Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:27:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081695.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_SRR3081695 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081695.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:27:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081695.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,080,847
Mapped reads	1,863,045 / 89.53%
Unmapped reads	217,802 / 10.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,437 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	89,341 / 4.29%
Duplication rate	4.06%
Clipped reads	775,604 / 37.27%

2.2. ACGT Content

Number/percentage of A's	35,468,107 / 28.18%
Number/percentage of C's	22,479,911 / 17.86%
Number/percentage of T's	40,863,116 / 32.46%
Number/percentage of G's	26,974,577 / 21.43%
Number/percentage of N's	92,717 / 0.07%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.3147

2.4. Mapping Quality

Mean Mapping Quality	47.54

2.5. Mismatches and indels

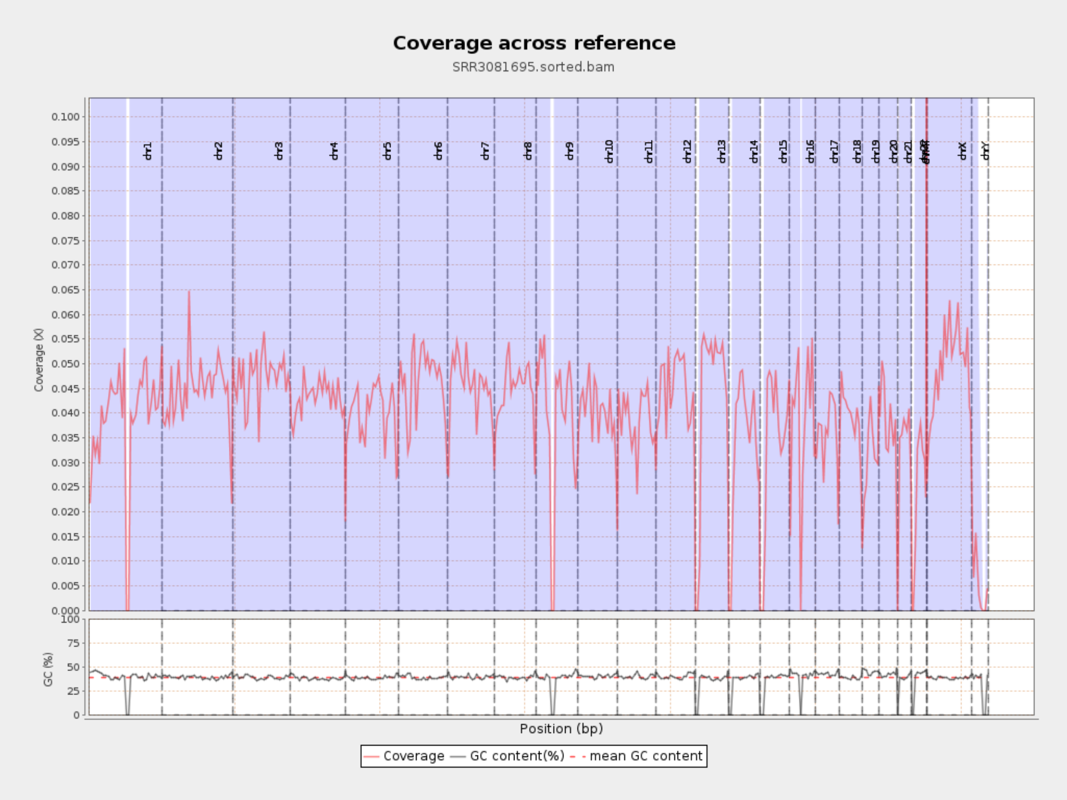
General error rate	0.88%
Mismatches	1,088,739
Insertions	10,630
Mapped reads with at least one insertion	0.57%
Deletions	28,481
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.87%

2.6. Chromosome stats

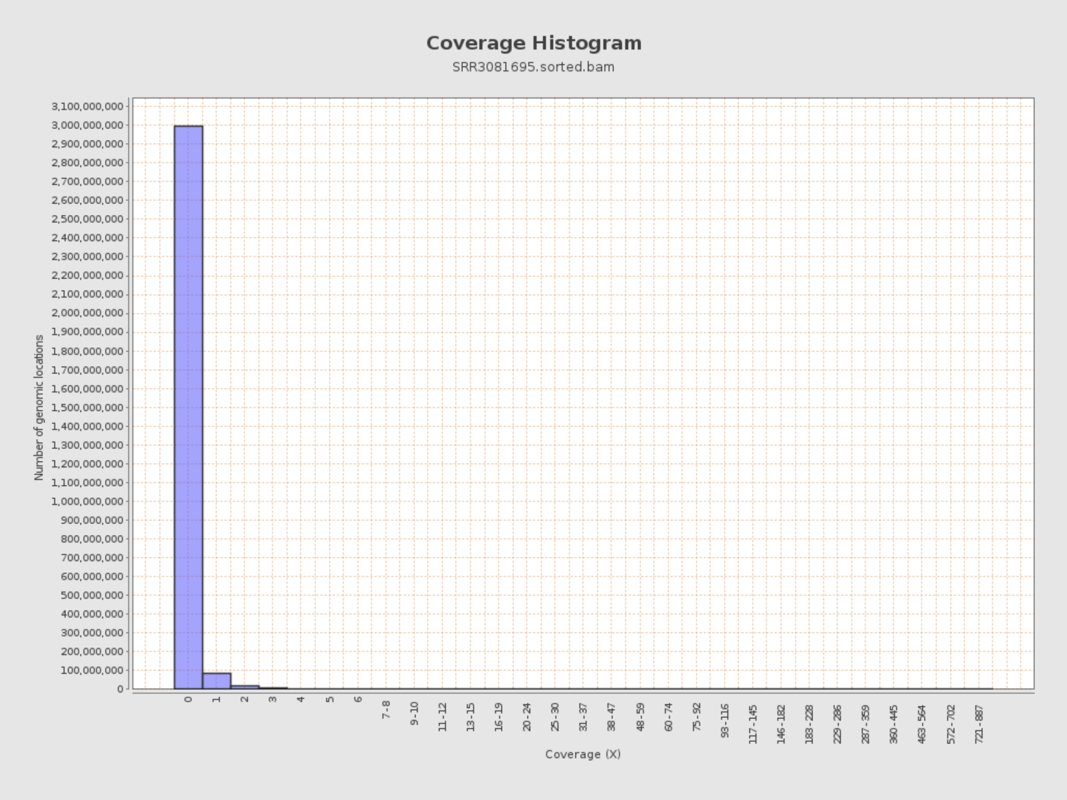
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9710196	0.039	0.3918
chr2	243199373	10863600	0.0447	0.3398
chr3	198022430	9394043	0.0474	0.2622
chr4	191154276	8237575	0.0431	0.2589
chr5	180915260	7253462	0.0401	0.2417
chr6	171115067	7969416	0.0466	0.2919
chr7	159138663	7349202	0.0462	0.3656

chr8	146364022	6515795	0.0445	0.5932
chr9	141213431	5513650	0.039	0.2948
chr10	135534747	5498560	0.0406	0.2963
chr11	135006516	5168440	0.0383	0.2686
chr12	133851895	6013818	0.0449	0.2571
chr13	115169878	4956897	0.043	0.2511
chr14	107349540	3634564	0.0339	0.2276
chr15	102531392	3426355	0.0334	0.2203
chr16	90354753	3476502	0.0385	0.2449
chr17	81195210	2892086	0.0356	0.2365
chr18	78077248	3079197	0.0394	0.4818
chr19	59128983	1868343	0.0316	0.3266
chr20	63025520	2427231	0.0385	0.2395
chr21	48129895	1566204	0.0325	0.2253
chr22	51304566	1181235	0.023	0.1819
chrMT	16571	2638	0.1592	0.4192
chrX	155270560	7624032	0.0491	0.2805
chrY	59373566	301753	0.0051	0.1155

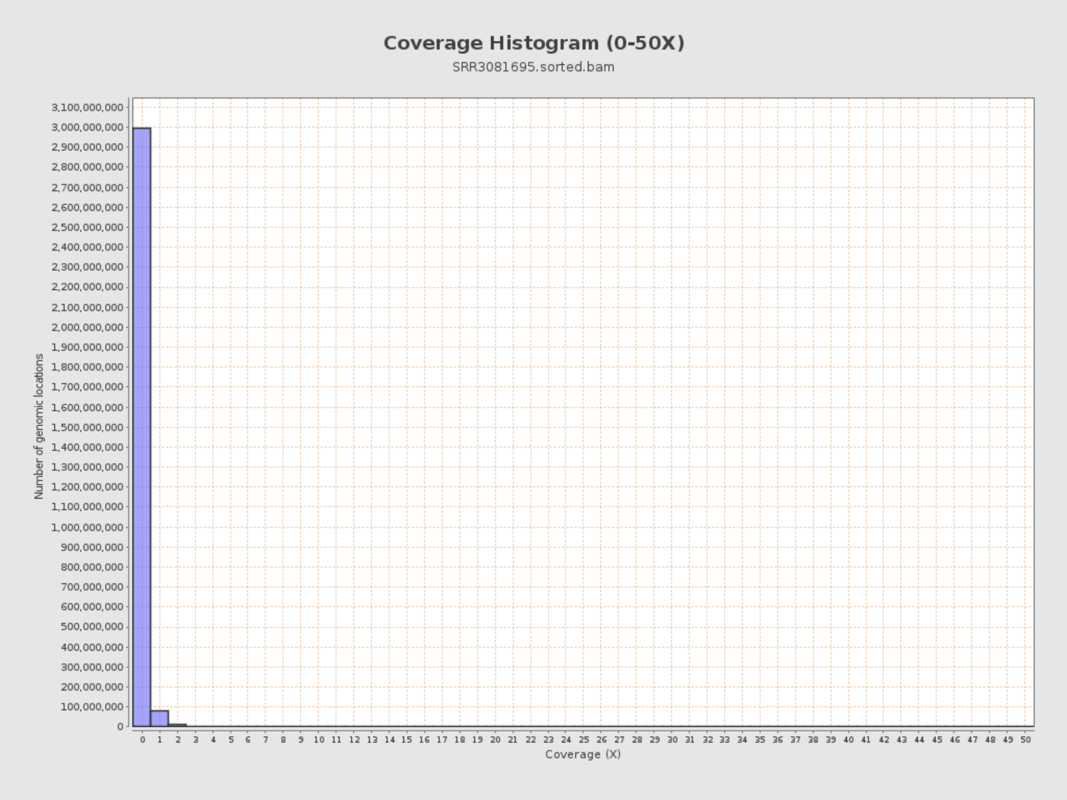
3. Results : Coverage across reference



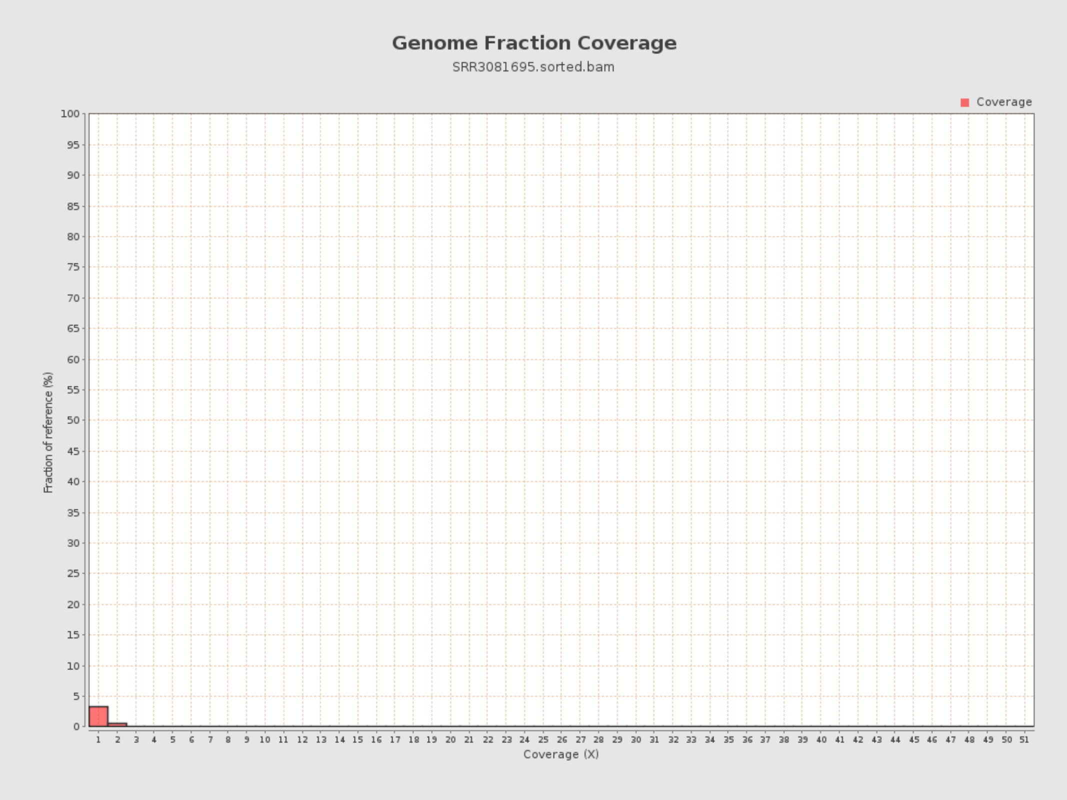
4. Results : Coverage Histogram



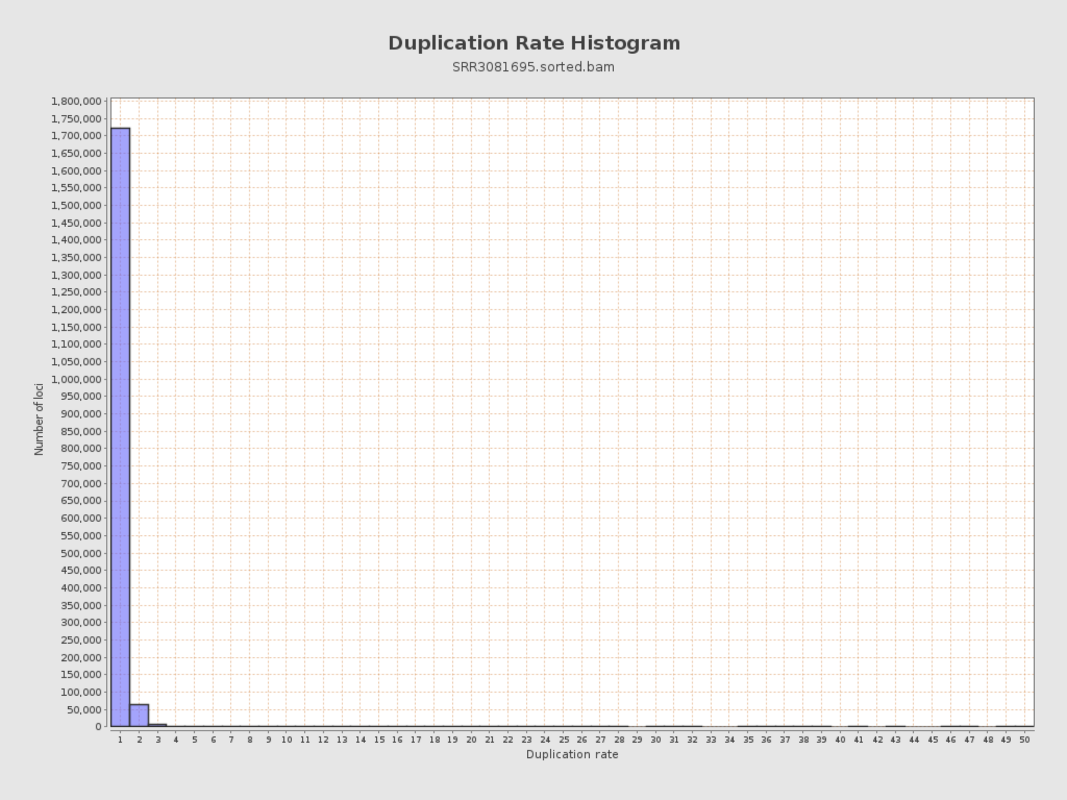
5. Results : Coverage Histogram (0-50X)



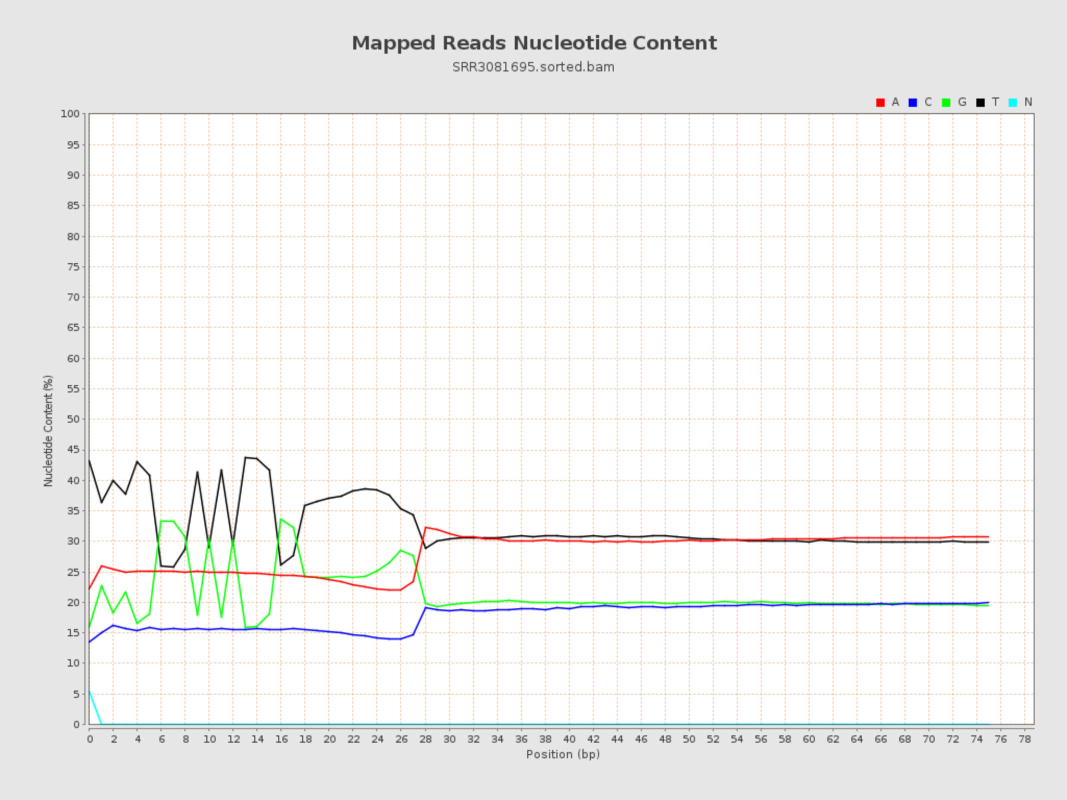
6. Results : Genome Fraction Coverage



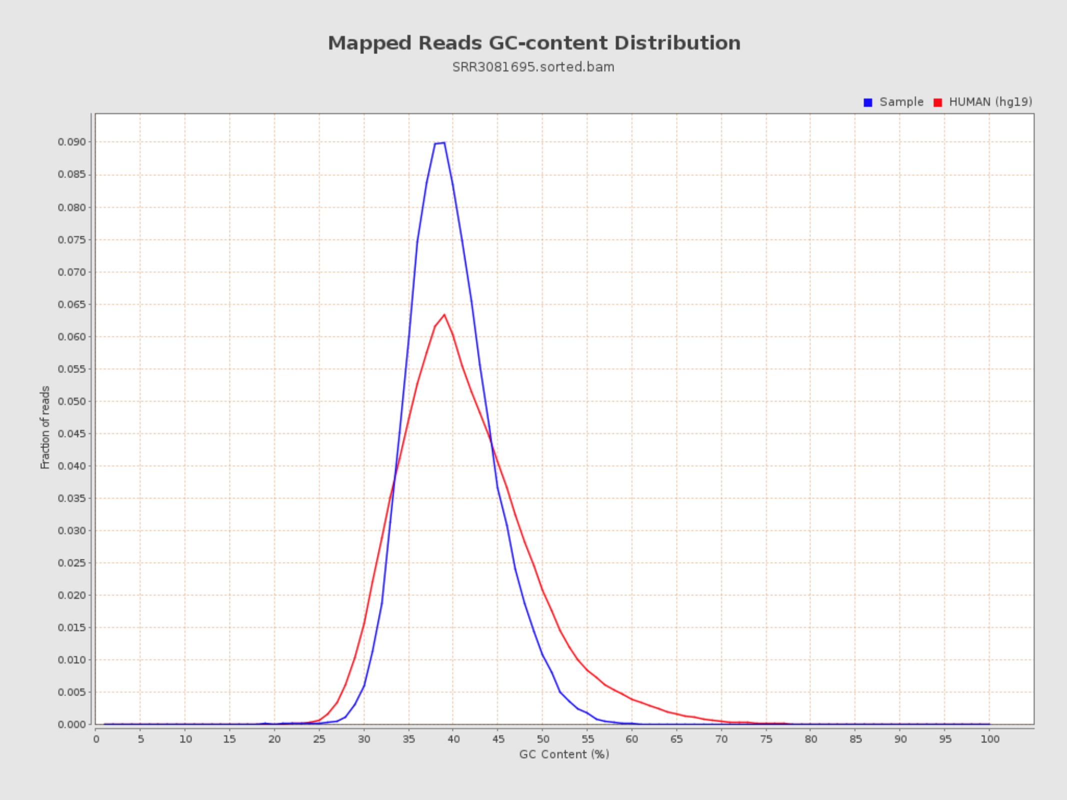
7. Results : Duplication Rate Histogram



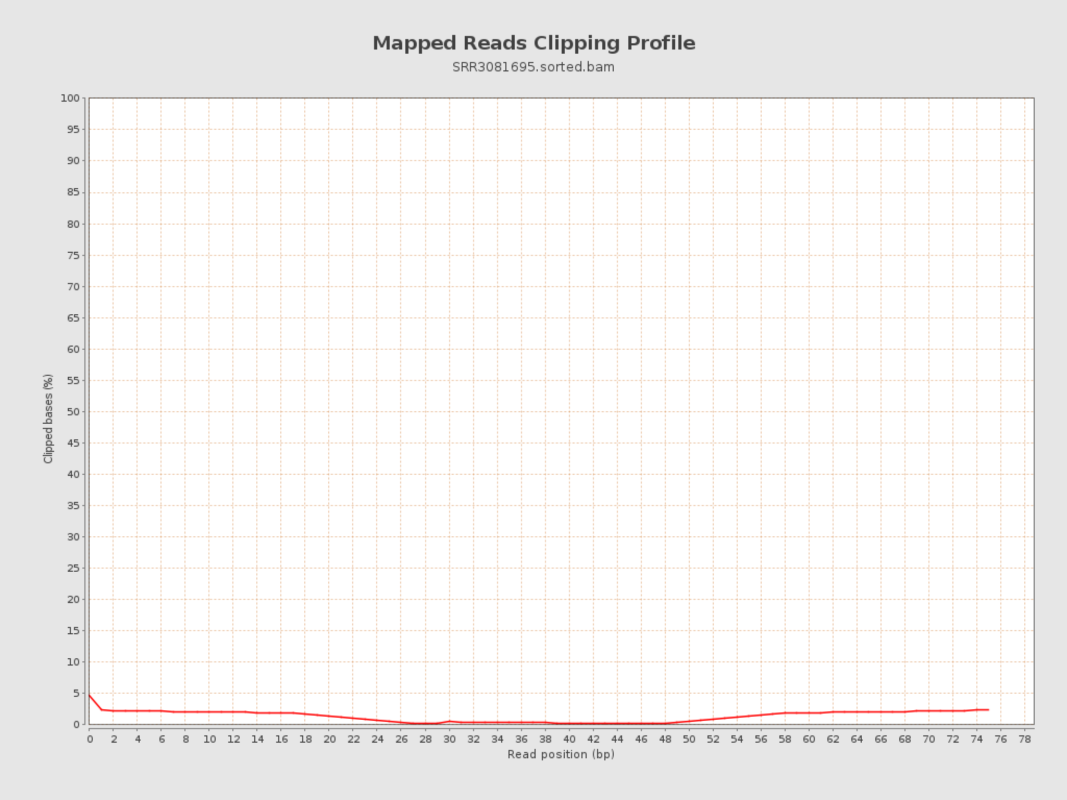
8. Results : Mapped Reads Nucleotide Content



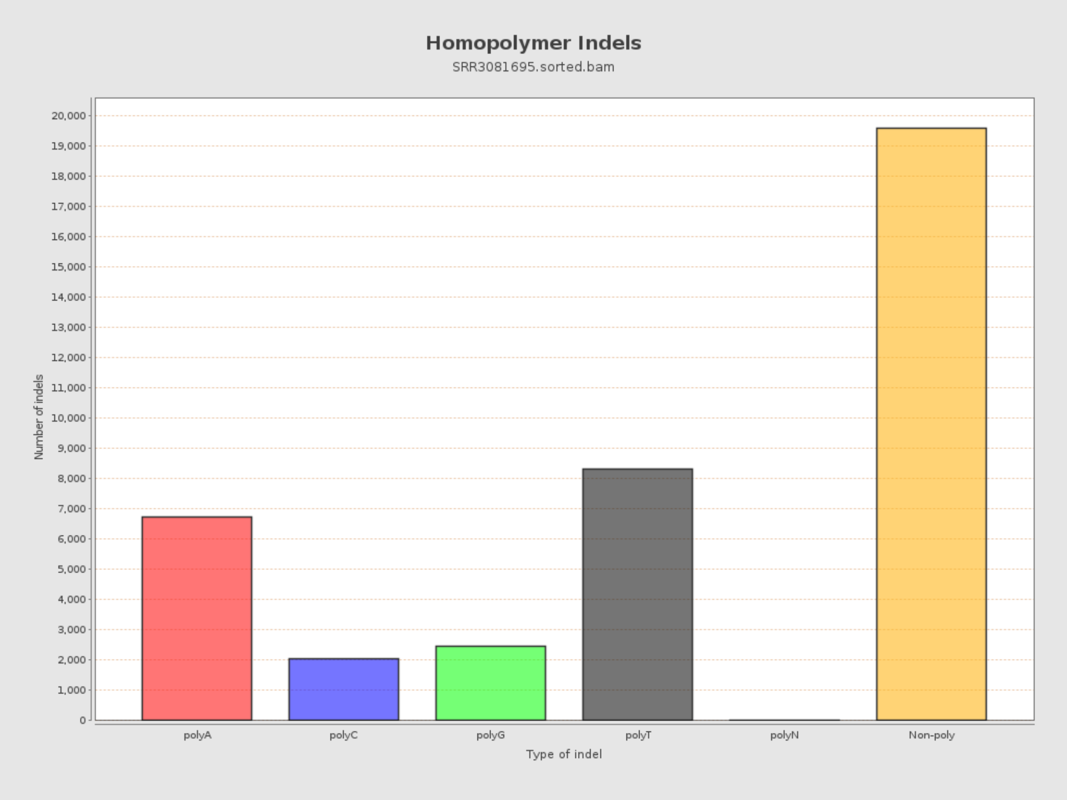
9. Results : Mapped Reads GC-content Distribution



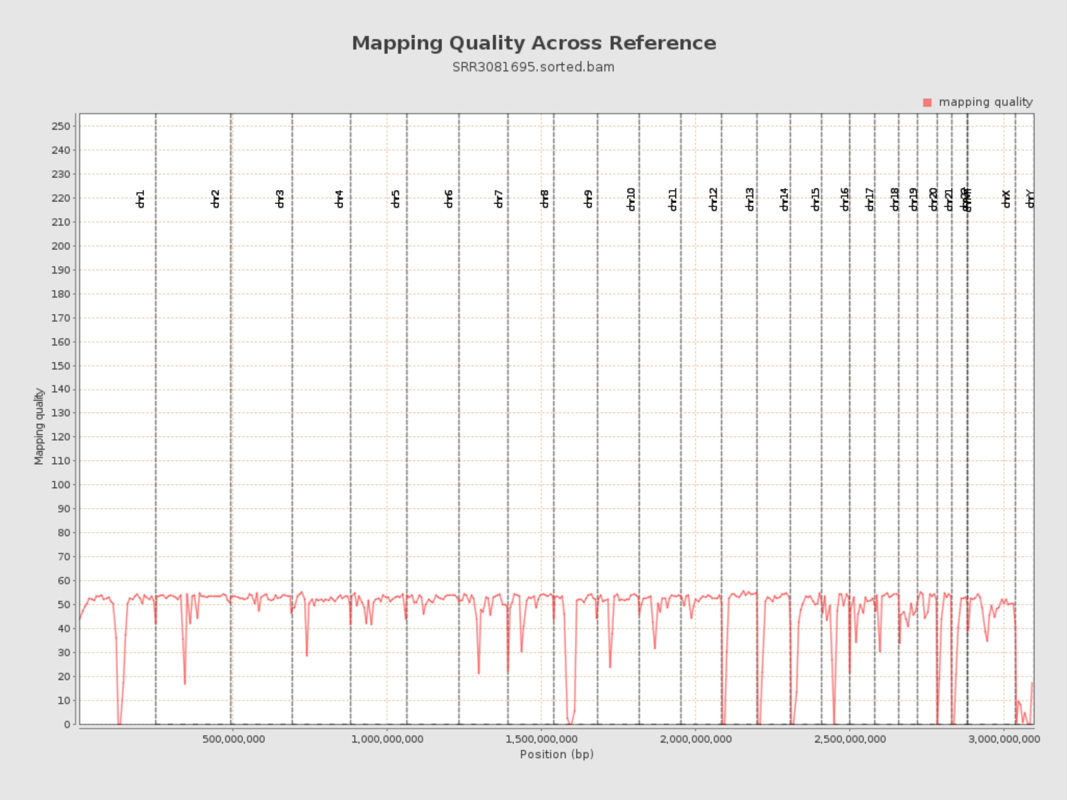
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram