Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:03:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081690.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_SRR3081690 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081690.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:03:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081690.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,145,270
Mapped reads	1,921,742 / 89.58%
Unmapped reads	223,528 / 10.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,723 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	85,038 / 3.96%
Duplication rate	3.74%
Clipped reads	796,002 / 37.1%

2.2. ACGT Content

Number/percentage of A's	36,488,073 / 28.07%
Number/percentage of C's	23,482,059 / 18.07%
Number/percentage of T's	41,754,751 / 32.12%
Number/percentage of G's	28,157,062 / 21.66%
Number/percentage of N's	94,357 / 0.07%
GC Percentage	39.73%

2.3. Coverage

Mean	0.042

Standard Deviation	0.3158

2.4. Mapping Quality

Mean Mapping Quality	47.54

2.5. Mismatches and indels

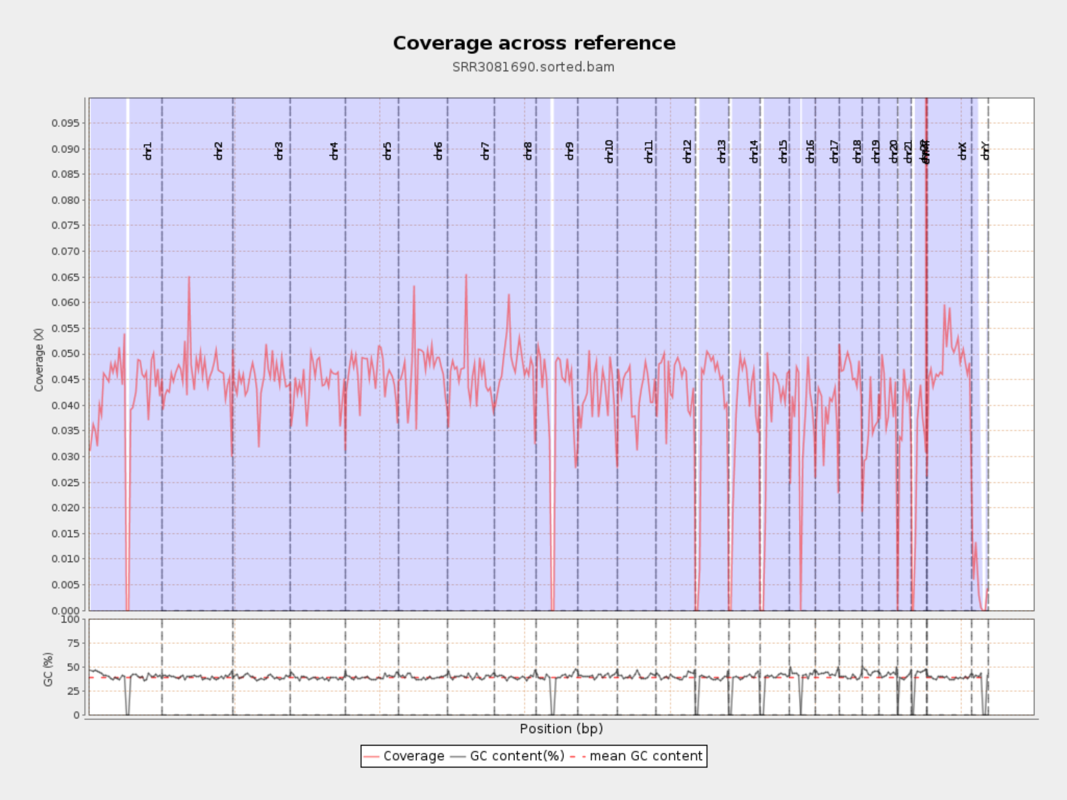
General error rate	0.87%
Mismatches	1,117,503
Insertions	10,759
Mapped reads with at least one insertion	0.56%
Deletions	29,668
Mapped reads with at least one deletion	1.53%
Homopolymer indels	49.74%

2.6. Chromosome stats

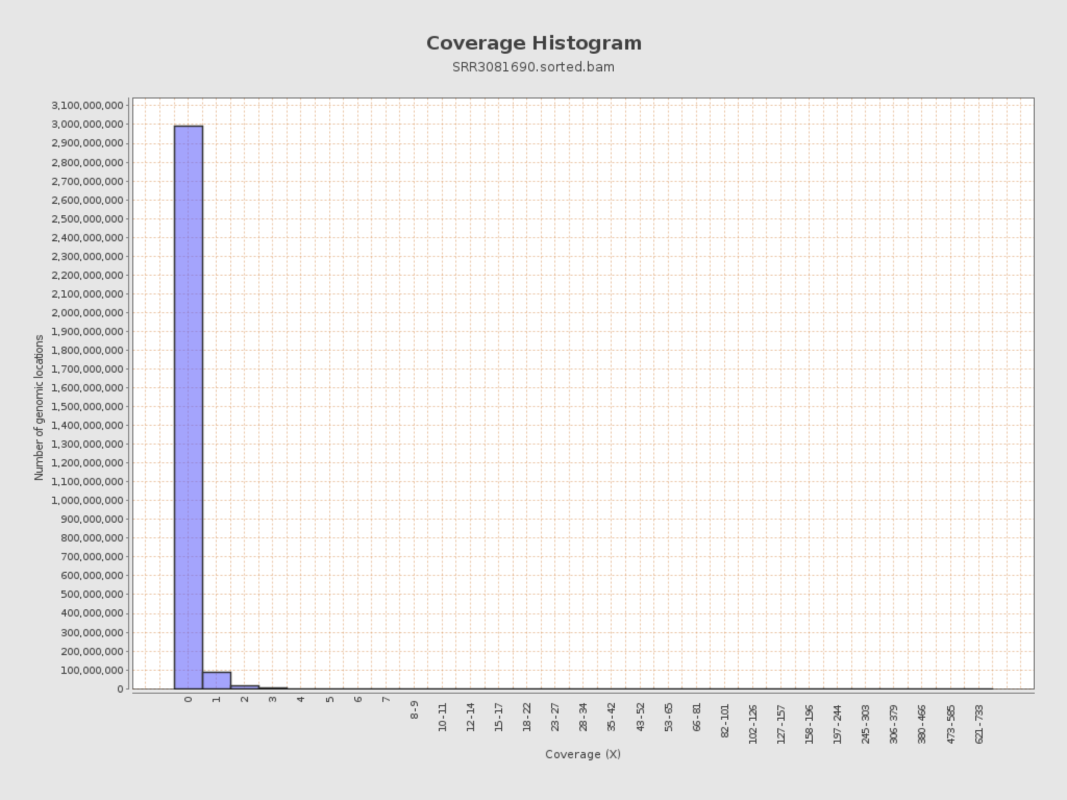
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10227916	0.041	0.4097
chr2	243199373	11228817	0.0462	0.3343
chr3	198022430	8941202	0.0452	0.2504
chr4	191154276	8432452	0.0441	0.2534
chr5	180915260	8375452	0.0463	0.2543
chr6	171115067	8068919	0.0472	0.2984
chr7	159138663	7301854	0.0459	0.4308

chr8	146364022	6958194	0.0475	0.5249
chr9	141213431	5601041	0.0397	0.2943
chr10	135534747	5736035	0.0423	0.2952
chr11	135006516	5763890	0.0427	0.2928
chr12	133851895	5903752	0.0441	0.2489
chr13	115169878	4427776	0.0384	0.2315
chr14	107349540	3914066	0.0365	0.2322
chr15	102531392	3648009	0.0356	0.2233
chr16	90354753	3295979	0.0365	0.2372
chr17	81195210	3072025	0.0378	0.2428
chr18	78077248	3662927	0.0469	0.5148
chr19	59128983	2047683	0.0346	0.3215
chr20	63025520	2582978	0.041	0.2428
chr21	48129895	1693556	0.0352	0.2307
chr22	51304566	1346786	0.0263	0.191
chrMT	16571	16879	1.0186	1.2795
chrX	155270560	7501095	0.0483	0.2734
chrY	59373566	274988	0.0046	0.0991

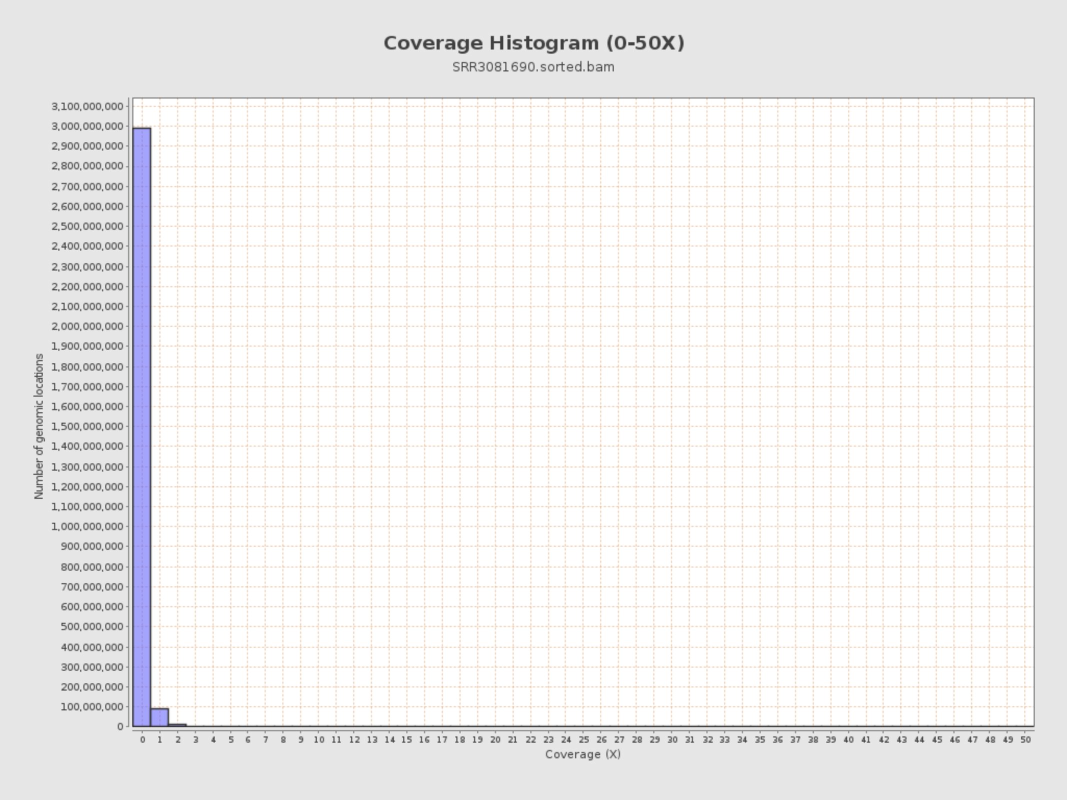
3. Results : Coverage across reference



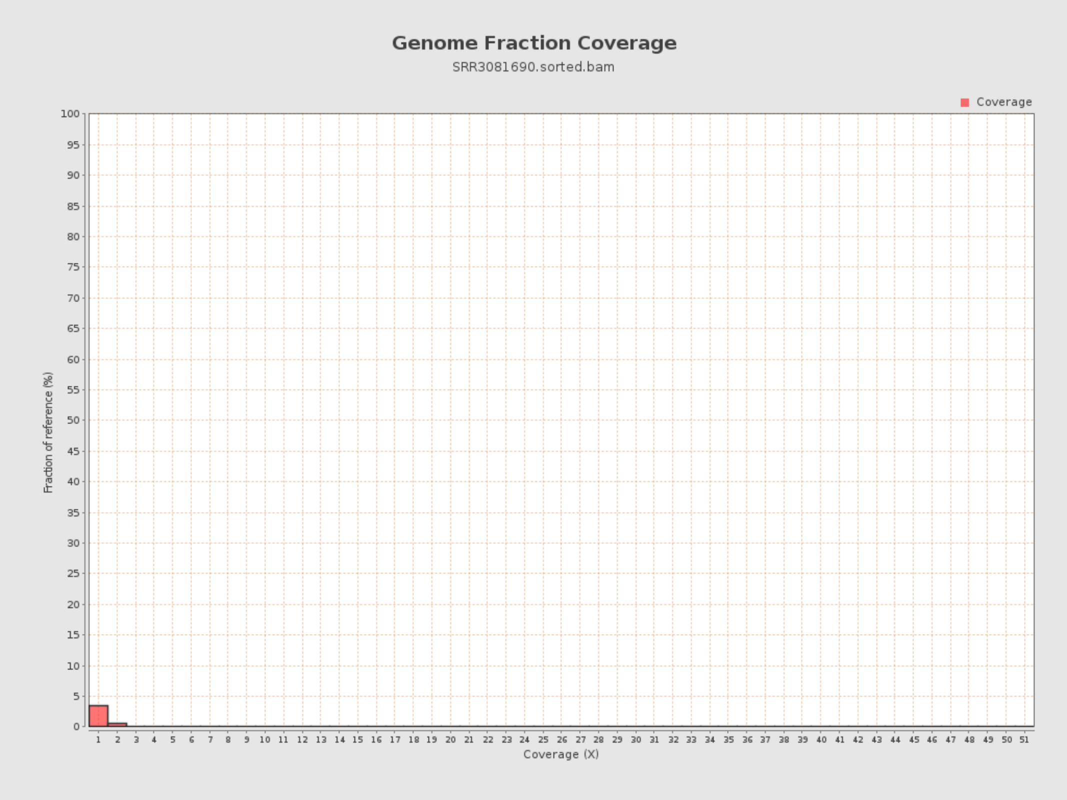
4. Results : Coverage Histogram



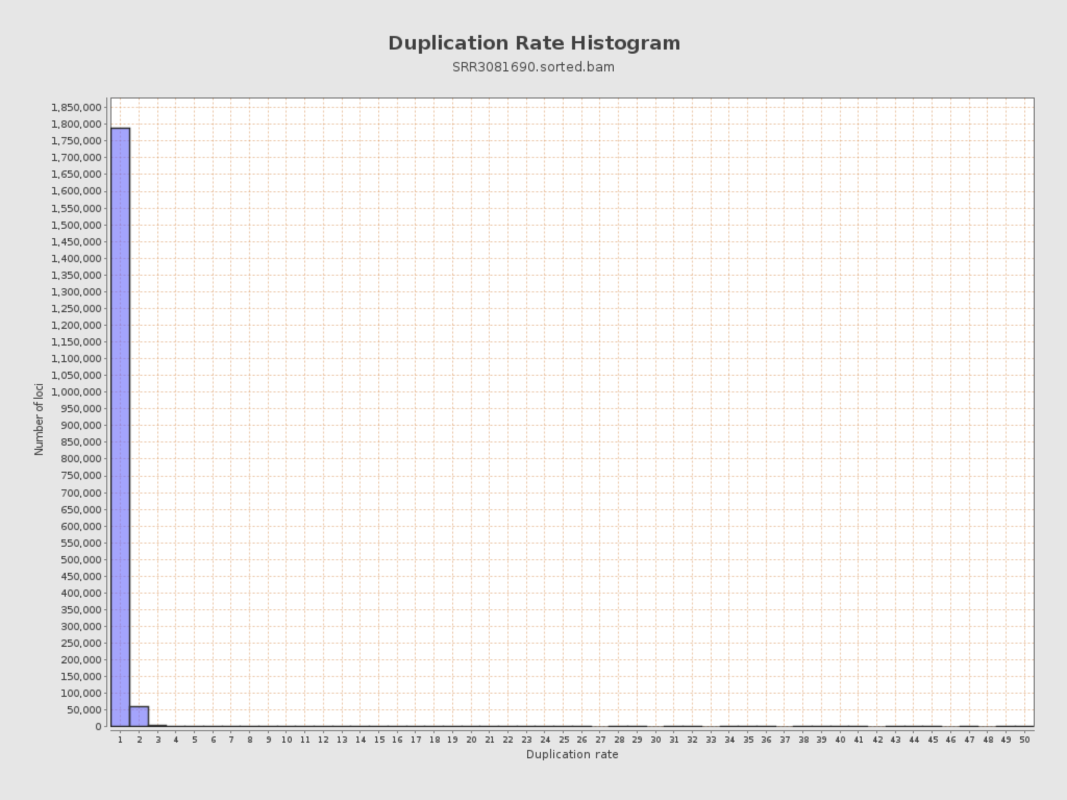
5. Results : Coverage Histogram (0-50X)



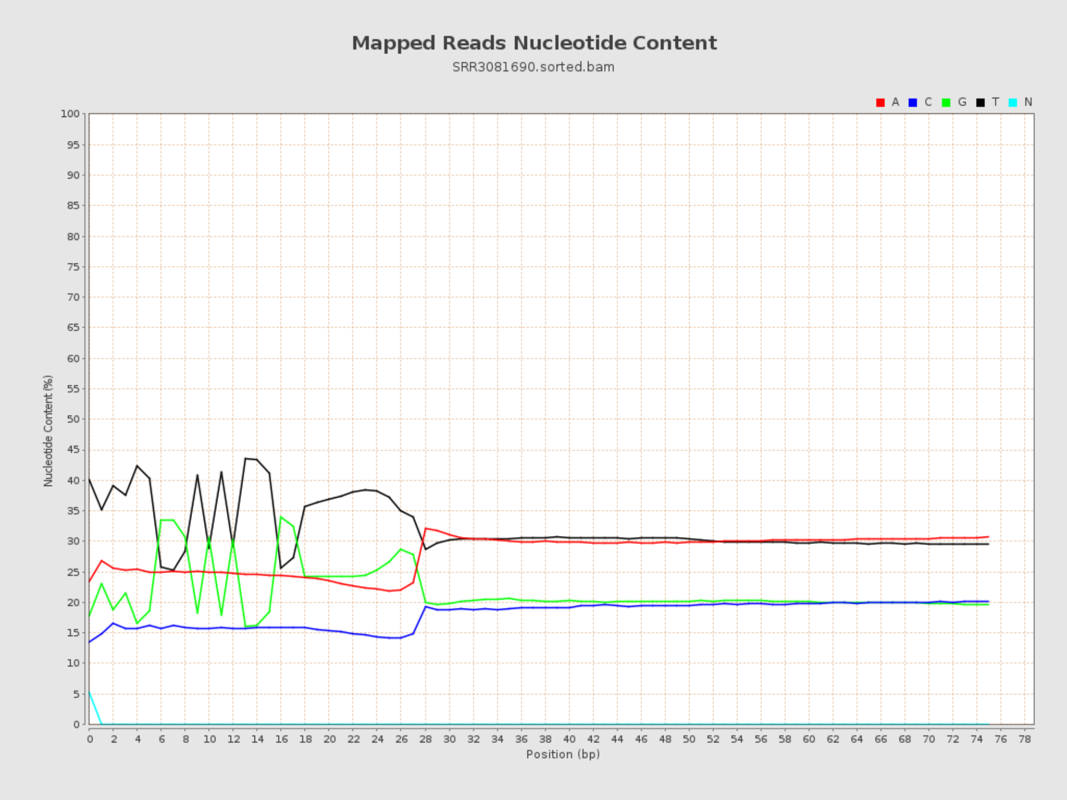
6. Results : Genome Fraction Coverage



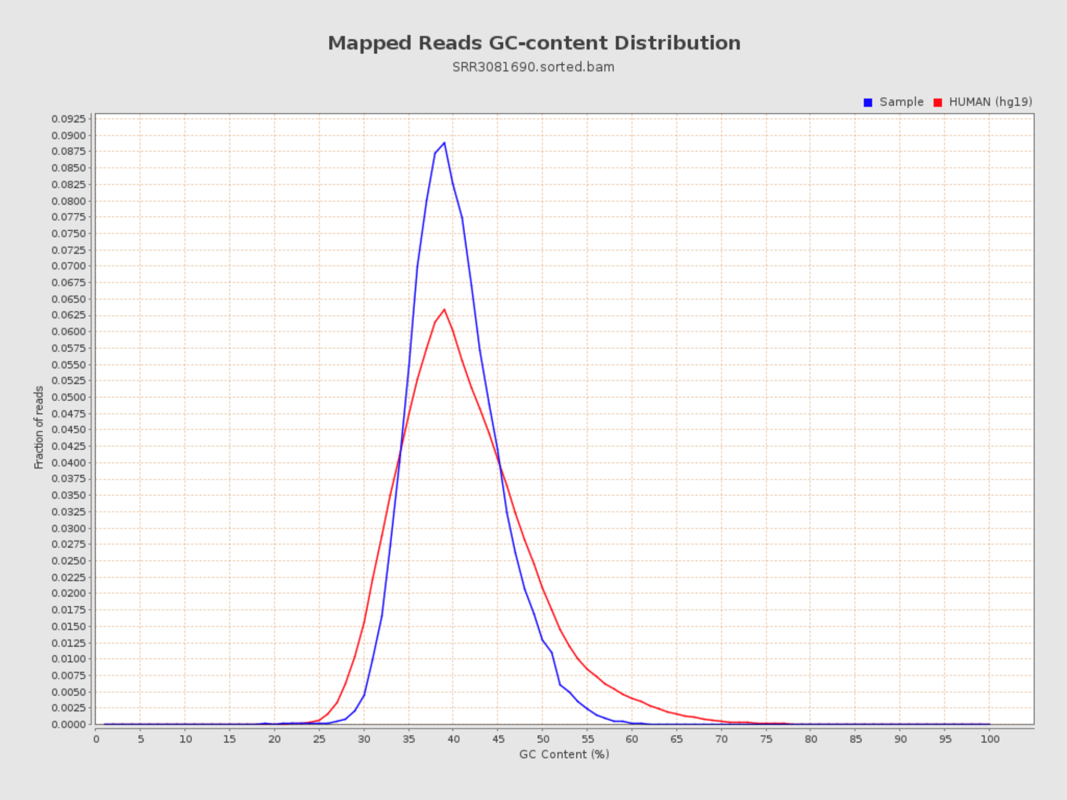
7. Results : Duplication Rate Histogram



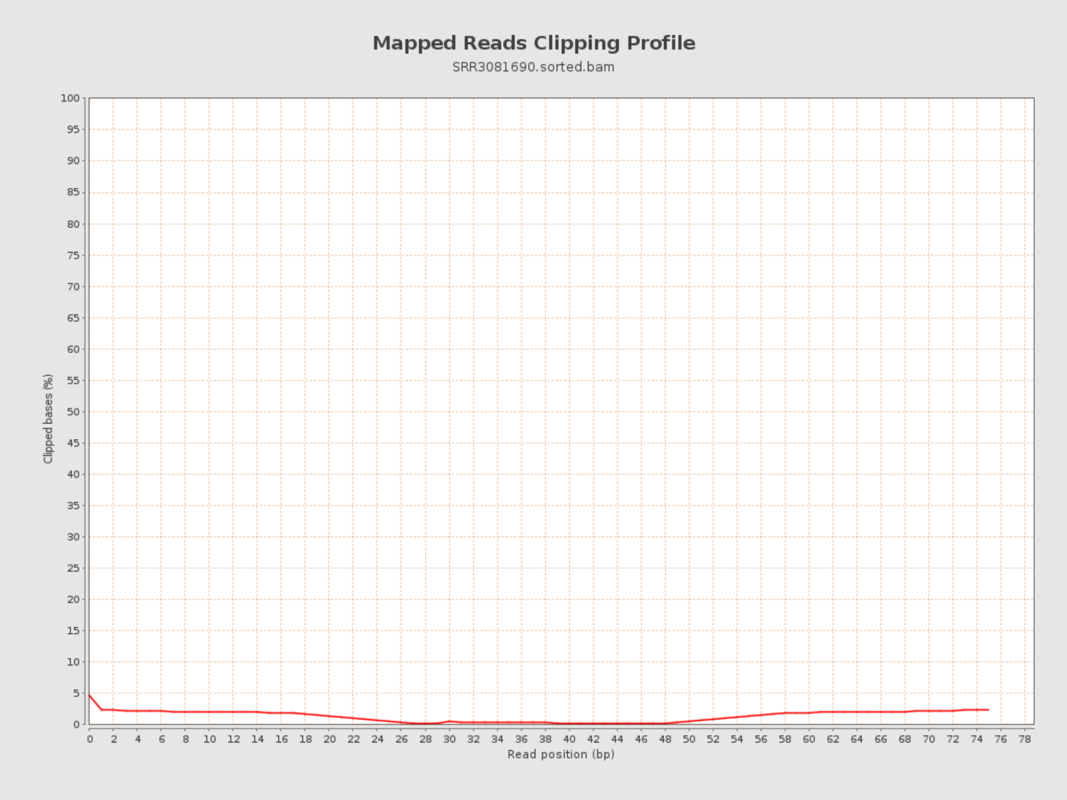
8. Results : Mapped Reads Nucleotide Content



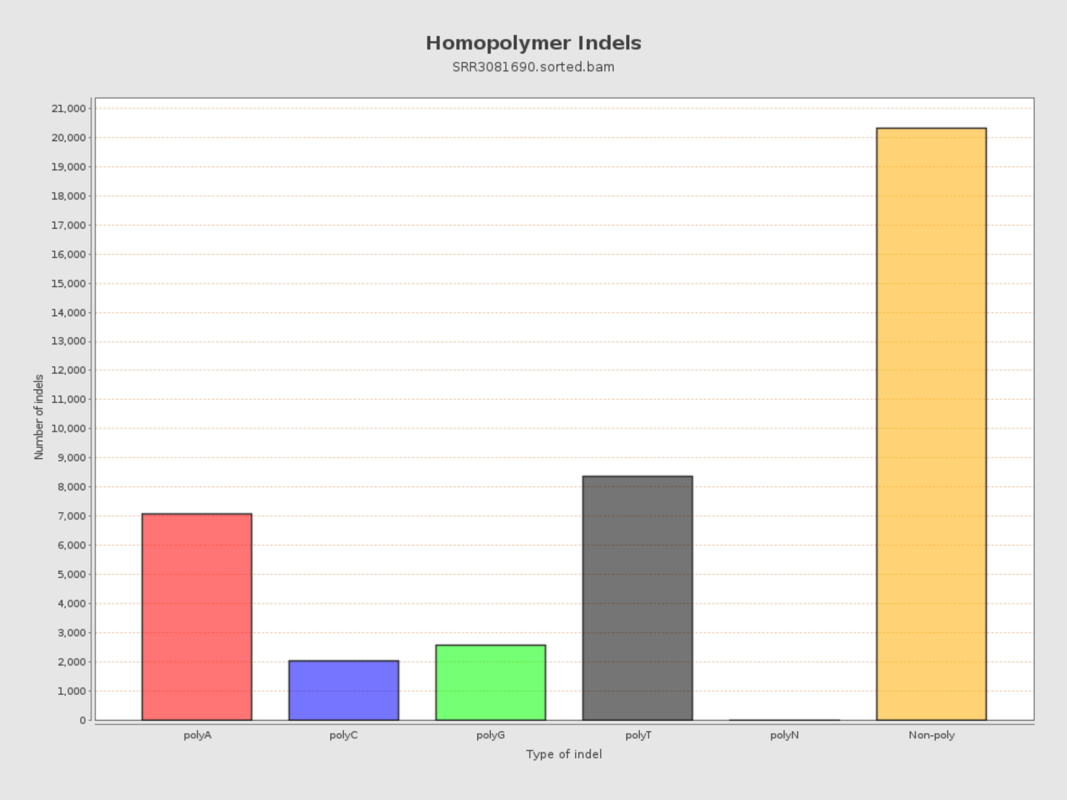
9. Results : Mapped Reads GC-content Distribution



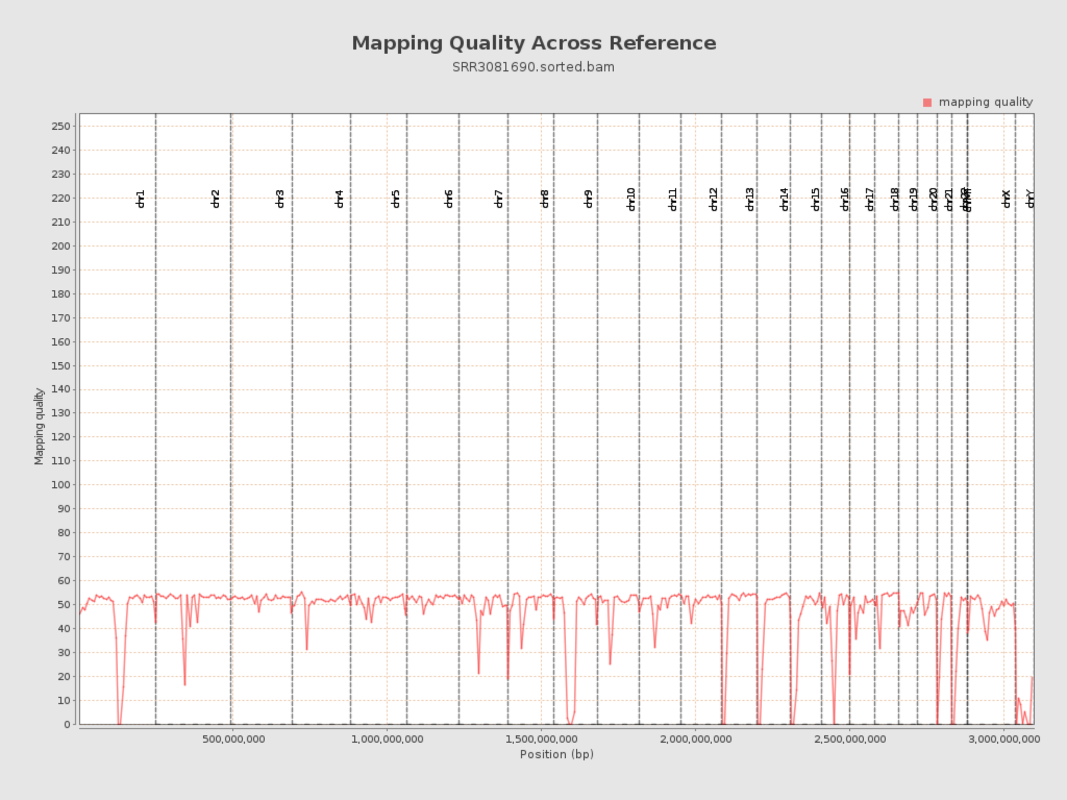
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram