Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:12:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081053.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_SRR3081053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:12:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,340,395
Mapped reads	1,083,040 / 80.8%
Unmapped reads	257,355 / 19.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,262 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	18,148 / 1.35%
Duplication rate	1.13%
Clipped reads	411,835 / 30.72%

2.2. ACGT Content

Number/percentage of A's	22,293,705 / 30.3%
Number/percentage of C's	13,921,079 / 18.92%
Number/percentage of T's	21,258,453 / 28.89%
Number/percentage of G's	16,100,309 / 21.88%
Number/percentage of N's	924 / 0%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.2231

2.4. Mapping Quality

Mean Mapping Quality	46.95

2.5. Mismatches and indels

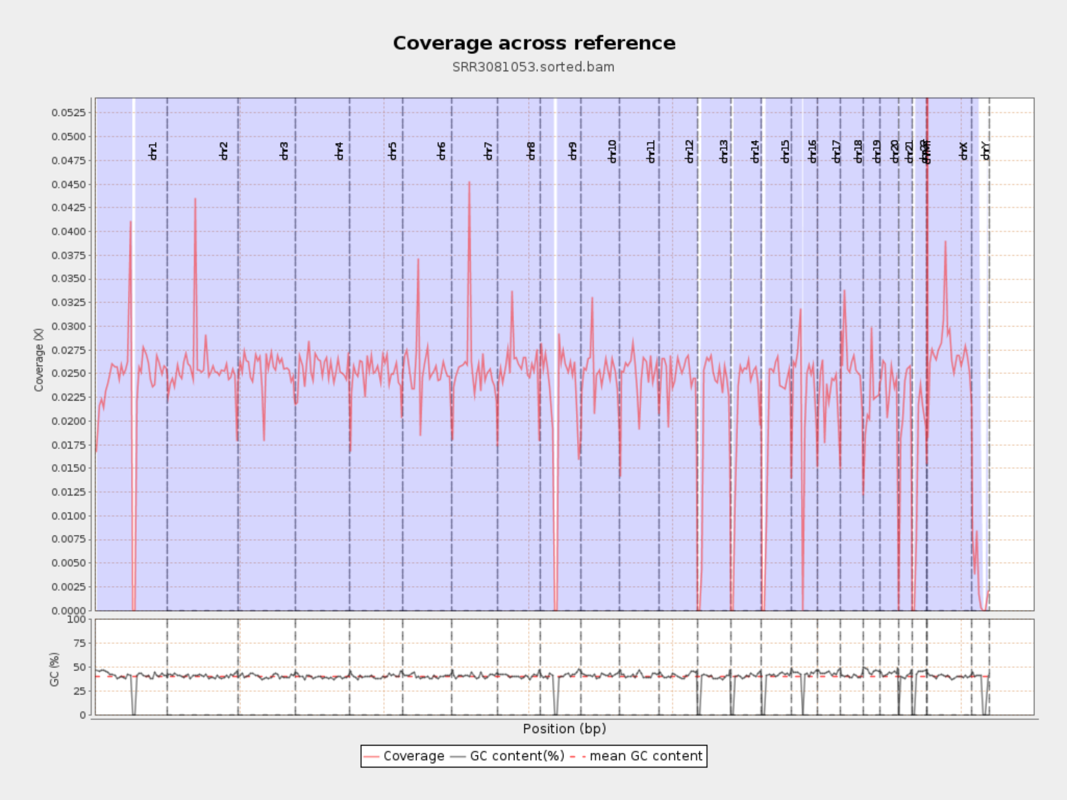
General error rate	0.77%
Mismatches	559,054
Insertions	4,909
Mapped reads with at least one insertion	0.45%
Deletions	12,423
Mapped reads with at least one deletion	1.14%
Homopolymer indels	45.36%

2.6. Chromosome stats

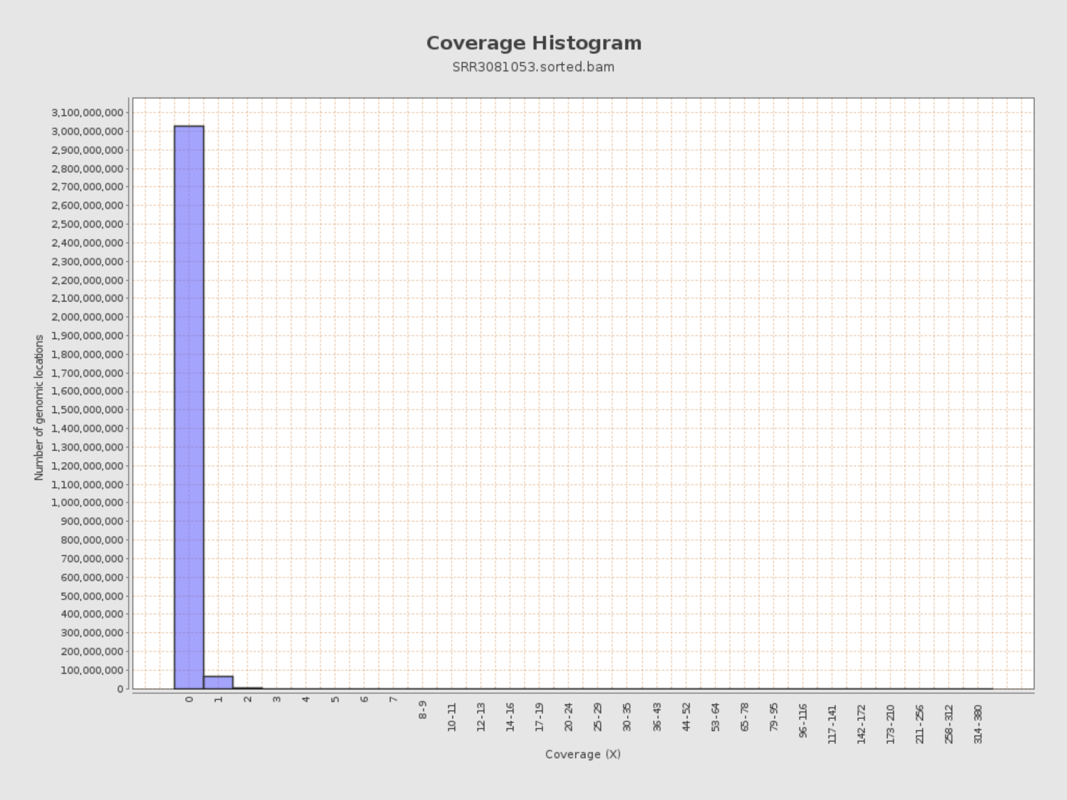
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5880434	0.0236	0.3608
chr2	243199373	6245040	0.0257	0.2354
chr3	198022430	5042123	0.0255	0.1635
chr4	191154276	4859830	0.0254	0.1669
chr5	180915260	4552421	0.0252	0.1635
chr6	171115067	4365906	0.0255	0.2056
chr7	159138663	4089885	0.0257	0.3296

chr8	146364022	3779909	0.0258	0.2127
chr9	141213431	3124111	0.0221	0.2124
chr10	135534747	3411810	0.0252	0.2065
chr11	135006516	3374462	0.025	0.2103
chr12	133851895	3324703	0.0248	0.1637
chr13	115169878	2391750	0.0208	0.1475
chr14	107349540	2213054	0.0206	0.1627
chr15	102531392	2068868	0.0202	0.1506
chr16	90354753	2021407	0.0224	0.1707
chr17	81195210	1837629	0.0226	0.1741
chr18	78077248	2054458	0.0263	0.4237
chr19	59128983	1299082	0.022	0.2475
chr20	63025520	1490394	0.0236	0.1605
chr21	48129895	972748	0.0202	0.1533
chr22	51304566	761227	0.0148	0.1256
chrMT	16571	15798	0.9534	1.111
chrX	155270560	4252341	0.0274	0.1881
chrY	59373566	166347	0.0028	0.0675

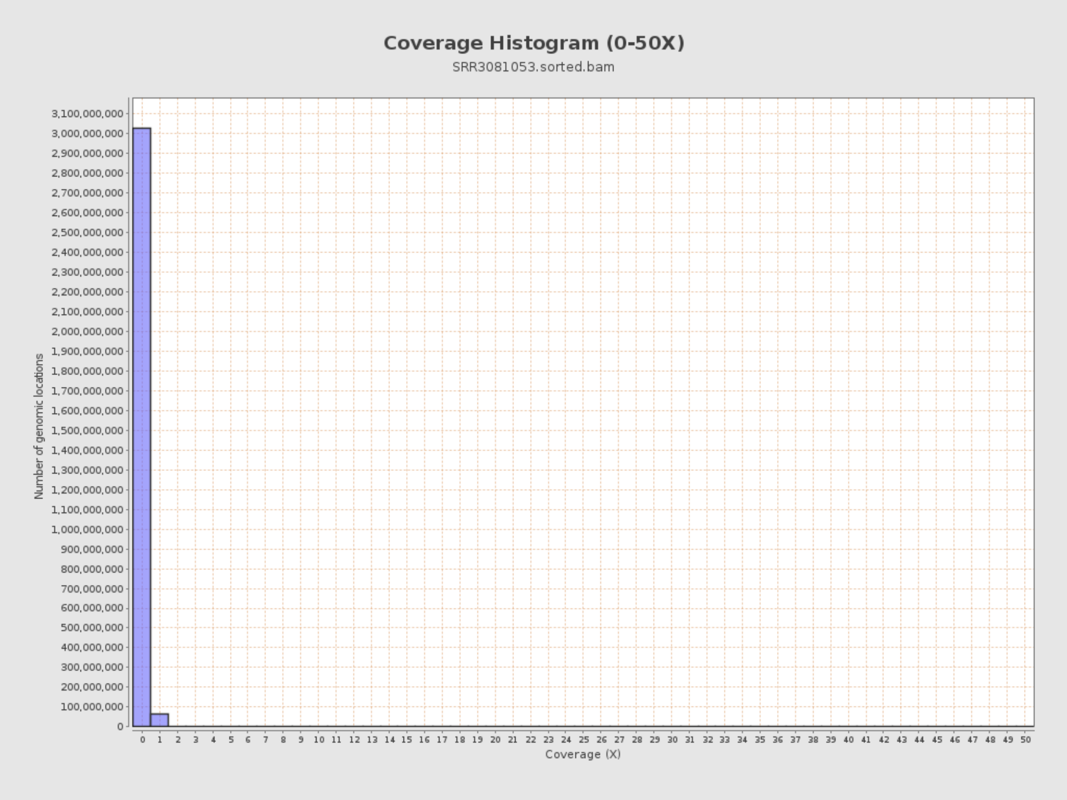
3. Results : Coverage across reference



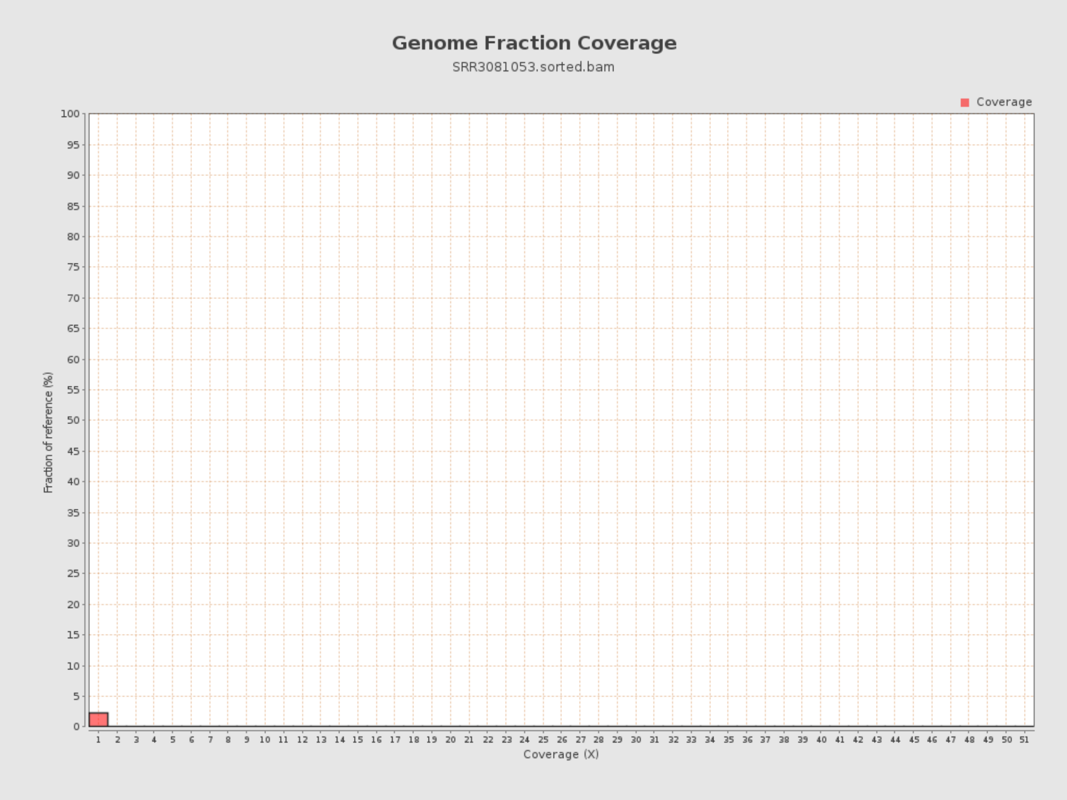
4. Results : Coverage Histogram



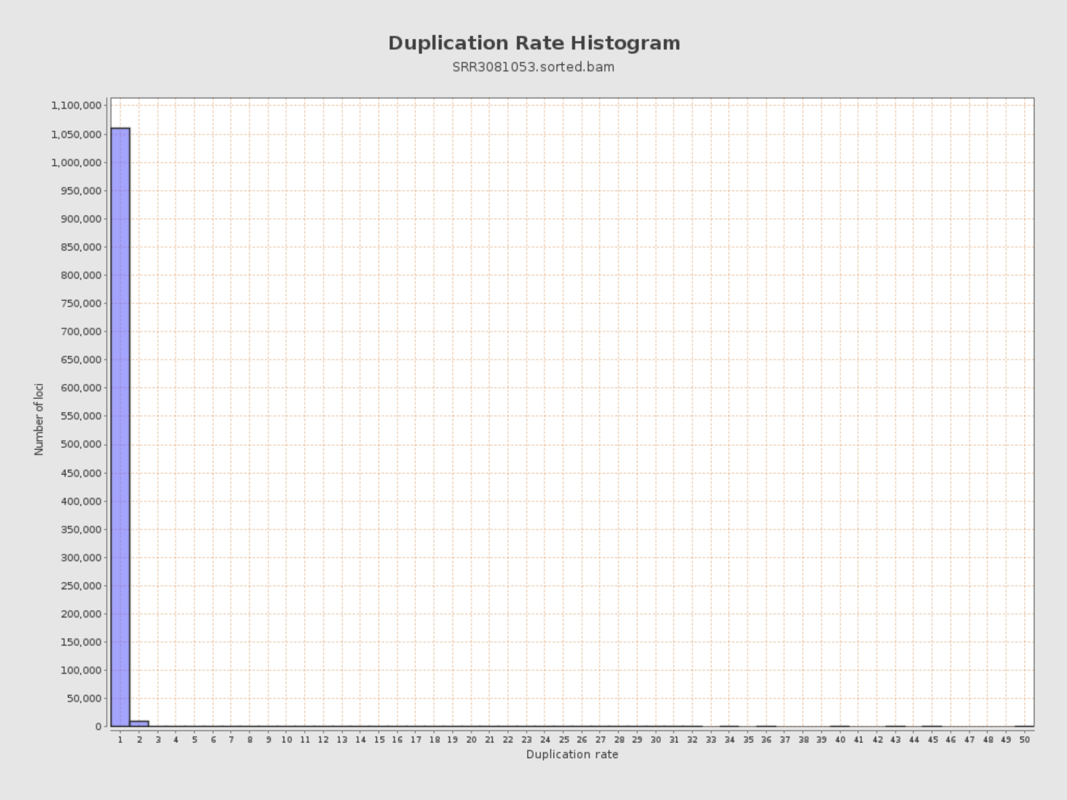
5. Results : Coverage Histogram (0-50X)



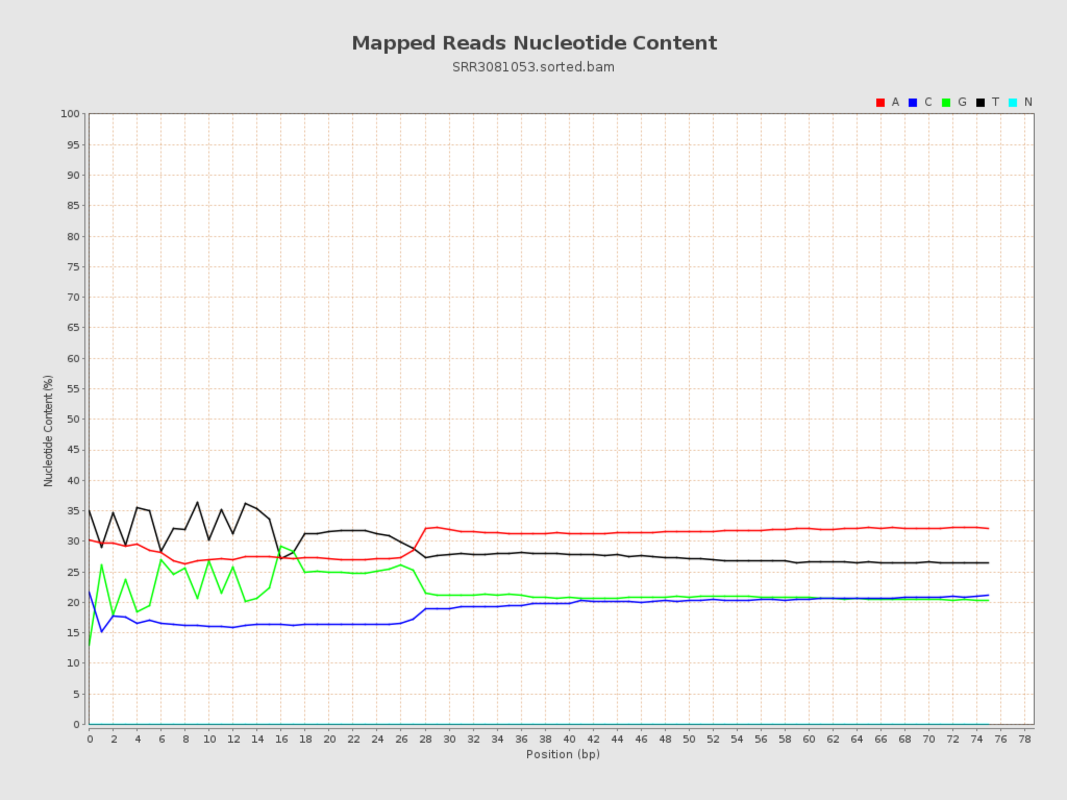
6. Results : Genome Fraction Coverage



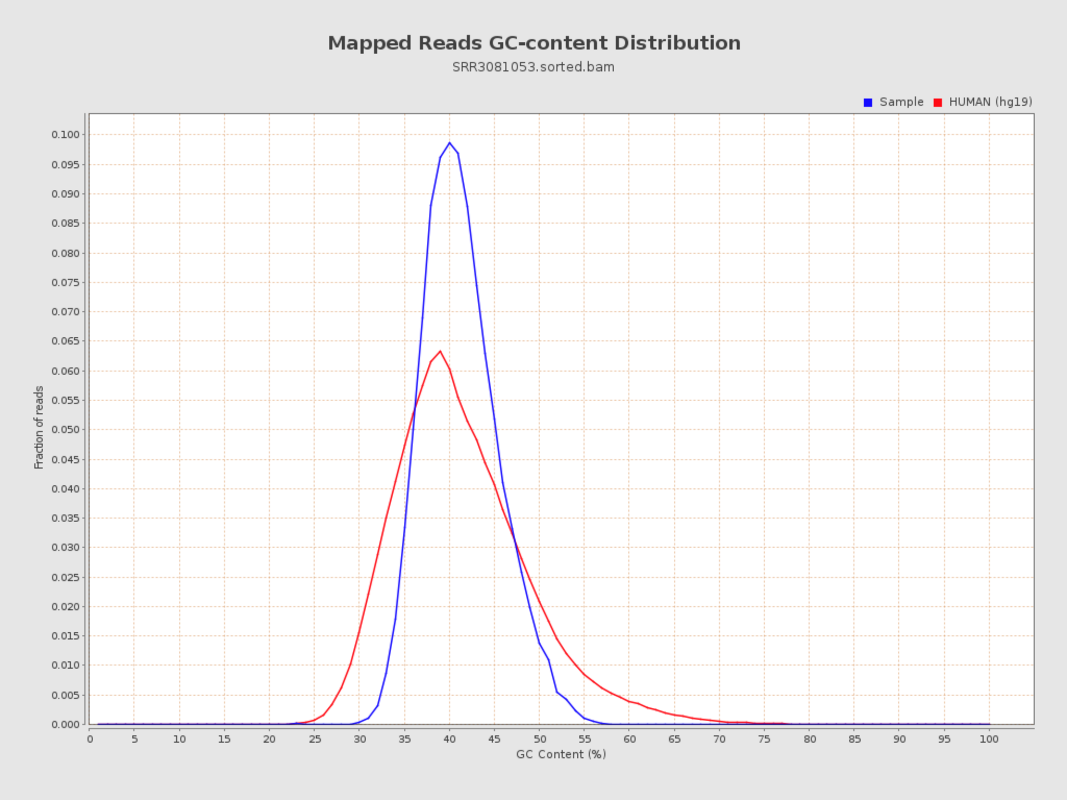
7. Results : Duplication Rate Histogram



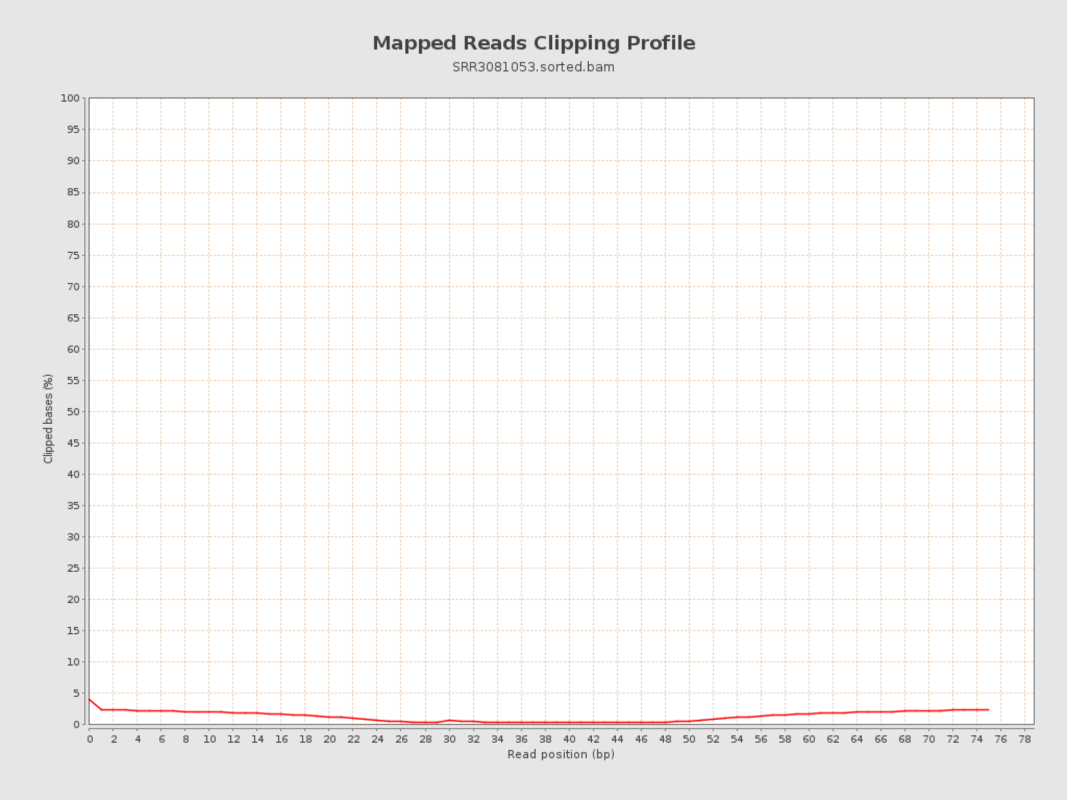
8. Results : Mapped Reads Nucleotide Content



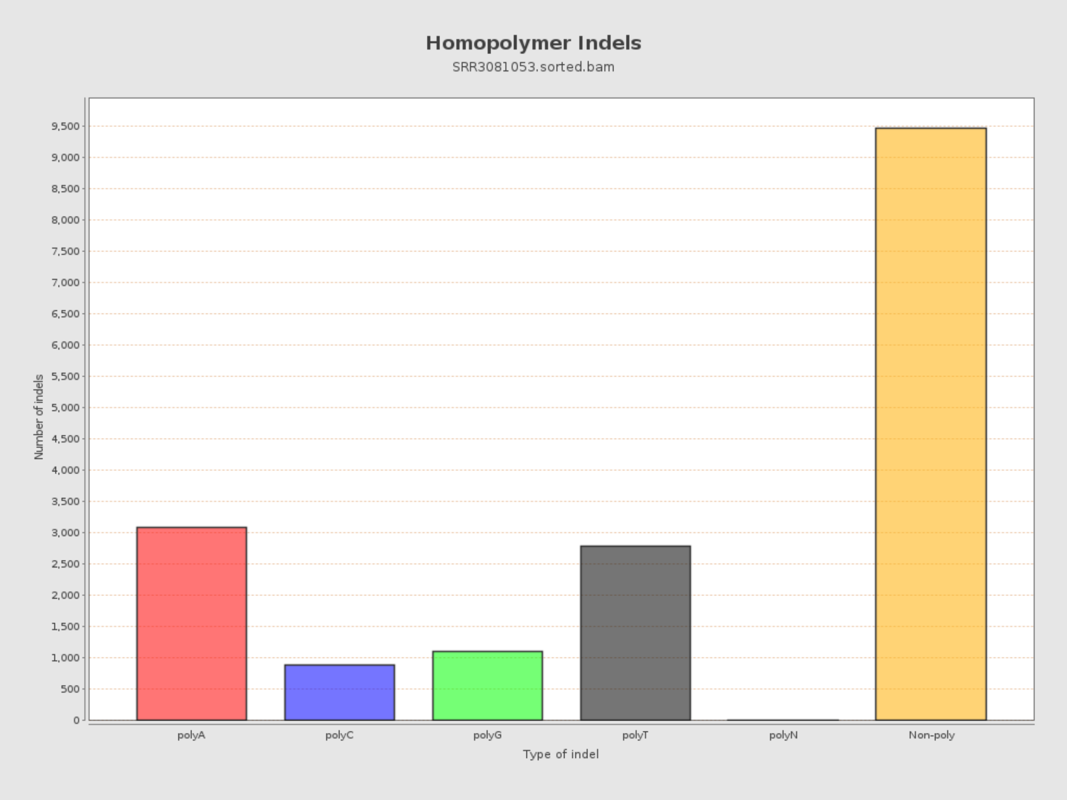
9. Results : Mapped Reads GC-content Distribution



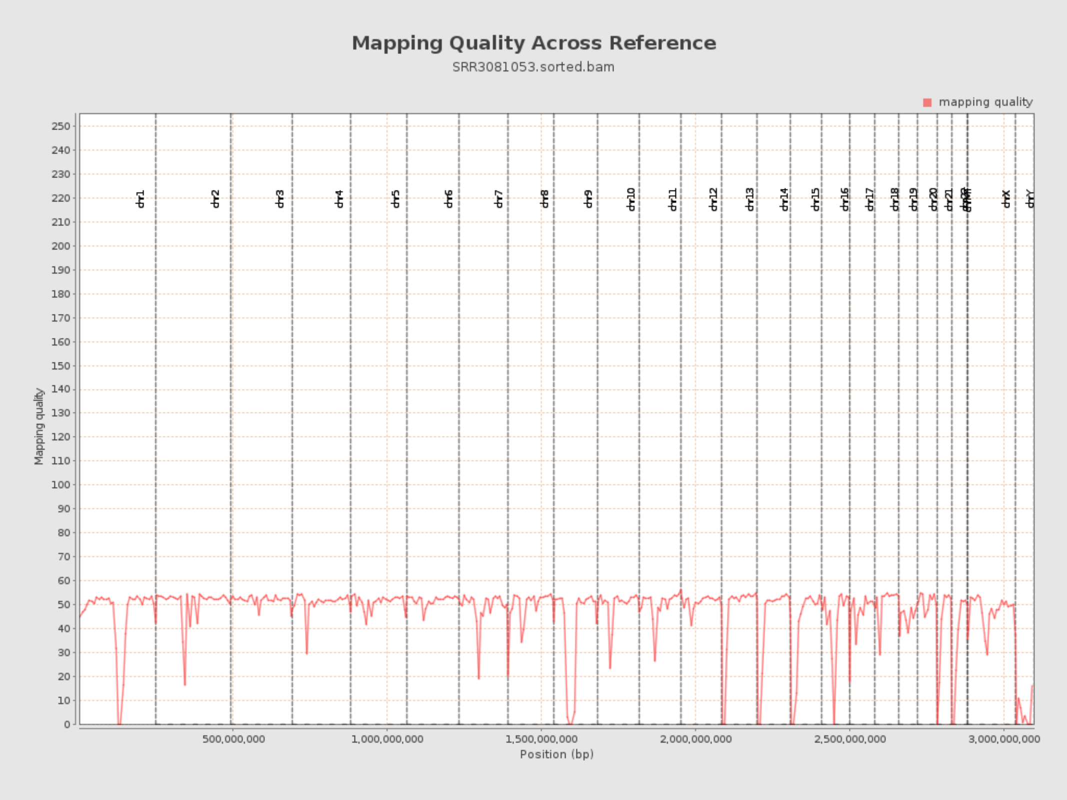
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram