Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 13:21:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472699.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_SRR3472699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472699_1.fastq.gz SRR3472699_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 13:21:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,664,150
Mapped reads	14,533,314 / 99.11%
Unmapped reads	130,836 / 0.89%
Mapped paired reads	14,533,314 / 99.11%
Mapped reads, first in pair	7,308,069 / 49.84%
Mapped reads, second in pair	7,225,245 / 49.27%
Mapped reads, both in pair	14,442,770 / 98.49%
Mapped reads, singletons	90,544 / 0.62%
Secondary alignments	0
Supplementary alignments	24,399 / 0.17%
Read min/max/mean length	30 / 101 / 99.76
Duplicated reads (estimated)	7,593,938 / 51.79%
Duplication rate	46.31%
Clipped reads	615,481 / 4.2%

2.2. ACGT Content

Number/percentage of A's	390,789,230 / 27.18%
Number/percentage of C's	327,294,720 / 22.76%
Number/percentage of T's	398,493,794 / 27.72%
Number/percentage of G's	320,837,454 / 22.32%
Number/percentage of N's	328,753 / 0.02%

GC Percentage	45.08%

2.3. Coverage

Mean	0.4645
Standard Deviation	9.3751

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	21,695.72
Standard Deviation	1,480,928.06
P25/Median/P75	179 / 240 / 317

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	6,576,869
Insertions	68,359
Mapped reads with at least one insertion	0.46%
Deletions	81,583
Mapped reads with at least one deletion	0.55%
Homopolymer indels	44.52%

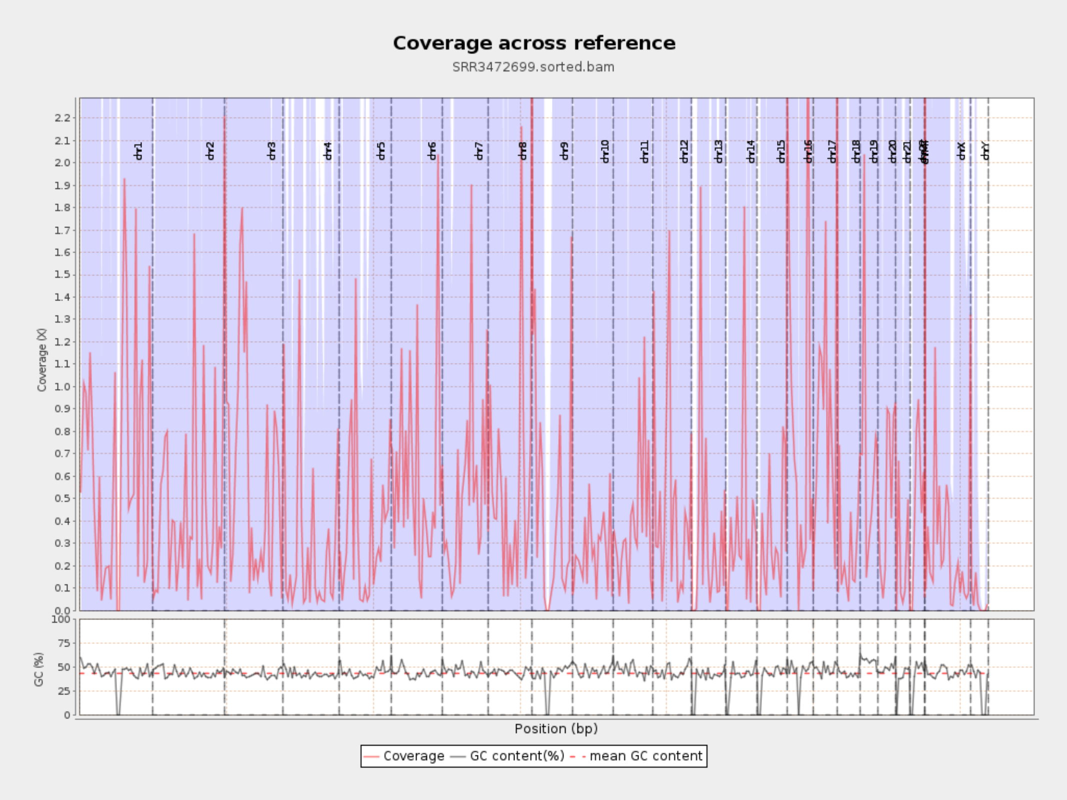
2.7. Chromosome stats

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

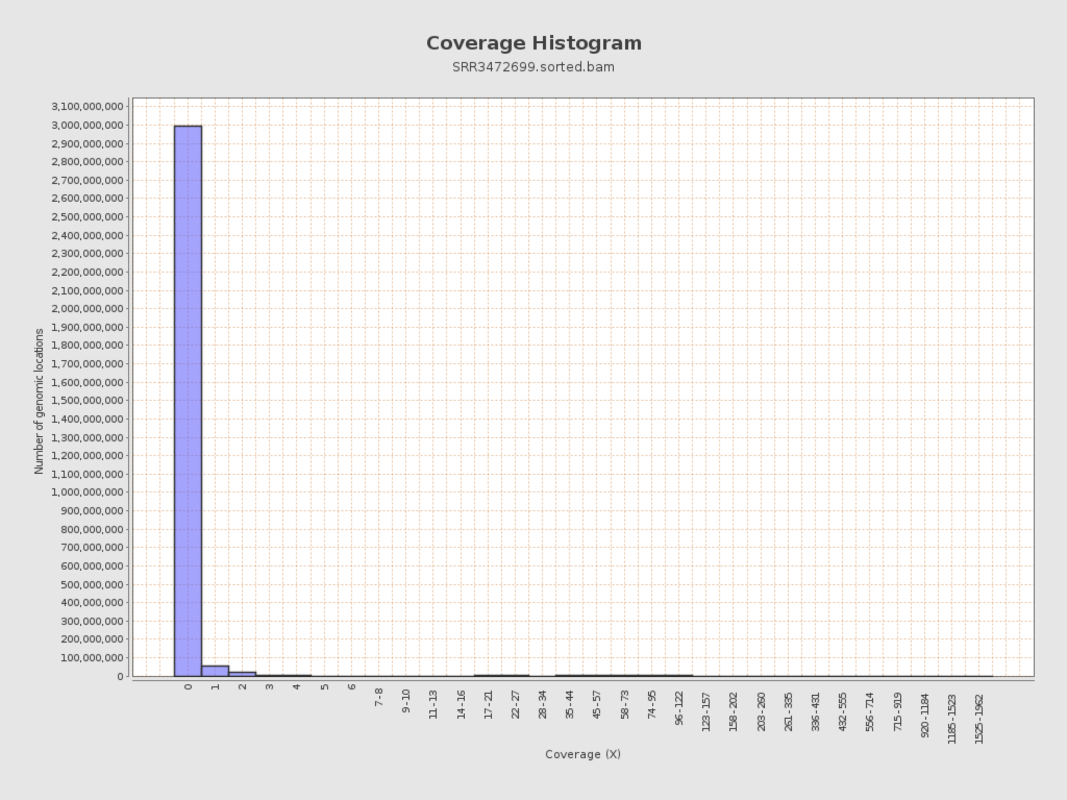
		bases	coverage	deviation
chr1	249250621	163467393	0.6558	11.6241
chr2	243199373	102477761	0.4214	9.278
chr3	198022430	126257004	0.6376	10.1914
chr4	191154276	50440917	0.2639	7.2386
chr5	180915260	67953965	0.3756	8.3207
chr6	171115067	100576797	0.5878	9.9652
chr7	159138663	86148403	0.5413	11.2633
chr8	146364022	79408808	0.5425	10.0326
chr9	141213431	70605255	0.5	8.728
chr10	135534747	36080534	0.2662	6.4701
chr11	135006516	54441455	0.4033	8.6333
chr12	133851895	65079863	0.4862	8.3666
chr13	115169878	37138621	0.3225	8.8167
chr14	107349540	37895472	0.353	7.9609
chr15	102531392	31078261	0.3031	6.8671
chr16	90354753	78758288	0.8717	16.0724
chr17	81195210	73093687	0.9002	13.6943
chr18	78077248	21446387	0.2747	6.0642
chr19	59128983	42352906	0.7163	9.7514
chr20	63025520	32220903	0.5112	9.8432
chr21	48129895	11218166	0.2331	9.7439
chr22	51304566	24543877	0.4784	9.7898
chrMT	16571	76913	4.6414	3.0278
chrX	155270560	42680958	0.2749	4.4957

chrY	59373566	2506903	0.0422	1.3493

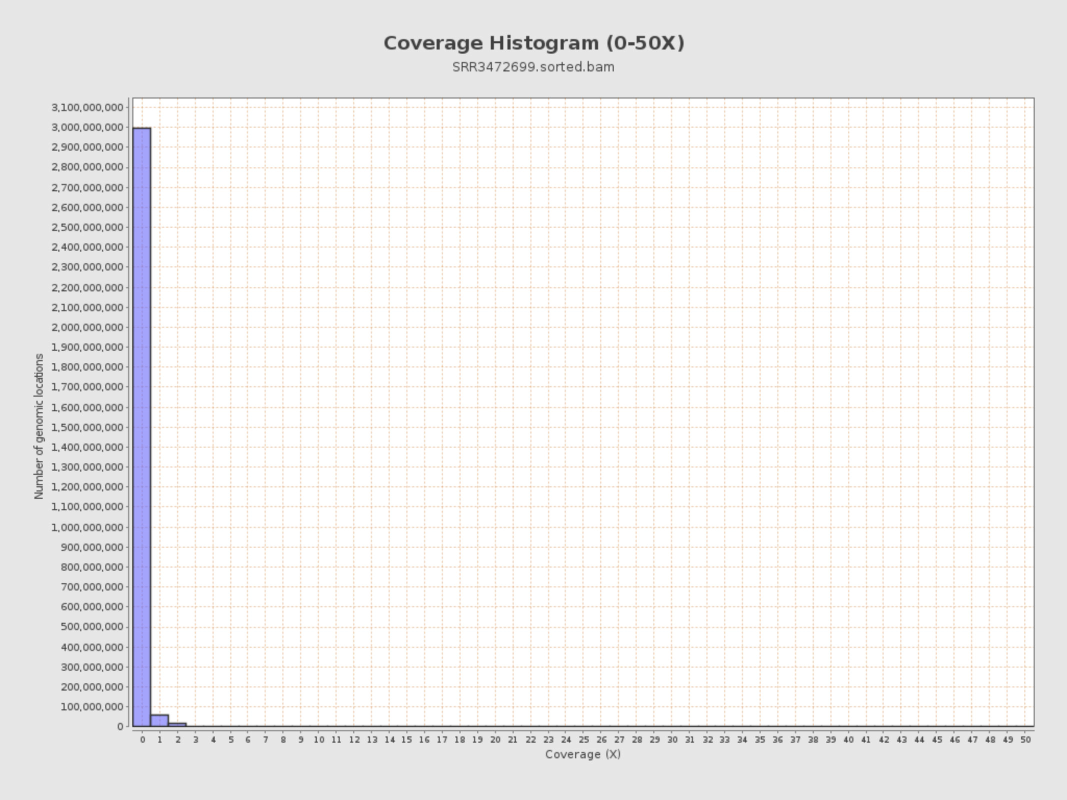
3. Results : Coverage across reference



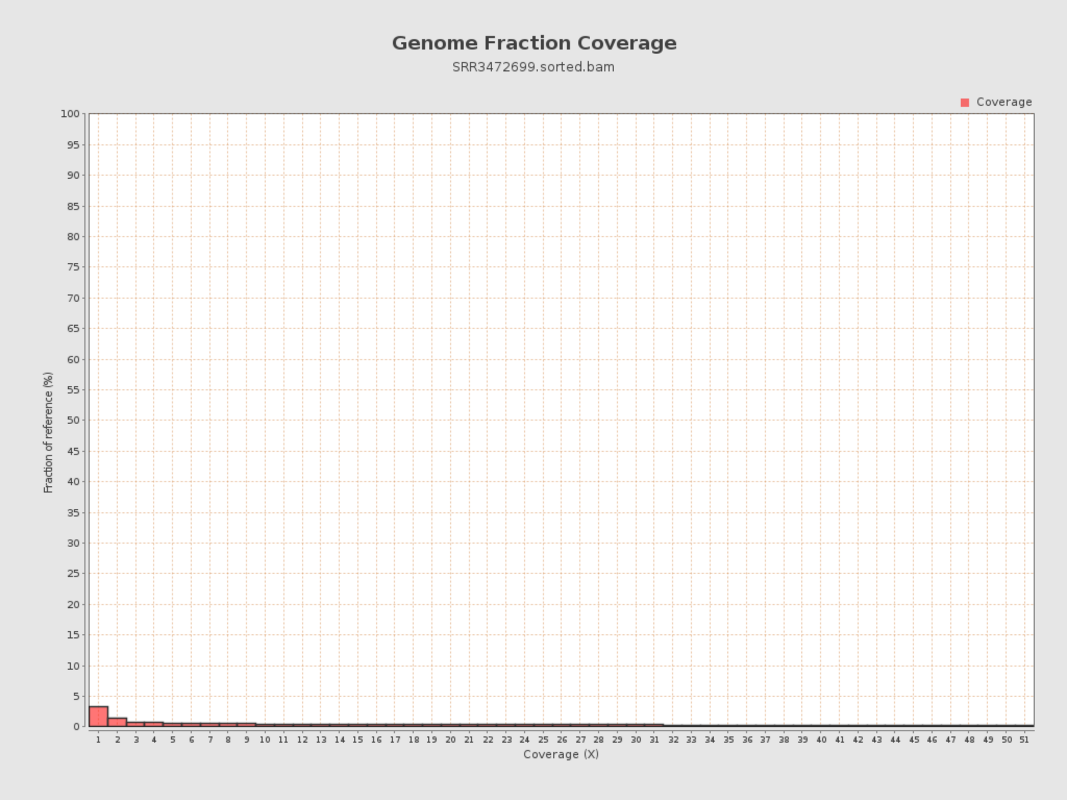
4. Results : Coverage Histogram



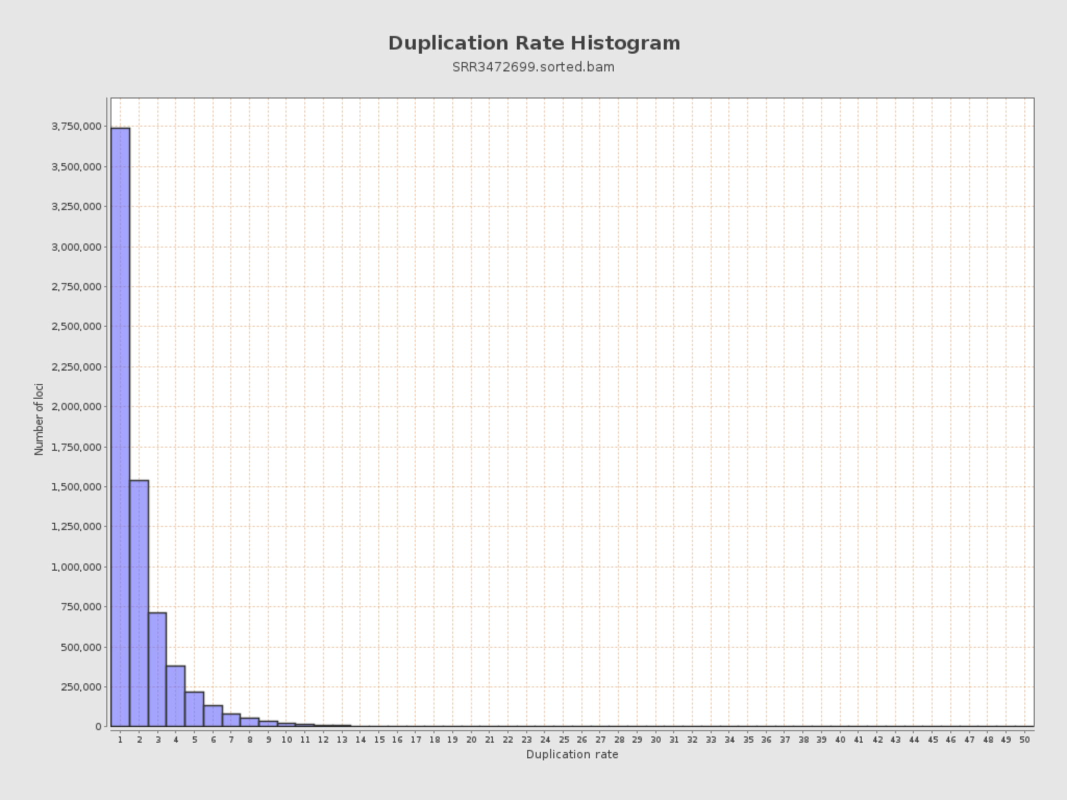
5. Results : Coverage Histogram (0-50X)



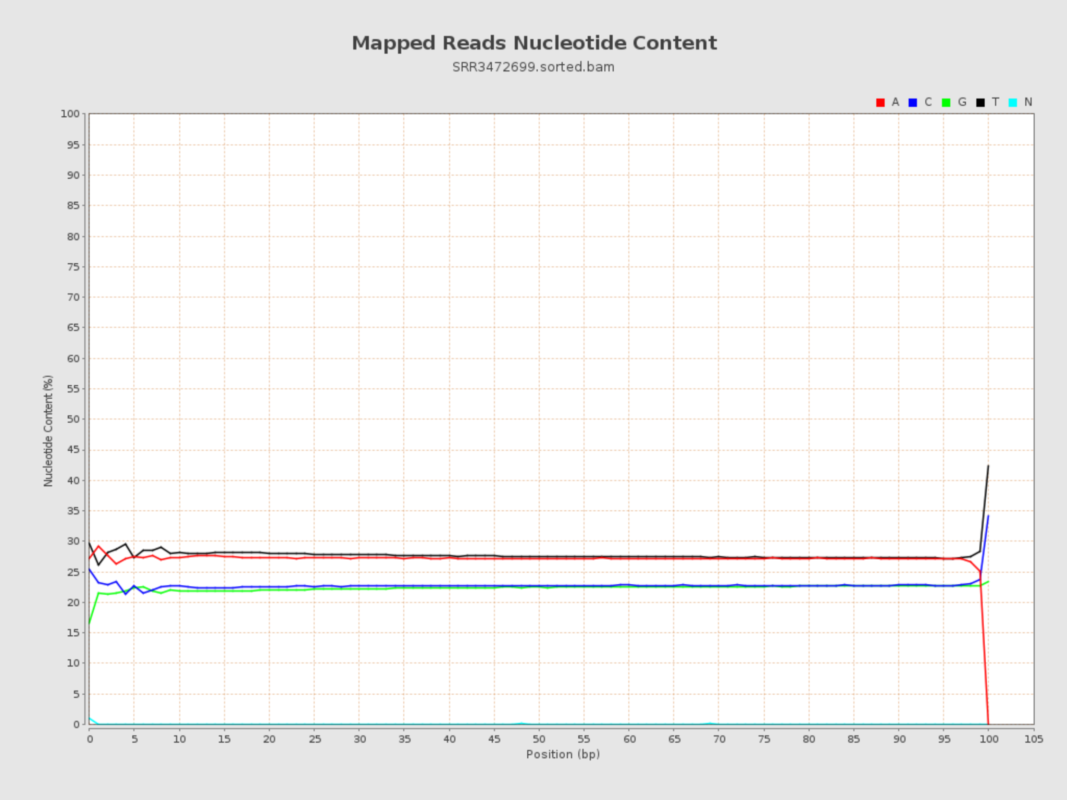
6. Results : Genome Fraction Coverage



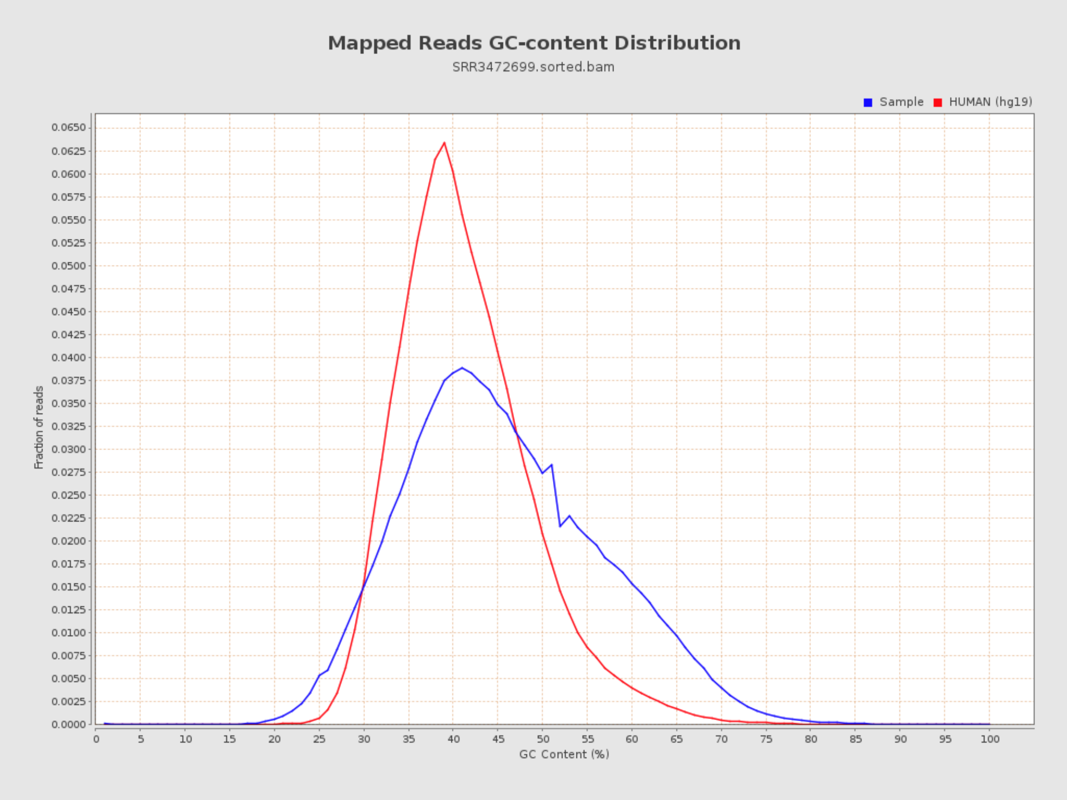
7. Results : Duplication Rate Histogram



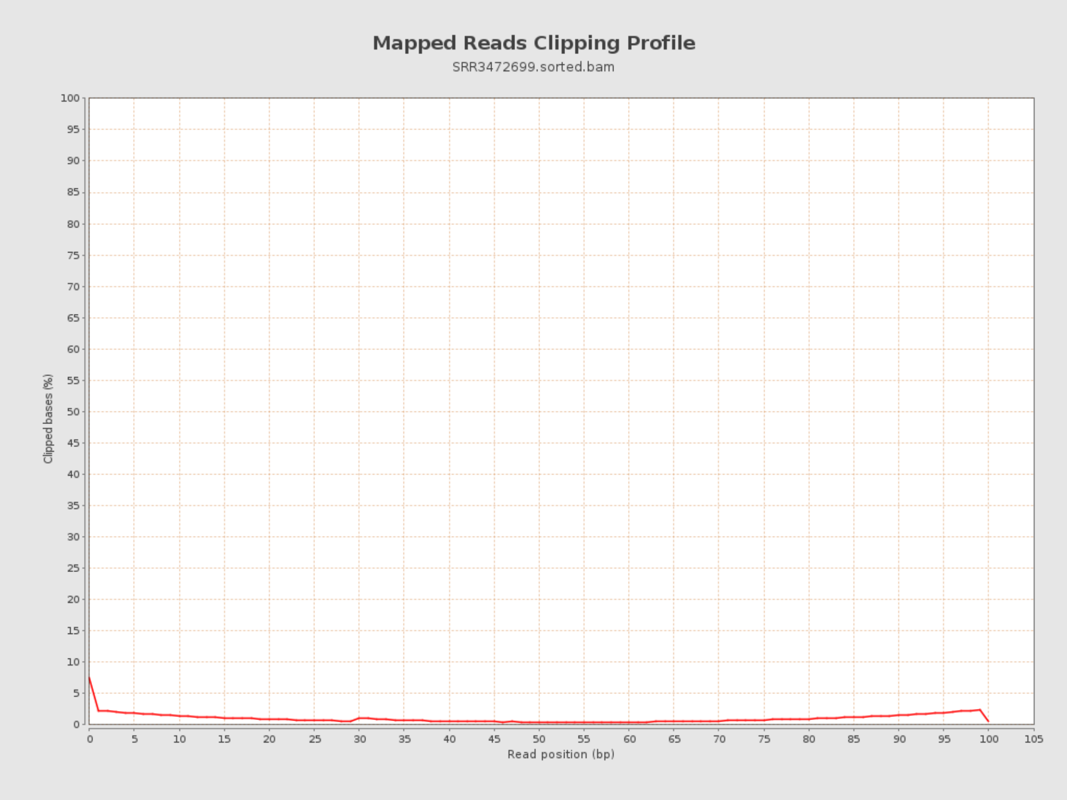
8. Results : Mapped Reads Nucleotide Content



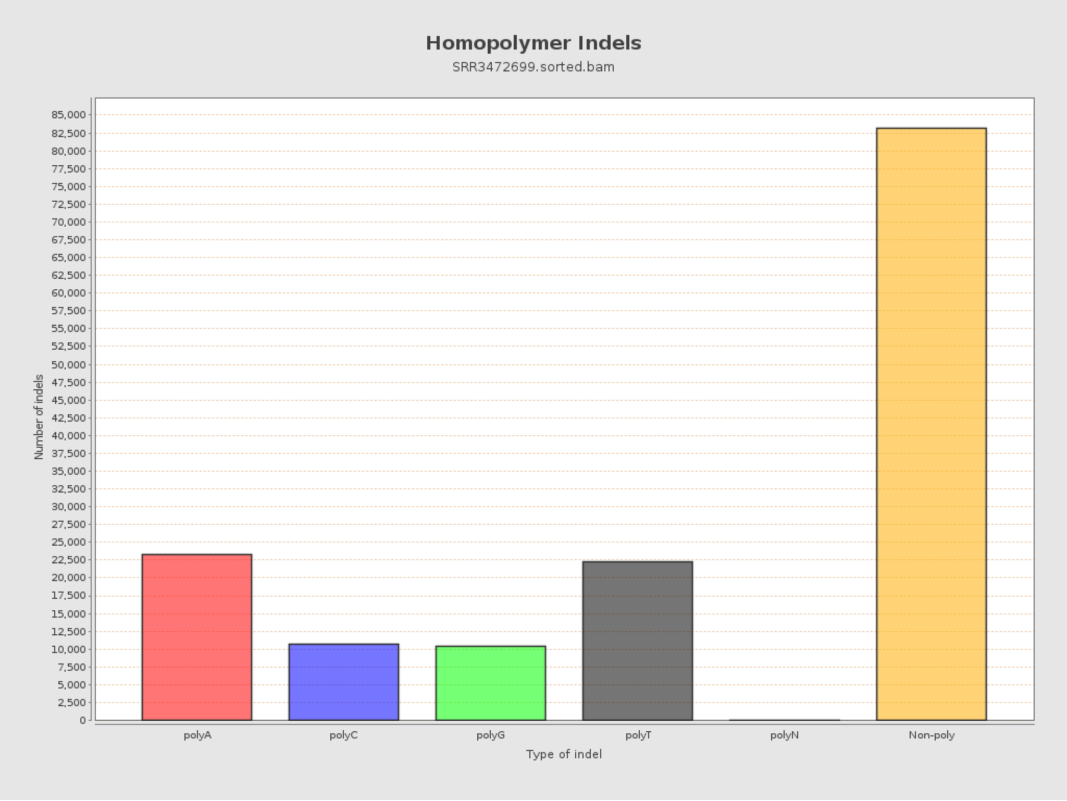
9. Results : Mapped Reads GC-content Distribution



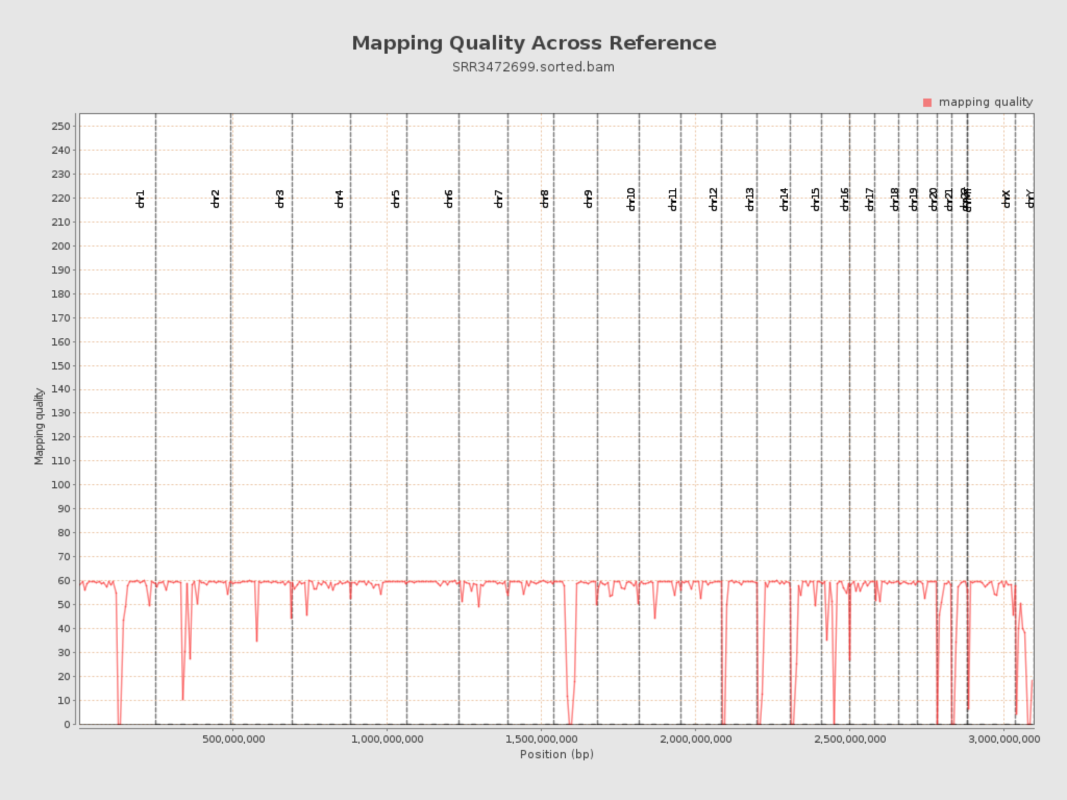
10. Results : Mapped Reads Clipping Profile



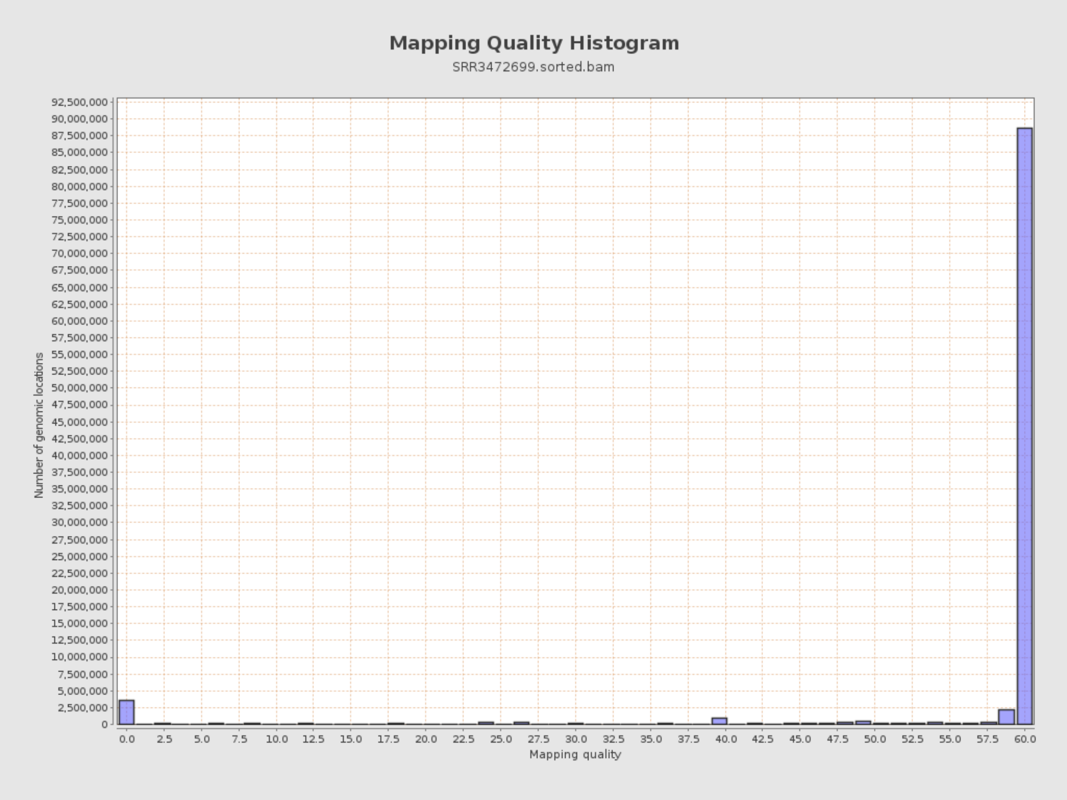
11. Results : Homopolymer Indels



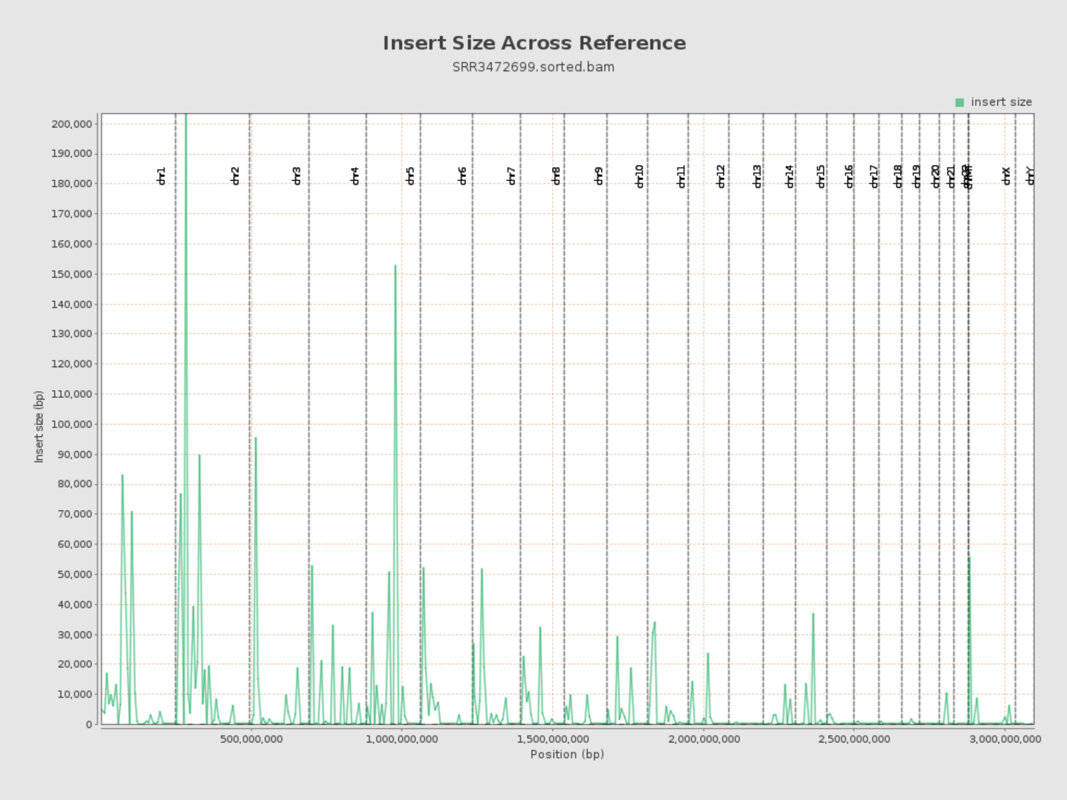
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram