Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:47:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085047.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_SRR3085047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:47:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,121
Mapped reads	1,443 / 35.02%
Unmapped reads	2,678 / 64.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	666 / 16.16%

2.2. ACGT Content

Number/percentage of A's	28,176 / 29.31%
Number/percentage of C's	18,404 / 19.14%
Number/percentage of T's	29,047 / 30.21%
Number/percentage of G's	20,490 / 21.31%
Number/percentage of N's	18 / 0.02%
GC Percentage	40.46%

2.3. Coverage

Mean	0

Standard Deviation	0.0056

2.4. Mapping Quality

Mean Mapping Quality	42.79

2.5. Mismatches and indels

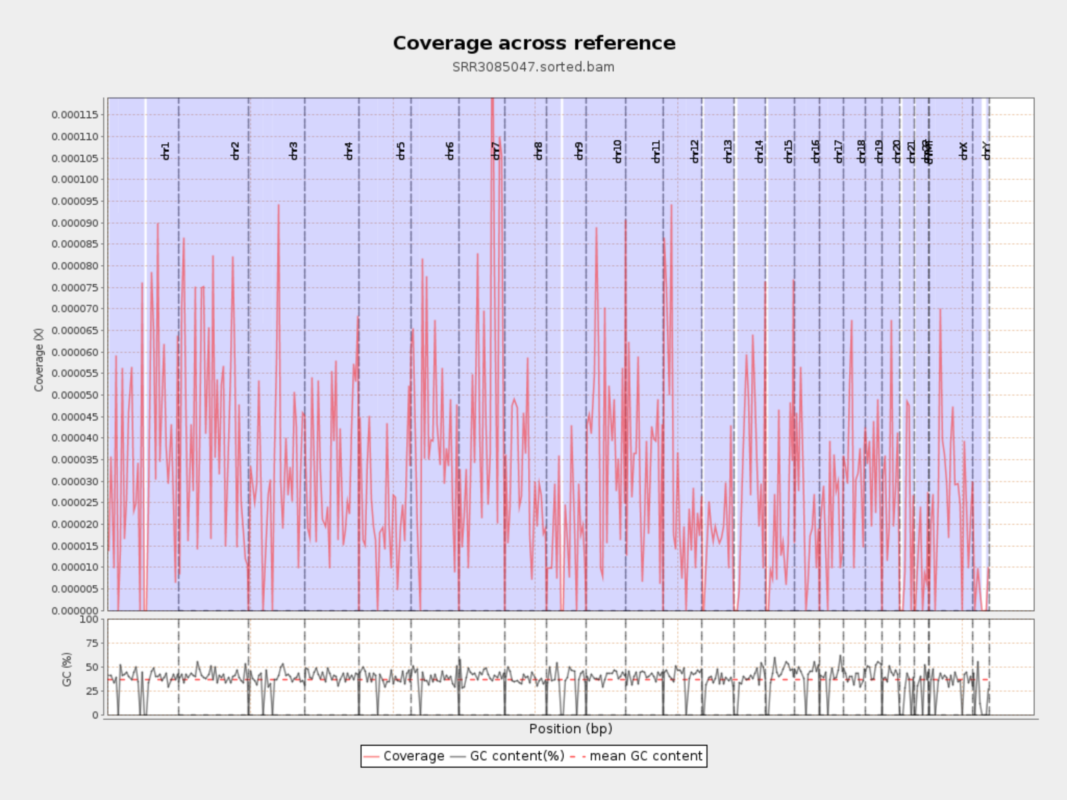
General error rate	1.13%
Mismatches	1,081
Insertions	6
Mapped reads with at least one insertion	0.42%
Deletions	15
Mapped reads with at least one deletion	1.04%
Homopolymer indels	66.67%

2.6. Chromosome stats

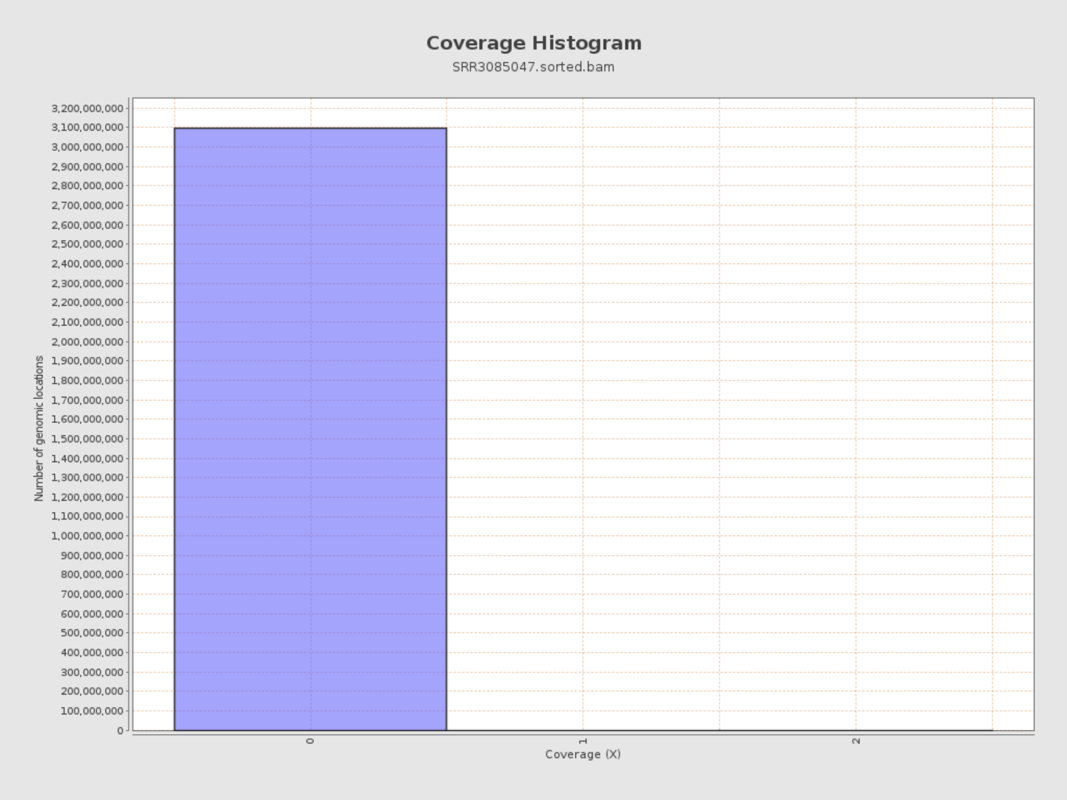
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8841	0	0.006
chr2	243199373	10699	0	0.0067
chr3	198022430	6413	0	0.0057
chr4	191154276	6478	0	0.0058
chr5	180915260	4317	0	0.0049
chr6	171115067	7043	0	0.0064
chr7	159138663	8022	0.0001	0.0071

chr8	146364022	4460	0	0.0055
chr9	141213431	2245	0	0.004
chr10	135534747	5617	0	0.0064
chr11	135006516	4606	0	0.0058
chr12	133851895	4171	0	0.0056
chr13	115169878	1953	0	0.0041
chr14	107349540	3244	0	0.0055
chr15	102531392	2012	0	0.0044
chr16	90354753	2045	0	0.0048
chr17	81195210	1724	0	0.0046
chr18	78077248	2692	0	0.0059
chr19	59128983	1853	0	0.0056
chr20	63025520	1904	0	0.0055
chr21	48129895	945	0	0.0044
chr22	51304566	434	0	0.0029
chrMT	16571	0	0	0
chrX	155270560	4176	0	0.0052
chrY	59373566	263	0	0.0021

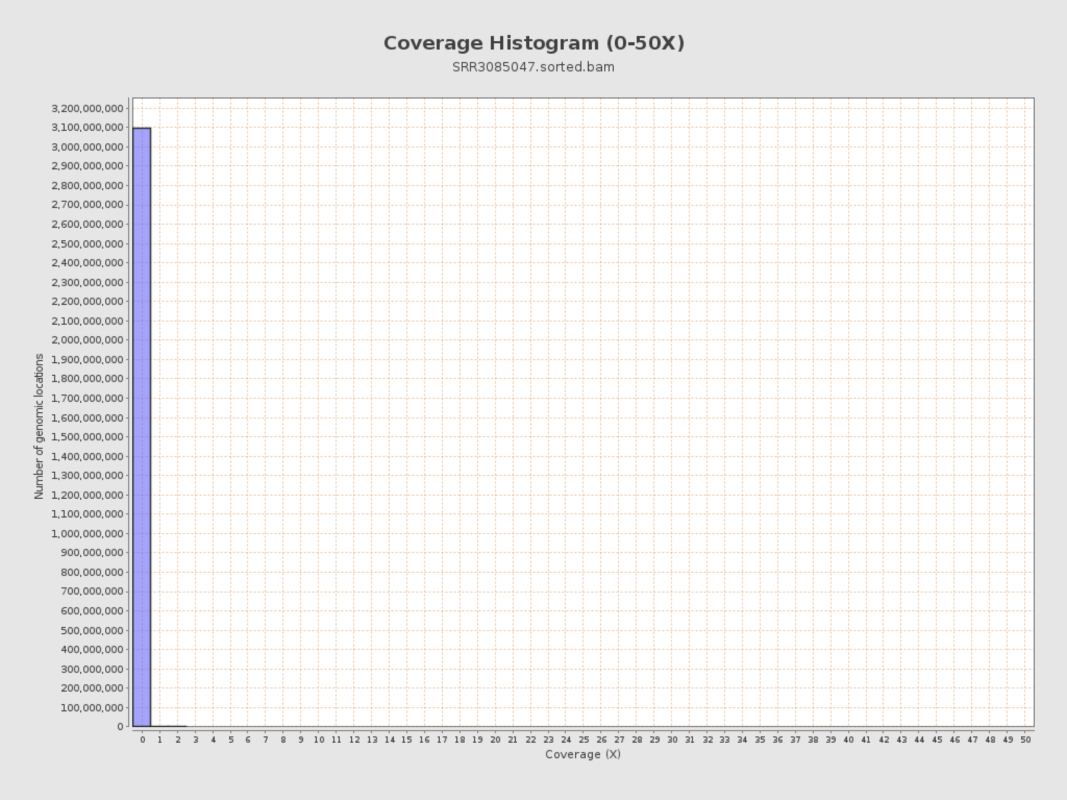
3. Results : Coverage across reference



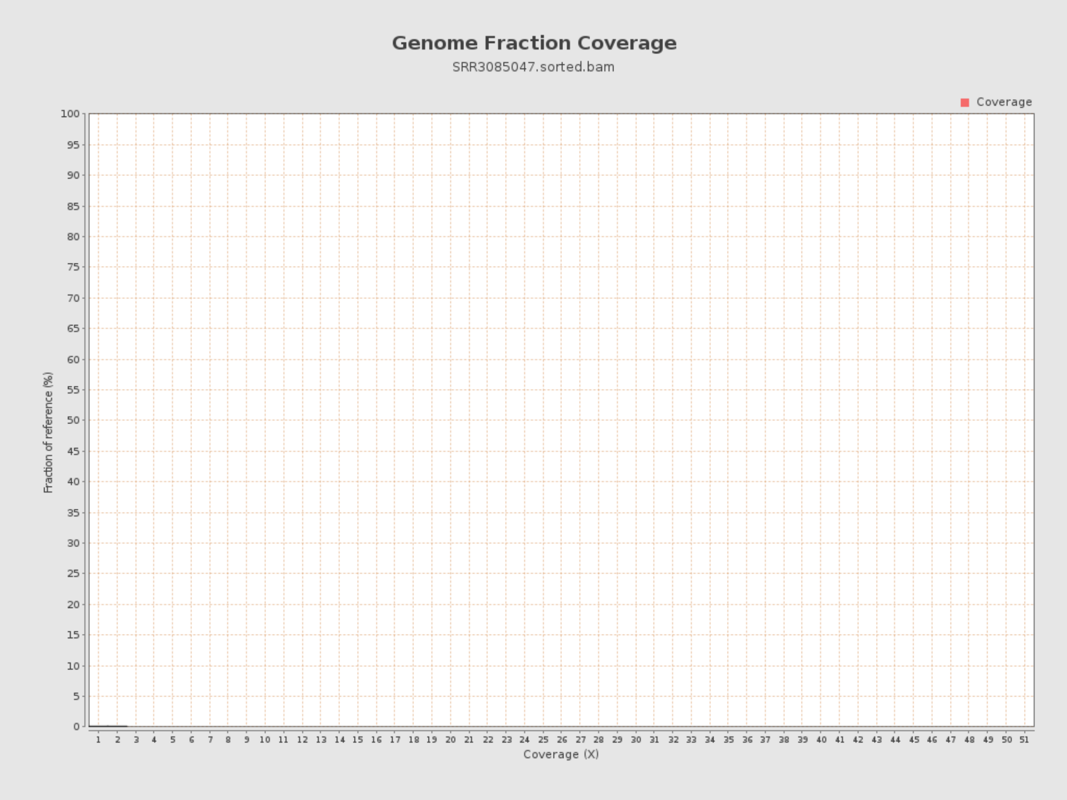
4. Results : Coverage Histogram



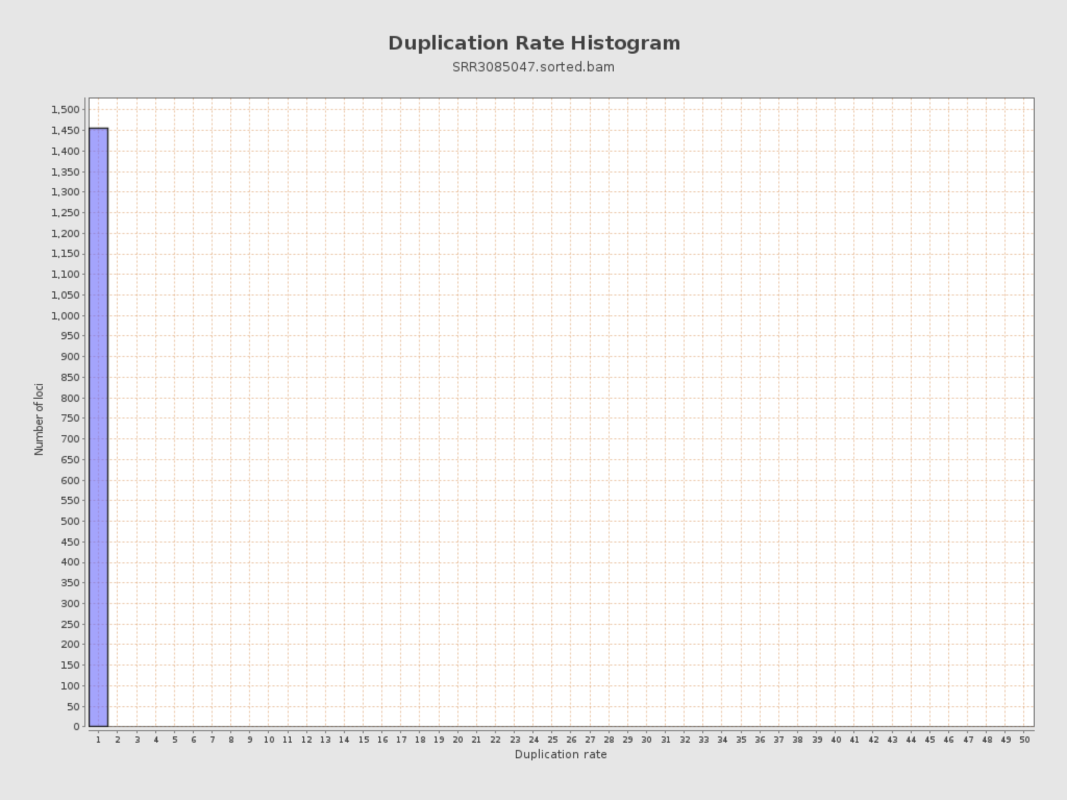
5. Results : Coverage Histogram (0-50X)



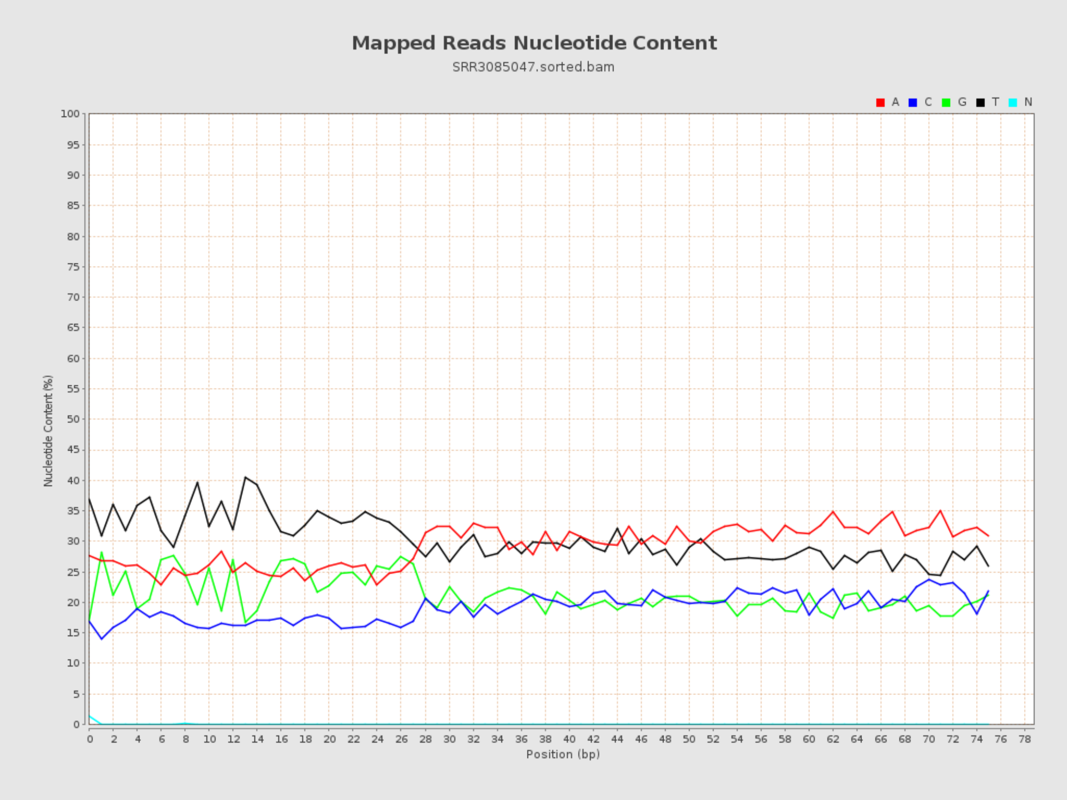
6. Results : Genome Fraction Coverage



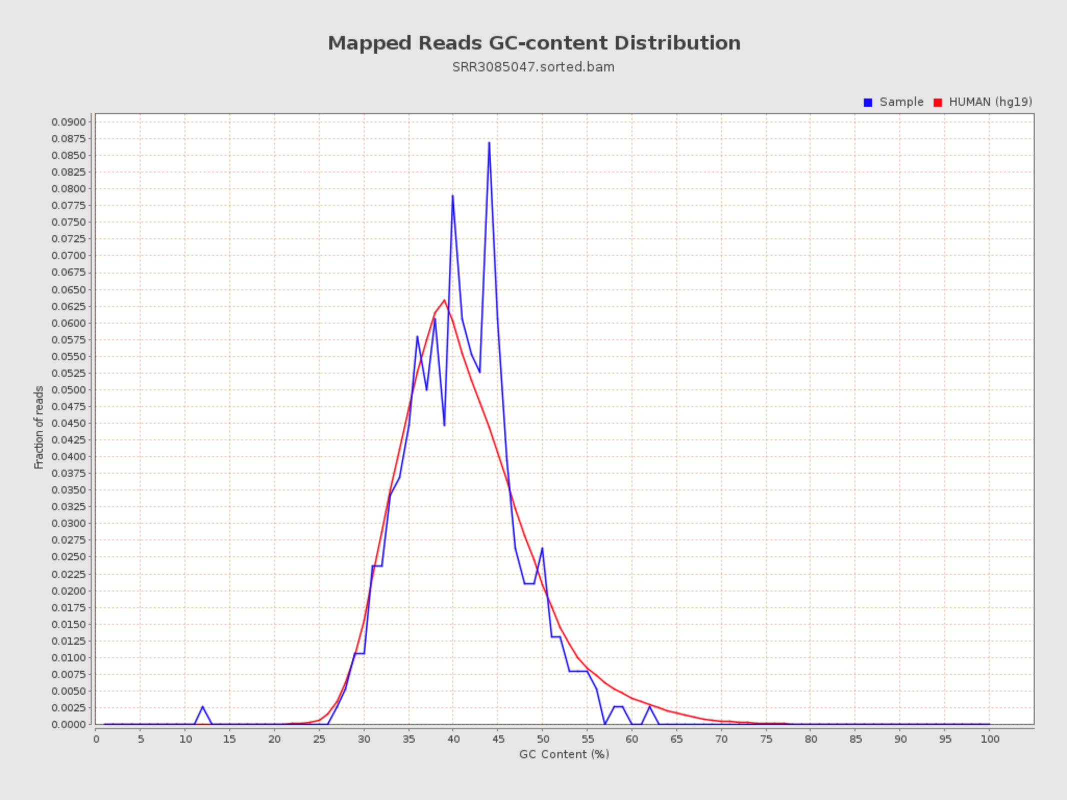
7. Results : Duplication Rate Histogram



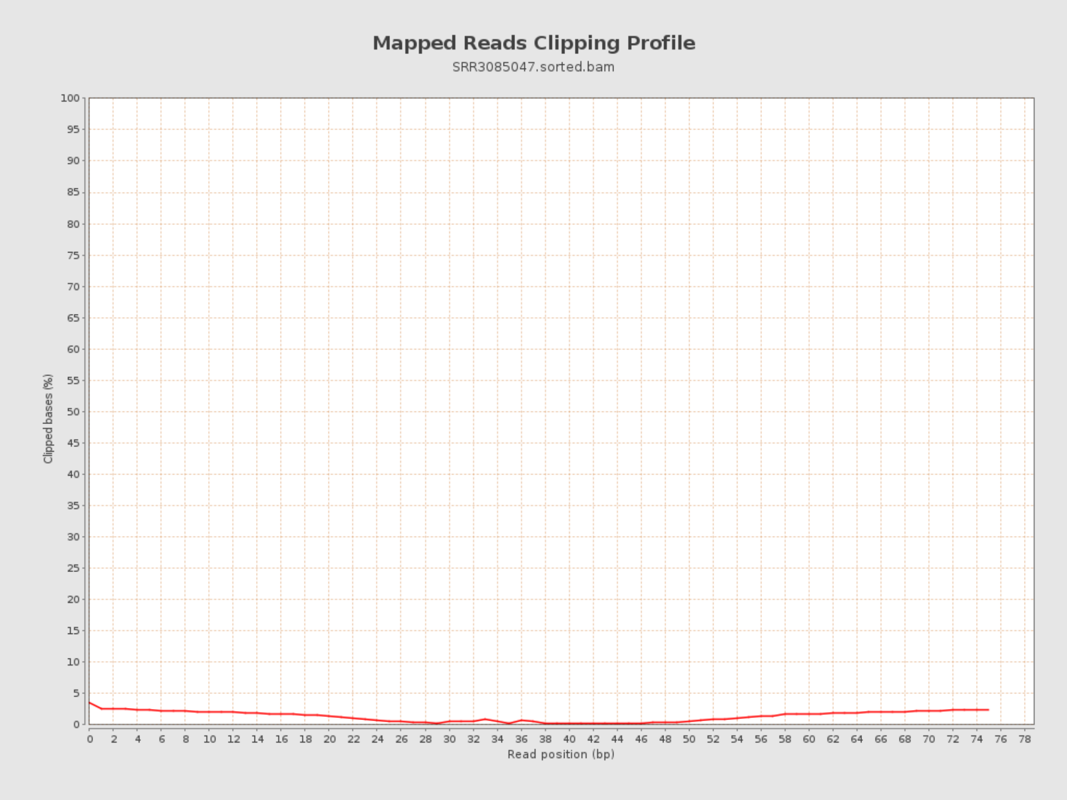
8. Results : Mapped Reads Nucleotide Content



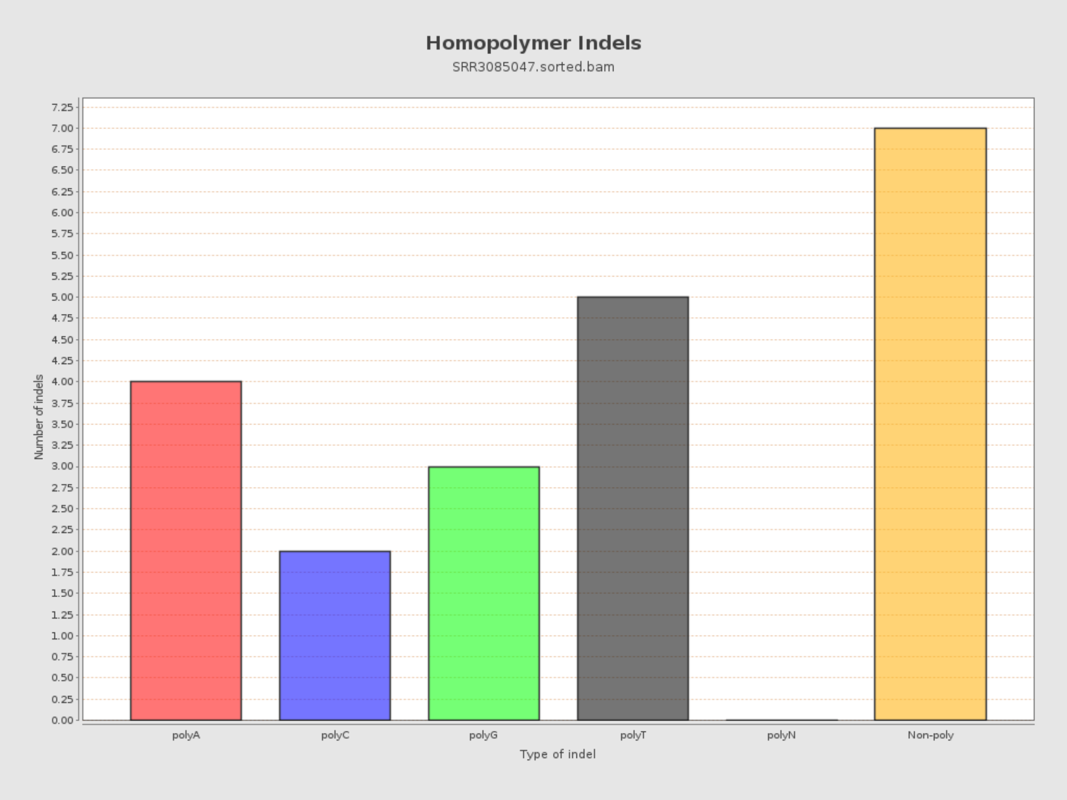
9. Results : Mapped Reads GC-content Distribution



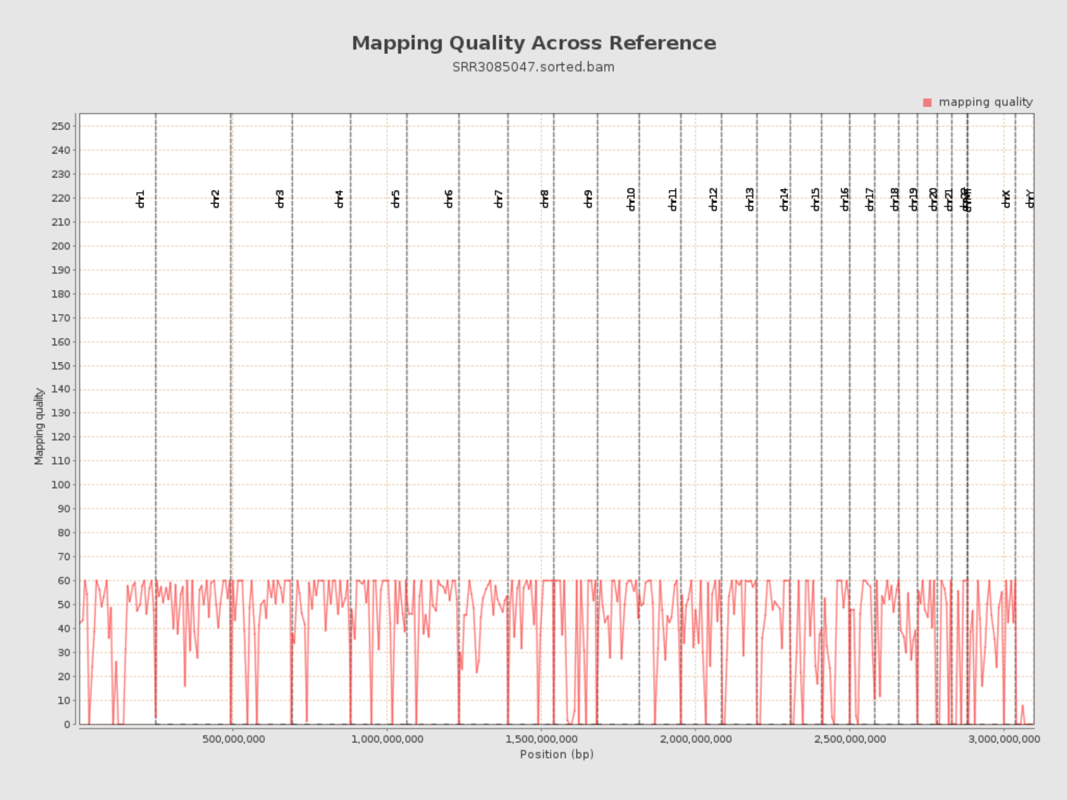
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram