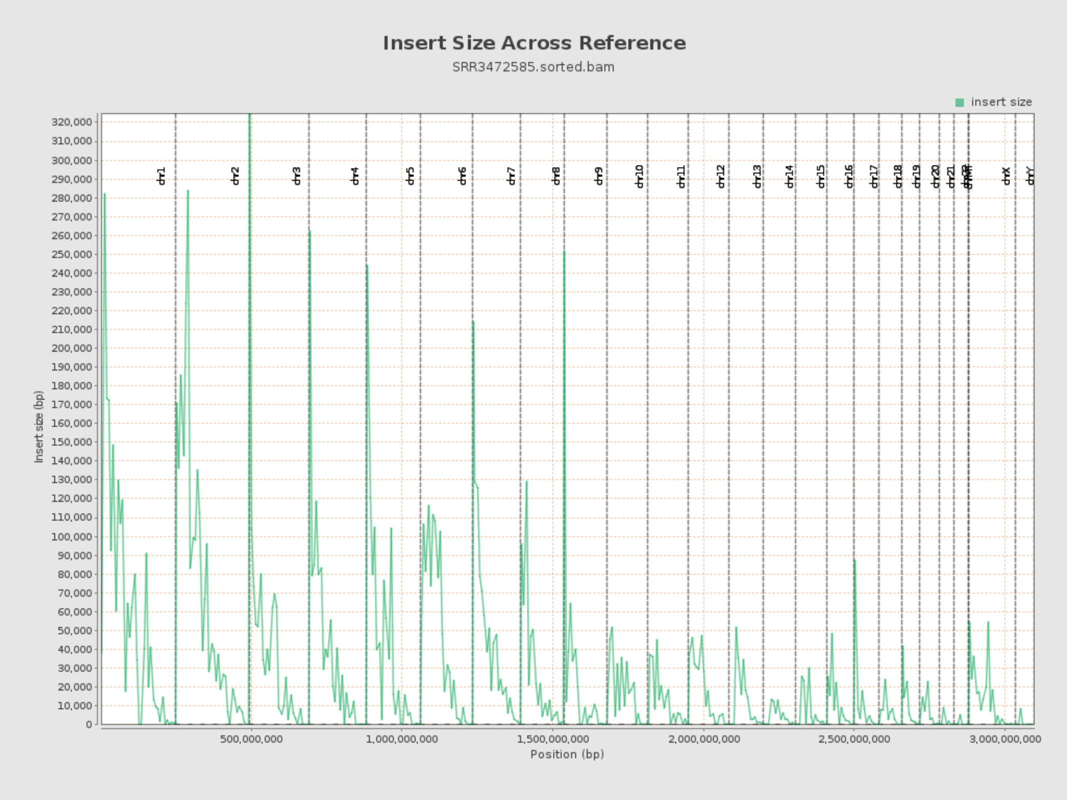
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram