Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:23:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081778.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_SRR3081778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:23:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,454,988
Mapped reads	2,191,547 / 89.27%
Unmapped reads	263,441 / 10.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,388 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	91,227 / 3.72%
Duplication rate	3.28%
Clipped reads	898,070 / 36.58%

2.2. ACGT Content

Number/percentage of A's	39,997,191 / 27.08%
Number/percentage of C's	29,112,816 / 19.71%
Number/percentage of T's	44,644,631 / 30.23%
Number/percentage of G's	33,925,180 / 22.97%
Number/percentage of N's	1,698 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.387

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

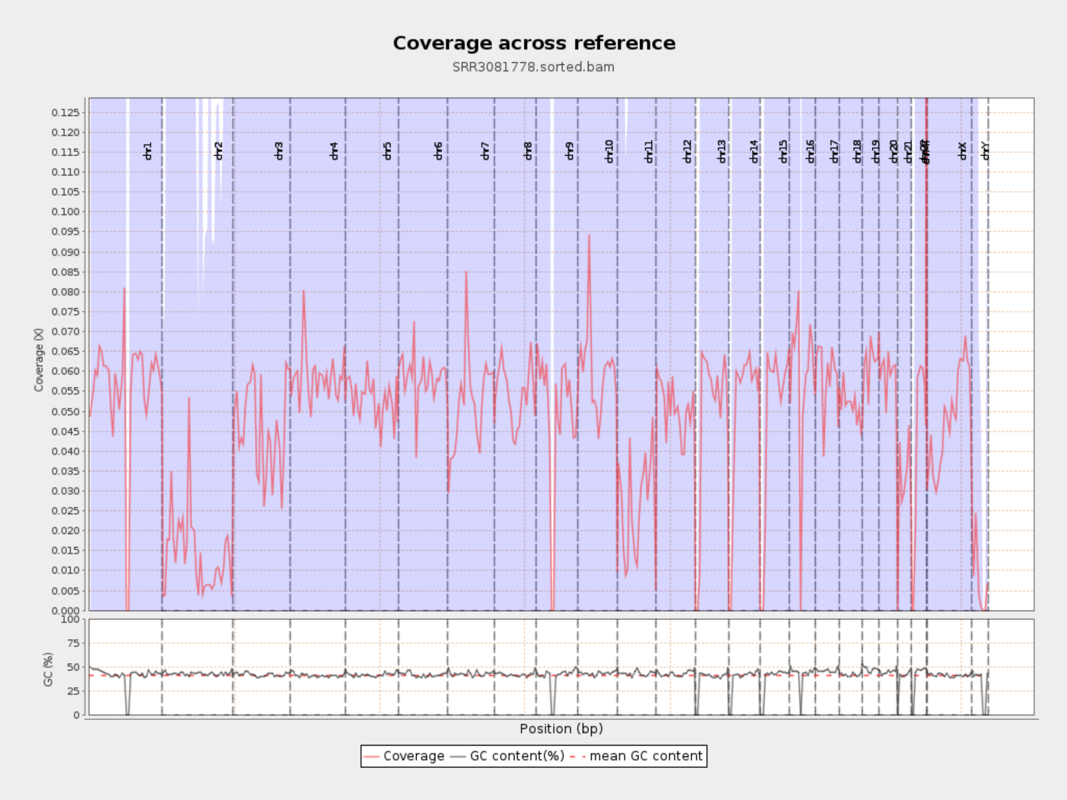
General error rate	0.91%
Mismatches	1,316,862
Insertions	10,618
Mapped reads with at least one insertion	0.48%
Deletions	32,323
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.23%

2.6. Chromosome stats

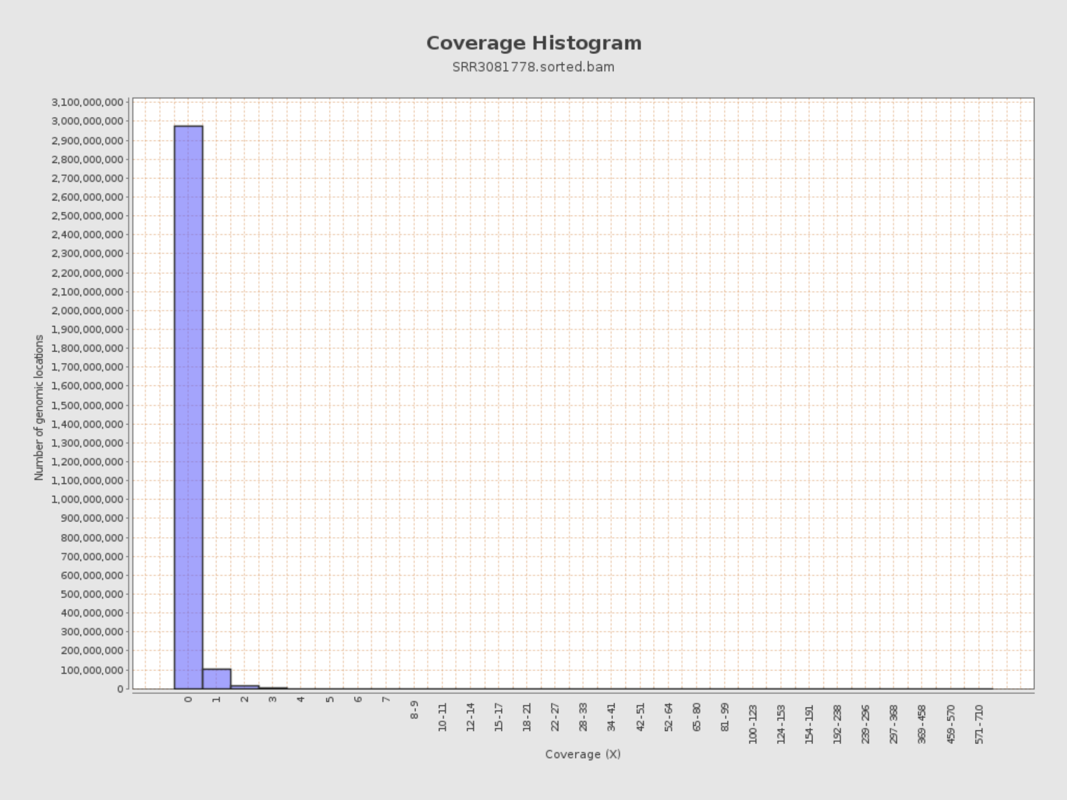
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13842647	0.0555	0.6897
chr2	243199373	3481180	0.0143	0.3754
chr3	198022430	8943730	0.0452	0.2492
chr4	191154276	11163052	0.0584	0.3129
chr5	180915260	9597874	0.0531	0.2675
chr6	171115067	10049718	0.0587	0.3361
chr7	159138663	8399871	0.0528	0.5313

chr8	146364022	7964531	0.0544	0.4211
chr9	141213431	6829513	0.0484	0.3715
chr10	135534747	8170674	0.0603	0.4486
chr11	135006516	3573255	0.0265	0.2584
chr12	133851895	6798696	0.0508	0.2624
chr13	115169878	5583368	0.0485	0.2547
chr14	107349540	5327607	0.0496	0.2727
chr15	102531392	4975751	0.0485	0.2589
chr16	90354753	5324259	0.0589	0.3126
chr17	81195210	4759746	0.0586	0.2951
chr18	78077248	4035522	0.0517	0.6562
chr19	59128983	3670808	0.0621	0.4926
chr20	63025520	3725177	0.0591	0.2913
chr21	48129895	1528929	0.0318	0.2382
chr22	51304566	2081797	0.0406	0.2343
chrMT	16571	6600	0.3983	0.6724
chrX	155270560	7474142	0.0481	0.2758
chrY	59373566	432743	0.0073	0.1909

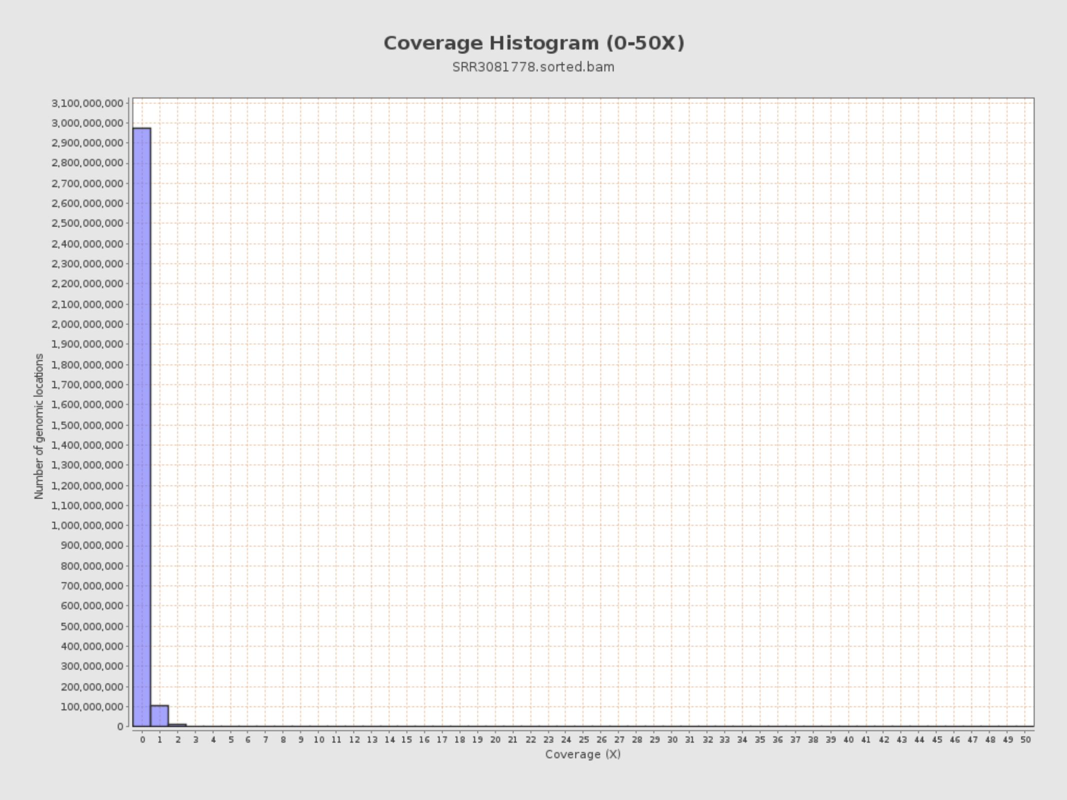
3. Results : Coverage across reference



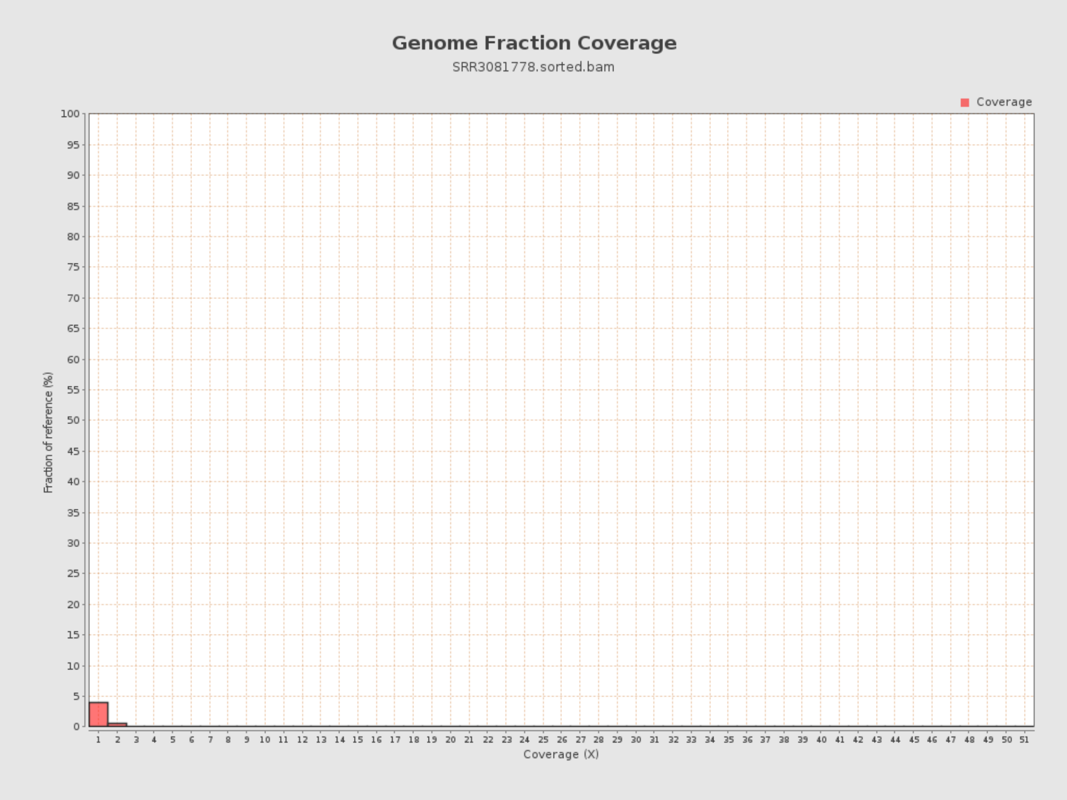
4. Results : Coverage Histogram



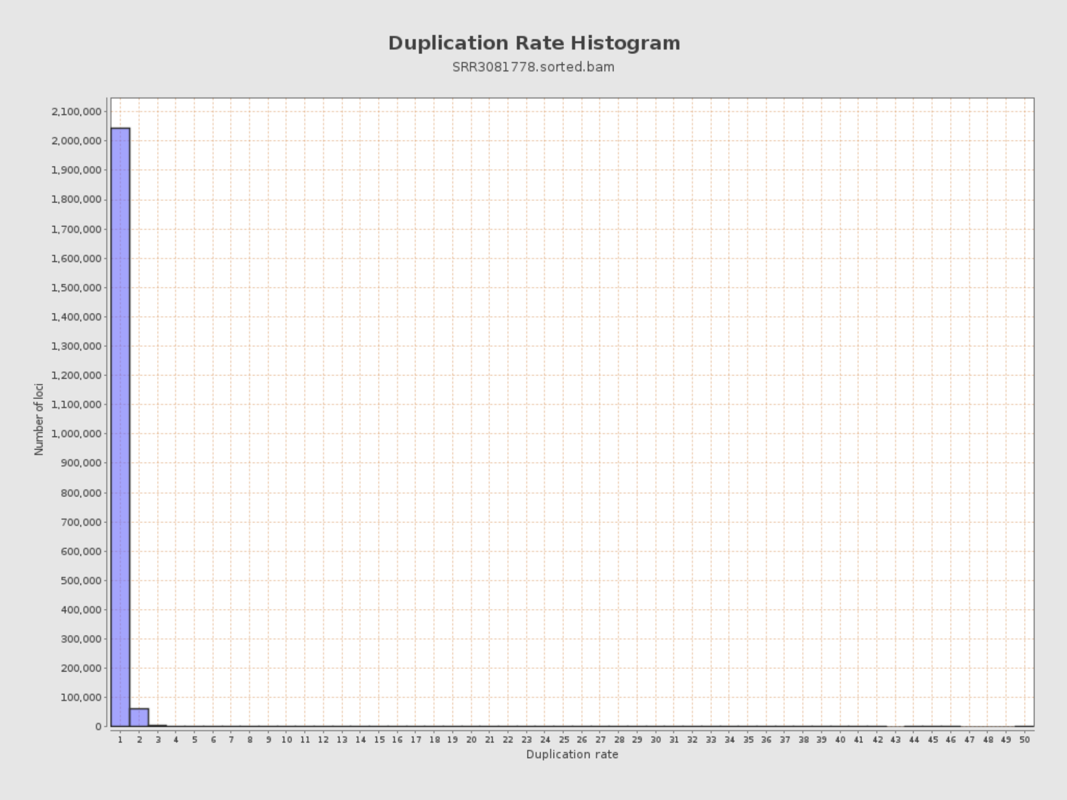
5. Results : Coverage Histogram (0-50X)



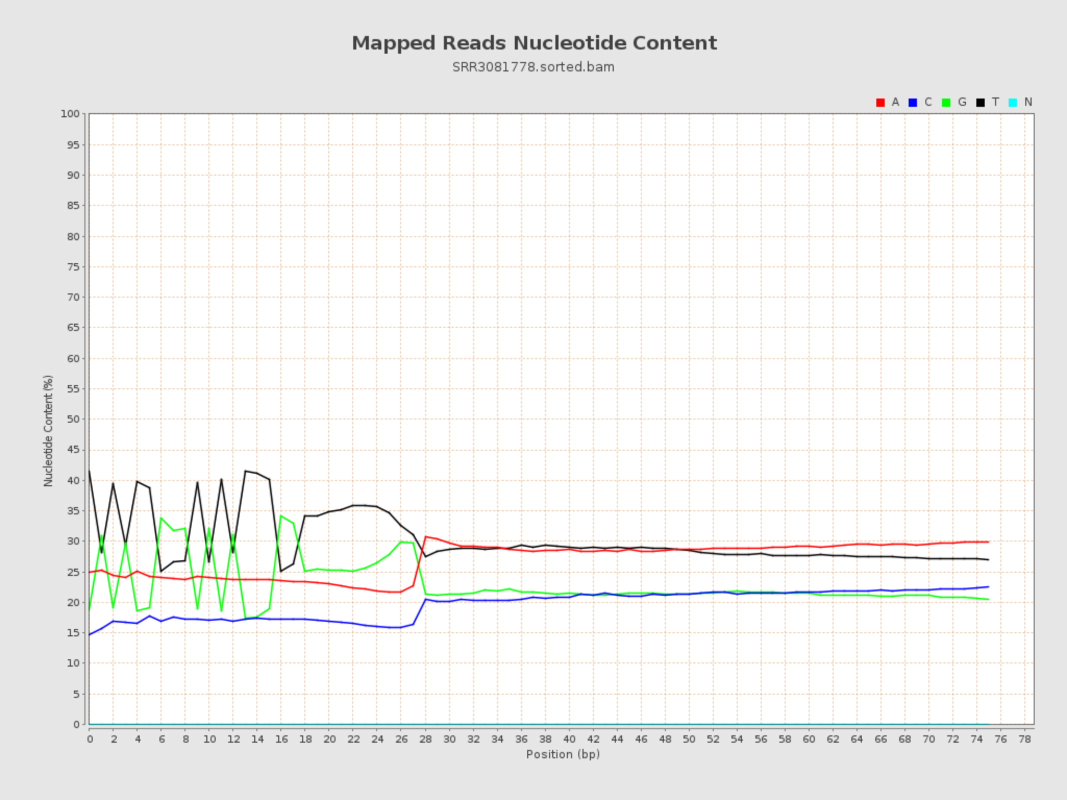
6. Results : Genome Fraction Coverage



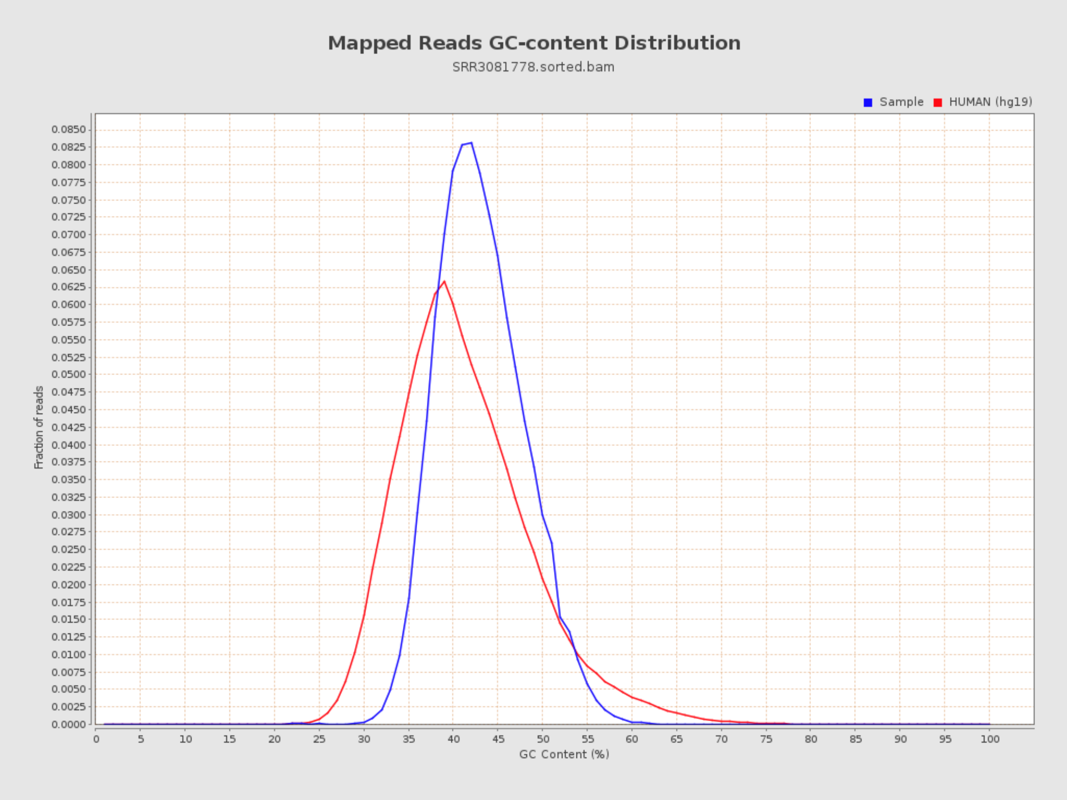
7. Results : Duplication Rate Histogram



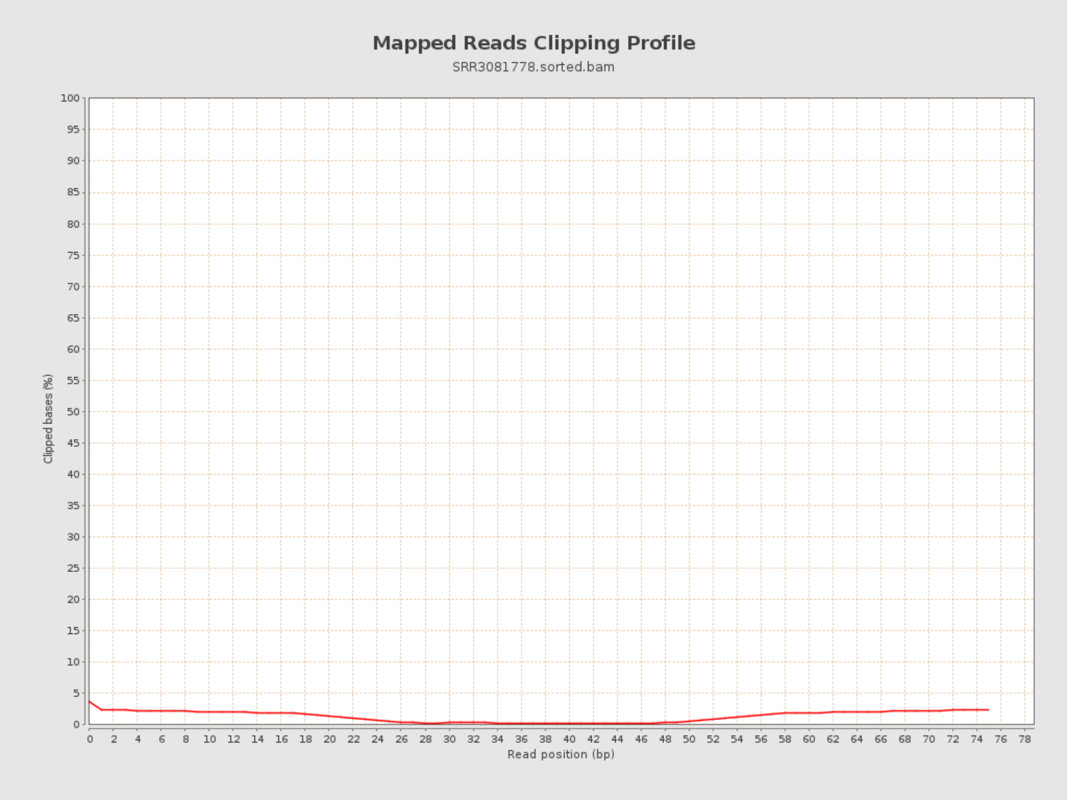
8. Results : Mapped Reads Nucleotide Content



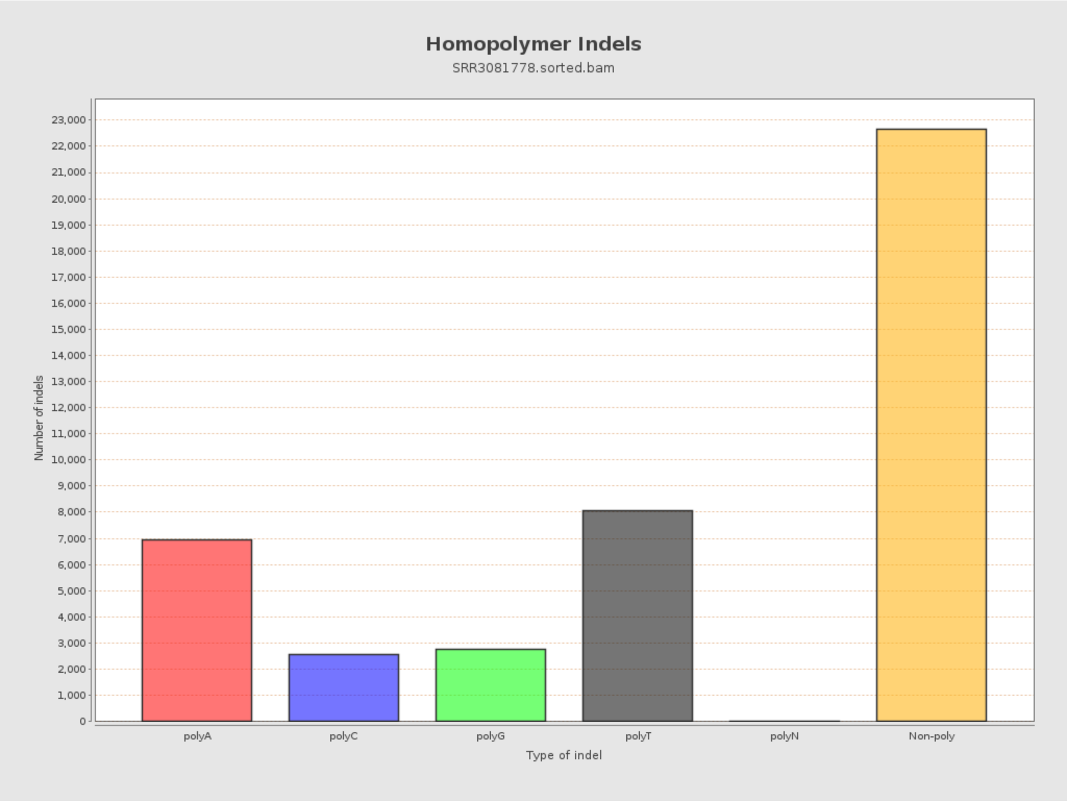
9. Results : Mapped Reads GC-content Distribution



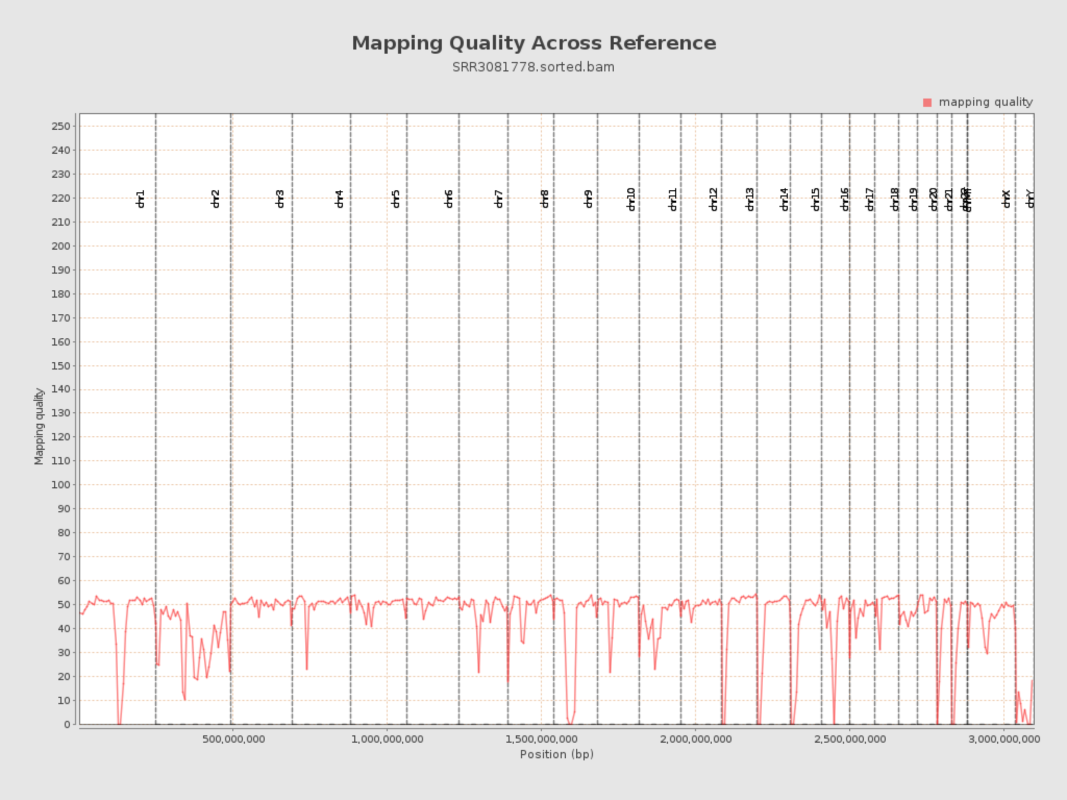
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram