Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:49:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080964.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_SRR3080964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:49:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,499,691
Mapped reads	5,737,156 / 88.27%
Unmapped reads	762,535 / 11.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	59,873 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	453,368 / 6.98%
Duplication rate	6.23%
Clipped reads	2,503,497 / 38.52%

2.2. ACGT Content

Number/percentage of A's	108,104,674 / 28.05%
Number/percentage of C's	67,915,475 / 17.62%
Number/percentage of T's	125,222,206 / 32.5%
Number/percentage of G's	83,348,762 / 21.63%
Number/percentage of N's	756,701 / 0.2%
GC Percentage	39.25%

2.3. Coverage

Mean	0.1245

Standard Deviation	0.8095

2.4. Mapping Quality

Mean Mapping Quality	46.94

2.5. Mismatches and indels

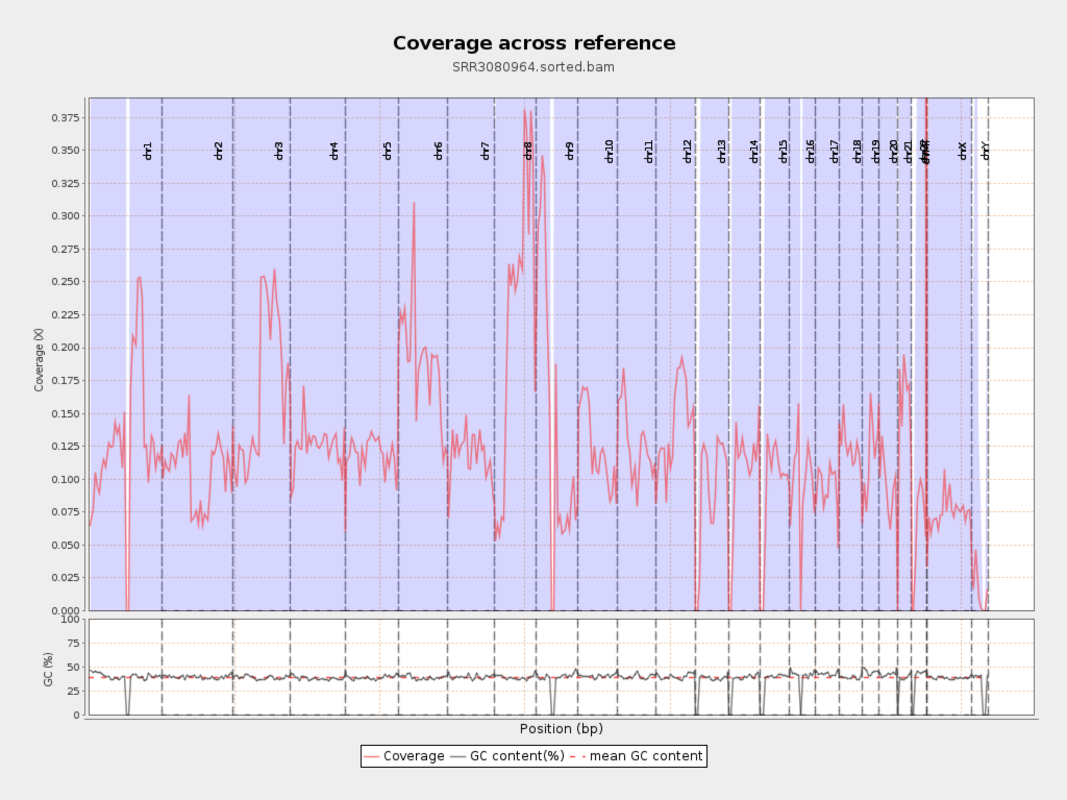
General error rate	1.01%
Mismatches	3,850,507
Insertions	30,863
Mapped reads with at least one insertion	0.53%
Deletions	86,716
Mapped reads with at least one deletion	1.5%
Homopolymer indels	49.02%

2.6. Chromosome stats

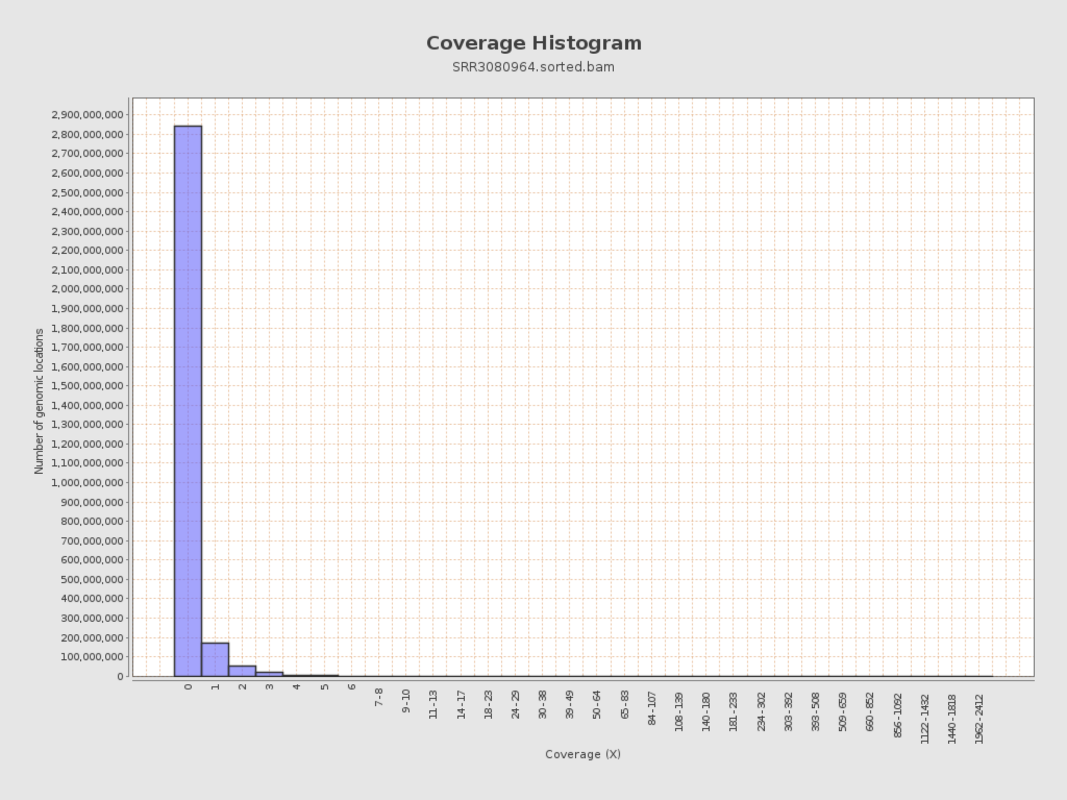
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31860460	0.1278	1.0773
chr2	243199373	25716246	0.1057	0.7749
chr3	198022430	33274021	0.168	0.5831
chr4	191154276	23828051	0.1247	0.5408
chr5	180915260	21543478	0.1191	0.4869
chr6	171115067	32582898	0.1904	0.92
chr7	159138663	18894678	0.1187	0.7226

chr8	146364022	32662938	0.2232	1.6394
chr9	141213431	19774446	0.14	1.0299
chr10	135534747	16947040	0.125	0.6701
chr11	135006516	17094359	0.1266	0.6337
chr12	133851895	18985332	0.1418	0.5623
chr13	115169878	10308372	0.0895	0.4171
chr14	107349540	10829506	0.1009	0.6049
chr15	102531392	9508395	0.0927	0.4264
chr16	90354753	8796433	0.0974	0.5755
chr17	81195210	7507737	0.0925	0.4463
chr18	78077248	9733888	0.1247	1.7716
chr19	59128983	6944012	0.1174	0.8992
chr20	63025520	6009908	0.0954	0.4851
chr21	48129895	7212407	0.1499	0.676
chr22	51304566	3071865	0.0599	0.3343
chrMT	16571	99981	6.0335	4.3519
chrX	155270560	11482942	0.074	0.4356
chrY	59373566	822036	0.0138	0.2717

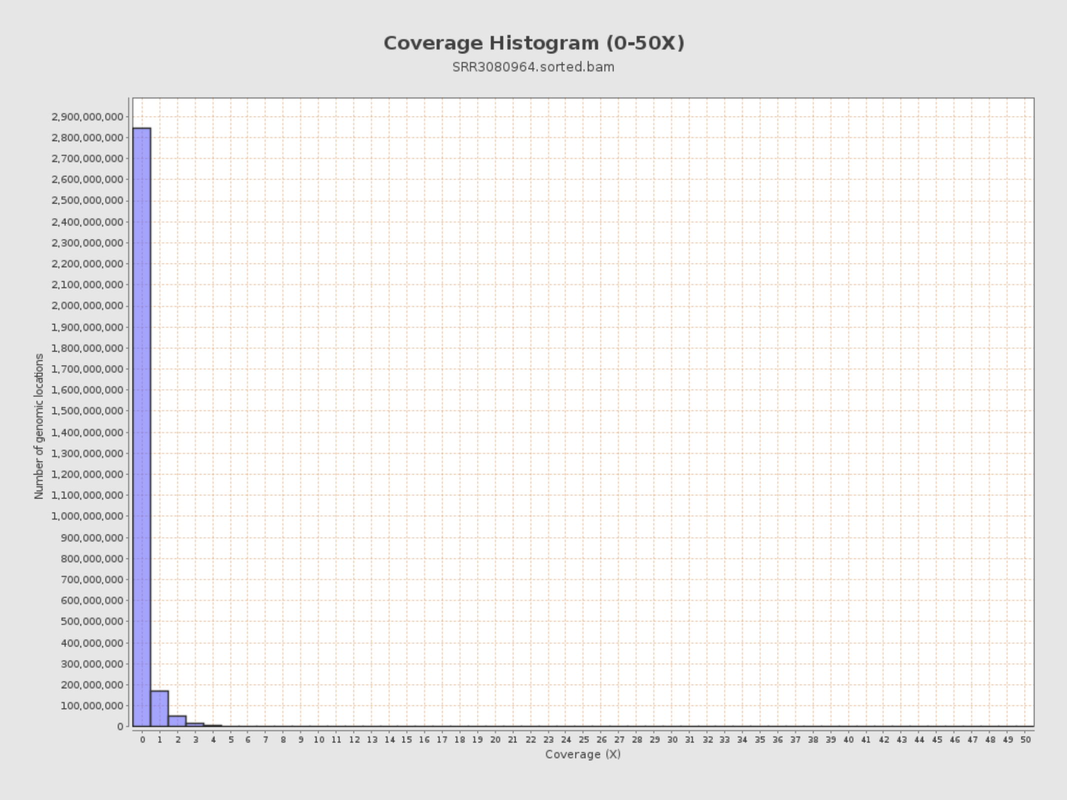
3. Results : Coverage across reference



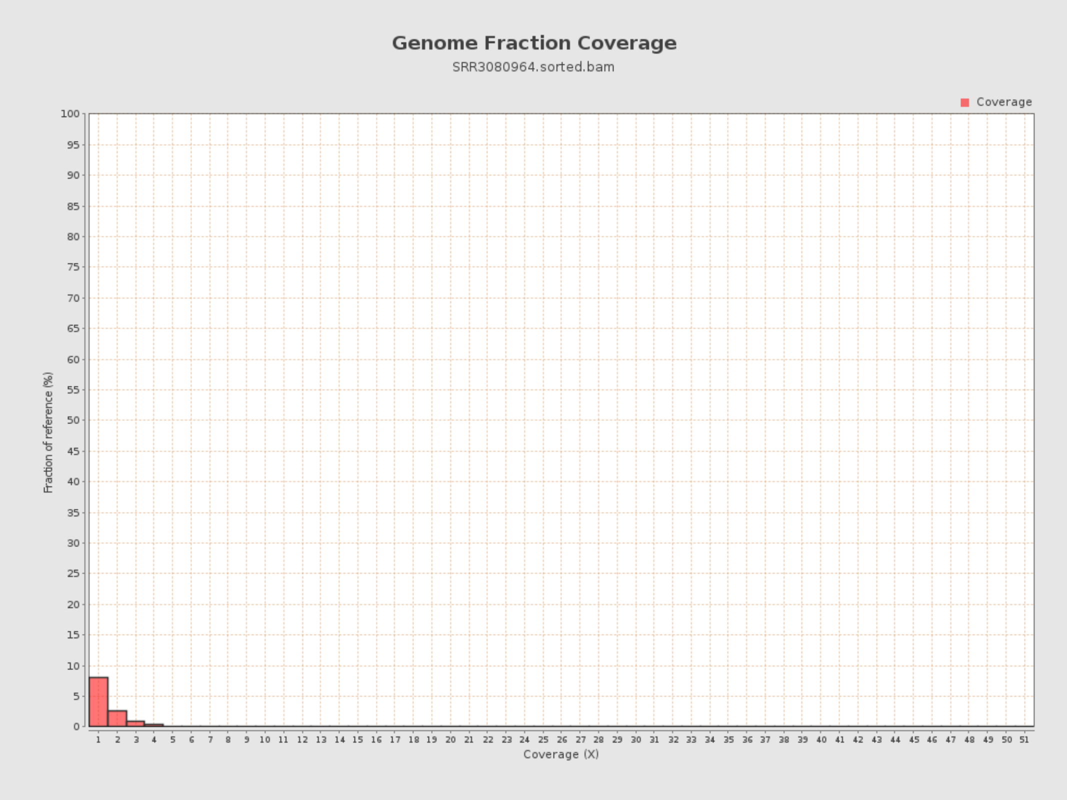
4. Results : Coverage Histogram



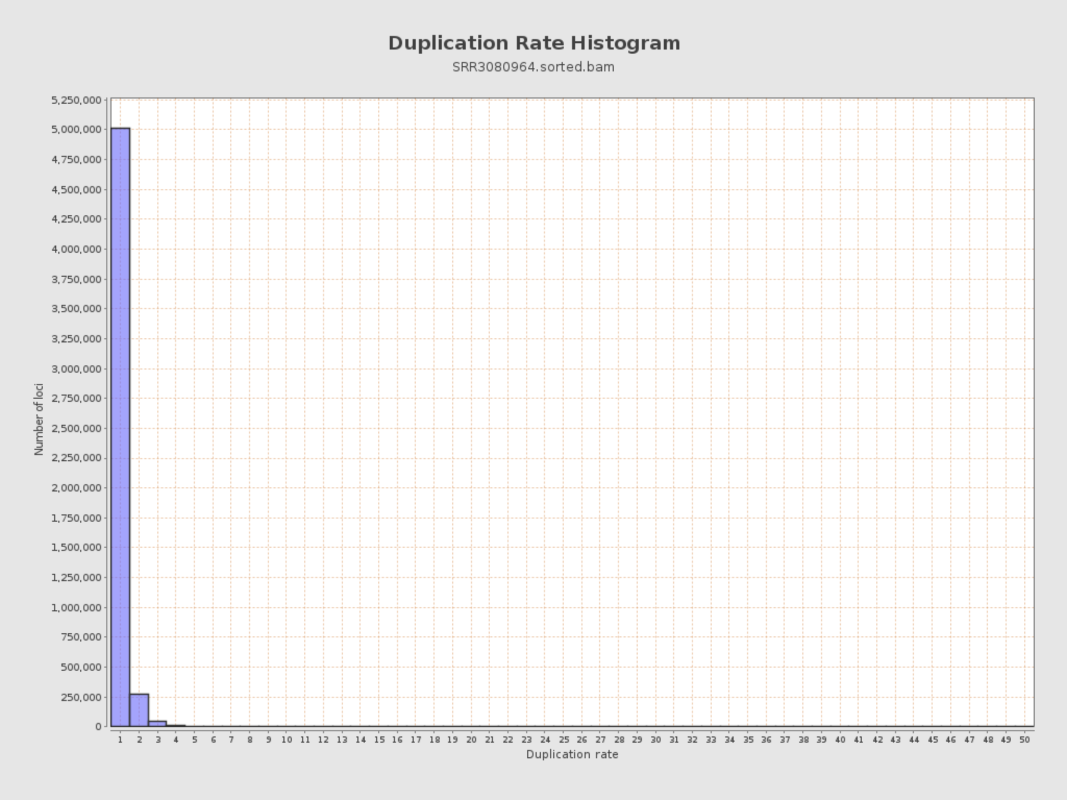
5. Results : Coverage Histogram (0-50X)



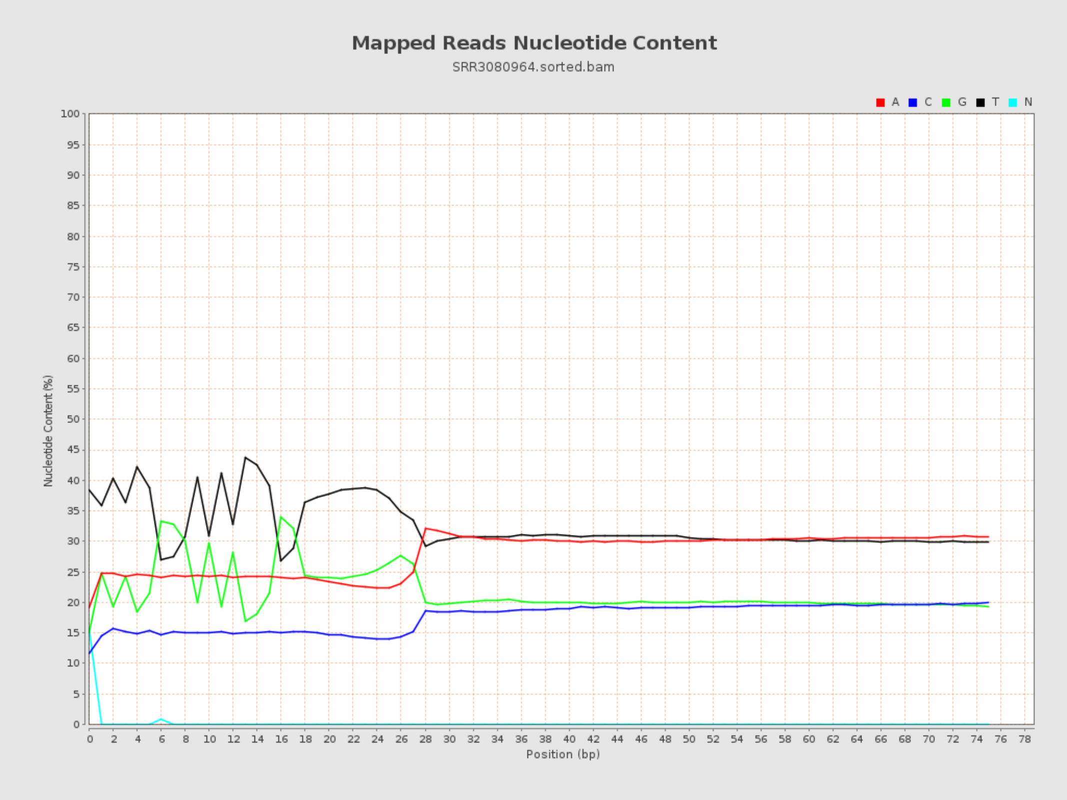
6. Results : Genome Fraction Coverage



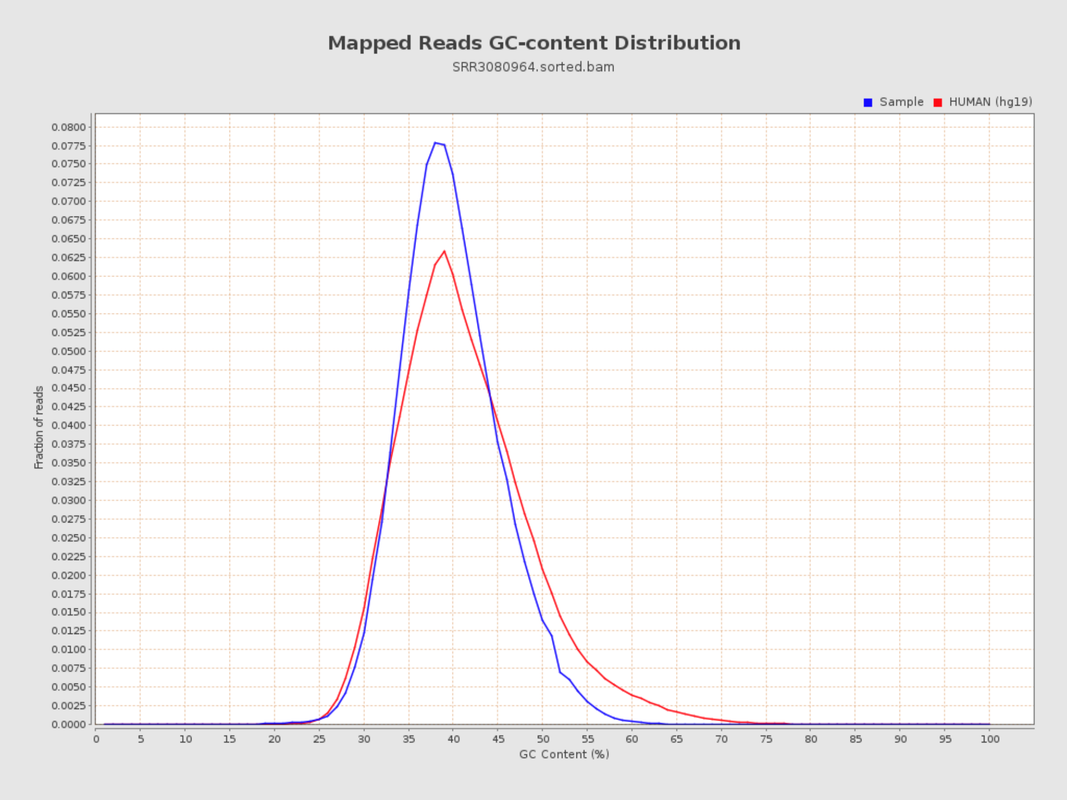
7. Results : Duplication Rate Histogram



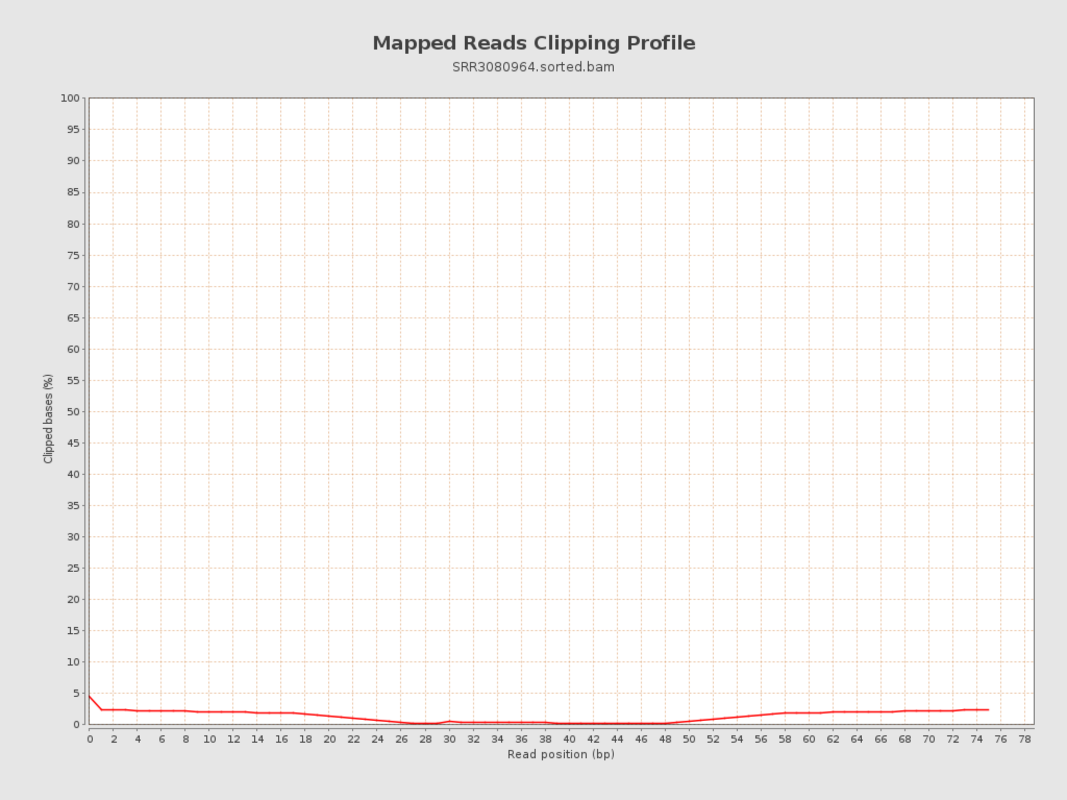
8. Results : Mapped Reads Nucleotide Content



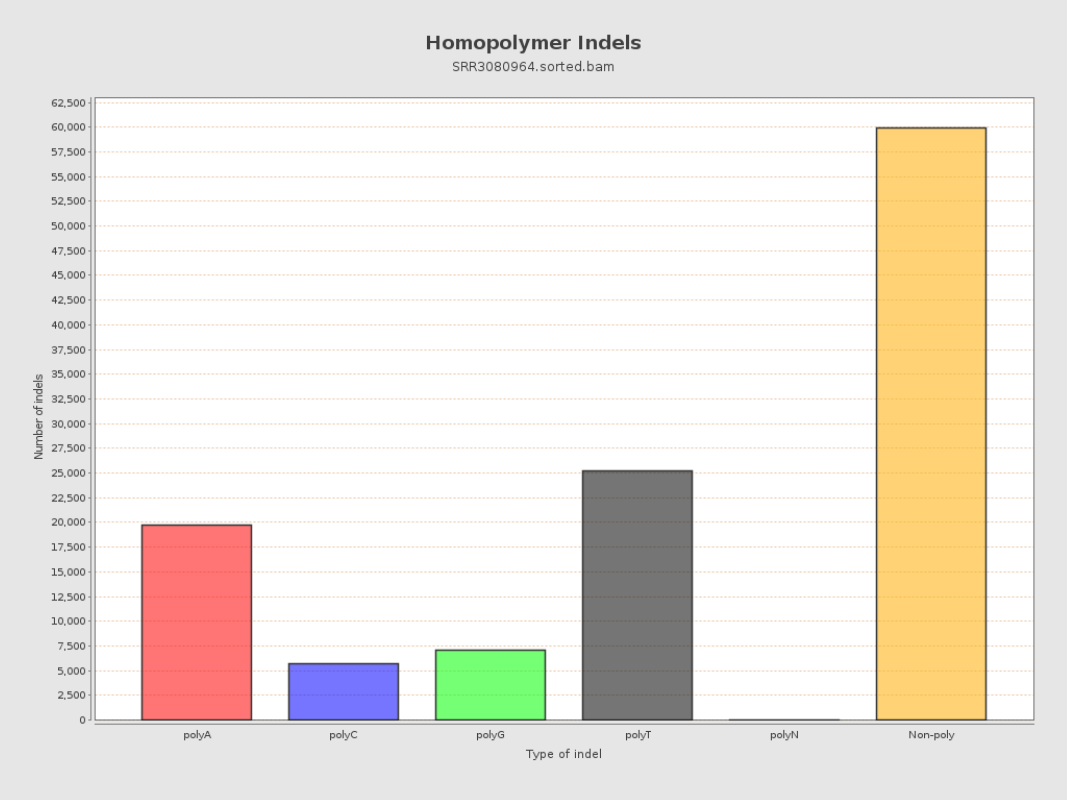
9. Results : Mapped Reads GC-content Distribution



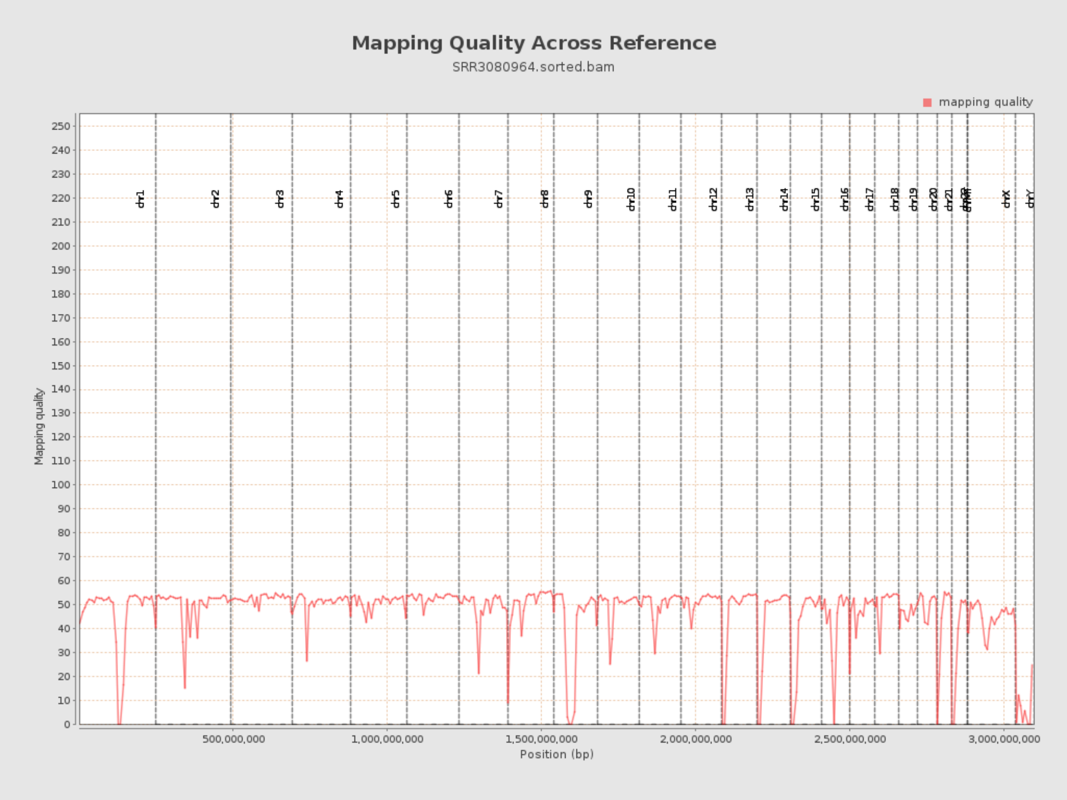
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram