Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 04:55:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617386.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_SRR617386 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617386_1.fastq.gz SRR617386_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 04:55:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617386.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,287,829 / 94.65%
Unmapped reads	1,712,171 / 5.35%
Mapped paired reads	30,287,829 / 94.65%
Mapped reads, first in pair	15,232,158 / 47.6%
Mapped reads, second in pair	15,055,671 / 47.05%
Mapped reads, both in pair	29,724,184 / 92.89%
Mapped reads, singletons	563,645 / 1.76%
Secondary alignments	0
Supplementary alignments	94,813 / 0.3%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	1,614,376 / 5.04%
Duplication rate	1.52%
Clipped reads	2,541,190 / 7.94%

2.2. ACGT Content

Number/percentage of A's	899,586,120 / 30.33%
Number/percentage of C's	588,047,009 / 19.82%
Number/percentage of T's	887,897,836 / 29.93%
Number/percentage of G's	589,931,706 / 19.89%
Number/percentage of N's	793,654 / 0.03%

GC Percentage	39.71%

2.3. Coverage

Mean	0.9585
Standard Deviation	9.883

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	64,306.98
Standard Deviation	2,419,057.36
P25/Median/P75	171 / 211 / 273

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	29,220,417
Insertions	301,066
Mapped reads with at least one insertion	0.96%
Deletions	365,100
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.27%

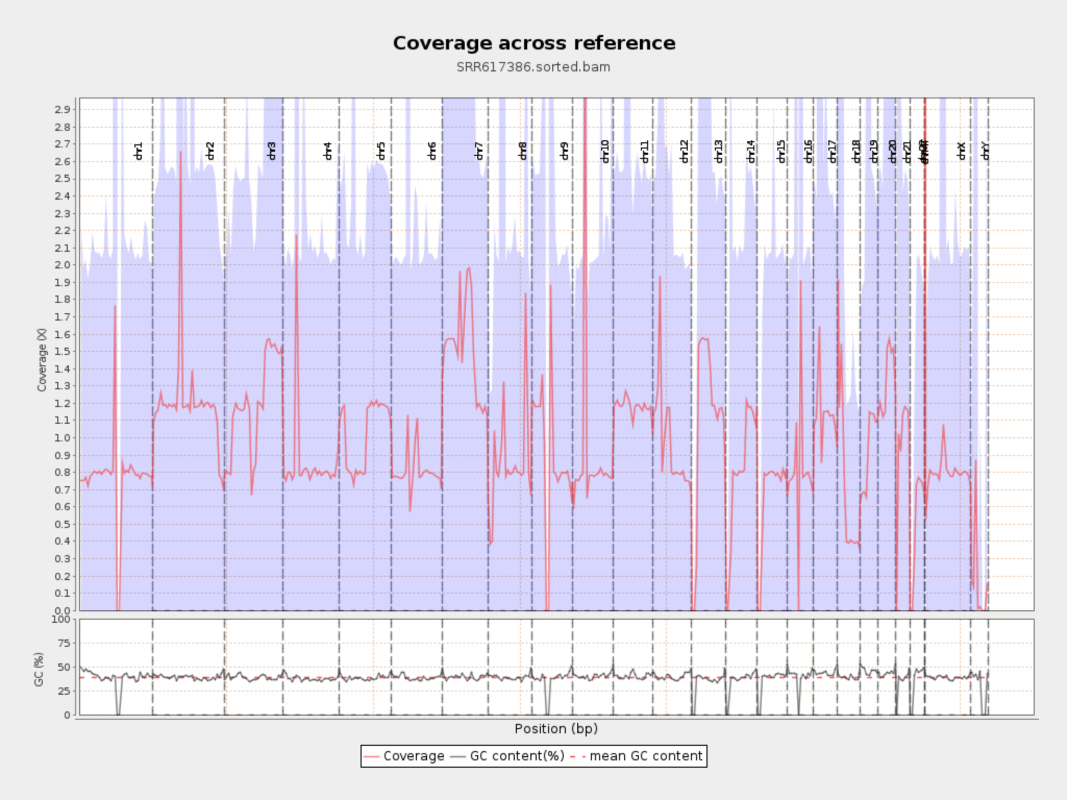
2.7. Chromosome stats

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

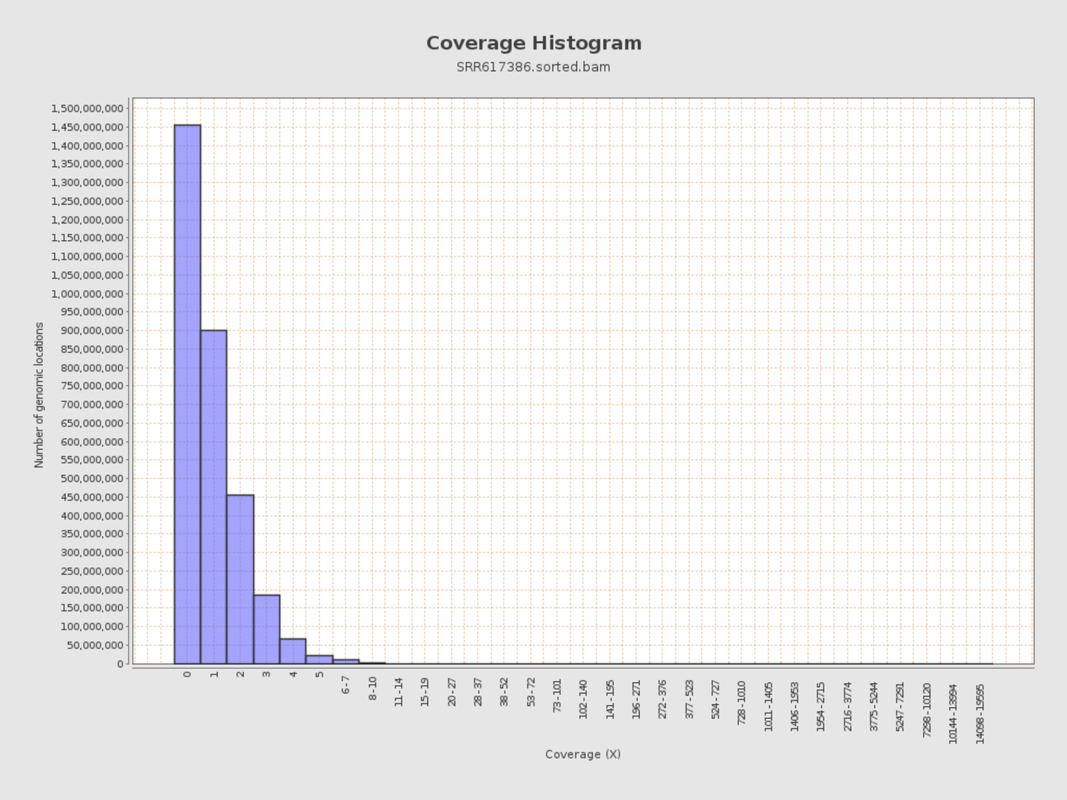
		bases	coverage	deviation
chr1	249250621	192722928	0.7732	20.1023
chr2	243199373	293015021	1.2048	8.945
chr3	198022430	236273888	1.1932	1.4829
chr4	191154276	162925148	0.8523	9.4329
chr5	180915260	186127950	1.0288	1.468
chr6	171115067	139091862	0.8129	3.6908
chr7	159138663	240804426	1.5132	10.8656
chr8	146364022	124977197	0.8539	7.7592
chr9	141213431	125048738	0.8855	15.0731
chr10	135534747	125292992	0.9244	20.3871
chr11	135006516	159270807	1.1797	5.7064
chr12	133851895	130651779	0.9761	1.4044
chr13	115169878	129233796	1.1221	1.3358
chr14	107349540	85774454	0.799	1.3747
chr15	102531392	66777698	0.6513	1.1008
chr16	90354753	74283599	0.8221	7.9527
chr17	81195210	92348658	1.1374	7.1309
chr18	78077248	53646213	0.6871	15.3475
chr19	59128983	54801203	0.9268	9.6354
chr20	63025520	84793792	1.3454	2.4569
chr21	48129895	47103761	0.9787	3.2083
chr22	51304566	26285926	0.5124	0.9274
chrMT	16571	2011264	121.3725	21.625
chrX	155270560	123706962	0.7967	3.097

chrY	59373566	10167061	0.1712	8.4595

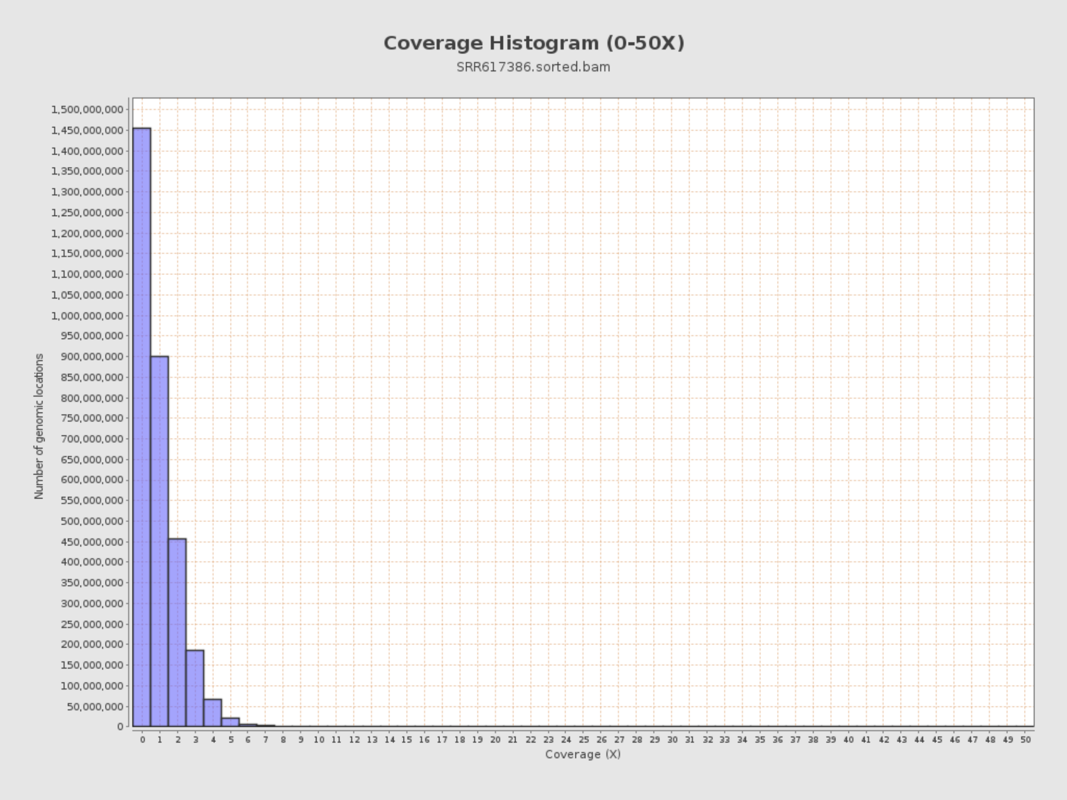
3. Results : Coverage across reference



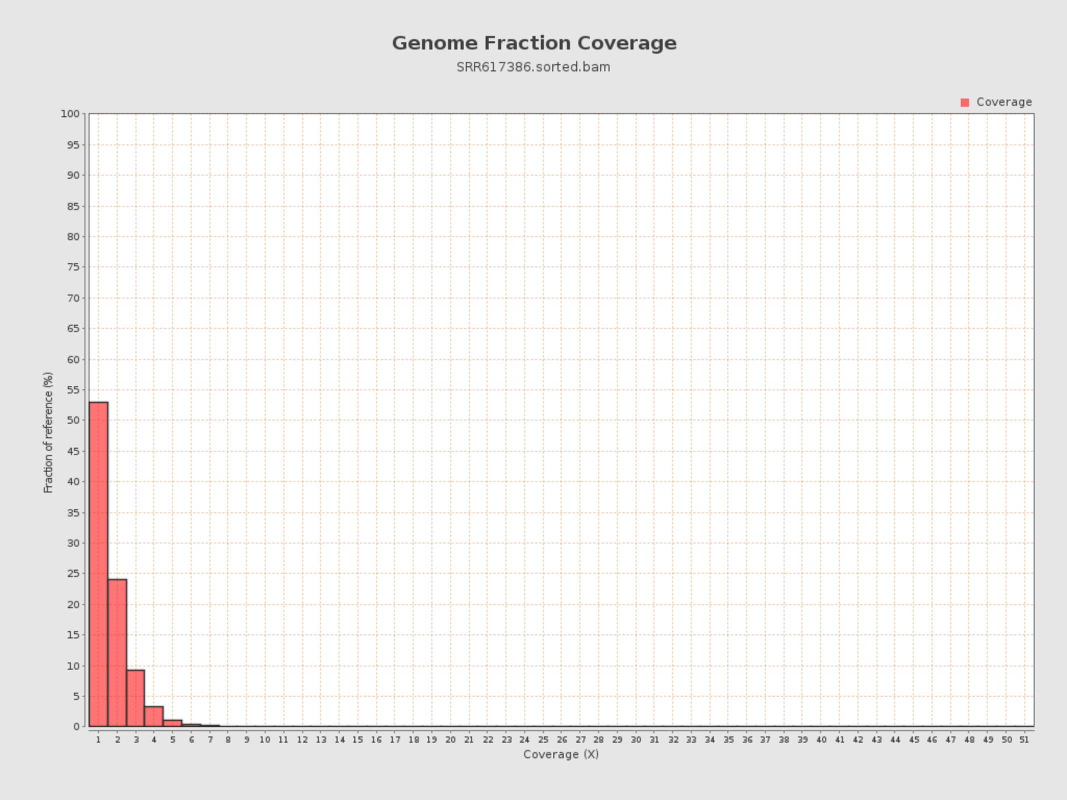
4. Results : Coverage Histogram



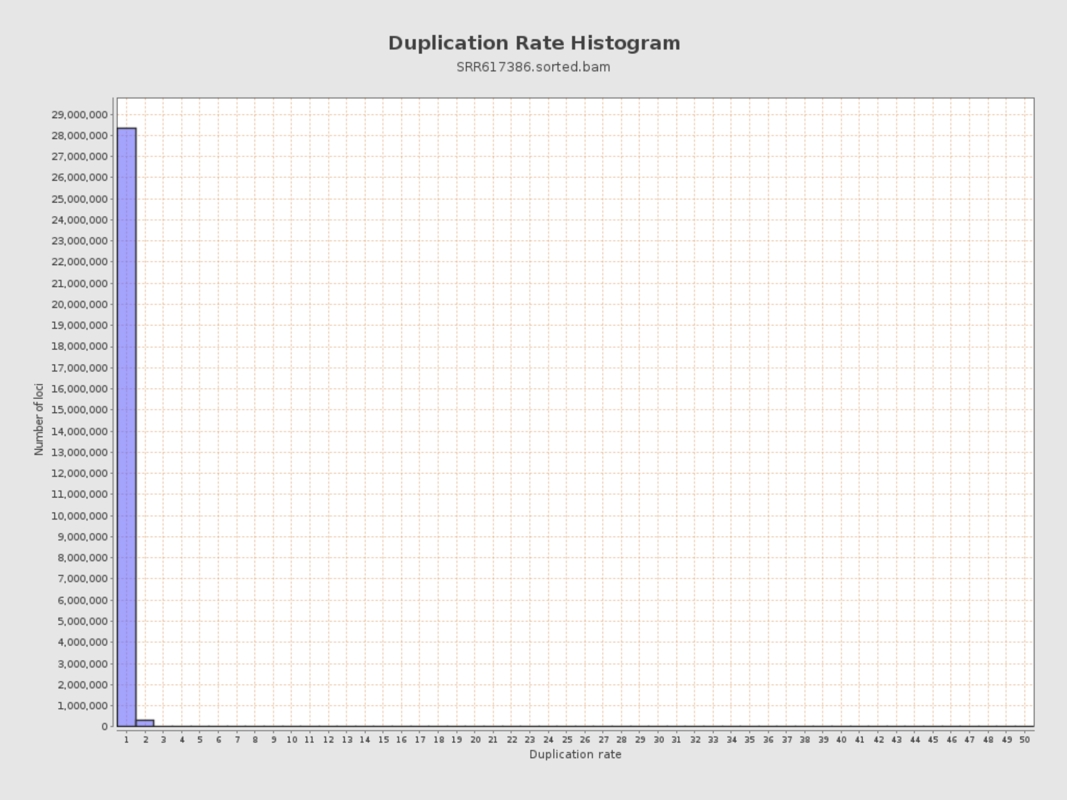
5. Results : Coverage Histogram (0-50X)



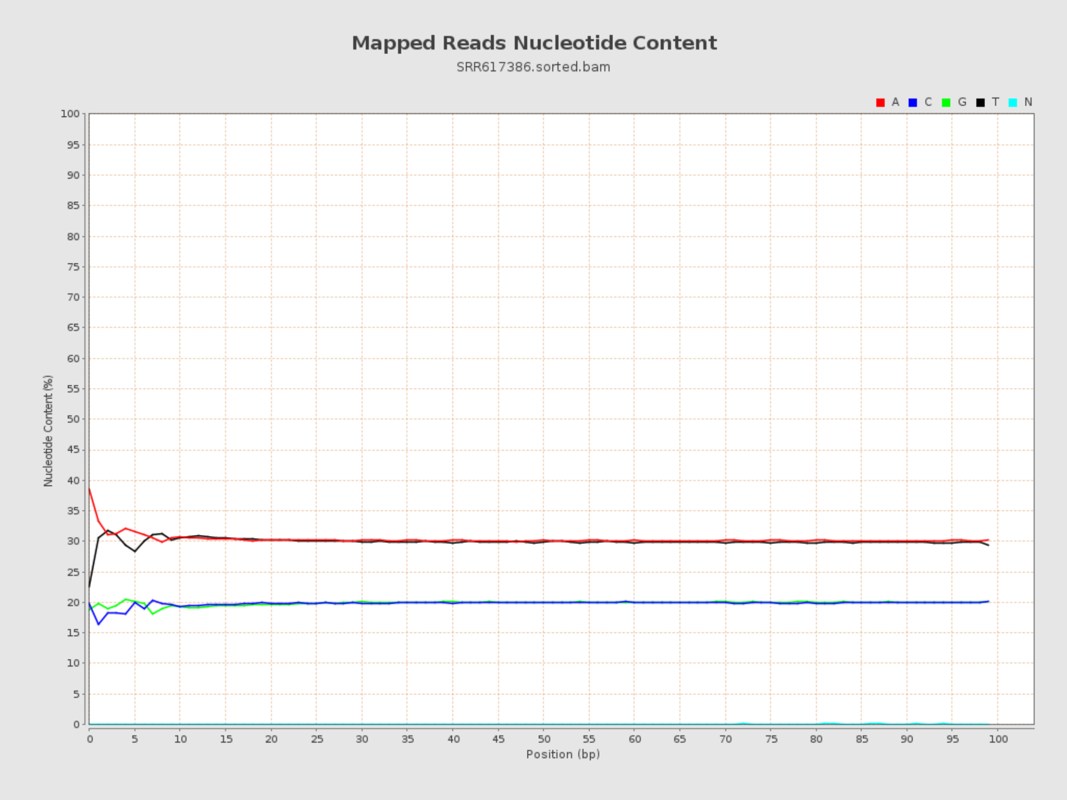
6. Results : Genome Fraction Coverage



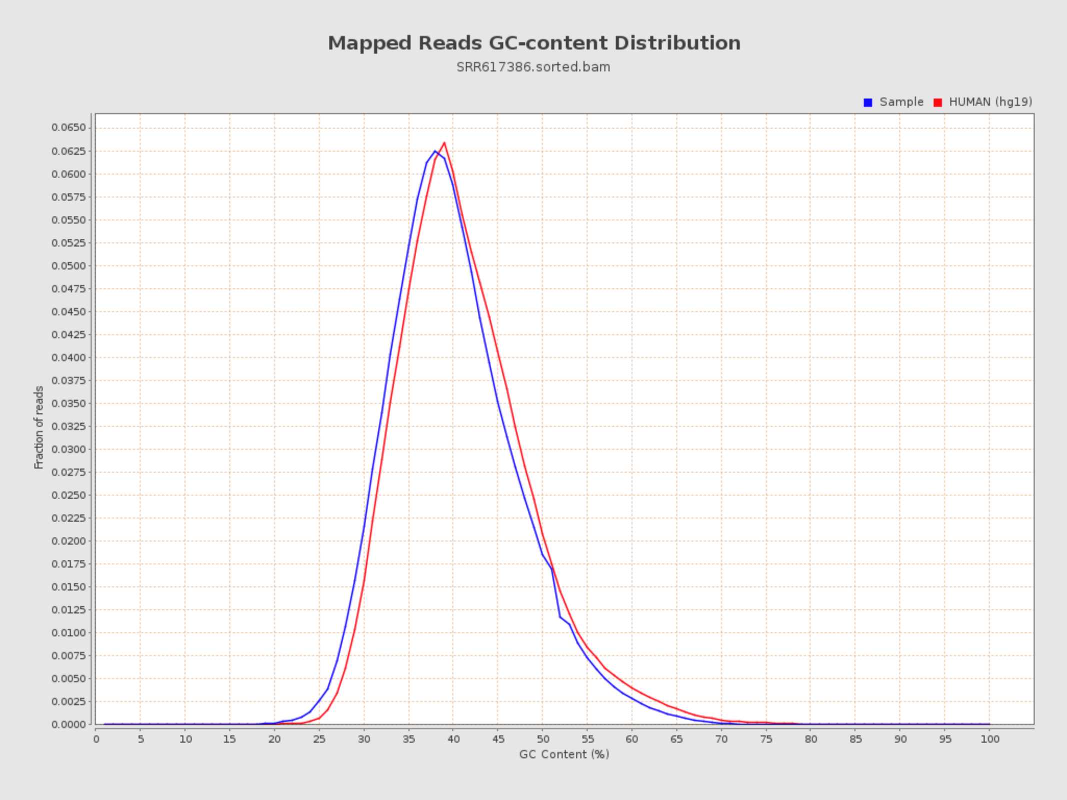
7. Results : Duplication Rate Histogram



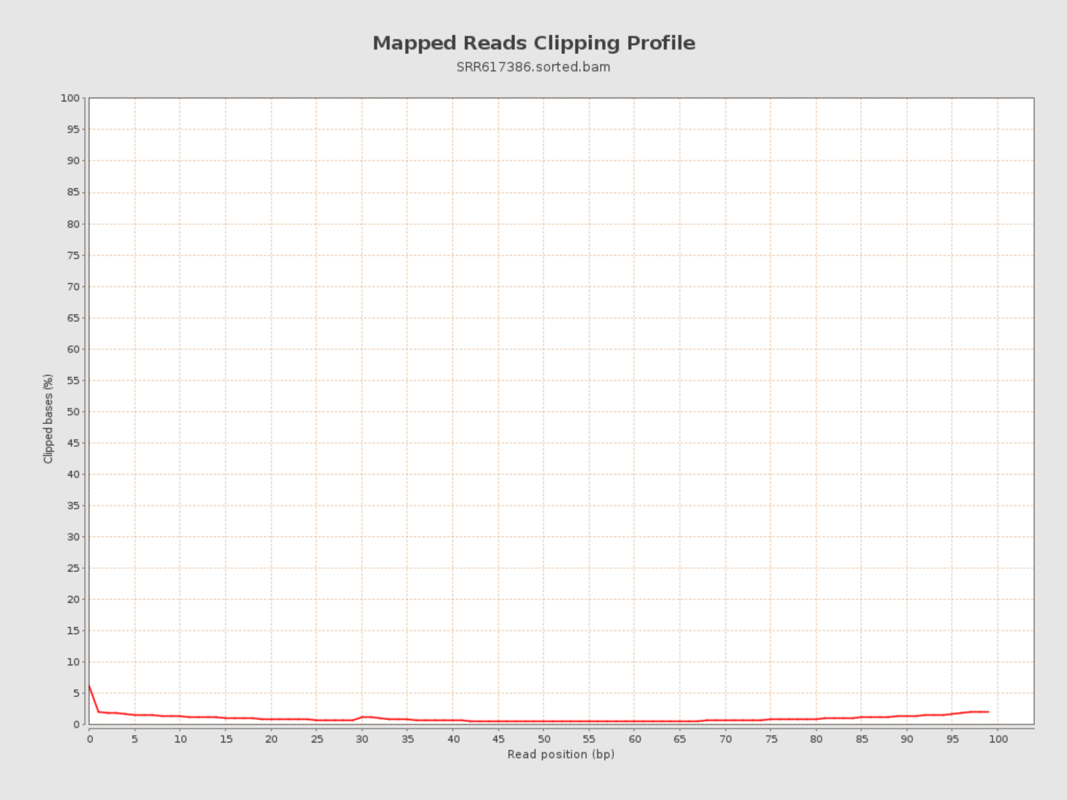
8. Results : Mapped Reads Nucleotide Content



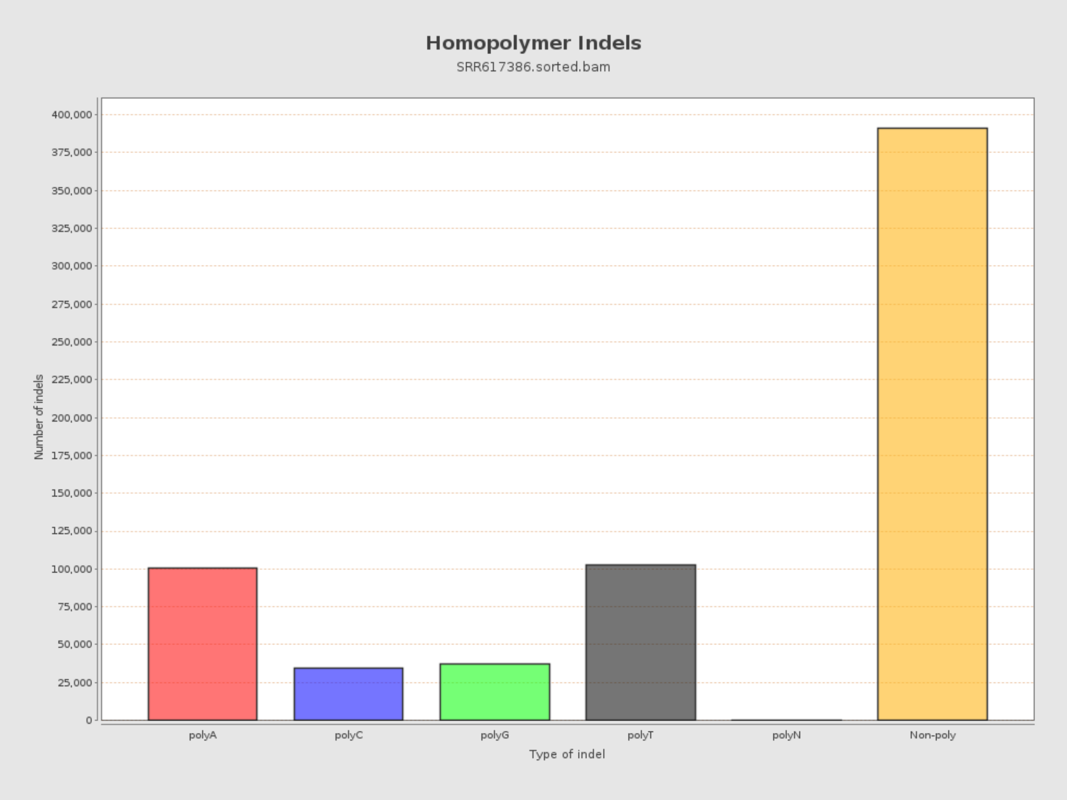
9. Results : Mapped Reads GC-content Distribution



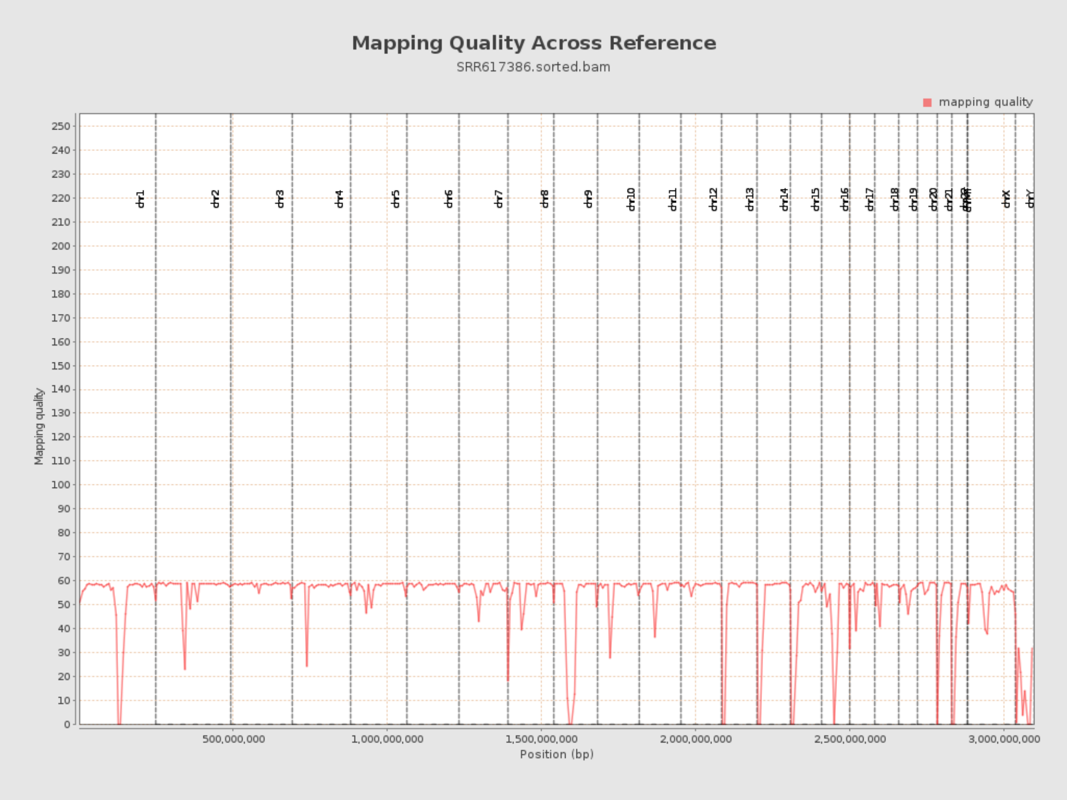
10. Results : Mapped Reads Clipping Profile



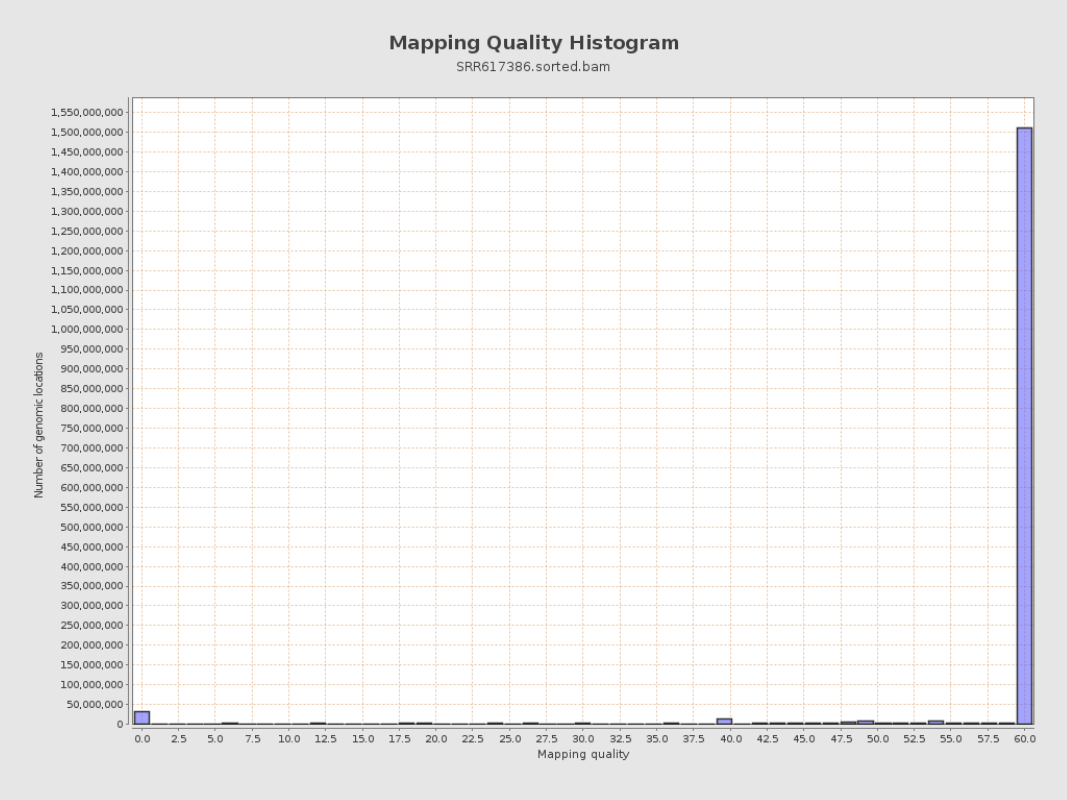
11. Results : Homopolymer Indels



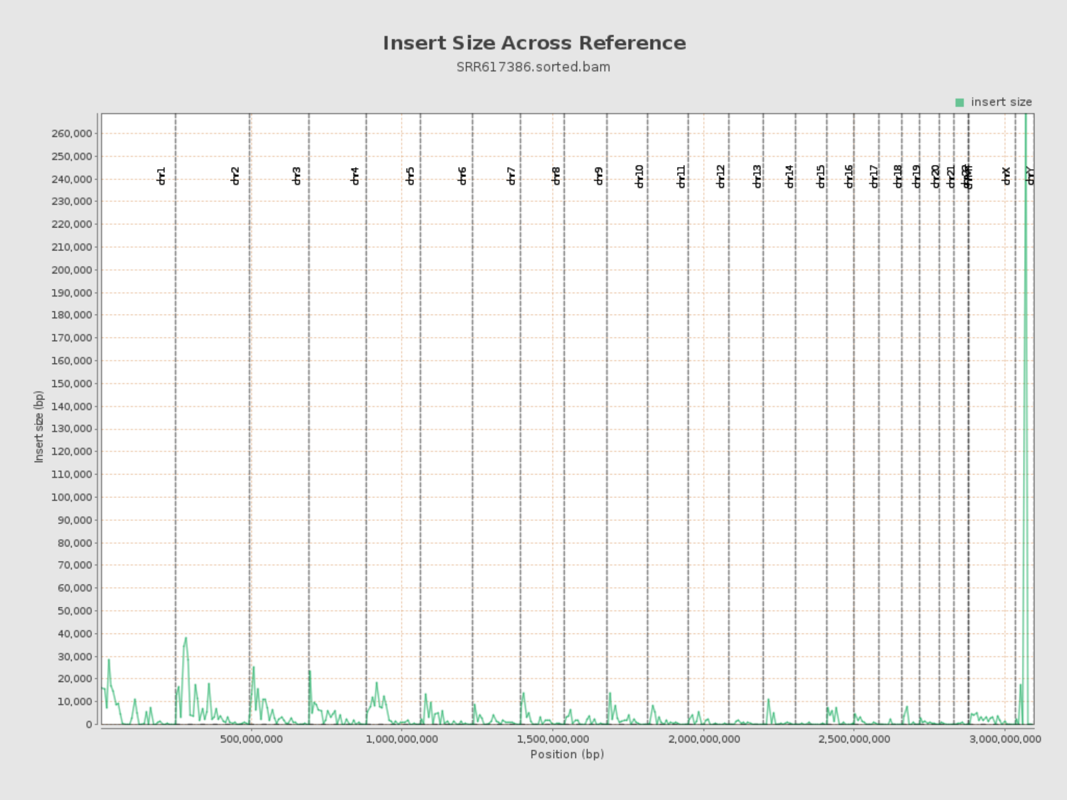
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram