Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:37:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004066.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_SRR6004066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:37:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,942,814
Mapped reads	2,428,895 / 82.54%
Unmapped reads	513,919 / 17.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,634 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	209,992 / 7.14%
Duplication rate	6.87%
Clipped reads	1,362,883 / 46.31%

2.2. ACGT Content

Number/percentage of A's	42,906,178 / 27.7%
Number/percentage of C's	27,616,286 / 17.83%
Number/percentage of T's	49,984,336 / 32.27%
Number/percentage of G's	34,282,450 / 22.13%
Number/percentage of N's	113,269 / 0.07%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0501

Standard Deviation	0.4892

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

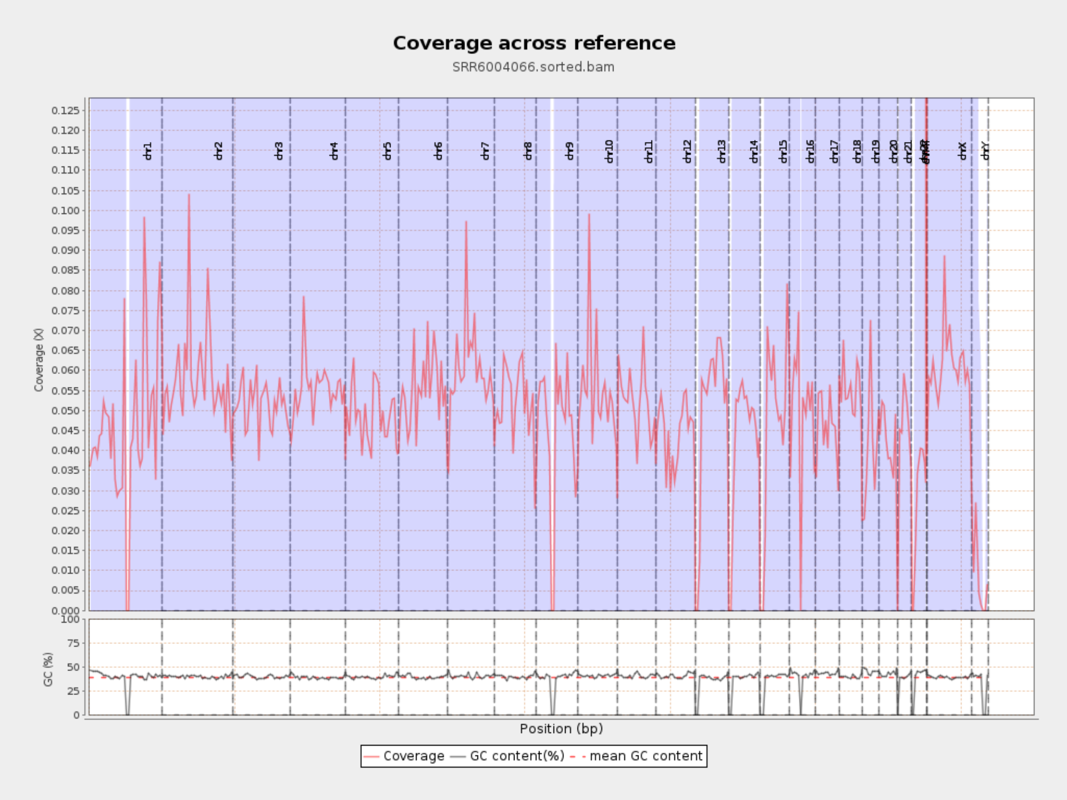
General error rate	0.93%
Mismatches	1,423,597
Insertions	12,212
Mapped reads with at least one insertion	0.5%
Deletions	51,552
Mapped reads with at least one deletion	2.1%
Homopolymer indels	44.62%

2.6. Chromosome stats

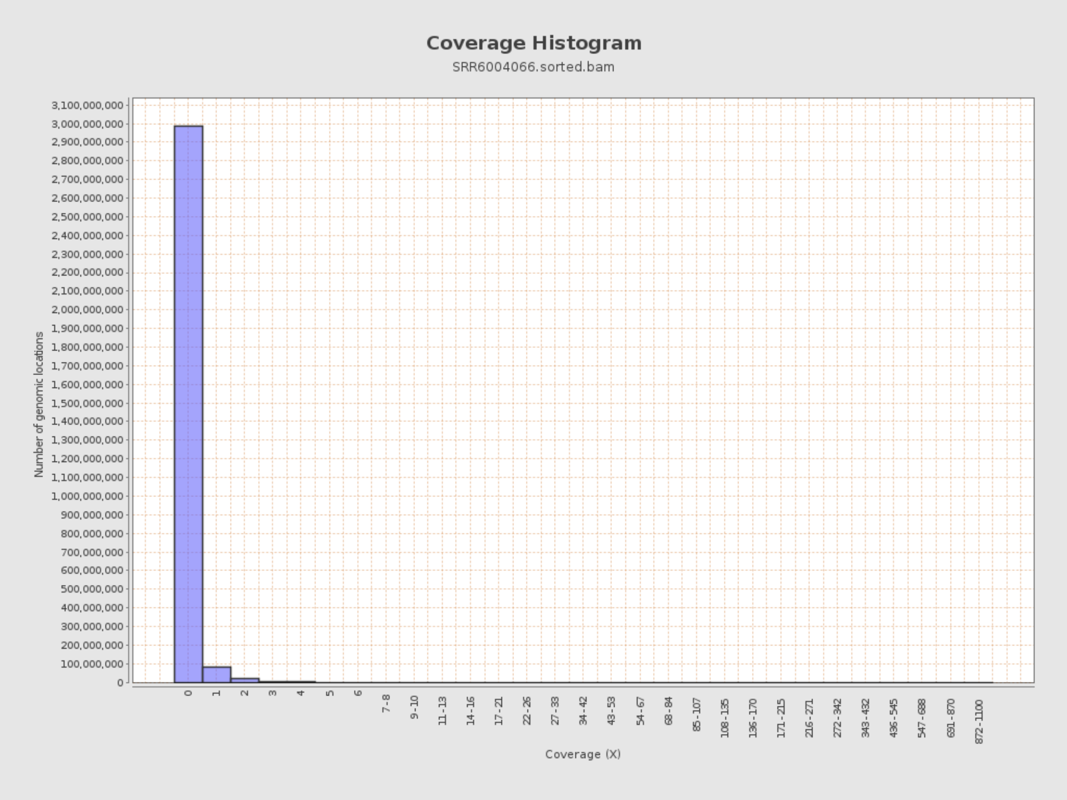
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11435057	0.0459	0.8937
chr2	243199373	14095276	0.058	0.5522
chr3	198022430	10207781	0.0515	0.3033
chr4	191154276	10593970	0.0554	0.3416
chr5	180915260	8834711	0.0488	0.2965
chr6	171115067	9395371	0.0549	0.3911
chr7	159138663	9684293	0.0609	0.5597

chr8	146364022	7600991	0.0519	0.7127
chr9	141213431	6416878	0.0454	0.4235
chr10	135534747	7522780	0.0555	0.4768
chr11	135006516	7033485	0.0521	0.412
chr12	133851895	5930098	0.0443	0.2882
chr13	115169878	5731660	0.0498	0.2977
chr14	107349540	4542820	0.0423	0.3094
chr15	102531392	4828115	0.0471	0.3109
chr16	90354753	4459950	0.0494	0.353
chr17	81195210	3661494	0.0451	0.3427
chr18	78077248	4339975	0.0556	0.8453
chr19	59128983	2435975	0.0412	0.6131
chr20	63025520	2683711	0.0426	0.2866
chr21	48129895	2074839	0.0431	0.3044
chr22	51304566	1354457	0.0264	0.21
chrMT	16571	257332	15.5291	9.4529
chrX	155270560	9401281	0.0605	0.3699
chrY	59373566	467352	0.0079	0.204

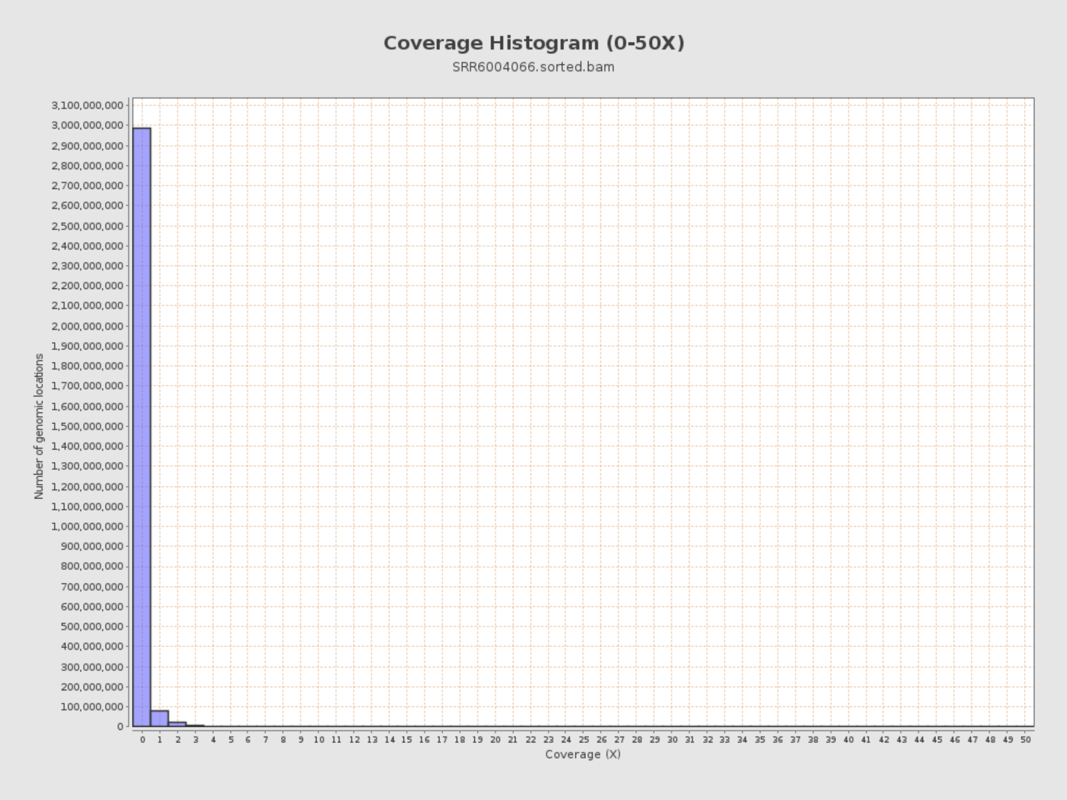
3. Results : Coverage across reference



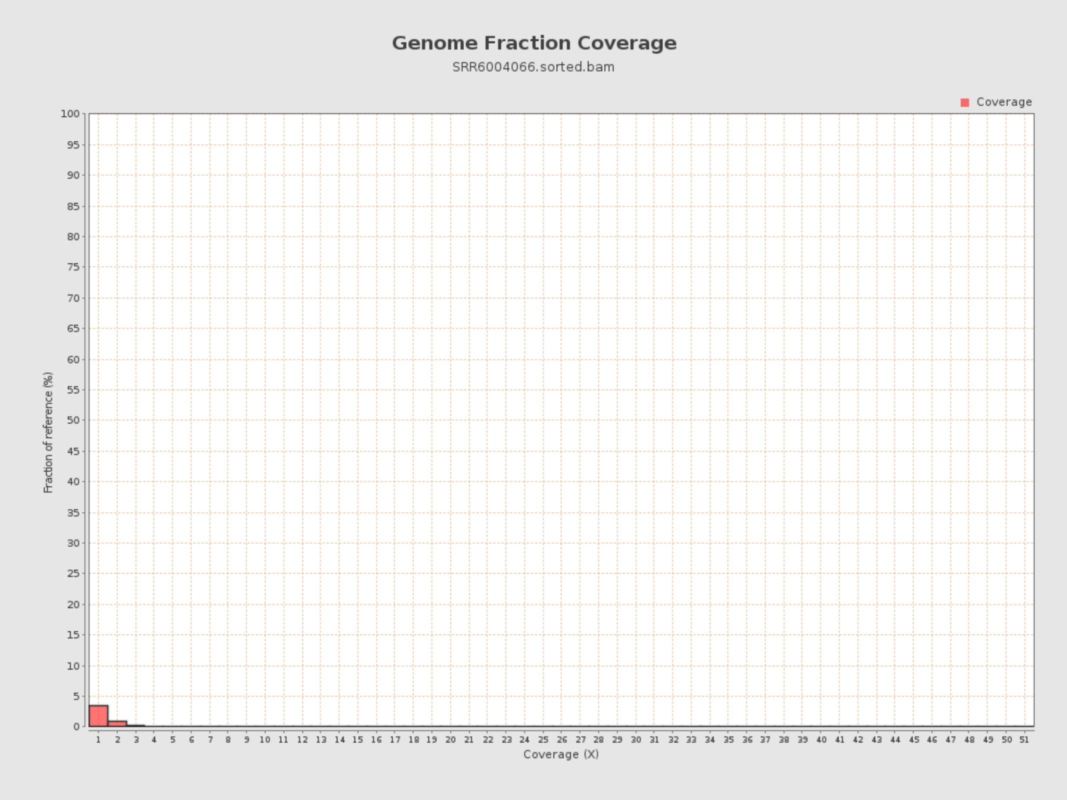
4. Results : Coverage Histogram



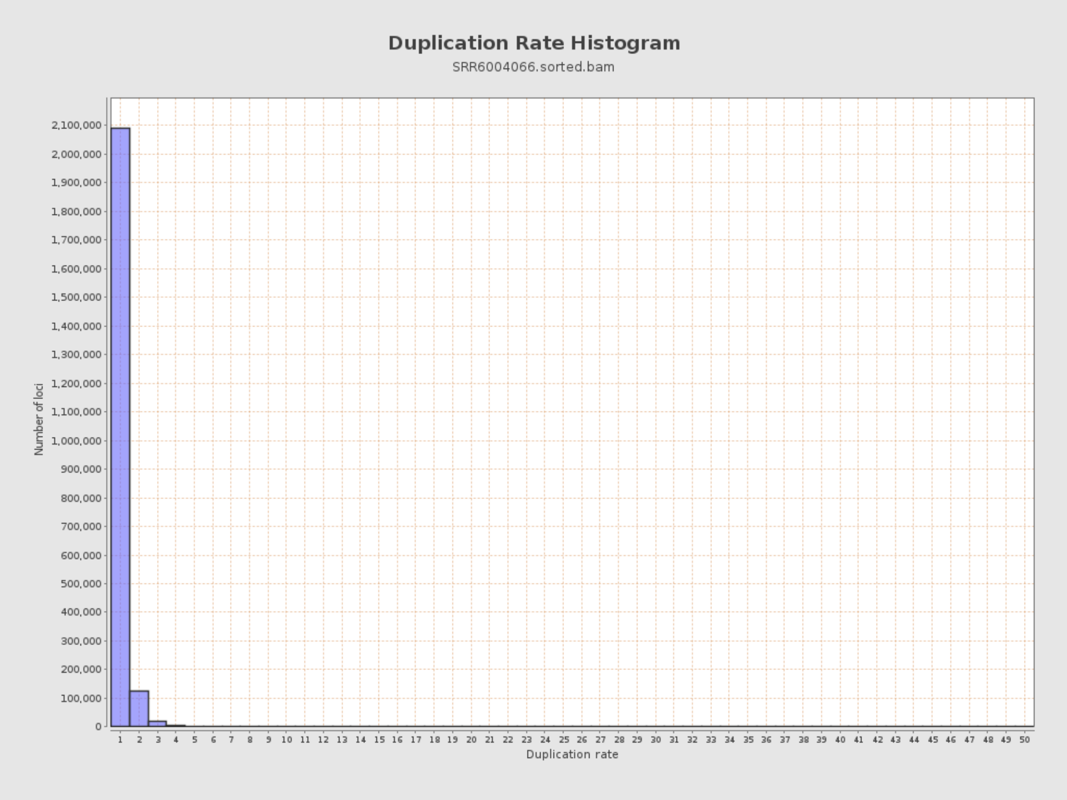
5. Results : Coverage Histogram (0-50X)



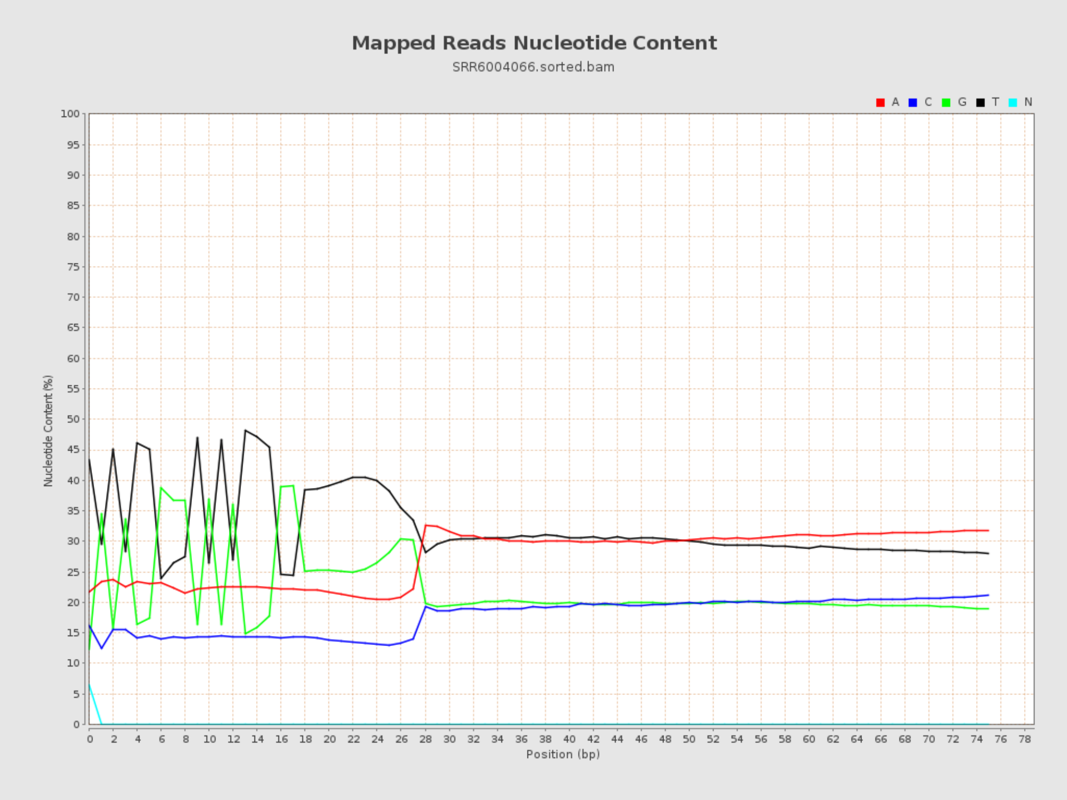
6. Results : Genome Fraction Coverage



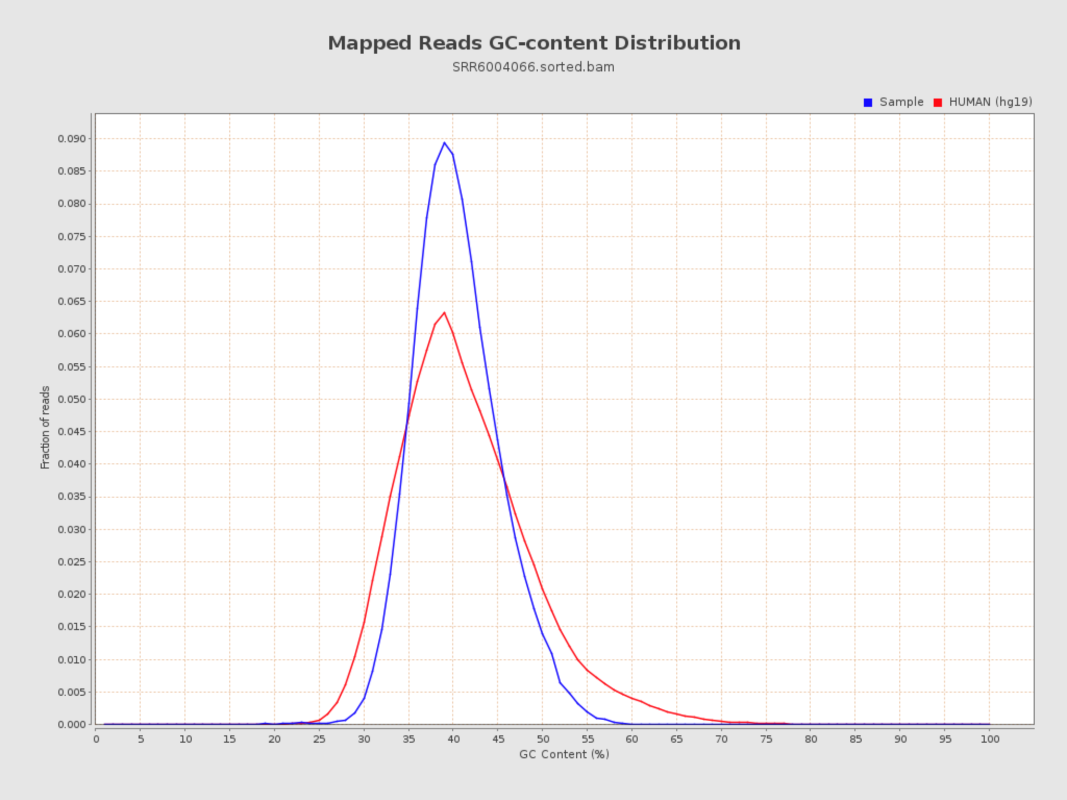
7. Results : Duplication Rate Histogram



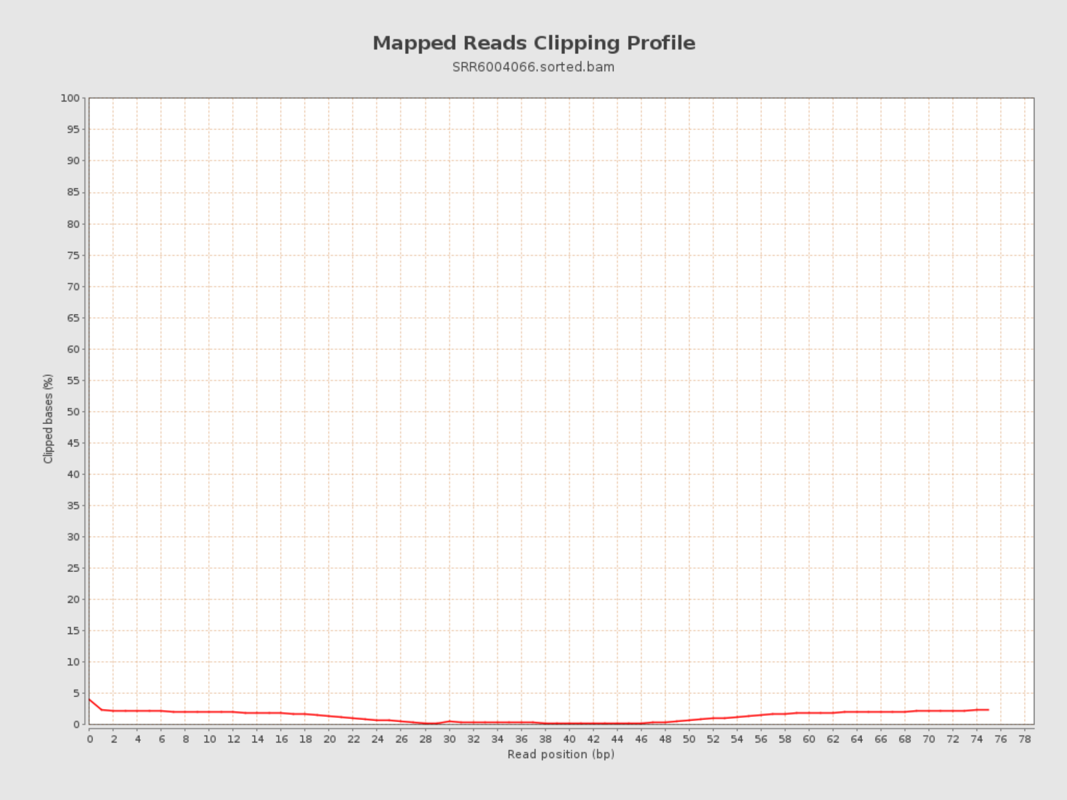
8. Results : Mapped Reads Nucleotide Content



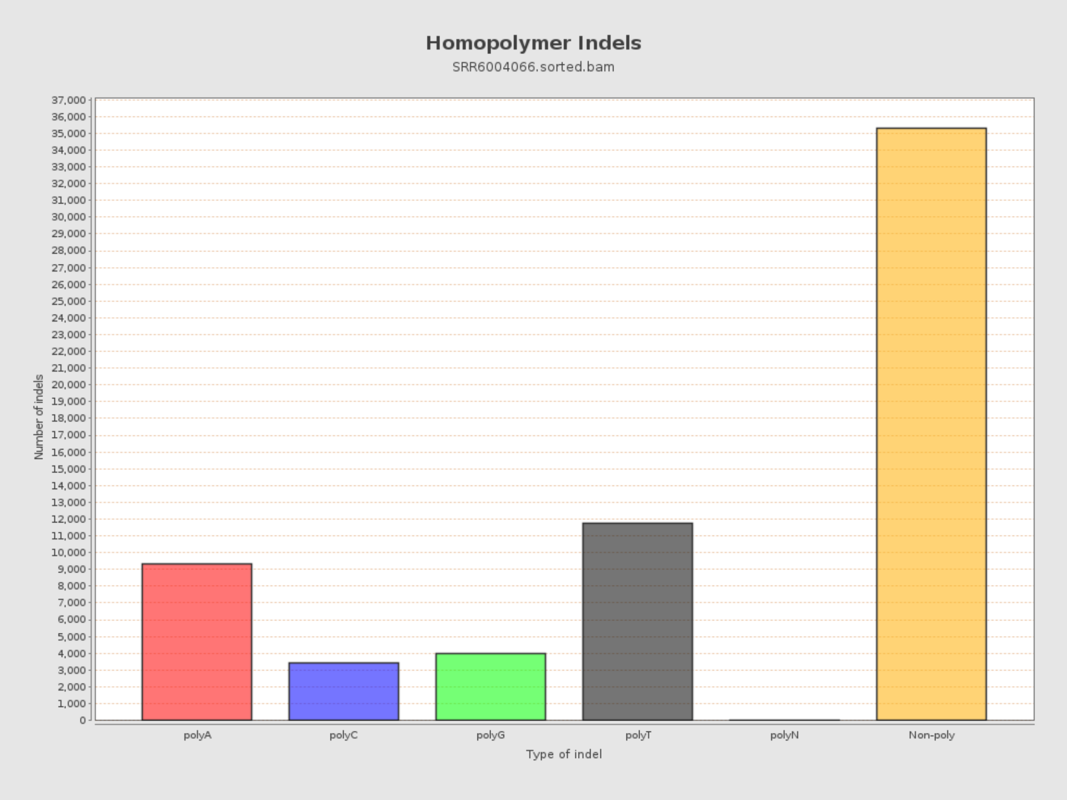
9. Results : Mapped Reads GC-content Distribution



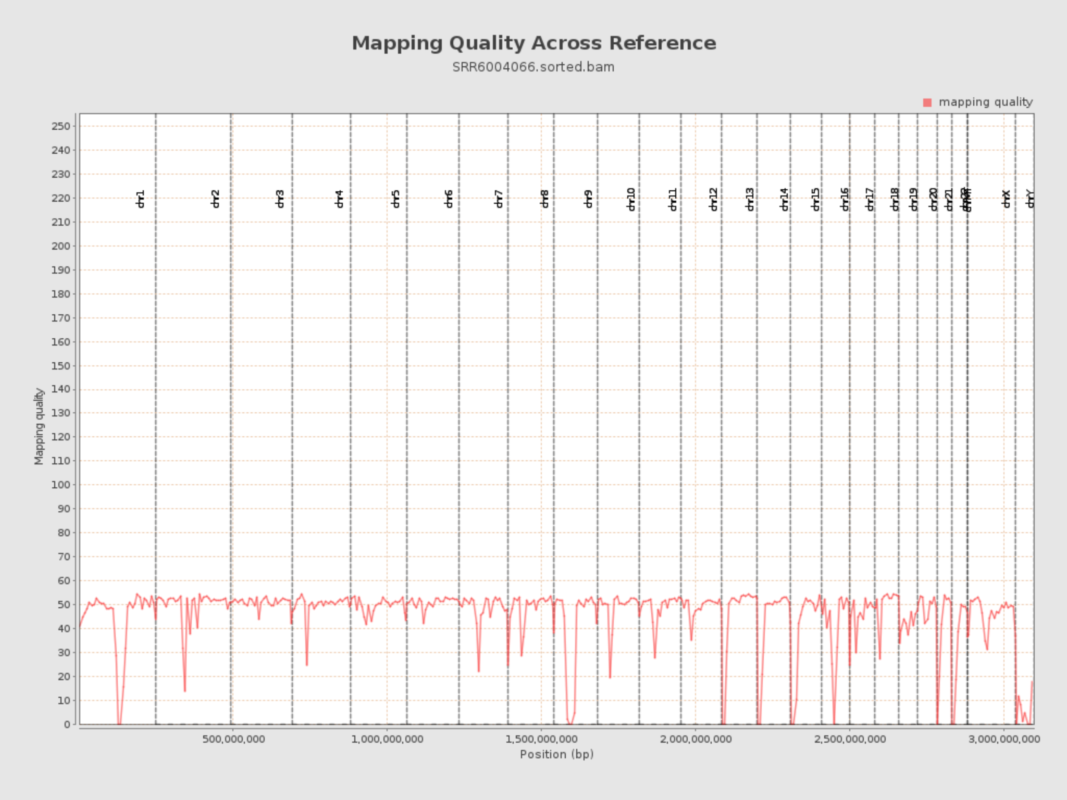
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram