Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 17:23:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472787.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_SRR3472787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472787_1.fastq.gz SRR3472787_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 17:23:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,790,200
Mapped reads	14,672,303 / 99.2%
Unmapped reads	117,897 / 0.8%
Mapped paired reads	14,672,303 / 99.2%
Mapped reads, first in pair	7,356,956 / 49.74%
Mapped reads, second in pair	7,315,347 / 49.46%
Mapped reads, both in pair	14,602,536 / 98.73%
Mapped reads, singletons	69,767 / 0.47%
Secondary alignments	0
Supplementary alignments	52,022 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	8,923,666 / 60.33%
Duplication rate	46.48%
Clipped reads	1,239,328 / 8.38%

2.2. ACGT Content

Number/percentage of A's	392,174,092 / 27.16%
Number/percentage of C's	331,778,916 / 22.98%
Number/percentage of T's	390,085,969 / 27.01%
Number/percentage of G's	329,678,565 / 22.83%
Number/percentage of N's	281,086 / 0.02%

GC Percentage	45.81%

2.3. Coverage

Mean	0.4665
Standard Deviation	15.5521

2.4. Mapping Quality

Mean Mapping Quality	55.31

2.5. Insert size

Mean	24,579.98
Standard Deviation	1,512,815.85
P25/Median/P75	165 / 230 / 310

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	8,363,634
Insertions	82,269
Mapped reads with at least one insertion	0.55%
Deletions	75,911
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.42%

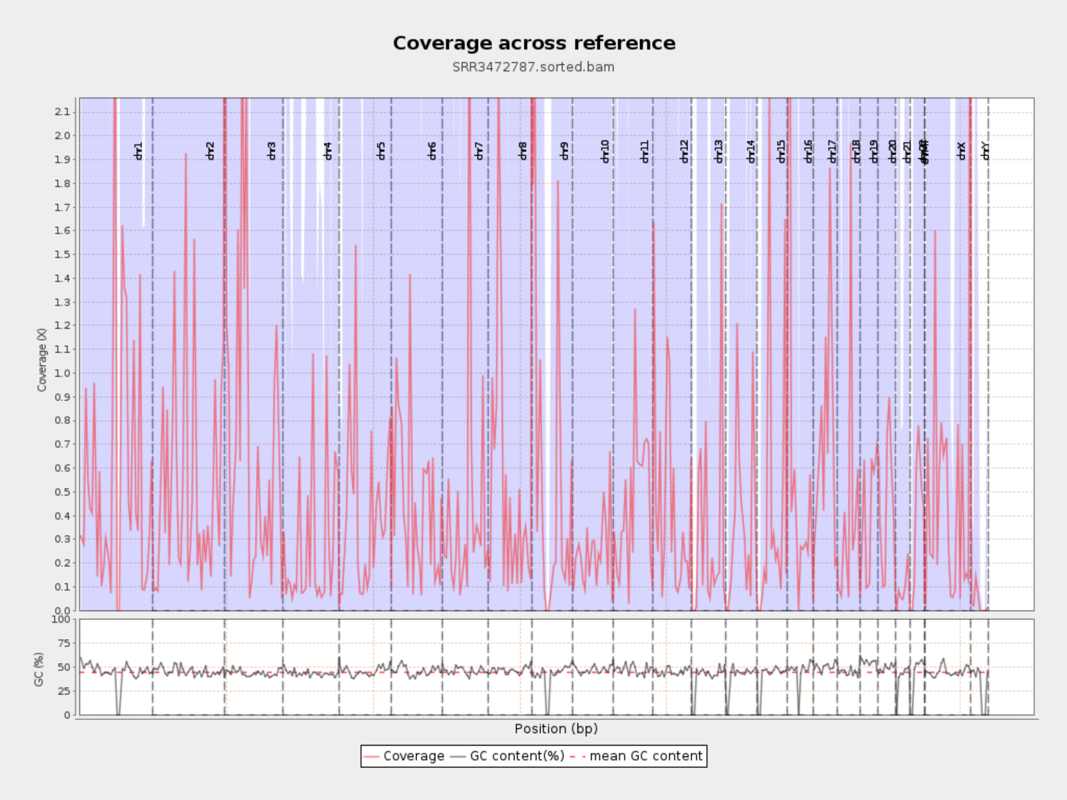
2.7. Chromosome stats

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

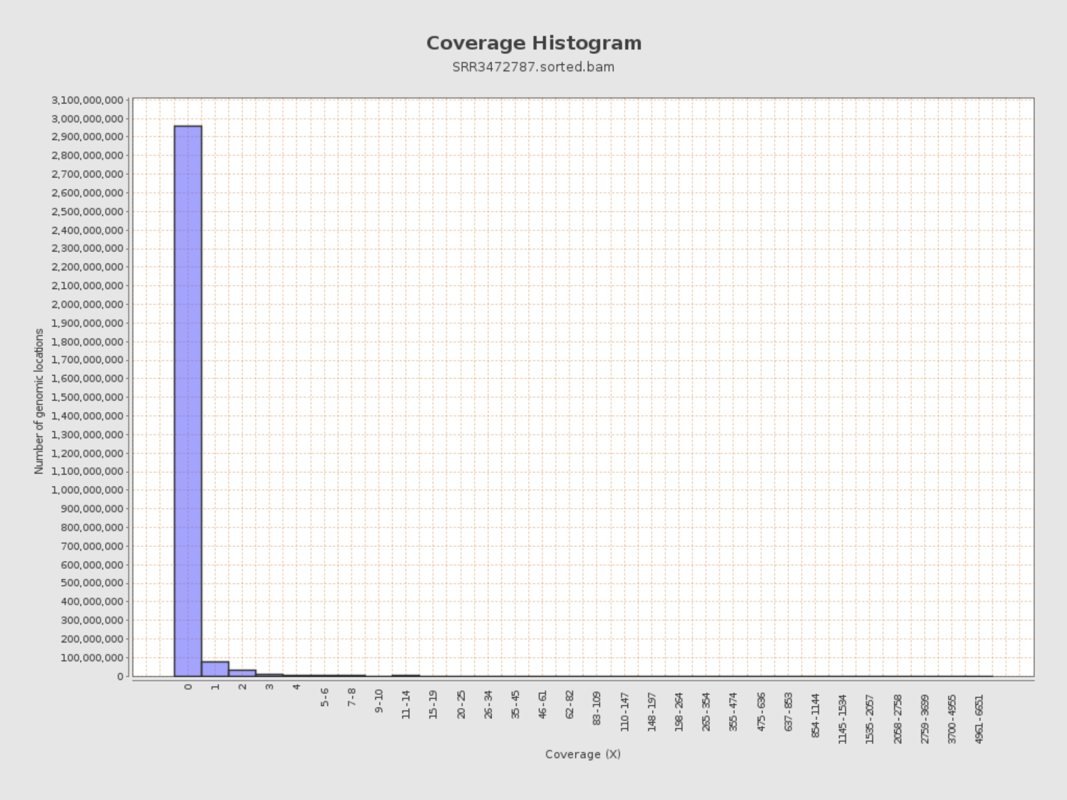
		bases	coverage	deviation
chr1	249250621	148135621	0.5943	18.8878
chr2	243199373	129507329	0.5325	17.2399
chr3	198022430	152433135	0.7698	18.0465
chr4	191154276	51651623	0.2702	10.9038
chr5	180915260	75040612	0.4148	12.4687
chr6	171115067	78827469	0.4607	11.8854
chr7	159138663	69310985	0.4355	16.2599
chr8	146364022	73541086	0.5025	16.1997
chr9	141213431	84752369	0.6002	18.9627
chr10	135534747	33483126	0.247	7.8758
chr11	135006516	63445739	0.4699	13.2402
chr12	133851895	59619460	0.4454	11.7756
chr13	115169878	37144110	0.3225	17.0741
chr14	107349540	40138295	0.3739	12.1809
chr15	102531392	46064841	0.4493	21.5014
chr16	90354753	57870275	0.6405	19.0975
chr17	81195210	57693212	0.7105	18.3311
chr18	78077248	32308828	0.4138	25.1075
chr19	59128983	24897748	0.4211	10.1313
chr20	63025520	29064184	0.4611	13.419
chr21	48129895	4456100	0.0926	3.1374
chr22	51304566	19110300	0.3725	9.6905
chrMT	16571	773	0.0466	0.2271
chrX	155270560	73605542	0.474	15.4149

chrY	59373566	2081266	0.0351	1.2816

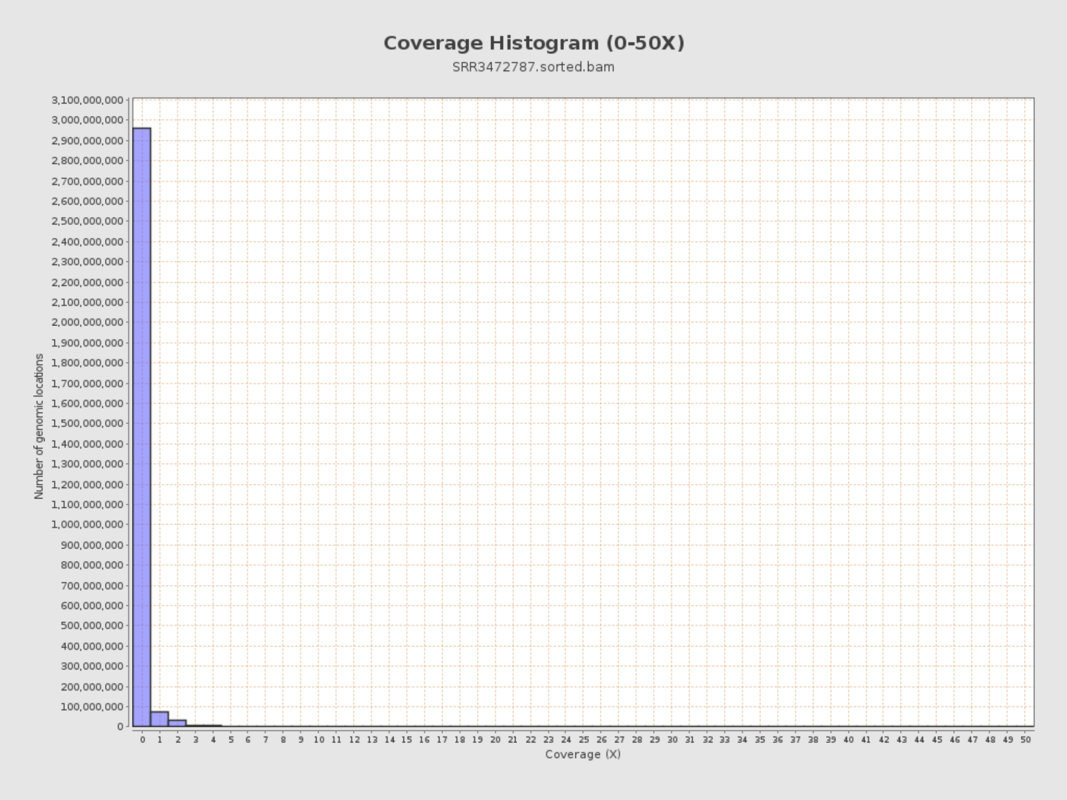
3. Results : Coverage across reference



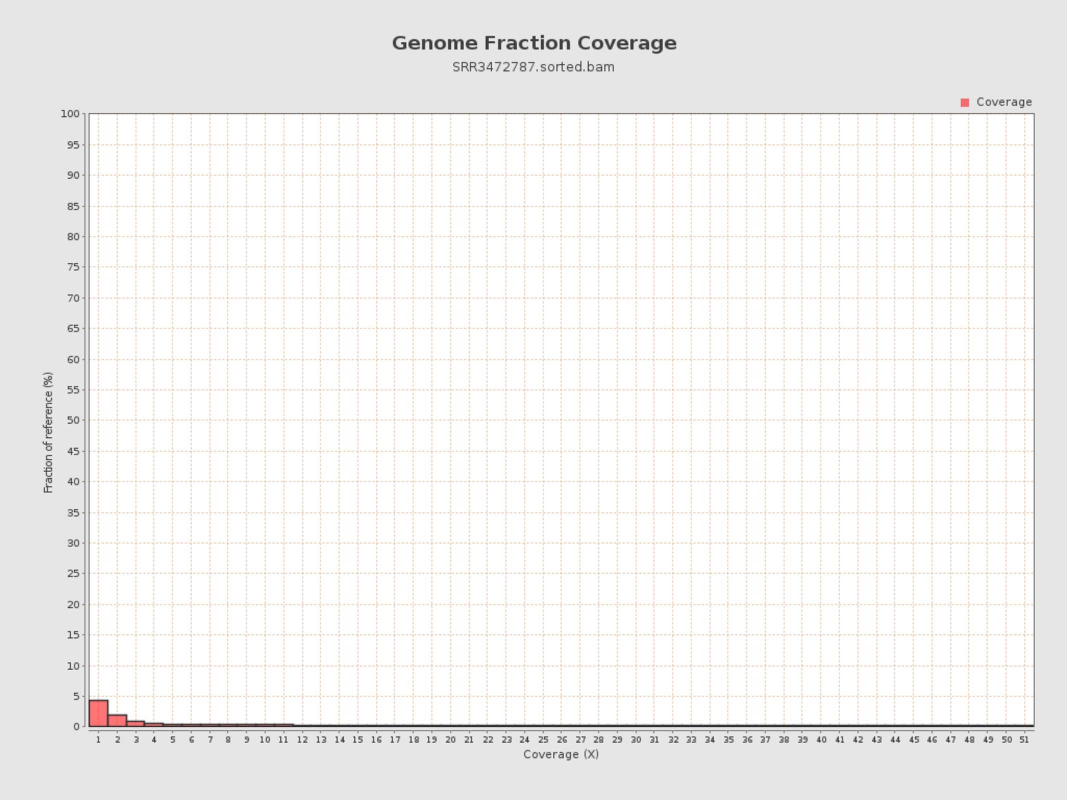
4. Results : Coverage Histogram



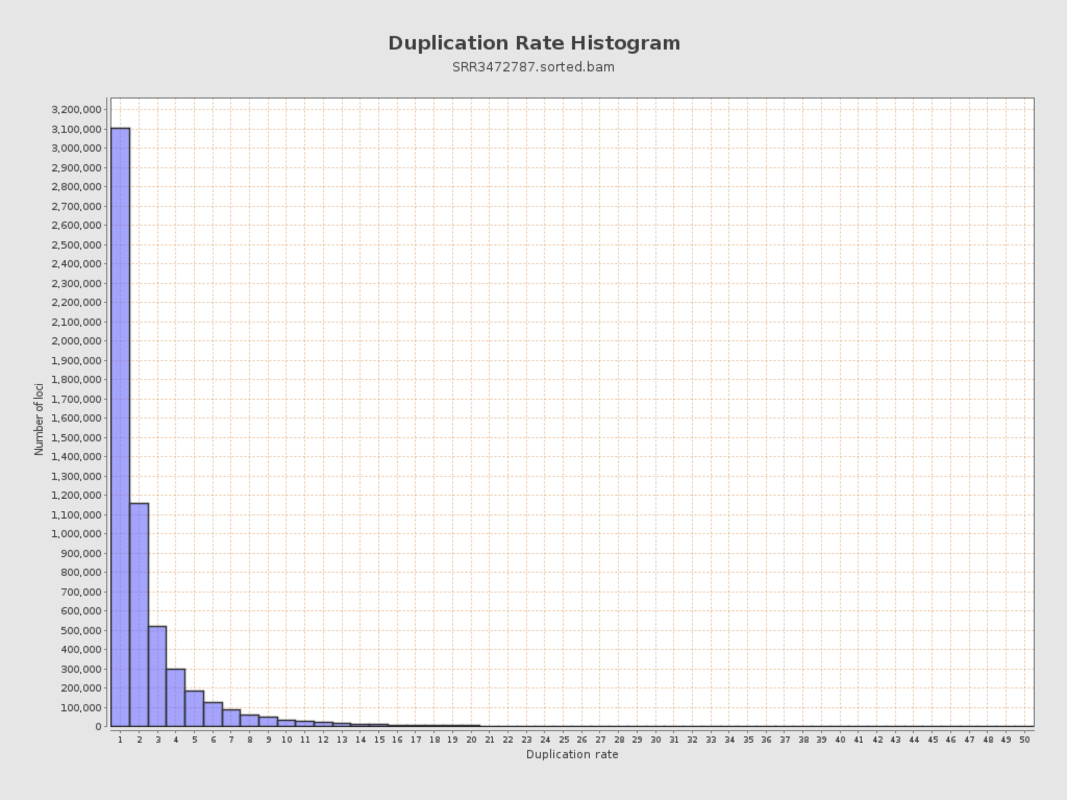
5. Results : Coverage Histogram (0-50X)



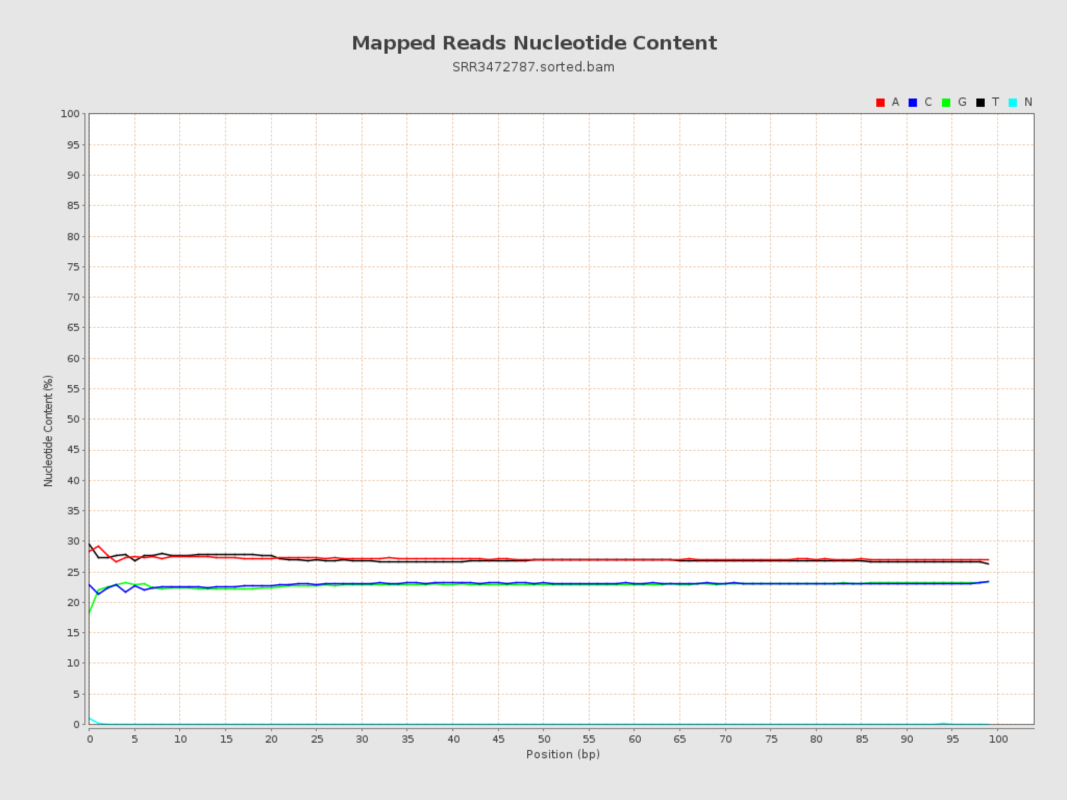
6. Results : Genome Fraction Coverage



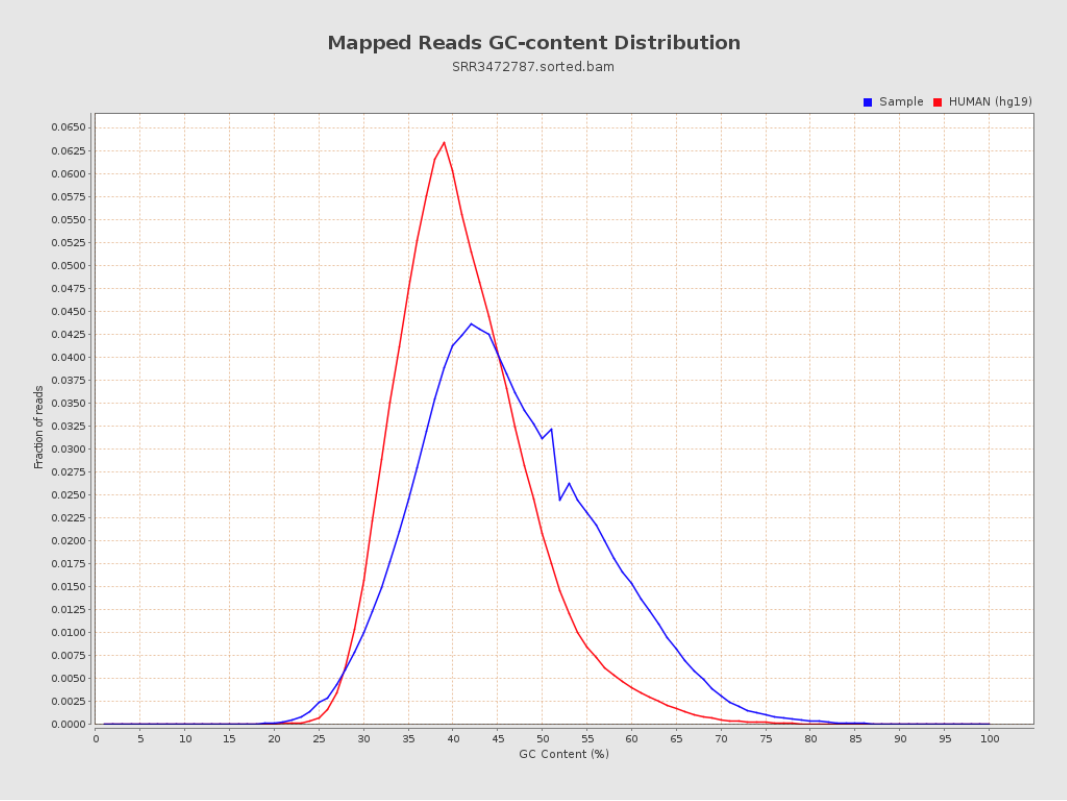
7. Results : Duplication Rate Histogram



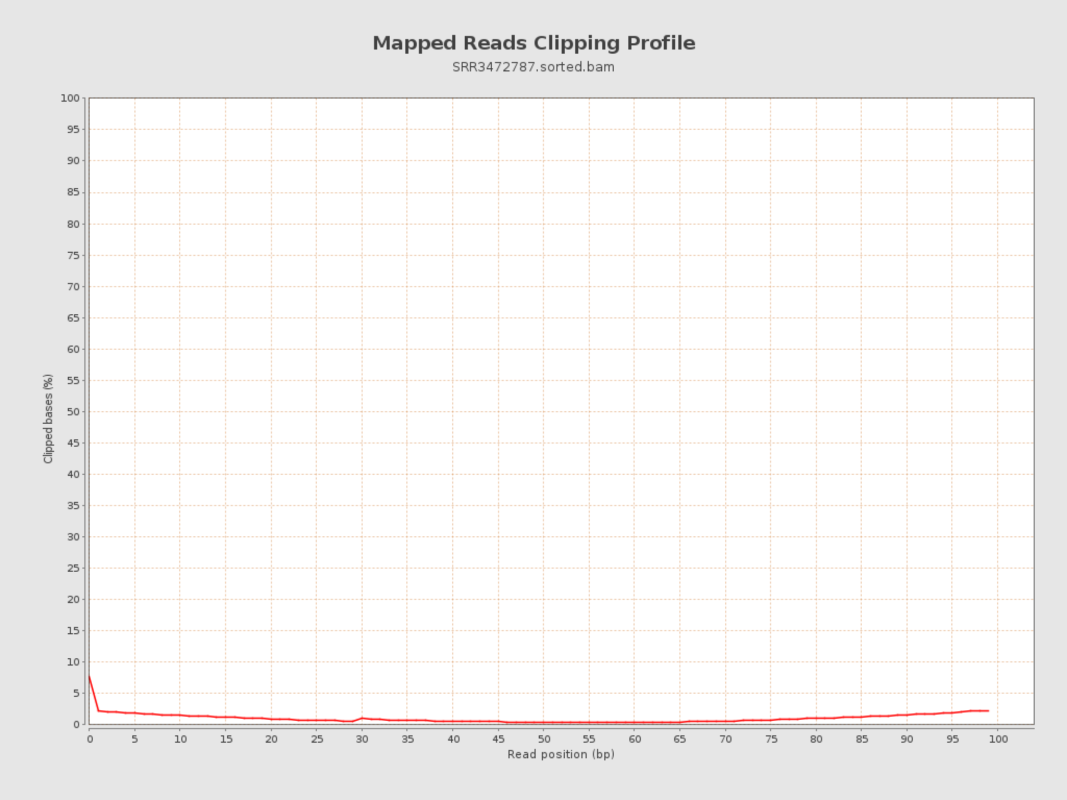
8. Results : Mapped Reads Nucleotide Content



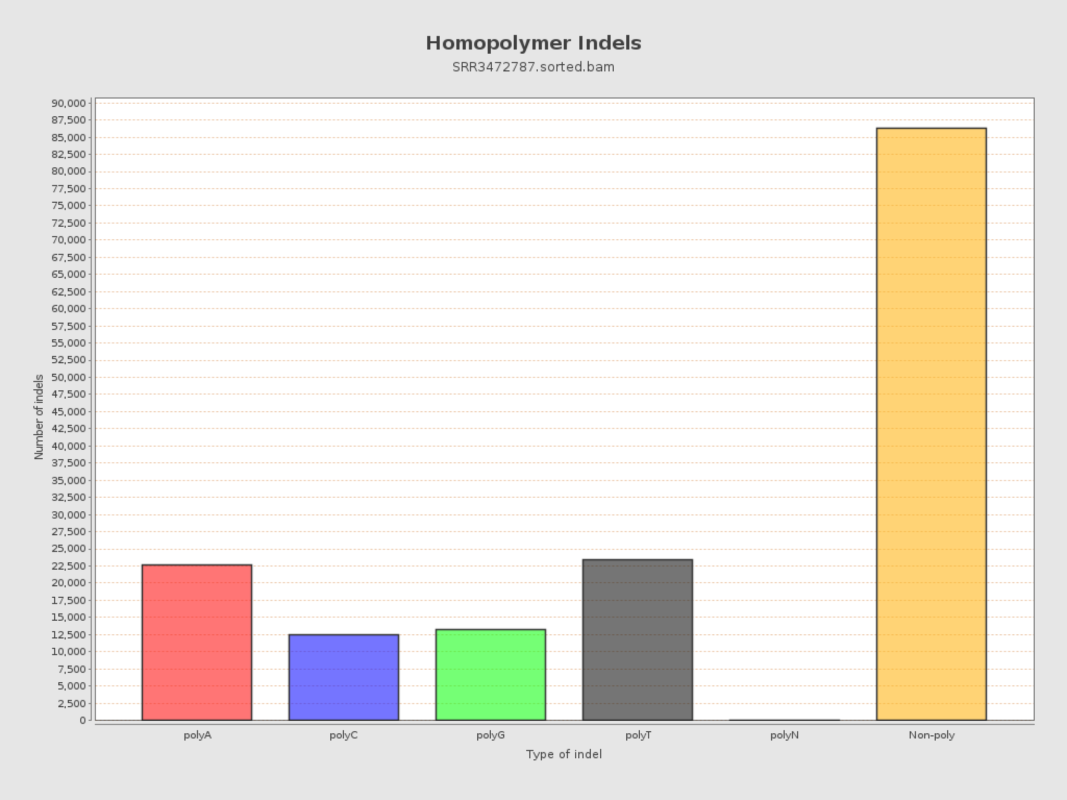
9. Results : Mapped Reads GC-content Distribution



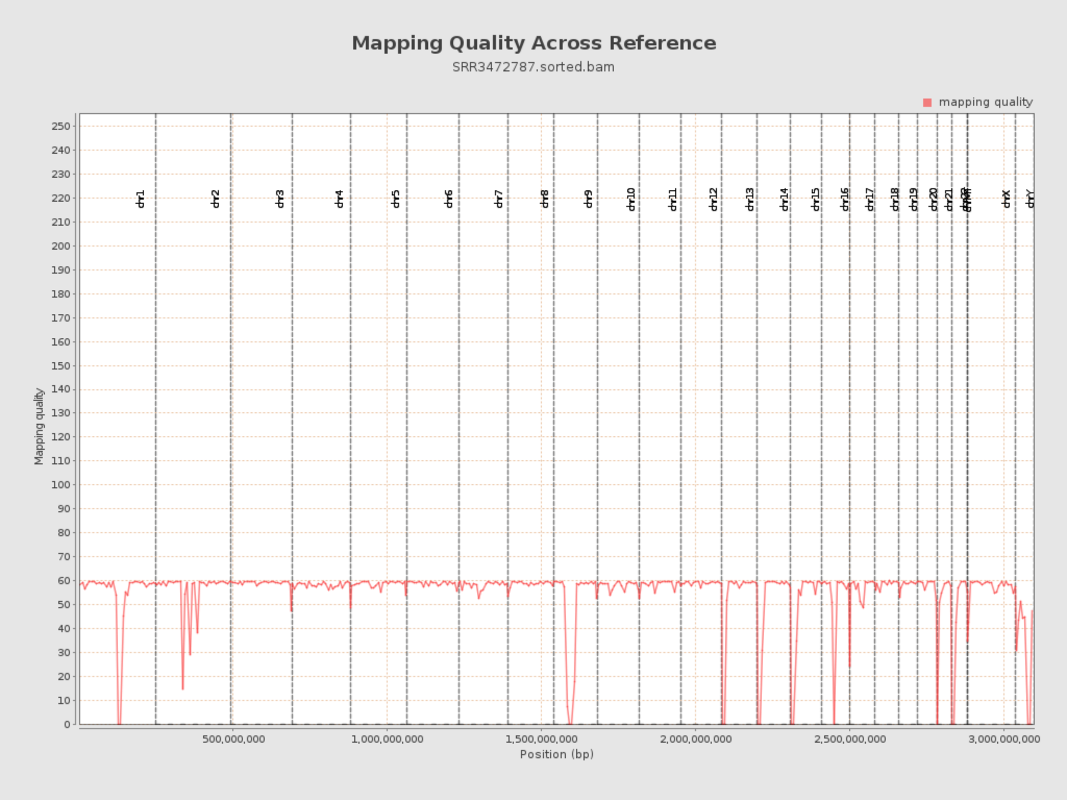
10. Results : Mapped Reads Clipping Profile



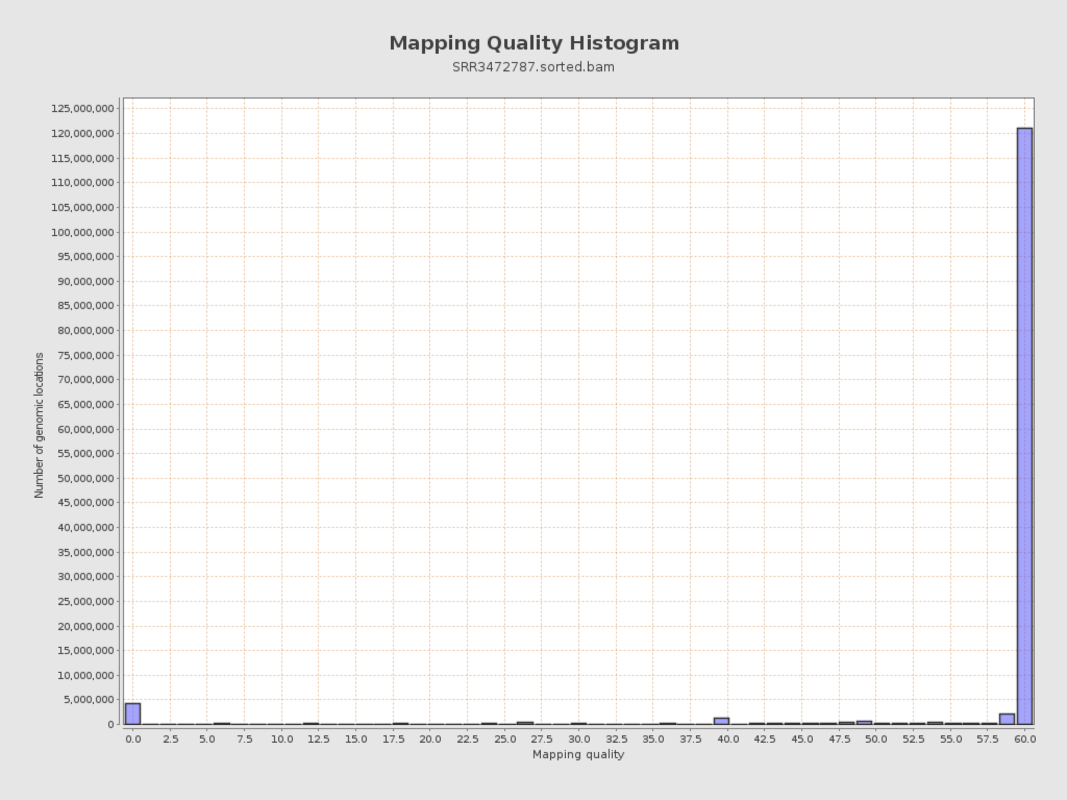
11. Results : Homopolymer Indels



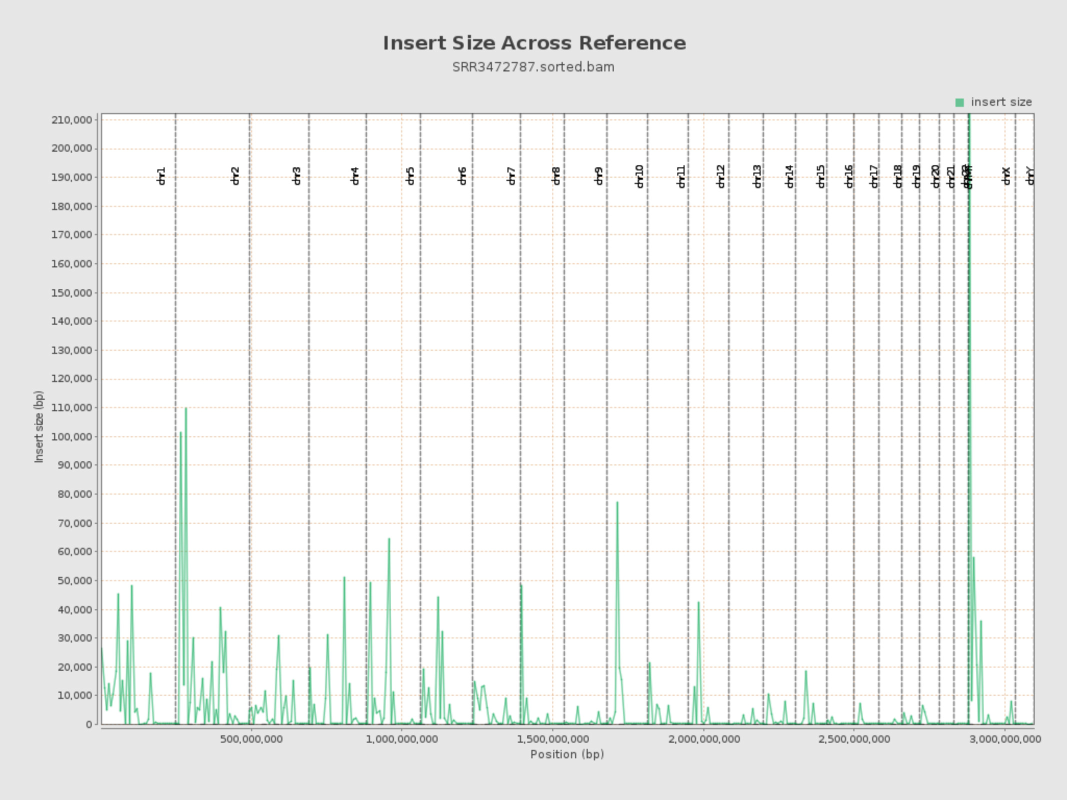
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram