Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:46:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081025.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_SRR3081025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081025.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:46:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,385,588
Mapped reads	1,615,108 / 67.7%
Unmapped reads	770,480 / 32.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,289 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	42,171 / 1.77%
Duplication rate	2.14%
Clipped reads	1,053,377 / 44.16%

2.2. ACGT Content

Number/percentage of A's	27,626,563 / 28.56%
Number/percentage of C's	19,556,996 / 20.22%
Number/percentage of T's	27,760,651 / 28.7%
Number/percentage of G's	21,793,871 / 22.53%
Number/percentage of N's	1,240 / 0%
GC Percentage	42.74%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.2405

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

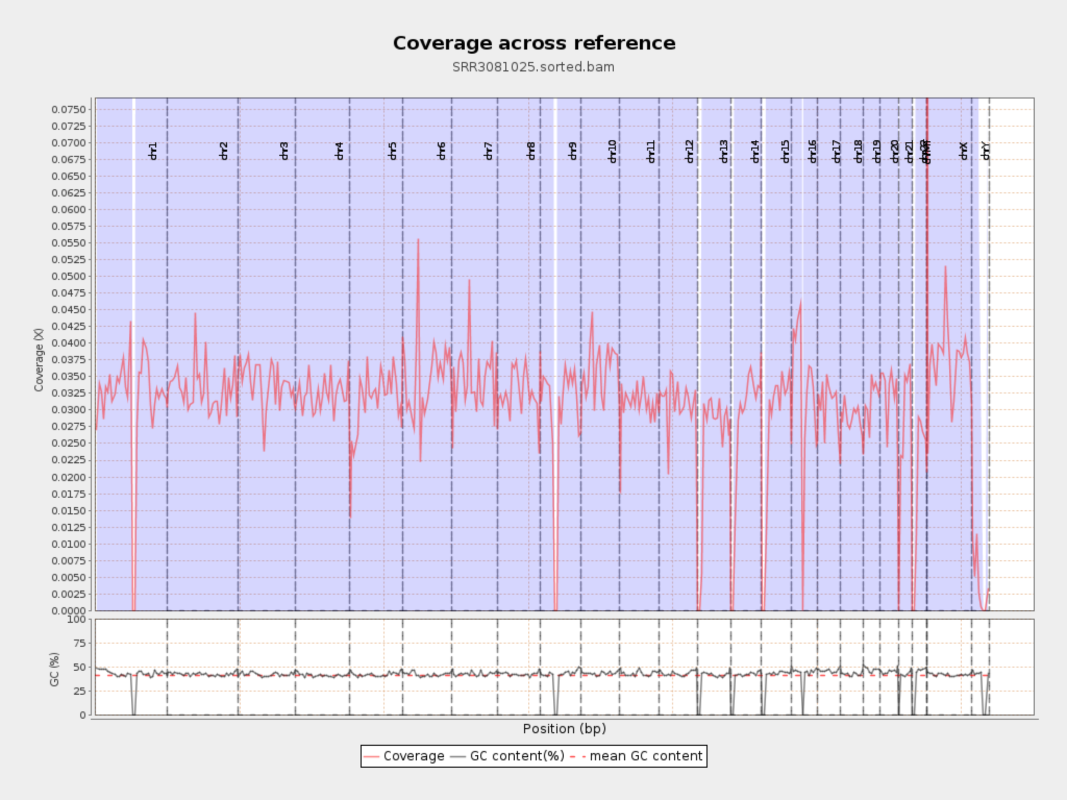
General error rate	0.68%
Mismatches	650,512
Insertions	6,060
Mapped reads with at least one insertion	0.37%
Deletions	17,757
Mapped reads with at least one deletion	1.09%
Homopolymer indels	45.69%

2.6. Chromosome stats

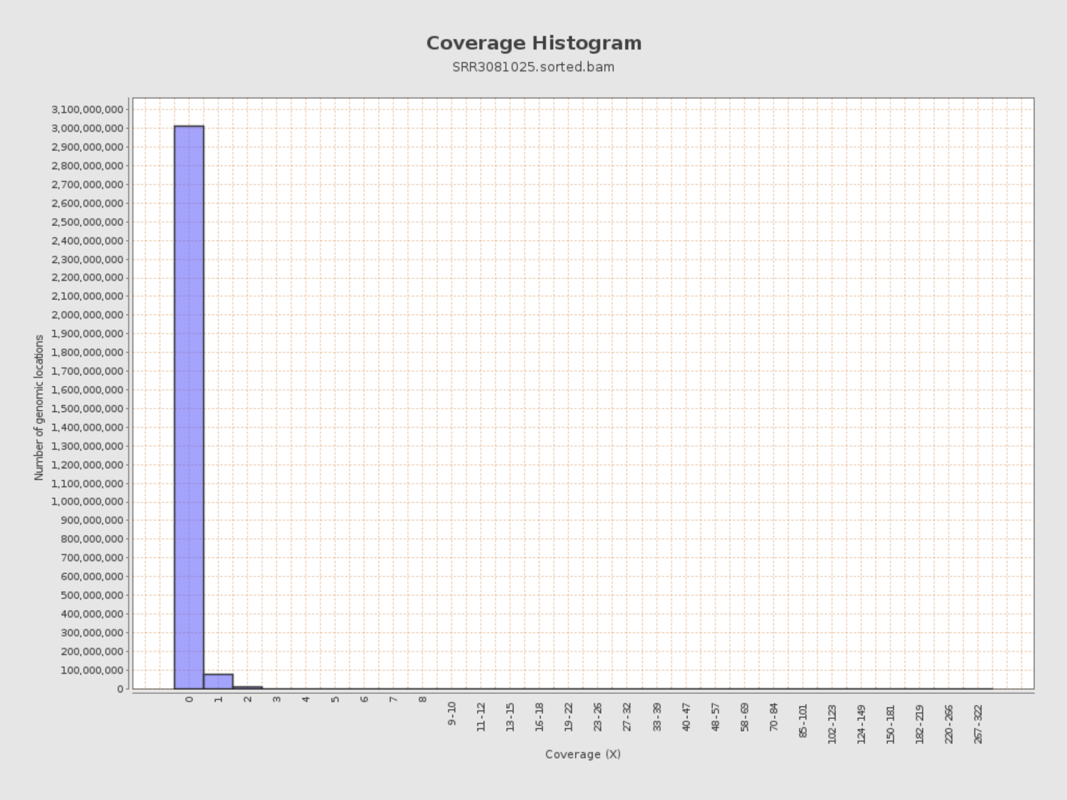
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7840105	0.0315	0.3247
chr2	243199373	8069236	0.0332	0.2546
chr3	198022430	6746309	0.0341	0.2029
chr4	191154276	6209397	0.0325	0.2035
chr5	180915260	5734893	0.0317	0.1967
chr6	171115067	6030380	0.0352	0.2682
chr7	159138663	5551962	0.0349	0.3362

chr8	146364022	4780009	0.0327	0.2415
chr9	141213431	4093227	0.029	0.2304
chr10	135534747	4900883	0.0362	0.2444
chr11	135006516	4209035	0.0312	0.2284
chr12	133851895	4173745	0.0312	0.1964
chr13	115169878	2814644	0.0244	0.1722
chr14	107349540	2889432	0.0269	0.1861
chr15	102531392	2721597	0.0265	0.1888
chr16	90354753	2932291	0.0325	0.2064
chr17	81195210	2506467	0.0309	0.2092
chr18	78077248	2266841	0.029	0.3566
chr19	59128983	1850839	0.0313	0.2813
chr20	63025520	2061613	0.0327	0.2025
chr21	48129895	1307668	0.0272	0.192
chr22	51304566	977432	0.0191	0.1512
chrMT	16571	31186	1.882	1.7371
chrX	155270560	5837267	0.0376	0.2316
chrY	59373566	233592	0.0039	0.0883

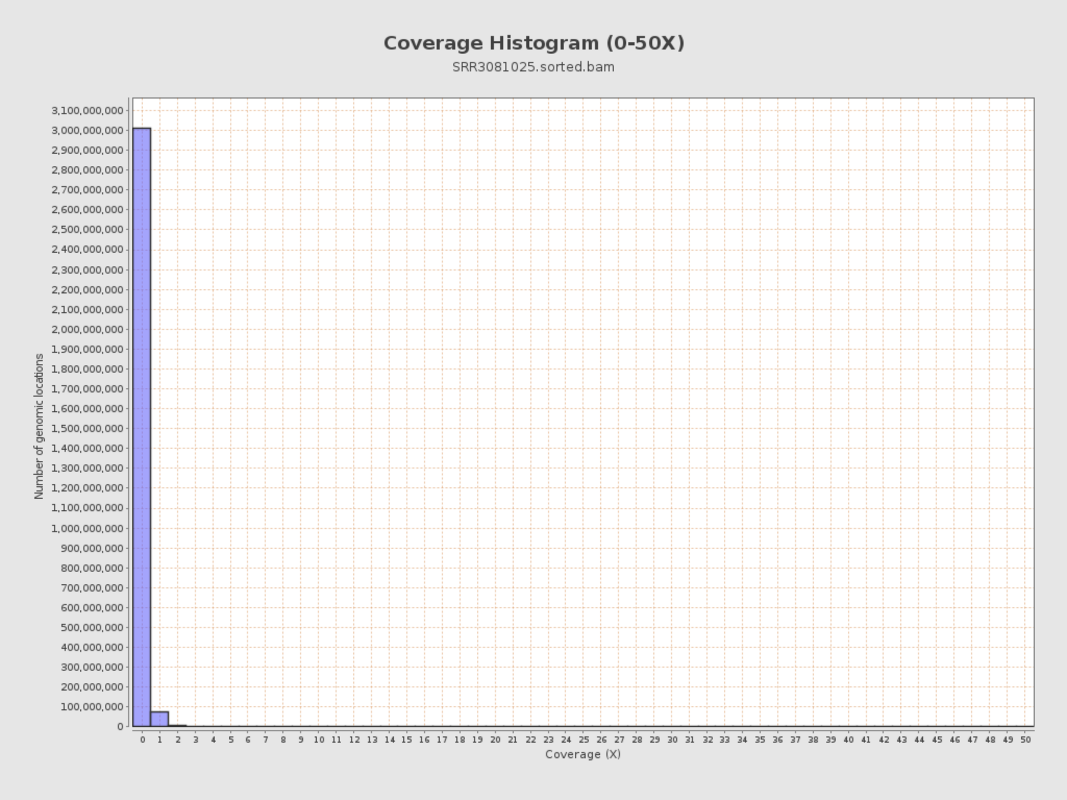
3. Results : Coverage across reference



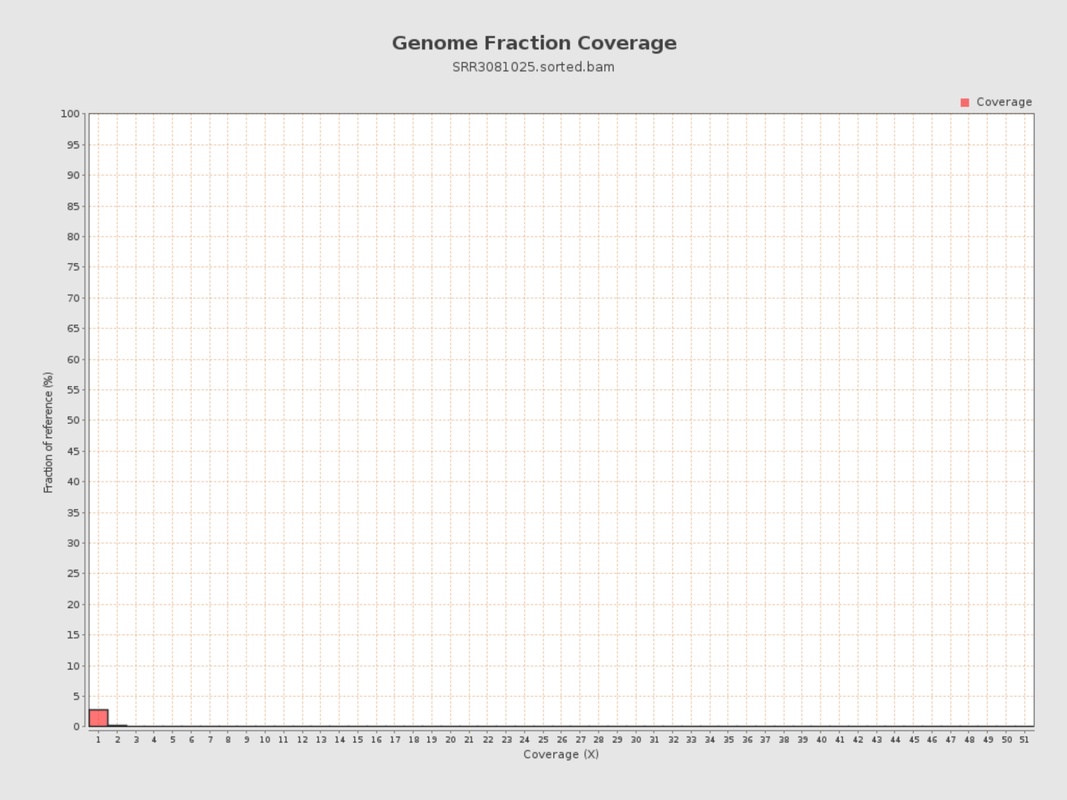
4. Results : Coverage Histogram



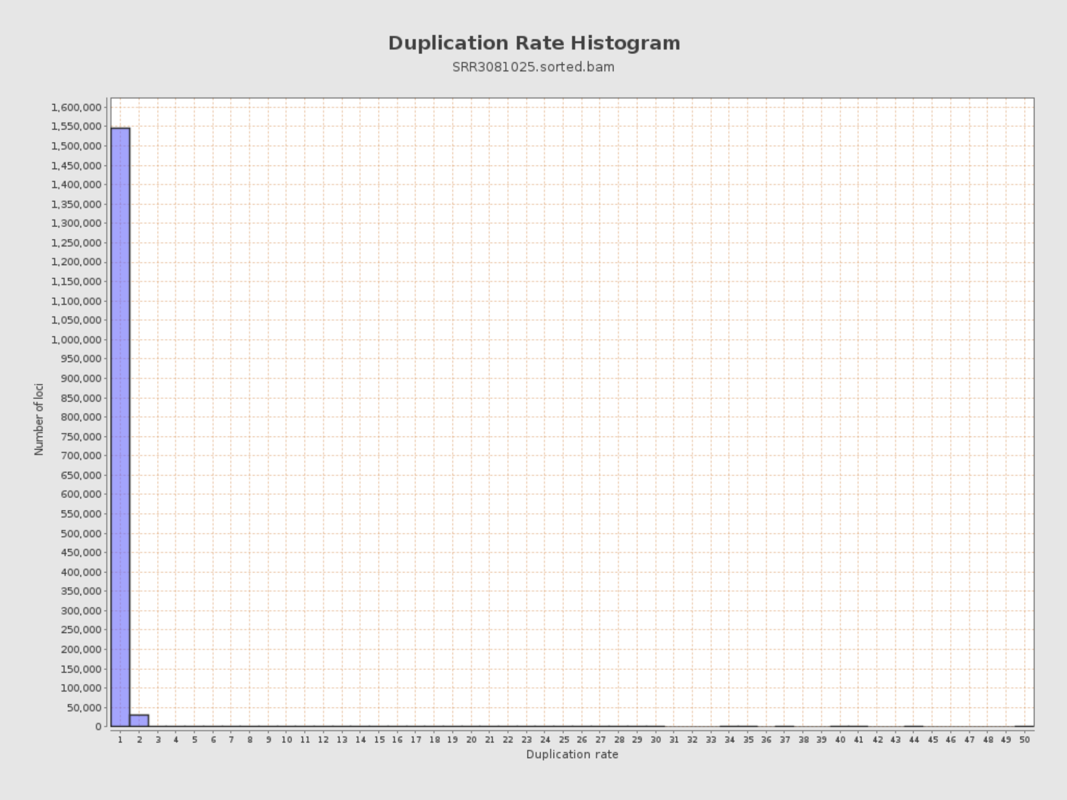
5. Results : Coverage Histogram (0-50X)



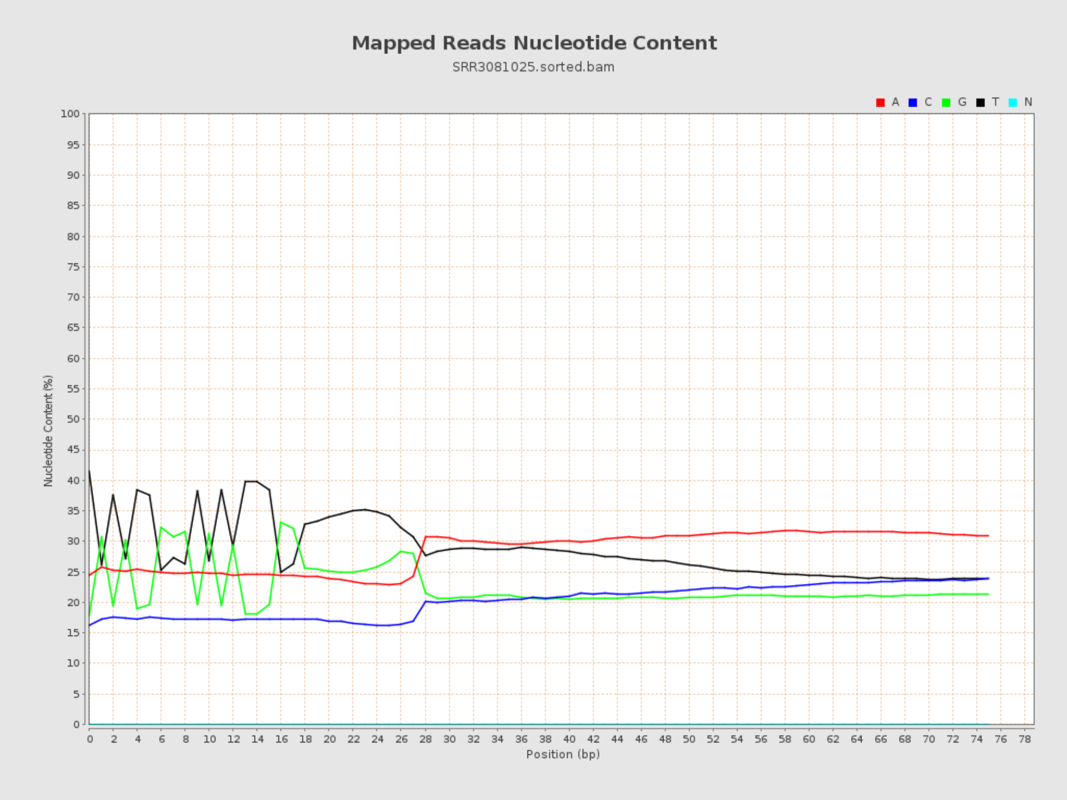
6. Results : Genome Fraction Coverage



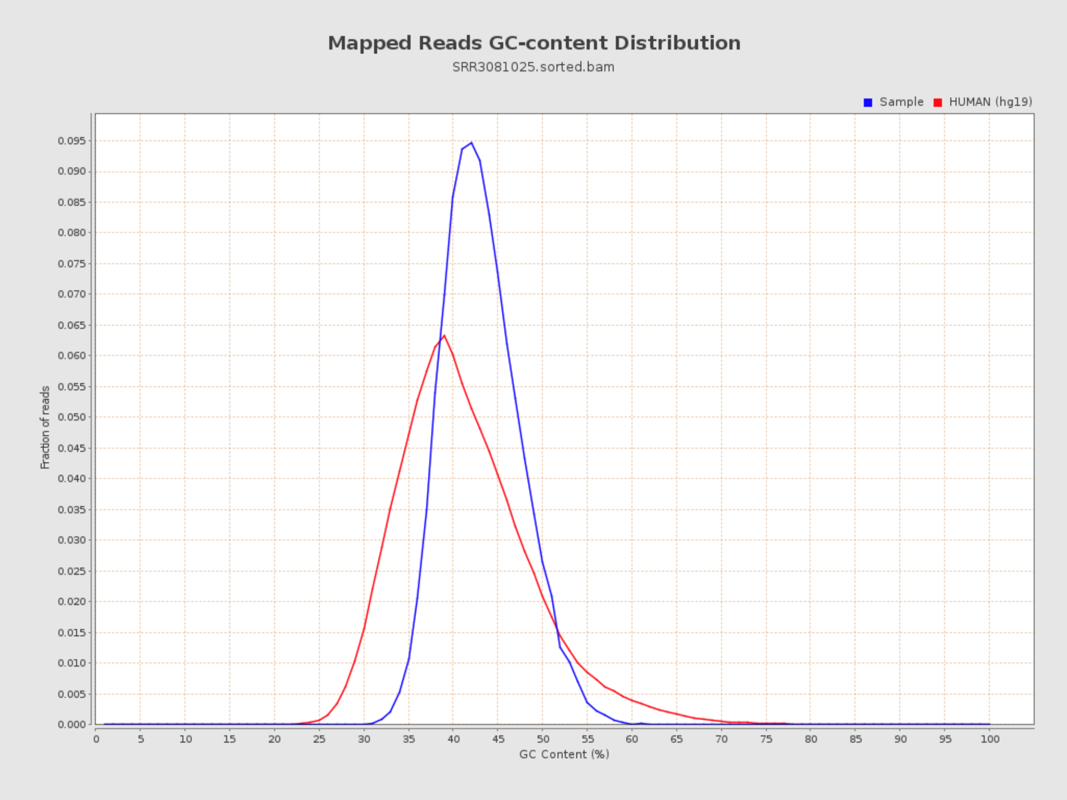
7. Results : Duplication Rate Histogram



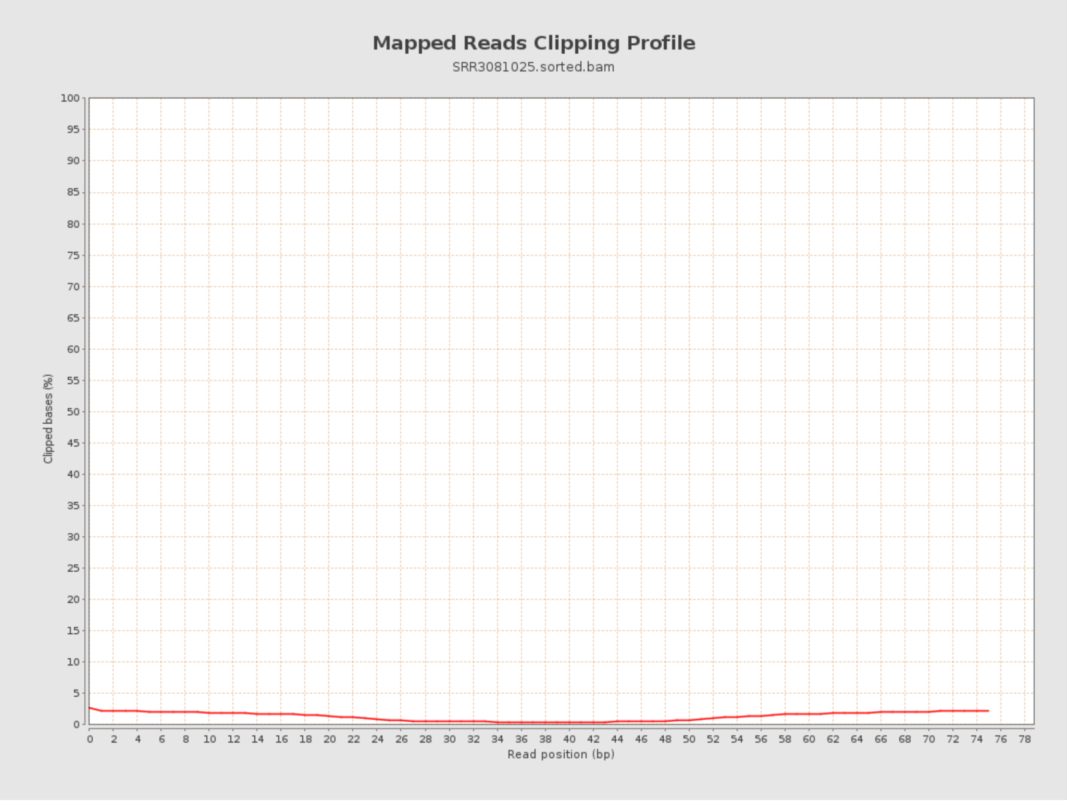
8. Results : Mapped Reads Nucleotide Content



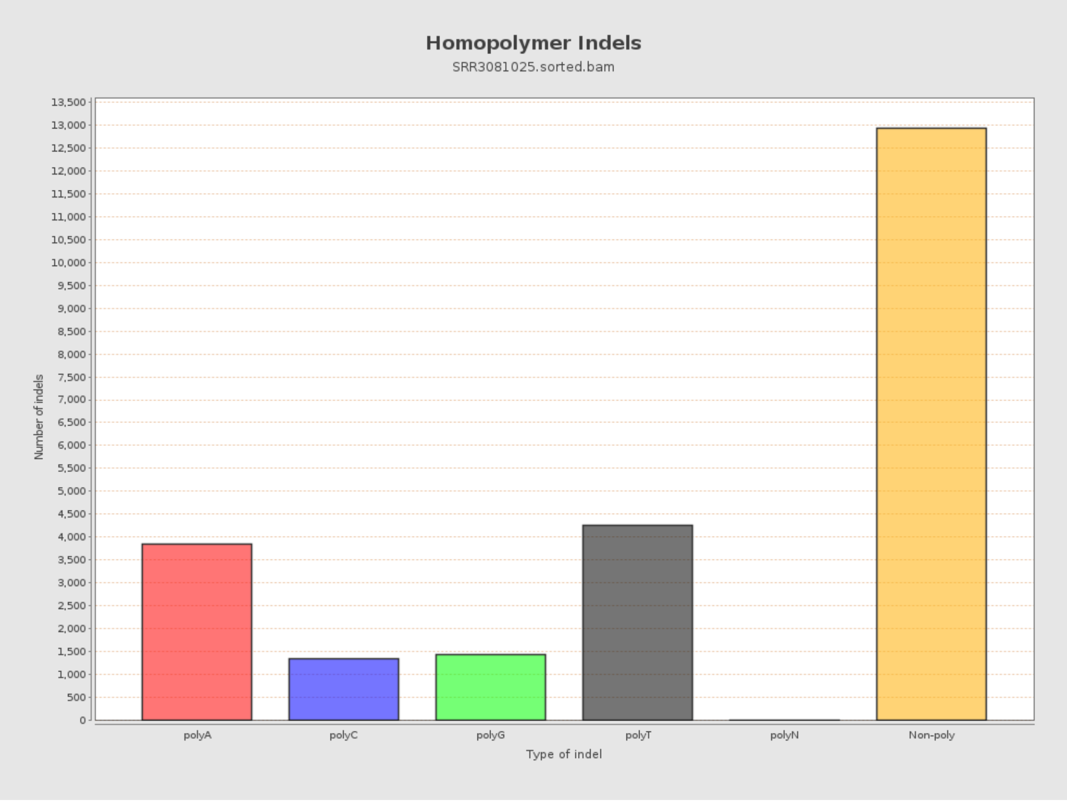
9. Results : Mapped Reads GC-content Distribution



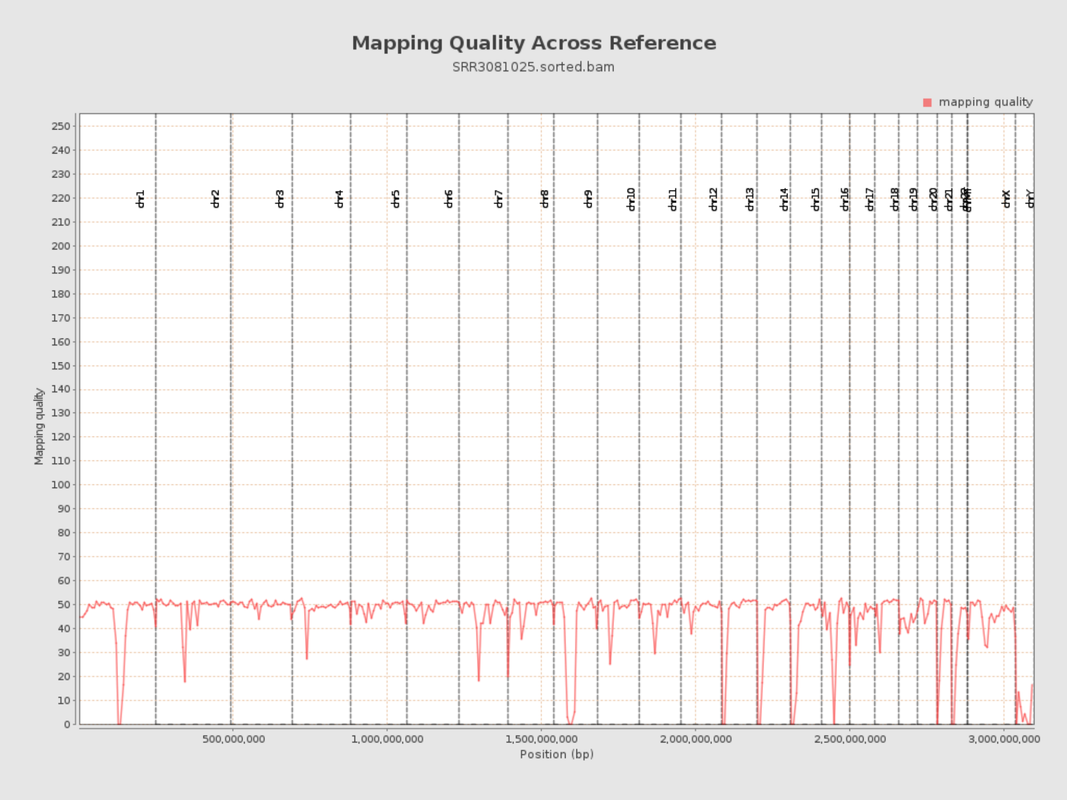
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram