Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 14:10:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617396.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_SRR617396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617396_1.fastq.gz SRR617396_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 14:10:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	28,725,495 / 89.77%
Unmapped reads	3,274,505 / 10.23%
Mapped paired reads	28,725,495 / 89.77%
Mapped reads, first in pair	14,582,246 / 45.57%
Mapped reads, second in pair	14,143,249 / 44.2%
Mapped reads, both in pair	27,965,620 / 87.39%
Mapped reads, singletons	759,875 / 2.37%
Secondary alignments	0
Supplementary alignments	396,188 / 1.24%
Read min/max/mean length	30 / 100 / 100.51
Duplicated reads (estimated)	1,242,825 / 3.88%
Duplication rate	3.96%
Clipped reads	4,627,733 / 14.46%

2.2. ACGT Content

Number/percentage of A's	836,390,501 / 29.84%
Number/percentage of C's	562,862,434 / 20.08%
Number/percentage of T's	827,251,353 / 29.52%
Number/percentage of G's	574,193,913 / 20.49%
Number/percentage of N's	1,869,254 / 0.07%

GC Percentage	40.57%

2.3. Coverage

Mean	0.9055
Standard Deviation	2.767

2.4. Mapping Quality

Mean Mapping Quality	53.74

2.5. Insert size

Mean	49,640.22
Standard Deviation	2,127,999.43
P25/Median/P75	169 / 208 / 268

2.6. Mismatches and indels

General error rate	1.58%
Mismatches	43,860,704
Insertions	229,364
Mapped reads with at least one insertion	0.79%
Deletions	277,505
Mapped reads with at least one deletion	0.95%
Homopolymer indels	43.72%

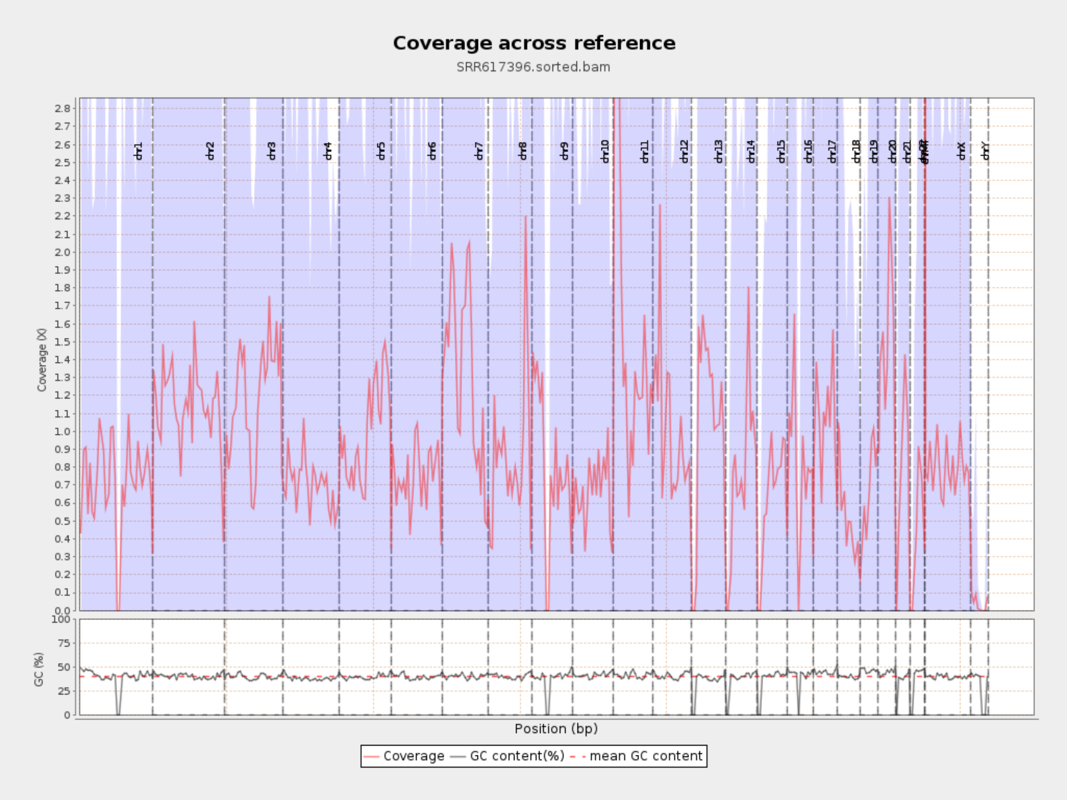
2.7. Chromosome stats

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

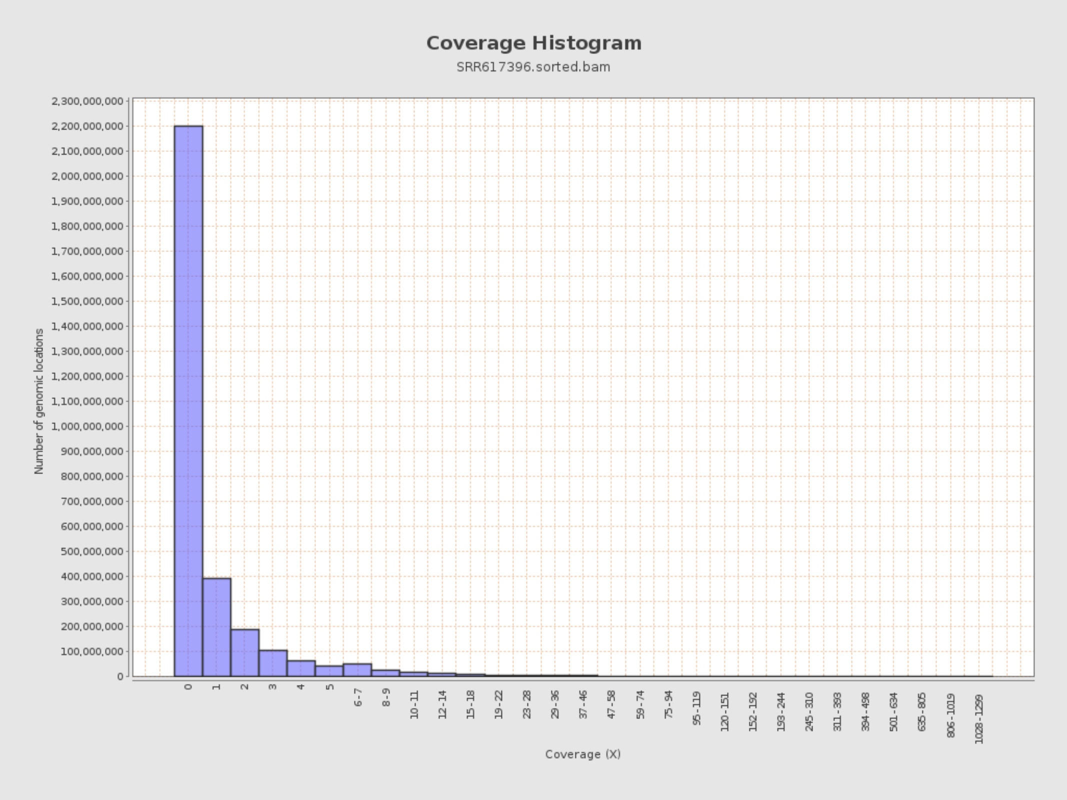
		bases	coverage	deviation
chr1	249250621	180375505	0.7237	2.5886
chr2	243199373	279969517	1.1512	2.9139
chr3	198022430	237214744	1.1979	3.2385
chr4	191154276	135462158	0.7087	2.1644
chr5	180915260	179708655	0.9933	2.7364
chr6	171115067	128764184	0.7525	2.4619
chr7	159138663	209937750	1.3192	3.0701
chr8	146364022	124036137	0.8474	3.0685
chr9	141213431	112160264	0.7943	2.4625
chr10	135534747	89781644	0.6624	2.2735
chr11	135006516	207307275	1.5355	3.6276
chr12	133851895	133744778	0.9992	2.6388
chr13	115169878	122110940	1.0603	2.6352
chr14	107349540	81395860	0.7582	2.7419
chr15	102531392	64093682	0.6251	2.2236
chr16	90354753	70107498	0.7759	3.1144
chr17	81195210	85917898	1.0582	3.4932
chr18	78077248	40337741	0.5166	1.8916
chr19	59128983	39651642	0.6706	2.1945
chr20	63025520	94849495	1.5049	4.4473
chr21	48129895	38374918	0.7973	2.3977
chr22	51304566	22303019	0.4347	1.9462
chrMT	16571	165733	10.0014	5.0635
chrX	155270560	123167749	0.7932	2.4346

chrY	59373566	2235190	0.0376	0.518

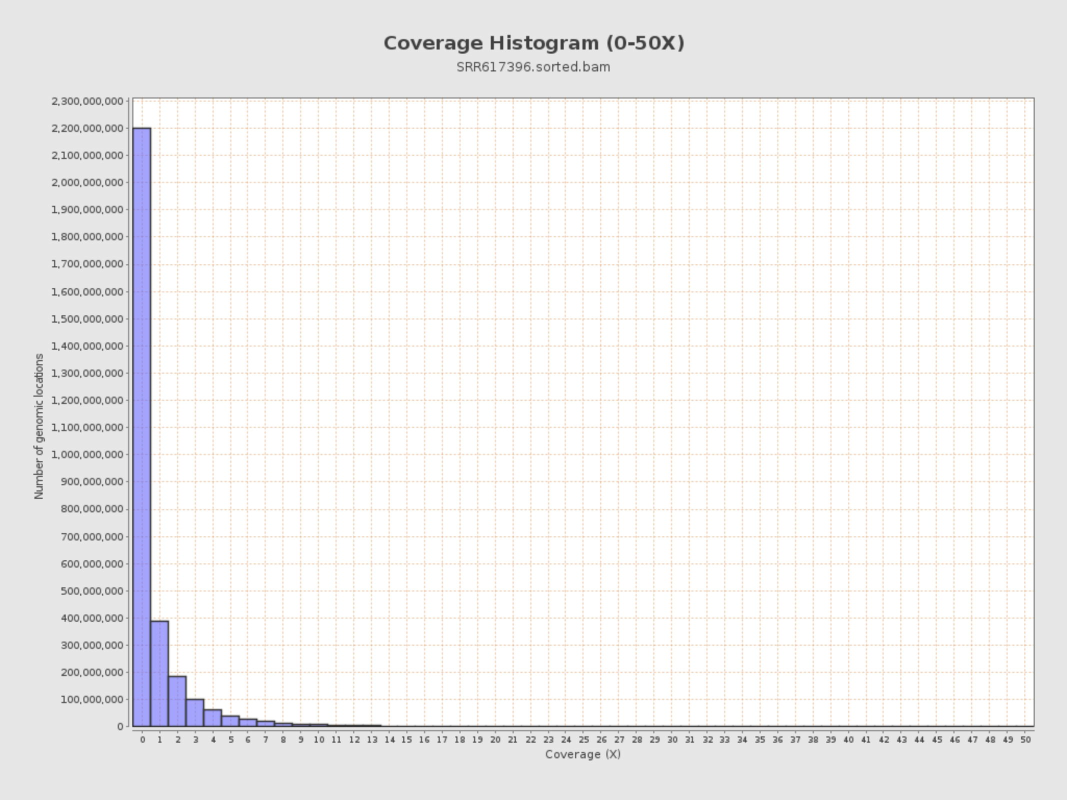
3. Results : Coverage across reference



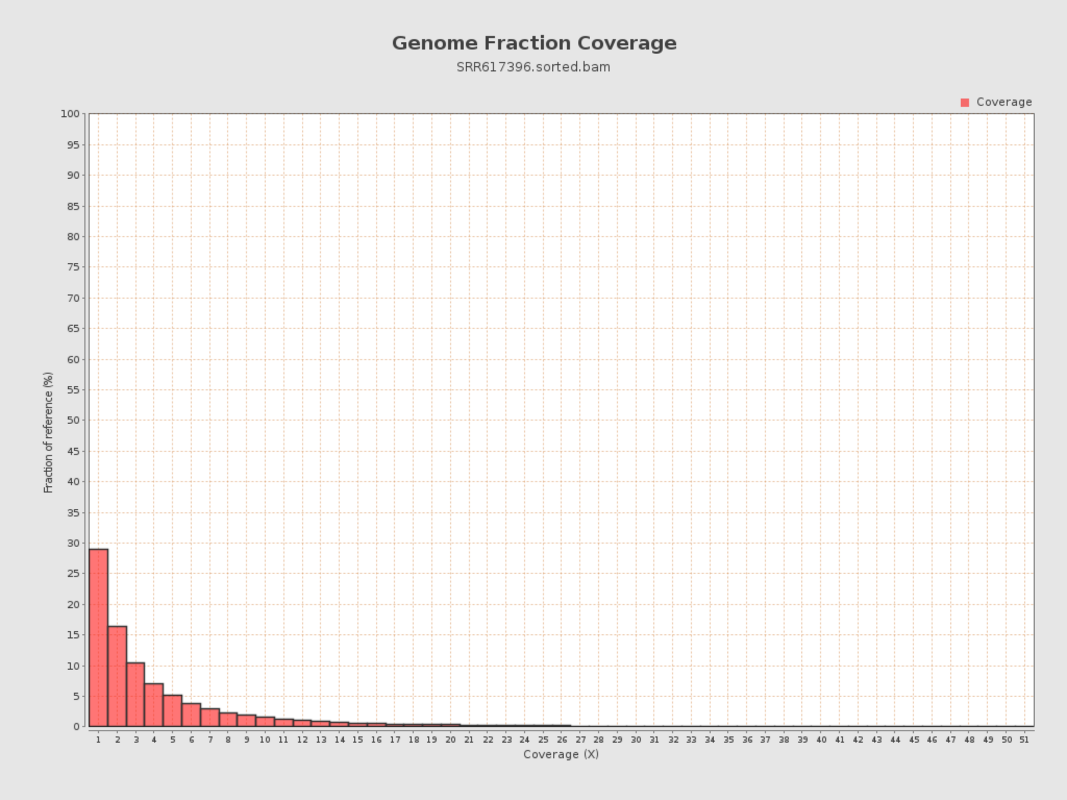
4. Results : Coverage Histogram



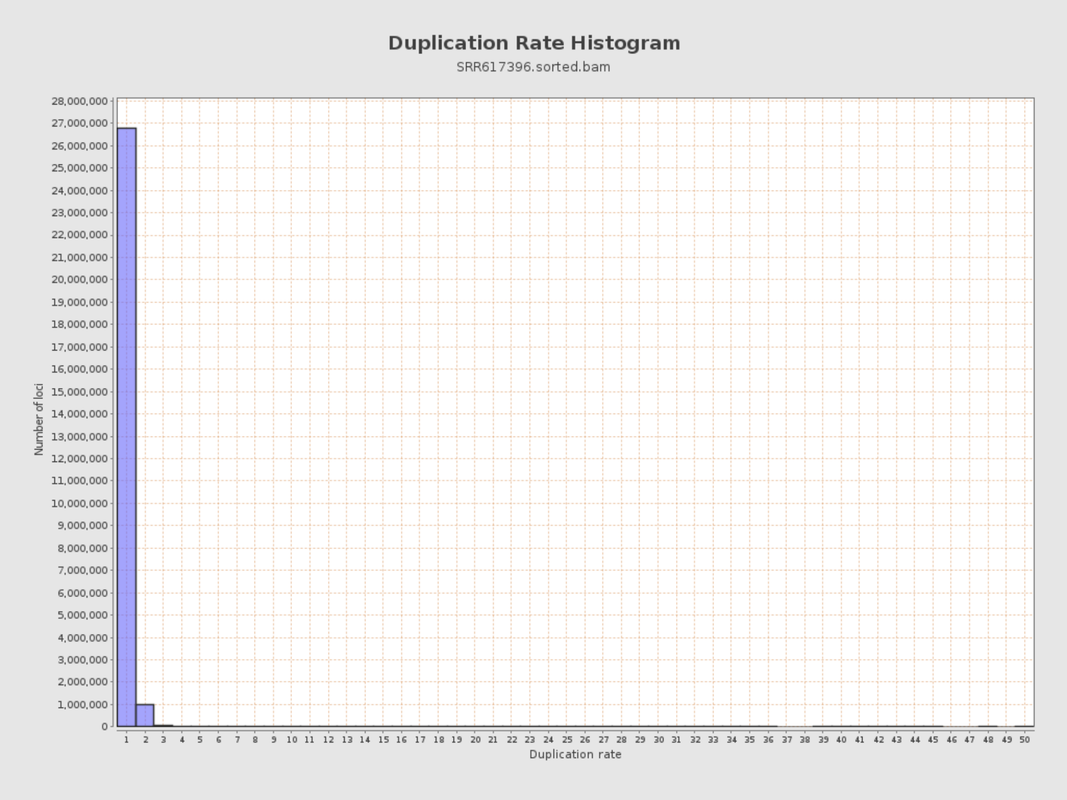
5. Results : Coverage Histogram (0-50X)



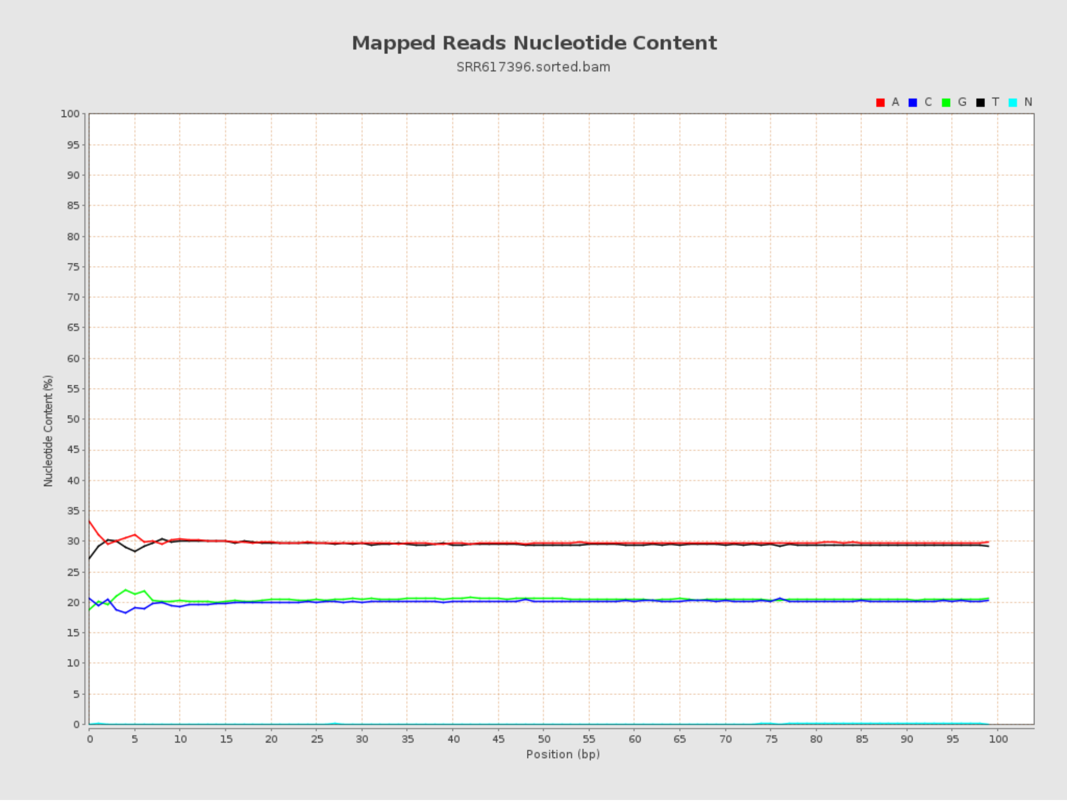
6. Results : Genome Fraction Coverage



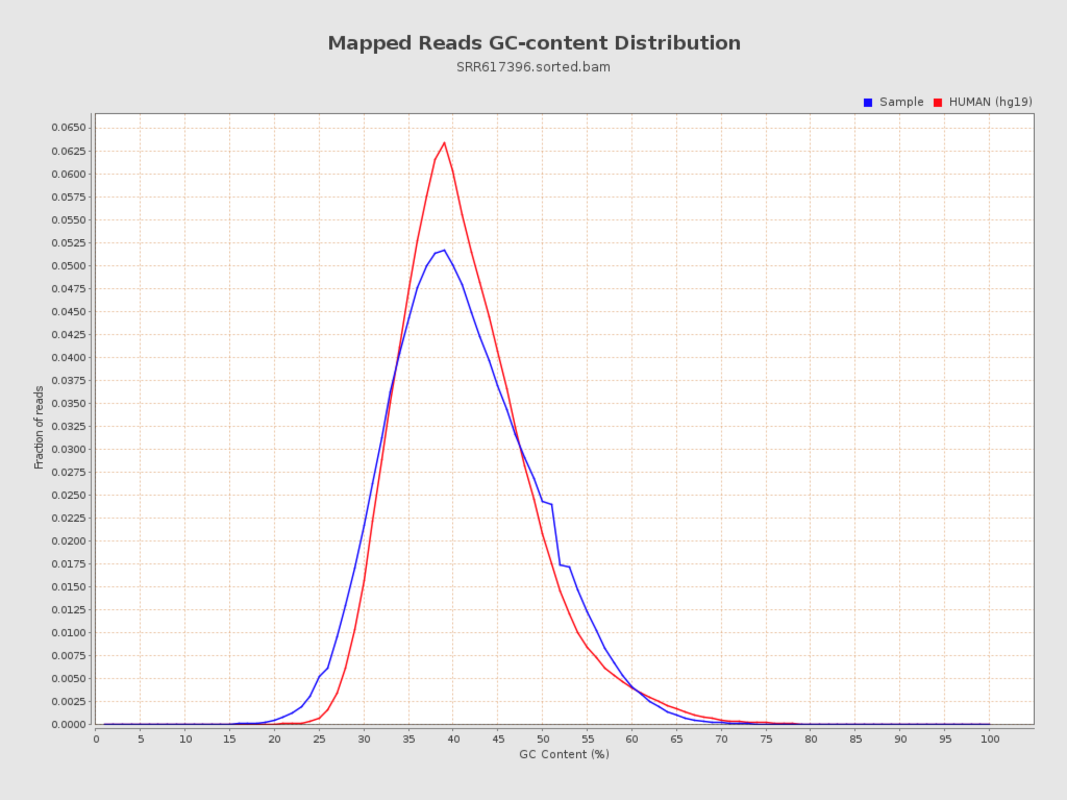
7. Results : Duplication Rate Histogram



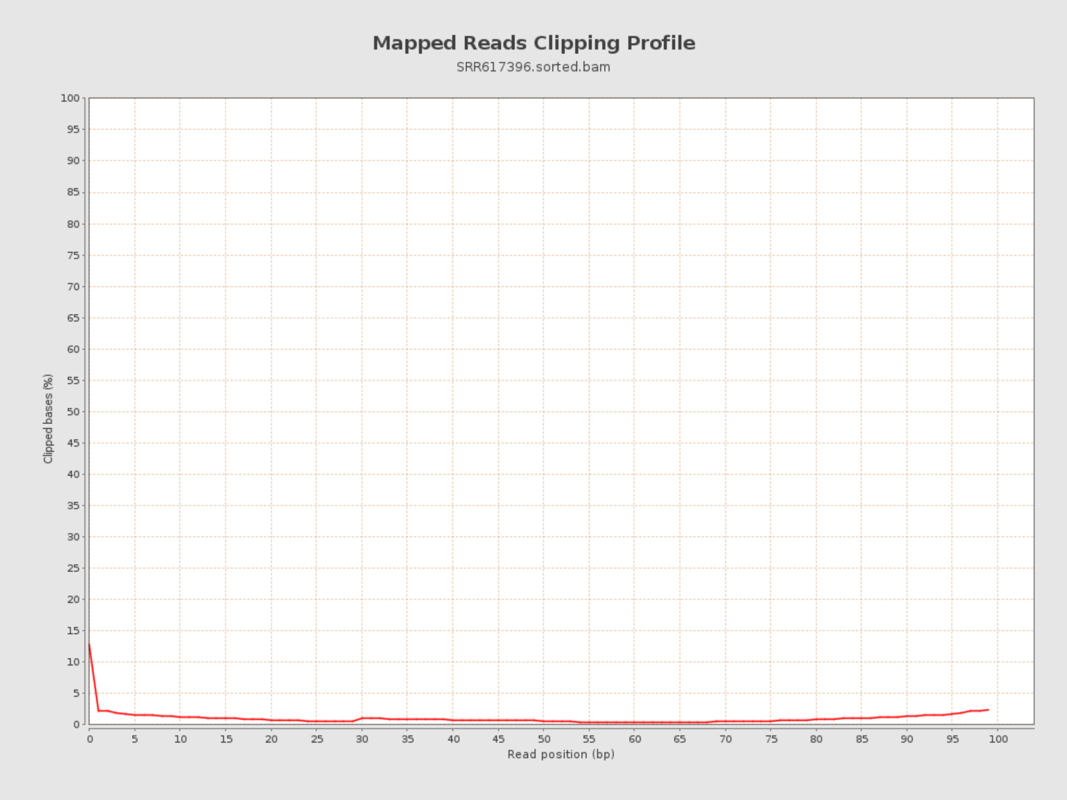
8. Results : Mapped Reads Nucleotide Content



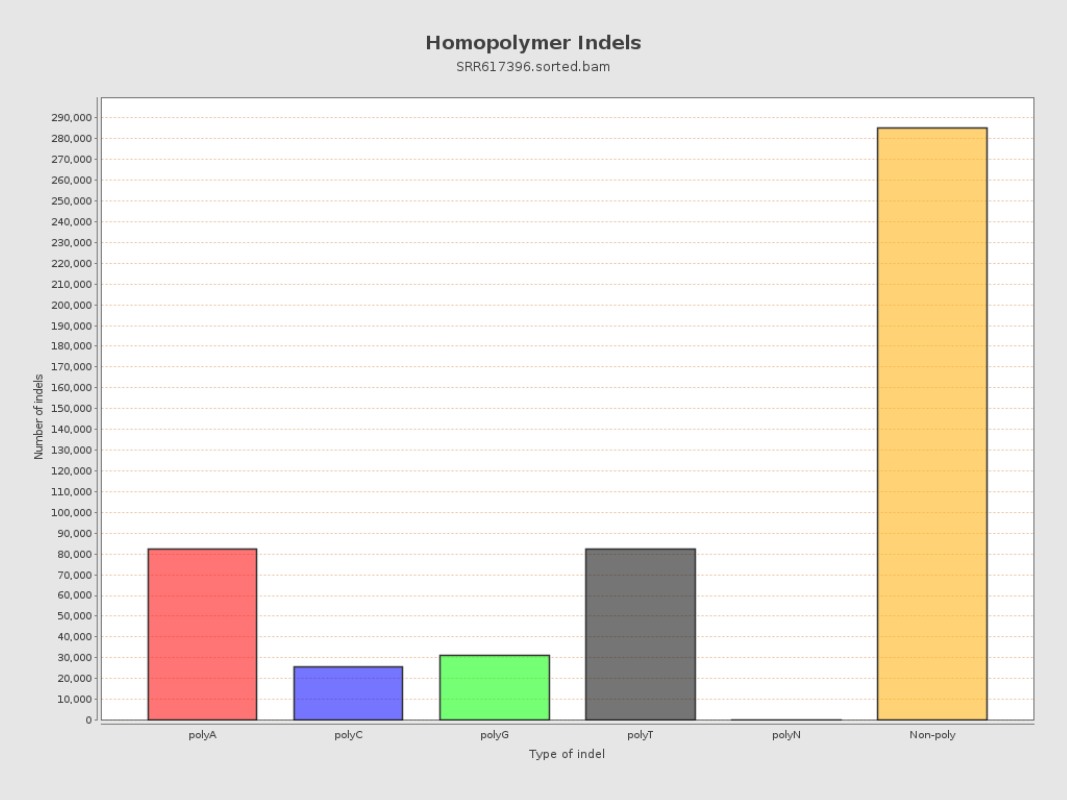
9. Results : Mapped Reads GC-content Distribution



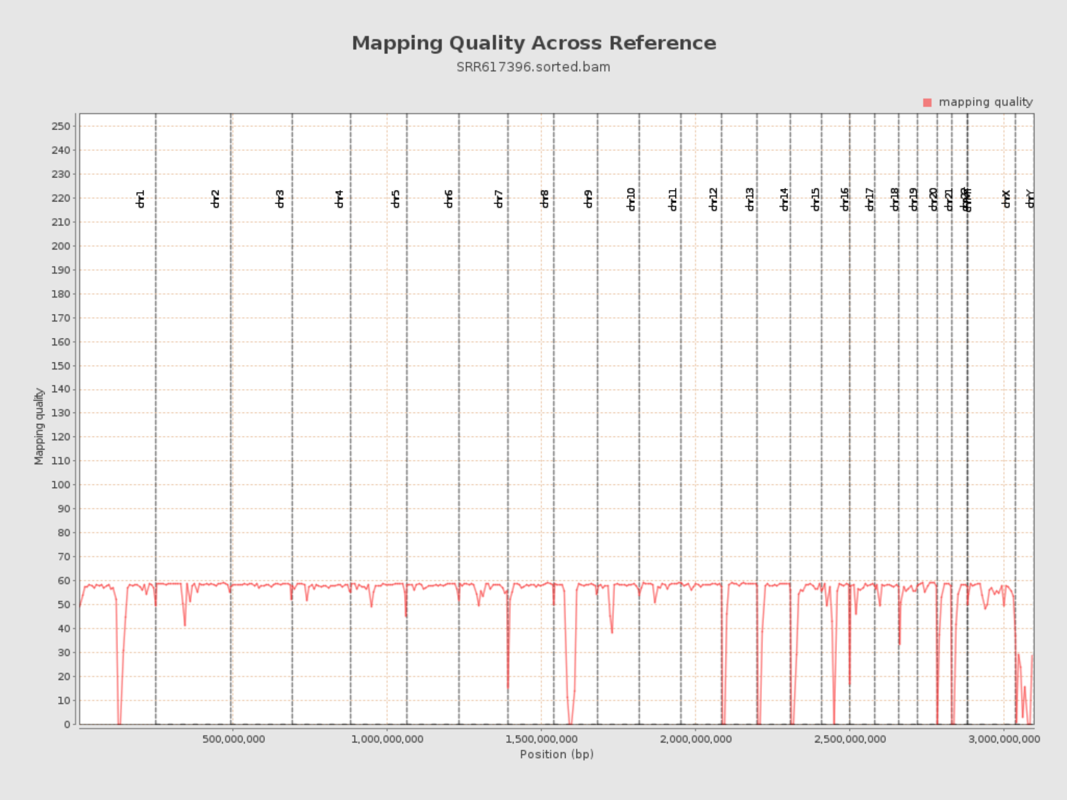
10. Results : Mapped Reads Clipping Profile



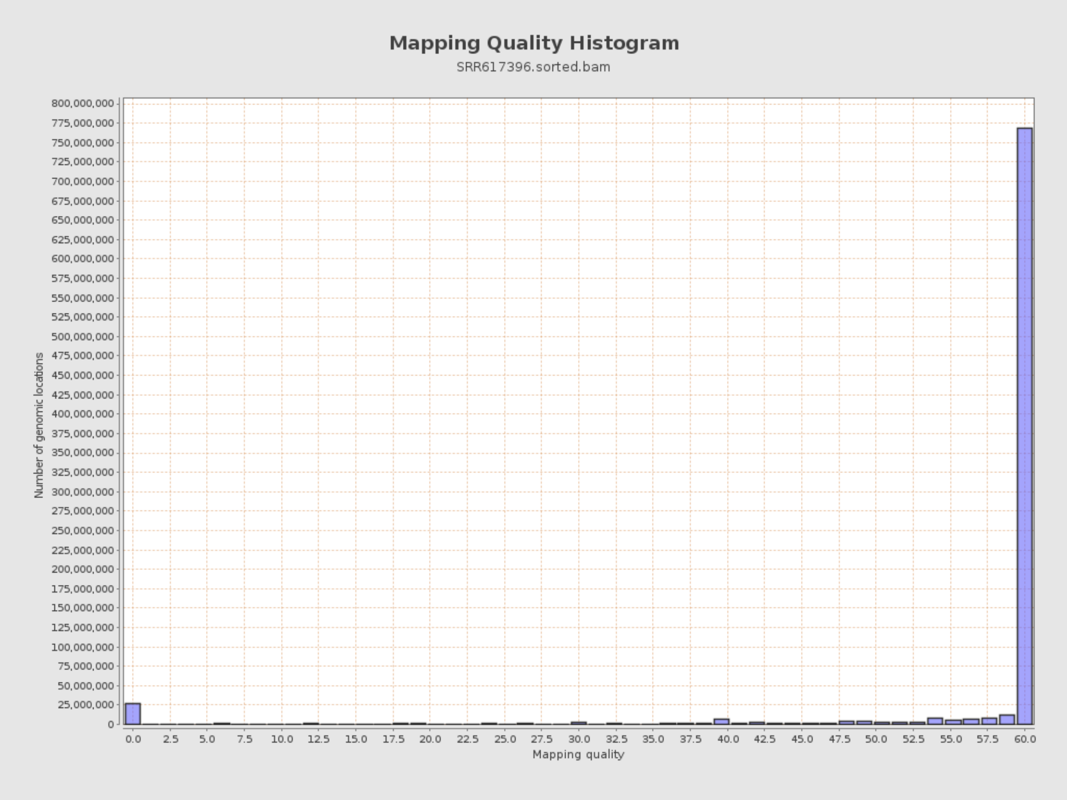
11. Results : Homopolymer Indels



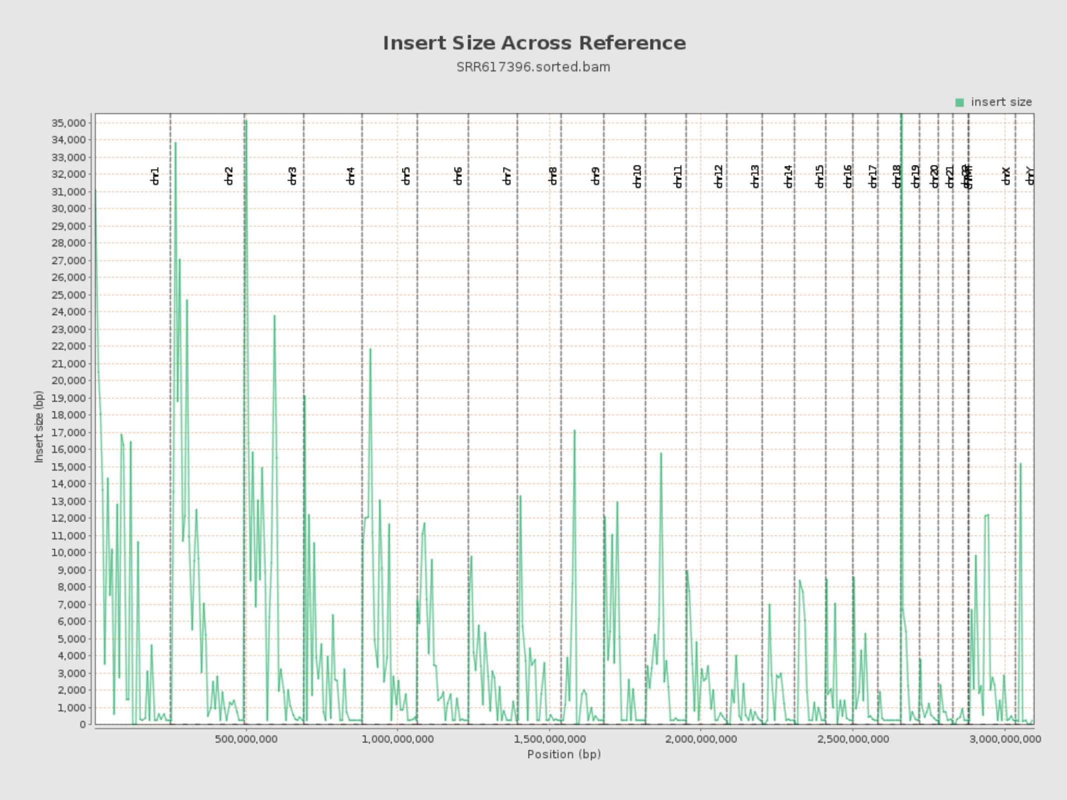
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram