Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:52:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081040.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_SRR3081040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:52:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,115,910
Mapped reads	1,710,492 / 80.84%
Unmapped reads	405,418 / 19.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,045 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	43,226 / 2.04%
Duplication rate	1.97%
Clipped reads	934,519 / 44.17%

2.2. ACGT Content

Number/percentage of A's	31,646,295 / 29.13%
Number/percentage of C's	20,809,208 / 19.15%
Number/percentage of T's	32,159,379 / 29.6%
Number/percentage of G's	24,025,874 / 22.11%
Number/percentage of N's	1,380 / 0%
GC Percentage	41.27%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.2756

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

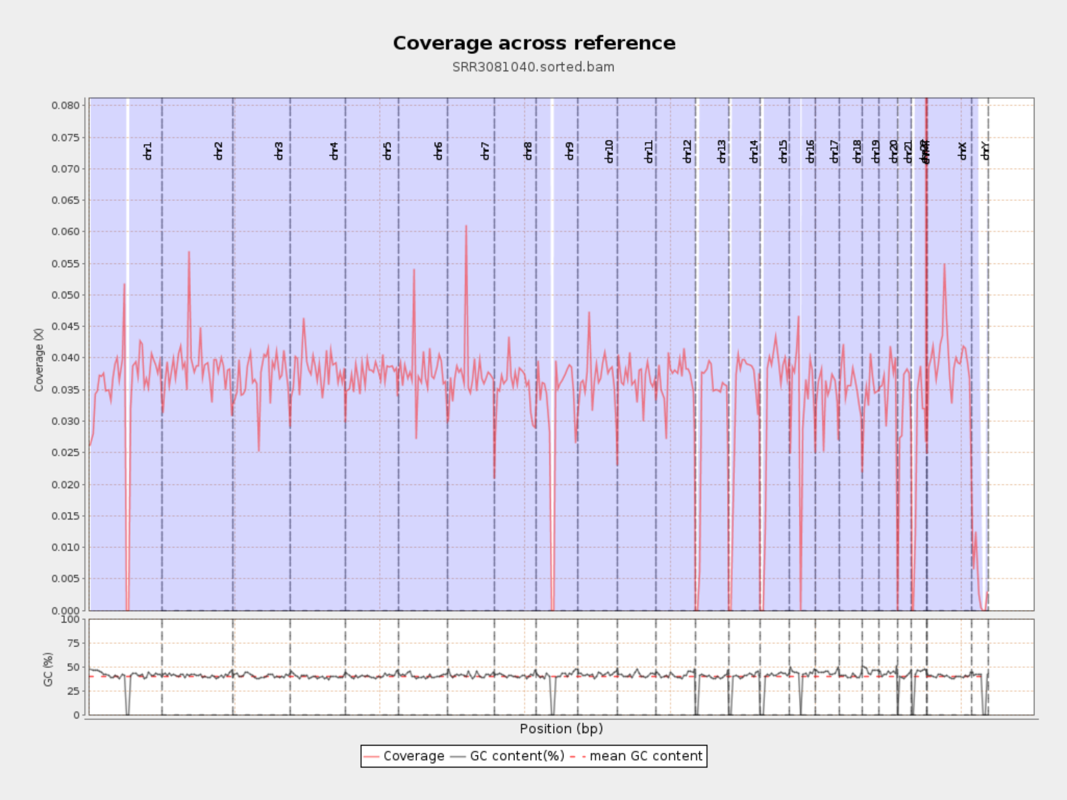
General error rate	0.82%
Mismatches	877,425
Insertions	7,102
Mapped reads with at least one insertion	0.41%
Deletions	22,252
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.29%

2.6. Chromosome stats

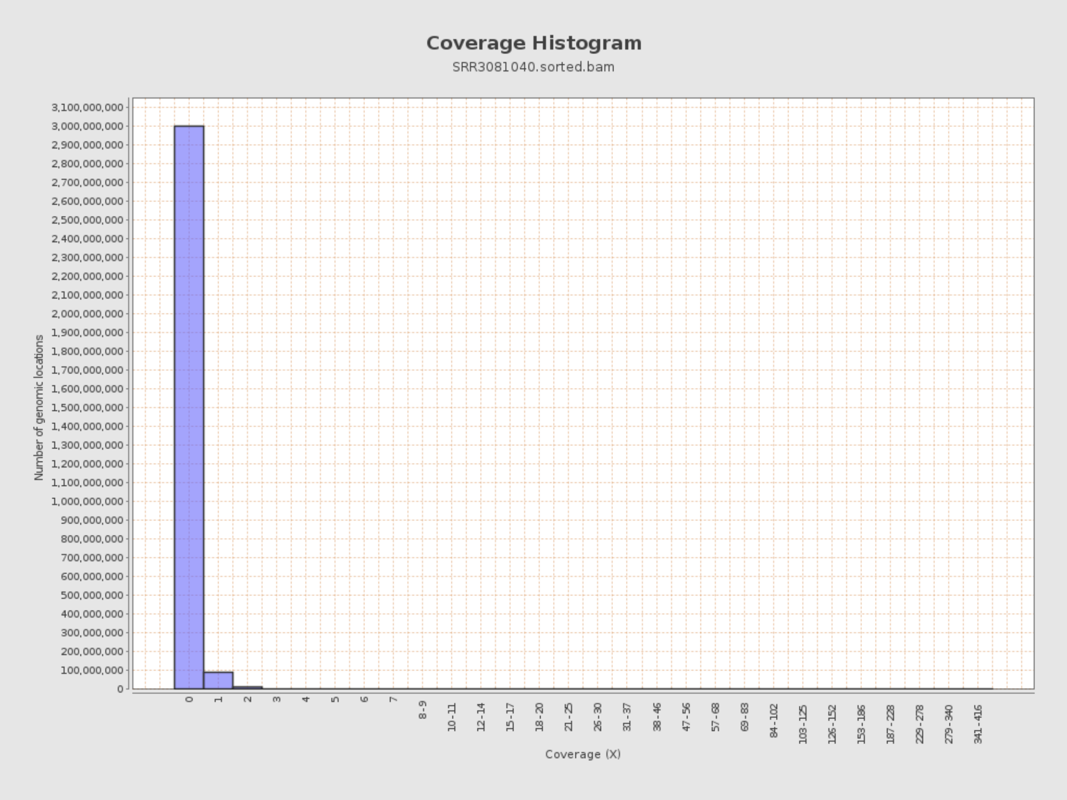
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8713546	0.035	0.4161
chr2	243199373	9401538	0.0387	0.2923
chr3	198022430	7302972	0.0369	0.208
chr4	191154276	7300852	0.0382	0.2209
chr5	180915260	6785256	0.0375	0.2109
chr6	171115067	6482491	0.0379	0.2648
chr7	159138663	6015042	0.0378	0.4162

chr8	146364022	5184032	0.0354	0.2896
chr9	141213431	4469300	0.0316	0.2548
chr10	135534747	5027414	0.0371	0.2534
chr11	135006516	4922430	0.0365	0.2668
chr12	133851895	4933556	0.0369	0.2099
chr13	115169878	3496507	0.0304	0.1887
chr14	107349540	3380978	0.0315	0.2023
chr15	102531392	3258288	0.0318	0.2034
chr16	90354753	3013254	0.0333	0.2148
chr17	81195210	2772201	0.0341	0.2232
chr18	78077248	2818035	0.0361	0.4758
chr19	59128983	2048132	0.0346	0.31
chr20	63025520	2256700	0.0358	0.2089
chr21	48129895	1443210	0.03	0.1976
chr22	51304566	1211089	0.0236	0.1661
chrMT	16571	31172	1.8811	1.8539
chrX	155270560	6163016	0.0397	0.2402
chrY	59373566	249471	0.0042	0.0957

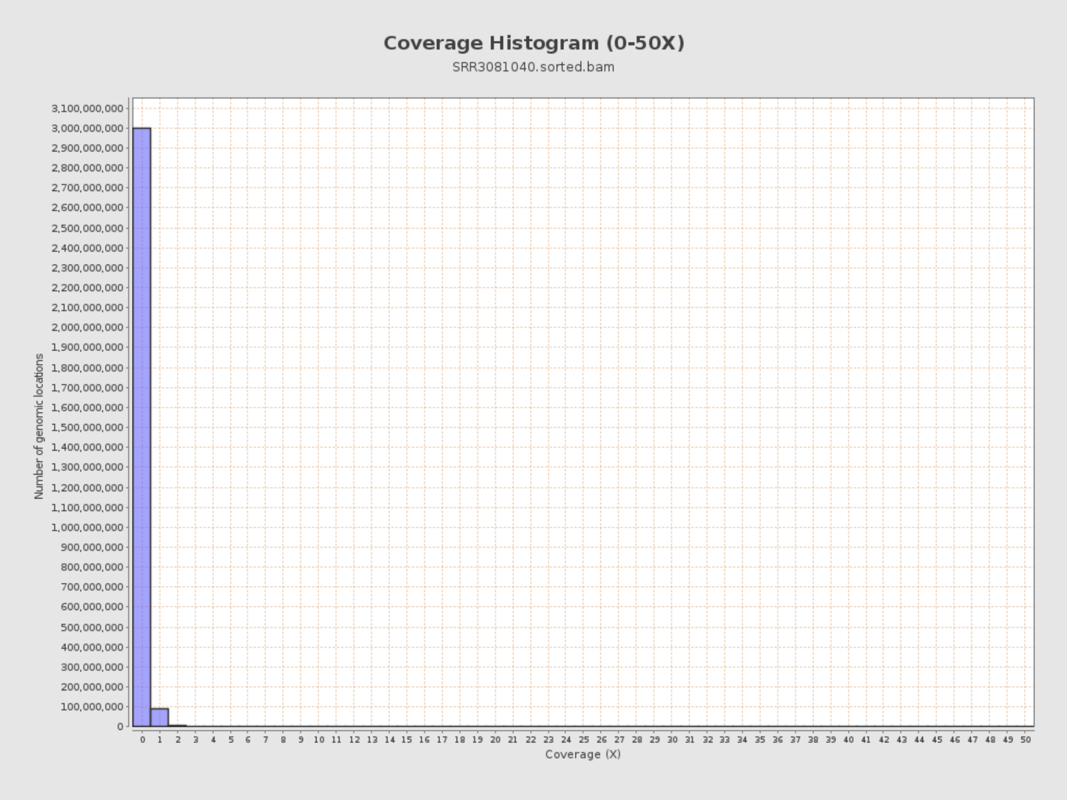
3. Results : Coverage across reference



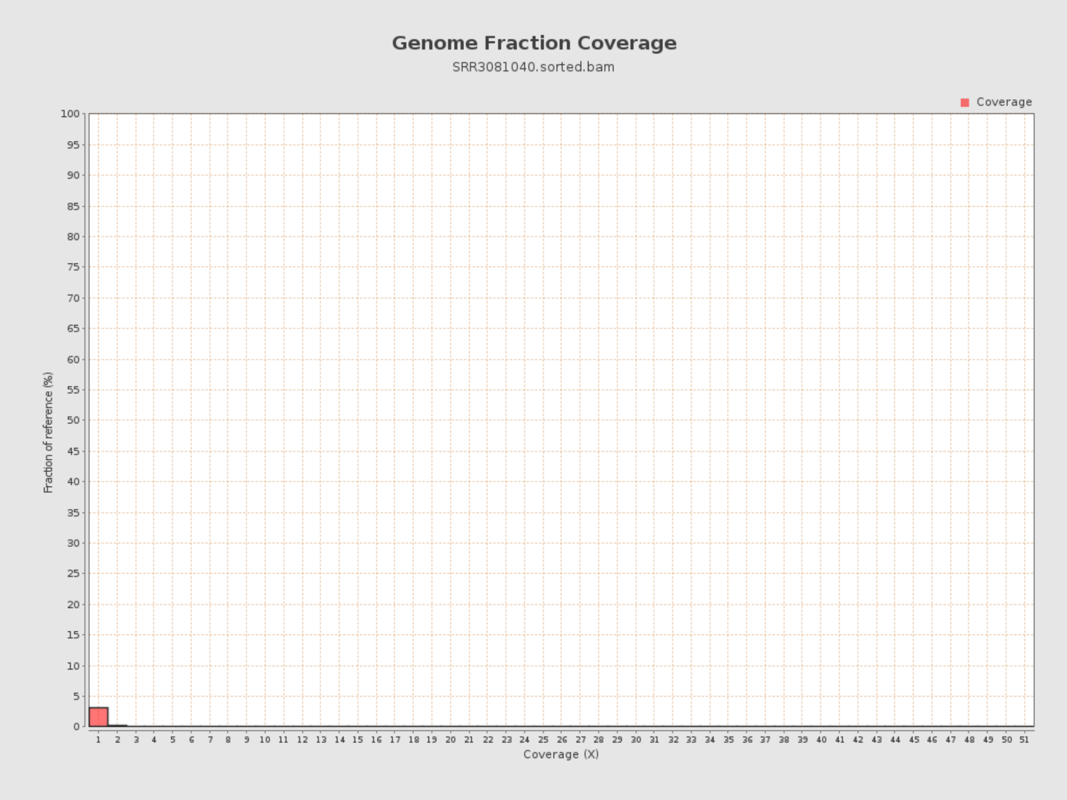
4. Results : Coverage Histogram



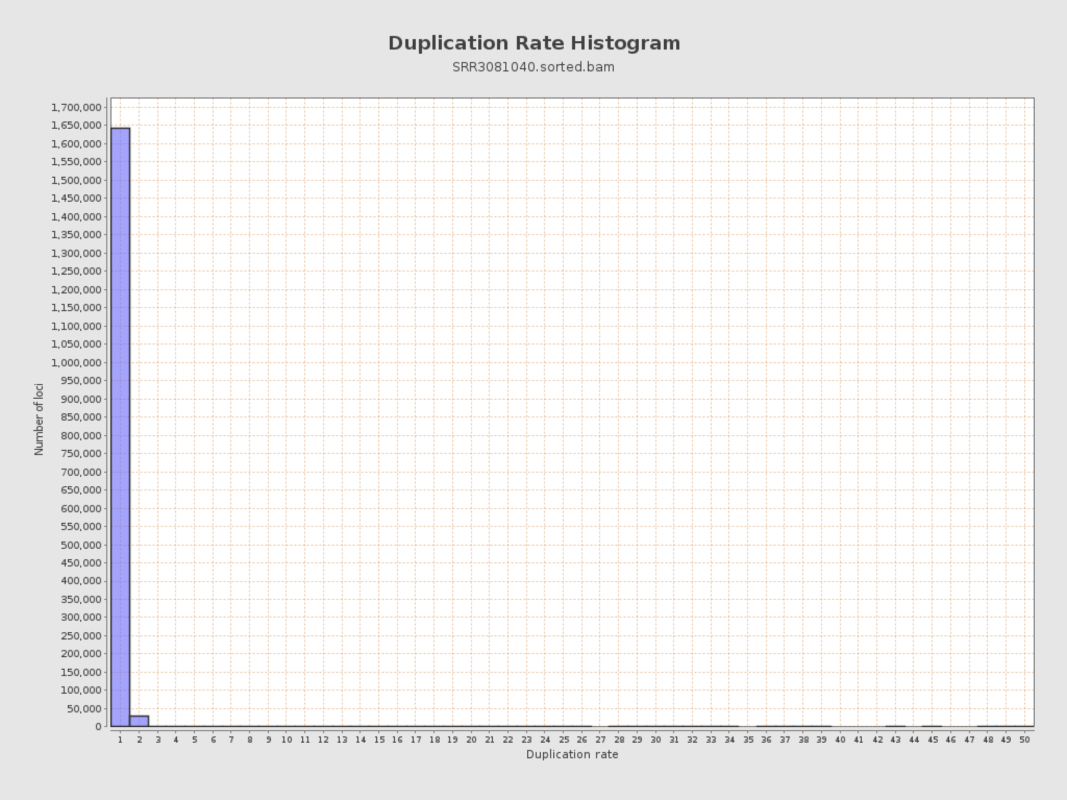
5. Results : Coverage Histogram (0-50X)



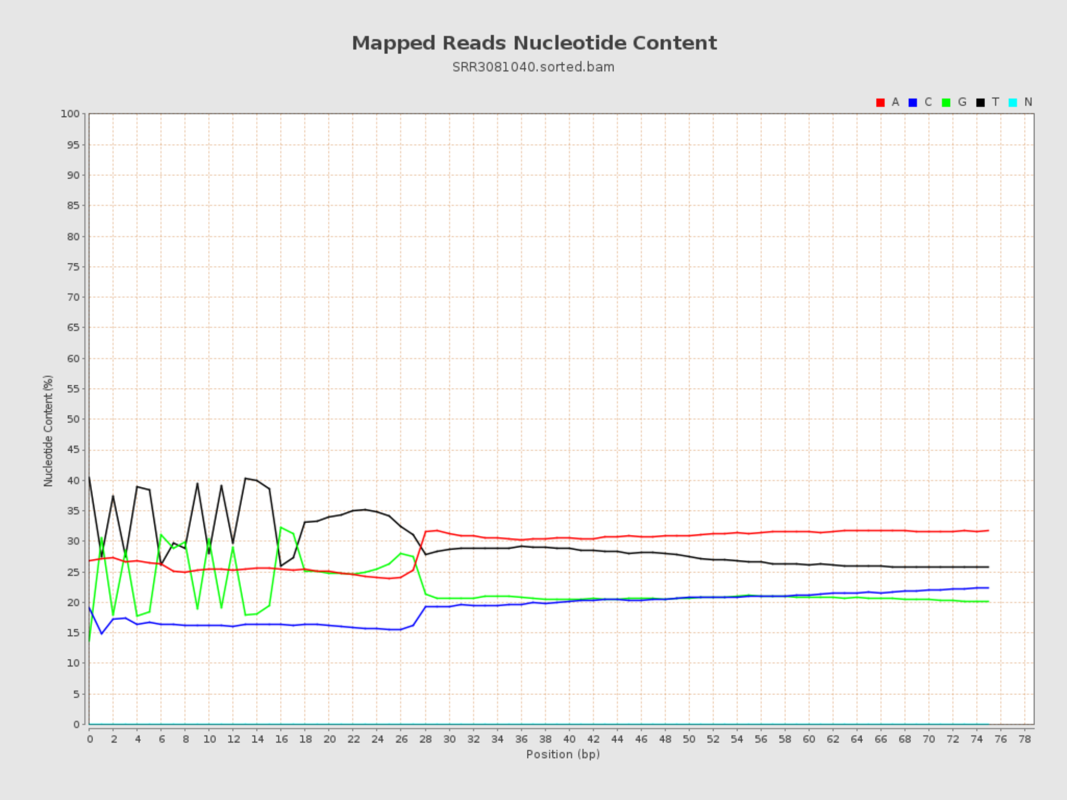
6. Results : Genome Fraction Coverage



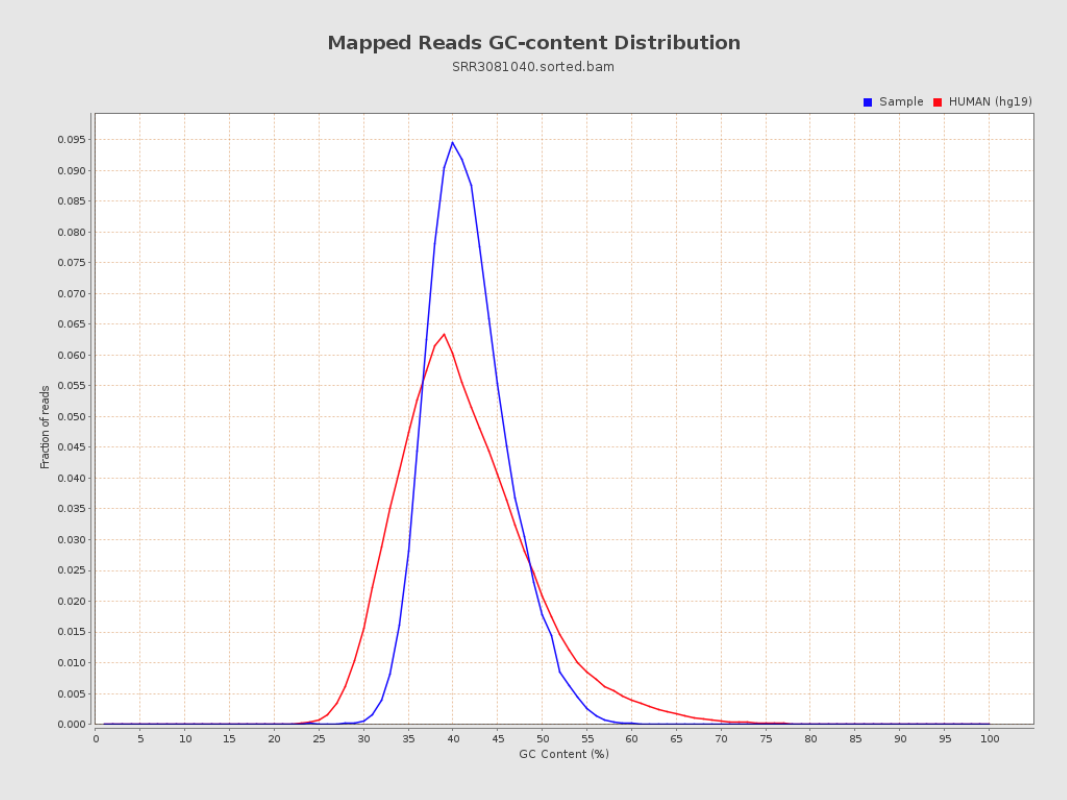
7. Results : Duplication Rate Histogram



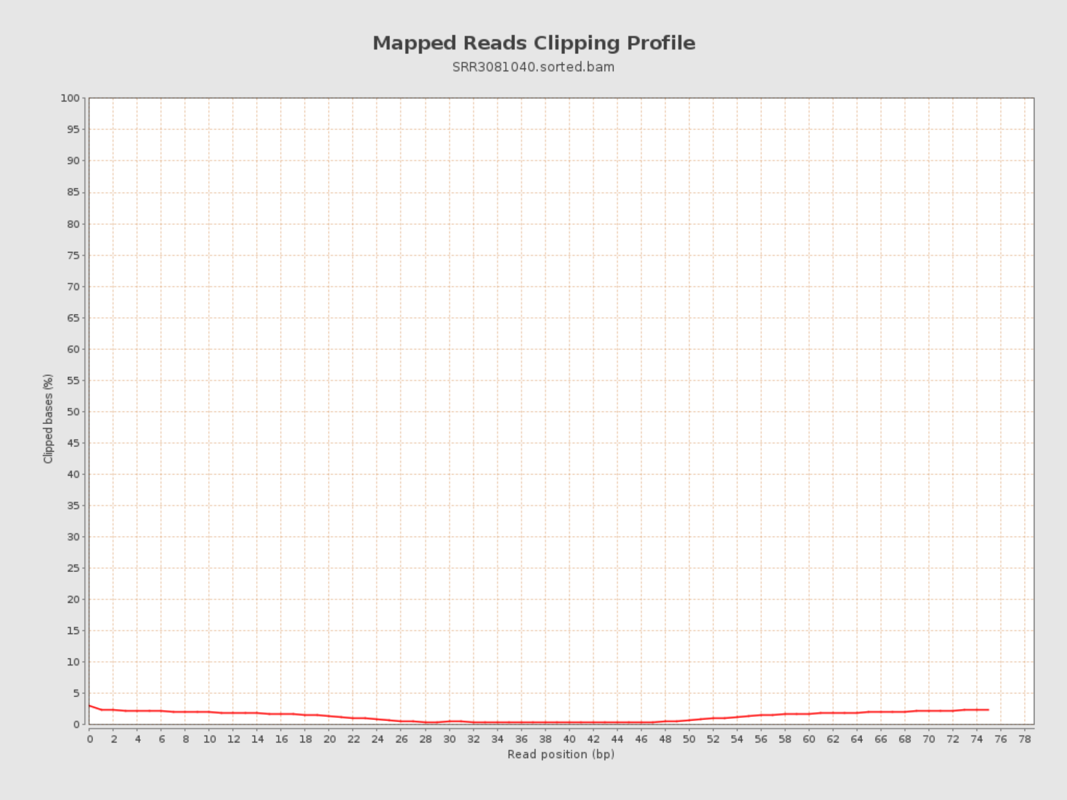
8. Results : Mapped Reads Nucleotide Content



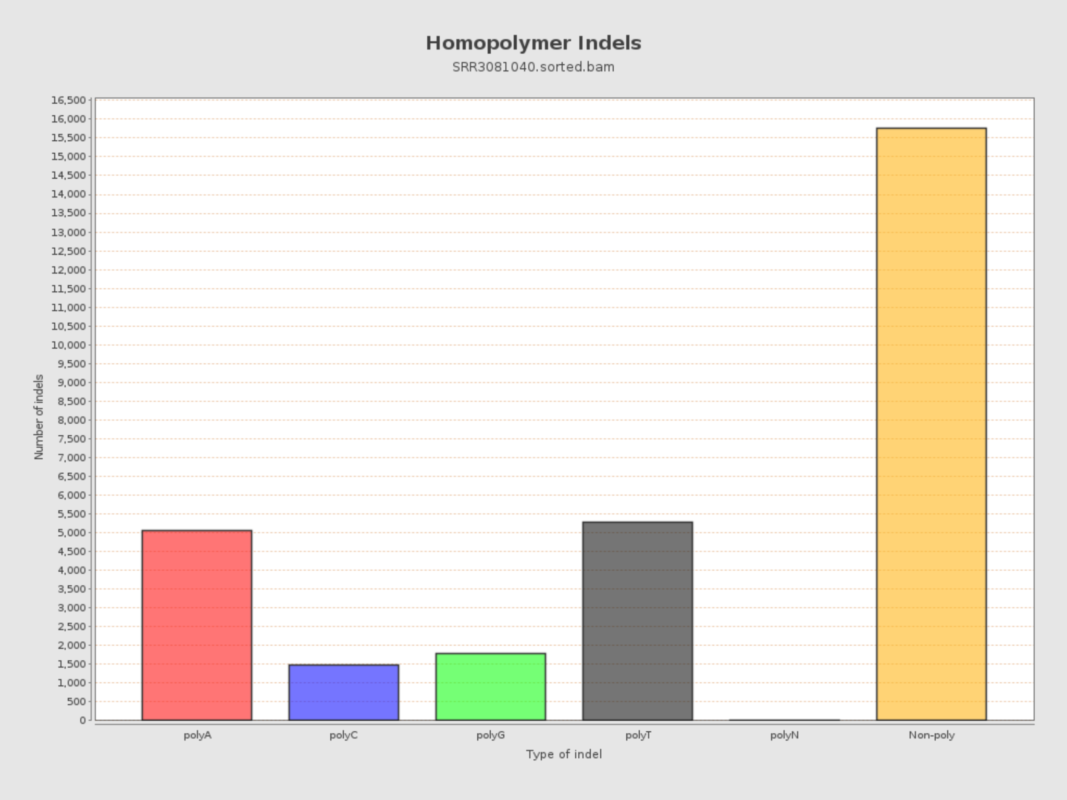
9. Results : Mapped Reads GC-content Distribution



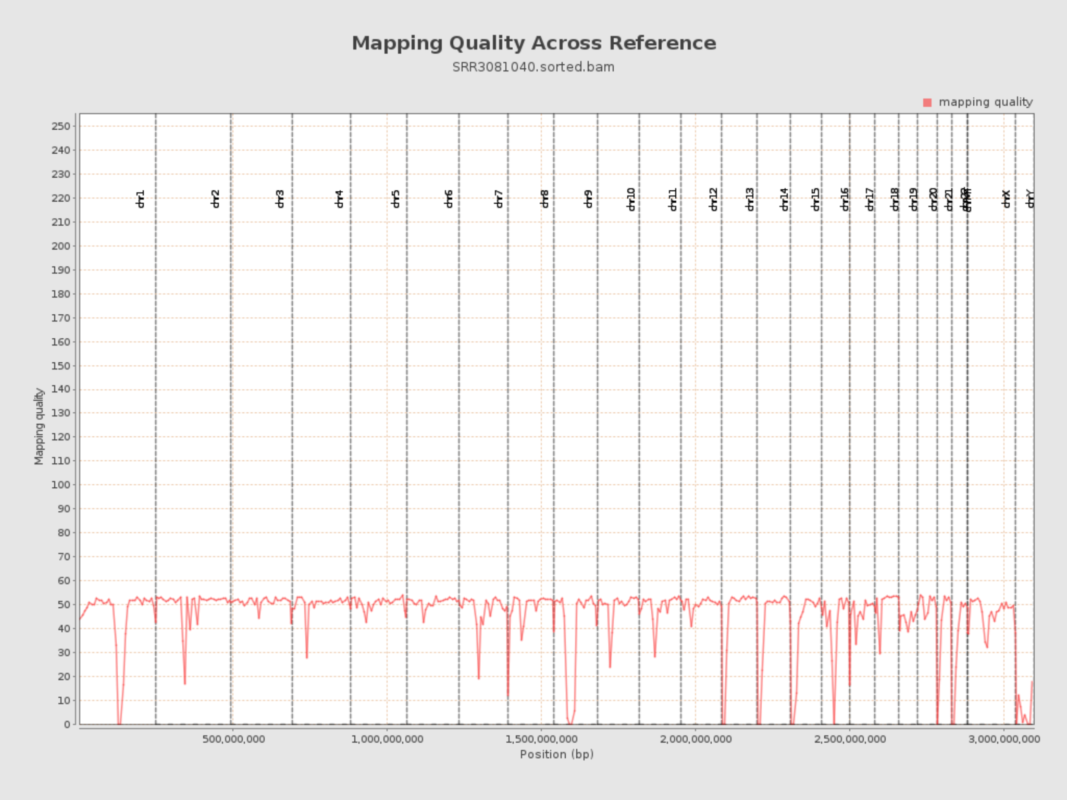
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram