Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:12:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080651.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_SRR3080651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080651.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:12:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,256,263
Mapped reads	1,139,288 / 90.69%
Unmapped reads	116,975 / 9.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,186 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	37,284 / 2.97%
Duplication rate	2.85%
Clipped reads	519,659 / 41.37%

2.2. ACGT Content

Number/percentage of A's	20,269,236 / 26.81%
Number/percentage of C's	14,168,233 / 18.74%
Number/percentage of T's	23,656,580 / 31.3%
Number/percentage of G's	17,492,437 / 23.14%
Number/percentage of N's	3,263 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2074

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

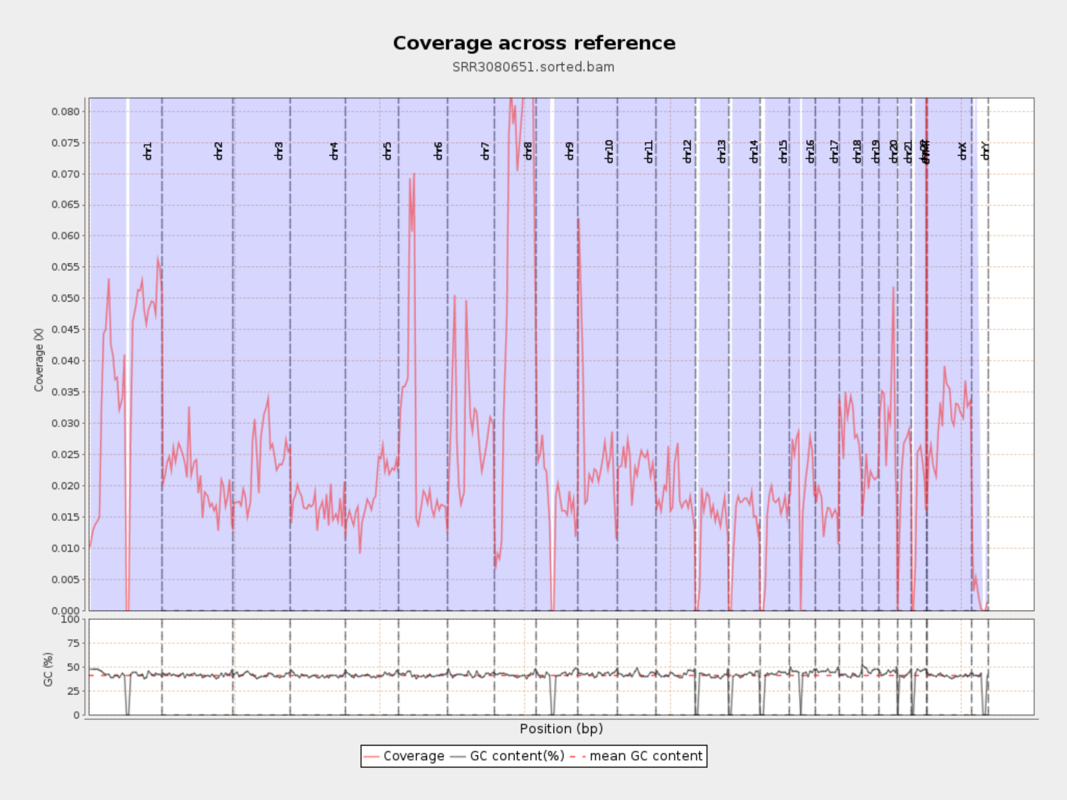
General error rate	0.69%
Mismatches	511,137
Insertions	5,608
Mapped reads with at least one insertion	0.49%
Deletions	17,582
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.72%

2.6. Chromosome stats

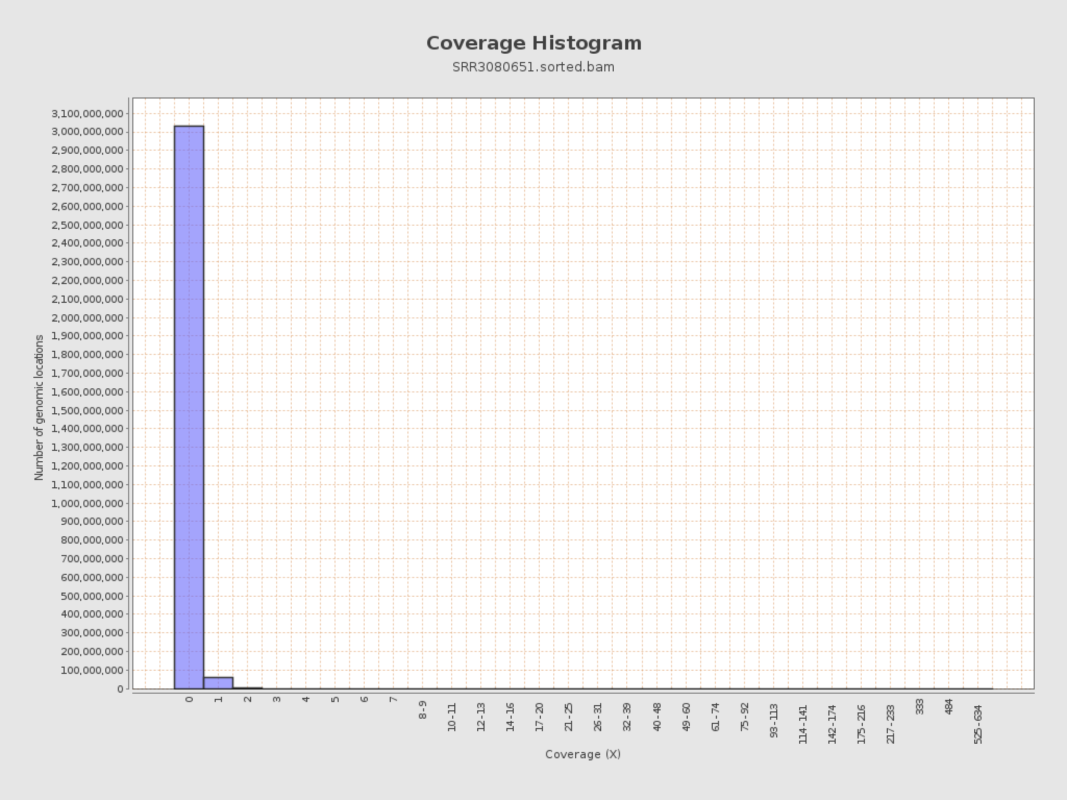
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9267060	0.0372	0.2482
chr2	243199373	5124936	0.0211	0.3135
chr3	198022430	4657013	0.0235	0.1688
chr4	191154276	3218082	0.0168	0.1448
chr5	180915260	3388552	0.0187	0.1502
chr6	171115067	4629674	0.0271	0.2124
chr7	159138663	4736314	0.0298	0.331

chr8	146364022	8855027	0.0605	0.2924
chr9	141213431	2407246	0.017	0.1588
chr10	135534747	3590686	0.0265	0.1858
chr11	135006516	3141032	0.0233	0.1749
chr12	133851895	2485847	0.0186	0.1499
chr13	115169878	1570926	0.0136	0.1284
chr14	107349540	1504456	0.014	0.1322
chr15	102531392	1419899	0.0138	0.135
chr16	90354753	1969862	0.0218	0.1655
chr17	81195210	1286438	0.0158	0.1399
chr18	78077248	2326707	0.0298	0.2287
chr19	59128983	1255669	0.0212	0.1783
chr20	63025520	2013269	0.0319	0.1992
chr21	48129895	1049937	0.0218	0.1645
chr22	51304566	829353	0.0162	0.14
chrMT	16571	5024	0.3032	0.6337
chrX	155270560	4745364	0.0306	0.1986
chrY	59373566	139890	0.0024	0.0542

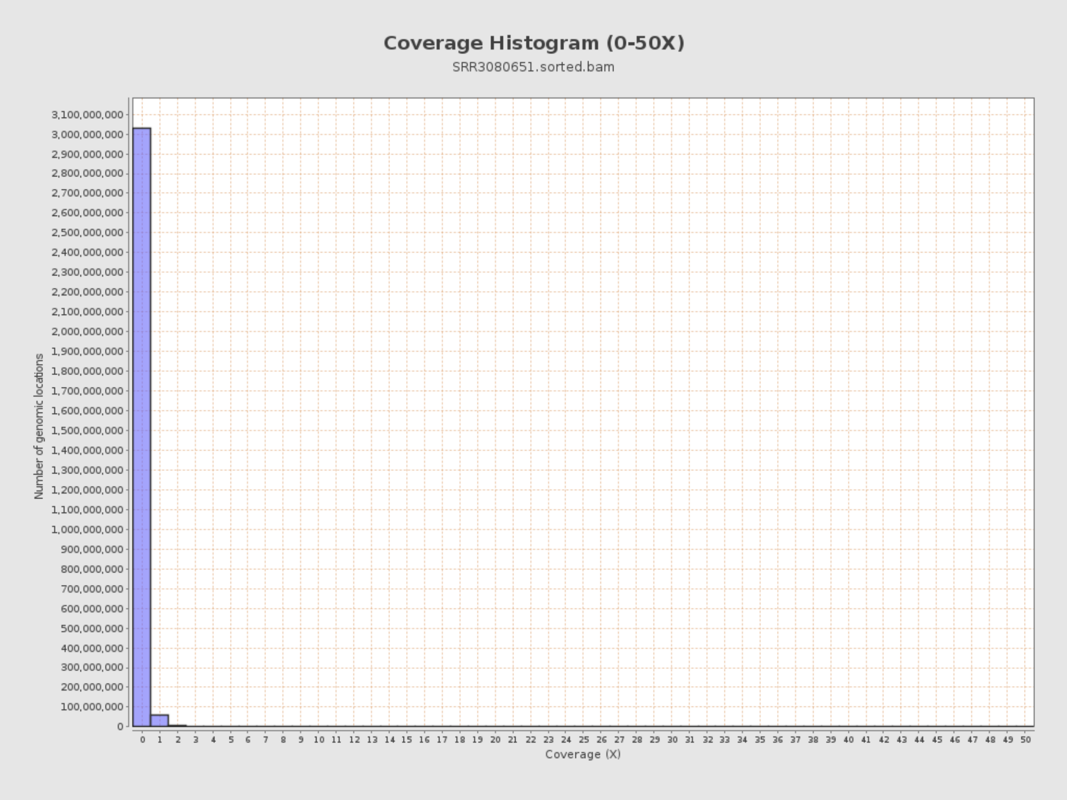
3. Results : Coverage across reference



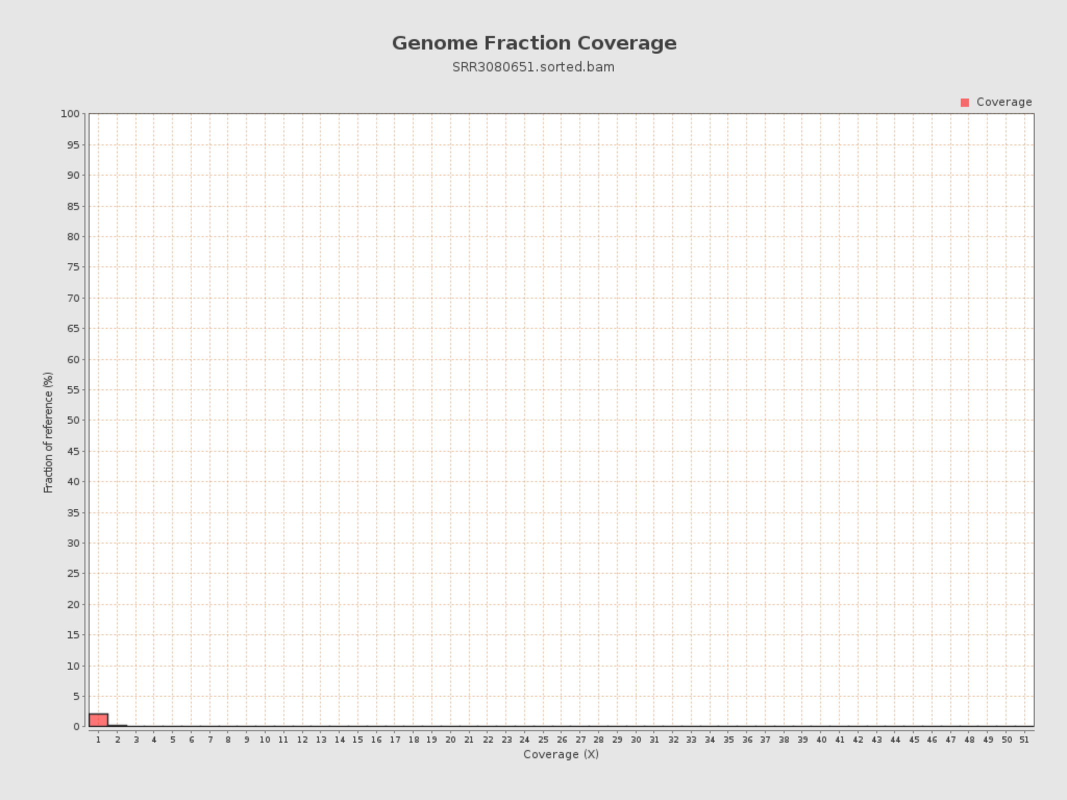
4. Results : Coverage Histogram



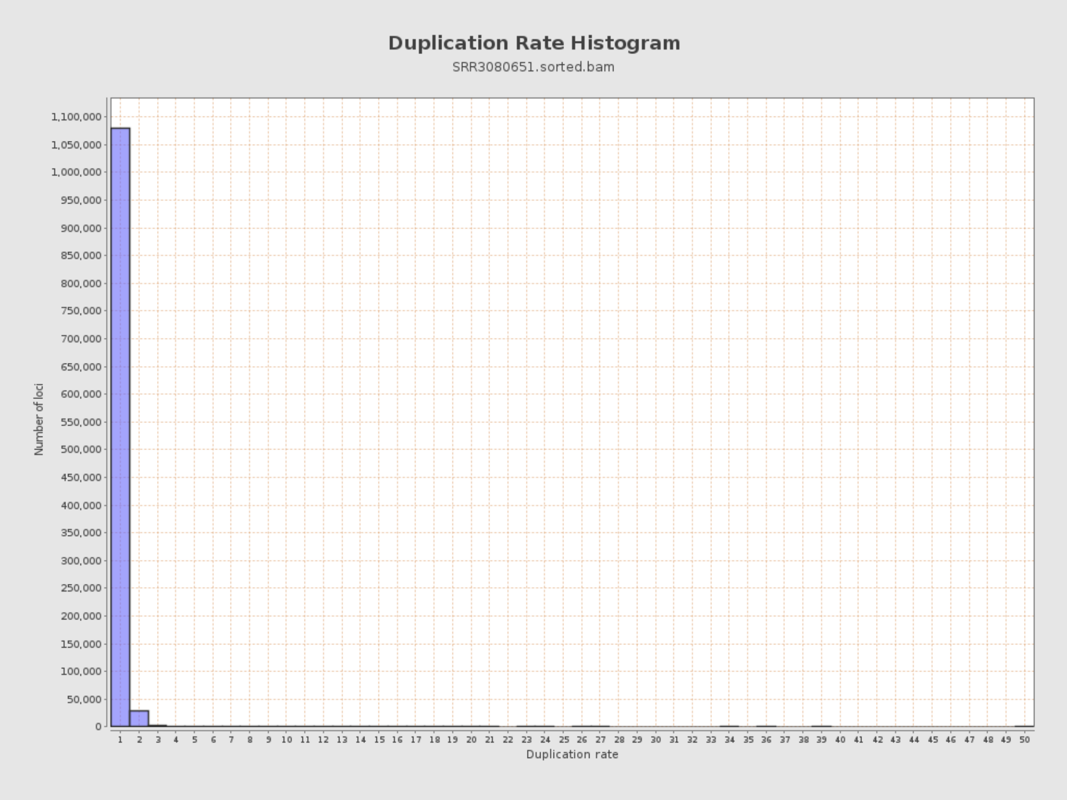
5. Results : Coverage Histogram (0-50X)



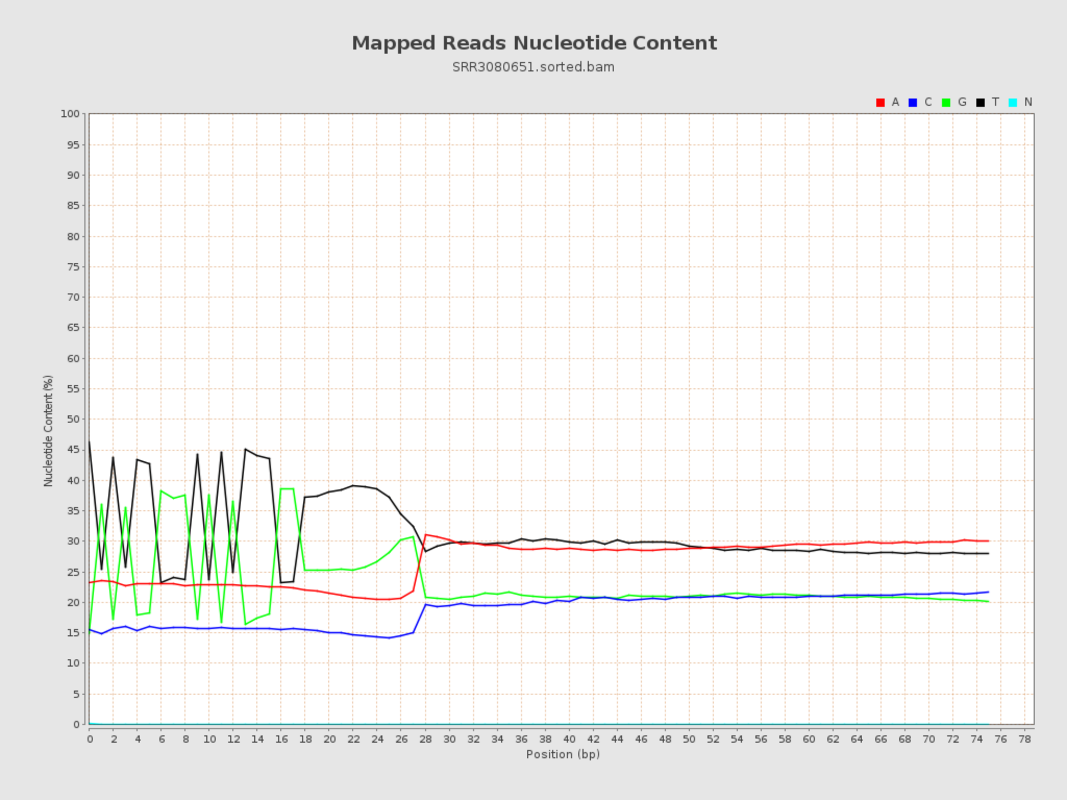
6. Results : Genome Fraction Coverage



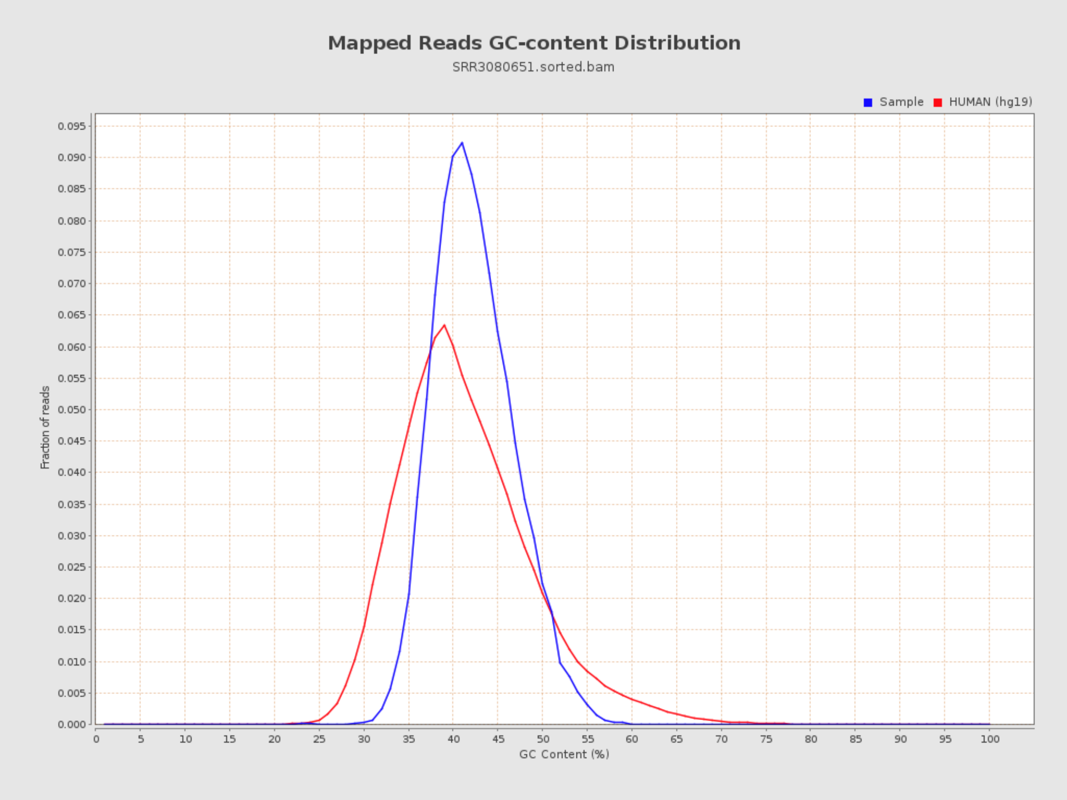
7. Results : Duplication Rate Histogram



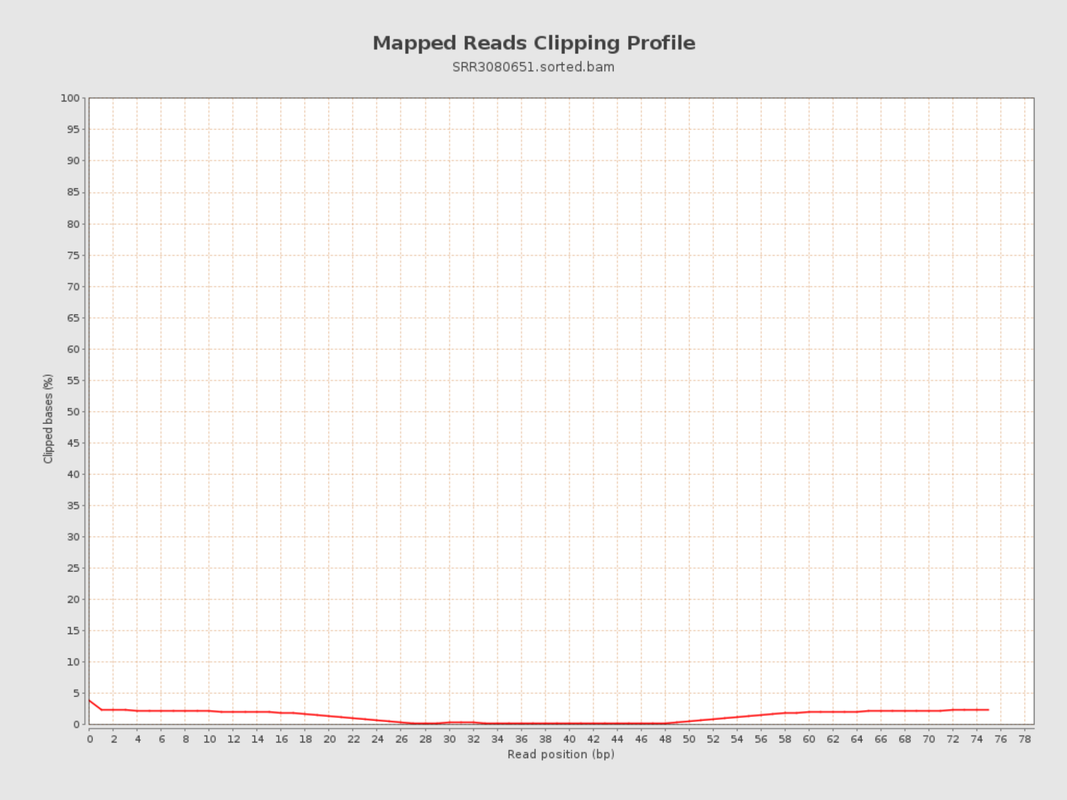
8. Results : Mapped Reads Nucleotide Content



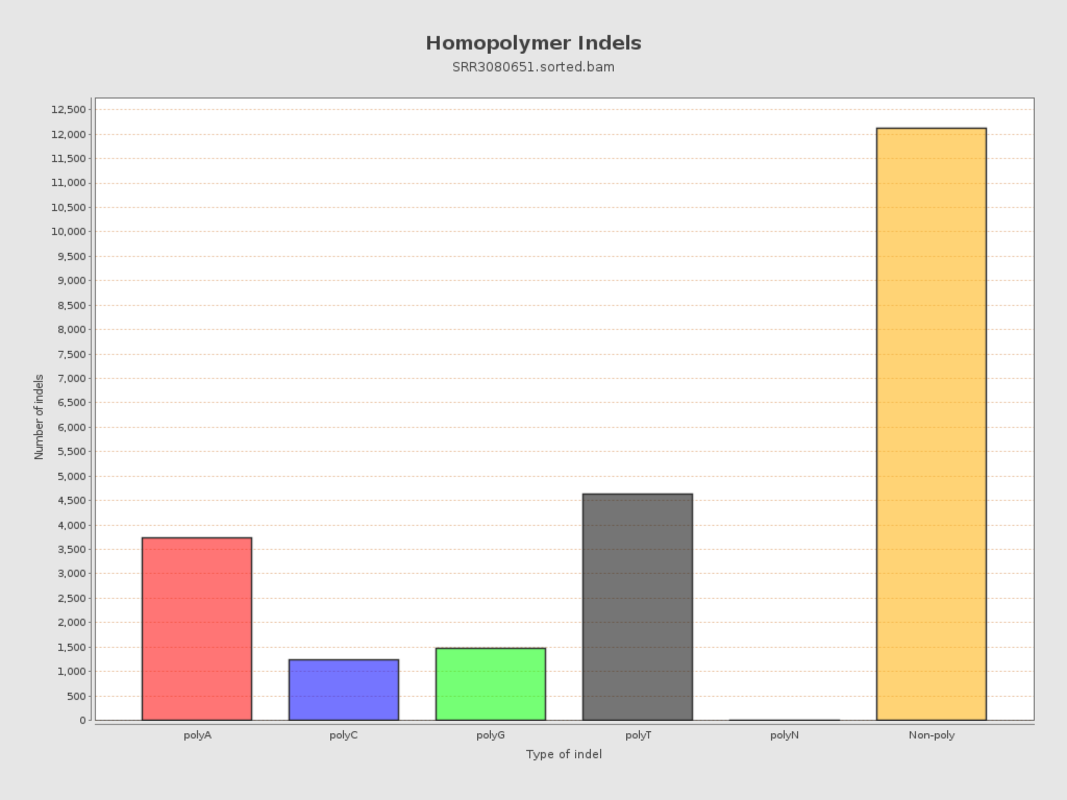
9. Results : Mapped Reads GC-content Distribution



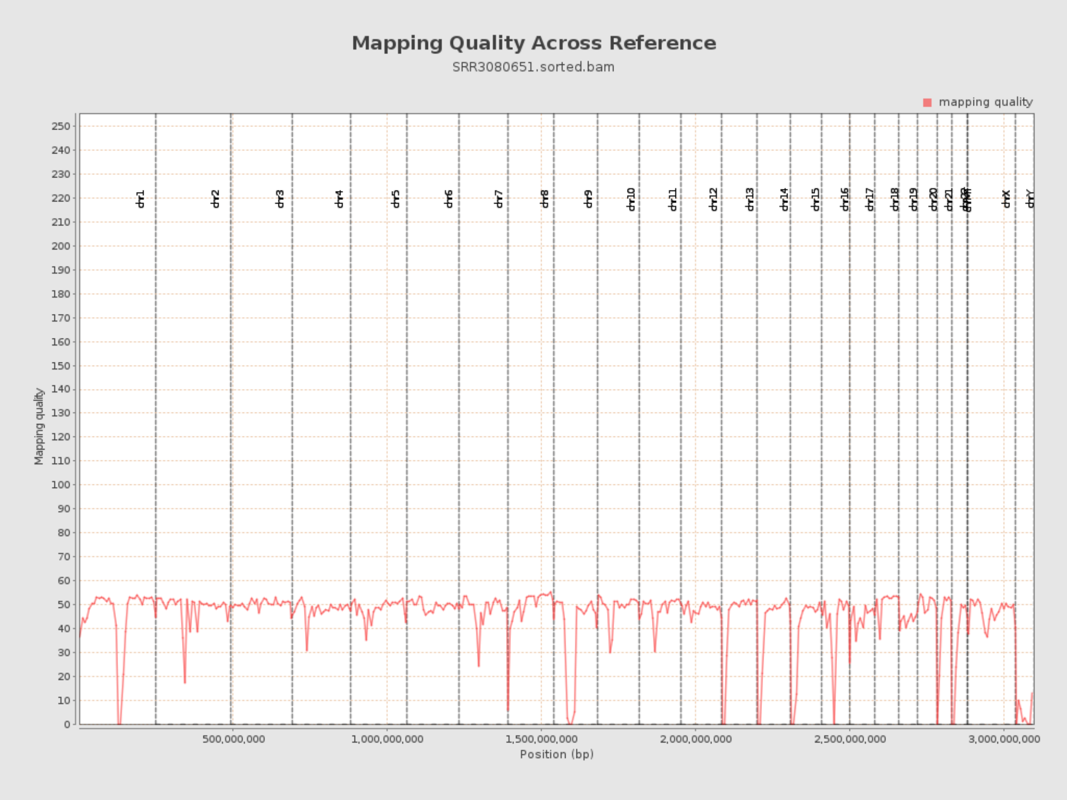
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram