Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:34:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085026.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_SRR3085026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:34:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,176,489
Mapped reads	1,936,076 / 88.95%
Unmapped reads	240,413 / 11.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,325 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	64,868 / 2.98%
Duplication rate	2.58%
Clipped reads	887,374 / 40.77%

2.2. ACGT Content

Number/percentage of A's	35,611,161 / 27.59%
Number/percentage of C's	24,821,896 / 19.23%
Number/percentage of T's	39,573,542 / 30.66%
Number/percentage of G's	29,041,155 / 22.5%
Number/percentage of N's	6,275 / 0%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.3369

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

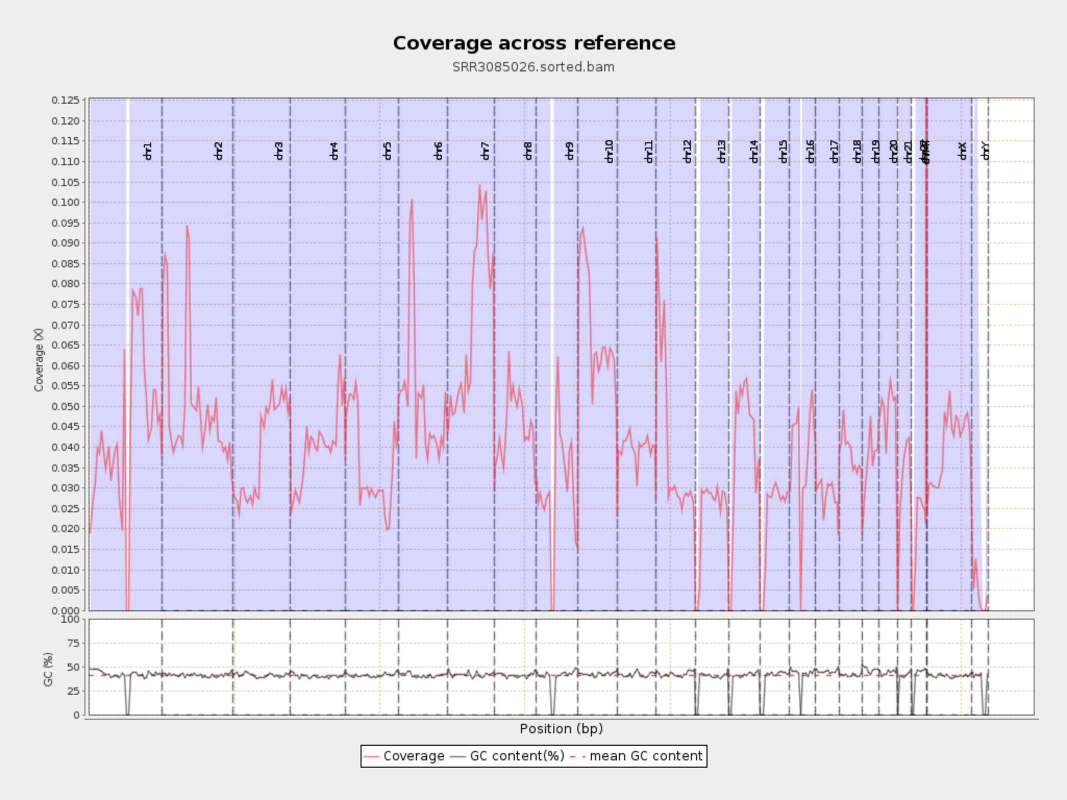
General error rate	0.86%
Mismatches	1,100,404
Insertions	8,995
Mapped reads with at least one insertion	0.46%
Deletions	27,042
Mapped reads with at least one deletion	1.38%
Homopolymer indels	46.57%

2.6. Chromosome stats

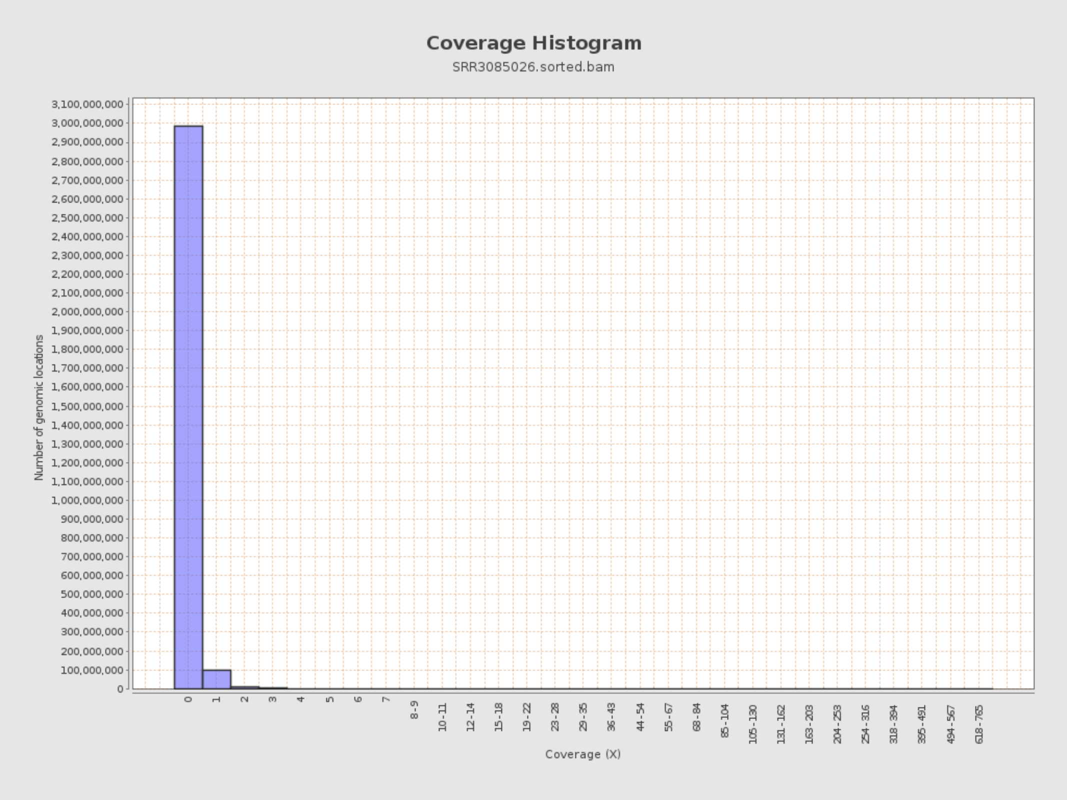
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10963260	0.044	0.4621
chr2	243199373	12383916	0.0509	0.4754
chr3	198022430	7830614	0.0395	0.2235
chr4	191154276	7660385	0.0401	0.2275
chr5	180915260	6413897	0.0355	0.2109
chr6	171115067	9001432	0.0526	0.3377
chr7	159138663	11365181	0.0714	0.3879

chr8	146364022	6637130	0.0453	0.5194
chr9	141213431	4269624	0.0302	0.3295
chr10	135534747	9457009	0.0698	0.4139
chr11	135006516	5358160	0.0397	0.3356
chr12	133851895	5418004	0.0405	0.2324
chr13	115169878	2698147	0.0234	0.169
chr14	107349540	4281647	0.0399	0.2409
chr15	102531392	2360119	0.023	0.1726
chr16	90354753	3512890	0.0389	0.2363
chr17	81195210	2293636	0.0282	0.2155
chr18	78077248	3023164	0.0387	0.5421
chr19	59128983	2164724	0.0366	0.3707
chr20	63025520	3074308	0.0488	0.2524
chr21	48129895	1471998	0.0306	0.2096
chr22	51304566	944338	0.0184	0.1489
chrMT	16571	11144	0.6725	0.889
chrX	155270560	6244015	0.0402	0.2612
chrY	59373566	261034	0.0044	0.0913

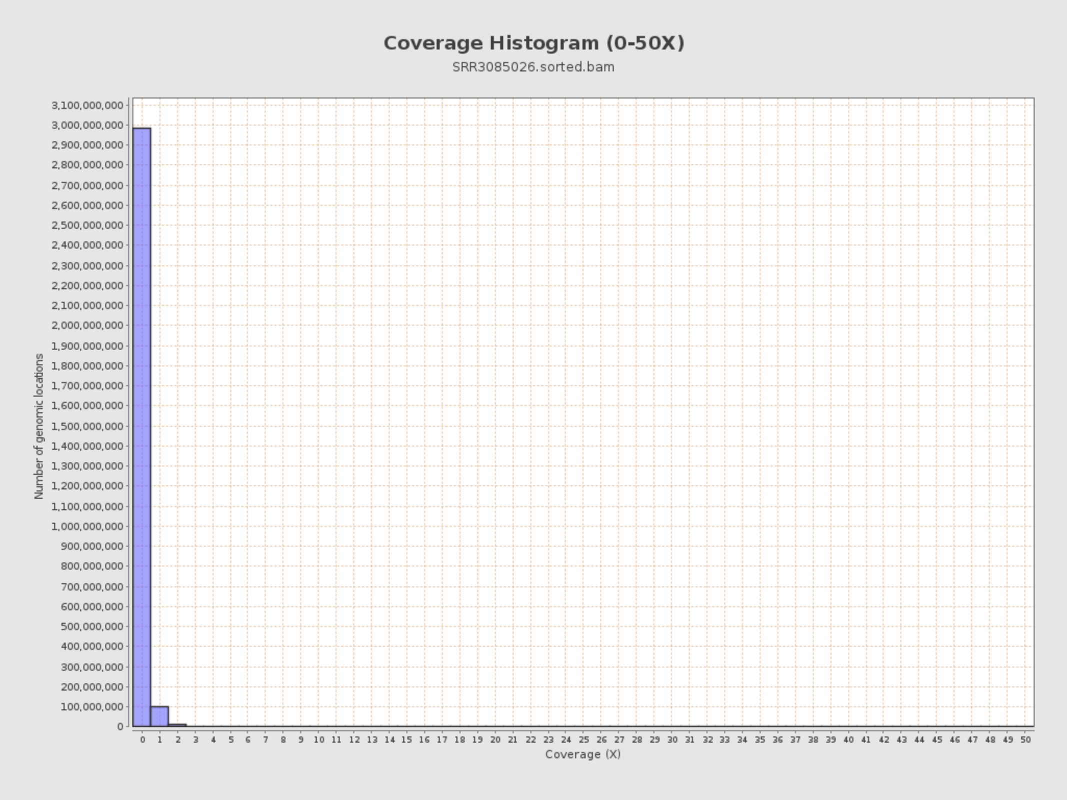
3. Results : Coverage across reference



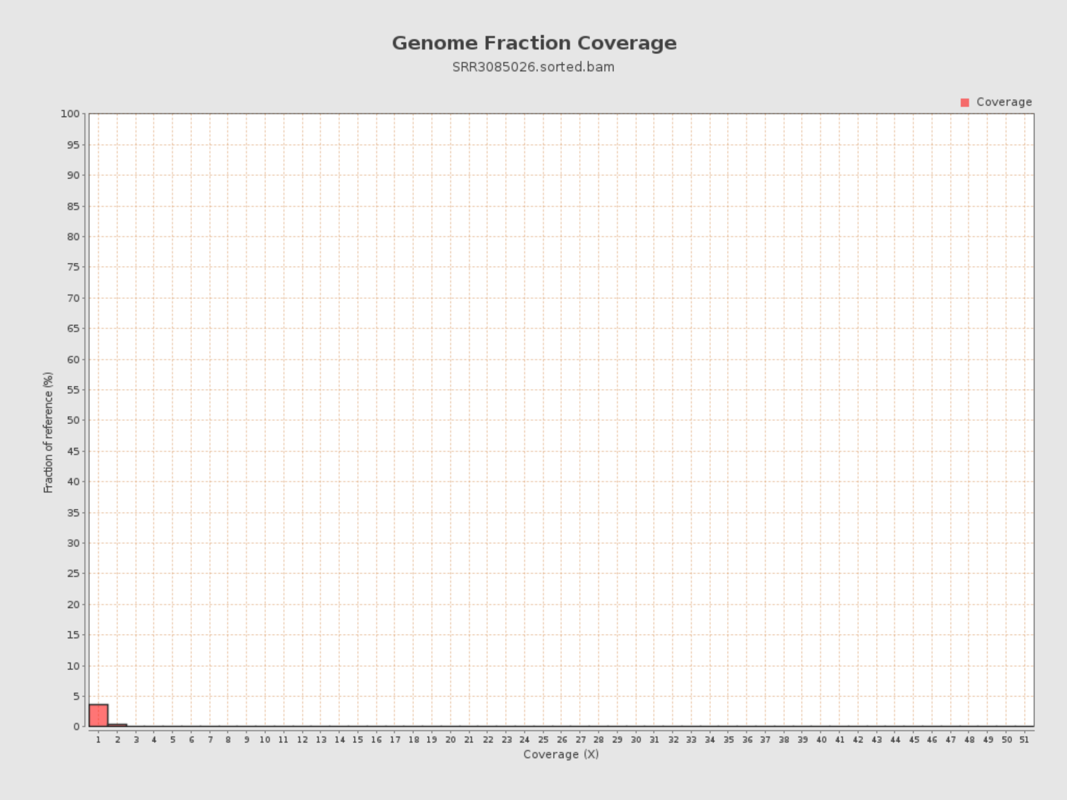
4. Results : Coverage Histogram



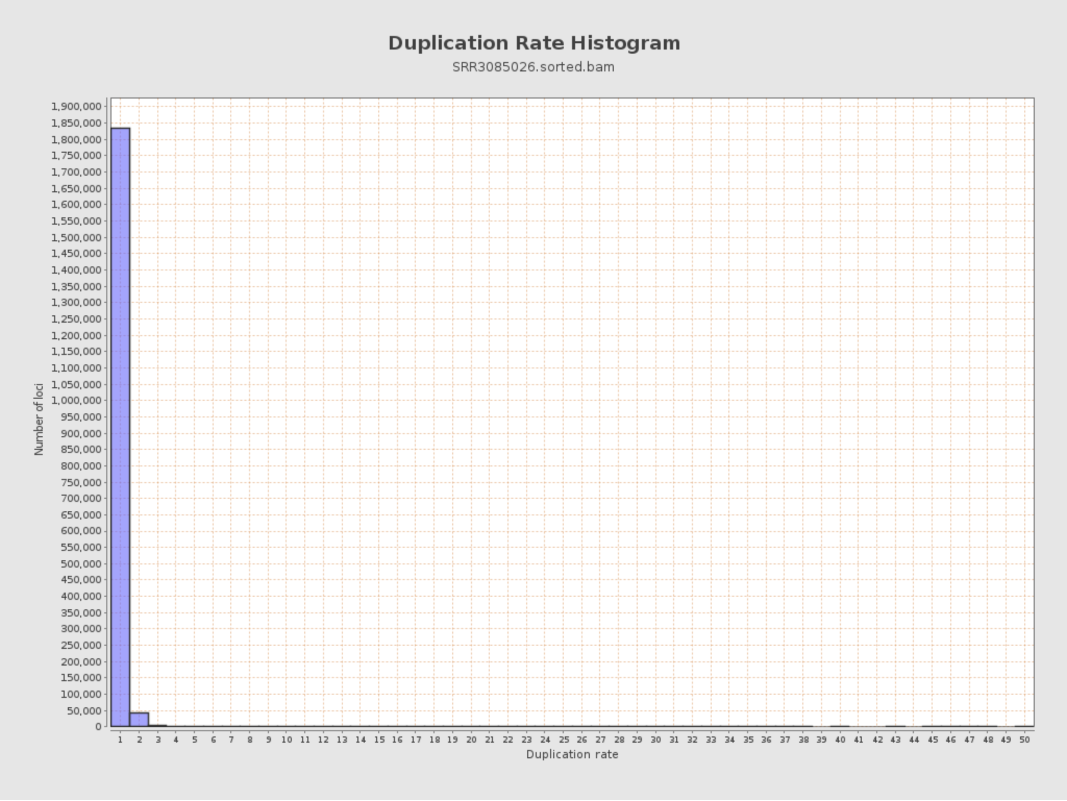
5. Results : Coverage Histogram (0-50X)



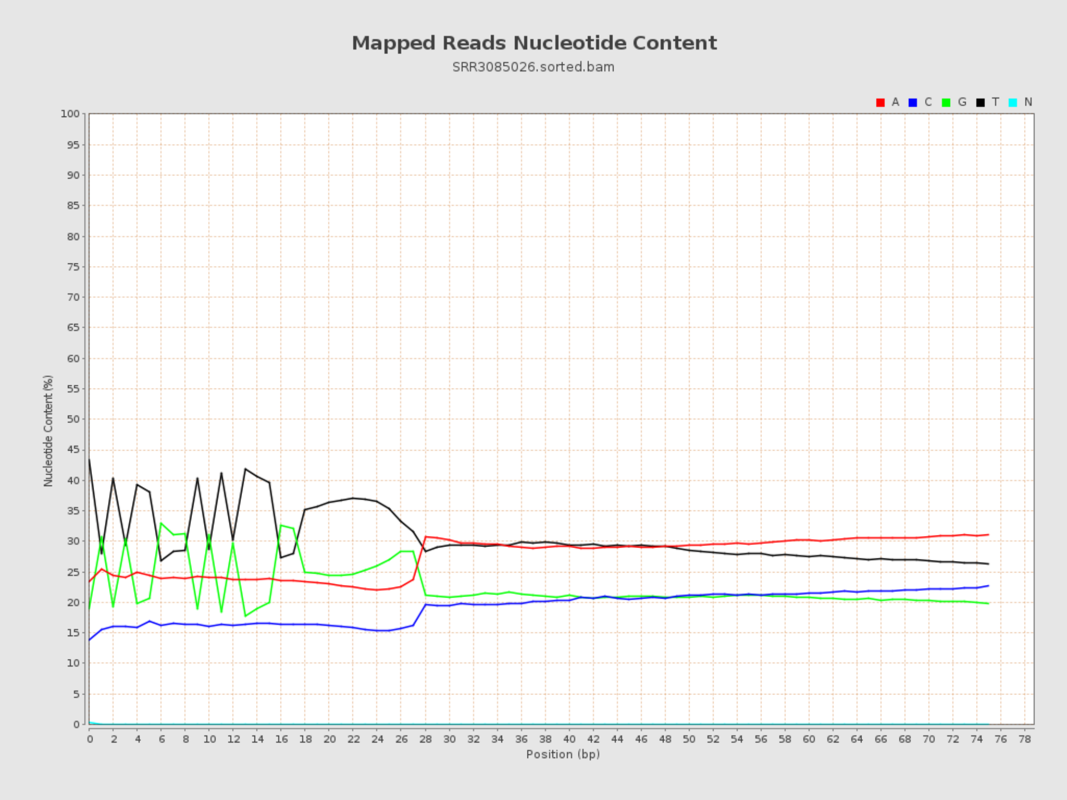
6. Results : Genome Fraction Coverage



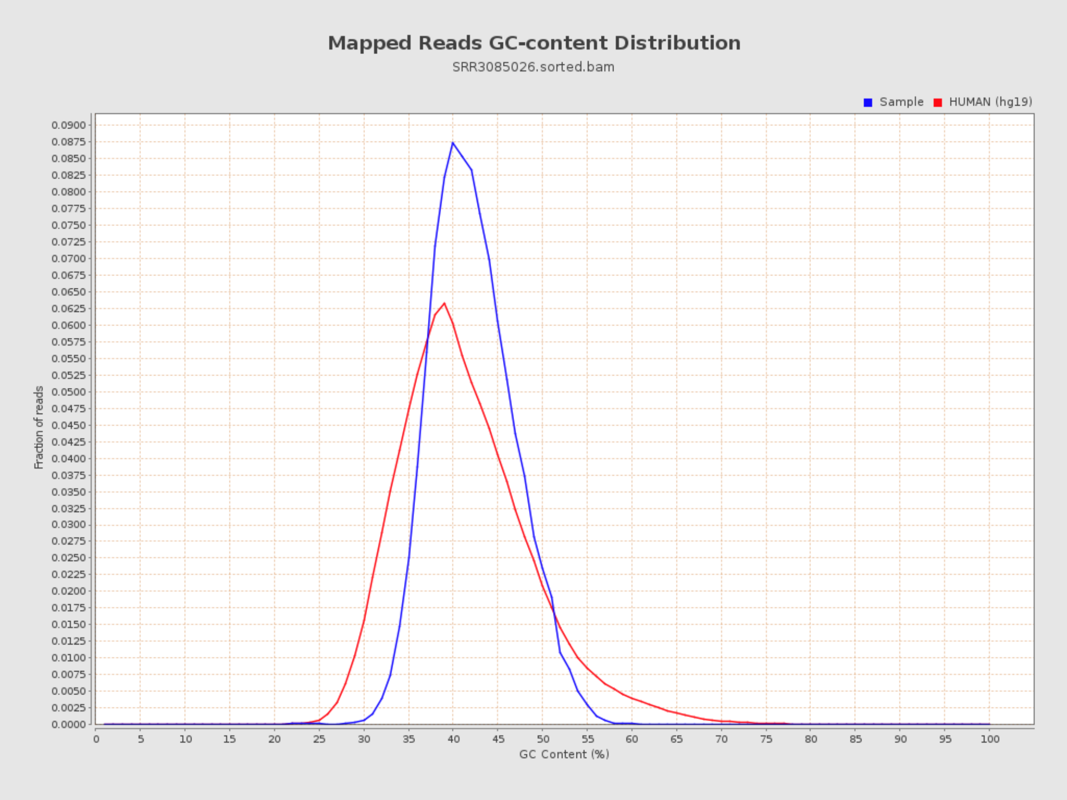
7. Results : Duplication Rate Histogram



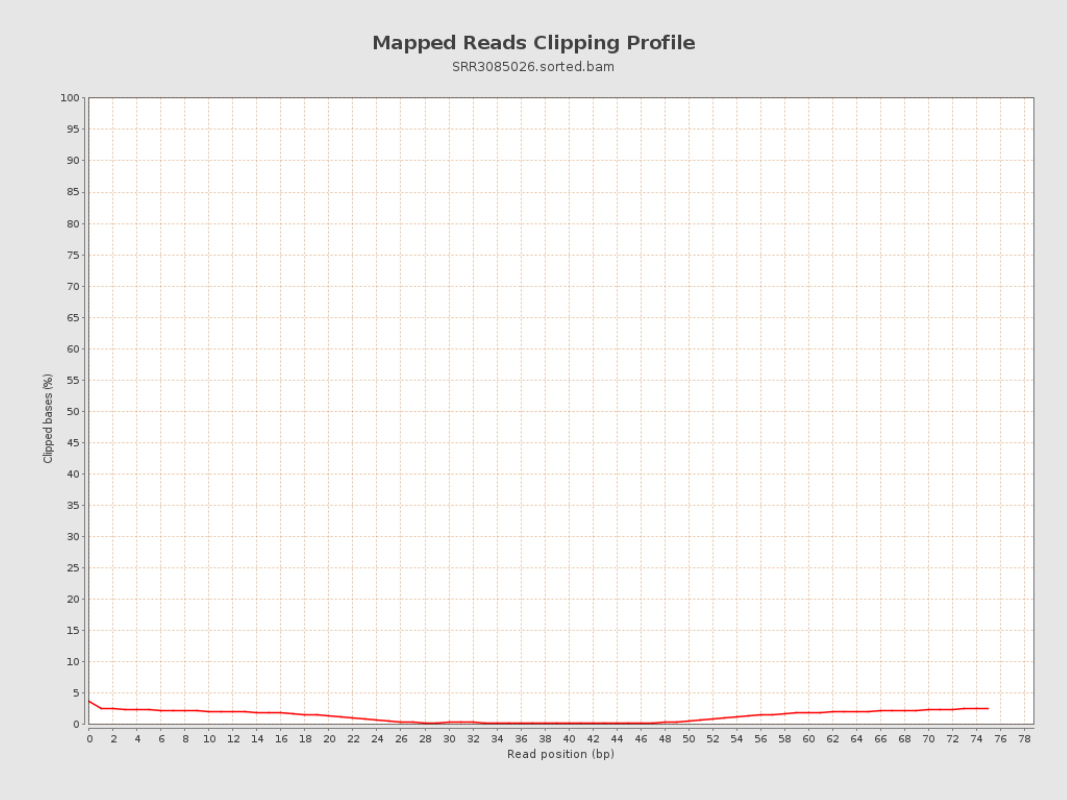
8. Results : Mapped Reads Nucleotide Content



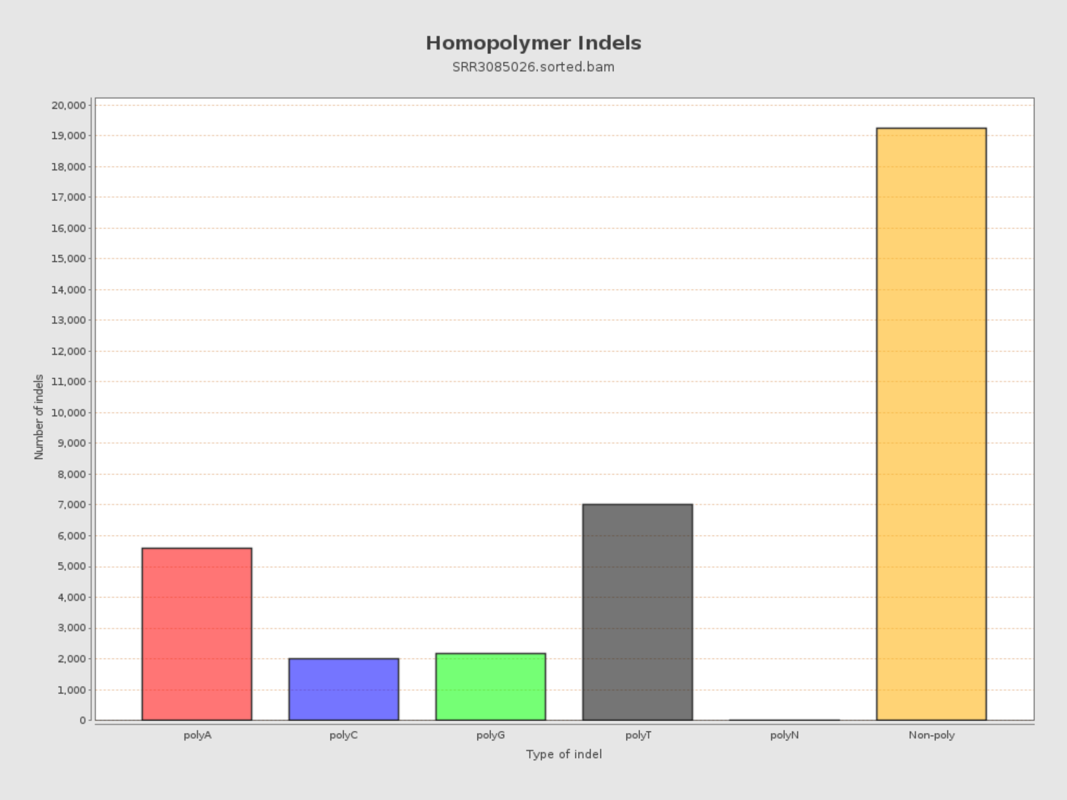
9. Results : Mapped Reads GC-content Distribution



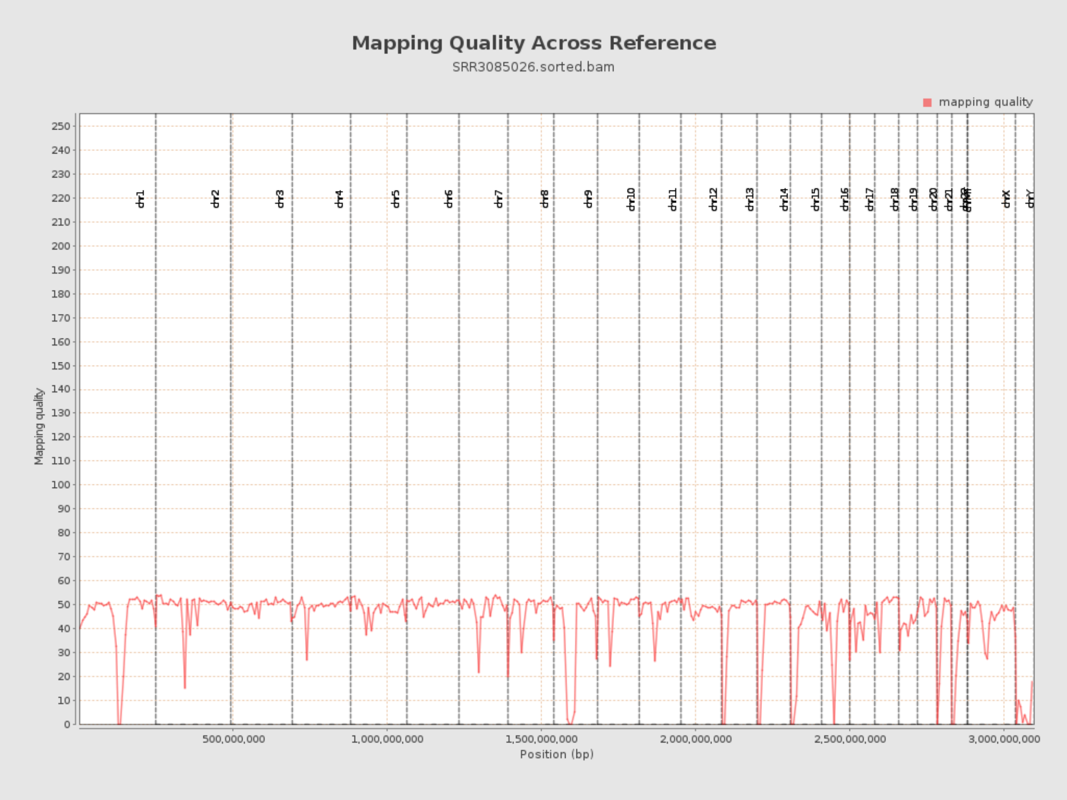
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram