Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:09:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472557.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_SRR3472557 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472557_1.fastq.gz SRR3472557_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:09:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472557.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,610,648
Mapped reads	17,412,165 / 98.87%
Unmapped reads	198,483 / 1.13%
Mapped paired reads	17,412,165 / 98.87%
Mapped reads, first in pair	8,737,018 / 49.61%
Mapped reads, second in pair	8,675,147 / 49.26%
Mapped reads, both in pair	17,304,878 / 98.26%
Mapped reads, singletons	107,287 / 0.61%
Secondary alignments	0
Supplementary alignments	65,897 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	11,142,757 / 63.27%
Duplication rate	46.31%
Clipped reads	1,557,760 / 8.85%

2.2. ACGT Content

Number/percentage of A's	472,939,846 / 27.65%
Number/percentage of C's	385,277,251 / 22.52%
Number/percentage of T's	469,110,995 / 27.43%
Number/percentage of G's	382,858,219 / 22.38%
Number/percentage of N's	264,850 / 0.02%

GC Percentage	44.91%

2.3. Coverage

Mean	0.5526
Standard Deviation	20.1585

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	27,882.9
Standard Deviation	1,633,864.59
P25/Median/P75	166 / 235 / 319

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	10,397,401
Insertions	93,884
Mapped reads with at least one insertion	0.53%
Deletions	91,652
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.61%

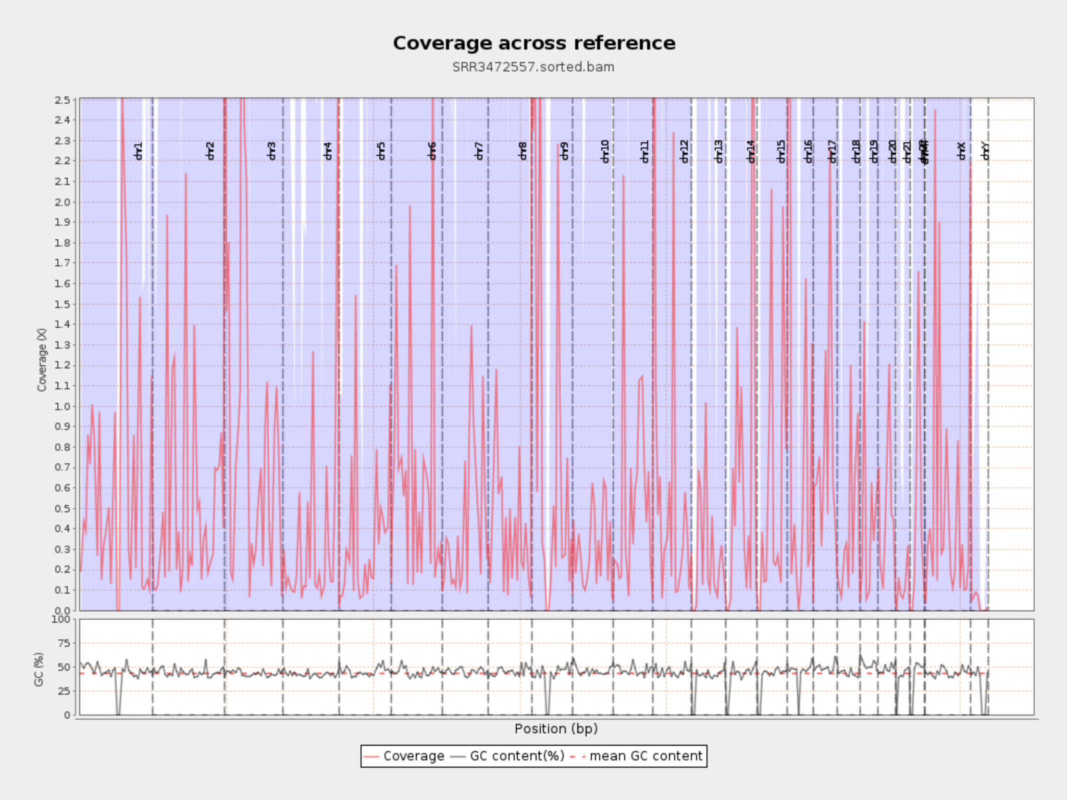
2.7. Chromosome stats

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

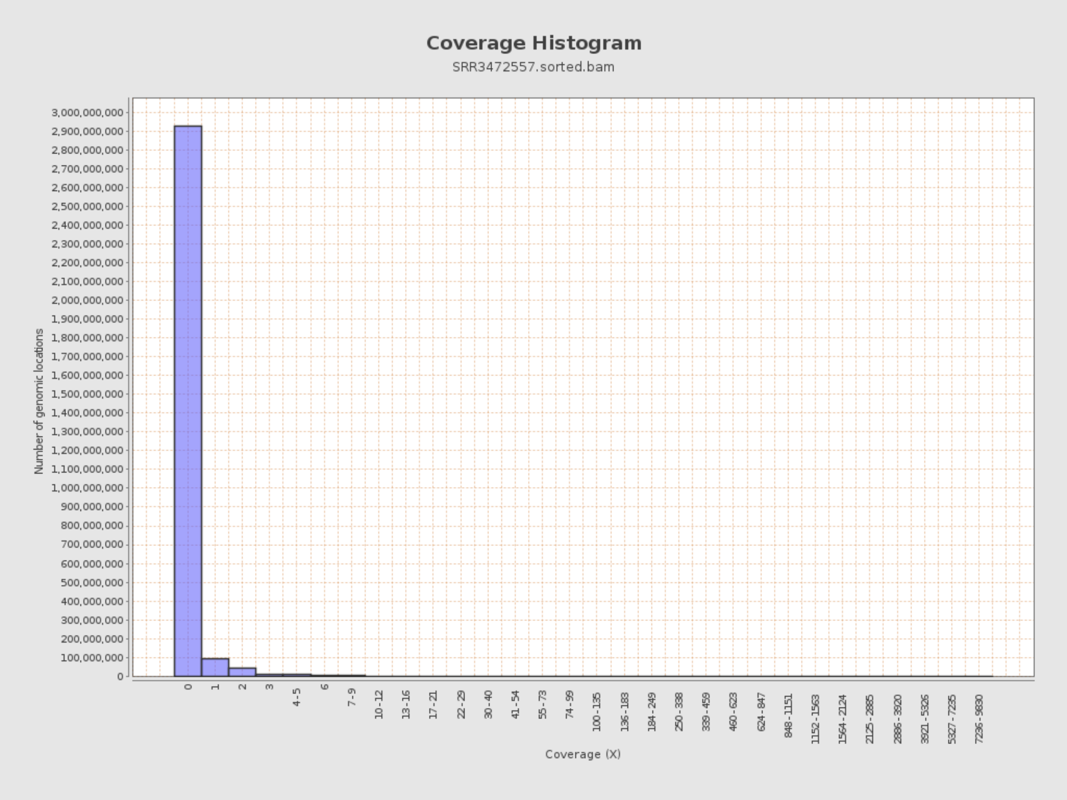
		bases	coverage	deviation
chr1	249250621	161192604	0.6467	17.835
chr2	243199373	129663526	0.5332	19.116
chr3	198022430	198748209	1.0037	24.0333
chr4	191154276	67444452	0.3528	14.3196
chr5	180915260	64673288	0.3575	15.2957
chr6	171115067	116754391	0.6823	26.8517
chr7	159138663	70605896	0.4437	13.8705
chr8	146364022	58889321	0.4023	13.808
chr9	141213431	123796498	0.8767	26.0665
chr10	135534747	42293054	0.312	10.4425
chr11	135006516	76615407	0.5675	21.7663
chr12	133851895	91033207	0.6801	32.5396
chr13	115169878	31963486	0.2775	8.5783
chr14	107349540	70084163	0.6529	32.0279
chr15	102531392	61417952	0.599	20.6828
chr16	90354753	81064233	0.8972	30.1135
chr17	81195210	62693459	0.7721	21.3709
chr18	78077248	32410868	0.4151	15.9428
chr19	59128983	26406168	0.4466	11.8364
chr20	63025520	32281554	0.5122	17.9076
chr21	48129895	5876578	0.1221	5.8342
chr22	51304566	23034360	0.449	15.1432
chrMT	16571	1670	0.1008	0.4255
chrX	155270560	79603921	0.5127	18.3373

chrY	59373566	2121891	0.0357	0.8146

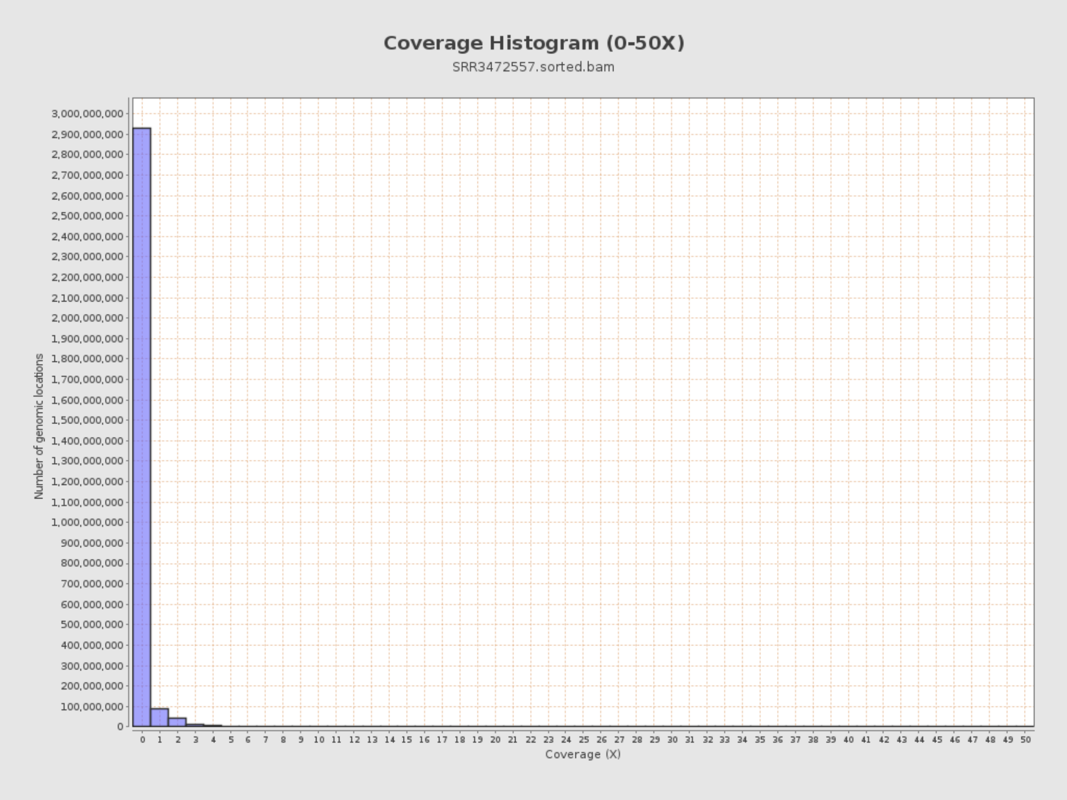
3. Results : Coverage across reference



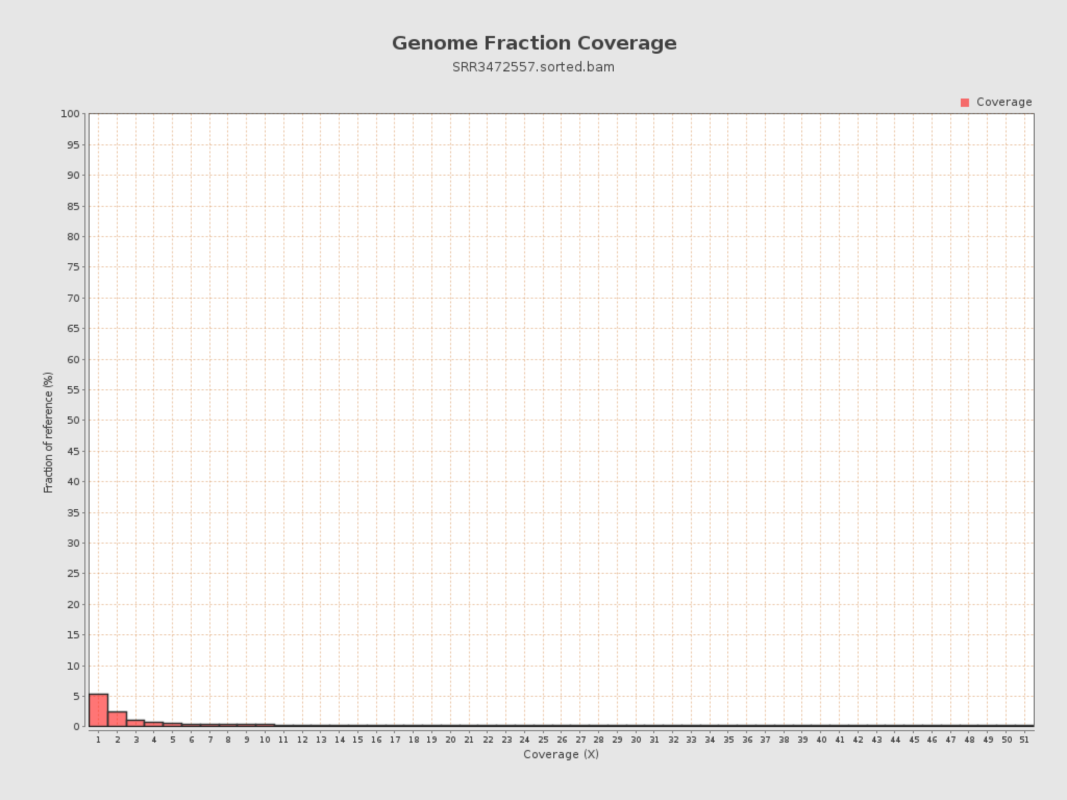
4. Results : Coverage Histogram



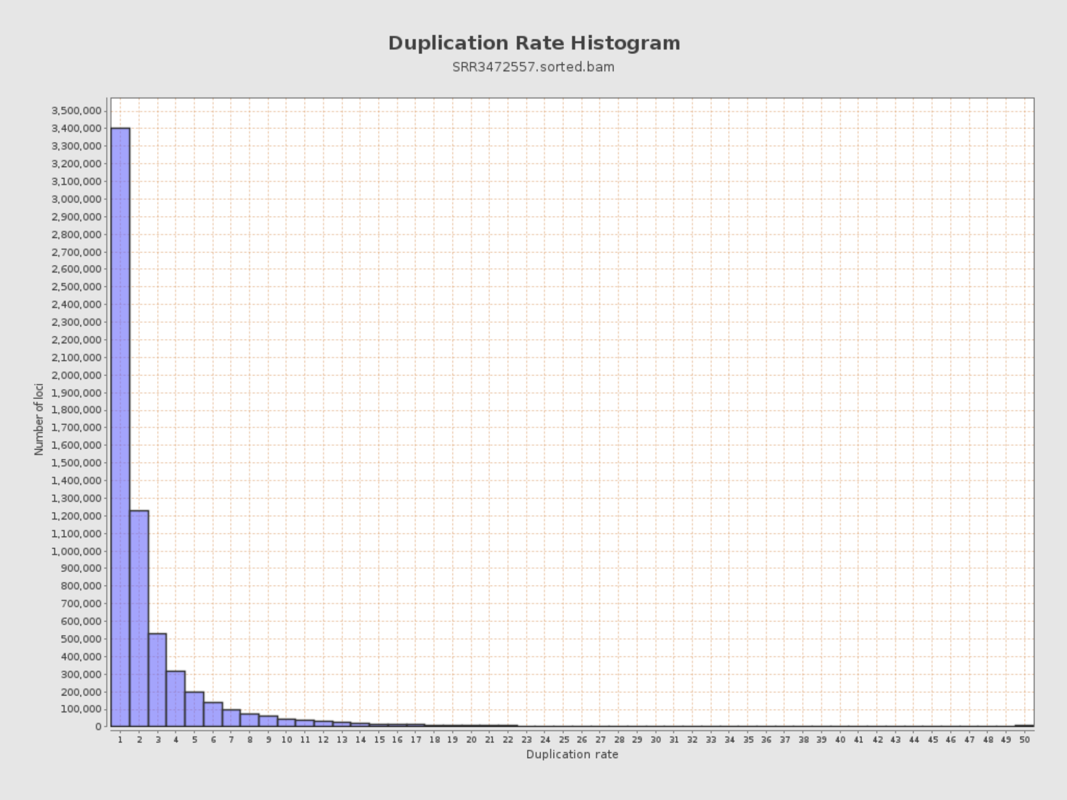
5. Results : Coverage Histogram (0-50X)



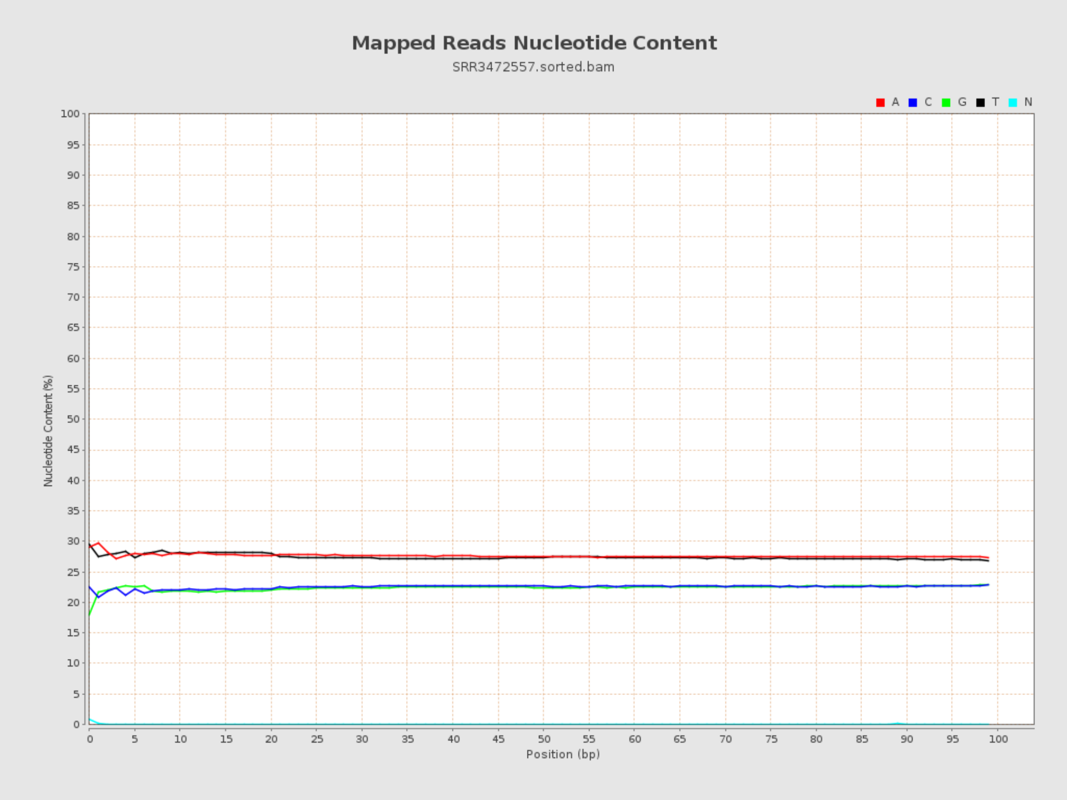
6. Results : Genome Fraction Coverage



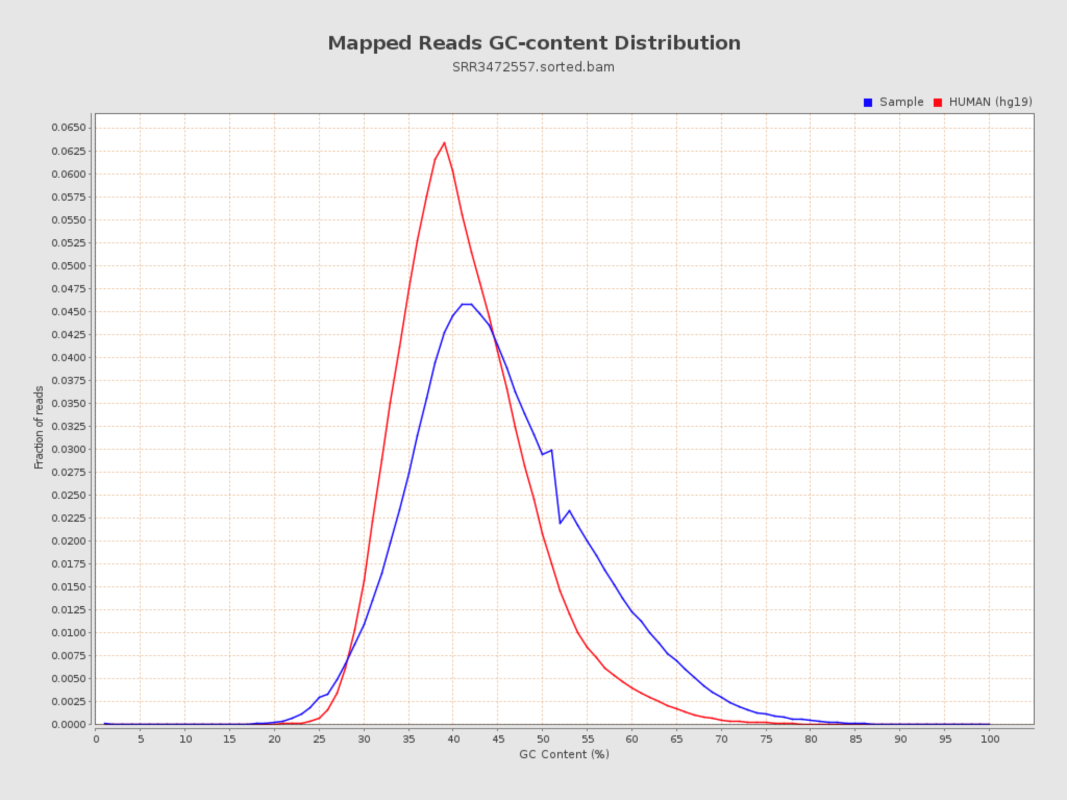
7. Results : Duplication Rate Histogram



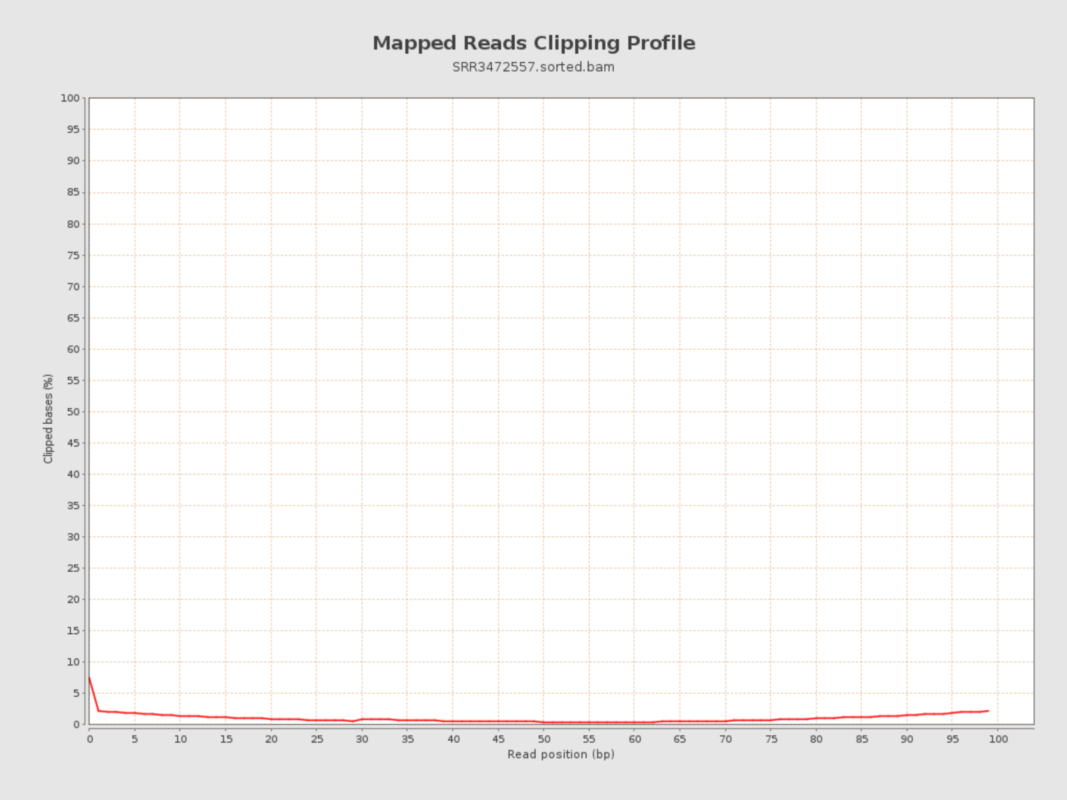
8. Results : Mapped Reads Nucleotide Content



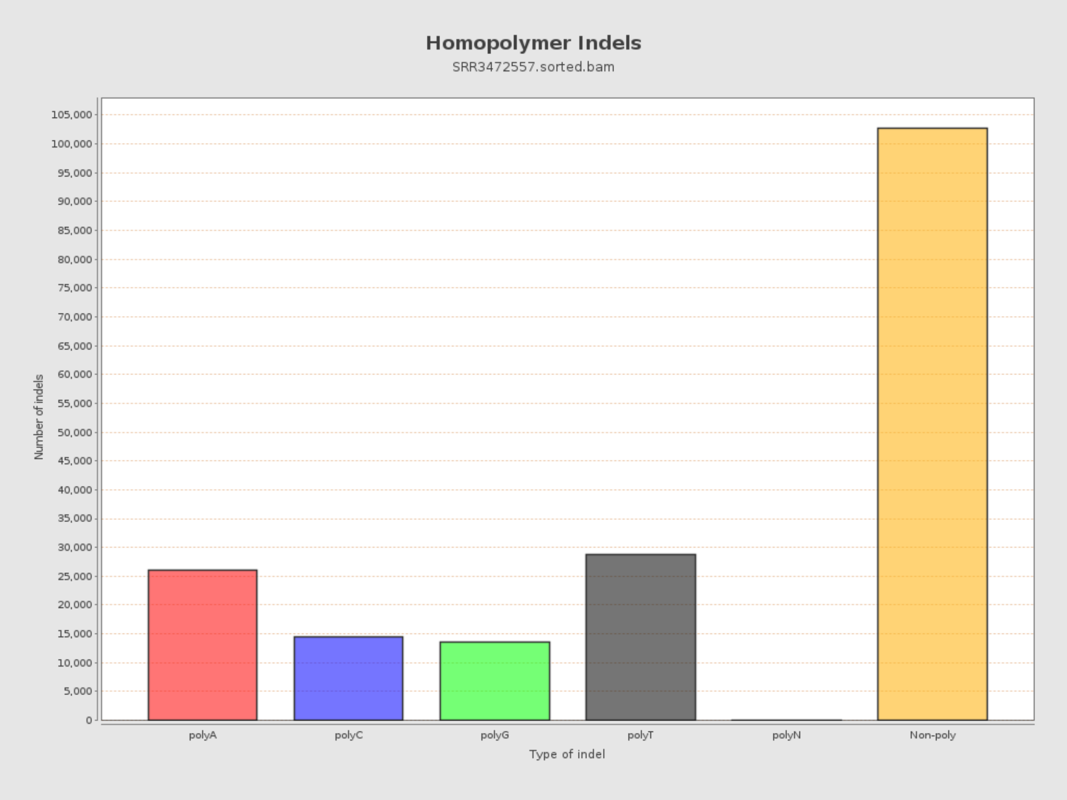
9. Results : Mapped Reads GC-content Distribution



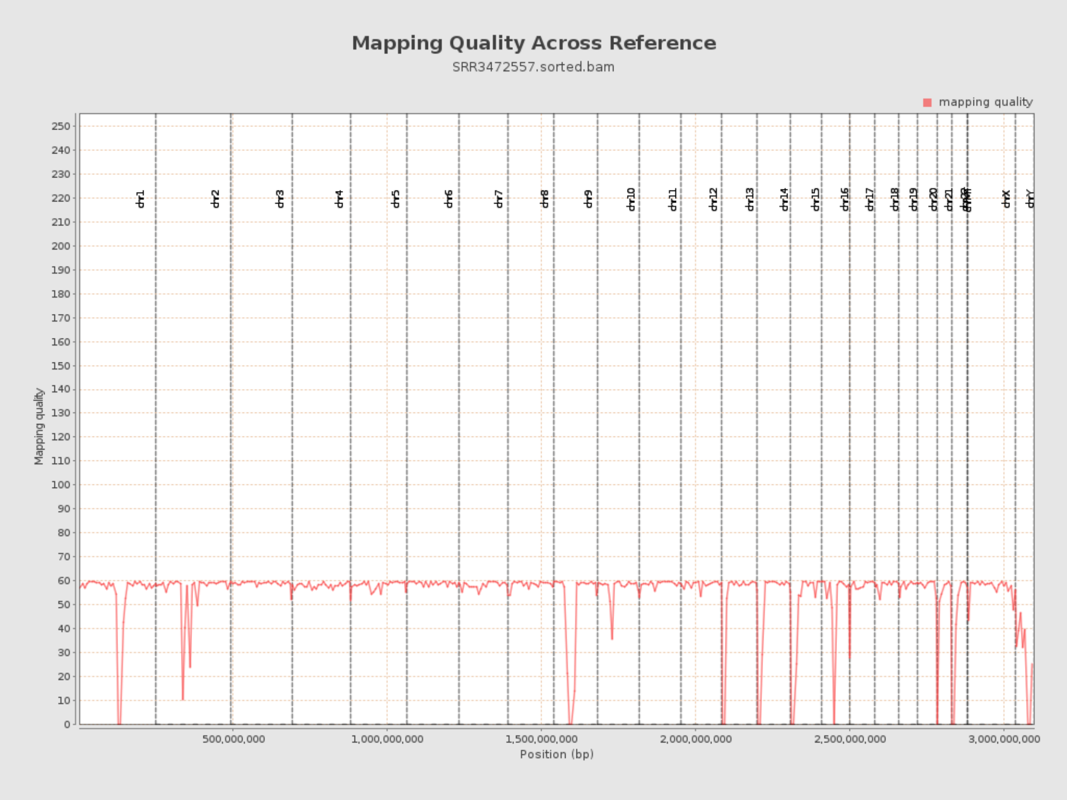
10. Results : Mapped Reads Clipping Profile



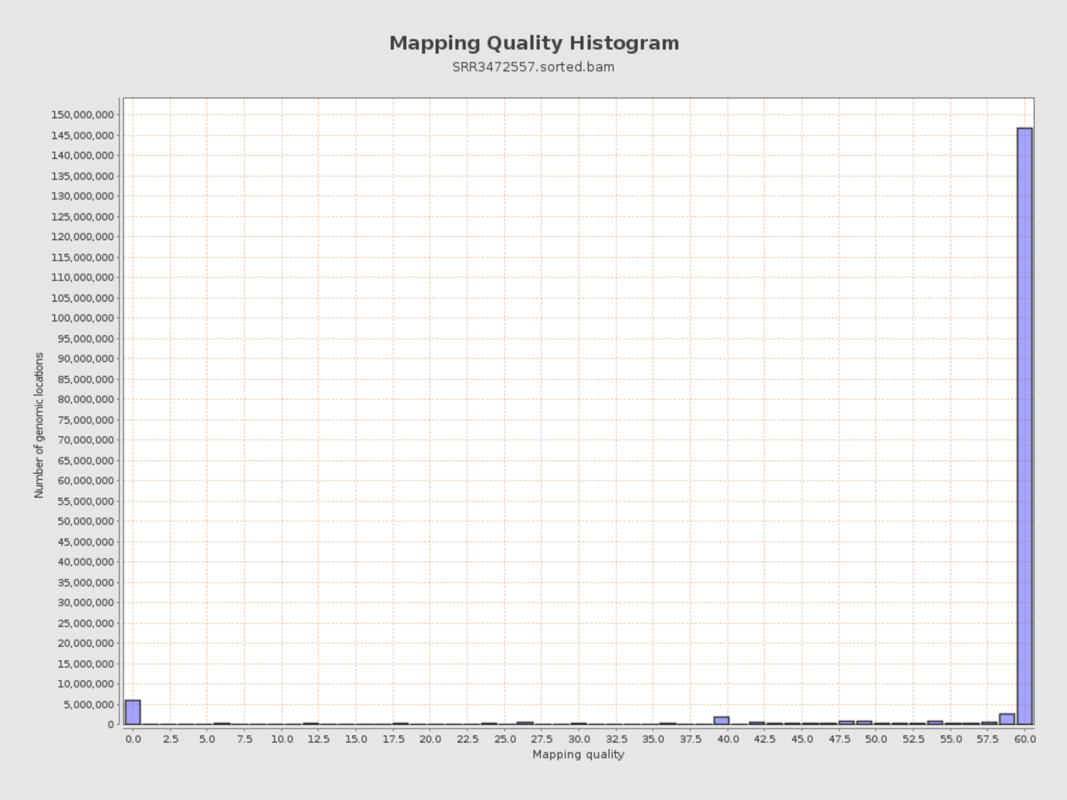
11. Results : Homopolymer Indels



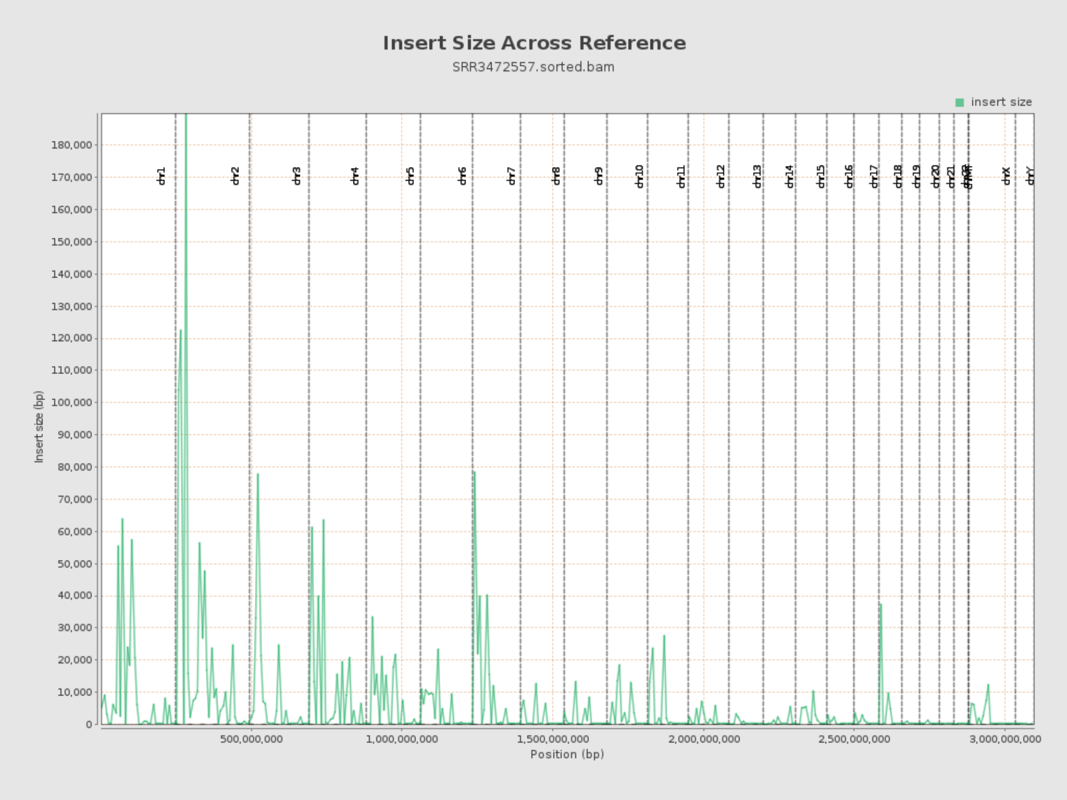
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram