Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:33:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082908.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_SRR3082908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082908.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:33:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,952,138
Mapped reads	1,729,115 / 88.58%
Unmapped reads	223,023 / 11.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,405 / 1.25%
Read min/max/mean length	30 / 76 / 76.44
Duplicated reads (estimated)	109,762 / 5.62%
Duplication rate	5.4%
Clipped reads	827,403 / 42.38%

2.2. ACGT Content

Number/percentage of A's	31,256,668 / 27.33%
Number/percentage of C's	21,266,197 / 18.6%
Number/percentage of T's	36,202,557 / 31.66%
Number/percentage of G's	25,620,029 / 22.4%
Number/percentage of N's	5,299 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.037

Standard Deviation	0.3012

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

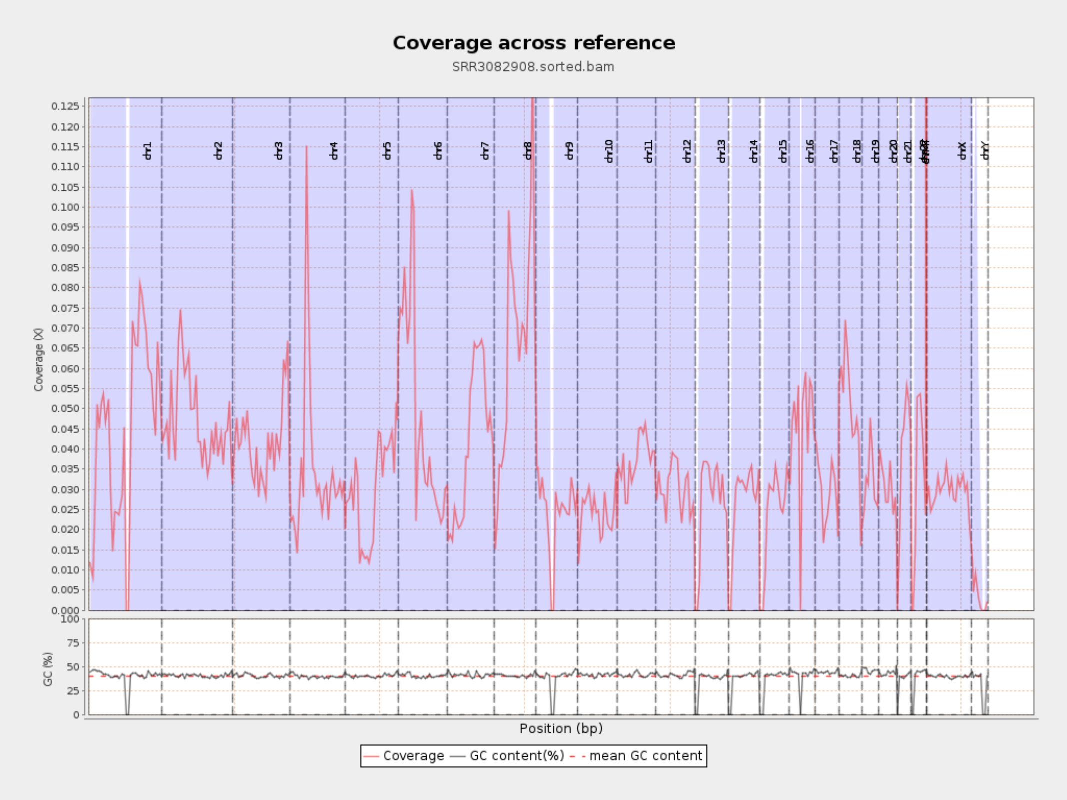
General error rate	0.74%
Mismatches	834,755
Insertions	9,353
Mapped reads with at least one insertion	0.54%
Deletions	26,252
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.81%

2.6. Chromosome stats

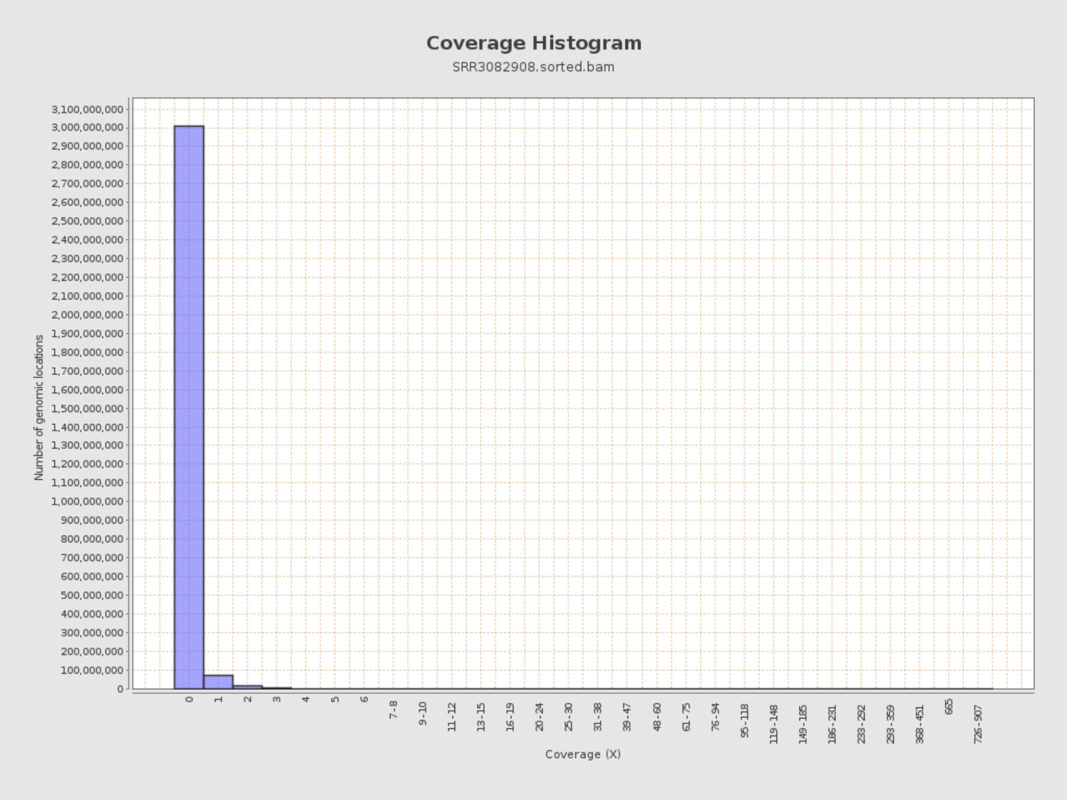
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11047680	0.0443	0.4143
chr2	243199373	11564575	0.0476	0.4759
chr3	198022430	8260848	0.0417	0.252
chr4	191154276	6631661	0.0347	0.2331
chr5	180915260	5401026	0.0299	0.2135
chr6	171115067	8287180	0.0484	0.3094
chr7	159138663	6664625	0.0419	0.2978

chr8	146364022	9794037	0.0669	0.3779
chr9	141213431	3402444	0.0241	0.2523
chr10	135534747	3233831	0.0239	0.2149
chr11	135006516	5029657	0.0373	0.2682
chr12	133851895	4038468	0.0302	0.2184
chr13	115169878	3036667	0.0264	0.2041
chr14	107349540	2829069	0.0264	0.2108
chr15	102531392	2447916	0.0239	0.1916
chr16	90354753	4079437	0.0451	0.2692
chr17	81195210	2347041	0.0289	0.2166
chr18	78077248	3994384	0.0512	0.4796
chr19	59128983	1903495	0.0322	0.317
chr20	63025520	1932680	0.0307	0.2231
chr21	48129895	1851663	0.0385	0.2447
chr22	51304566	1579116	0.0308	0.2164
chrMT	16571	227904	13.7532	9.3513
chrX	155270560	4594500	0.0296	0.2236
chrY	59373566	213762	0.0036	0.0747

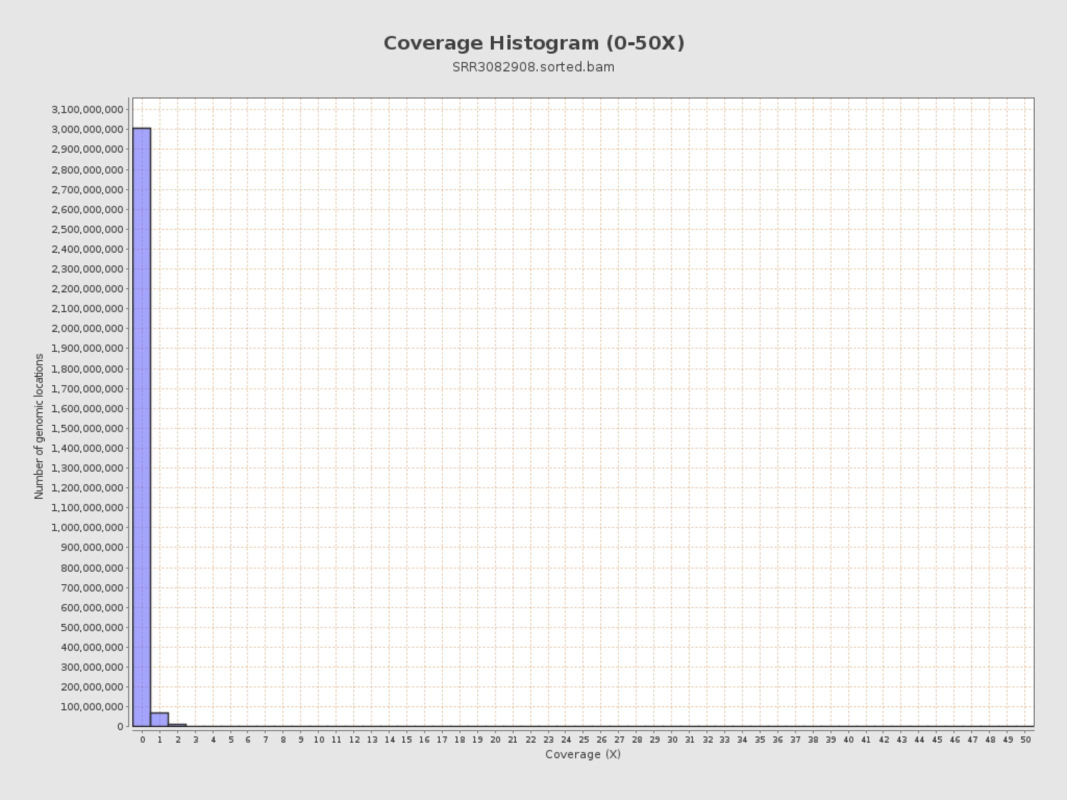
3. Results : Coverage across reference



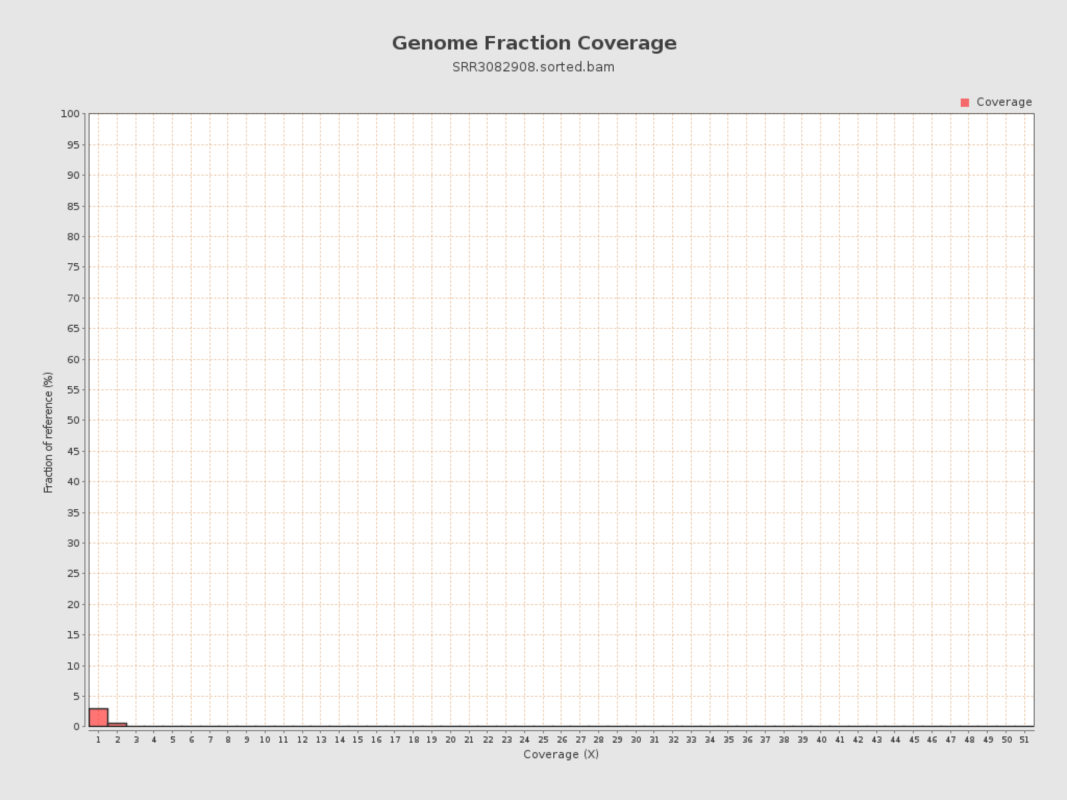
4. Results : Coverage Histogram



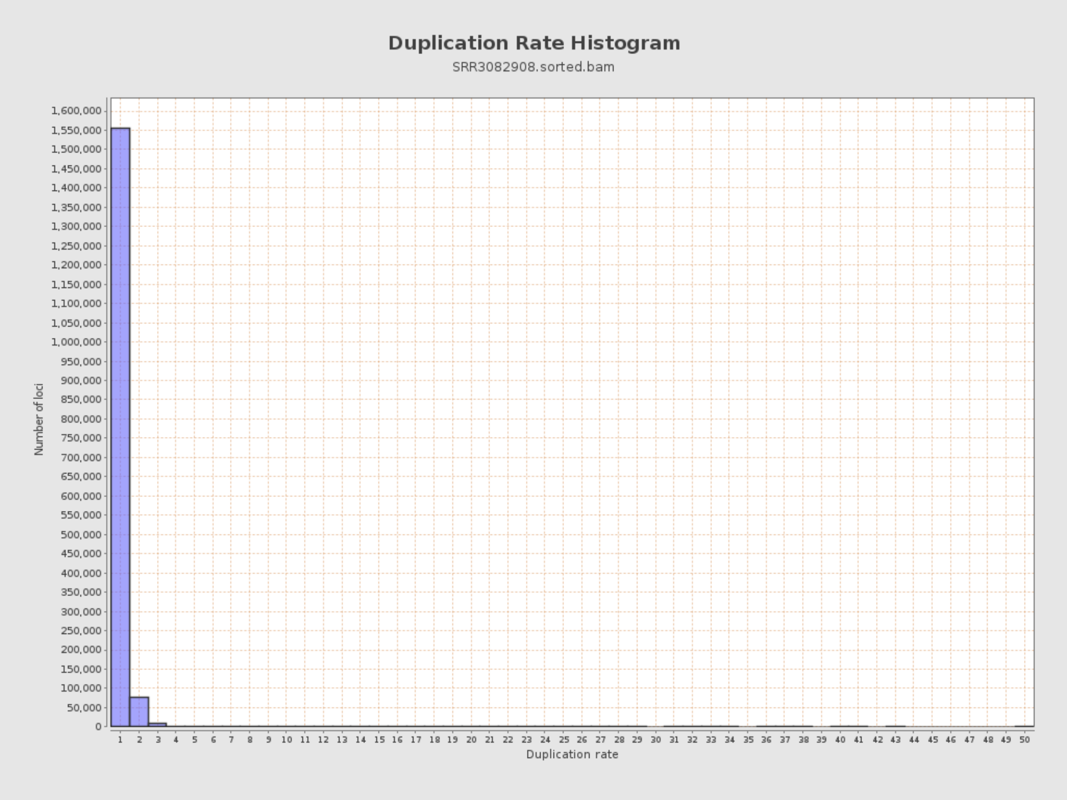
5. Results : Coverage Histogram (0-50X)



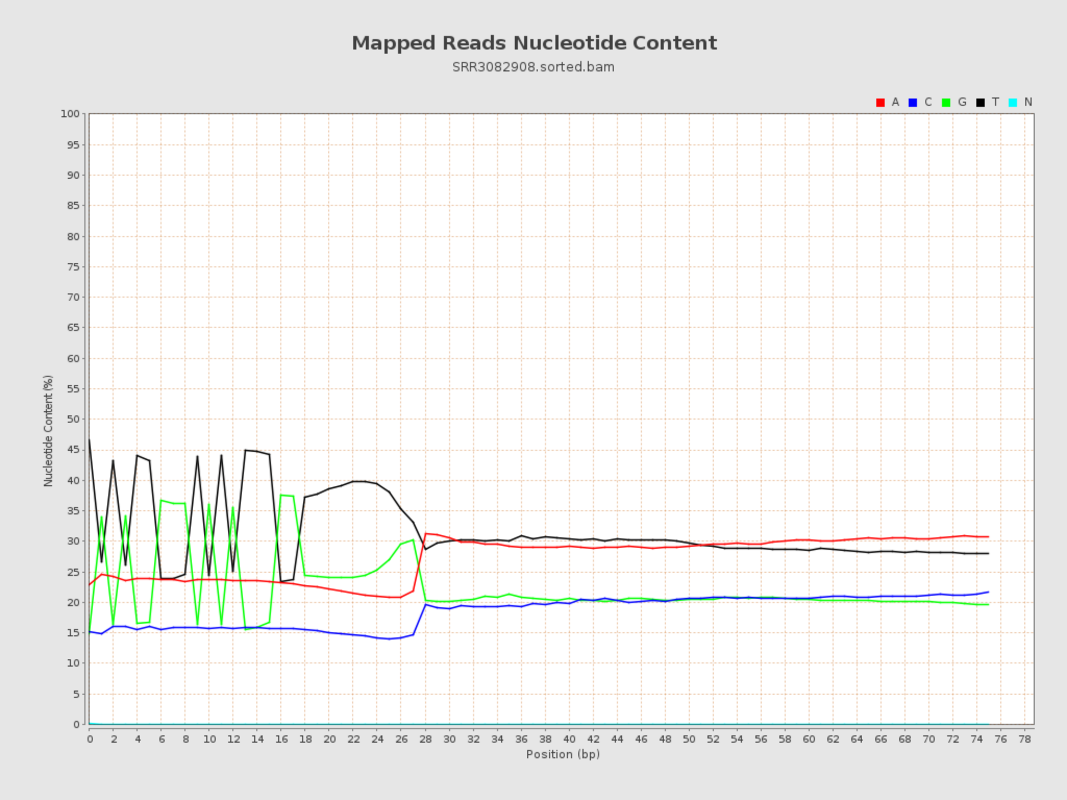
6. Results : Genome Fraction Coverage



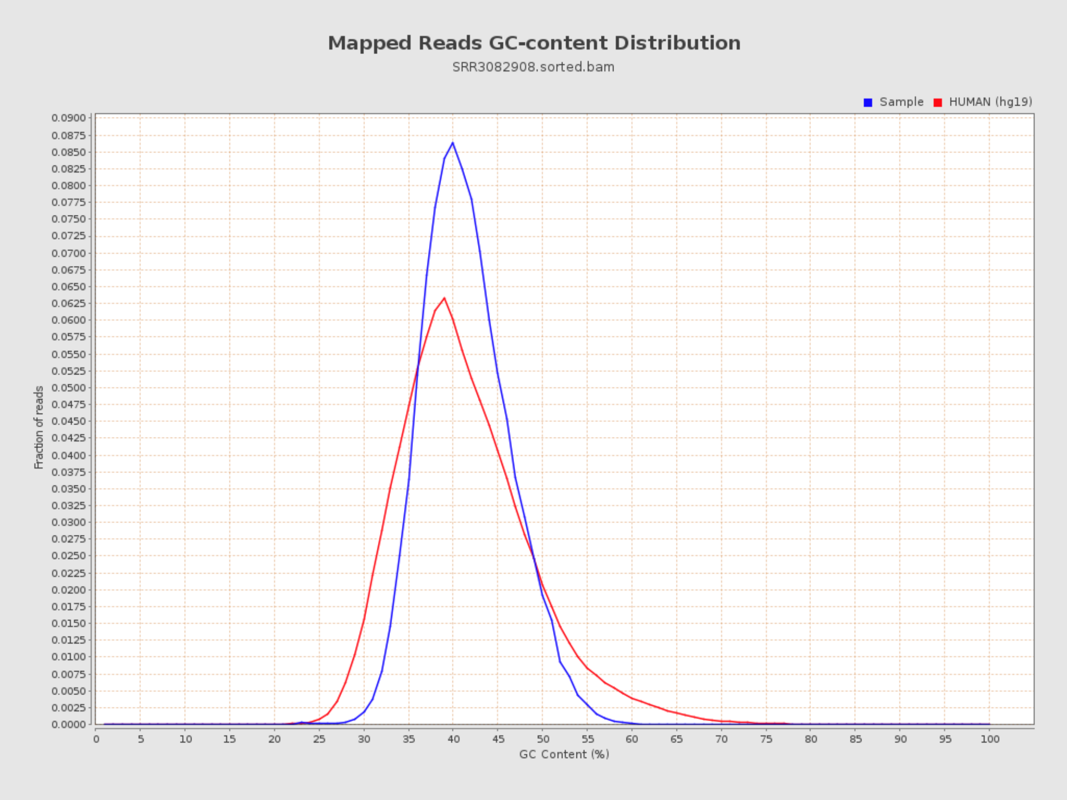
7. Results : Duplication Rate Histogram



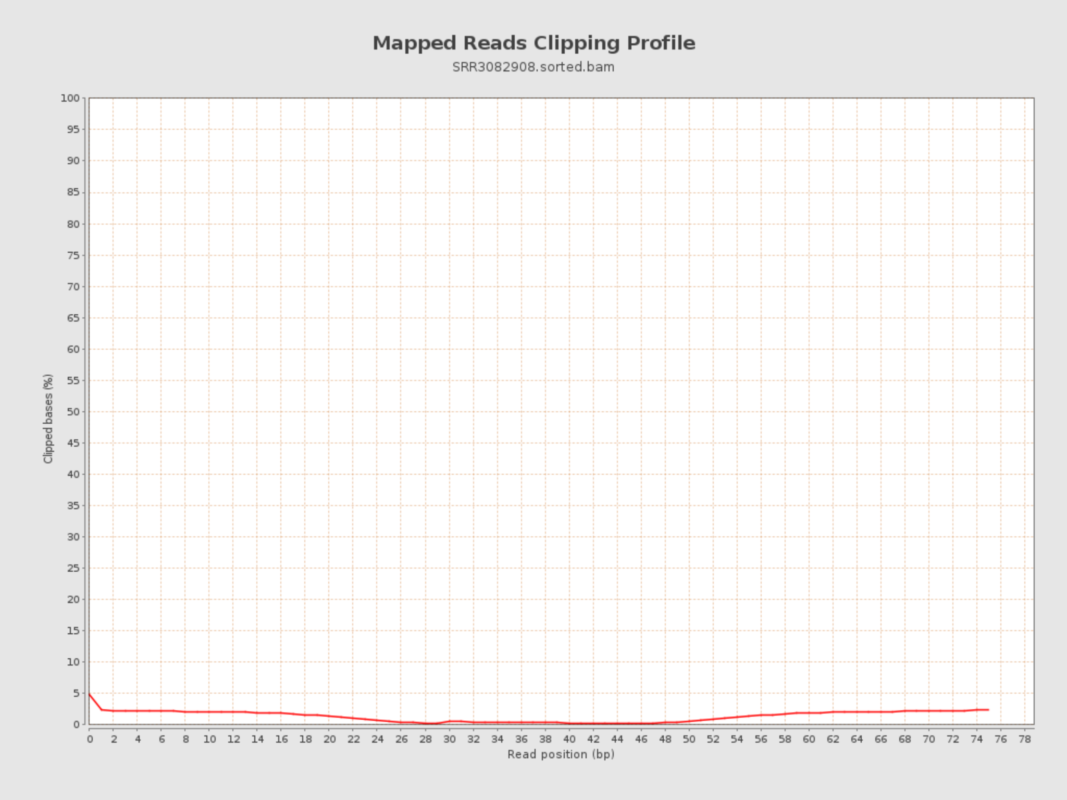
8. Results : Mapped Reads Nucleotide Content



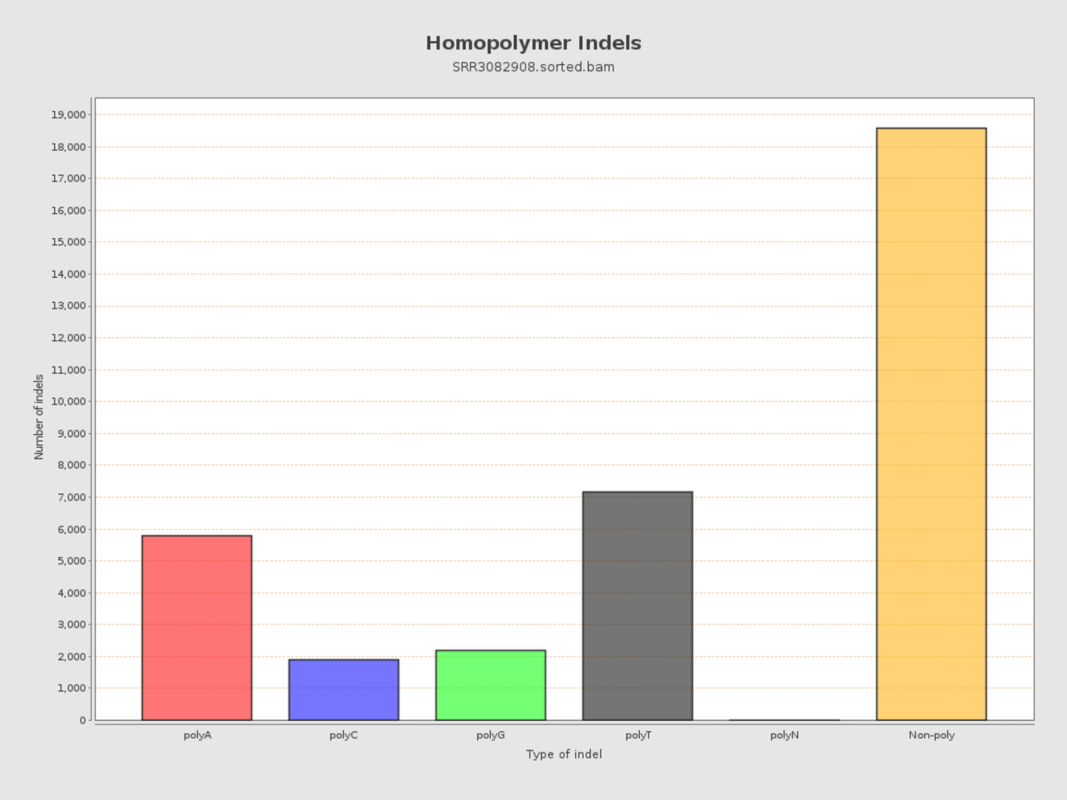
9. Results : Mapped Reads GC-content Distribution



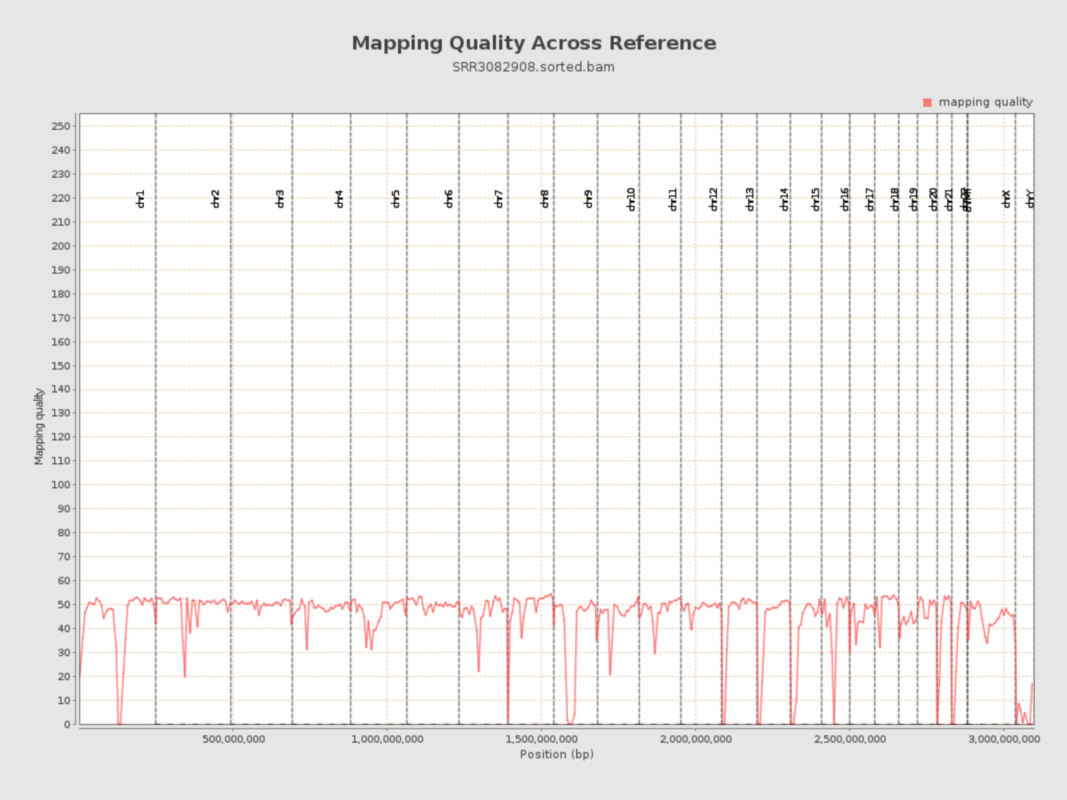
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram