Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:38:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063563.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_SRR6063563 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063563.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:38:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063563.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,208,946
Mapped reads	116,294 / 9.62%
Unmapped reads	1,092,652 / 90.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,022 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	15,499 / 1.28%
Duplication rate	8.8%
Clipped reads	69,632 / 5.76%

2.2. ACGT Content

Number/percentage of A's	1,965,691 / 27.29%
Number/percentage of C's	1,345,242 / 18.68%
Number/percentage of T's	2,255,352 / 31.31%
Number/percentage of G's	1,636,982 / 22.73%
Number/percentage of N's	120 / 0%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0023

Standard Deviation	0.1163

2.4. Mapping Quality

Mean Mapping Quality	43.3

2.5. Mismatches and indels

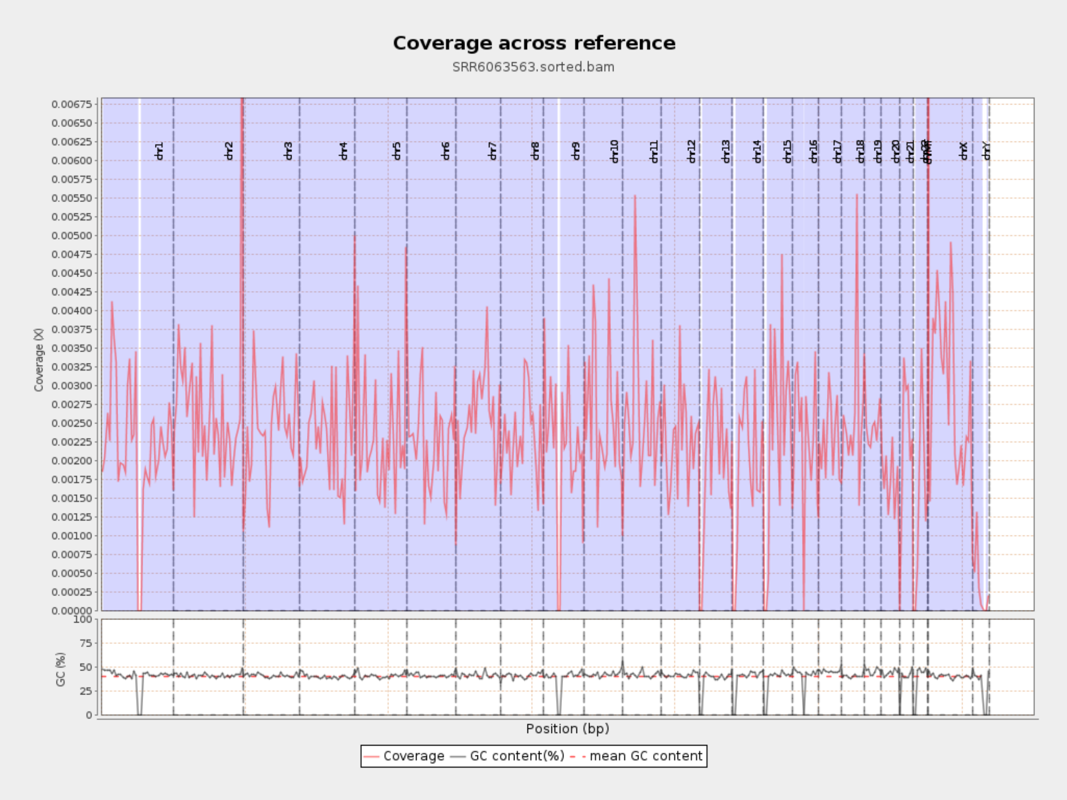
General error rate	0.88%
Mismatches	60,283
Insertions	1,078
Mapped reads with at least one insertion	0.86%
Deletions	2,394
Mapped reads with at least one deletion	1.87%
Homopolymer indels	47.24%

2.6. Chromosome stats

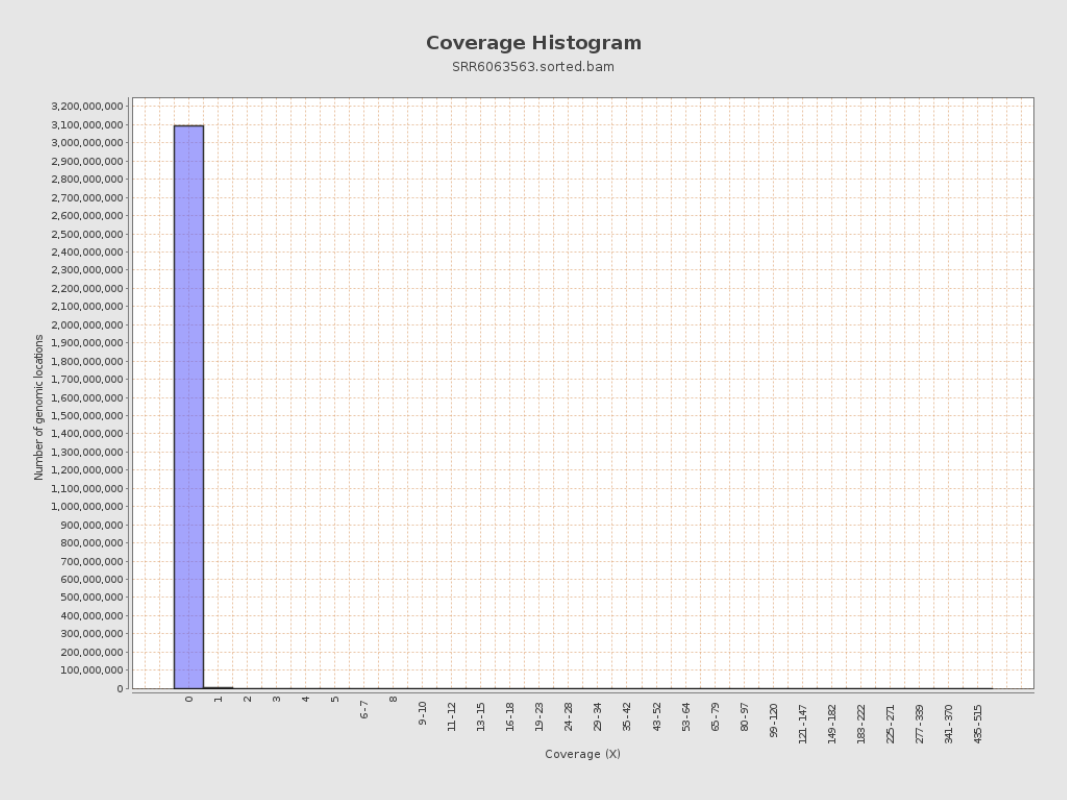
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	557895	0.0022	0.0992
chr2	243199373	661994	0.0027	0.2262
chr3	198022430	478542	0.0024	0.0844
chr4	191154276	439461	0.0023	0.0912
chr5	180915260	413480	0.0023	0.1915
chr6	171115067	392485	0.0023	0.1082
chr7	159138663	406772	0.0026	0.0866

chr8	146364022	342082	0.0023	0.0895
chr9	141213431	307837	0.0022	0.0775
chr10	135534747	358780	0.0026	0.0956
chr11	135006516	359600	0.0027	0.0939
chr12	133851895	304273	0.0023	0.0793
chr13	115169878	223374	0.0019	0.0901
chr14	107349540	204625	0.0019	0.1172
chr15	102531392	234172	0.0023	0.1294
chr16	90354753	208820	0.0023	0.0776
chr17	81195210	186854	0.0023	0.0893
chr18	78077248	201305	0.0026	0.0862
chr19	59128983	146076	0.0025	0.0856
chr20	63025520	109073	0.0017	0.0638
chr21	48129895	109846	0.0023	0.0852
chr22	51304566	78306	0.0015	0.0649
chrMT	16571	1036	0.0625	0.3412
chrX	155270560	458839	0.003	0.0987
chrY	59373566	22199	0.0004	0.051

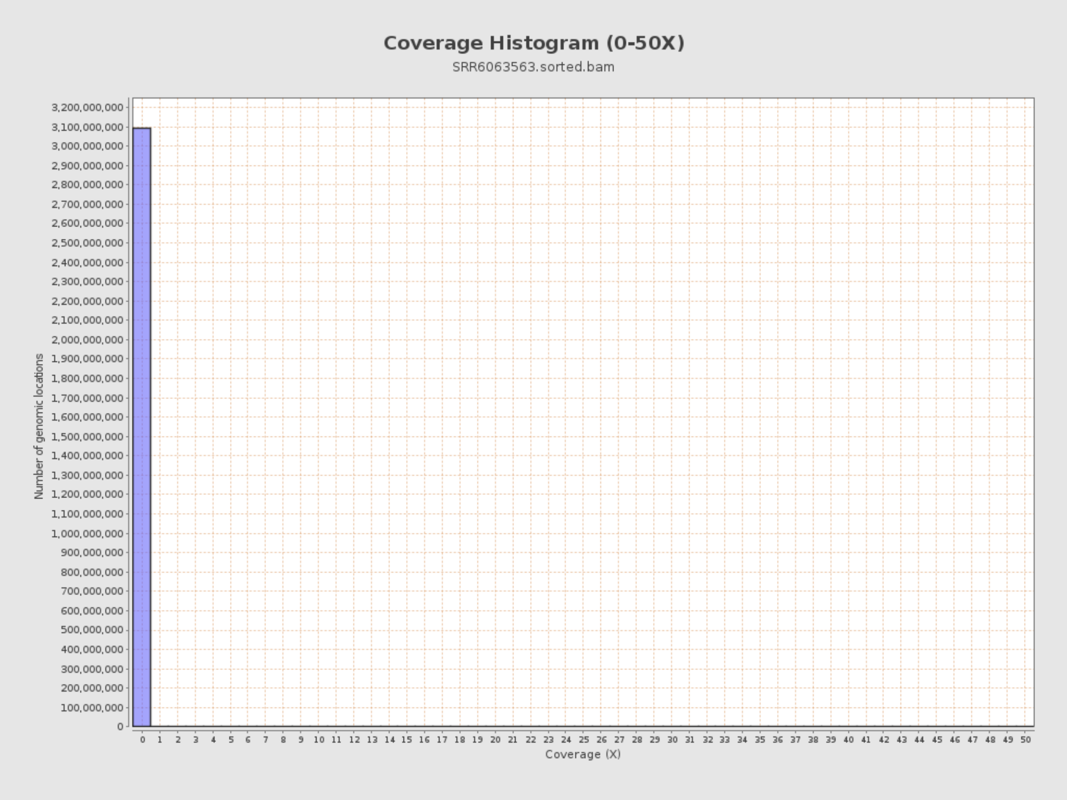
3. Results : Coverage across reference



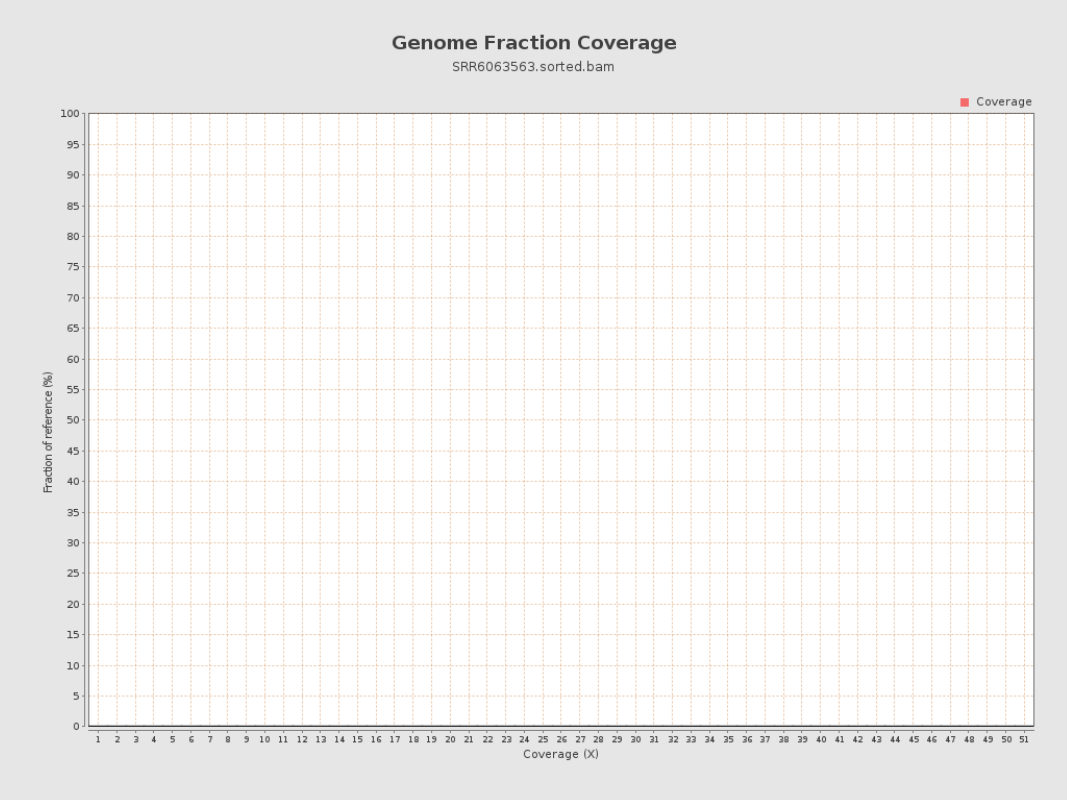
4. Results : Coverage Histogram



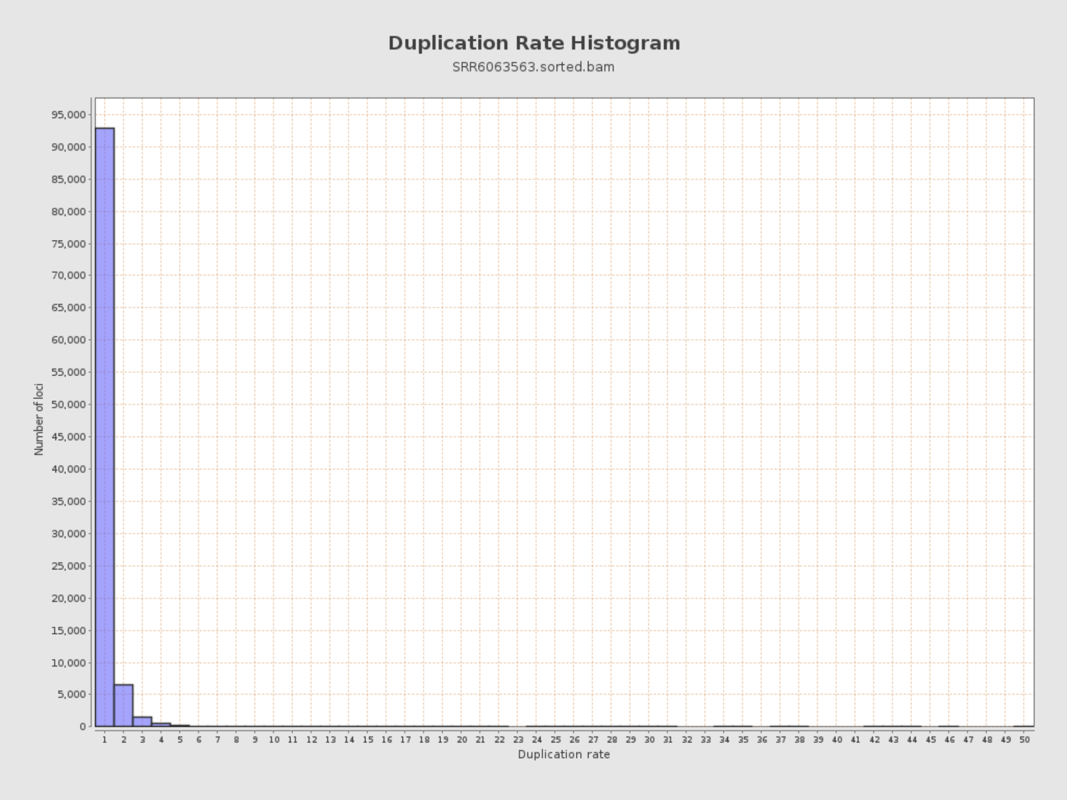
5. Results : Coverage Histogram (0-50X)



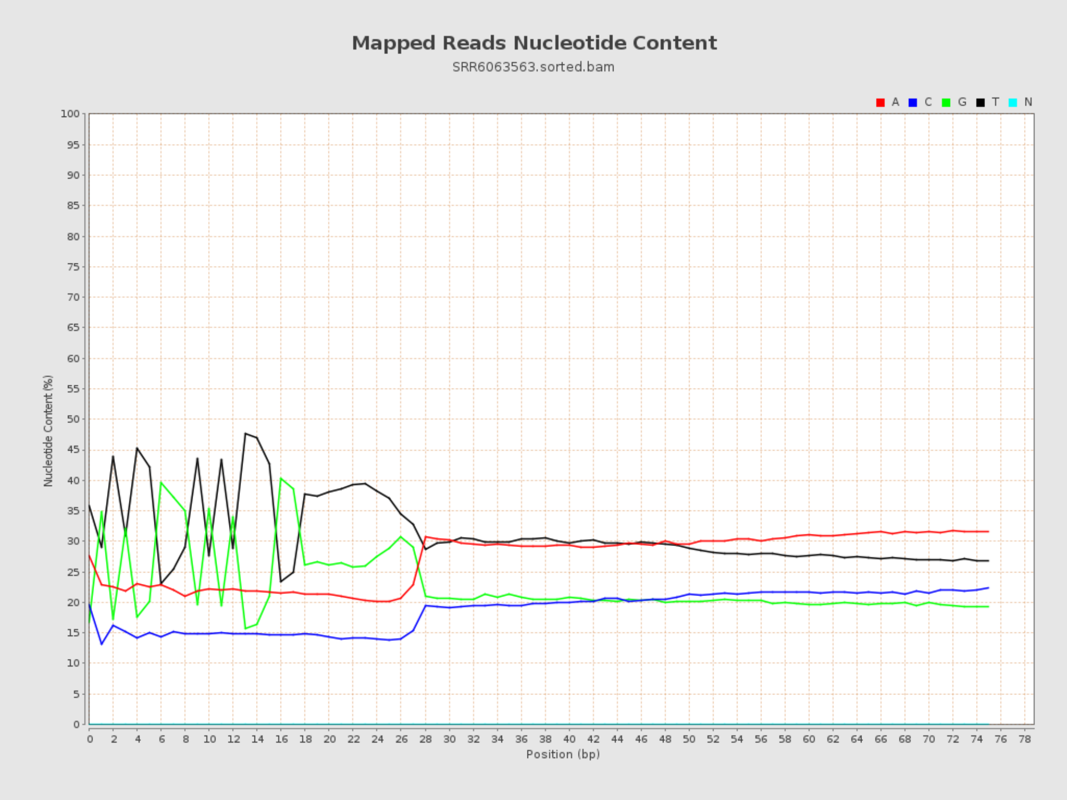
6. Results : Genome Fraction Coverage



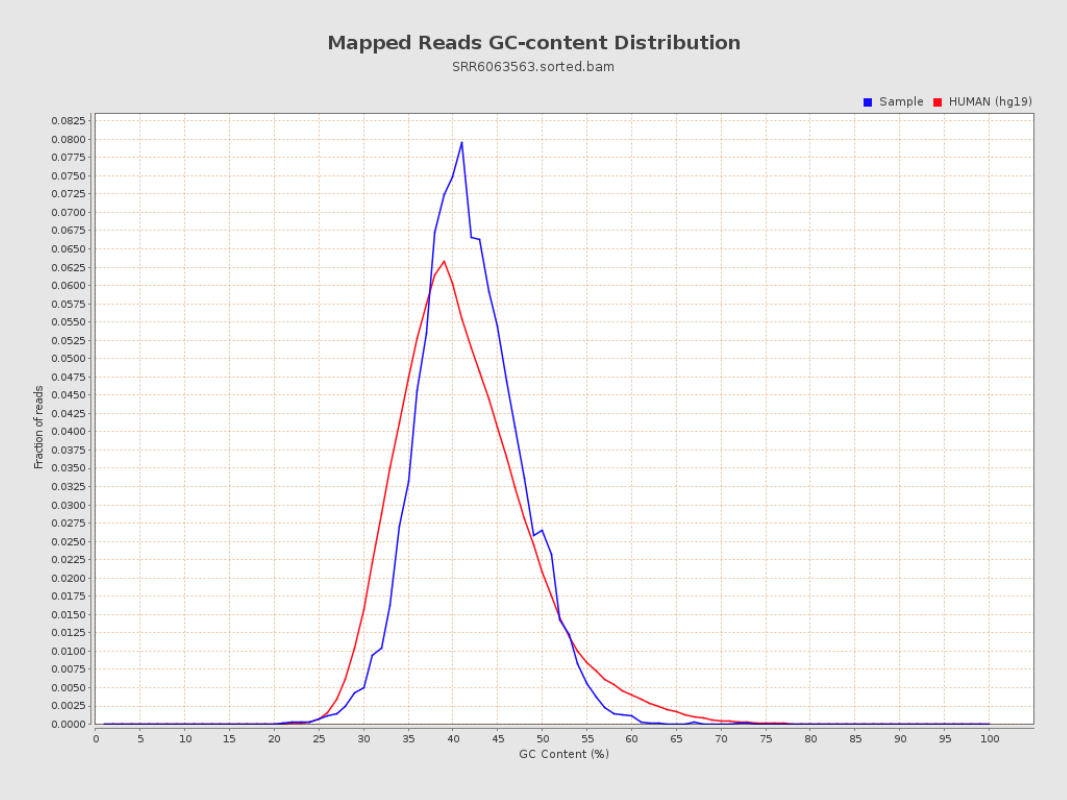
7. Results : Duplication Rate Histogram



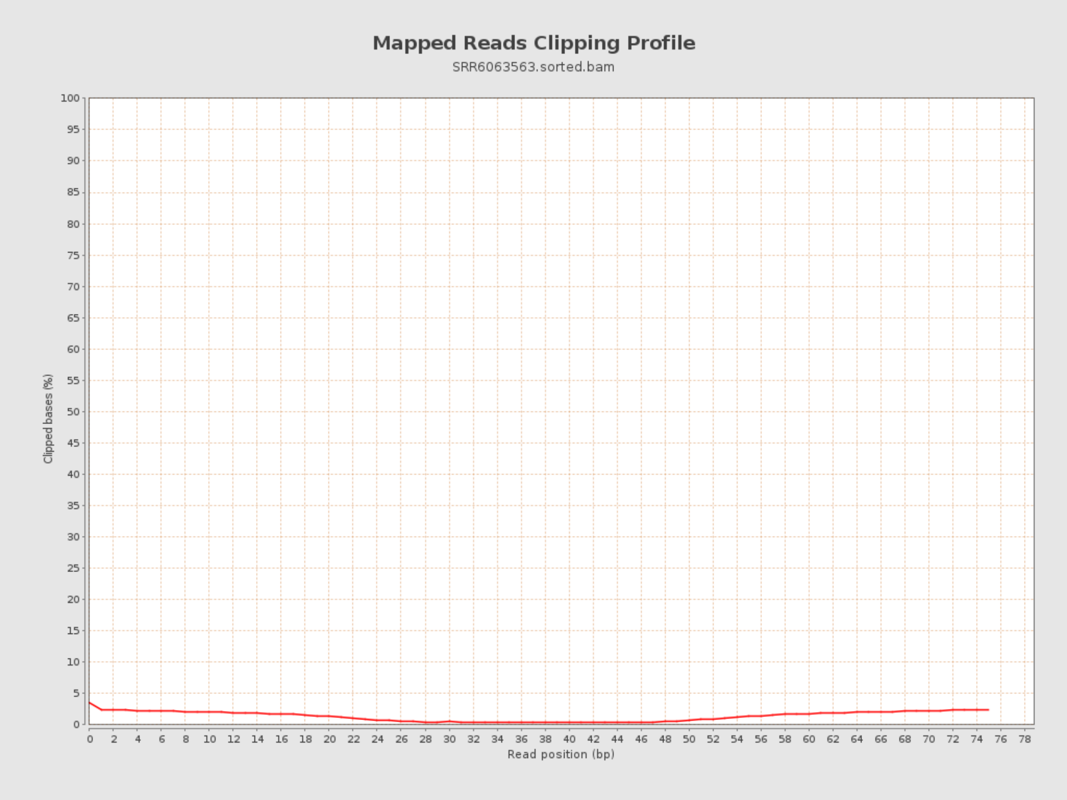
8. Results : Mapped Reads Nucleotide Content



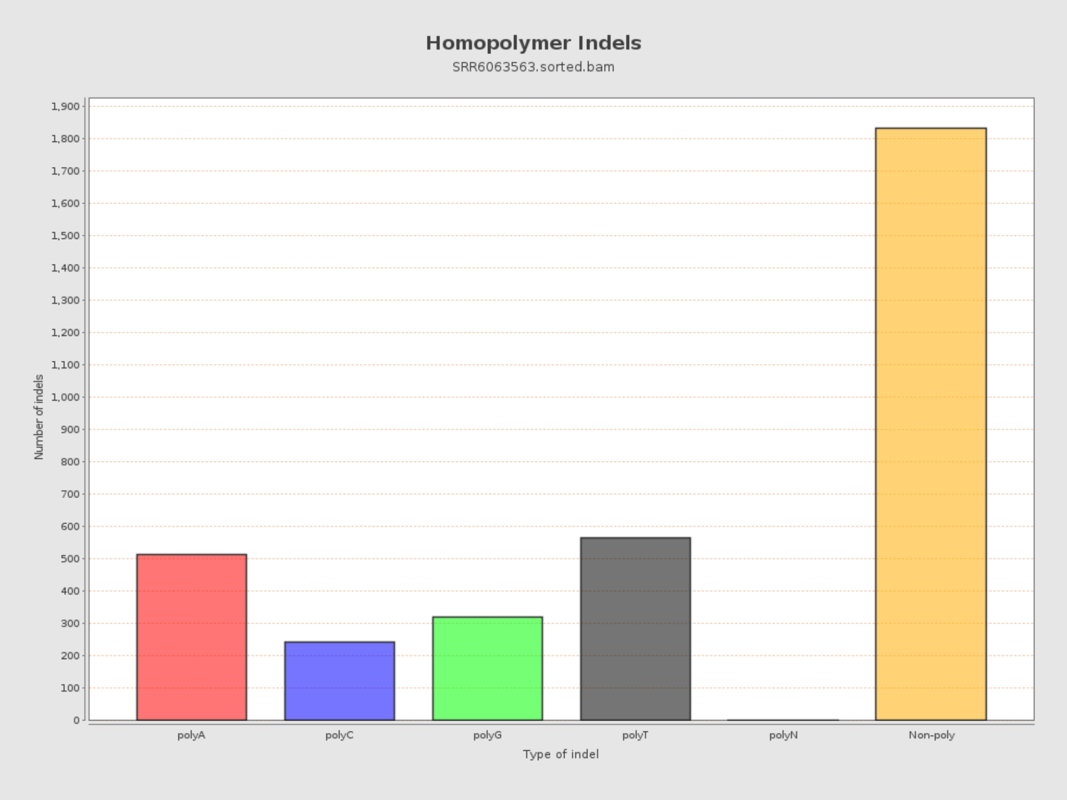
9. Results : Mapped Reads GC-content Distribution



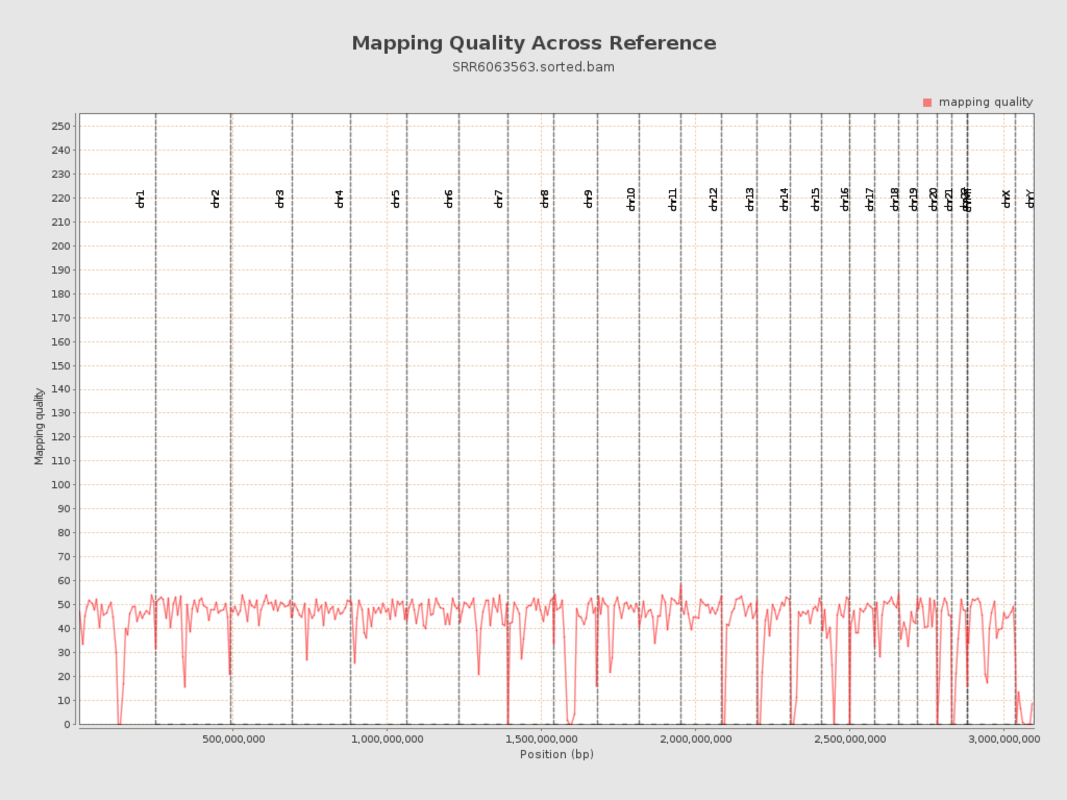
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram