Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 00:10:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472735.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_SRR3472735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472735_1.fastq.gz SRR3472735_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 00:10:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,388,404
Mapped reads	14,651,886 / 95.21%
Unmapped reads	736,518 / 4.79%
Mapped paired reads	14,651,886 / 95.21%
Mapped reads, first in pair	7,153,273 / 46.48%
Mapped reads, second in pair	7,498,613 / 48.73%
Mapped reads, both in pair	14,115,372 / 91.73%
Mapped reads, singletons	536,514 / 3.49%
Secondary alignments	0
Supplementary alignments	69,215 / 0.45%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	8,563,386 / 55.65%
Duplication rate	44.4%
Clipped reads	1,680,924 / 10.92%

2.2. ACGT Content

Number/percentage of A's	408,730,579 / 28.89%
Number/percentage of C's	322,376,383 / 22.79%
Number/percentage of T's	367,174,661 / 25.95%
Number/percentage of G's	316,236,513 / 22.35%
Number/percentage of N's	244,411 / 0.02%

GC Percentage	45.14%

2.3. Coverage

Mean	0.4571
Standard Deviation	14.0154

2.4. Mapping Quality

Mean Mapping Quality	54.45

2.5. Insert size

Mean	33,553.34
Standard Deviation	1,796,451.28
P25/Median/P75	177 / 250 / 336

2.6. Mismatches and indels

General error rate	1.83%
Mismatches	25,753,524
Insertions	77,283
Mapped reads with at least one insertion	0.52%
Deletions	76,110
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.57%

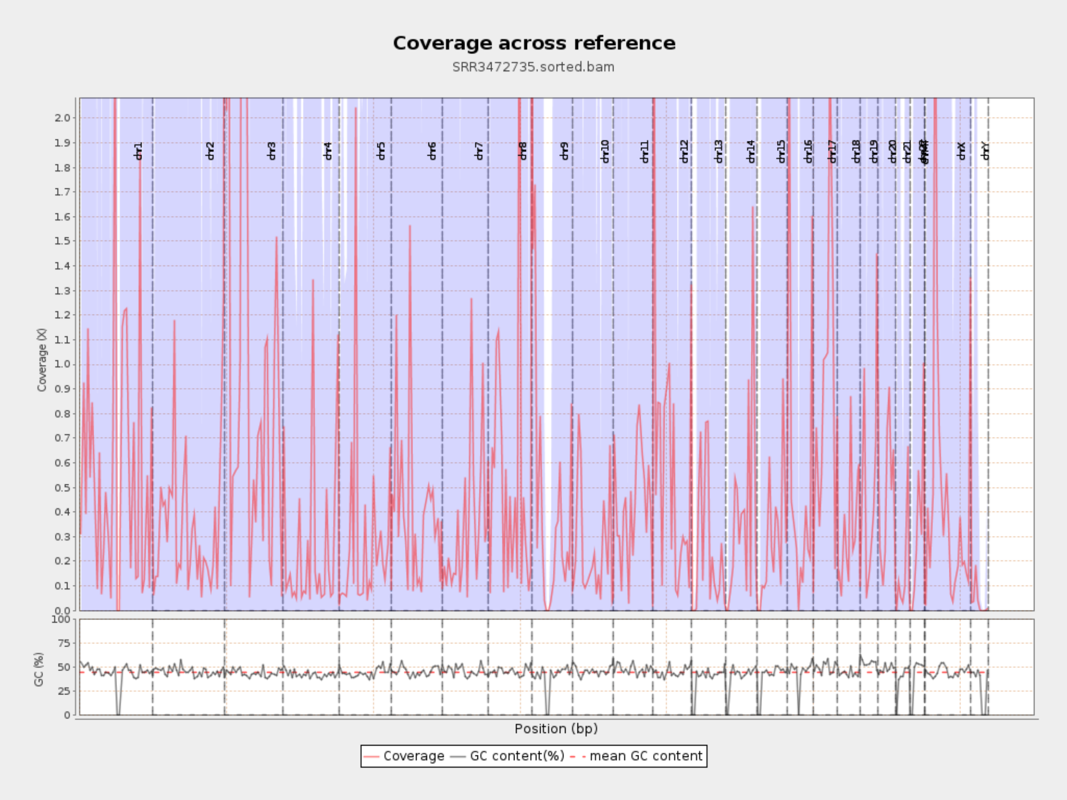
2.7. Chromosome stats

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

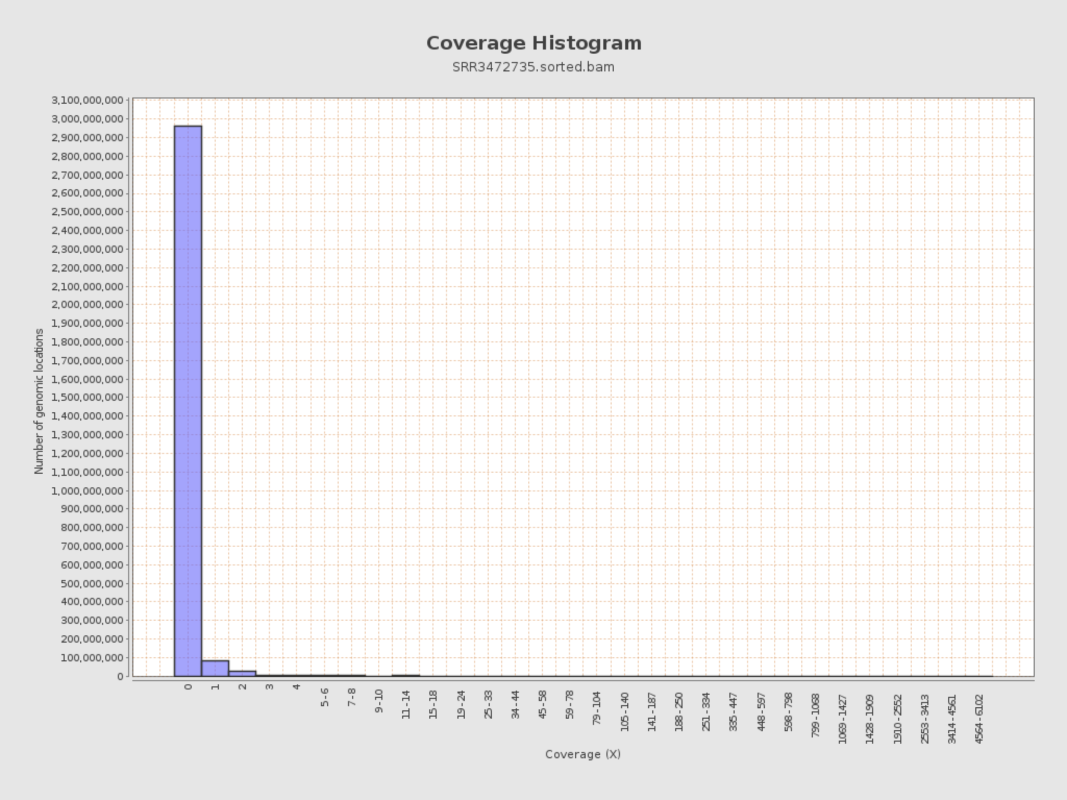
		bases	**coverage**	**deviation**
chr1	249250621	146056466	0.586	18.1232
chr2	243199373	82256340	0.3382	9.6738
chr3	198022430	239766574	1.2108	26.1114
chr4	191154276	48405635	0.2532	8.5151
chr5	180915260	52665853	0.2911	9.6982
chr6	171115067	71017166	0.415	11.7477
chr7	159138663	55267800	0.3473	9.3027
chr8	146364022	79418308	0.5426	18.7368
chr9	141213431	62149525	0.4401	10.0149
chr10	135534747	34464167	0.2543	9.3958
chr11	135006516	58430035	0.4328	12.332
chr12	133851895	82249438	0.6145	14.1122
chr13	115169878	29135801	0.253	9.0038
chr14	107349540	40703295	0.3792	19.6396
chr15	102531392	29154371	0.2843	7.4942
chr16	90354753	50003247	0.5534	18.8791
chr17	81195210	71837849	0.8848	18.8818
chr18	78077248	25806896	0.3305	10.5823
chr19	59128983	26879961	0.4546	10.2828
chr20	63025520	29160690	0.4627	10.1559
chr21	48129895	7875450	0.1636	7.6732
chr22	51304566	17158077	0.3344	12.4112
chrMT	16571	2004	0.1209	0.5423
chrX	155270560	72830228	0.4691	12.7652

chrY	59373566	2259117	0.038	1.399

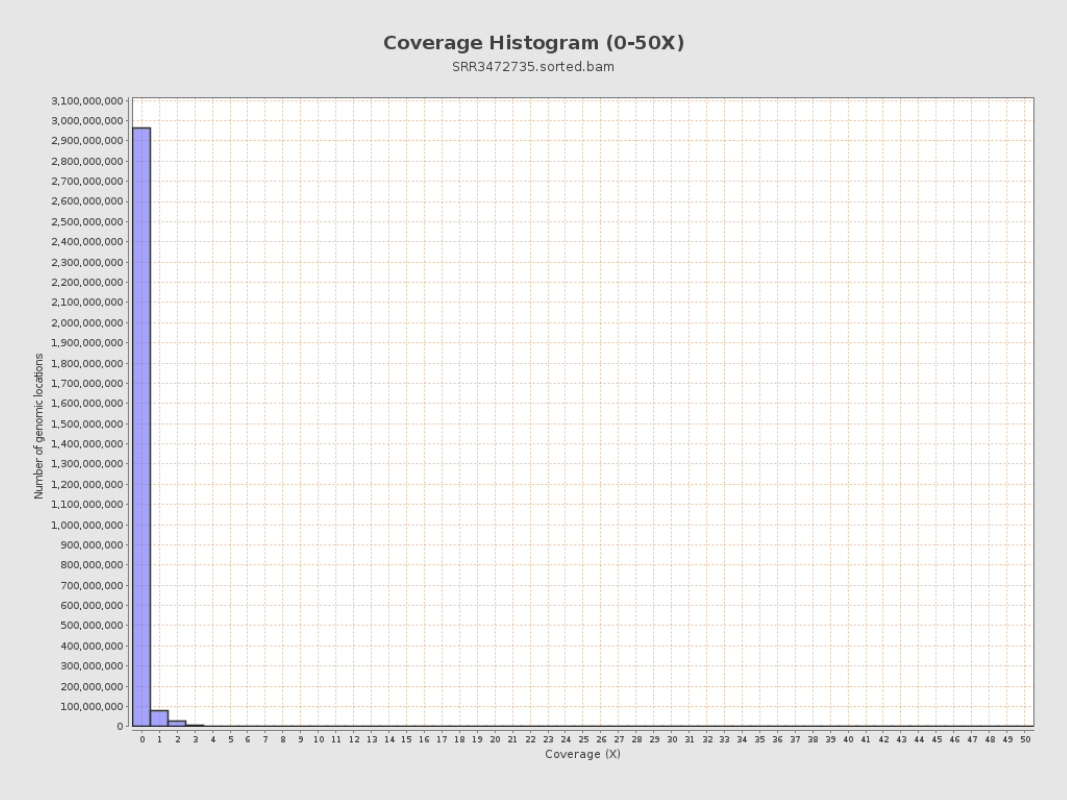
3. Results : Coverage across reference



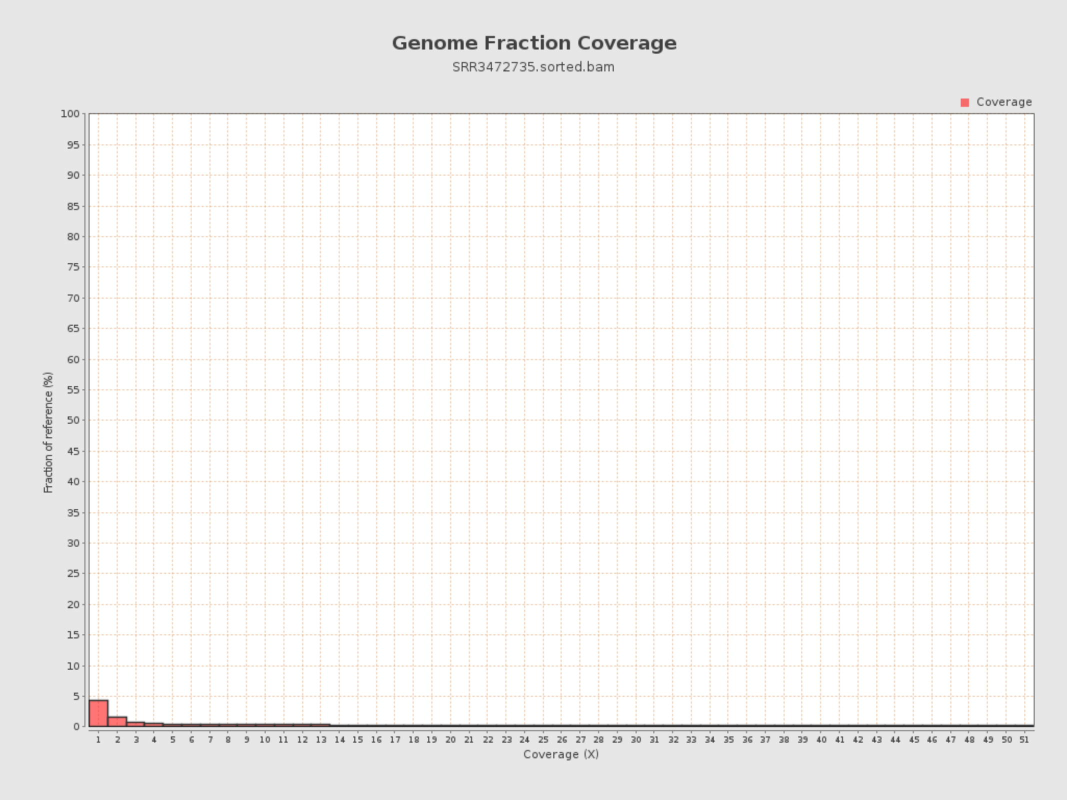
4. Results : Coverage Histogram



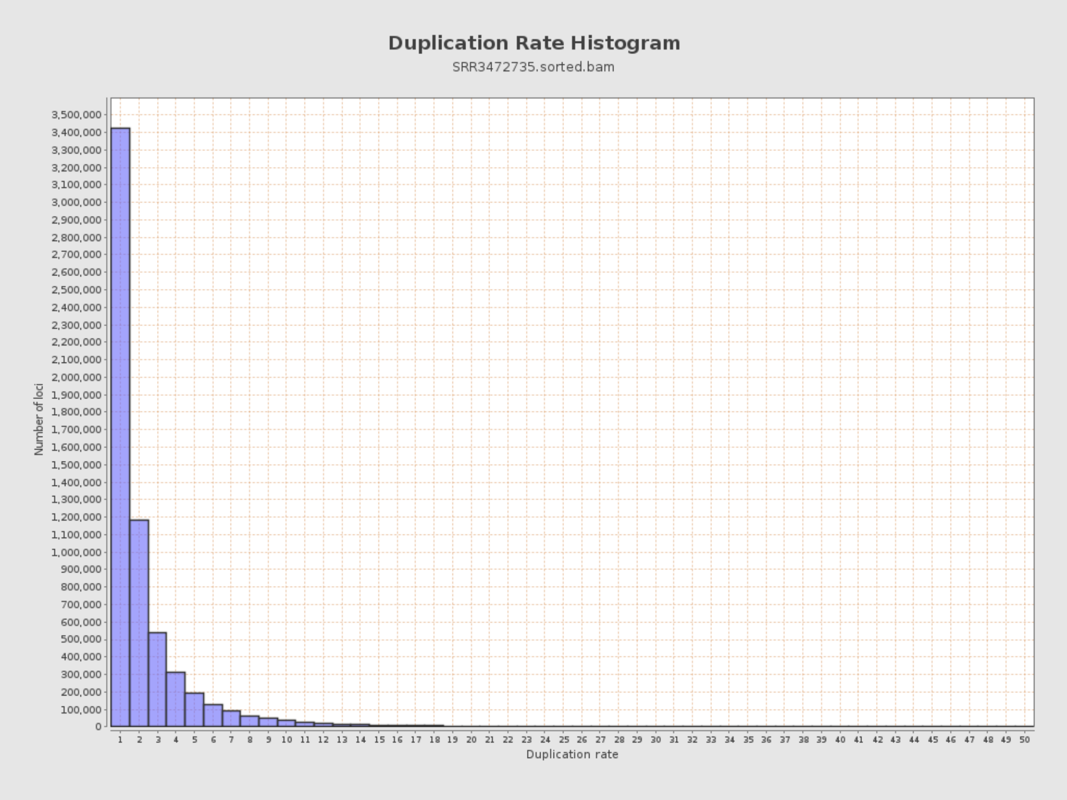
5. Results : Coverage Histogram (0-50X)



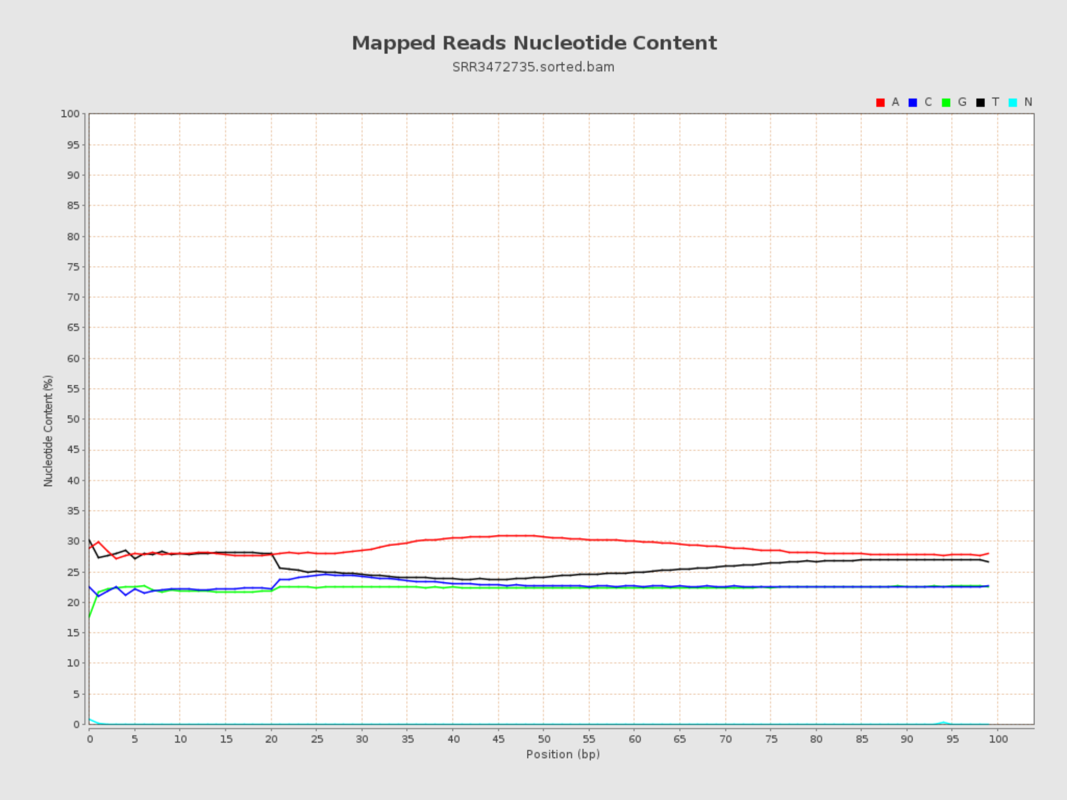
6. Results : Genome Fraction Coverage



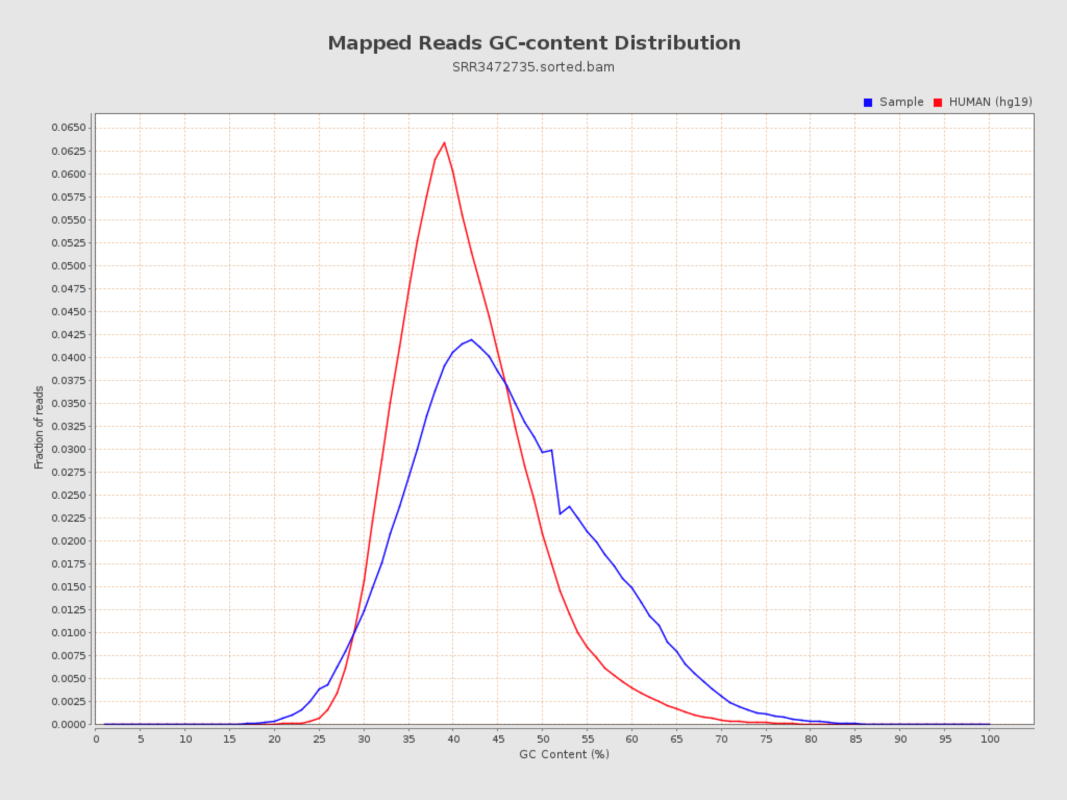
7. Results : Duplication Rate Histogram



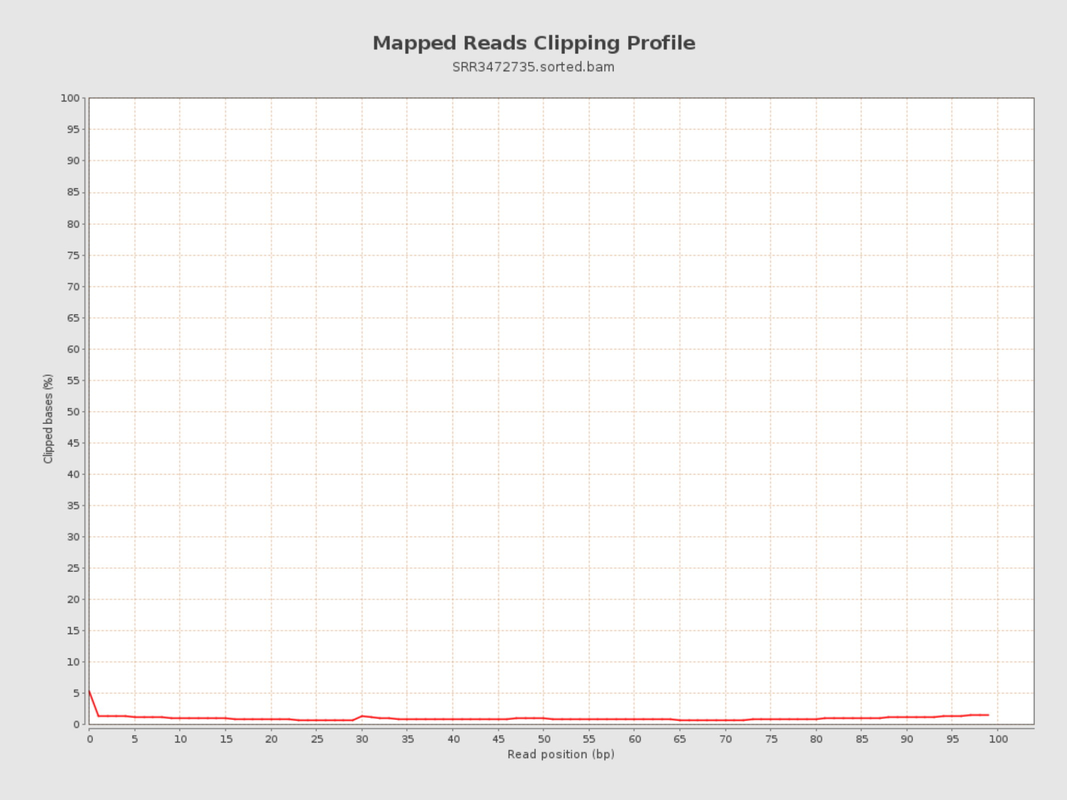
8. Results : Mapped Reads Nucleotide Content



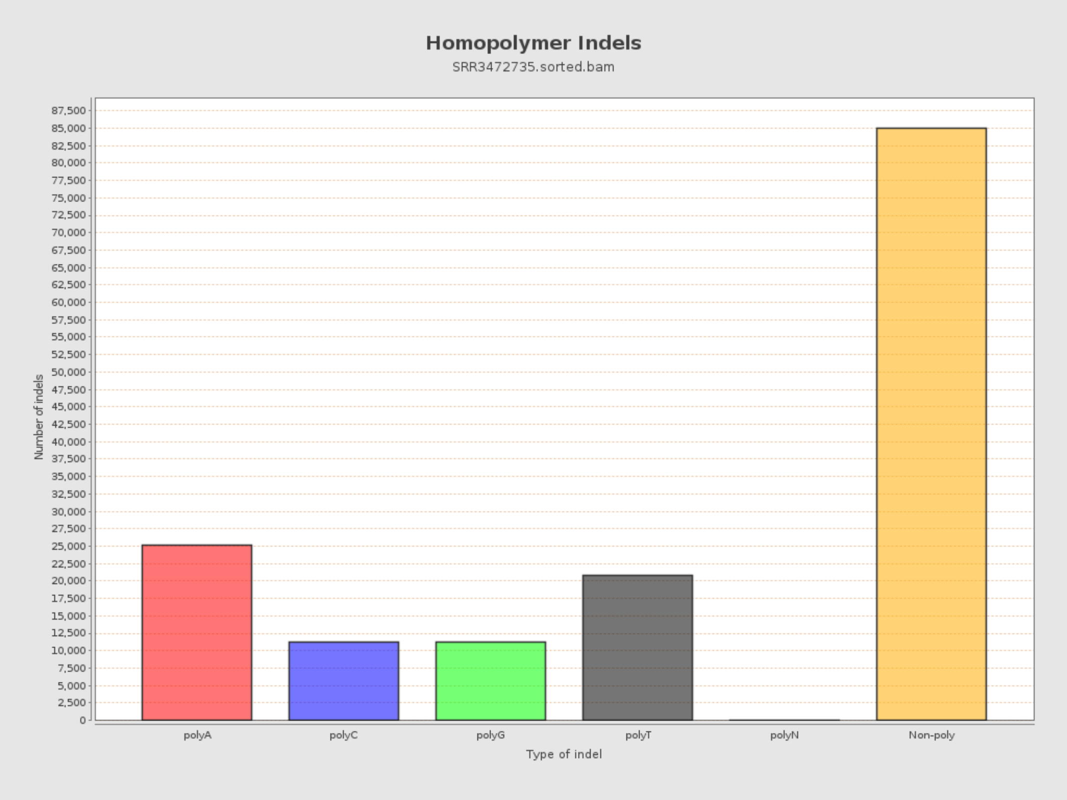
9. Results : Mapped Reads GC-content Distribution



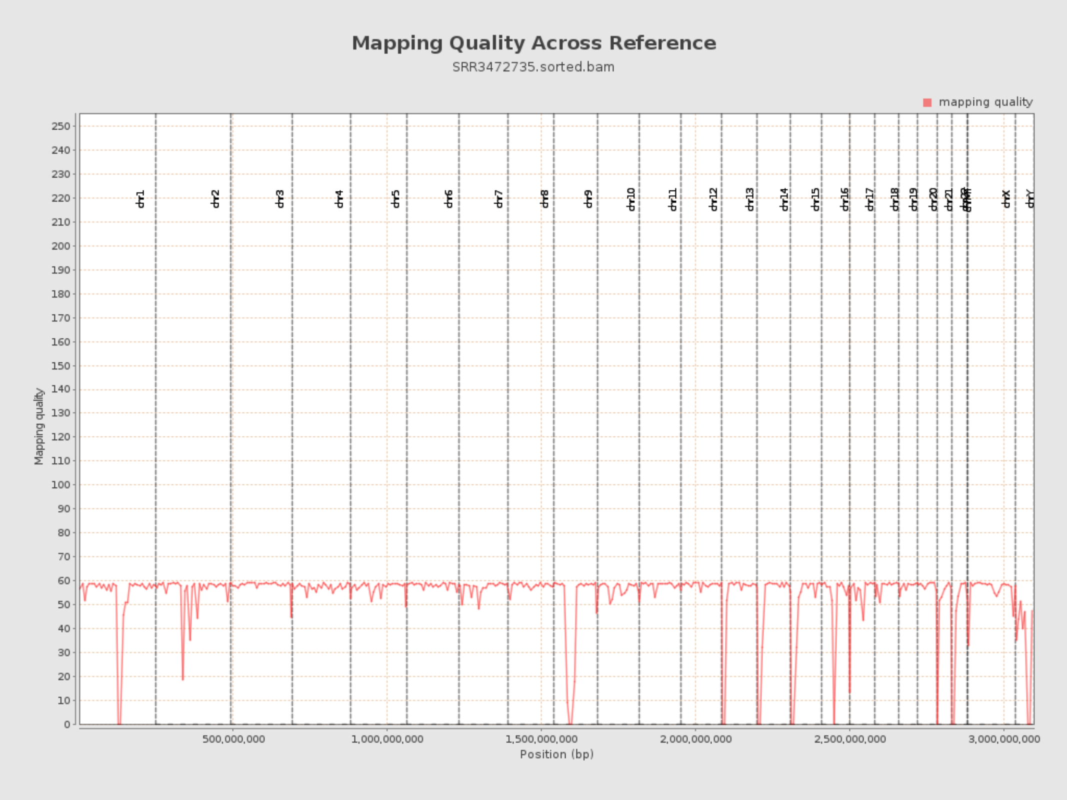
10. Results : Mapped Reads Clipping Profile



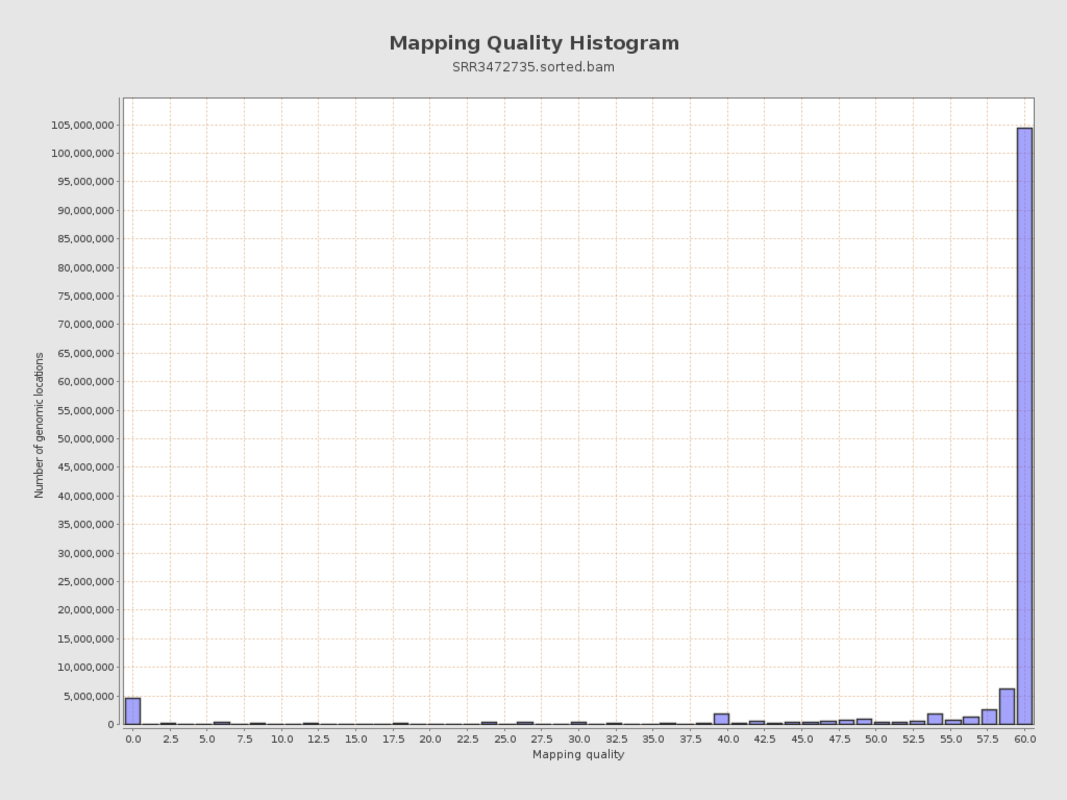
11. Results : Homopolymer Indels



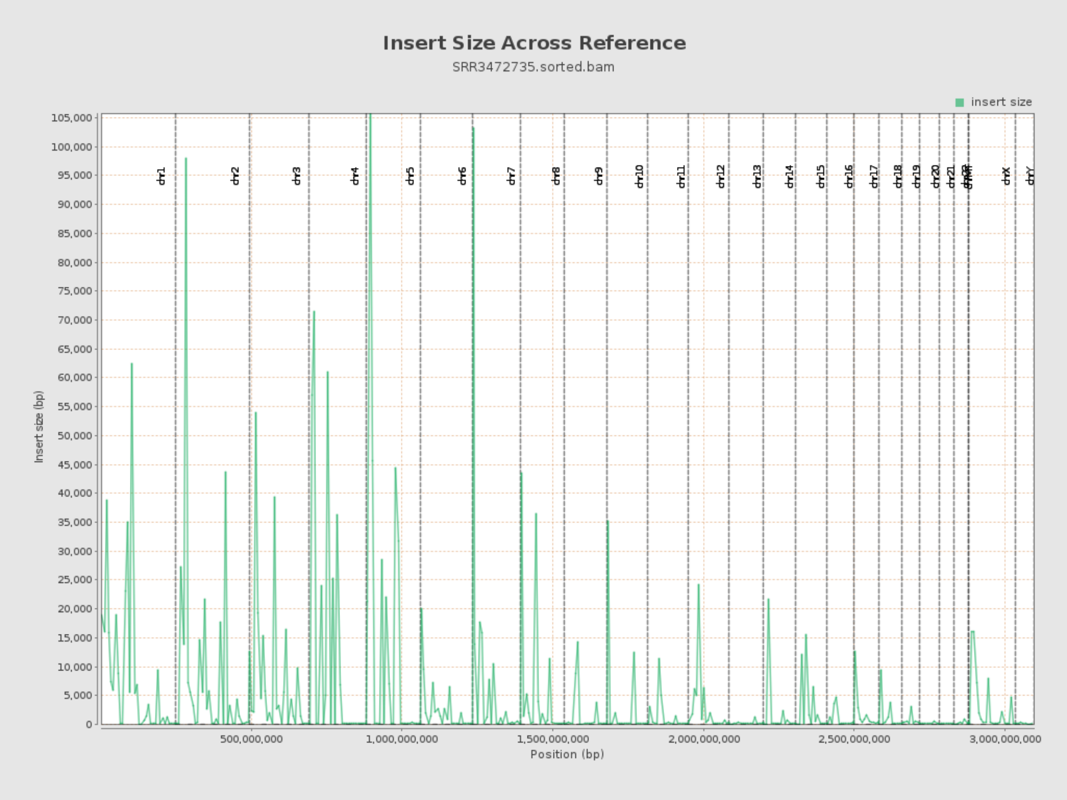
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram