Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:07:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081943.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_SRR3081943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081943.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:07:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,386,896
Mapped reads	3,108,136 / 91.77%
Unmapped reads	278,760 / 8.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,072 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	166,124 / 4.9%
Duplication rate	3.58%
Clipped reads	1,164,994 / 34.4%

2.2. ACGT Content

Number/percentage of A's	60,218,648 / 28.38%
Number/percentage of C's	39,473,522 / 18.6%
Number/percentage of T's	66,427,991 / 31.31%
Number/percentage of G's	46,038,019 / 21.7%
Number/percentage of N's	27,004 / 0.01%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0686

Standard Deviation	0.7705

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

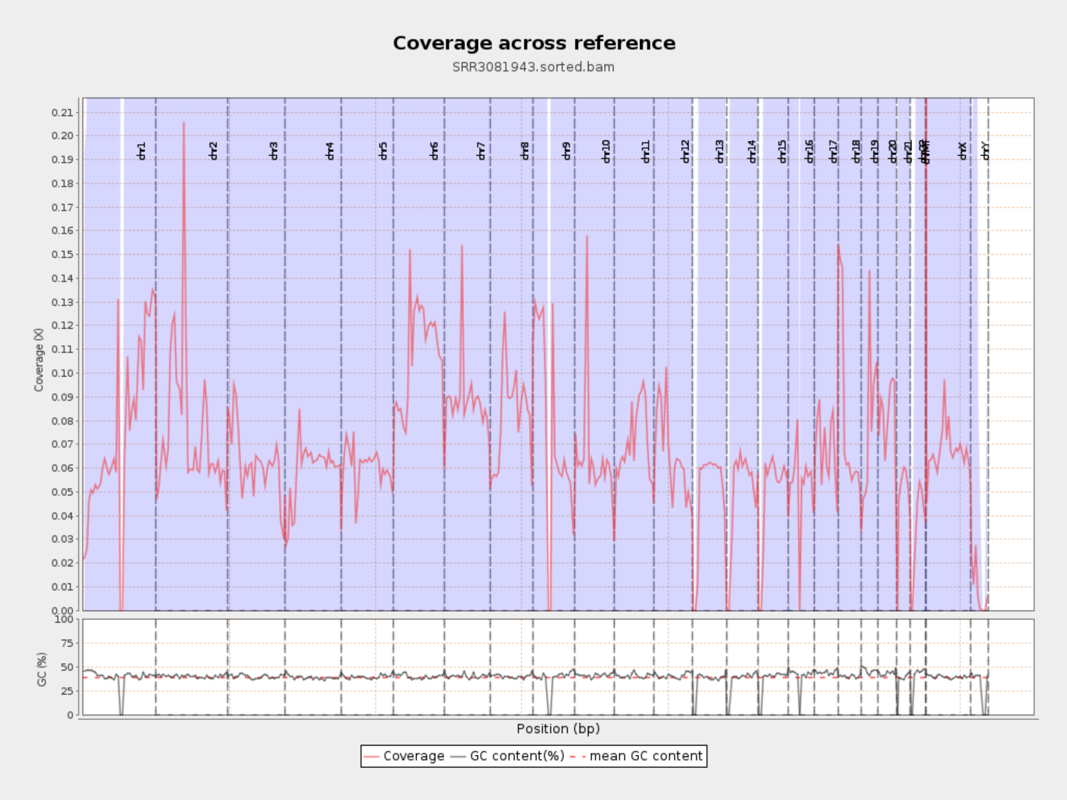
General error rate	0.82%
Mismatches	1,704,527
Insertions	15,996
Mapped reads with at least one insertion	0.51%
Deletions	49,517
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47%

2.6. Chromosome stats

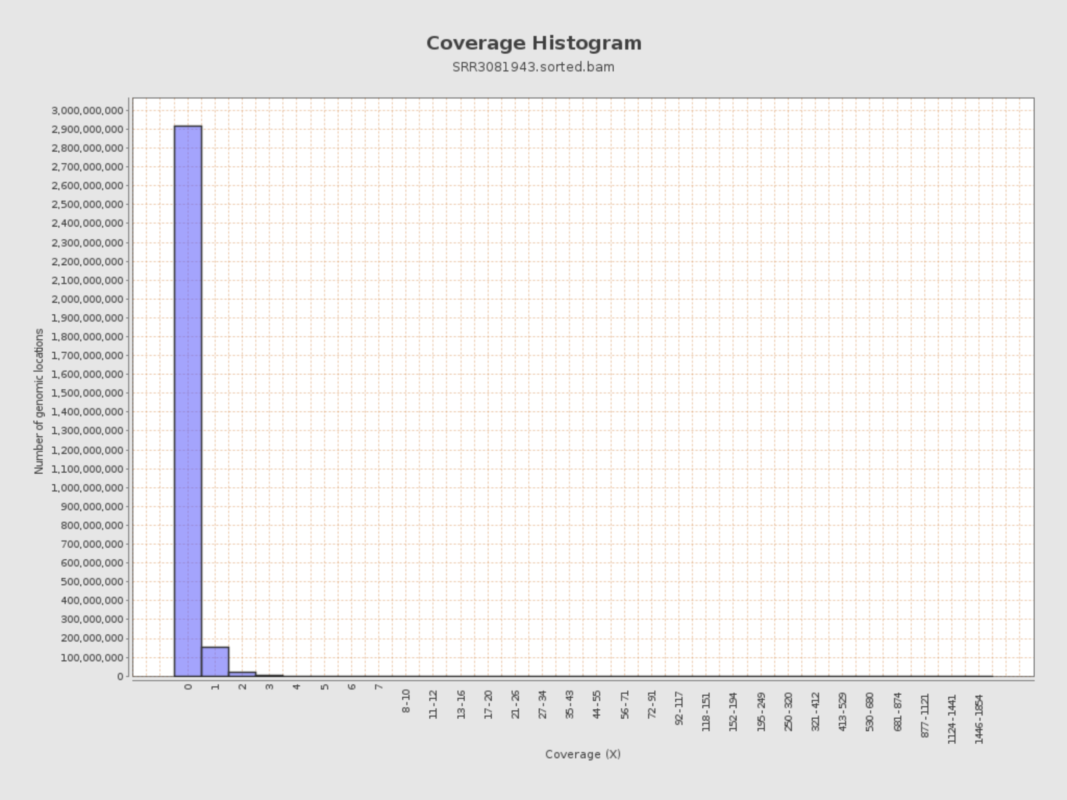
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18612505	0.0747	1.5647
chr2	243199373	18761193	0.0771	1.0405
chr3	198022430	12480336	0.063	0.2957
chr4	191154276	11381505	0.0595	0.3189
chr5	180915260	10882679	0.0602	0.2906
chr6	171115067	18660508	0.1091	0.5566
chr7	159138663	14147764	0.0889	1.0519

chr8	146364022	12127652	0.0829	0.9278
chr9	141213431	10718689	0.0759	0.8182
chr10	135534747	8839823	0.0652	0.7586
chr11	135006516	9586289	0.071	0.497
chr12	133851895	8757720	0.0654	0.3299
chr13	115169878	5580517	0.0485	0.2482
chr14	107349540	5274639	0.0491	0.3499
chr15	102531392	4893939	0.0477	0.2543
chr16	90354753	4666358	0.0516	0.3936
chr17	81195210	5629718	0.0693	0.3514
chr18	78077248	6295576	0.0806	1.4
chr19	59128983	4702591	0.0795	1.2099
chr20	63025520	5279213	0.0838	0.3474
chr21	48129895	2298574	0.0478	0.3339
chr22	51304566	1730190	0.0337	0.2056
chrMT	16571	6953	0.4196	0.7068
chrX	155270560	10448560	0.0673	0.4159
chrY	59373566	508832	0.0086	0.2273

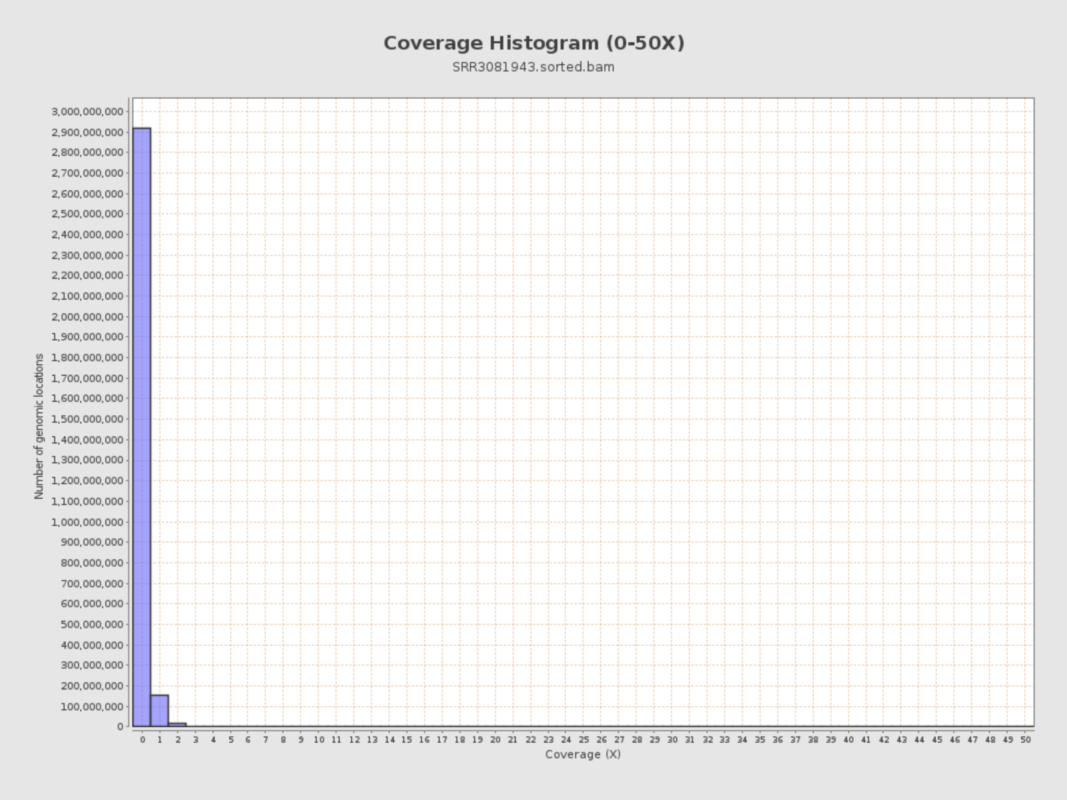
3. Results : Coverage across reference



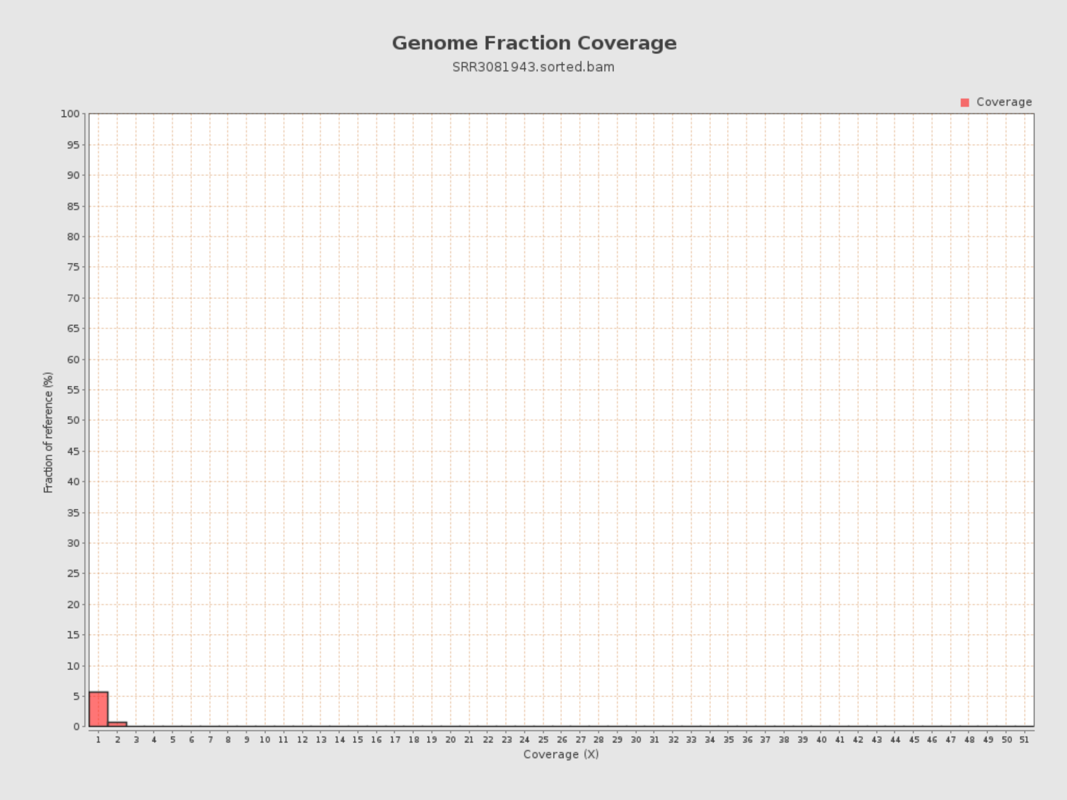
4. Results : Coverage Histogram



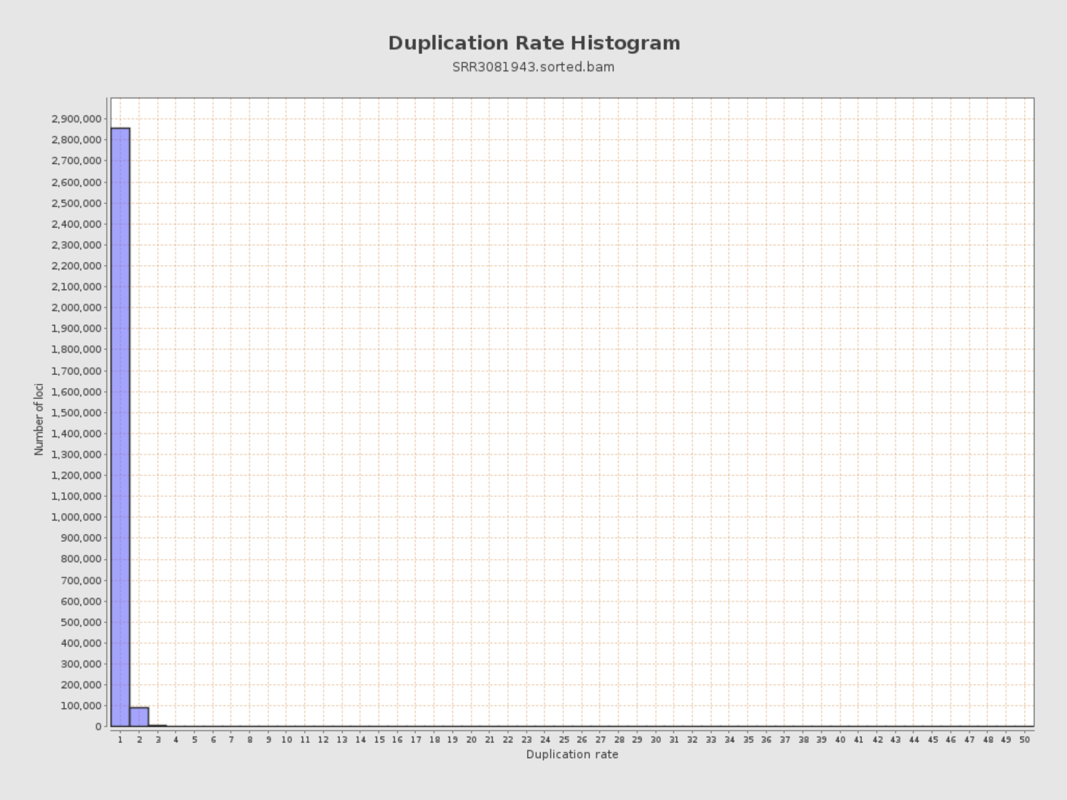
5. Results : Coverage Histogram (0-50X)



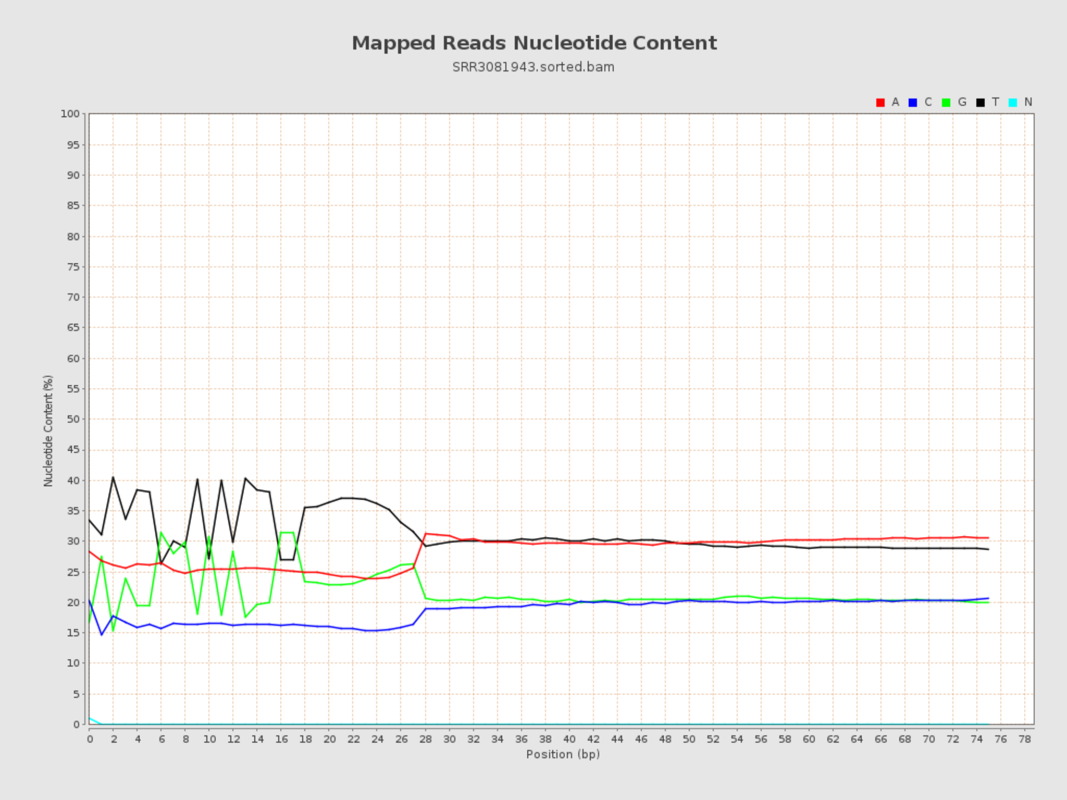
6. Results : Genome Fraction Coverage



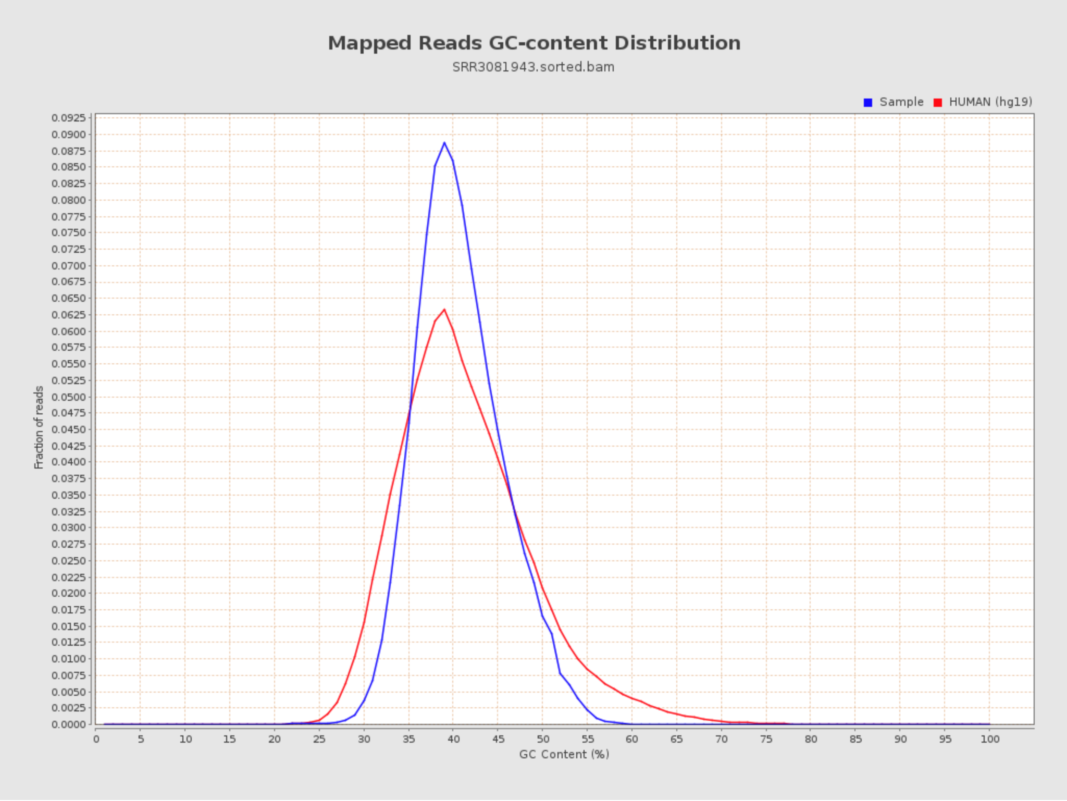
7. Results : Duplication Rate Histogram



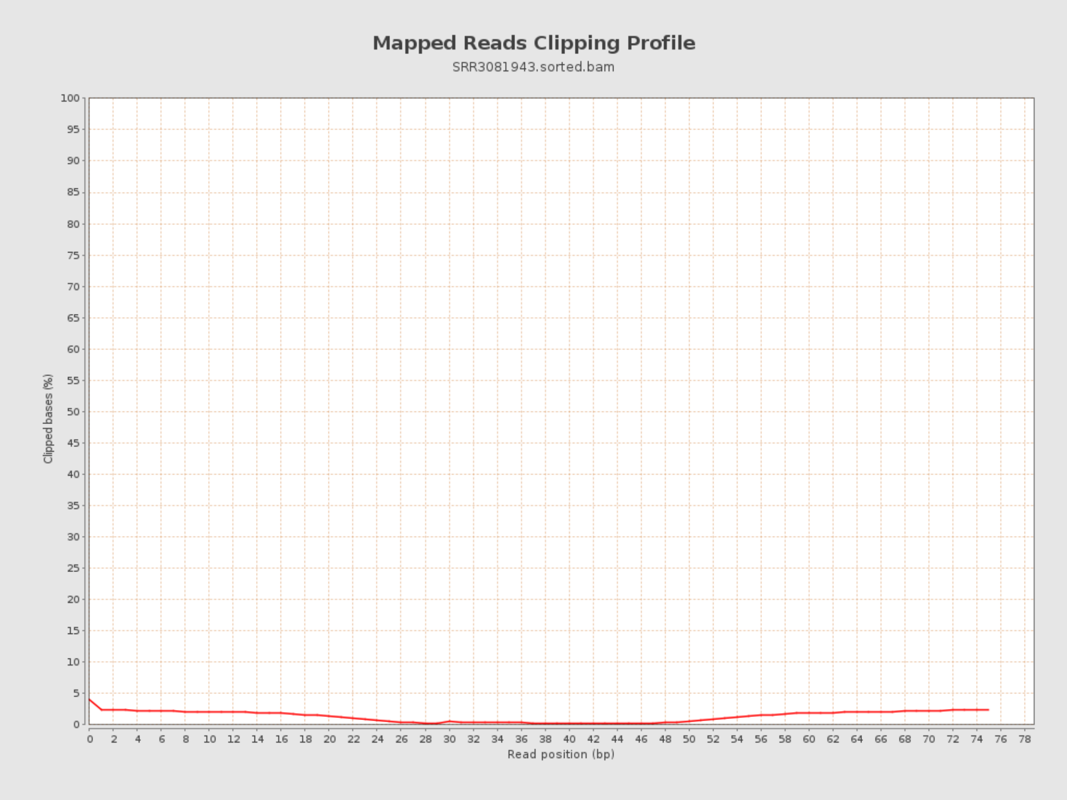
8. Results : Mapped Reads Nucleotide Content



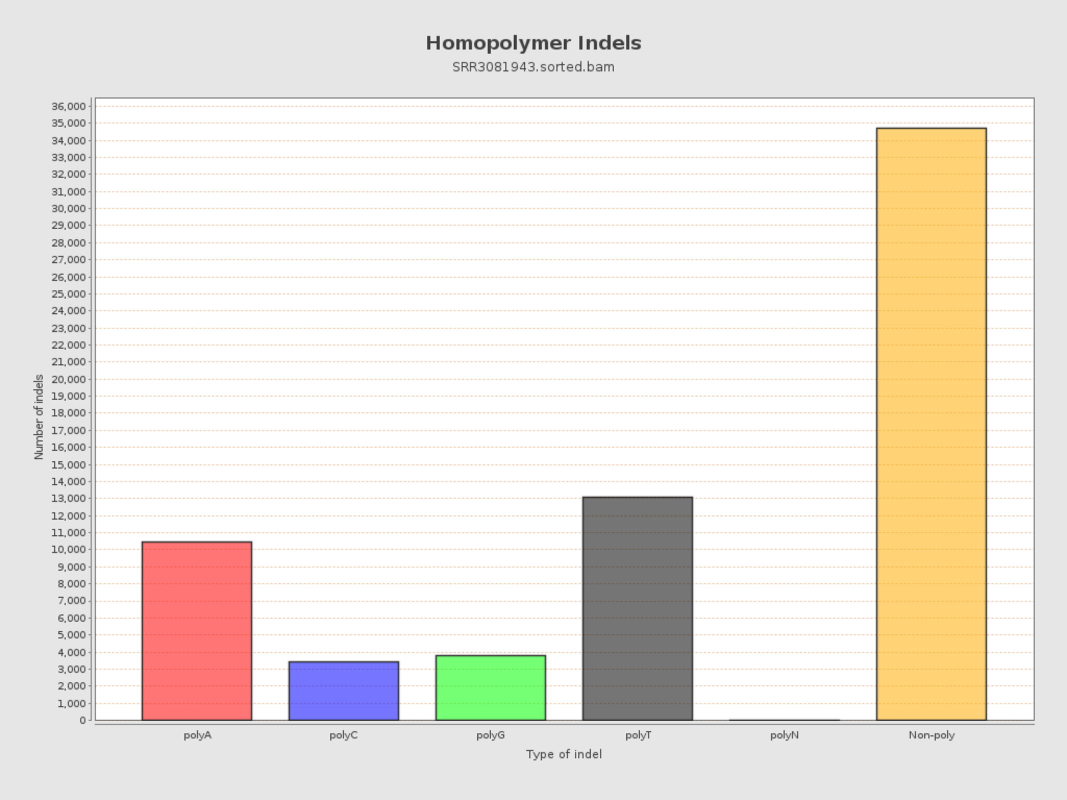
9. Results : Mapped Reads GC-content Distribution



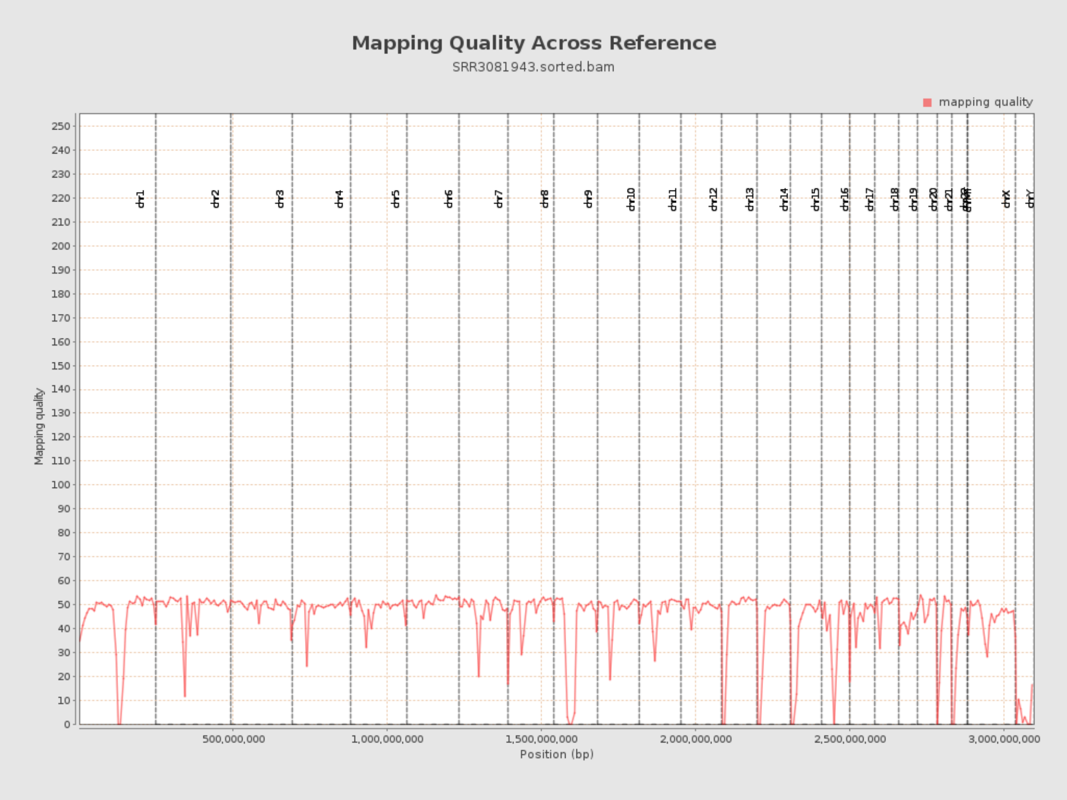
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram