Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 16:44:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472784.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_SRR3472784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472784_1.fastq.gz SRR3472784_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 16:44:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,647,230
Mapped reads	10,546,033 / 99.05%
Unmapped reads	101,197 / 0.95%
Mapped paired reads	10,546,033 / 99.05%
Mapped reads, first in pair	5,289,722 / 49.68%
Mapped reads, second in pair	5,256,311 / 49.37%
Mapped reads, both in pair	10,489,652 / 98.52%
Mapped reads, singletons	56,381 / 0.53%
Secondary alignments	0
Supplementary alignments	43,126 / 0.41%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	6,162,597 / 57.88%
Duplication rate	44.65%
Clipped reads	945,561 / 8.88%

2.2. ACGT Content

Number/percentage of A's	284,326,183 / 27.41%
Number/percentage of C's	235,613,737 / 22.72%
Number/percentage of T's	282,699,988 / 27.26%
Number/percentage of G's	234,310,584 / 22.59%
Number/percentage of N's	203,936 / 0.02%

GC Percentage	45.31%

2.3. Coverage

Mean	0.3351
Standard Deviation	12.7967

2.4. Mapping Quality

Mean Mapping Quality	55.09

2.5. Insert size

Mean	27,246.86
Standard Deviation	1,619,435.85
P25/Median/P75	161 / 226 / 307

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	6,058,131
Insertions	64,618
Mapped reads with at least one insertion	0.61%
Deletions	54,481
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.33%

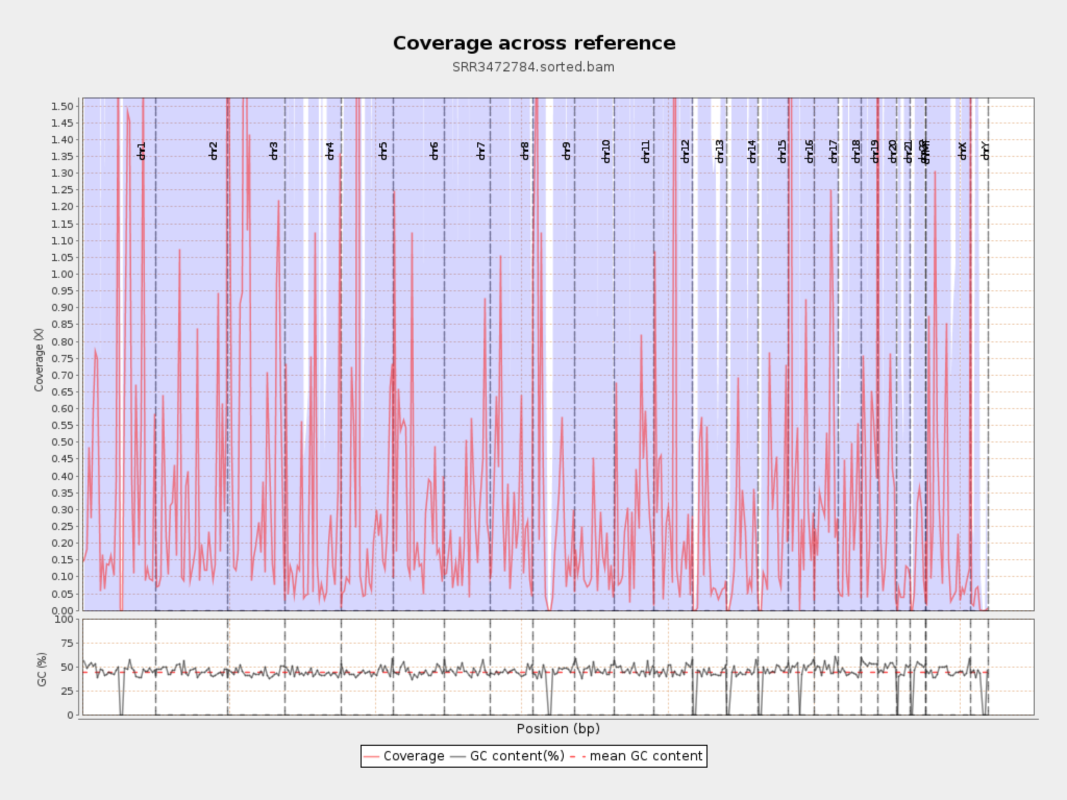
2.7. Chromosome stats

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

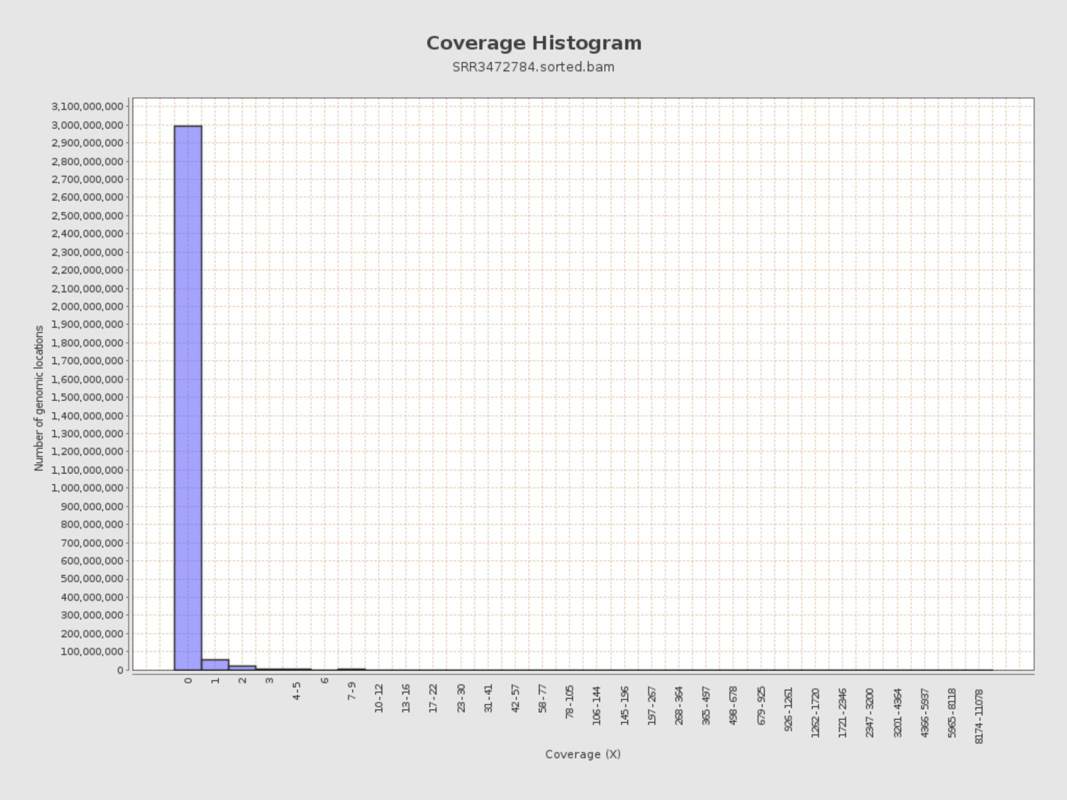
		bases	coverage	deviation
chr1	249250621	110537906	0.4435	19.4525
chr2	243199373	71837381	0.2954	11.7256
chr3	198022430	131728999	0.6652	15.4699
chr4	191154276	49762224	0.2603	10.6227
chr5	180915260	70517515	0.3898	16.7522
chr6	171115067	59726449	0.349	10.0031
chr7	159138663	41679985	0.2619	7.6186
chr8	146364022	45429693	0.3104	10.5479
chr9	141213431	56280597	0.3985	12.1242
chr10	135534747	21527846	0.1588	6.6784
chr11	135006516	40706665	0.3015	9.9977
chr12	133851895	53562129	0.4002	18.637
chr13	115169878	18208365	0.1581	6.2471
chr14	107349540	21116625	0.1967	7.8725
chr15	102531392	27152933	0.2648	13.5982
chr16	90354753	52380326	0.5797	21.5914
chr17	81195210	35945005	0.4427	12.2792
chr18	78077248	18530367	0.2373	8.5179
chr19	59128983	29905710	0.5058	16.3596
chr20	63025520	19444919	0.3085	10.5124
chr21	48129895	3586135	0.0745	2.8647
chr22	51304566	8746467	0.1705	6.0849
chrMT	16571	3441	0.2077	0.5404
chrX	155270560	47650394	0.3069	9.7272

chrY	59373566	1320724	0.0222	0.8974

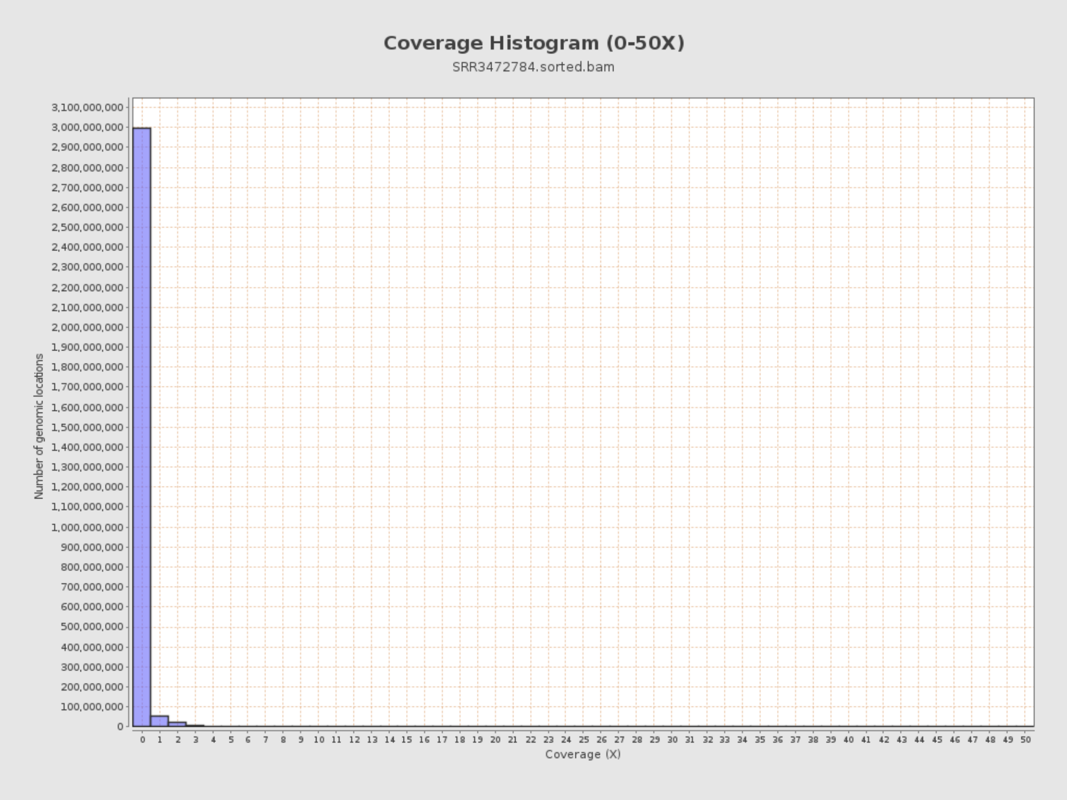
3. Results : Coverage across reference



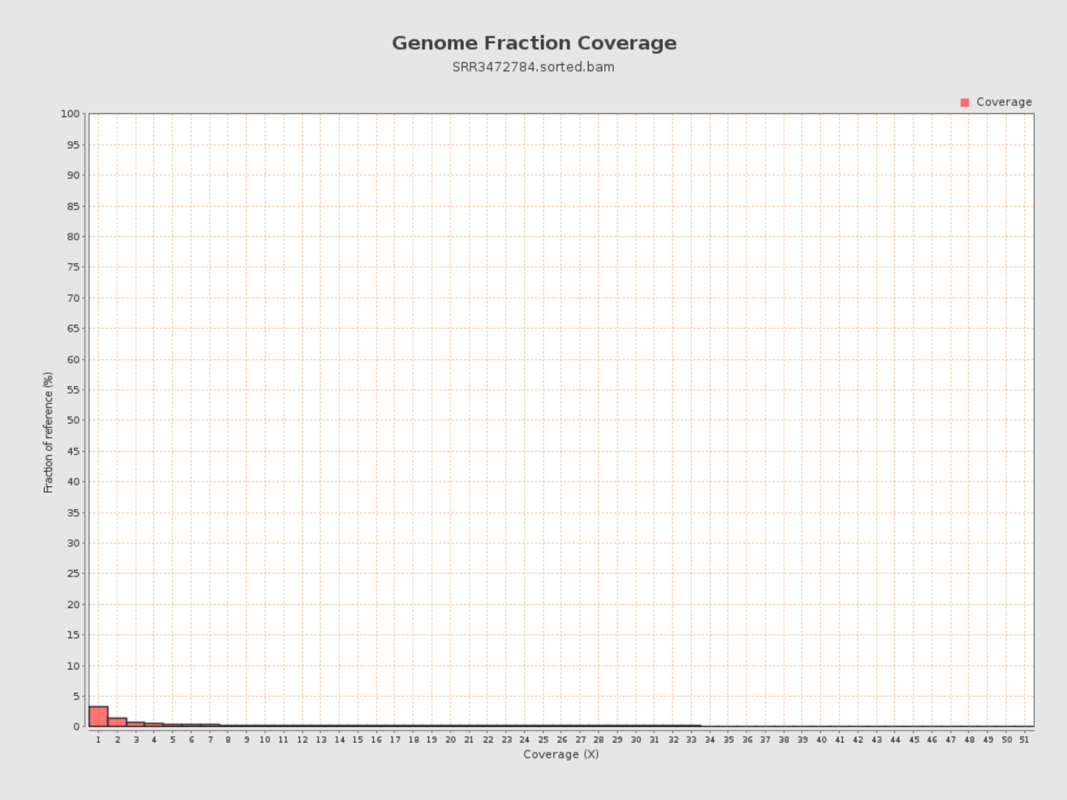
4. Results : Coverage Histogram



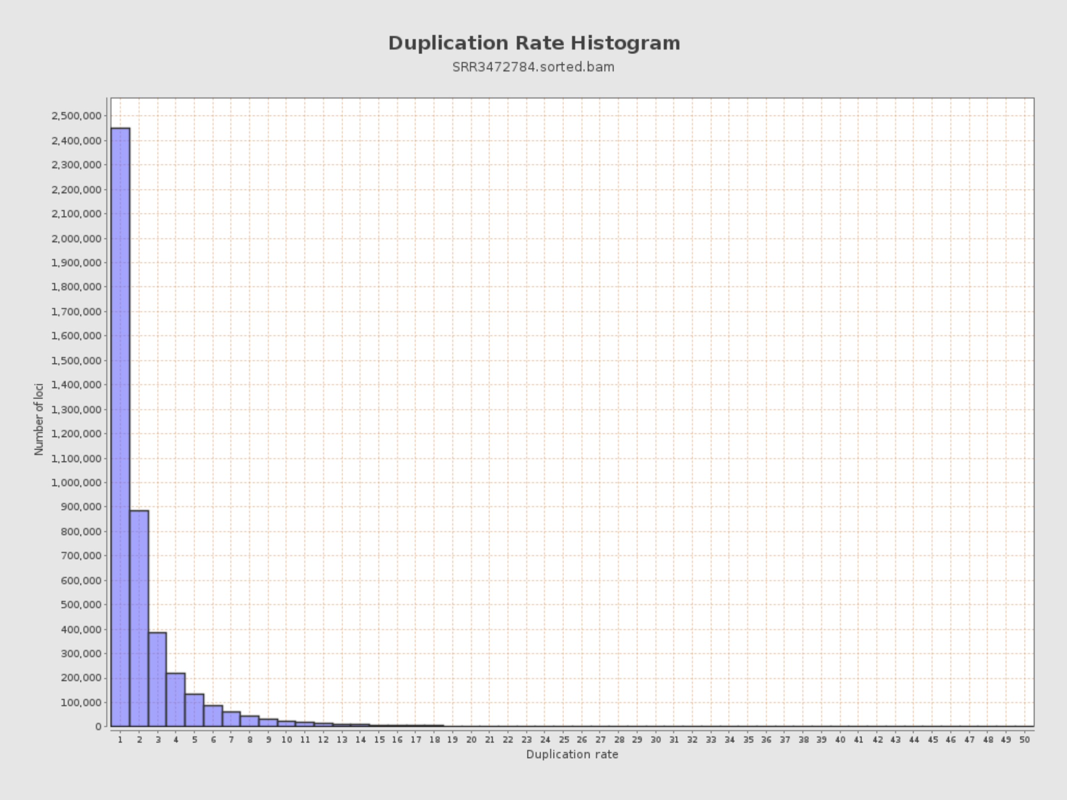
5. Results : Coverage Histogram (0-50X)



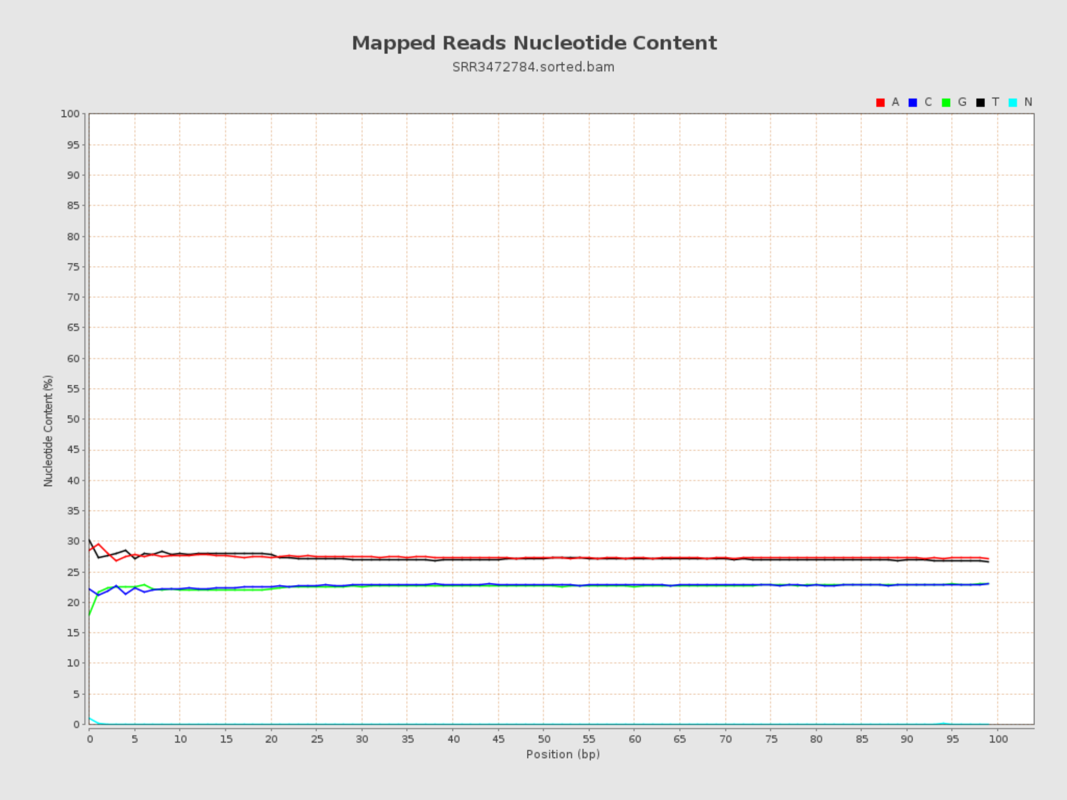
6. Results : Genome Fraction Coverage



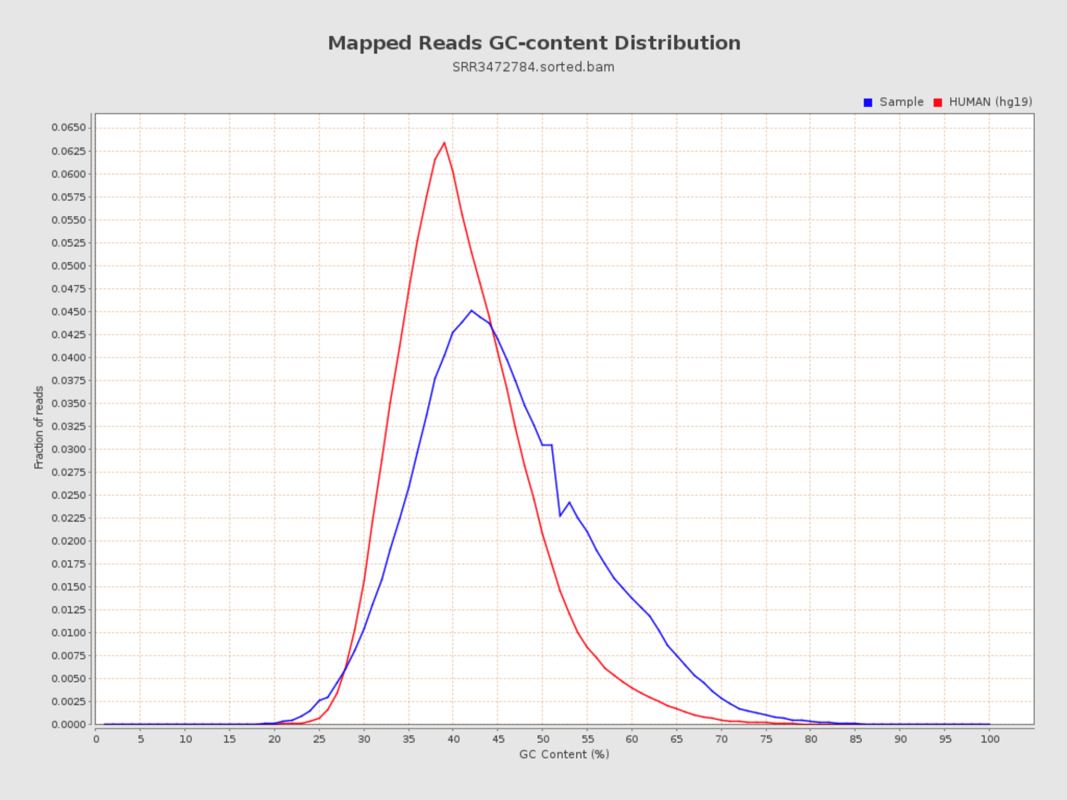
7. Results : Duplication Rate Histogram



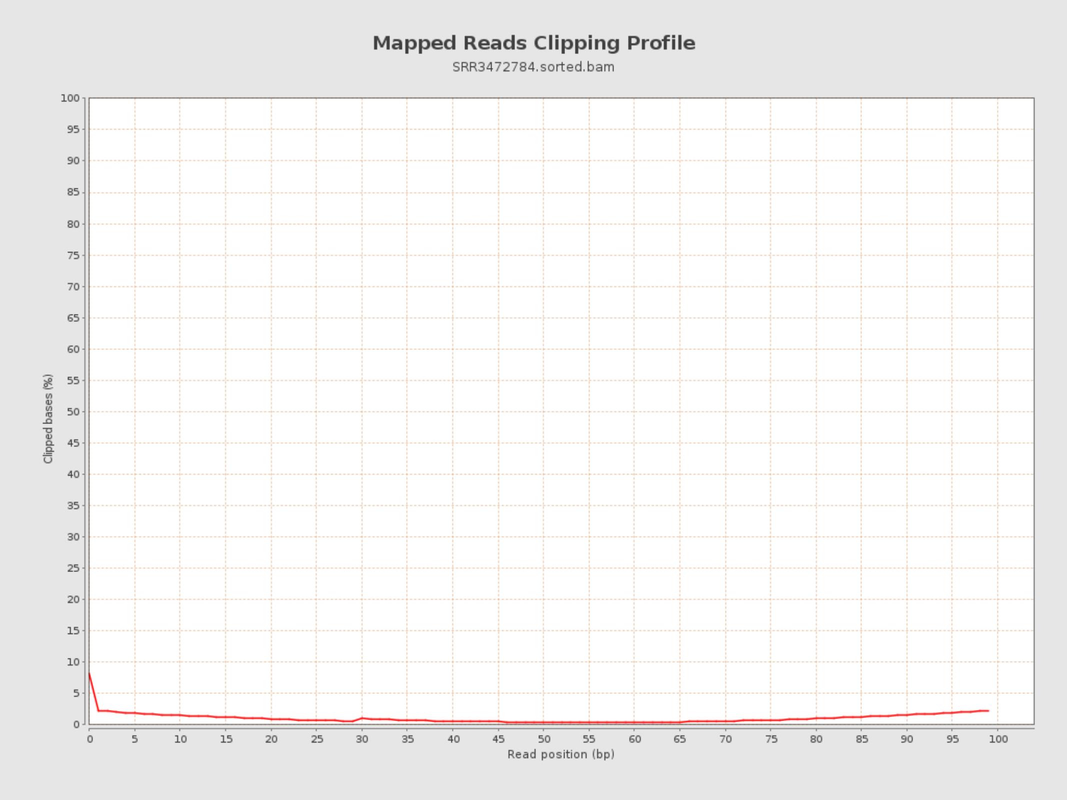
8. Results : Mapped Reads Nucleotide Content



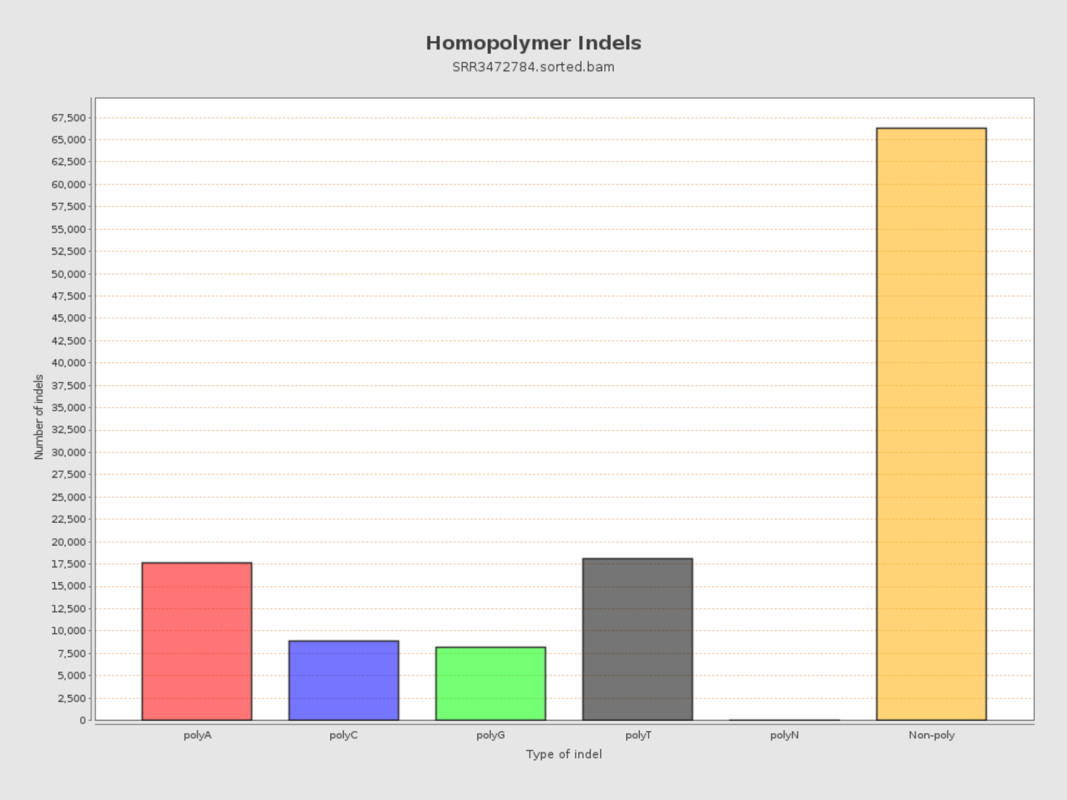
9. Results : Mapped Reads GC-content Distribution



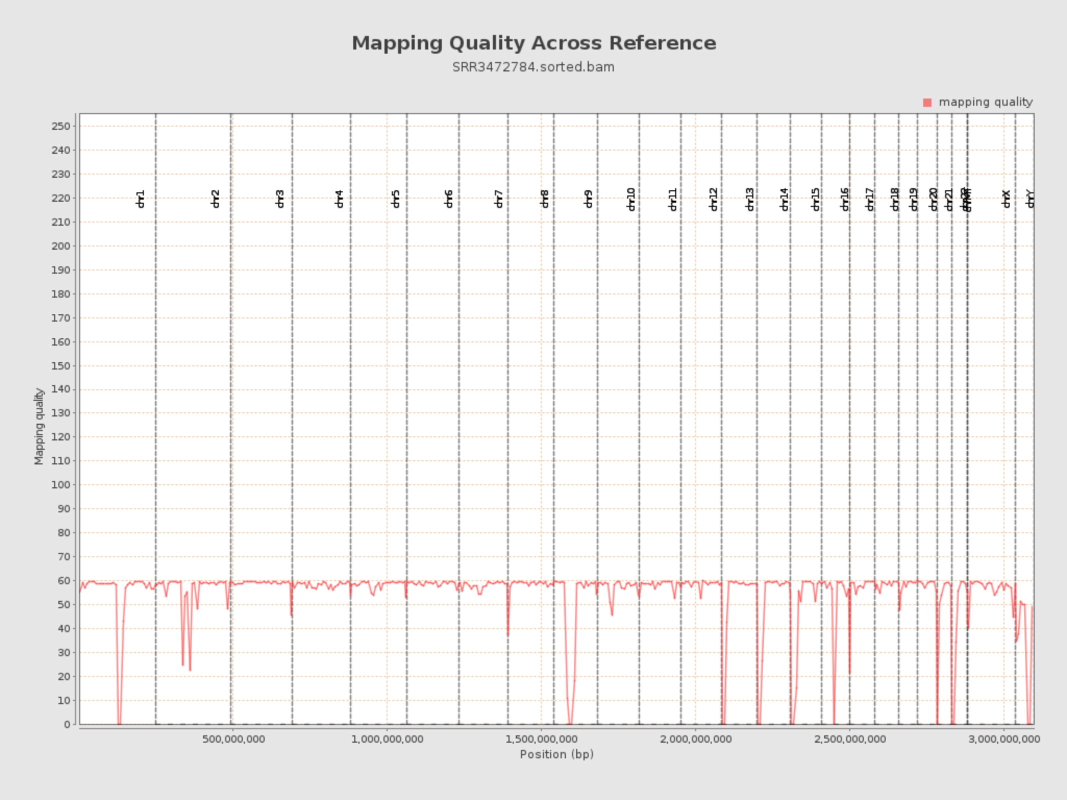
10. Results : Mapped Reads Clipping Profile



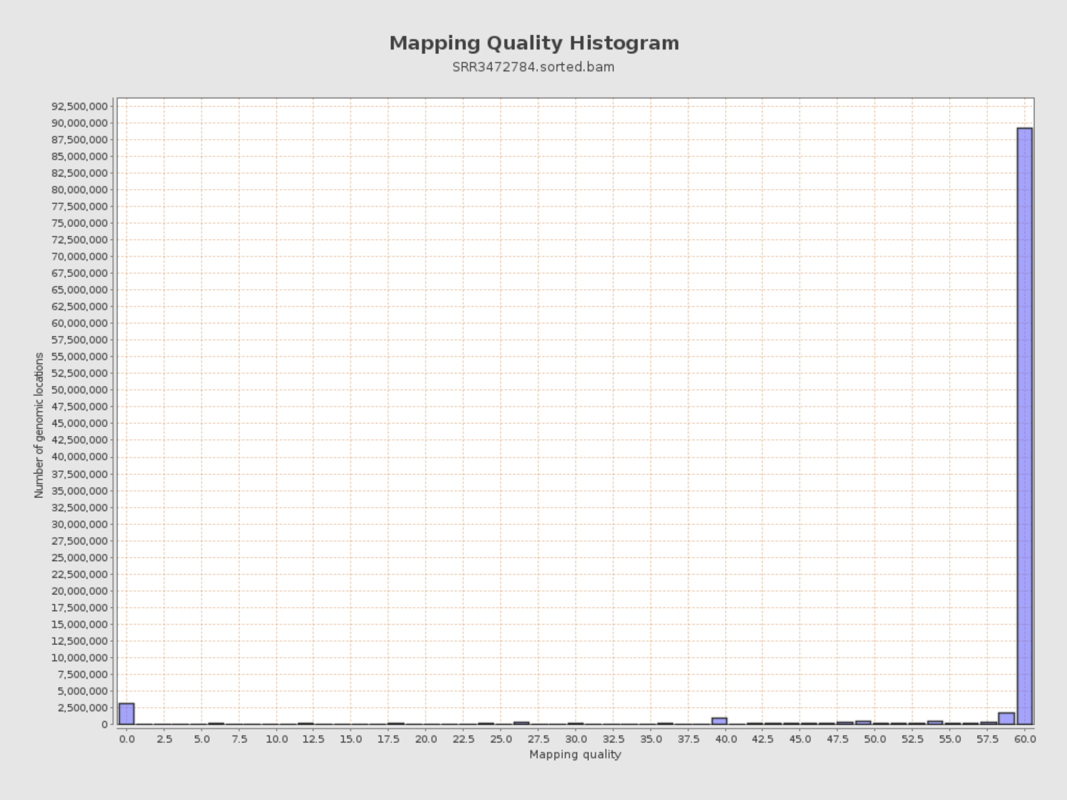
11. Results : Homopolymer Indels



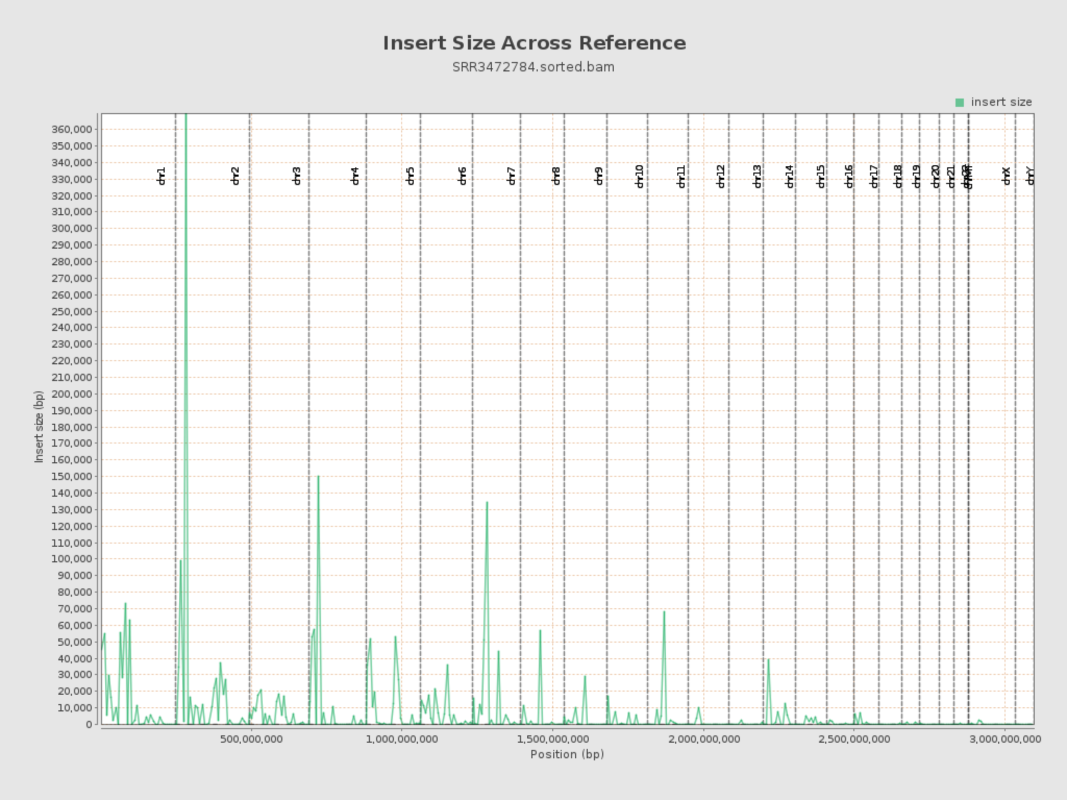
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram