Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:59:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082704.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_SRR3082704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082704.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:59:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,350,825
Mapped reads	3,106,246 / 92.7%
Unmapped reads	244,579 / 7.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,157 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	129,367 / 3.86%
Duplication rate	3.07%
Clipped reads	1,463,440 / 43.67%

2.2. ACGT Content

Number/percentage of A's	56,604,247 / 27.49%
Number/percentage of C's	35,444,531 / 17.22%
Number/percentage of T's	68,498,691 / 33.27%
Number/percentage of G's	45,286,943 / 22%
Number/percentage of N's	56,150 / 0.03%
GC Percentage	39.21%

2.3. Coverage

Mean	0.0665

Standard Deviation	0.5324

2.4. Mapping Quality

Mean Mapping Quality	46.44

2.5. Mismatches and indels

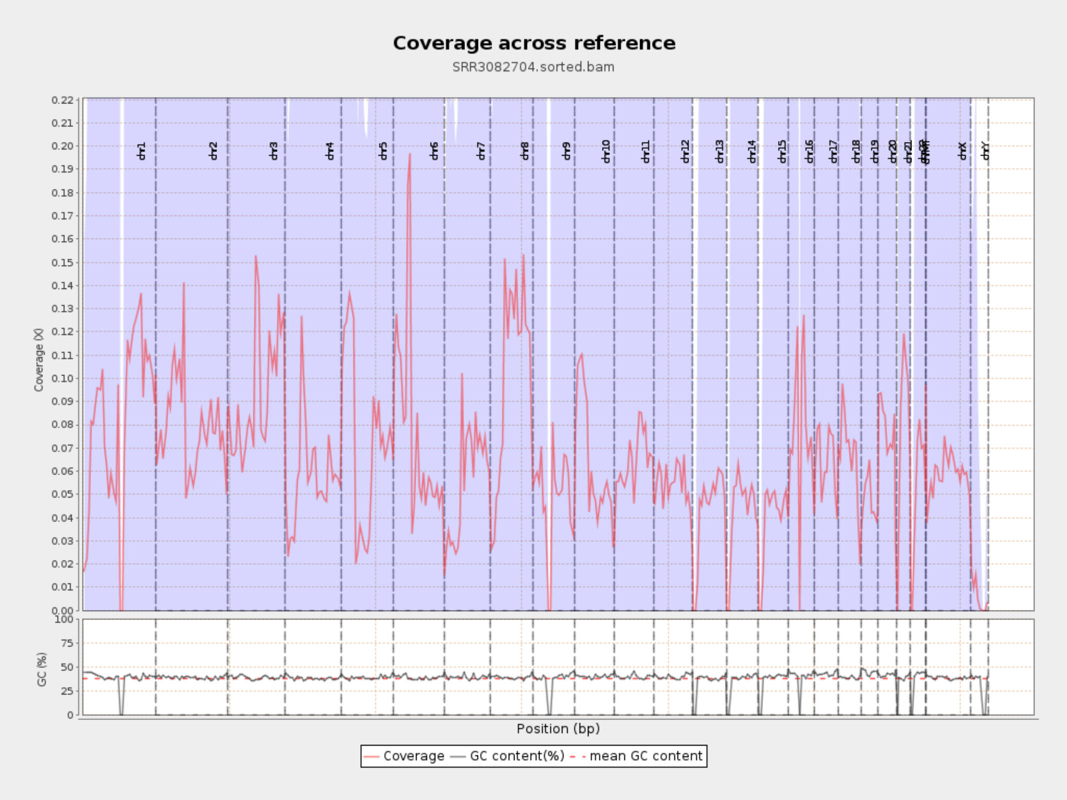
General error rate	0.93%
Mismatches	1,881,406
Insertions	18,618
Mapped reads with at least one insertion	0.59%
Deletions	49,169
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.88%

2.6. Chromosome stats

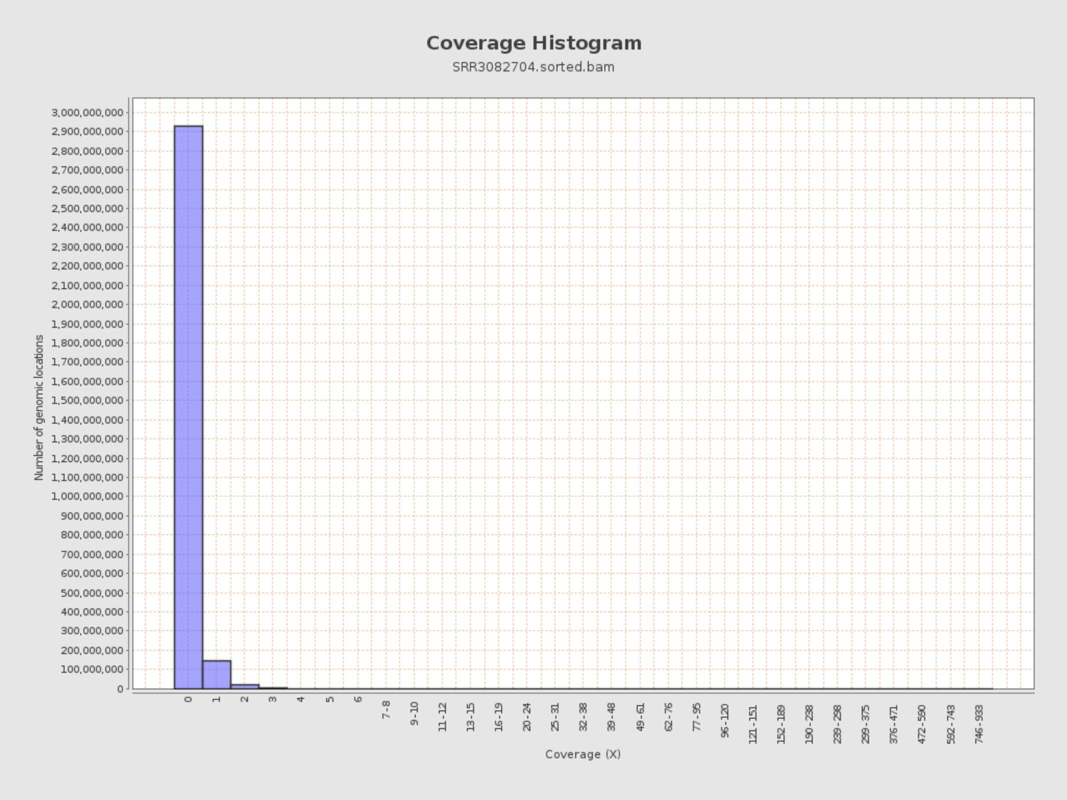
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20330611	0.0816	0.8625
chr2	243199373	19292917	0.0793	0.7192
chr3	198022430	18333946	0.0926	0.3594
chr4	191154276	11157532	0.0584	0.2911
chr5	180915260	13293450	0.0735	0.3213
chr6	171115067	13301049	0.0777	0.5069
chr7	159138663	8905333	0.056	0.7644

chr8	146364022	14950731	0.1021	0.5184
chr9	141213431	6929177	0.0491	0.5597
chr10	135534747	8833650	0.0652	0.4618
chr11	135006516	8699718	0.0644	0.4787
chr12	133851895	7258809	0.0542	0.2777
chr13	115169878	4957590	0.043	0.2374
chr14	107349540	4659828	0.0434	0.2846
chr15	102531392	3942449	0.0385	0.2252
chr16	90354753	6832670	0.0756	0.3614
chr17	81195210	5309487	0.0654	0.4023
chr18	78077248	5322683	0.0682	1.1901
chr19	59128983	2861388	0.0484	0.5889
chr20	63025520	4933104	0.0783	0.3523
chr21	48129895	3783920	0.0786	0.3444
chr22	51304566	2627449	0.0512	0.263
chrMT	16571	1611	0.0972	0.329
chrX	155270560	9094042	0.0586	0.3572
chrY	59373566	355668	0.006	0.1167

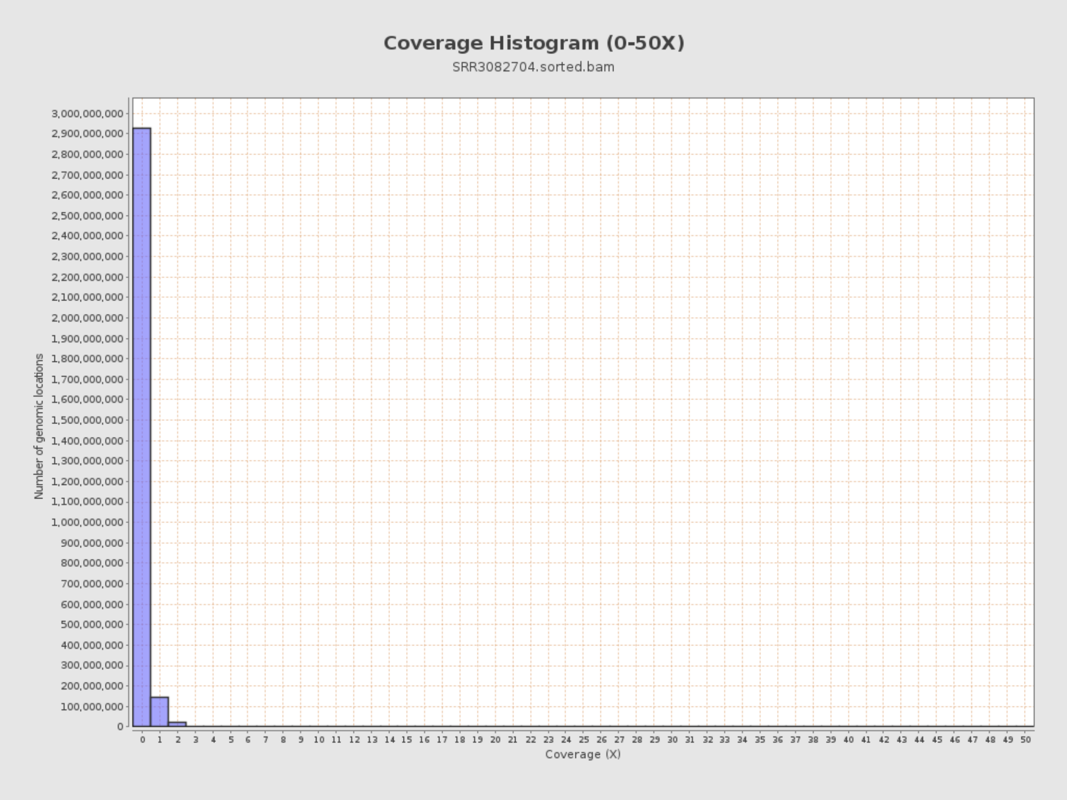
3. Results : Coverage across reference



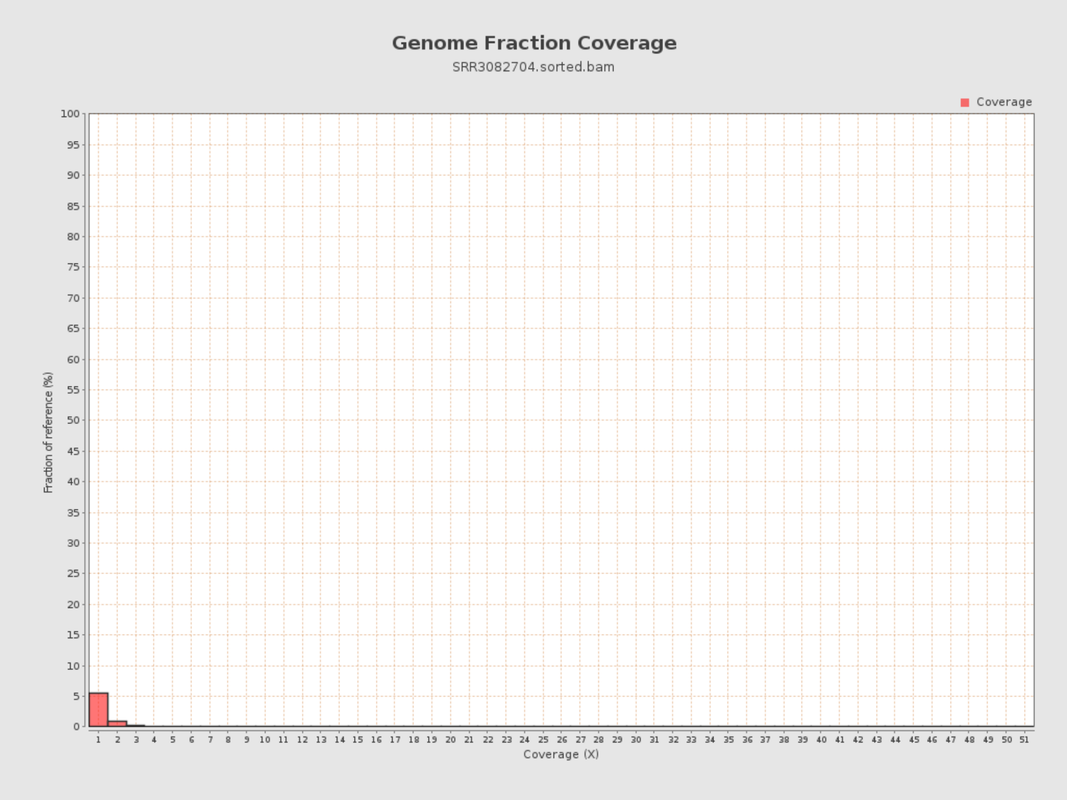
4. Results : Coverage Histogram



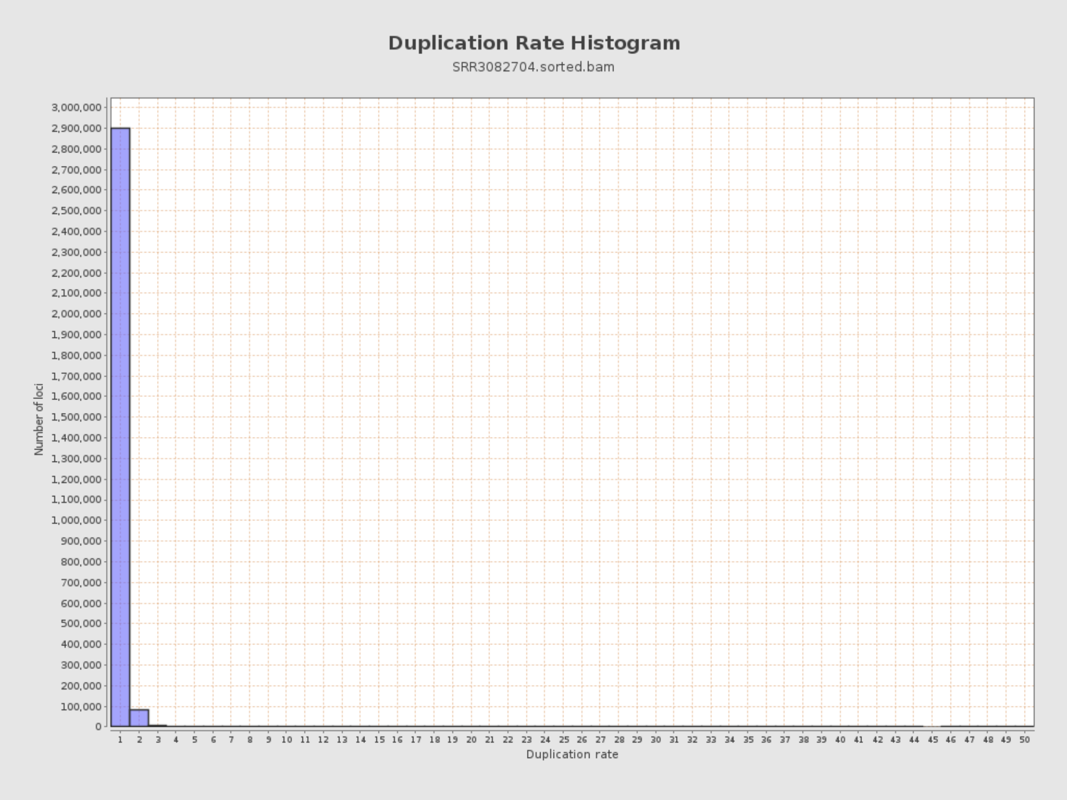
5. Results : Coverage Histogram (0-50X)



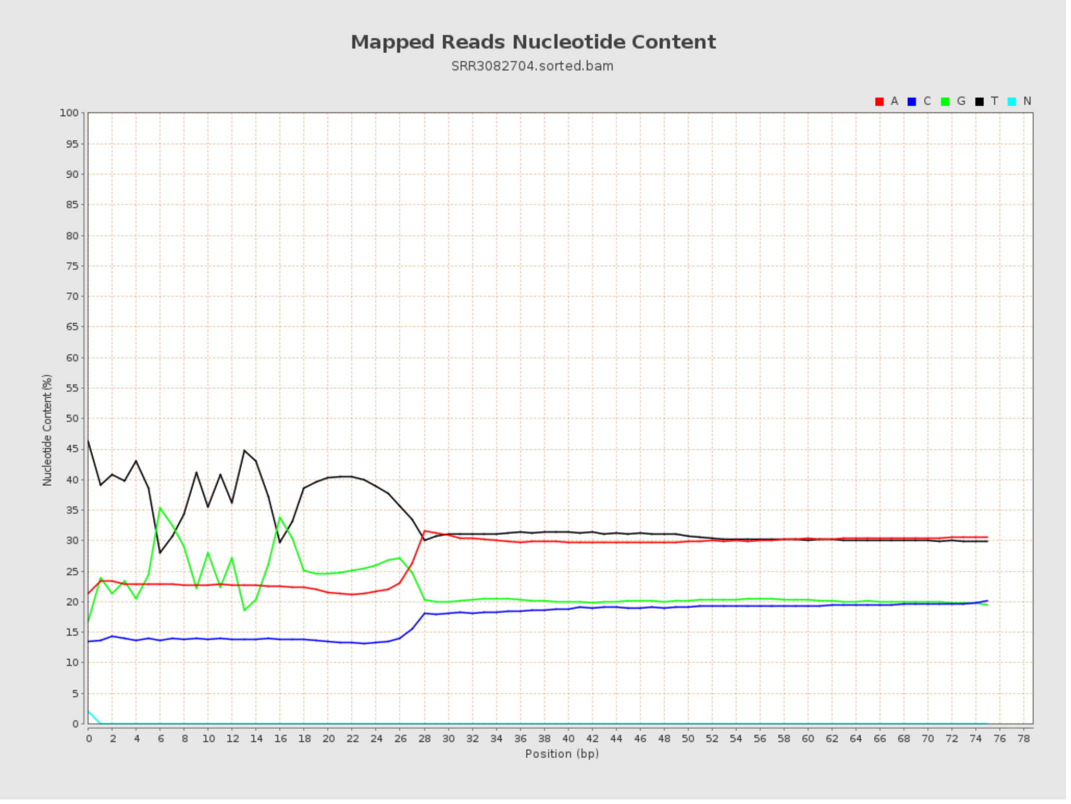
6. Results : Genome Fraction Coverage



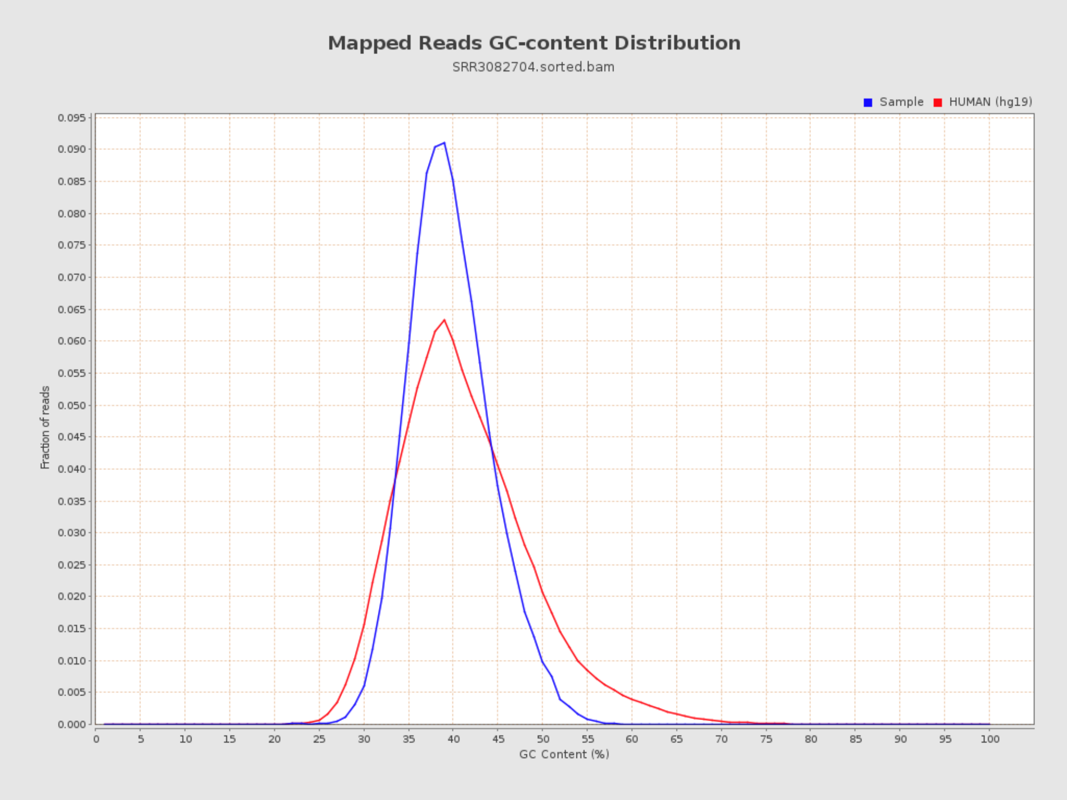
7. Results : Duplication Rate Histogram



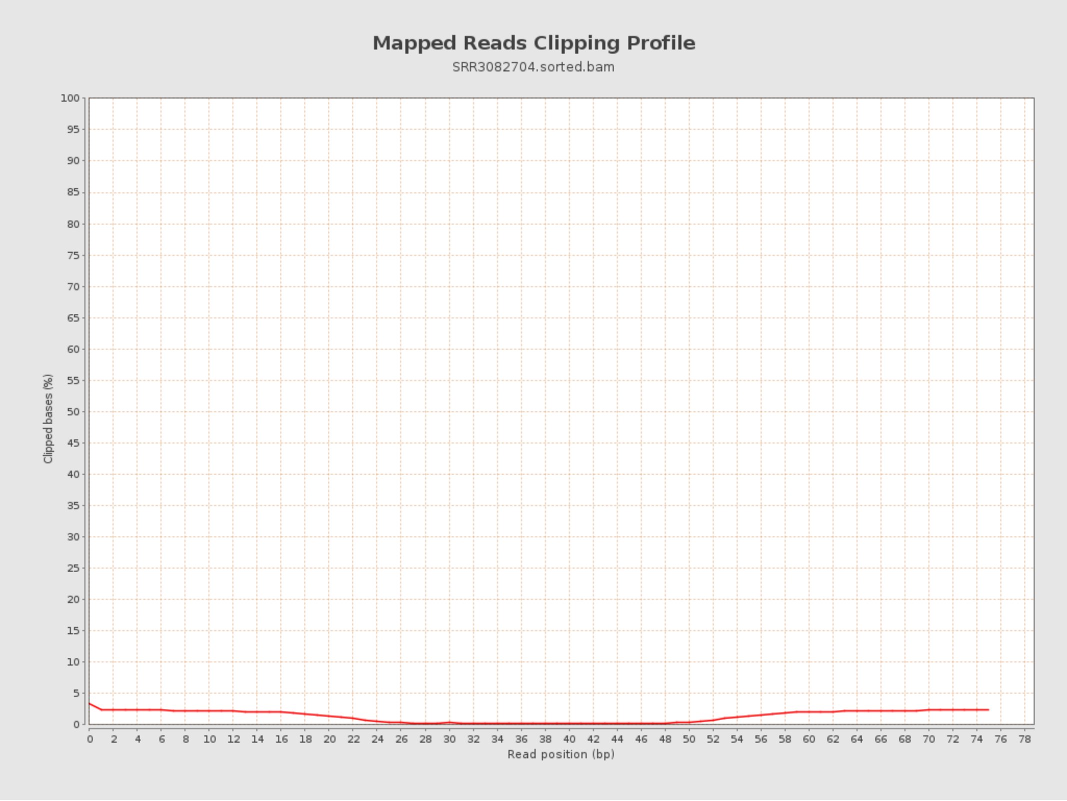
8. Results : Mapped Reads Nucleotide Content



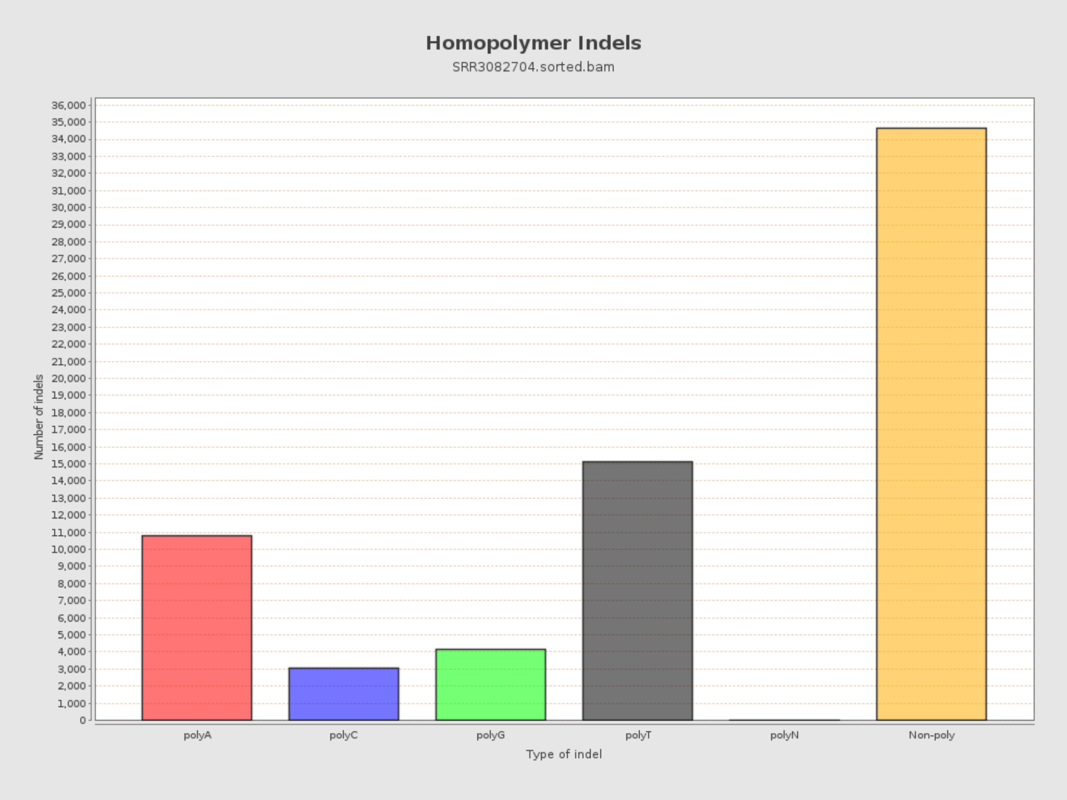
9. Results : Mapped Reads GC-content Distribution



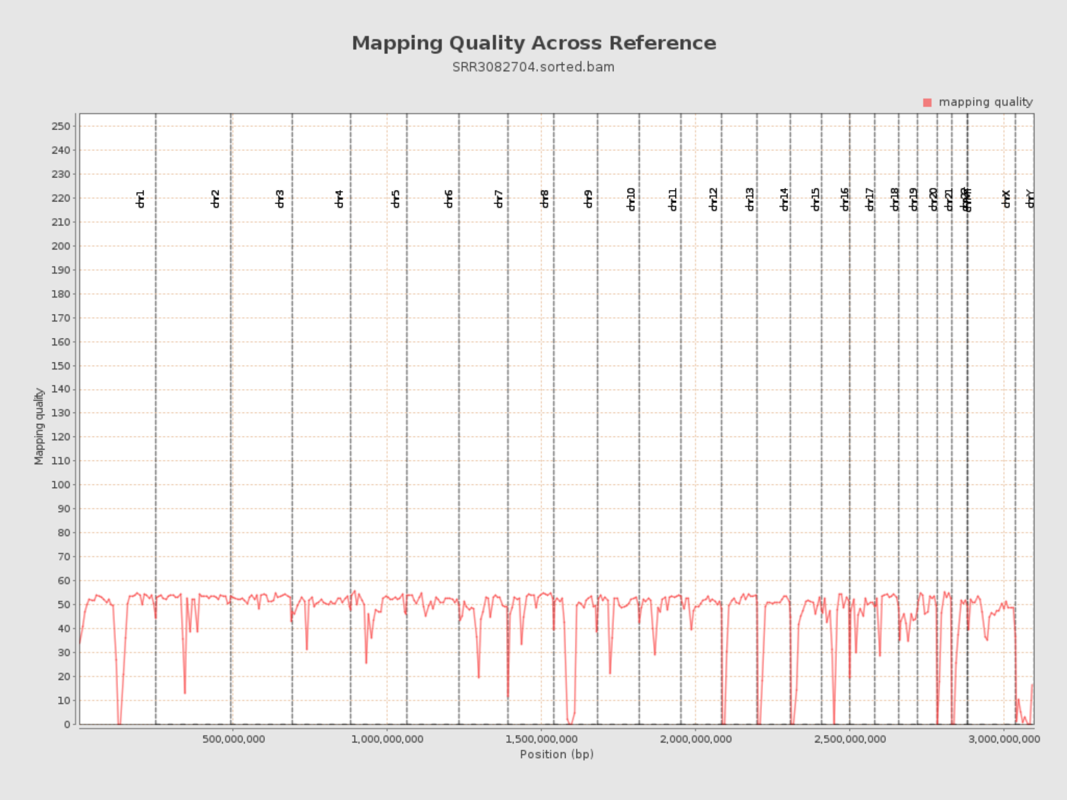
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram