Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:19:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081155.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_SRR3081155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:19:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,566,920
Mapped reads	2,271,595 / 88.49%
Unmapped reads	295,325 / 11.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,732 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	92,118 / 3.59%
Duplication rate	3.21%
Clipped reads	1,055,806 / 41.13%

2.2. ACGT Content

Number/percentage of A's	41,649,769 / 27.62%
Number/percentage of C's	27,791,348 / 18.43%
Number/percentage of T's	47,256,194 / 31.34%
Number/percentage of G's	34,039,089 / 22.58%
Number/percentage of N's	44,500 / 0.03%
GC Percentage	41.01%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.3814

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

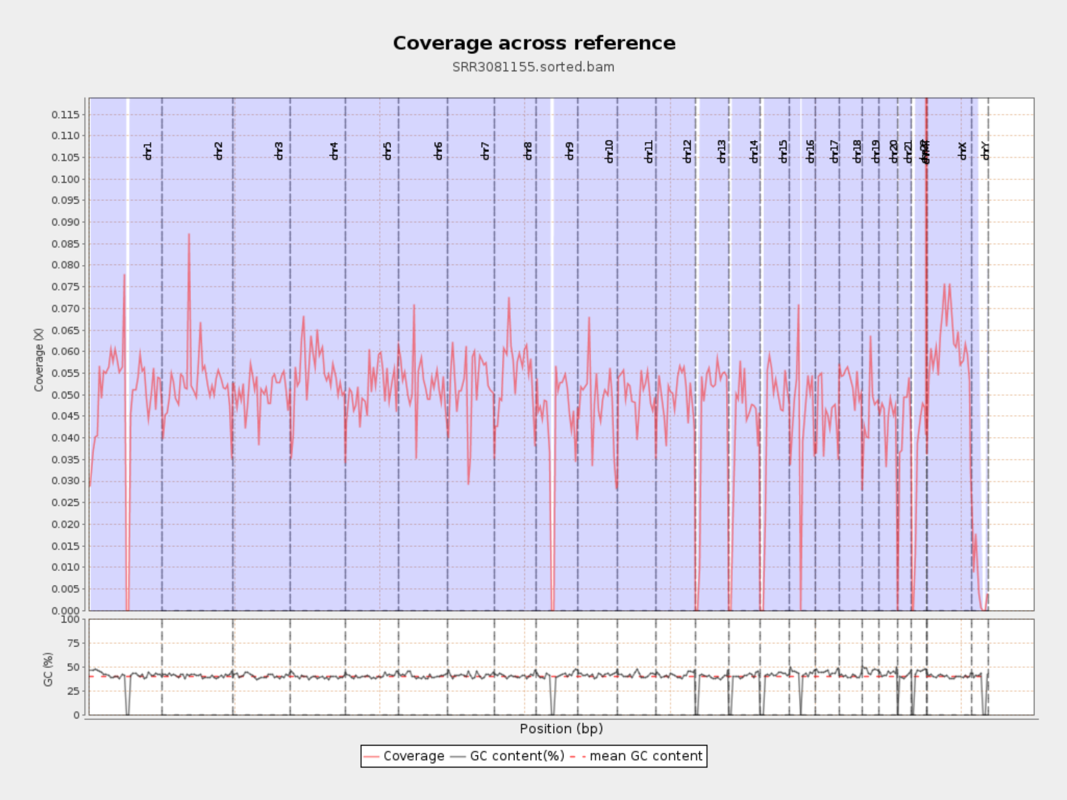
General error rate	0.84%
Mismatches	1,243,977
Insertions	11,538
Mapped reads with at least one insertion	0.5%
Deletions	33,957
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47%

2.6. Chromosome stats

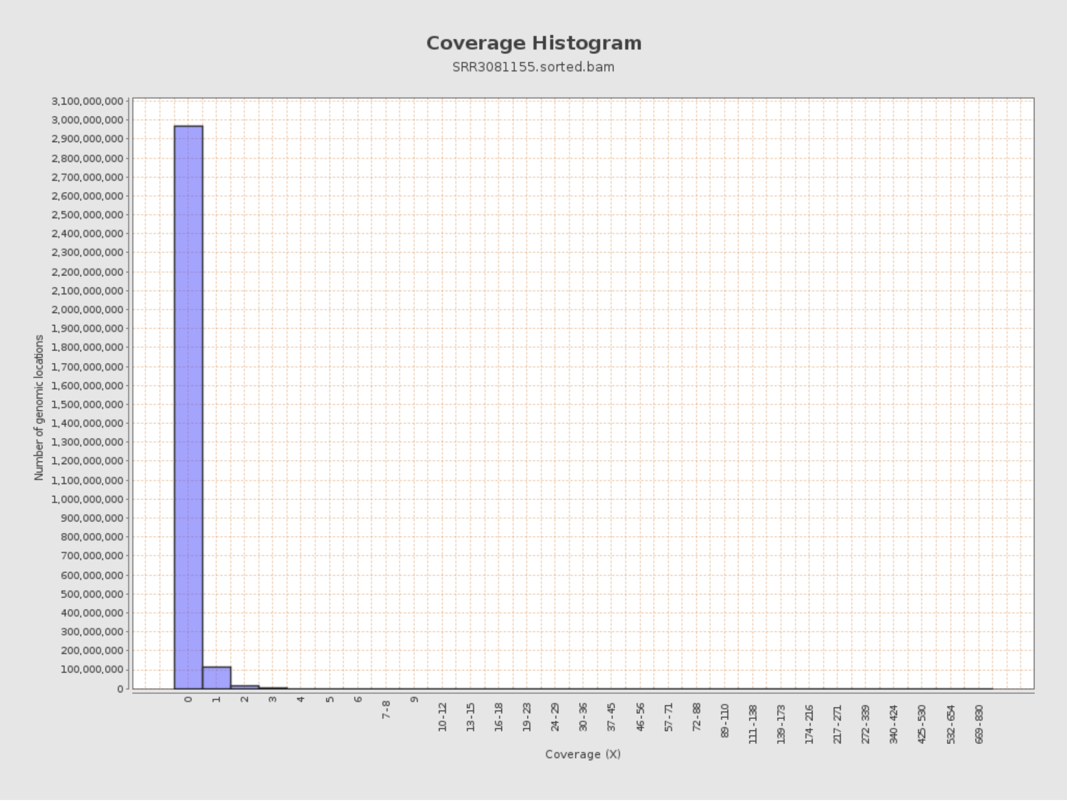
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12256957	0.0492	0.6478
chr2	243199373	12822777	0.0527	0.5045
chr3	198022430	10048743	0.0507	0.2537
chr4	191154276	10490376	0.0549	0.2753
chr5	180915260	9274363	0.0513	0.256
chr6	171115067	8978004	0.0525	0.3282
chr7	159138663	8303004	0.0522	0.4298

chr8	146364022	8028968	0.0549	0.4772
chr9	141213431	5979526	0.0423	0.3507
chr10	135534747	6578227	0.0485	0.3485
chr11	135006516	6758323	0.0501	0.3532
chr12	133851895	6661981	0.0498	0.2547
chr13	115169878	5155024	0.0448	0.239
chr14	107349540	4326578	0.0403	0.245
chr15	102531392	4355823	0.0425	0.2376
chr16	90354753	4038265	0.0447	0.262
chr17	81195210	3618972	0.0446	0.2792
chr18	78077248	4135104	0.053	0.6523
chr19	59128983	2753640	0.0466	0.4644
chr20	63025520	2788795	0.0442	0.2481
chr21	48129895	1948004	0.0405	0.2405
chr22	51304566	1568314	0.0306	0.195
chrMT	16571	154512	9.3242	5.8425
chrX	155270560	9437095	0.0608	0.3125
chrY	59373566	375007	0.0063	0.126

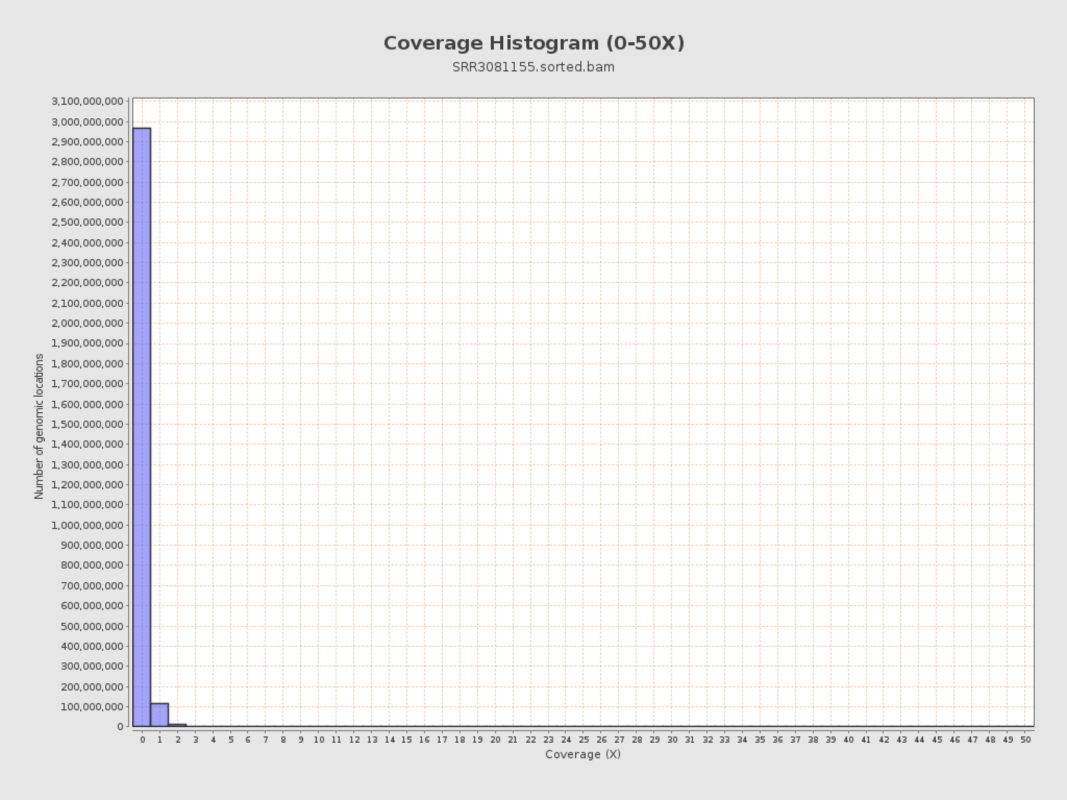
3. Results : Coverage across reference



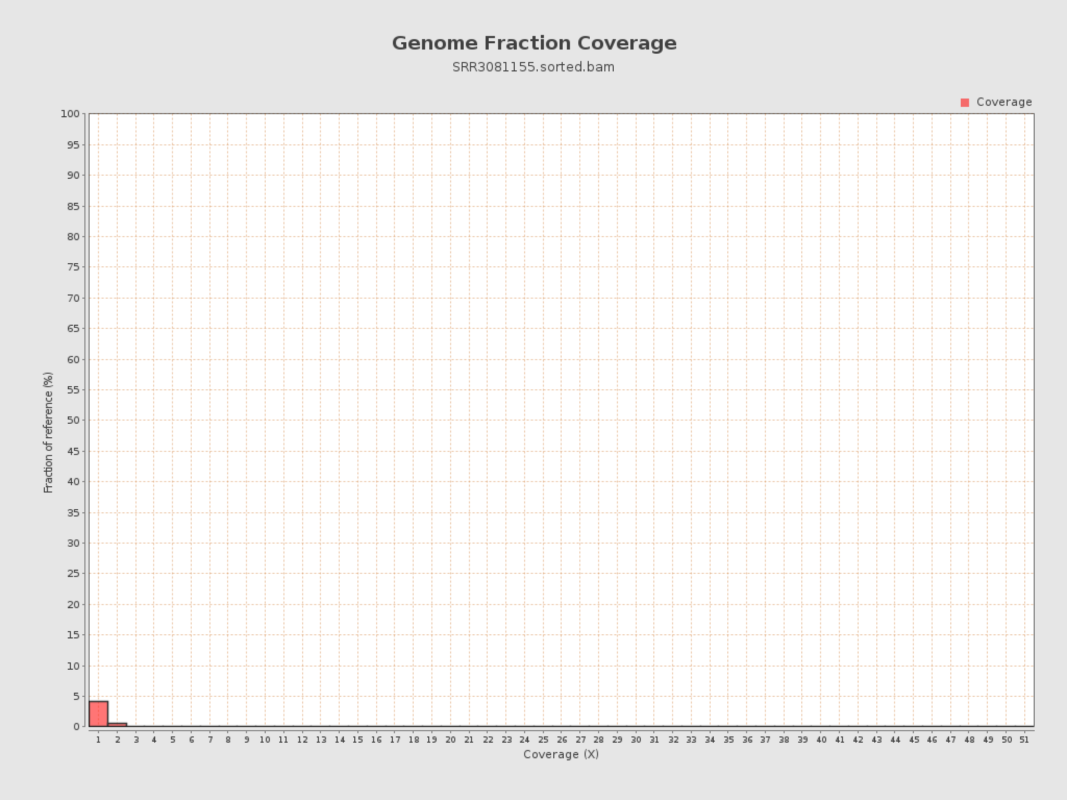
4. Results : Coverage Histogram



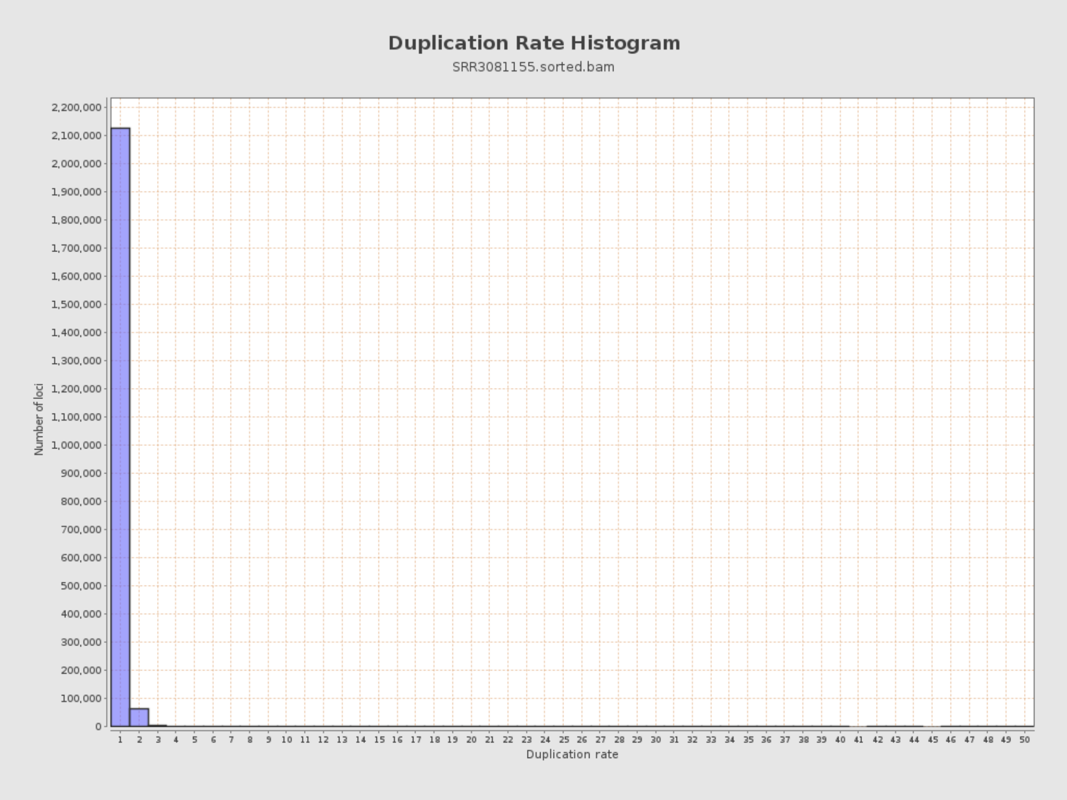
5. Results : Coverage Histogram (0-50X)



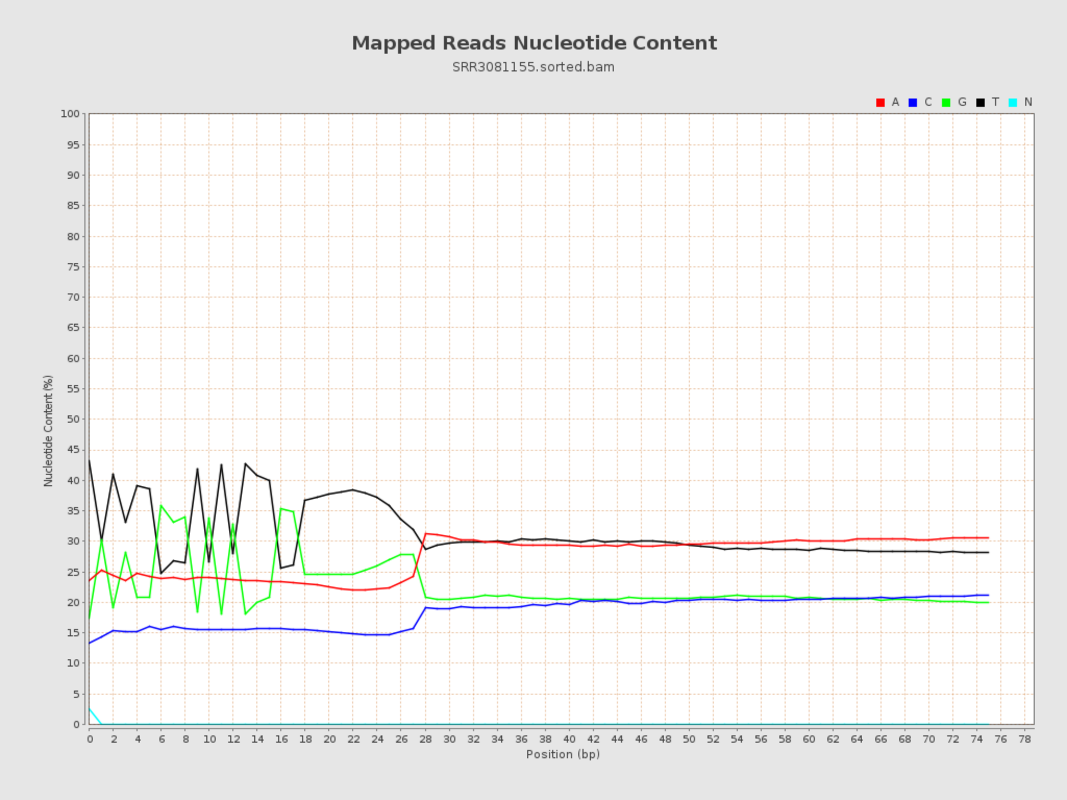
6. Results : Genome Fraction Coverage



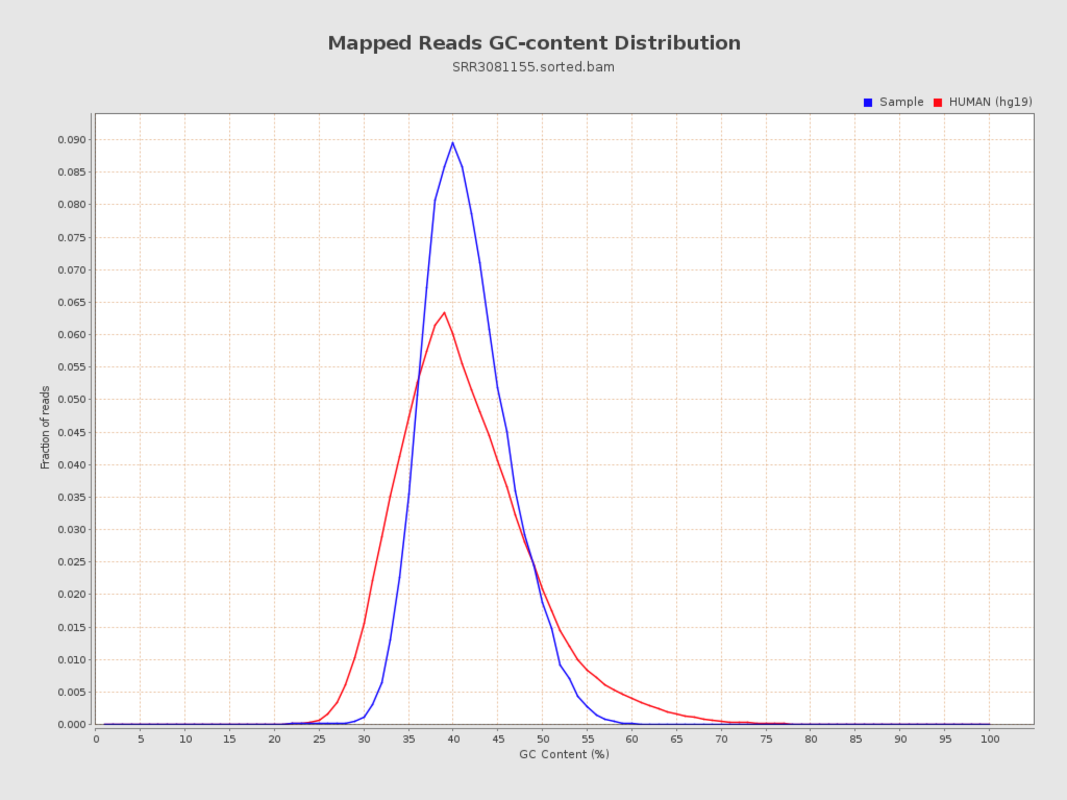
7. Results : Duplication Rate Histogram



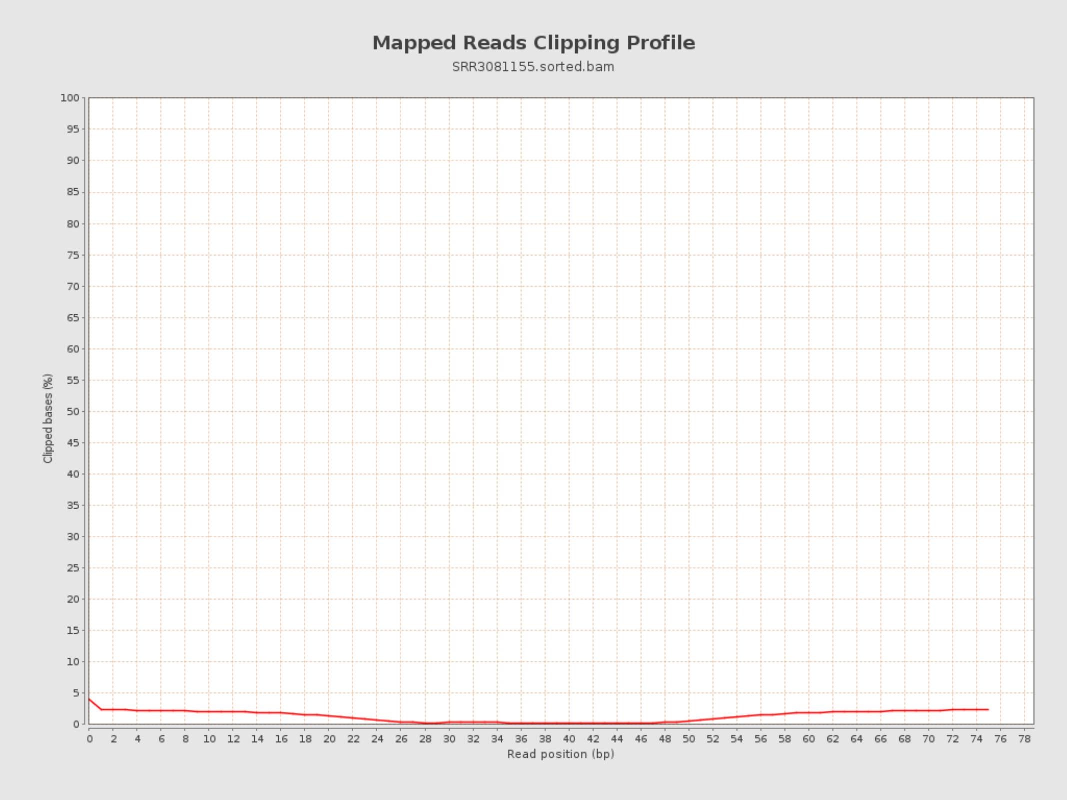
8. Results : Mapped Reads Nucleotide Content



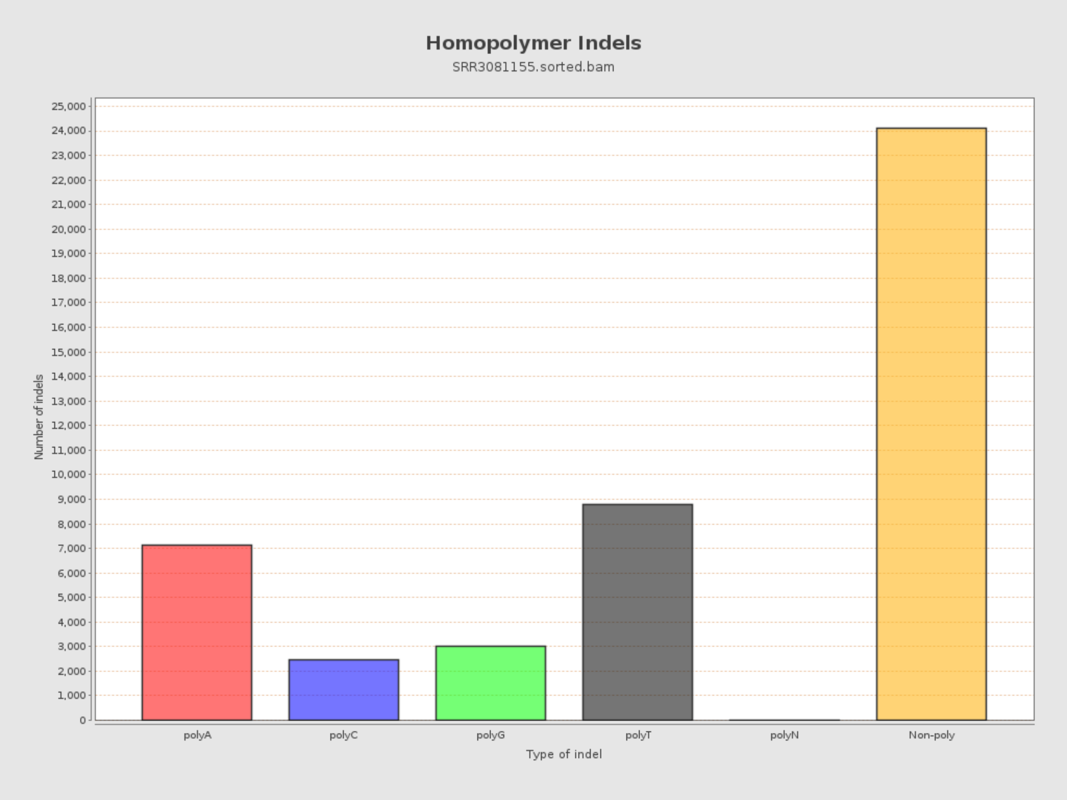
9. Results : Mapped Reads GC-content Distribution



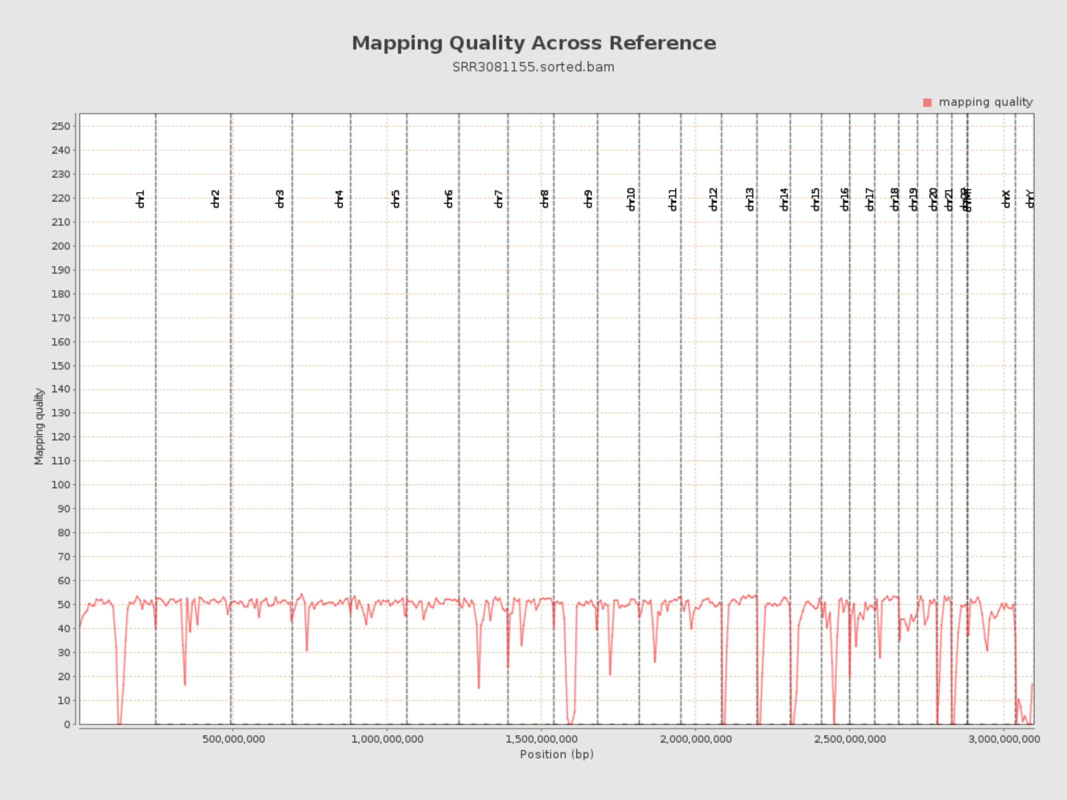
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram