Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:55:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080710.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_SRR3080710 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080710.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:55:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080710.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,158,424
Mapped reads	1,966,346 / 91.1%
Unmapped reads	192,078 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,309 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	102,619 / 4.75%
Duplication rate	4.49%
Clipped reads	756,227 / 35.04%

2.2. ACGT Content

Number/percentage of A's	37,687,384 / 28.14%
Number/percentage of C's	24,743,641 / 18.48%
Number/percentage of T's	42,629,069 / 31.84%
Number/percentage of G's	28,842,865 / 21.54%
Number/percentage of N's	2,094 / 0%
GC Percentage	40.02%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.3405

2.4. Mapping Quality

Mean Mapping Quality	46.64

2.5. Mismatches and indels

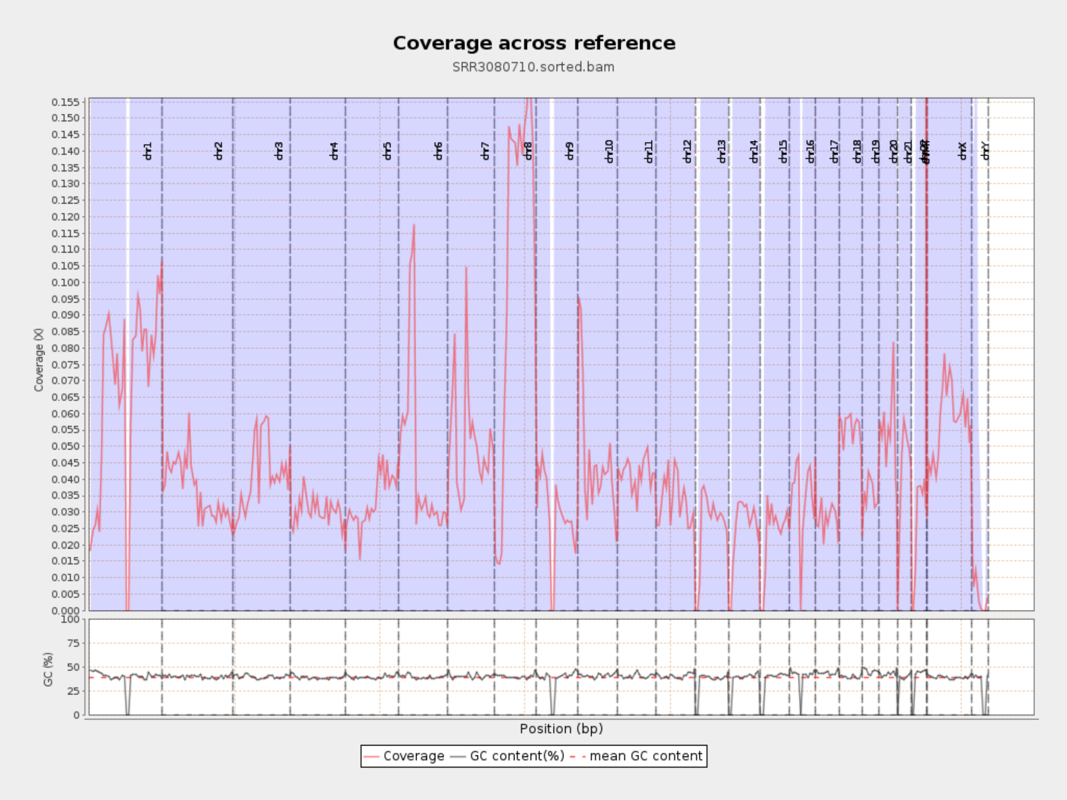
General error rate	0.8%
Mismatches	1,054,127
Insertions	9,533
Mapped reads with at least one insertion	0.48%
Deletions	28,027
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.92%

2.6. Chromosome stats

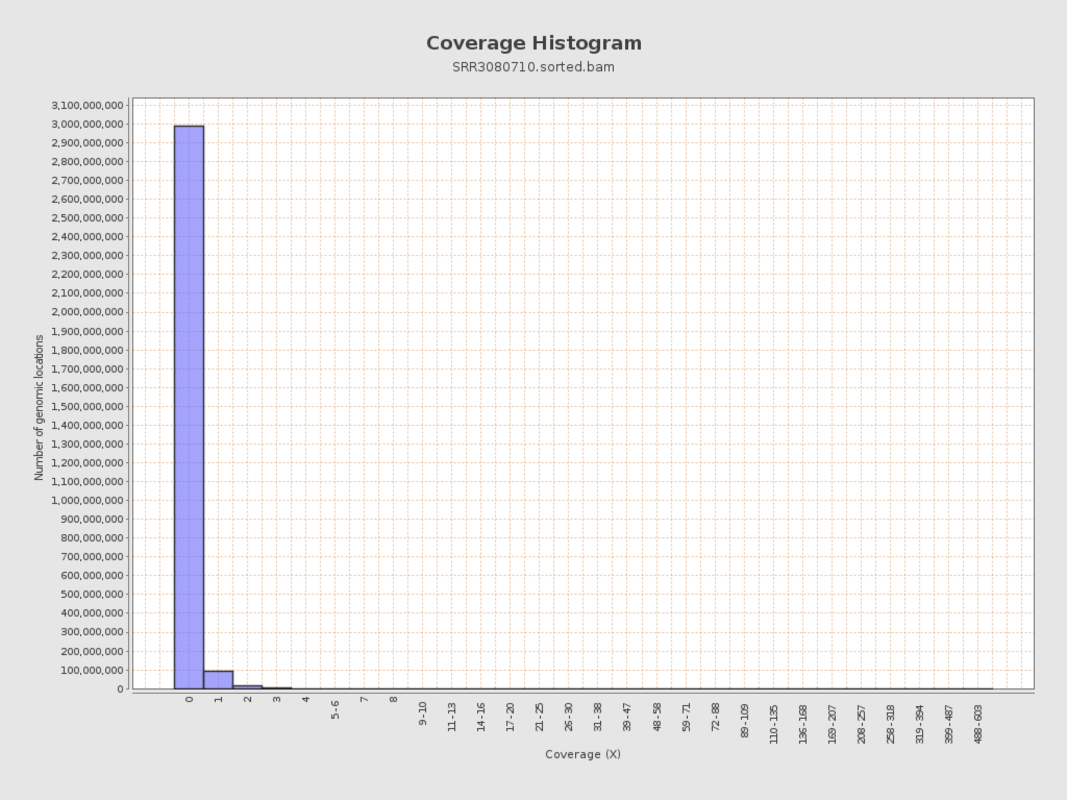
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16659113	0.0668	0.4626
chr2	243199373	8938445	0.0368	0.3486
chr3	198022430	8167949	0.0412	0.2378
chr4	191154276	5810162	0.0304	0.2092
chr5	180915260	6037445	0.0334	0.213
chr6	171115067	7914622	0.0463	0.3168
chr7	159138663	8311208	0.0522	0.7659

chr8	146364022	15909681	0.1087	0.5028
chr9	141213431	4103749	0.0291	0.247
chr10	135534747	6325415	0.0467	0.3011
chr11	135006516	5608406	0.0415	0.2789
chr12	133851895	4435614	0.0331	0.2147
chr13	115169878	2931722	0.0255	0.1873
chr14	107349540	2656733	0.0247	0.1931
chr15	102531392	2337033	0.0228	0.1779
chr16	90354753	3094856	0.0343	0.2289
chr17	81195210	2254427	0.0278	0.2145
chr18	78077248	4376189	0.056	0.4009
chr19	59128983	2124347	0.0359	0.2982
chr20	63025520	3438706	0.0546	0.278
chr21	48129895	2016187	0.0419	0.2479
chr22	51304566	1325439	0.0258	0.1869
chrMT	16571	9776	0.5899	0.8798
chrX	155270560	8880190	0.0572	0.3011
chrY	59373566	287568	0.0048	0.1006

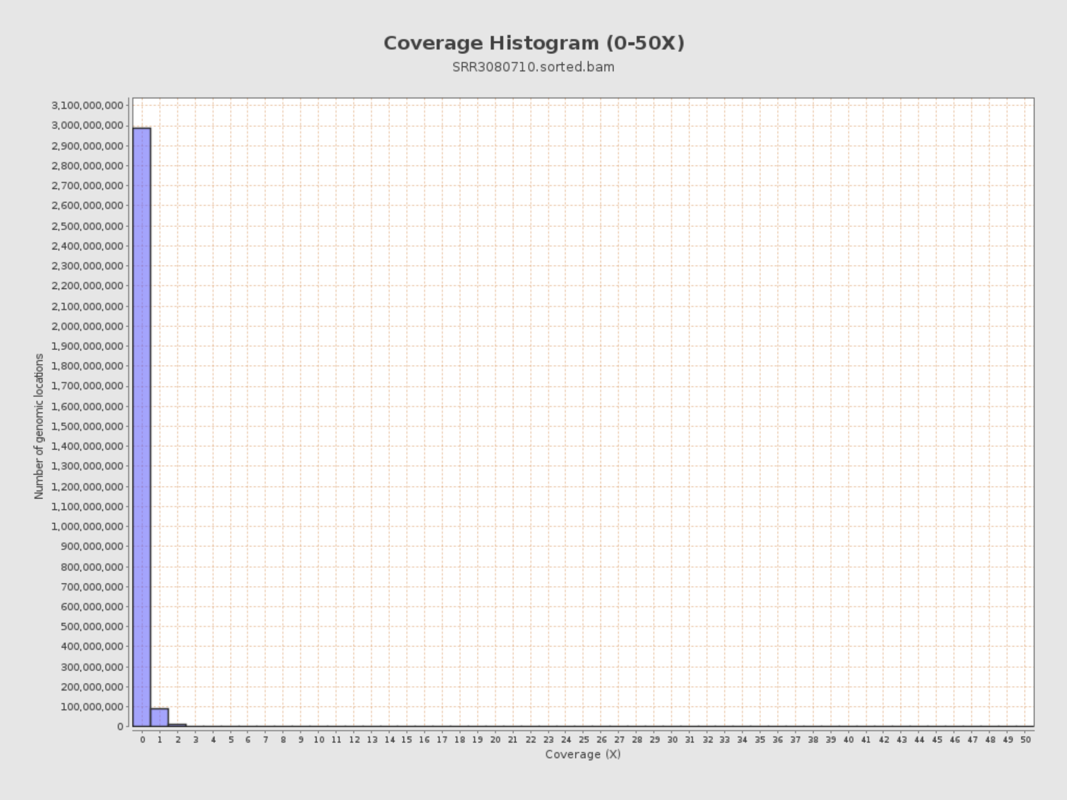
3. Results : Coverage across reference



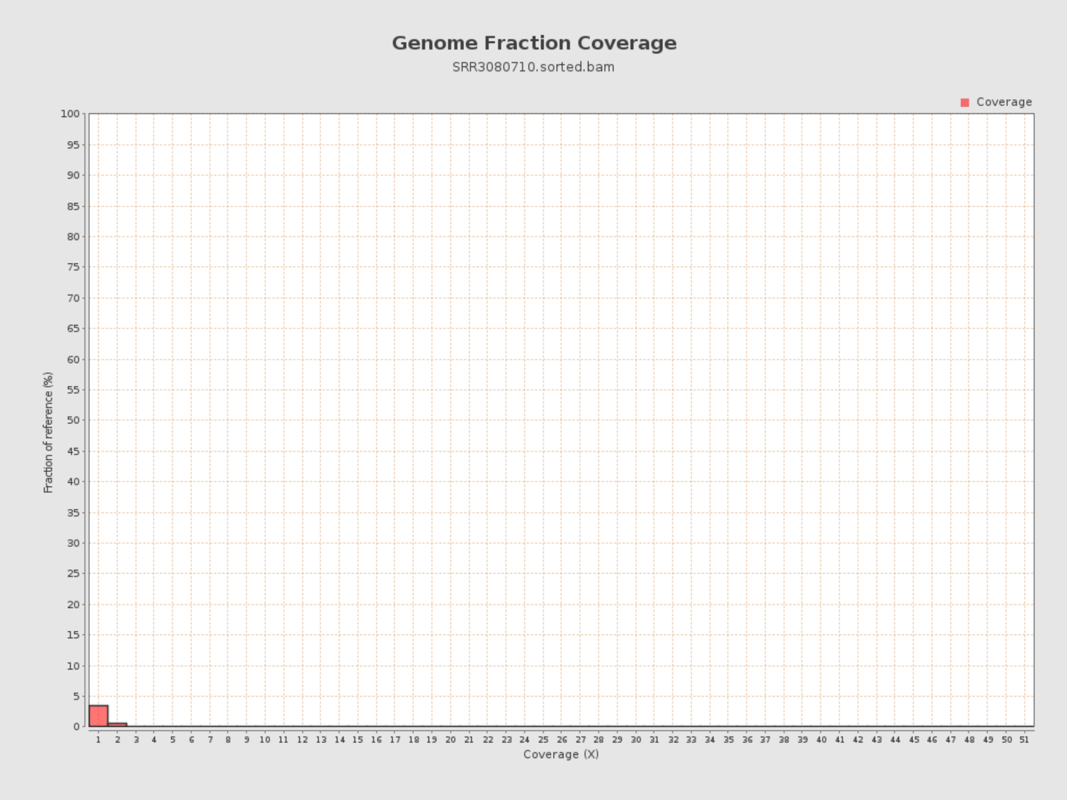
4. Results : Coverage Histogram



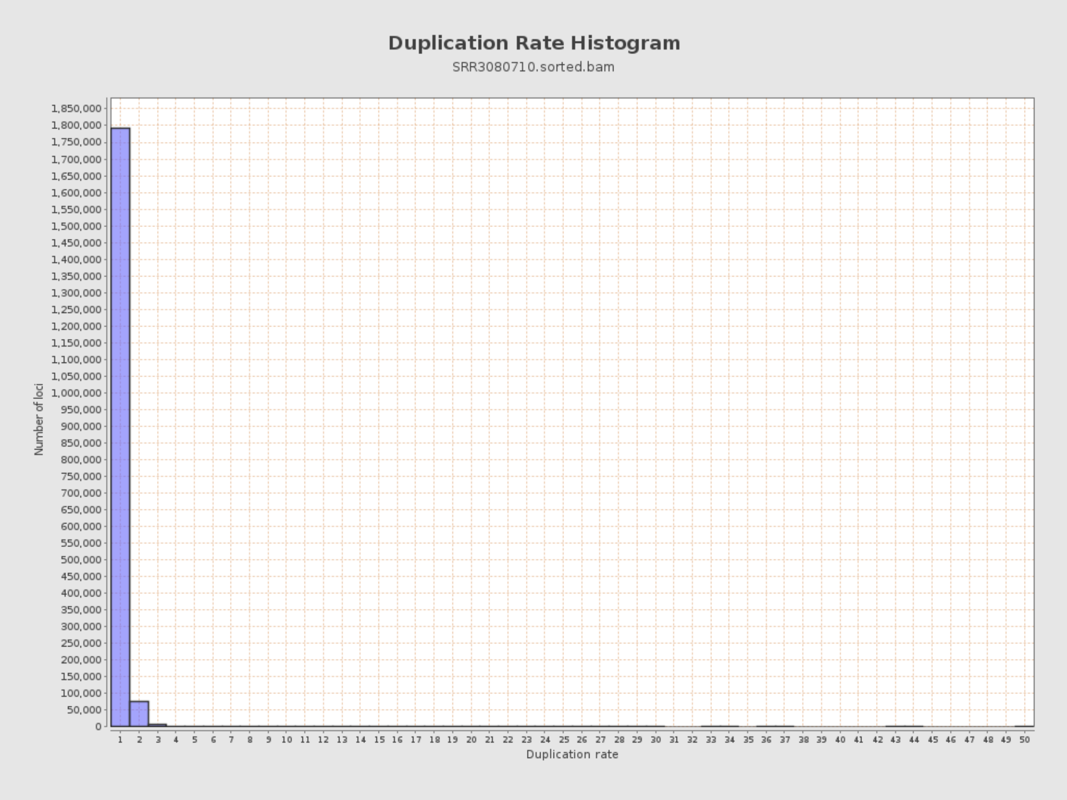
5. Results : Coverage Histogram (0-50X)



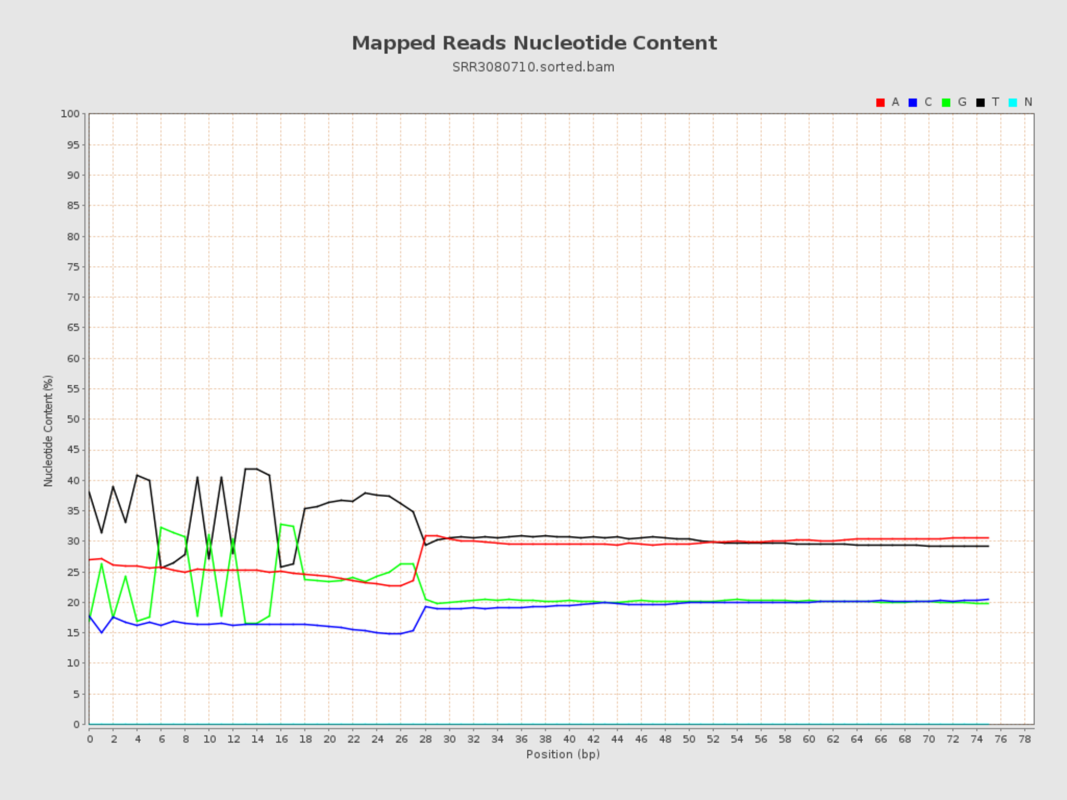
6. Results : Genome Fraction Coverage



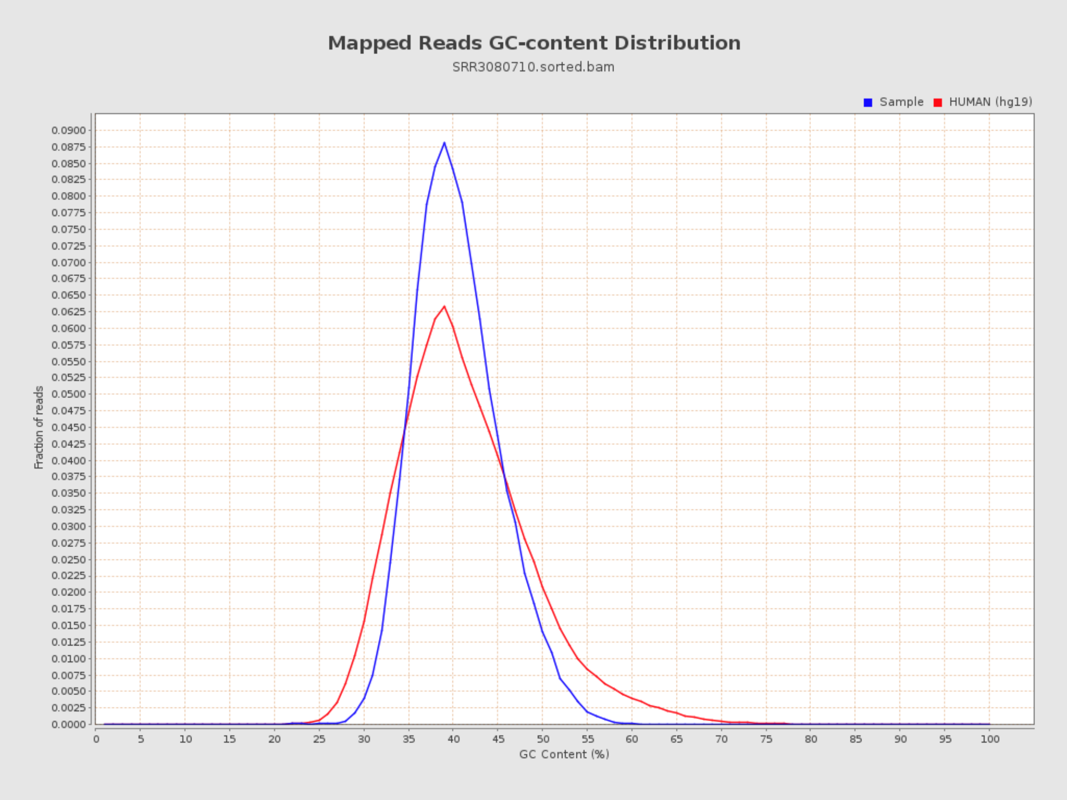
7. Results : Duplication Rate Histogram



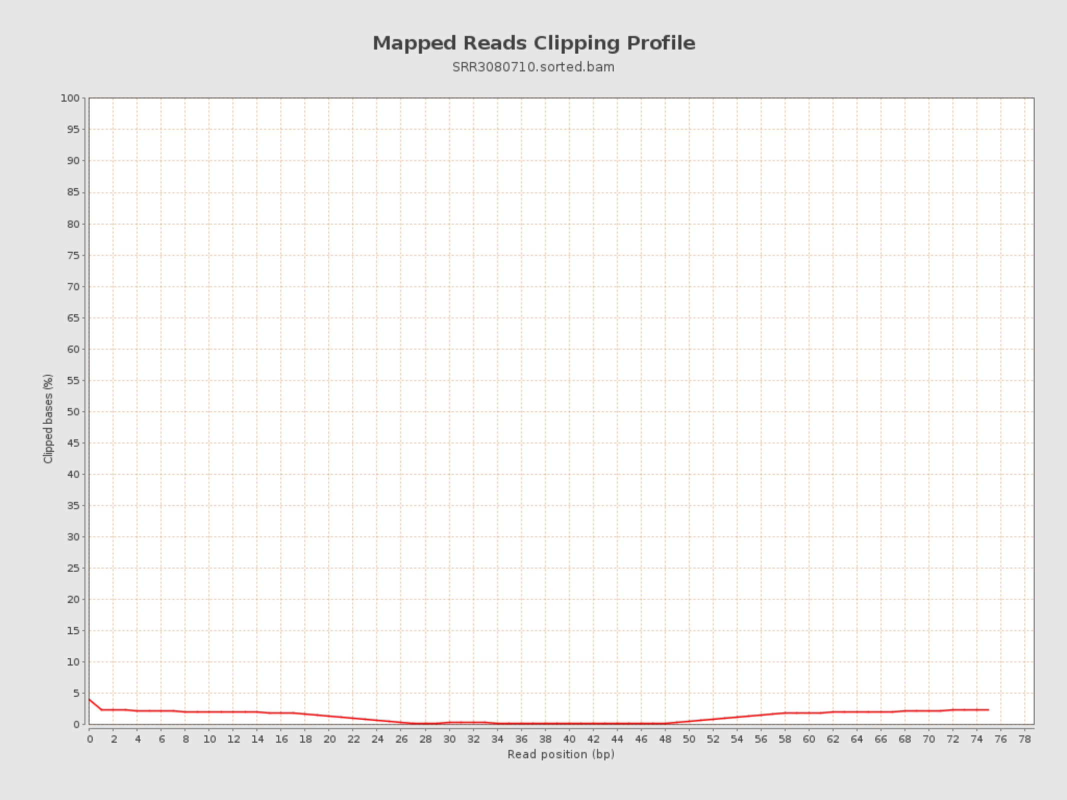
8. Results : Mapped Reads Nucleotide Content



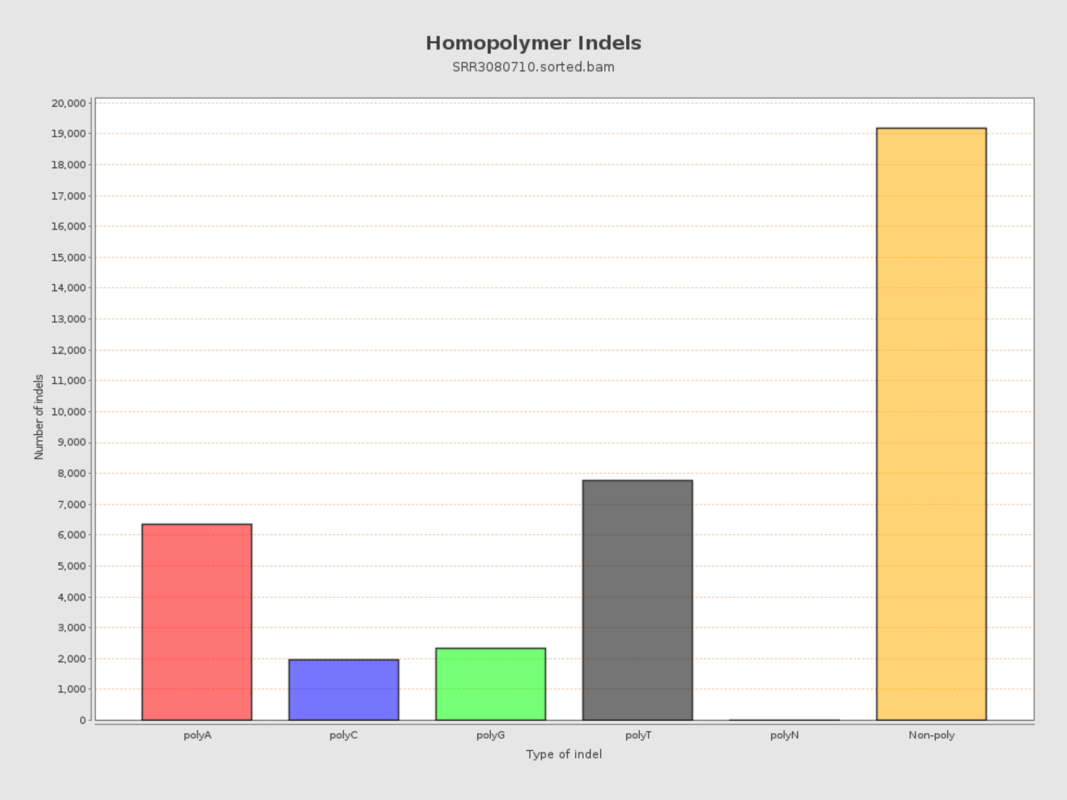
9. Results : Mapped Reads GC-content Distribution



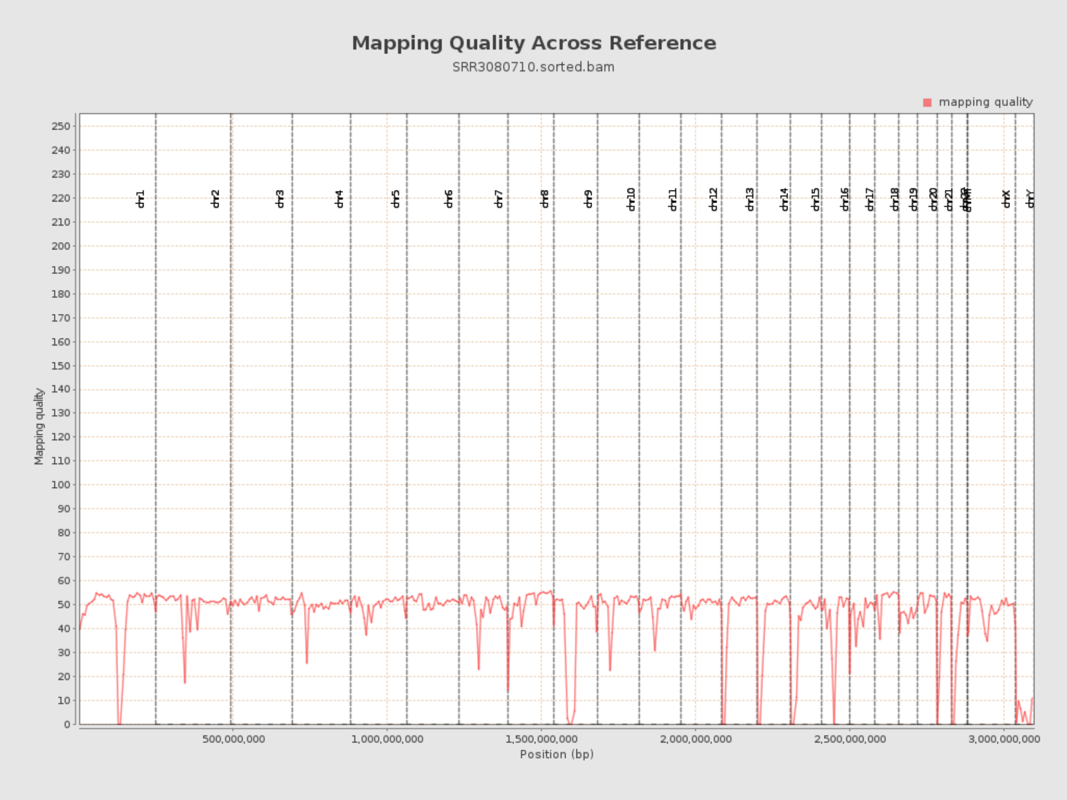
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram