Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 12:25:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472695.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_SRR3472695 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472695_1.fastq.gz SRR3472695_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 12:25:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472695.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,303,046
Mapped reads	15,169,653 / 99.13%
Unmapped reads	133,393 / 0.87%
Mapped paired reads	15,169,653 / 99.13%
Mapped reads, first in pair	7,617,819 / 49.78%
Mapped reads, second in pair	7,551,834 / 49.35%
Mapped reads, both in pair	15,096,056 / 98.65%
Mapped reads, singletons	73,597 / 0.48%
Secondary alignments	0
Supplementary alignments	95,118 / 0.62%
Read min/max/mean length	30 / 101 / 99.58
Duplicated reads (estimated)	11,356,594 / 74.21%
Duplication rate	47.52%
Clipped reads	949,328 / 6.2%

2.2. ACGT Content

Number/percentage of A's	400,342,370 / 26.81%
Number/percentage of C's	344,929,221 / 23.1%
Number/percentage of T's	406,722,890 / 27.24%
Number/percentage of G's	340,756,078 / 22.82%
Number/percentage of N's	340,464 / 0.02%

GC Percentage	45.92%

2.3. Coverage

Mean	0.4824
Standard Deviation	38.5506

2.4. Mapping Quality

Mean Mapping Quality	54.73

2.5. Insert size

Mean	18,431.03
Standard Deviation	1,294,960.38
P25/Median/P75	153 / 208 / 275

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	5,974,680
Insertions	88,325
Mapped reads with at least one insertion	0.58%
Deletions	76,454
Mapped reads with at least one deletion	0.5%
Homopolymer indels	47.32%

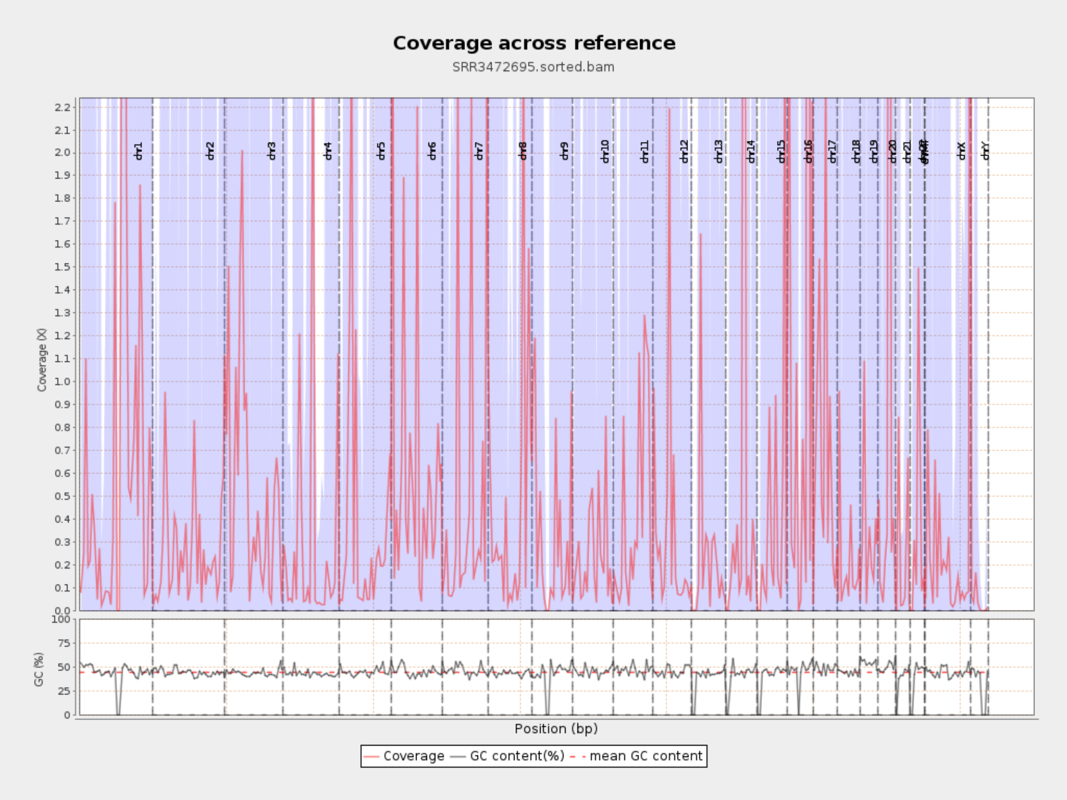
2.7. Chromosome stats

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

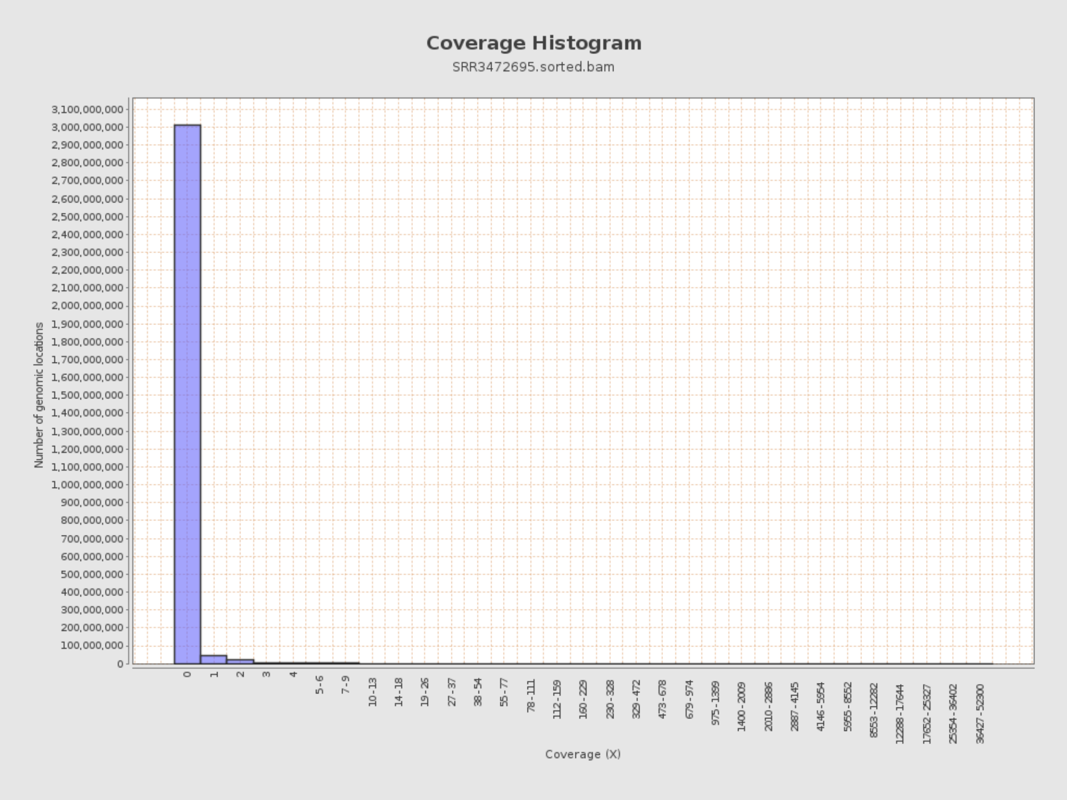
		bases	**coverage**	**deviation**
chr1	249250621	187216828	0.7511	49.8881
chr2	243199373	62394005	0.2566	17.2738
chr3	198022430	110227950	0.5566	19.8853
chr4	191154276	55542629	0.2906	21.5387
chr5	180915260	68249506	0.3772	22.2659
chr6	171115067	111980359	0.6544	29.9141
chr7	159138663	86337416	0.5425	32.7815
chr8	146364022	65288668	0.4461	27.9701
chr9	141213431	48538929	0.3437	18.975
chr10	135534747	32432257	0.2393	14.7559
chr11	135006516	58677018	0.4346	28.8625
chr12	133851895	47334125	0.3536	26.7336
chr13	115169878	27911806	0.2424	15.4015
chr14	107349540	59913293	0.5581	38.7491
chr15	102531392	48102472	0.4691	31.3638
chr16	90354753	180756682	2.0005	149.5425
chr17	81195210	58982186	0.7264	33.2895
chr18	78077248	17979686	0.2303	10.5977
chr19	59128983	19900631	0.3366	17.7629
chr20	63025520	69986825	1.1105	77.8142
chr21	48129895	12660814	0.2631	19.5346
chr22	51304566	16660335	0.3247	23.5217
chrMT	16571	3172	0.1914	0.4788
chrX	155270560	43939924	0.283	20.8502

chrY	59373566	2252751	0.0379	2.5489

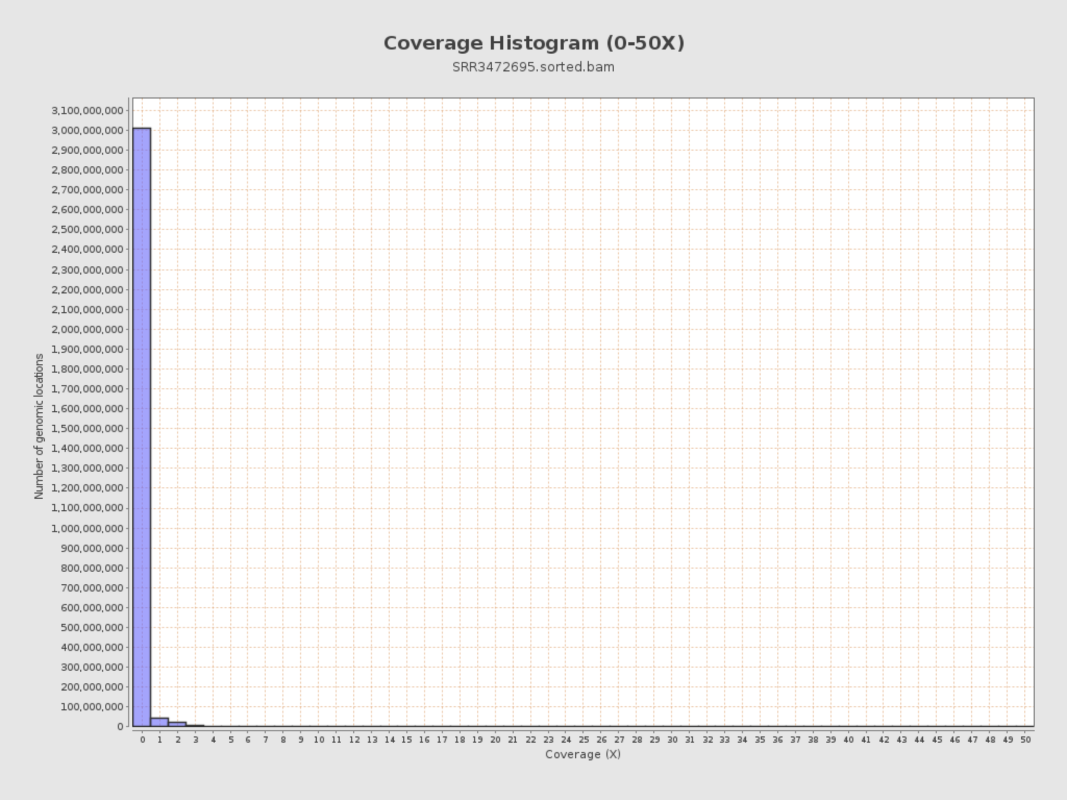
3. Results : Coverage across reference



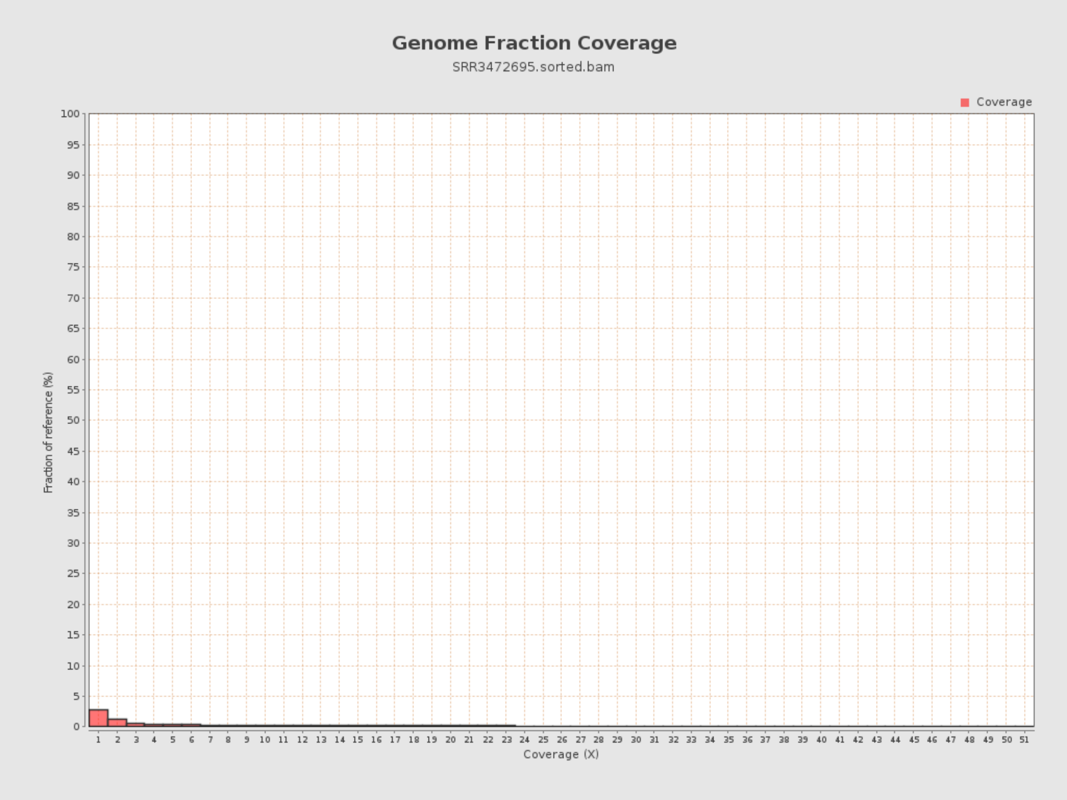
4. Results : Coverage Histogram



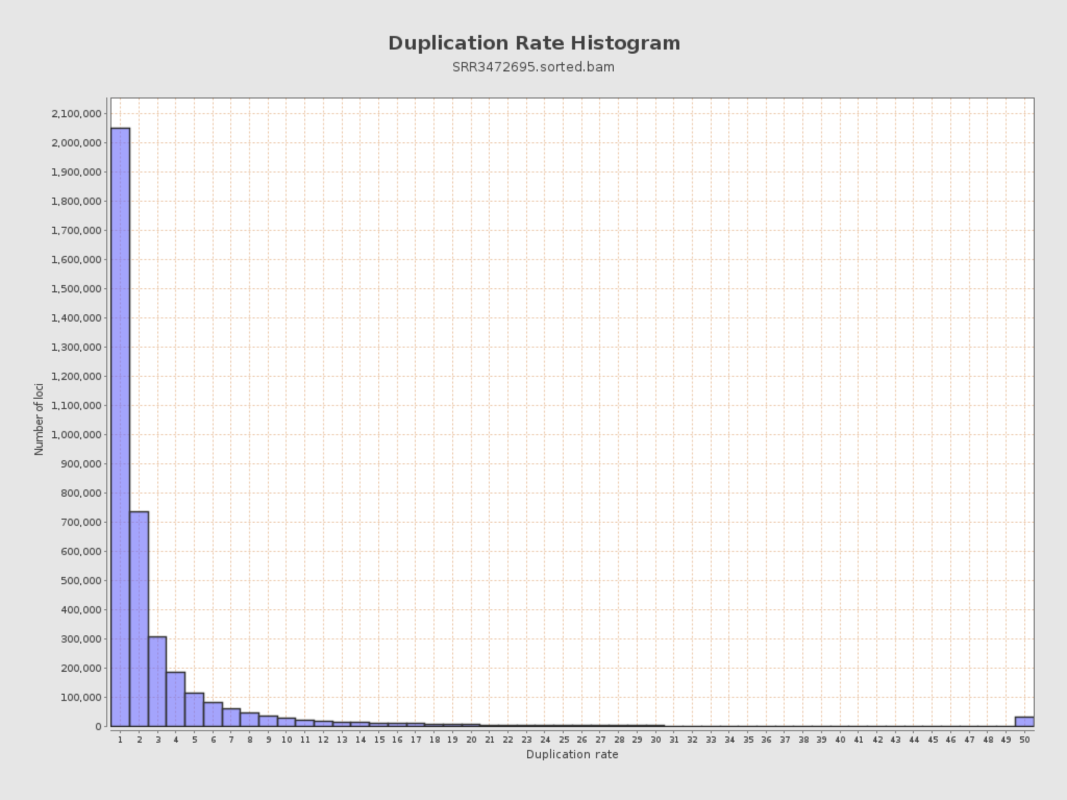
5. Results : Coverage Histogram (0-50X)



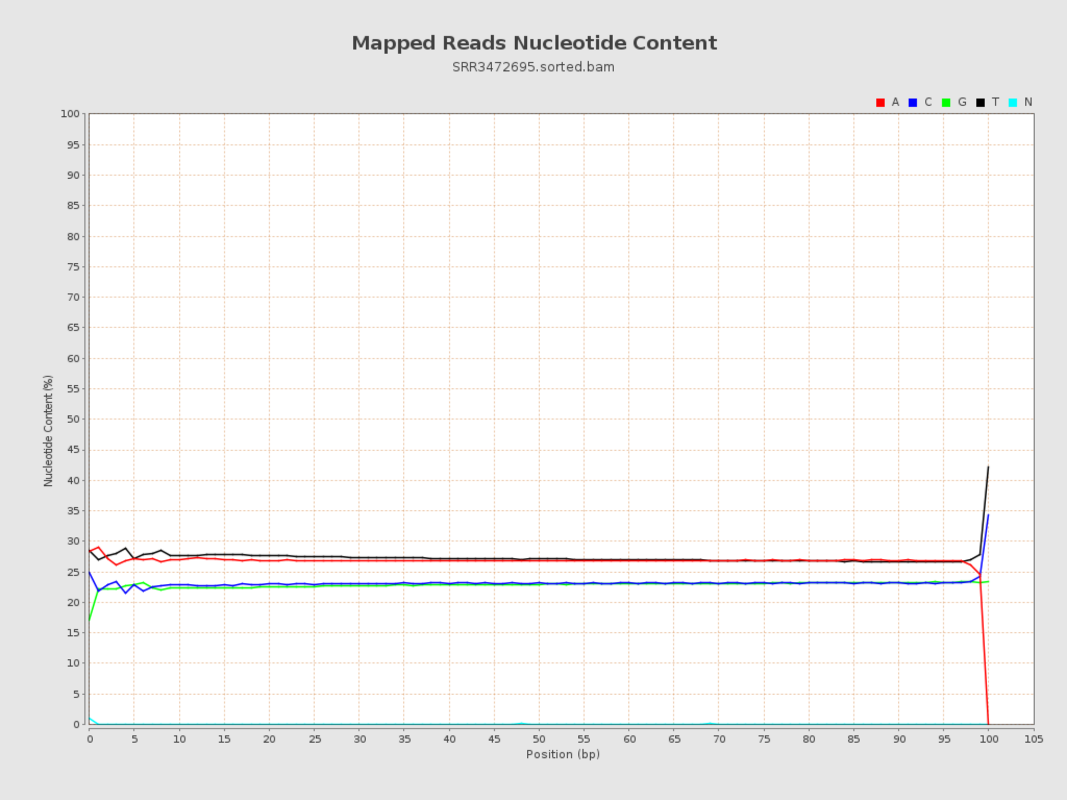
6. Results : Genome Fraction Coverage



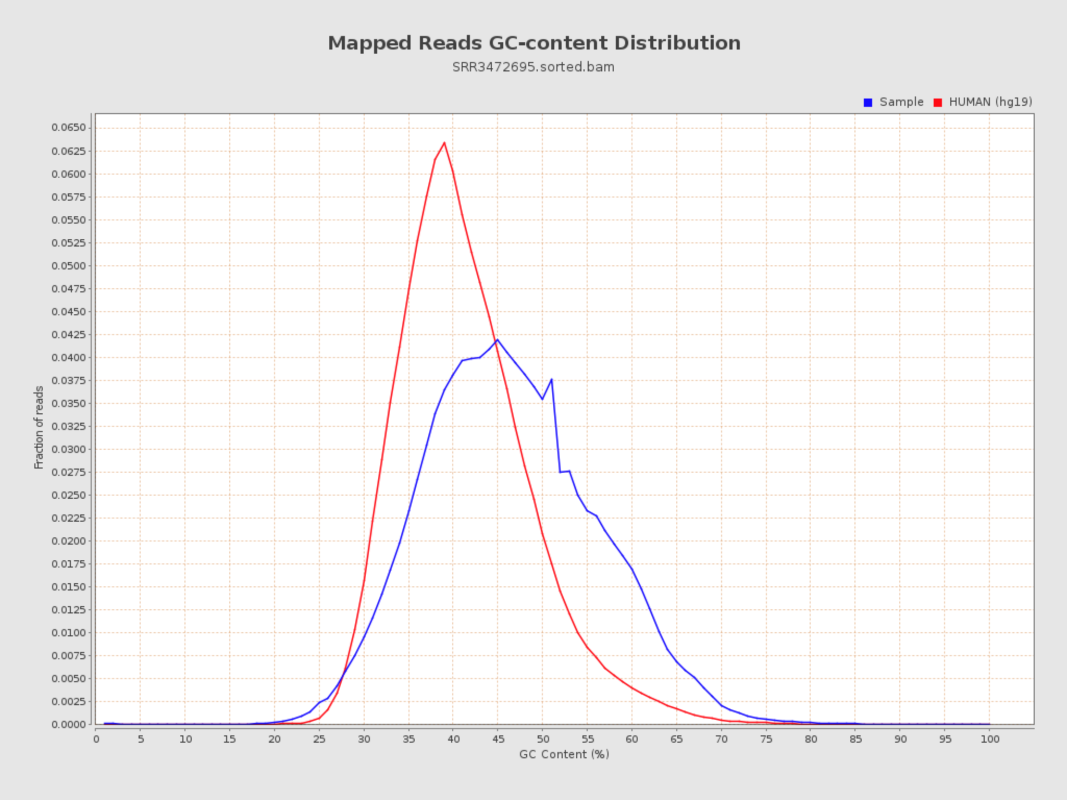
7. Results : Duplication Rate Histogram



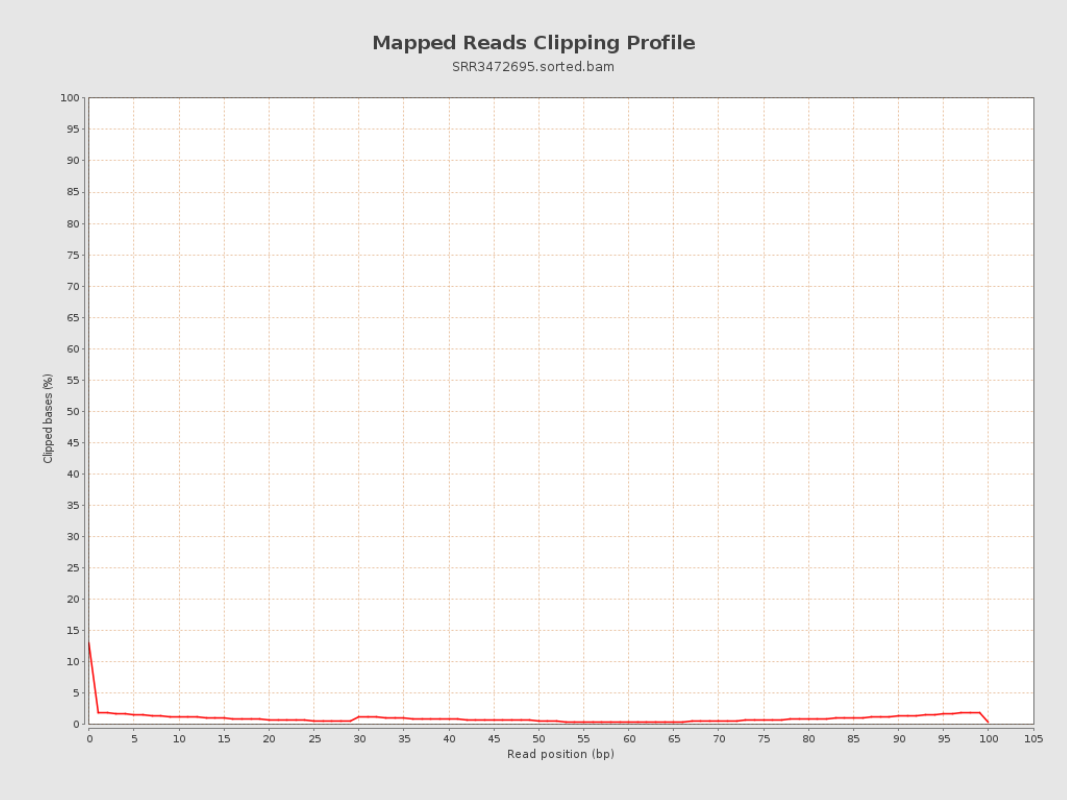
8. Results : Mapped Reads Nucleotide Content



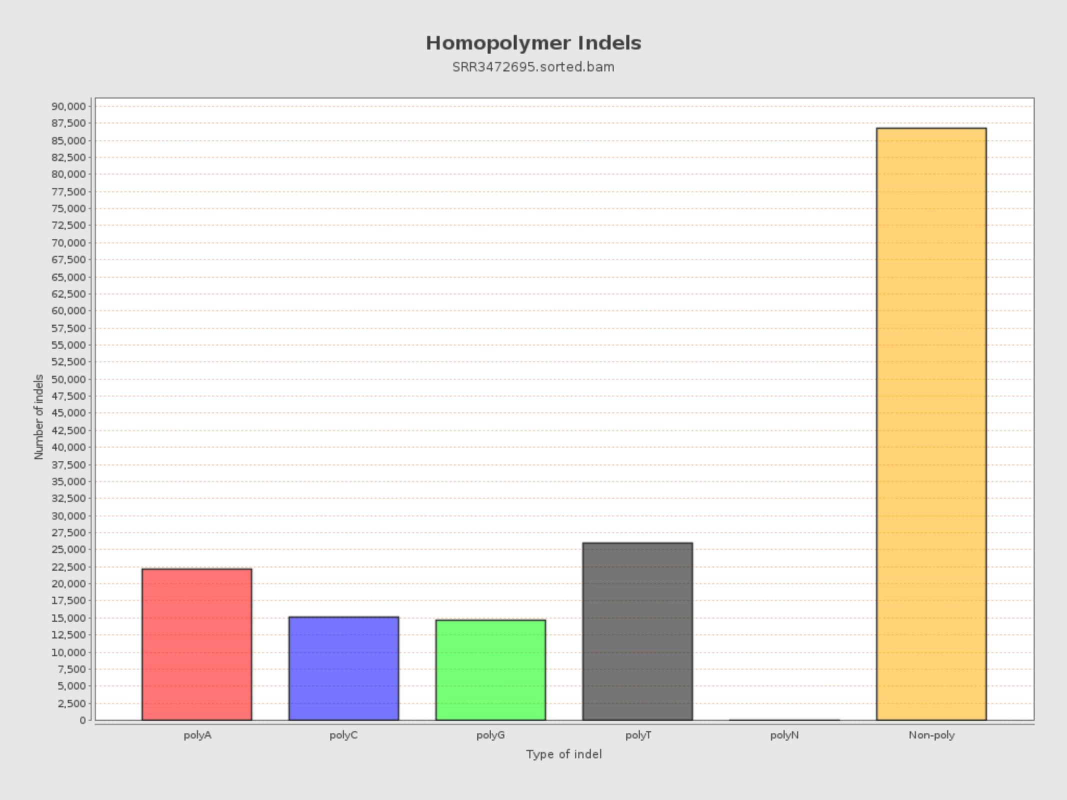
9. Results : Mapped Reads GC-content Distribution



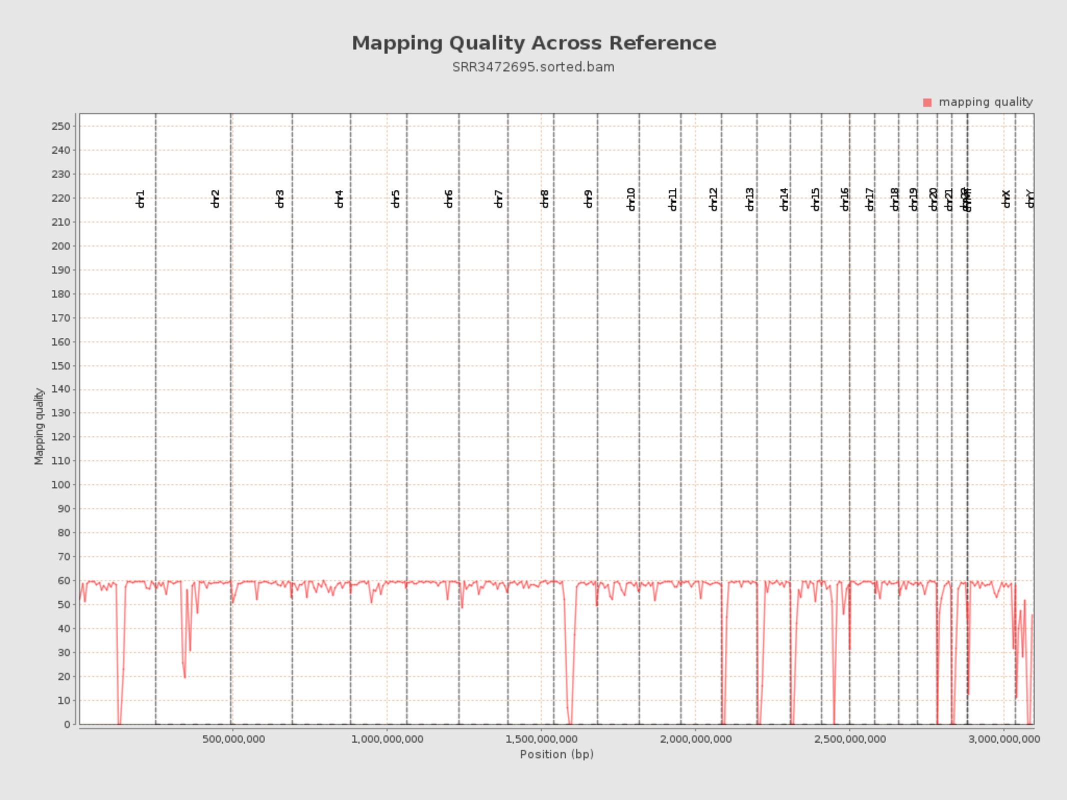
10. Results : Mapped Reads Clipping Profile



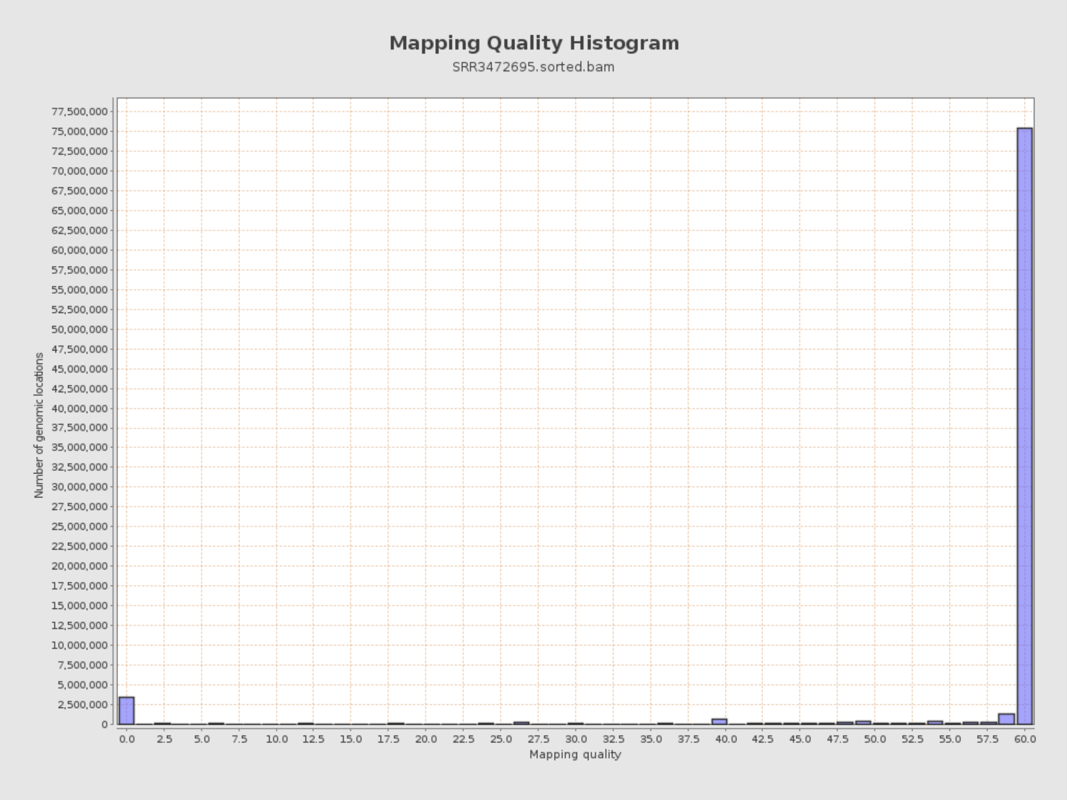
11. Results : Homopolymer Indels



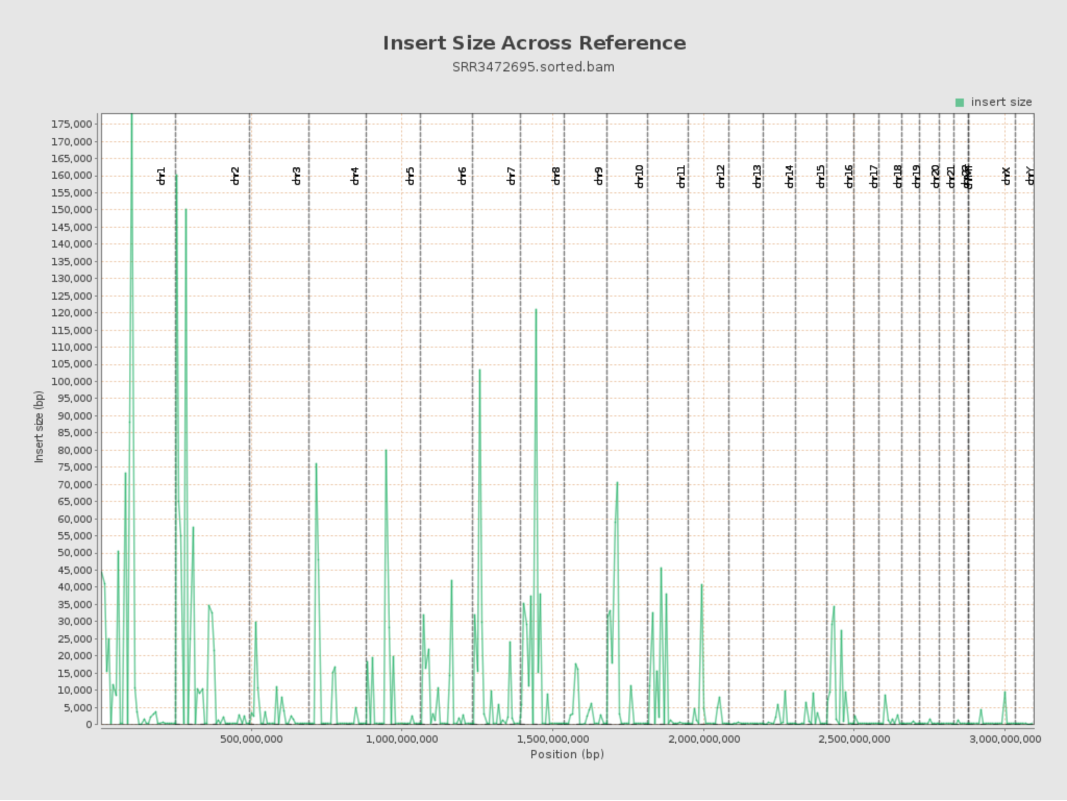
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram