Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:34:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084966.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_SRR3084966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084966.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:34:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,562,052
Mapped reads	2,282,084 / 89.07%
Unmapped reads	279,968 / 10.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,946 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	98,891 / 3.86%
Duplication rate	3.18%
Clipped reads	1,115,227 / 43.53%

2.2. ACGT Content

Number/percentage of A's	41,532,243 / 27.65%
Number/percentage of C's	28,516,534 / 18.98%
Number/percentage of T's	46,118,906 / 30.7%
Number/percentage of G's	34,036,674 / 22.66%
Number/percentage of N's	19,959 / 0.01%
GC Percentage	41.64%

2.3. Coverage

Mean	0.0485

Standard Deviation	0.4445

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

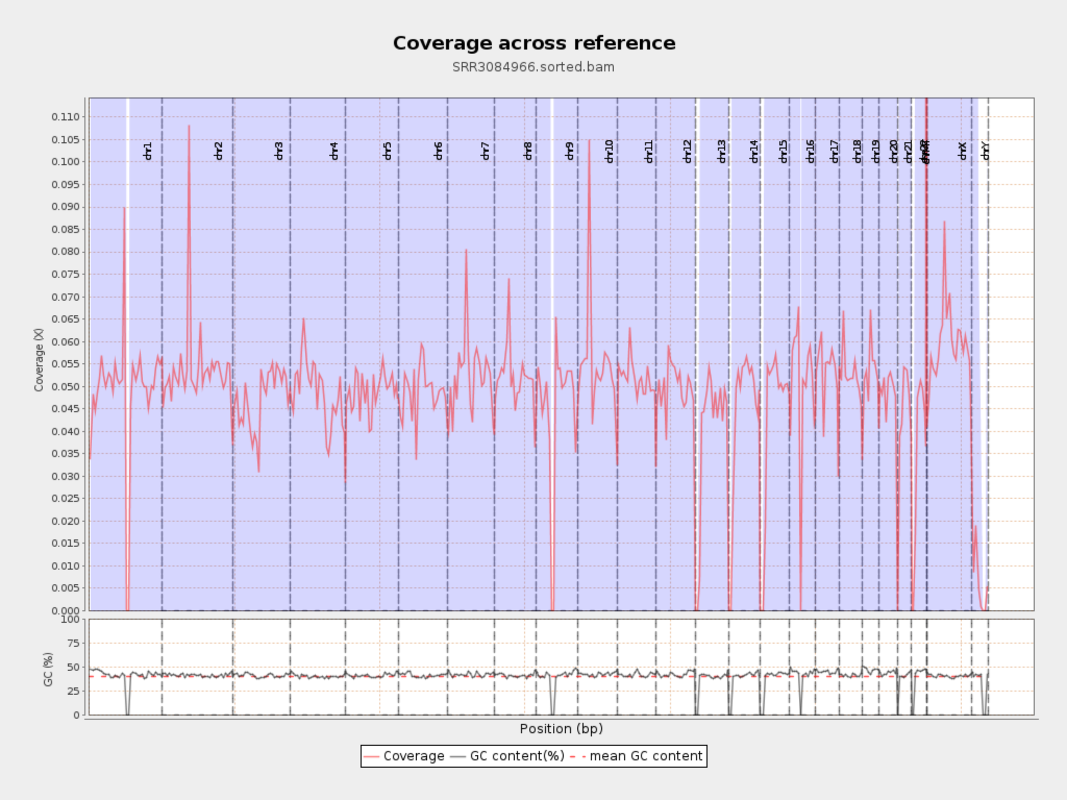
General error rate	0.88%
Mismatches	1,298,188
Insertions	12,457
Mapped reads with at least one insertion	0.54%
Deletions	36,401
Mapped reads with at least one deletion	1.58%
Homopolymer indels	46.18%

2.6. Chromosome stats

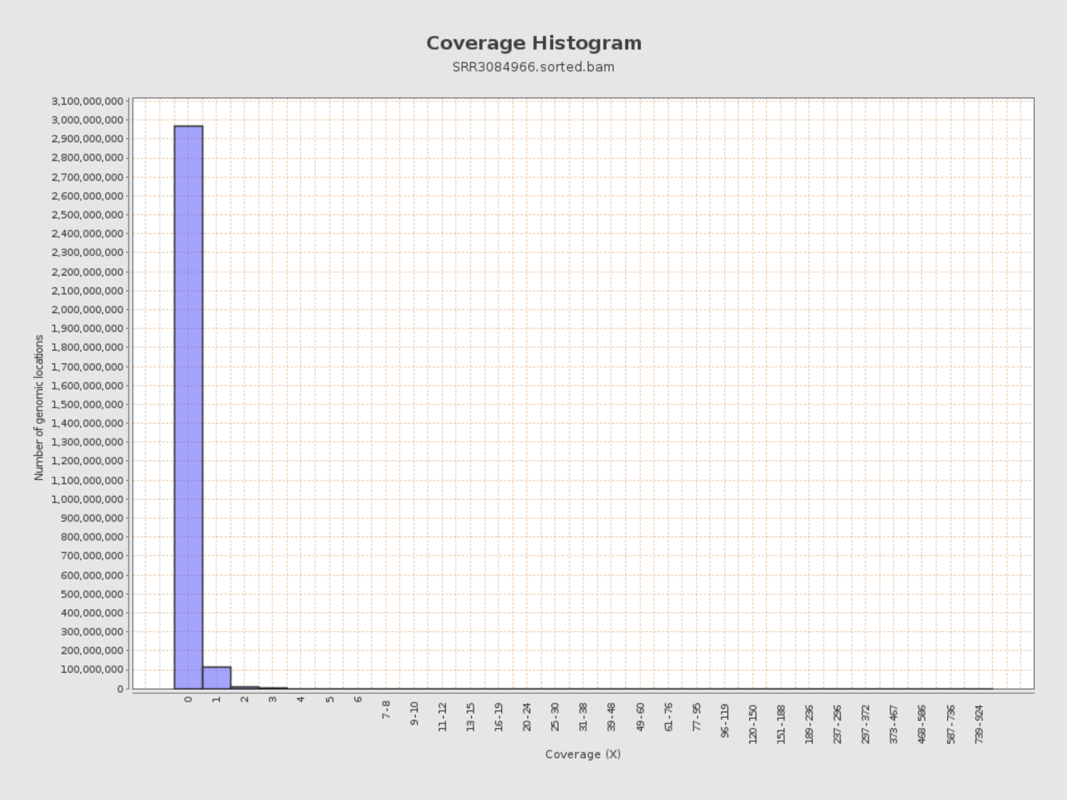
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12181532	0.0489	0.8094
chr2	243199373	13149894	0.0541	0.5863
chr3	198022430	9286317	0.0469	0.2516
chr4	191154276	9270178	0.0485	0.2617
chr5	180915260	8844291	0.0489	0.2501
chr6	171115067	8314621	0.0486	0.3139
chr7	159138663	8366447	0.0526	0.4332

chr8	146364022	7620332	0.0521	0.5442
chr9	141213431	6306176	0.0447	0.444
chr10	135534747	7470996	0.0551	0.5468
chr11	135006516	6944996	0.0514	0.4173
chr12	133851895	6625298	0.0495	0.255
chr13	115169878	4479243	0.0389	0.2193
chr14	107349540	4612646	0.043	0.2663
chr15	102531392	4330418	0.0422	0.2354
chr16	90354753	4539785	0.0502	0.3018
chr17	81195210	4276142	0.0527	0.3139
chr18	78077248	4145733	0.0531	0.8264
chr19	59128983	3134521	0.053	0.5923
chr20	63025520	3043943	0.0483	0.2587
chr21	48129895	2020728	0.042	0.2536
chr22	51304566	1692811	0.033	0.202
chrMT	16571	12845	0.7751	1.0765
chrX	155270560	9220606	0.0594	0.3346
chrY	59373566	392402	0.0066	0.139

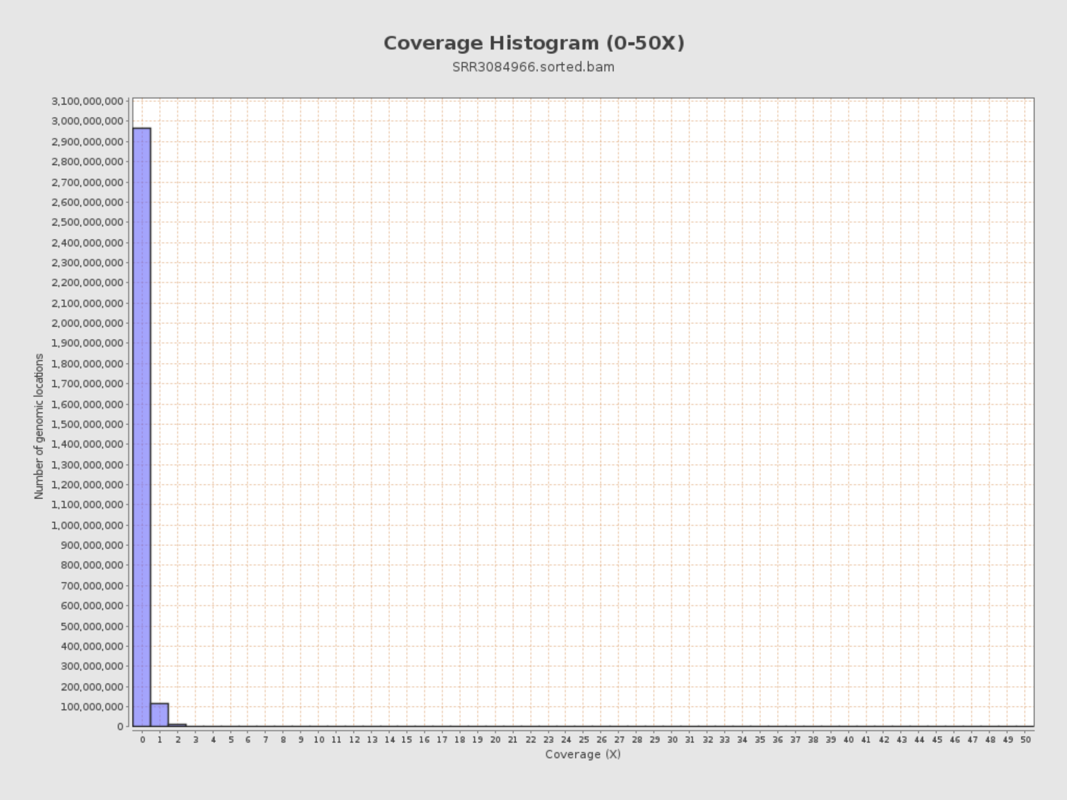
3. Results : Coverage across reference



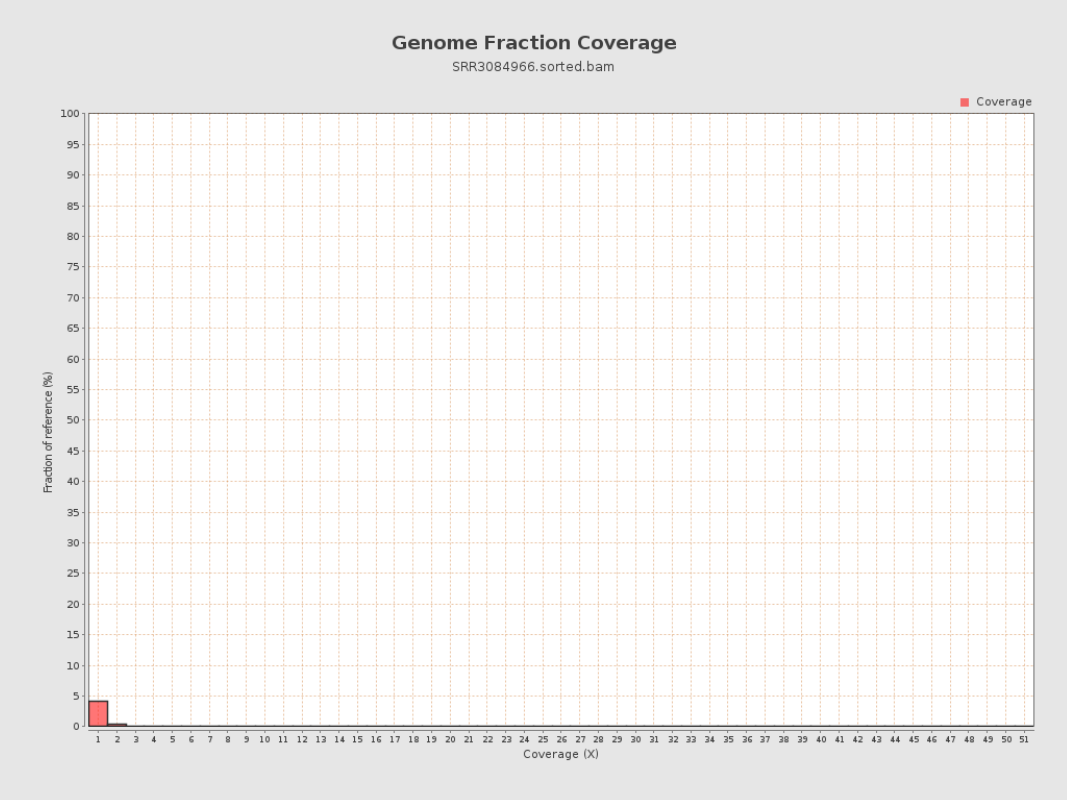
4. Results : Coverage Histogram



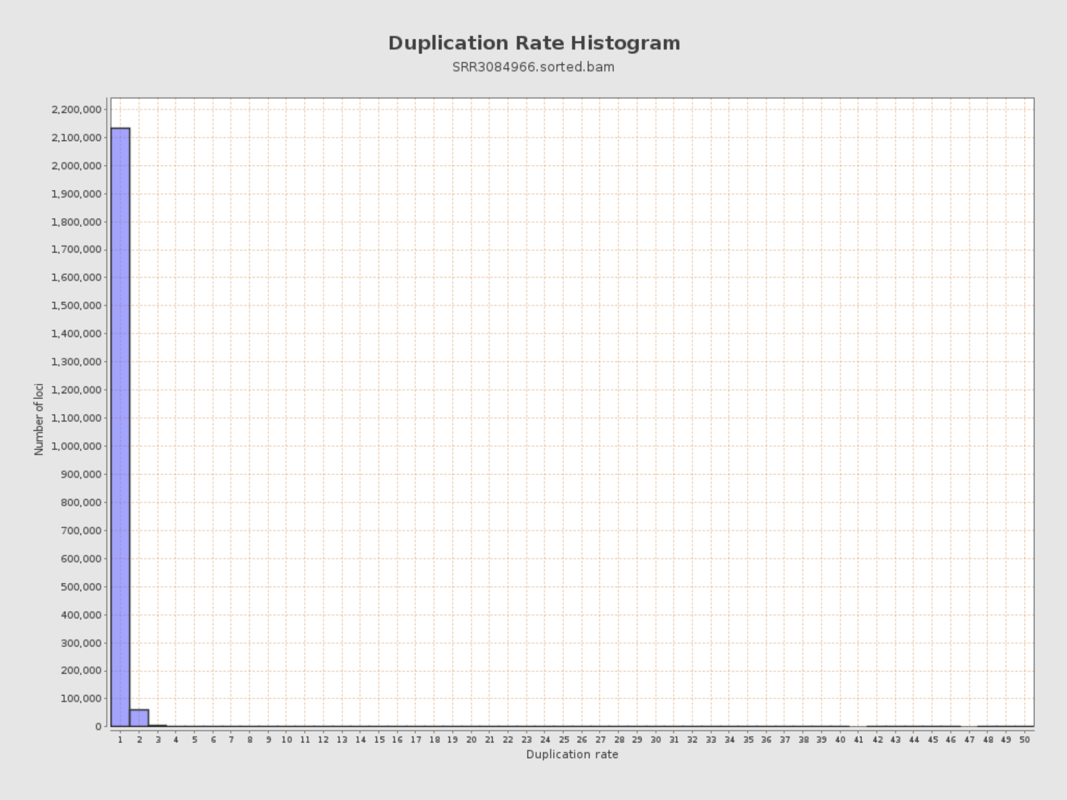
5. Results : Coverage Histogram (0-50X)



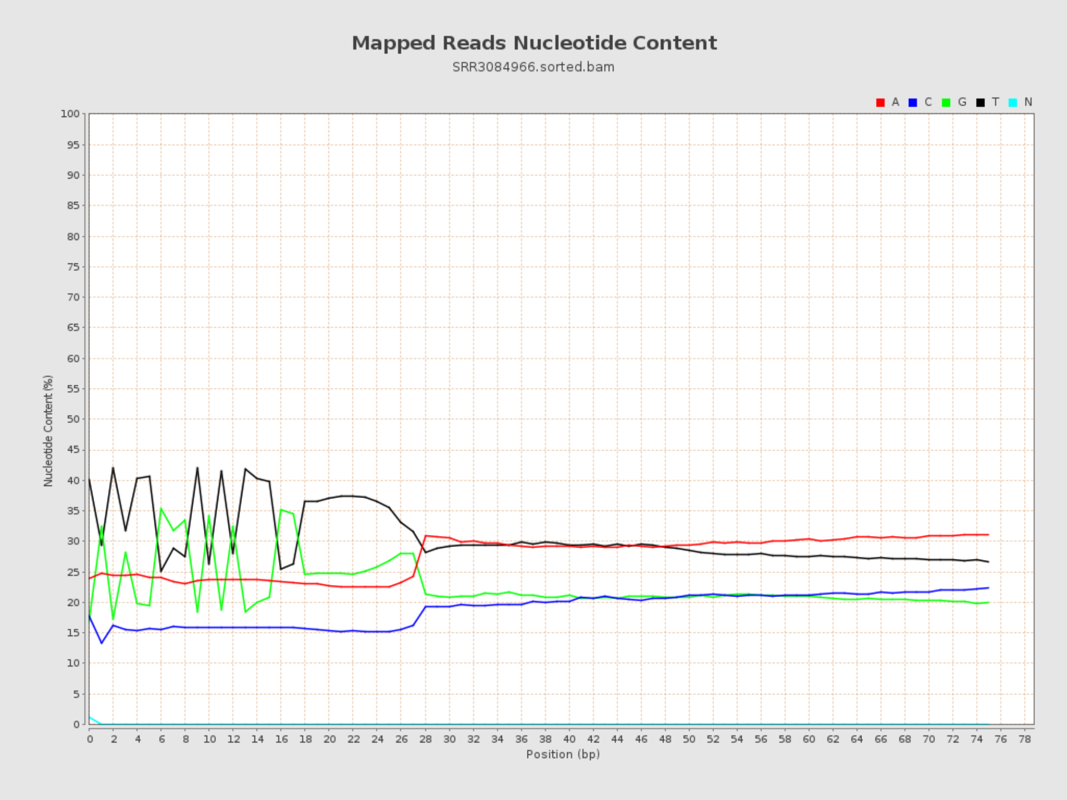
6. Results : Genome Fraction Coverage



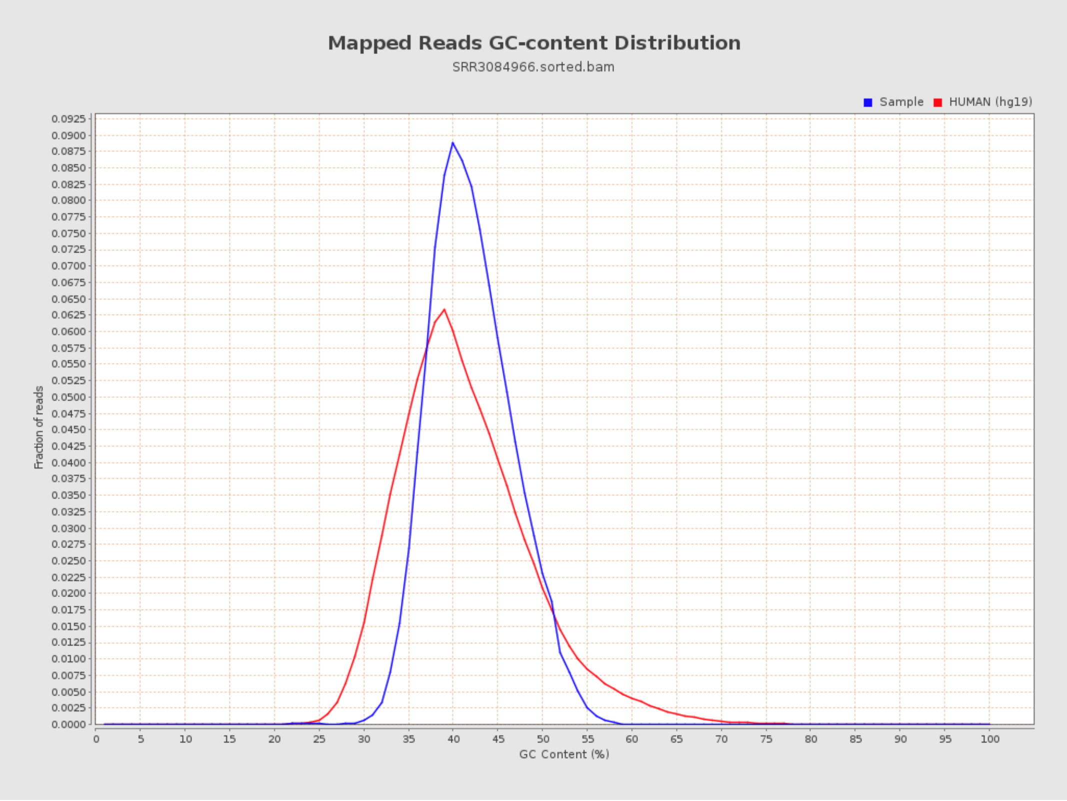
7. Results : Duplication Rate Histogram



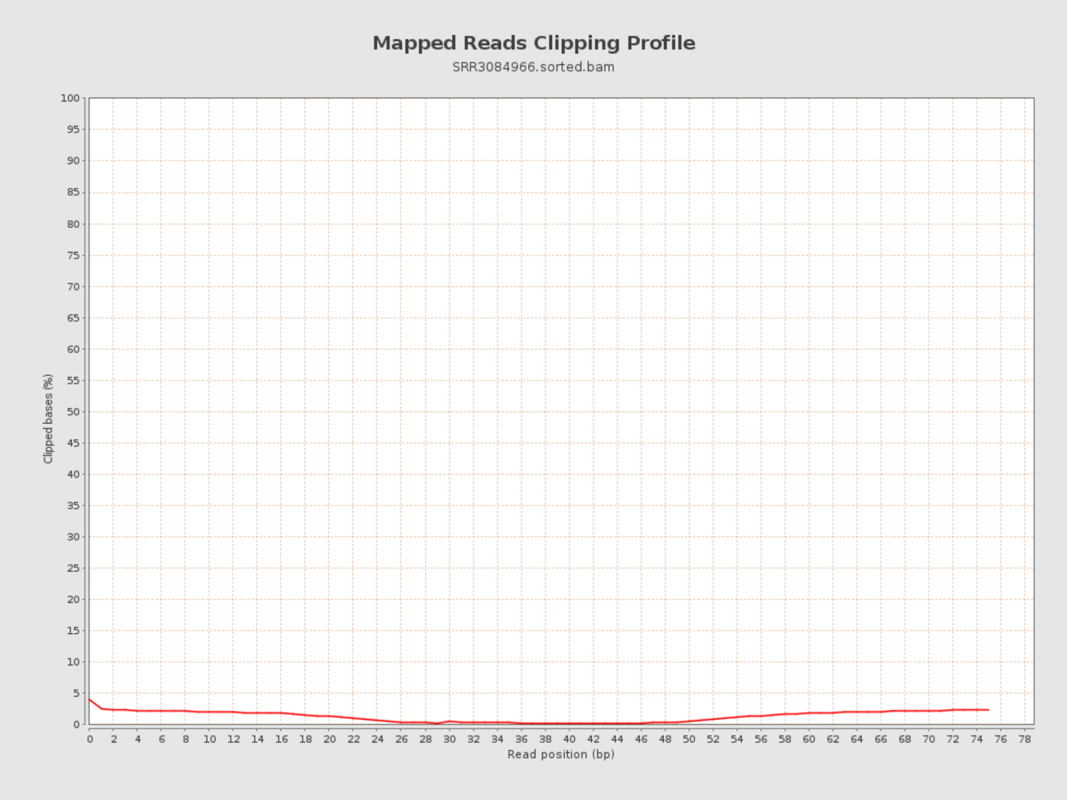
8. Results : Mapped Reads Nucleotide Content



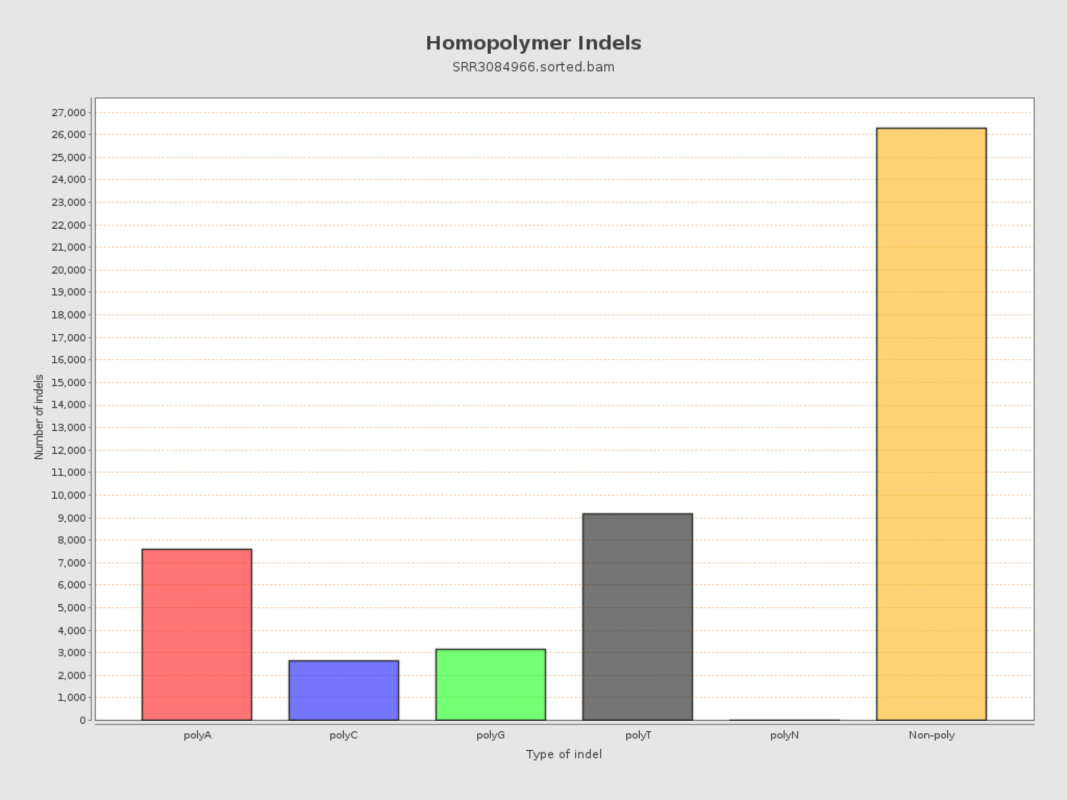
9. Results : Mapped Reads GC-content Distribution



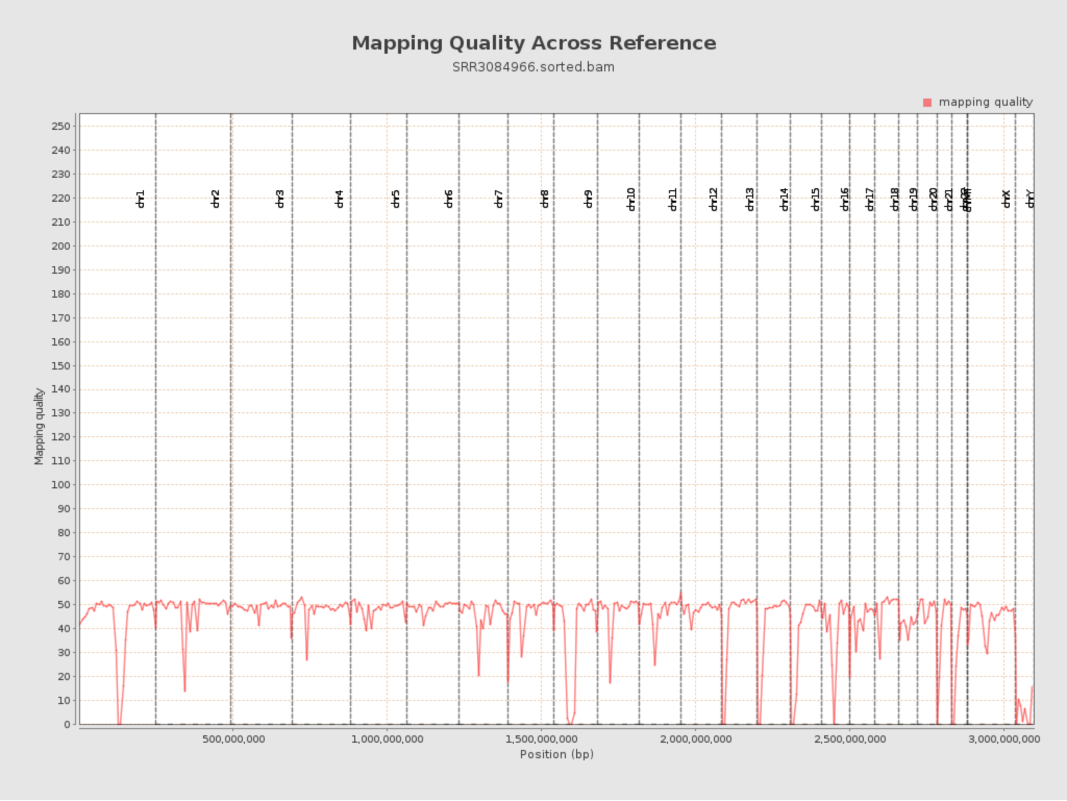
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram