Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 12:08:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617673.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_SRR617673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617673_1.fastq.gz SRR617673_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 12:08:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,964,600 / 93.64%
Unmapped reads	2,035,400 / 6.36%
Mapped paired reads	29,964,600 / 93.64%
Mapped reads, first in pair	15,206,709 / 47.52%
Mapped reads, second in pair	14,757,891 / 46.12%
Mapped reads, both in pair	29,125,182 / 91.02%
Mapped reads, singletons	839,418 / 2.62%
Secondary alignments	0
Supplementary alignments	171,794 / 0.54%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,830,891 / 21.35%
Duplication rate	10.64%
Clipped reads	6,667,666 / 20.84%

2.2. ACGT Content

Number/percentage of A's	859,515,246 / 29.76%
Number/percentage of C's	574,091,149 / 19.88%
Number/percentage of T's	858,965,770 / 29.74%
Number/percentage of G's	592,835,814 / 20.52%
Number/percentage of N's	2,998,278 / 0.1%

GC Percentage	40.4%

2.3. Coverage

Mean	0.9336
Standard Deviation	10.2891

2.4. Mapping Quality

Mean Mapping Quality	52.49

2.5. Insert size

Mean	47,463.97
Standard Deviation	2,040,893.24
P25/Median/P75	180 / 225 / 293

2.6. Mismatches and indels

General error rate	1.58%
Mismatches	44,660,317
Insertions	453,178
Mapped reads with at least one insertion	1.48%
Deletions	1,057,189
Mapped reads with at least one deletion	3.45%
Homopolymer indels	47.6%

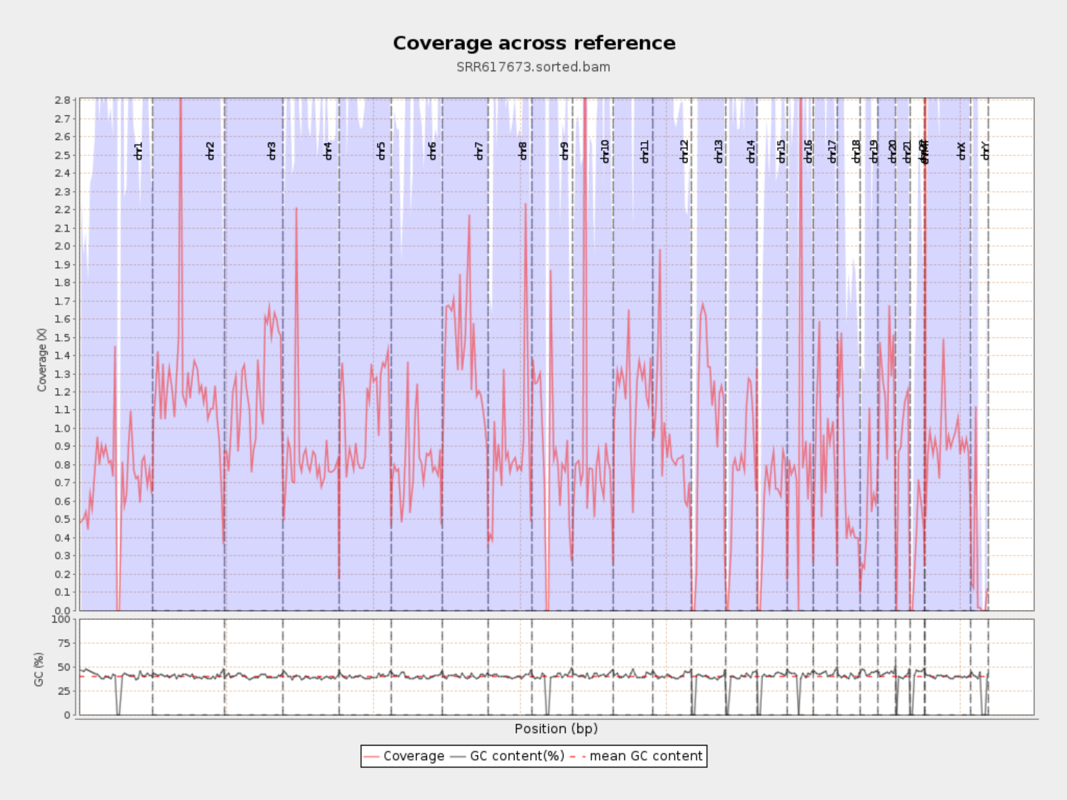
2.7. Chromosome stats

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

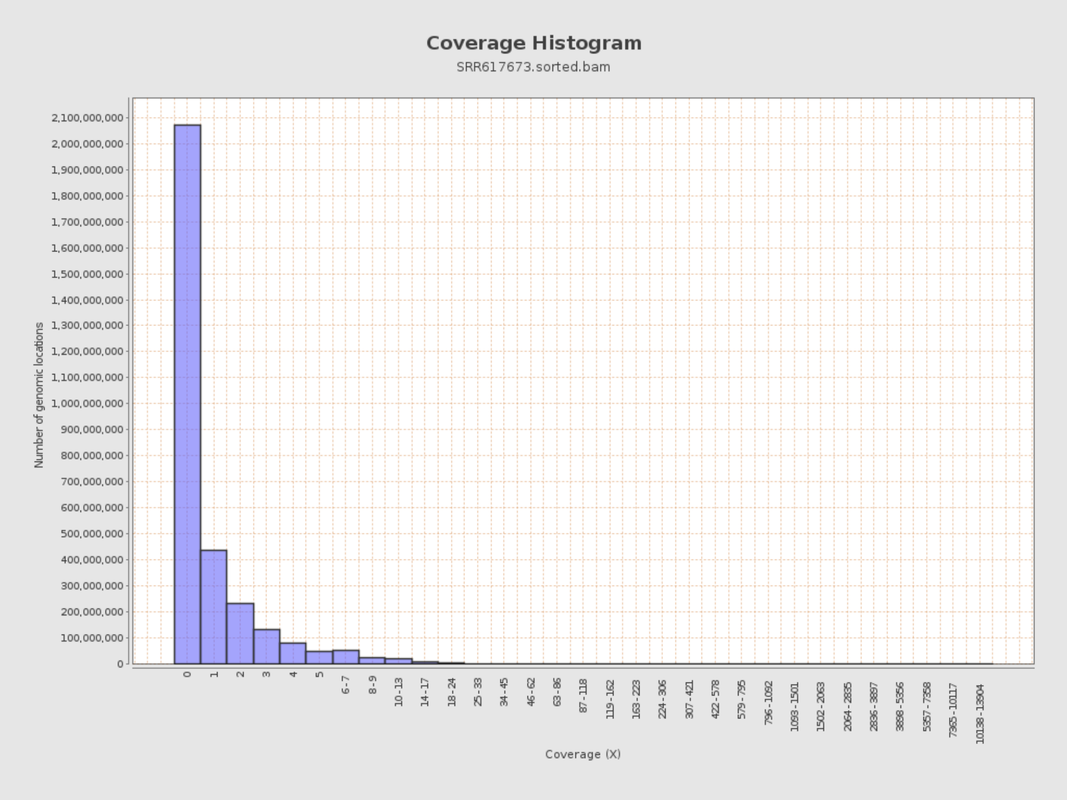
		bases	coverage	deviation
chr1	249250621	177455369	0.712	10.0251
chr2	243199373	298598155	1.2278	11.837
chr3	198022430	242031618	1.2222	2.4726
chr4	191154276	161401540	0.8444	8.1285
chr5	180915260	191148897	1.0566	2.3175
chr6	171115067	140335492	0.8201	5.6183
chr7	159138663	226540930	1.4235	13.1782
chr8	146364022	128501637	0.878	4.0302
chr9	141213431	118192559	0.837	19.3388
chr10	135534747	122352274	0.9027	20.9566
chr11	135006516	158908802	1.177	11.5435
chr12	133851895	123408691	0.922	2.218
chr13	115169878	124143547	1.0779	2.3074
chr14	107349540	82755754	0.7709	2.4432
chr15	102531392	61679175	0.6016	1.762
chr16	90354753	80152867	0.8871	16.4504
chr17	81195210	71302772	0.8782	12.3472
chr18	78077248	53291038	0.6825	17.9379
chr19	59128983	30848448	0.5217	5.9592
chr20	63025520	77838227	1.235	2.9818
chr21	48129895	42167388	0.8761	4.314
chr22	51304566	18731154	0.3651	1.2736
chrMT	16571	3051952	184.1743	128.629
chrX	155270560	143760274	0.9259	4.281

chrY	59373566	11553121	0.1946	16.5998

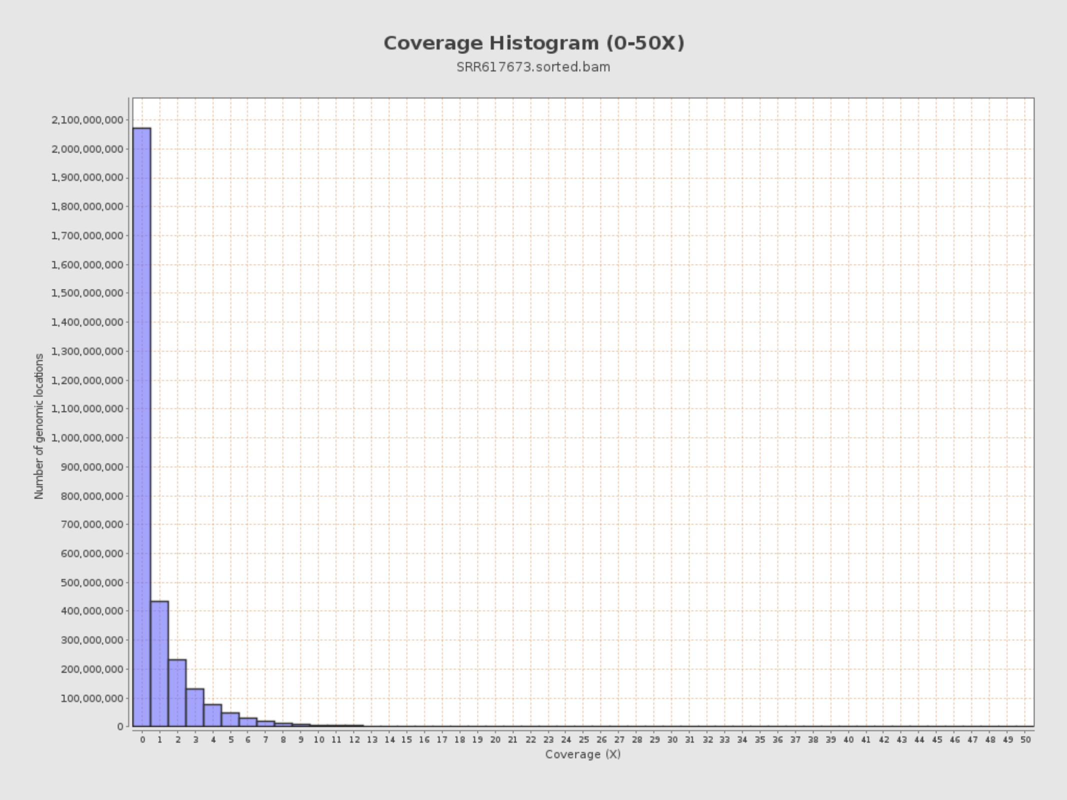
3. Results : Coverage across reference



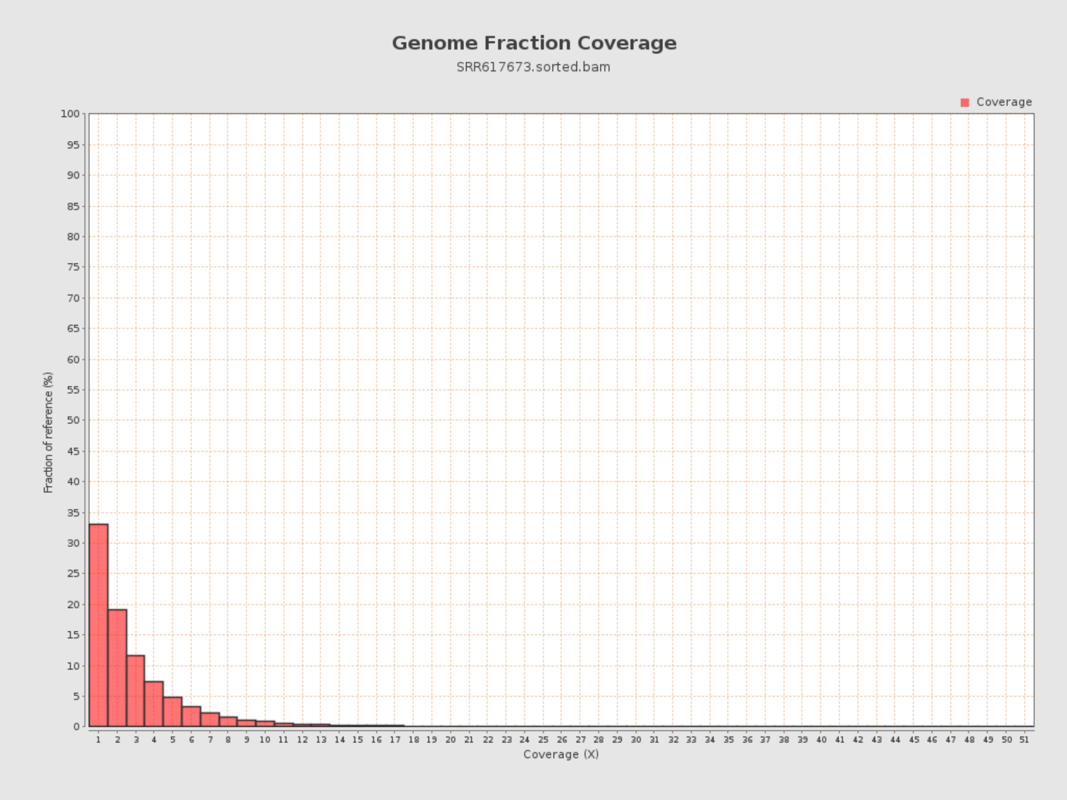
4. Results : Coverage Histogram



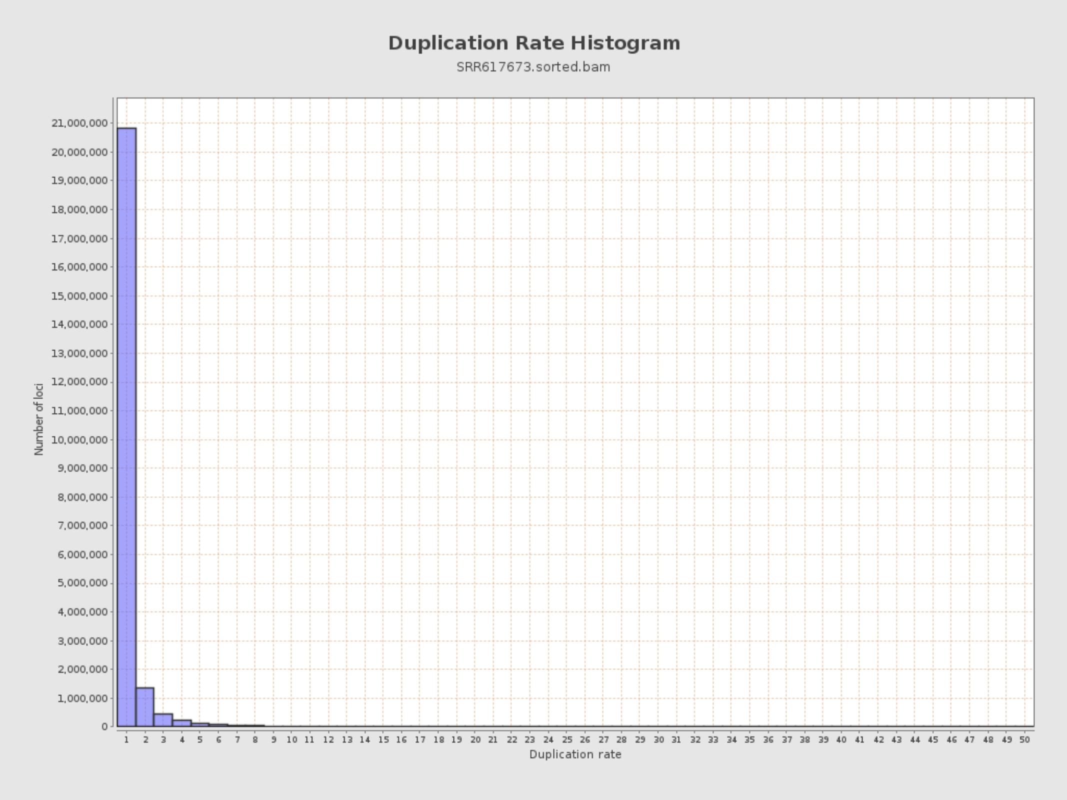
5. Results : Coverage Histogram (0-50X)



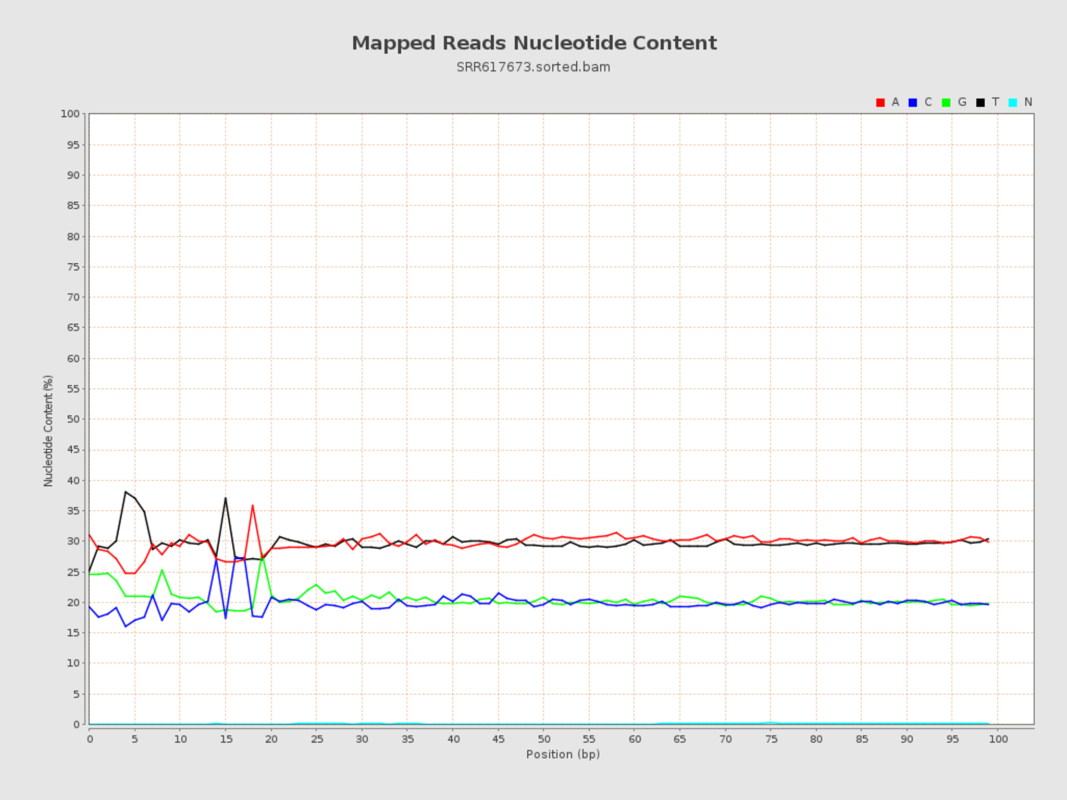
6. Results : Genome Fraction Coverage



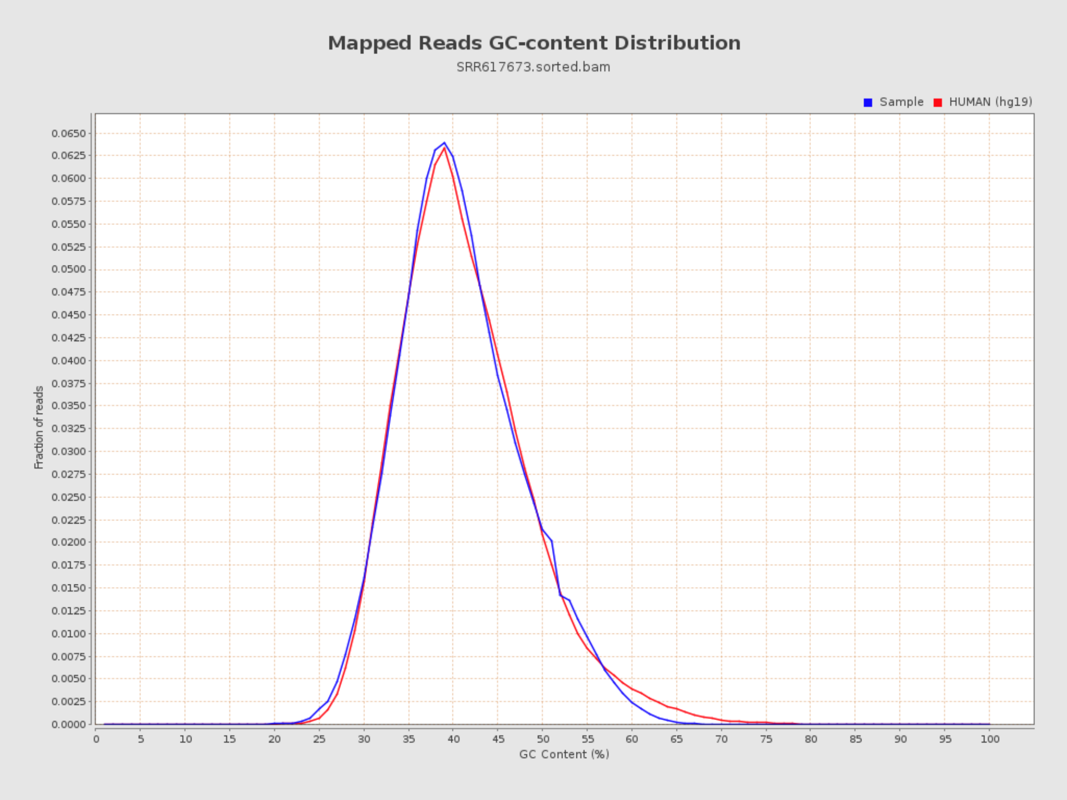
7. Results : Duplication Rate Histogram



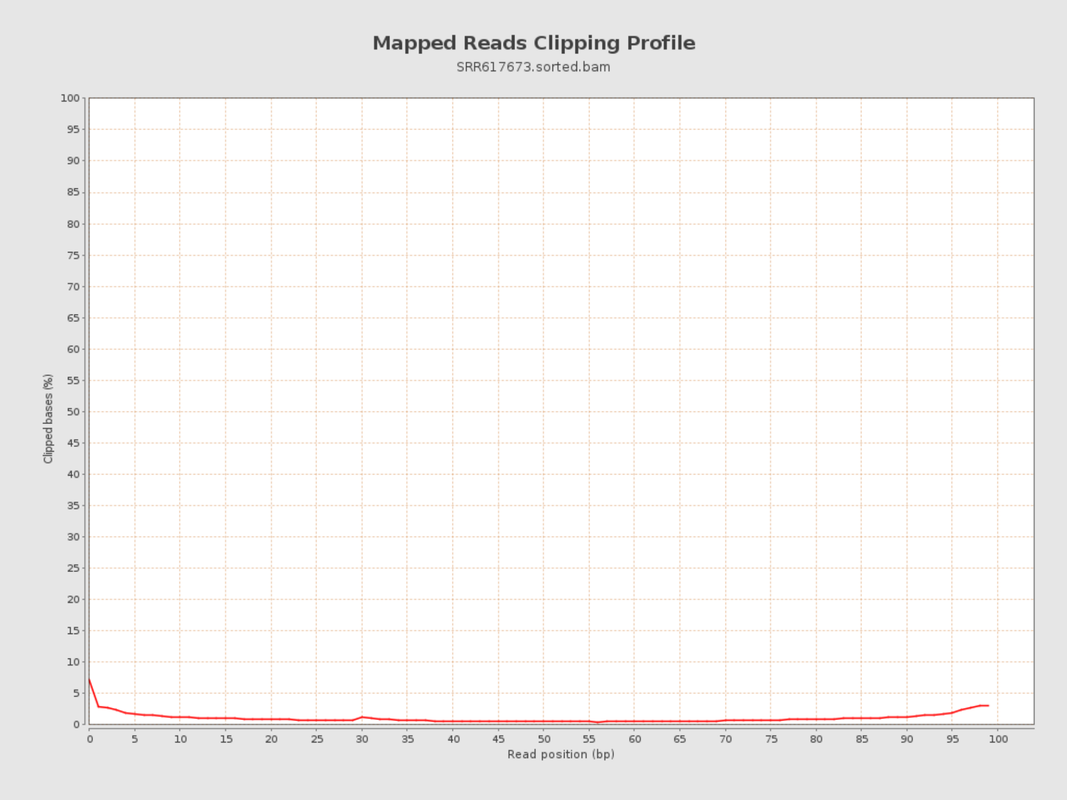
8. Results : Mapped Reads Nucleotide Content



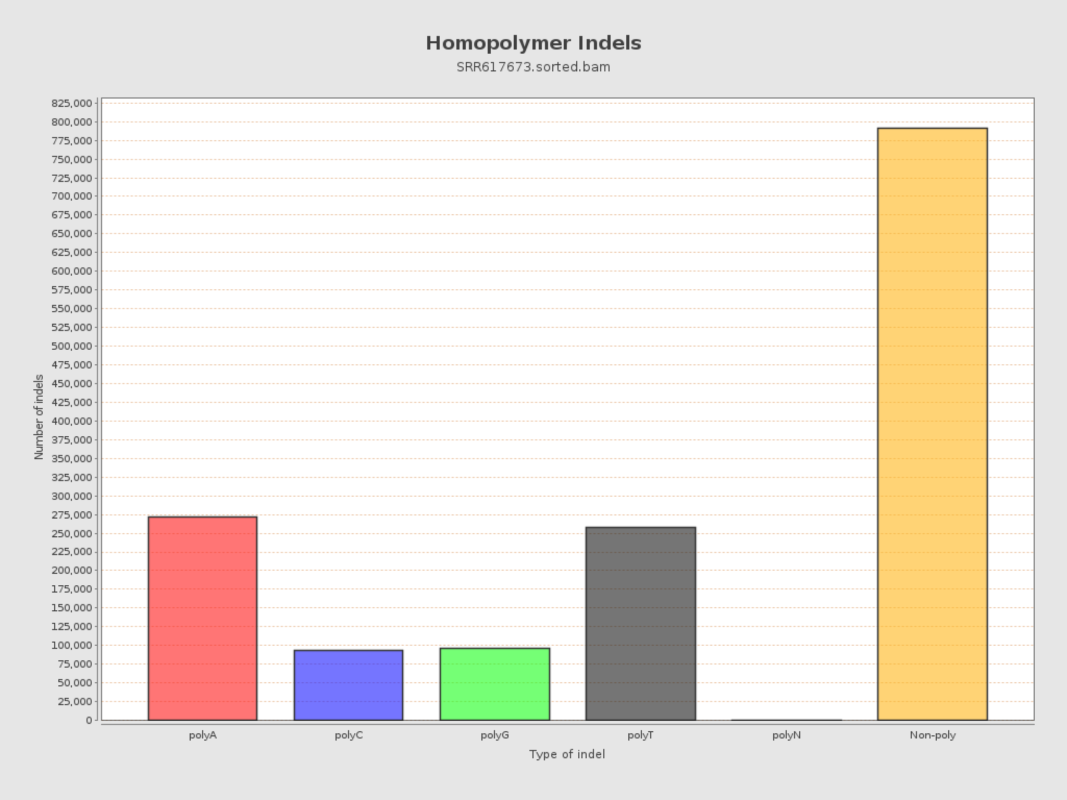
9. Results : Mapped Reads GC-content Distribution



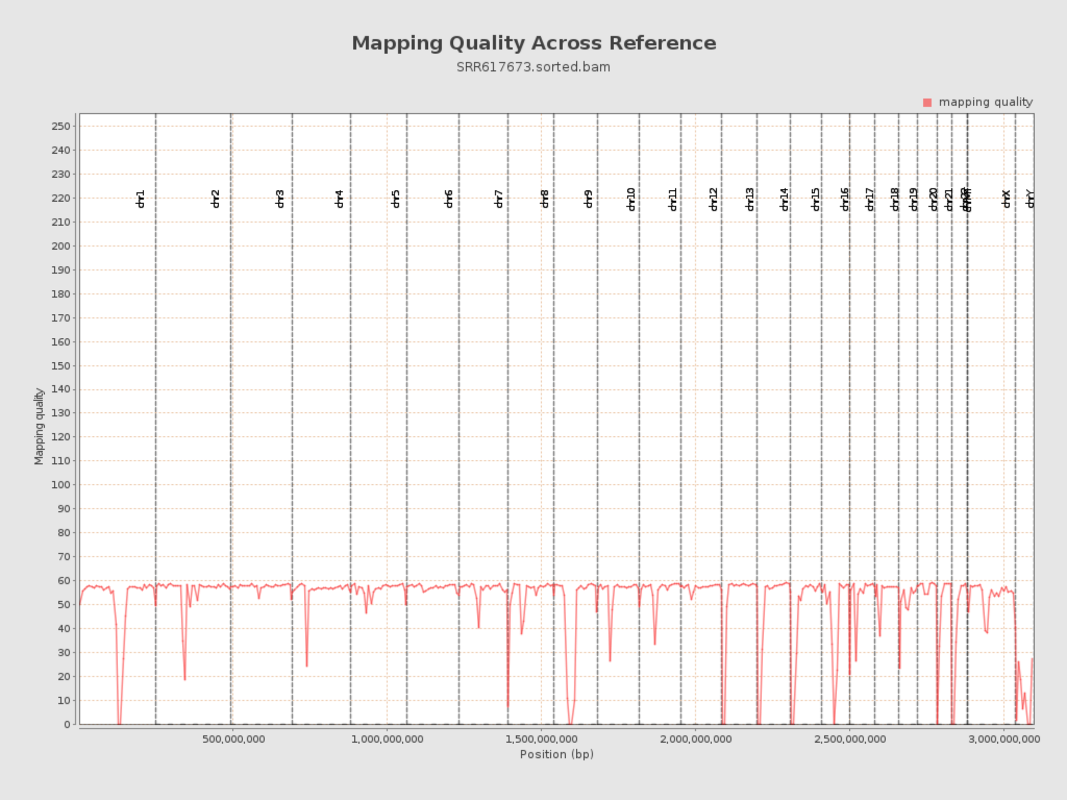
10. Results : Mapped Reads Clipping Profile



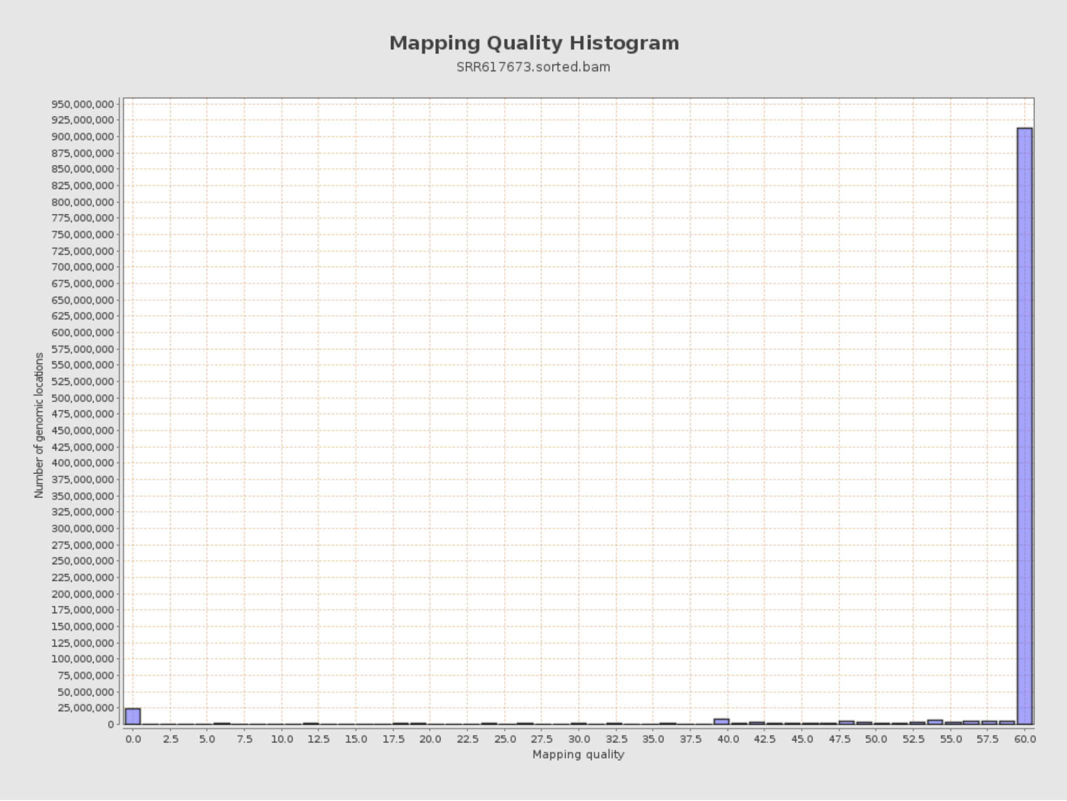
11. Results : Homopolymer Indels



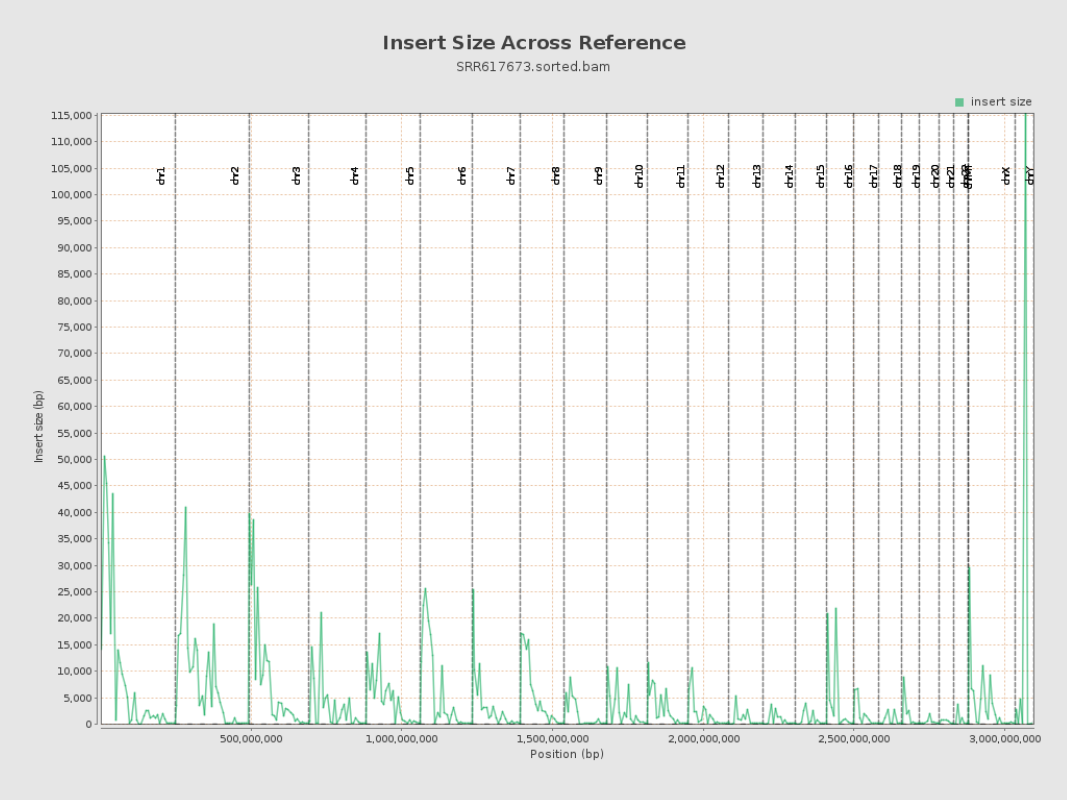
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram