Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:23:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081169.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_SRR3081169 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081169.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:23:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,798,239
Mapped reads	1,506,092 / 83.75%
Unmapped reads	292,147 / 16.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,384 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	59,588 / 3.31%
Duplication rate	3.28%
Clipped reads	764,705 / 42.53%

2.2. ACGT Content

Number/percentage of A's	27,059,102 / 27.45%
Number/percentage of C's	17,895,210 / 18.15%
Number/percentage of T's	31,383,655 / 31.83%
Number/percentage of G's	22,222,078 / 22.54%
Number/percentage of N's	28,427 / 0.03%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.2716

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

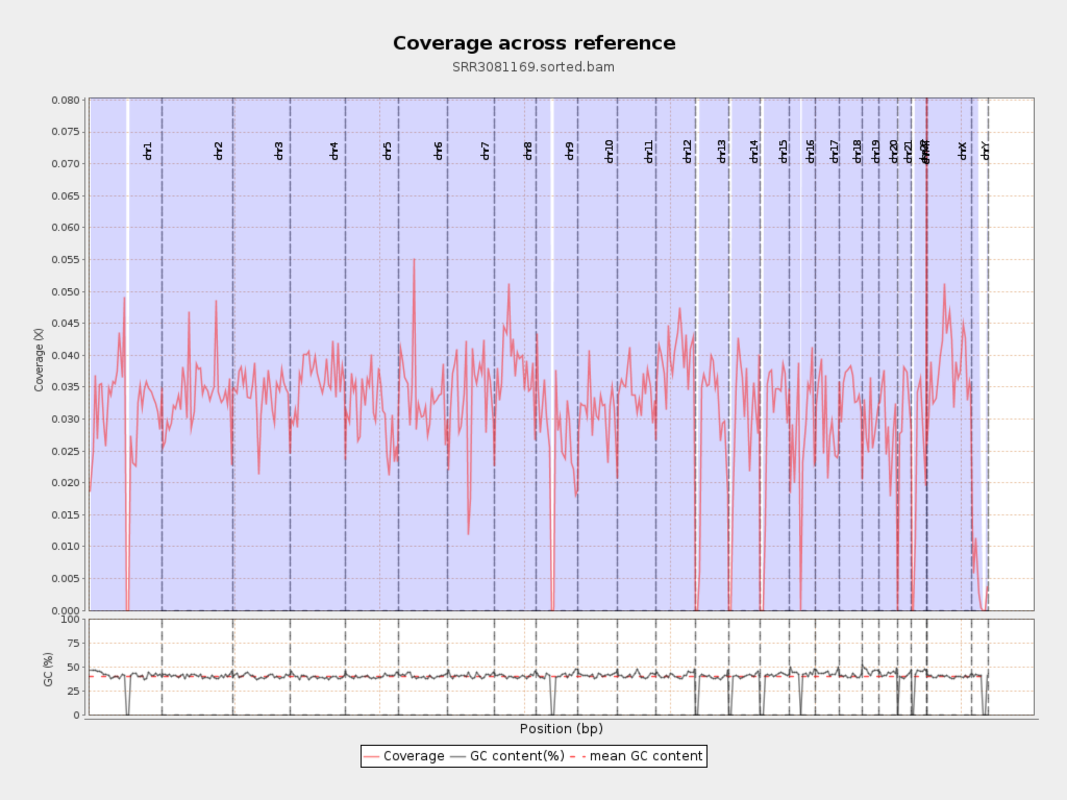
General error rate	0.87%
Mismatches	845,166
Insertions	7,339
Mapped reads with at least one insertion	0.48%
Deletions	21,987
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.81%

2.6. Chromosome stats

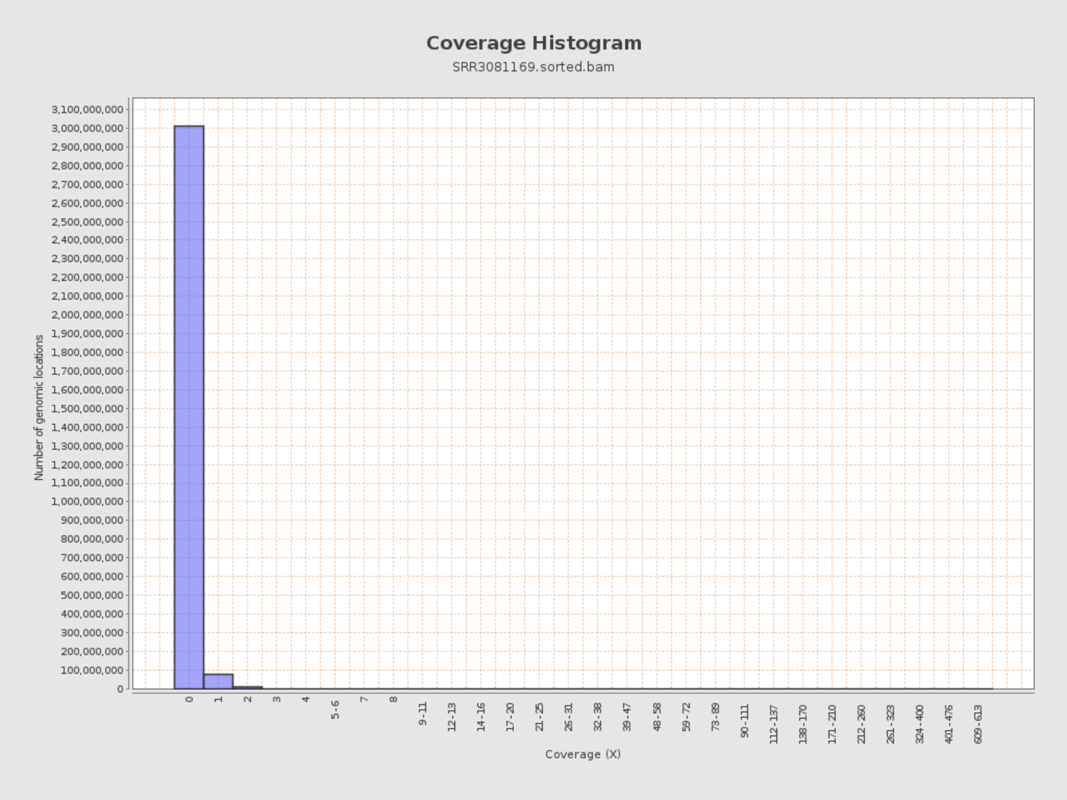
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7626224	0.0306	0.4071
chr2	243199373	8201469	0.0337	0.3492
chr3	198022430	6767226	0.0342	0.203
chr4	191154276	6944182	0.0363	0.2158
chr5	180915260	5669207	0.0313	0.1953
chr6	171115067	5797753	0.0339	0.266
chr7	159138663	5310729	0.0334	0.3314

chr8	146364022	5577969	0.0381	0.3614
chr9	141213431	3605679	0.0255	0.2352
chr10	135534747	4253984	0.0314	0.238
chr11	135006516	4631295	0.0343	0.2604
chr12	133851895	5331054	0.0398	0.2214
chr13	115169878	3185976	0.0277	0.1835
chr14	107349540	3023905	0.0282	0.1927
chr15	102531392	2919731	0.0285	0.1912
chr16	90354753	2452945	0.0271	0.1936
chr17	81195210	2373332	0.0292	0.2148
chr18	78077248	2714956	0.0348	0.4342
chr19	59128983	1719390	0.0291	0.298
chr20	63025520	1827167	0.029	0.1938
chr21	48129895	1407697	0.0292	0.1956
chr22	51304566	1076640	0.021	0.1584
chrMT	16571	1343	0.081	0.296
chrX	155270560	5953762	0.0383	0.2382
chrY	59373566	249911	0.0042	0.0857

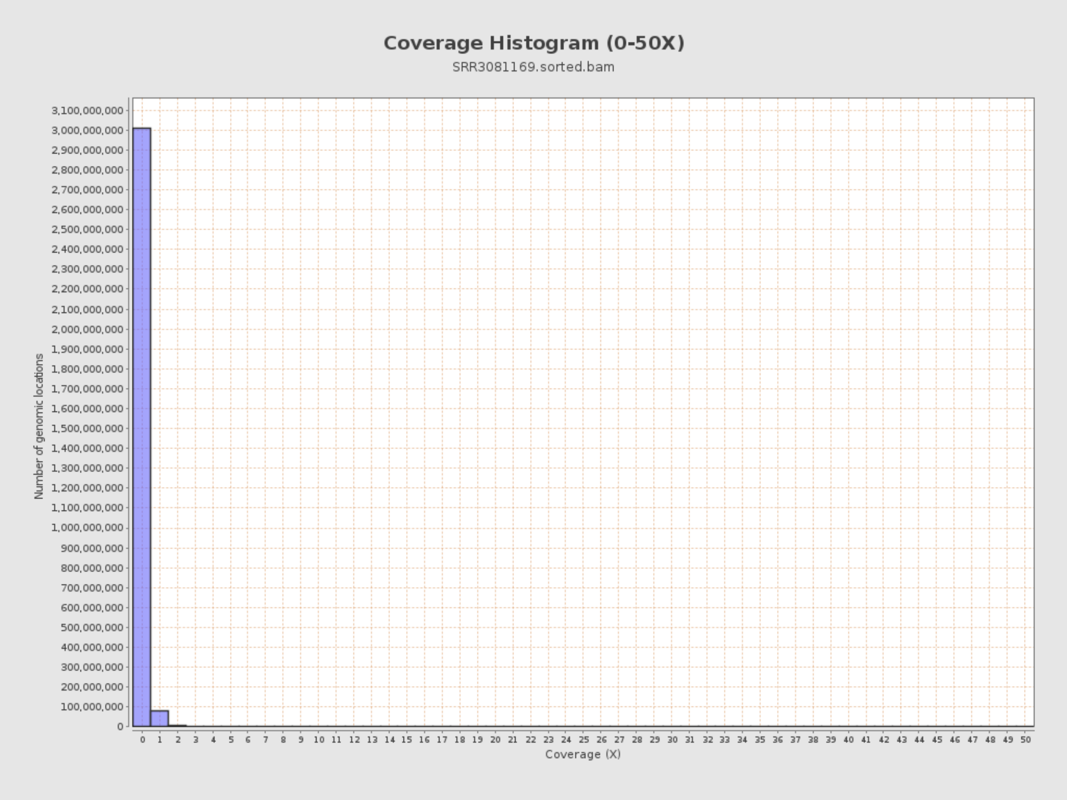
3. Results : Coverage across reference



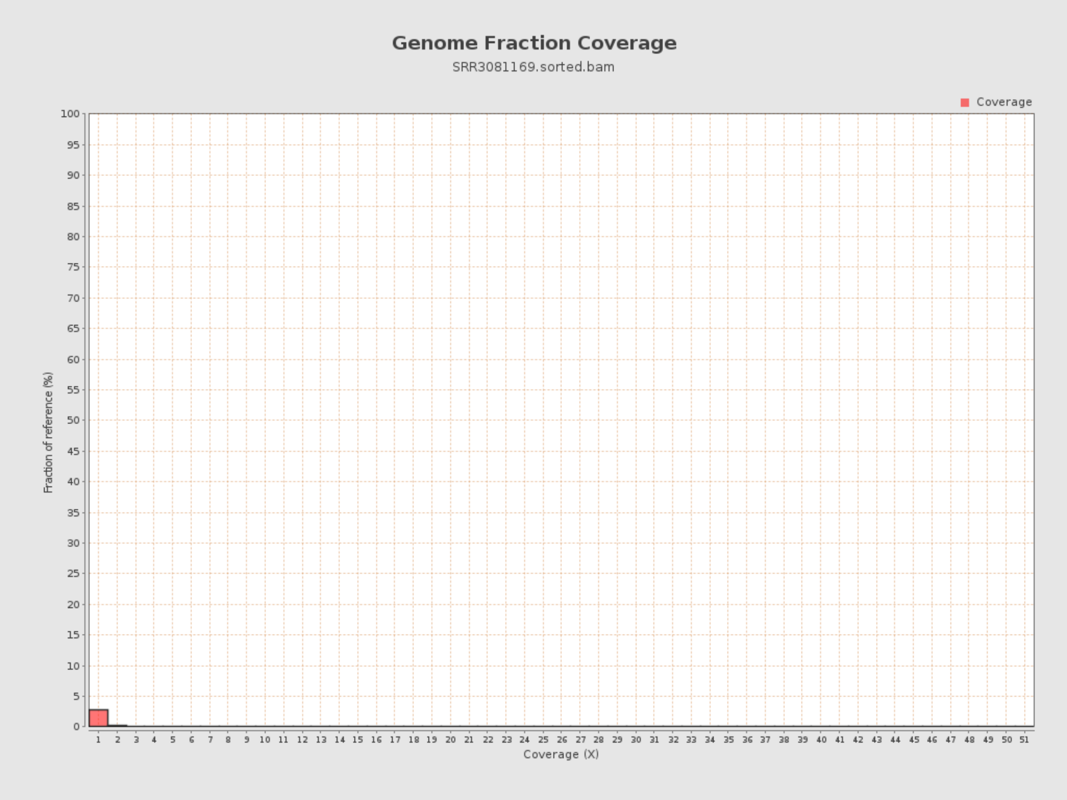
4. Results : Coverage Histogram



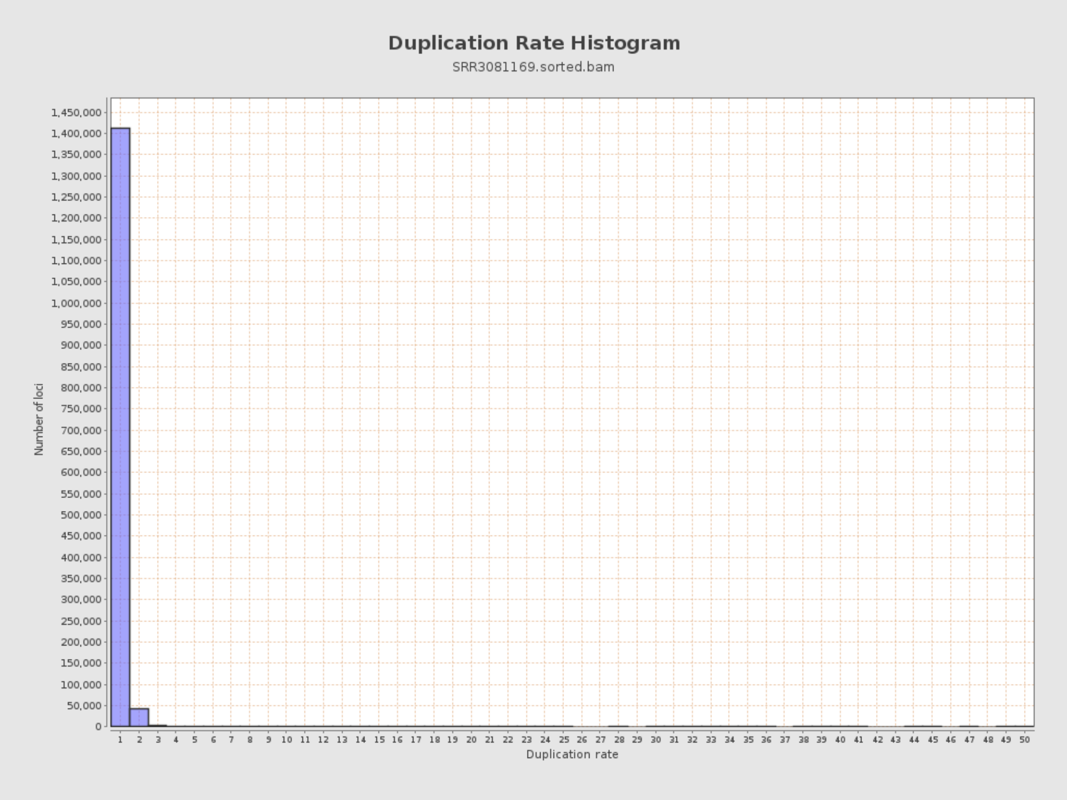
5. Results : Coverage Histogram (0-50X)



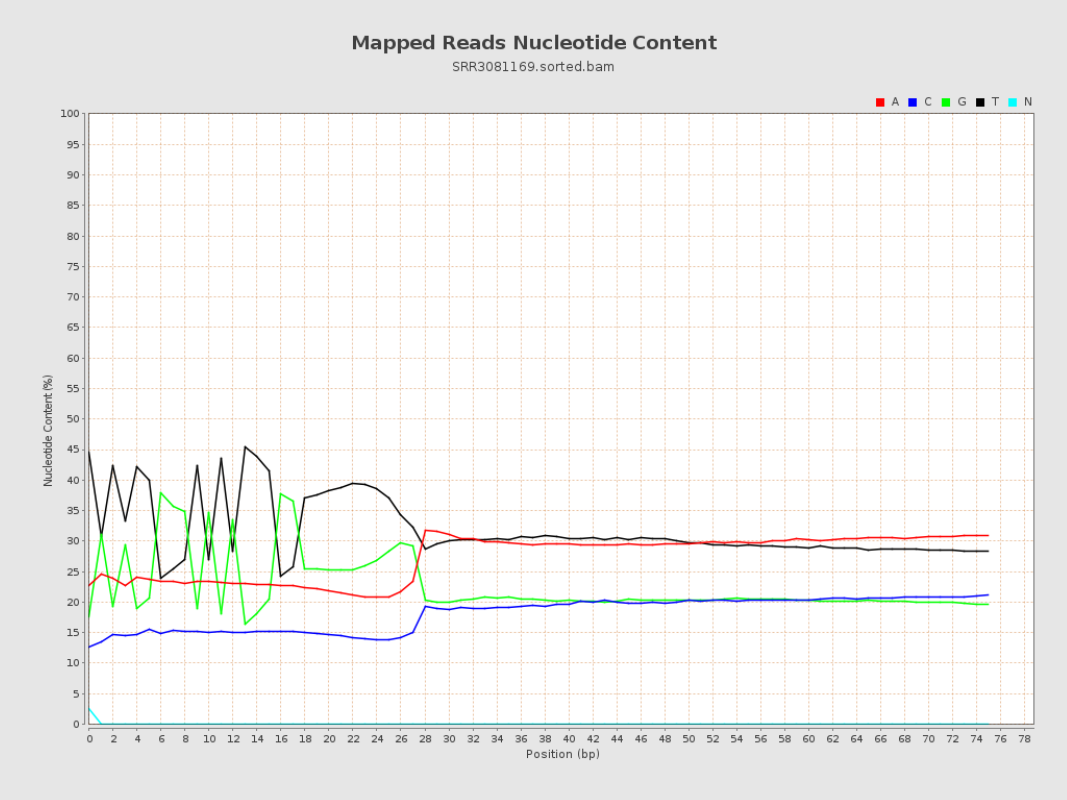
6. Results : Genome Fraction Coverage



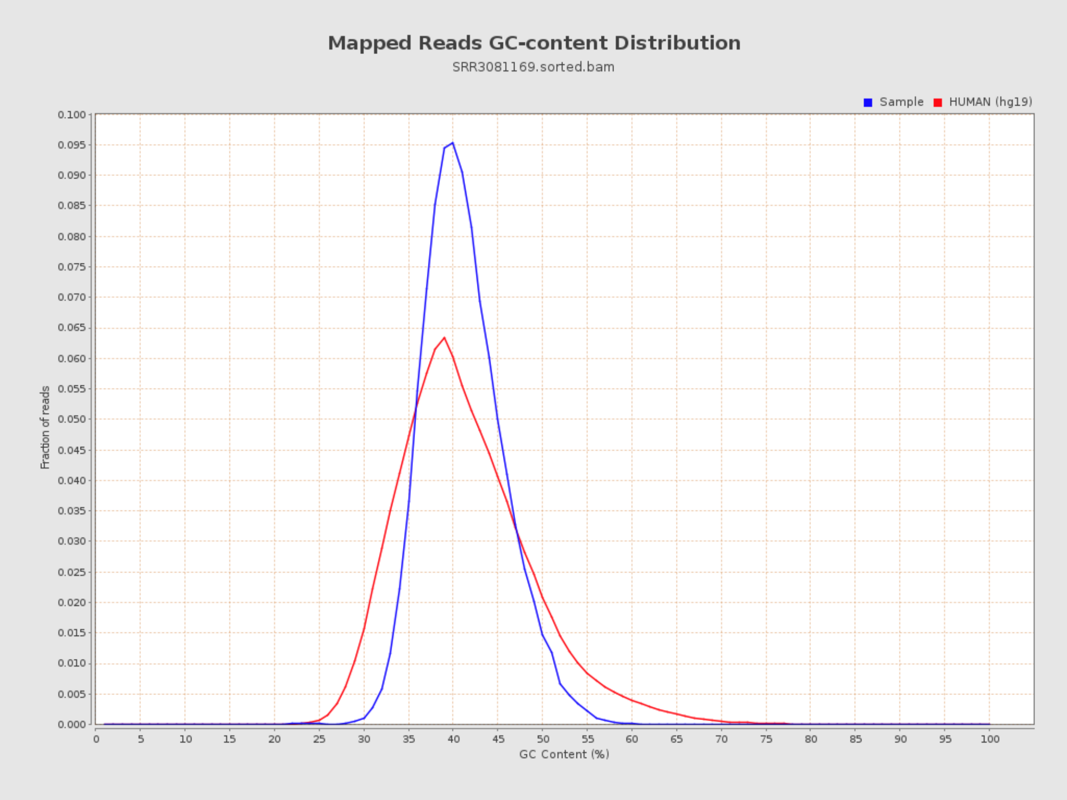
7. Results : Duplication Rate Histogram



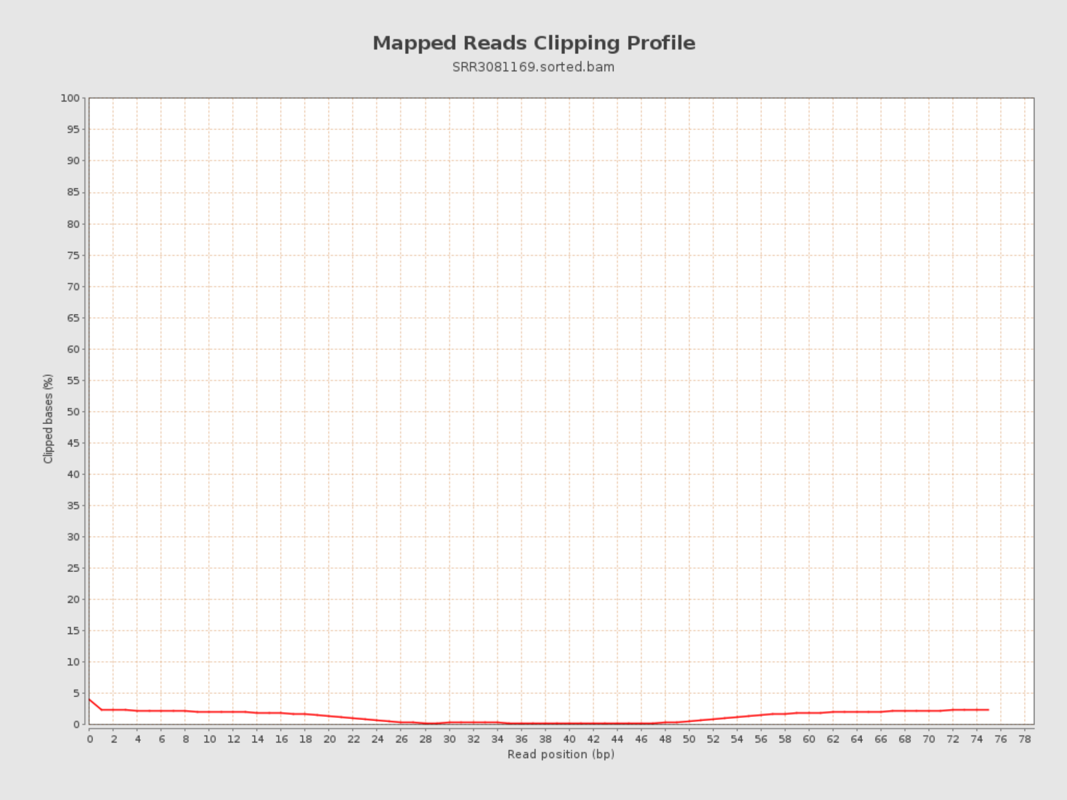
8. Results : Mapped Reads Nucleotide Content



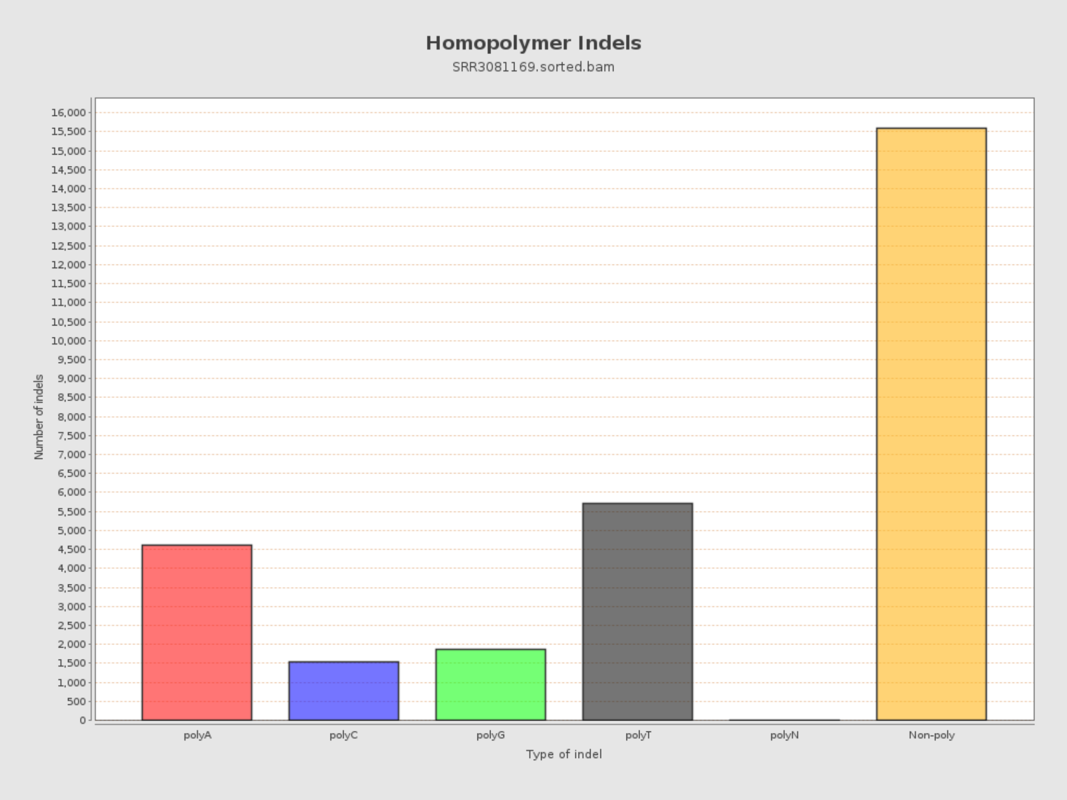
9. Results : Mapped Reads GC-content Distribution



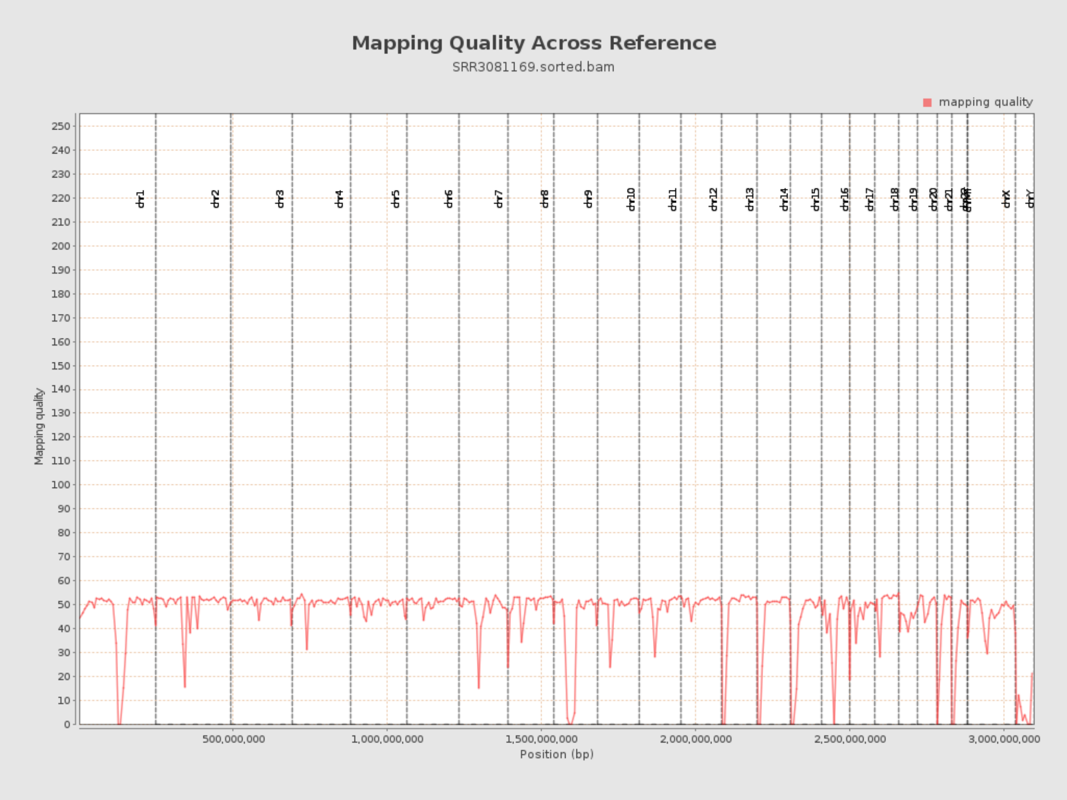
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram