Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:17:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081250.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_SRR3081250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:17:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,235,614
Mapped reads	1,916,427 / 85.72%
Unmapped reads	319,187 / 14.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,612 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	74,430 / 3.33%
Duplication rate	2.89%
Clipped reads	825,354 / 36.92%

2.2. ACGT Content

Number/percentage of A's	35,204,766 / 27.48%
Number/percentage of C's	22,854,345 / 17.84%
Number/percentage of T's	41,451,247 / 32.36%
Number/percentage of G's	28,564,158 / 22.3%
Number/percentage of N's	33,086 / 0.03%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0414

Standard Deviation	0.389

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

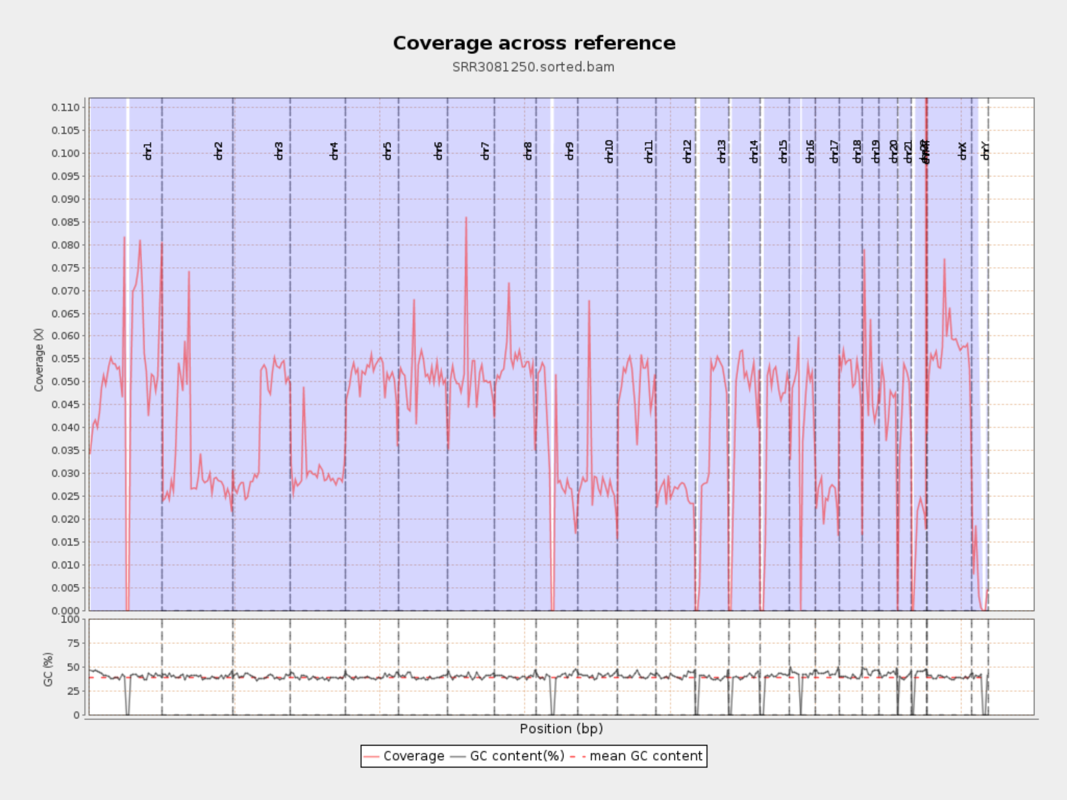
General error rate	0.88%
Mismatches	1,104,259
Insertions	10,670
Mapped reads with at least one insertion	0.55%
Deletions	34,673
Mapped reads with at least one deletion	1.79%
Homopolymer indels	50.07%

2.6. Chromosome stats

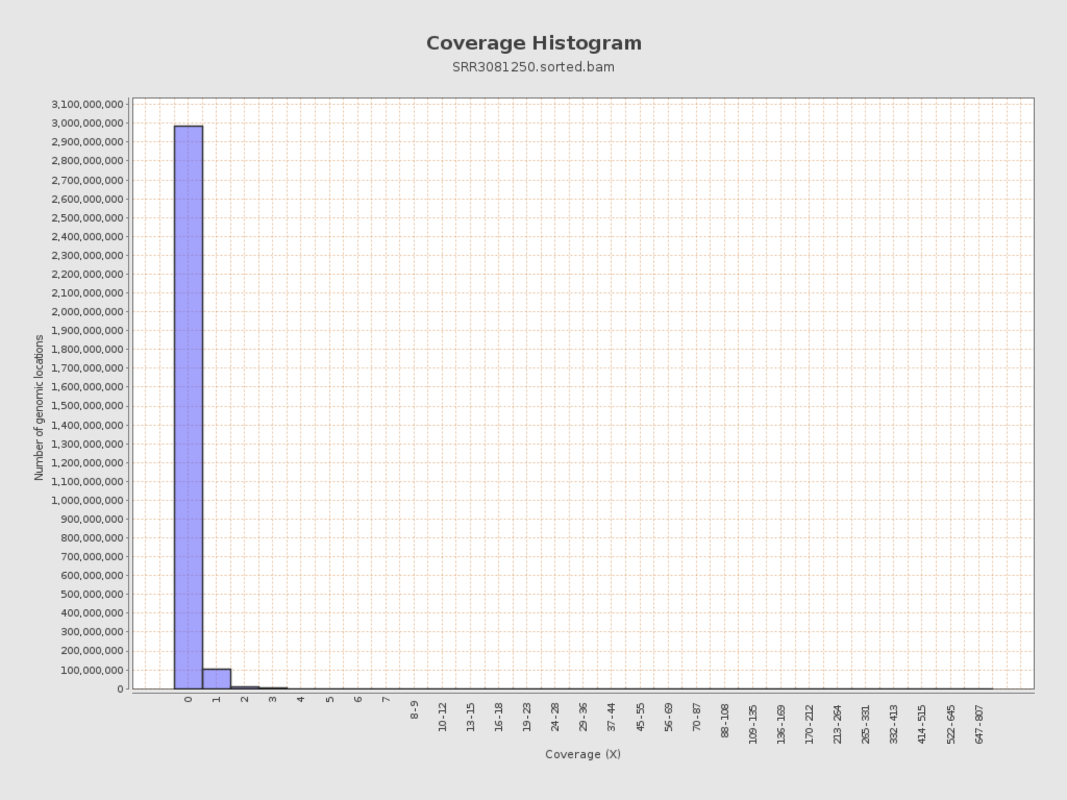
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12798520	0.0513	0.7377
chr2	243199373	8010432	0.0329	0.413
chr3	198022430	7974321	0.0403	0.225
chr4	191154276	5732540	0.03	0.2095
chr5	180915260	9300624	0.0514	0.2529
chr6	171115067	8789953	0.0514	0.3201
chr7	159138663	8187824	0.0515	0.5796

chr8	146364022	7868414	0.0538	0.4821
chr9	141213431	4467220	0.0316	0.3717
chr10	135534747	3964035	0.0292	0.3532
chr11	135006516	6640064	0.0492	0.3727
chr12	133851895	3452199	0.0258	0.1874
chr13	115169878	4243612	0.0368	0.2093
chr14	107349540	4563392	0.0425	0.2404
chr15	102531392	4130691	0.0403	0.2201
chr16	90354753	3972059	0.044	0.2486
chr17	81195210	1986446	0.0245	0.2057
chr18	78077248	4116764	0.0527	0.6165
chr19	59128983	2993293	0.0506	0.5522
chr20	63025520	2864418	0.0454	0.24
chr21	48129895	1989624	0.0413	0.2481
chr22	51304566	815437	0.0159	0.135
chrMT	16571	57415	3.4648	2.5538
chrX	155270560	8891371	0.0573	0.3006
chrY	59373566	354977	0.006	0.1443

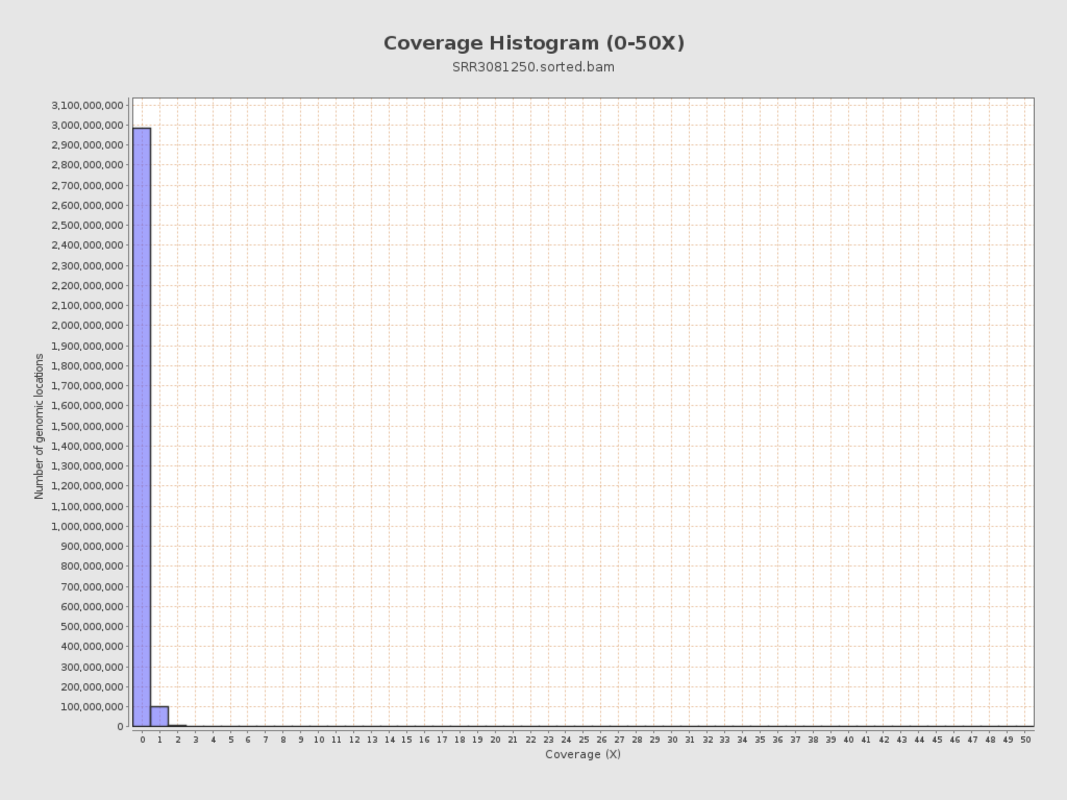
3. Results : Coverage across reference



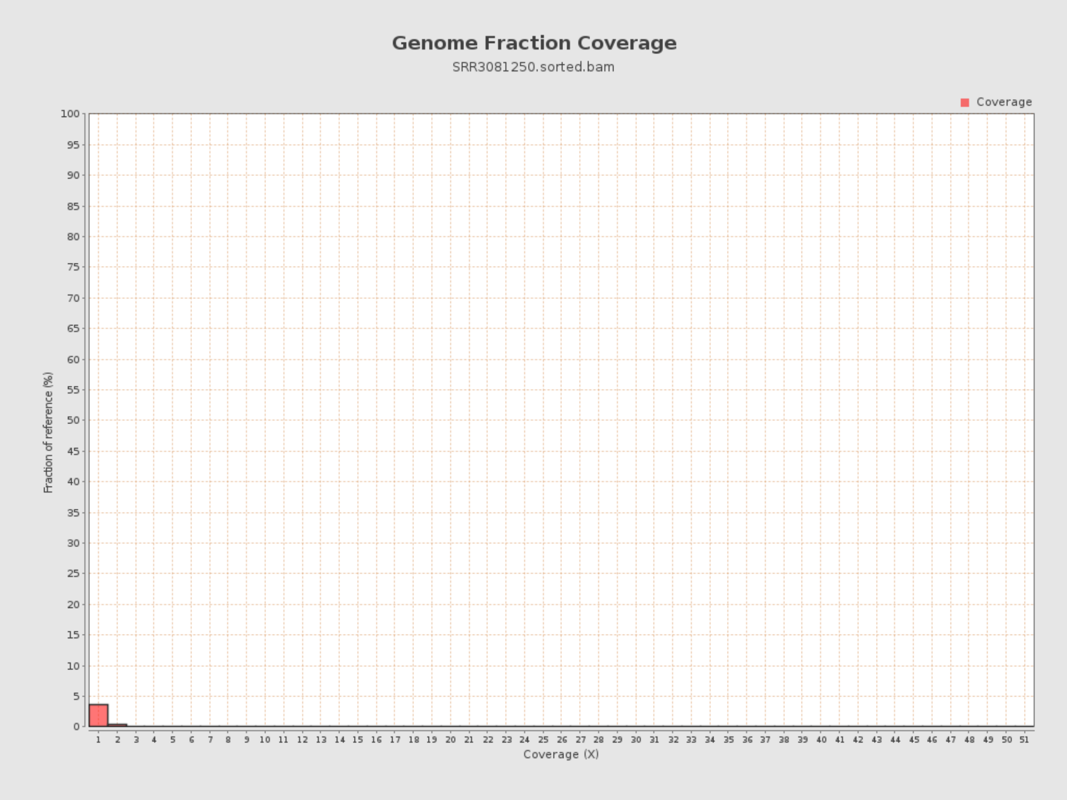
4. Results : Coverage Histogram



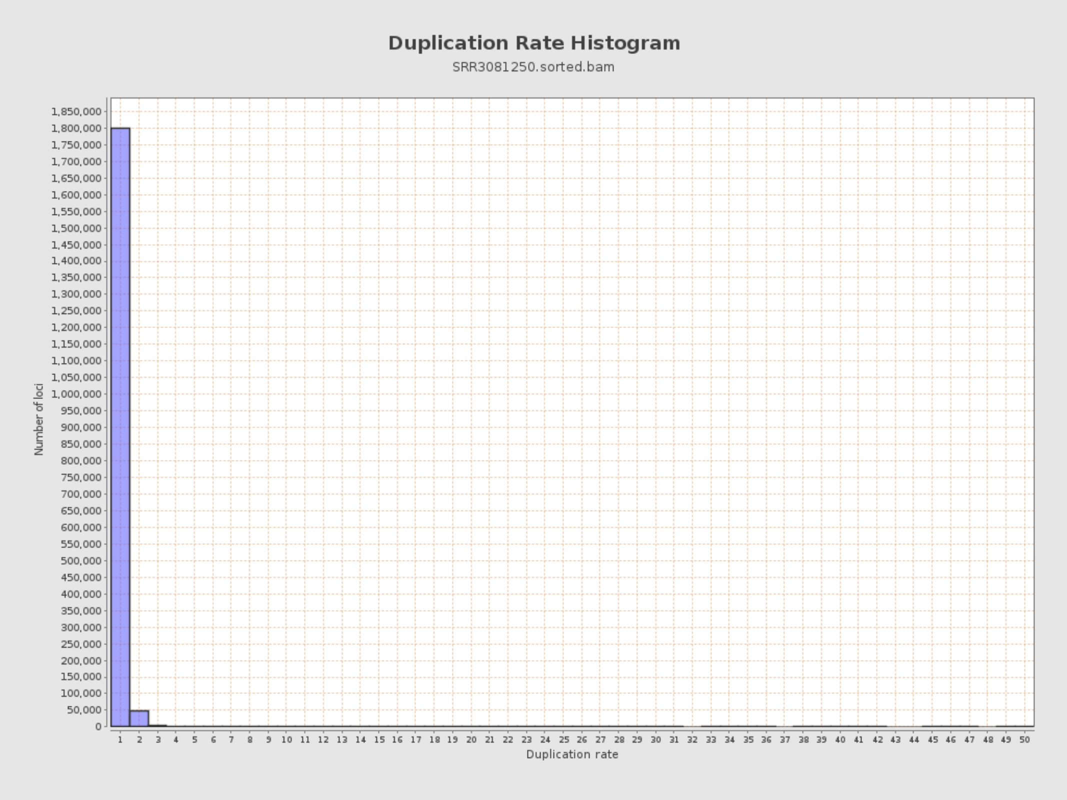
5. Results : Coverage Histogram (0-50X)



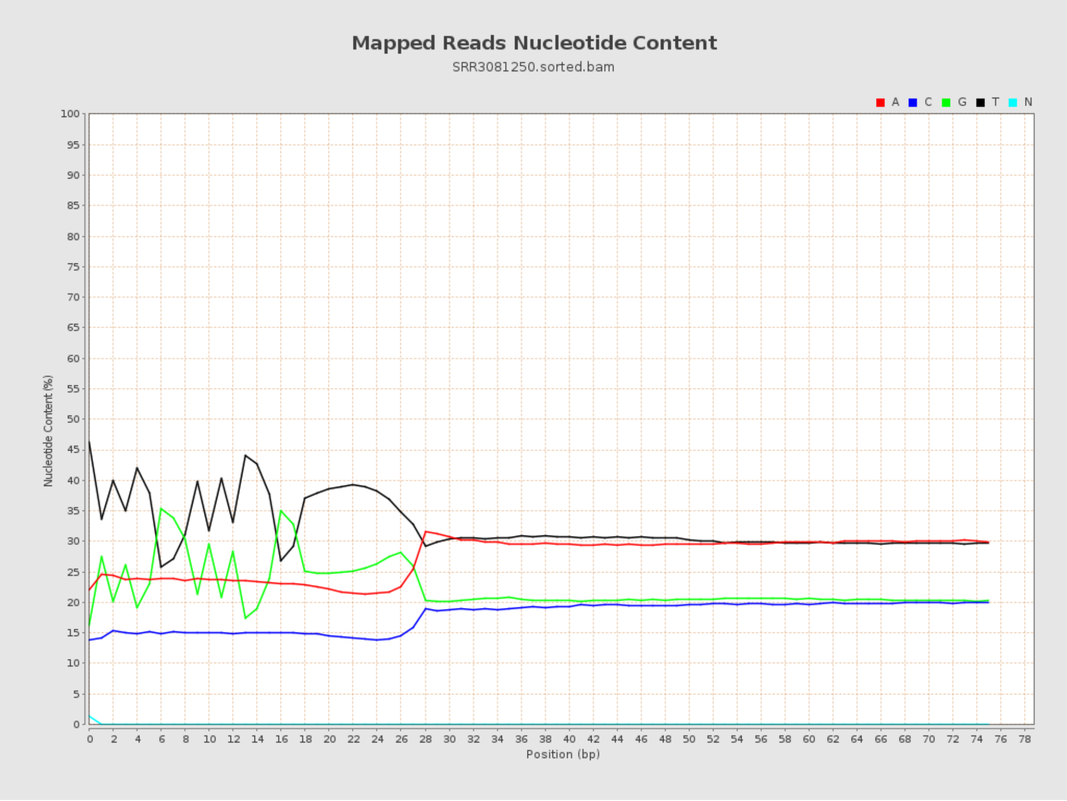
6. Results : Genome Fraction Coverage



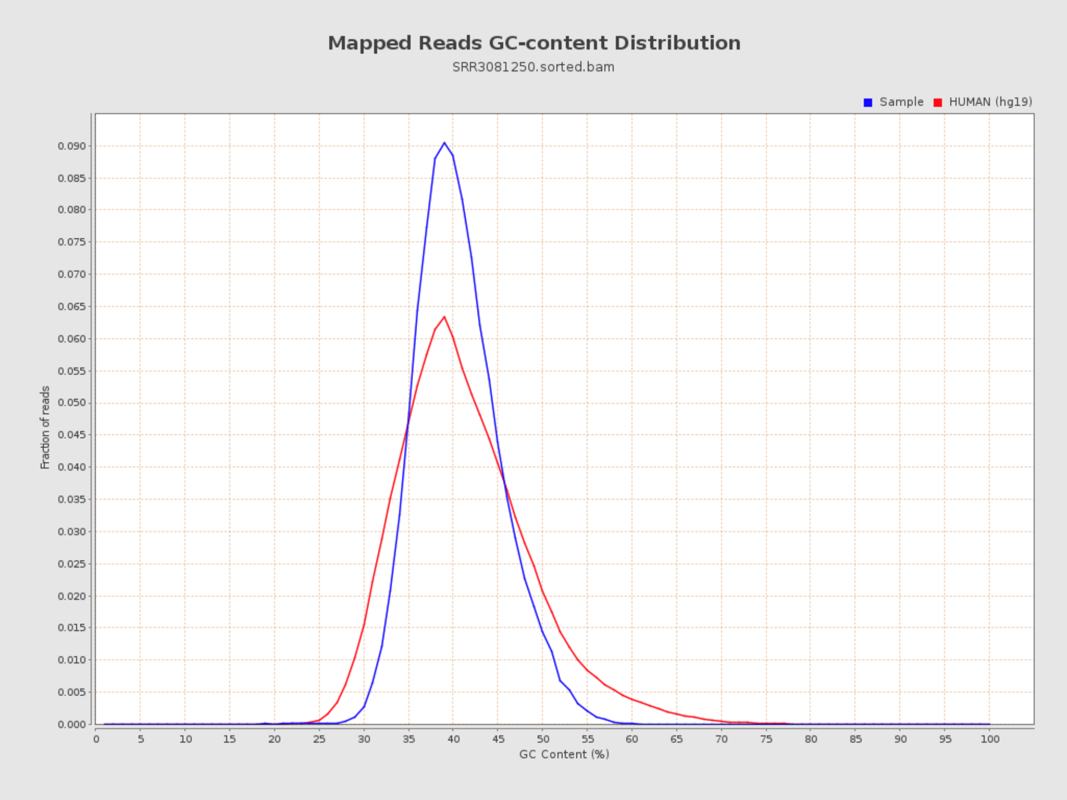
7. Results : Duplication Rate Histogram



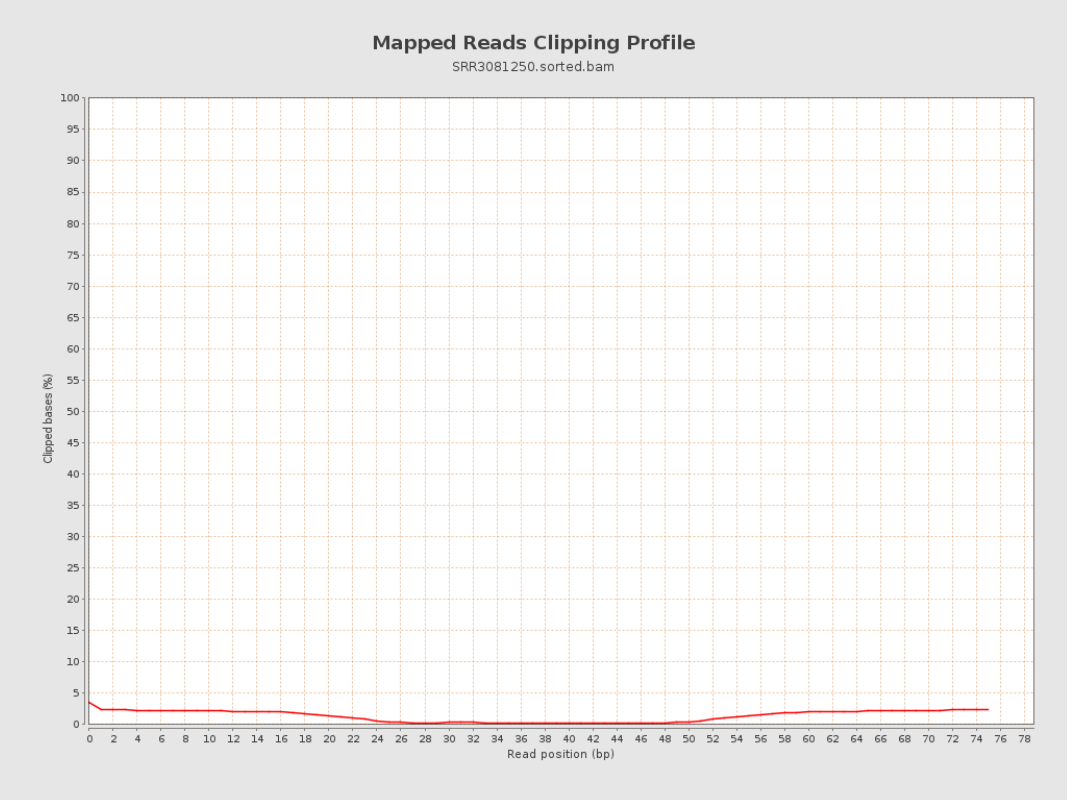
8. Results : Mapped Reads Nucleotide Content



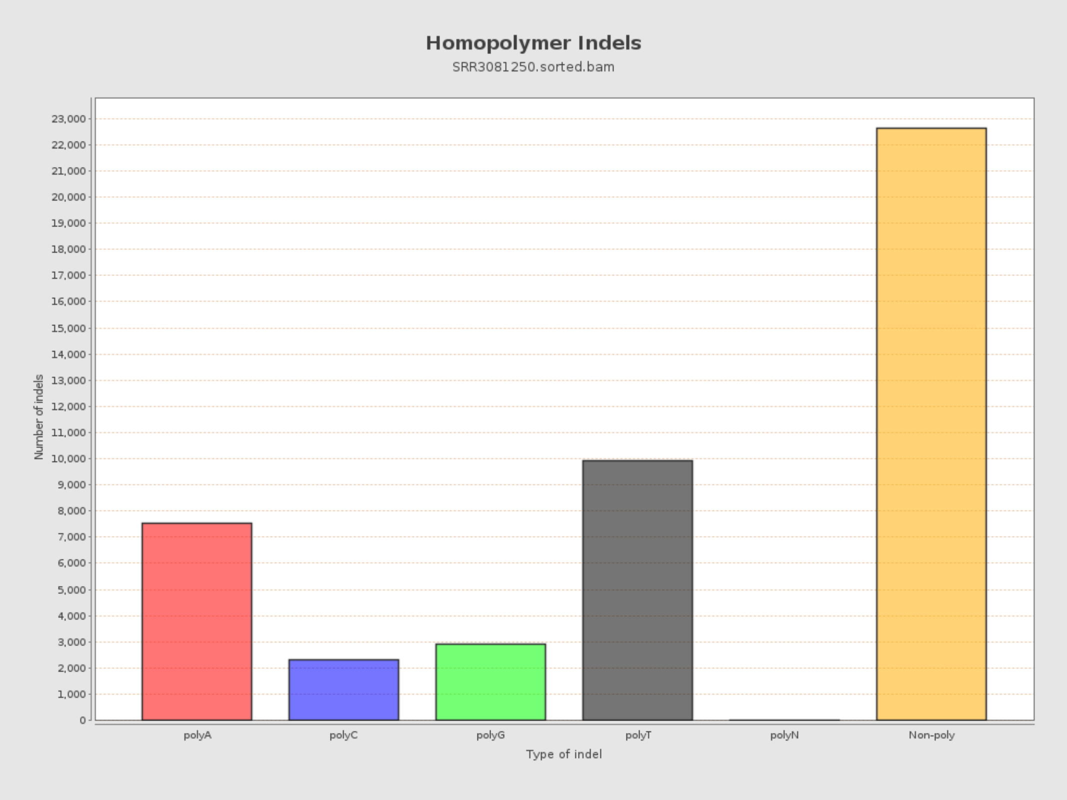
9. Results : Mapped Reads GC-content Distribution



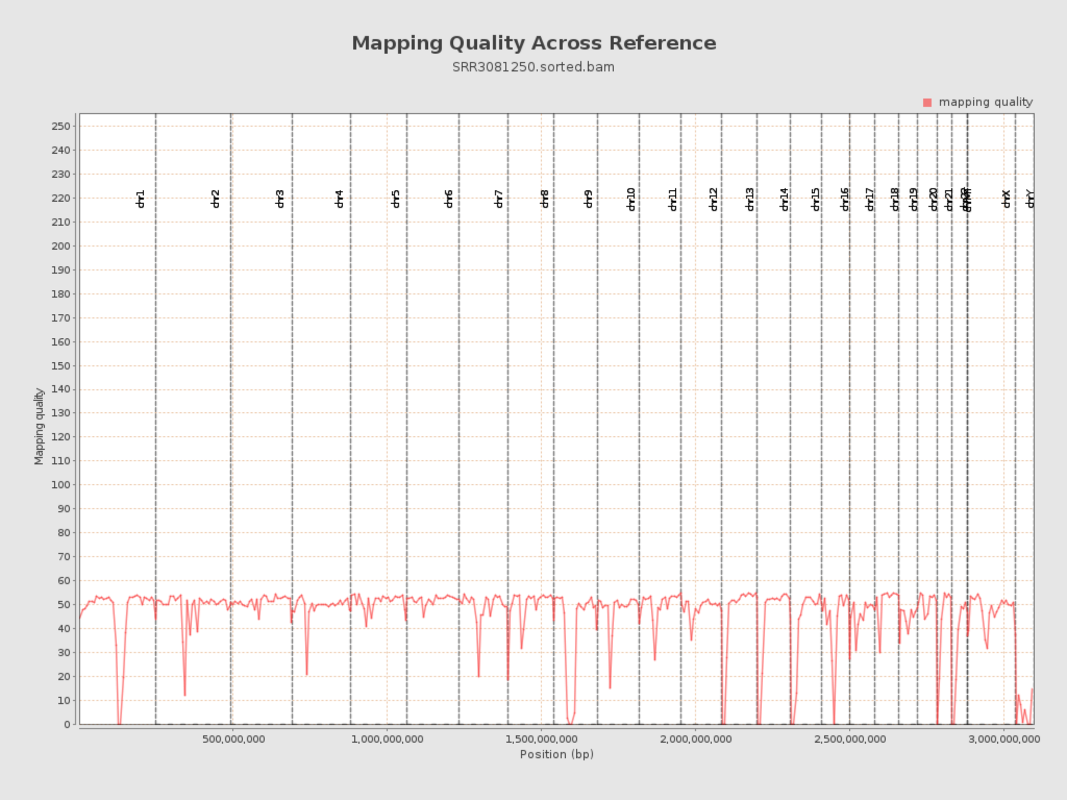
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram