Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 02:12:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472580.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_SRR3472580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472580_1.fastq.gz SRR3472580_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 02:12:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,371,370
Mapped reads	6,720,702 / 91.17%
Unmapped reads	650,668 / 8.83%
Mapped paired reads	6,720,702 / 91.17%
Mapped reads, first in pair	3,390,882 / 46%
Mapped reads, second in pair	3,329,820 / 45.17%
Mapped reads, both in pair	6,545,968 / 88.8%
Mapped reads, singletons	174,734 / 2.37%
Secondary alignments	0
Supplementary alignments	218,787 / 2.97%
Read min/max/mean length	30 / 100 / 101.16
Duplicated reads (estimated)	993,186 / 13.47%
Duplication rate	12.88%
Clipped reads	5,223,955 / 70.87%

2.2. ACGT Content

Number/percentage of A's	140,057,261 / 25.77%
Number/percentage of C's	108,394,790 / 19.95%
Number/percentage of T's	162,136,352 / 29.83%
Number/percentage of G's	132,504,682 / 24.38%
Number/percentage of N's	363,123 / 0.07%

GC Percentage	44.33%

2.3. Coverage

Mean	0.1756
Standard Deviation	1.7744

2.4. Mapping Quality

Mean Mapping Quality	50.31

2.5. Insert size

Mean	257,971.59
Standard Deviation	4,913,032.79
P25/Median/P75	90 / 128 / 179

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	6,547,912
Insertions	52,138
Mapped reads with at least one insertion	0.76%
Deletions	124,118
Mapped reads with at least one deletion	1.81%
Homopolymer indels	42.43%

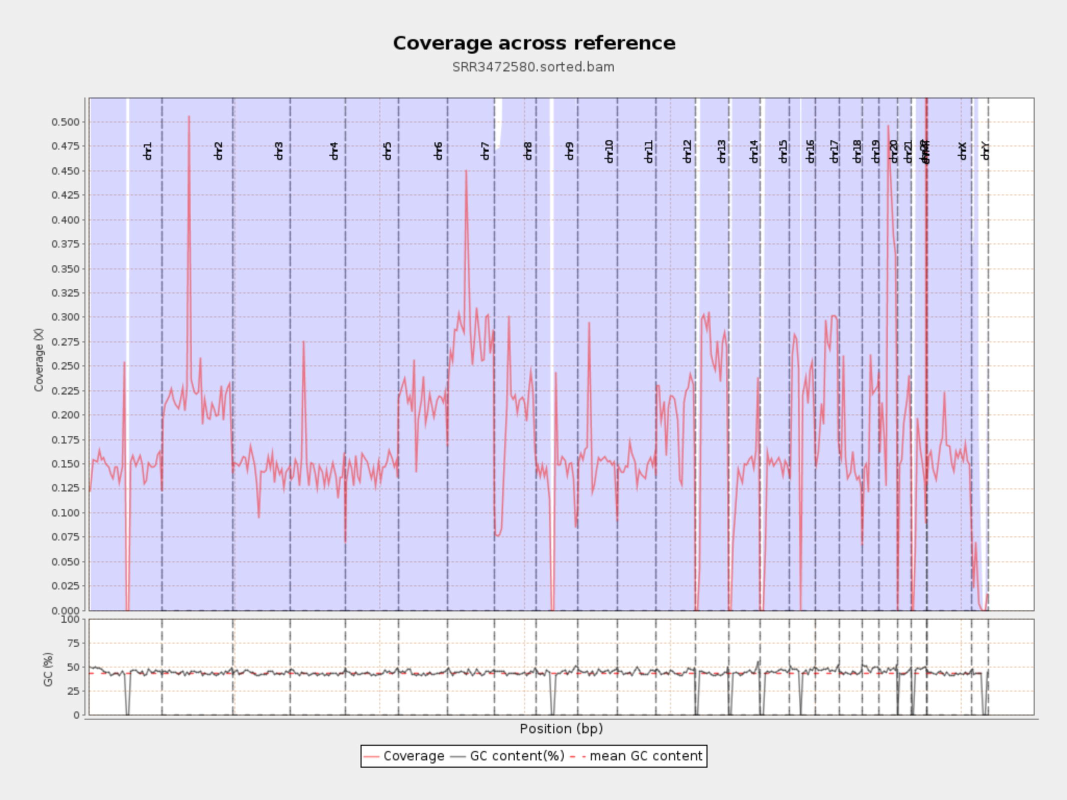
2.7. Chromosome stats

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

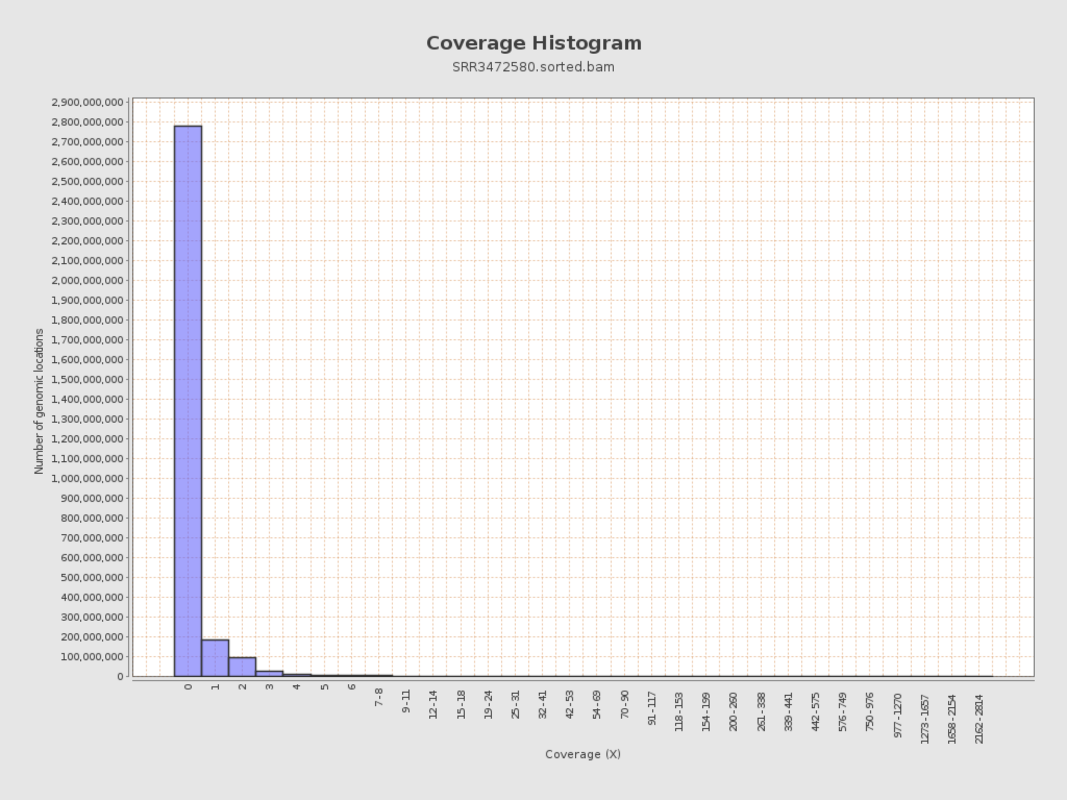
		bases	coverage	deviation
chr1	249250621	35457467	0.1423	2.1553
chr2	243199373	54483955	0.224	2.3888
chr3	198022430	28744903	0.1452	0.5504
chr4	191154276	27898670	0.1459	0.9371
chr5	180915260	26359462	0.1457	0.5839
chr6	171115067	36462662	0.2131	1.023
chr7	159138663	46381949	0.2915	3.2753
chr8	146364022	27096465	0.1851	1.6066
chr9	141213431	18365926	0.1301	1.8713
chr10	135534747	21450366	0.1583	1.5874
chr11	135006516	19762987	0.1464	1.3436
chr12	133851895	27339298	0.2043	0.6807
chr13	115169878	26142661	0.227	0.7265
chr14	107349540	13737518	0.128	4.3039
chr15	102531392	12593618	0.1228	0.5142
chr16	90354753	19579465	0.2167	0.9672
chr17	81195210	19666628	0.2422	1.3059
chr18	78077248	12223122	0.1566	3.1832
chr19	59128983	11195177	0.1893	1.5568
chr20	63025520	18860919	0.2993	1.088
chr21	48129895	8124394	0.1688	0.7572
chr22	51304566	5634742	0.1098	0.4974
chrMT	16571	227321	13.718	9.8431
chrX	155270560	24698626	0.1591	0.862

chrY	59373566	1199818	0.0202	0.699

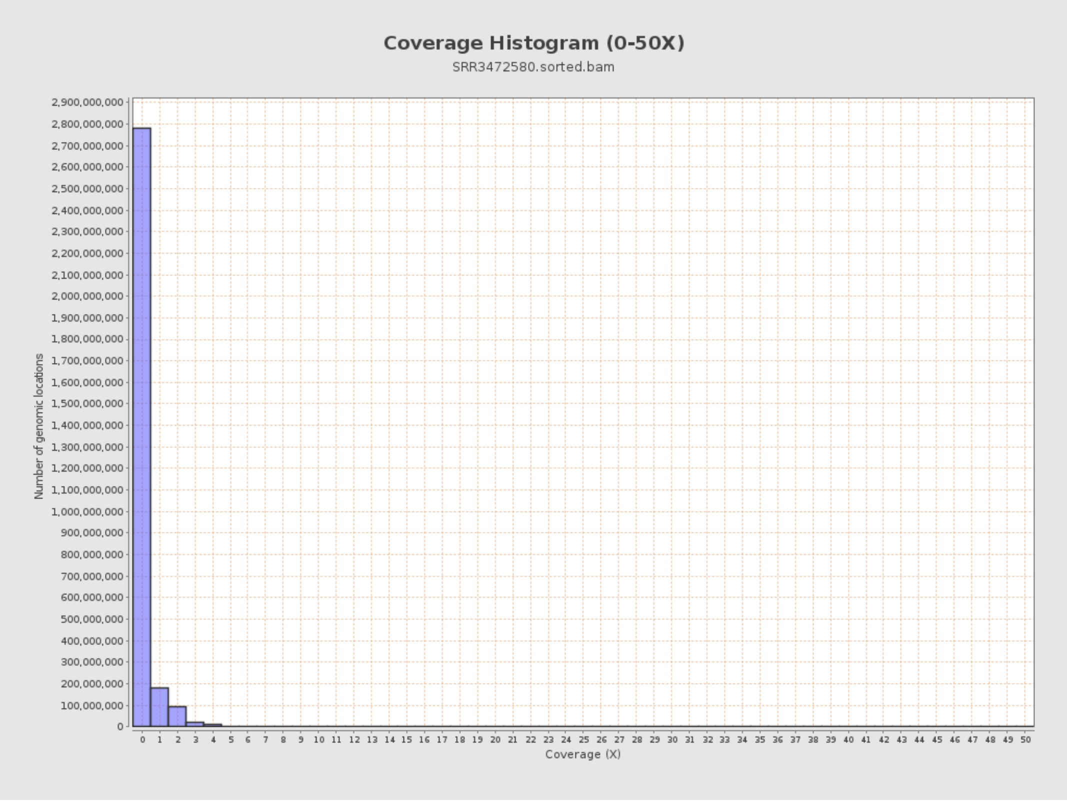
3. Results : Coverage across reference



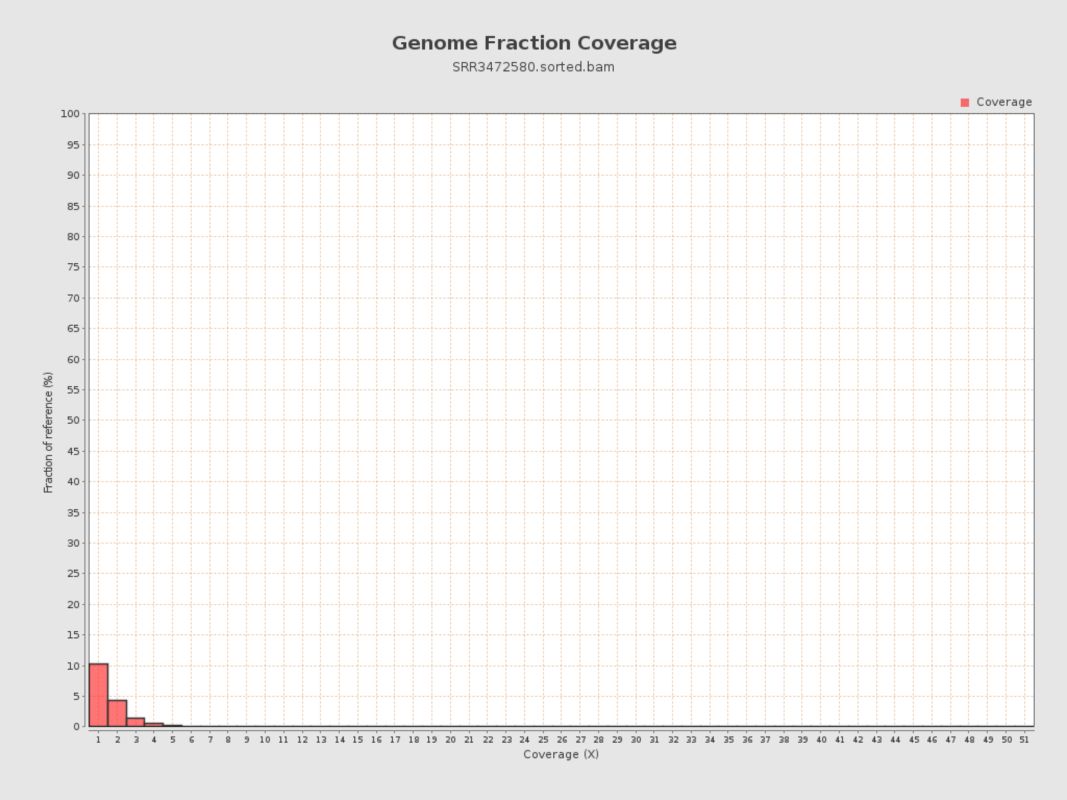
4. Results : Coverage Histogram



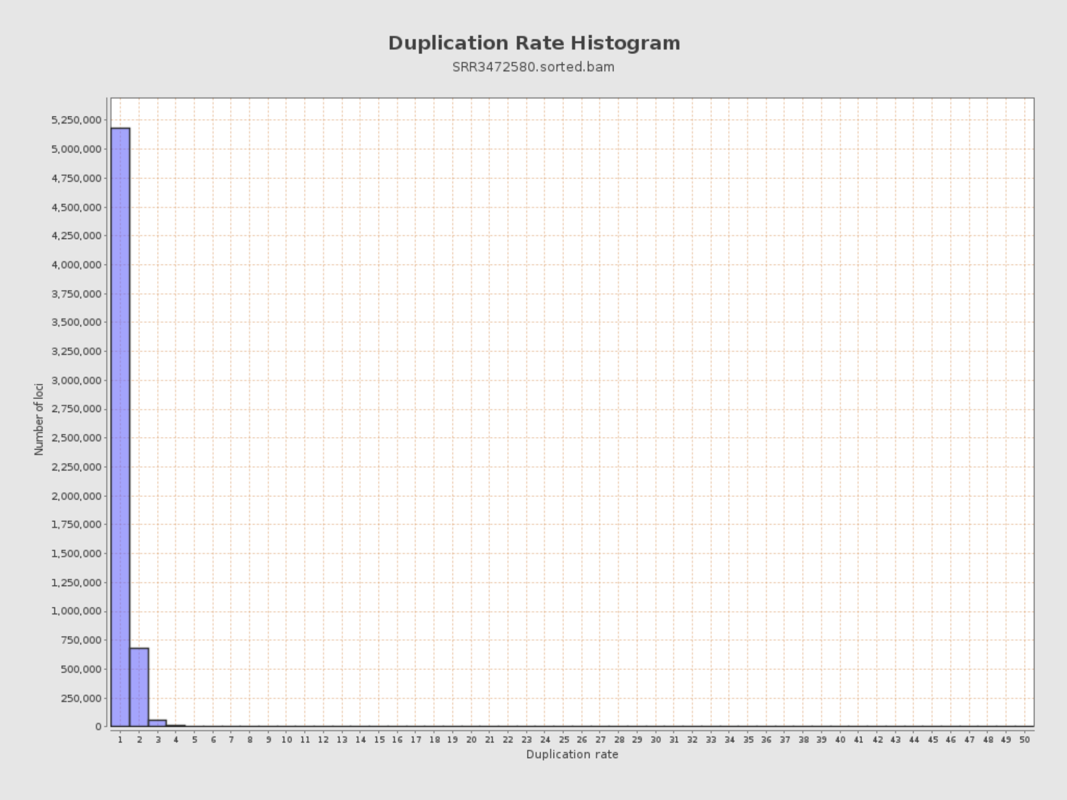
5. Results : Coverage Histogram (0-50X)



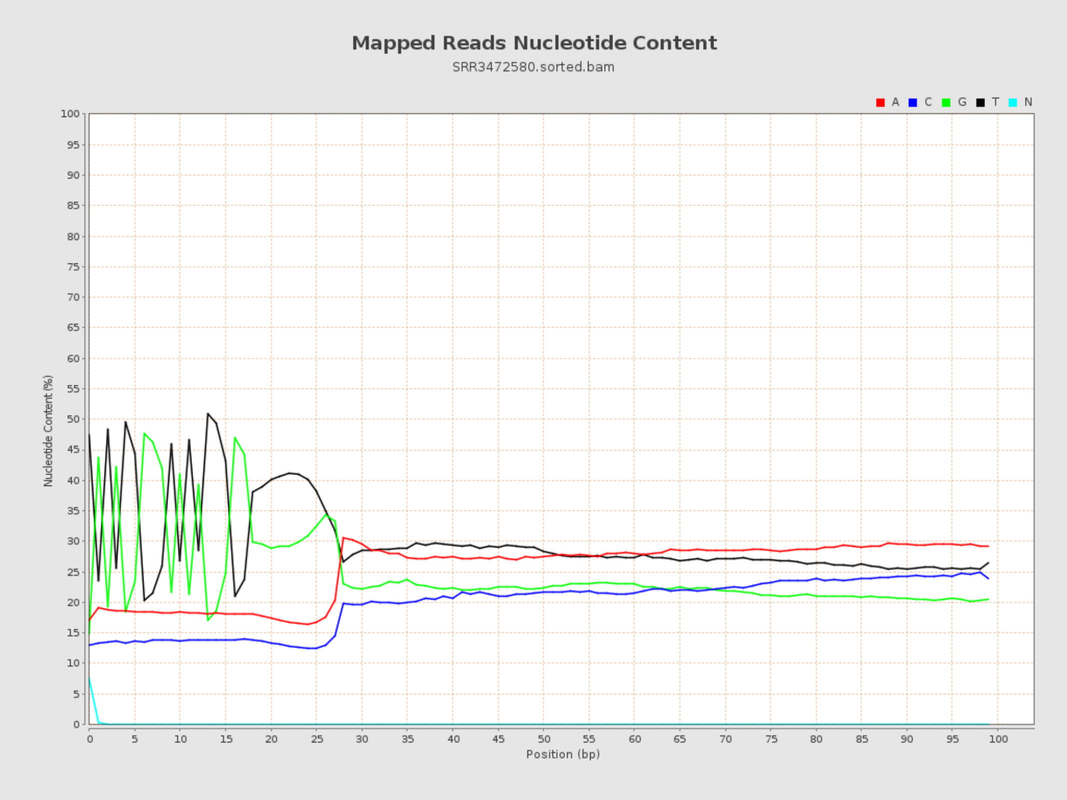
6. Results : Genome Fraction Coverage



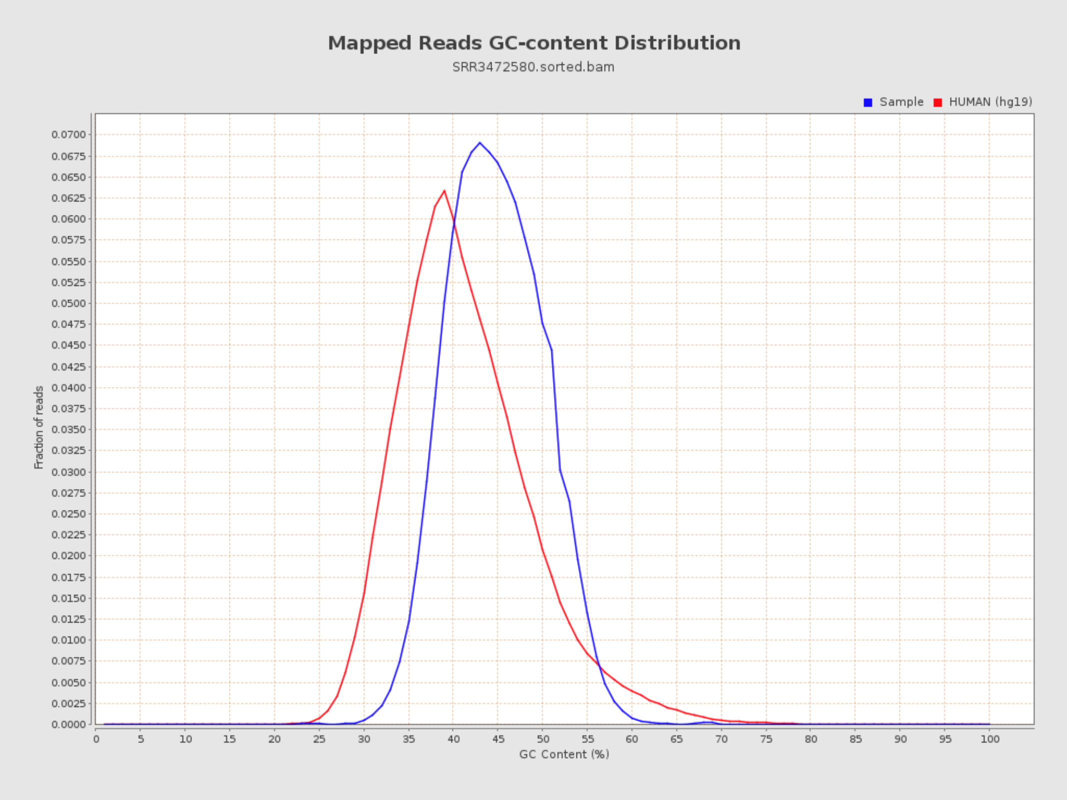
7. Results : Duplication Rate Histogram



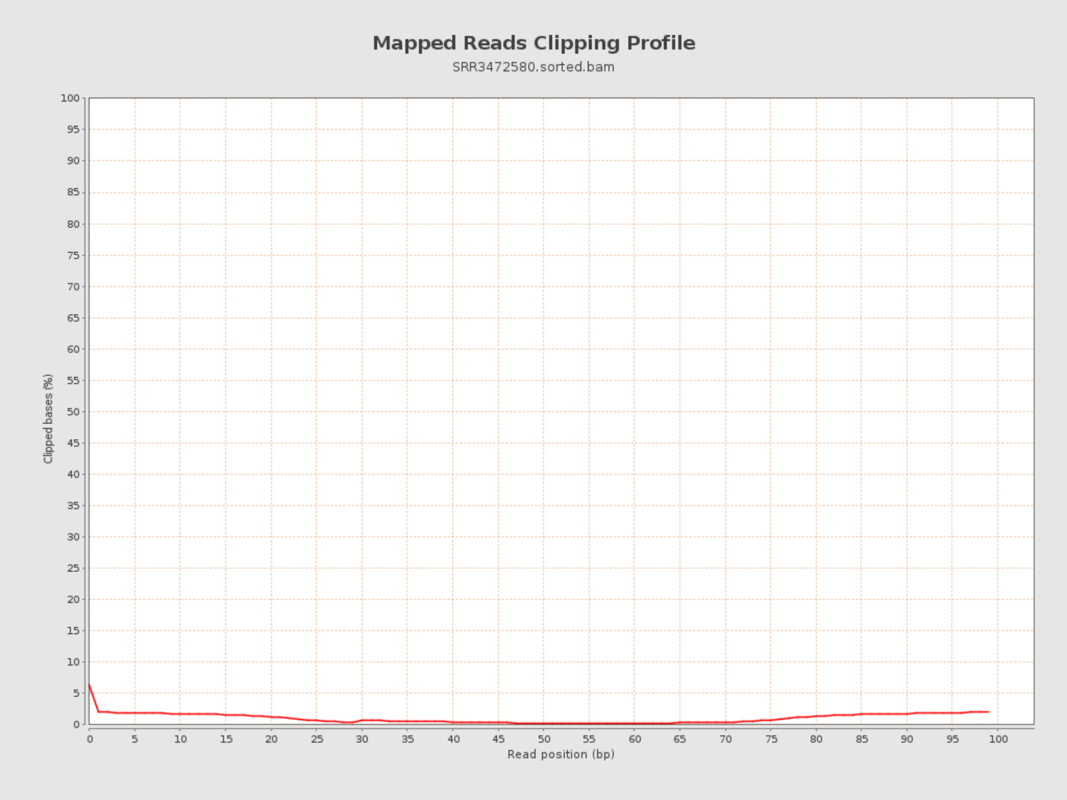
8. Results : Mapped Reads Nucleotide Content



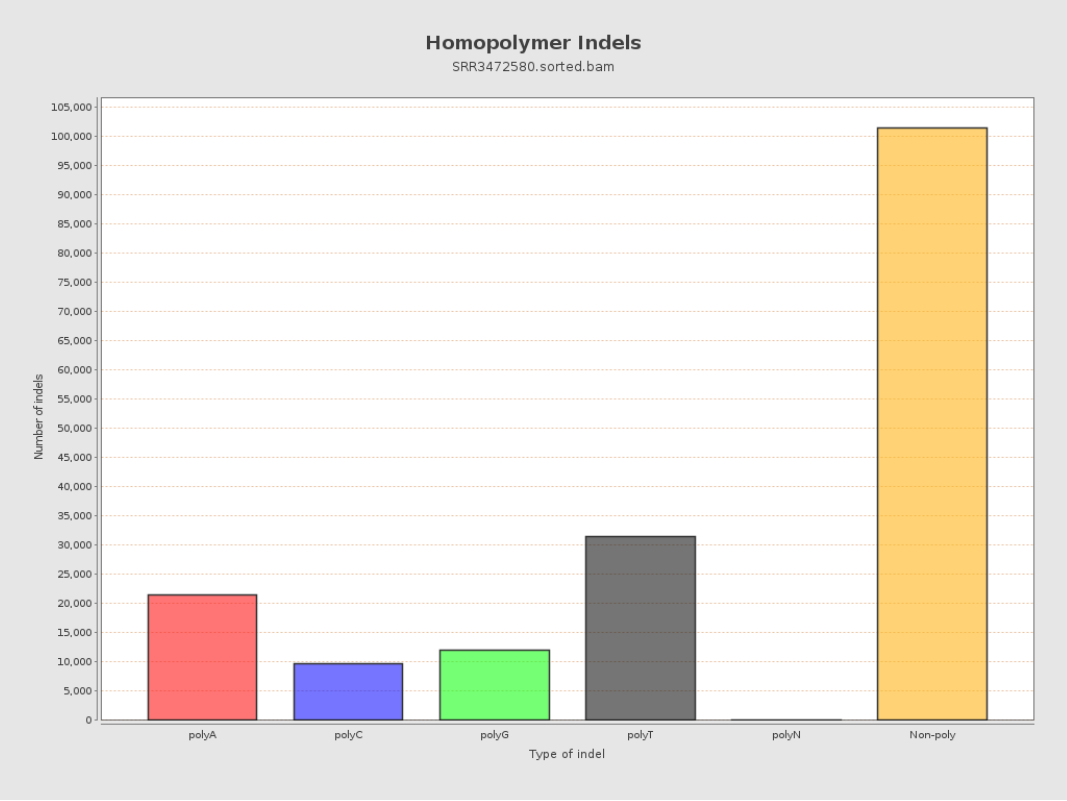
9. Results : Mapped Reads GC-content Distribution



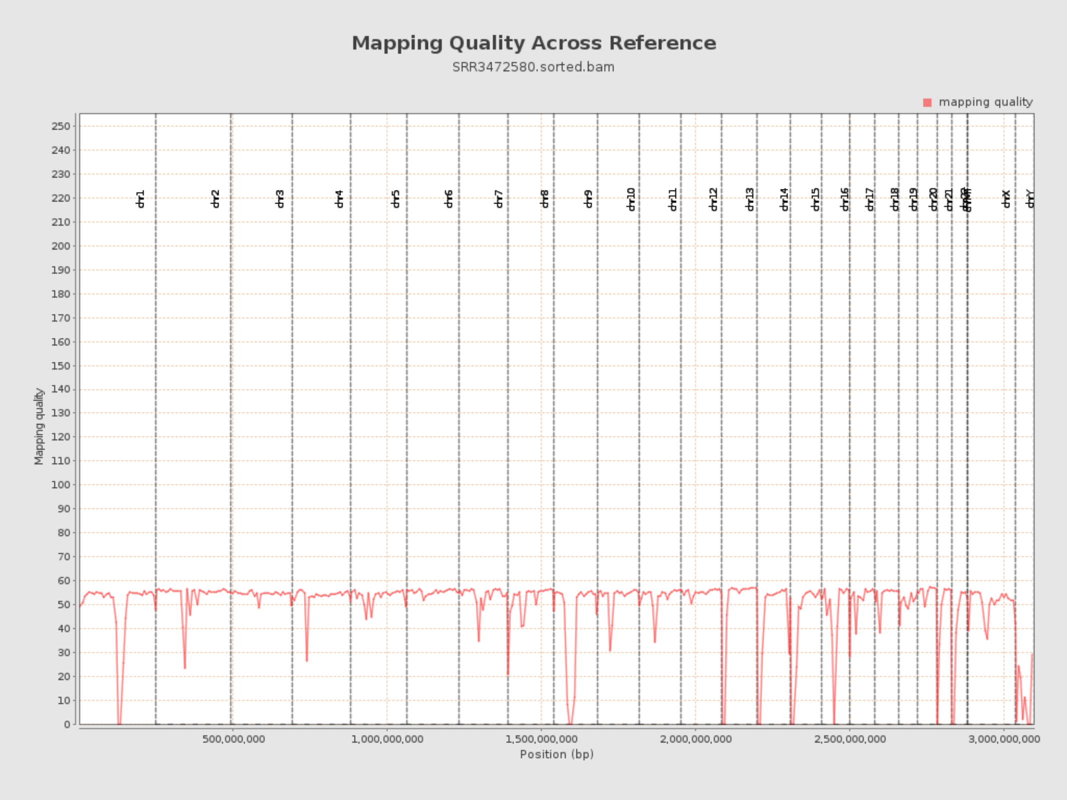
10. Results : Mapped Reads Clipping Profile



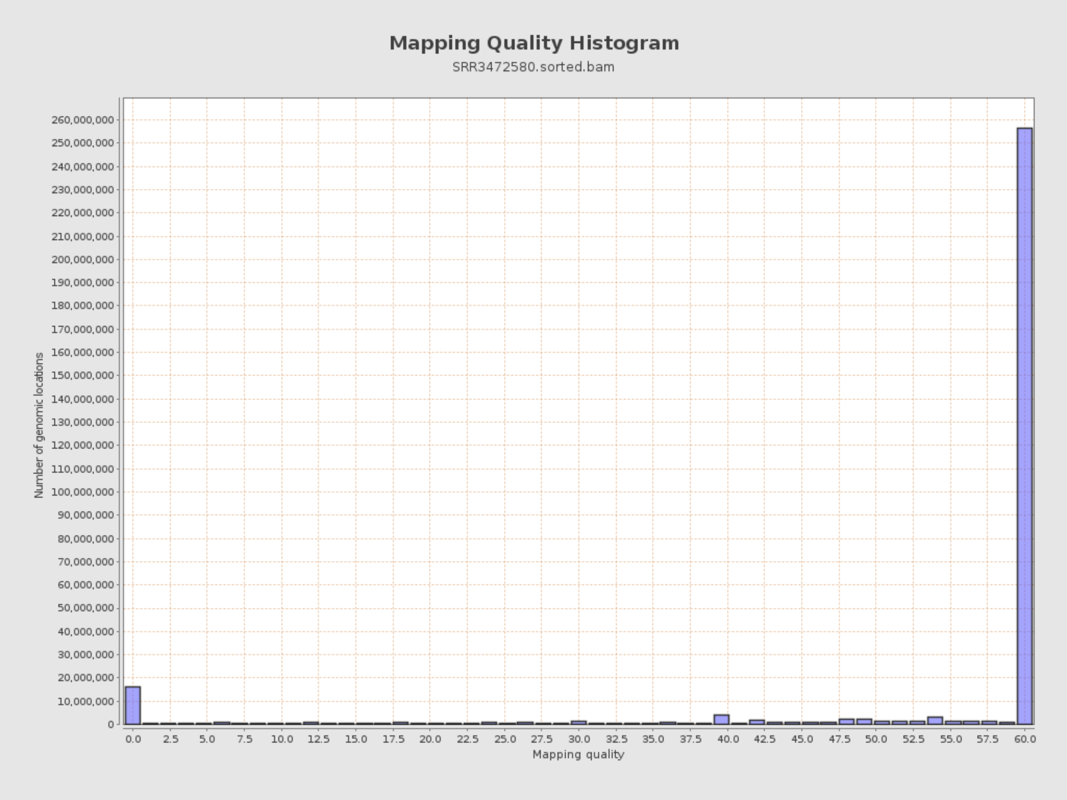
11. Results : Homopolymer Indels



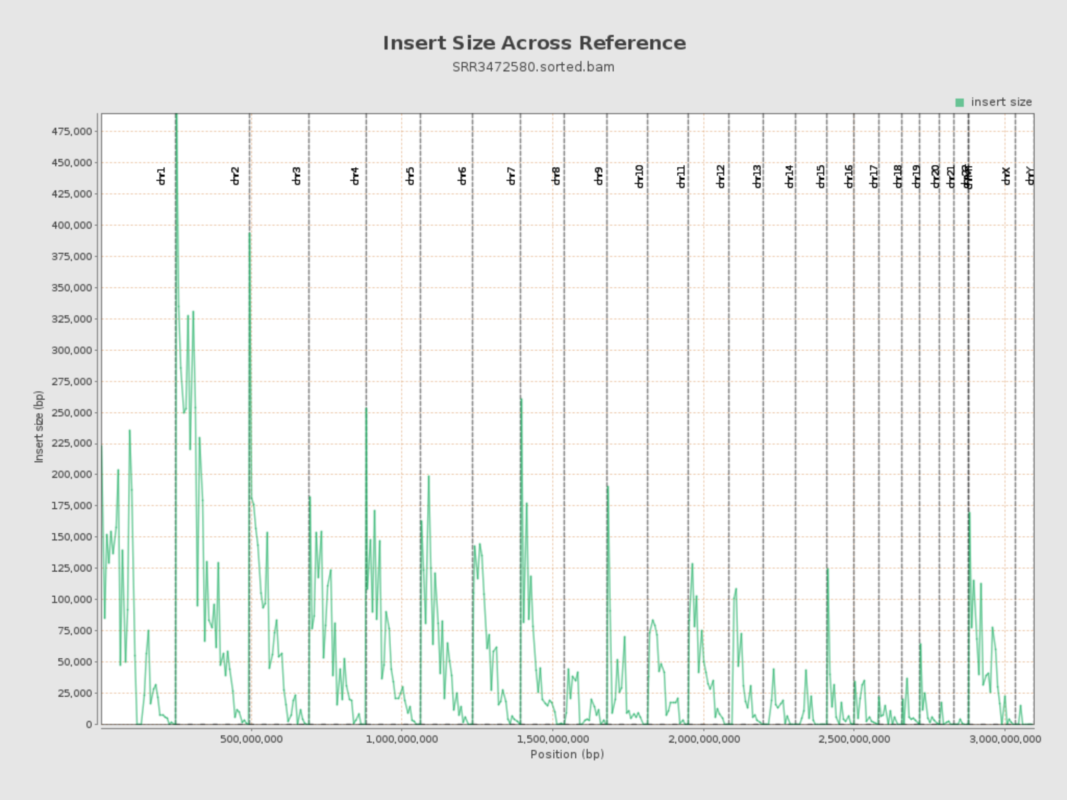
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram