Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:57:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080965.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_SRR3080965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080965.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:57:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,251,386
Mapped reads	5,487,842 / 87.79%
Unmapped reads	763,544 / 12.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	65,778 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	481,851 / 7.71%
Duplication rate	6.98%
Clipped reads	2,354,803 / 37.67%

2.2. ACGT Content

Number/percentage of A's	104,578,192 / 28.29%
Number/percentage of C's	65,223,810 / 17.64%
Number/percentage of T's	120,179,609 / 32.51%
Number/percentage of G's	78,985,231 / 21.36%
Number/percentage of N's	729,003 / 0.2%
GC Percentage	39.01%

2.3. Coverage

Mean	0.1195

Standard Deviation	0.7545

2.4. Mapping Quality

Mean Mapping Quality	47.04

2.5. Mismatches and indels

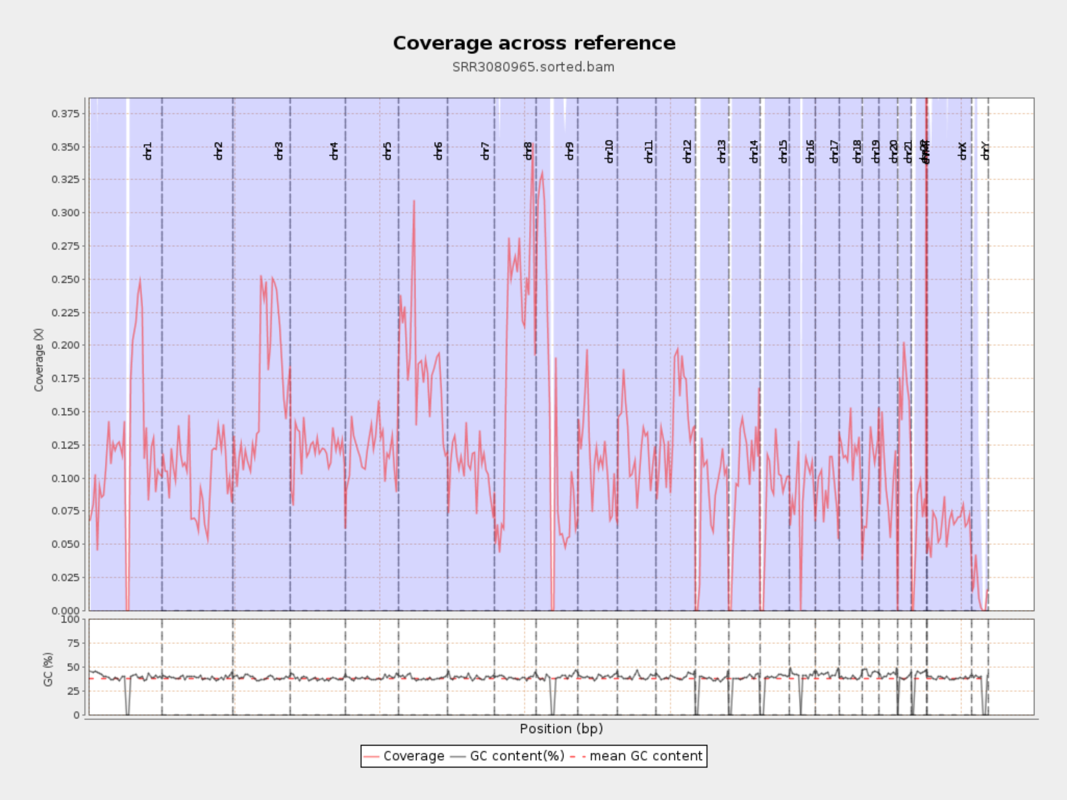
General error rate	1.01%
Mismatches	3,696,708
Insertions	29,087
Mapped reads with at least one insertion	0.52%
Deletions	81,853
Mapped reads with at least one deletion	1.48%
Homopolymer indels	49.38%

2.6. Chromosome stats

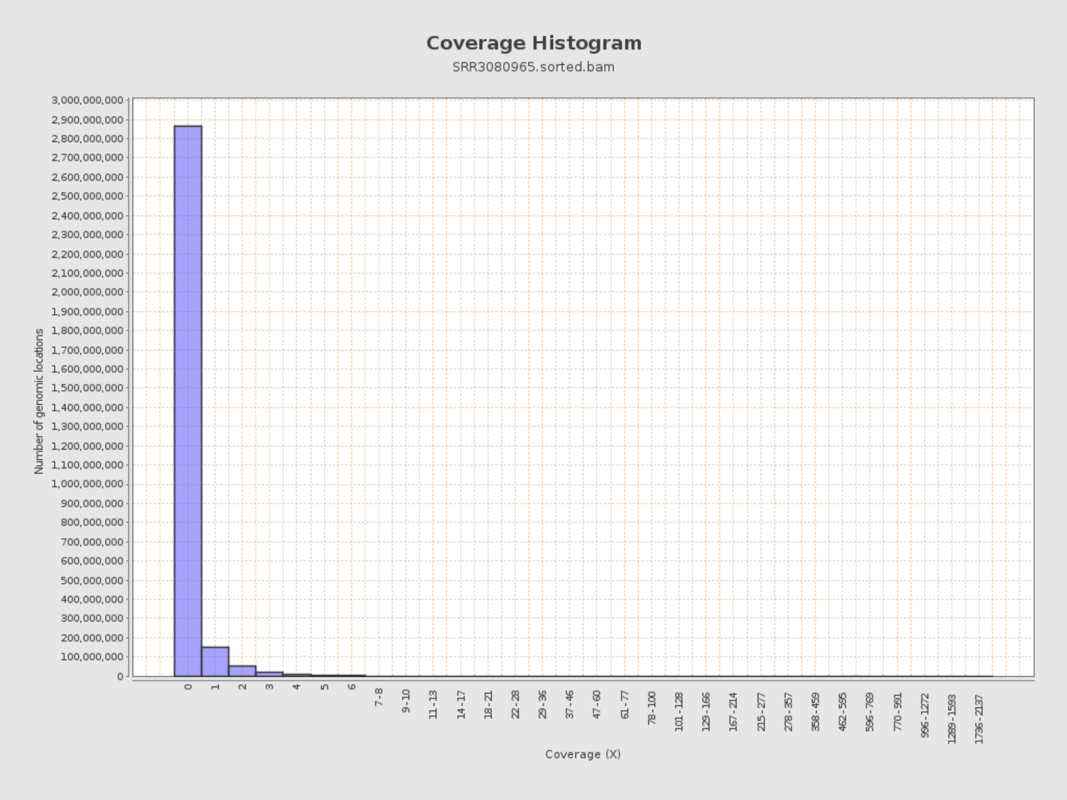
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30212331	0.1212	1.0224
chr2	243199373	24976910	0.1027	0.7257
chr3	198022430	32773723	0.1655	0.603
chr4	191154276	23133059	0.121	0.5339
chr5	180915260	21871258	0.1209	0.5094
chr6	171115067	32064784	0.1874	0.886
chr7	159138663	17426521	0.1095	0.6992

chr8	146364022	29778084	0.2035	1.4997
chr9	141213431	19521182	0.1382	0.9178
chr10	135534747	15721679	0.116	0.6206
chr11	135006516	16643422	0.1233	0.6283
chr12	133851895	18872025	0.141	0.5726
chr13	115169878	9451666	0.0821	0.4189
chr14	107349540	10726413	0.0999	0.5832
chr15	102531392	8758225	0.0854	0.4281
chr16	90354753	8001978	0.0886	0.5283
chr17	81195210	7317884	0.0901	0.4594
chr18	78077248	9365365	0.1199	1.3993
chr19	59128983	6008853	0.1016	0.8548
chr20	63025520	6194680	0.0983	0.486
chr21	48129895	7126896	0.1481	0.664
chr22	51304566	3086512	0.0602	0.3539
chrMT	16571	29072	1.7544	1.8443
chrX	155270560	10014610	0.0645	0.4098
chrY	59373566	753474	0.0127	0.2473

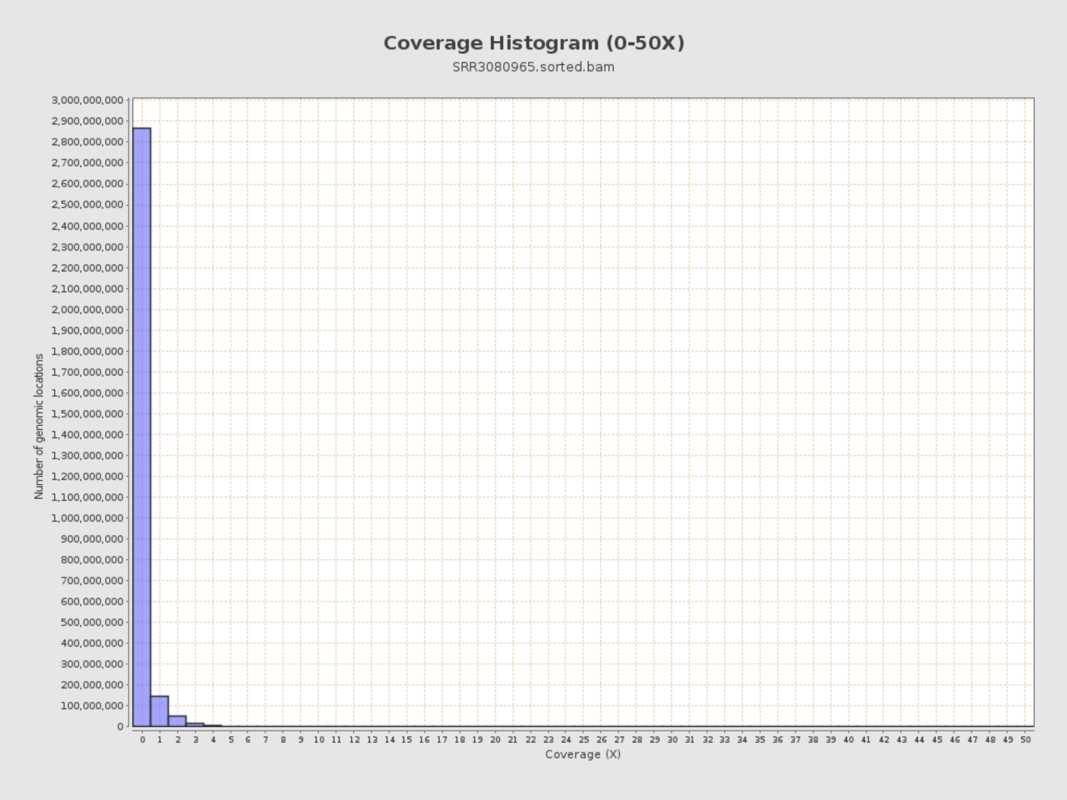
3. Results : Coverage across reference



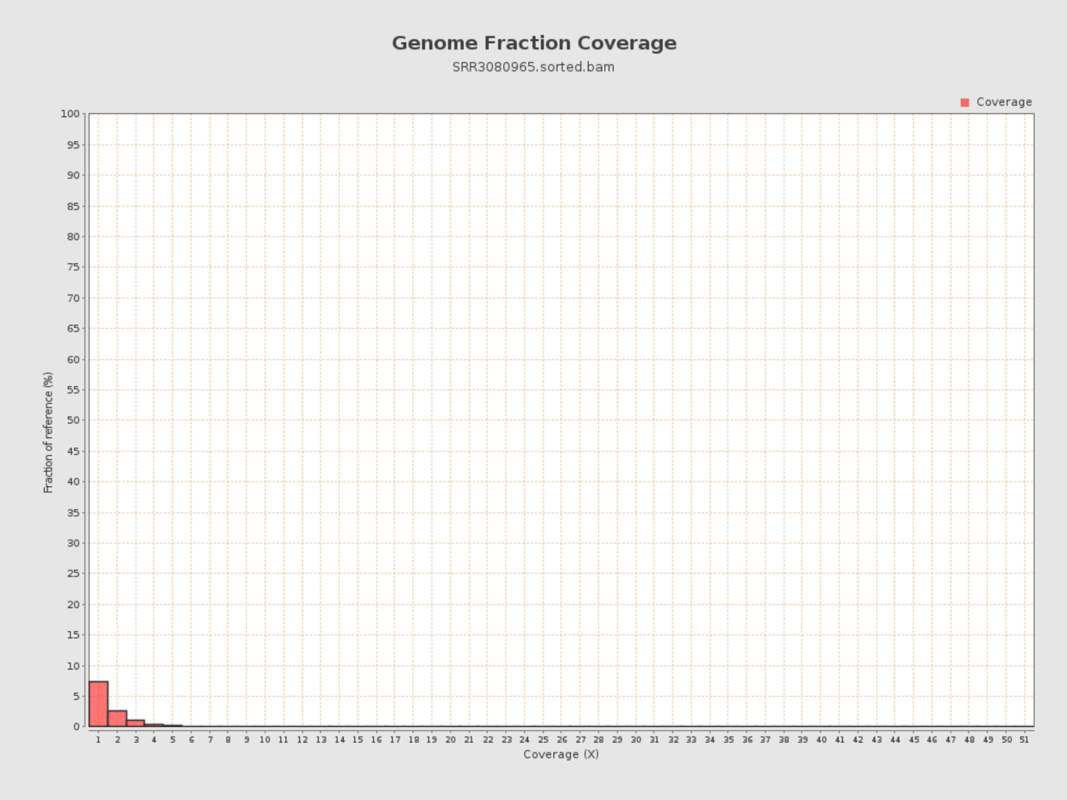
4. Results : Coverage Histogram



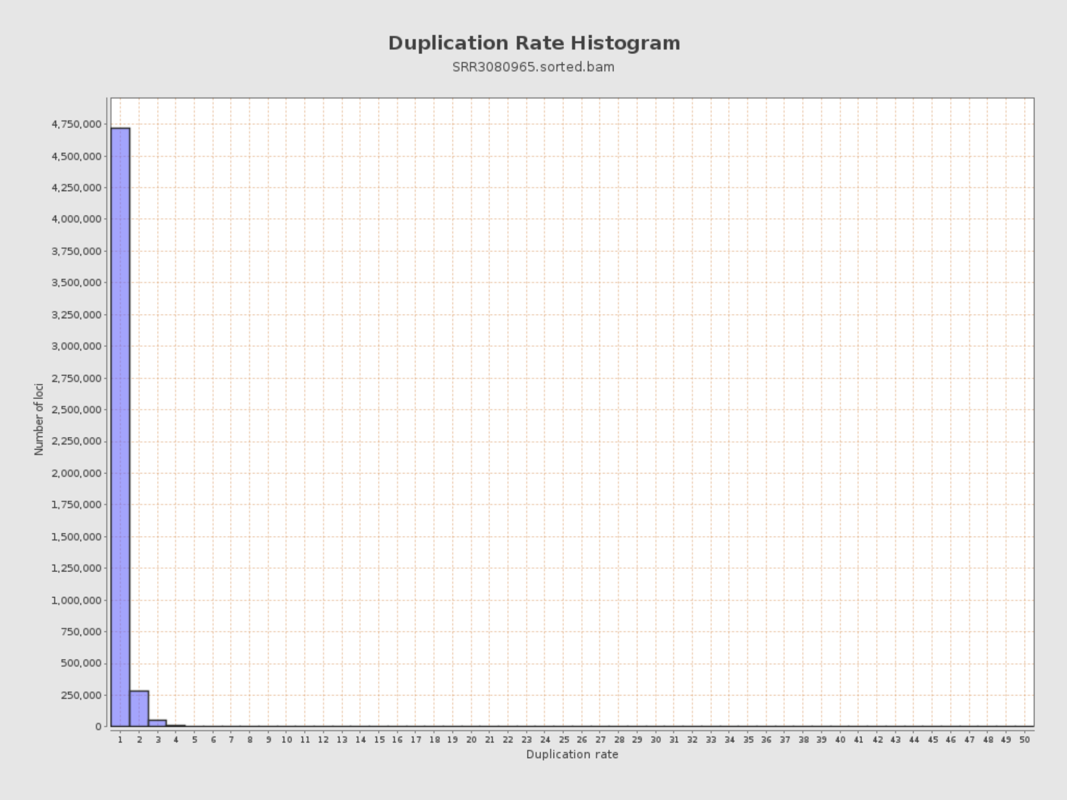
5. Results : Coverage Histogram (0-50X)



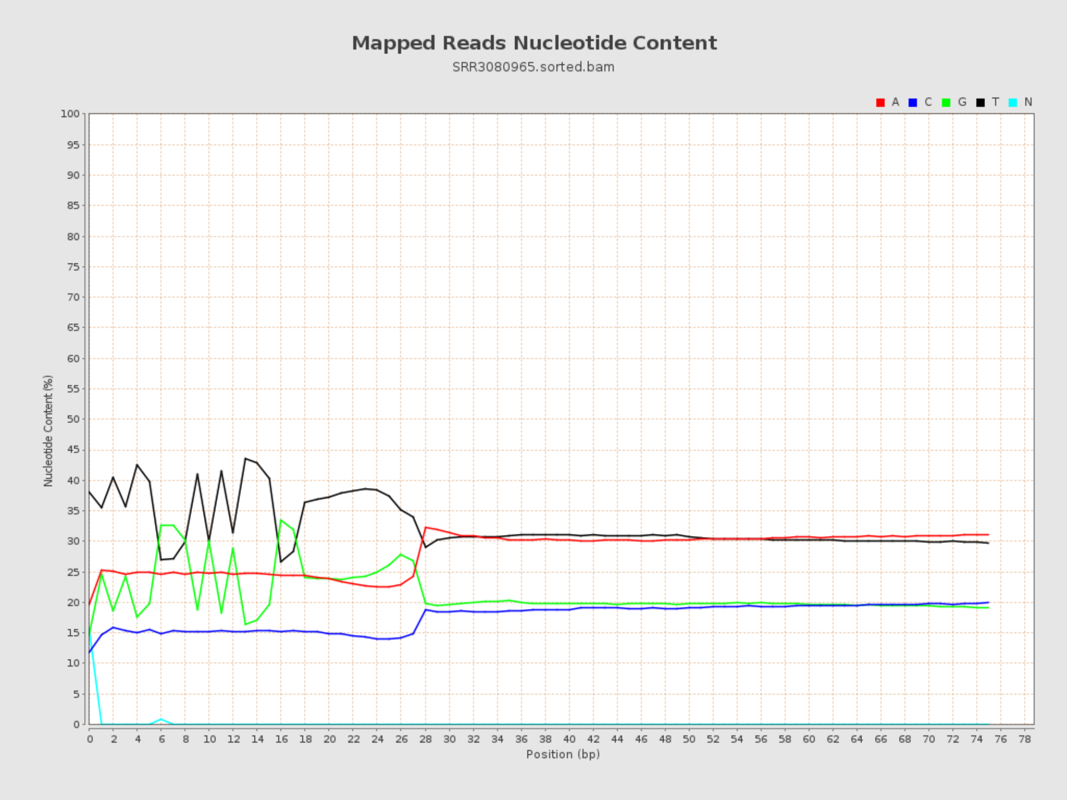
6. Results : Genome Fraction Coverage



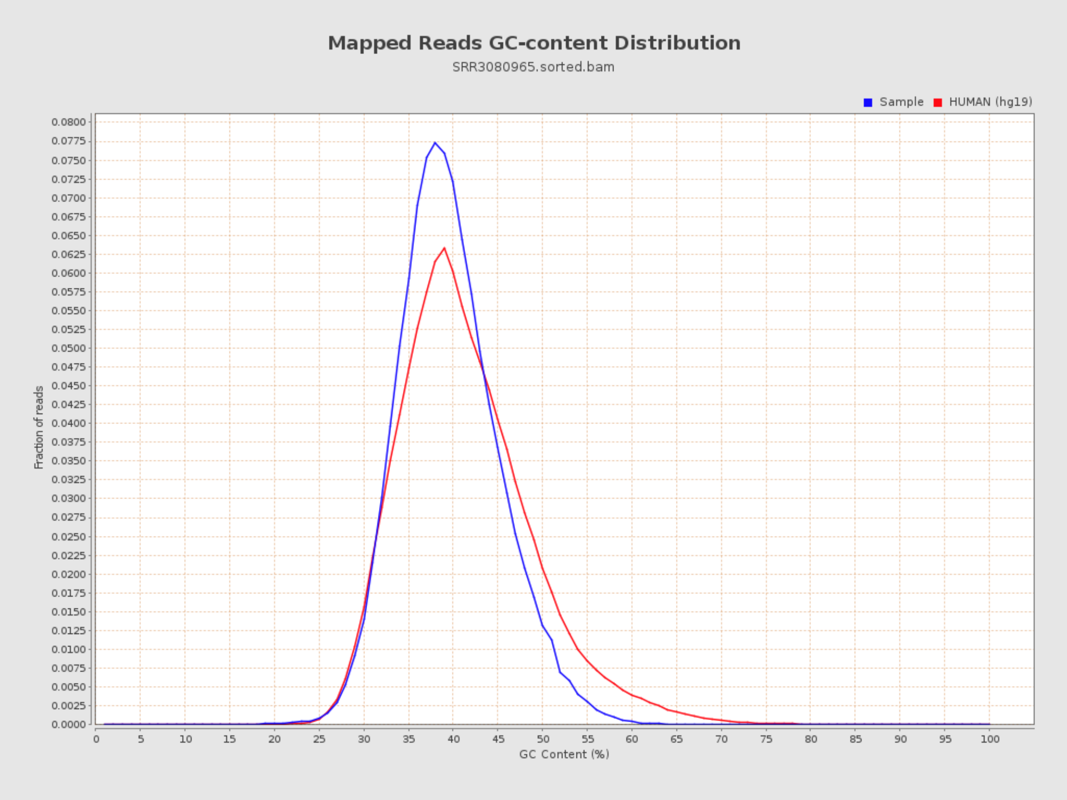
7. Results : Duplication Rate Histogram



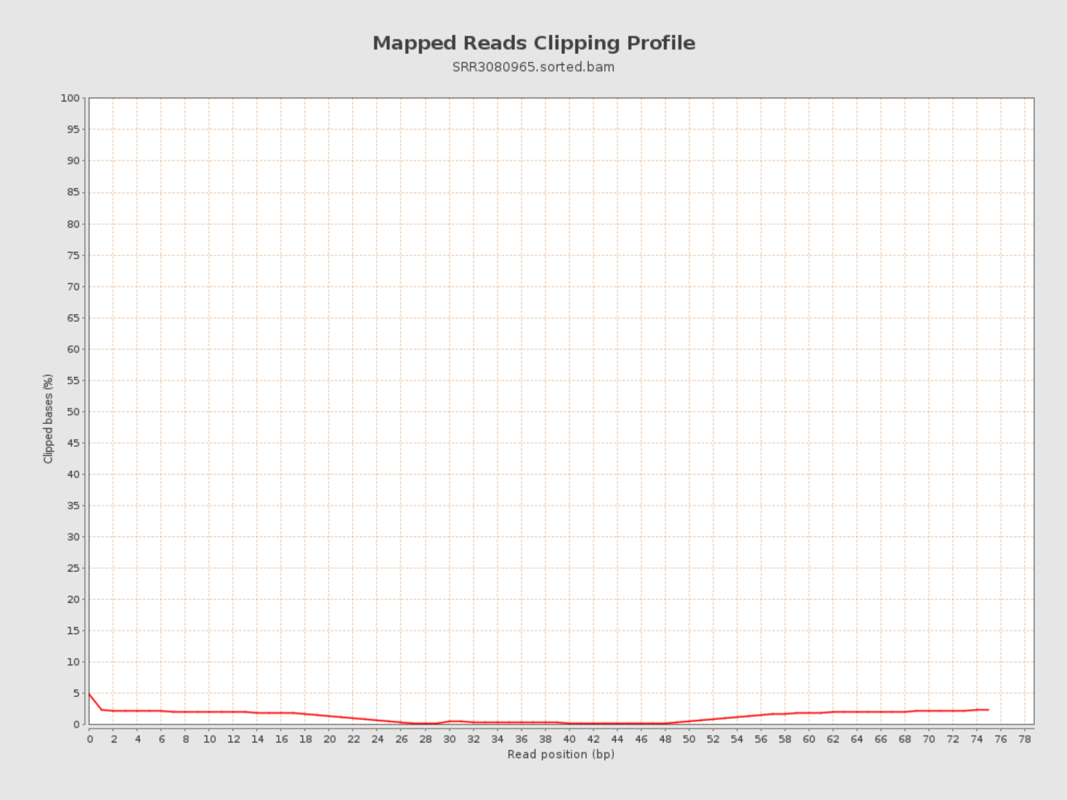
8. Results : Mapped Reads Nucleotide Content



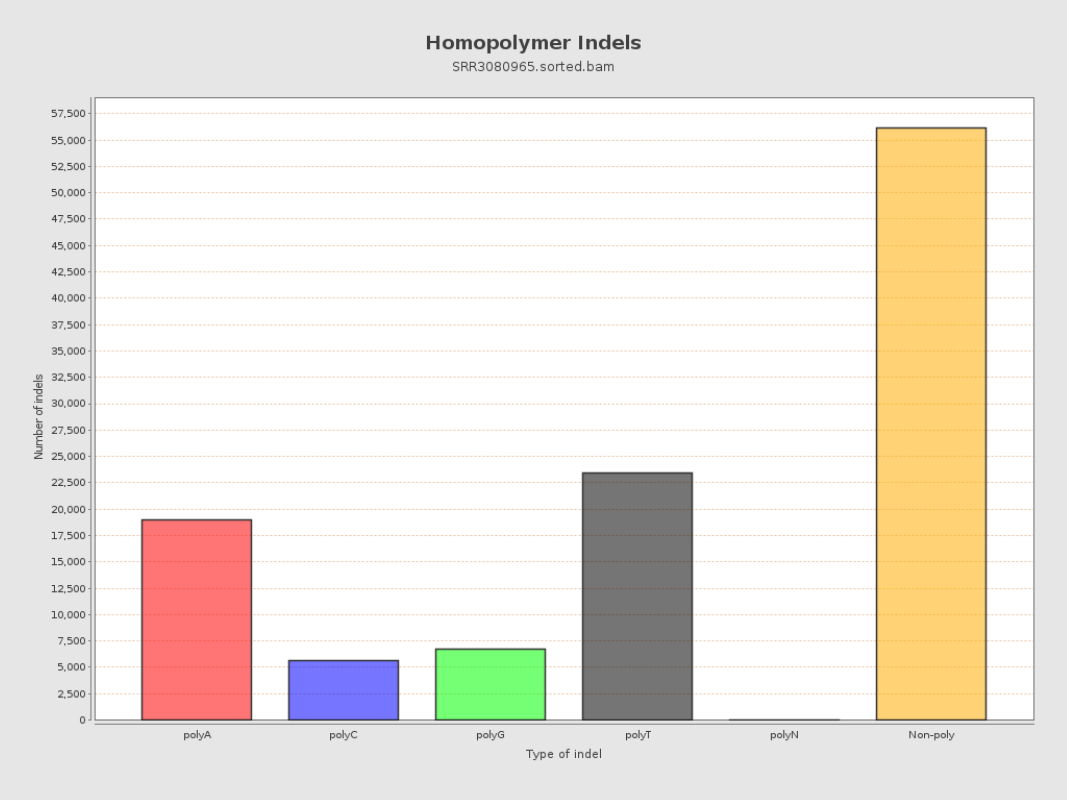
9. Results : Mapped Reads GC-content Distribution



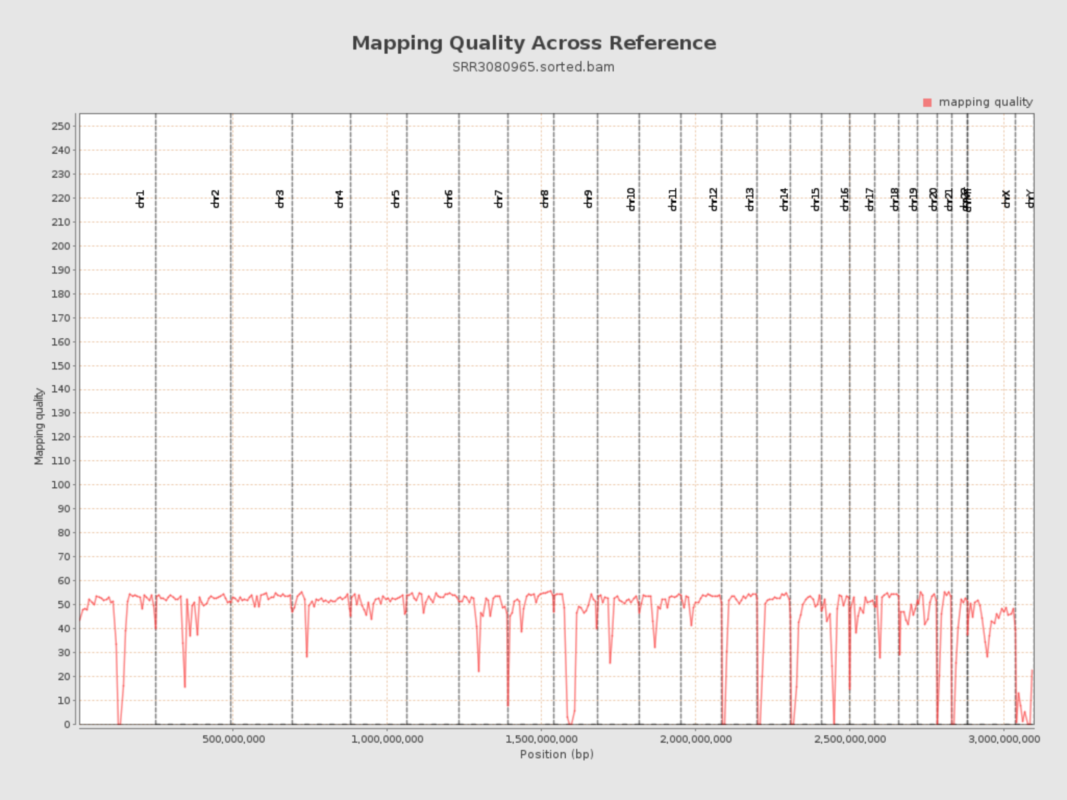
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram