Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:36:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081035.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_SRR3081035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:36:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,855,323
Mapped reads	1,511,544 / 81.47%
Unmapped reads	343,779 / 18.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,660 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	33,127 / 1.79%
Duplication rate	1.75%
Clipped reads	803,665 / 43.32%

2.2. ACGT Content

Number/percentage of A's	29,100,795 / 29.96%
Number/percentage of C's	18,701,171 / 19.25%
Number/percentage of T's	28,664,385 / 29.51%
Number/percentage of G's	20,666,725 / 21.28%
Number/percentage of N's	1,251 / 0%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.2485

2.4. Mapping Quality

Mean Mapping Quality	46.95

2.5. Mismatches and indels

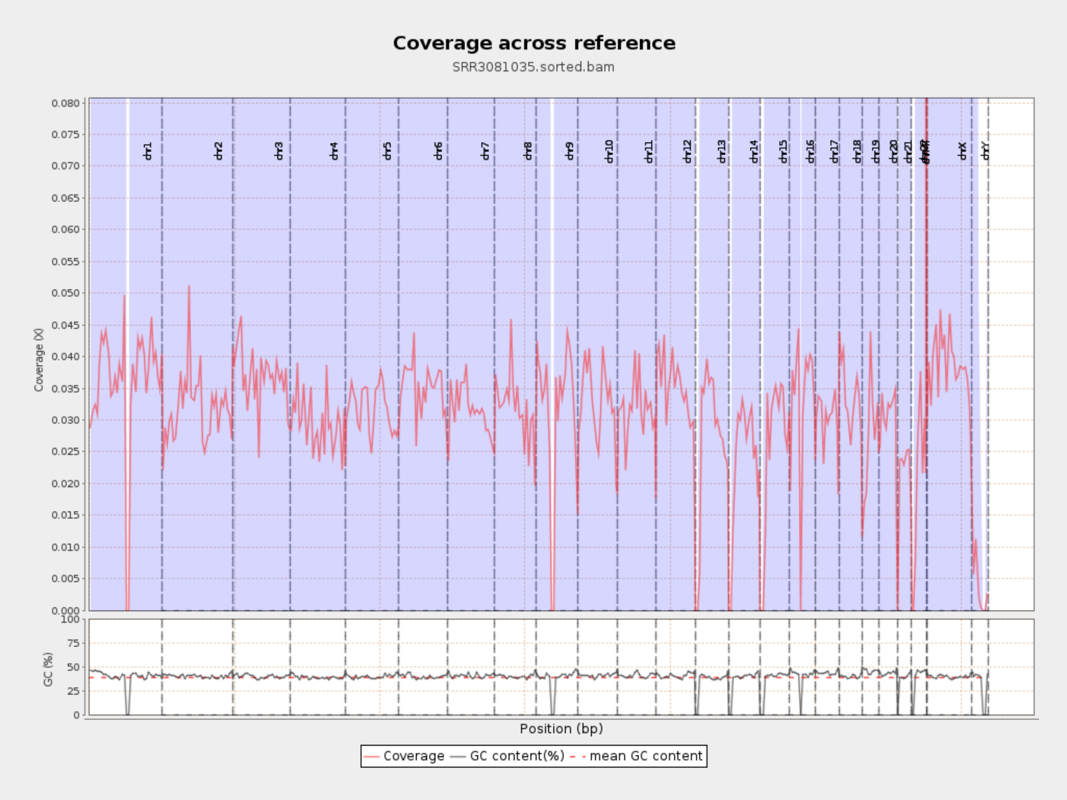
General error rate	0.79%
Mismatches	758,439
Insertions	6,570
Mapped reads with at least one insertion	0.43%
Deletions	19,799
Mapped reads with at least one deletion	1.3%
Homopolymer indels	47.4%

2.6. Chromosome stats

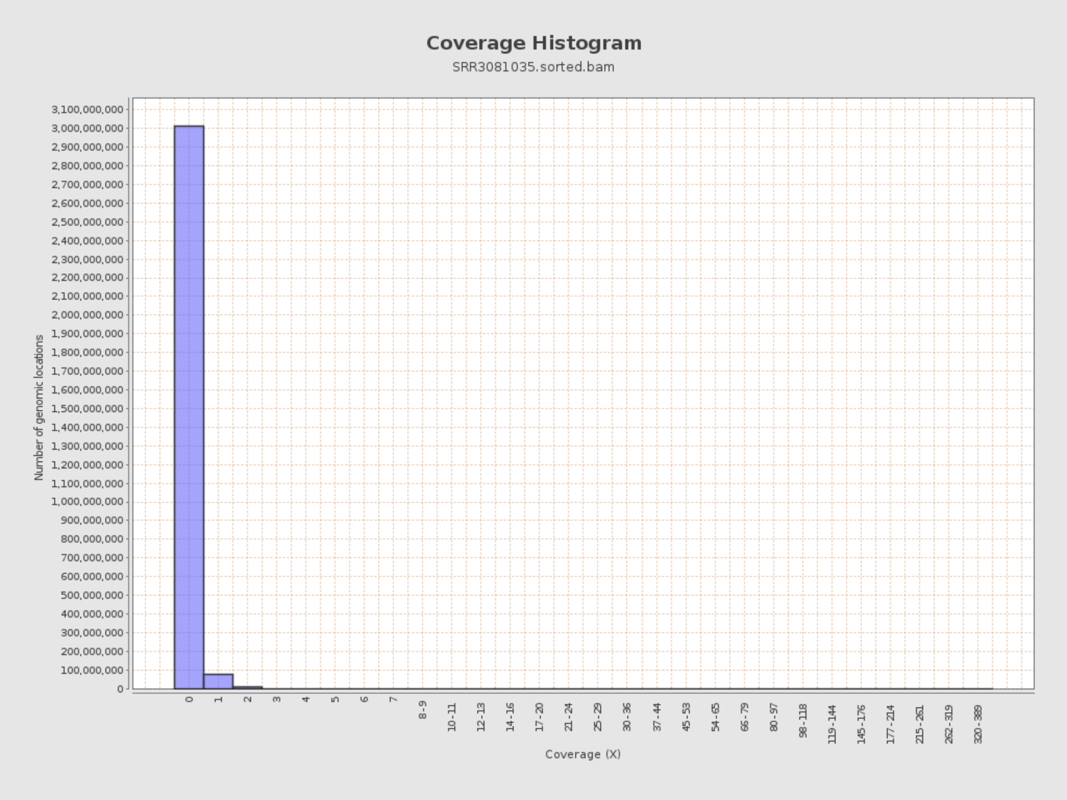
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8895090	0.0357	0.3913
chr2	243199373	7769326	0.0319	0.2651
chr3	198022430	7337020	0.0371	0.213
chr4	191154276	5657925	0.0296	0.1983
chr5	180915260	5758312	0.0318	0.1972
chr6	171115067	6006753	0.0351	0.2367
chr7	159138663	5046060	0.0317	0.2739

chr8	146364022	4686636	0.032	0.2873
chr9	141213431	4440400	0.0314	0.237
chr10	135534747	4499331	0.0332	0.2443
chr11	135006516	4254609	0.0315	0.2347
chr12	133851895	4715197	0.0352	0.2089
chr13	115169878	3027656	0.0263	0.1781
chr14	107349540	2514319	0.0234	0.1745
chr15	102531392	2618820	0.0255	0.1792
chr16	90354753	3015061	0.0334	0.2147
chr17	81195210	2441485	0.0301	0.2023
chr18	78077248	2656263	0.034	0.4105
chr19	59128983	1629688	0.0276	0.2796
chr20	63025520	1934792	0.0307	0.1975
chr21	48129895	1015561	0.0211	0.1723
chr22	51304566	992847	0.0194	0.1527
chrMT	16571	37222	2.2462	2.0611
chrX	155270560	5980789	0.0385	0.228
chrY	59373566	236878	0.004	0.092

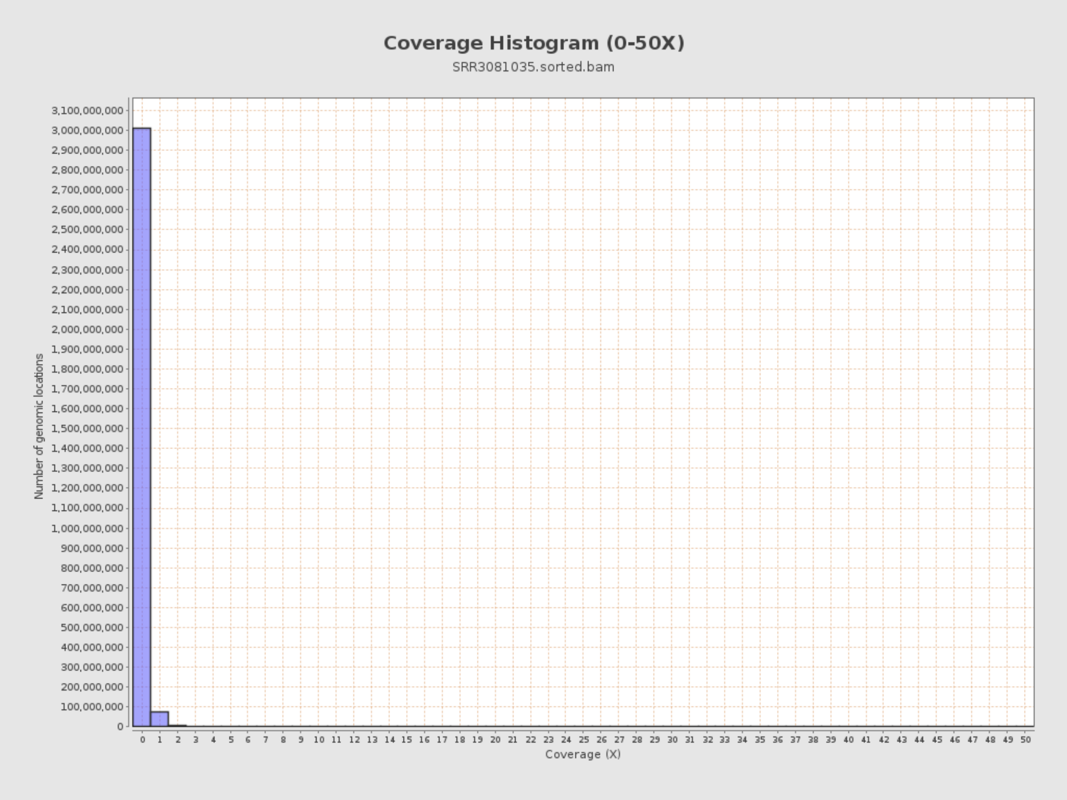
3. Results : Coverage across reference



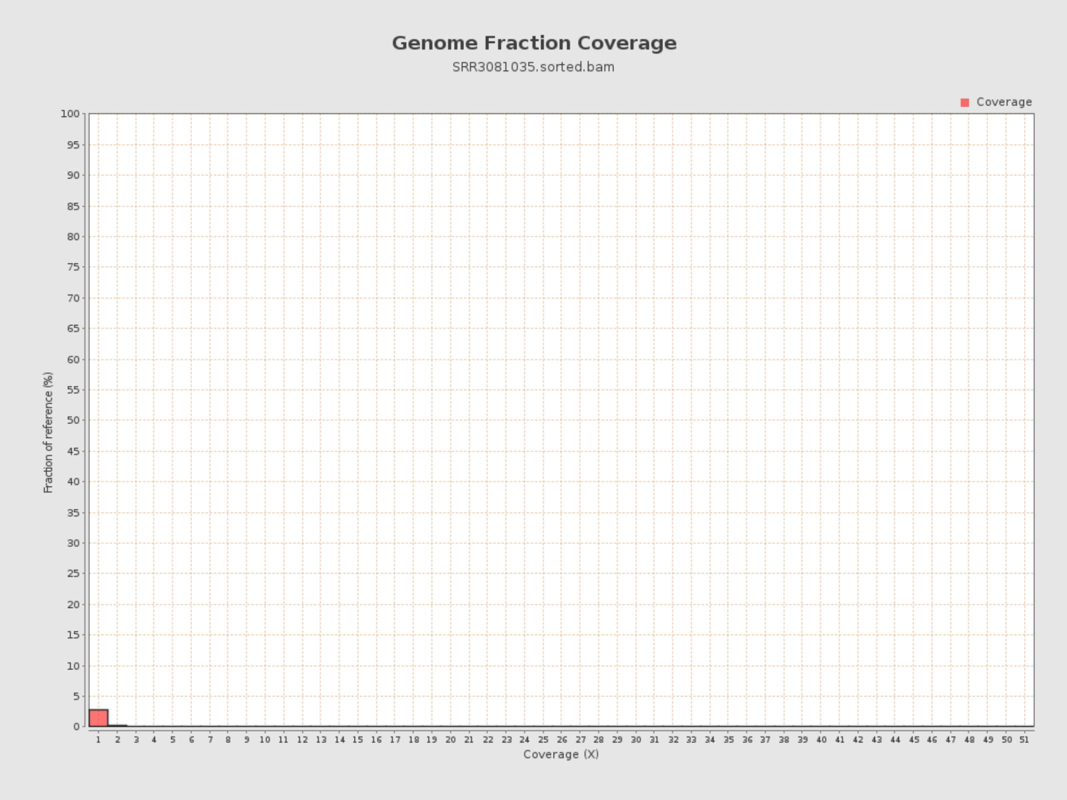
4. Results : Coverage Histogram



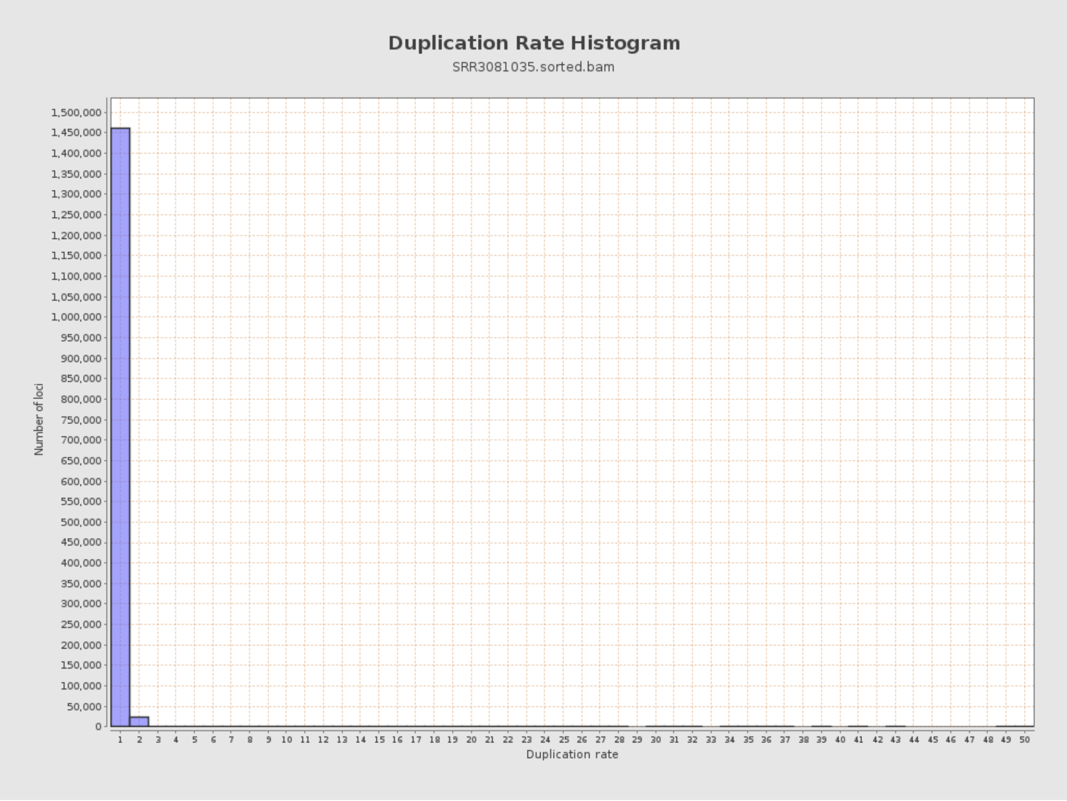
5. Results : Coverage Histogram (0-50X)



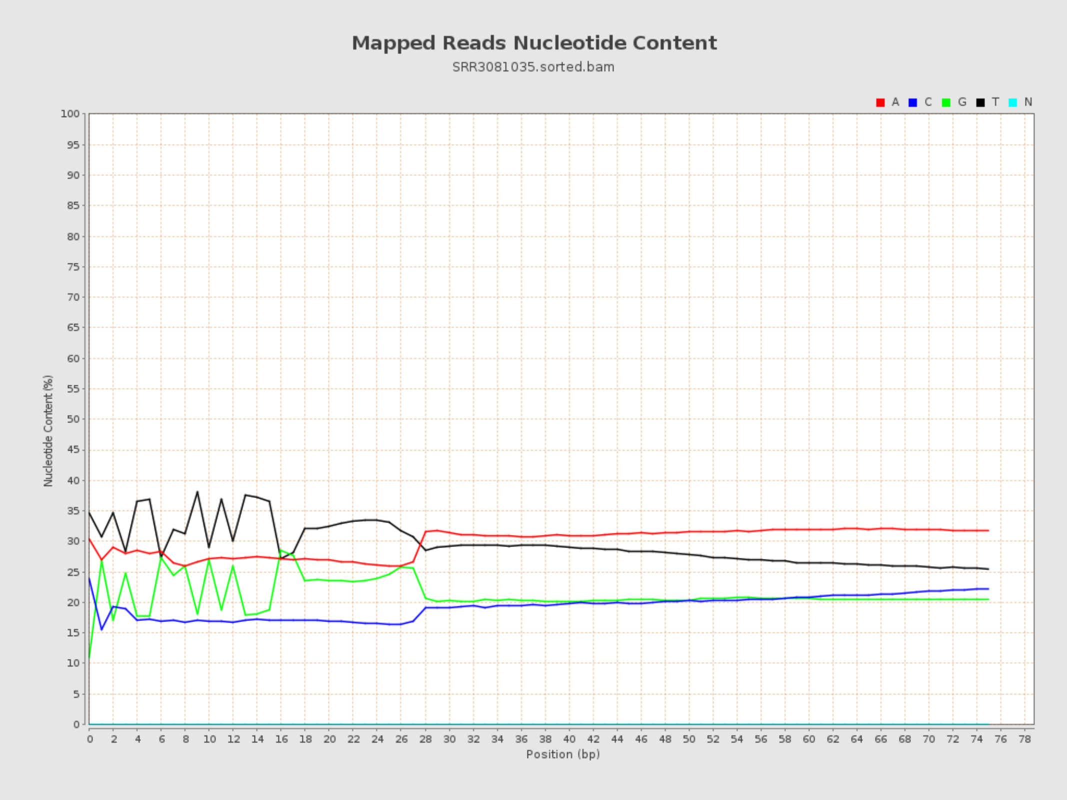
6. Results : Genome Fraction Coverage



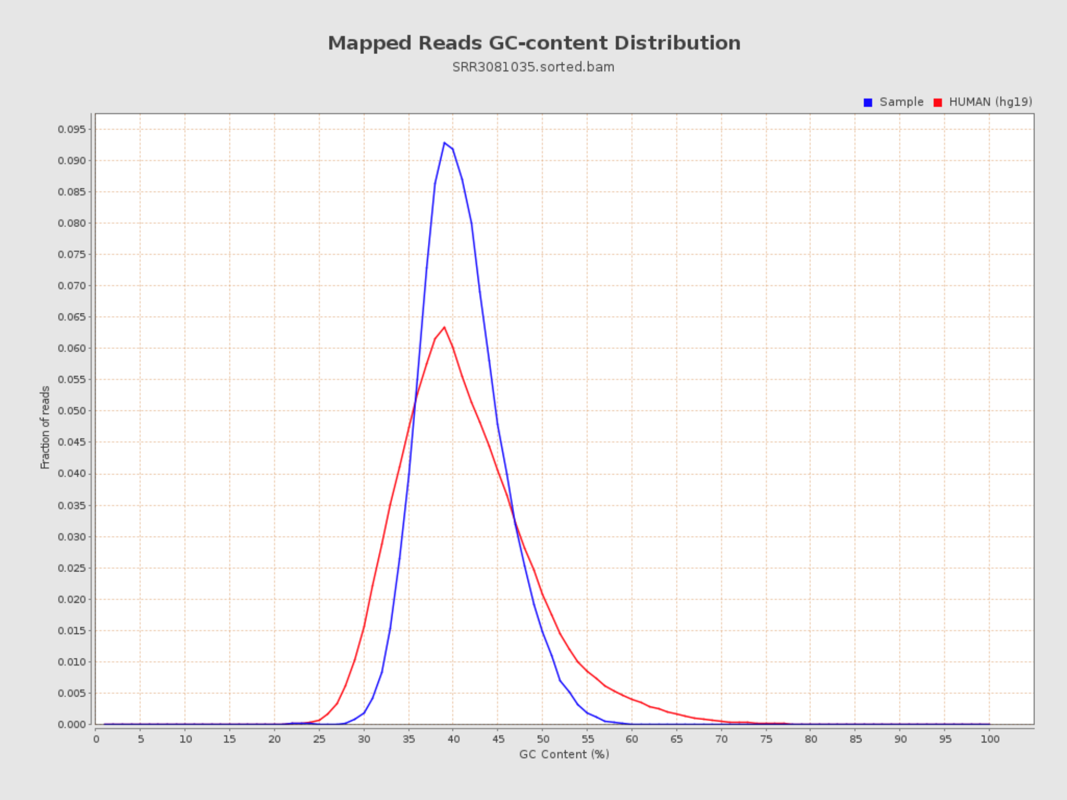
7. Results : Duplication Rate Histogram



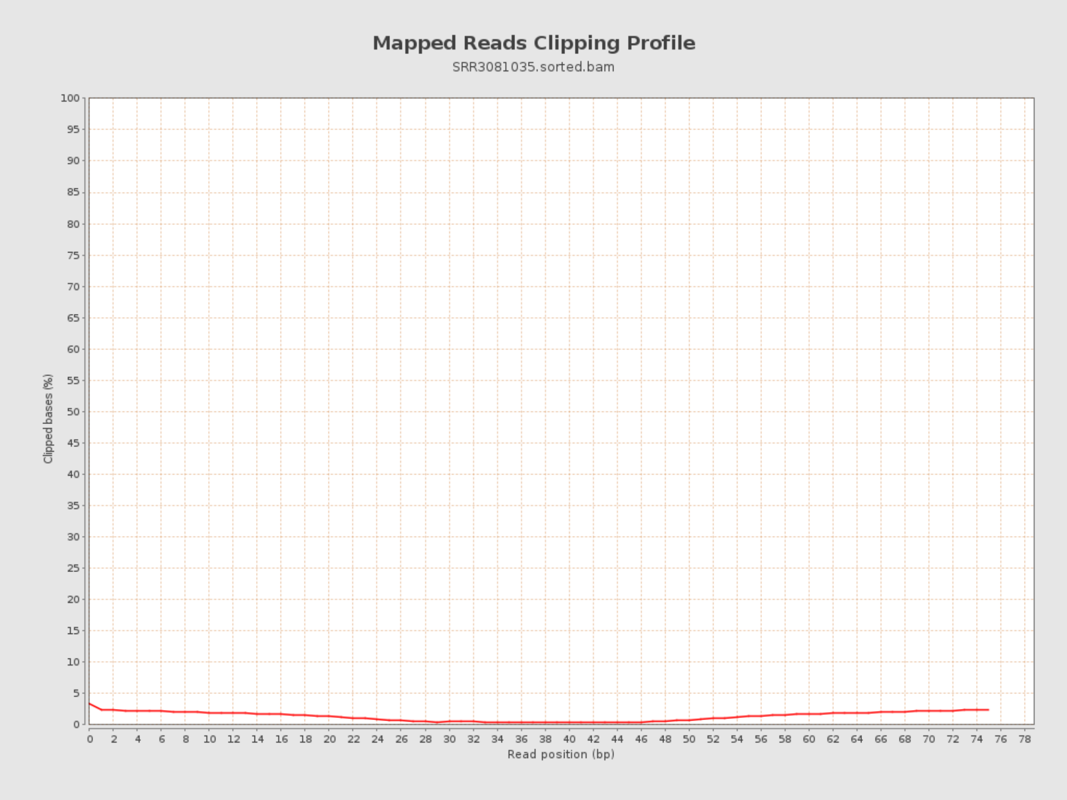
8. Results : Mapped Reads Nucleotide Content



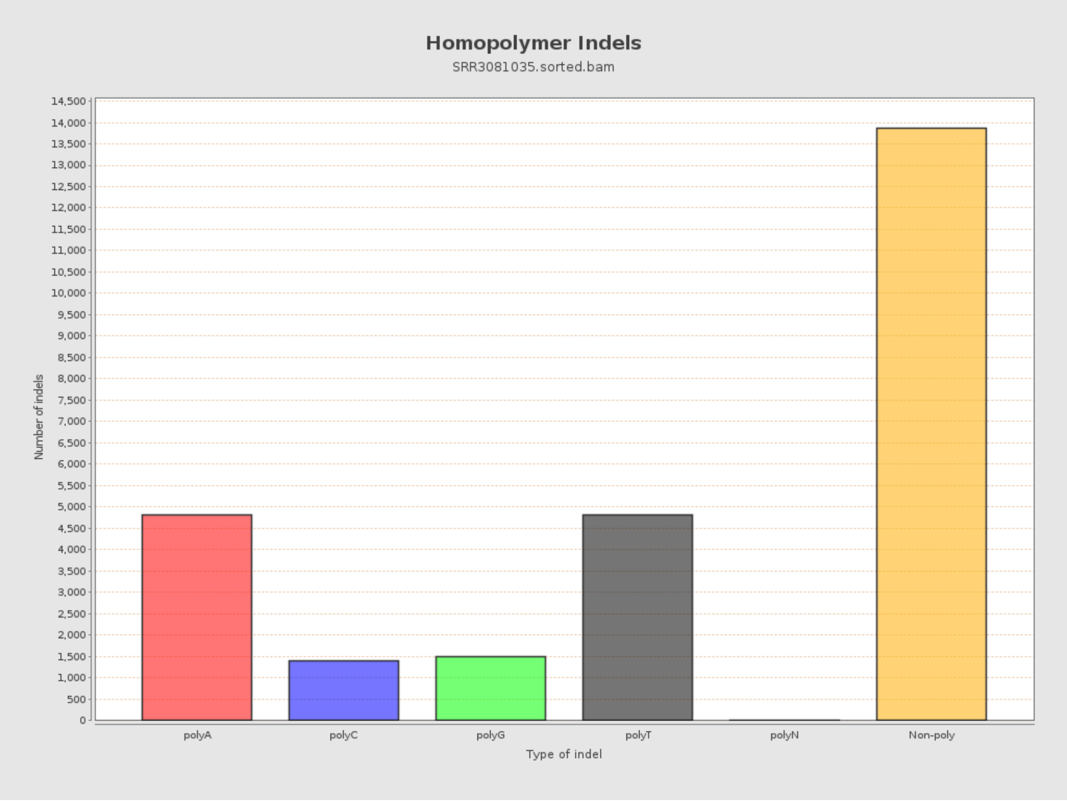
9. Results : Mapped Reads GC-content Distribution



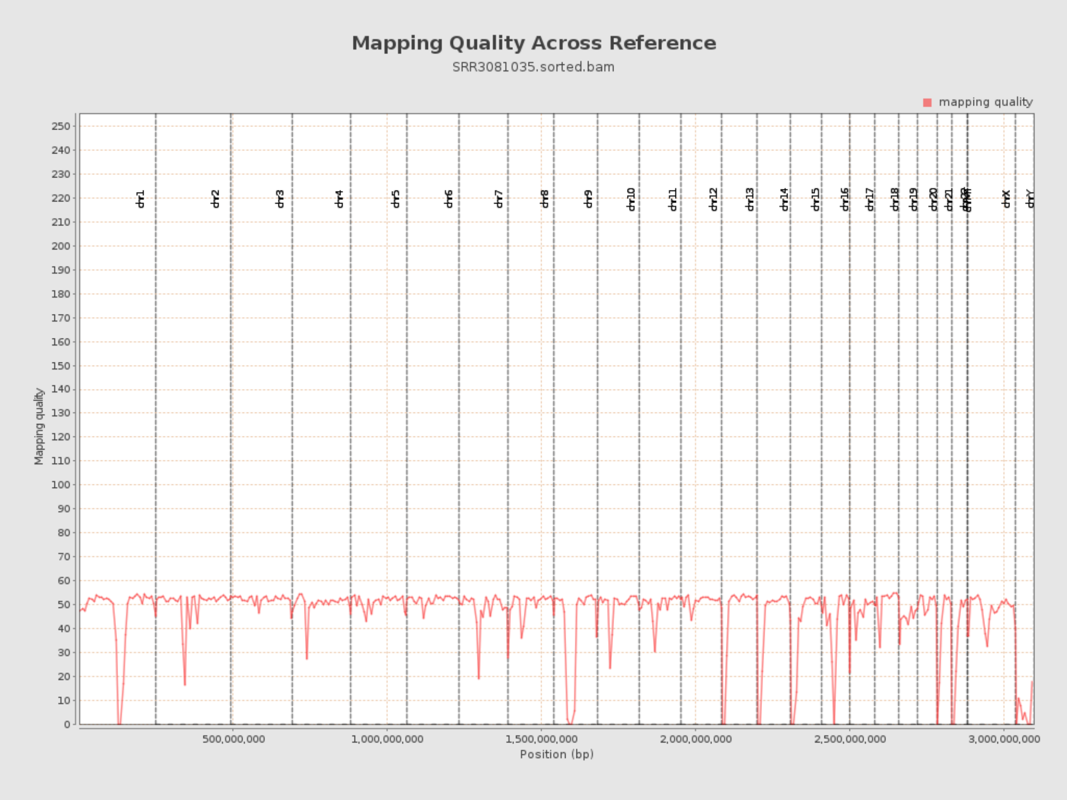
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram