Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 16:13:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472782.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_SRR3472782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472782_1.fastq.gz SRR3472782_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 16:13:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,460,250
Mapped reads	14,342,442 / 99.19%
Unmapped reads	117,808 / 0.81%
Mapped paired reads	14,342,442 / 99.19%
Mapped reads, first in pair	7,190,561 / 49.73%
Mapped reads, second in pair	7,151,881 / 49.46%
Mapped reads, both in pair	14,274,658 / 98.72%
Mapped reads, singletons	67,784 / 0.47%
Secondary alignments	0
Supplementary alignments	56,046 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	9,142,716 / 63.23%
Duplication rate	46.15%
Clipped reads	1,311,057 / 9.07%

2.2. ACGT Content

Number/percentage of A's	387,823,447 / 27.51%
Number/percentage of C's	318,746,338 / 22.61%
Number/percentage of T's	385,265,913 / 27.33%
Number/percentage of G's	317,761,443 / 22.54%
Number/percentage of N's	274,333 / 0.02%

GC Percentage	45.15%

2.3. Coverage

Mean	0.4555
Standard Deviation	18.0139

2.4. Mapping Quality

Mean Mapping Quality	54.88

2.5. Insert size

Mean	25,020.07
Standard Deviation	1,587,861.45
P25/Median/P75	160 / 226 / 308

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	8,112,869
Insertions	81,826
Mapped reads with at least one insertion	0.56%
Deletions	76,726
Mapped reads with at least one deletion	0.53%
Homopolymer indels	43.42%

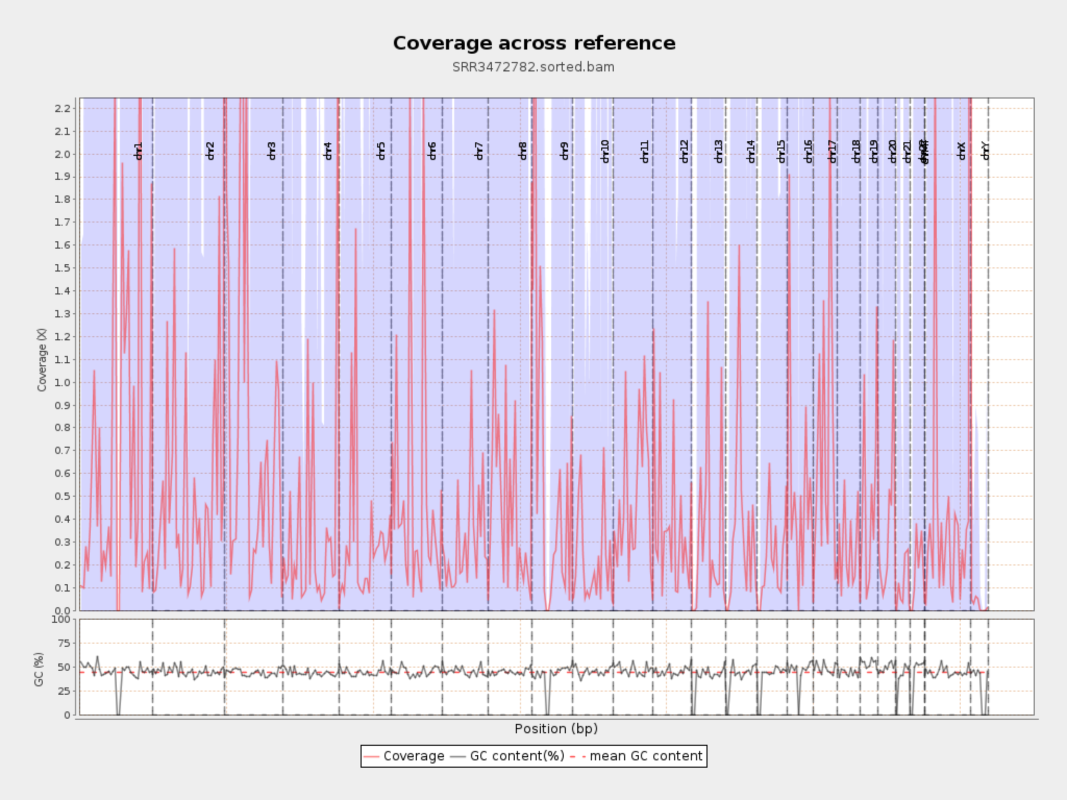
2.7. Chromosome stats

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

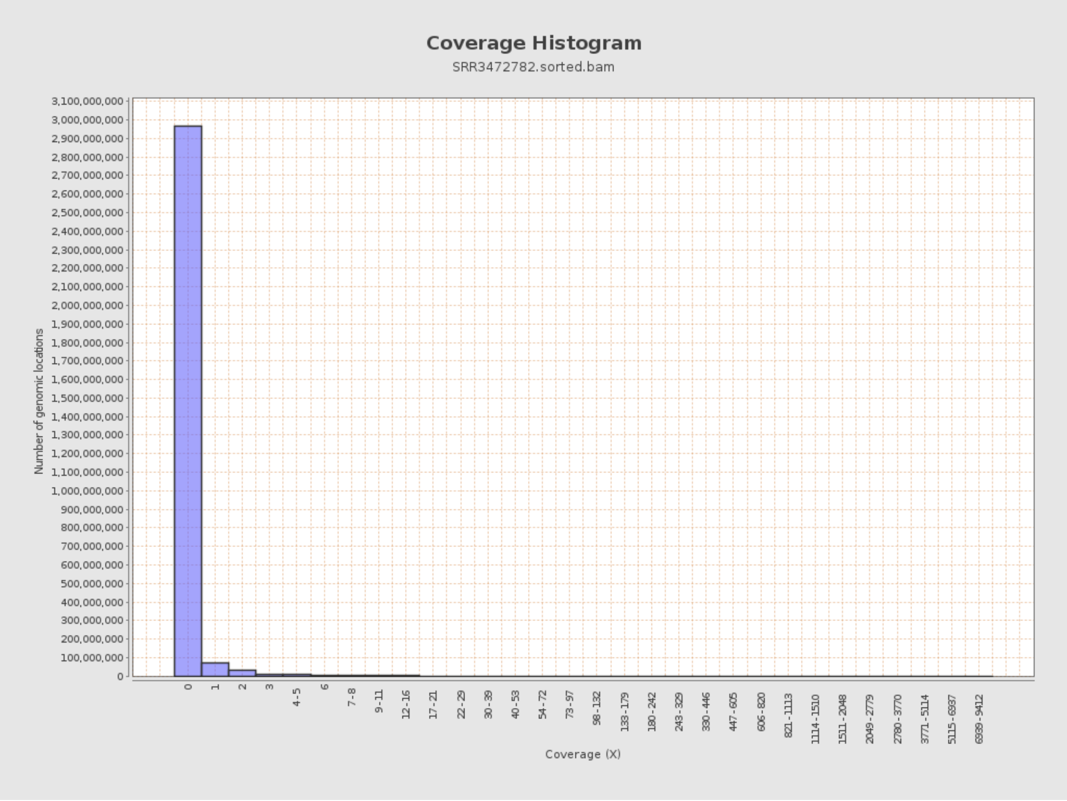
		bases	coverage	deviation
chr1	249250621	176182286	0.7068	30.0828
chr2	243199373	116487170	0.479	17.8521
chr3	198022430	181631531	0.9172	24.0291
chr4	191154276	67462813	0.3529	19.7922
chr5	180915260	57353170	0.317	11.0429
chr6	171115067	85935236	0.5022	19.2486
chr7	159138663	49975838	0.314	10.1319
chr8	146364022	65726138	0.4491	15.7349
chr9	141213431	89915674	0.6367	17.7938
chr10	135534747	30054622	0.2217	10.1761
chr11	135006516	68157346	0.5048	18.416
chr12	133851895	50738065	0.3791	12.0348
chr13	115169878	38089975	0.3307	15.5294
chr14	107349540	40321787	0.3756	14.5331
chr15	102531392	22660075	0.221	7.3635
chr16	90354753	46230464	0.5117	16.5092
chr17	81195210	58412840	0.7194	20.6479
chr18	78077248	21110664	0.2704	13.1745
chr19	59128983	27484412	0.4648	12.6047
chr20	63025520	22690730	0.36	12.592
chr21	48129895	5735309	0.1192	6.5891
chr22	51304566	8957827	0.1746	7.3705
chrMT	16571	1138	0.0687	0.3
chrX	155270560	77256240	0.4976	25.007

chrY	59373566	1490639	0.0251	0.6064

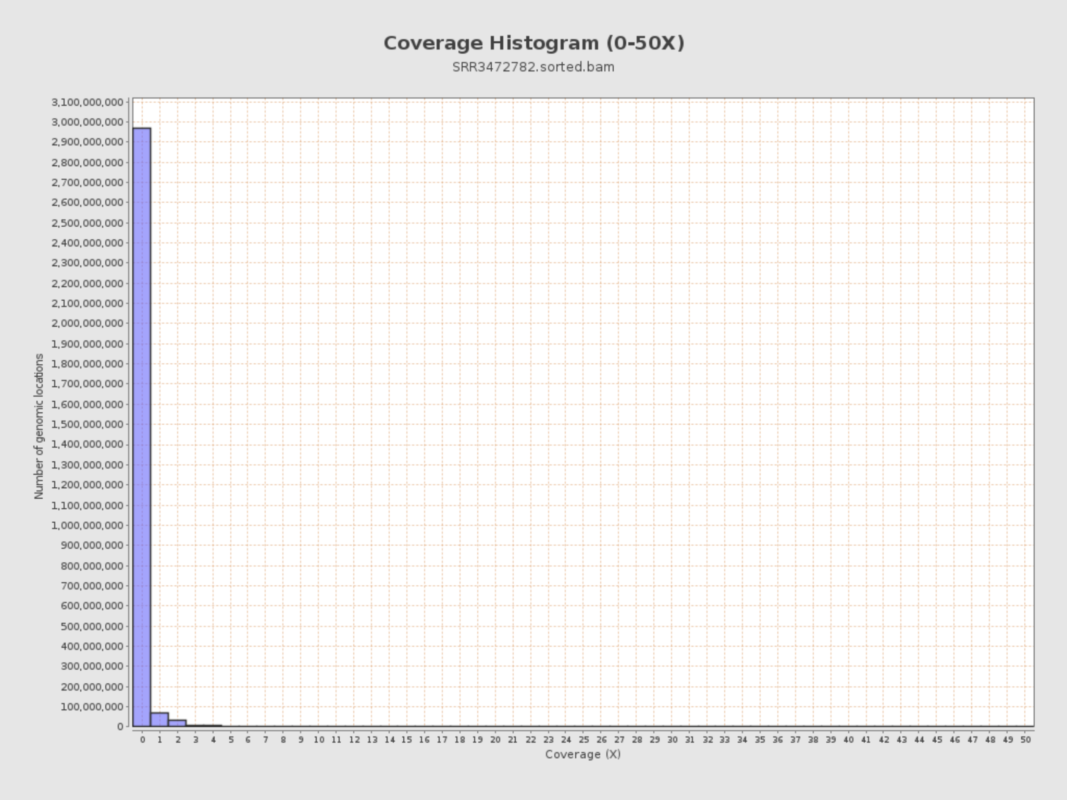
3. Results : Coverage across reference



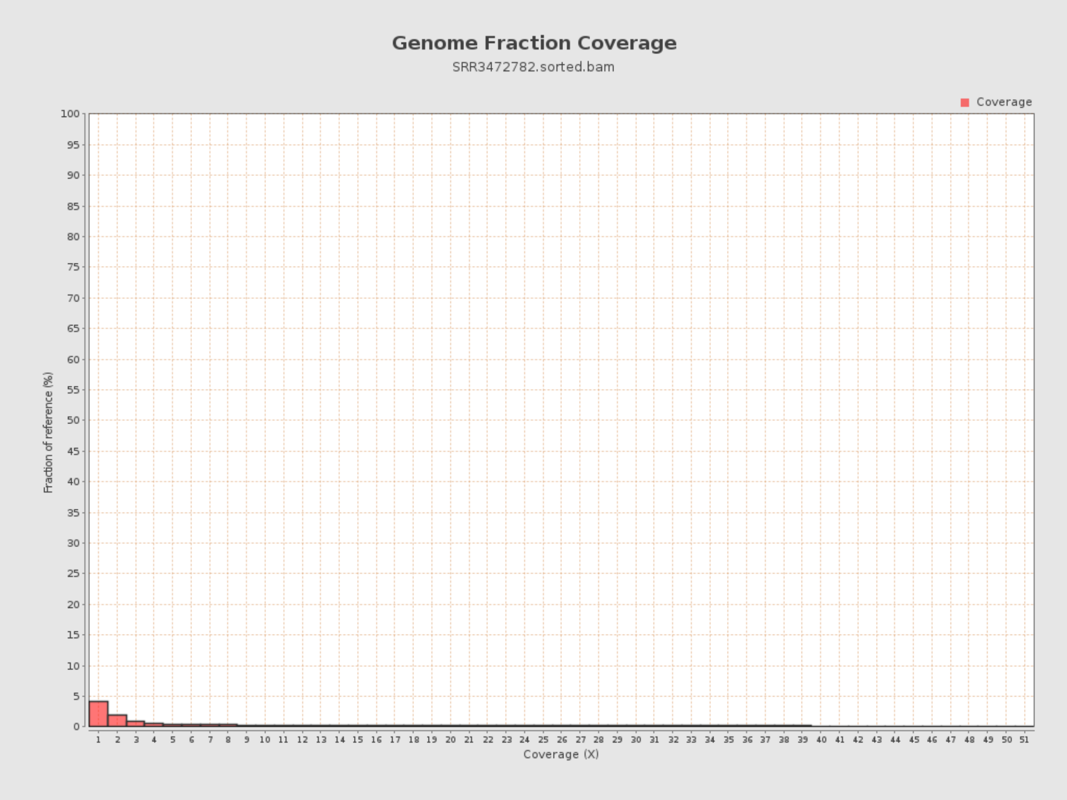
4. Results : Coverage Histogram



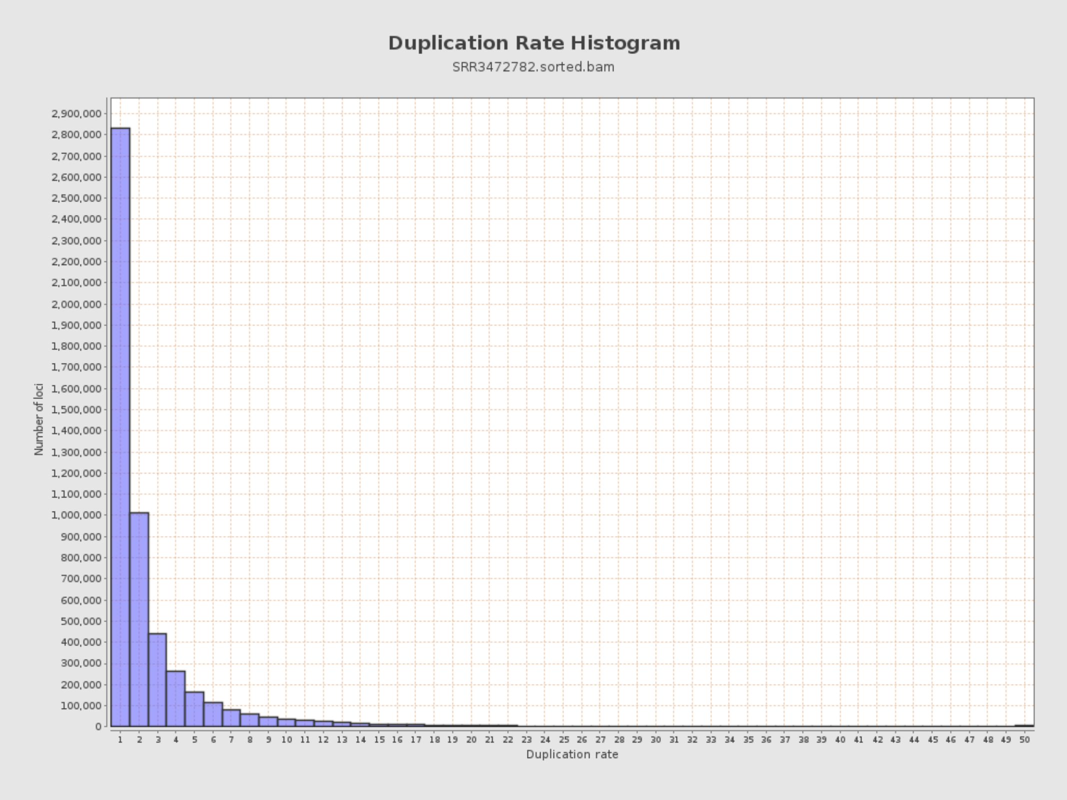
5. Results : Coverage Histogram (0-50X)



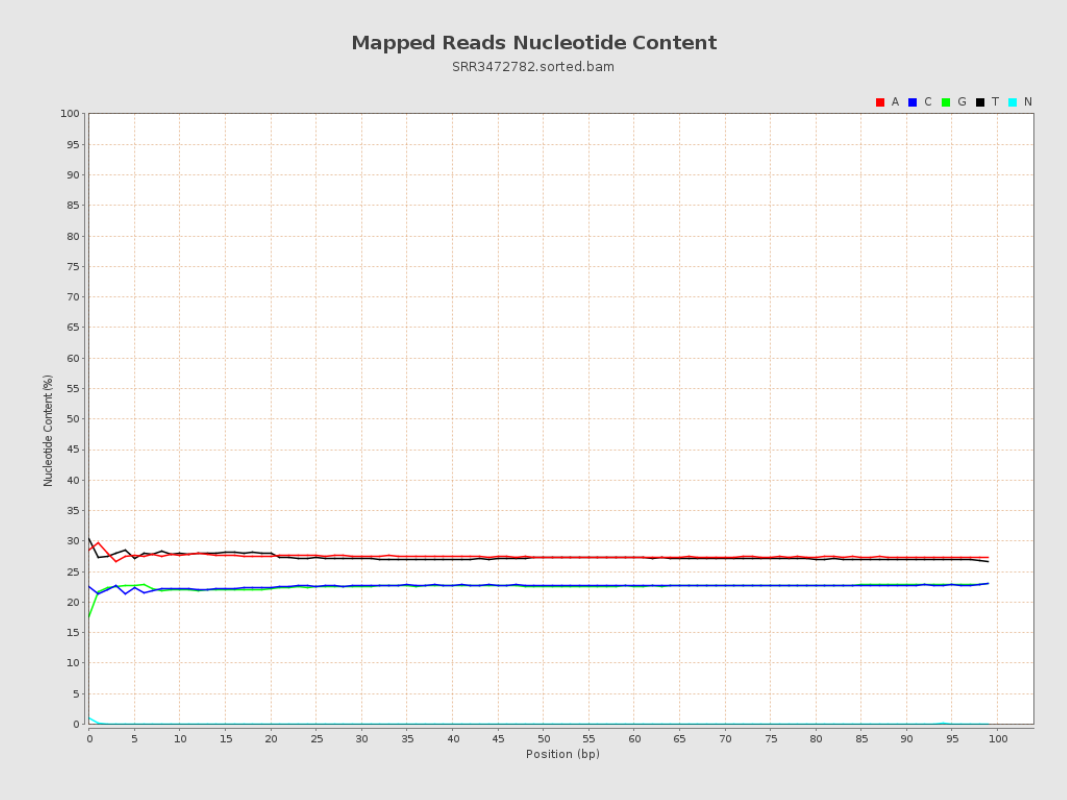
6. Results : Genome Fraction Coverage



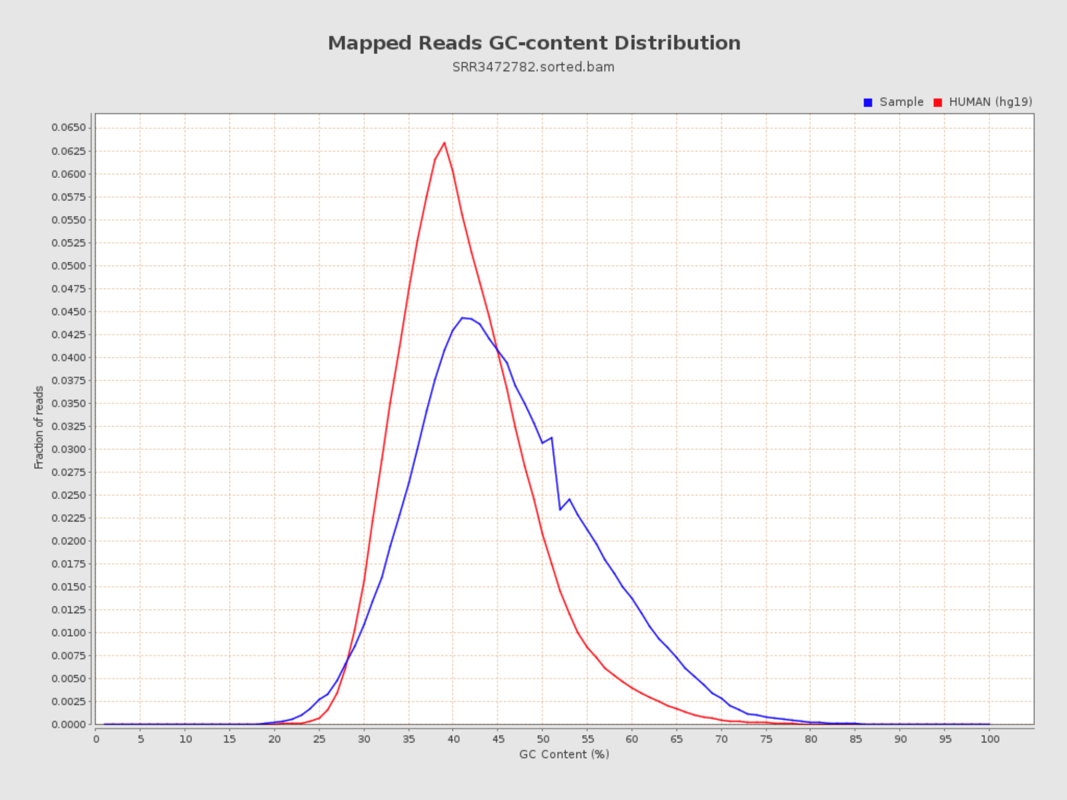
7. Results : Duplication Rate Histogram



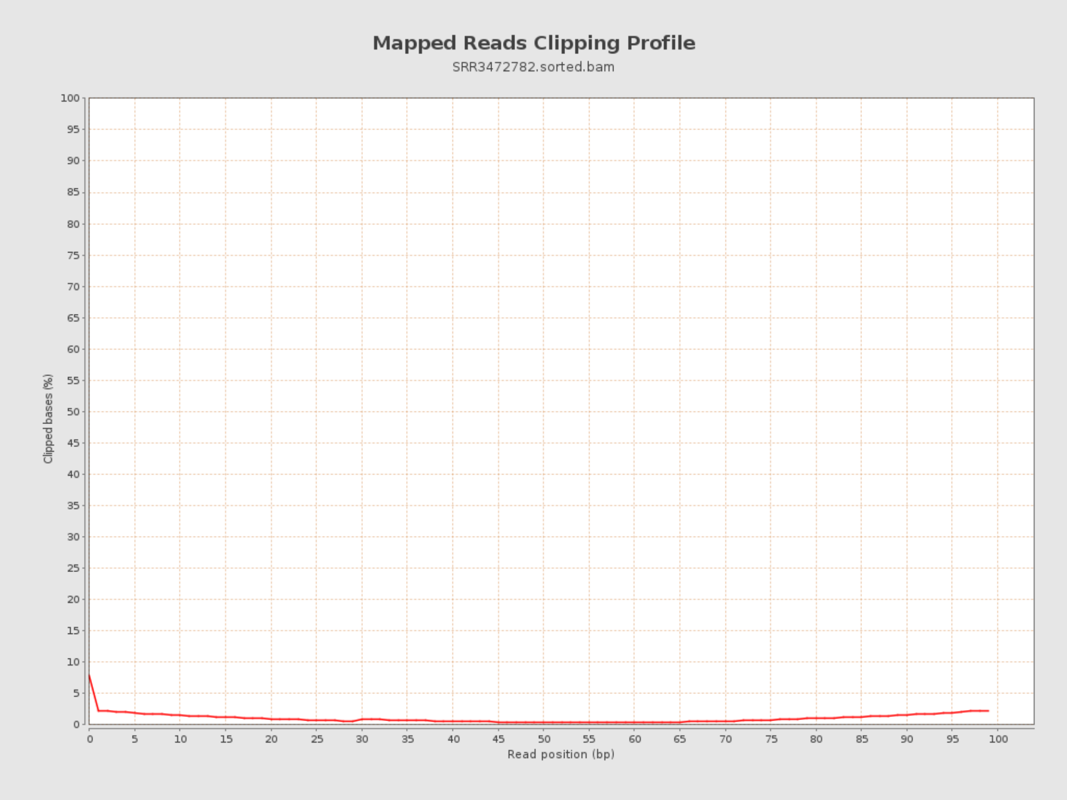
8. Results : Mapped Reads Nucleotide Content



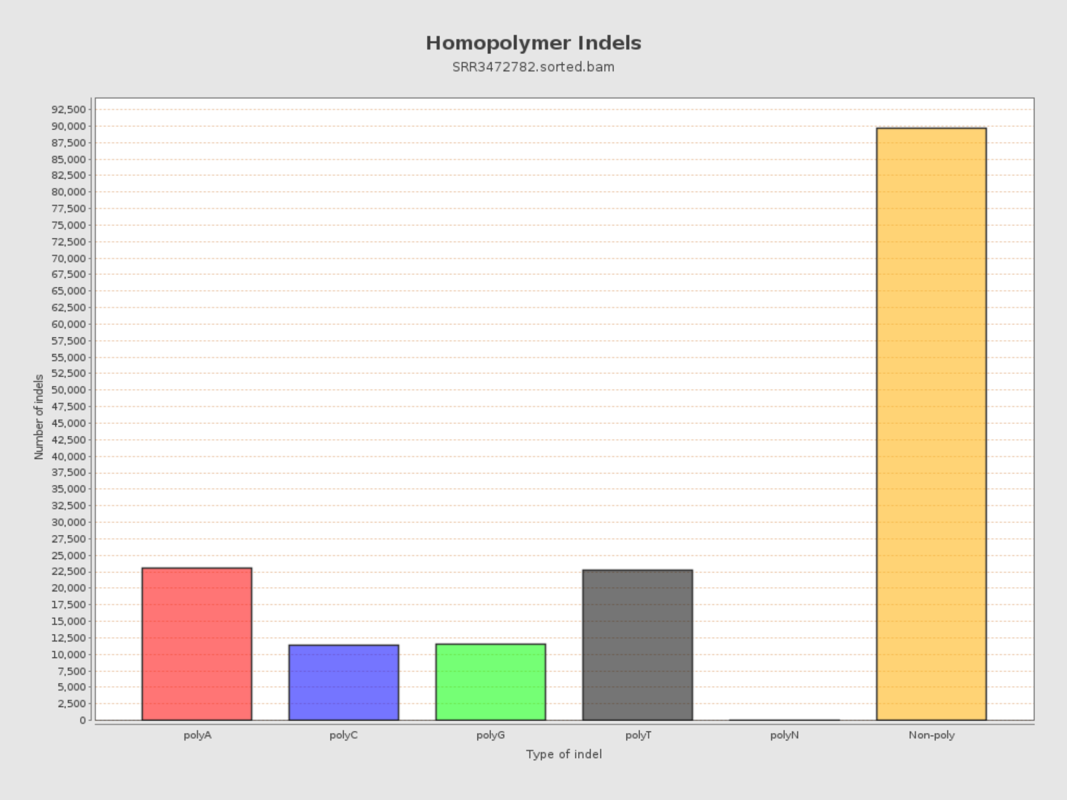
9. Results : Mapped Reads GC-content Distribution



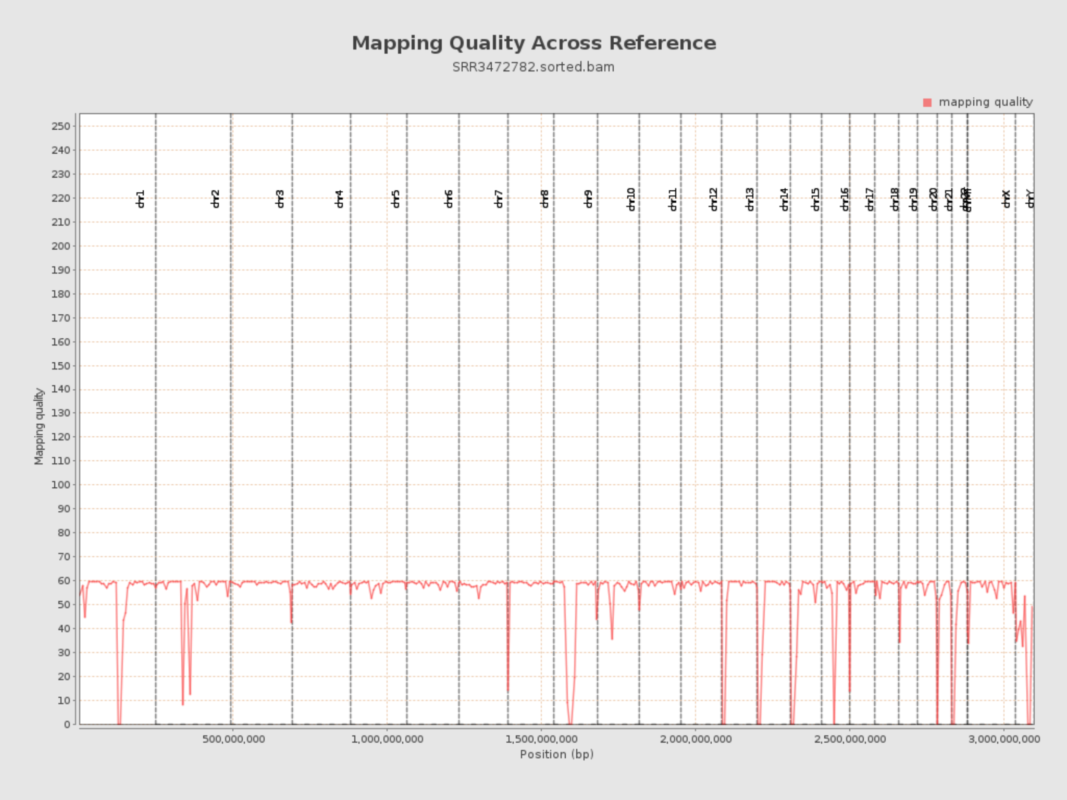
10. Results : Mapped Reads Clipping Profile



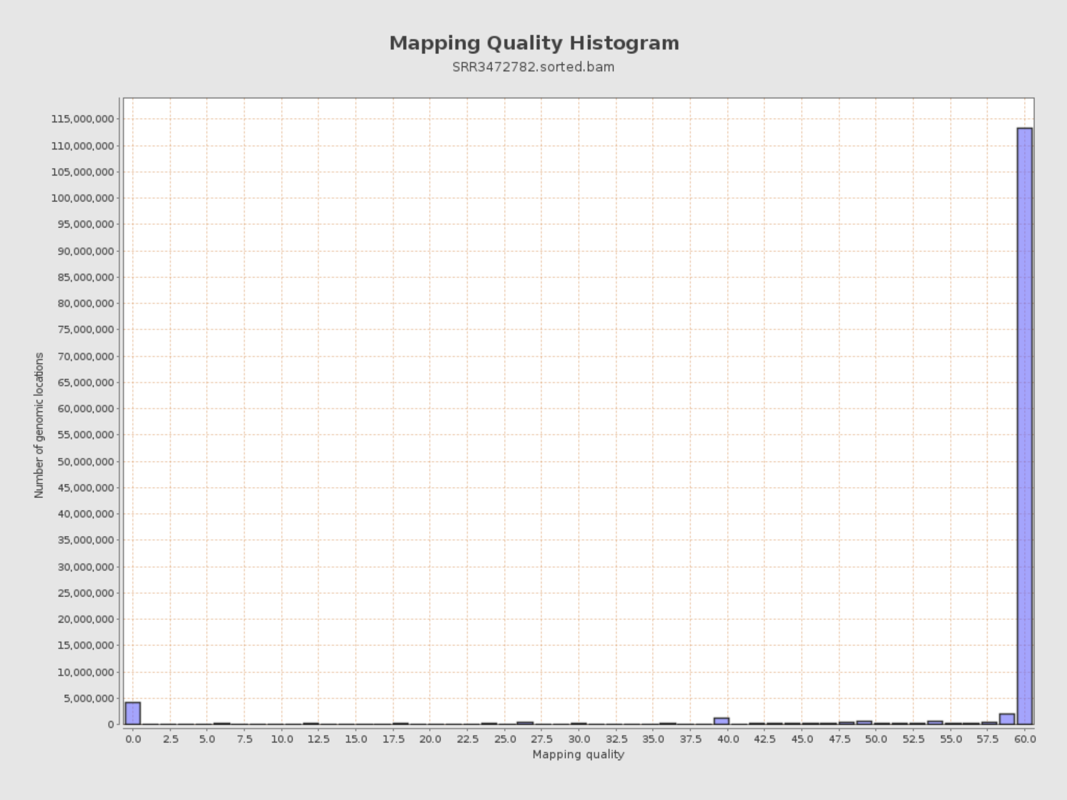
11. Results : Homopolymer Indels



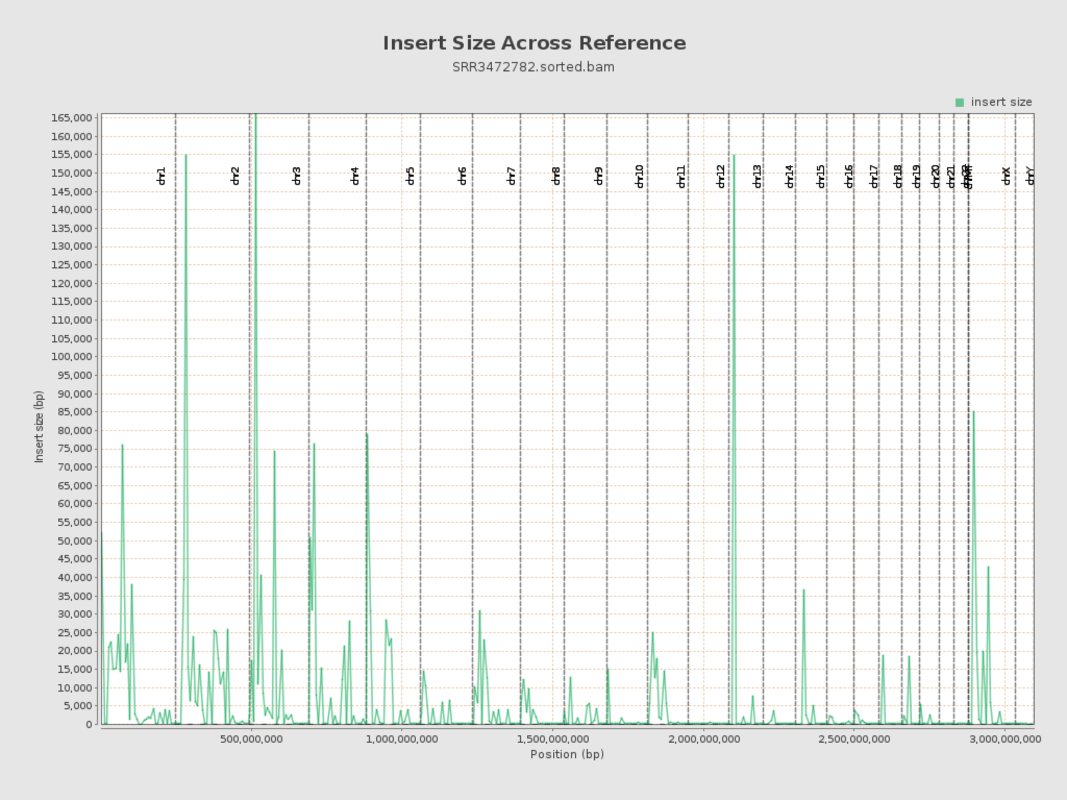
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram