Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:32:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063543.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_SRR6063543 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063543.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:32:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063543.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,599,950
Mapped reads	2,366,911 / 91.04%
Unmapped reads	233,039 / 8.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,684 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	102,071 / 3.93%
Duplication rate	3.02%
Clipped reads	1,078,631 / 41.49%

2.2. ACGT Content

Number/percentage of A's	44,815,747 / 28.38%
Number/percentage of C's	29,260,443 / 18.53%
Number/percentage of T's	49,332,256 / 31.24%
Number/percentage of G's	34,526,494 / 21.86%
Number/percentage of N's	3,409 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.051

Standard Deviation	0.5609

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

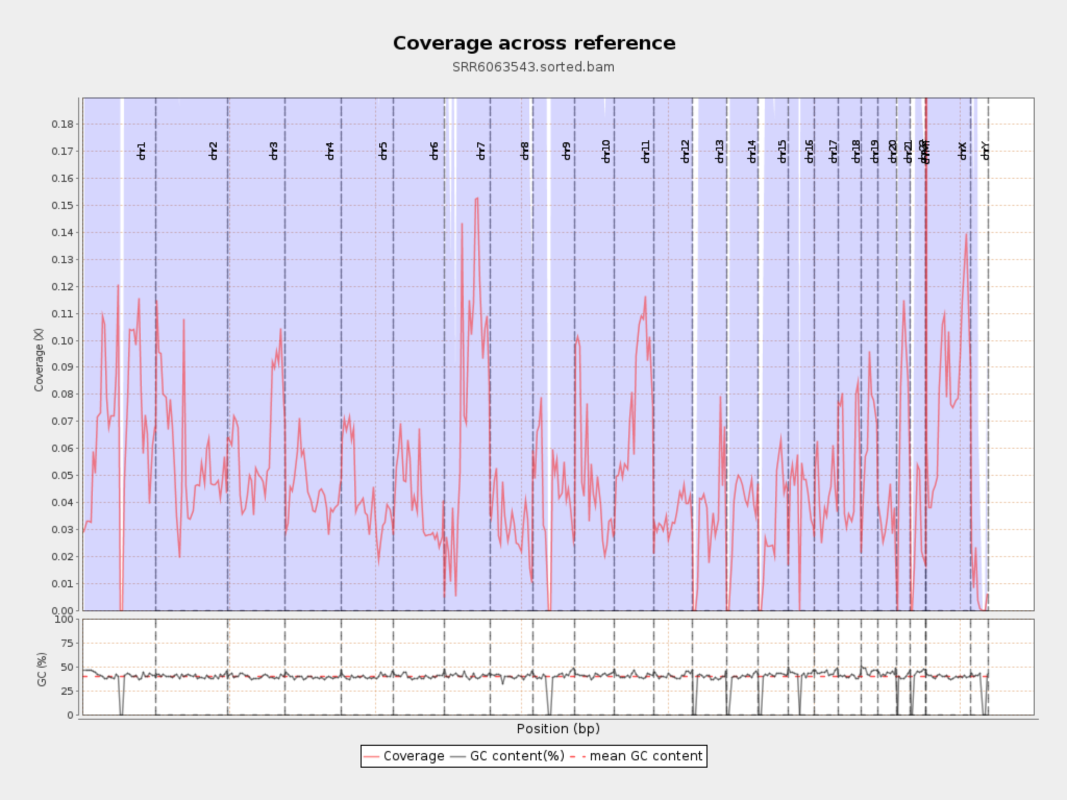
General error rate	0.82%
Mismatches	1,270,267
Insertions	12,545
Mapped reads with at least one insertion	0.53%
Deletions	45,441
Mapped reads with at least one deletion	1.9%
Homopolymer indels	45.58%

2.6. Chromosome stats

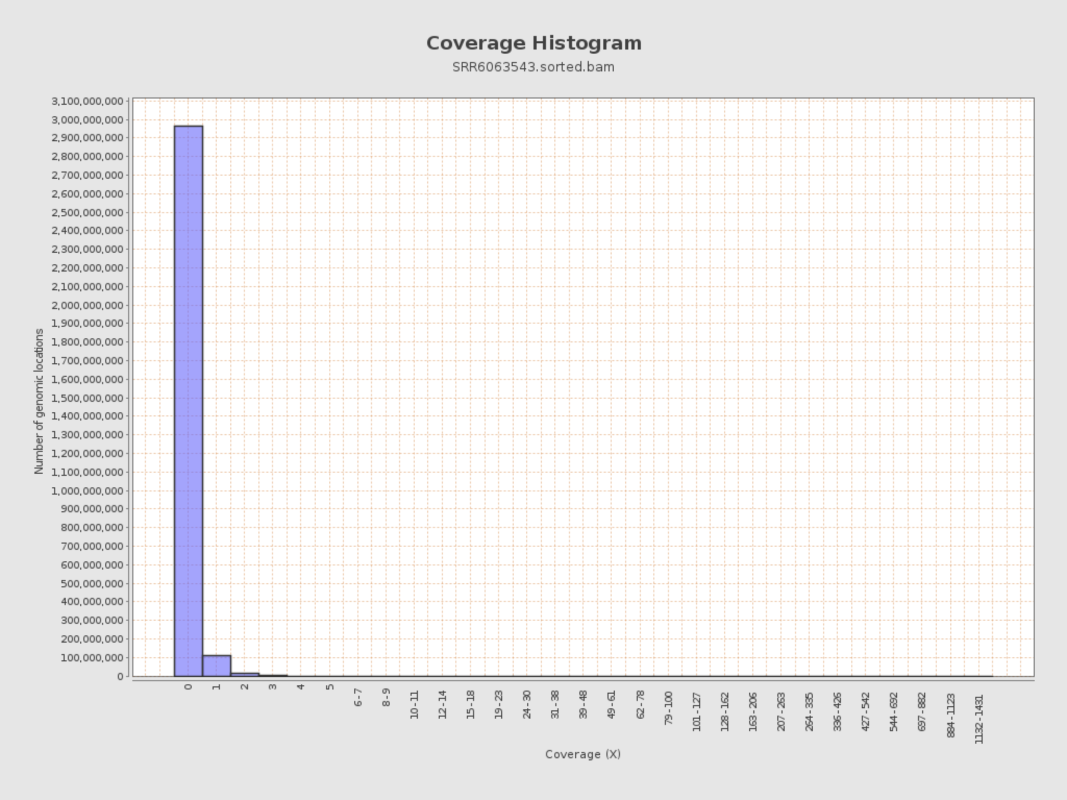
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17075031	0.0685	1.1673
chr2	243199373	13864178	0.057	0.5769
chr3	198022430	12104159	0.0611	0.2896
chr4	191154276	8382646	0.0439	0.2594
chr5	180915260	7727378	0.0427	0.2418
chr6	171115067	7071605	0.0413	0.2641
chr7	159138663	12539031	0.0788	0.9918

chr8	146364022	4644397	0.0317	0.8708
chr9	141213431	6126931	0.0434	0.4343
chr10	135534747	6689505	0.0494	0.4109
chr11	135006516	10326791	0.0765	0.4354
chr12	133851895	4707992	0.0352	0.2354
chr13	115169878	4004972	0.0348	0.2164
chr14	107349540	3907440	0.0364	0.2752
chr15	102531392	3164178	0.0309	0.2098
chr16	90354753	3701305	0.041	0.278
chr17	81195210	3602325	0.0444	0.2772
chr18	78077248	4340177	0.0556	0.7861
chr19	59128983	3862962	0.0653	0.7585
chr20	63025520	2094475	0.0332	0.2315
chr21	48129895	3483633	0.0724	0.3351
chr22	51304566	1290487	0.0252	0.1798
chrMT	16571	62221	3.7548	3.1134
chrX	155270560	12789965	0.0824	0.3934
chrY	59373566	449618	0.0076	0.1915

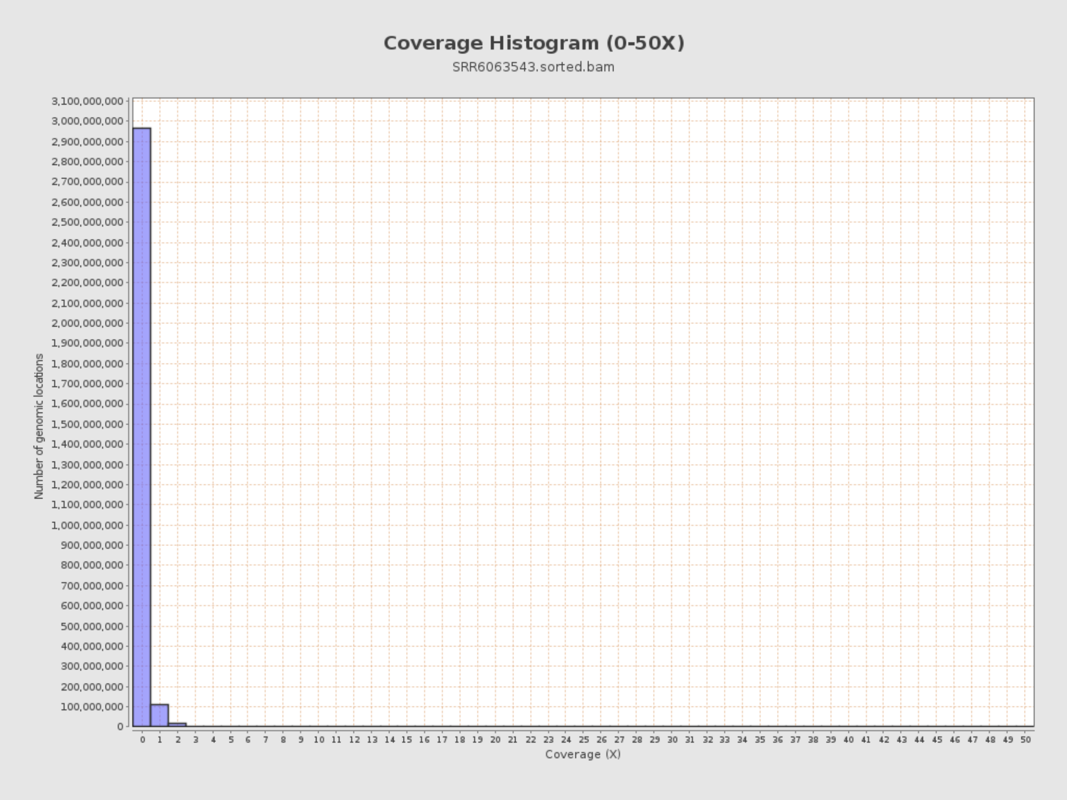
3. Results : Coverage across reference



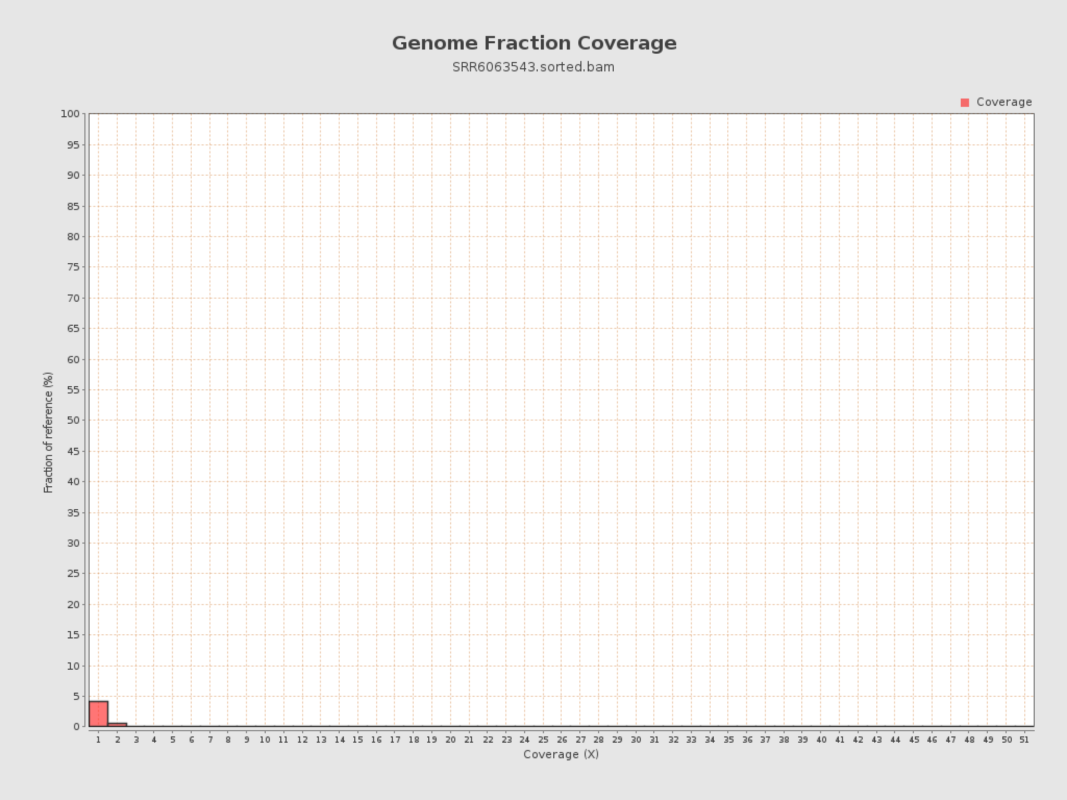
4. Results : Coverage Histogram



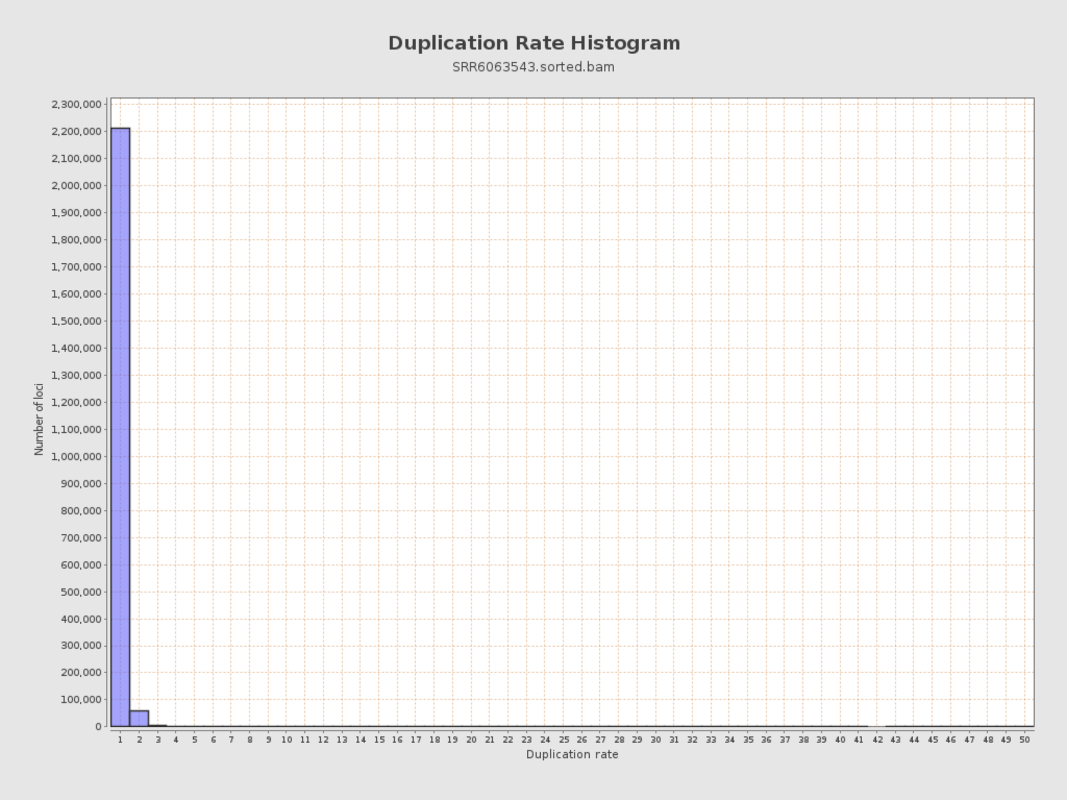
5. Results : Coverage Histogram (0-50X)



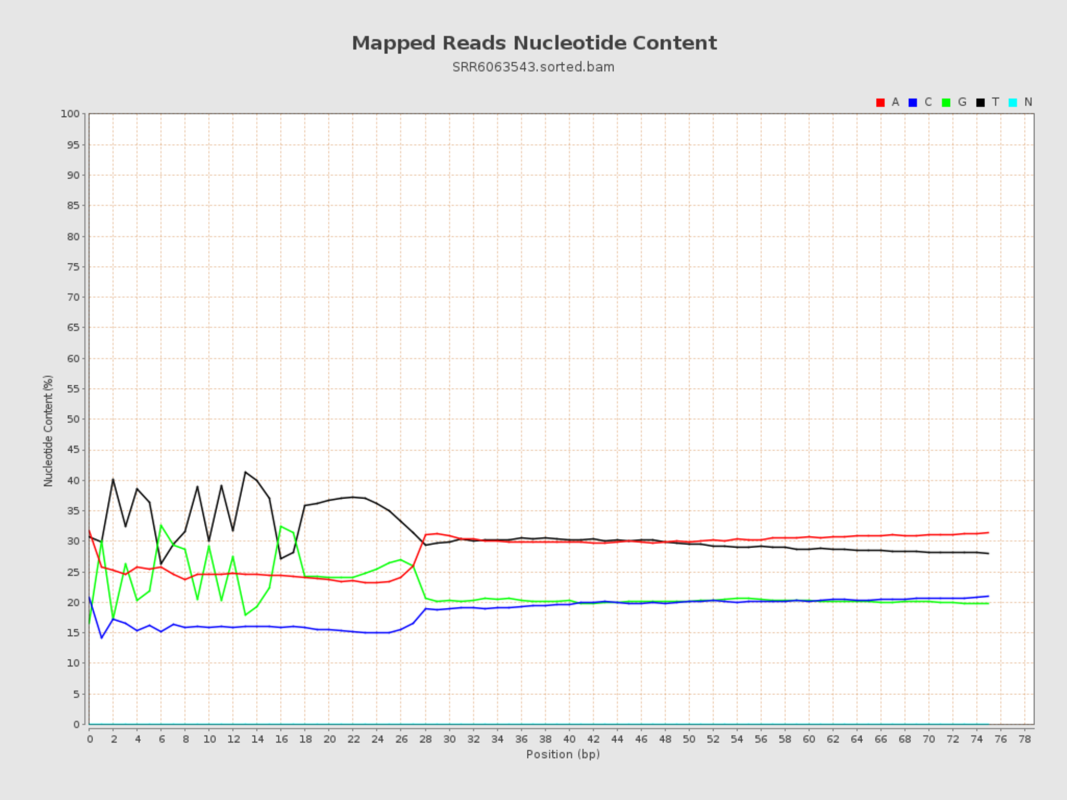
6. Results : Genome Fraction Coverage



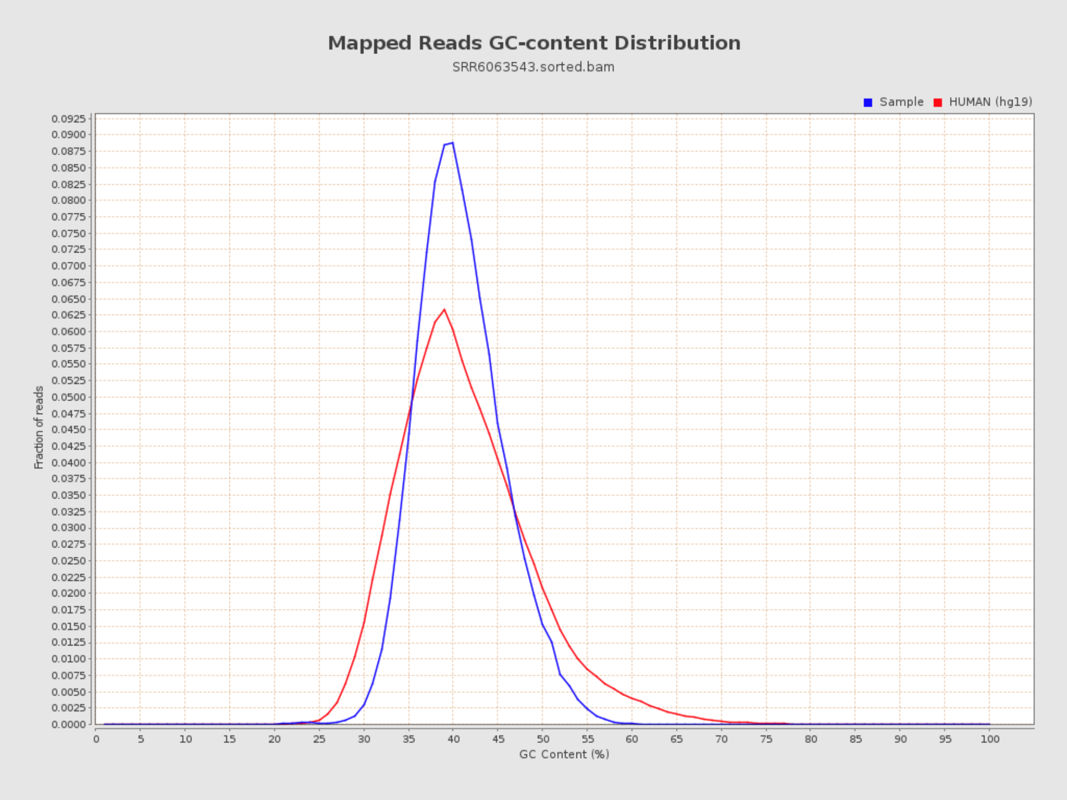
7. Results : Duplication Rate Histogram



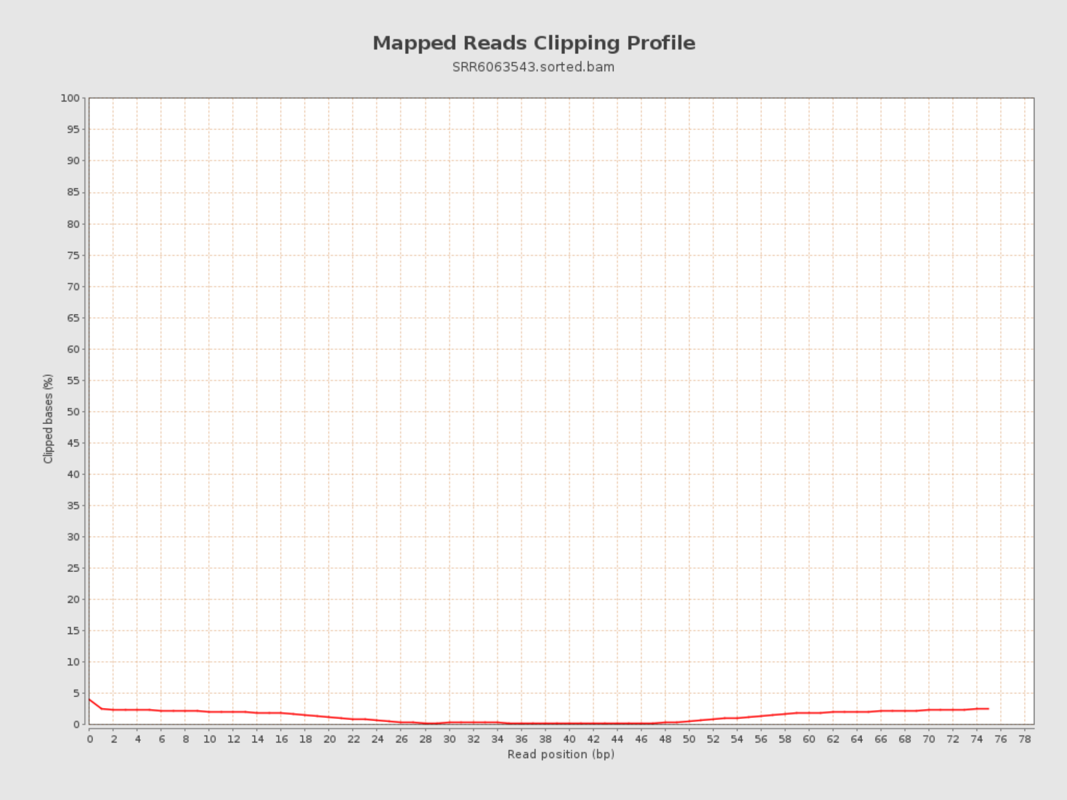
8. Results : Mapped Reads Nucleotide Content



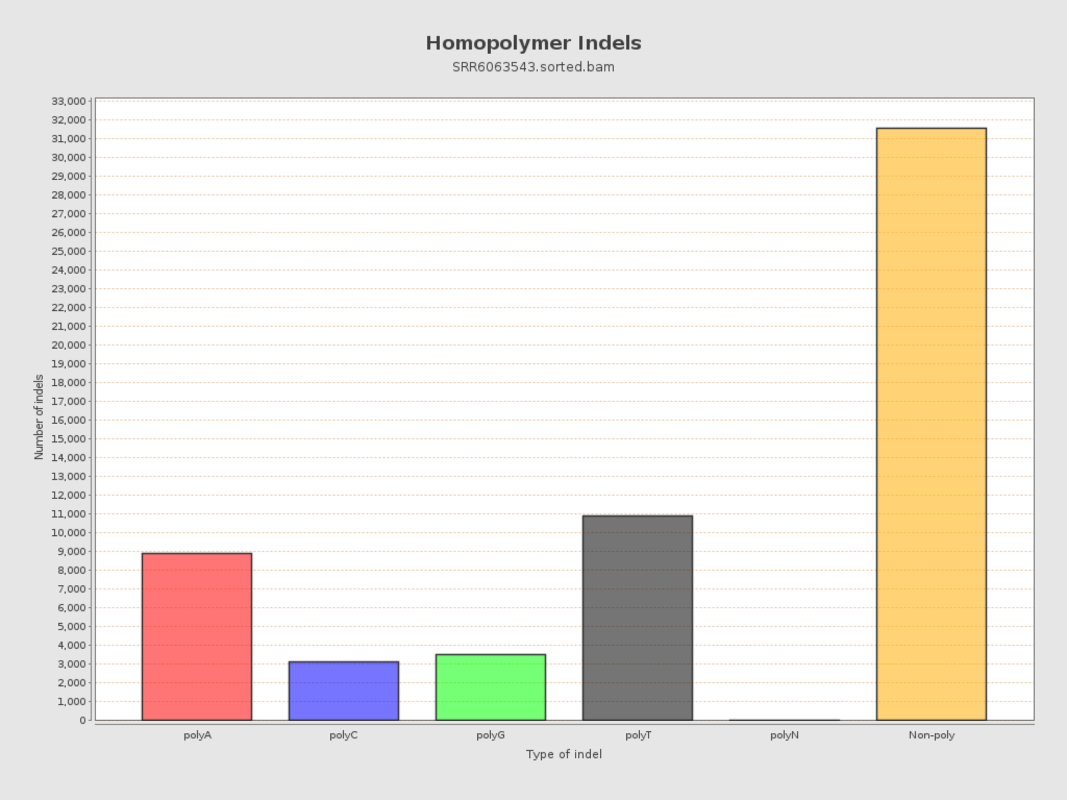
9. Results : Mapped Reads GC-content Distribution



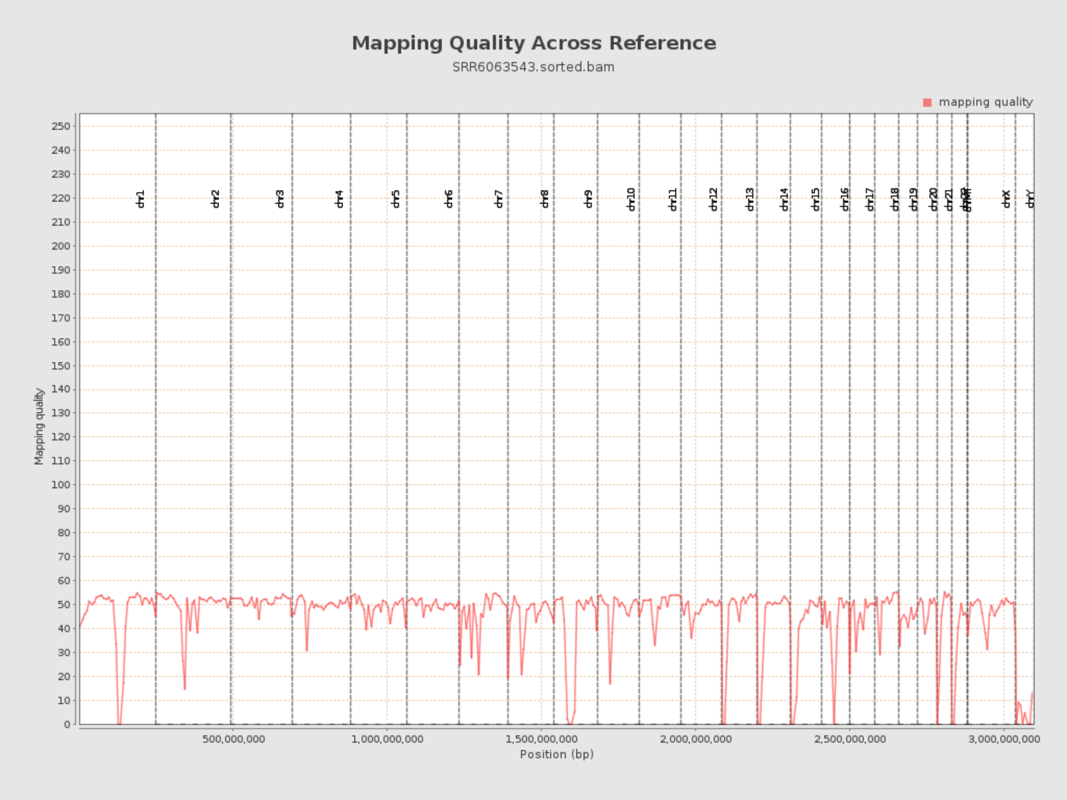
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram