Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:38:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081699.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_SRR3081699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081699.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:38:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,863,723
Mapped reads	2,658,702 / 92.84%
Unmapped reads	205,021 / 7.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,660 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	112,102 / 3.91%
Duplication rate	3.23%
Clipped reads	1,016,045 / 35.48%

2.2. ACGT Content

Number/percentage of A's	51,743,978 / 28.51%
Number/percentage of C's	33,804,899 / 18.63%
Number/percentage of T's	57,281,299 / 31.56%
Number/percentage of G's	38,655,095 / 21.3%
Number/percentage of N's	2,073 / 0%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0586

Standard Deviation	0.467

2.4. Mapping Quality

Mean Mapping Quality	47.12

2.5. Mismatches and indels

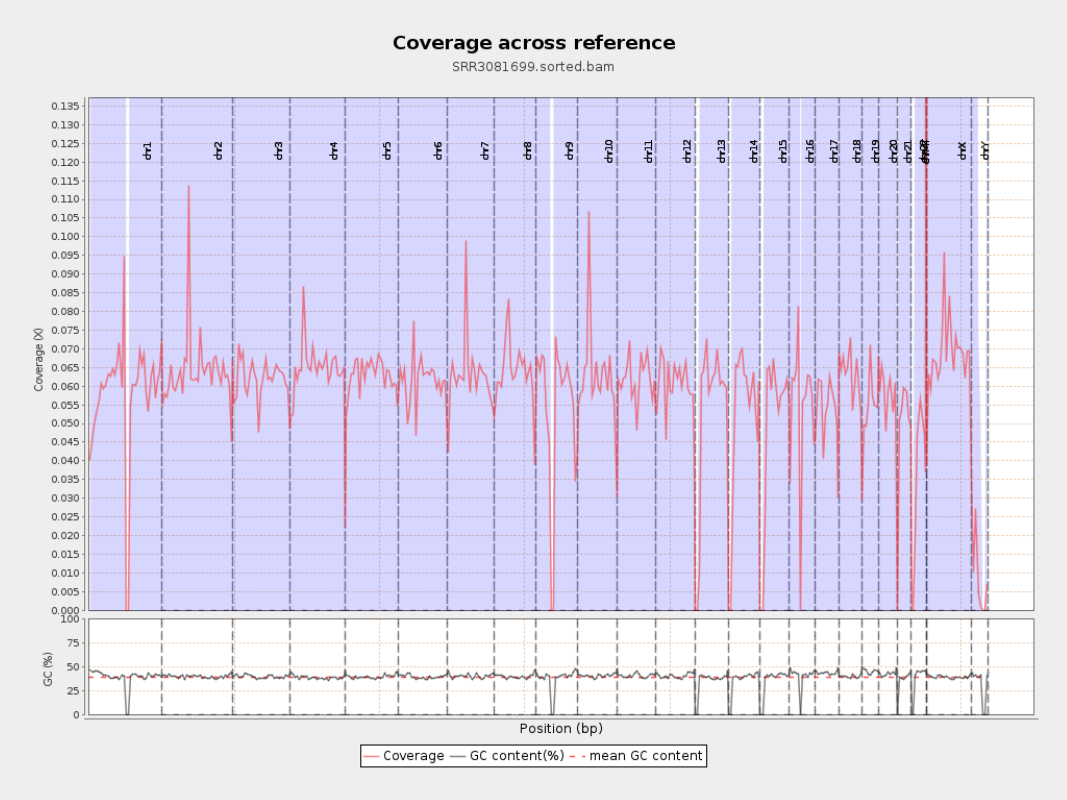
General error rate	0.86%
Mismatches	1,533,174
Insertions	14,654
Mapped reads with at least one insertion	0.55%
Deletions	41,102
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.81%

2.6. Chromosome stats

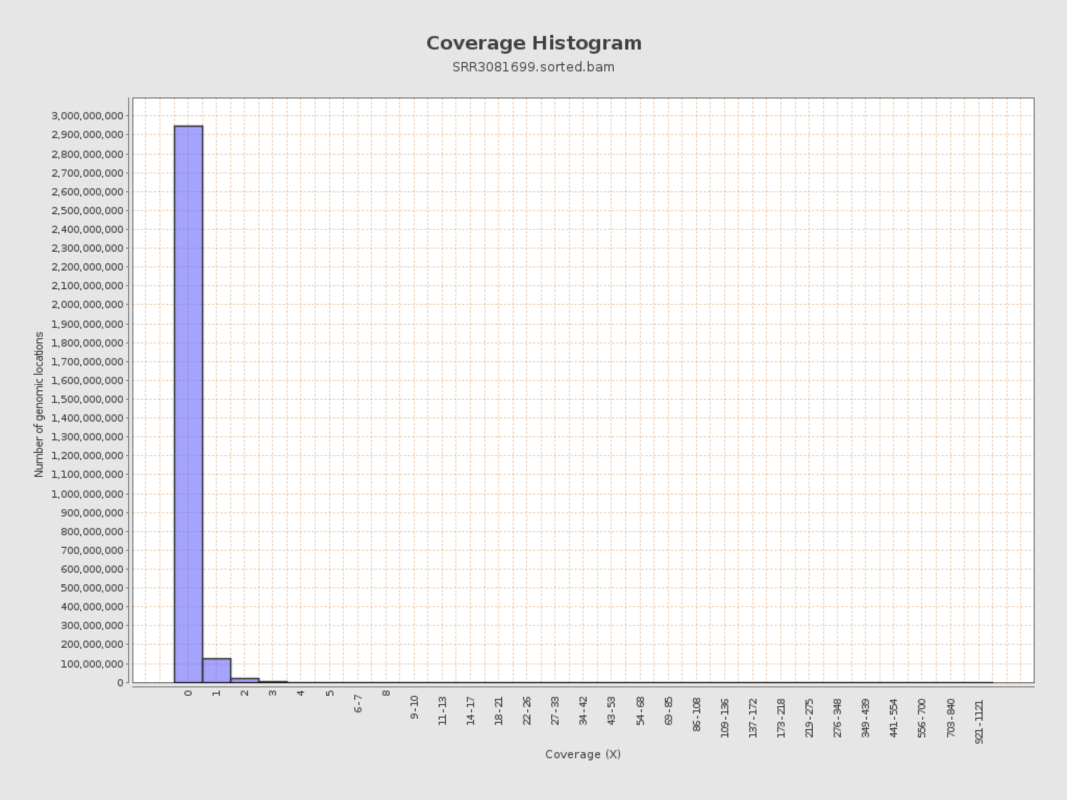
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14341809	0.0575	0.7596
chr2	243199373	15647578	0.0643	0.5548
chr3	198022430	12320186	0.0622	0.2922
chr4	191154276	12431388	0.065	0.3314
chr5	180915260	11413916	0.0631	0.2949
chr6	171115067	10508016	0.0614	0.341
chr7	159138663	10088770	0.0634	0.6365

chr8	146364022	9333321	0.0638	0.7568
chr9	141213431	7624485	0.054	0.4385
chr10	135534747	8555089	0.0631	0.4821
chr11	135006516	8300178	0.0615	0.3834
chr12	133851895	8118650	0.0607	0.2917
chr13	115169878	6005102	0.0521	0.2663
chr14	107349540	5483278	0.0511	0.2856
chr15	102531392	5052439	0.0493	0.2617
chr16	90354753	4914407	0.0544	0.3172
chr17	81195210	4352765	0.0536	0.3021
chr18	78077248	4948666	0.0634	0.7959
chr19	59128983	3258803	0.0551	0.596
chr20	63025520	3610756	0.0573	0.2933
chr21	48129895	2358911	0.049	0.2895
chr22	51304566	1782167	0.0347	0.2137
chrMT	16571	16388	0.989	1.1708
chrX	155270560	10593235	0.0682	0.3511
chrY	59373566	495005	0.0083	0.2131

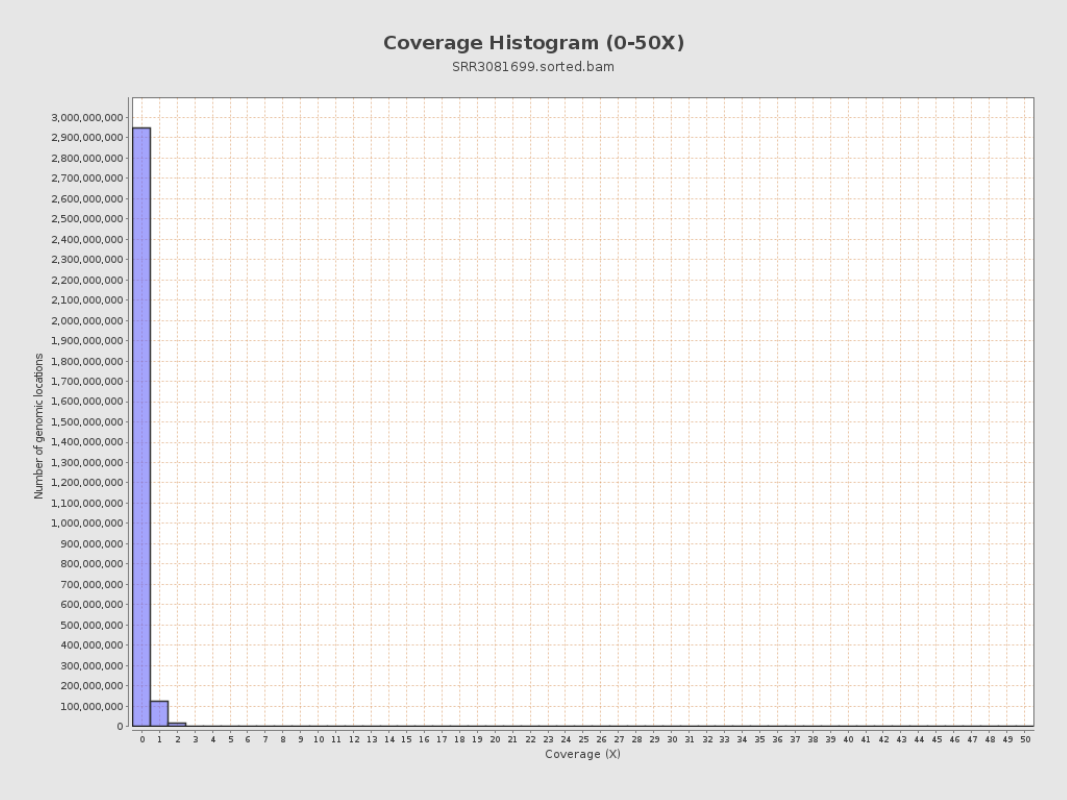
3. Results : Coverage across reference



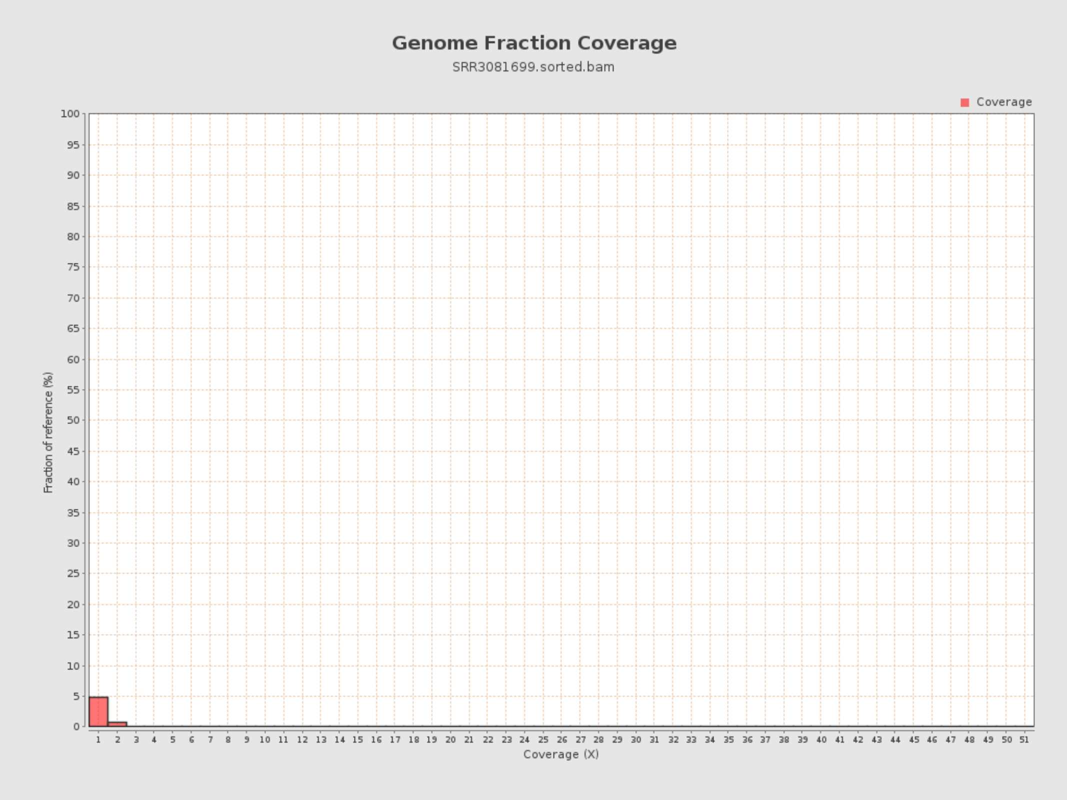
4. Results : Coverage Histogram



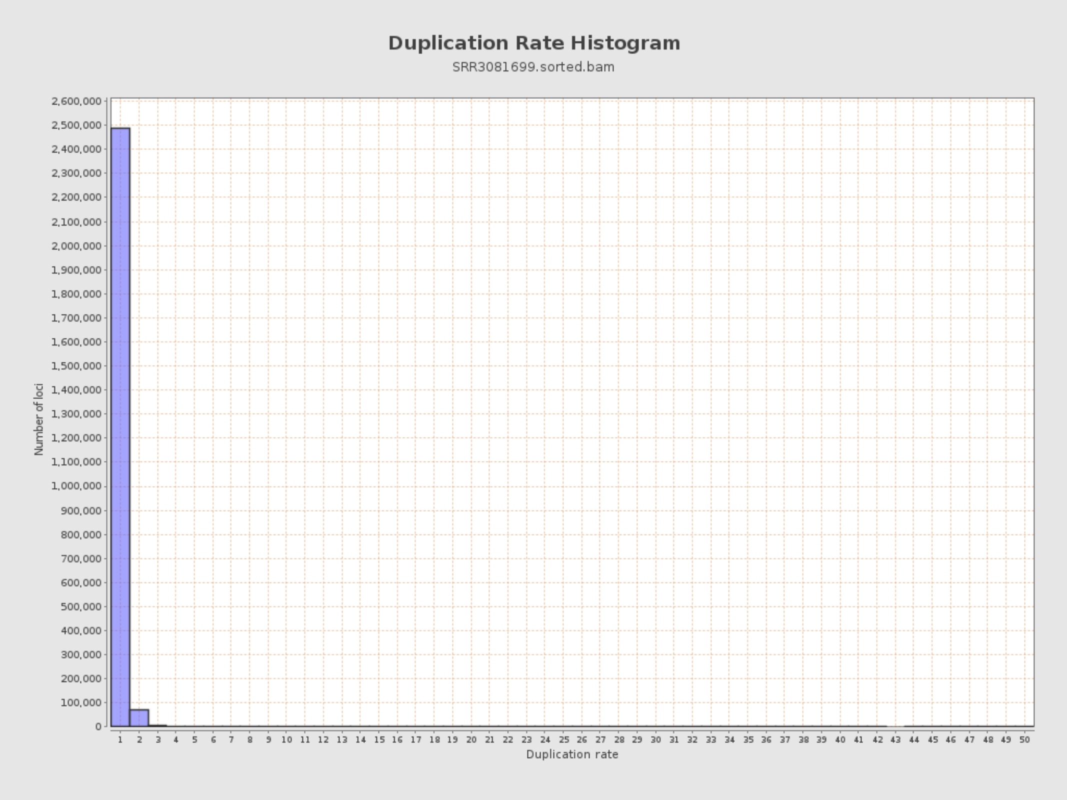
5. Results : Coverage Histogram (0-50X)



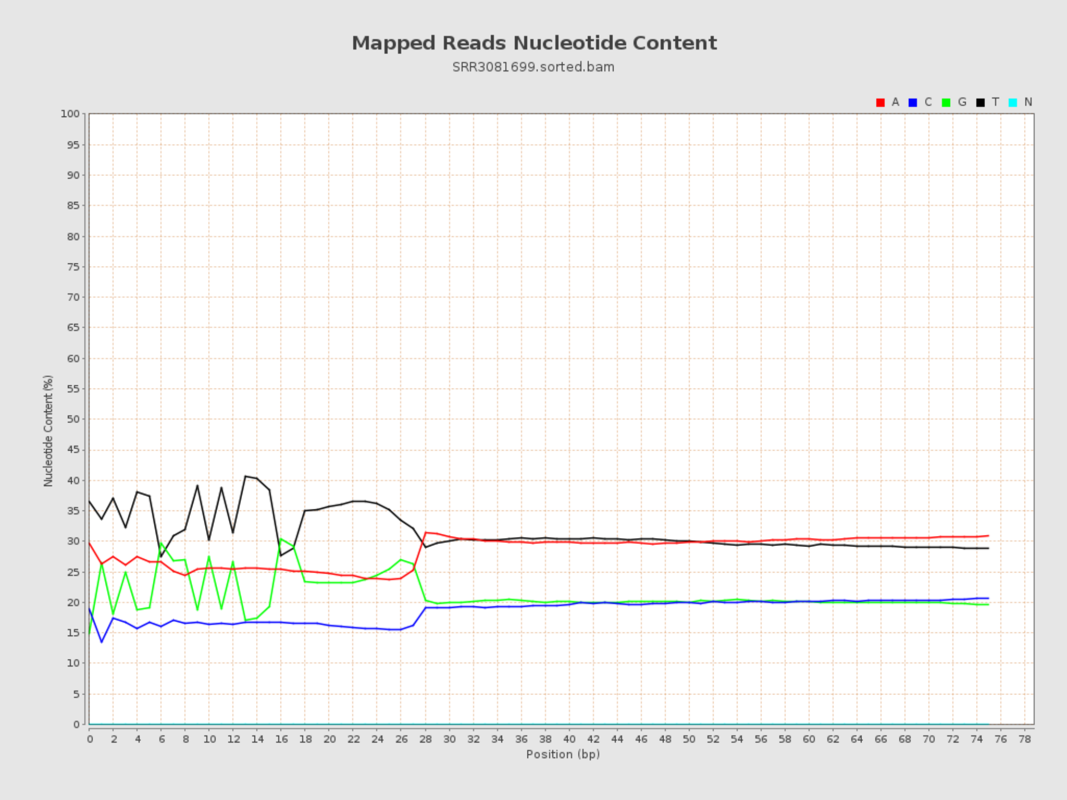
6. Results : Genome Fraction Coverage



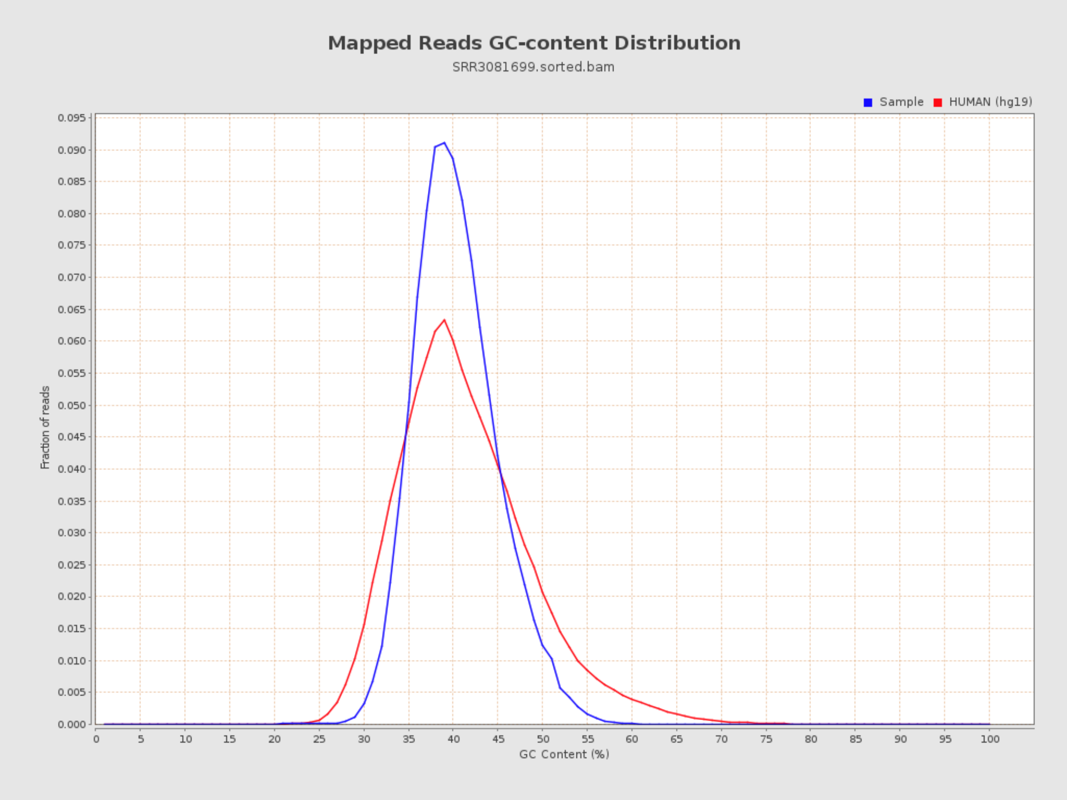
7. Results : Duplication Rate Histogram



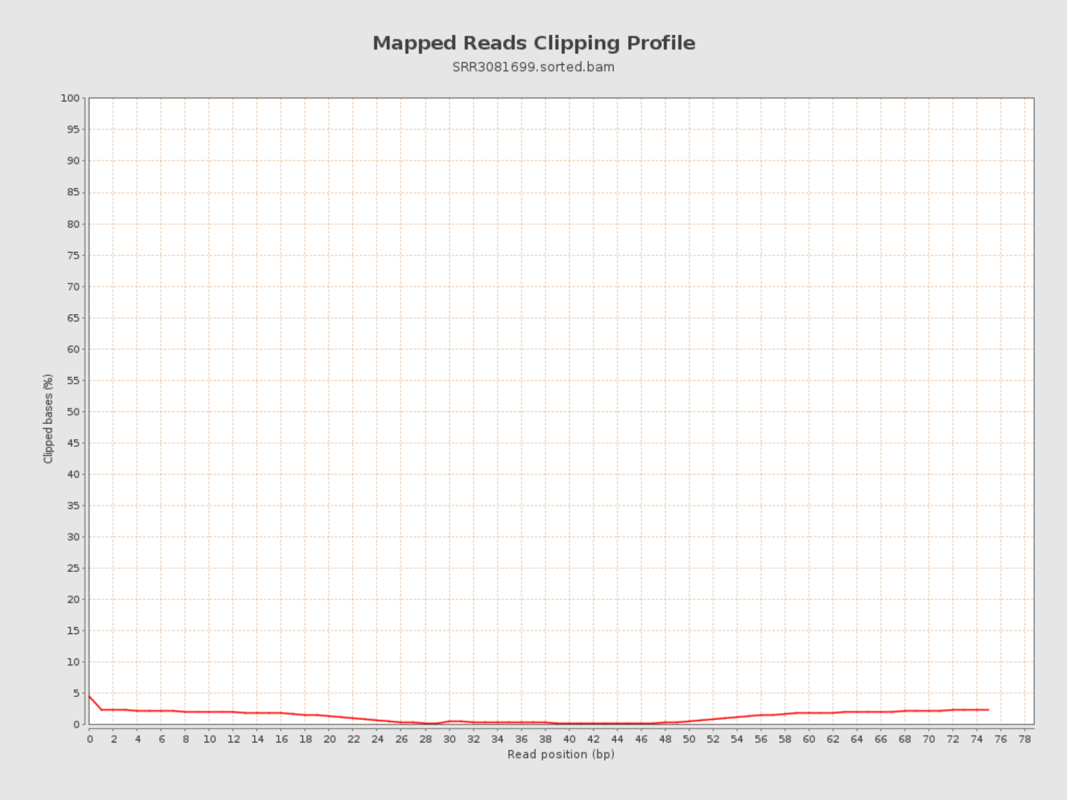
8. Results : Mapped Reads Nucleotide Content



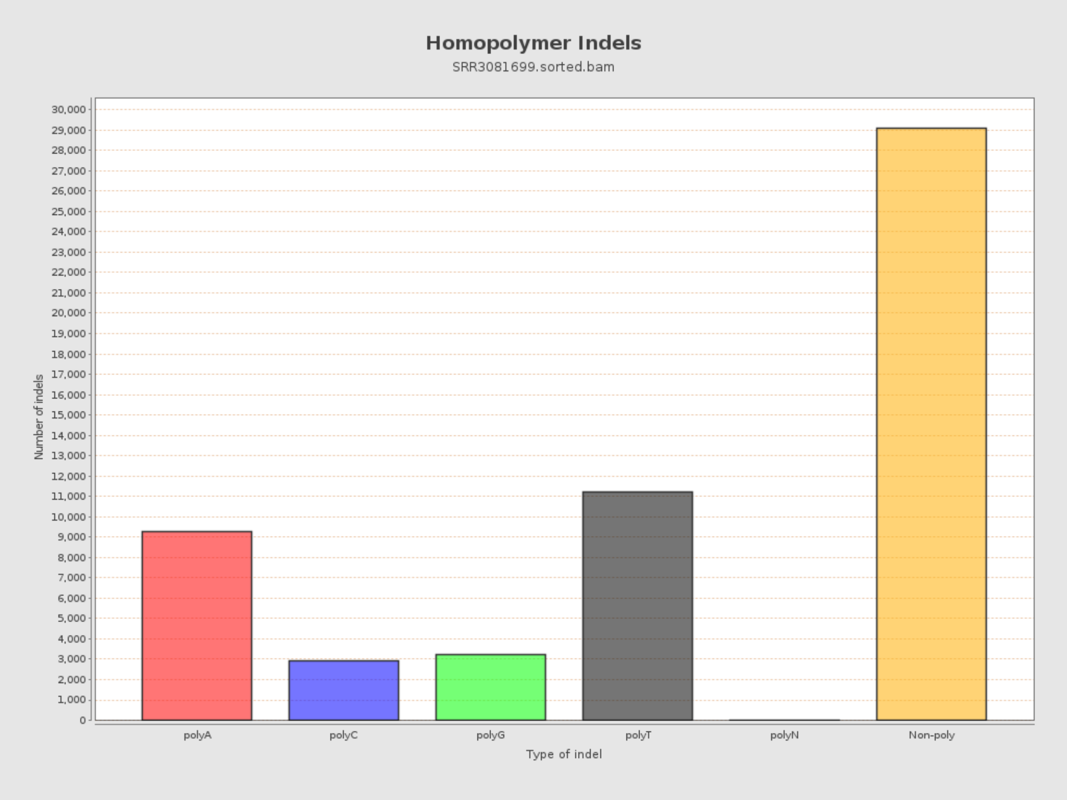
9. Results : Mapped Reads GC-content Distribution



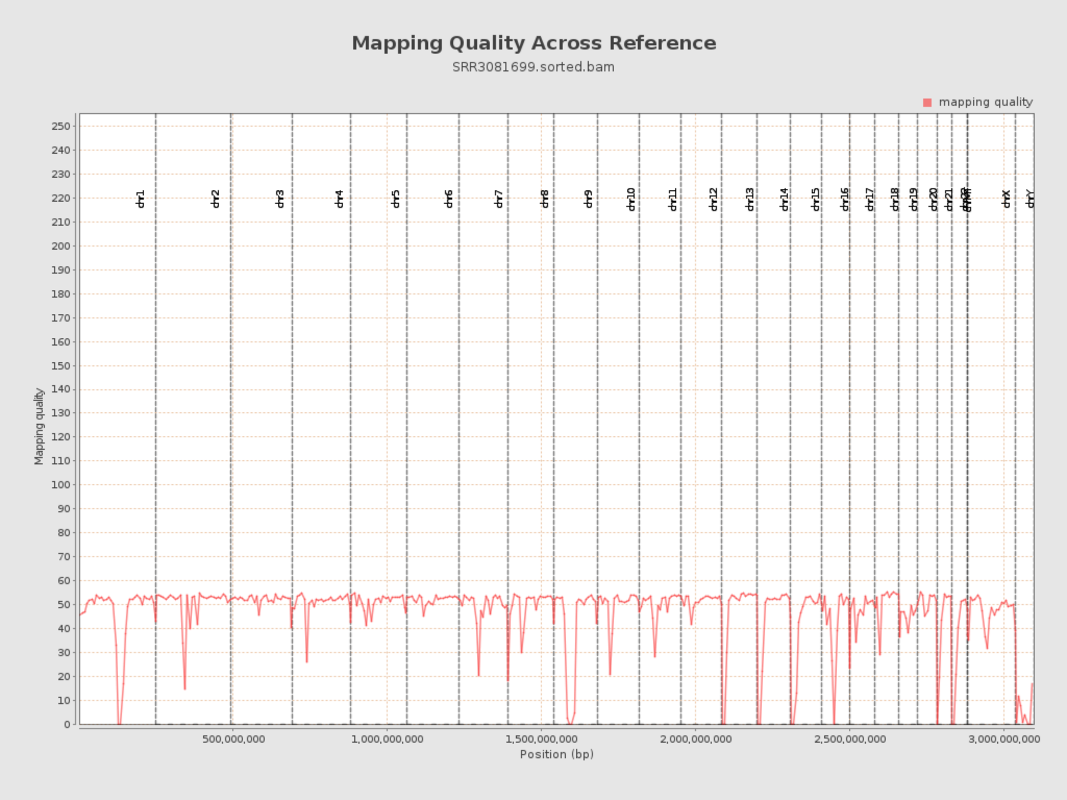
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram