Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:56:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063535.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_SRR6063535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063535.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:56:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,715,643
Mapped reads	2,352,688 / 86.63%
Unmapped reads	362,955 / 13.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,192 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	187,232 / 6.89%
Duplication rate	6.36%
Clipped reads	1,342,386 / 49.43%

2.2. ACGT Content

Number/percentage of A's	40,370,590 / 26.93%
Number/percentage of C's	26,466,330 / 17.65%
Number/percentage of T's	48,828,470 / 32.57%
Number/percentage of G's	34,247,753 / 22.84%
Number/percentage of N's	2,874 / 0%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0485

Standard Deviation	0.5266

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

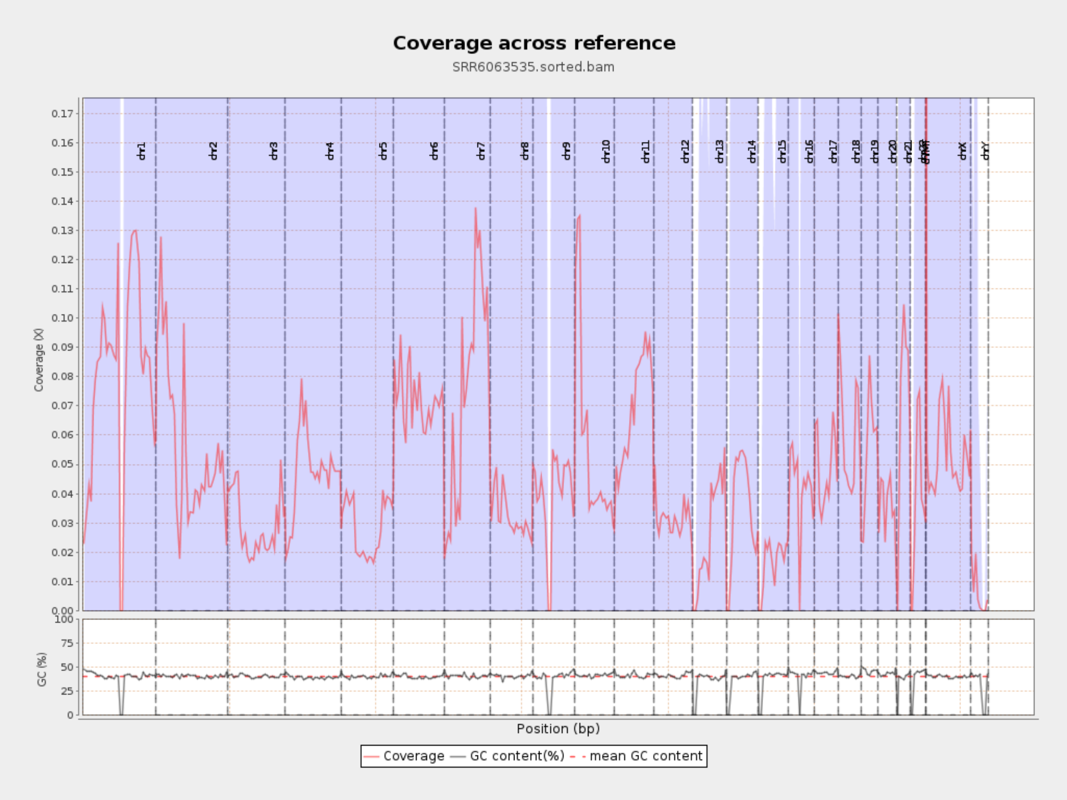
General error rate	0.84%
Mismatches	1,235,366
Insertions	11,306
Mapped reads with at least one insertion	0.48%
Deletions	46,483
Mapped reads with at least one deletion	1.95%
Homopolymer indels	45.11%

2.6. Chromosome stats

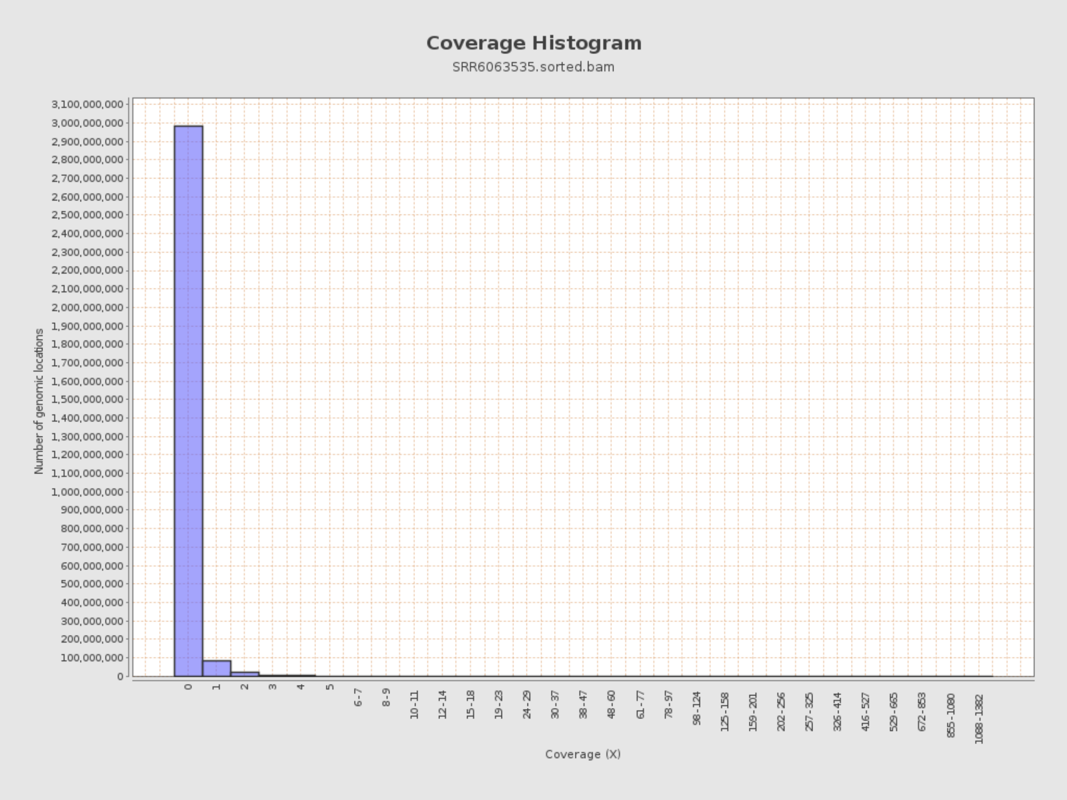
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20023064	0.0803	1.0854
chr2	243199373	13801633	0.0568	0.698
chr3	198022430	5763063	0.0291	0.2176
chr4	191154276	9123667	0.0477	0.2938
chr5	180915260	5142994	0.0284	0.2174
chr6	171115067	12362736	0.0722	0.4019
chr7	159138663	11933021	0.075	0.6997

chr8	146364022	4697403	0.0321	0.8112
chr9	141213431	5587433	0.0396	0.4182
chr10	135534747	7656605	0.0565	0.3924
chr11	135006516	9310280	0.069	0.4483
chr12	133851895	4236650	0.0317	0.2523
chr13	115169878	3094454	0.0269	0.2105
chr14	107349540	3784239	0.0353	0.2773
chr15	102531392	1655154	0.0161	0.1783
chr16	90354753	3678989	0.0407	0.2805
chr17	81195210	4011068	0.0494	0.3066
chr18	78077248	4734730	0.0606	0.686
chr19	59128983	3329127	0.0563	0.6814
chr20	63025520	2273883	0.0361	0.2611
chr21	48129895	3337179	0.0693	0.3525
chr22	51304566	1927933	0.0376	0.2417
chrMT	16571	22630	1.3656	1.6629
chrX	155270560	8143120	0.0524	0.3327
chrY	59373566	360783	0.0061	0.1709

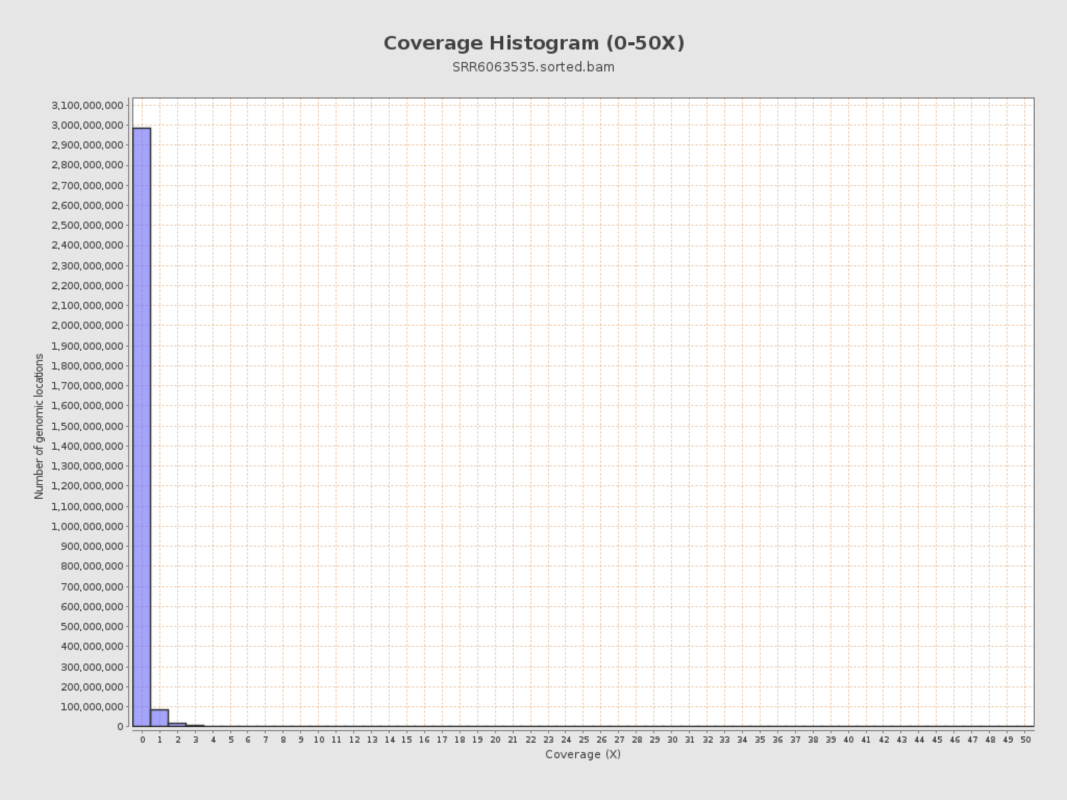
3. Results : Coverage across reference



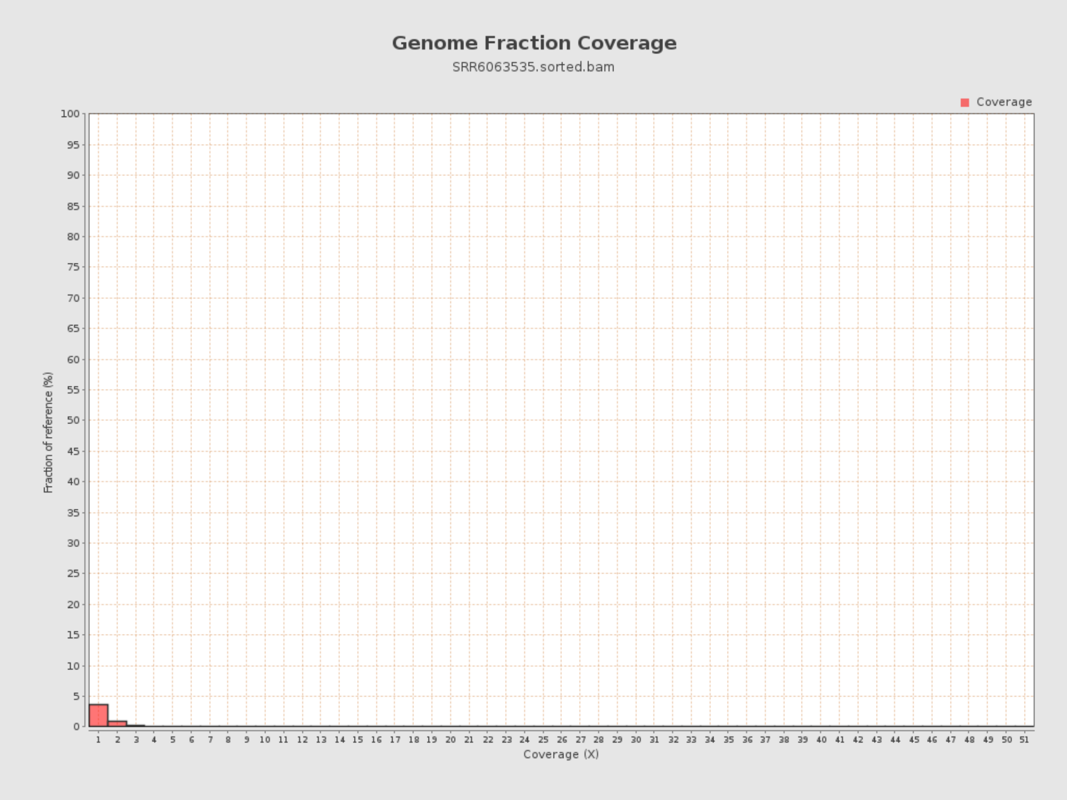
4. Results : Coverage Histogram



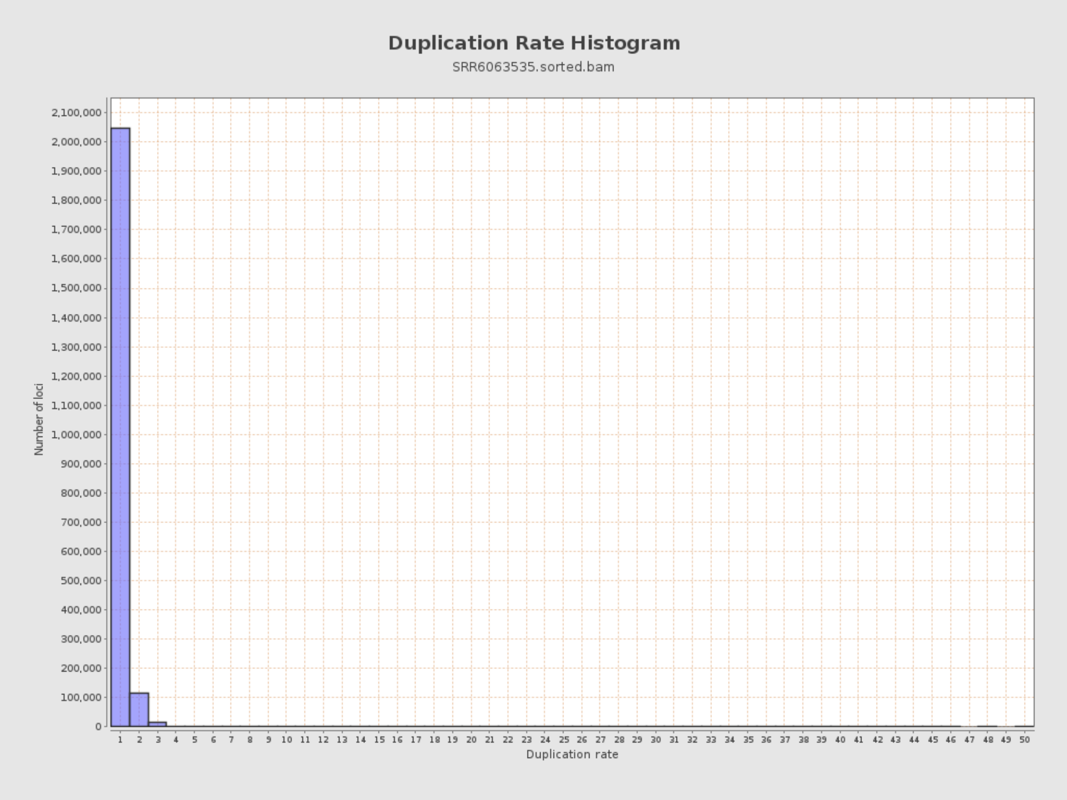
5. Results : Coverage Histogram (0-50X)



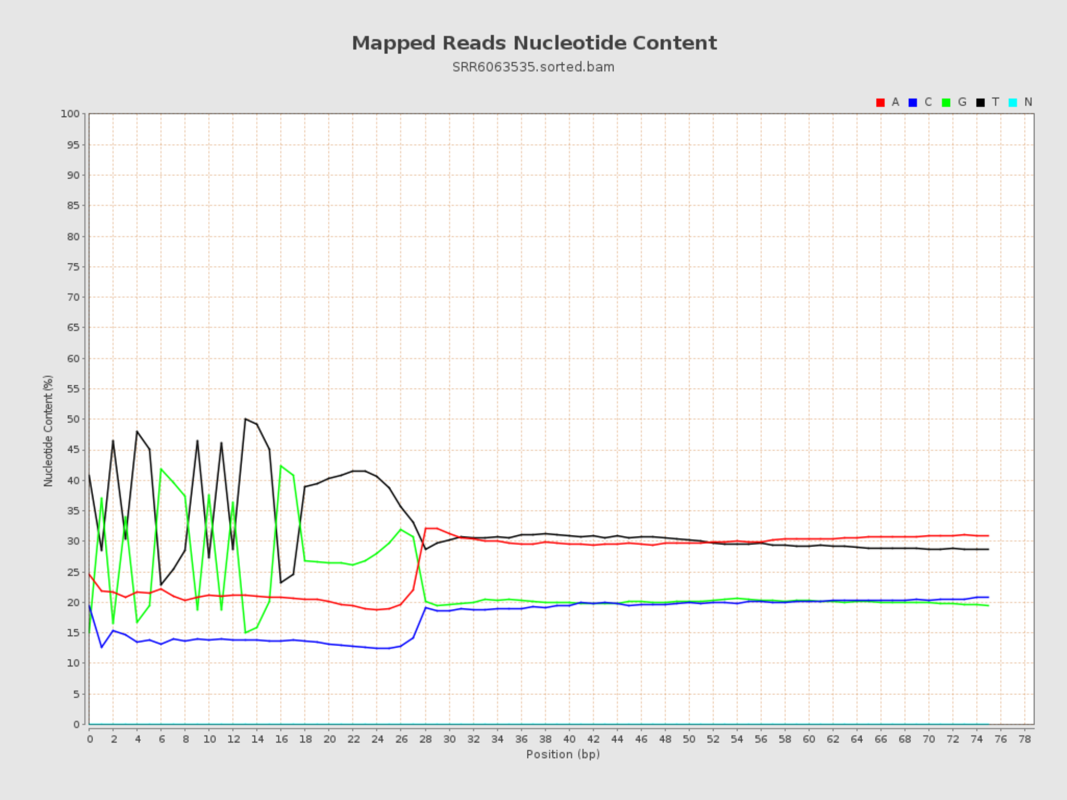
6. Results : Genome Fraction Coverage



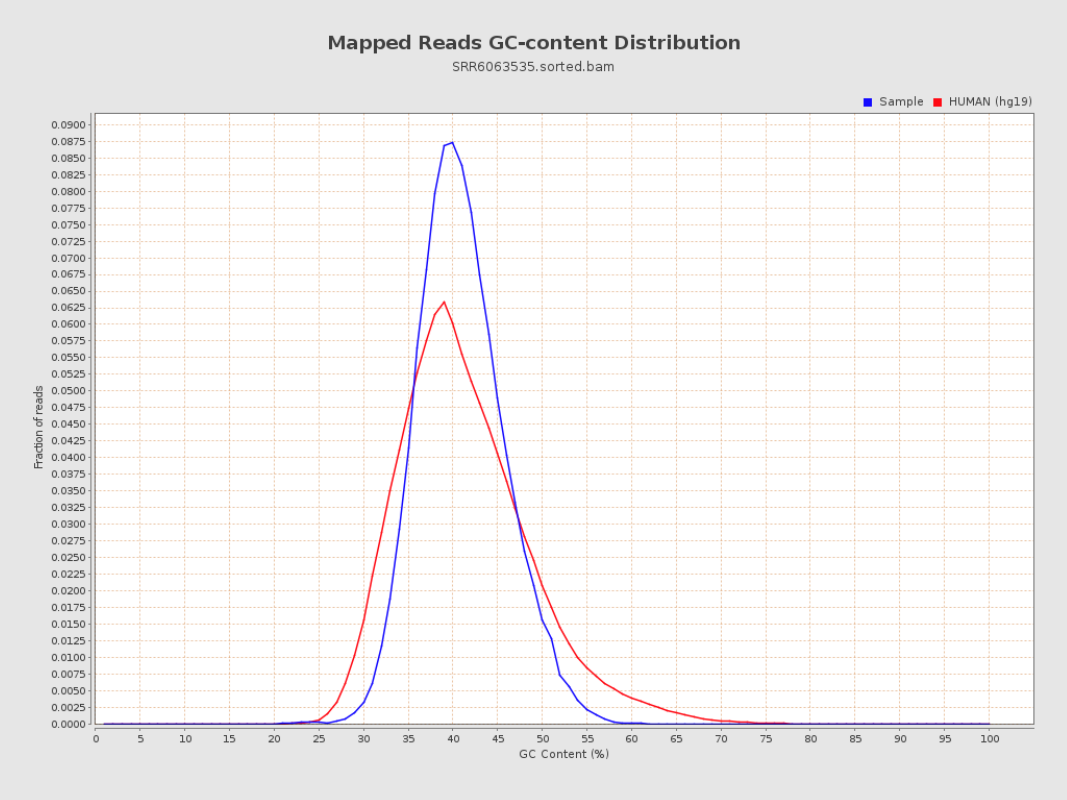
7. Results : Duplication Rate Histogram



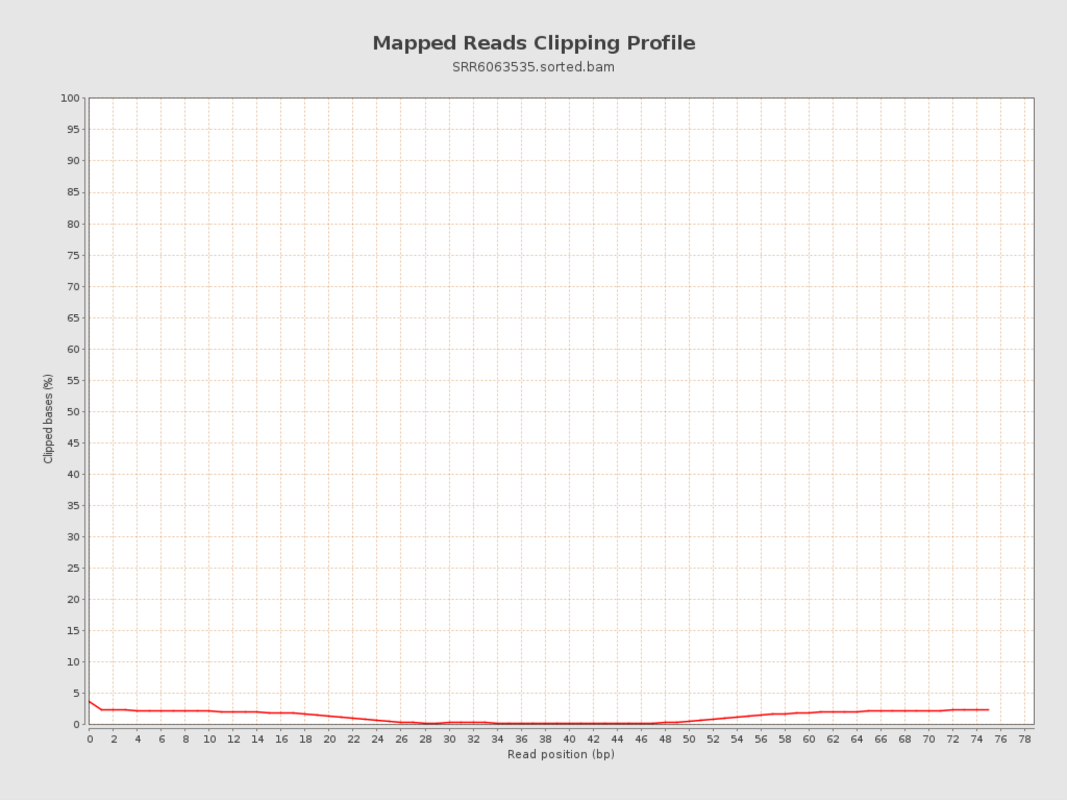
8. Results : Mapped Reads Nucleotide Content



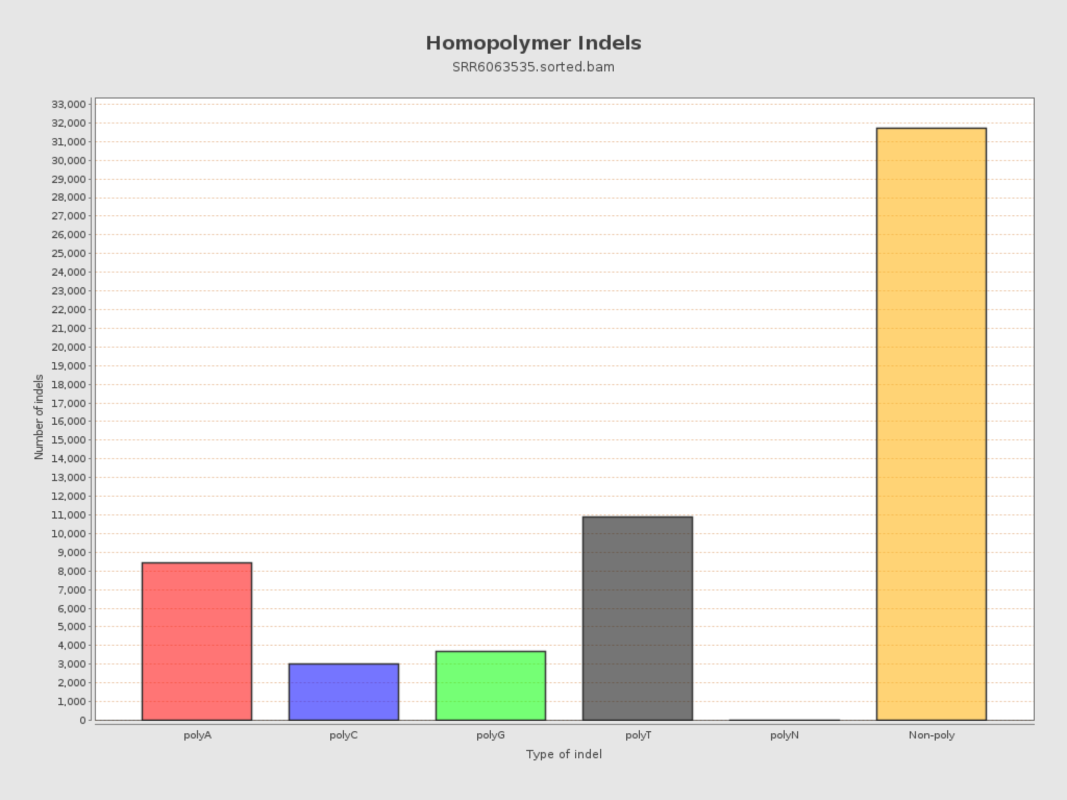
9. Results : Mapped Reads GC-content Distribution



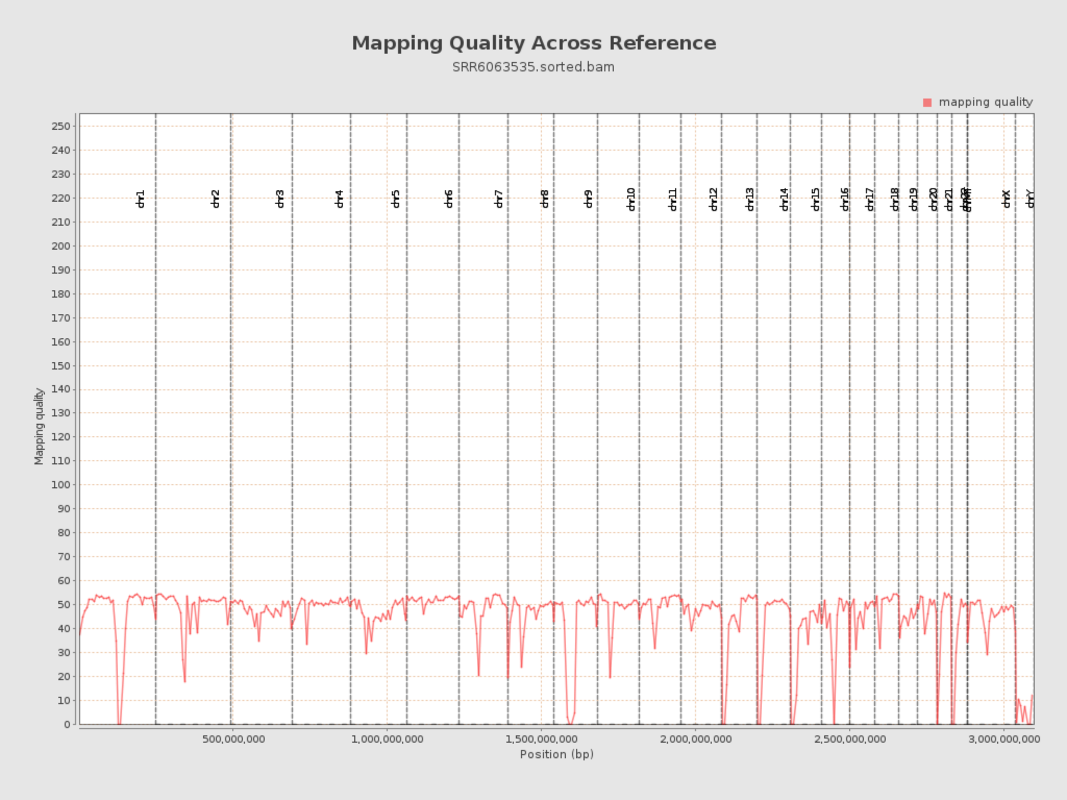
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram