Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:40:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081746.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_SRR3081746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:40:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,150,668
Mapped reads	1,932,702 / 89.87%
Unmapped reads	217,966 / 10.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,533 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	78,883 / 3.67%
Duplication rate	3.08%
Clipped reads	851,080 / 39.57%

2.2. ACGT Content

Number/percentage of A's	35,390,747 / 27.44%
Number/percentage of C's	24,318,640 / 18.86%
Number/percentage of T's	40,345,407 / 31.28%
Number/percentage of G's	28,914,362 / 22.42%
Number/percentage of N's	1,468 / 0%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.372

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

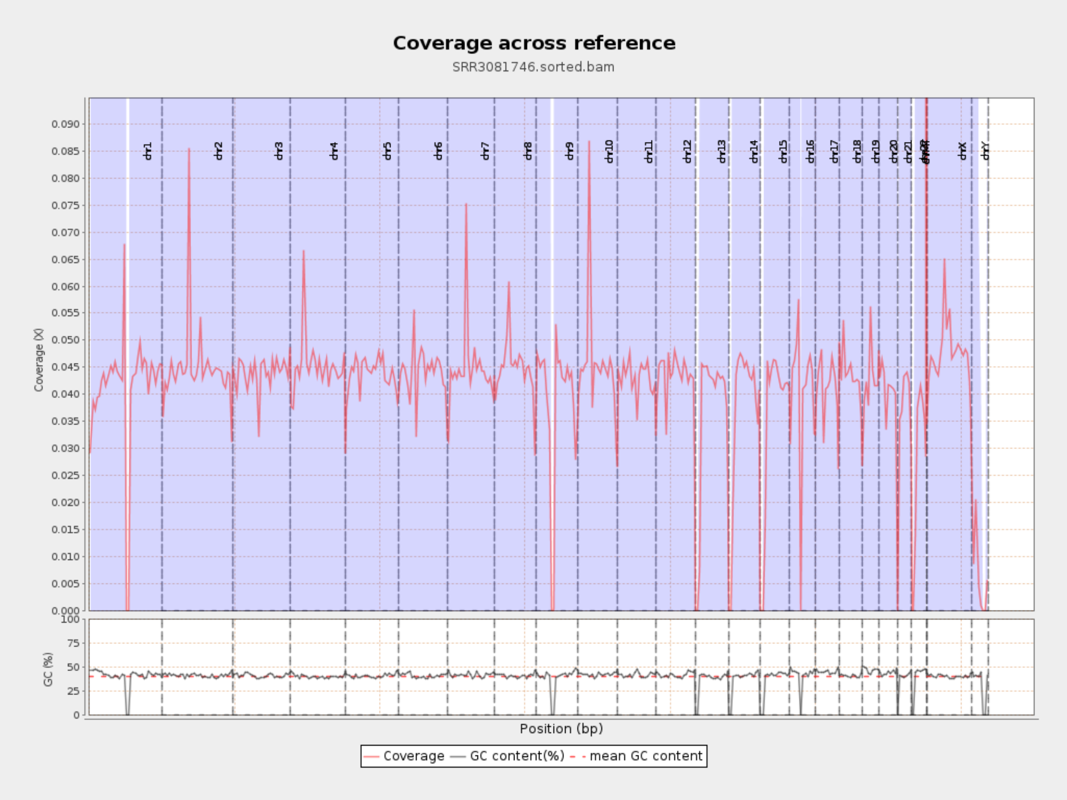
General error rate	0.82%
Mismatches	1,034,116
Insertions	9,425
Mapped reads with at least one insertion	0.48%
Deletions	26,094
Mapped reads with at least one deletion	1.34%
Homopolymer indels	47.17%

2.6. Chromosome stats

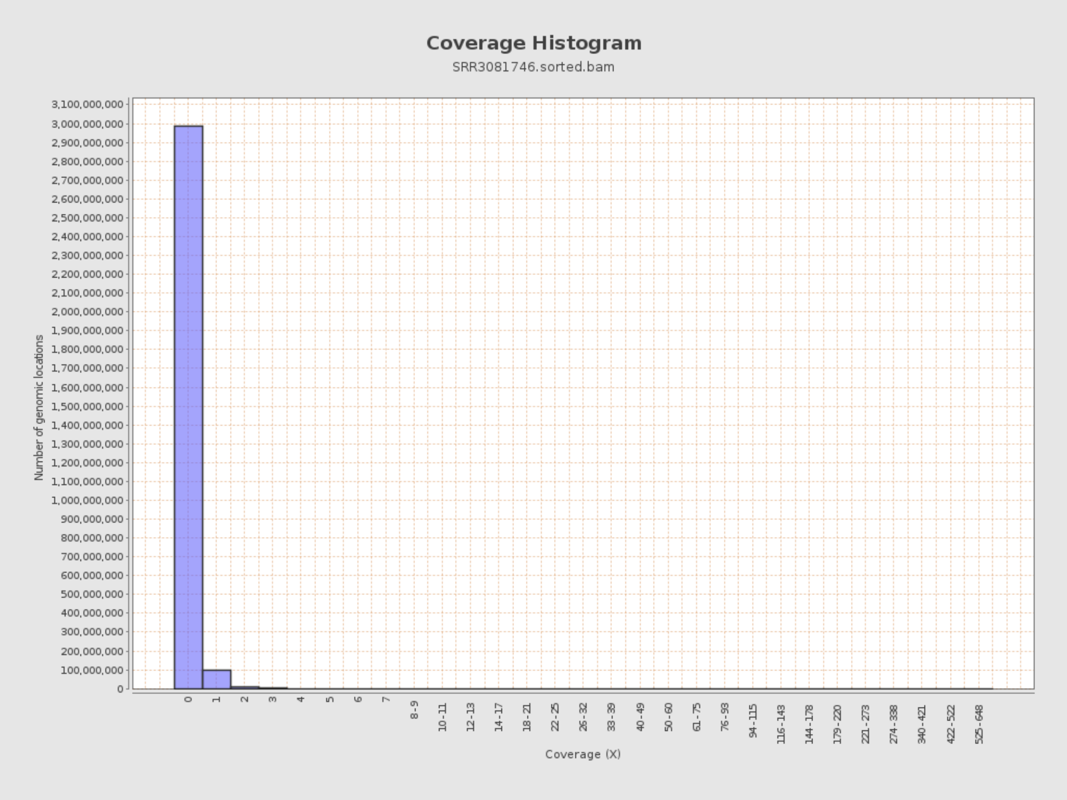
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10241303	0.0411	0.6082
chr2	243199373	10970650	0.0451	0.4706
chr3	198022430	8694389	0.0439	0.239
chr4	191154276	8647504	0.0452	0.2652
chr5	180915260	7947719	0.0439	0.2363
chr6	171115067	7534617	0.044	0.2776
chr7	159138663	7180259	0.0451	0.5212

chr8	146364022	6550514	0.0448	0.4666
chr9	141213431	5395284	0.0382	0.3554
chr10	135534747	6231756	0.046	0.435
chr11	135006516	5787058	0.0429	0.3169
chr12	133851895	5817786	0.0435	0.2367
chr13	115169878	4109873	0.0357	0.2101
chr14	107349540	3905092	0.0364	0.2341
chr15	102531392	3614021	0.0352	0.2136
chr16	90354753	3648160	0.0404	0.2627
chr17	81195210	3314978	0.0408	0.244
chr18	78077248	3439583	0.0441	0.6436
chr19	59128983	2521720	0.0426	0.4786
chr20	63025520	2552096	0.0405	0.2358
chr21	48129895	1708682	0.0355	0.2363
chr22	51304566	1348338	0.0263	0.1799
chrMT	16571	49958	3.0148	2.615
chrX	155270560	7408004	0.0477	0.2793
chrY	59373566	397733	0.0067	0.1706

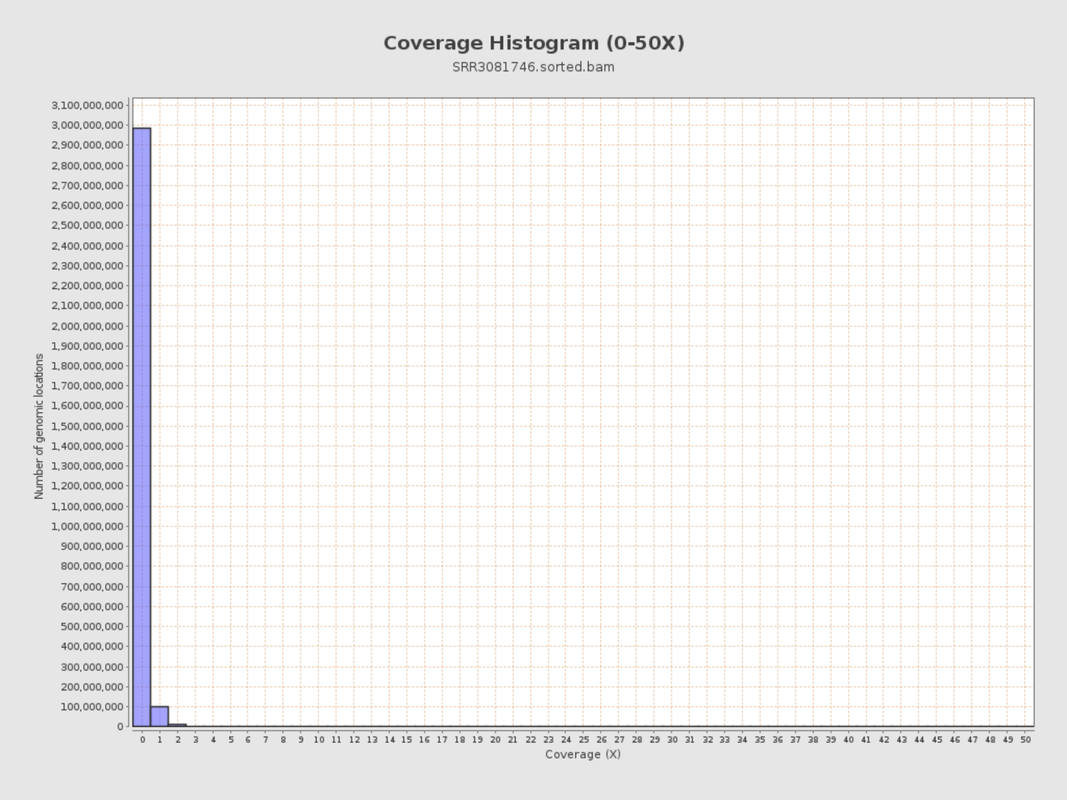
3. Results : Coverage across reference



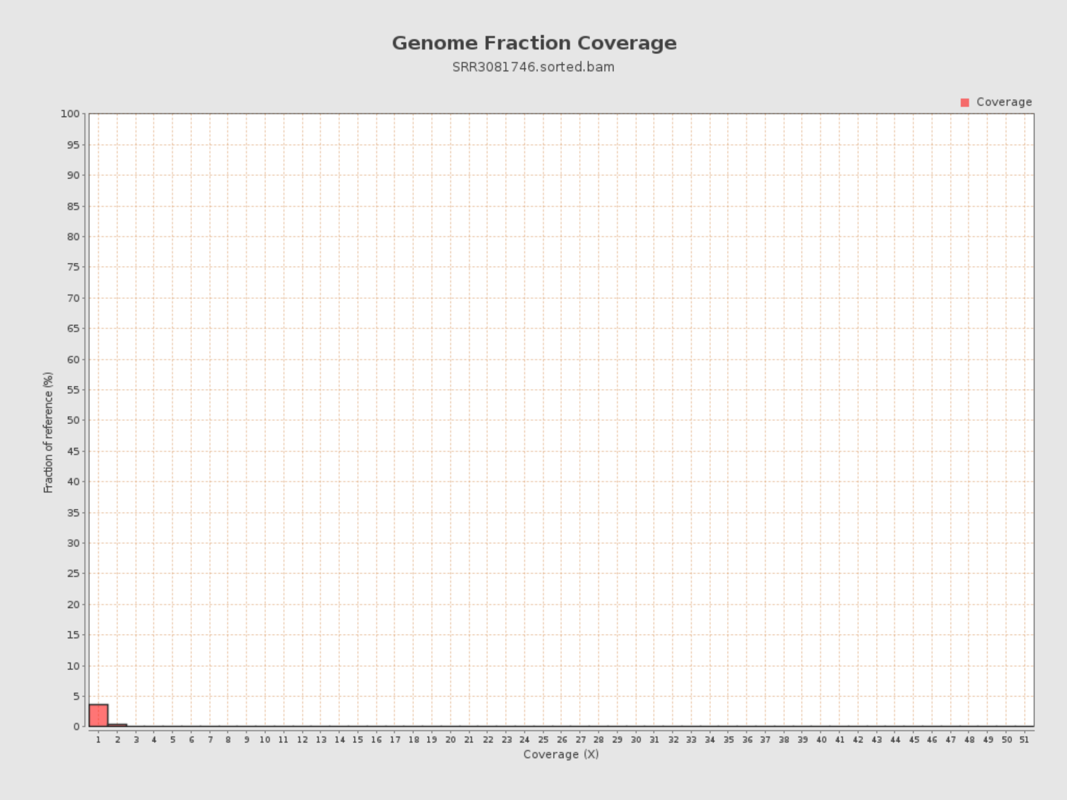
4. Results : Coverage Histogram



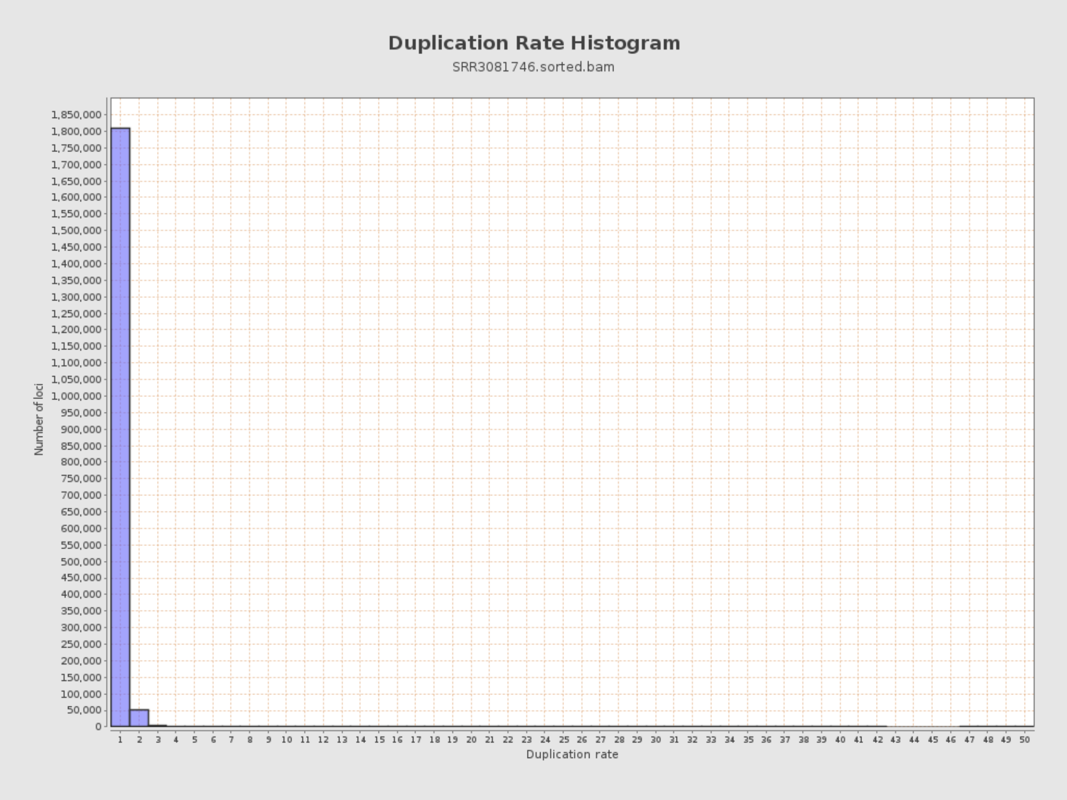
5. Results : Coverage Histogram (0-50X)



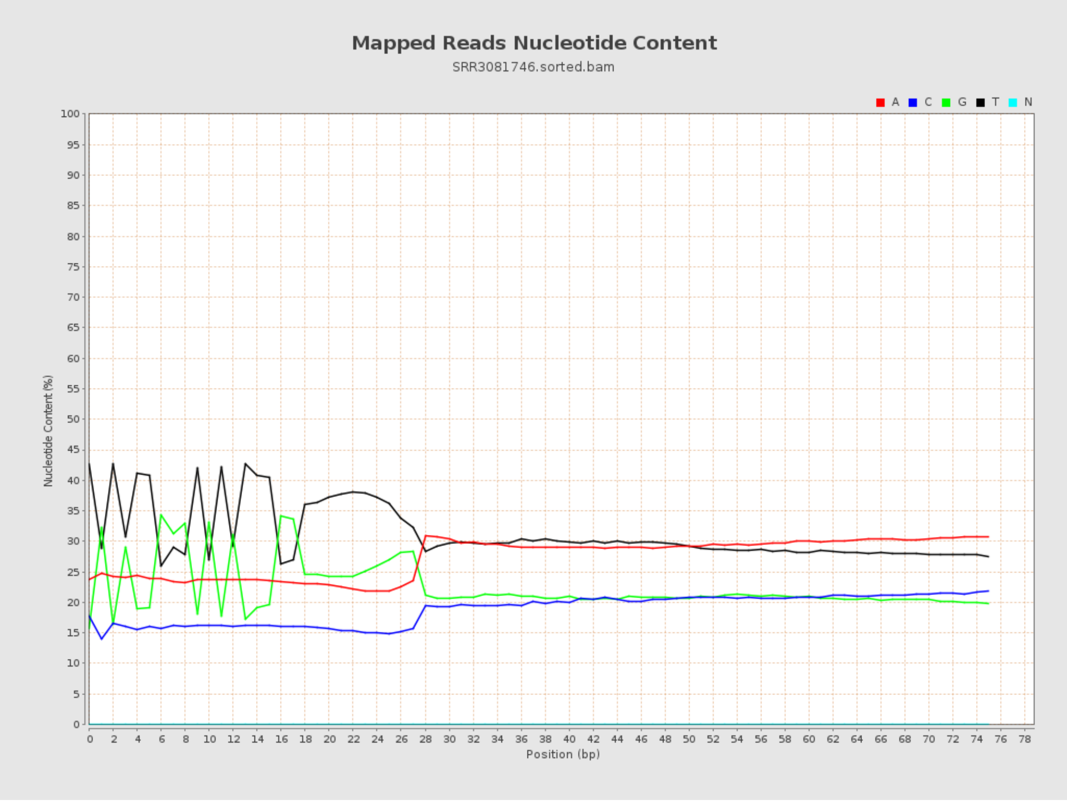
6. Results : Genome Fraction Coverage



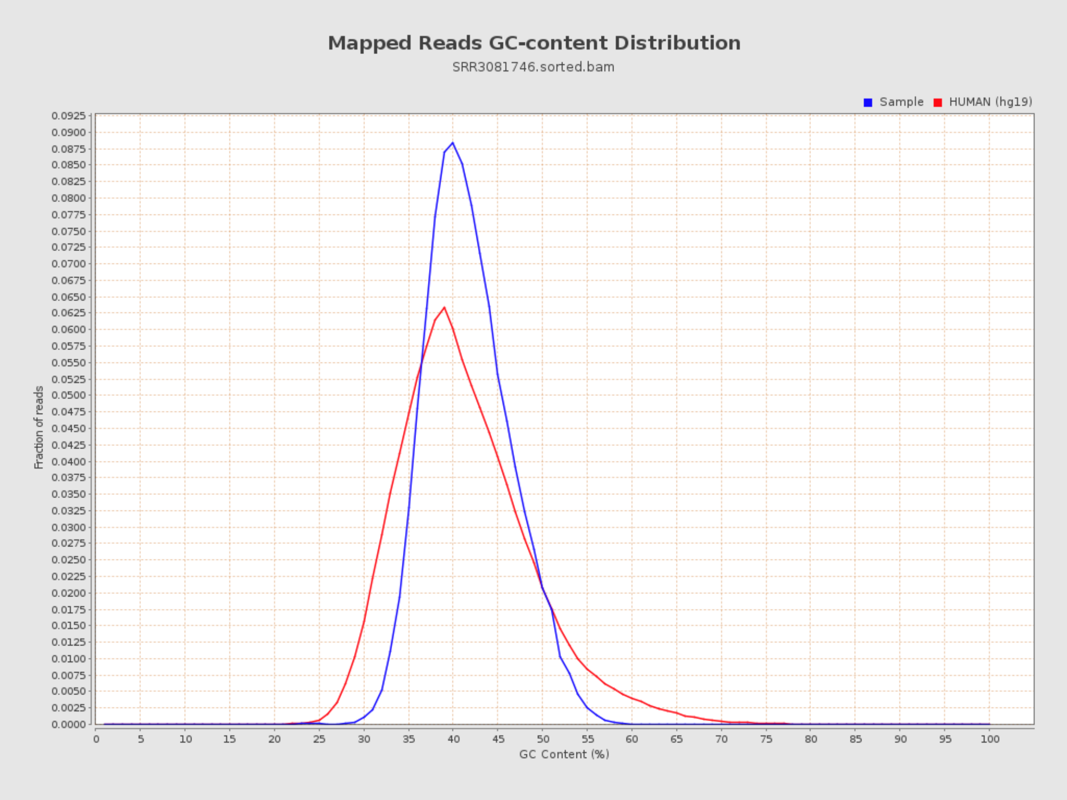
7. Results : Duplication Rate Histogram



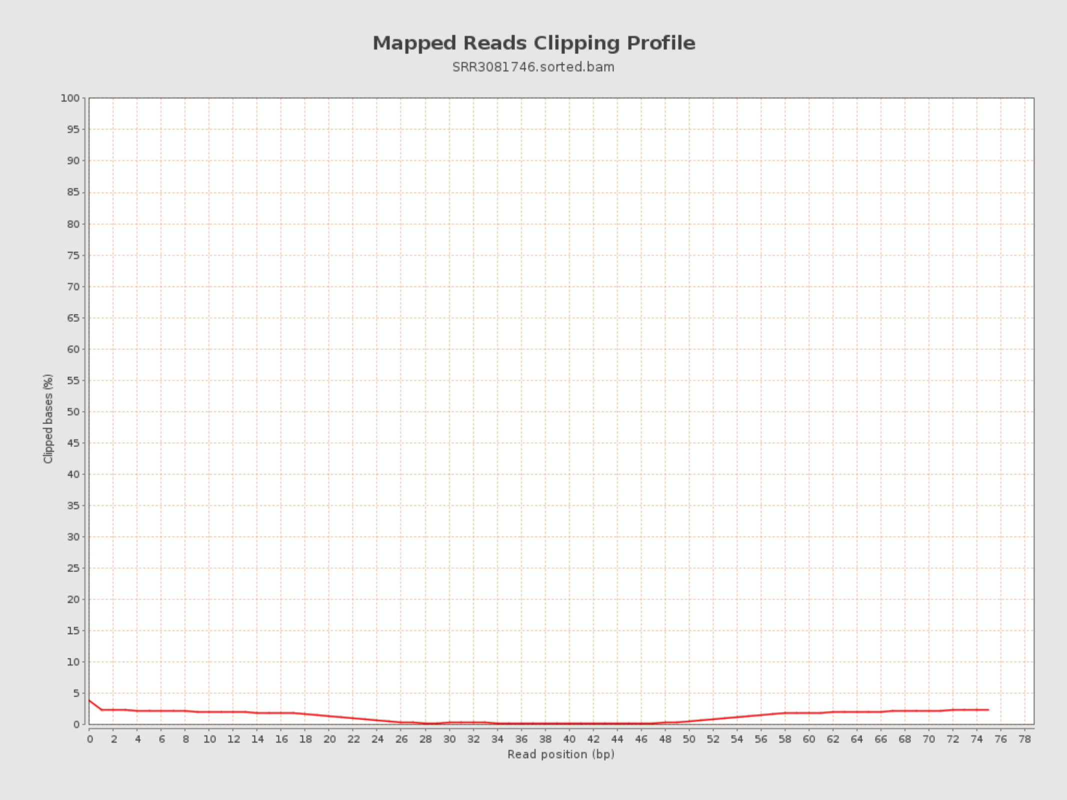
8. Results : Mapped Reads Nucleotide Content



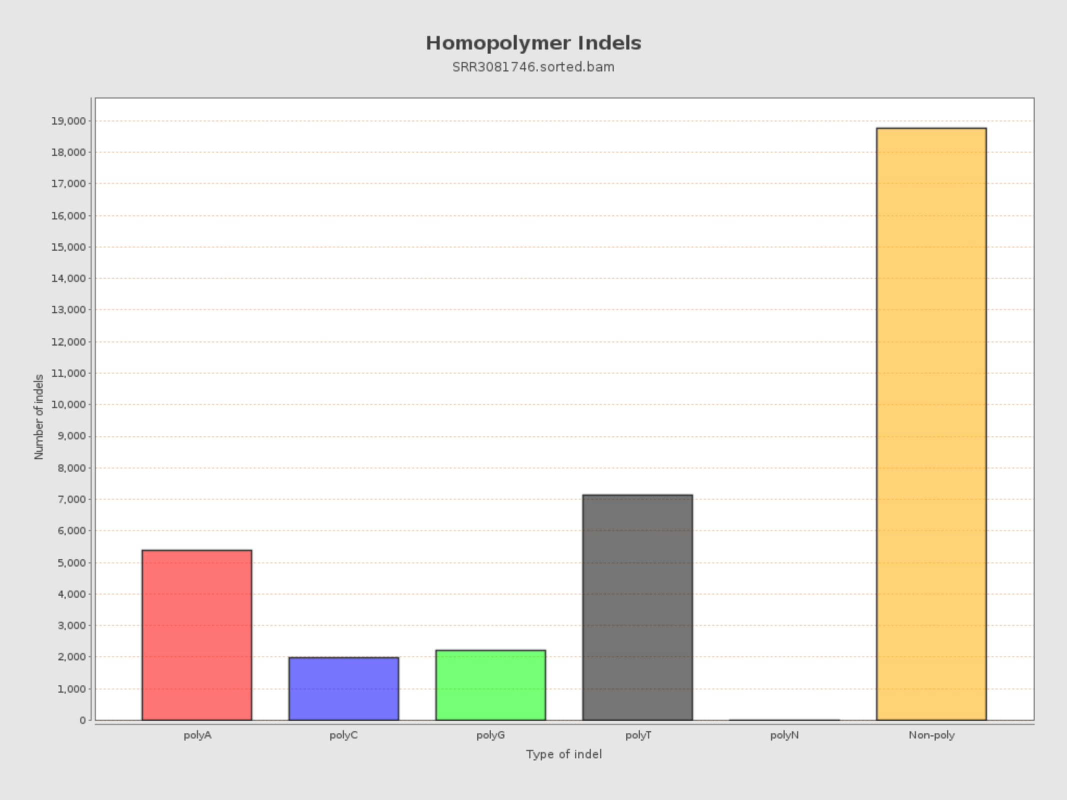
9. Results : Mapped Reads GC-content Distribution



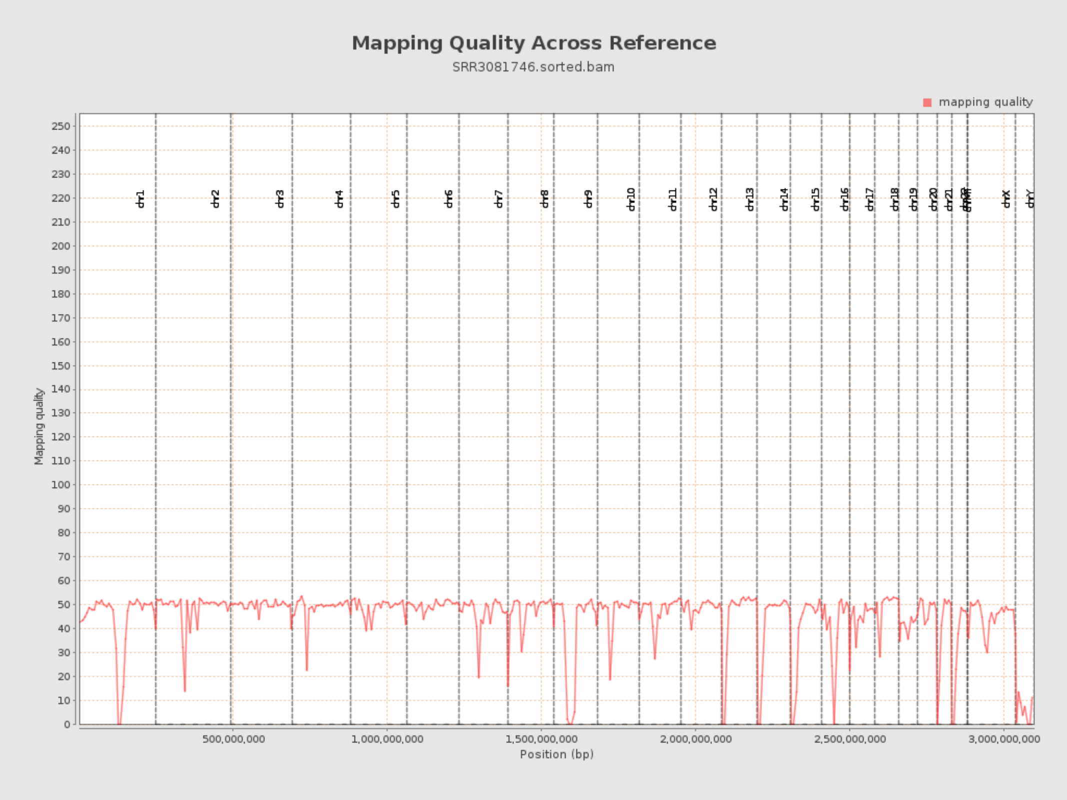
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram