Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:02:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472388.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_SRR3472388 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472388_1.fastq.gz SRR3472388_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:02:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472388.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,438,998
Mapped reads	17,271,569 / 99.04%
Unmapped reads	167,429 / 0.96%
Mapped paired reads	17,271,569 / 99.04%
Mapped reads, first in pair	8,659,304 / 49.65%
Mapped reads, second in pair	8,612,265 / 49.39%
Mapped reads, both in pair	17,172,848 / 98.47%
Mapped reads, singletons	98,721 / 0.57%
Secondary alignments	0
Supplementary alignments	68,486 / 0.39%
Read min/max/mean length	30 / 100 / 99.49
Duplicated reads (estimated)	10,706,501 / 61.39%
Duplication rate	47.32%
Clipped reads	1,219,983 / 7%

2.2. ACGT Content

Number/percentage of A's	455,387,586 / 26.87%
Number/percentage of C's	393,492,860 / 23.22%
Number/percentage of T's	456,088,752 / 26.91%
Number/percentage of G's	389,761,075 / 23%
Number/percentage of N's	213,956 / 0.01%

GC Percentage	46.21%

2.3. Coverage

Mean	0.5476
Standard Deviation	17.1403

2.4. Mapping Quality

Mean Mapping Quality	54.77

2.5. Insert size

Mean	17,885.79
Standard Deviation	1,312,898.97
P25/Median/P75	158 / 218 / 292

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,521,979
Insertions	97,938
Mapped reads with at least one insertion	0.56%
Deletions	79,167
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.28%

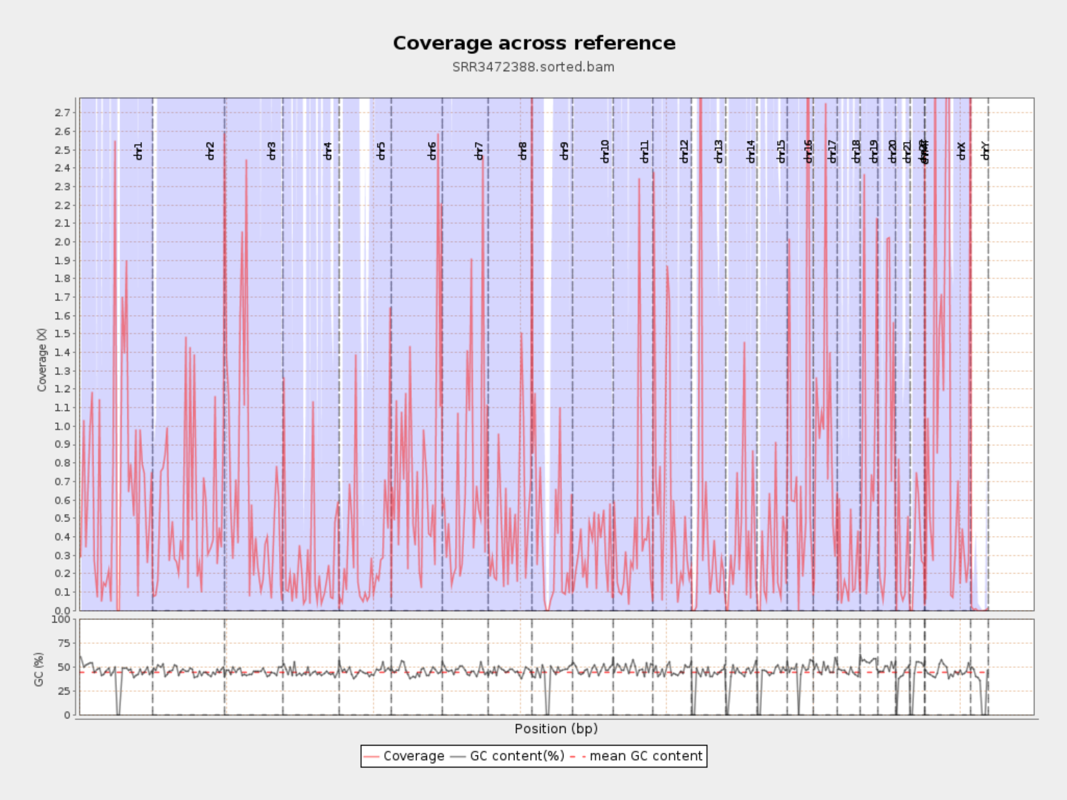
2.7. Chromosome stats

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

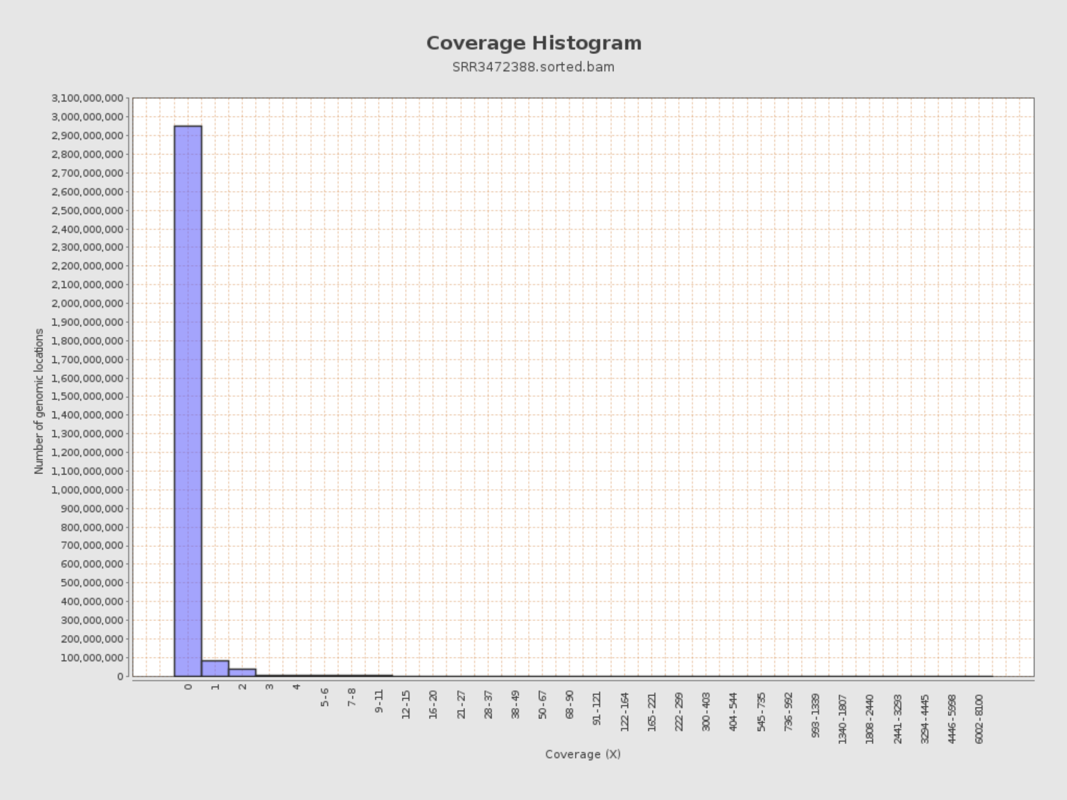
		bases	coverage	deviation
chr1	249250621	170029729	0.6822	20.3974
chr2	243199373	127934595	0.526	15.7243
chr3	198022430	135214089	0.6828	16.8292
chr4	191154276	46306881	0.2422	9.7834
chr5	180915260	61058652	0.3375	11.8272
chr6	171115067	131160606	0.7665	17.8794
chr7	159138663	113972410	0.7162	19.1034
chr8	146364022	72639445	0.4963	13.0716
chr9	141213431	56828960	0.4024	11.0647
chr10	135534747	43355317	0.3199	9.6362
chr11	135006516	52698783	0.3903	18.8768
chr12	133851895	84688277	0.6327	16.4112
chr13	115169878	53831919	0.4674	21.7729
chr14	107349540	40637451	0.3786	10.6934
chr15	102531392	29284645	0.2856	12.3146
chr16	90354753	81405548	0.901	24.7434
chr17	81195210	80228872	0.9881	26.3731
chr18	78077248	17935478	0.2297	7.5545
chr19	59128983	53391282	0.903	19.5898
chr20	63025520	54783177	0.8692	23.1805
chr21	48129895	12647206	0.2628	13.6577
chr22	51304566	17184020	0.3349	8.3144
chrMT	16571	41332	2.4942	2.0525
chrX	155270560	157589860	1.0149	28.51

chrY	59373566	323765	0.0055	0.3738

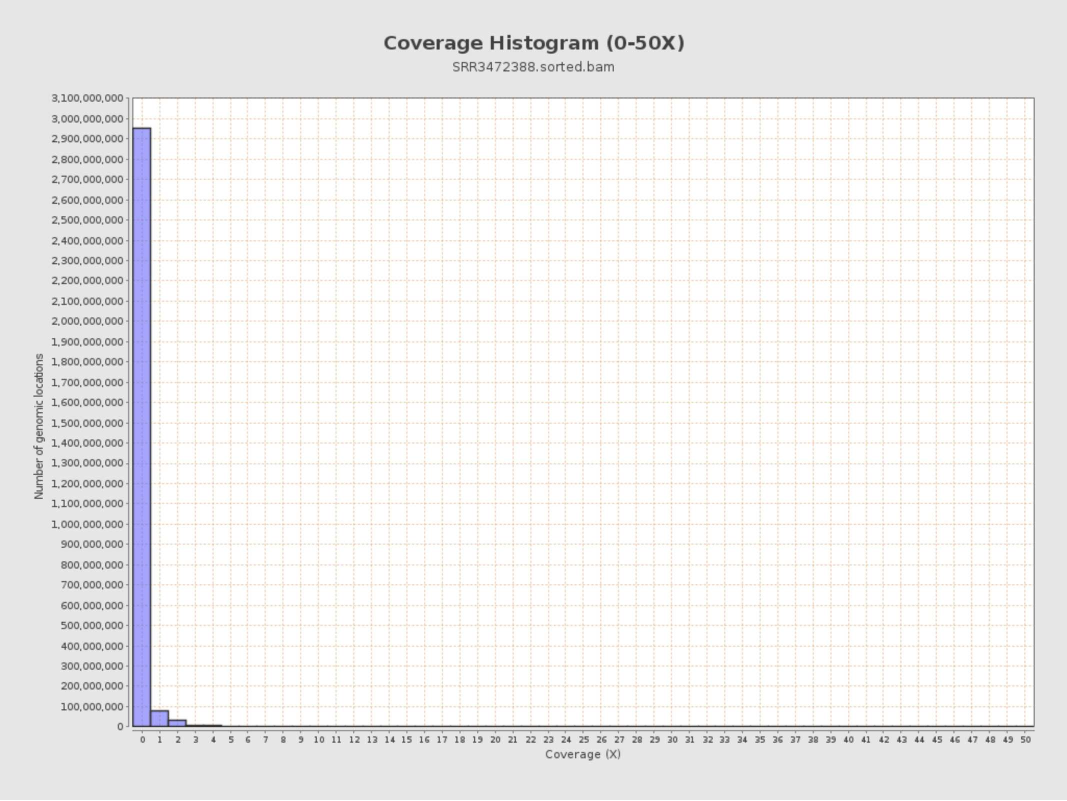
3. Results : Coverage across reference



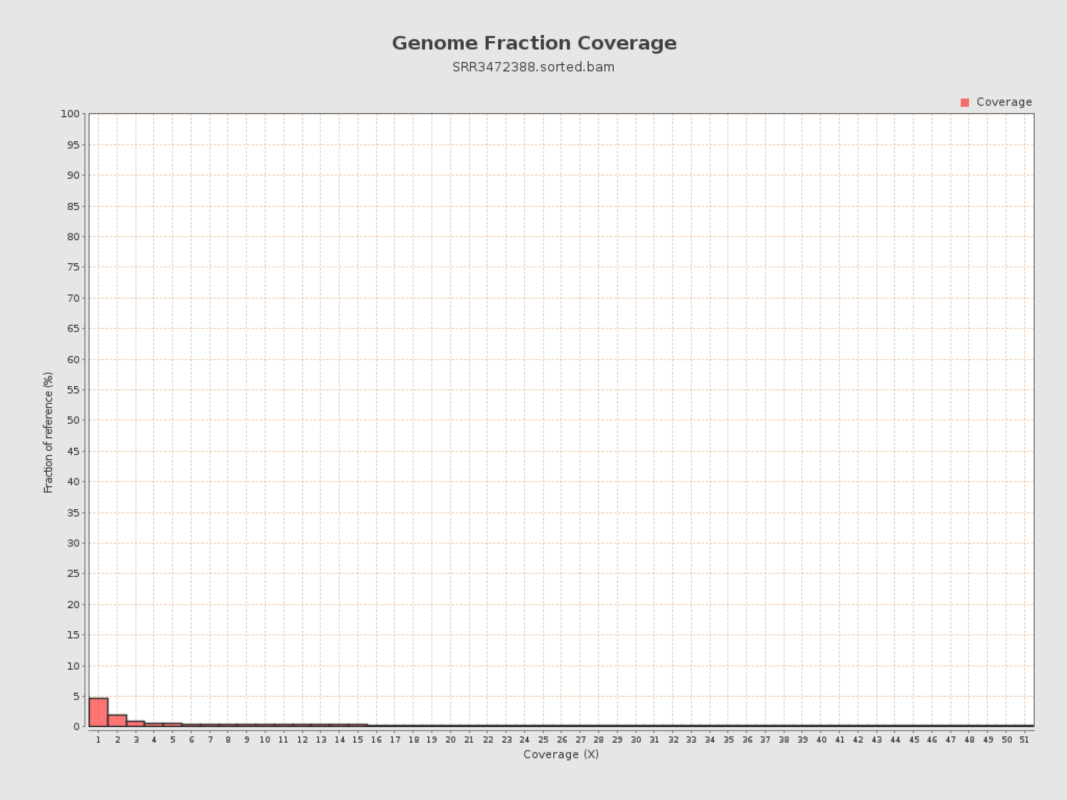
4. Results : Coverage Histogram



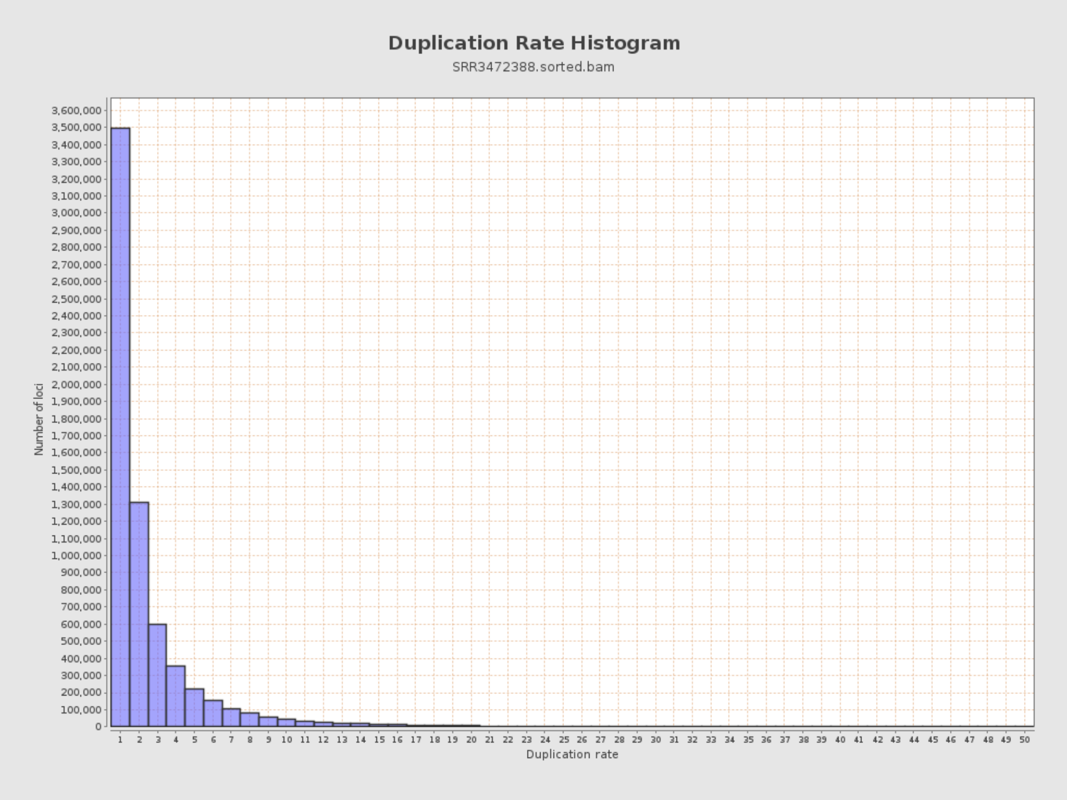
5. Results : Coverage Histogram (0-50X)



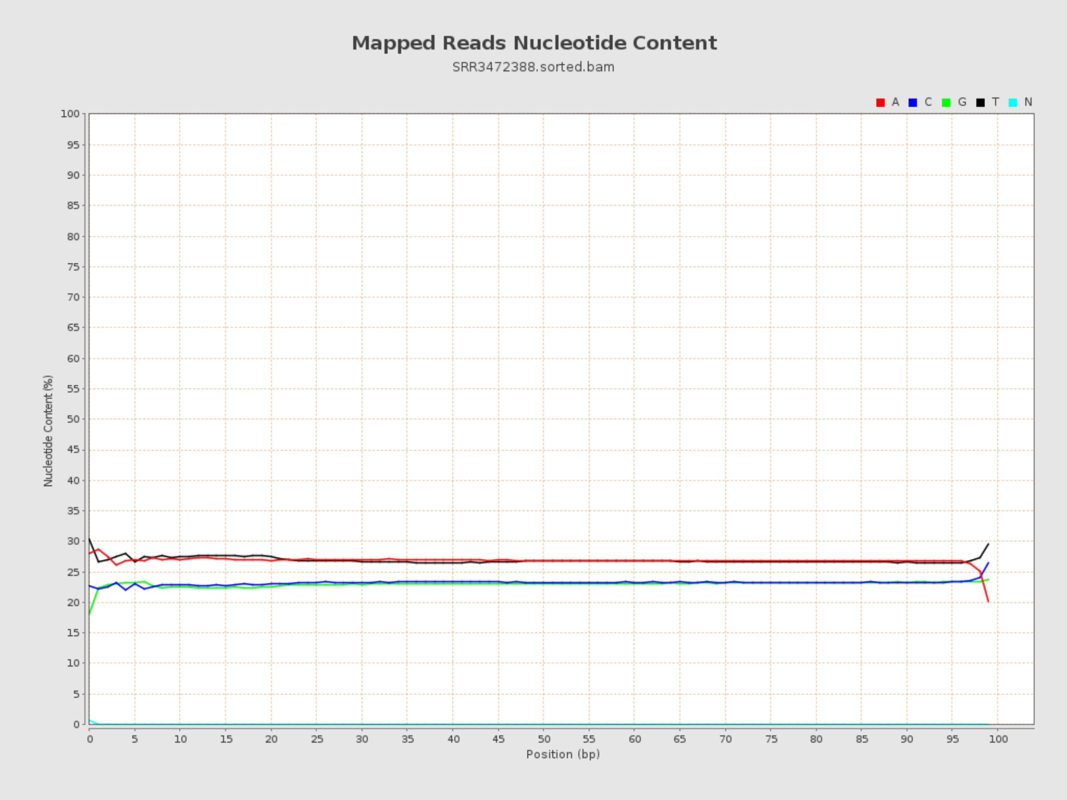
6. Results : Genome Fraction Coverage



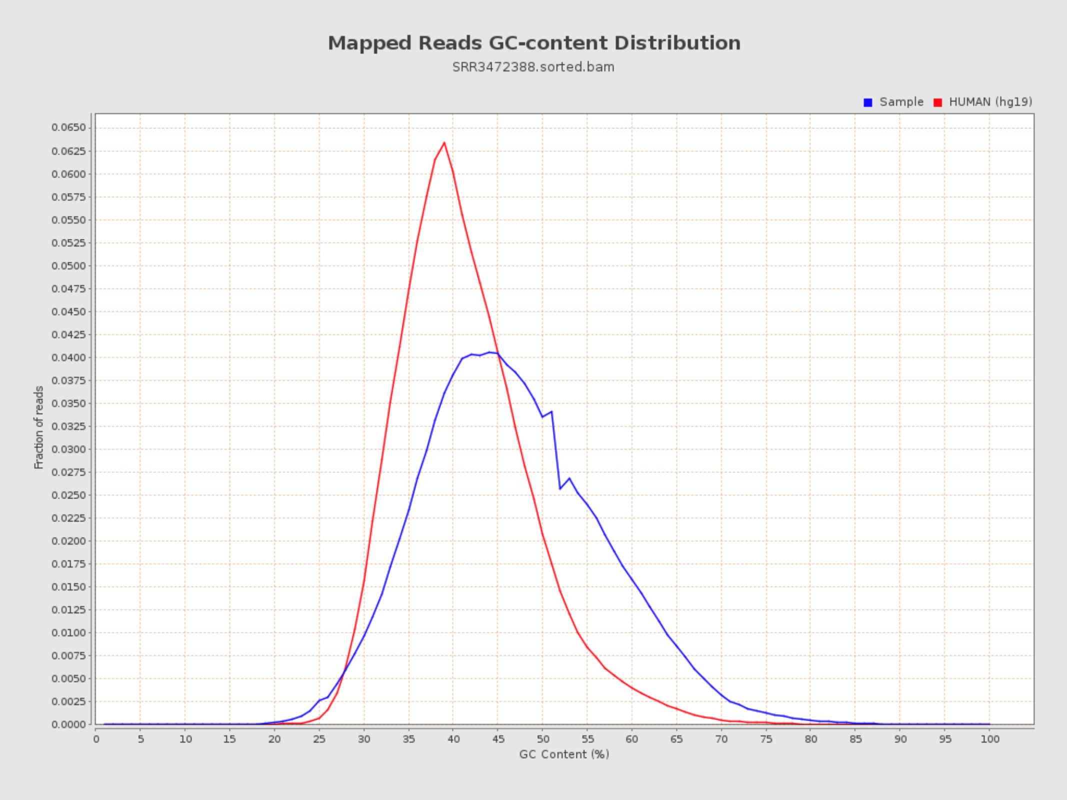
7. Results : Duplication Rate Histogram



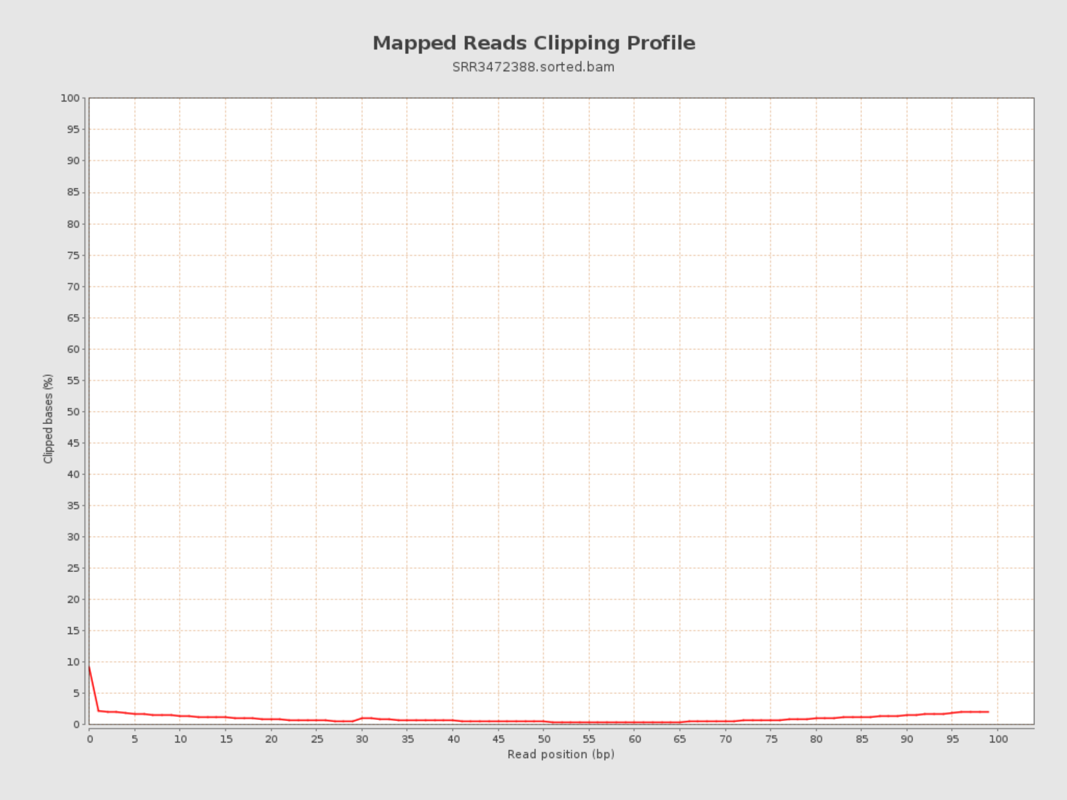
8. Results : Mapped Reads Nucleotide Content



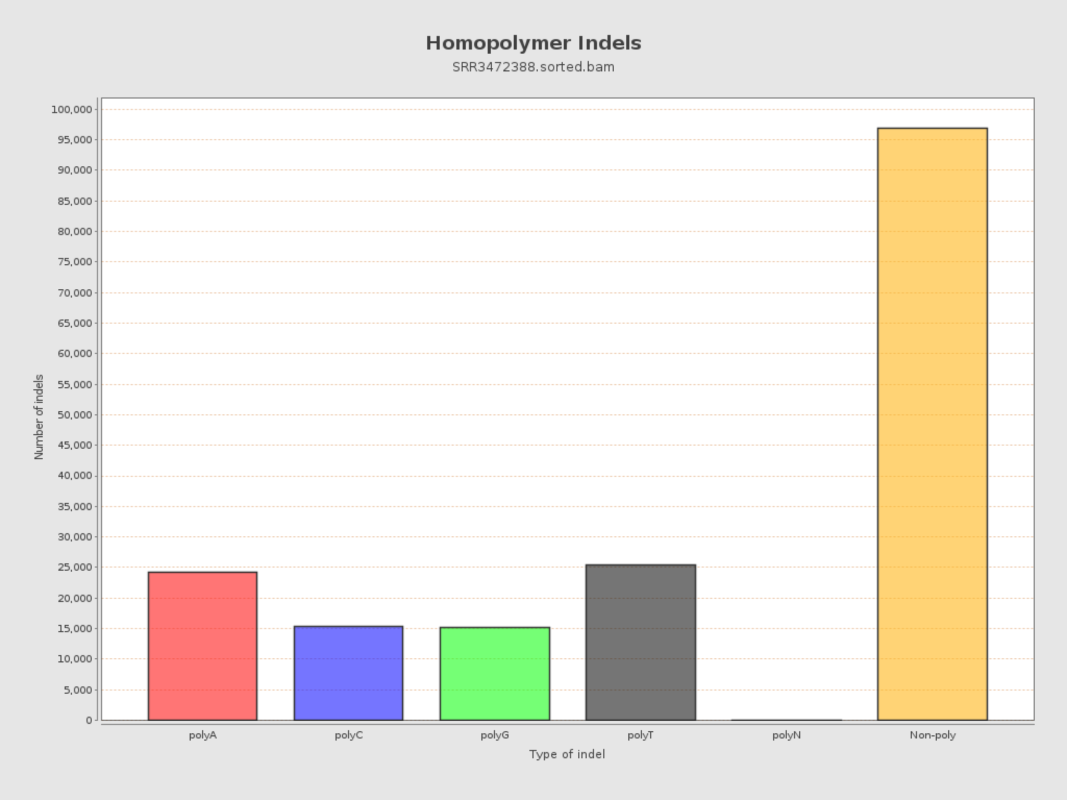
9. Results : Mapped Reads GC-content Distribution



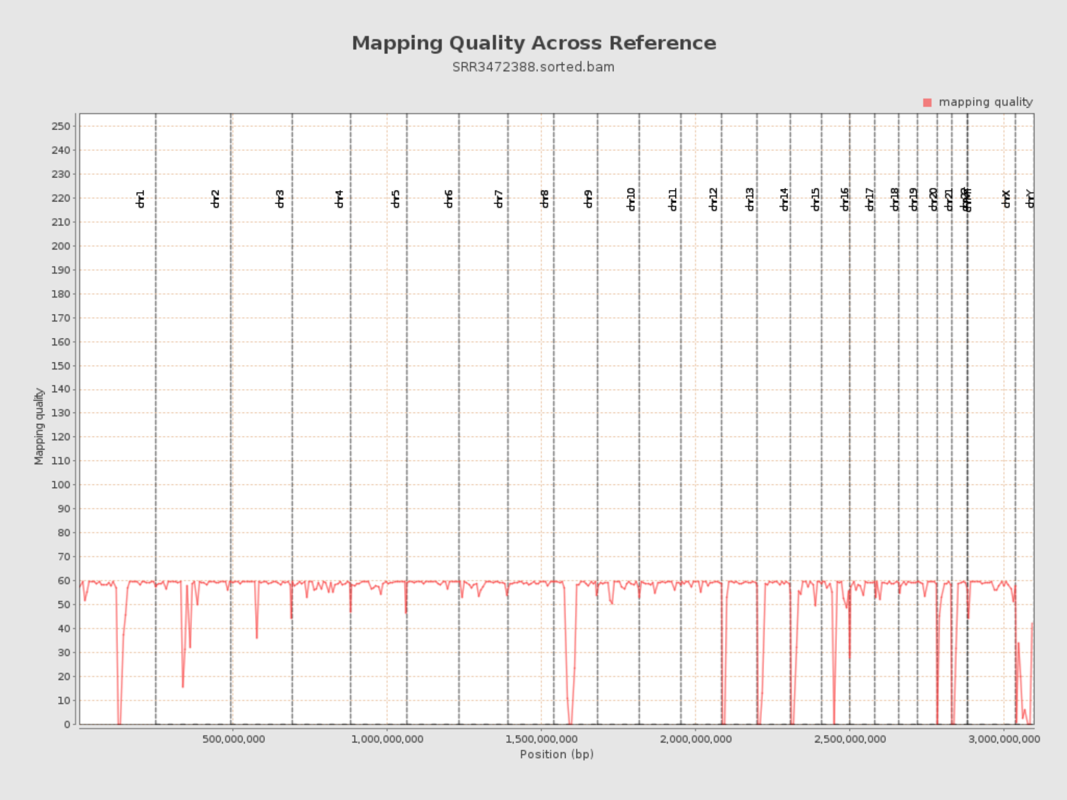
10. Results : Mapped Reads Clipping Profile



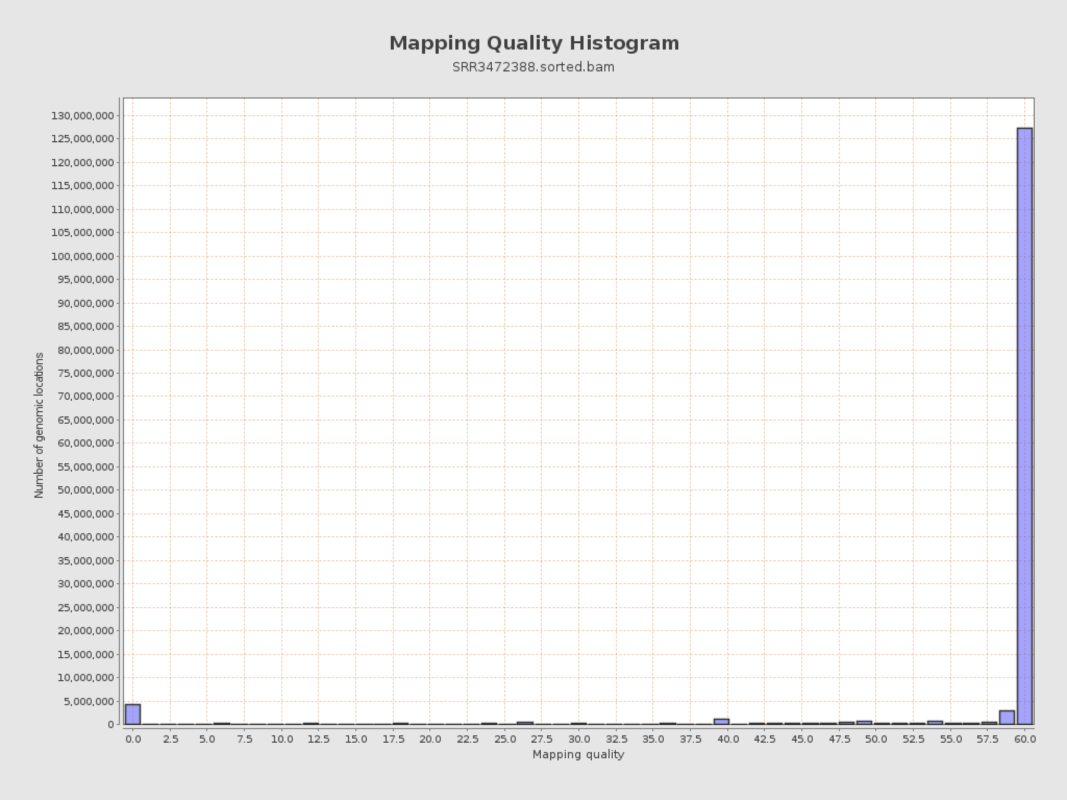
11. Results : Homopolymer Indels



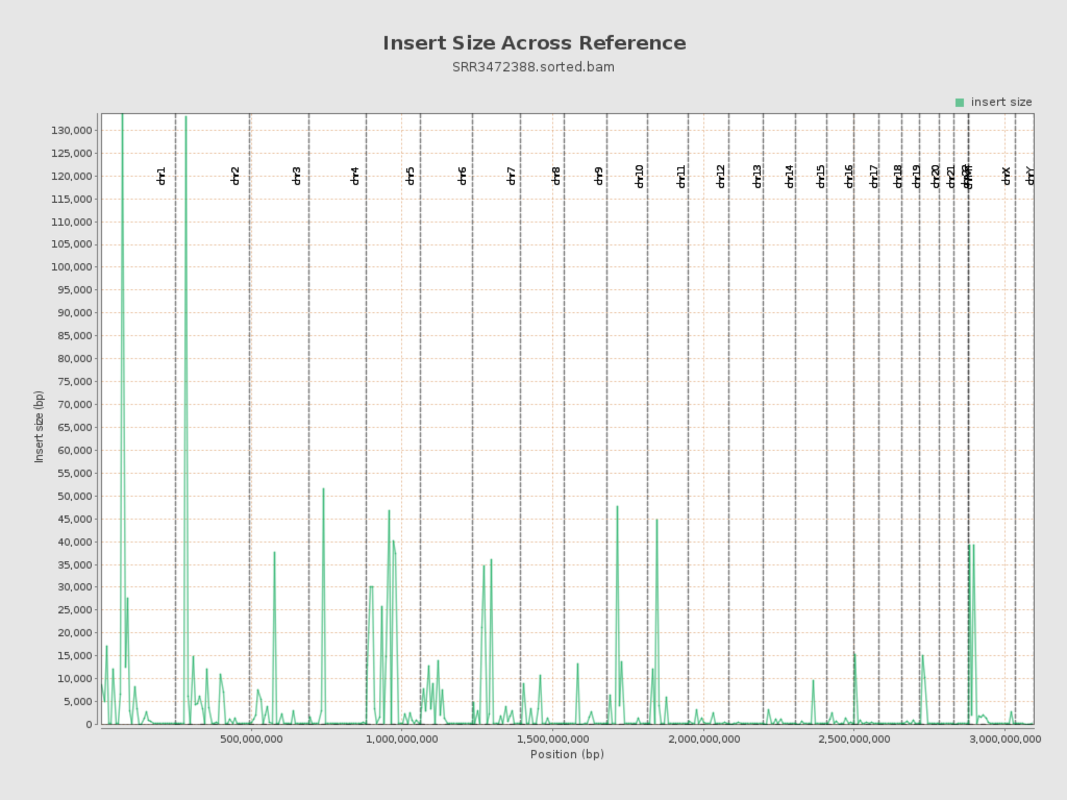
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram