Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:53:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081178.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_SRR3081178 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081178.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:53:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081178.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,021,456
Mapped reads	1,832,984 / 90.68%
Unmapped reads	188,472 / 9.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,672 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	73,245 / 3.62%
Duplication rate	3.28%
Clipped reads	789,481 / 39.06%

2.2. ACGT Content

Number/percentage of A's	35,018,744 / 28.39%
Number/percentage of C's	22,547,710 / 18.28%
Number/percentage of T's	39,261,974 / 31.83%
Number/percentage of G's	26,483,672 / 21.47%
Number/percentage of N's	36,511 / 0.03%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.3185

2.4. Mapping Quality

Mean Mapping Quality	47.15

2.5. Mismatches and indels

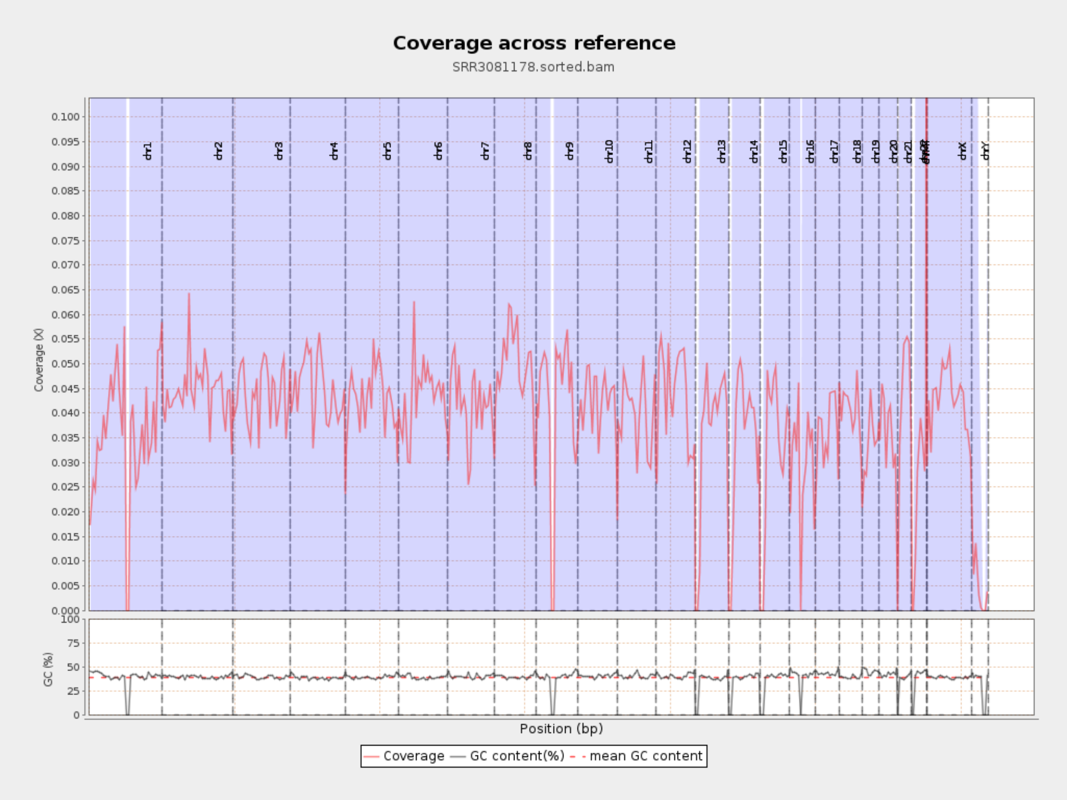
General error rate	0.82%
Mismatches	993,084
Insertions	9,785
Mapped reads with at least one insertion	0.53%
Deletions	27,676
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.44%

2.6. Chromosome stats

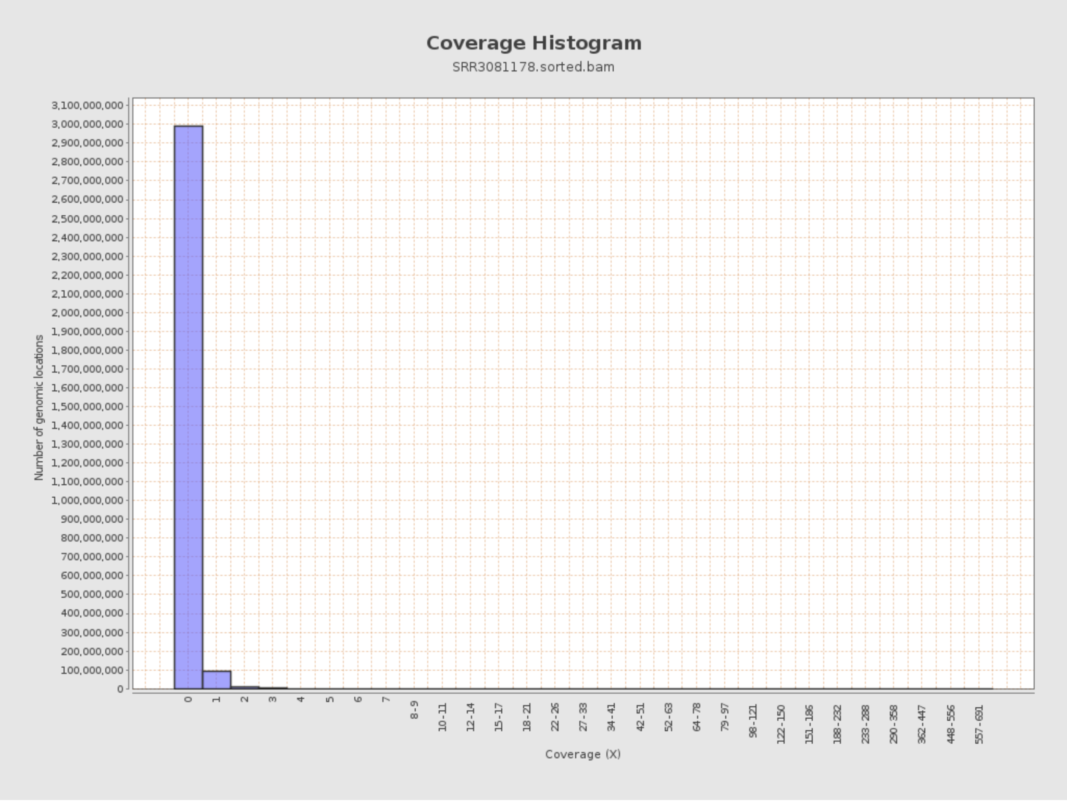
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8898110	0.0357	0.5383
chr2	243199373	10821639	0.0445	0.3808
chr3	198022430	8710203	0.044	0.2341
chr4	191154276	8576818	0.0449	0.2444
chr5	180915260	7824384	0.0432	0.234
chr6	171115067	7448948	0.0435	0.283
chr7	159138663	6661651	0.0419	0.2902

chr8	146364022	7275532	0.0497	0.4827
chr9	141213431	5889045	0.0417	0.3108
chr10	135534747	5778204	0.0426	0.2801
chr11	135006516	5405233	0.04	0.2997
chr12	133851895	5872157	0.0439	0.2378
chr13	115169878	4063377	0.0353	0.2096
chr14	107349540	3670154	0.0342	0.221
chr15	102531392	3320408	0.0324	0.2041
chr16	90354753	2665947	0.0295	0.2112
chr17	81195210	2940702	0.0362	0.2337
chr18	78077248	3206493	0.0411	0.5118
chr19	59128983	2011826	0.034	0.369
chr20	63025520	2261235	0.0359	0.2208
chr21	48129895	2046263	0.0425	0.2434
chr22	51304566	1155711	0.0225	0.1659
chrMT	16571	4534	0.2736	0.5985
chrX	155270560	6592235	0.0425	0.2474
chrY	59373566	292229	0.0049	0.1038

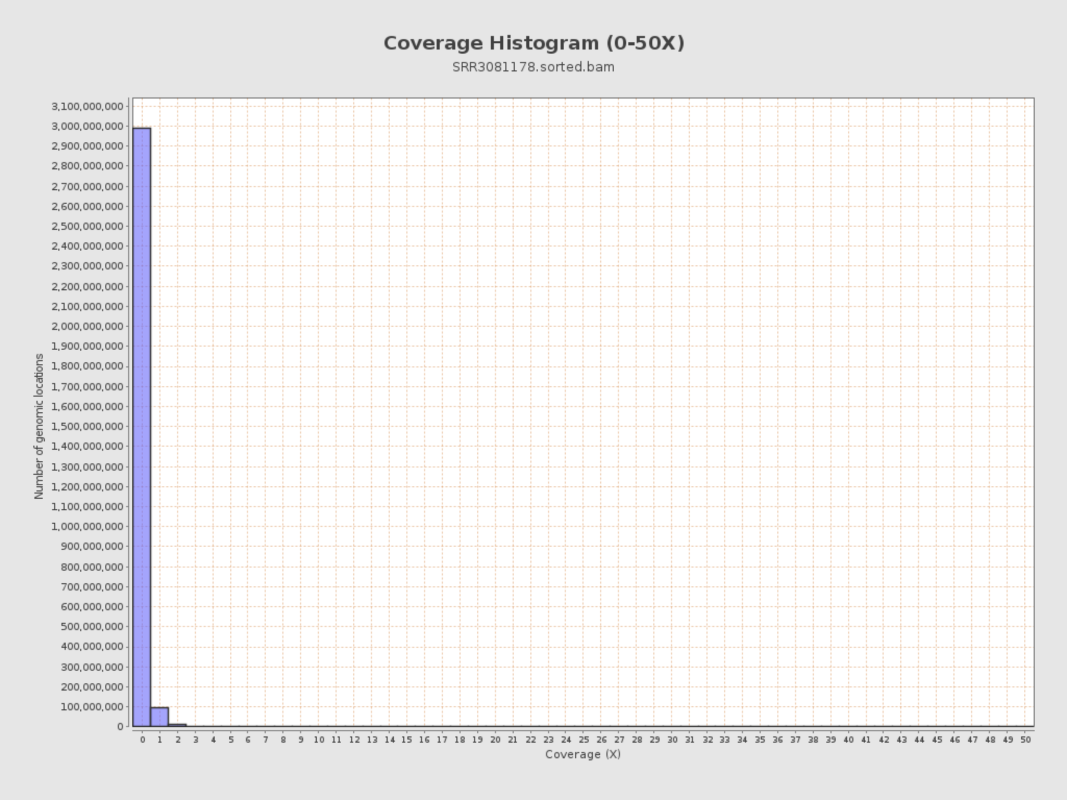
3. Results : Coverage across reference



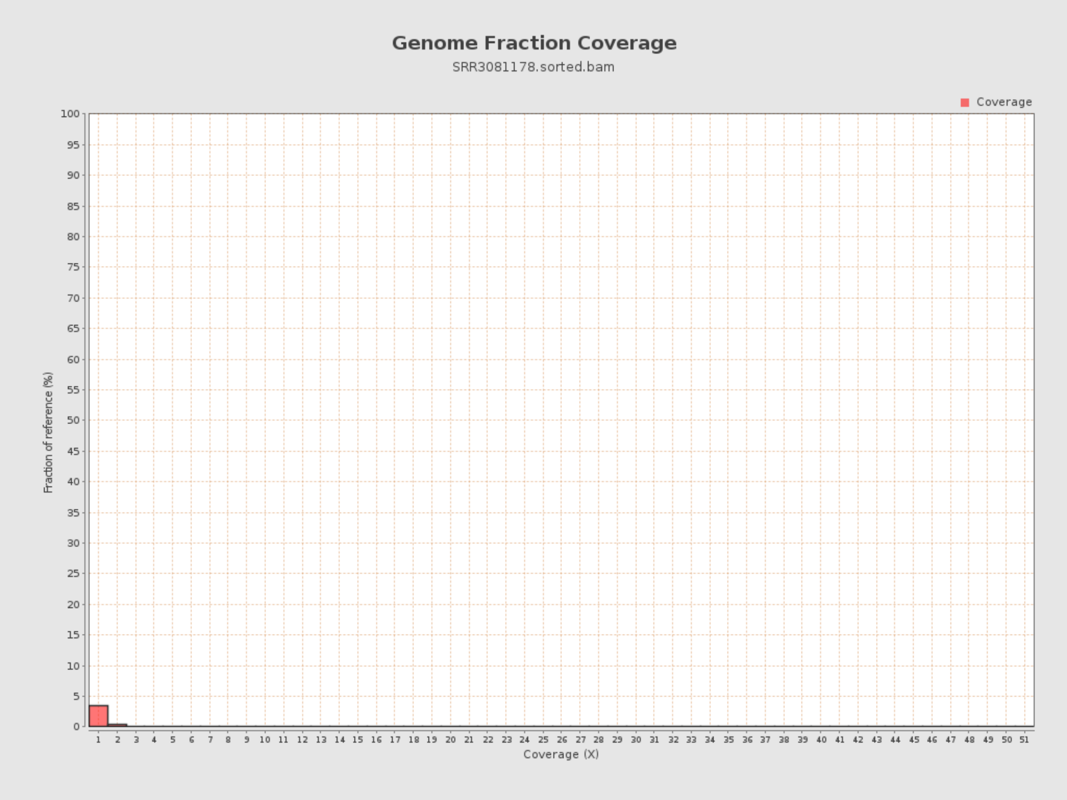
4. Results : Coverage Histogram



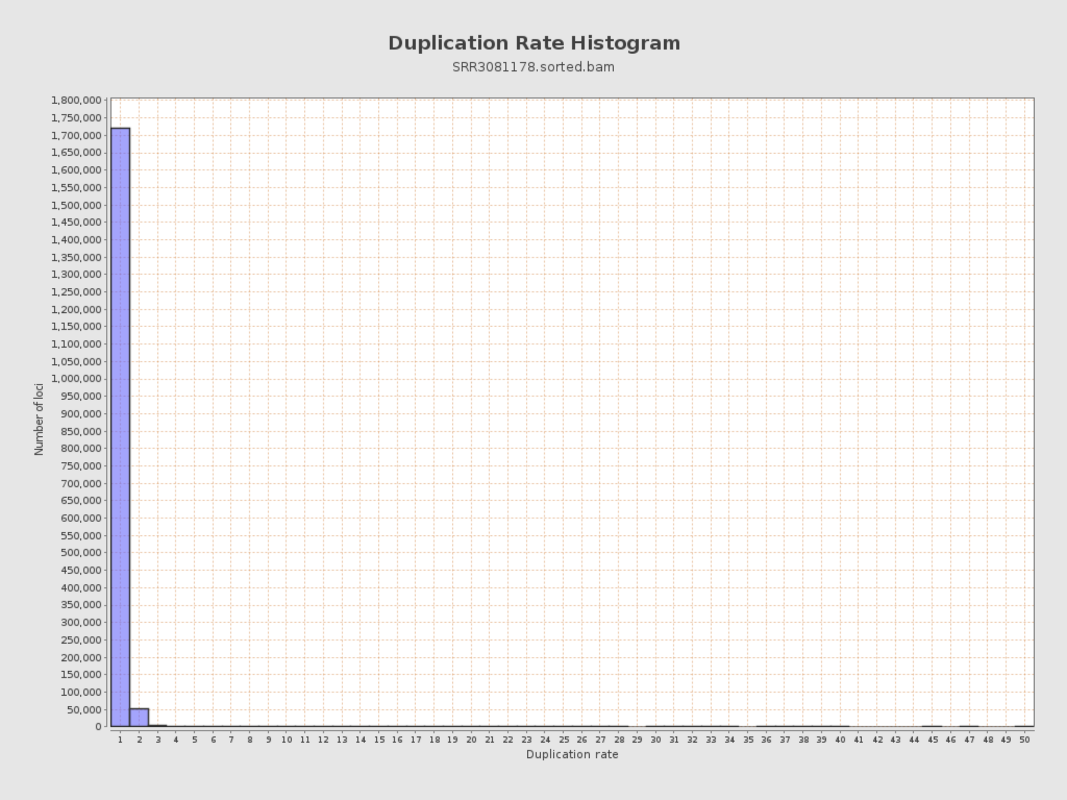
5. Results : Coverage Histogram (0-50X)



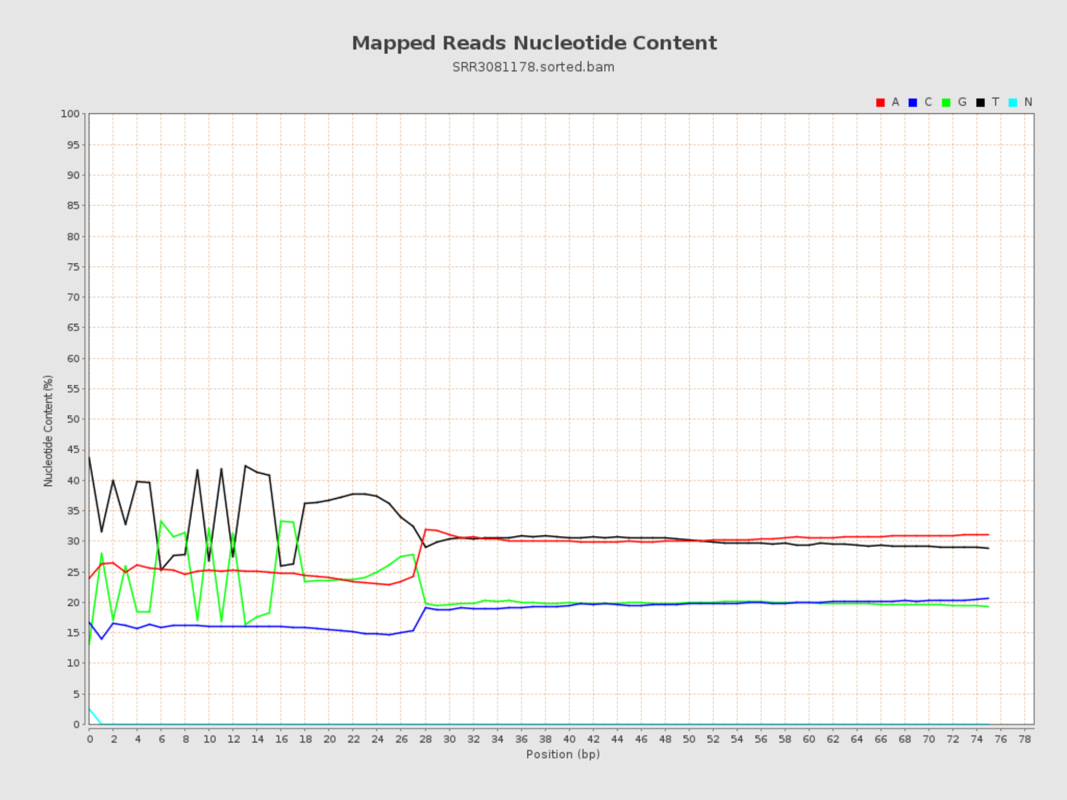
6. Results : Genome Fraction Coverage



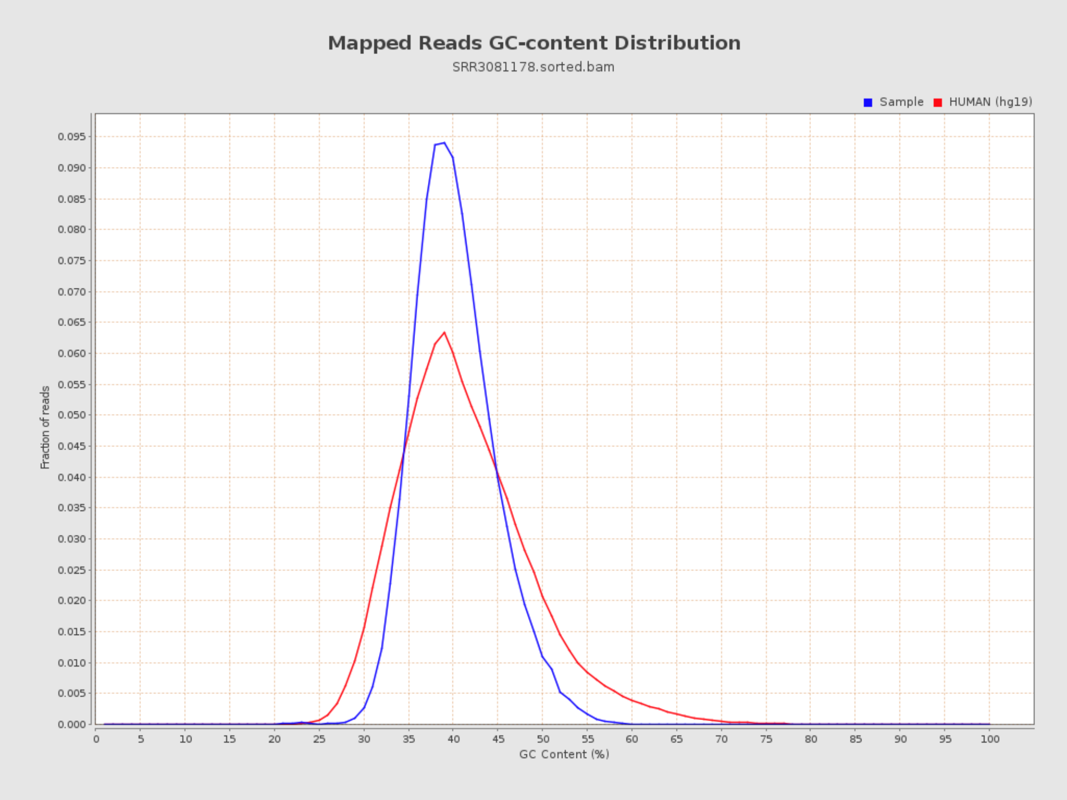
7. Results : Duplication Rate Histogram



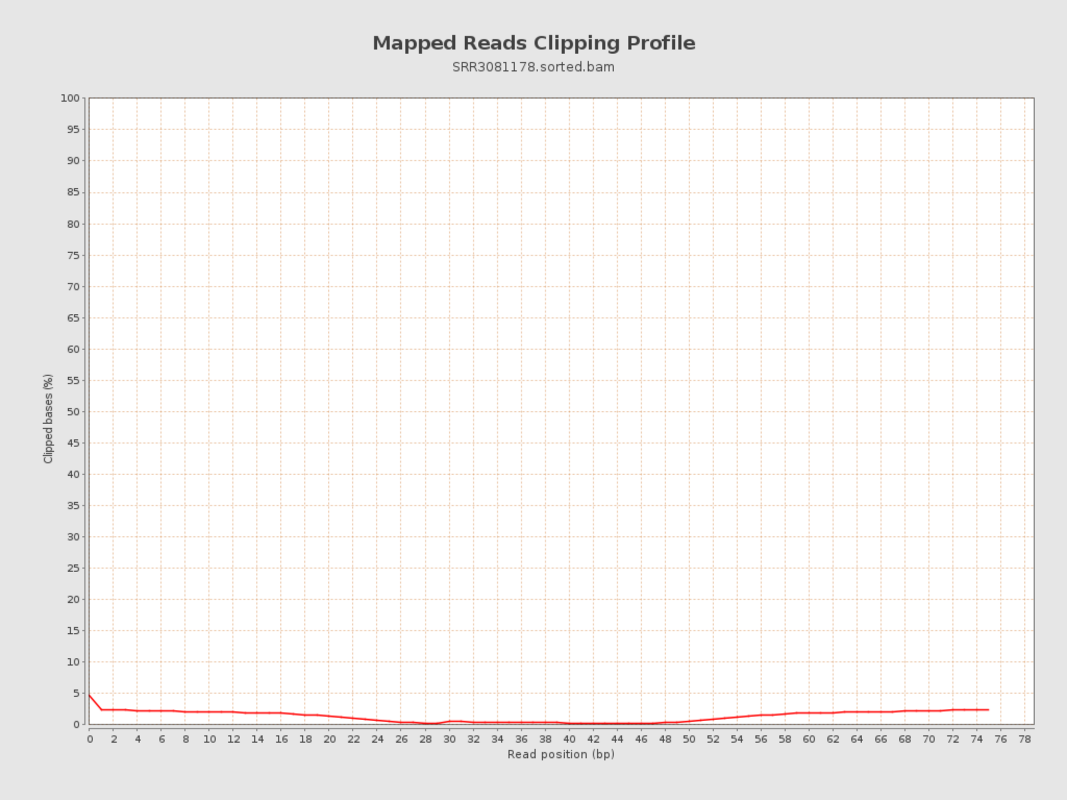
8. Results : Mapped Reads Nucleotide Content



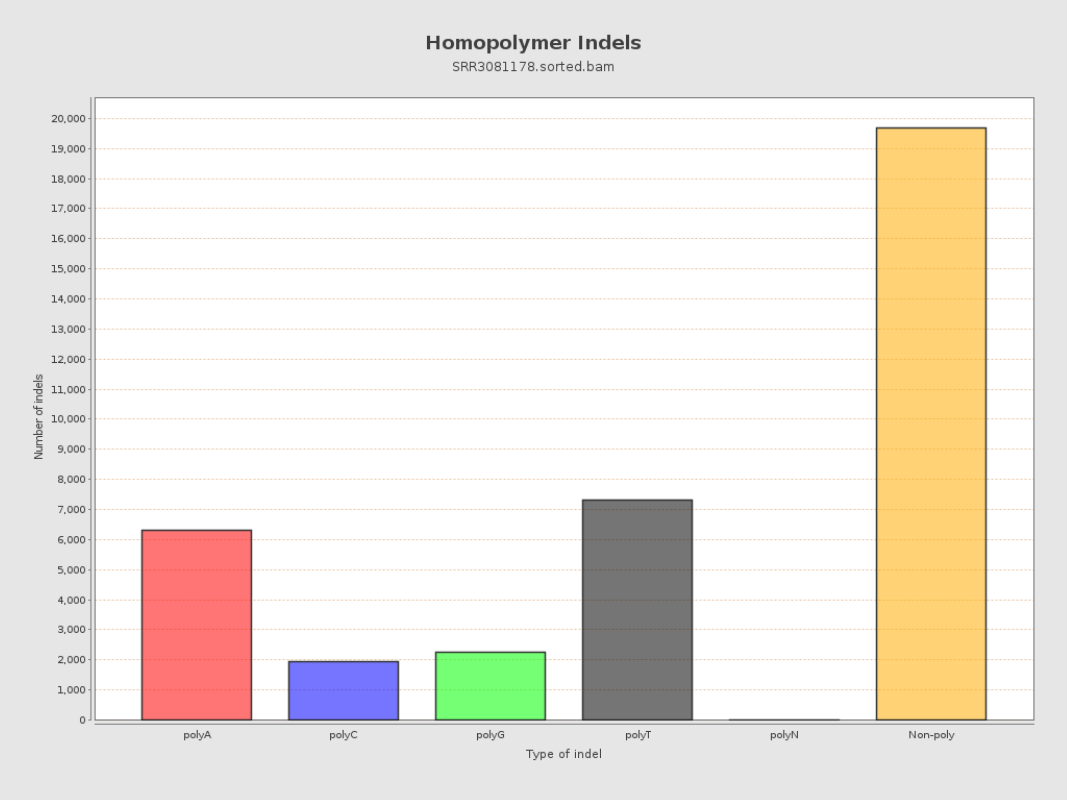
9. Results : Mapped Reads GC-content Distribution



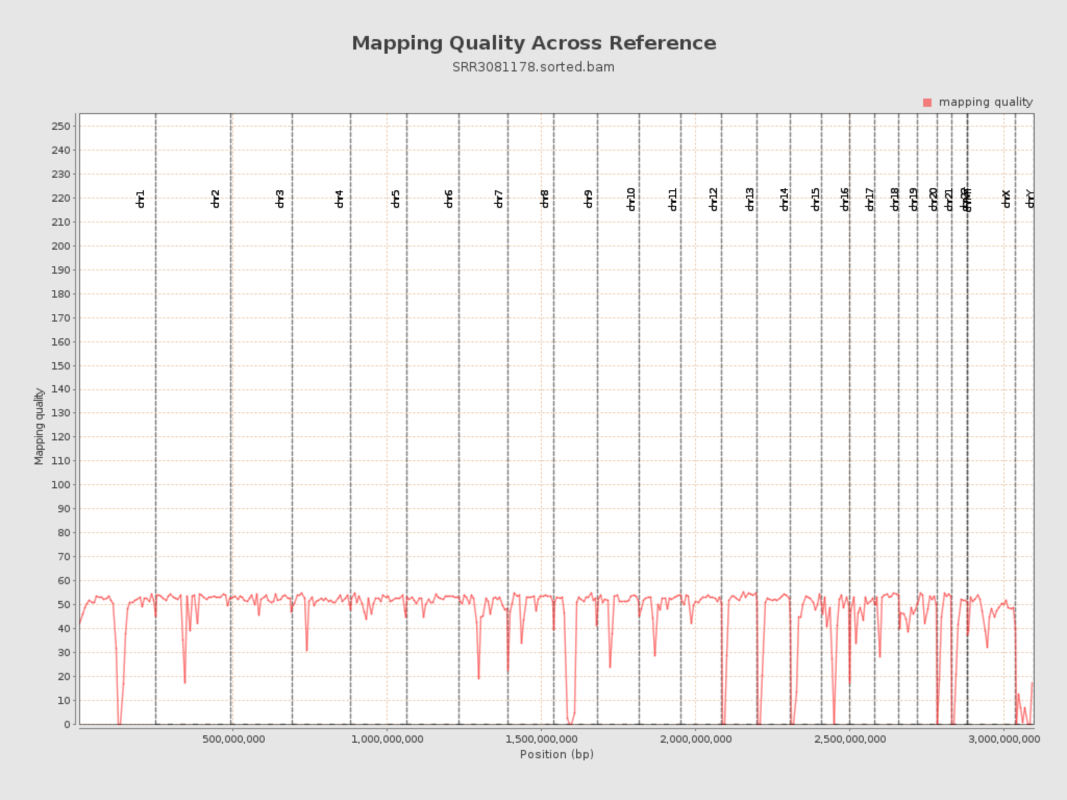
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram