Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:34:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081698.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_SRR3081698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081698.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:34:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,848,205
Mapped reads	2,594,635 / 91.1%
Unmapped reads	253,570 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,388 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	101,773 / 3.57%
Duplication rate	3.13%
Clipped reads	1,079,733 / 37.91%

2.2. ACGT Content

Number/percentage of A's	48,173,539 / 27.54%
Number/percentage of C's	33,741,666 / 19.29%
Number/percentage of T's	53,553,170 / 30.61%
Number/percentage of G's	39,462,476 / 22.56%
Number/percentage of N's	1,968 / 0%
GC Percentage	41.85%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.3959

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

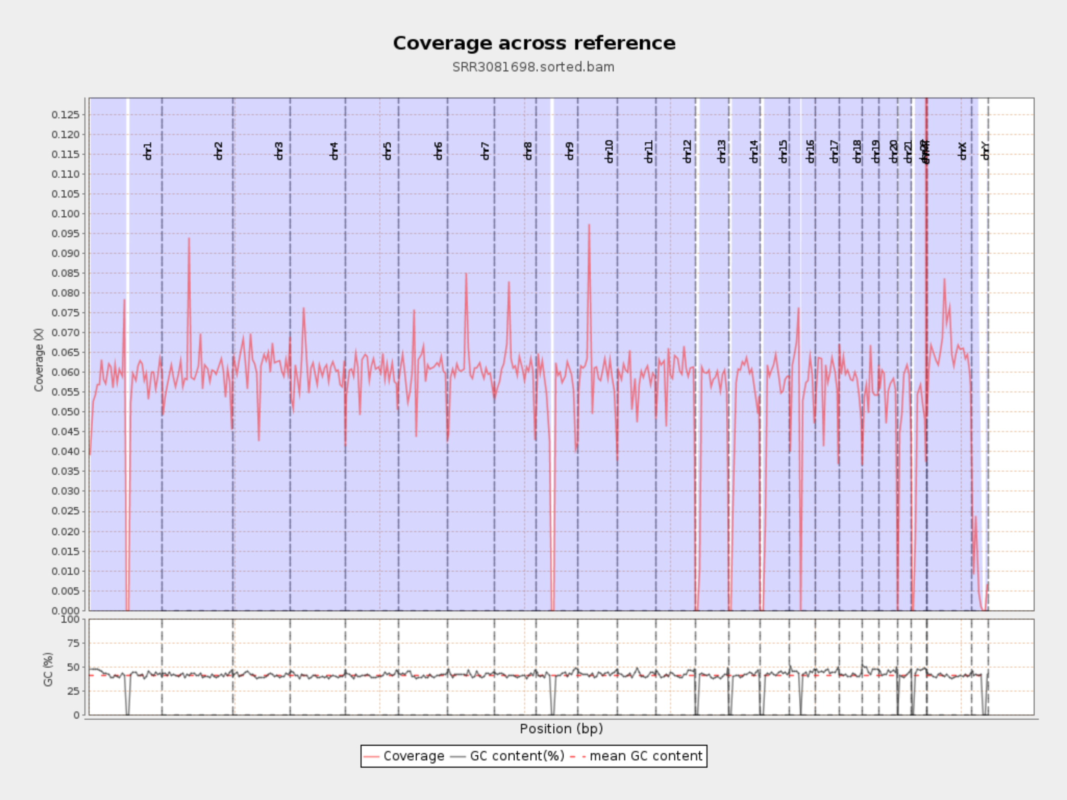
General error rate	0.82%
Mismatches	1,406,973
Insertions	12,474
Mapped reads with at least one insertion	0.48%
Deletions	33,588
Mapped reads with at least one deletion	1.28%
Homopolymer indels	46.68%

2.6. Chromosome stats

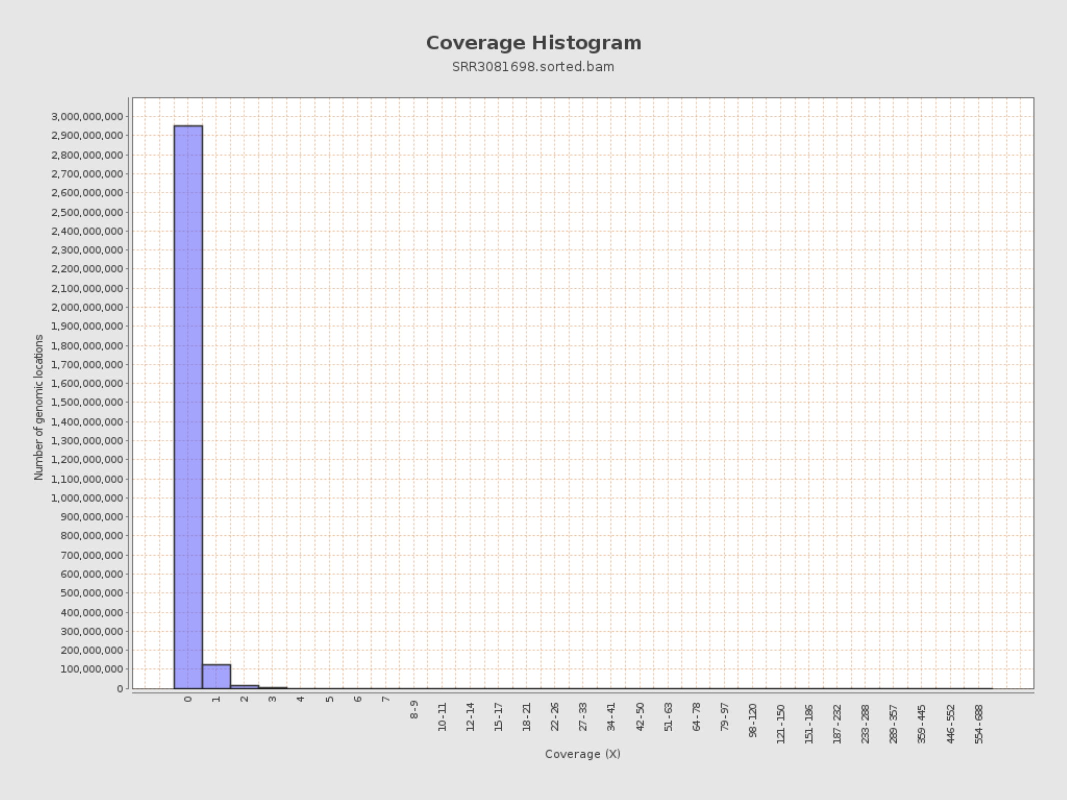
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13734521	0.0551	0.5914
chr2	243199373	14602766	0.06	0.4905
chr3	198022430	12282169	0.062	0.2888
chr4	191154276	11470891	0.06	0.3067
chr5	180915260	10877752	0.0601	0.2835
chr6	171115067	10342084	0.0604	0.3259
chr7	159138663	9704992	0.061	0.52

chr8	146364022	8935082	0.061	0.5306
chr9	141213431	7227376	0.0512	0.3671
chr10	135534747	8287974	0.0612	0.4649
chr11	135006516	7857974	0.0582	0.3529
chr12	133851895	8053497	0.0602	0.2865
chr13	115169878	5612548	0.0487	0.2545
chr14	107349540	5273553	0.0491	0.2698
chr15	102531392	4933435	0.0481	0.2563
chr16	90354753	4933599	0.0546	0.3078
chr17	81195210	4645094	0.0572	0.3009
chr18	78077248	4598674	0.0589	0.6129
chr19	59128983	3262540	0.0552	0.5041
chr20	63025520	3474395	0.0551	0.2799
chr21	48129895	2343716	0.0487	0.2813
chr22	51304566	1854537	0.0361	0.219
chrMT	16571	25726	1.5525	1.5768
chrX	155270560	10194767	0.0657	0.3246
chrY	59373566	463065	0.0078	0.1757

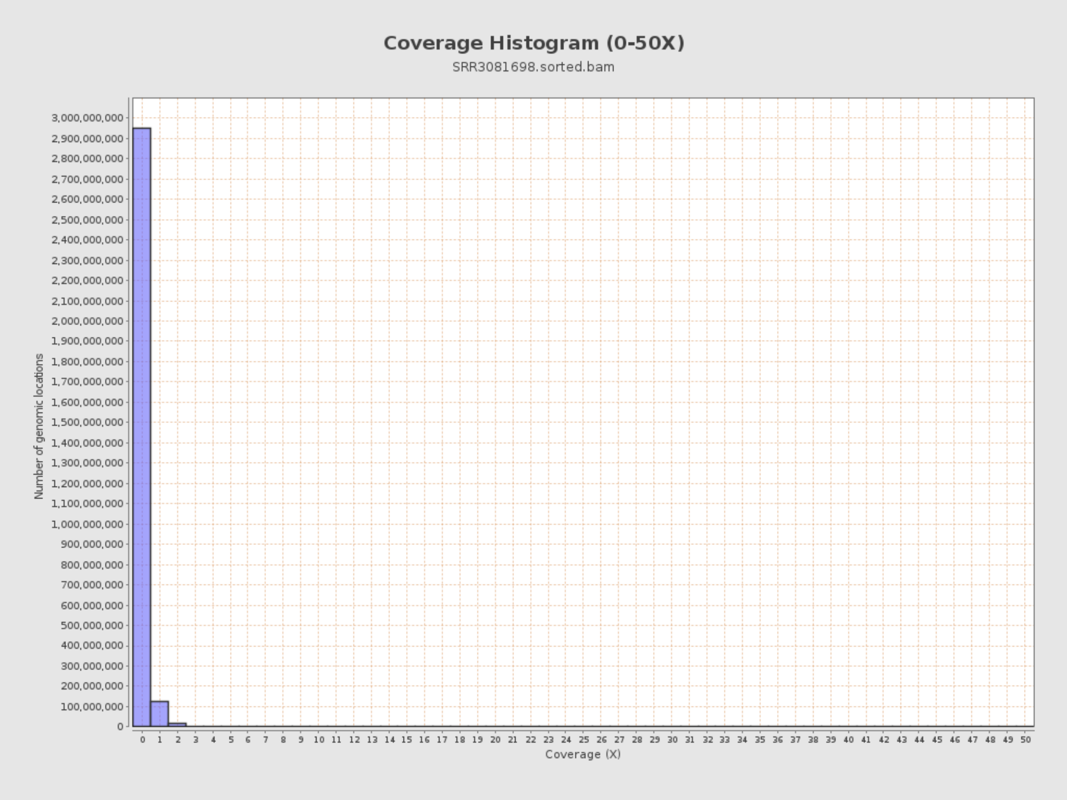
3. Results : Coverage across reference



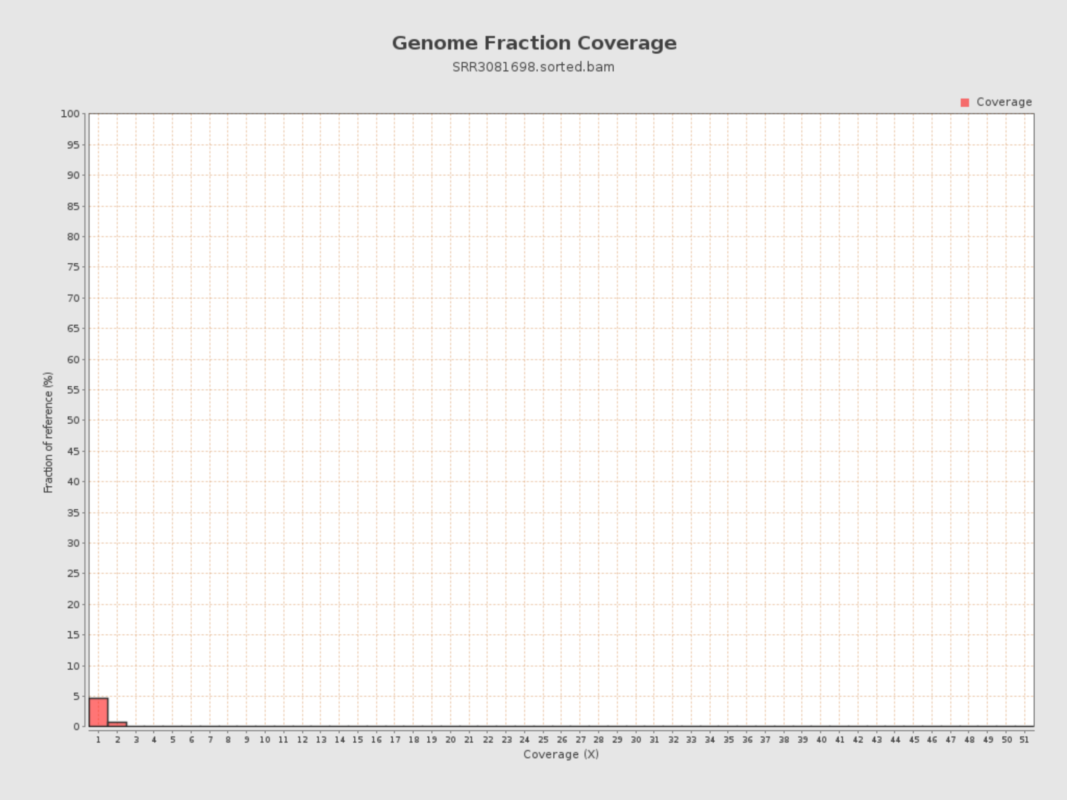
4. Results : Coverage Histogram



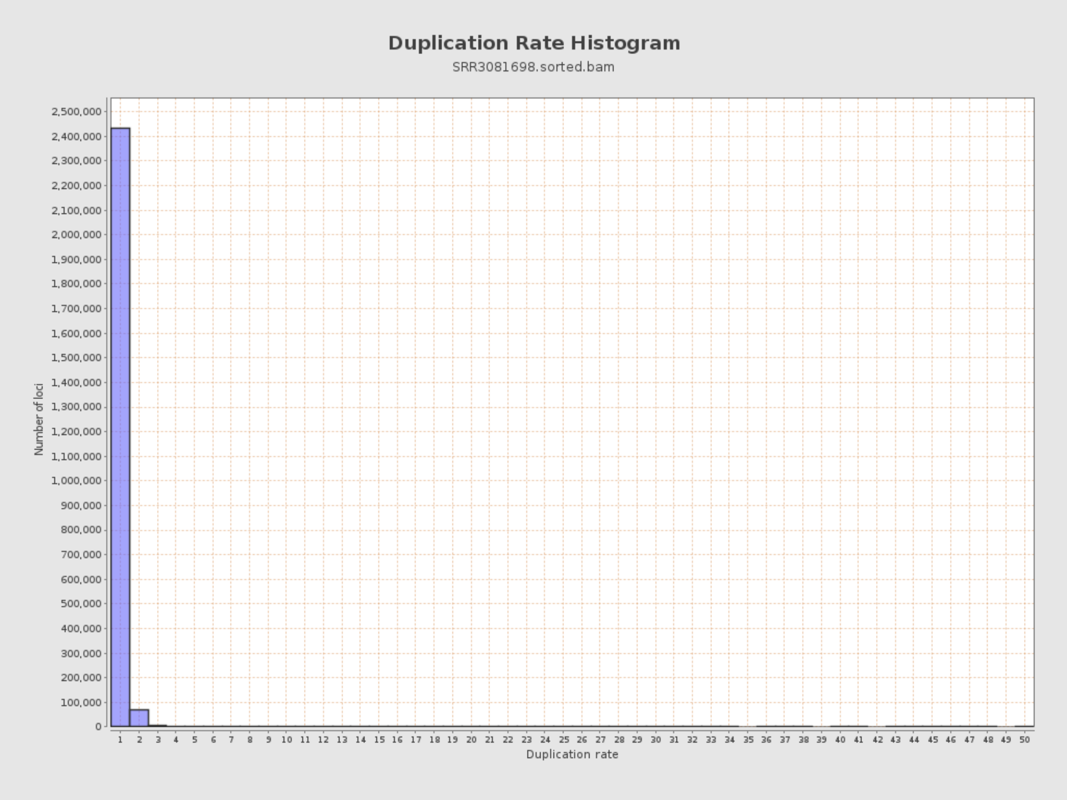
5. Results : Coverage Histogram (0-50X)



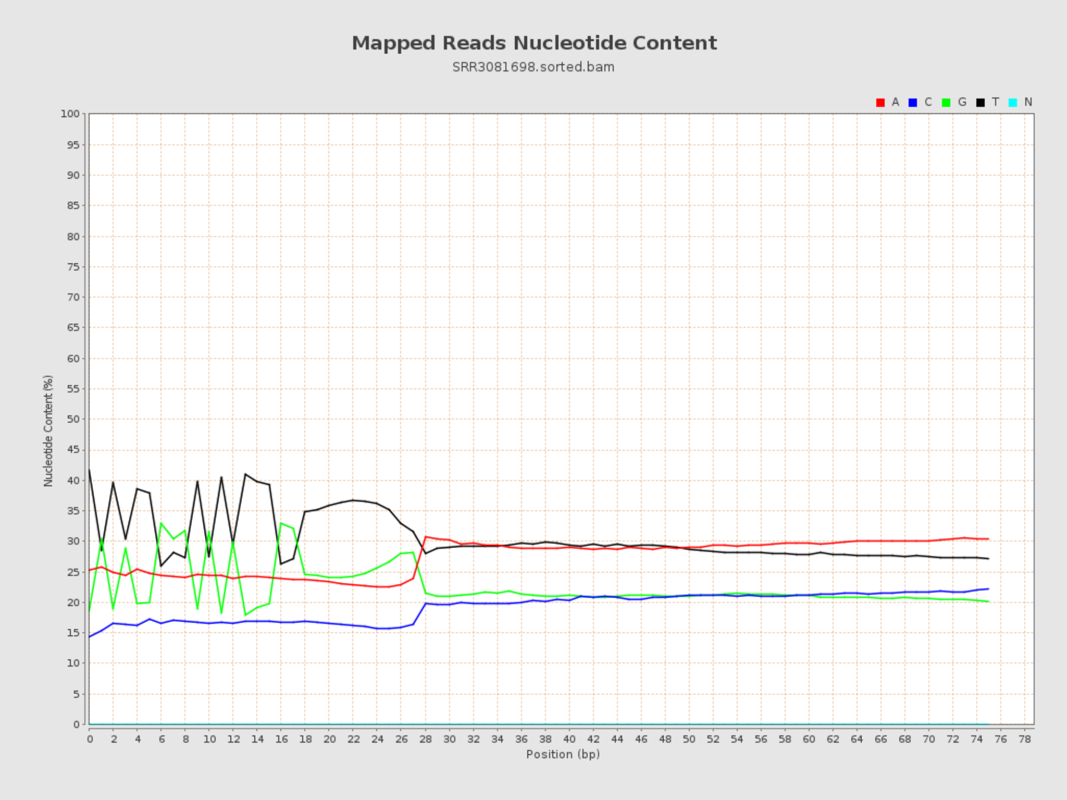
6. Results : Genome Fraction Coverage



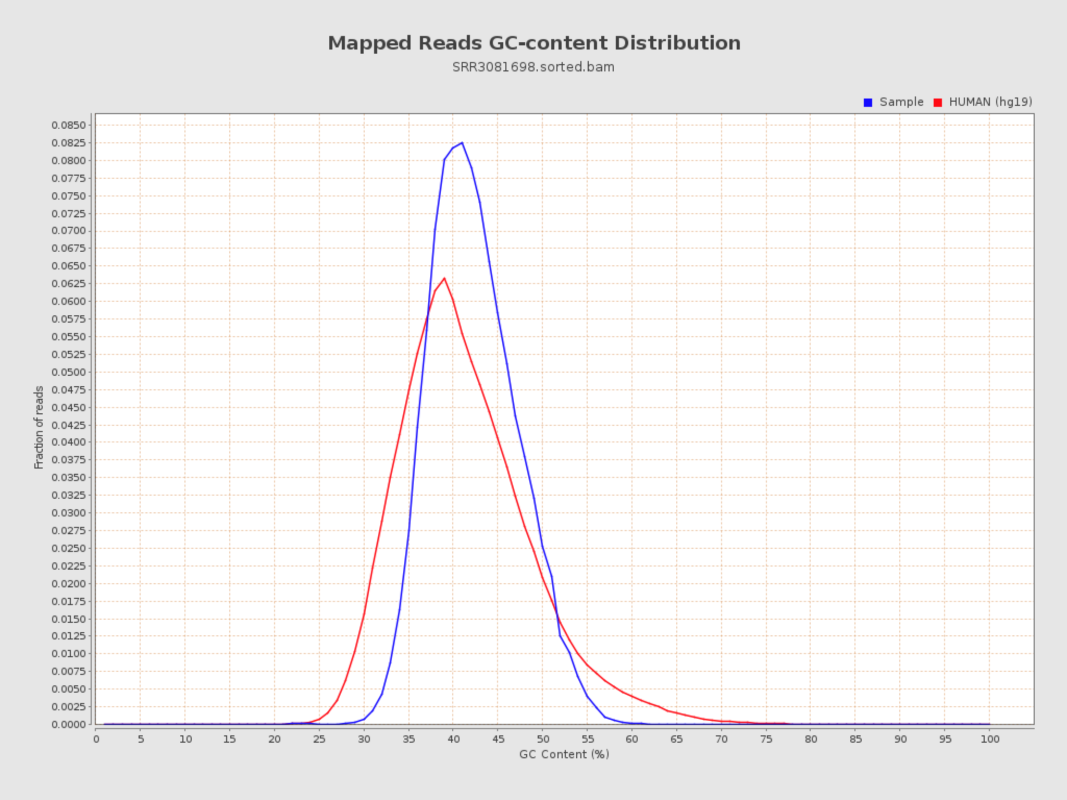
7. Results : Duplication Rate Histogram



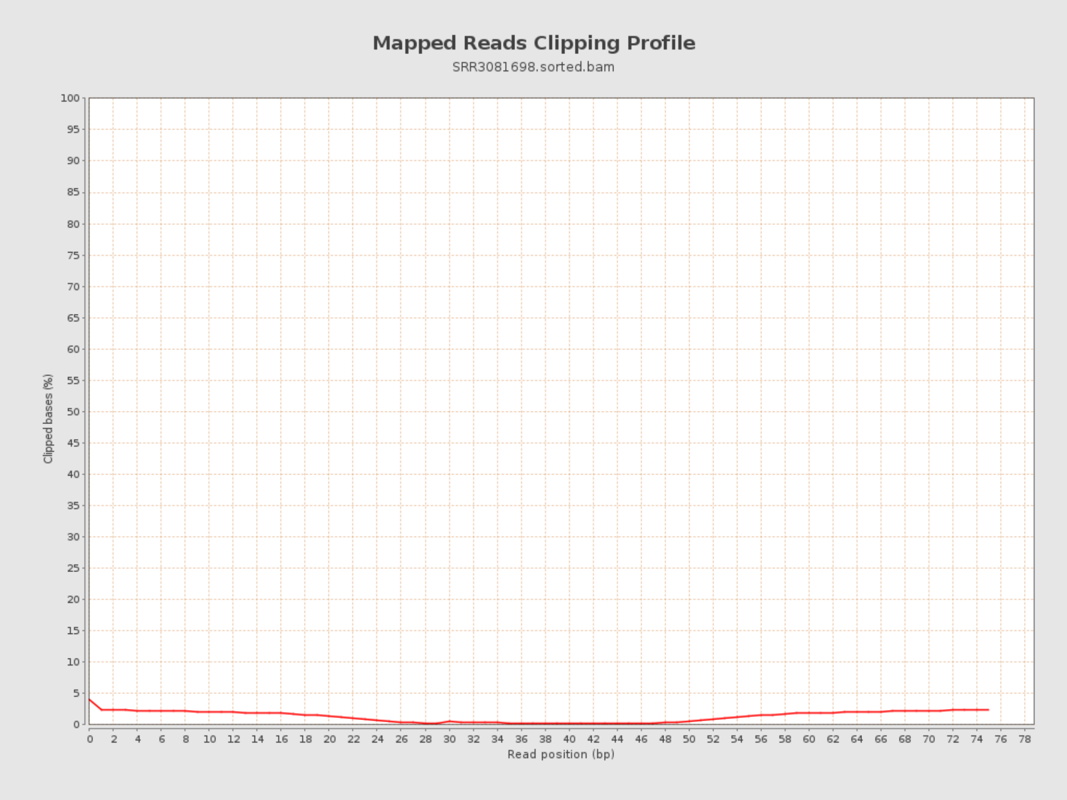
8. Results : Mapped Reads Nucleotide Content



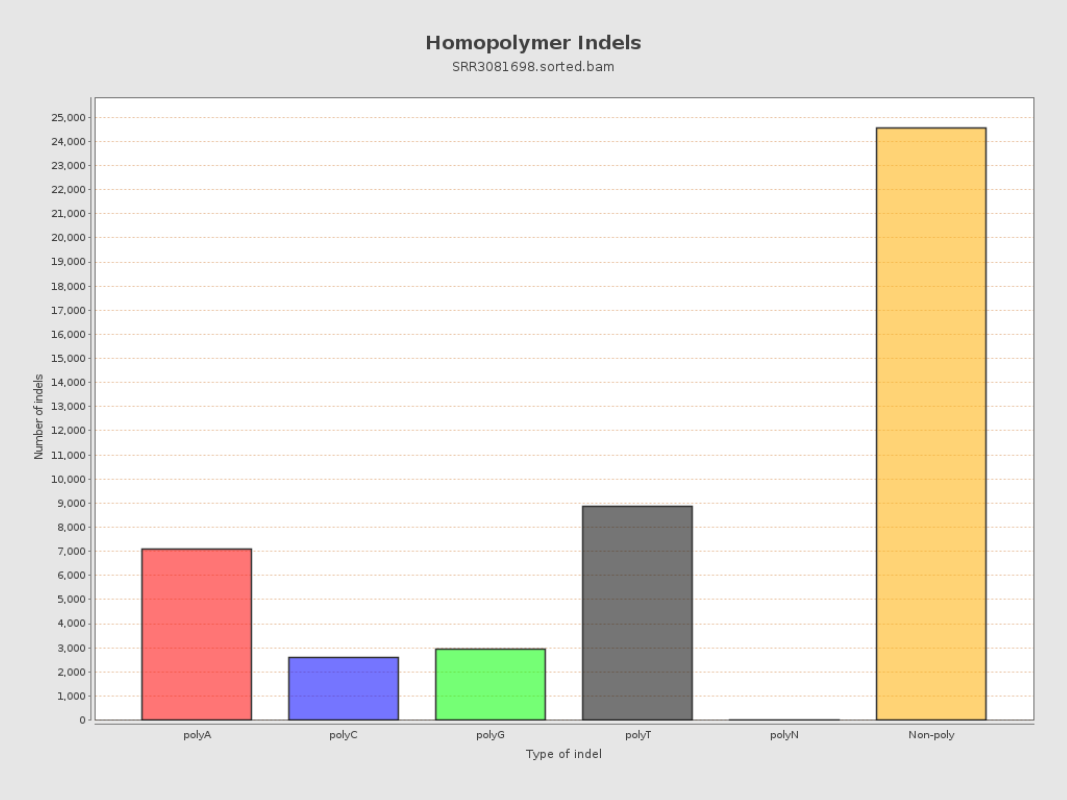
9. Results : Mapped Reads GC-content Distribution



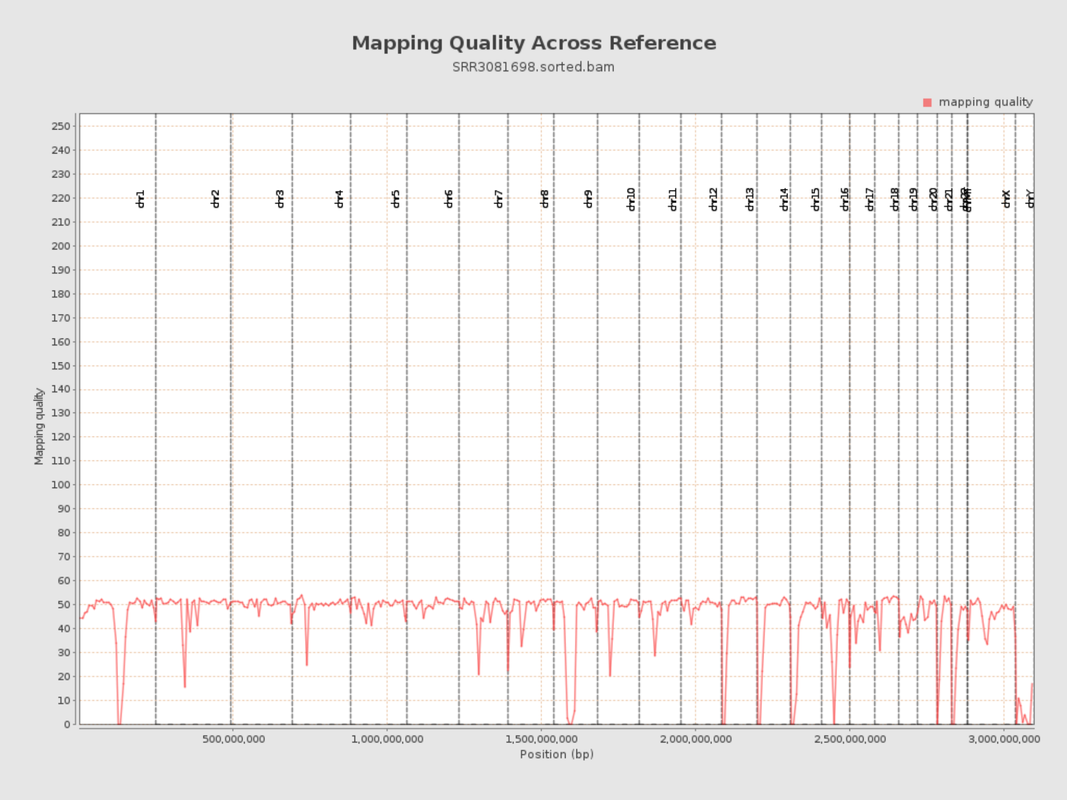
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram