Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:31:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081172.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_SRR3081172 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081172.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:31:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081172.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,310,221
Mapped reads	2,117,730 / 91.67%
Unmapped reads	192,491 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,222 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	71,867 / 3.11%
Duplication rate	2.61%
Clipped reads	840,210 / 36.37%

2.2. ACGT Content

Number/percentage of A's	42,101,385 / 29.08%
Number/percentage of C's	27,007,894 / 18.65%
Number/percentage of T's	45,213,427 / 31.23%
Number/percentage of G's	30,430,918 / 21.02%
Number/percentage of N's	43,298 / 0.03%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0468

Standard Deviation	0.3888

2.4. Mapping Quality

Mean Mapping Quality	47.48

2.5. Mismatches and indels

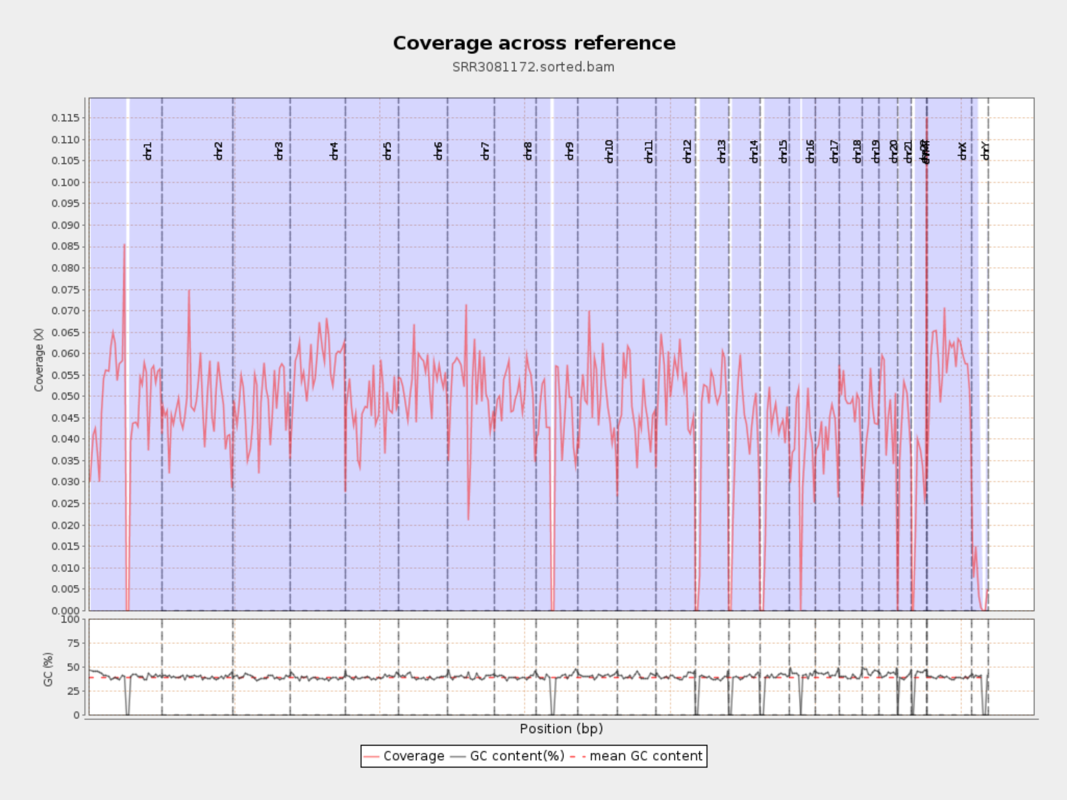
General error rate	0.85%
Mismatches	1,204,809
Insertions	11,340
Mapped reads with at least one insertion	0.53%
Deletions	34,396
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47%

2.6. Chromosome stats

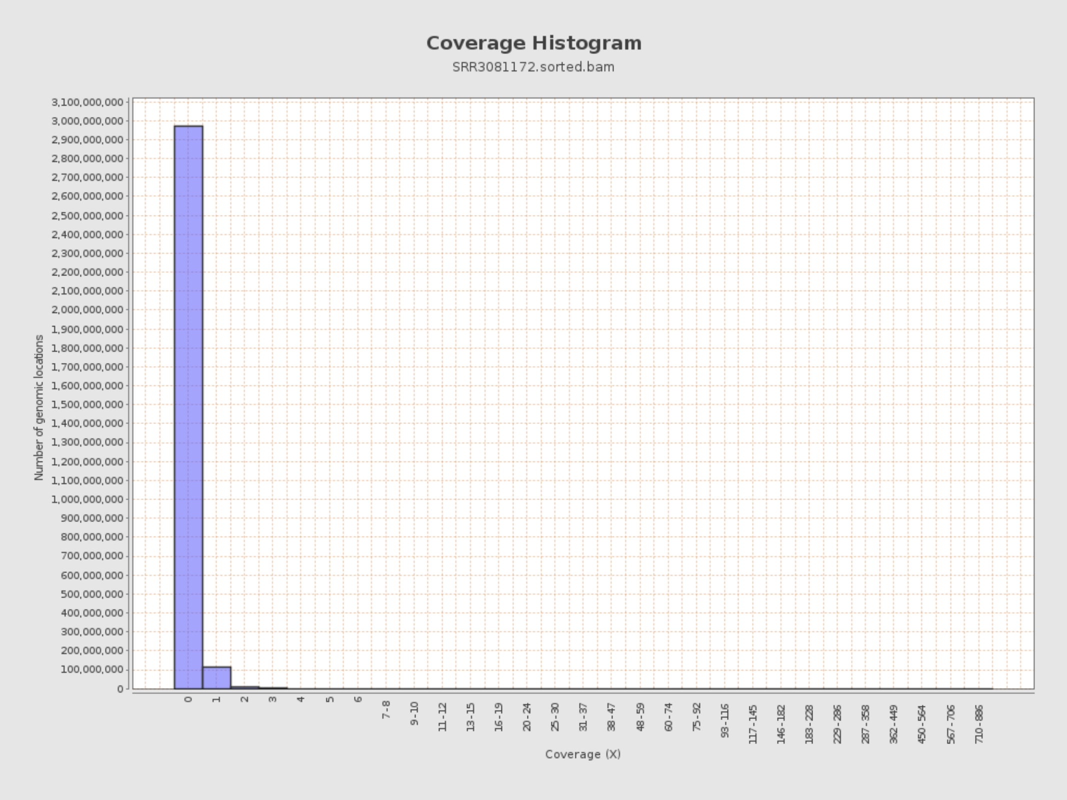
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12025458	0.0482	0.7261
chr2	243199373	11544636	0.0475	0.4027
chr3	198022430	9525206	0.0481	0.2414
chr4	191154276	11066733	0.0579	0.271
chr5	180915260	8548562	0.0473	0.242
chr6	171115067	9233557	0.054	0.3164
chr7	159138663	8204846	0.0516	0.538

chr8	146364022	7387853	0.0505	0.5944
chr9	141213431	5920093	0.0419	0.3272
chr10	135534747	6742888	0.0498	0.3351
chr11	135006516	6387357	0.0473	0.3362
chr12	133851895	7033497	0.0525	0.2576
chr13	115169878	5003185	0.0434	0.2293
chr14	107349540	4197517	0.0391	0.2301
chr15	102531392	3732511	0.0364	0.2139
chr16	90354753	3287118	0.0364	0.2411
chr17	81195210	3235897	0.0399	0.257
chr18	78077248	3828950	0.049	0.612
chr19	59128983	2543156	0.043	0.4639
chr20	63025520	2958305	0.0469	0.2465
chr21	48129895	1937092	0.0402	0.2318
chr22	51304566	1247310	0.0243	0.1696
chrMT	16571	1909	0.1152	0.3546
chrX	155270560	8941398	0.0576	0.2961
chrY	59373566	317786	0.0054	0.1123

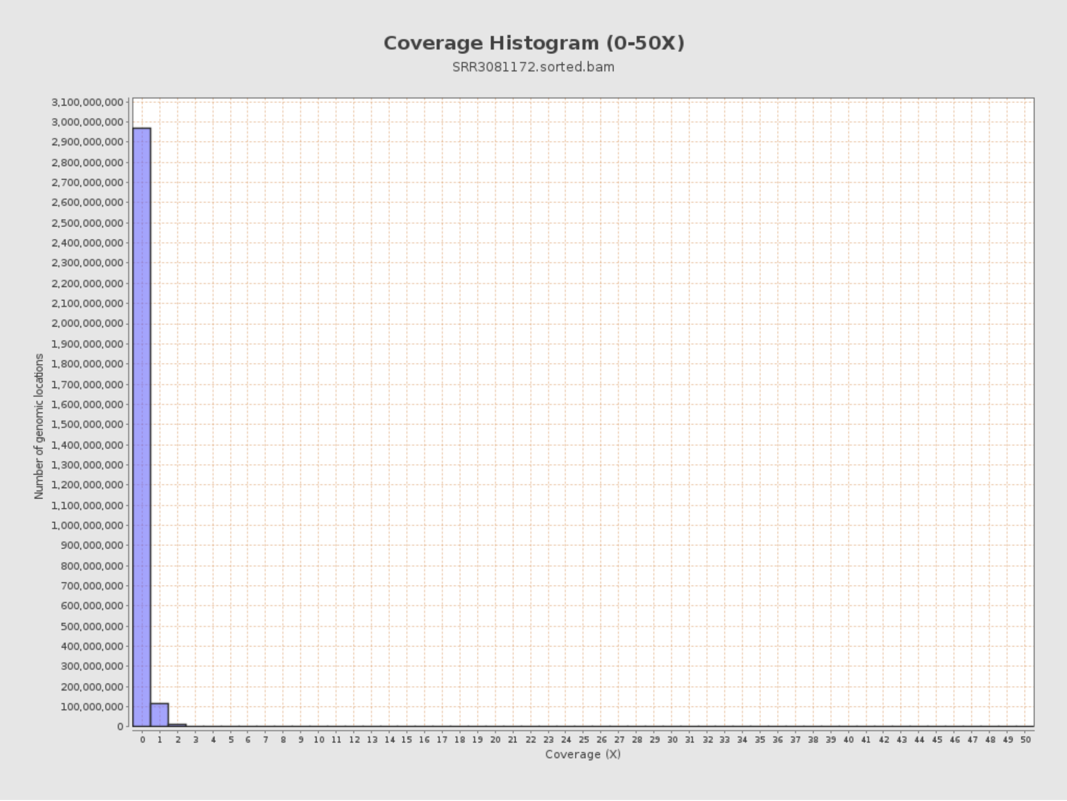
3. Results : Coverage across reference



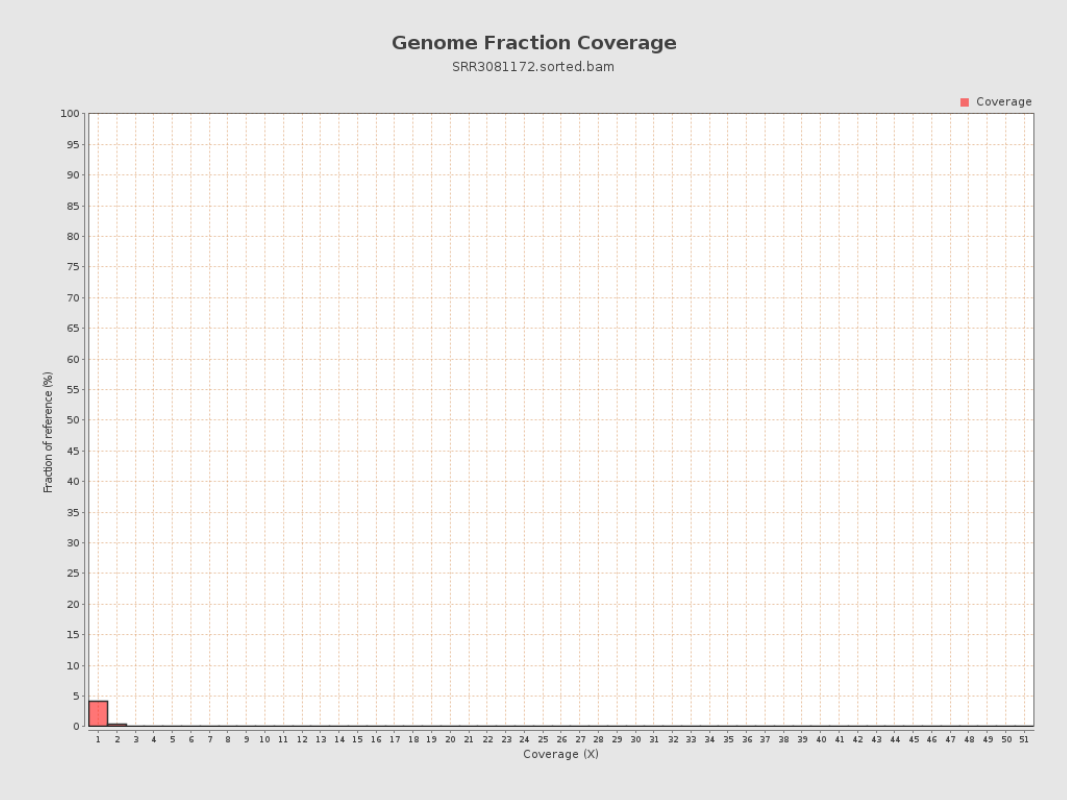
4. Results : Coverage Histogram



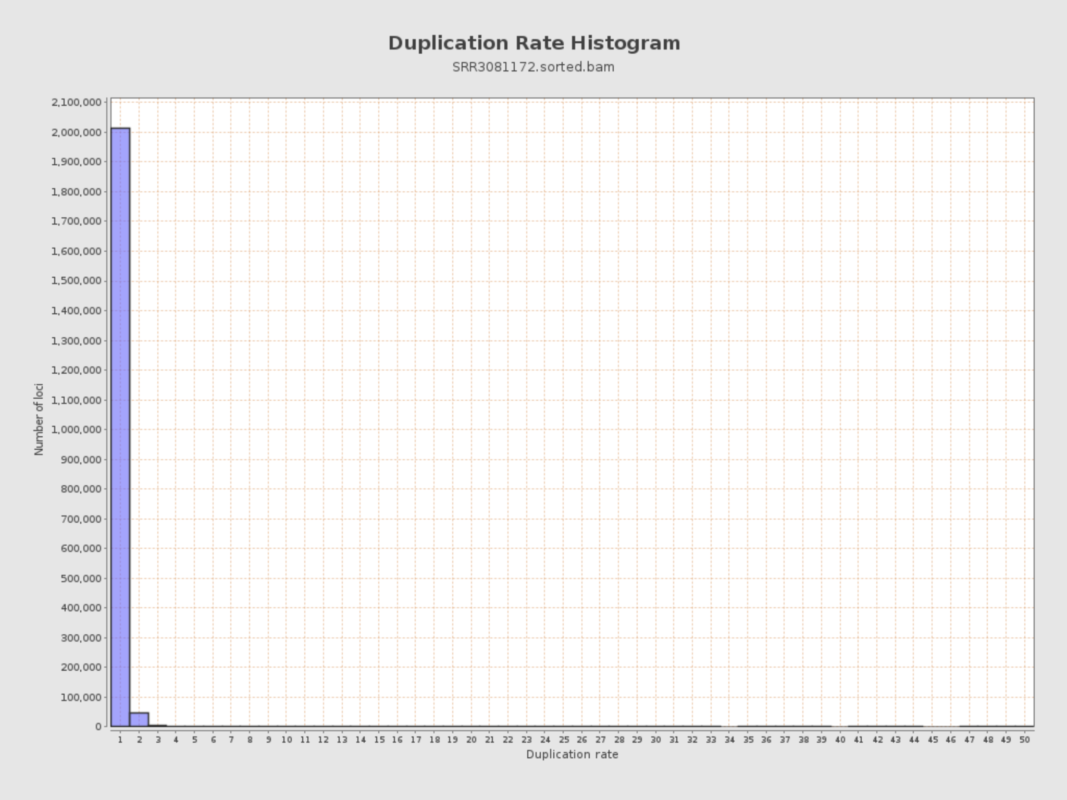
5. Results : Coverage Histogram (0-50X)



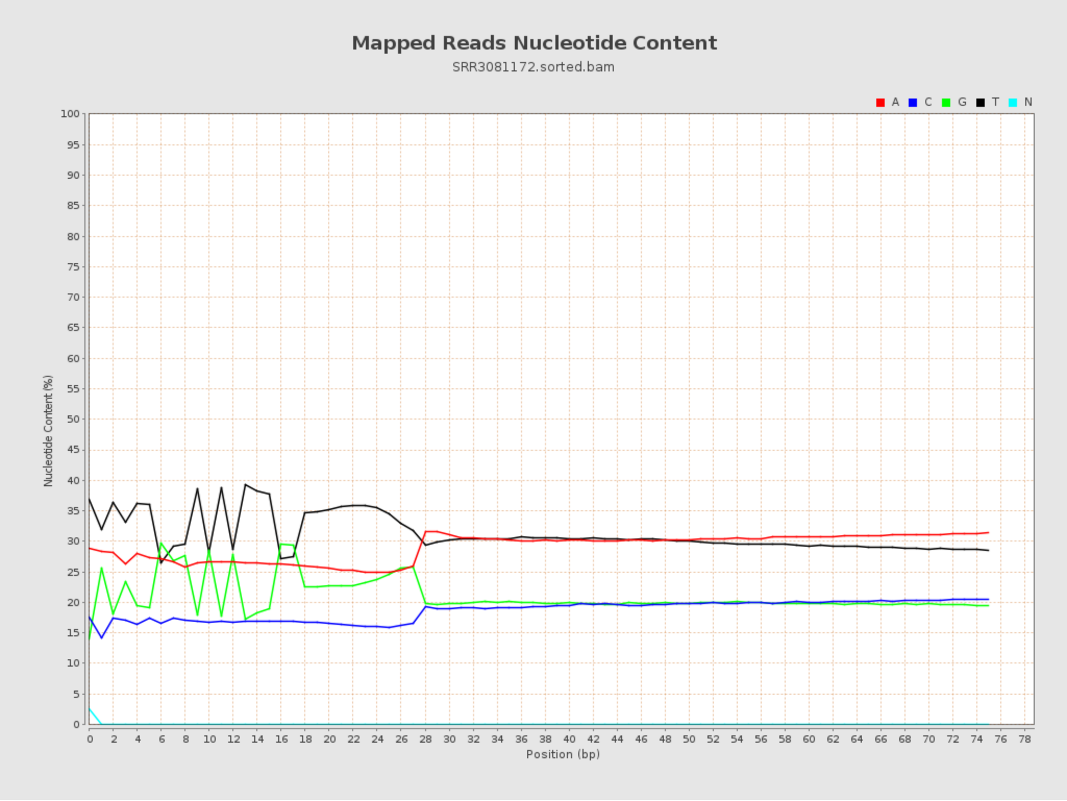
6. Results : Genome Fraction Coverage



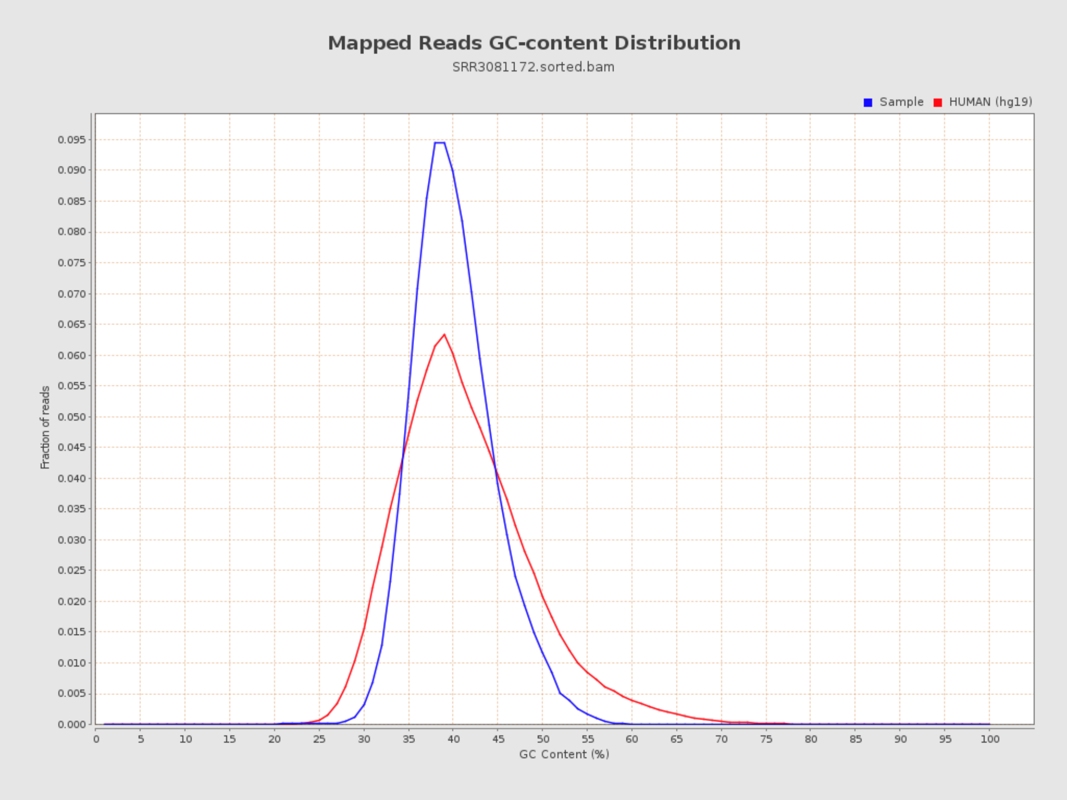
7. Results : Duplication Rate Histogram



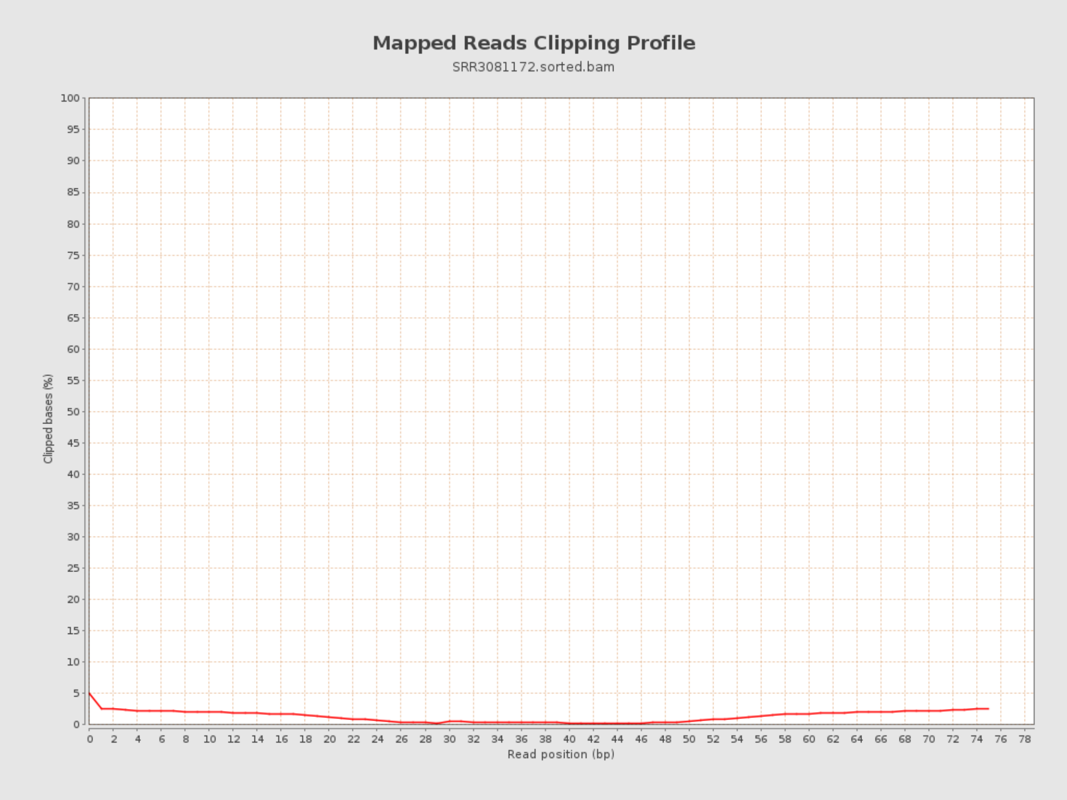
8. Results : Mapped Reads Nucleotide Content



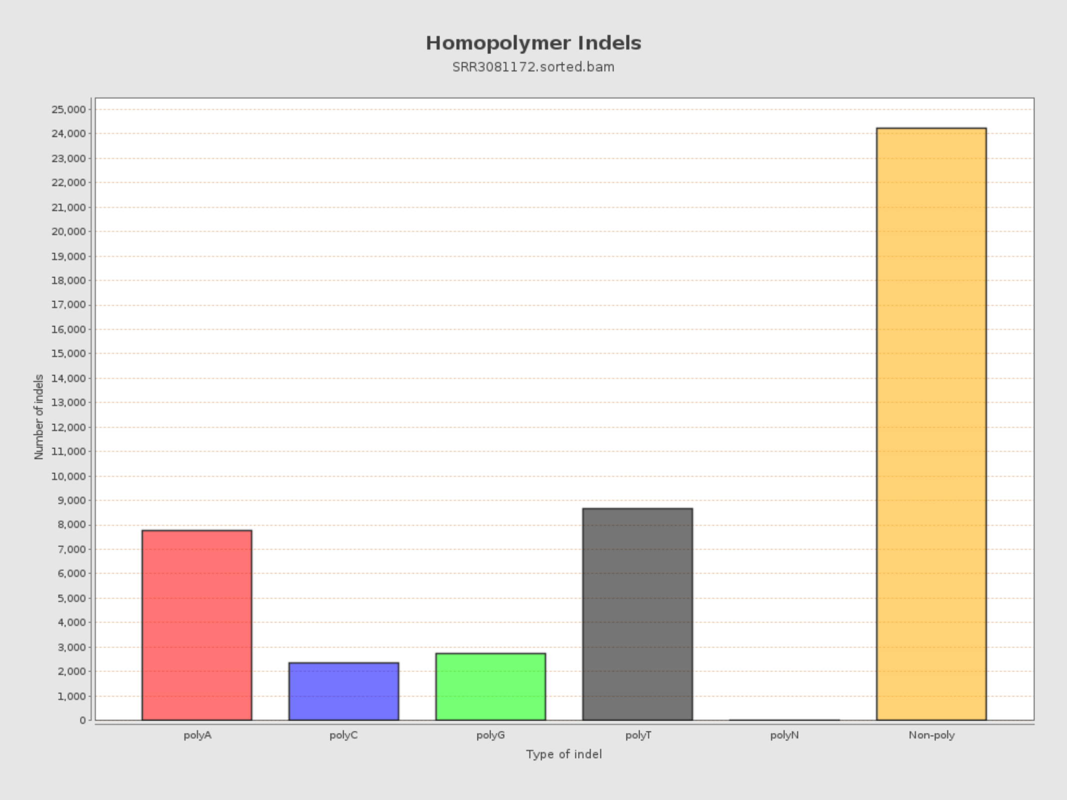
9. Results : Mapped Reads GC-content Distribution



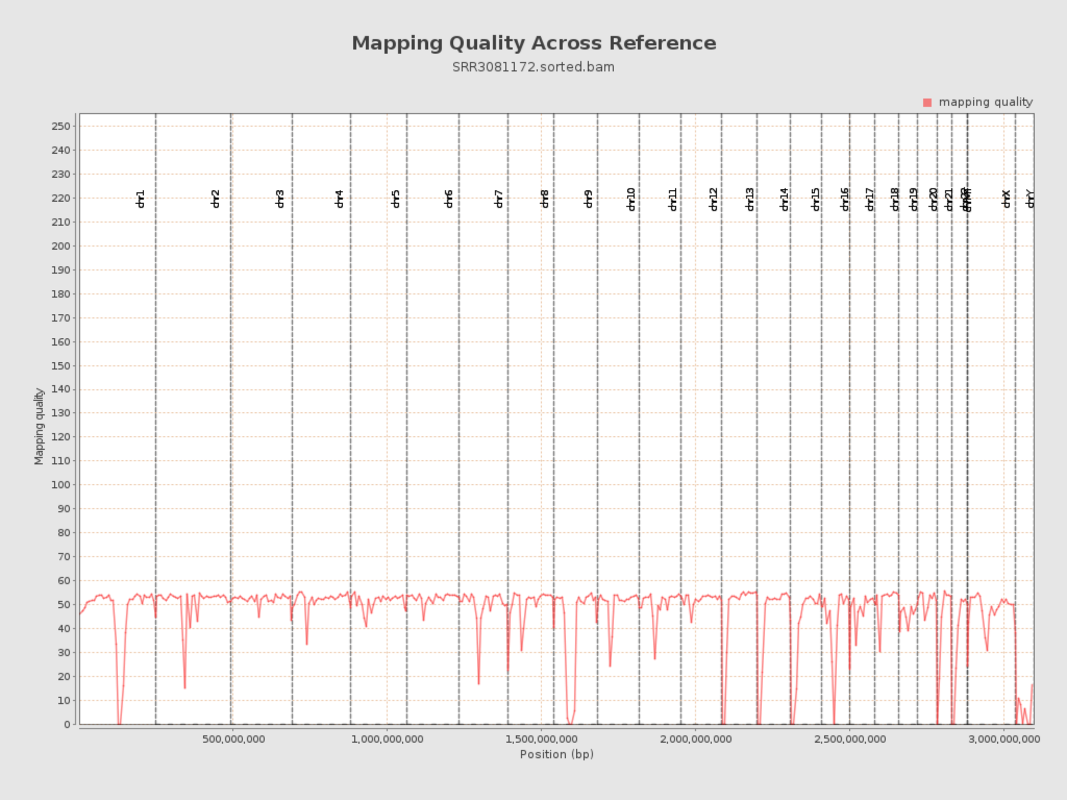
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram