Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 08:41:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472760.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_SRR3472760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472760_1.fastq.gz SRR3472760_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 08:41:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,673,064
Mapped reads	18,497,757 / 99.06%
Unmapped reads	175,307 / 0.94%
Mapped paired reads	18,497,757 / 99.06%
Mapped reads, first in pair	9,281,603 / 49.71%
Mapped reads, second in pair	9,216,154 / 49.36%
Mapped reads, both in pair	18,392,458 / 98.5%
Mapped reads, singletons	105,299 / 0.56%
Secondary alignments	0
Supplementary alignments	61,846 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	11,930,843 / 63.89%
Duplication rate	48.14%
Clipped reads	1,527,379 / 8.18%

2.2. ACGT Content

Number/percentage of A's	507,350,775 / 27.87%
Number/percentage of C's	404,873,319 / 22.24%
Number/percentage of T's	504,454,905 / 27.71%
Number/percentage of G's	403,259,879 / 22.15%
Number/percentage of N's	352,701 / 0.02%

GC Percentage	44.4%

2.3. Coverage

Mean	0.5881
Standard Deviation	19.2814

2.4. Mapping Quality

Mean Mapping Quality	55.16

2.5. Insert size

Mean	23,761.11
Standard Deviation	1,510,278.46
P25/Median/P75	171 / 241 / 327

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	11,121,459
Insertions	98,851
Mapped reads with at least one insertion	0.53%
Deletions	103,252
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.77%

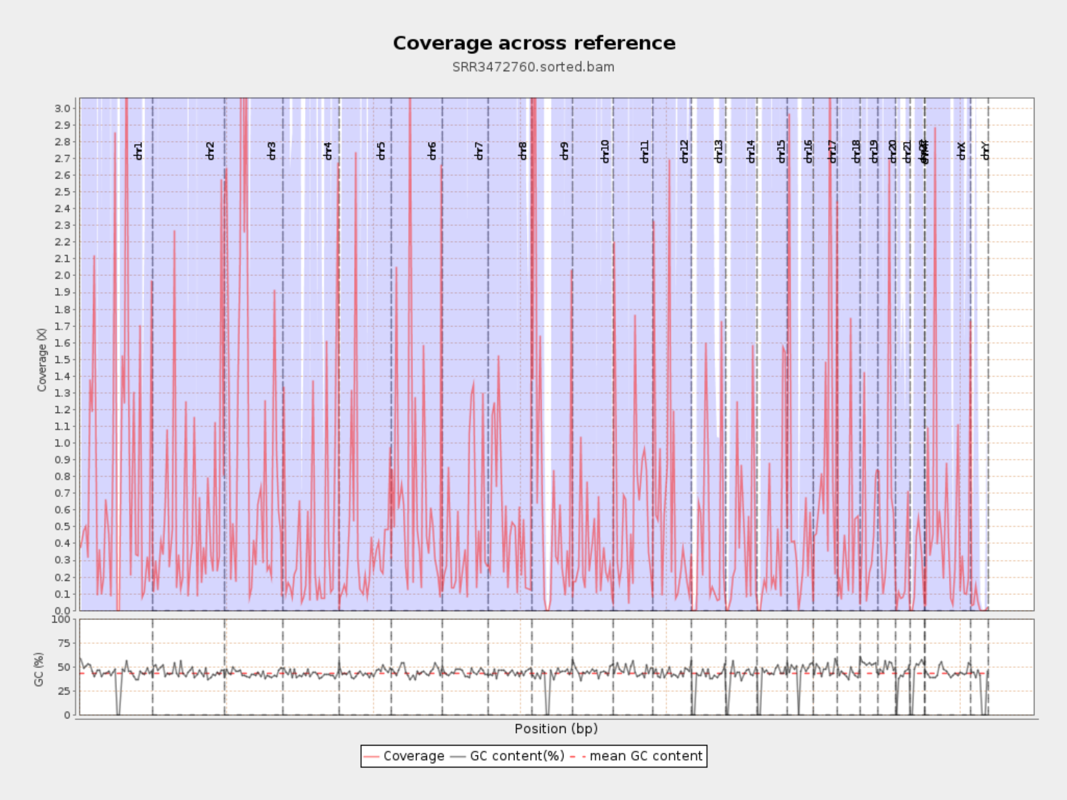
2.7. Chromosome stats

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

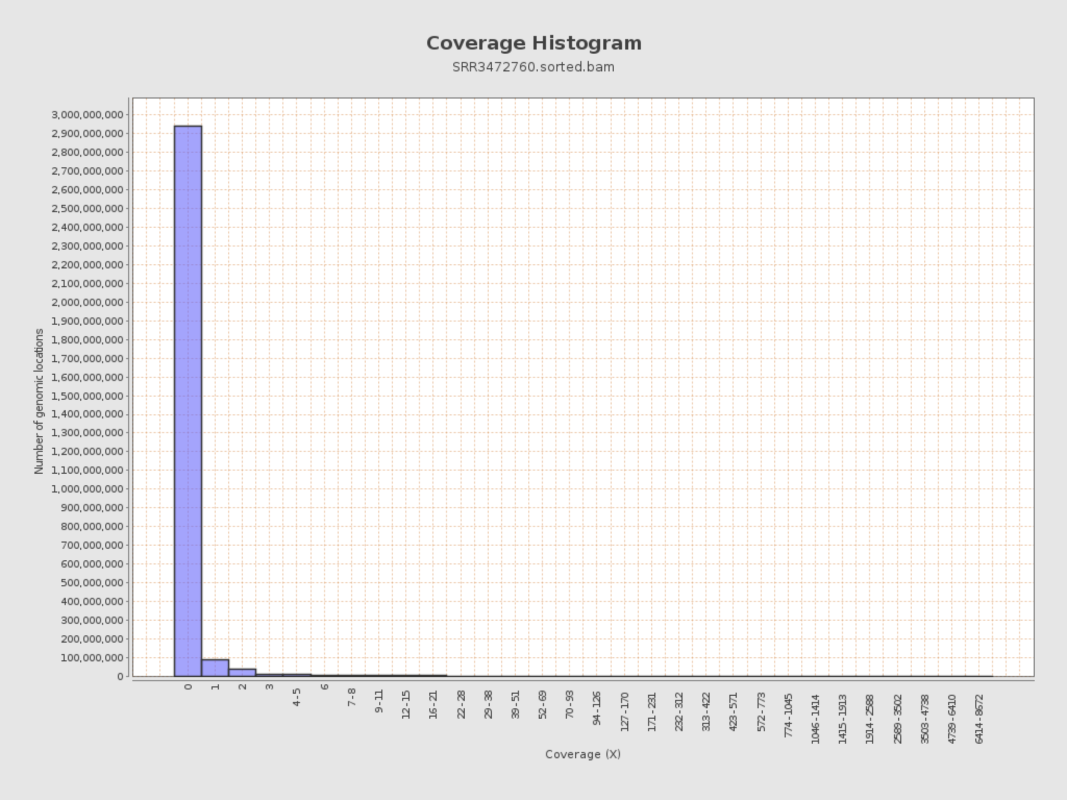
		bases	coverage	deviation
chr1	249250621	205320091	0.8237	25.8354
chr2	243199373	135940805	0.559	20.4348
chr3	198022430	218687497	1.1044	25.2478
chr4	191154276	86297186	0.4515	17.6595
chr5	180915260	81646450	0.4513	13.489
chr6	171115067	127577570	0.7456	21.1606
chr7	159138663	74459182	0.4679	14.5463
chr8	146364022	76988291	0.526	15.4567
chr9	141213431	107779850	0.7632	19.8523
chr10	135534747	45878785	0.3385	15.2105
chr11	135006516	88900734	0.6585	25.223
chr12	133851895	87470631	0.6535	18.3406
chr13	115169878	50157779	0.4355	23.0862
chr14	107349540	45442315	0.4233	15.5336
chr15	102531392	44617927	0.4352	15.6628
chr16	90354753	49470770	0.5475	15.0094
chr17	81195210	80616907	0.9929	23.2733
chr18	78077248	33190332	0.4251	21.0491
chr19	59128983	30027143	0.5078	10.0566
chr20	63025520	45368541	0.7198	28.3933
chr21	48129895	8940487	0.1858	6.8736
chr22	51304566	11835570	0.2307	6.594
chrMT	16571	4334	0.2615	0.6544
chrX	155270560	81778139	0.5267	13.4533

chrY	59373566	2135866	0.036	1.3156

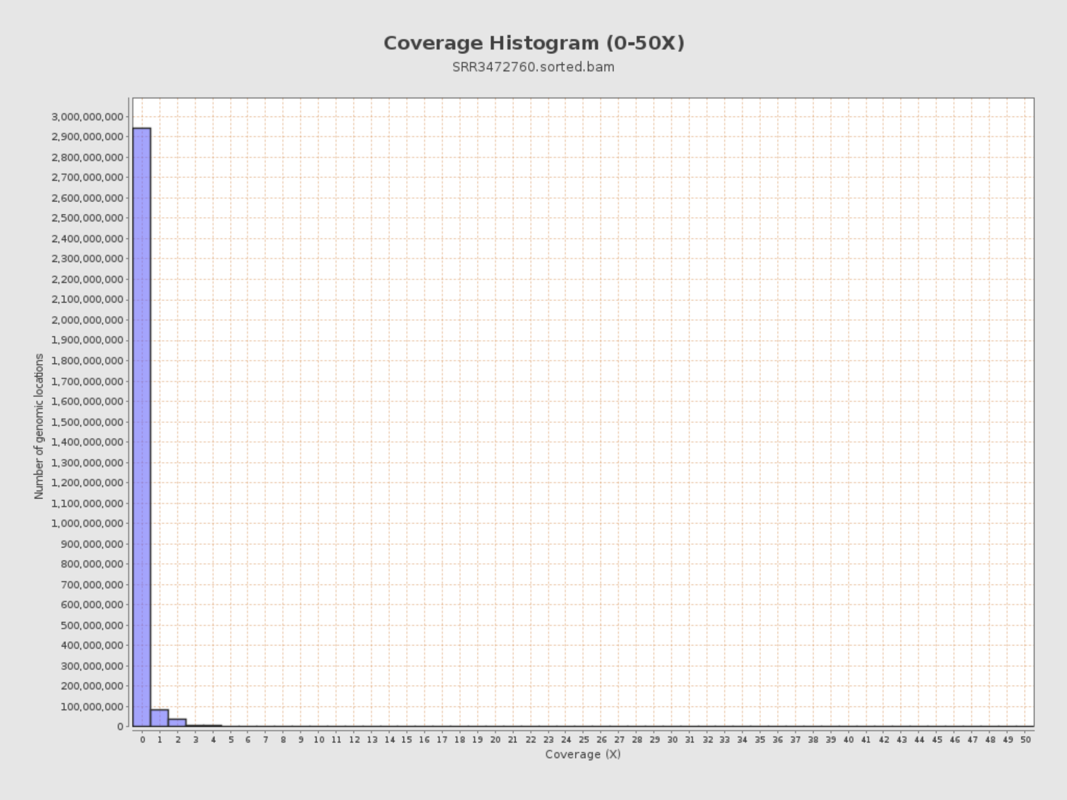
3. Results : Coverage across reference



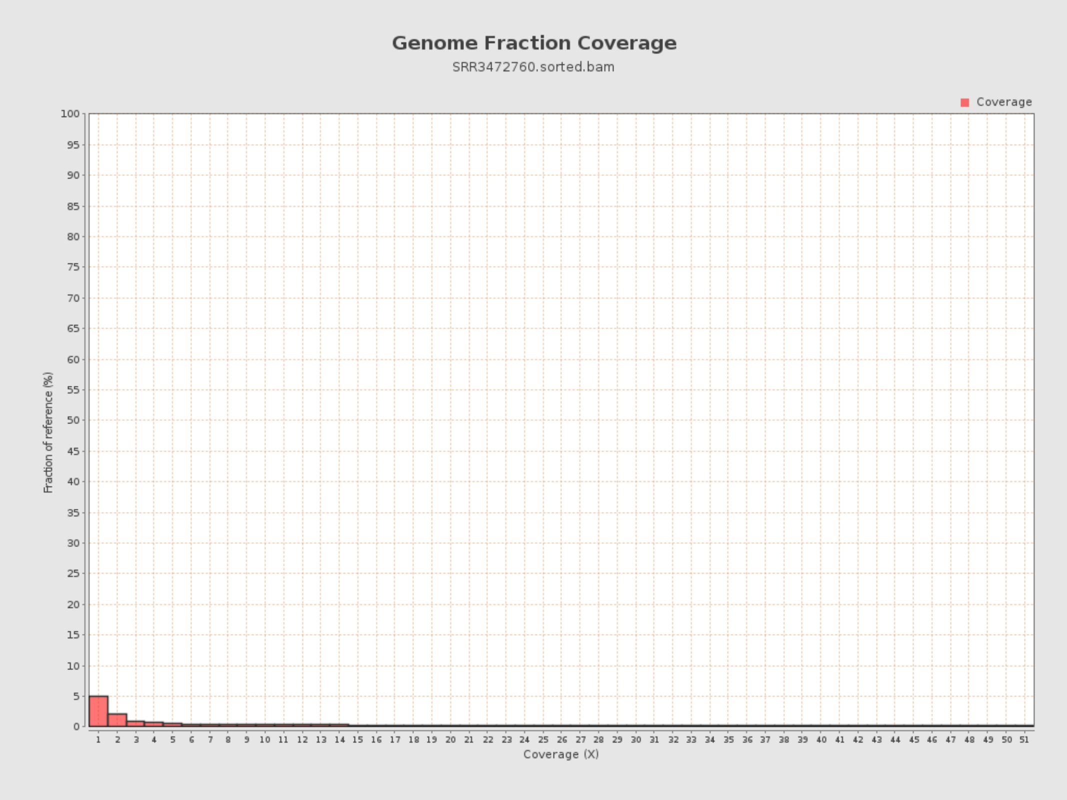
4. Results : Coverage Histogram



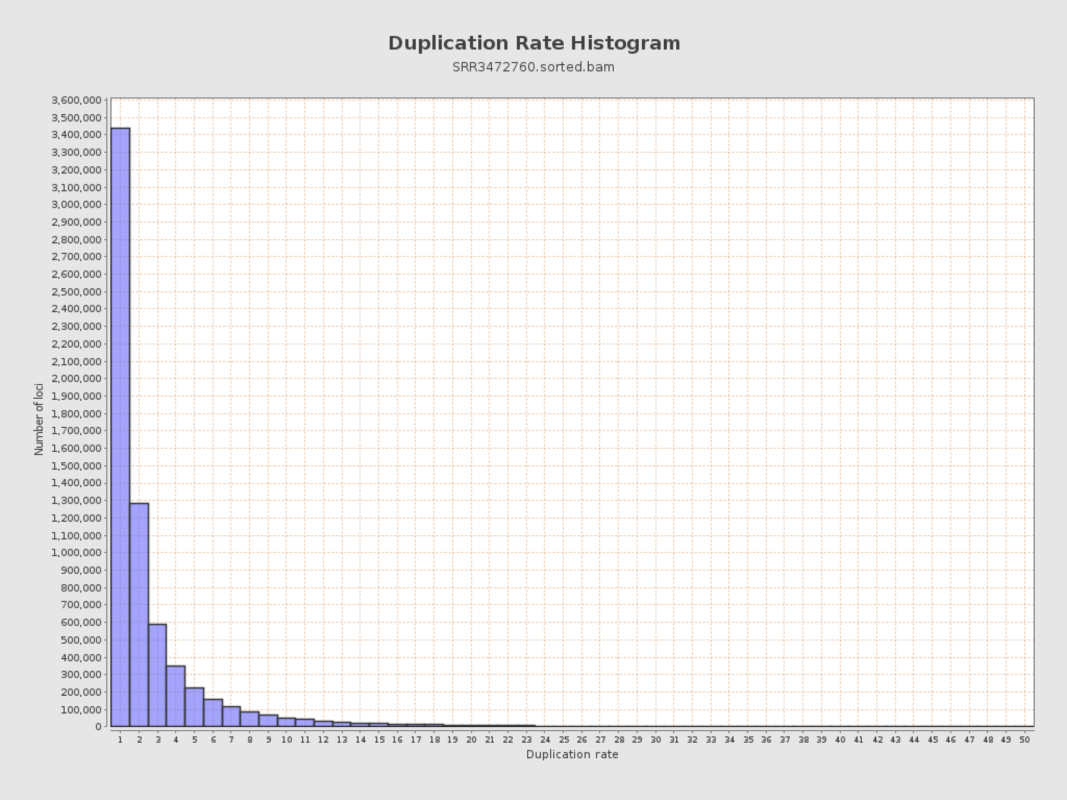
5. Results : Coverage Histogram (0-50X)



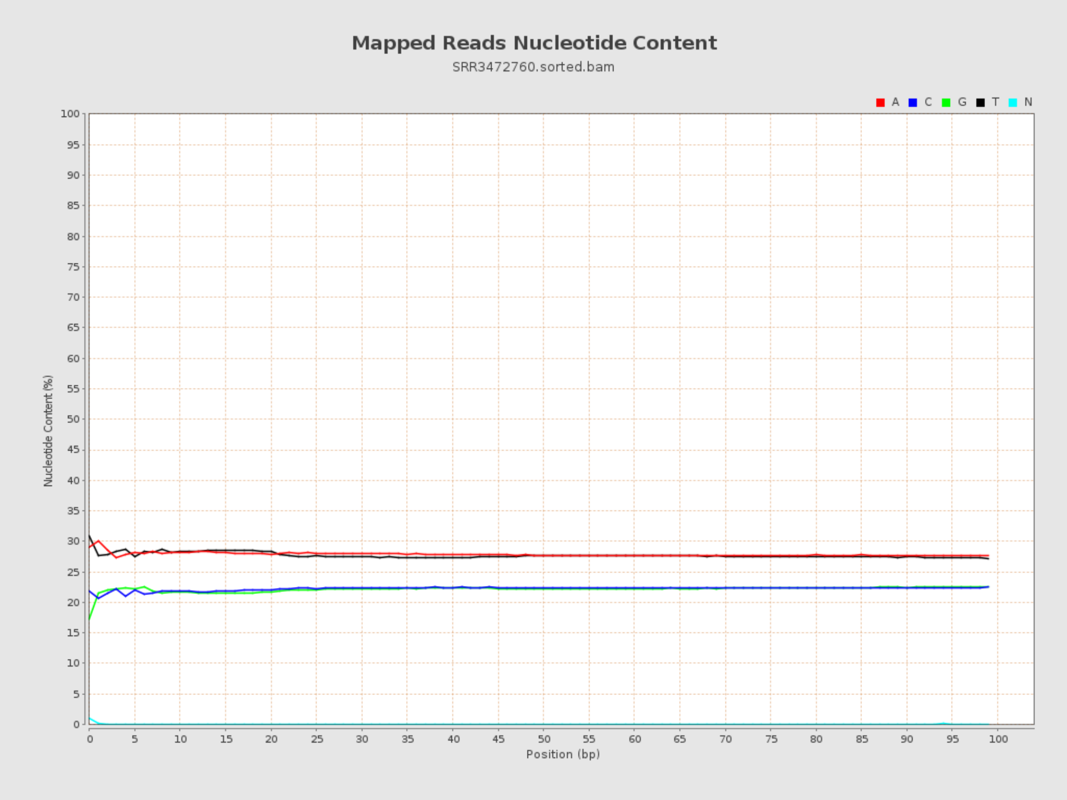
6. Results : Genome Fraction Coverage



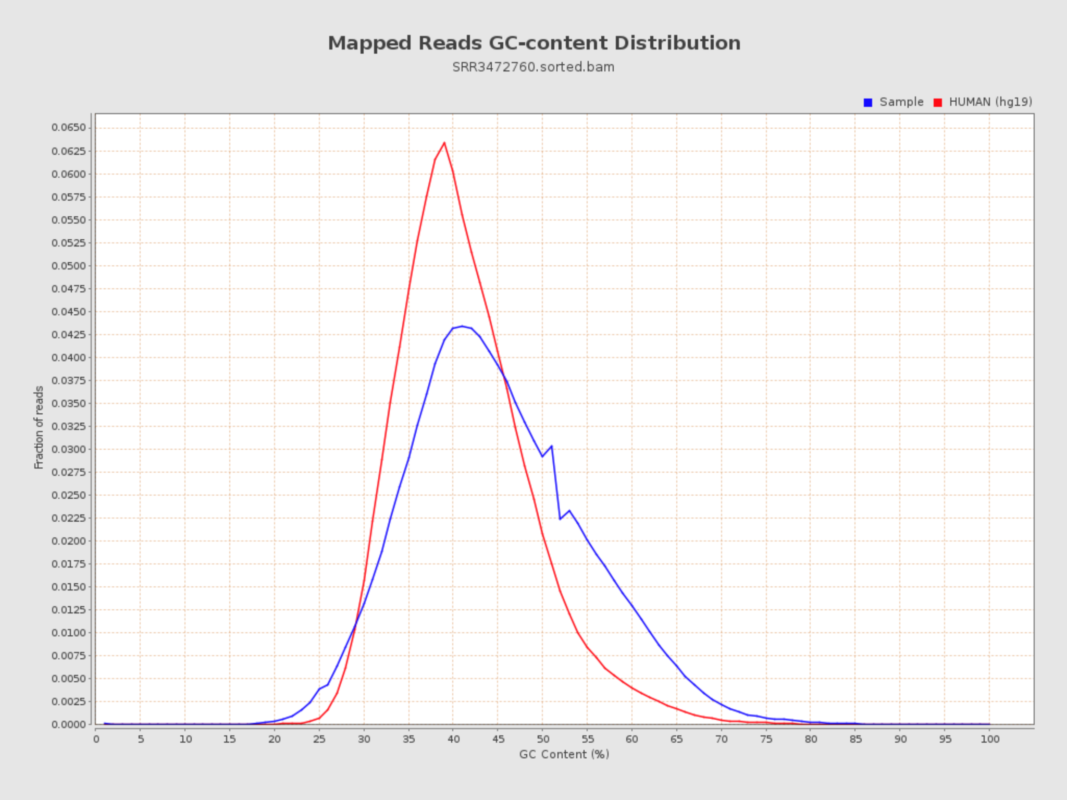
7. Results : Duplication Rate Histogram



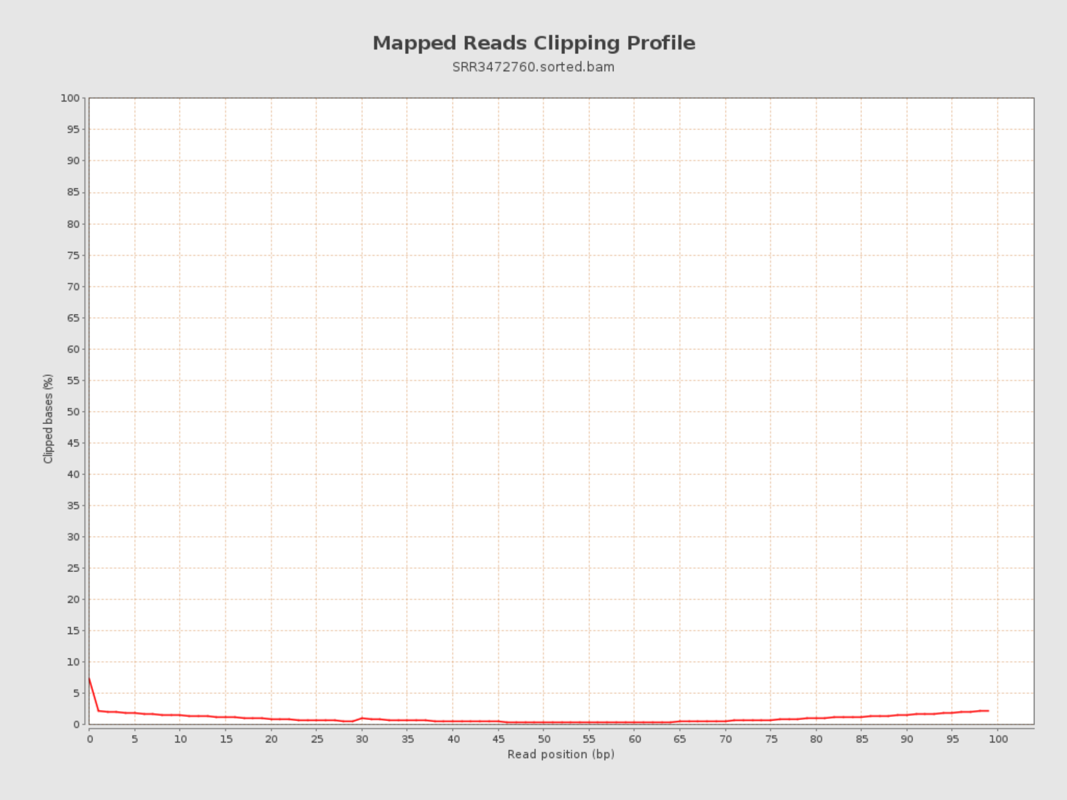
8. Results : Mapped Reads Nucleotide Content



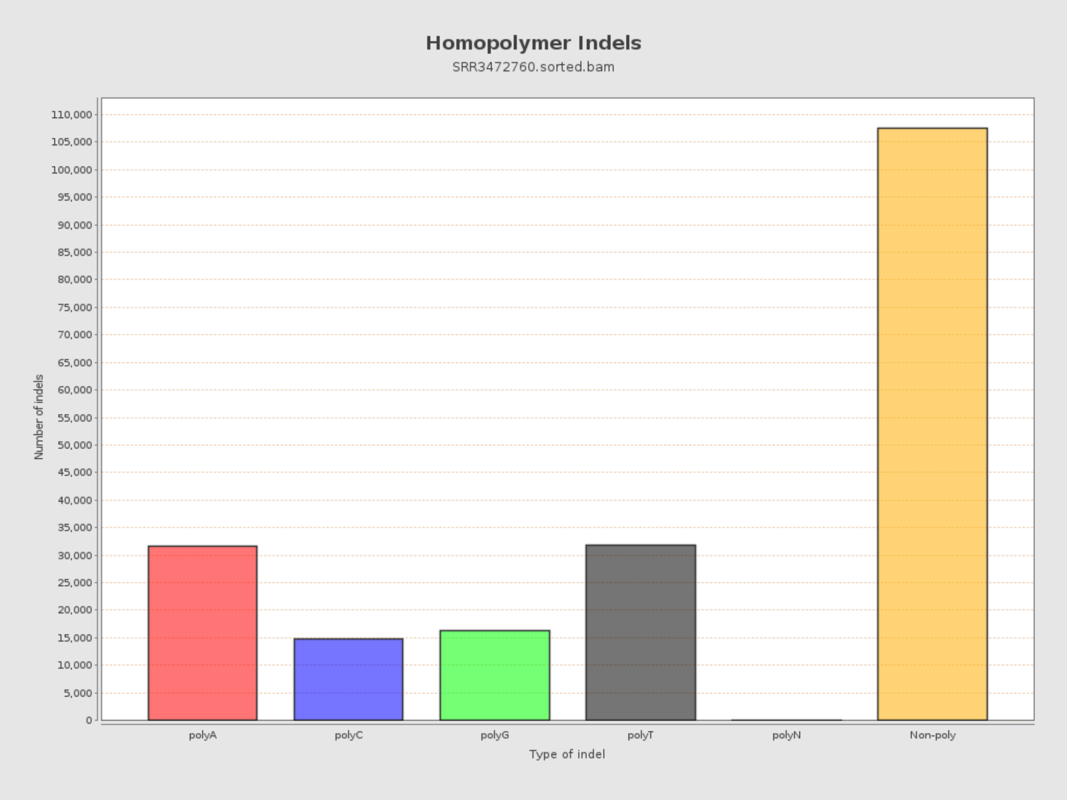
9. Results : Mapped Reads GC-content Distribution



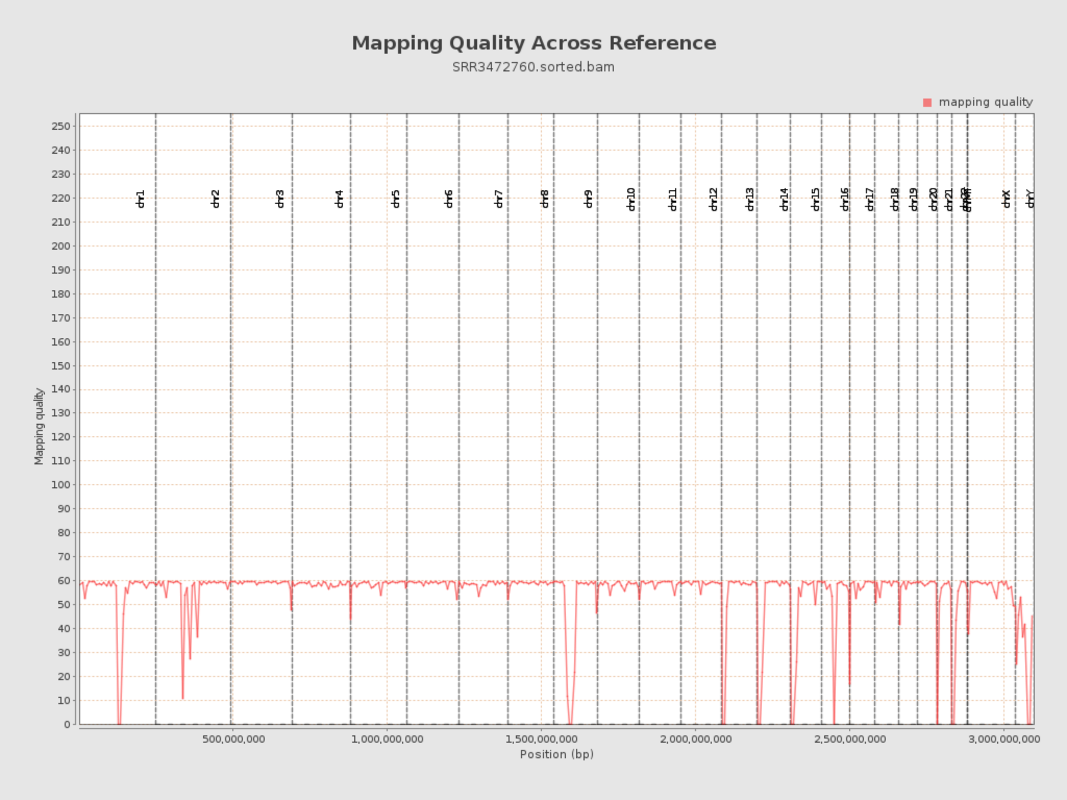
10. Results : Mapped Reads Clipping Profile



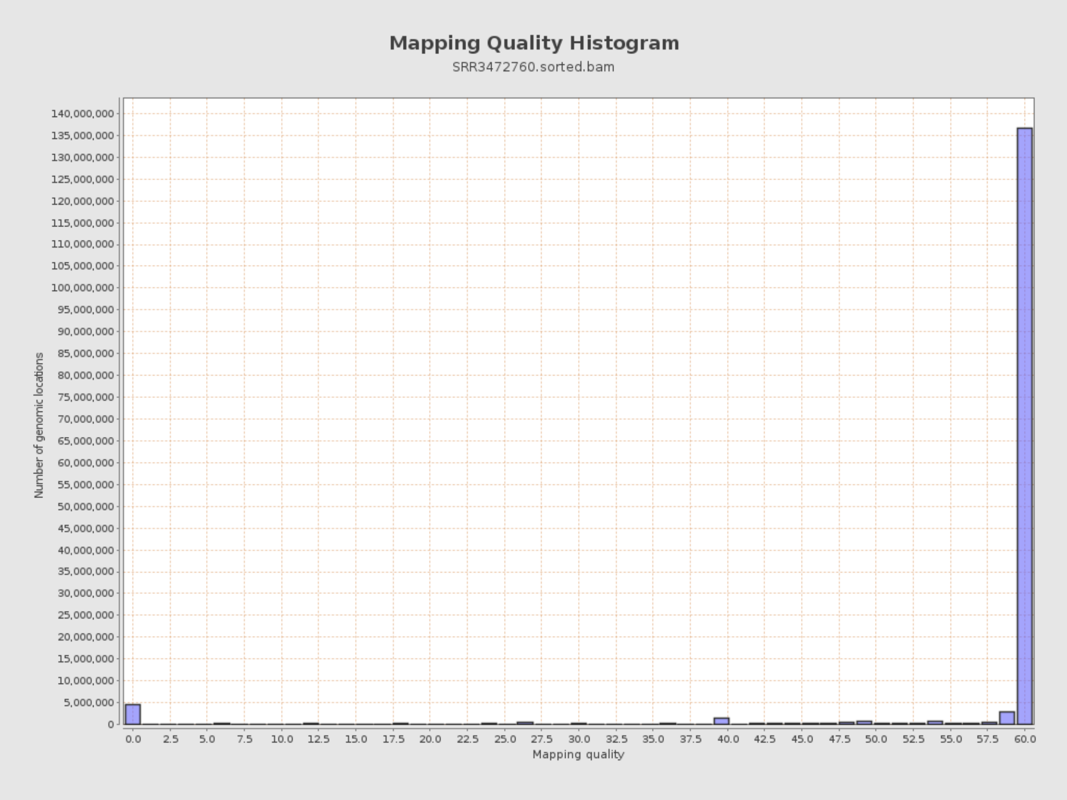
11. Results : Homopolymer Indels



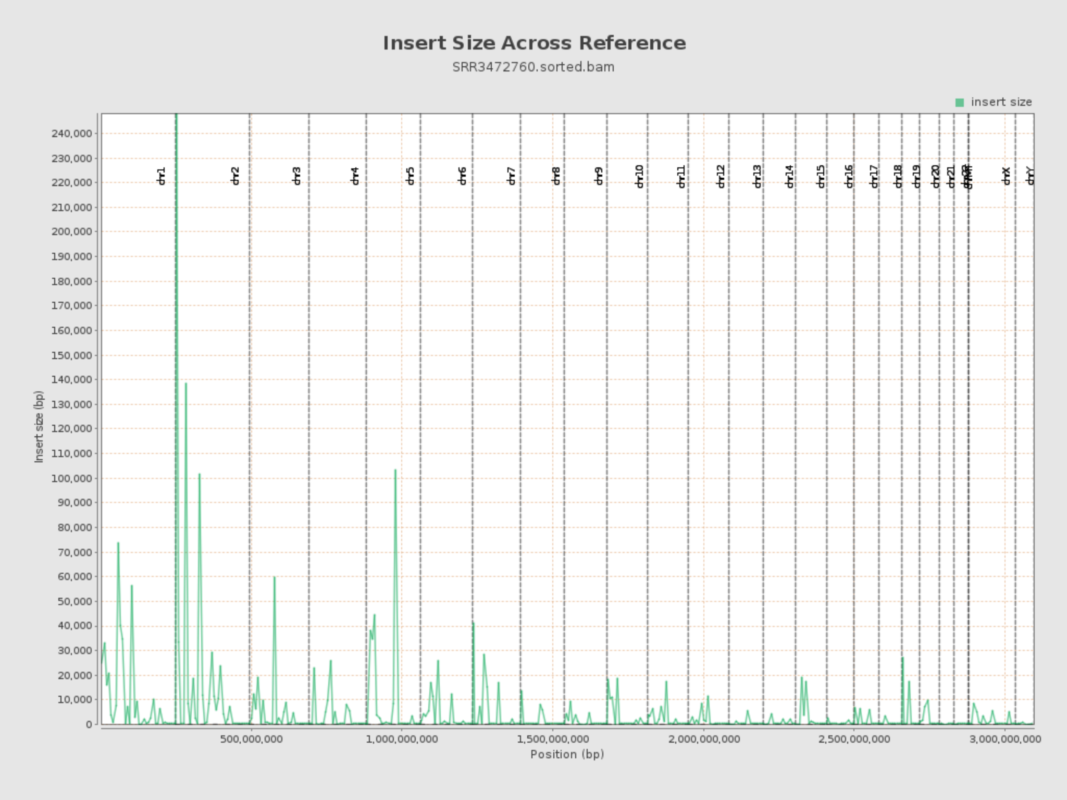
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram