Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:59:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081009.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_SRR3081009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081009.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:59:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,709,102
Mapped reads	2,209,465 / 81.56%
Unmapped reads	499,637 / 18.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,280 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	70,522 / 2.6%
Duplication rate	2.31%
Clipped reads	1,310,603 / 48.38%

2.2. ACGT Content

Number/percentage of A's	38,774,942 / 28.11%
Number/percentage of C's	27,849,370 / 20.19%
Number/percentage of T's	39,964,983 / 28.97%
Number/percentage of G's	31,373,109 / 22.74%
Number/percentage of N's	1,768 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.3806

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

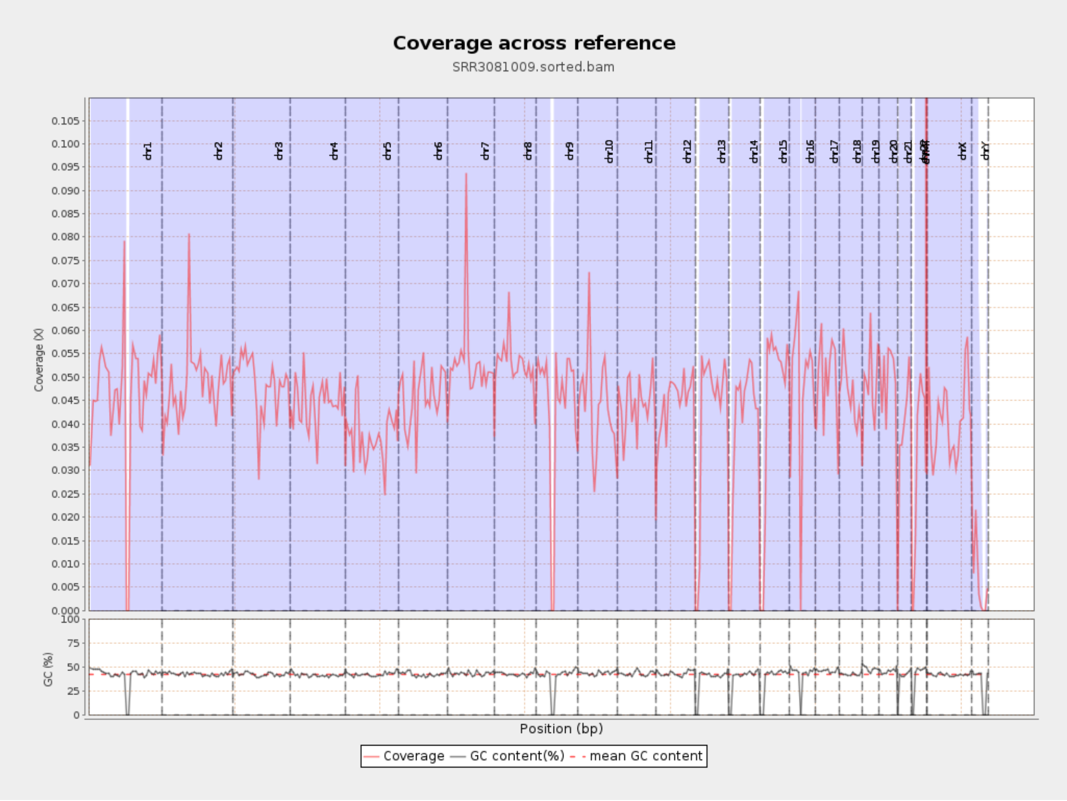
General error rate	0.75%
Mismatches	1,022,418
Insertions	9,491
Mapped reads with at least one insertion	0.43%
Deletions	27,432
Mapped reads with at least one deletion	1.23%
Homopolymer indels	45.49%

2.6. Chromosome stats

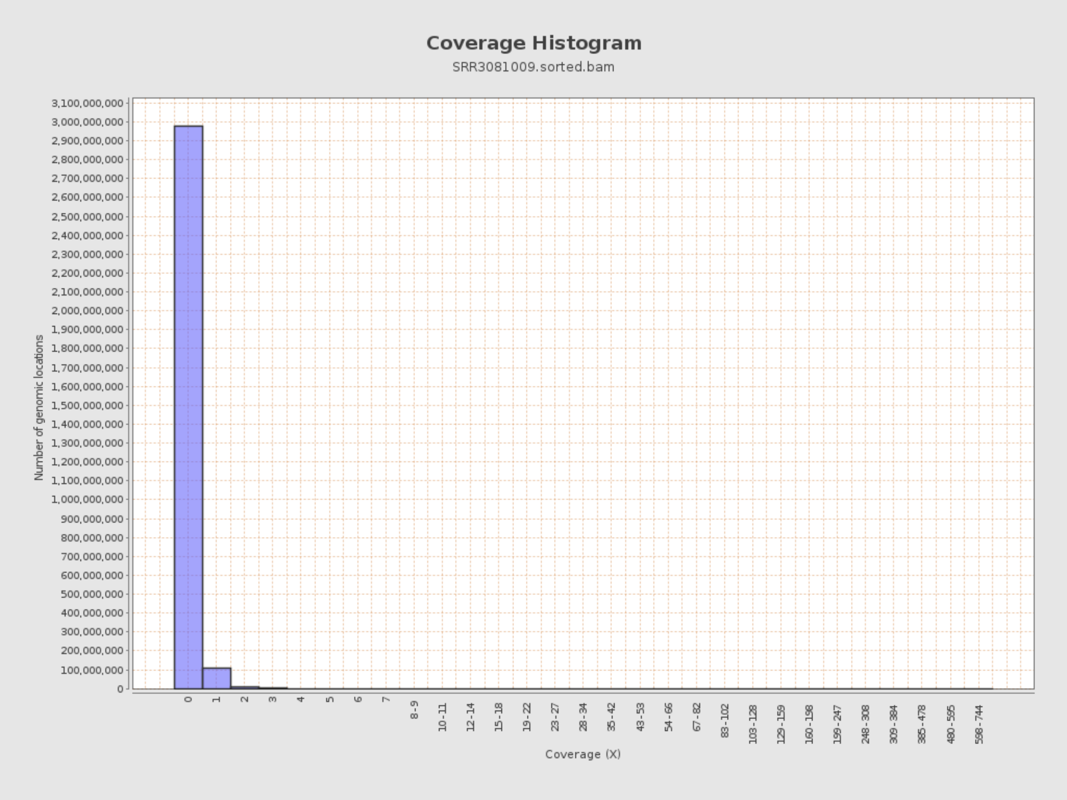
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11537587	0.0463	0.6526
chr2	243199373	11785731	0.0485	0.4023
chr3	198022430	9643666	0.0487	0.2456
chr4	191154276	8493975	0.0444	0.2602
chr5	180915260	6740704	0.0373	0.2171
chr6	171115067	7870264	0.046	0.3117
chr7	159138663	8493379	0.0534	0.7056

chr8	146364022	7718360	0.0527	0.3368
chr9	141213431	6173926	0.0437	0.3487
chr10	135534747	5968406	0.044	0.3312
chr11	135006516	5923763	0.0439	0.3234
chr12	133851895	5964724	0.0446	0.239
chr13	115169878	4776299	0.0415	0.2252
chr14	107349540	4241030	0.0395	0.2427
chr15	102531392	4560016	0.0445	0.242
chr16	90354753	4385083	0.0485	0.2919
chr17	81195210	3944279	0.0486	0.2908
chr18	78077248	3651733	0.0468	0.6856
chr19	59128983	2908077	0.0492	0.4598
chr20	63025520	3097161	0.0491	0.263
chr21	48129895	1842283	0.0383	0.2417
chr22	51304566	1601737	0.0312	0.196
chrMT	16571	17755	1.0715	1.3257
chrX	155270560	6298533	0.0406	0.2595
chrY	59373566	373606	0.0063	0.1586

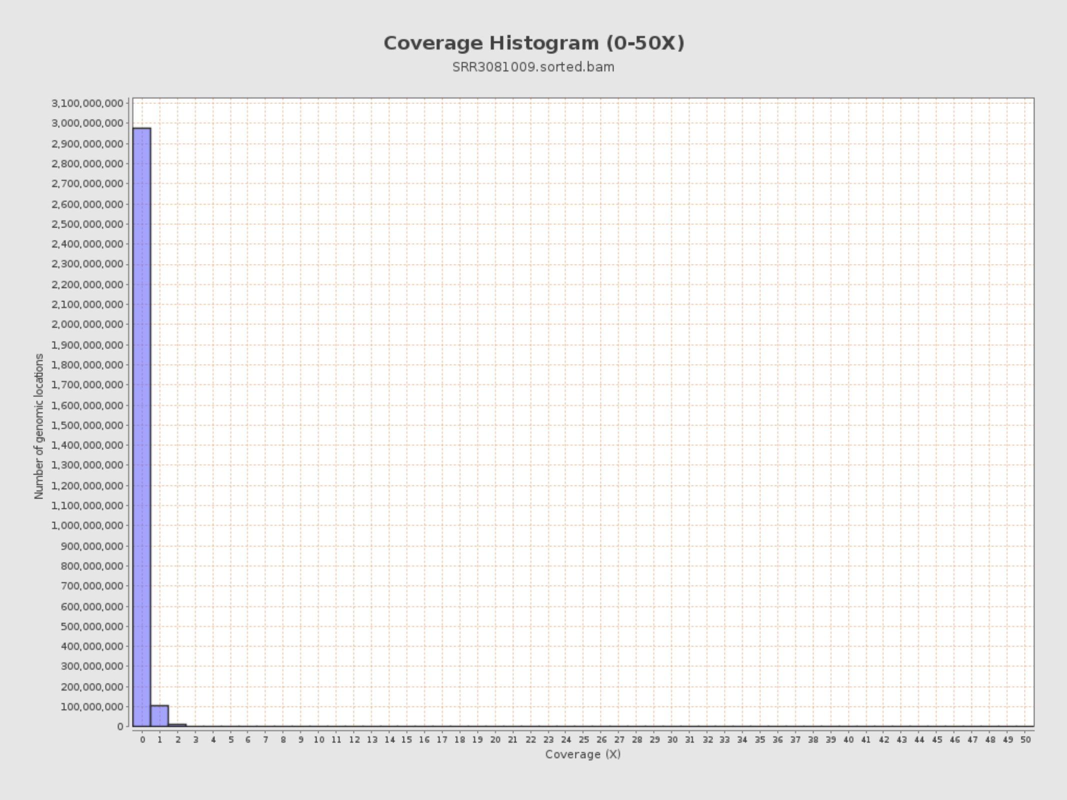
3. Results : Coverage across reference



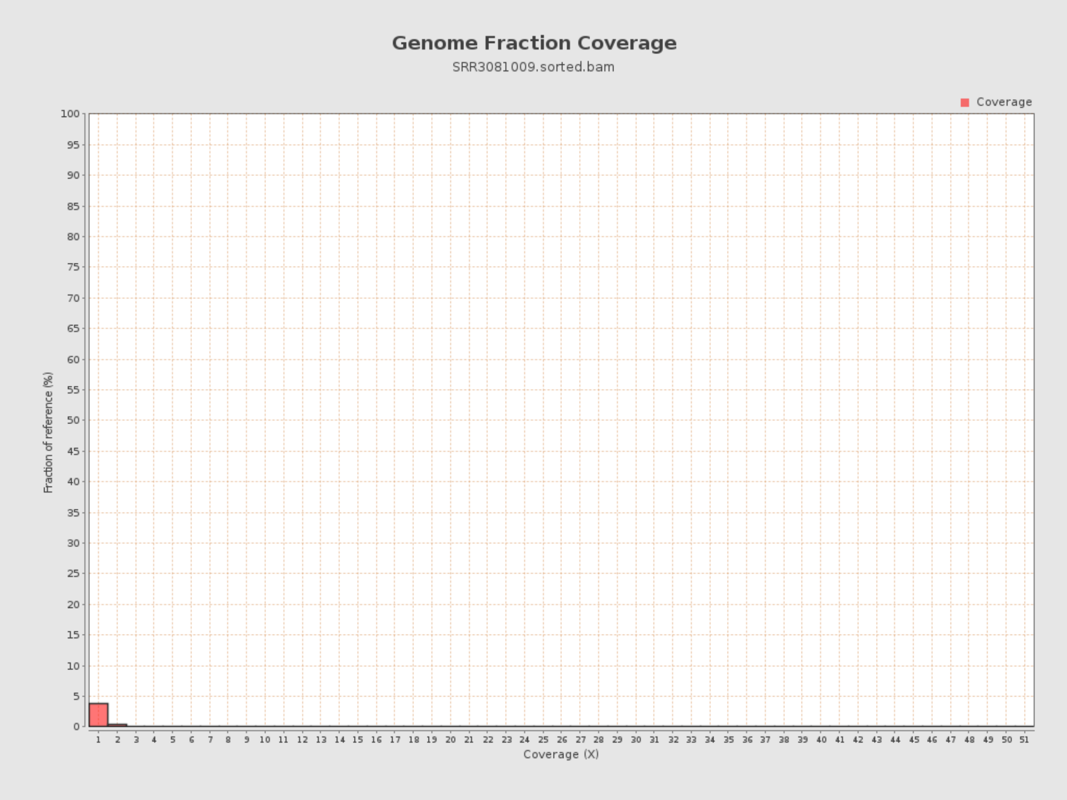
4. Results : Coverage Histogram



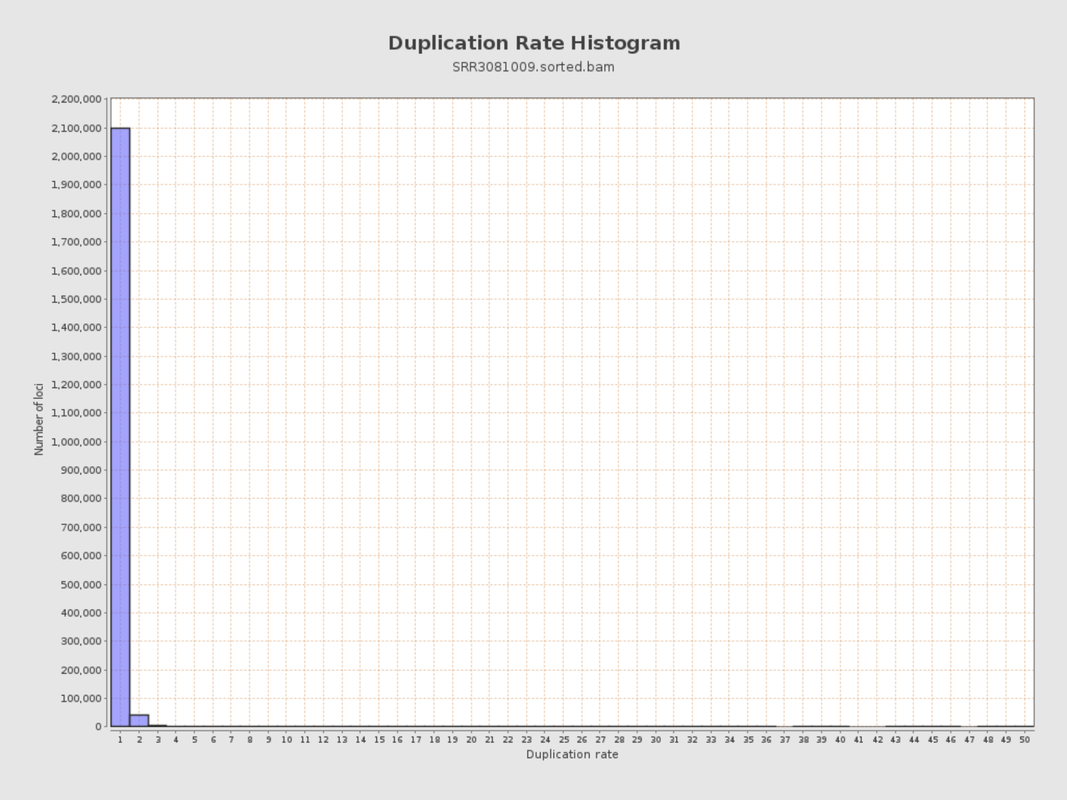
5. Results : Coverage Histogram (0-50X)



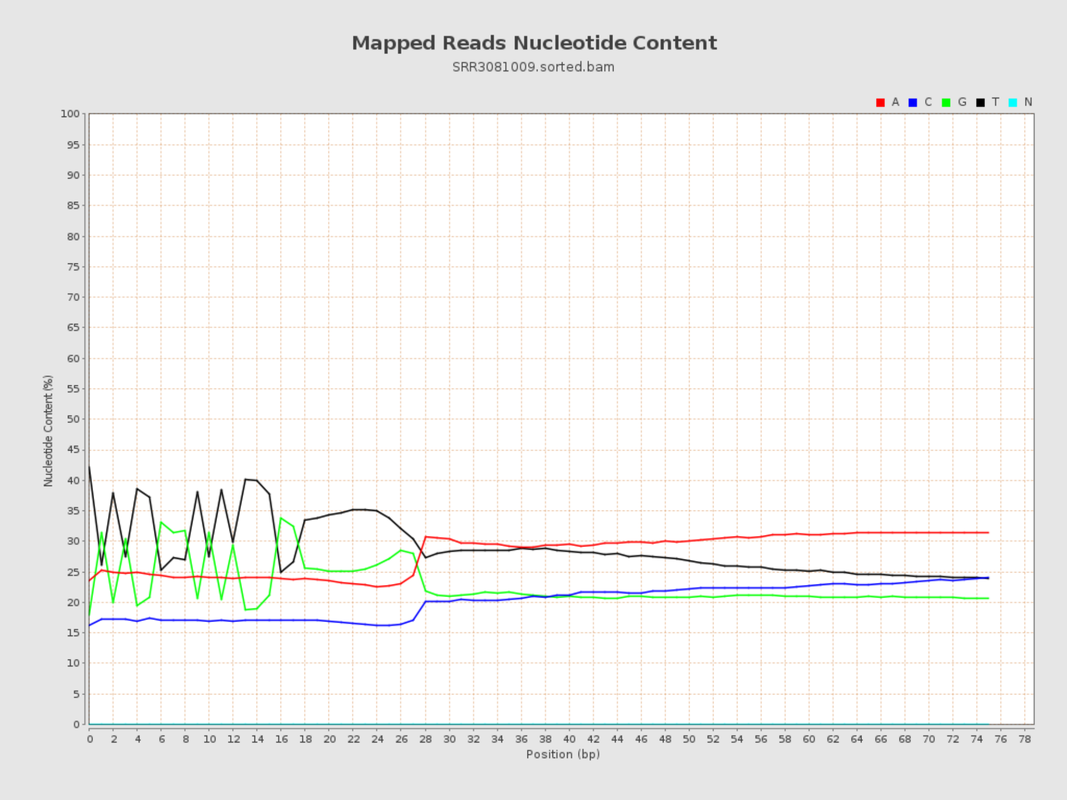
6. Results : Genome Fraction Coverage



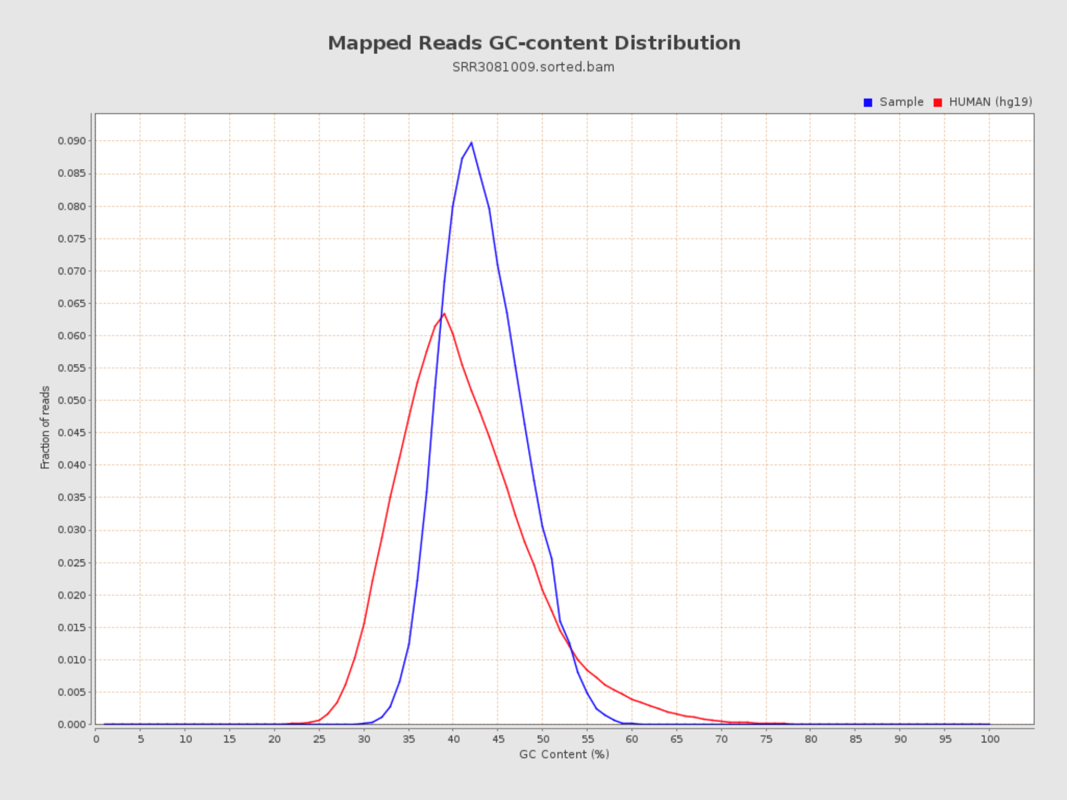
7. Results : Duplication Rate Histogram



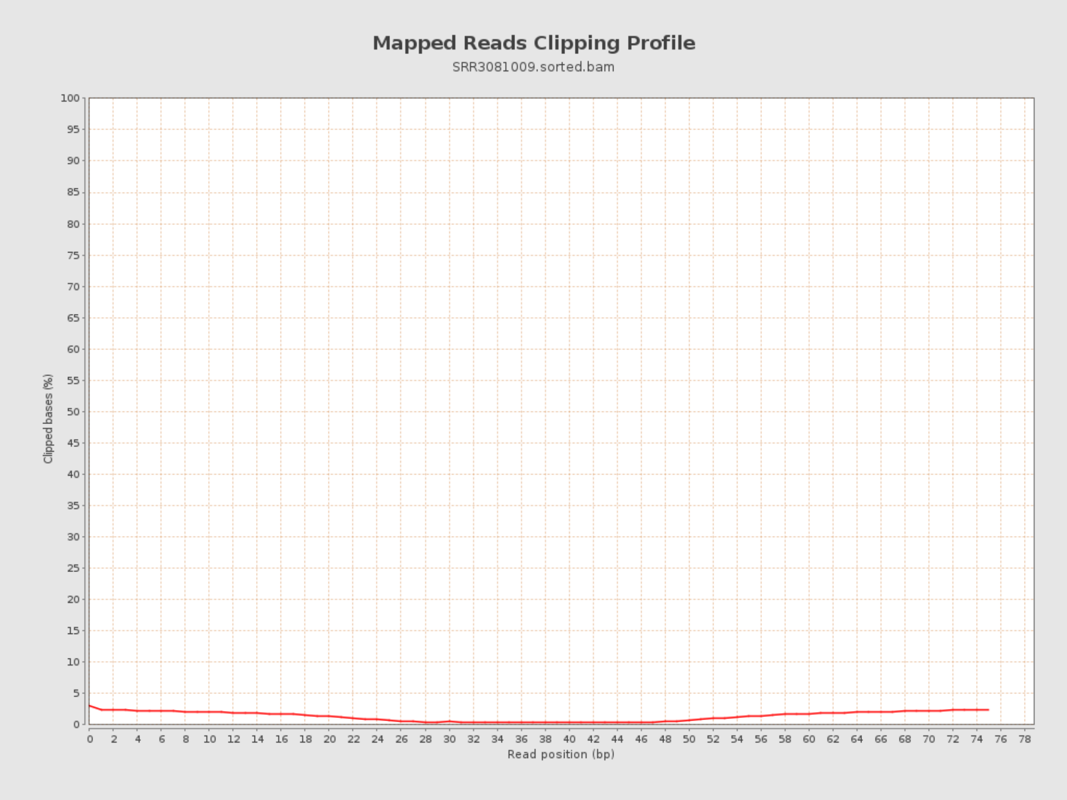
8. Results : Mapped Reads Nucleotide Content



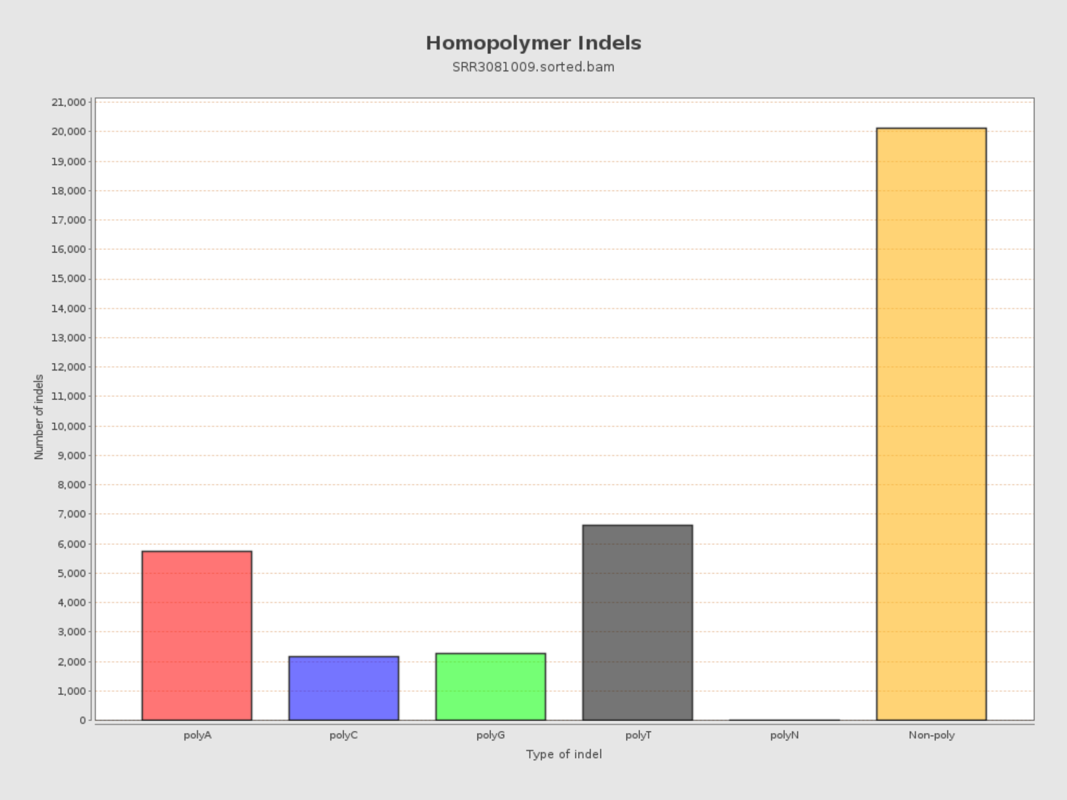
9. Results : Mapped Reads GC-content Distribution



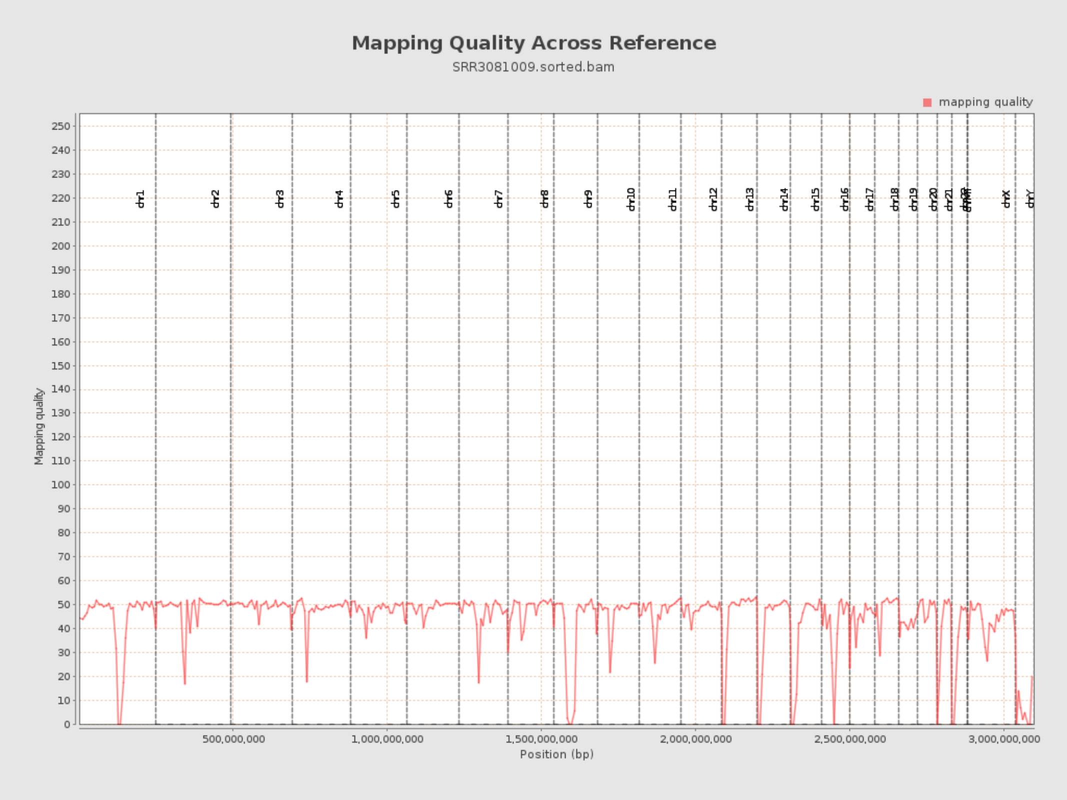
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram