Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:25:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085113.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_SRR3085113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:25:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,428,511
Mapped reads	2,204,925 / 90.79%
Unmapped reads	223,586 / 9.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,482 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	86,881 / 3.58%
Duplication rate	2.76%
Clipped reads	1,055,625 / 43.47%

2.2. ACGT Content

Number/percentage of A's	40,846,522 / 27.98%
Number/percentage of C's	27,030,611 / 18.52%
Number/percentage of T's	45,523,743 / 31.19%
Number/percentage of G's	32,539,114 / 22.29%
Number/percentage of N's	19,612 / 0.01%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0472

Standard Deviation	0.4727

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

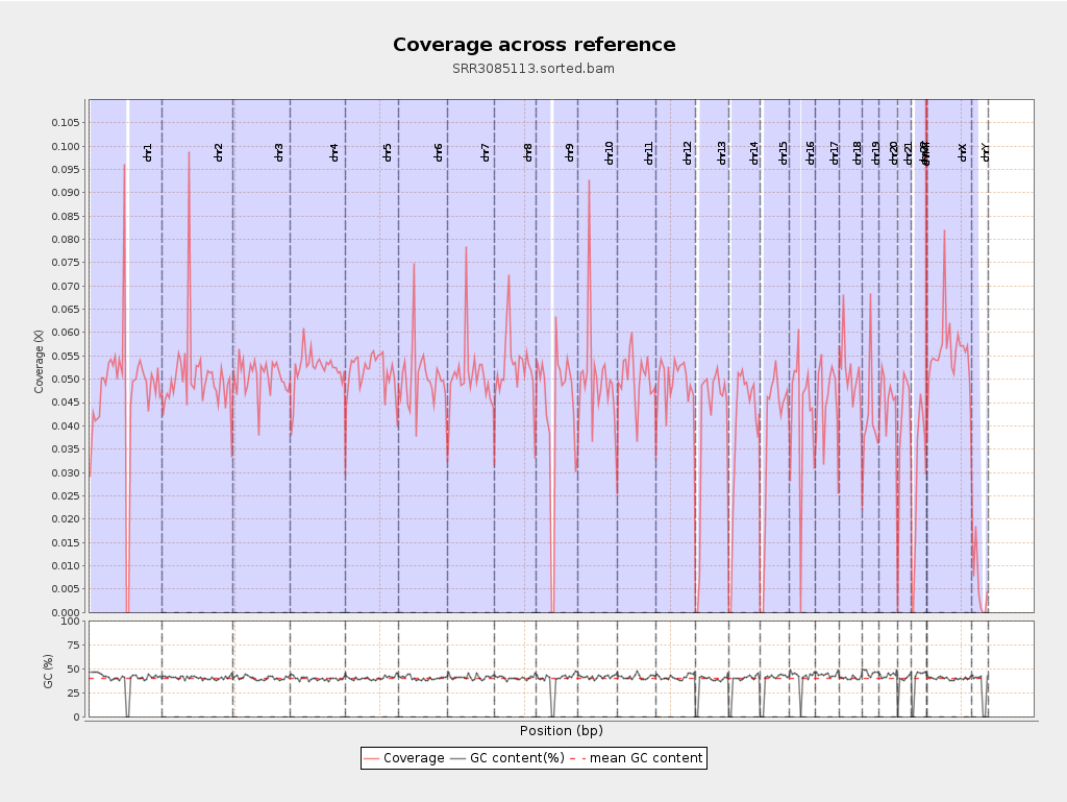
General error rate	0.85%
Mismatches	1,226,026
Insertions	11,566
Mapped reads with at least one insertion	0.52%
Deletions	33,621
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.72%

2.6. Chromosome stats

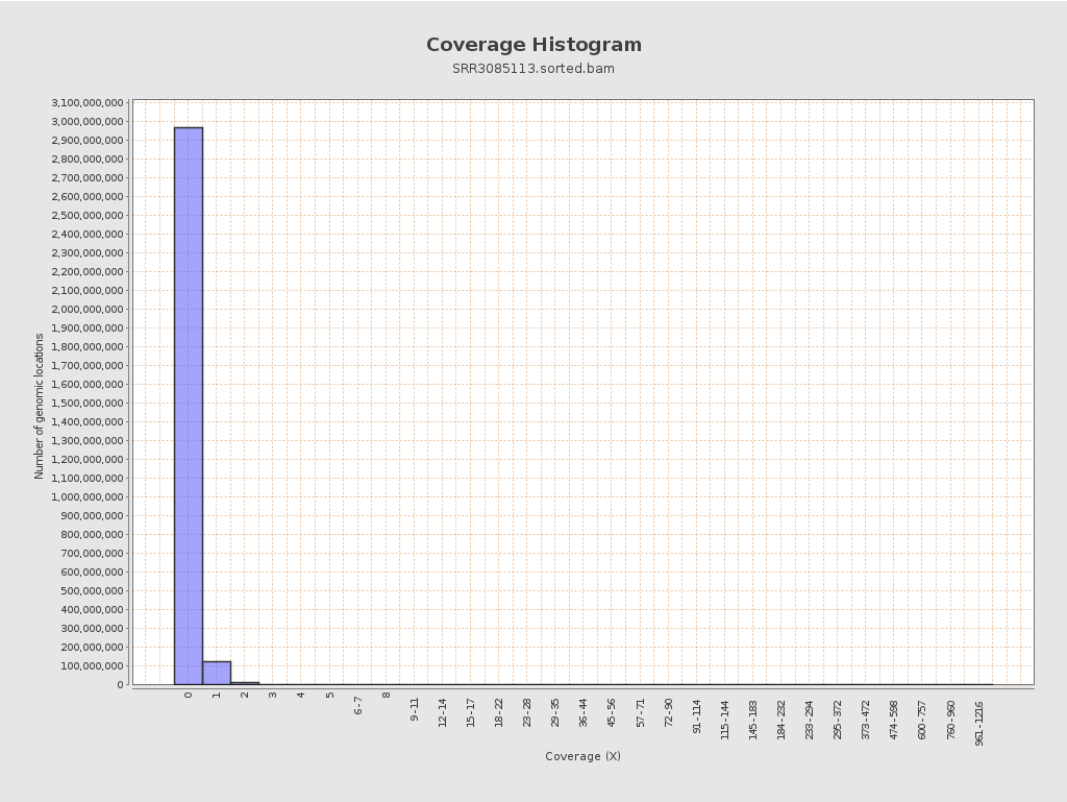
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11736940	0.0471	1.0078
chr2	243199373	12304288	0.0506	0.5392
chr3	198022430	10005222	0.0505	0.246
chr4	191154276	9979199	0.0522	0.2573
chr5	180915260	9347407	0.0517	0.2488
chr6	171115067	8579024	0.0501	0.3623
chr7	159138663	8115563	0.051	0.4268

chr8	146364022	7681625	0.0525	0.5913
chr9	141213431	6151382	0.0436	0.4158
chr10	135534747	6798533	0.0502	0.4973
chr11	135006516	6727608	0.0498	0.4347
chr12	133851895	6607323	0.0494	0.2472
chr13	115169878	4575517	0.0397	0.2141
chr14	107349540	4189855	0.039	0.2485
chr15	102531392	3904083	0.0381	0.2168
chr16	90354753	3846412	0.0426	0.2839
chr17	81195210	3663758	0.0451	0.293
chr18	78077248	4030045	0.0516	0.8249
chr19	59128983	2492525	0.0422	0.6948
chr20	63025520	2857190	0.0453	0.2448
chr21	48129895	1909196	0.0397	0.2369
chr22	51304566	1450342	0.0283	0.179
chrMT	16571	38992	2.353	1.9424
chrX	155270560	8662705	0.0558	0.3169
chrY	59373566	358501	0.006	0.1308

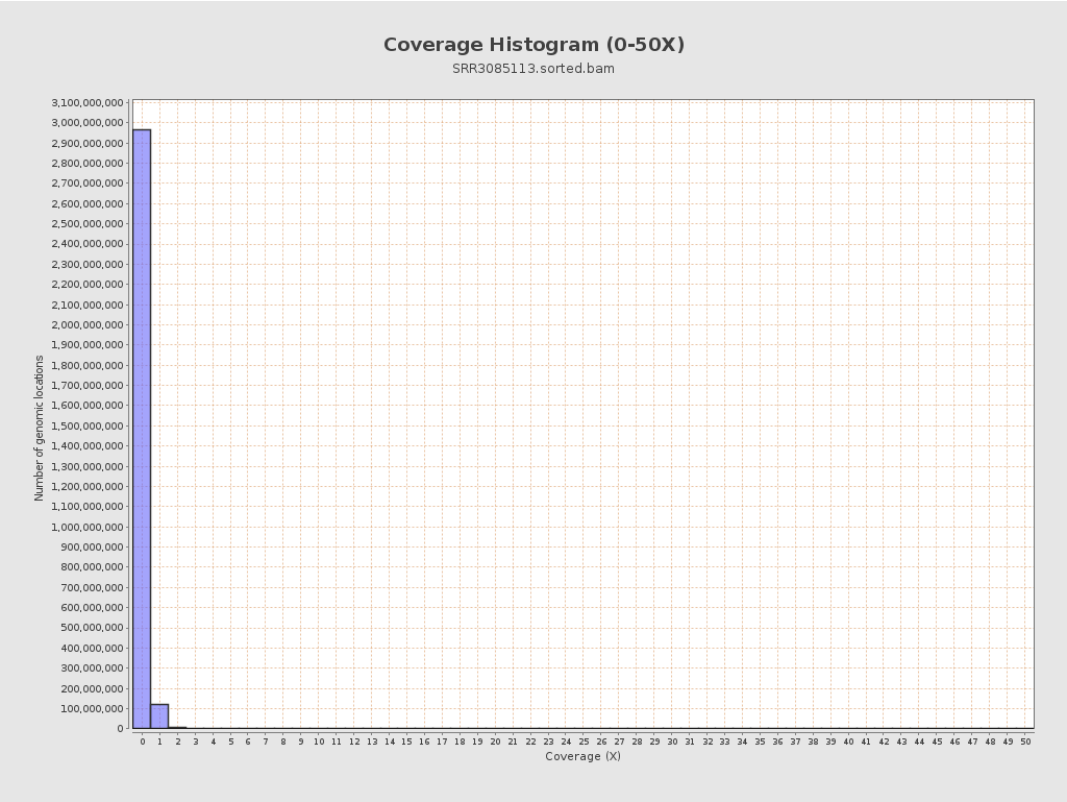
3. Results : Coverage across reference



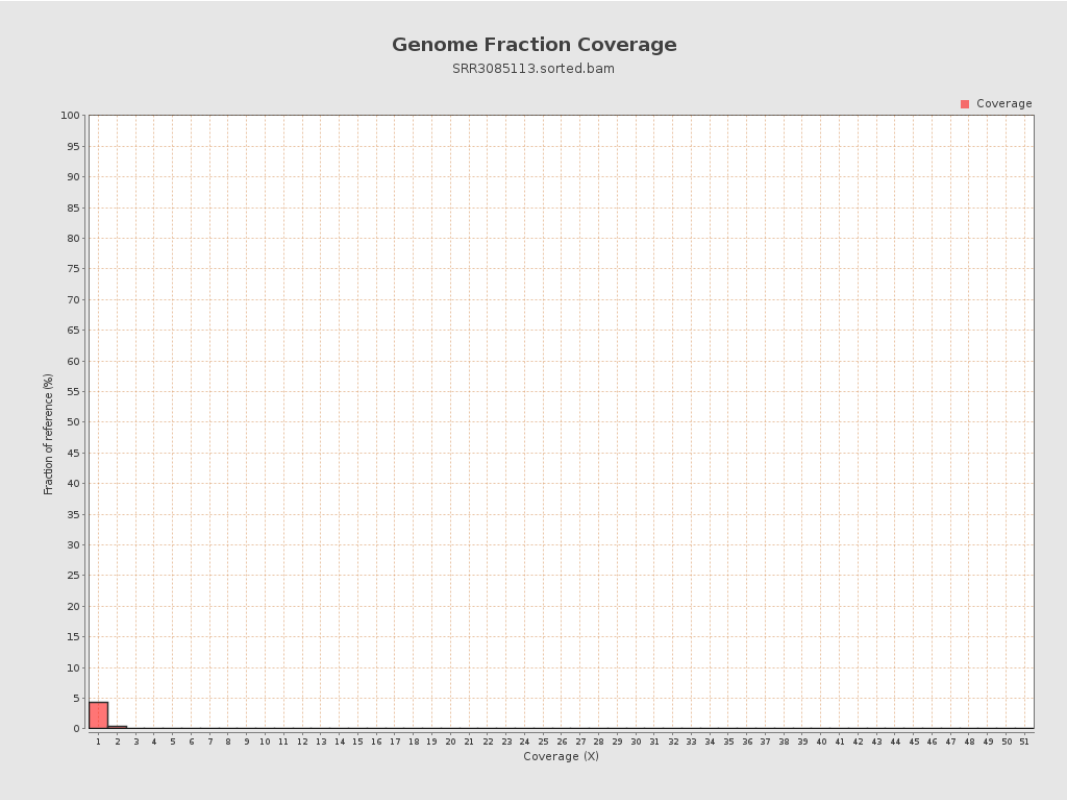
4. Results : Coverage Histogram



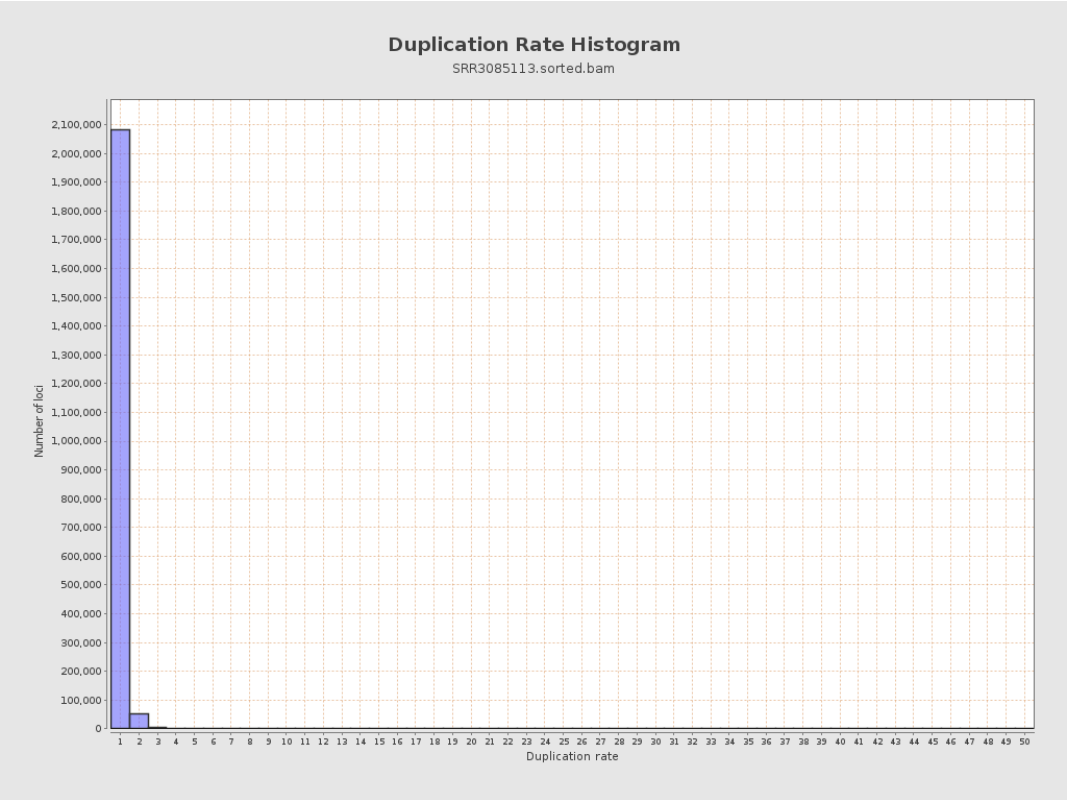
5. Results : Coverage Histogram (0-50X)



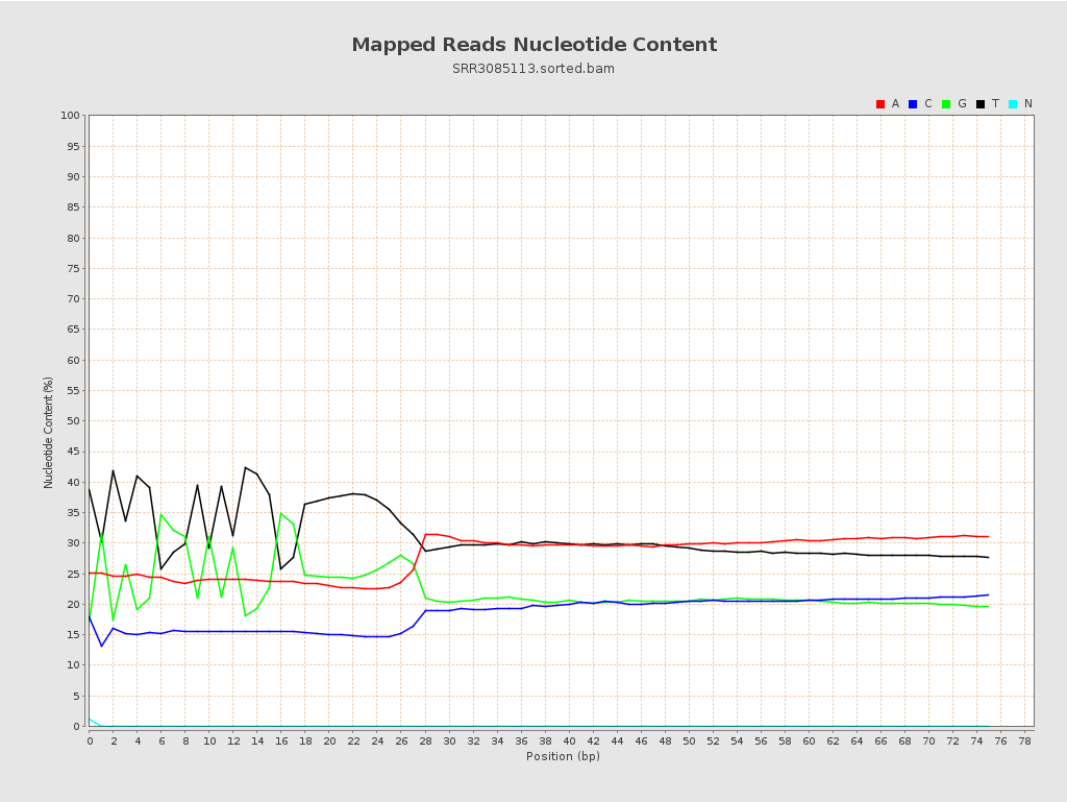
6. Results : Genome Fraction Coverage



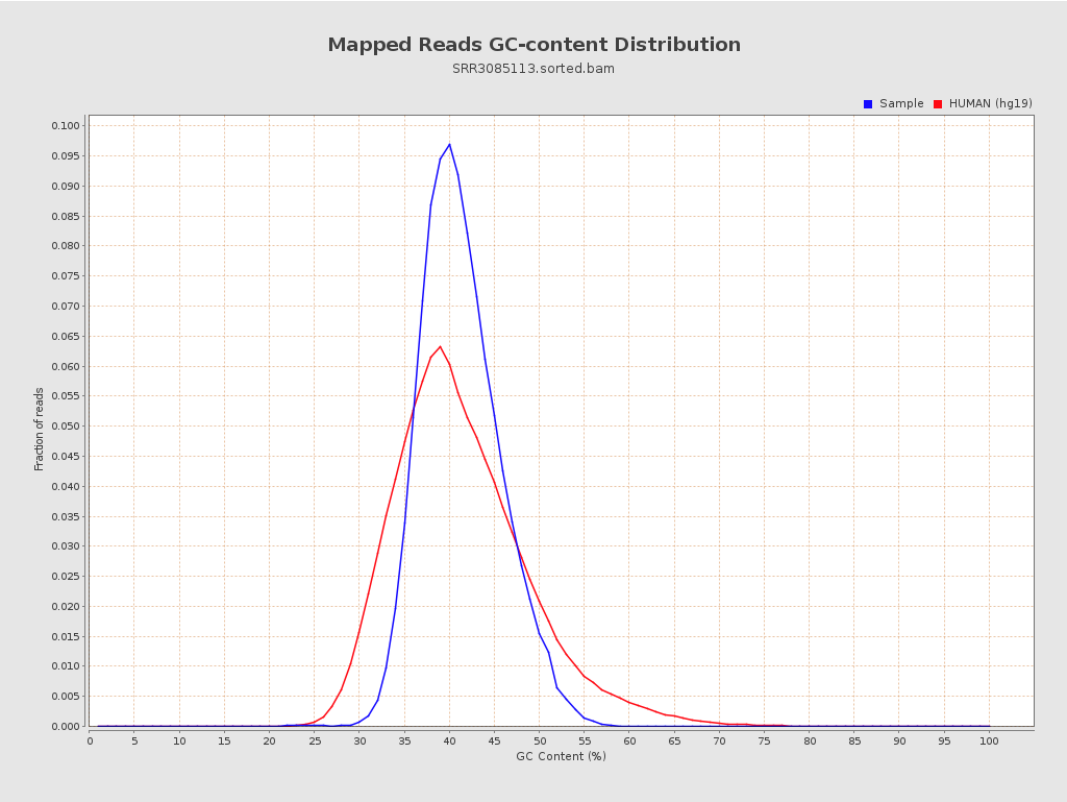
7. Results : Duplication Rate Histogram



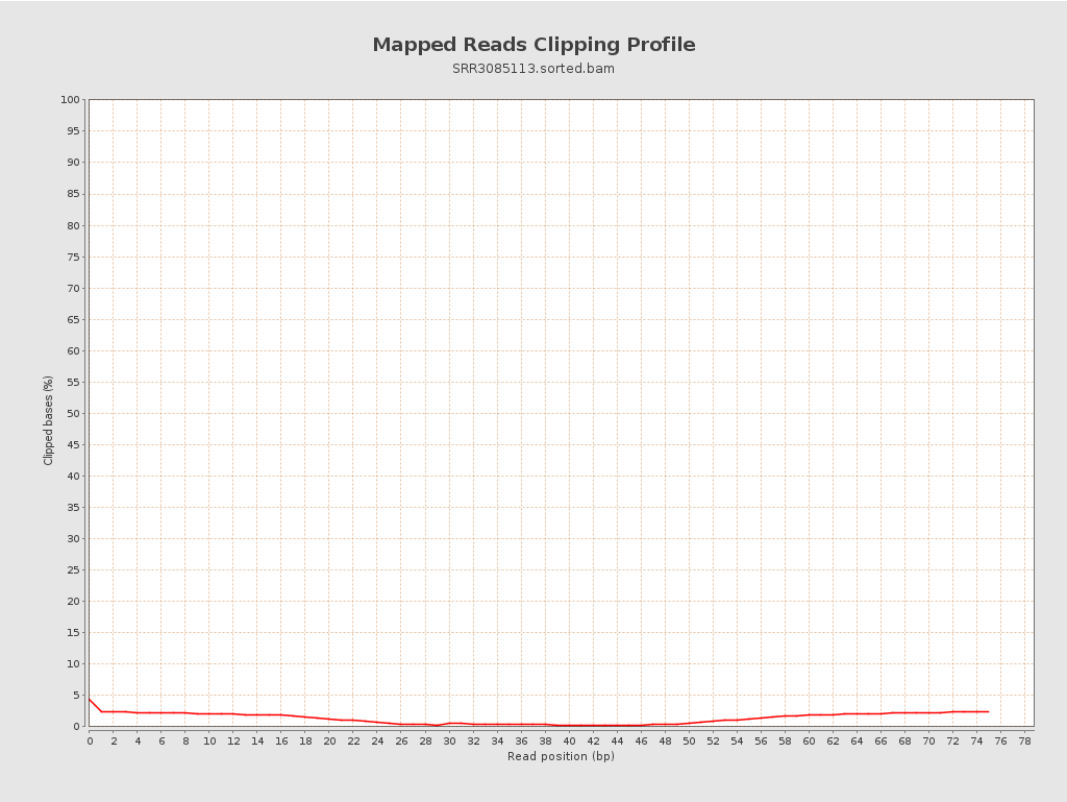
8. Results : Mapped Reads Nucleotide Content



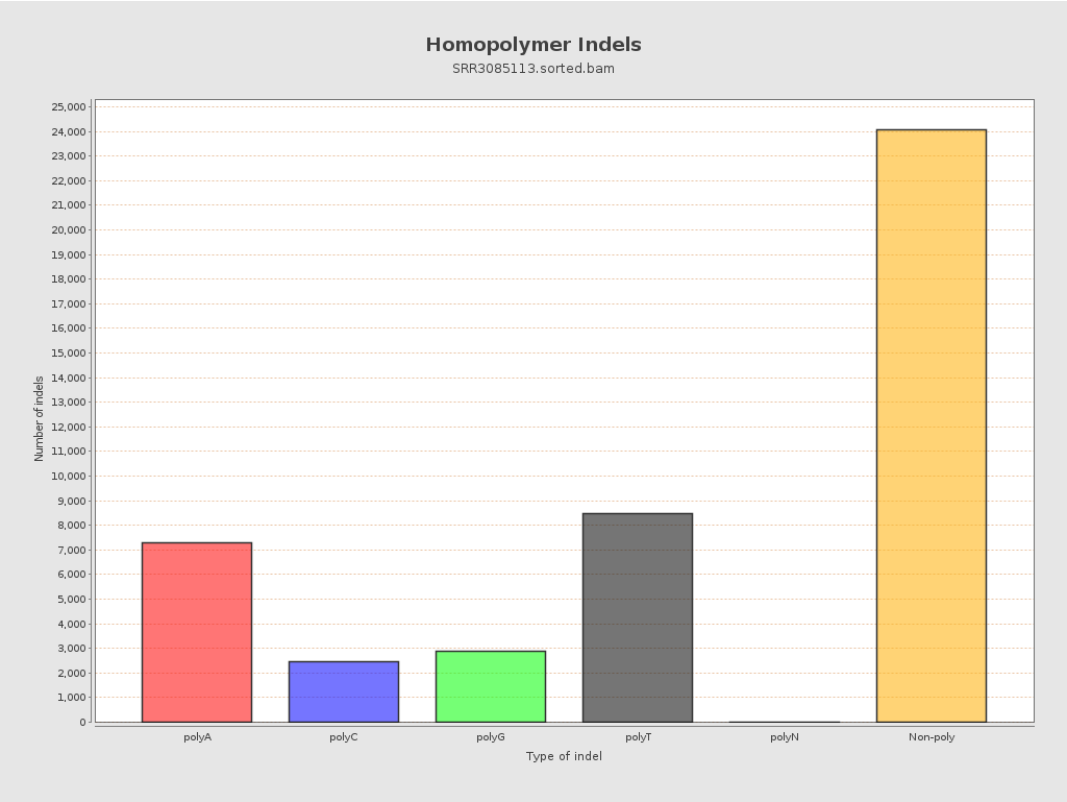
9. Results : Mapped Reads GC-content Distribution



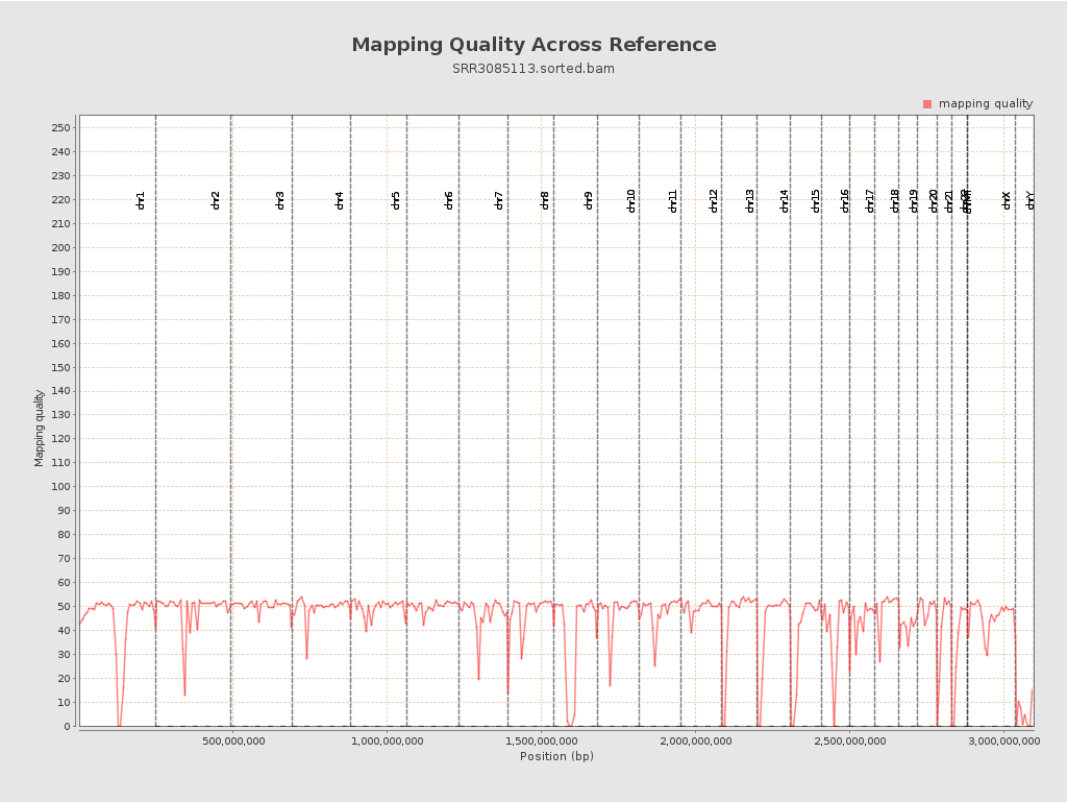
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram