Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 21:38:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472727.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_SRR3472727 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472727_1.fastq.gz SRR3472727_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 21:38:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472727.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,489,628
Mapped reads	17,339,278 / 99.14%
Unmapped reads	150,350 / 0.86%
Mapped paired reads	17,339,278 / 99.14%
Mapped reads, first in pair	8,695,148 / 49.72%
Mapped reads, second in pair	8,644,130 / 49.42%
Mapped reads, both in pair	17,253,614 / 98.65%
Mapped reads, singletons	85,664 / 0.49%
Secondary alignments	0
Supplementary alignments	59,789 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,034,399 / 63.09%
Duplication rate	47.48%
Clipped reads	1,431,107 / 8.18%

2.2. ACGT Content

Number/percentage of A's	457,760,093 / 26.81%
Number/percentage of C's	398,138,064 / 23.32%
Number/percentage of T's	455,337,044 / 26.67%
Number/percentage of G's	395,729,966 / 23.18%
Number/percentage of N's	332,612 / 0.02%

GC Percentage	46.5%

2.3. Coverage

Mean	0.5516
Standard Deviation	18.4226

2.4. Mapping Quality

Mean Mapping Quality	55.41

2.5. Insert size

Mean	22,589.36
Standard Deviation	1,481,021.43
P25/Median/P75	166 / 230 / 308

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	9,973,062
Insertions	95,226
Mapped reads with at least one insertion	0.54%
Deletions	97,768
Mapped reads with at least one deletion	0.56%
Homopolymer indels	42.2%

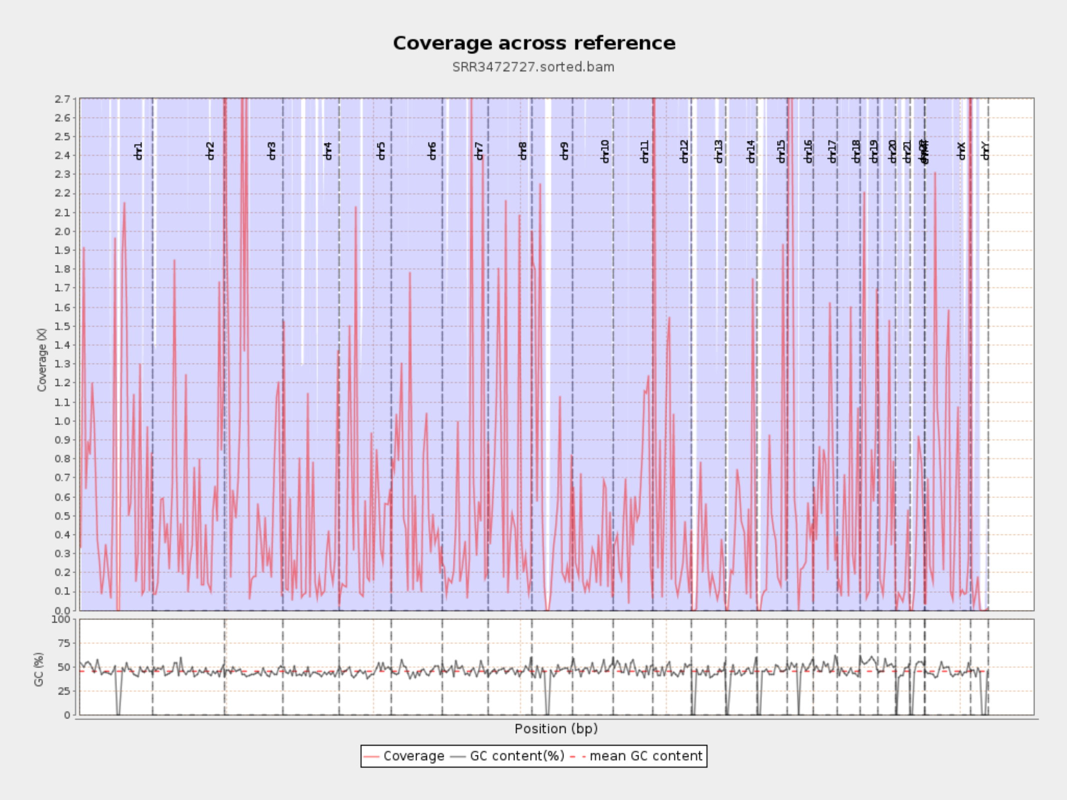
2.7. Chromosome stats

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

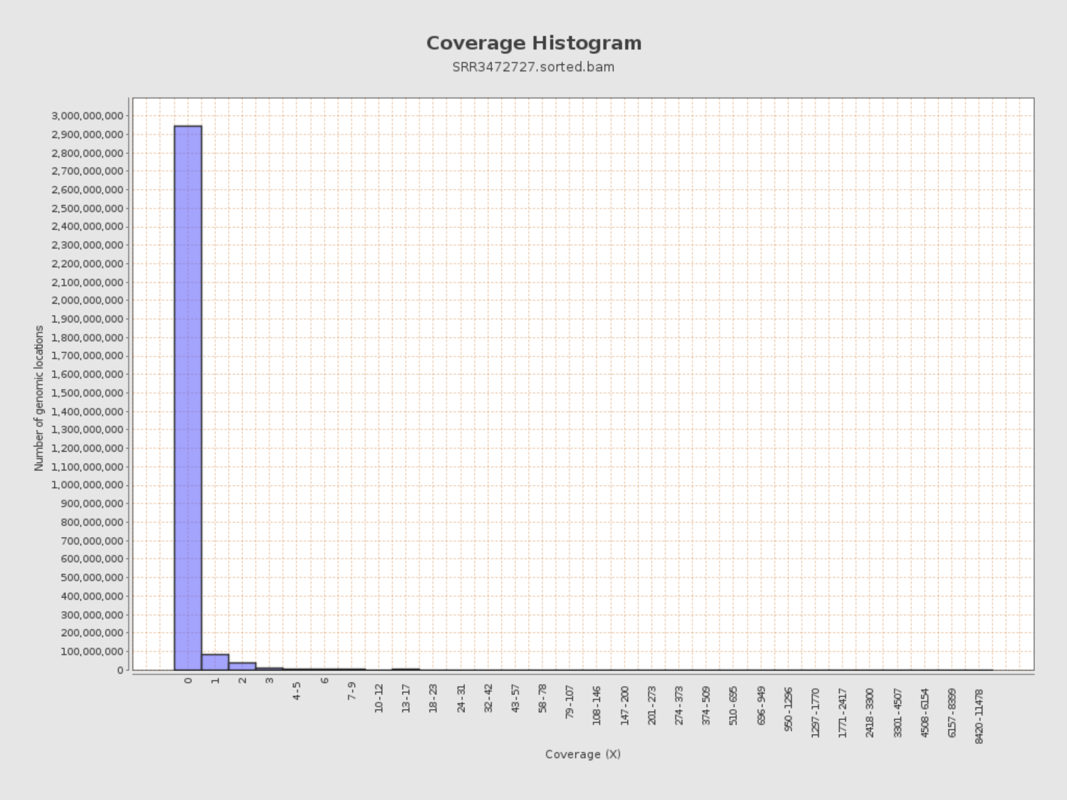
		bases	coverage	deviation
chr1	249250621	175217309	0.703	24.9534
chr2	243199373	125973403	0.518	19.3189
chr3	198022430	167575265	0.8462	18.6823
chr4	191154276	67151252	0.3513	13.3827
chr5	180915260	90970441	0.5028	17.9198
chr6	171115067	98619293	0.5763	15.1521
chr7	159138663	85411041	0.5367	23.8354
chr8	146364022	96450932	0.659	21.1288
chr9	141213431	88968721	0.63	15.6985
chr10	135534747	43042382	0.3176	13.2646
chr11	135006516	73595682	0.5451	15.6135
chr12	133851895	92139120	0.6884	19.4311
chr13	115169878	26939059	0.2339	8.1339
chr14	107349540	44845228	0.4177	14.412
chr15	102531392	43226587	0.4216	14.3057
chr16	90354753	79984069	0.8852	26.7354
chr17	81195210	54888795	0.676	16.6742
chr18	78077248	37888579	0.4853	20.5964
chr19	59128983	49069200	0.8299	21.6888
chr20	63025520	35213672	0.5587	18.8844
chr21	48129895	6892773	0.1432	6.7196
chr22	51304566	20508986	0.3997	11.9853
chrMT	16571	2348	0.1417	0.4814
chrX	155270560	99688358	0.642	21.7408

chrY	59373566	3277439	0.0552	5.1979

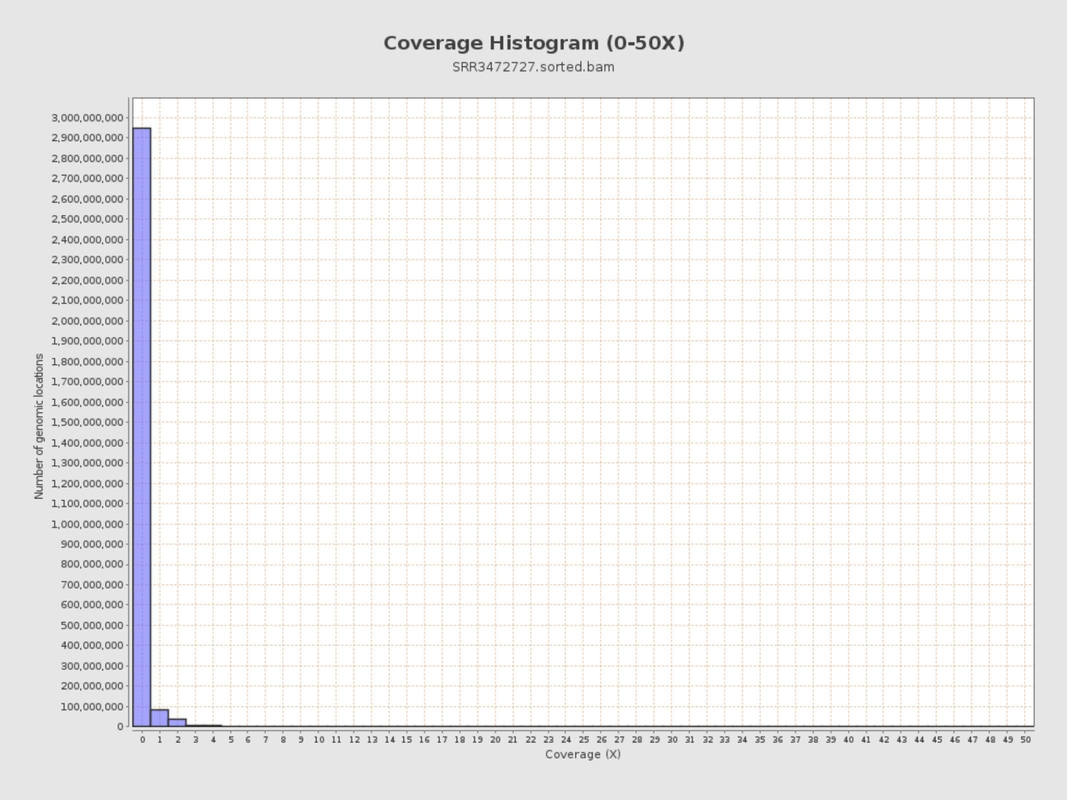
3. Results : Coverage across reference



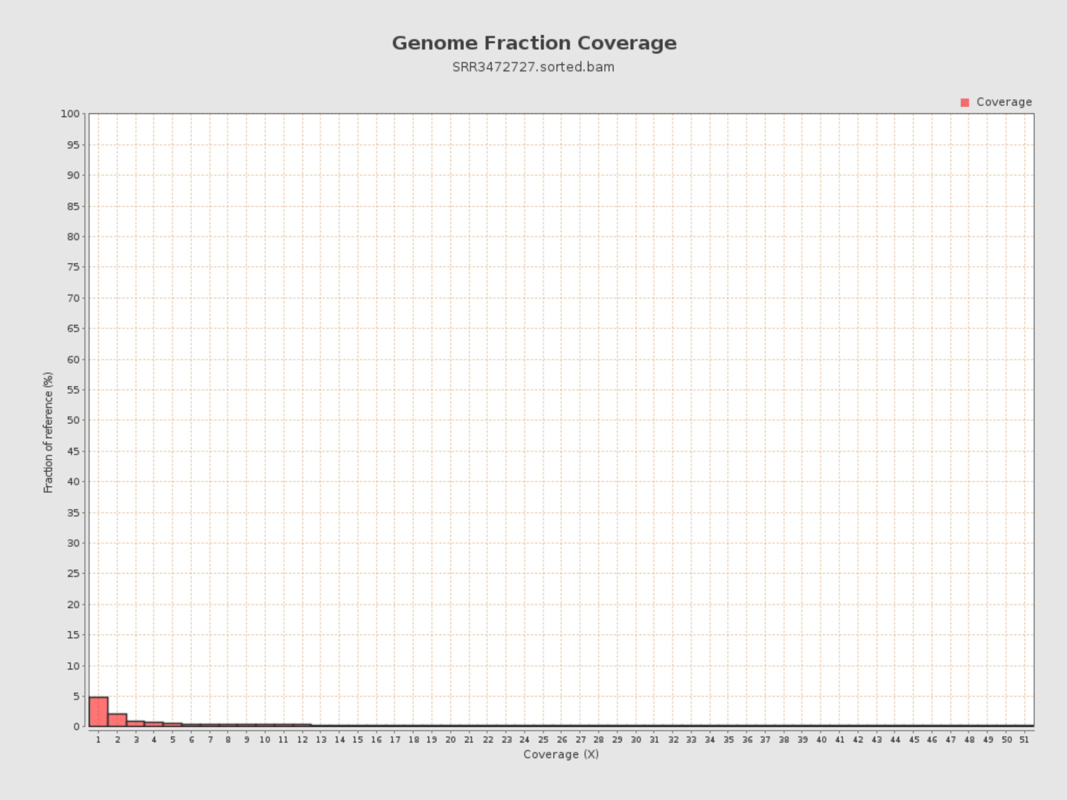
4. Results : Coverage Histogram



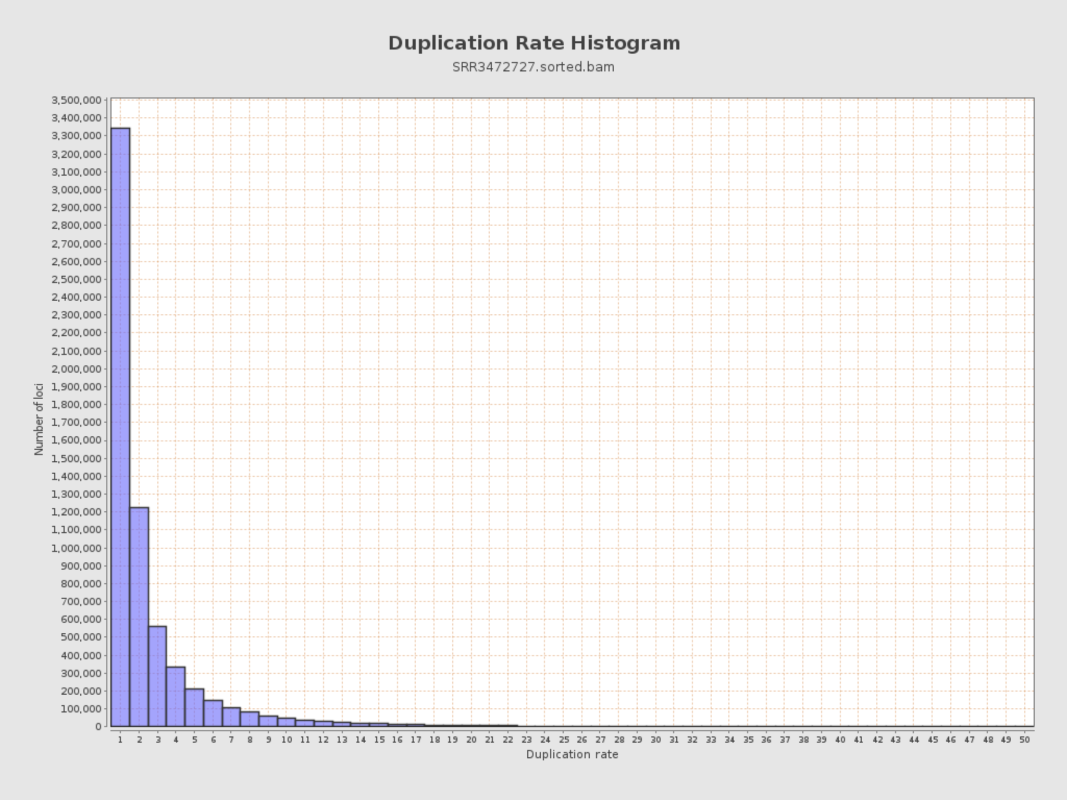
5. Results : Coverage Histogram (0-50X)



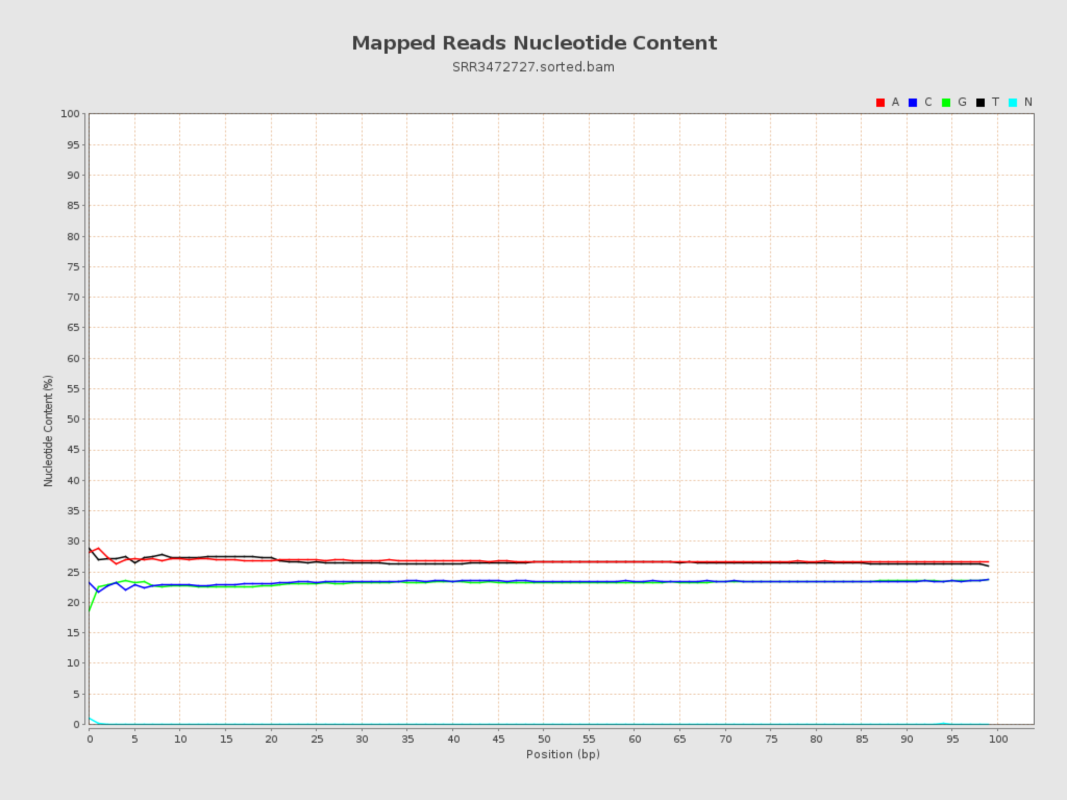
6. Results : Genome Fraction Coverage



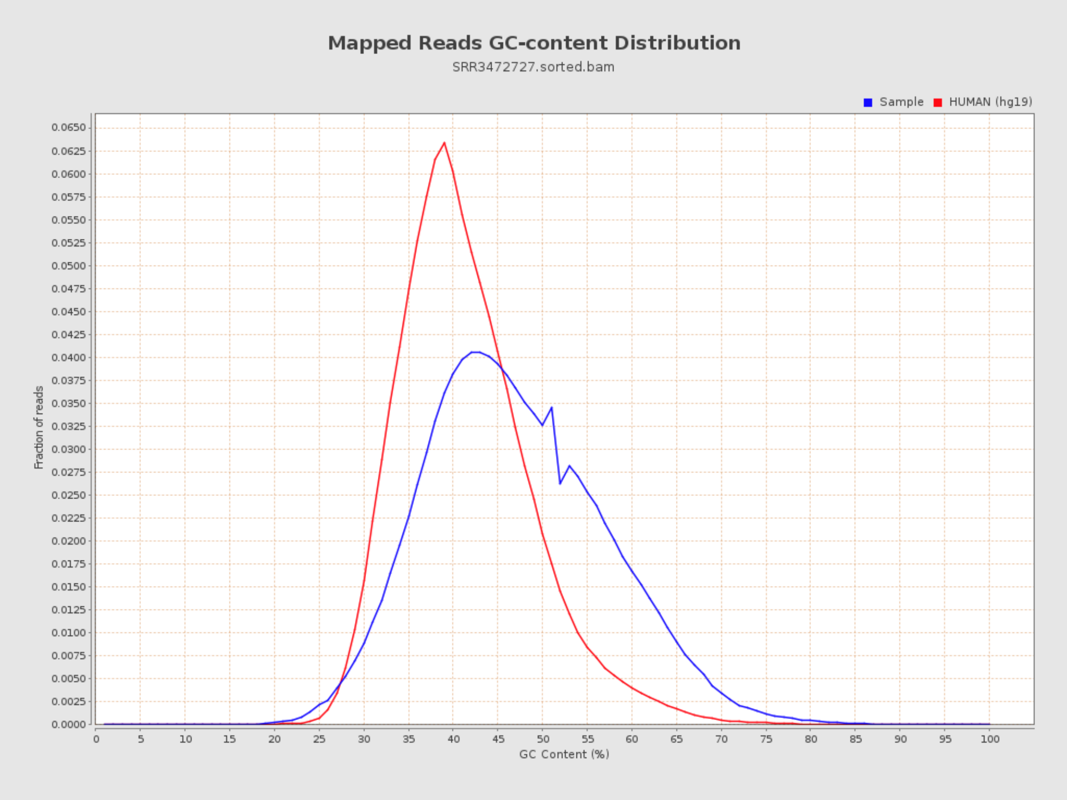
7. Results : Duplication Rate Histogram



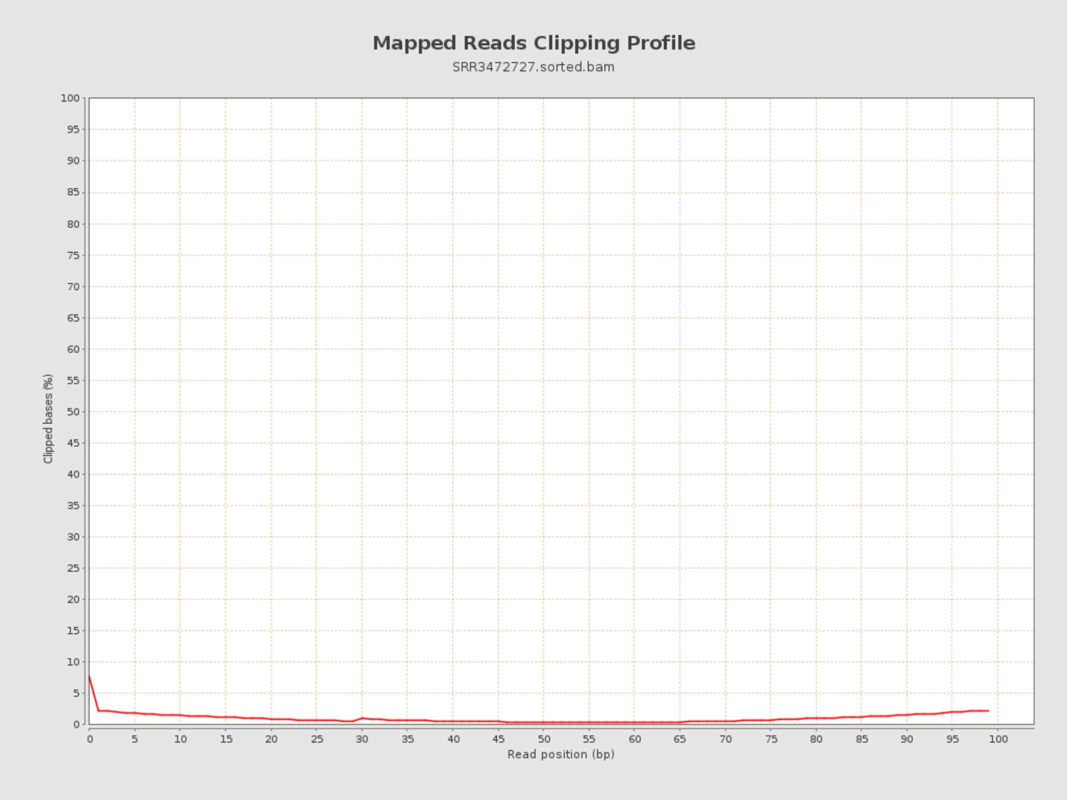
8. Results : Mapped Reads Nucleotide Content



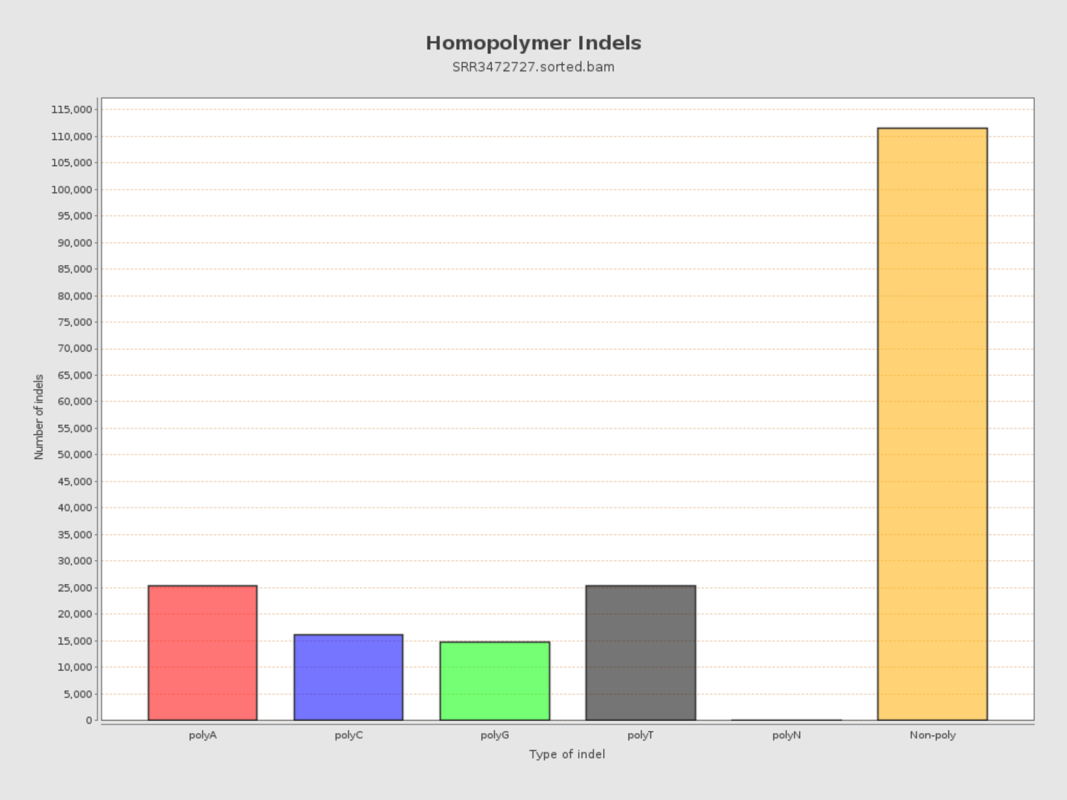
9. Results : Mapped Reads GC-content Distribution



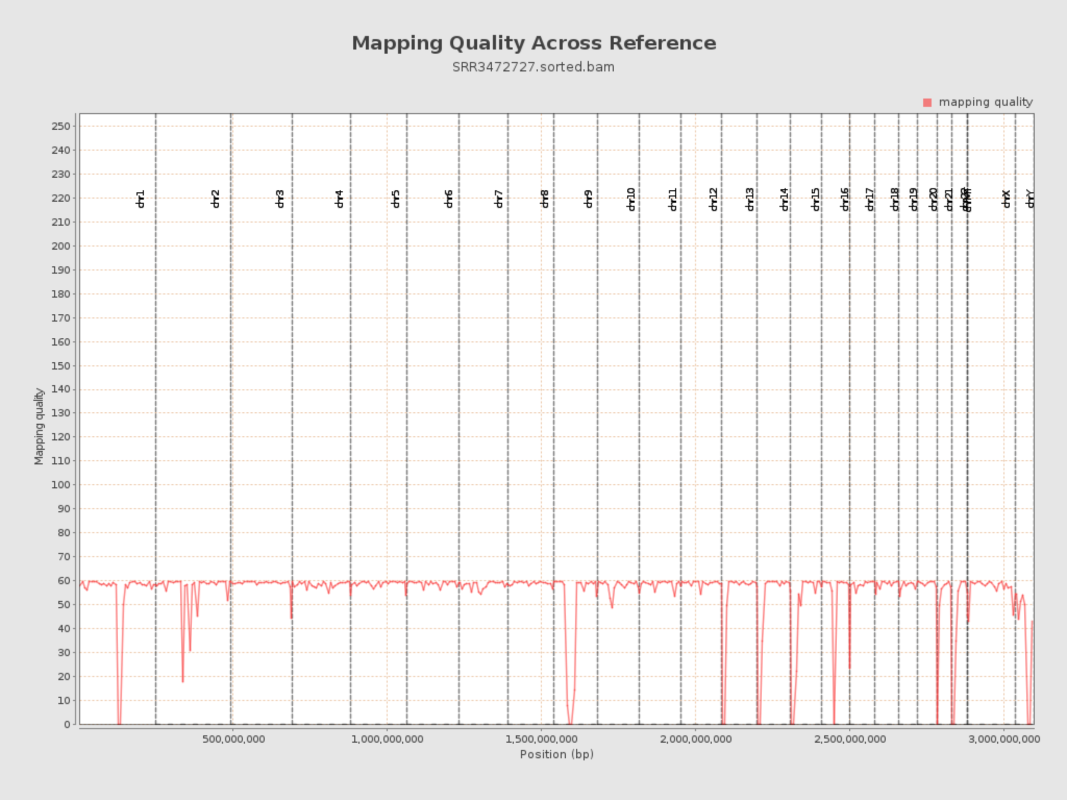
10. Results : Mapped Reads Clipping Profile



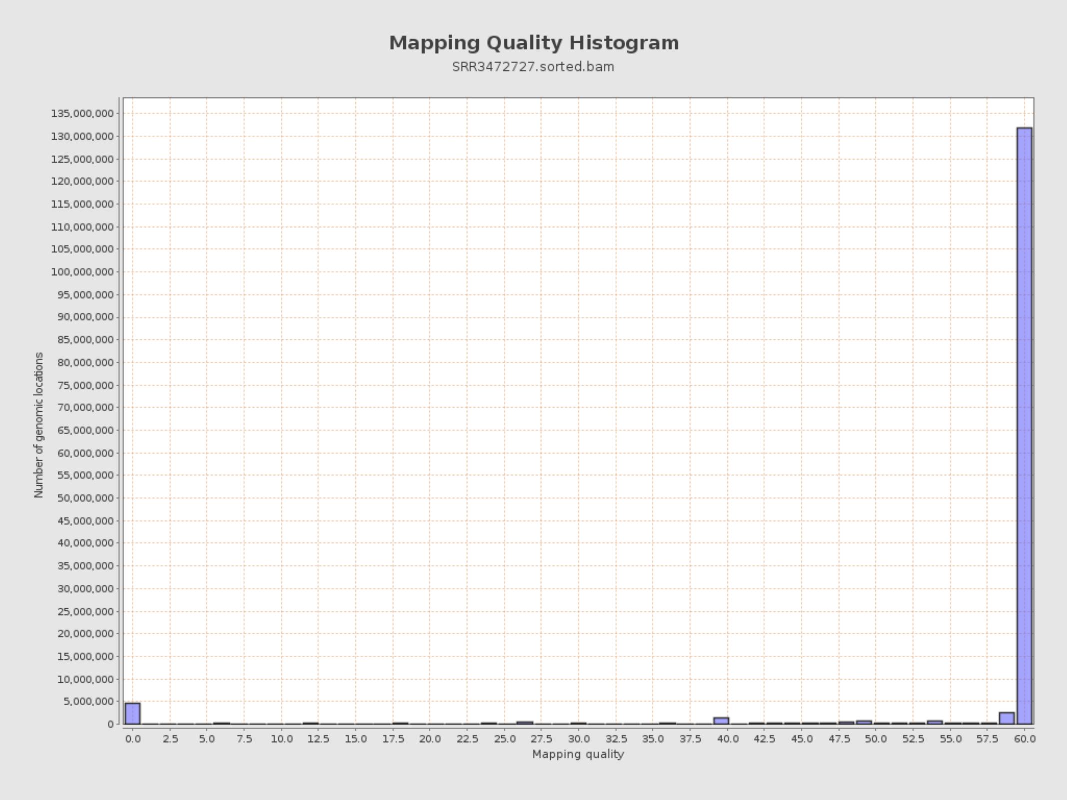
11. Results : Homopolymer Indels



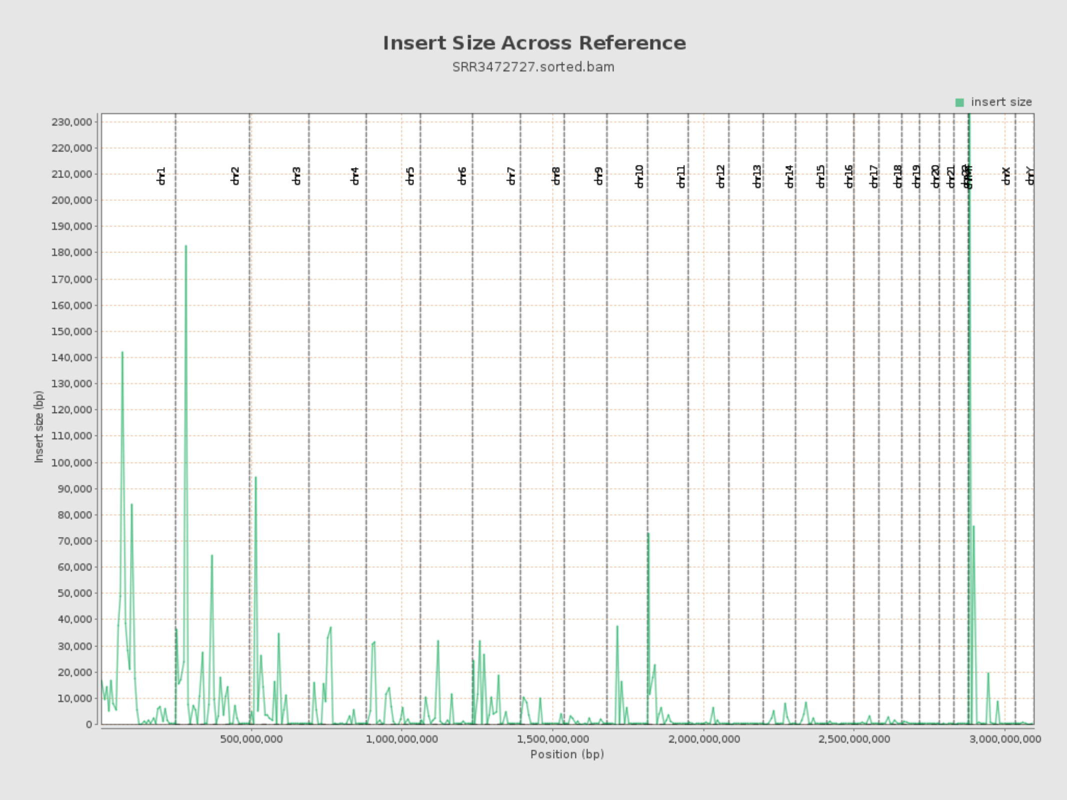
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram