Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 06:51:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472802.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_SRR3472802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 06:51:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,847,316
Mapped reads	1,399,385 / 75.75%
Unmapped reads	447,931 / 24.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,281 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	64,849 / 3.51%
Duplication rate	3.49%
Clipped reads	850,473 / 46.04%

2.2. ACGT Content

Number/percentage of A's	23,190,597 / 26.47%
Number/percentage of C's	17,572,379 / 20.06%
Number/percentage of T's	25,812,399 / 29.46%
Number/percentage of G's	21,032,608 / 24.01%
Number/percentage of N's	2,128 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.2521

2.4. Mapping Quality

Mean Mapping Quality	42.59

2.5. Mismatches and indels

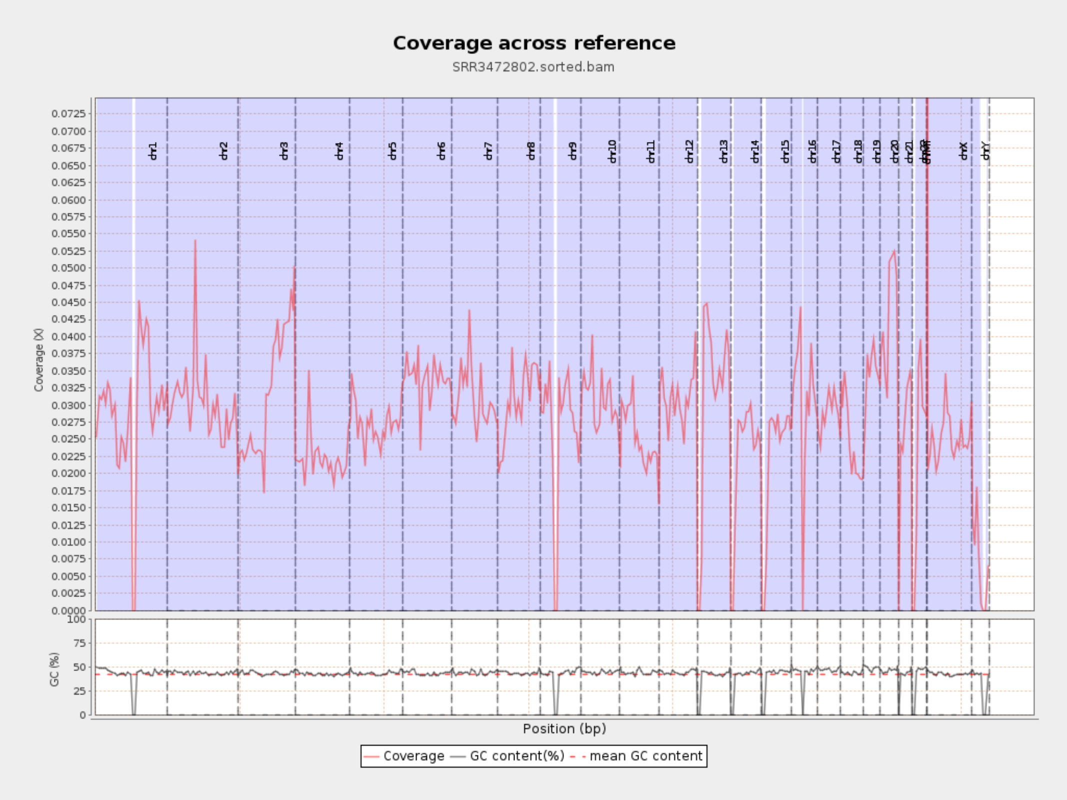
General error rate	0.92%
Mismatches	793,472
Insertions	6,605
Mapped reads with at least one insertion	0.47%
Deletions	21,256
Mapped reads with at least one deletion	1.5%
Homopolymer indels	44.63%

2.6. Chromosome stats

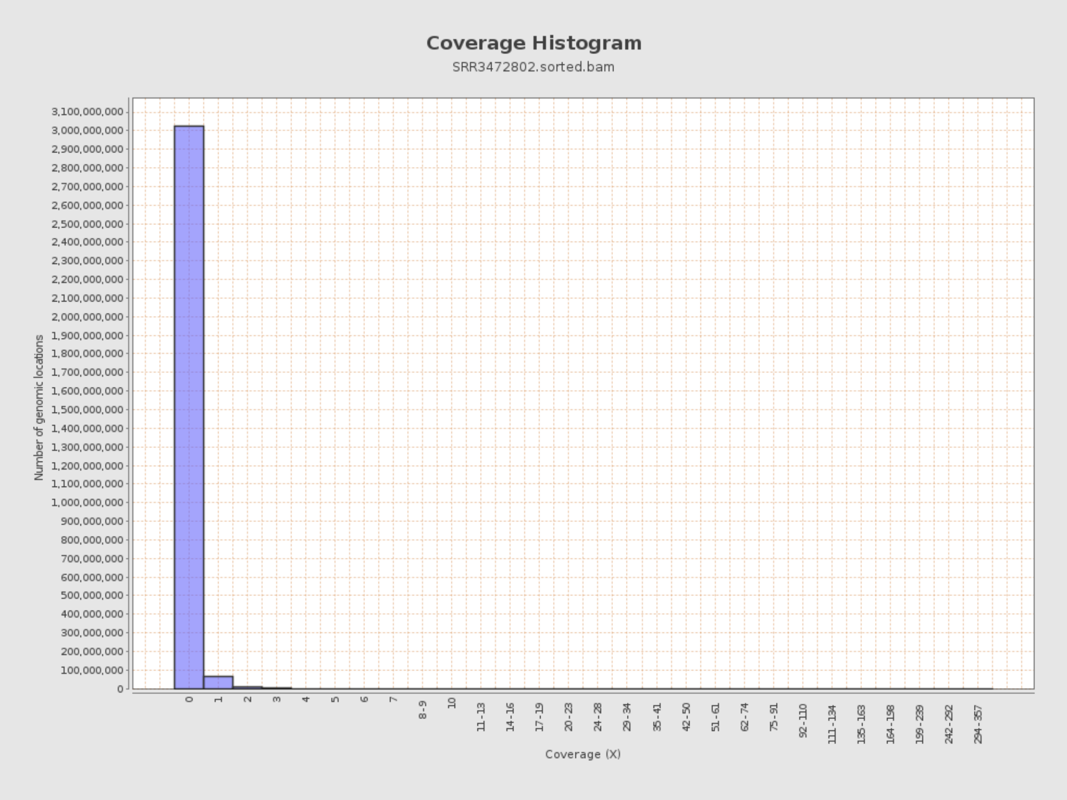
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7218102	0.029	0.3177
chr2	243199373	7418216	0.0305	0.3177
chr3	198022430	6208373	0.0314	0.2073
chr4	191154276	4258075	0.0223	0.1901
chr5	180915260	4957045	0.0274	0.1971
chr6	171115067	5785400	0.0338	0.2345
chr7	159138663	4946864	0.0311	0.3161

chr8	146364022	4488294	0.0307	0.2451
chr9	141213431	3724833	0.0264	0.2573
chr10	135534747	4206838	0.031	0.2525
chr11	135006516	3441252	0.0255	0.2631
chr12	133851895	4180842	0.0312	0.2171
chr13	115169878	3601076	0.0313	0.2119
chr14	107349540	2397029	0.0223	0.1994
chr15	102531392	2240215	0.0218	0.1944
chr16	90354753	2732597	0.0302	0.2192
chr17	81195210	2331455	0.0287	0.2194
chr18	78077248	1916427	0.0245	0.4347
chr19	59128983	2031374	0.0344	0.2761
chr20	63025520	2731257	0.0433	0.2536
chr21	48129895	1270728	0.0264	0.2082
chr22	51304566	1175584	0.0229	0.1826
chrMT	16571	76298	4.6043	3.9002
chrX	155270560	3910219	0.0252	0.2071
chrY	59373566	399995	0.0067	0.1131

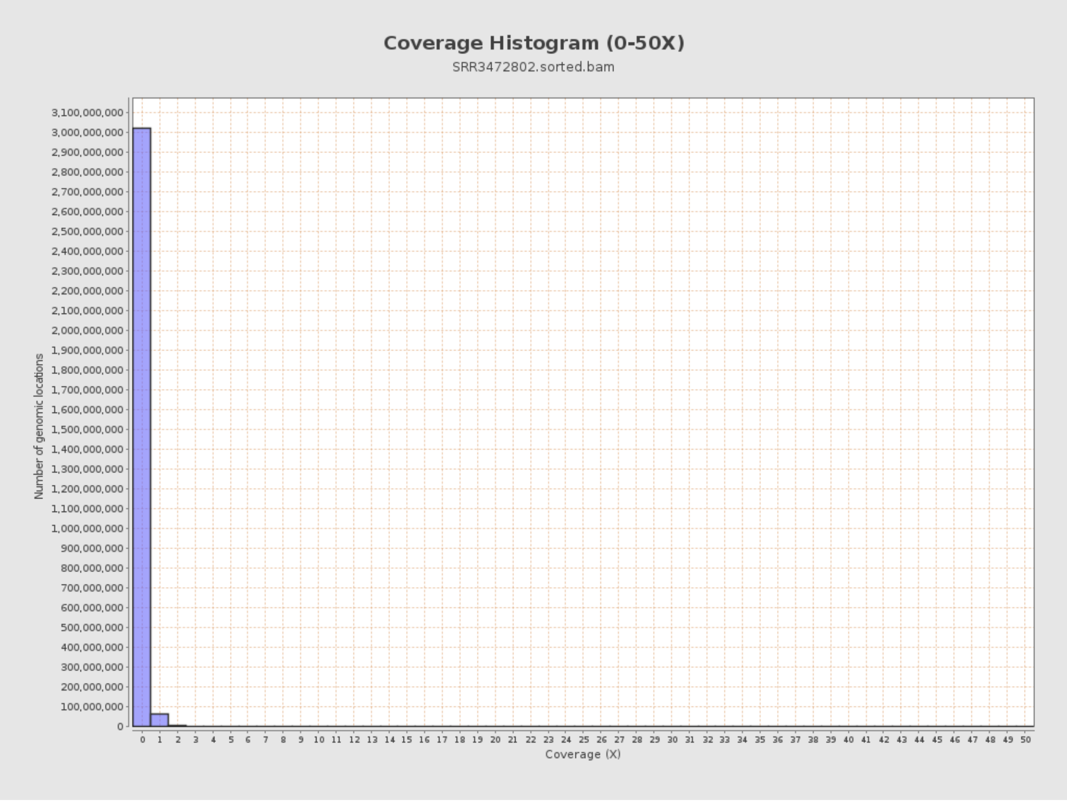
3. Results : Coverage across reference



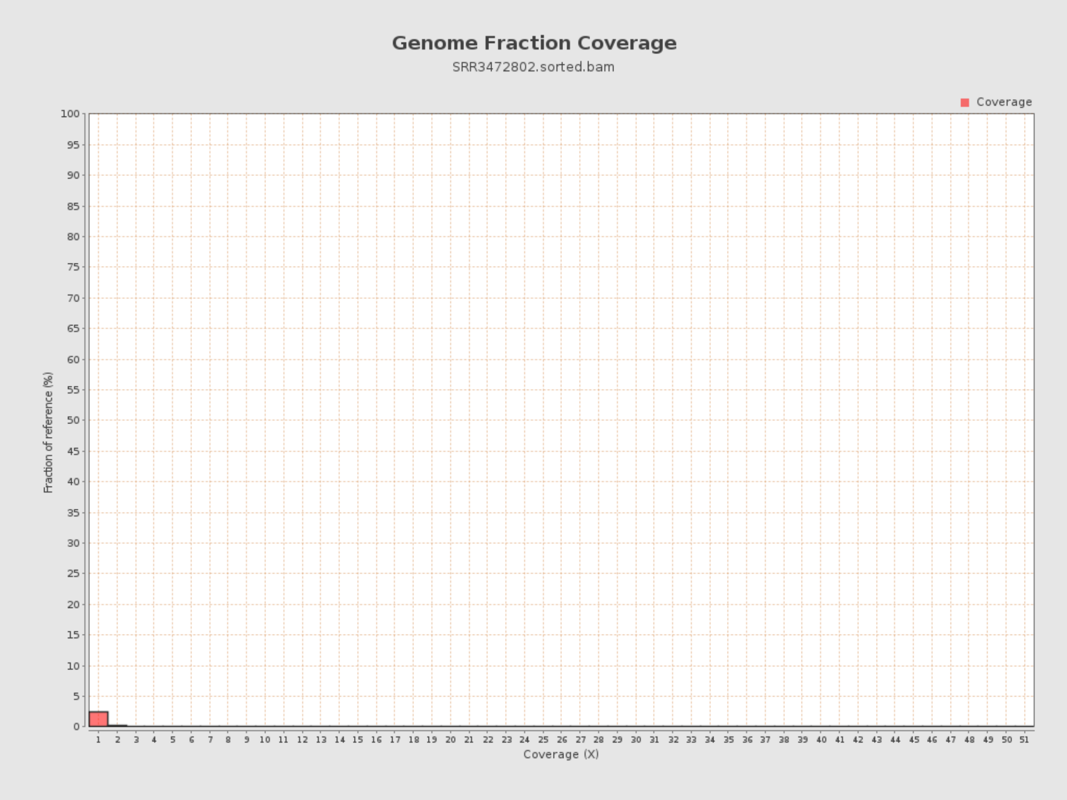
4. Results : Coverage Histogram



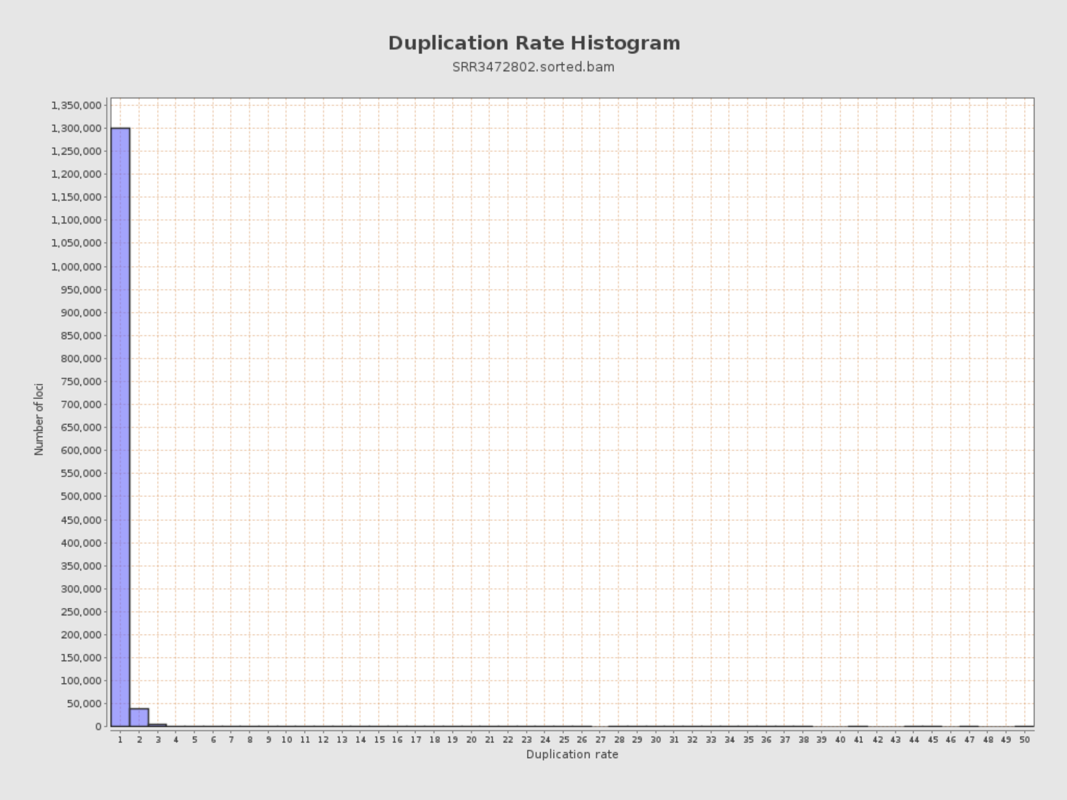
5. Results : Coverage Histogram (0-50X)



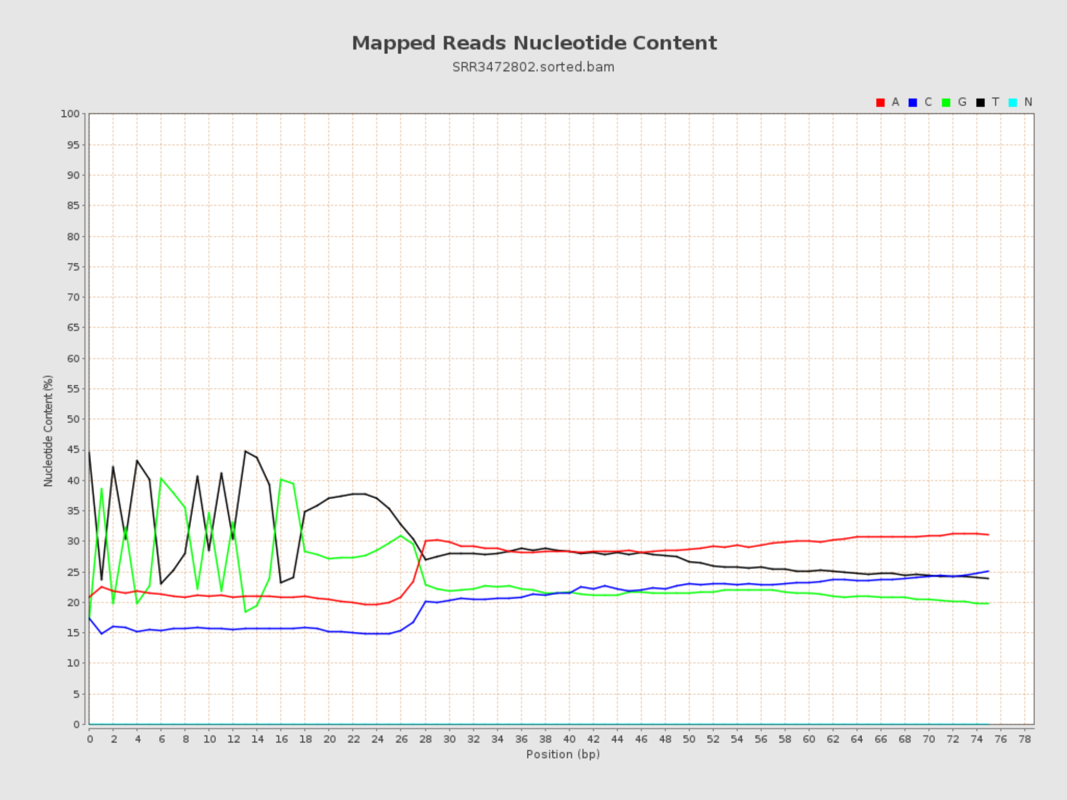
6. Results : Genome Fraction Coverage



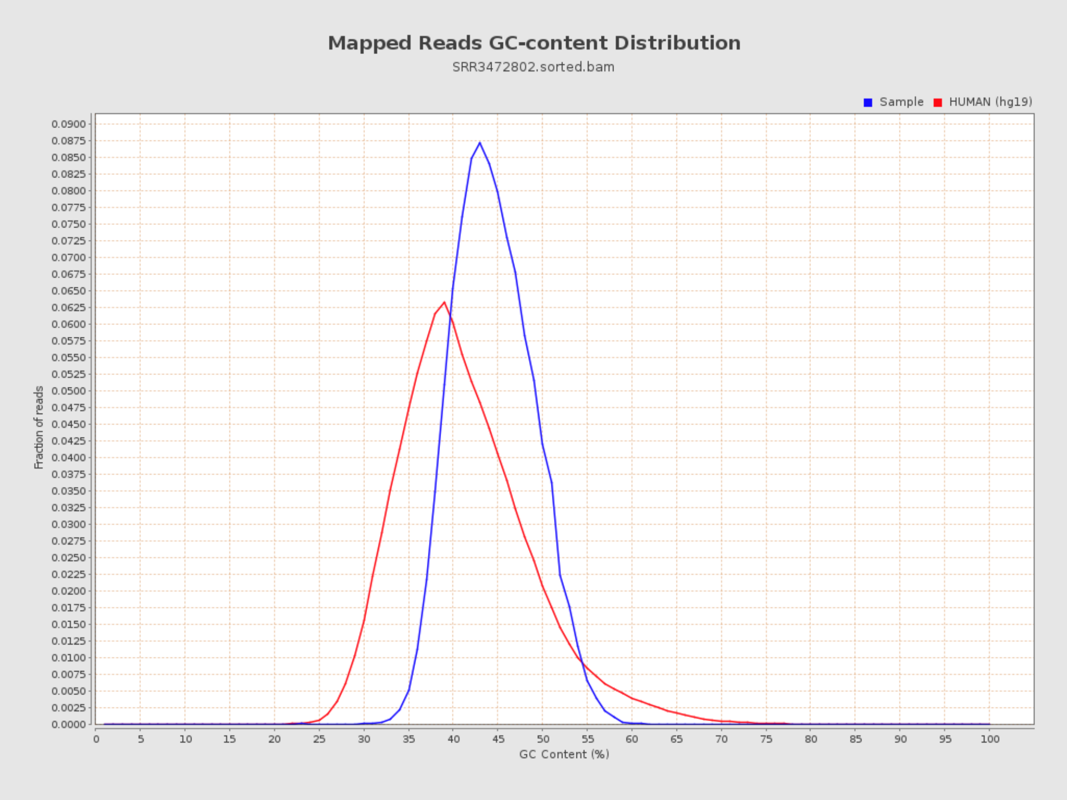
7. Results : Duplication Rate Histogram



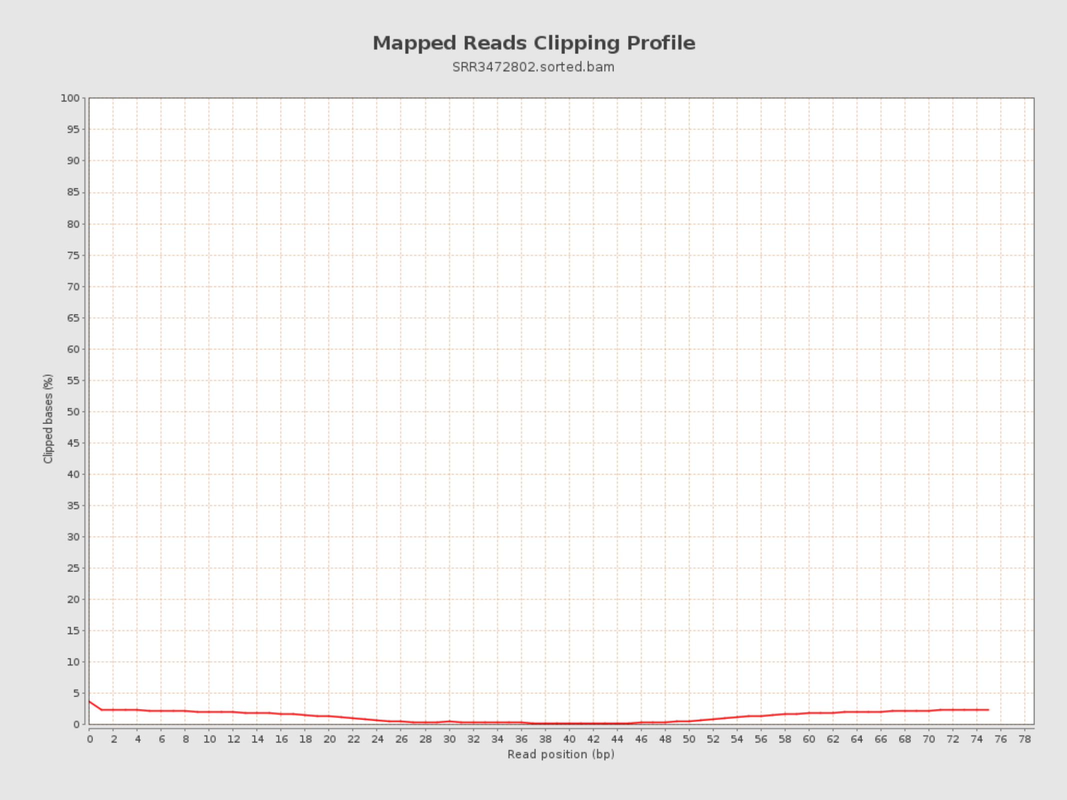
8. Results : Mapped Reads Nucleotide Content



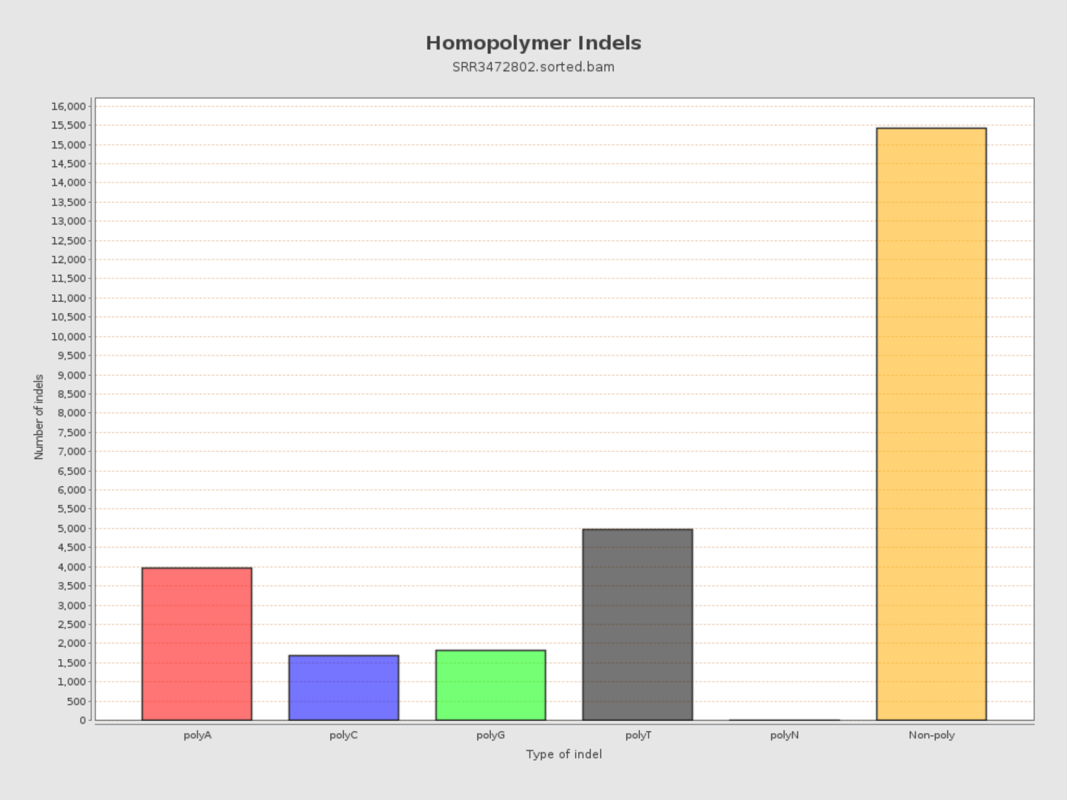
9. Results : Mapped Reads GC-content Distribution



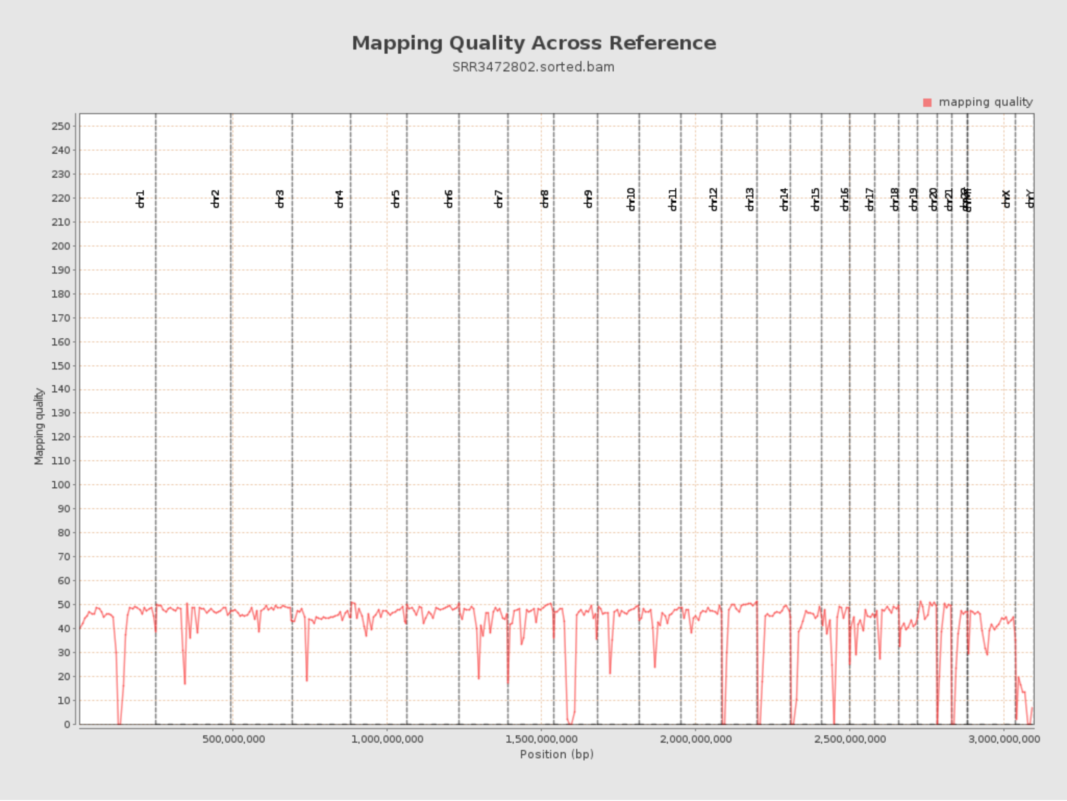
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram