Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 07:10:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617666.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_SRR617666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617666_1.fastq.gz SRR617666_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 07:10:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,666,374 / 95.83%
Unmapped reads	1,333,626 / 4.17%
Mapped paired reads	30,666,374 / 95.83%
Mapped reads, first in pair	15,388,784 / 48.09%
Mapped reads, second in pair	15,277,590 / 47.74%
Mapped reads, both in pair	30,142,080 / 94.19%
Mapped reads, singletons	524,294 / 1.64%
Secondary alignments	0
Supplementary alignments	140,964 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,165,414 / 22.39%
Duplication rate	10.89%
Clipped reads	6,151,418 / 19.22%

2.2. ACGT Content

Number/percentage of A's	888,046,157 / 29.74%
Number/percentage of C's	596,259,965 / 19.96%
Number/percentage of T's	887,375,161 / 29.71%
Number/percentage of G's	612,630,016 / 20.51%
Number/percentage of N's	2,215,972 / 0.07%

GC Percentage	40.48%

2.3. Coverage

Mean	0.9653
Standard Deviation	10.8674

2.4. Mapping Quality

Mean Mapping Quality	52.73

2.5. Insert size

Mean	31,354.27
Standard Deviation	1,610,718.77
P25/Median/P75	181 / 226 / 295

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	41,467,800
Insertions	464,386
Mapped reads with at least one insertion	1.49%
Deletions	1,098,558
Mapped reads with at least one deletion	3.51%
Homopolymer indels	47.78%

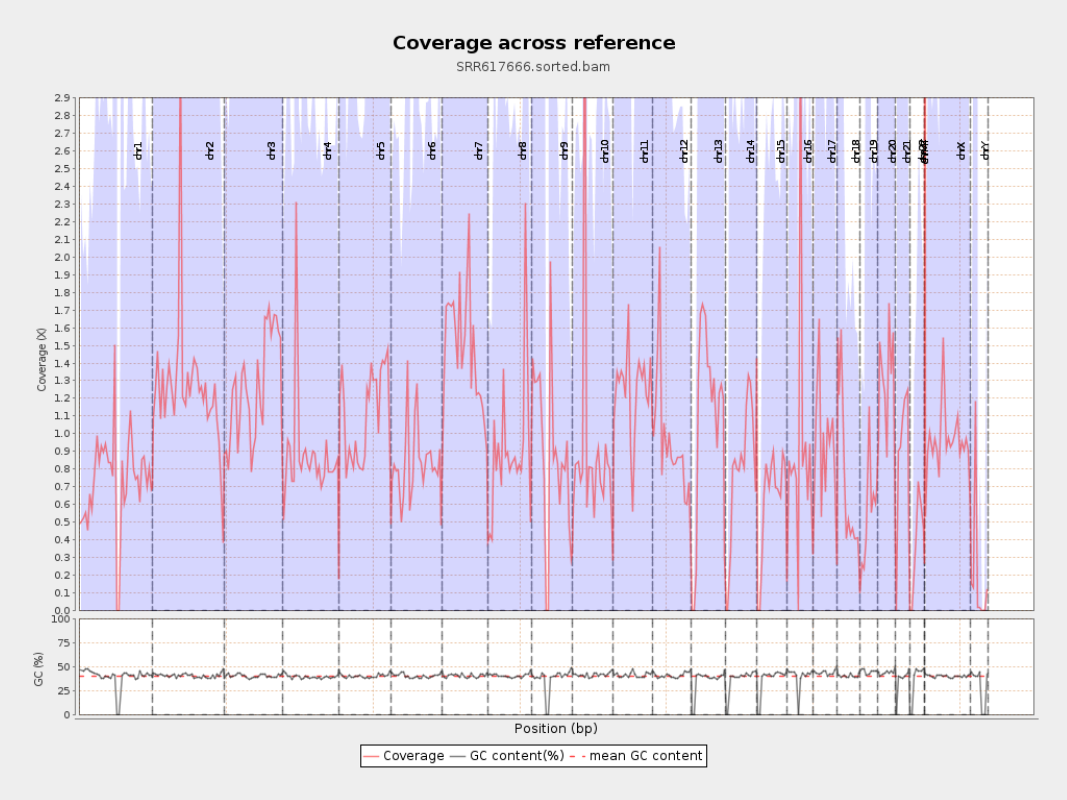
2.7. Chromosome stats

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

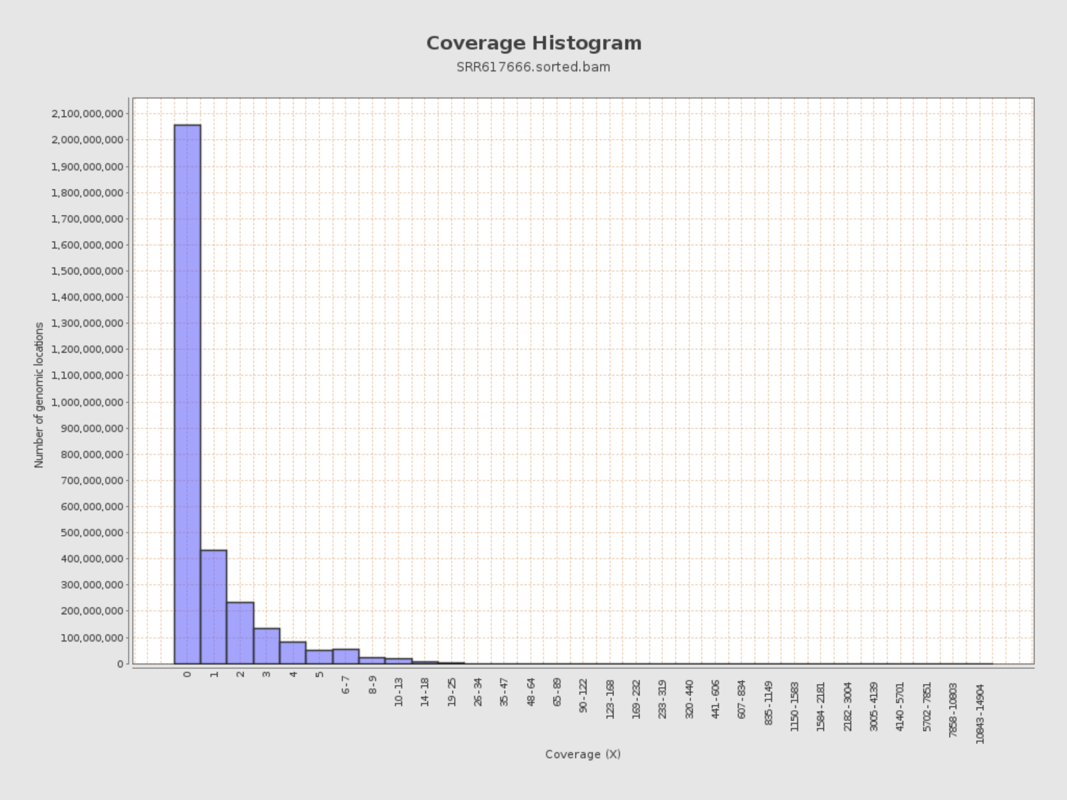
		bases	coverage	deviation
chr1	249250621	183324583	0.7355	10.3827
chr2	243199373	309013413	1.2706	12.5082
chr3	198022430	249970569	1.2623	2.4967
chr4	191154276	167071740	0.874	8.7633
chr5	180915260	197808928	1.0934	2.3727
chr6	171115067	144805683	0.8462	5.9039
chr7	159138663	234016041	1.4705	13.7801
chr8	146364022	132831149	0.9075	4.1543
chr9	141213431	122515923	0.8676	20.9614
chr10	135534747	126599898	0.9341	22.0355
chr11	135006516	164468896	1.2182	12.2485
chr12	133851895	127459159	0.9522	2.174
chr13	115169878	128378161	1.1147	2.3241
chr14	107349540	85449253	0.796	2.4987
chr15	102531392	63696119	0.6212	1.5891
chr16	90354753	82740635	0.9157	17.0465
chr17	81195210	73917099	0.9104	13.0973
chr18	78077248	55192960	0.7069	18.5957
chr19	59128983	31678289	0.5357	6.1978
chr20	63025520	80932321	1.2841	3.1119
chr21	48129895	43663940	0.9072	4.5334
chr22	51304566	19209671	0.3744	1.2793
chrMT	16571	3111765	187.7838	130.4461
chrX	155270560	148399094	0.9557	4.4385

chrY	59373566	12091690	0.2037	18.1161

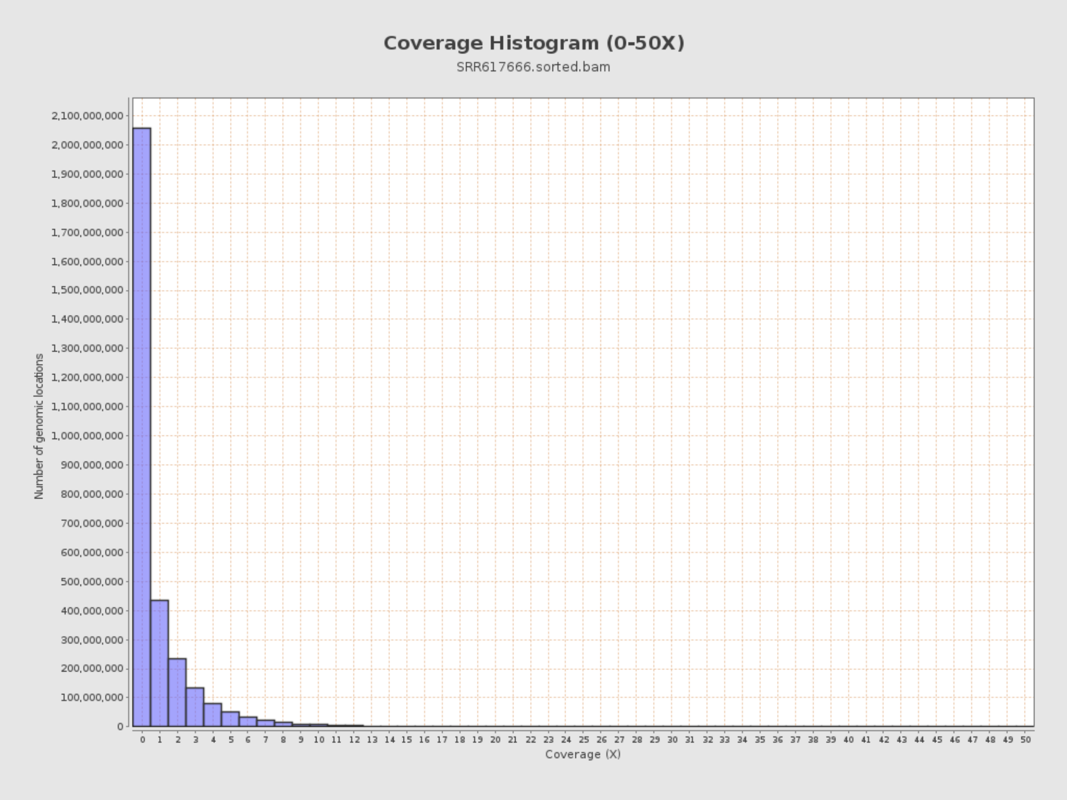
3. Results : Coverage across reference



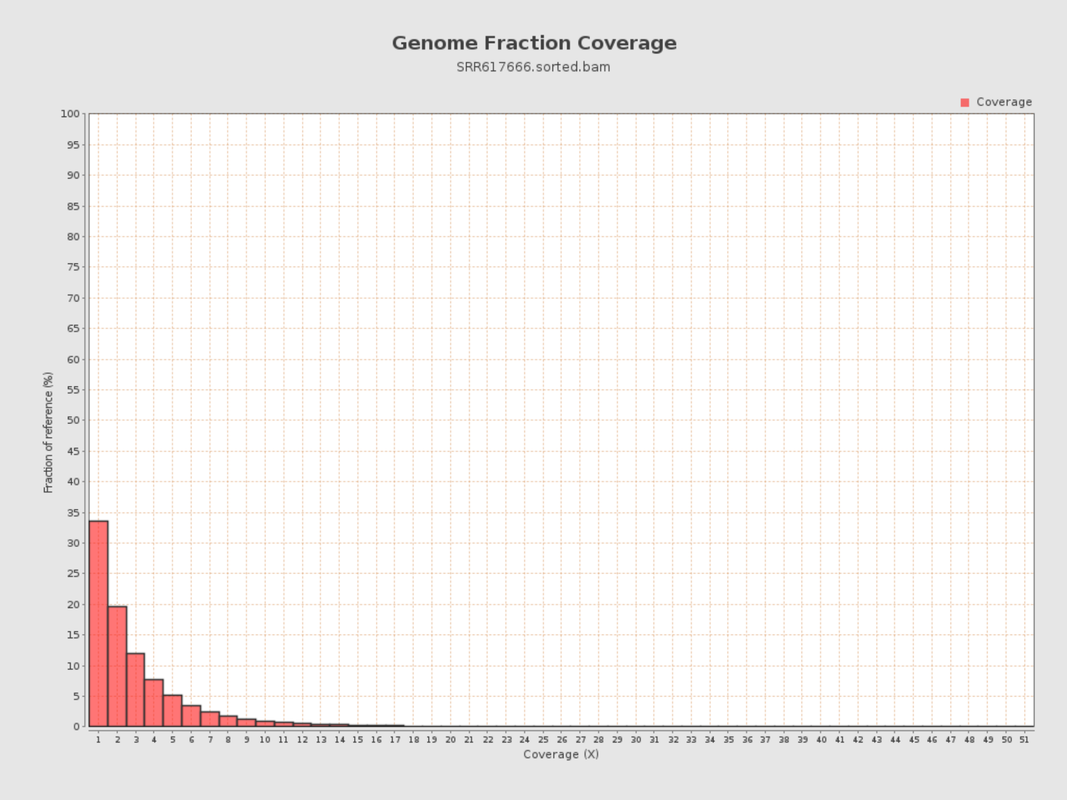
4. Results : Coverage Histogram



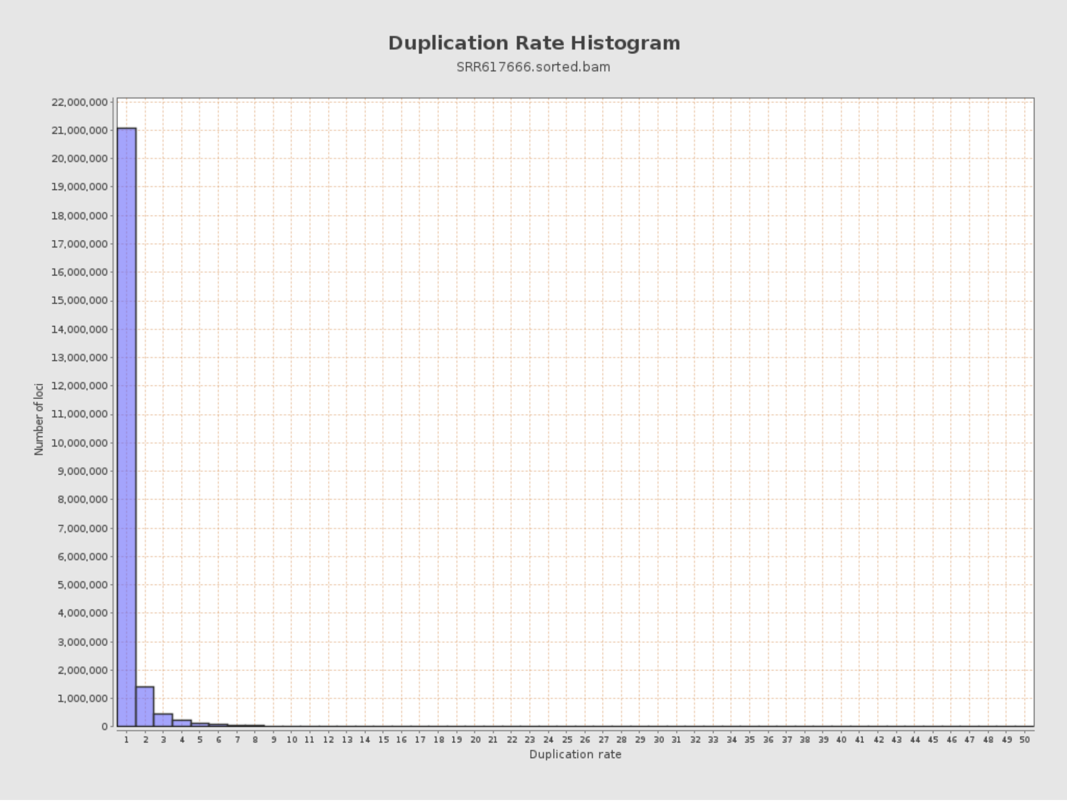
5. Results : Coverage Histogram (0-50X)



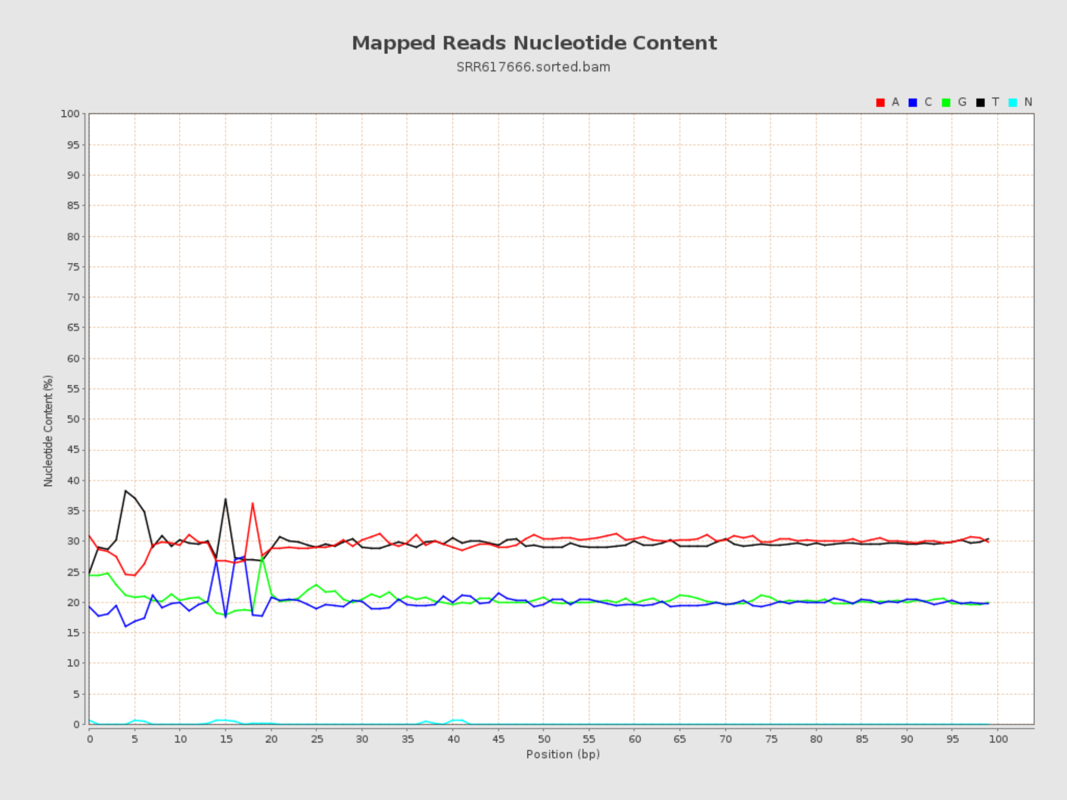
6. Results : Genome Fraction Coverage



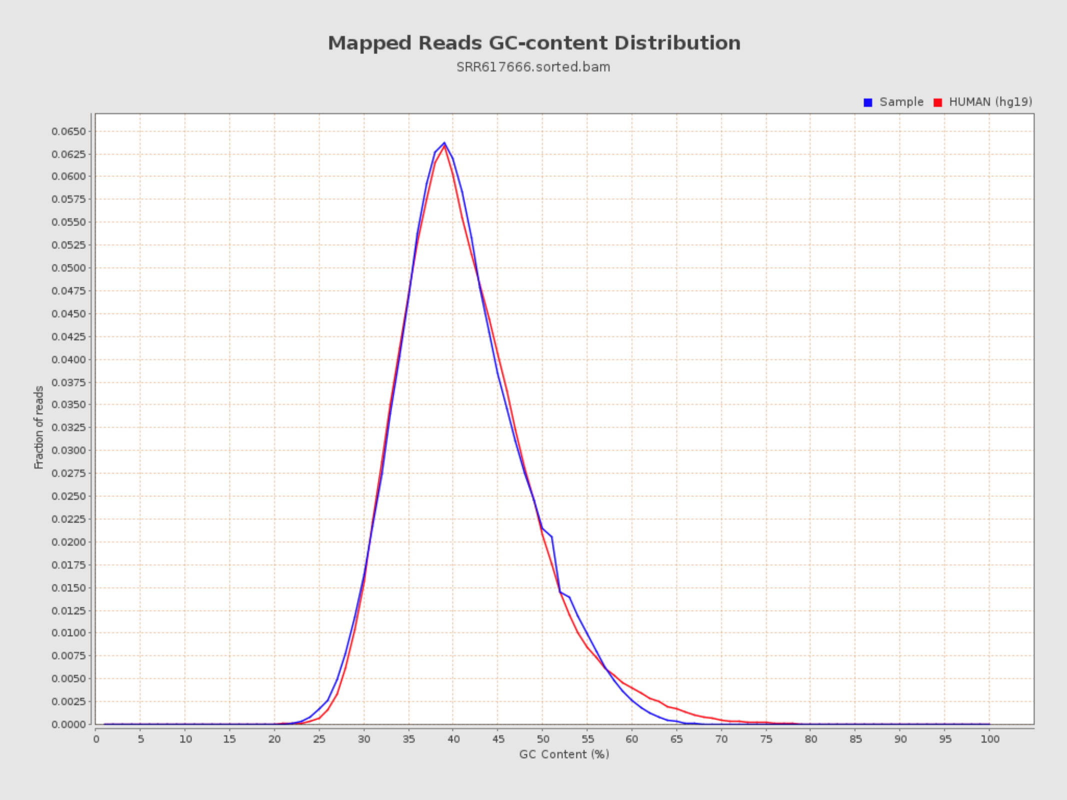
7. Results : Duplication Rate Histogram



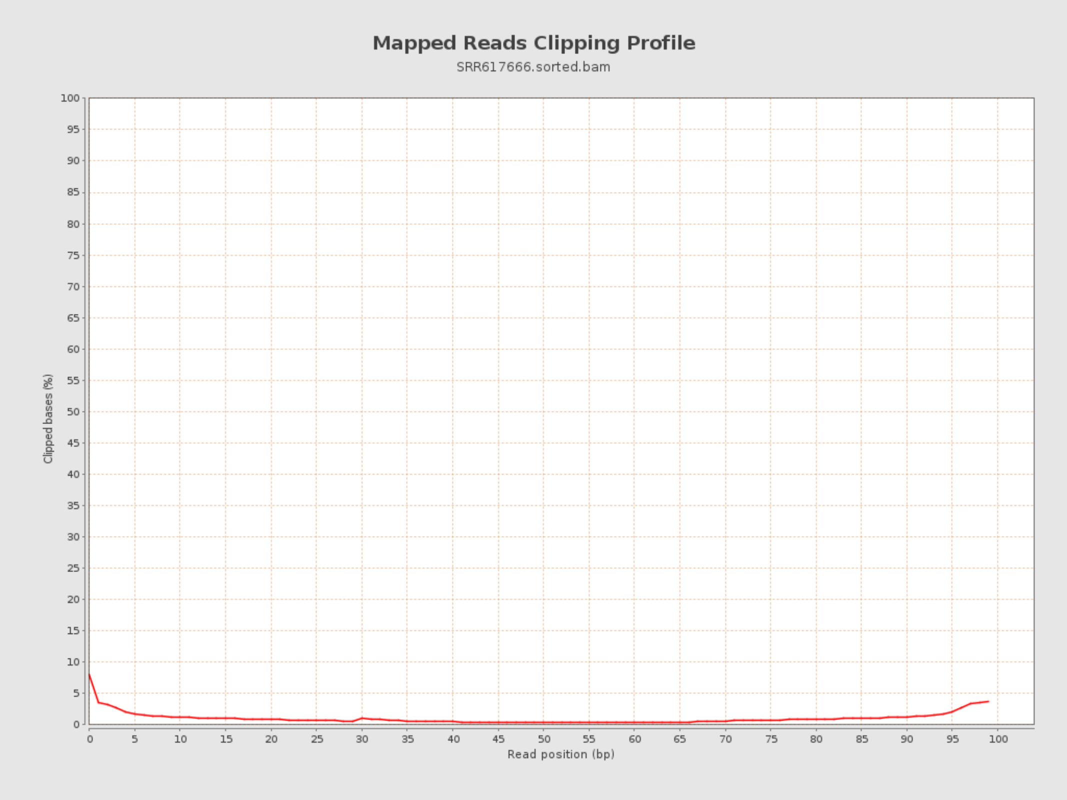
8. Results : Mapped Reads Nucleotide Content



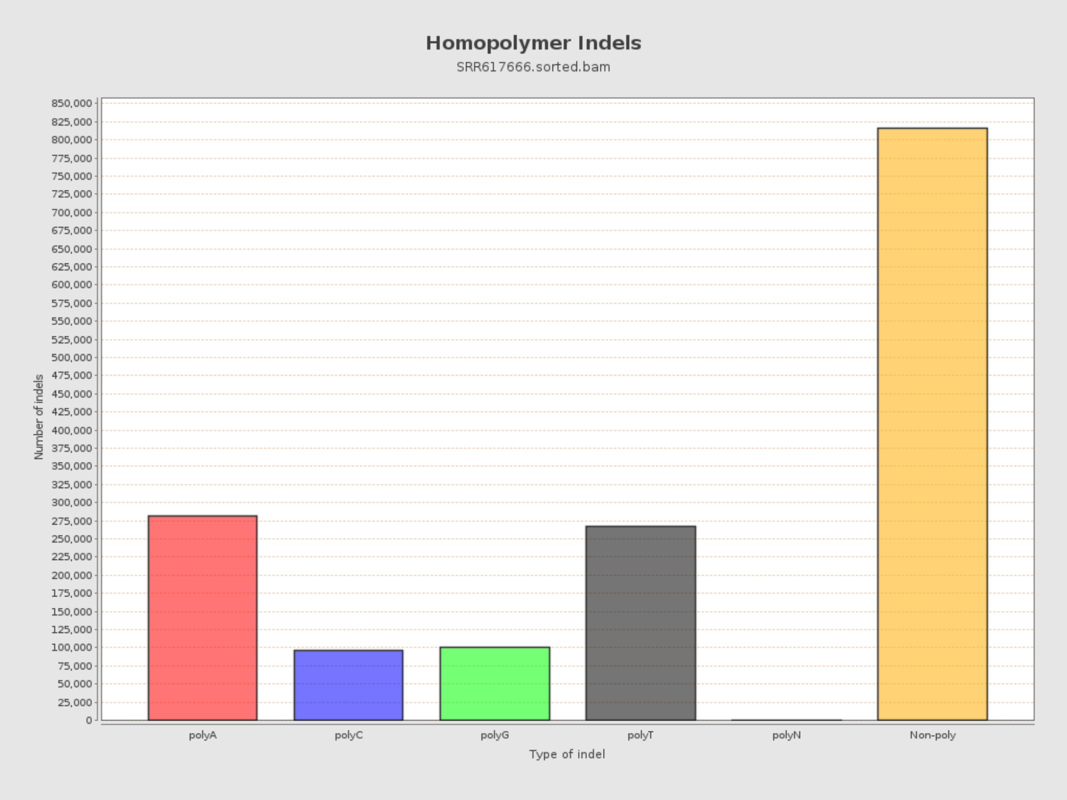
9. Results : Mapped Reads GC-content Distribution



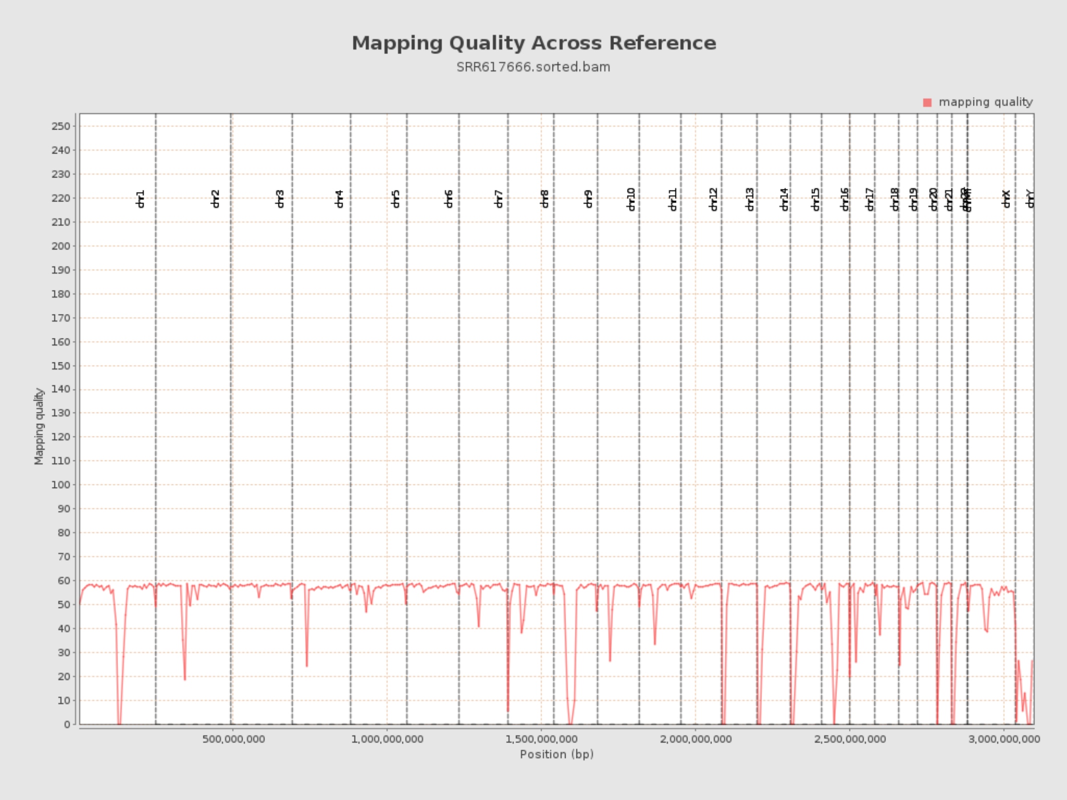
10. Results : Mapped Reads Clipping Profile



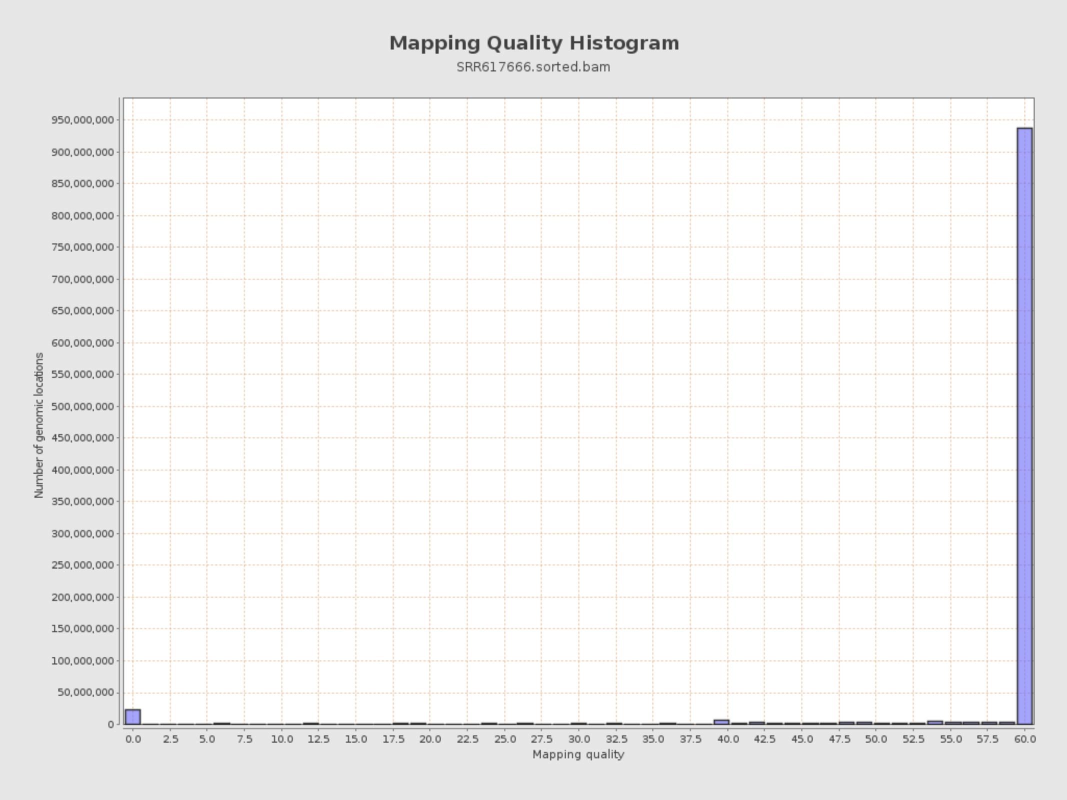
11. Results : Homopolymer Indels



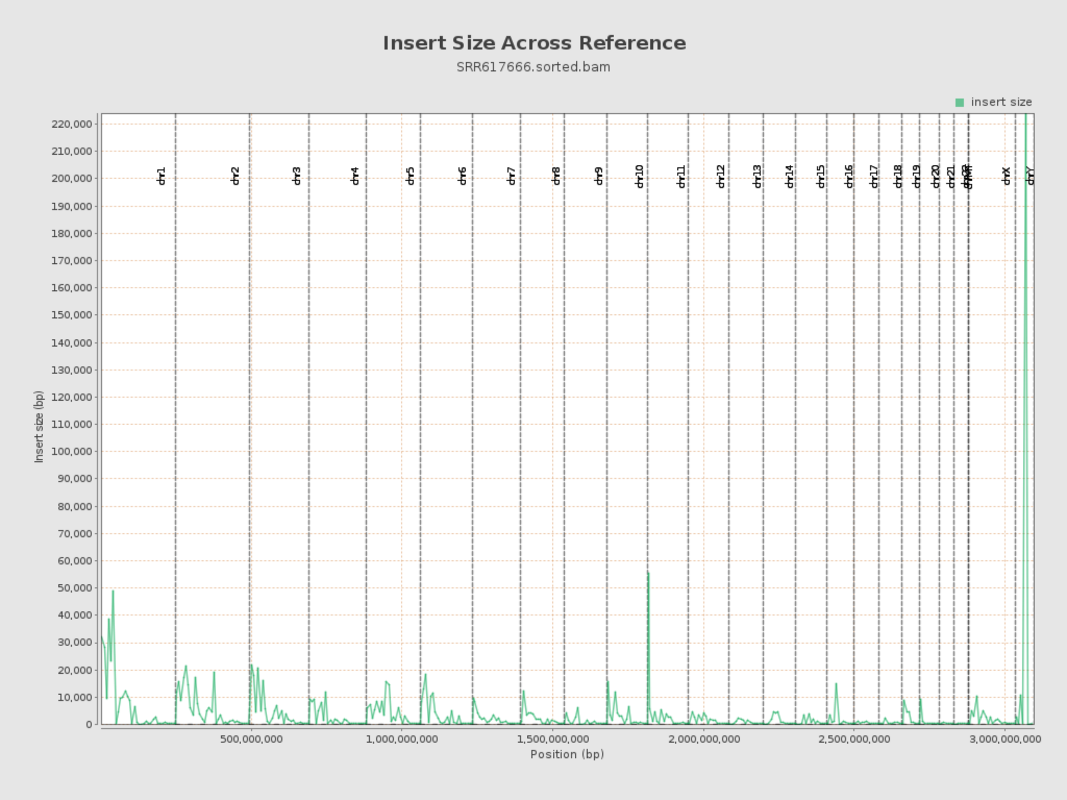
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram