Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:10:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081019.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_SRR3081019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:10:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,358,538
Mapped reads	2,724,402 / 81.12%
Unmapped reads	634,136 / 18.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,671 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	94,016 / 2.8%
Duplication rate	2.64%
Clipped reads	1,683,975 / 50.14%

2.2. ACGT Content

Number/percentage of A's	47,920,935 / 28.39%
Number/percentage of C's	34,439,100 / 20.4%
Number/percentage of T's	48,635,069 / 28.82%
Number/percentage of G's	37,780,864 / 22.38%
Number/percentage of N's	2,081 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0545

Standard Deviation	0.3945

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

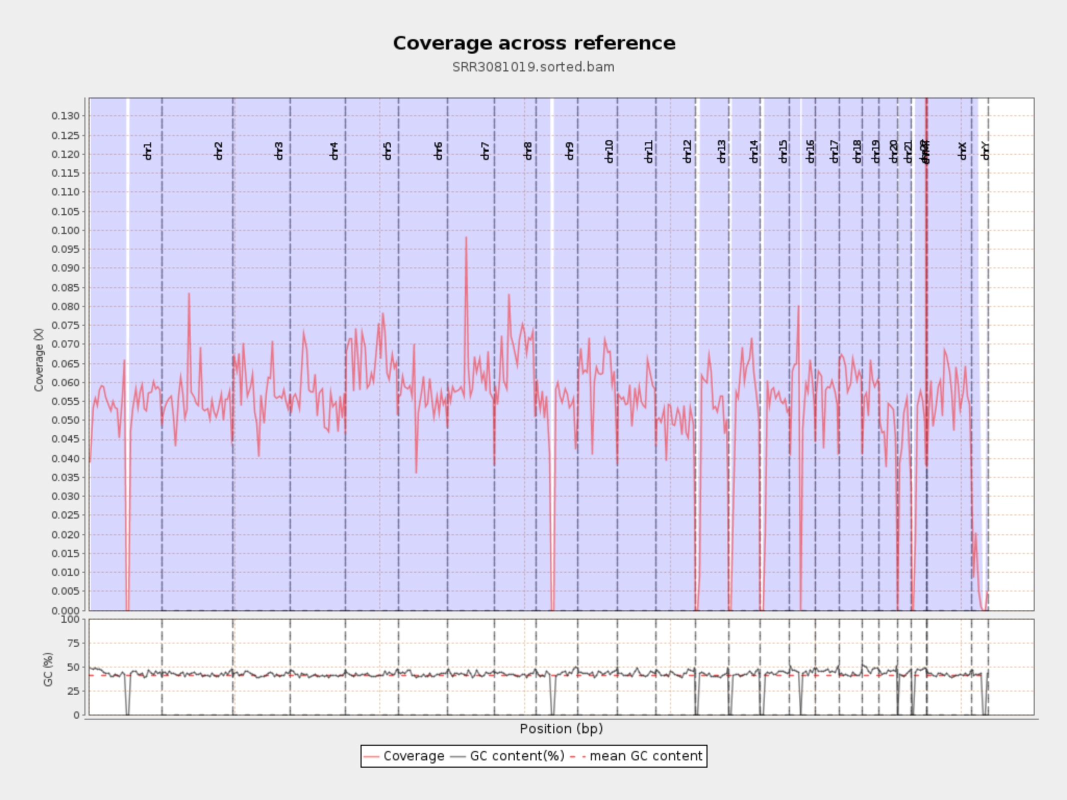
General error rate	0.79%
Mismatches	1,308,676
Insertions	11,676
Mapped reads with at least one insertion	0.43%
Deletions	34,870
Mapped reads with at least one deletion	1.27%
Homopolymer indels	45%

2.6. Chromosome stats

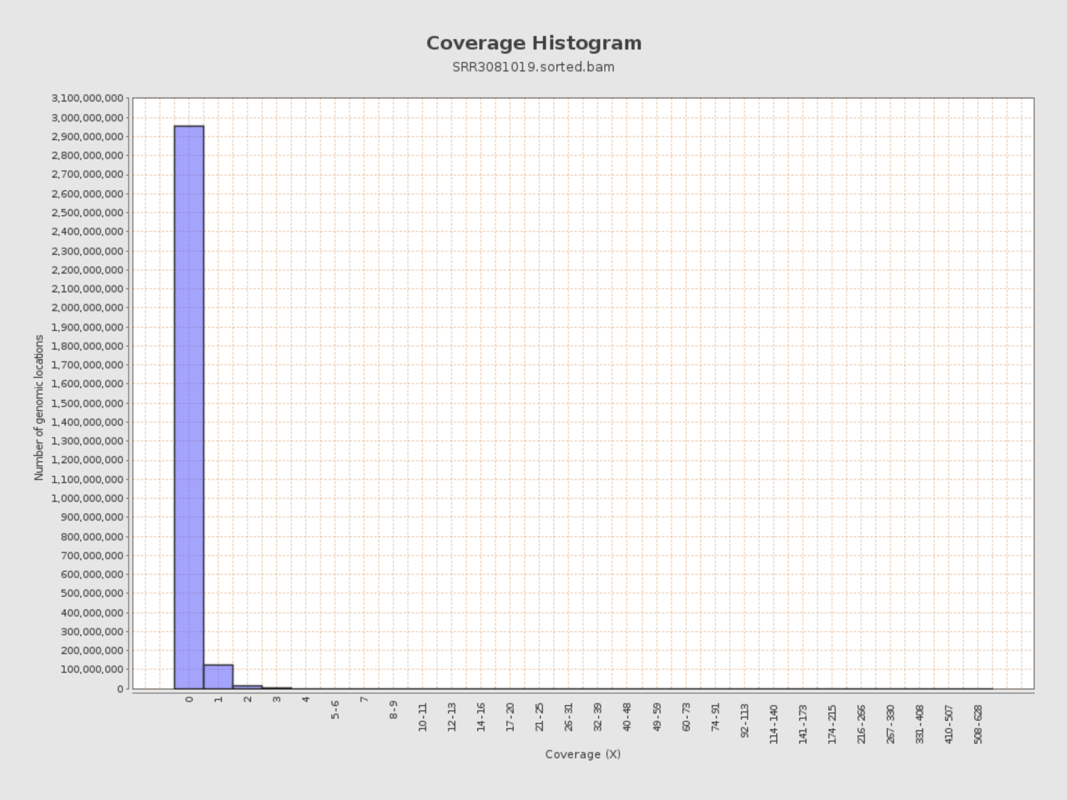
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12885919	0.0517	0.5615
chr2	243199373	13417563	0.0552	0.429
chr3	198022430	11457062	0.0579	0.2737
chr4	191154276	10710133	0.056	0.2889
chr5	180915260	11987153	0.0663	0.2957
chr6	171115067	9582727	0.056	0.3325
chr7	159138663	9828087	0.0618	0.7195

chr8	146364022	9841233	0.0672	0.4003
chr9	141213431	6814876	0.0483	0.3796
chr10	135534747	8486160	0.0626	0.3642
chr11	135006516	7595848	0.0563	0.3821
chr12	133851895	6626611	0.0495	0.2593
chr13	115169878	5411440	0.047	0.248
chr14	107349540	5502053	0.0513	0.2795
chr15	102531392	4660521	0.0455	0.2639
chr16	90354753	5001773	0.0554	0.2978
chr17	81195210	4576762	0.0564	0.3082
chr18	78077248	4929396	0.0631	0.7326
chr19	59128983	3423672	0.0579	0.4745
chr20	63025520	2979439	0.0473	0.2552
chr21	48129895	1961508	0.0408	0.2533
chr22	51304566	1893863	0.0369	0.2188
chrMT	16571	22505	1.3581	1.4526
chrX	155270560	8822228	0.0568	0.3139
chrY	59373566	419605	0.0071	0.1446

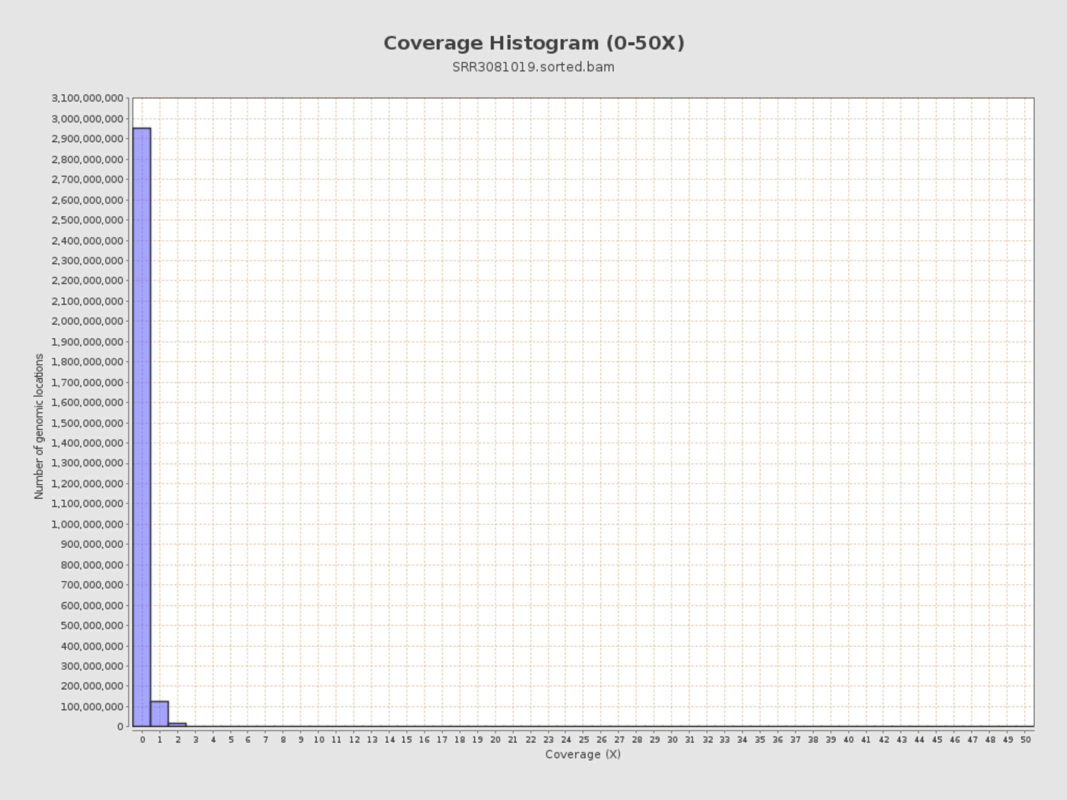
3. Results : Coverage across reference



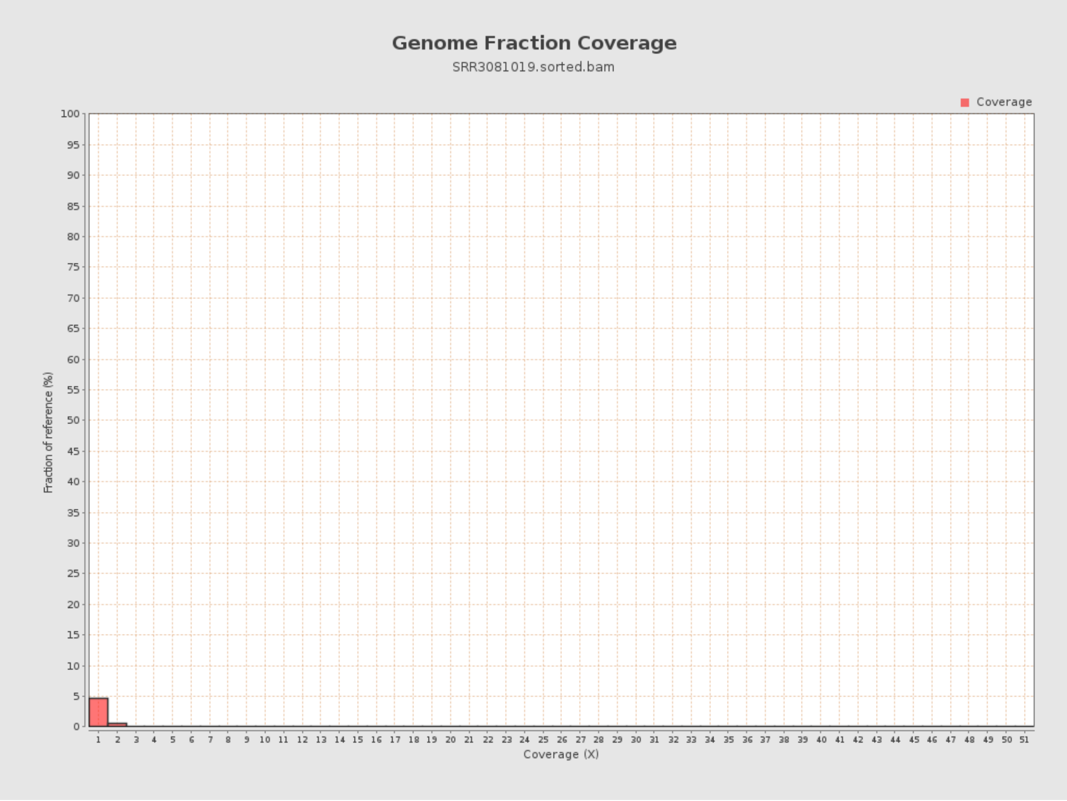
4. Results : Coverage Histogram



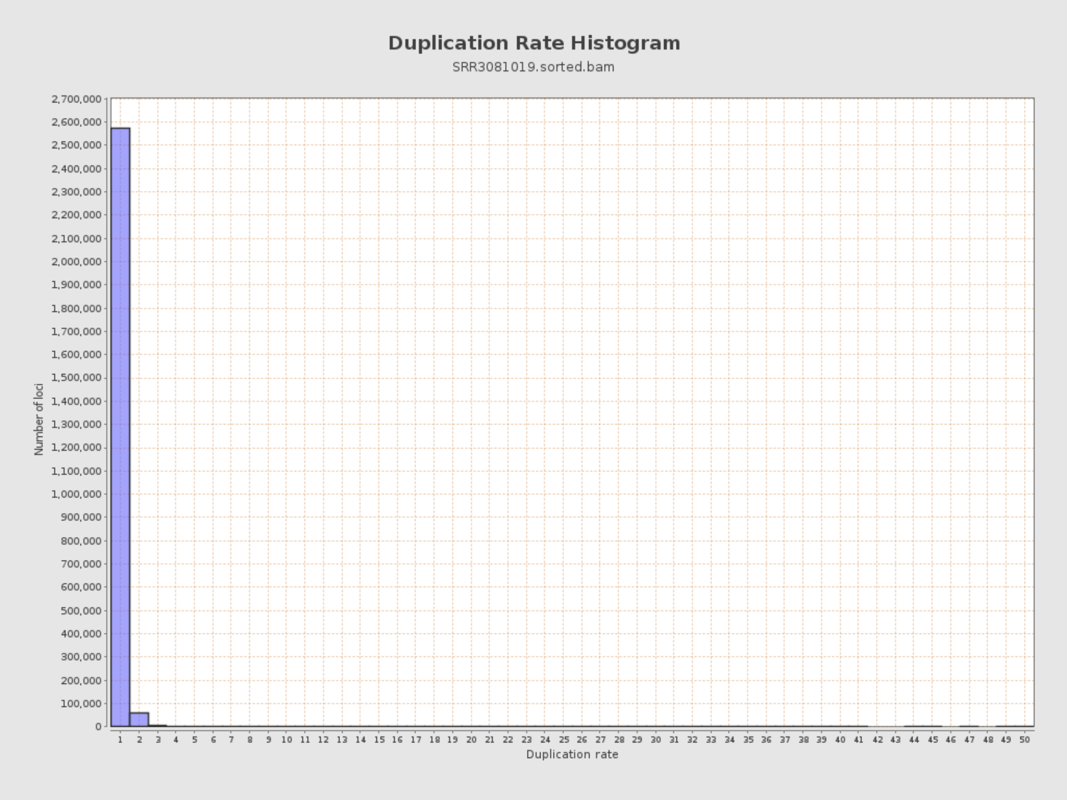
5. Results : Coverage Histogram (0-50X)



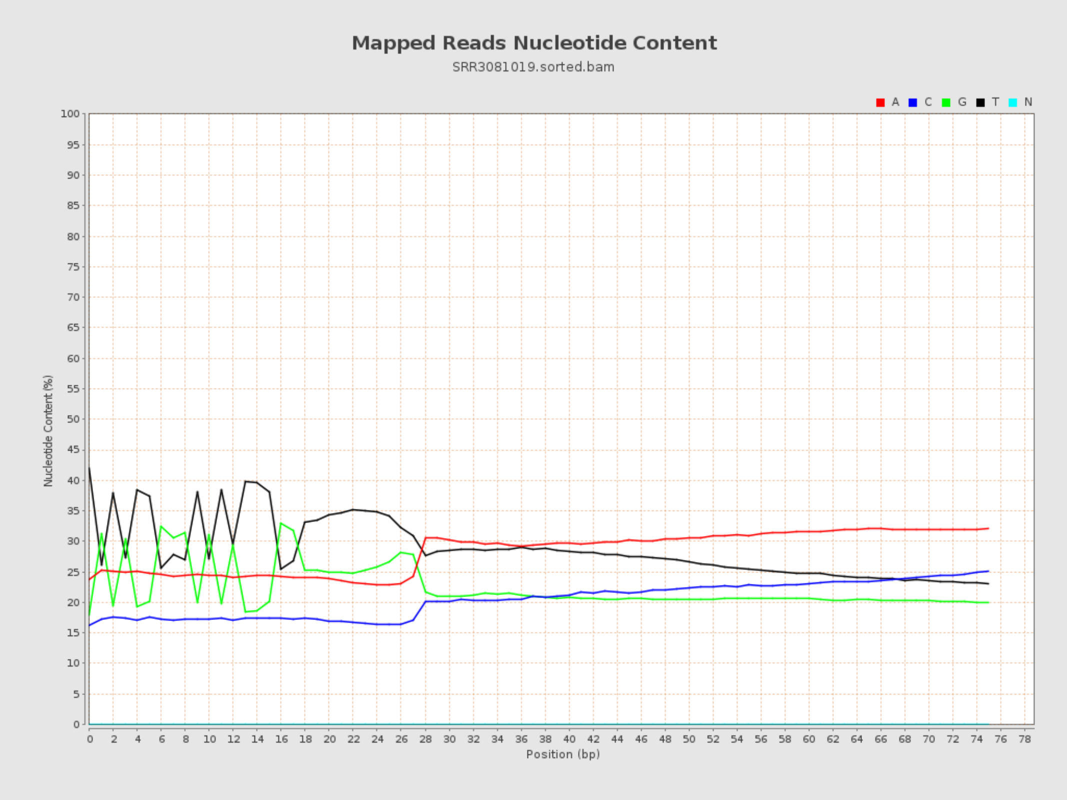
6. Results : Genome Fraction Coverage



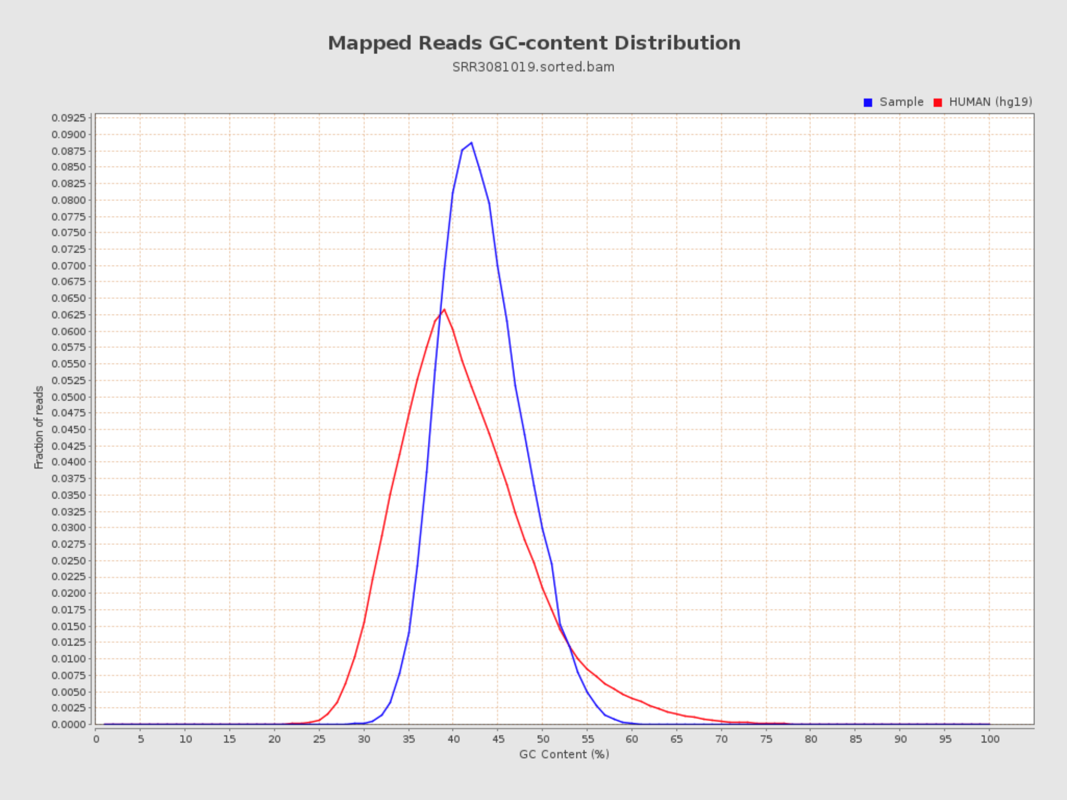
7. Results : Duplication Rate Histogram



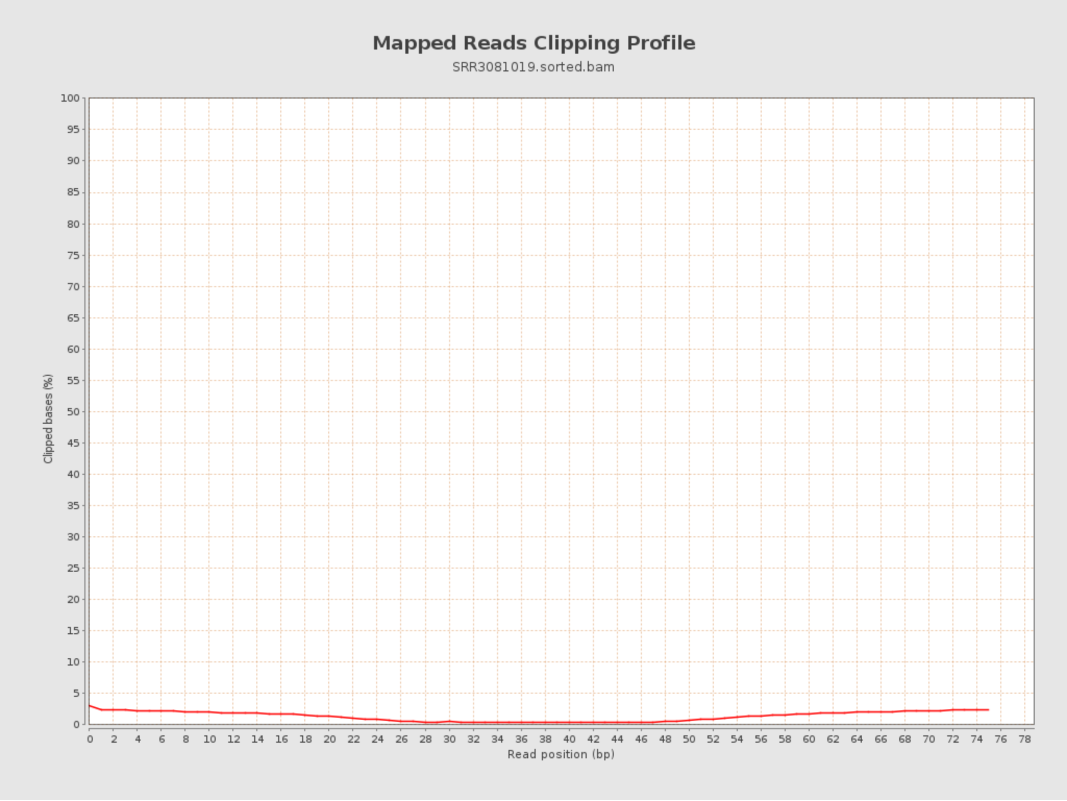
8. Results : Mapped Reads Nucleotide Content



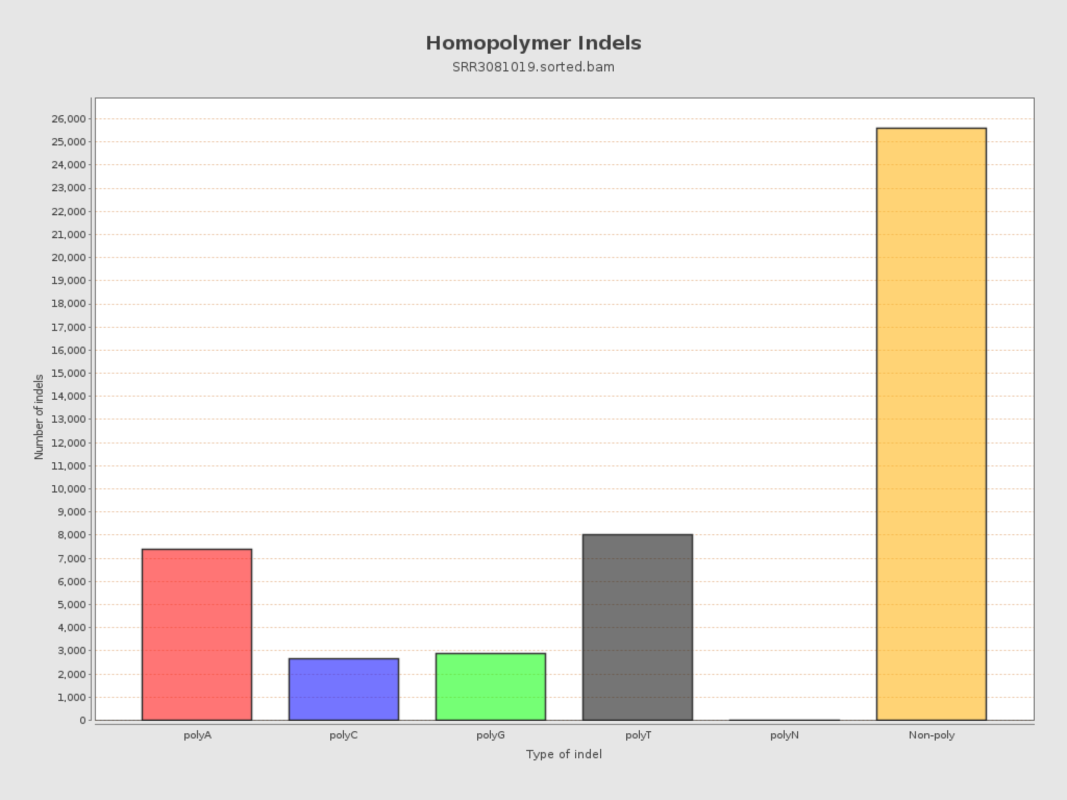
9. Results : Mapped Reads GC-content Distribution



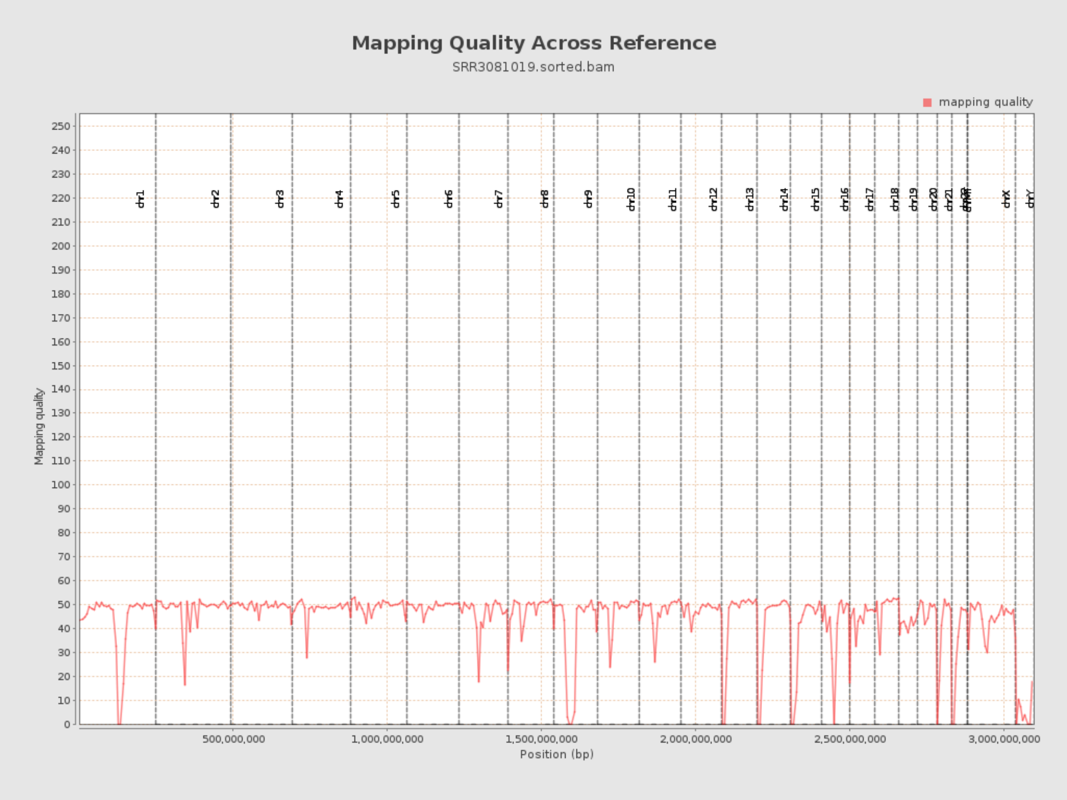
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram