Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:11:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081166.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_SRR3081166 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081166.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:11:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081166.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,074,223
Mapped reads	1,878,946 / 90.59%
Unmapped reads	195,277 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,914 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	72,397 / 3.49%
Duplication rate	3.15%
Clipped reads	766,994 / 36.98%

2.2. ACGT Content

Number/percentage of A's	36,756,715 / 28.8%
Number/percentage of C's	23,608,581 / 18.5%
Number/percentage of T's	40,169,146 / 31.47%
Number/percentage of G's	27,068,875 / 21.21%
Number/percentage of N's	38,480 / 0.03%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.3444

2.4. Mapping Quality

Mean Mapping Quality	47.46

2.5. Mismatches and indels

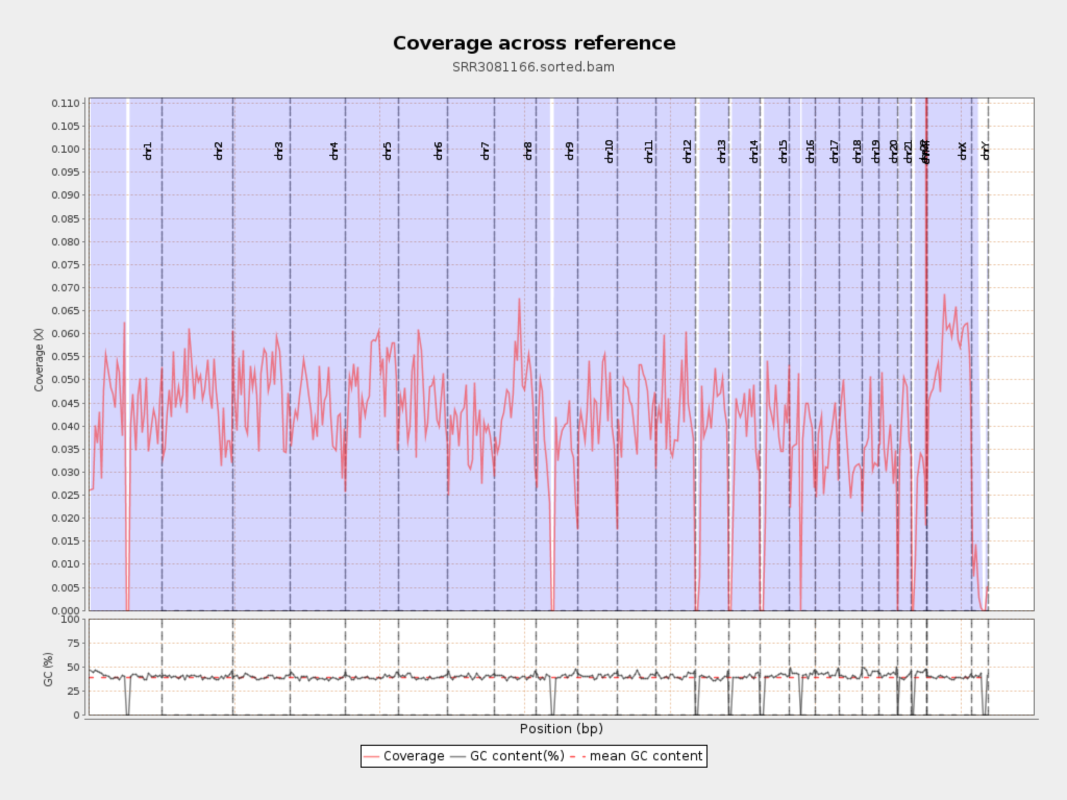
General error rate	0.83%
Mismatches	1,046,606
Insertions	9,951
Mapped reads with at least one insertion	0.52%
Deletions	29,022
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.05%

2.6. Chromosome stats

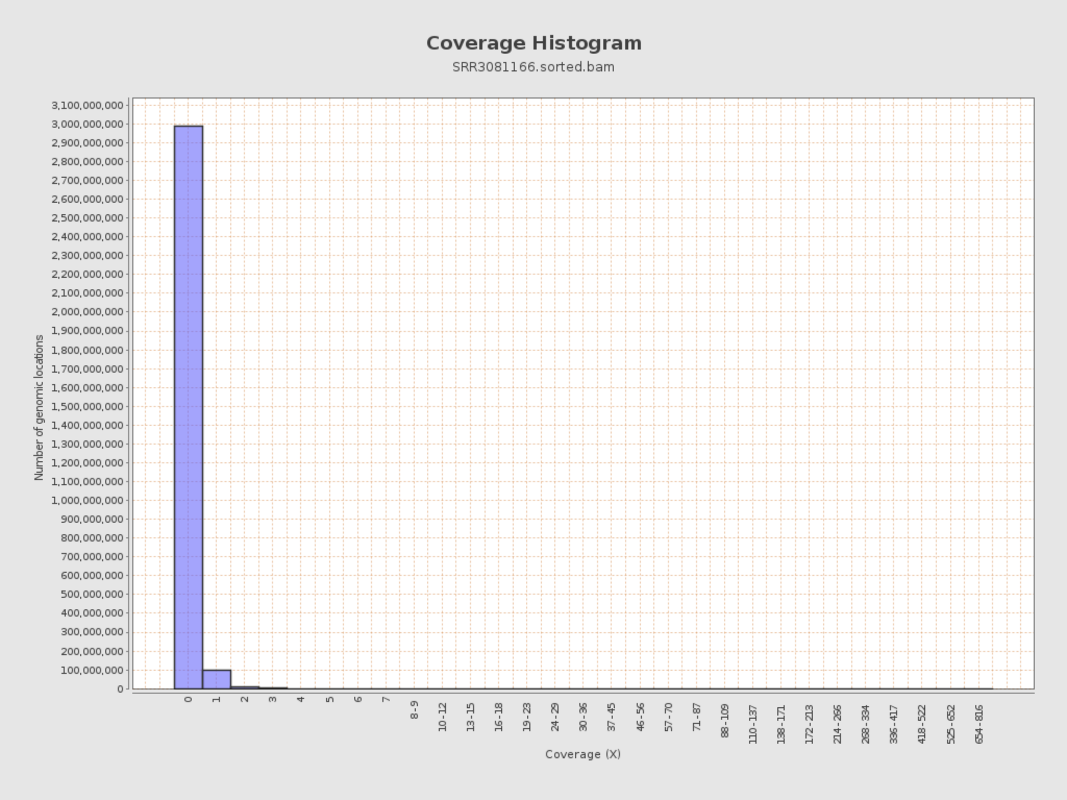
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10087221	0.0405	0.6497
chr2	243199373	11108611	0.0457	0.3303
chr3	198022430	9571985	0.0483	0.2471
chr4	191154276	8206407	0.0429	0.2404
chr5	180915260	9143151	0.0505	0.2537
chr6	171115067	7800274	0.0456	0.2689
chr7	159138663	6147219	0.0386	0.3186

chr8	146364022	6847389	0.0468	0.5342
chr9	141213431	4677350	0.0331	0.2961
chr10	135534747	5804075	0.0428	0.2931
chr11	135006516	6011147	0.0445	0.2978
chr12	133851895	5703365	0.0426	0.2358
chr13	115169878	4257883	0.037	0.2161
chr14	107349540	3768150	0.0351	0.2273
chr15	102531392	3566241	0.0348	0.2113
chr16	90354753	3170199	0.0351	0.2349
chr17	81195210	2819316	0.0347	0.2404
chr18	78077248	2764414	0.0354	0.6038
chr19	59128983	2096957	0.0355	0.4501
chr20	63025520	2260060	0.0359	0.2213
chr21	48129895	1800878	0.0374	0.2304
chr22	51304566	1086756	0.0212	0.1611
chrMT	16571	10868	0.6558	0.8925
chrX	155270560	8682508	0.0559	0.2947
chrY	59373566	296520	0.005	0.1074

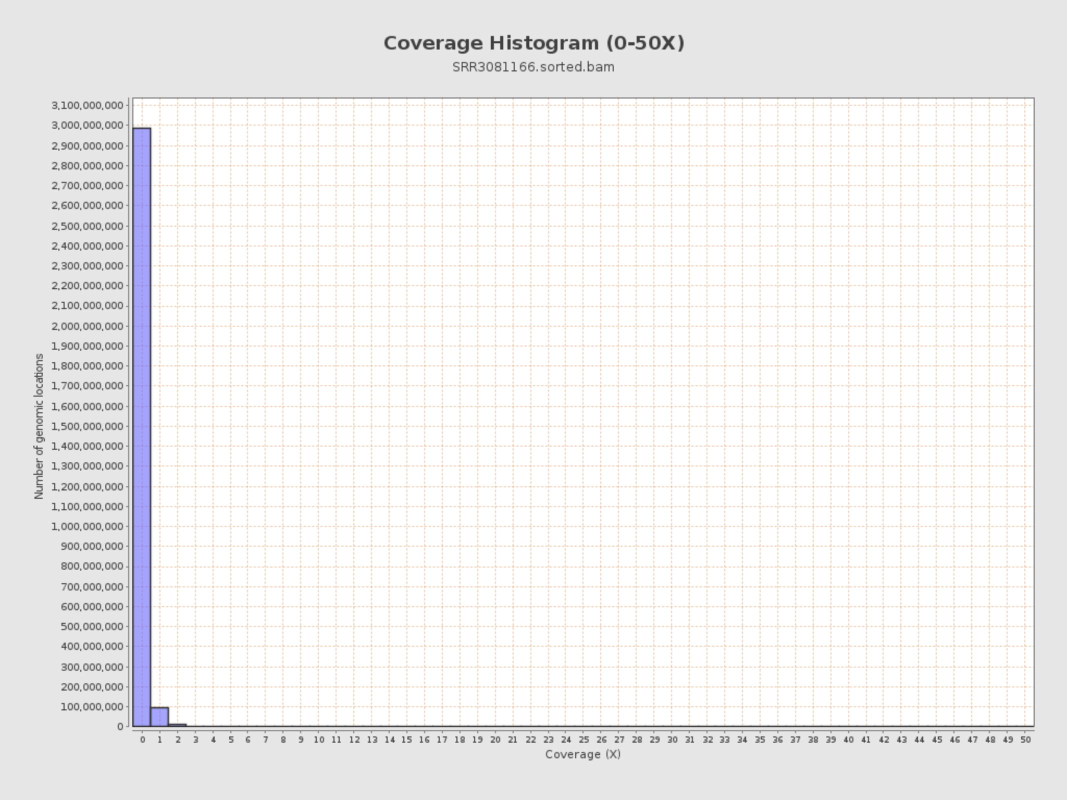
3. Results : Coverage across reference



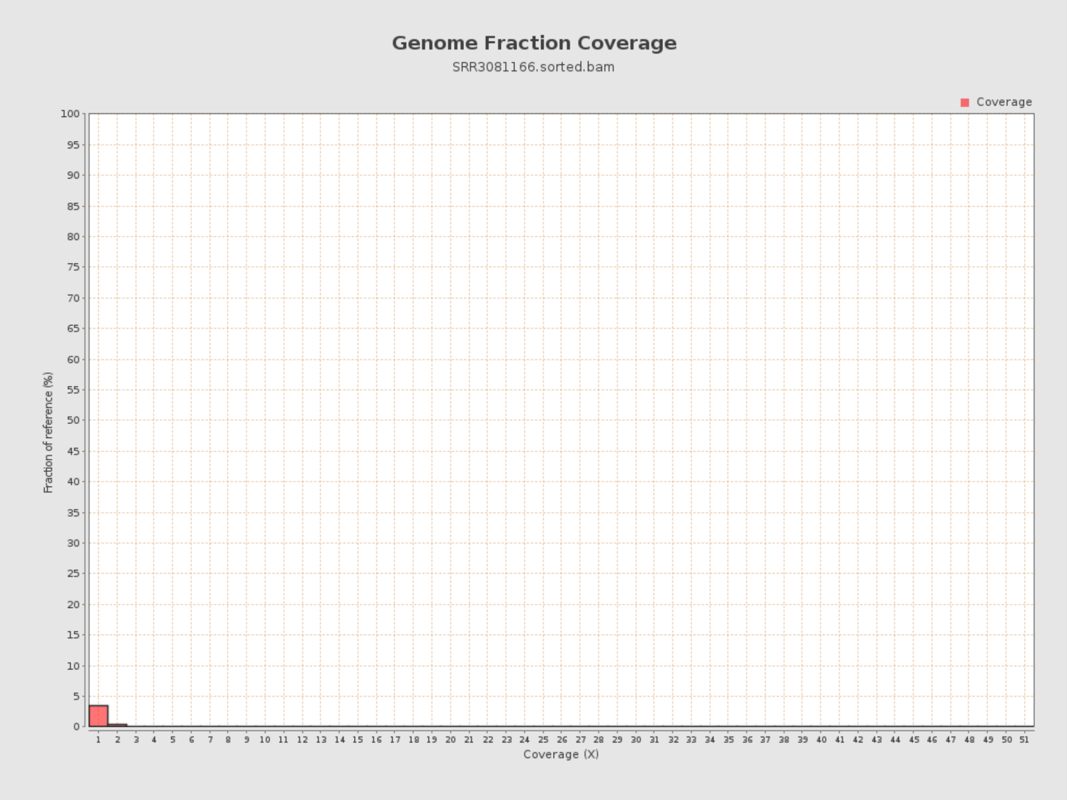
4. Results : Coverage Histogram



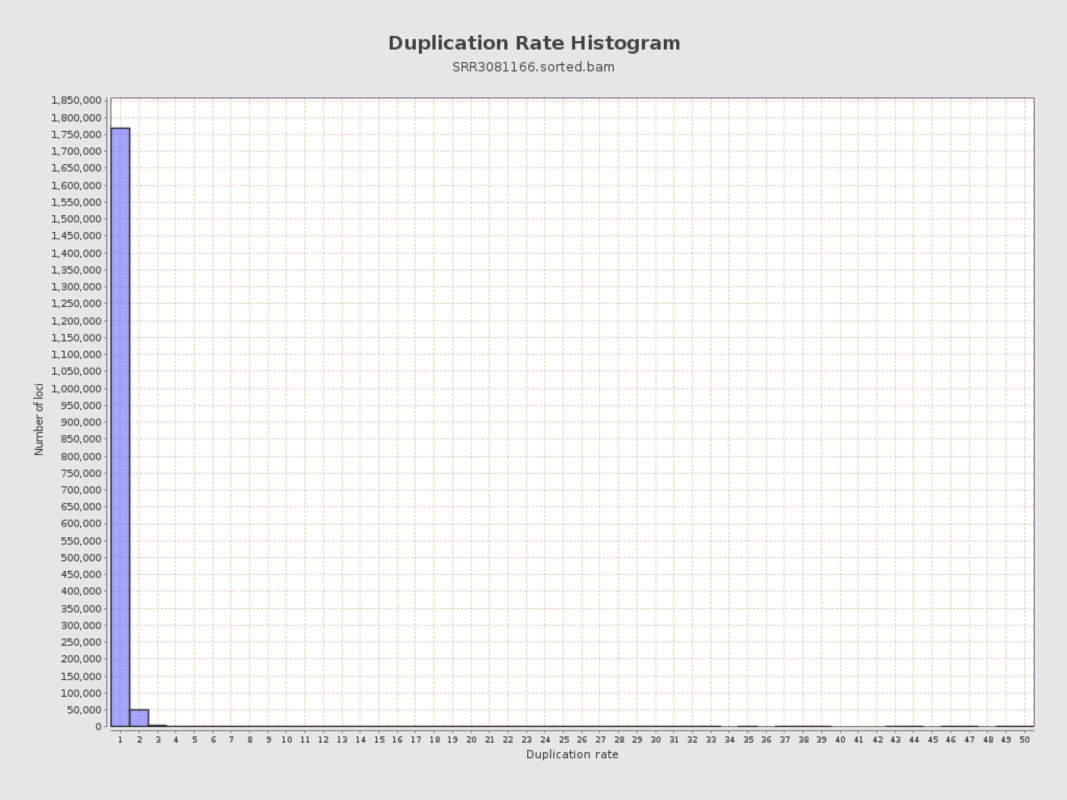
5. Results : Coverage Histogram (0-50X)



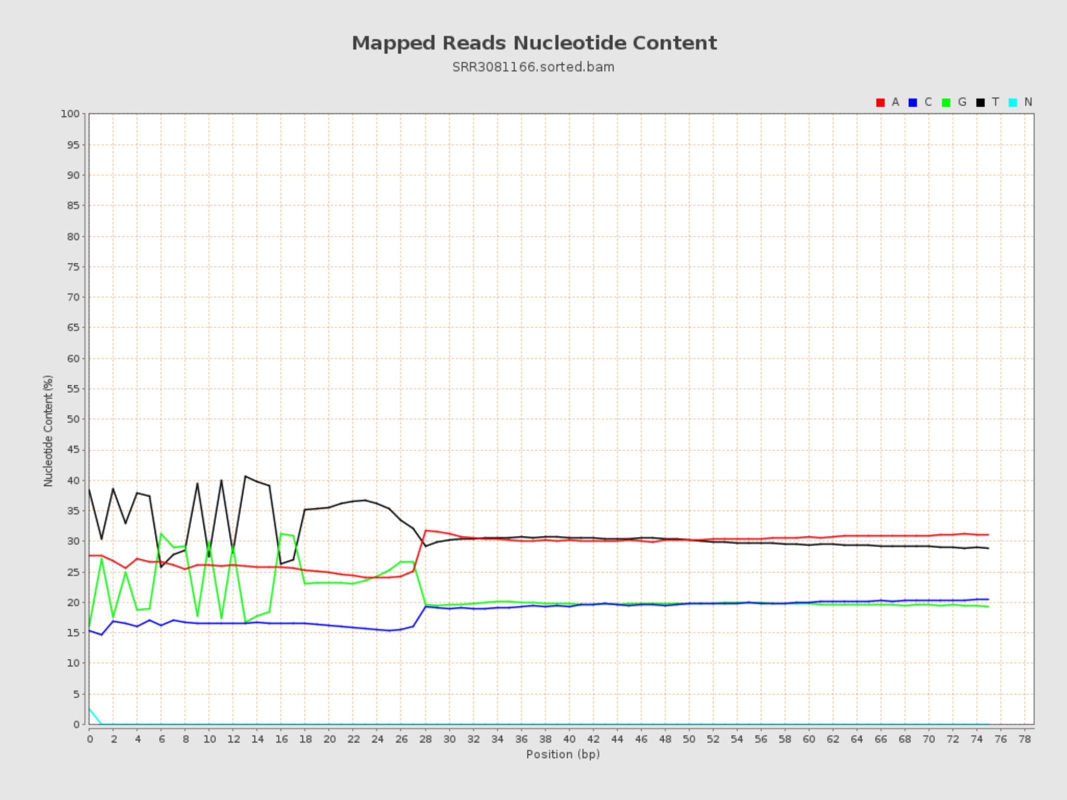
6. Results : Genome Fraction Coverage



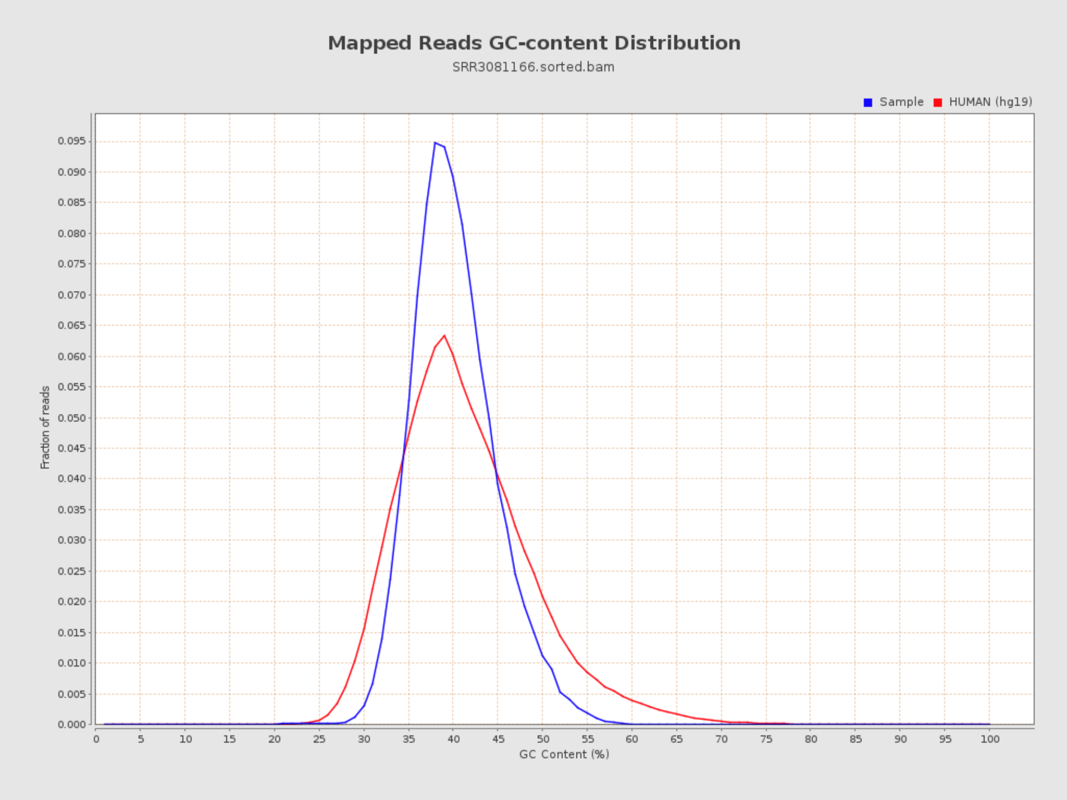
7. Results : Duplication Rate Histogram



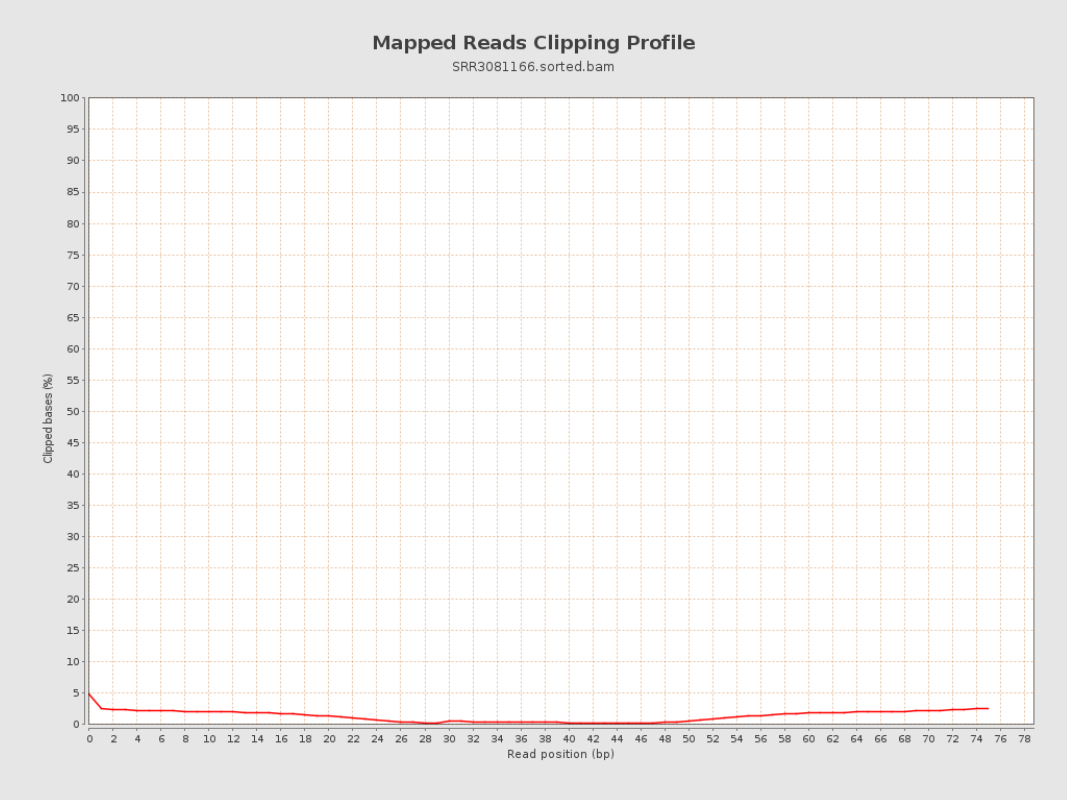
8. Results : Mapped Reads Nucleotide Content



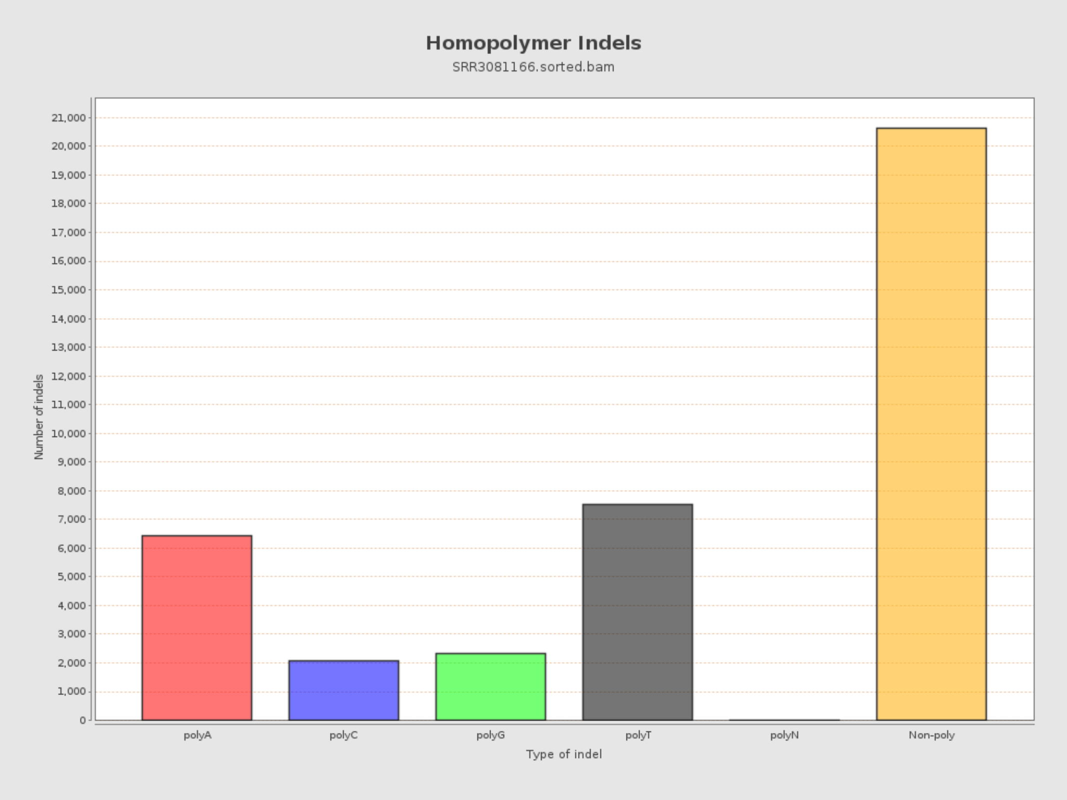
9. Results : Mapped Reads GC-content Distribution



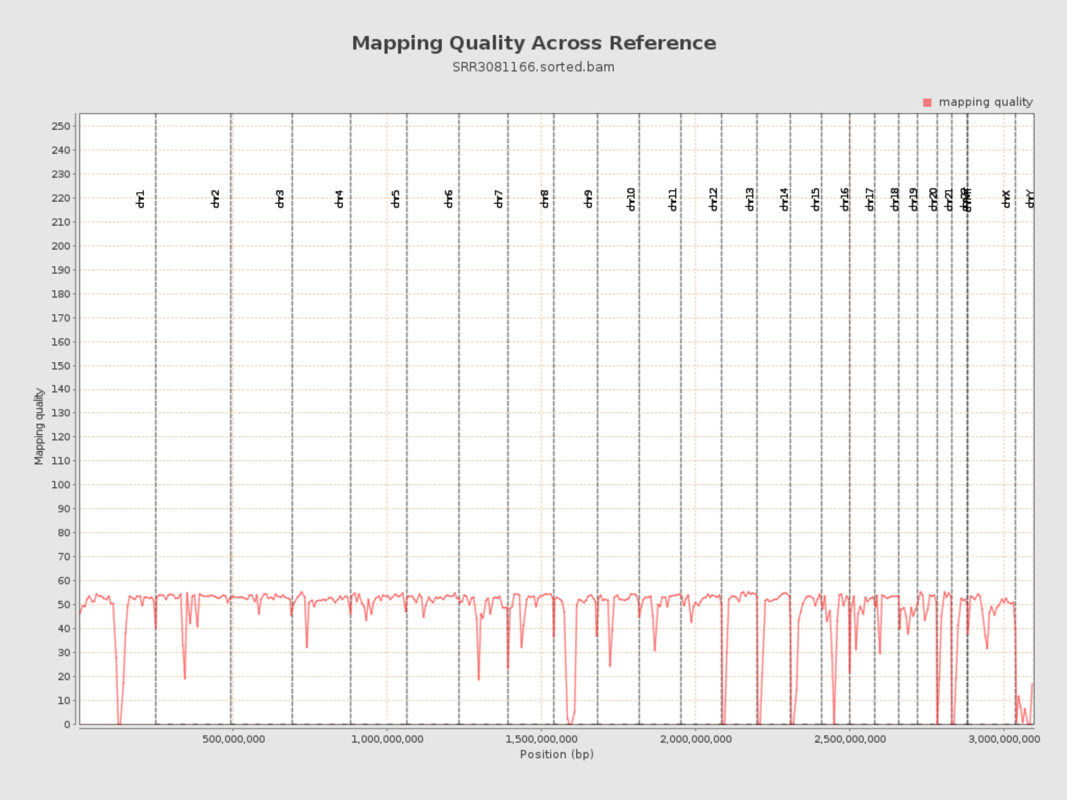
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram