Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:49:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081007.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_SRR3081007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081007.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:49:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,138,339
Mapped reads	2,518,882 / 80.26%
Unmapped reads	619,457 / 19.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,426 / 0.33%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	85,534 / 2.73%
Duplication rate	2.52%
Clipped reads	1,451,510 / 46.25%

2.2. ACGT Content

Number/percentage of A's	44,393,444 / 27.98%
Number/percentage of C's	32,286,479 / 20.35%
Number/percentage of T's	45,824,591 / 28.88%
Number/percentage of G's	36,173,644 / 22.8%
Number/percentage of N's	2,023 / 0%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.3974

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

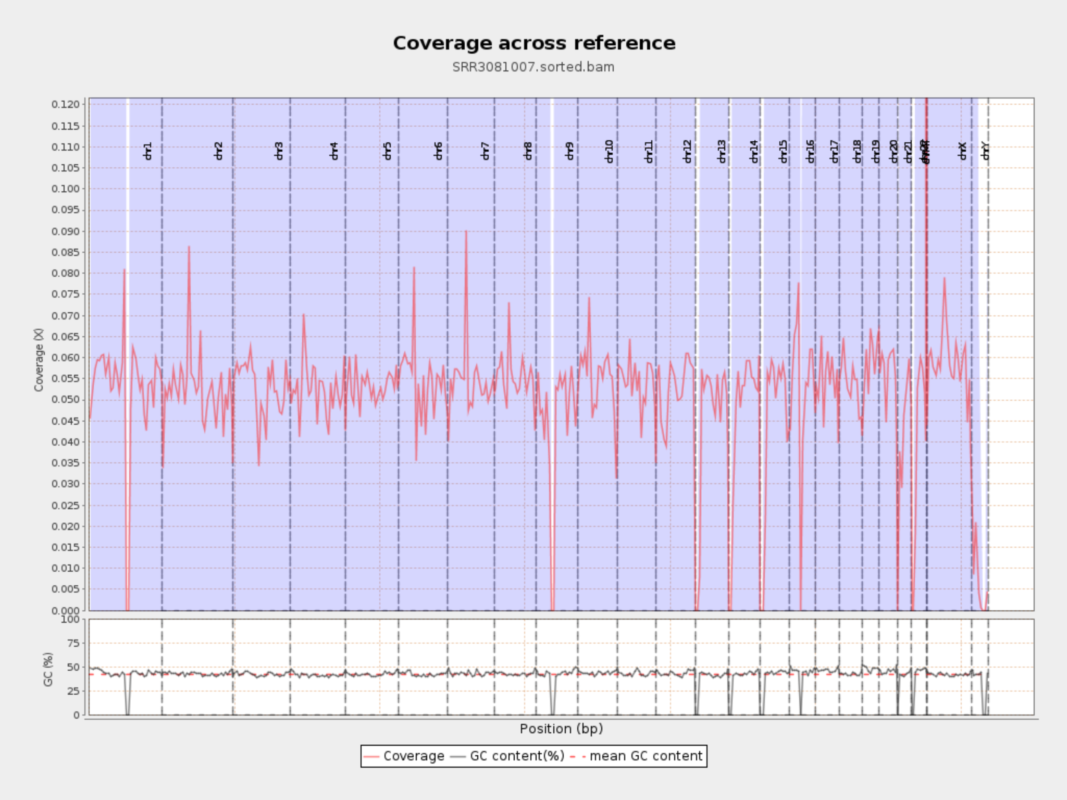
General error rate	0.76%
Mismatches	1,182,046
Insertions	10,996
Mapped reads with at least one insertion	0.43%
Deletions	33,088
Mapped reads with at least one deletion	1.3%
Homopolymer indels	45.3%

2.6. Chromosome stats

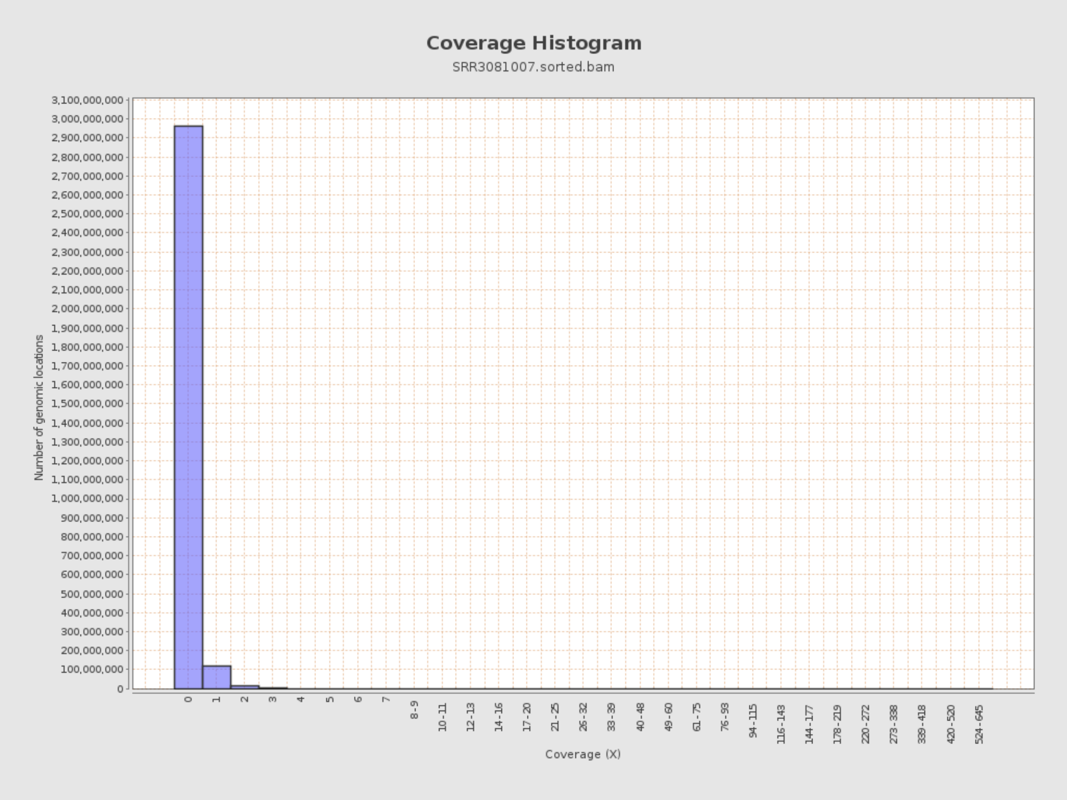
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13080679	0.0525	0.6198
chr2	243199373	12810367	0.0527	0.4726
chr3	198022430	10444008	0.0527	0.2597
chr4	191154276	10013751	0.0524	0.2794
chr5	180915260	9641644	0.0533	0.2774
chr6	171115067	9341061	0.0546	0.3818
chr7	159138663	8716507	0.0548	0.6478

chr8	146364022	8112993	0.0554	0.375
chr9	141213431	6253302	0.0443	0.3697
chr10	135534747	7512244	0.0554	0.3588
chr11	135006516	7288626	0.054	0.3847
chr12	133851895	7062421	0.0528	0.2641
chr13	115169878	5033833	0.0437	0.2391
chr14	107349540	4862030	0.0453	0.2642
chr15	102531392	4504354	0.0439	0.2548
chr16	90354753	4802750	0.0532	0.297
chr17	81195210	4415784	0.0544	0.3121
chr18	78077248	4253222	0.0545	0.7126
chr19	59128983	3490972	0.059	0.4739
chr20	63025520	3561861	0.0565	0.2954
chr21	48129895	2000671	0.0416	0.2558
chr22	51304566	1937502	0.0378	0.2211
chrMT	16571	34965	2.11	2.0106
chrX	155270560	9148485	0.0589	0.3184
chrY	59373566	414113	0.007	0.1529

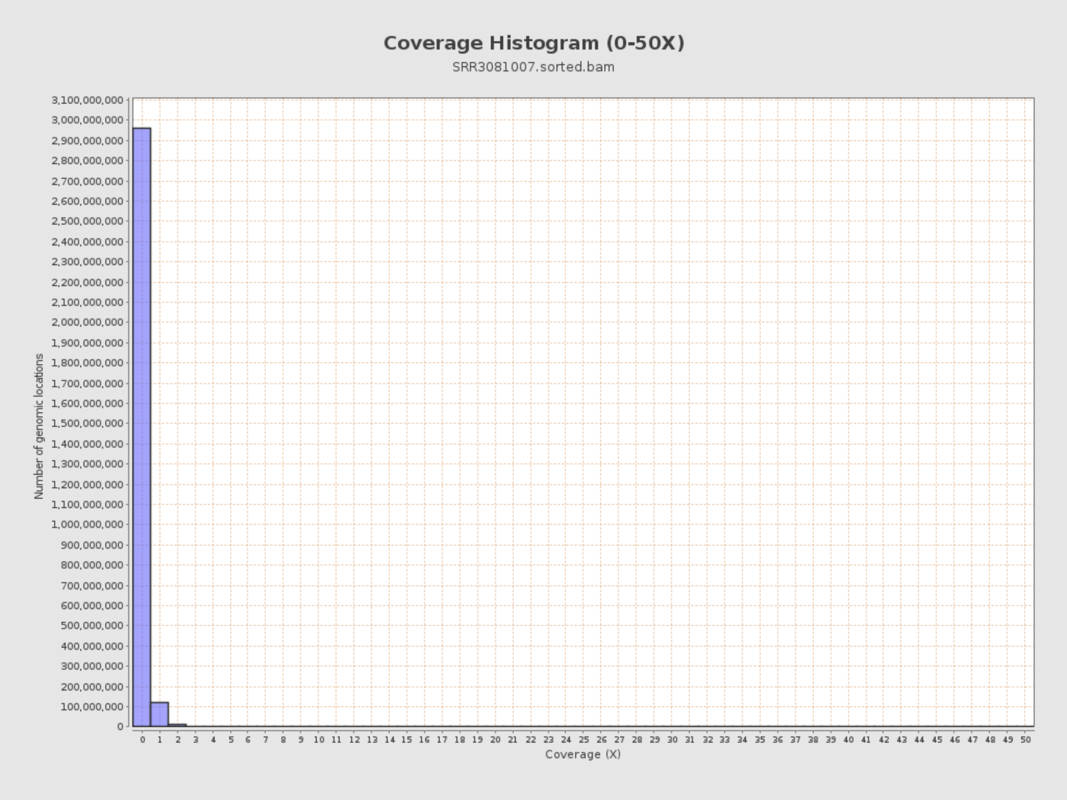
3. Results : Coverage across reference



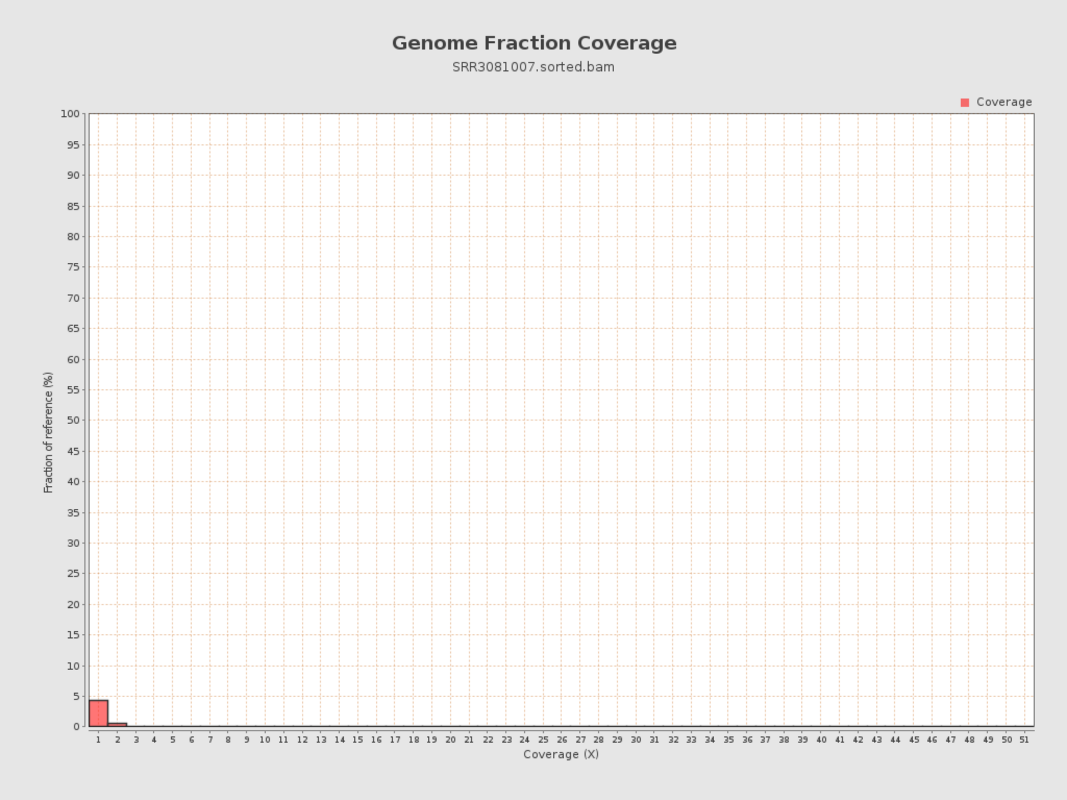
4. Results : Coverage Histogram



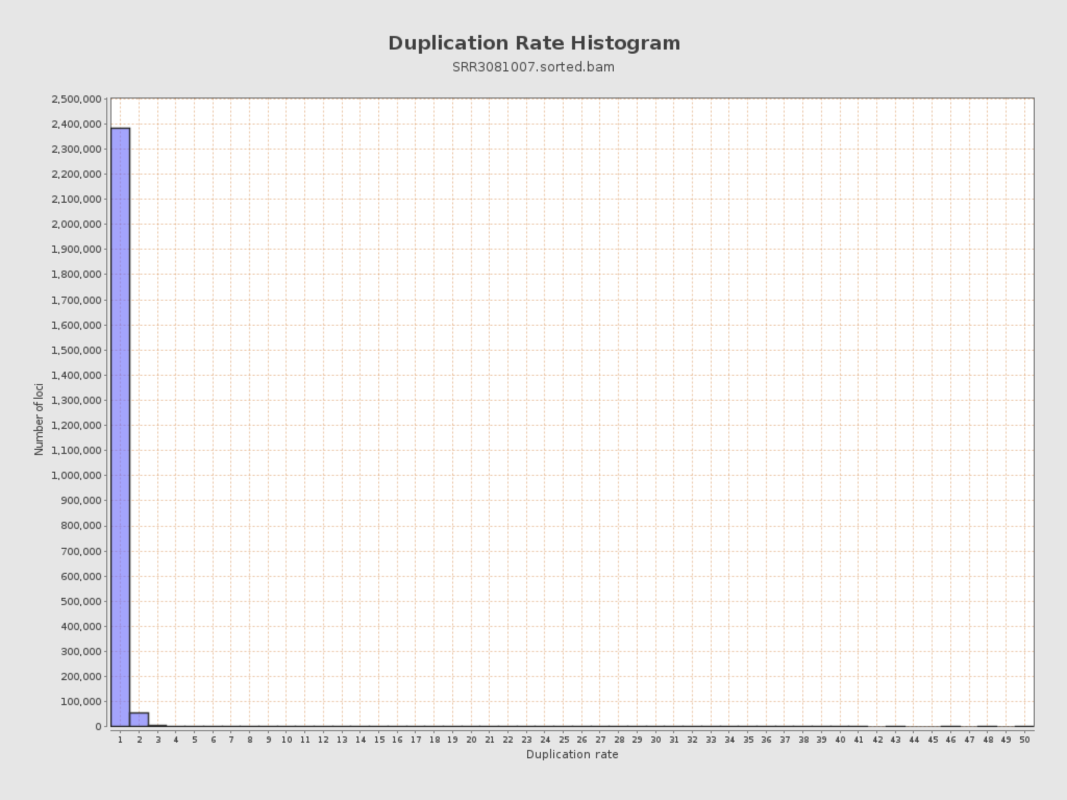
5. Results : Coverage Histogram (0-50X)



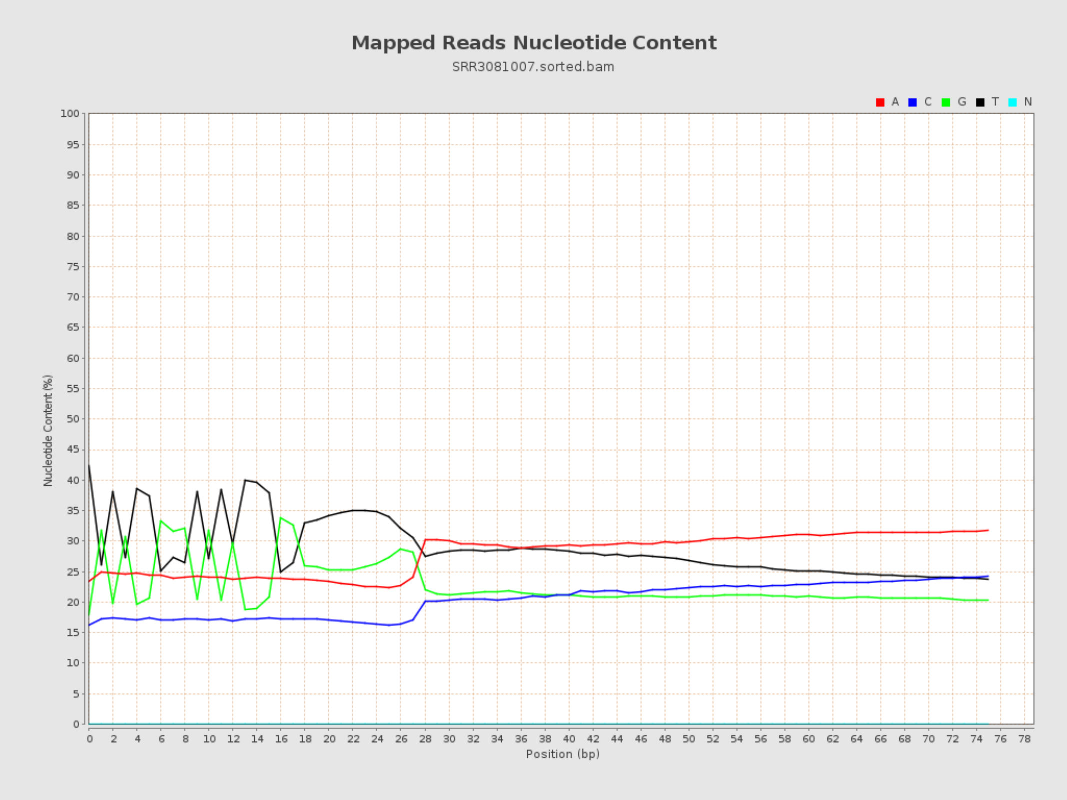
6. Results : Genome Fraction Coverage



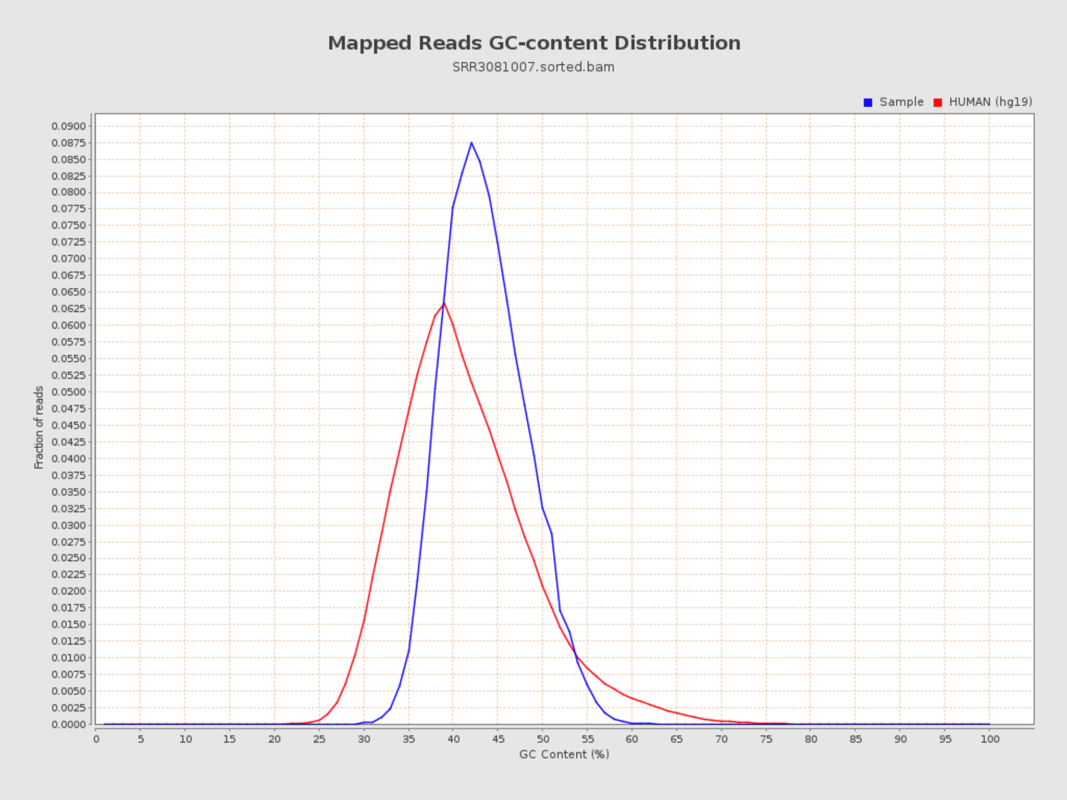
7. Results : Duplication Rate Histogram



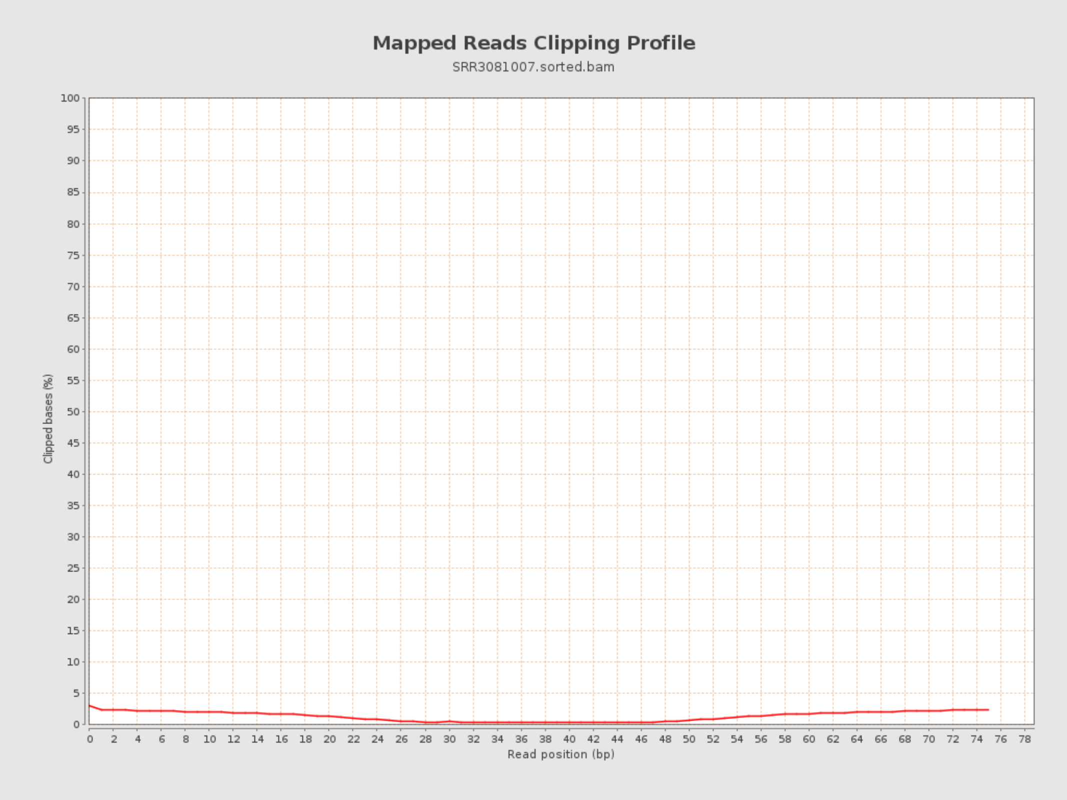
8. Results : Mapped Reads Nucleotide Content



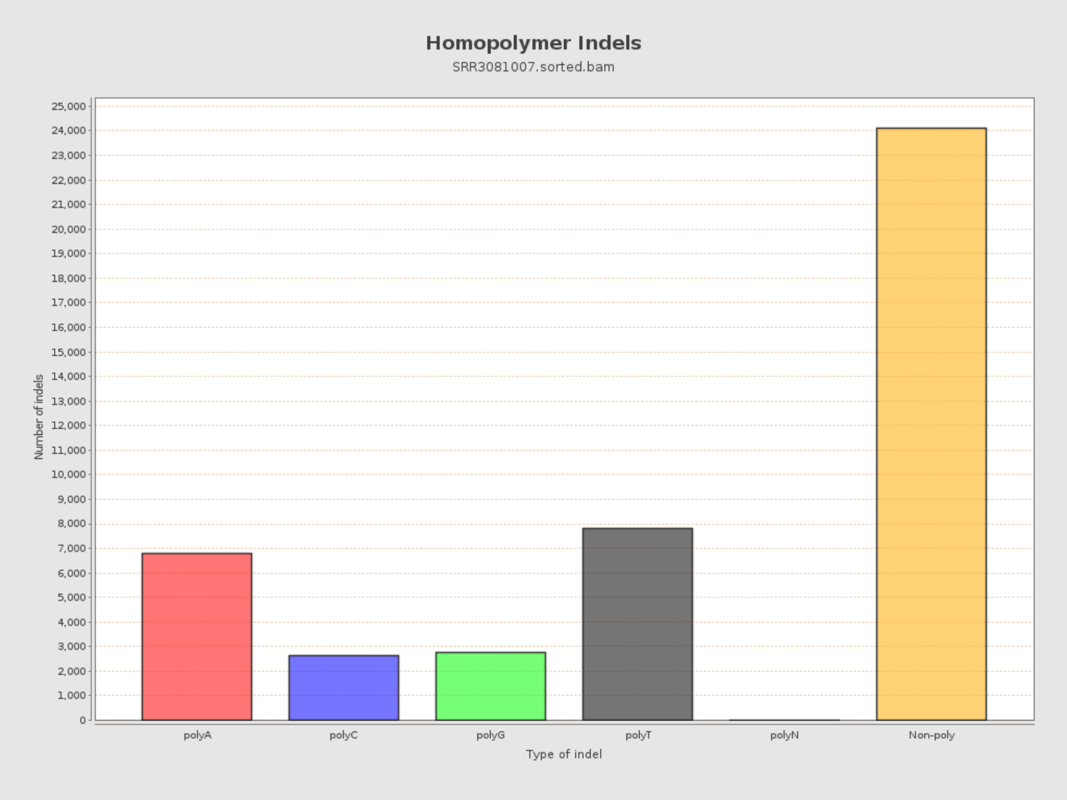
9. Results : Mapped Reads GC-content Distribution



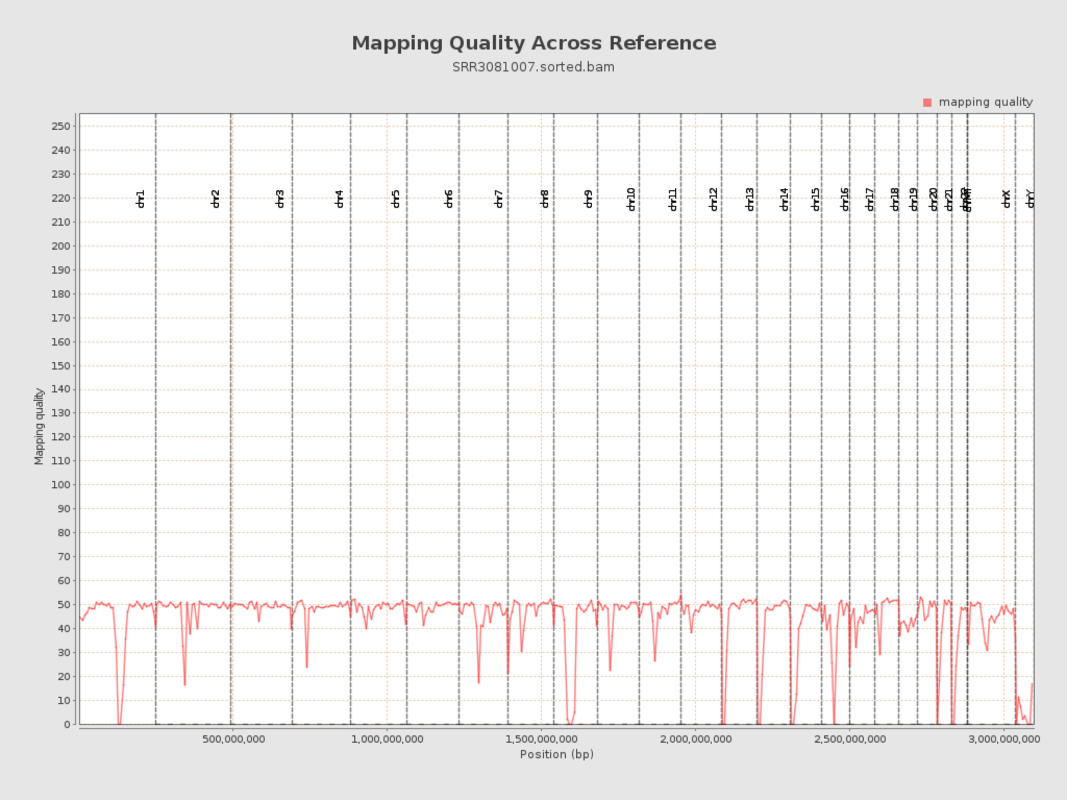
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram