Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 12:25:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617368.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_SRR617368 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617368_1.fastq.gz SRR617368_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 12:25:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617368.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,695,589 / 95.92%
Unmapped reads	1,304,411 / 4.08%
Mapped paired reads	30,695,589 / 95.92%
Mapped reads, first in pair	15,447,569 / 48.27%
Mapped reads, second in pair	15,248,020 / 47.65%
Mapped reads, both in pair	30,153,118 / 94.23%
Mapped reads, singletons	542,471 / 1.7%
Secondary alignments	0
Supplementary alignments	98,476 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	1,635,871 / 5.11%
Duplication rate	1.53%
Clipped reads	2,366,379 / 7.39%

2.2. ACGT Content

Number/percentage of A's	909,411,139 / 30.2%
Number/percentage of C's	599,719,514 / 19.91%
Number/percentage of T's	899,367,556 / 29.86%
Number/percentage of G's	601,769,898 / 19.98%
Number/percentage of N's	1,182,868 / 0.04%

GC Percentage	39.9%

2.3. Coverage

Mean	0.9731
Standard Deviation	9.9156

2.4. Mapping Quality

Mean Mapping Quality	53.44

2.5. Insert size

Mean	71,128.35
Standard Deviation	2,553,597.96
P25/Median/P75	173 / 215 / 281

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	26,000,366
Insertions	308,385
Mapped reads with at least one insertion	0.97%
Deletions	374,971
Mapped reads with at least one deletion	1.18%
Homopolymer indels	41.39%

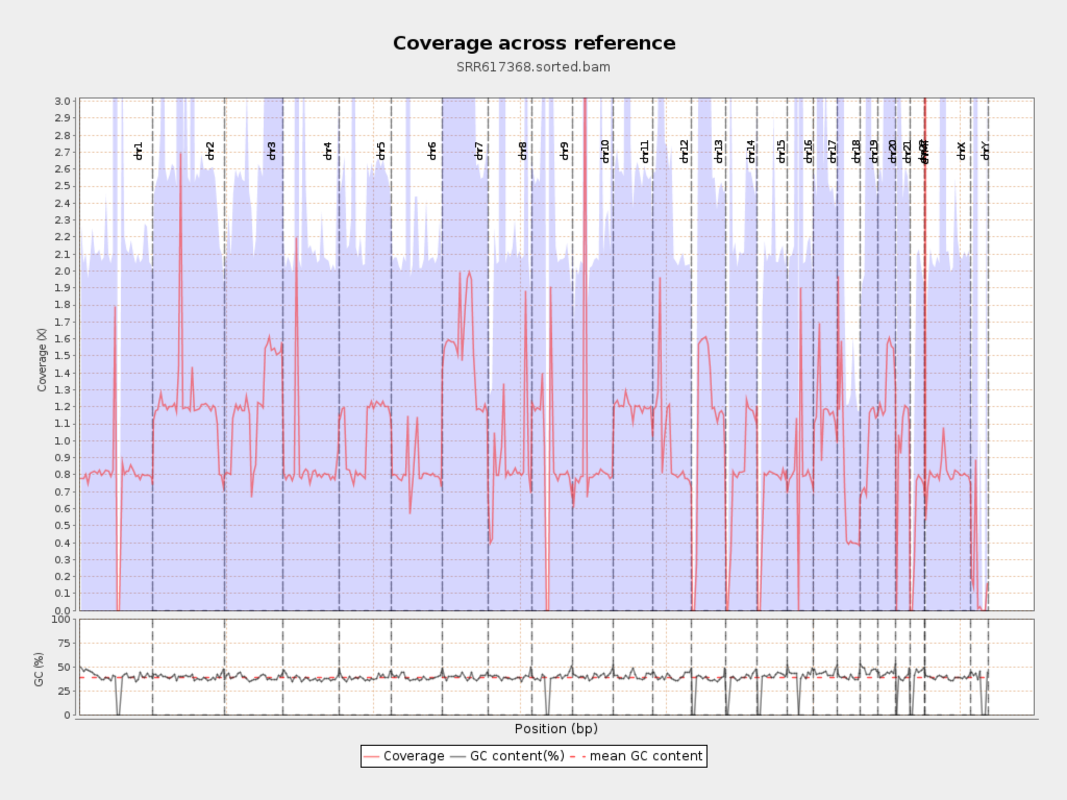
2.7. Chromosome stats

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

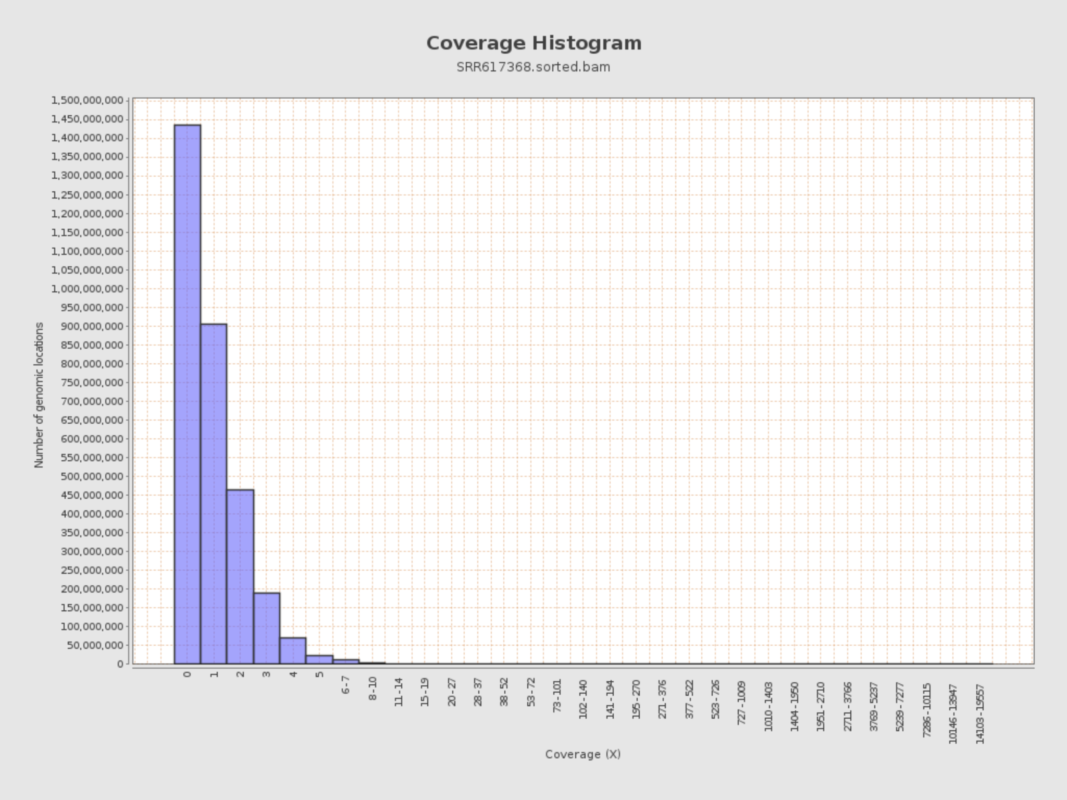
		bases	coverage	deviation
chr1	249250621	196057906	0.7866	20.0368
chr2	243199373	297173170	1.2219	9.0107
chr3	198022430	239127446	1.2076	1.492
chr4	191154276	164007091	0.858	9.6533
chr5	180915260	188584258	1.0424	1.4794
chr6	171115067	140592990	0.8216	3.7301
chr7	159138663	244062408	1.5336	10.9539
chr8	146364022	126581987	0.8648	7.7087
chr9	141213431	126786778	0.8978	15.2879
chr10	135534747	126904935	0.9363	20.2754
chr11	135006516	161734652	1.198	5.6638
chr12	133851895	132839589	0.9924	1.4056
chr13	115169878	130707576	1.1349	1.3409
chr14	107349540	87207088	0.8124	1.3976
chr15	102531392	67836407	0.6616	1.1037
chr16	90354753	76205592	0.8434	7.8661
chr17	81195210	95039614	1.1705	7.3183
chr18	78077248	54534861	0.6985	15.6914
chr19	59128983	56897989	0.9623	9.588
chr20	63025520	87061261	1.3814	2.4659
chr21	48129895	47963944	0.9966	3.3028
chr22	51304566	27310128	0.5323	0.9434
chrMT	16571	2112083	127.4566	19.5866
chrX	155270560	124615839	0.8026	3.054

chrY	59373566	10411231	0.1754	8.6143

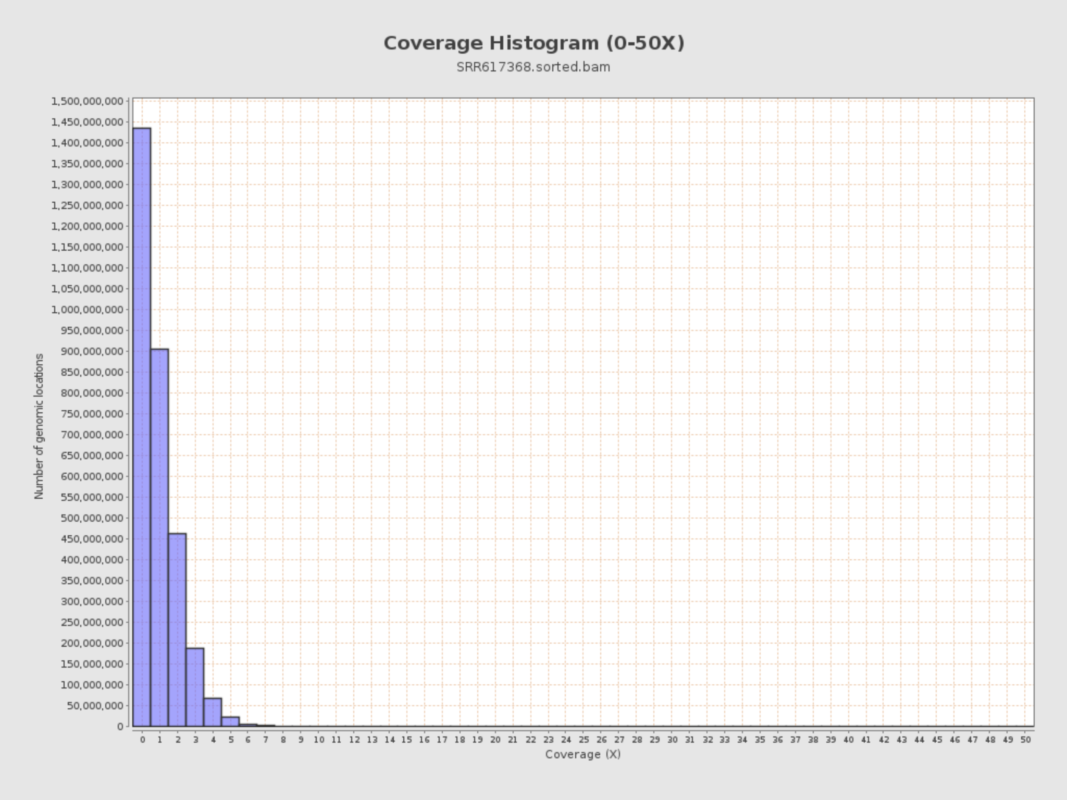
3. Results : Coverage across reference



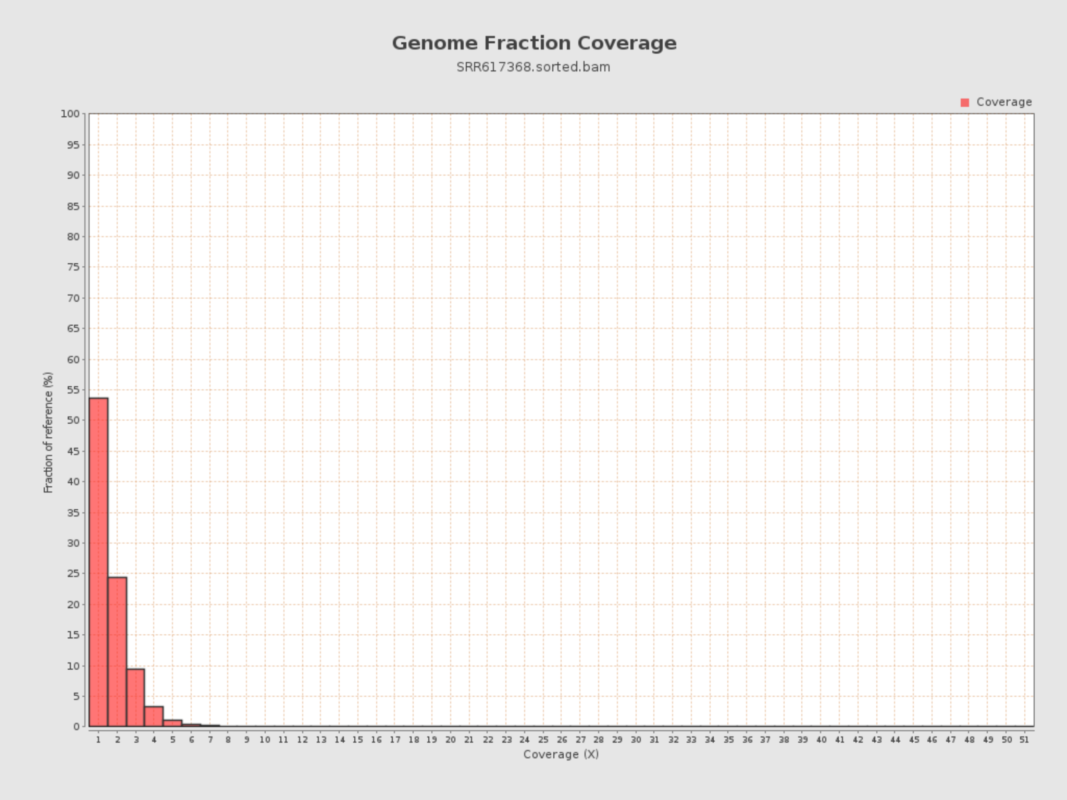
4. Results : Coverage Histogram



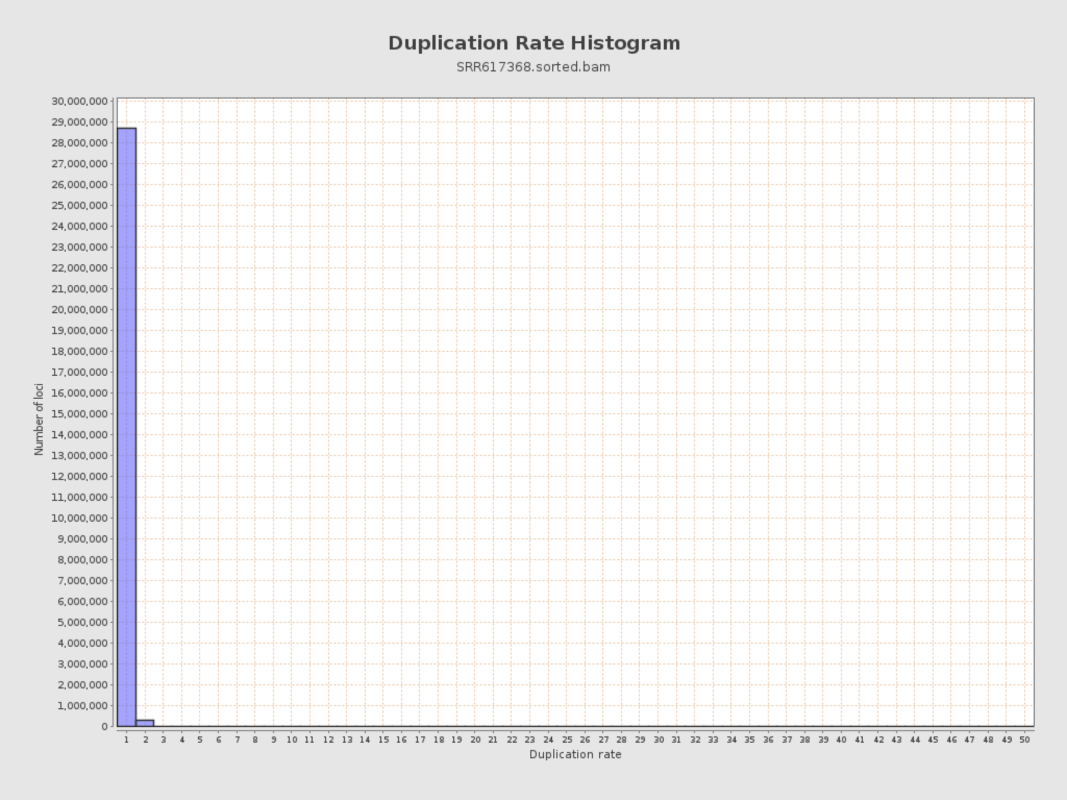
5. Results : Coverage Histogram (0-50X)



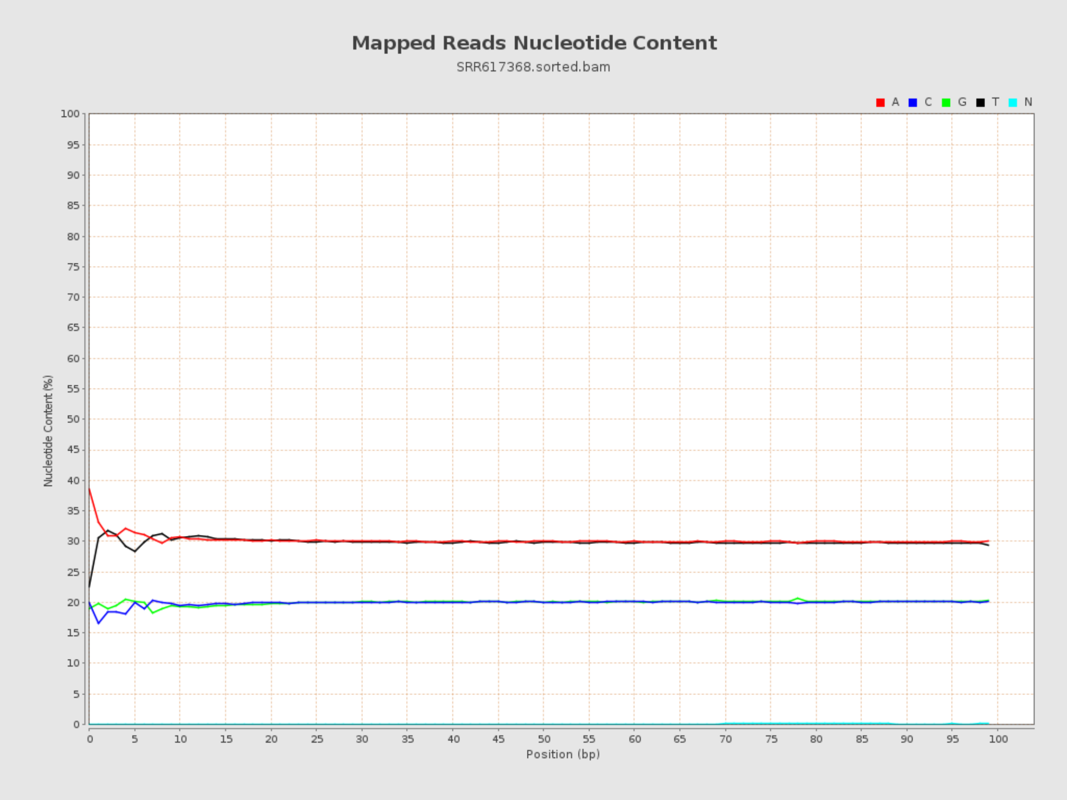
6. Results : Genome Fraction Coverage



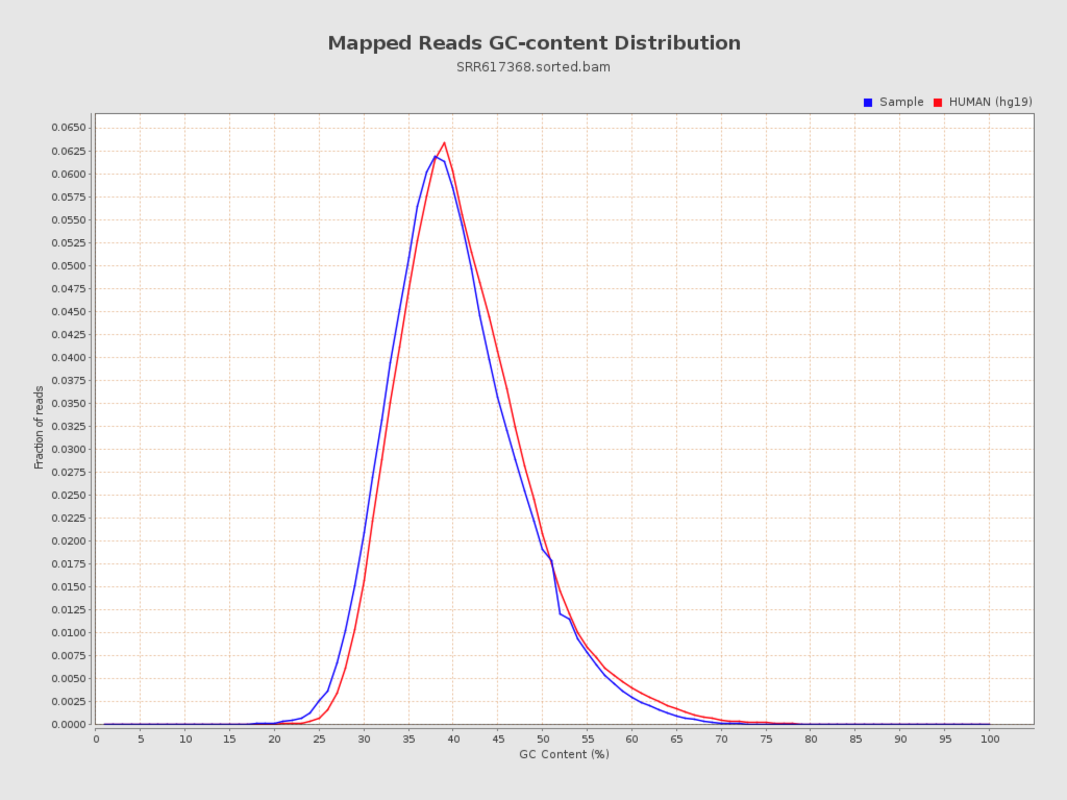
7. Results : Duplication Rate Histogram



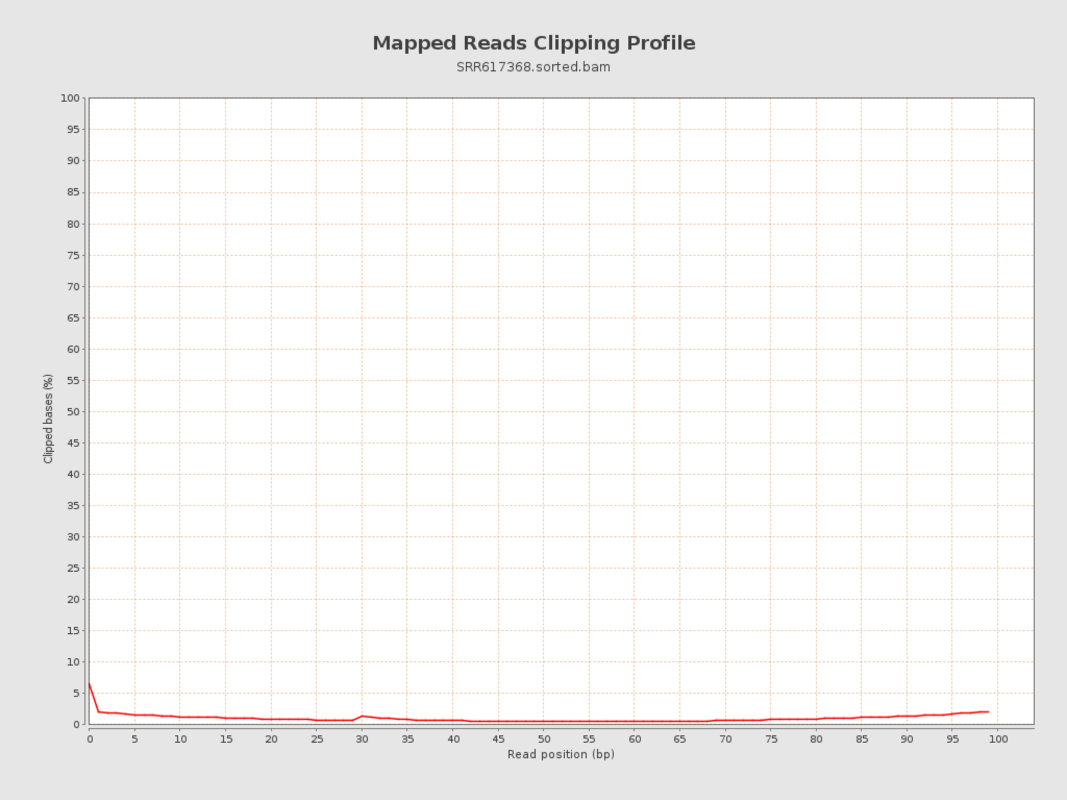
8. Results : Mapped Reads Nucleotide Content



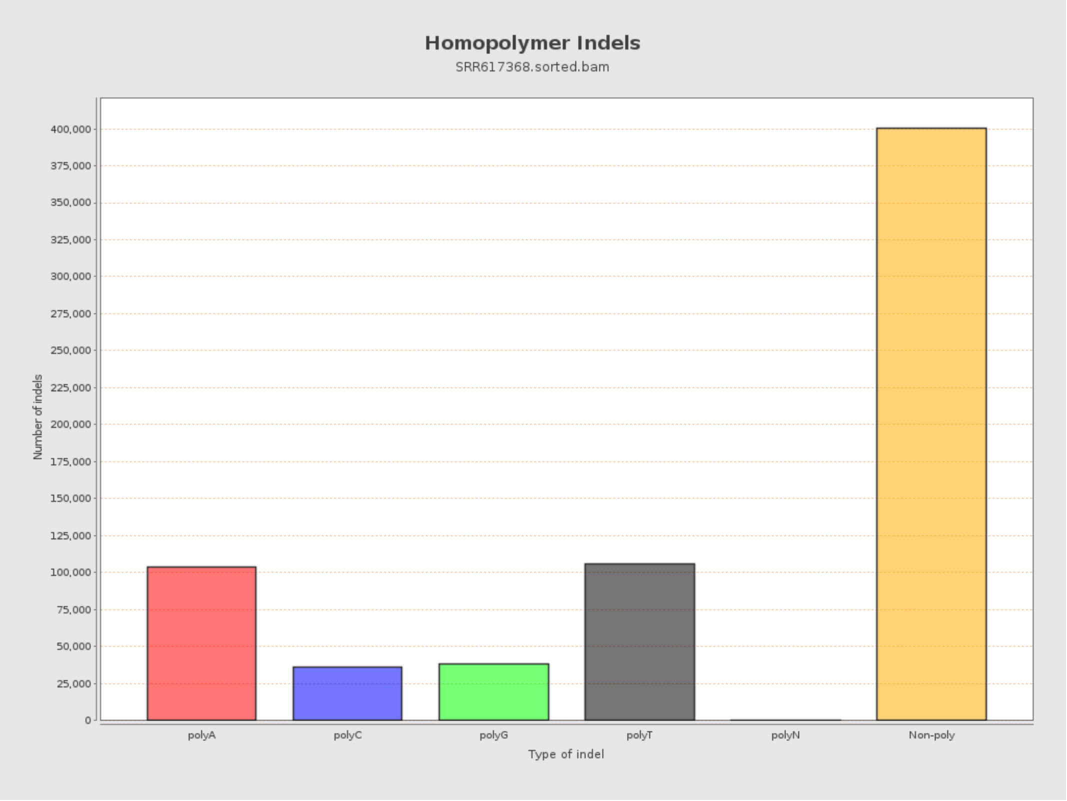
9. Results : Mapped Reads GC-content Distribution



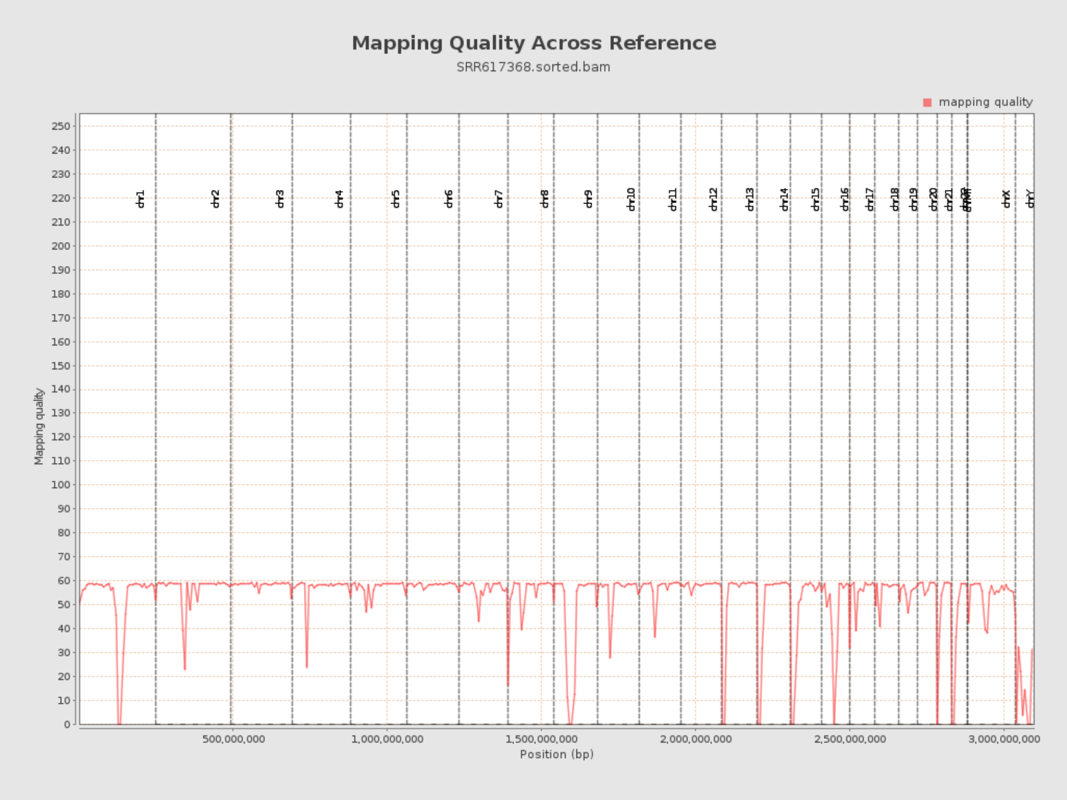
10. Results : Mapped Reads Clipping Profile



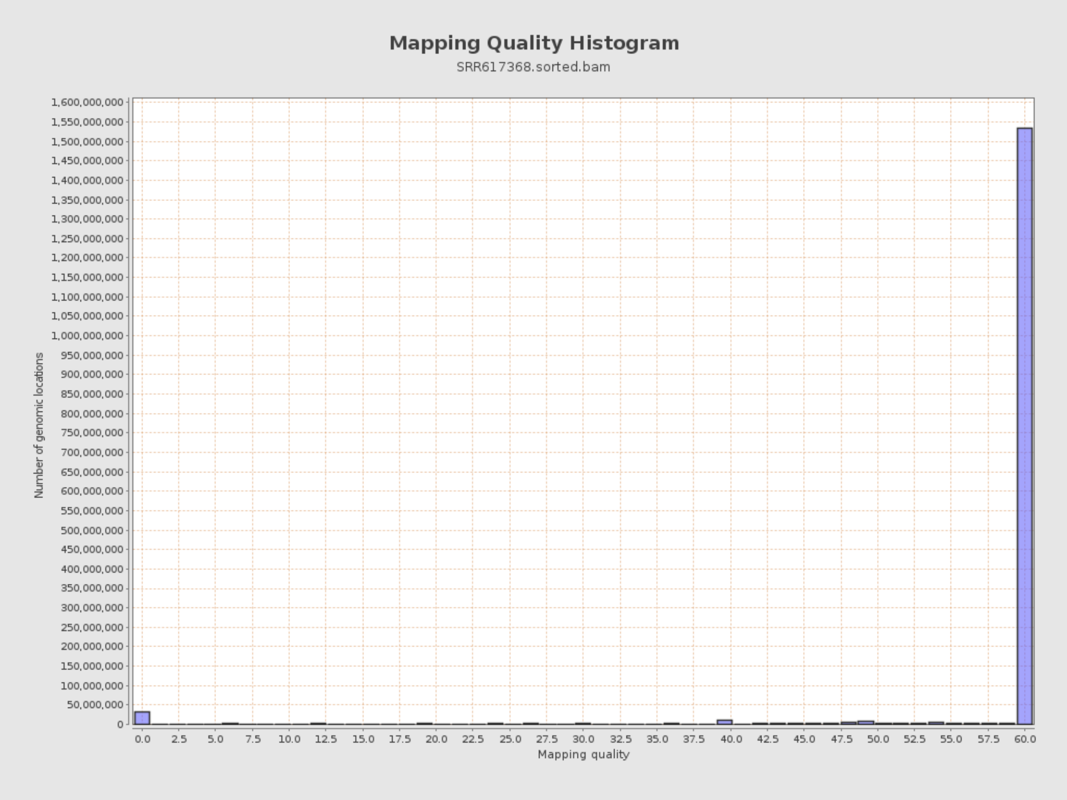
11. Results : Homopolymer Indels



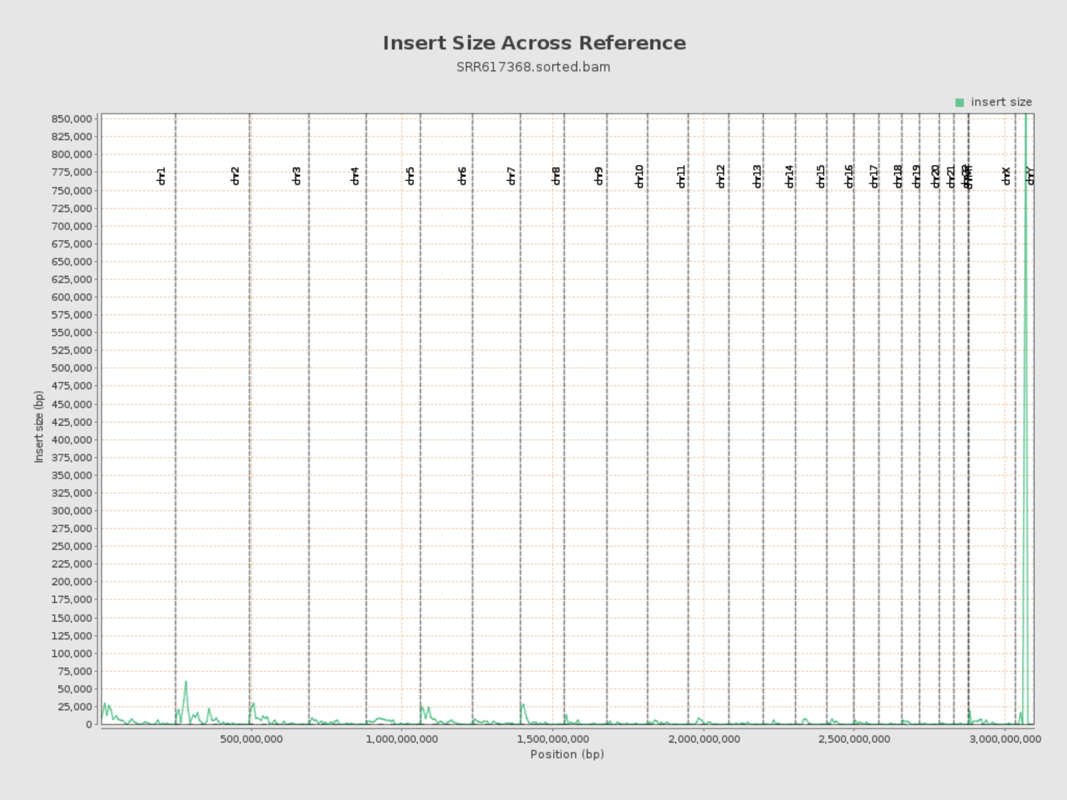
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram