Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 09:44:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472763.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_SRR3472763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472763_1.fastq.gz SRR3472763_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 09:44:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,712,950
Mapped reads	19,487,867 / 98.86%
Unmapped reads	225,083 / 1.14%
Mapped paired reads	19,487,867 / 98.86%
Mapped reads, first in pair	9,789,590 / 49.66%
Mapped reads, second in pair	9,698,277 / 49.2%
Mapped reads, both in pair	19,351,250 / 98.17%
Mapped reads, singletons	136,617 / 0.69%
Secondary alignments	0
Supplementary alignments	60,785 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	12,531,258 / 63.57%
Duplication rate	48.3%
Clipped reads	1,560,837 / 7.92%

2.2. ACGT Content

Number/percentage of A's	527,796,463 / 27.51%
Number/percentage of C's	434,623,053 / 22.66%
Number/percentage of T's	524,559,256 / 27.34%
Number/percentage of G's	430,973,684 / 22.47%
Number/percentage of N's	369,737 / 0.02%

GC Percentage	45.12%

2.3. Coverage

Mean	0.6198
Standard Deviation	19.8978

2.4. Mapping Quality

Mean Mapping Quality	55.22

2.5. Insert size

Mean	21,045.41
Standard Deviation	1,417,839.72
P25/Median/P75	174 / 246 / 332

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	12,184,887
Insertions	106,755
Mapped reads with at least one insertion	0.54%
Deletions	101,809
Mapped reads with at least one deletion	0.52%
Homopolymer indels	46.75%

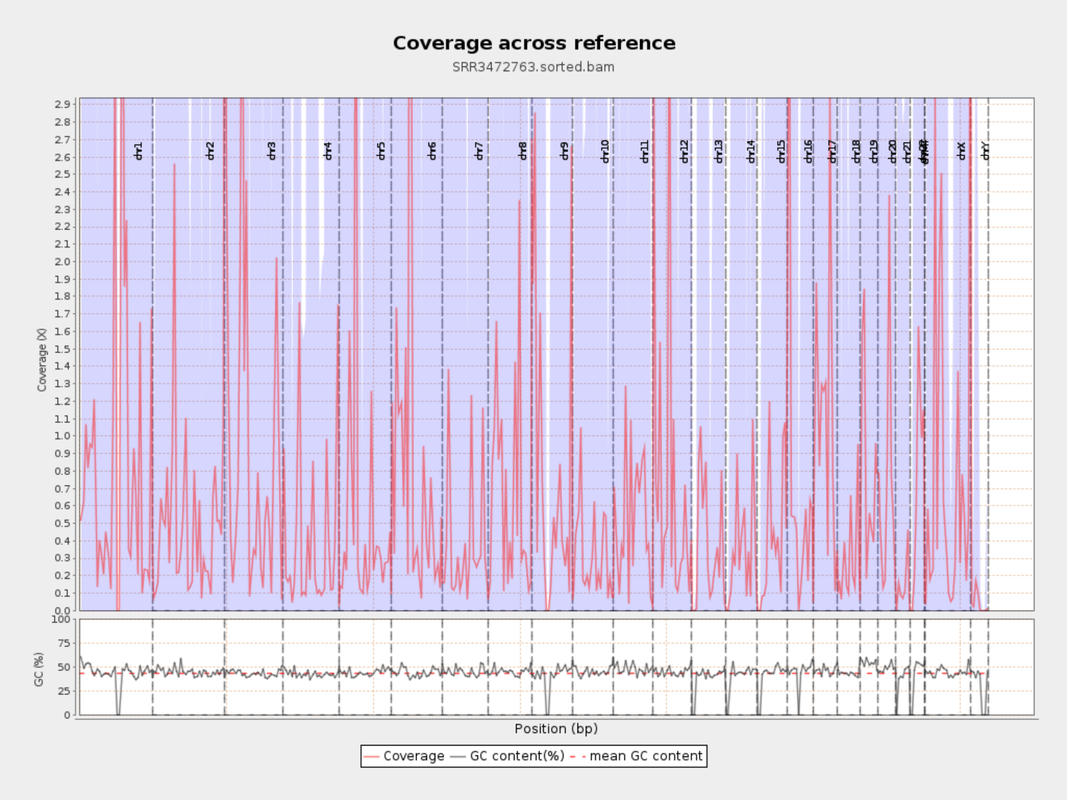
2.7. Chromosome stats

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

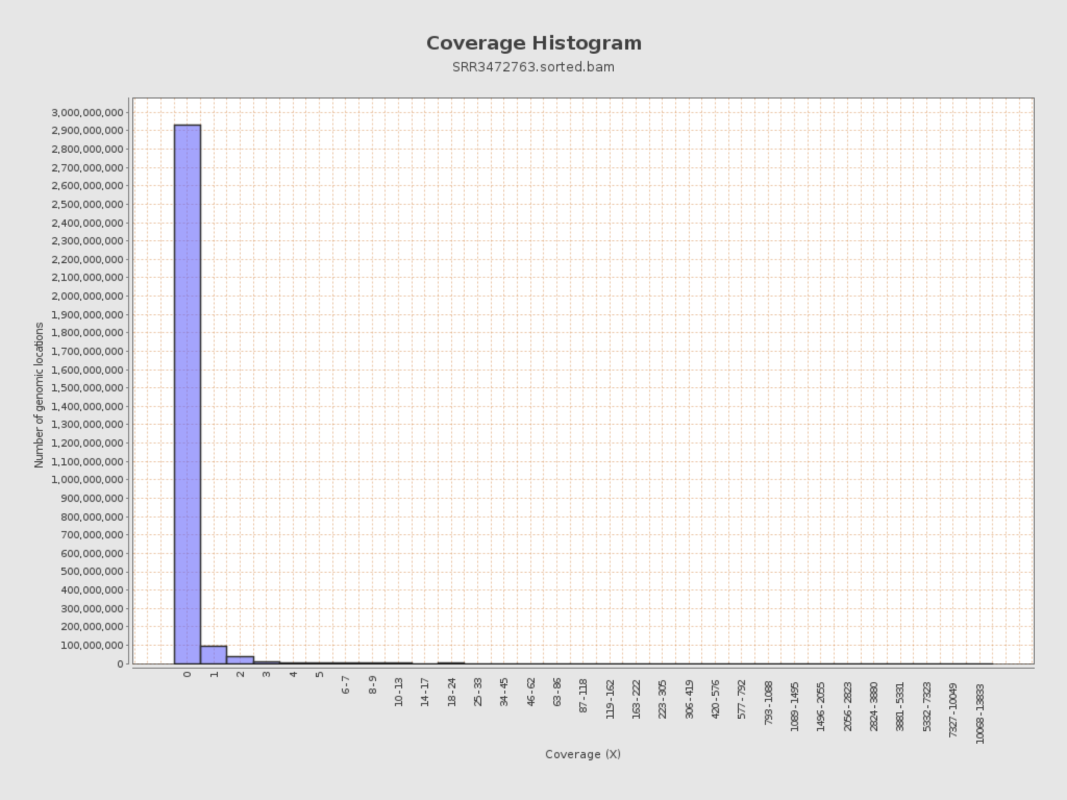
		bases	coverage	deviation
chr1	249250621	215418750	0.8643	29.9659
chr2	243199373	120649792	0.4961	16.3043
chr3	198022430	202026855	1.0202	22.0246
chr4	191154276	75886994	0.397	13.0251
chr5	180915260	103290797	0.5709	20.4379
chr6	171115067	143839092	0.8406	22.3723
chr7	159138663	60028201	0.3772	12.7063
chr8	146364022	98538011	0.6732	21.7336
chr9	141213431	111526649	0.7898	20.1514
chr10	135534747	43352507	0.3199	13.0545
chr11	135006516	72034753	0.5336	17.1583
chr12	133851895	110372458	0.8246	25.6532
chr13	115169878	43001089	0.3734	11.6337
chr14	107349540	36021088	0.3355	15.5104
chr15	102531392	42141738	0.411	13.001
chr16	90354753	68826132	0.7617	19.1874
chr17	81195210	89575221	1.1032	26.6097
chr18	78077248	23262948	0.2979	10.8078
chr19	59128983	48199809	0.8152	19.4911
chr20	63025520	46153665	0.7323	23.4535
chr21	48129895	7385080	0.1534	6.125
chr22	51304566	35558015	0.6931	19.8287
chrMT	16571	2141	0.1292	0.4631
chrX	155270560	118815571	0.7652	26.167

chrY	59373566	2685808	0.0452	1.5942

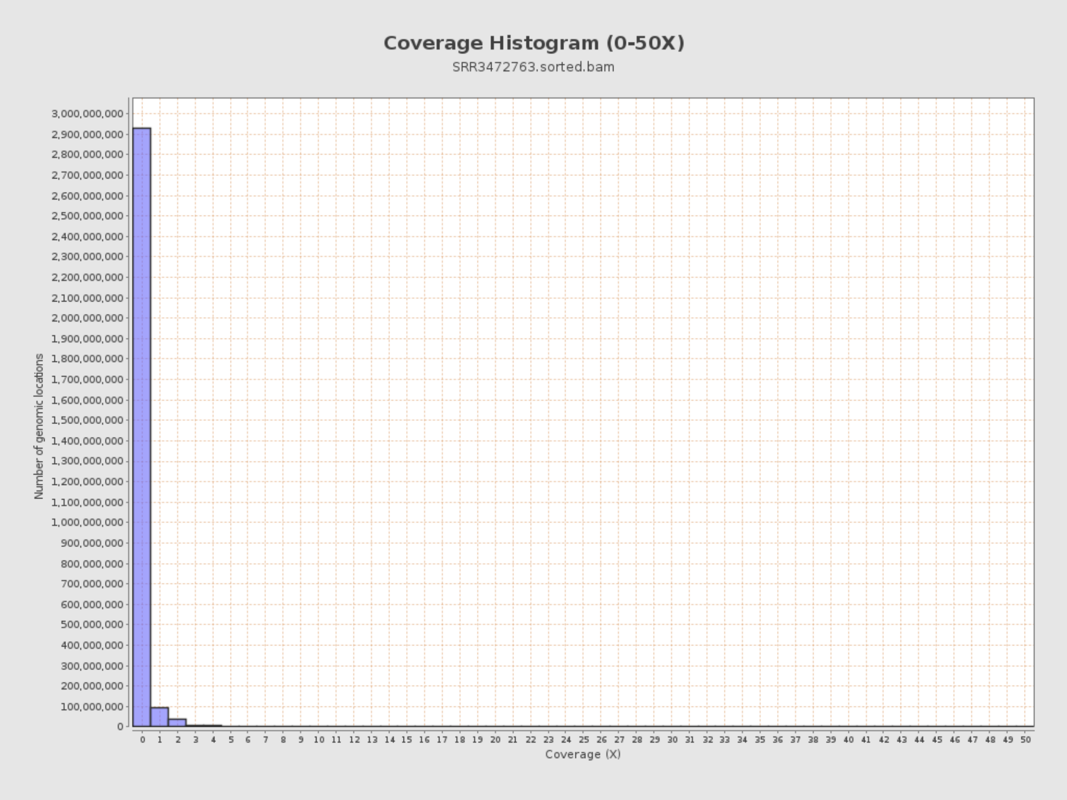
3. Results : Coverage across reference



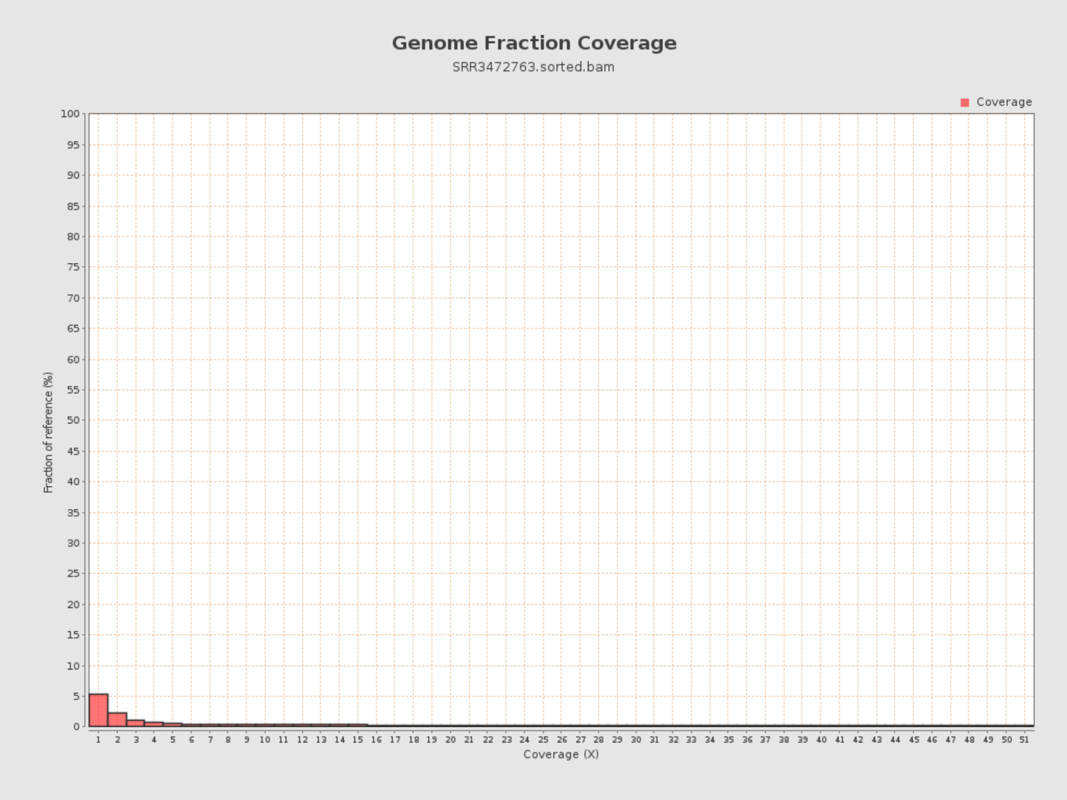
4. Results : Coverage Histogram



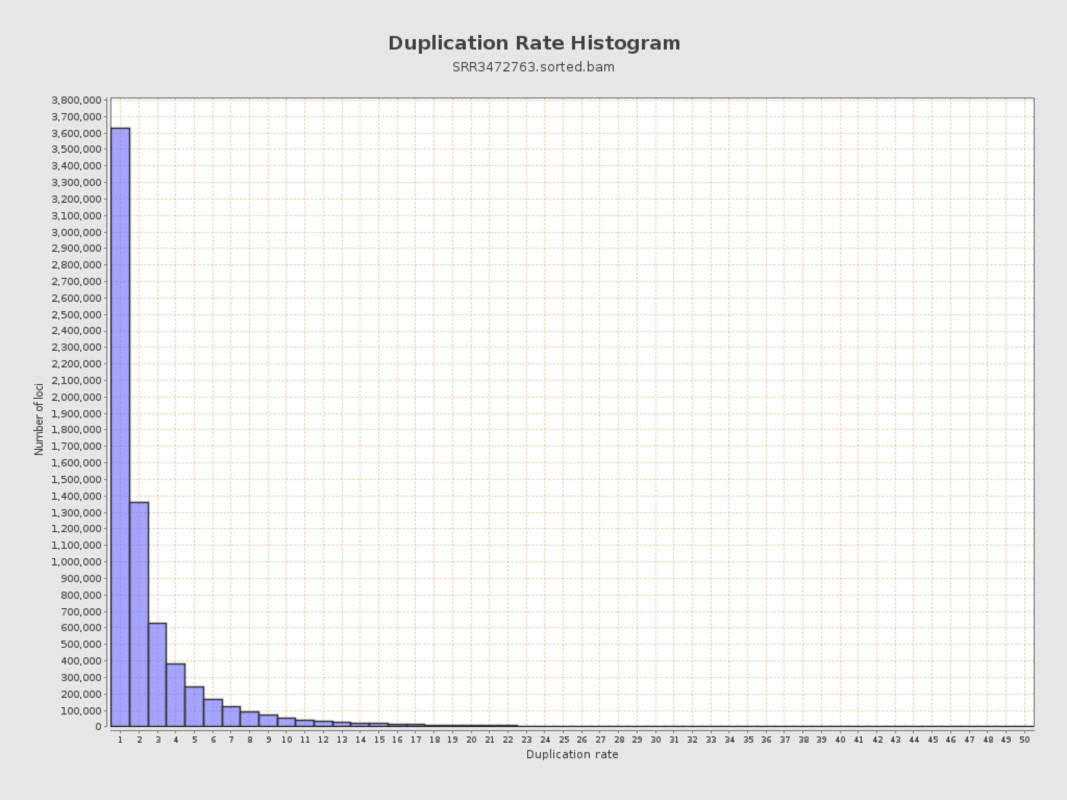
5. Results : Coverage Histogram (0-50X)



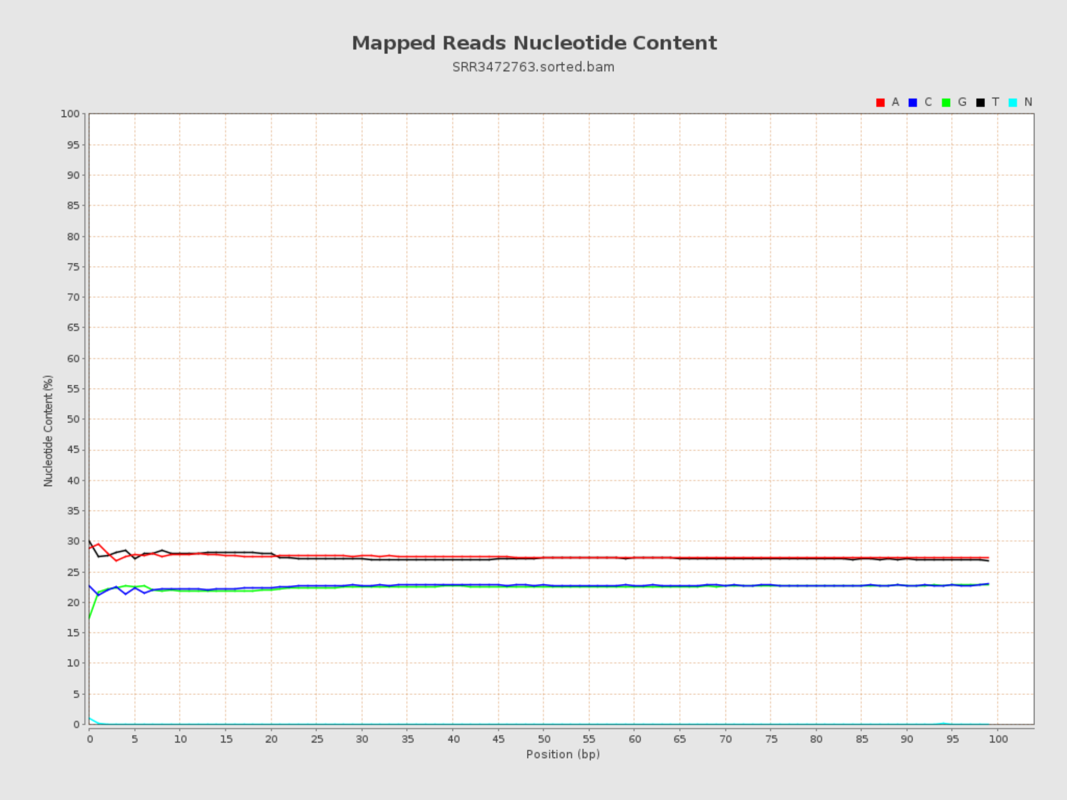
6. Results : Genome Fraction Coverage



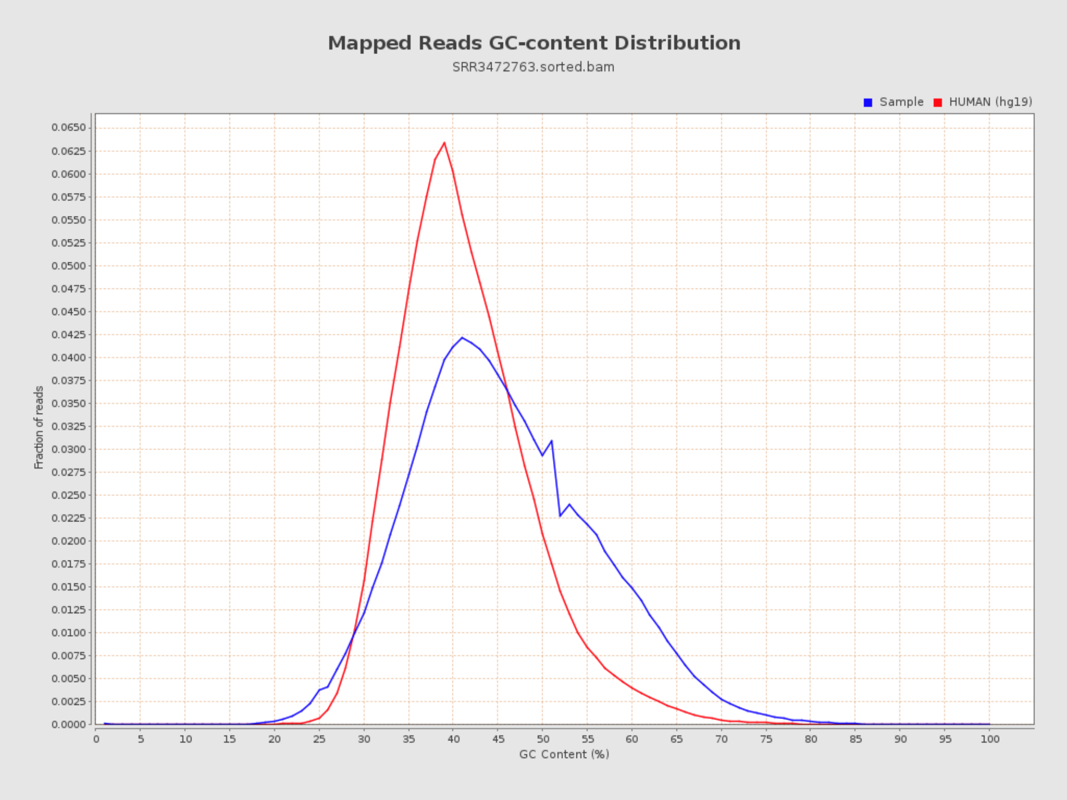
7. Results : Duplication Rate Histogram



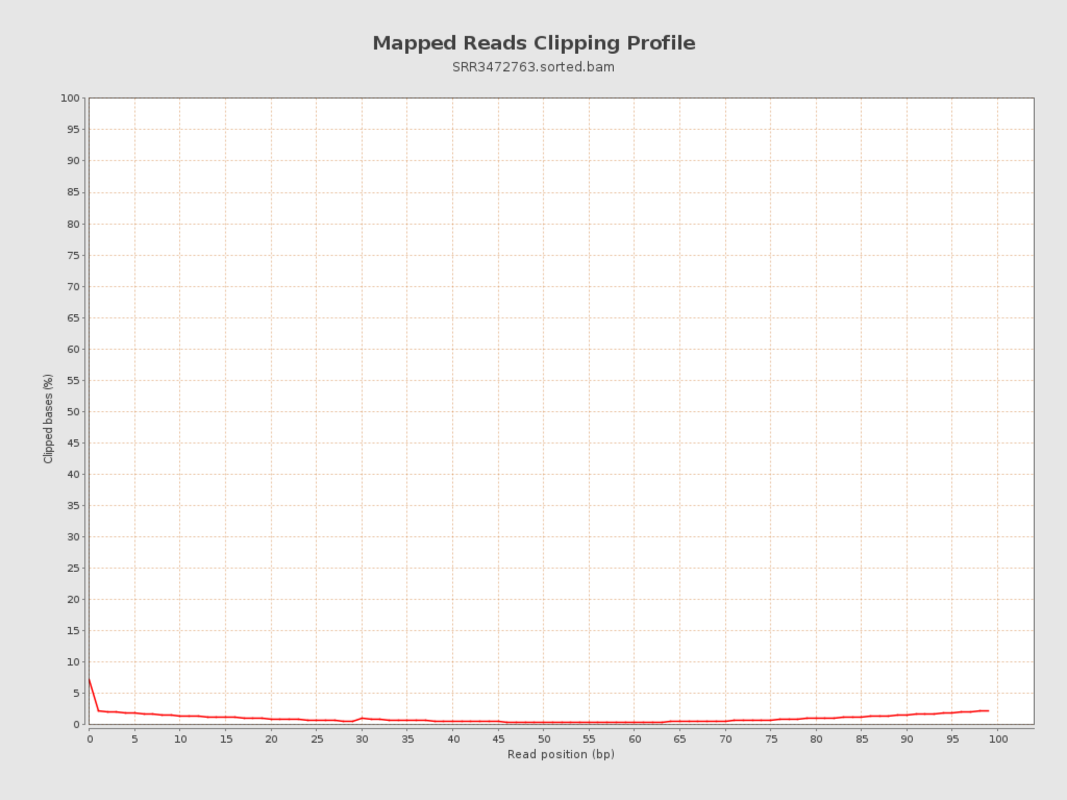
8. Results : Mapped Reads Nucleotide Content



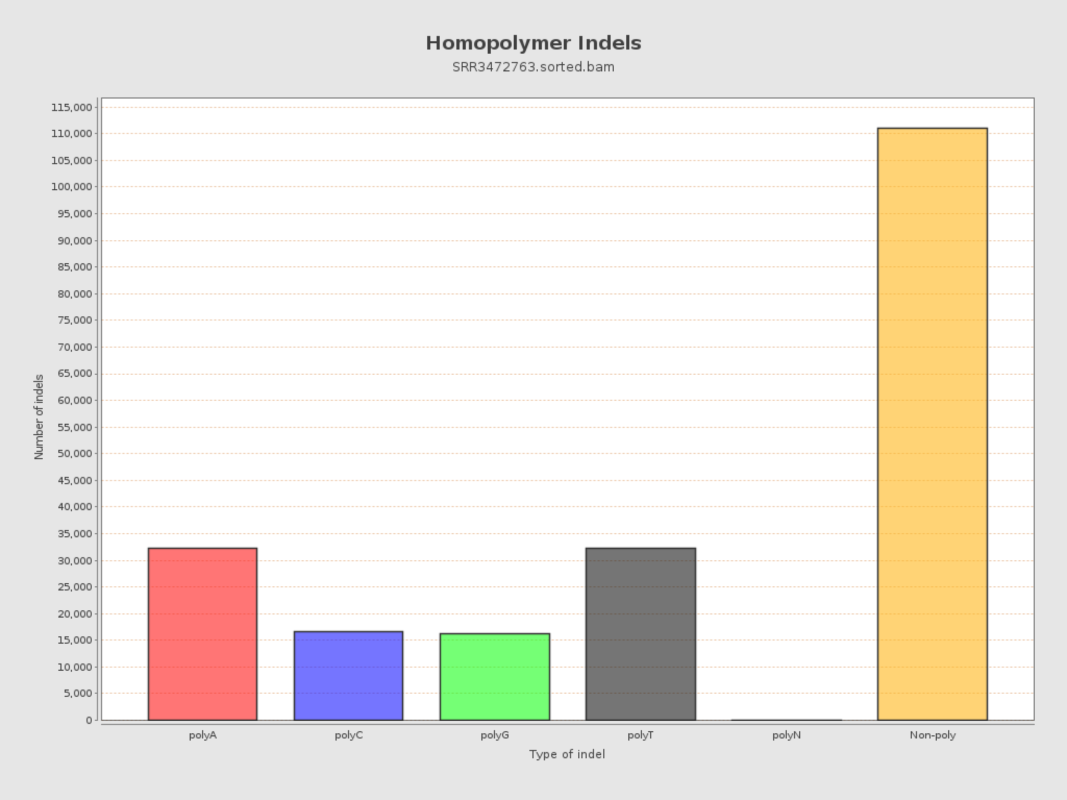
9. Results : Mapped Reads GC-content Distribution



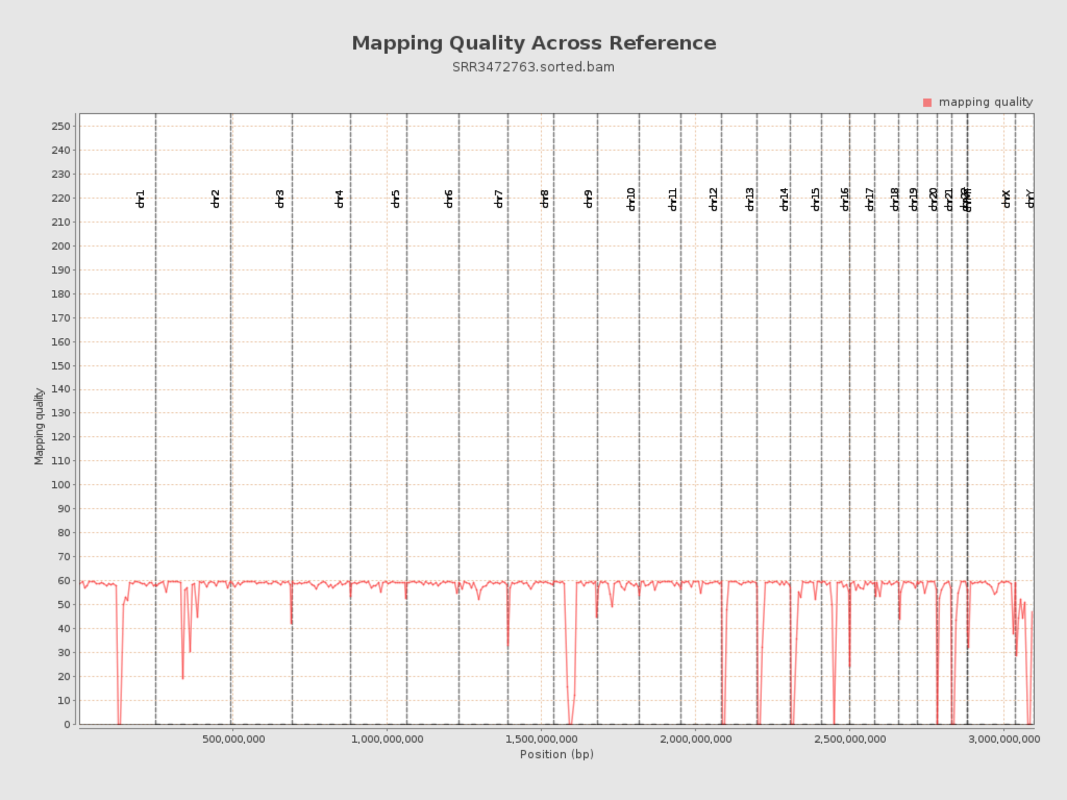
10. Results : Mapped Reads Clipping Profile



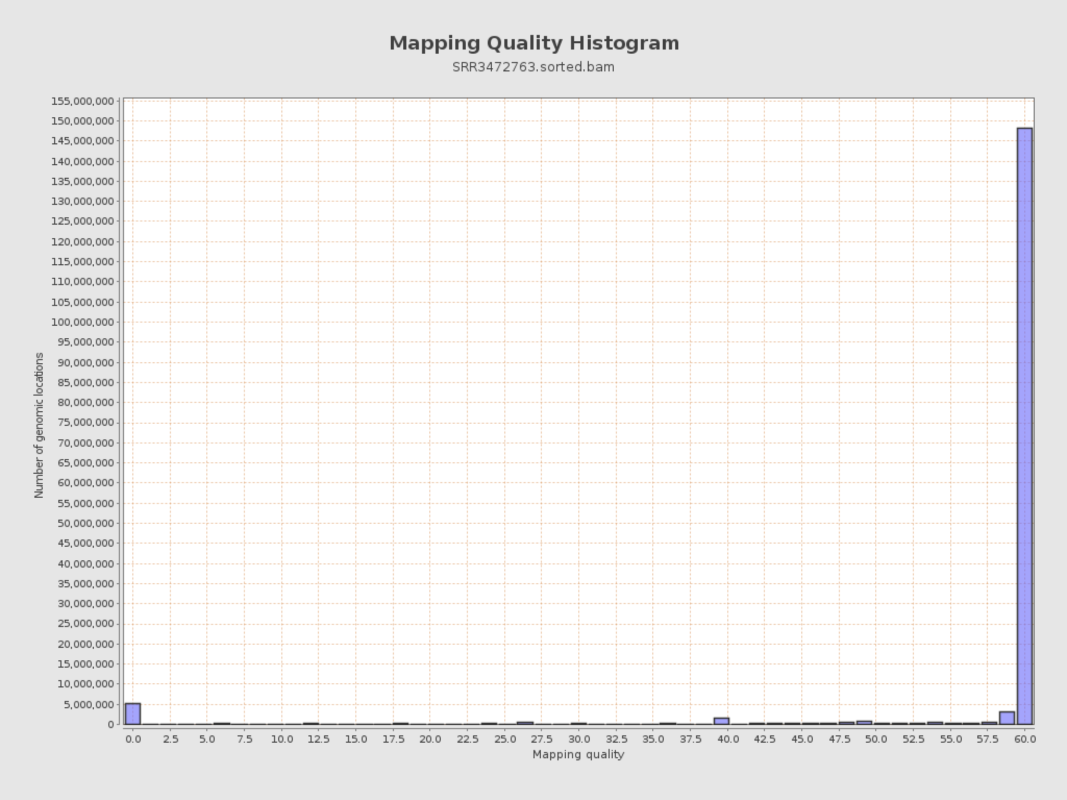
11. Results : Homopolymer Indels



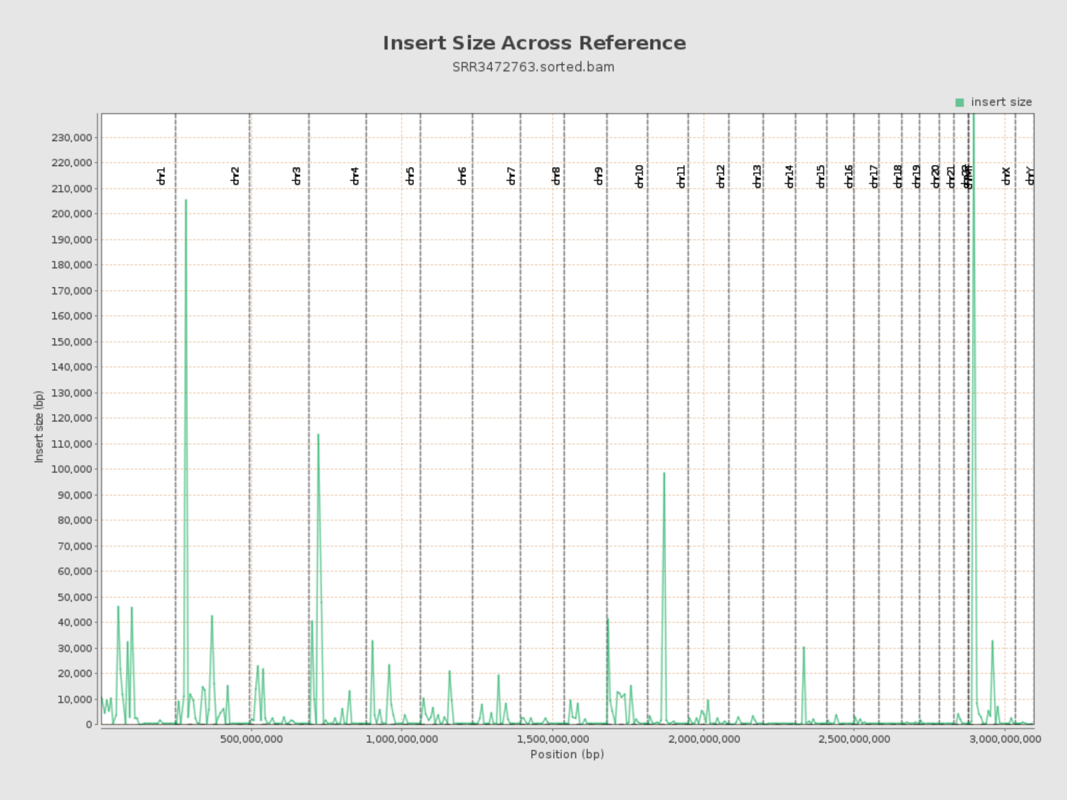
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram