Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 13:15:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617369.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_SRR617369 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617369_1.fastq.gz SRR617369_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 13:15:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617369.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,294,393 / 94.67%
Unmapped reads	1,705,607 / 5.33%
Mapped paired reads	30,294,393 / 94.67%
Mapped reads, first in pair	15,250,212 / 47.66%
Mapped reads, second in pair	15,044,181 / 47.01%
Mapped reads, both in pair	29,708,776 / 92.84%
Mapped reads, singletons	585,617 / 1.83%
Secondary alignments	0
Supplementary alignments	91,578 / 0.29%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	1,604,151 / 5.01%
Duplication rate	1.52%
Clipped reads	2,503,190 / 7.82%

2.2. ACGT Content

Number/percentage of A's	899,040,300 / 30.28%
Number/percentage of C's	589,529,757 / 19.86%
Number/percentage of T's	887,606,167 / 29.9%
Number/percentage of G's	591,510,593 / 19.92%
Number/percentage of N's	1,125,201 / 0.04%

GC Percentage	39.78%

2.3. Coverage

Mean	0.9593
Standard Deviation	9.862

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	62,800.87
Standard Deviation	2,390,941.6
P25/Median/P75	170 / 210 / 272

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	30,074,949
Insertions	300,094
Mapped reads with at least one insertion	0.96%
Deletions	364,881
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.4%

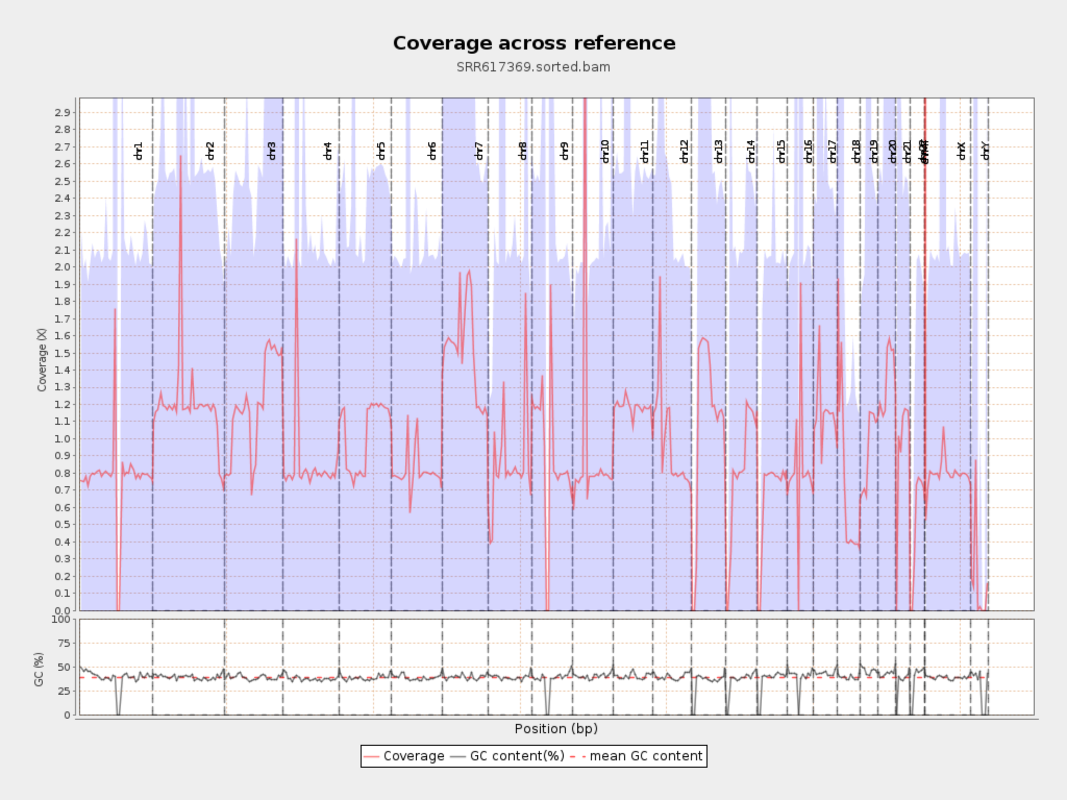
2.7. Chromosome stats

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

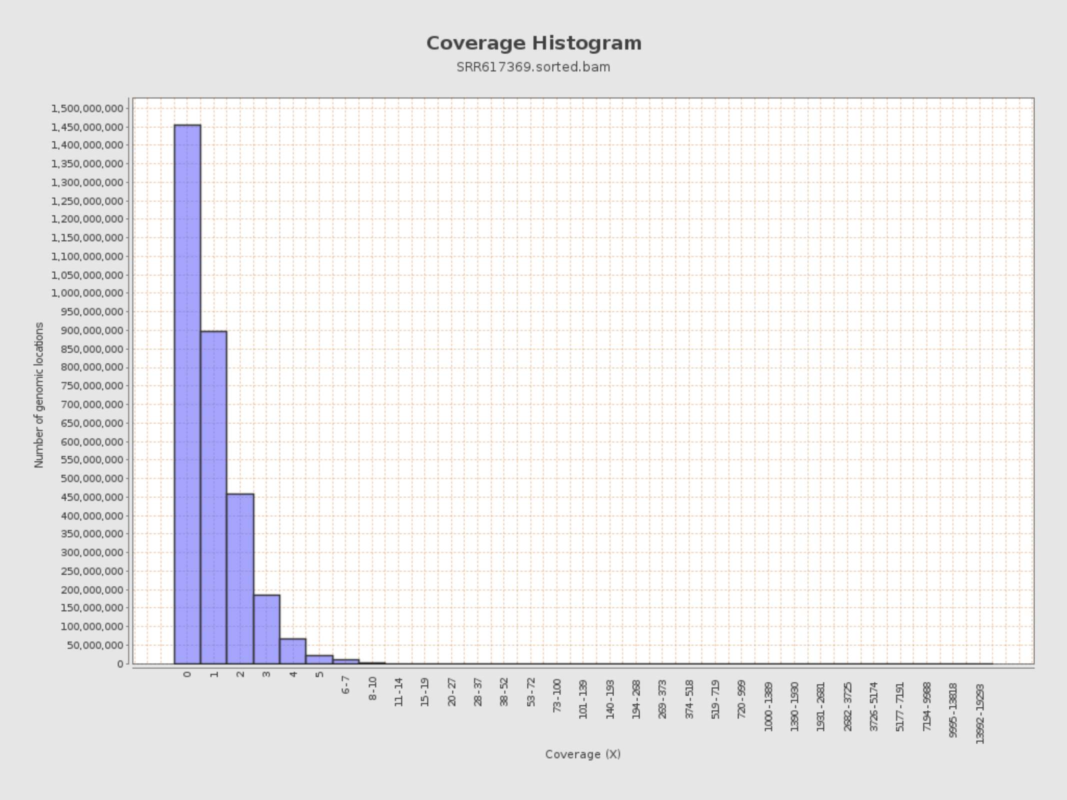
		bases	coverage	deviation
chr1	249250621	192810050	0.7736	20.0047
chr2	243199373	293129722	1.2053	8.8684
chr3	198022430	235917677	1.1914	1.4976
chr4	191154276	162391816	0.8495	9.3831
chr5	180915260	185872203	1.0274	1.4808
chr6	171115067	139488950	0.8152	3.702
chr7	159138663	240928110	1.514	10.9901
chr8	146364022	124867905	0.8531	7.7619
chr9	141213431	125266873	0.8871	15.0498
chr10	135534747	125027756	0.9225	20.2695
chr11	135006516	159460818	1.1811	5.5632
chr12	133851895	130888307	0.9779	1.3764
chr13	115169878	129241352	1.1222	1.3241
chr14	107349540	86053448	0.8016	1.3799
chr15	102531392	66669031	0.6502	1.0738
chr16	90354753	74797959	0.8278	7.9288
chr17	81195210	92937133	1.1446	7.222
chr18	78077248	53843694	0.6896	15.5757
chr19	59128983	55344028	0.936	9.7551
chr20	63025520	85247642	1.3526	2.4337
chr21	48129895	47130232	0.9792	3.1864
chr22	51304566	26499056	0.5165	0.9354
chrMT	16571	2027714	122.3652	21.9591
chrX	155270560	123622727	0.7962	3.0669

chrY	59373566	10226888	0.1722	8.4518

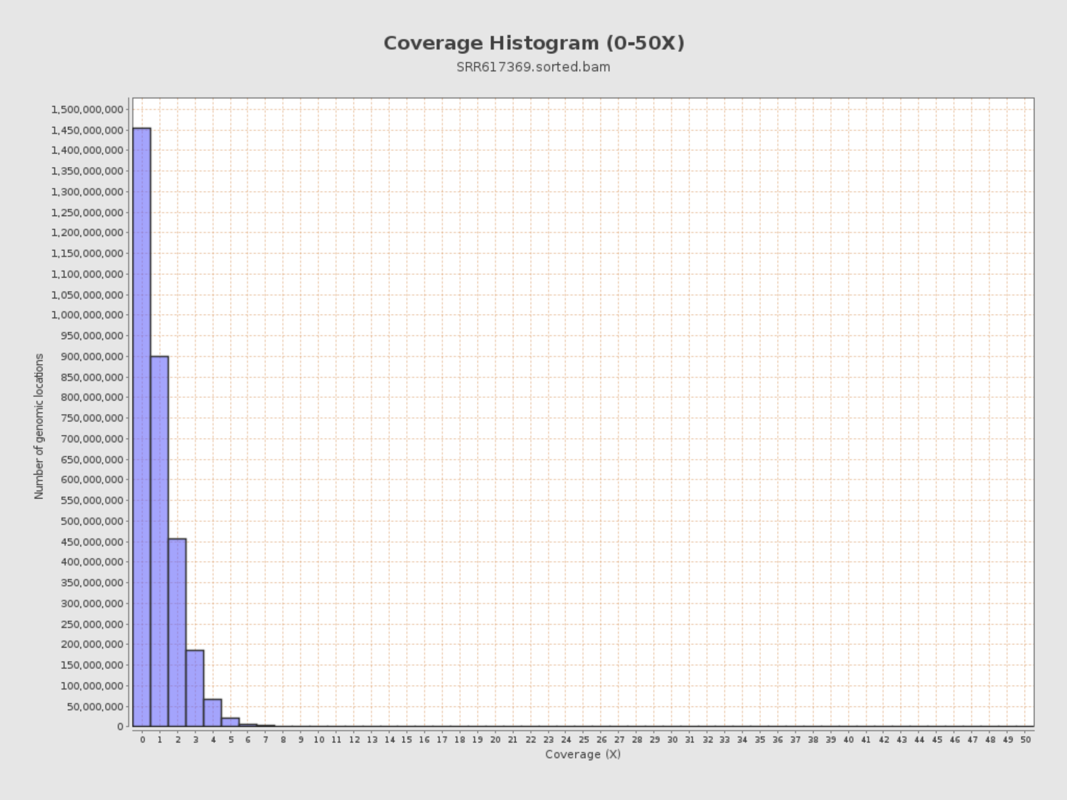
3. Results : Coverage across reference



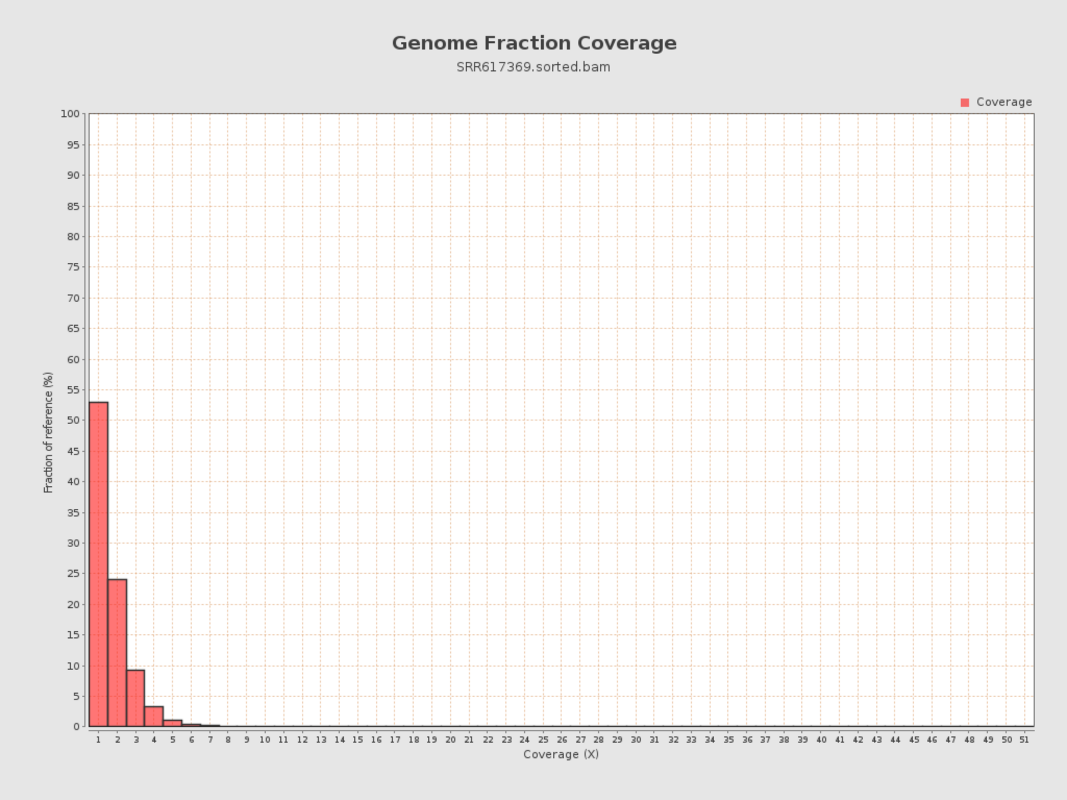
4. Results : Coverage Histogram



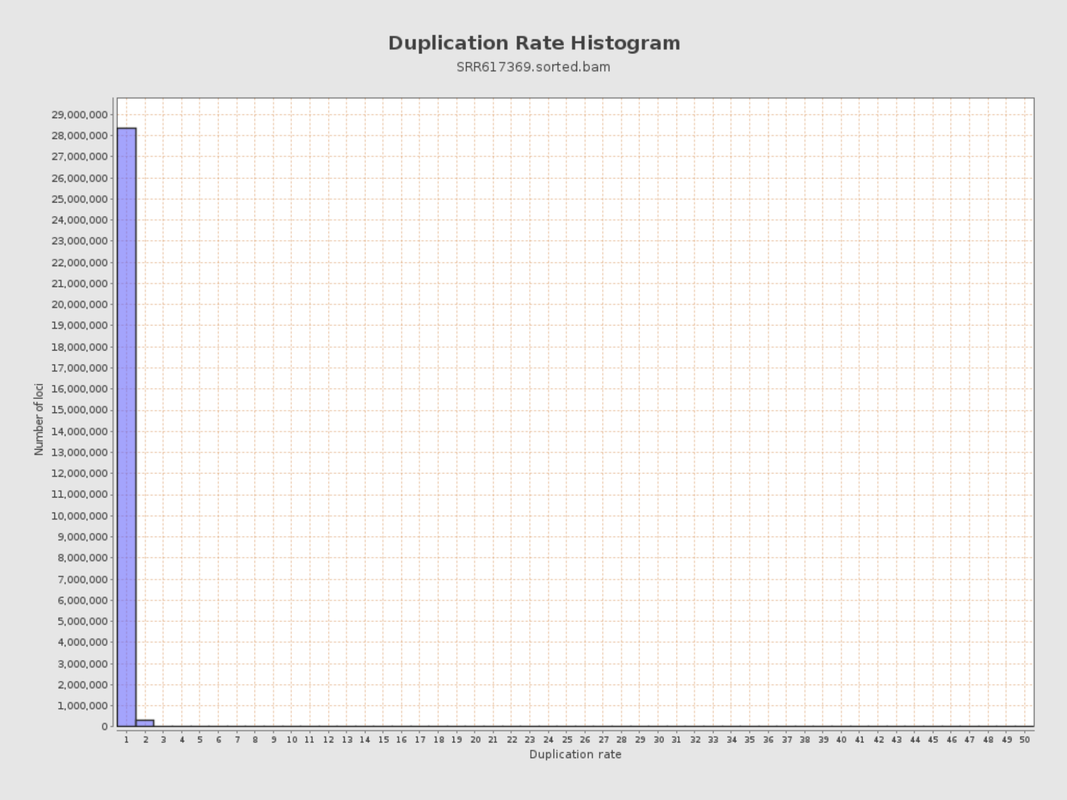
5. Results : Coverage Histogram (0-50X)



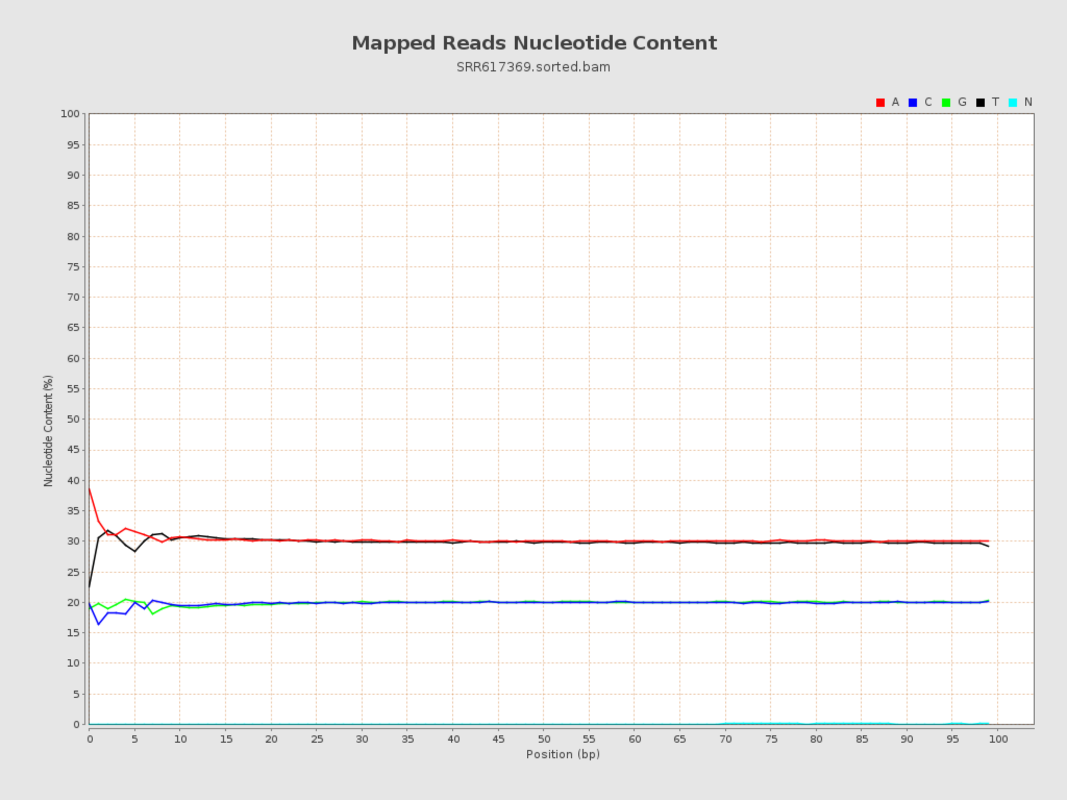
6. Results : Genome Fraction Coverage



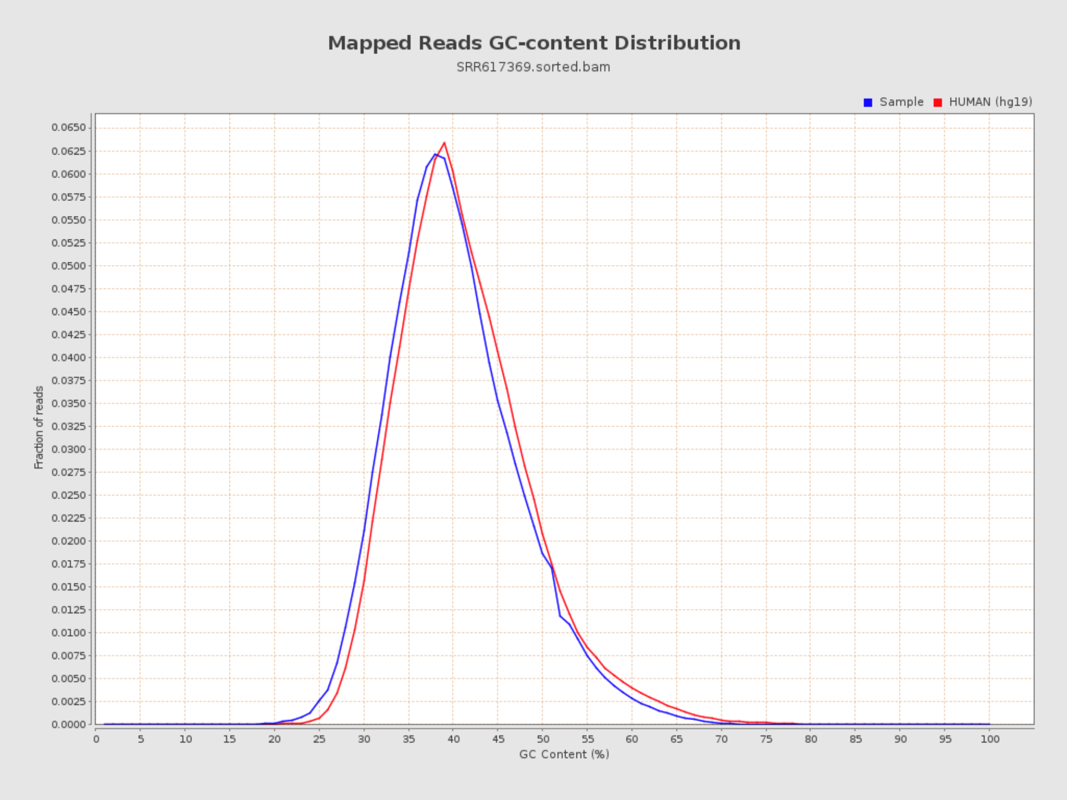
7. Results : Duplication Rate Histogram



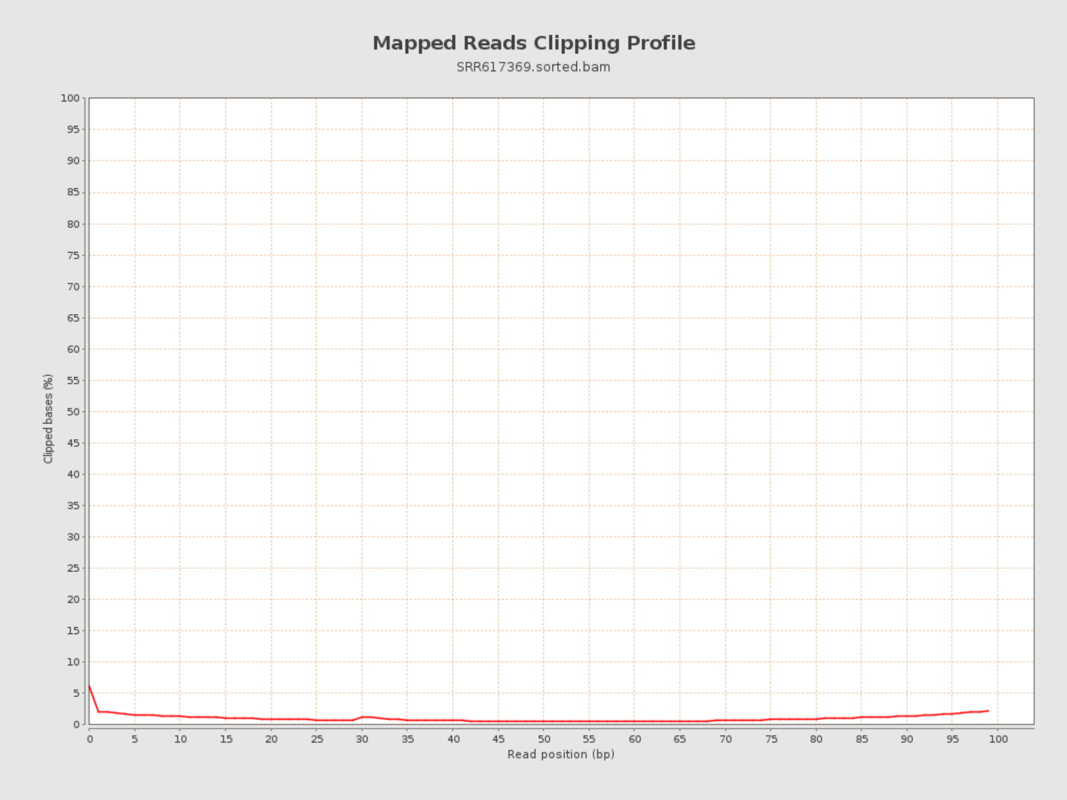
8. Results : Mapped Reads Nucleotide Content



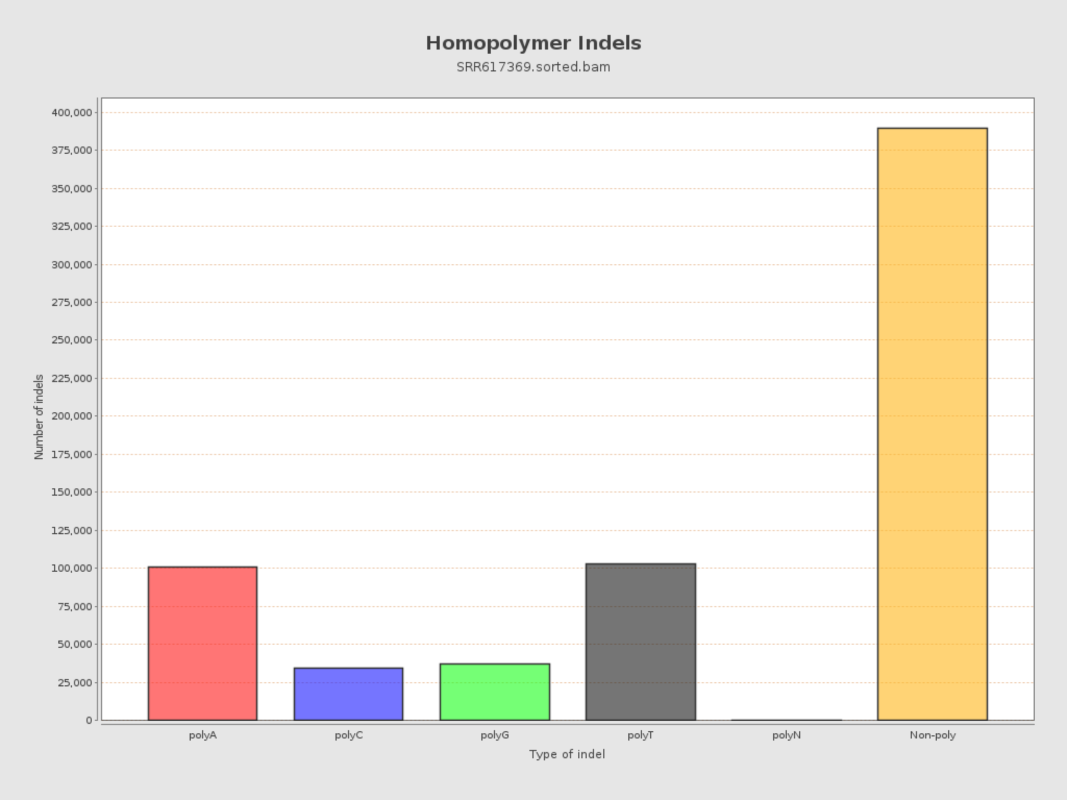
9. Results : Mapped Reads GC-content Distribution



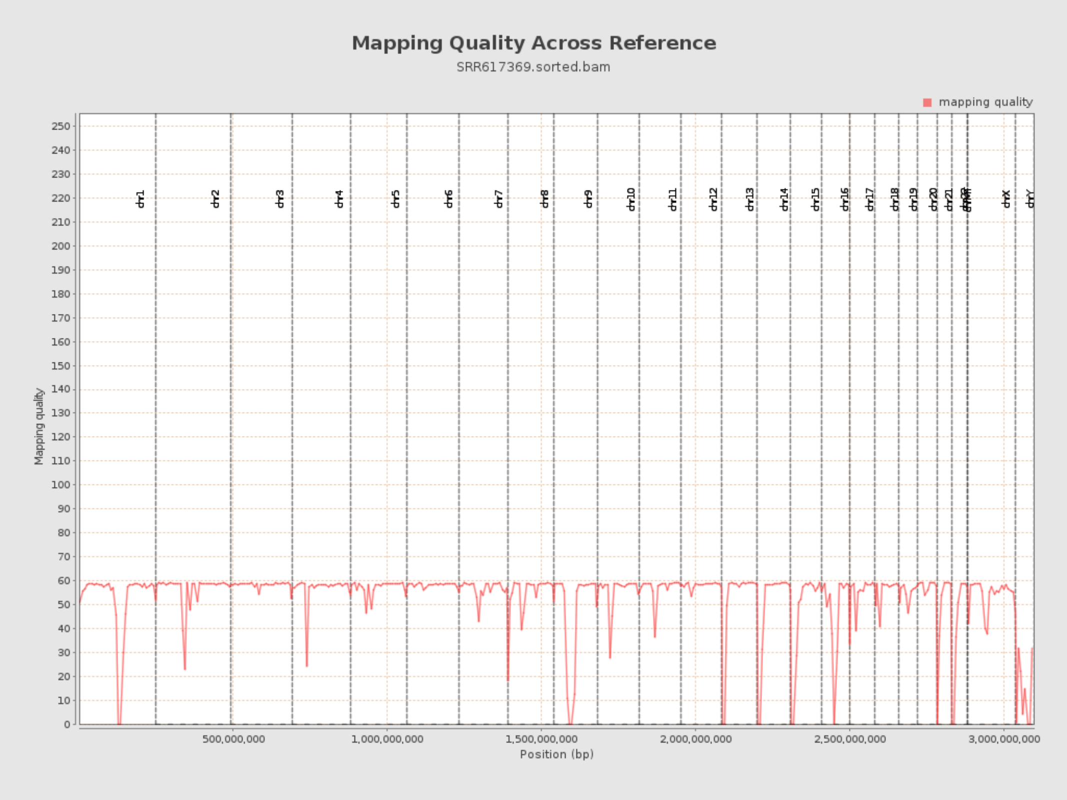
10. Results : Mapped Reads Clipping Profile



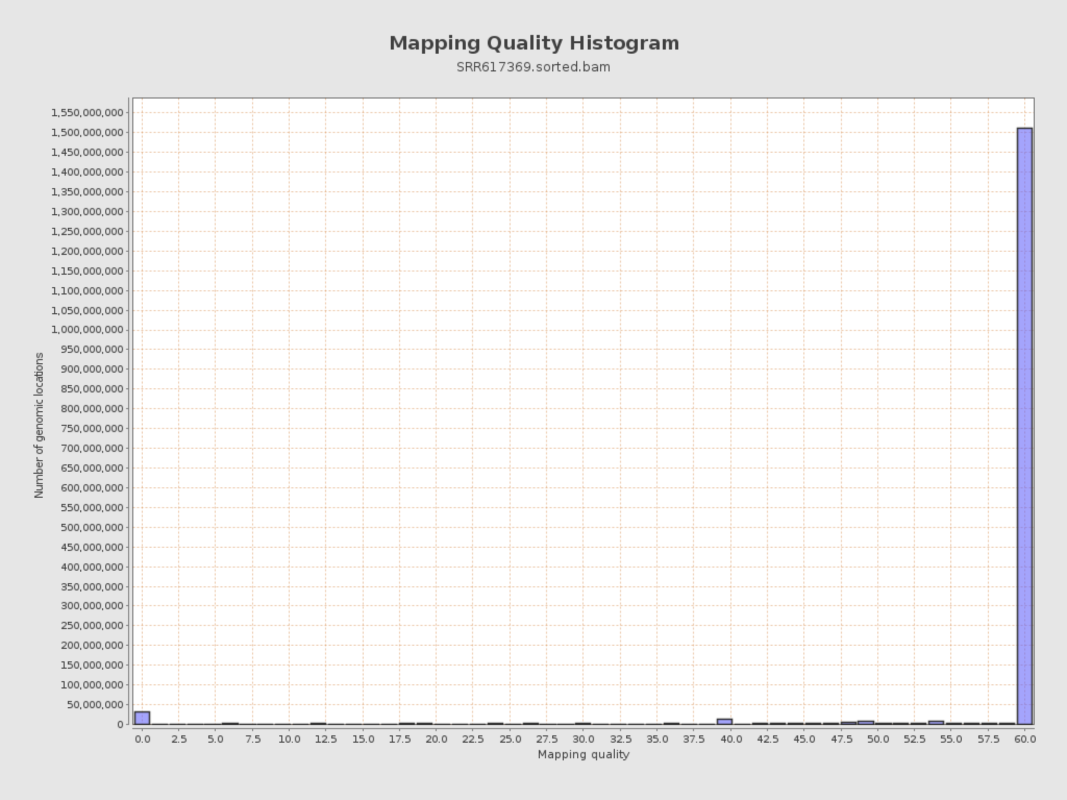
11. Results : Homopolymer Indels



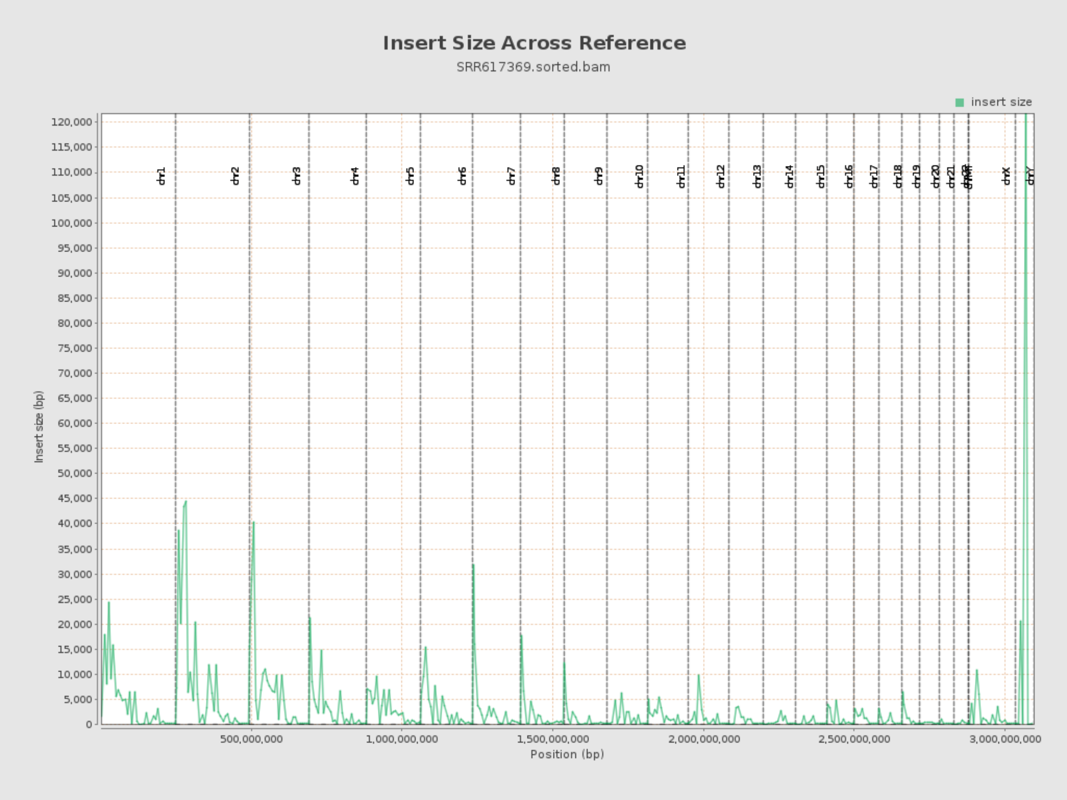
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram