Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:51:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081146.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_SRR3081146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081146.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:51:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,307,818
Mapped reads	2,026,037 / 87.79%
Unmapped reads	281,781 / 12.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,110 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	84,833 / 3.68%
Duplication rate	3.44%
Clipped reads	958,408 / 41.53%

2.2. ACGT Content

Number/percentage of A's	37,761,278 / 28.12%
Number/percentage of C's	24,736,550 / 18.42%
Number/percentage of T's	42,209,512 / 31.44%
Number/percentage of G's	29,521,595 / 21.99%
Number/percentage of N's	39,396 / 0.03%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.3311

2.4. Mapping Quality

Mean Mapping Quality	46.63

2.5. Mismatches and indels

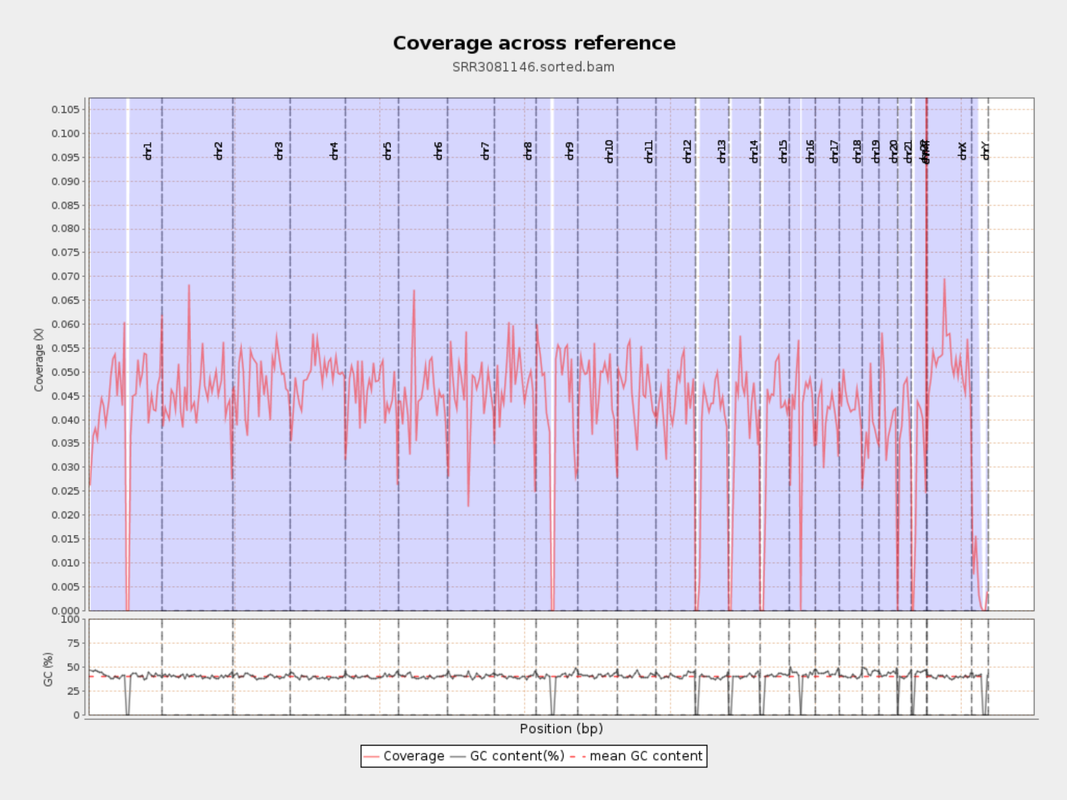
General error rate	0.85%
Mismatches	1,119,446
Insertions	10,428
Mapped reads with at least one insertion	0.51%
Deletions	29,305
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.4%

2.6. Chromosome stats

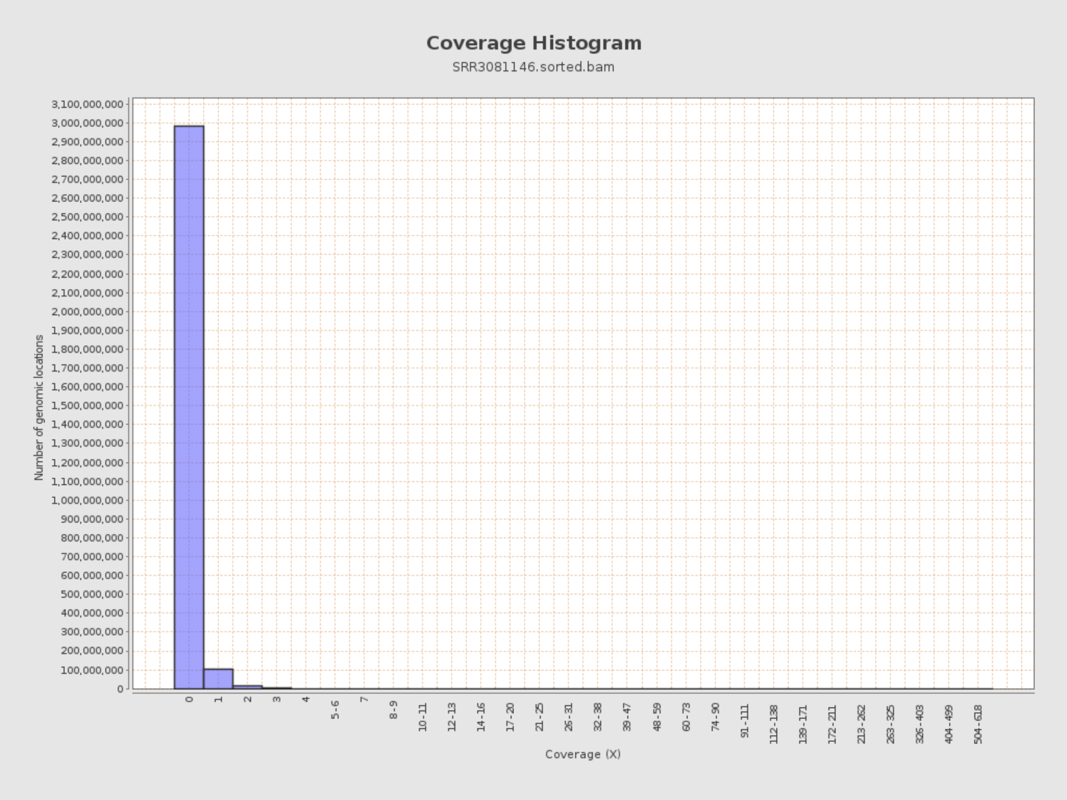
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10585477	0.0425	0.5033
chr2	243199373	11066774	0.0455	0.4216
chr3	198022430	9551942	0.0482	0.2468
chr4	191154276	9405591	0.0492	0.2582
chr5	180915260	8298716	0.0459	0.2421
chr6	171115067	7793255	0.0455	0.3162
chr7	159138663	7275947	0.0457	0.4008

chr8	146364022	6938044	0.0474	0.4171
chr9	141213431	6059368	0.0429	0.3252
chr10	135534747	6383661	0.0471	0.293
chr11	135006516	6254317	0.0463	0.3273
chr12	133851895	5929796	0.0443	0.2424
chr13	115169878	4152727	0.0361	0.2135
chr14	107349540	4054110	0.0378	0.2324
chr15	102531392	3818264	0.0372	0.2226
chr16	90354753	3710199	0.0411	0.2473
chr17	81195210	3262220	0.0402	0.2703
chr18	78077248	3442325	0.0441	0.5434
chr19	59128983	2198965	0.0372	0.396
chr20	63025520	2608822	0.0414	0.2337
chr21	48129895	1790113	0.0372	0.2304
chr22	51304566	1381235	0.0269	0.1837
chrMT	16571	3745	0.226	0.532
chrX	155270560	8035039	0.0517	0.278
chrY	59373566	314774	0.0053	0.1104

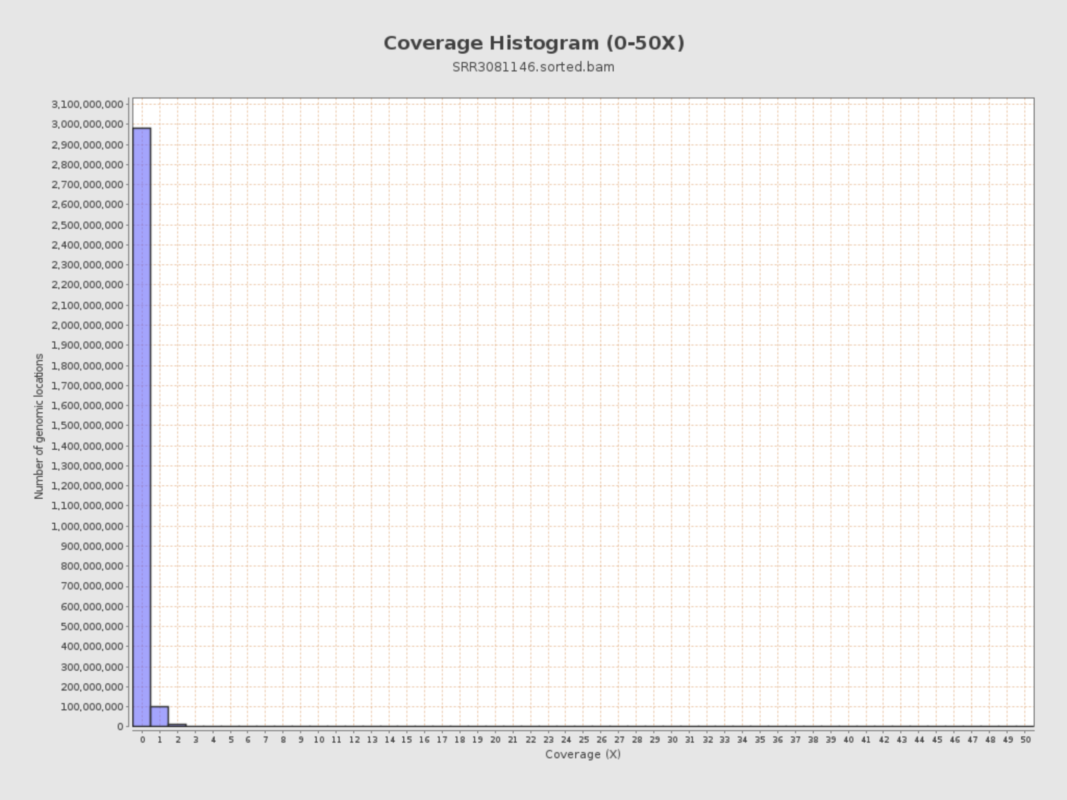
3. Results : Coverage across reference



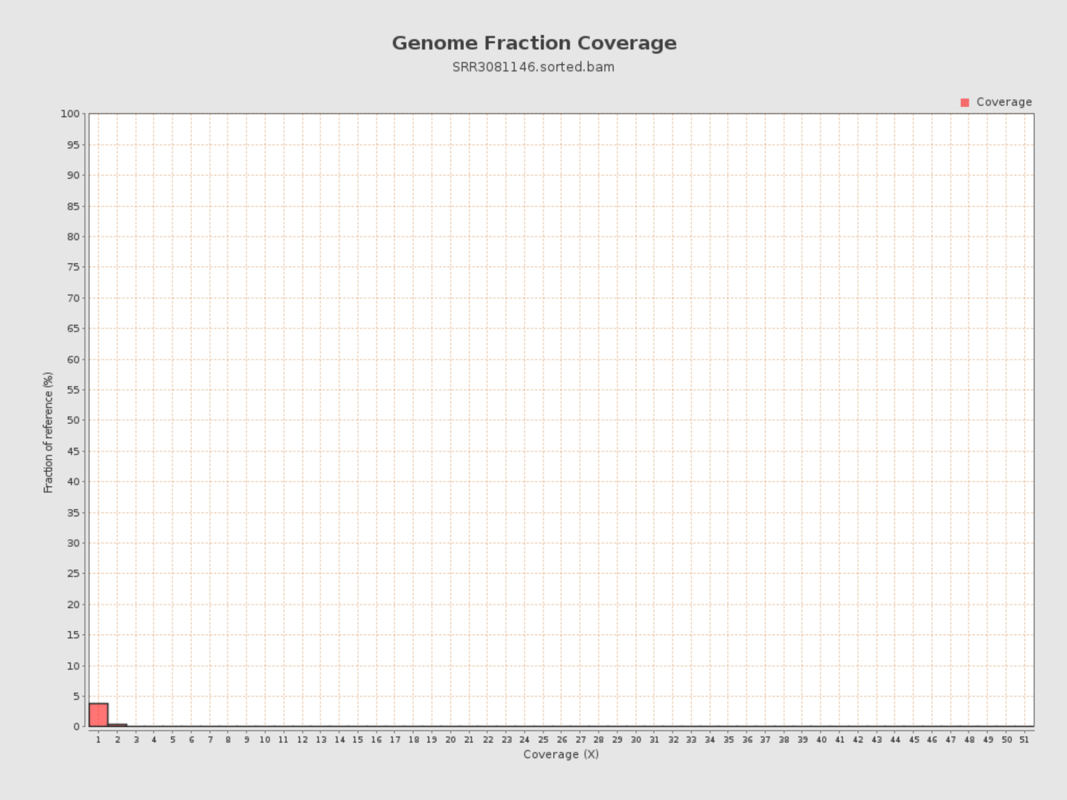
4. Results : Coverage Histogram



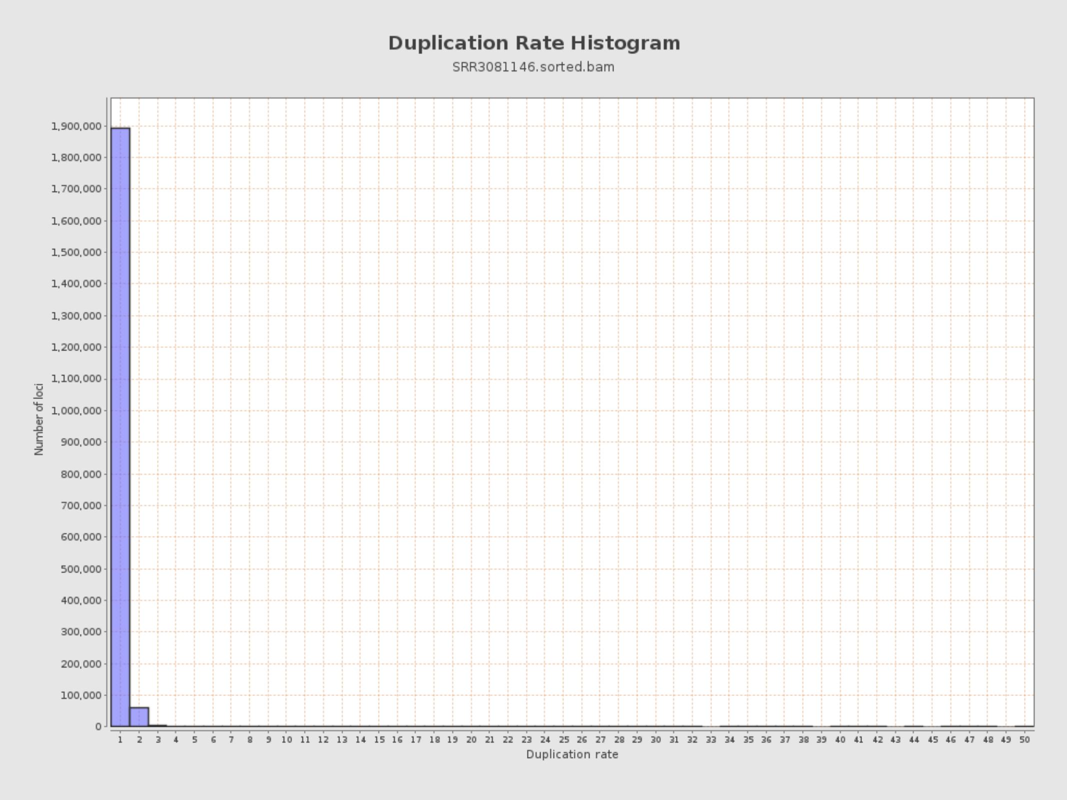
5. Results : Coverage Histogram (0-50X)



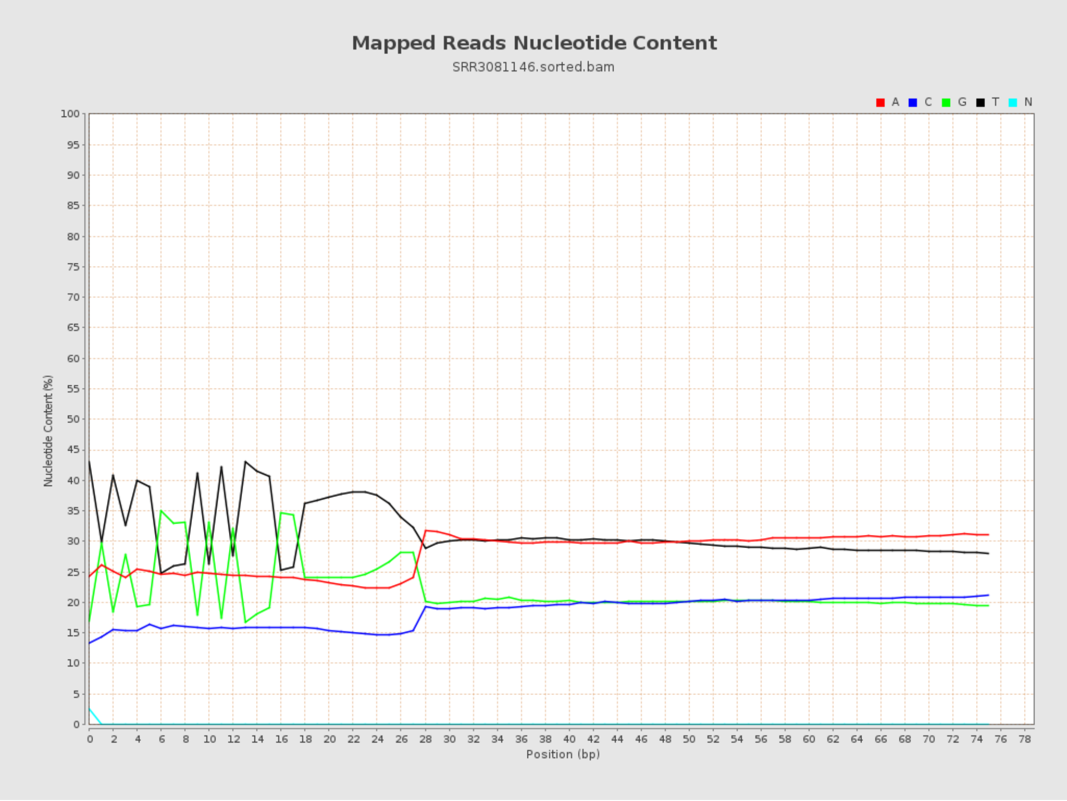
6. Results : Genome Fraction Coverage



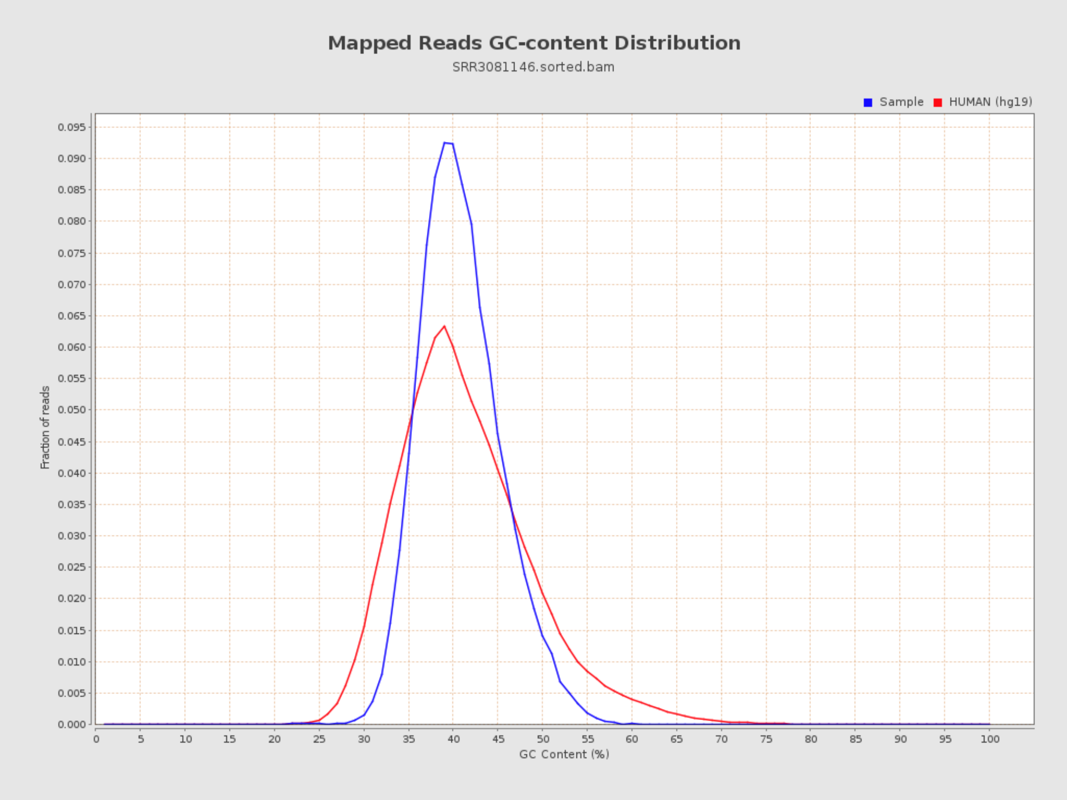
7. Results : Duplication Rate Histogram



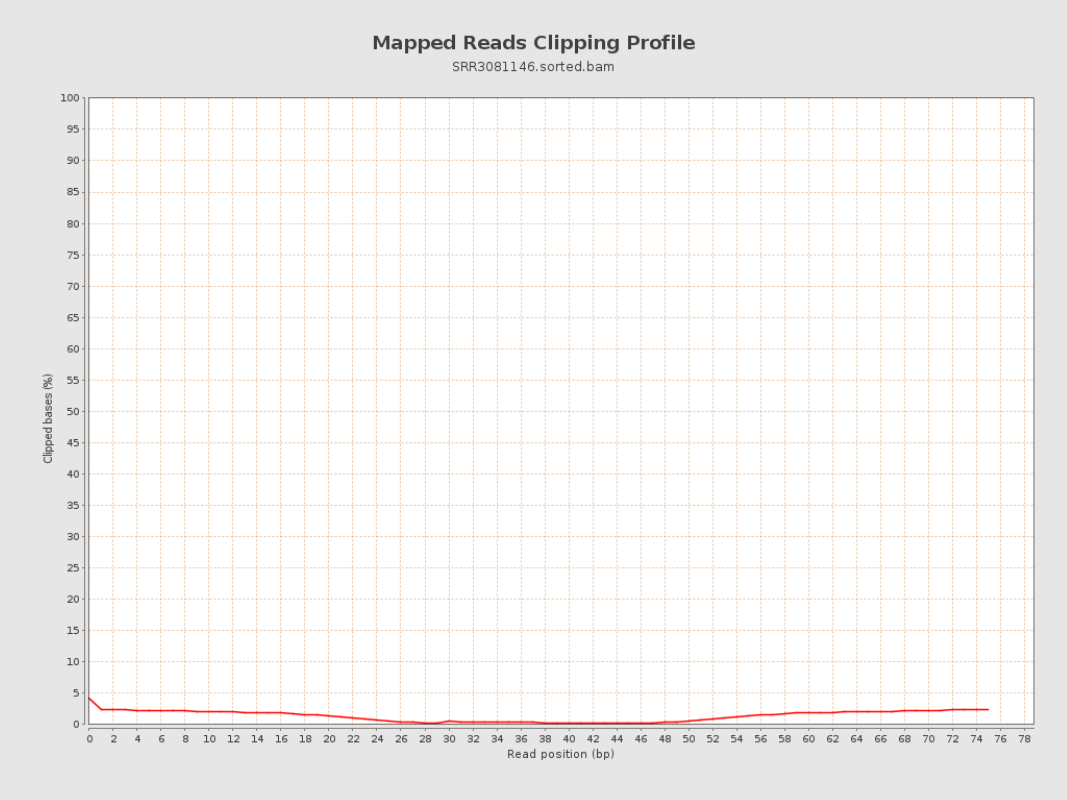
8. Results : Mapped Reads Nucleotide Content



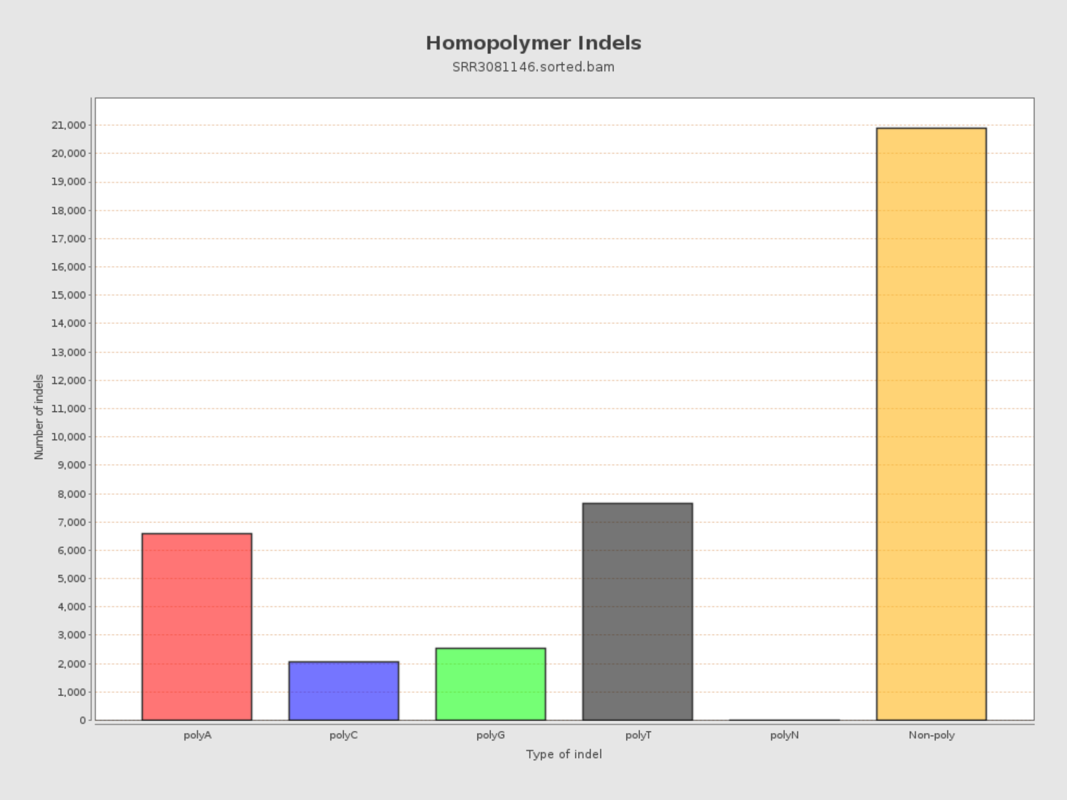
9. Results : Mapped Reads GC-content Distribution



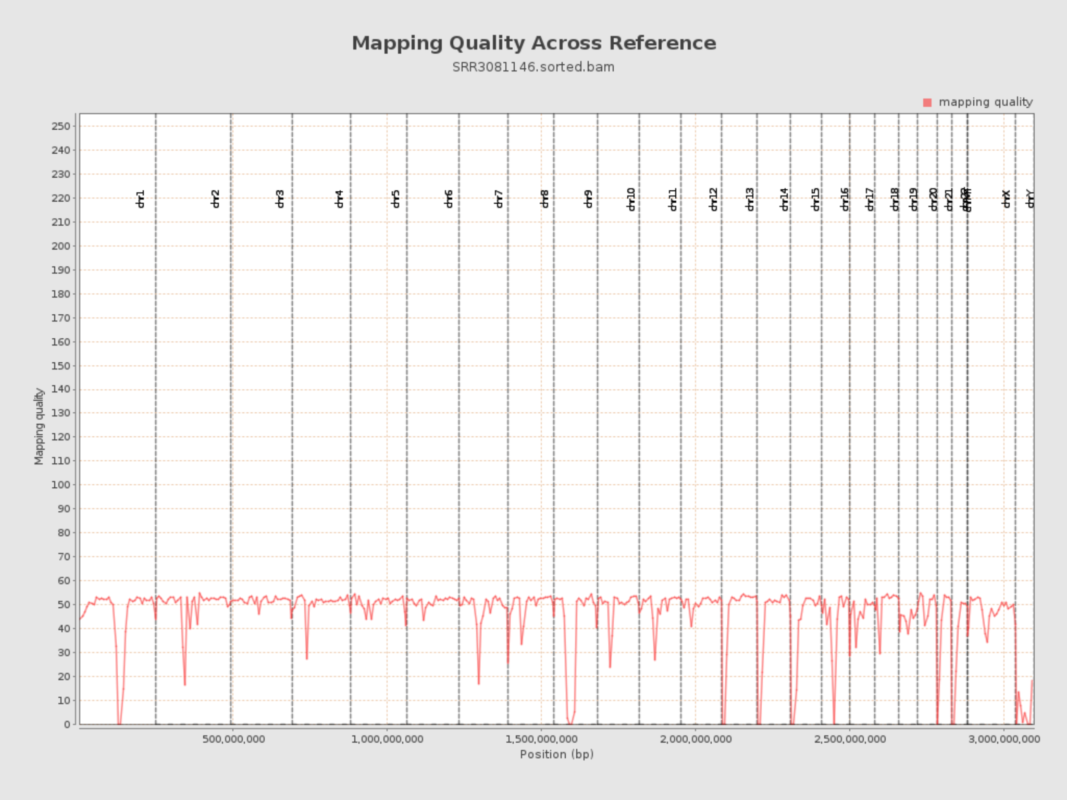
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram