Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:56:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081041.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_SRR3081041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:56:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,996,188
Mapped reads	1,645,814 / 82.45%
Unmapped reads	350,374 / 17.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,649 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	44,020 / 2.21%
Duplication rate	2.05%
Clipped reads	850,261 / 42.59%

2.2. ACGT Content

Number/percentage of A's	30,846,007 / 29.15%
Number/percentage of C's	20,053,687 / 18.95%
Number/percentage of T's	31,687,319 / 29.95%
Number/percentage of G's	23,218,781 / 21.94%
Number/percentage of N's	1,408 / 0%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.2848

2.4. Mapping Quality

Mean Mapping Quality	46.65

2.5. Mismatches and indels

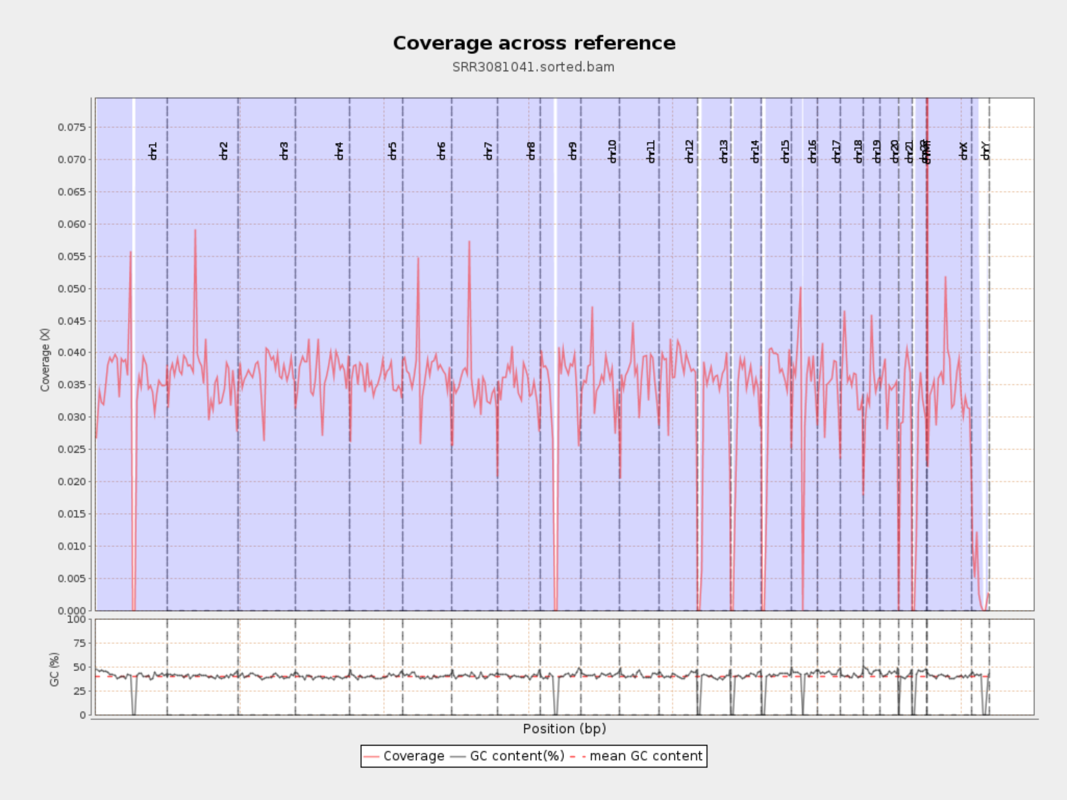
General error rate	0.8%
Mismatches	832,646
Insertions	7,097
Mapped reads with at least one insertion	0.43%
Deletions	22,962
Mapped reads with at least one deletion	1.38%
Homopolymer indels	46.88%

2.6. Chromosome stats

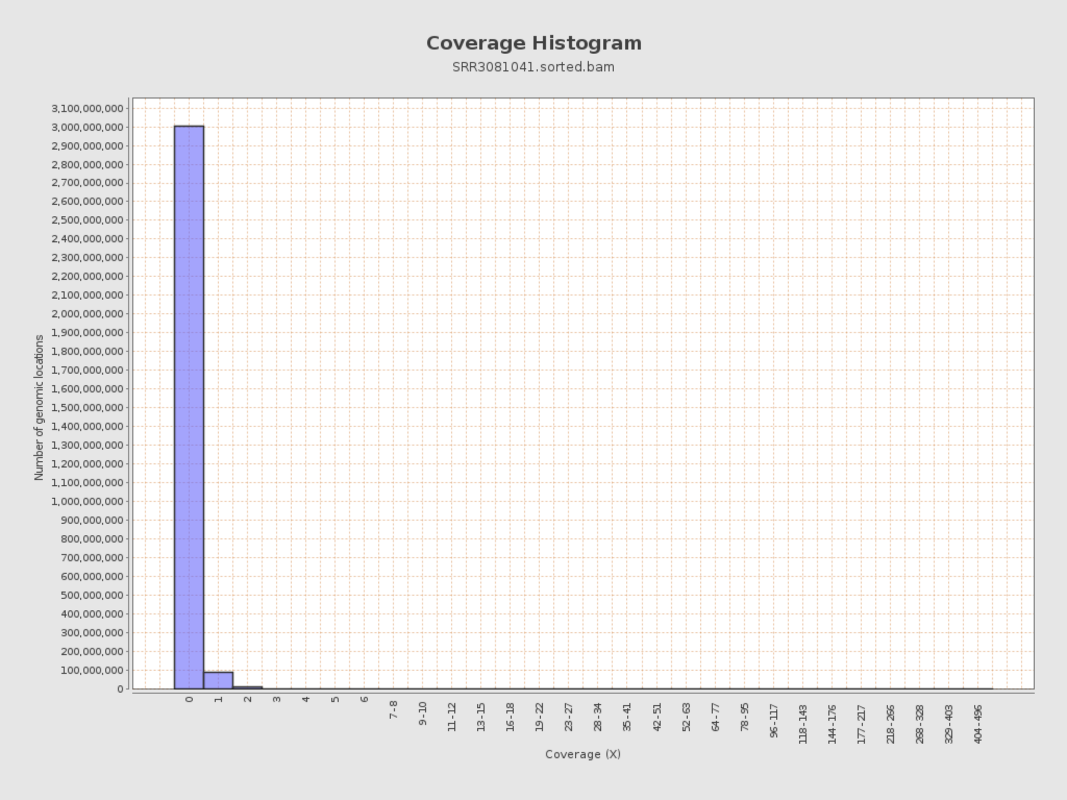
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8469201	0.034	0.483
chr2	243199373	8939413	0.0368	0.2956
chr3	198022430	7296646	0.0368	0.2084
chr4	191154276	7045957	0.0369	0.2151
chr5	180915260	6527827	0.0361	0.2079
chr6	171115067	6375344	0.0373	0.2656
chr7	159138663	5617072	0.0353	0.3809

chr8	146364022	5165082	0.0353	0.3019
chr9	141213431	4580123	0.0324	0.2713
chr10	135534747	4848404	0.0358	0.2536
chr11	135006516	4926338	0.0365	0.2761
chr12	133851895	5023616	0.0375	0.2126
chr13	115169878	3451491	0.03	0.1877
chr14	107349540	3204291	0.0298	0.2003
chr15	102531392	3209293	0.0313	0.2002
chr16	90354753	3054838	0.0338	0.2186
chr17	81195210	2838225	0.035	0.2296
chr18	78077248	2820781	0.0361	0.4998
chr19	59128983	2046811	0.0346	0.3429
chr20	63025520	2157425	0.0342	0.2054
chr21	48129895	1478667	0.0307	0.2261
chr22	51304566	1153898	0.0225	0.1629
chrMT	16571	15243	0.9199	1.08
chrX	155270560	5369670	0.0346	0.224
chrY	59373566	230809	0.0039	0.0912

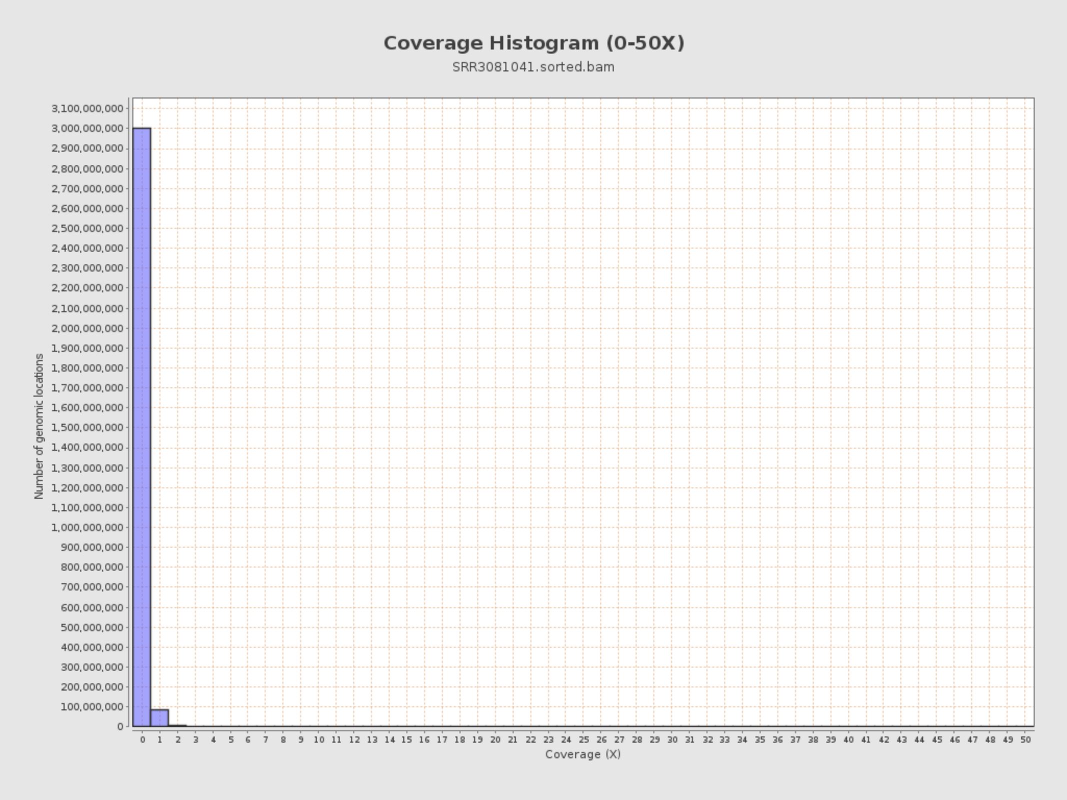
3. Results : Coverage across reference



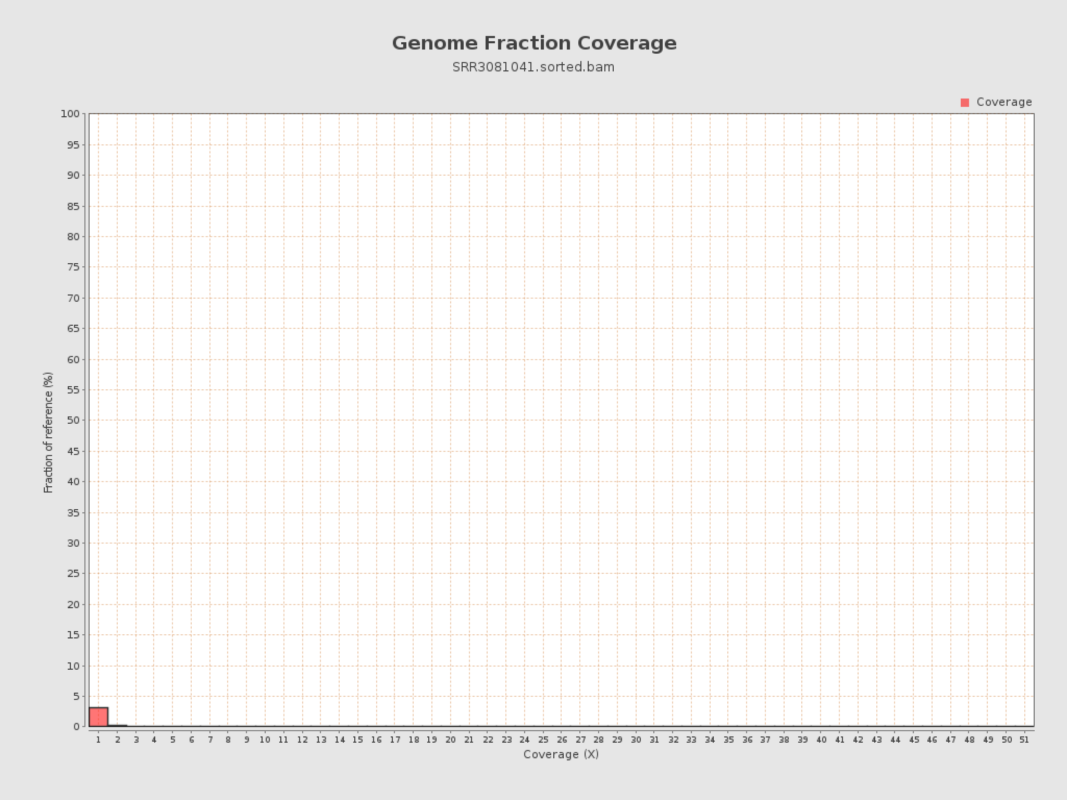
4. Results : Coverage Histogram



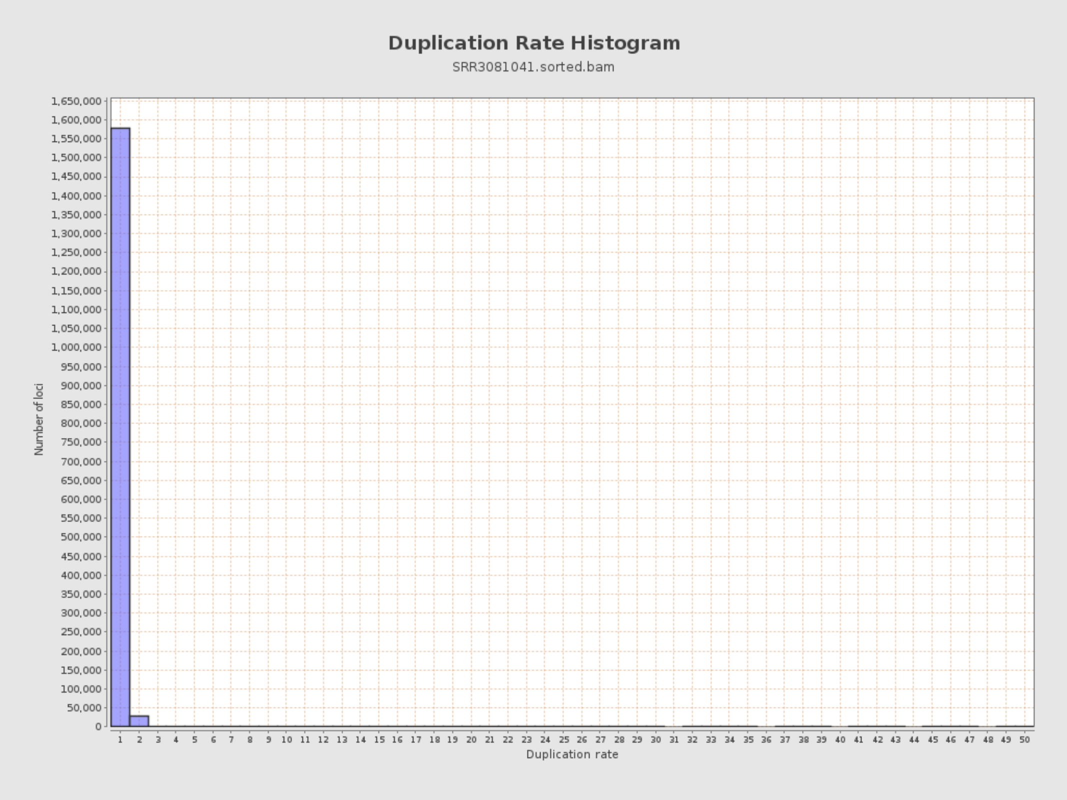
5. Results : Coverage Histogram (0-50X)



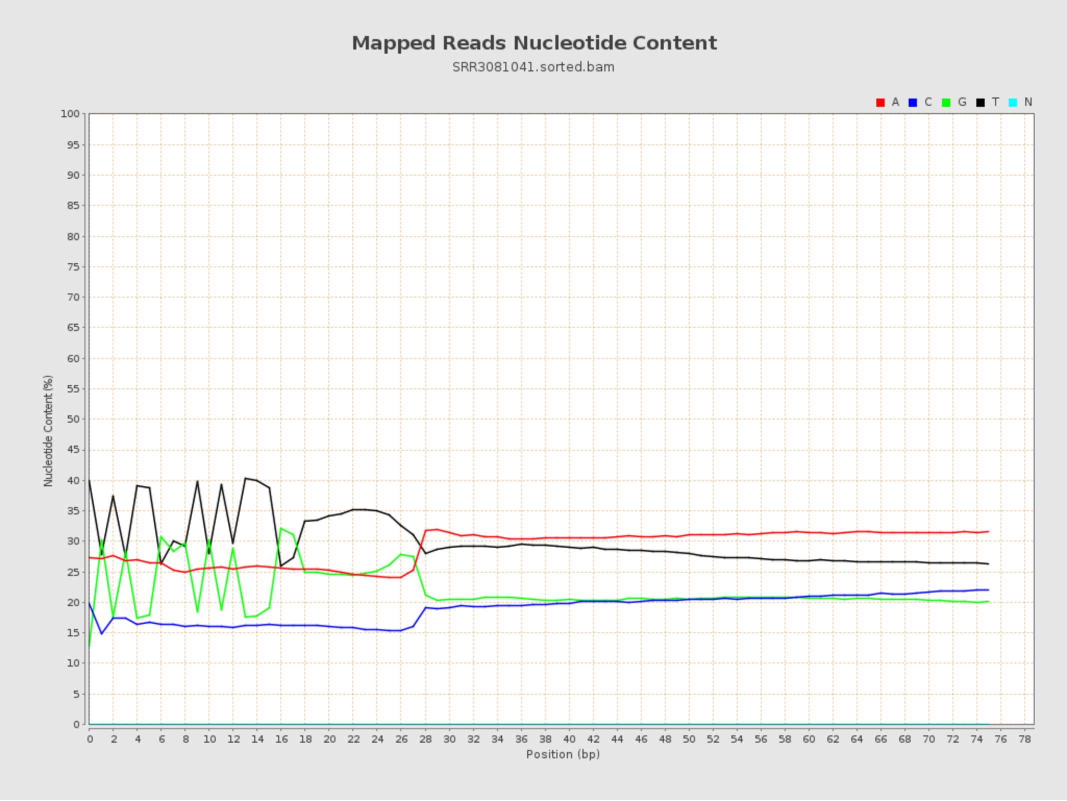
6. Results : Genome Fraction Coverage



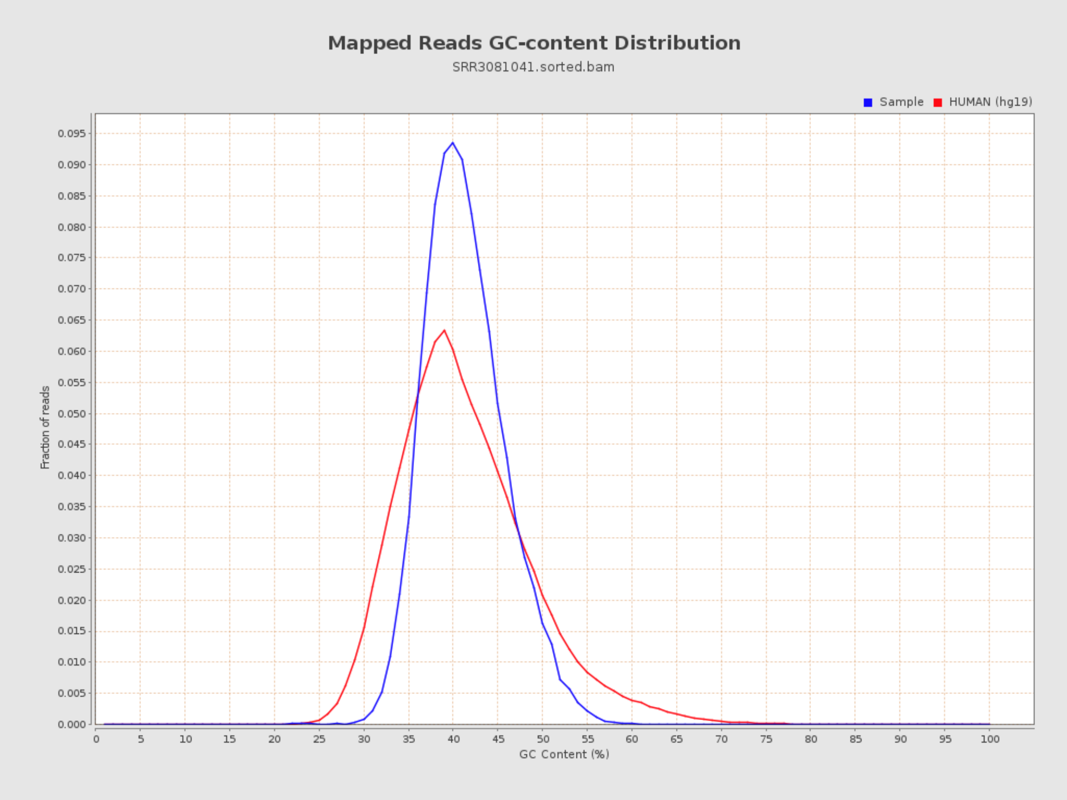
7. Results : Duplication Rate Histogram



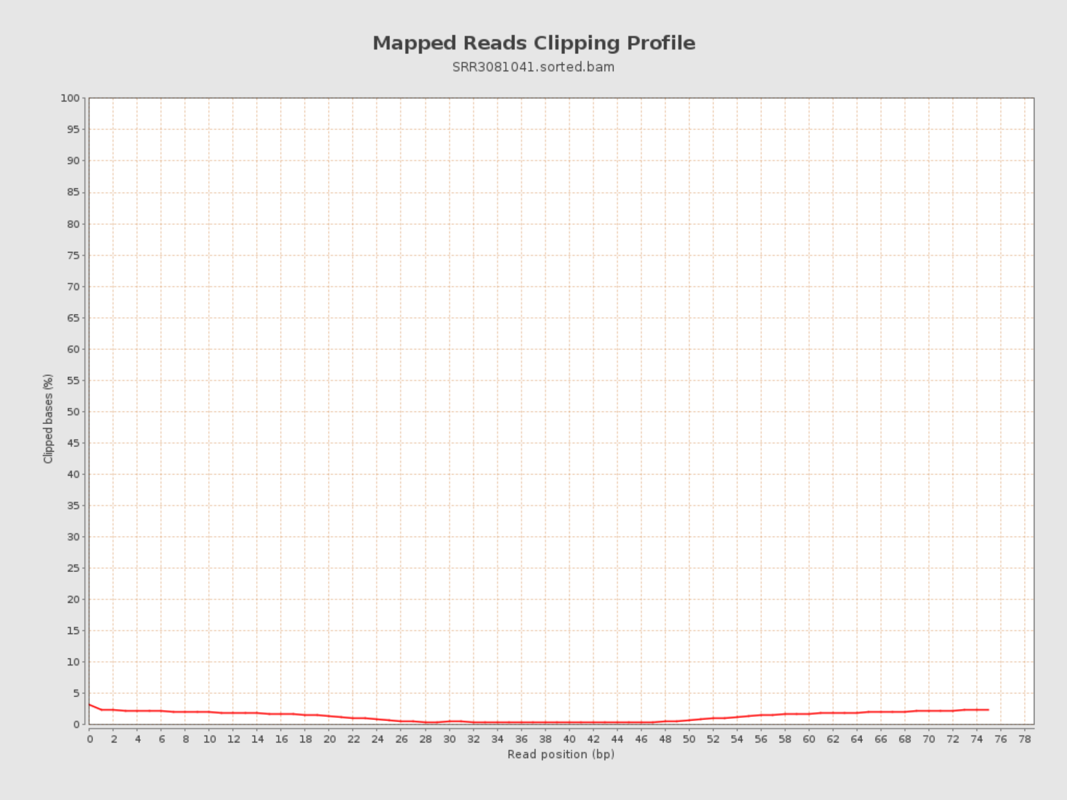
8. Results : Mapped Reads Nucleotide Content



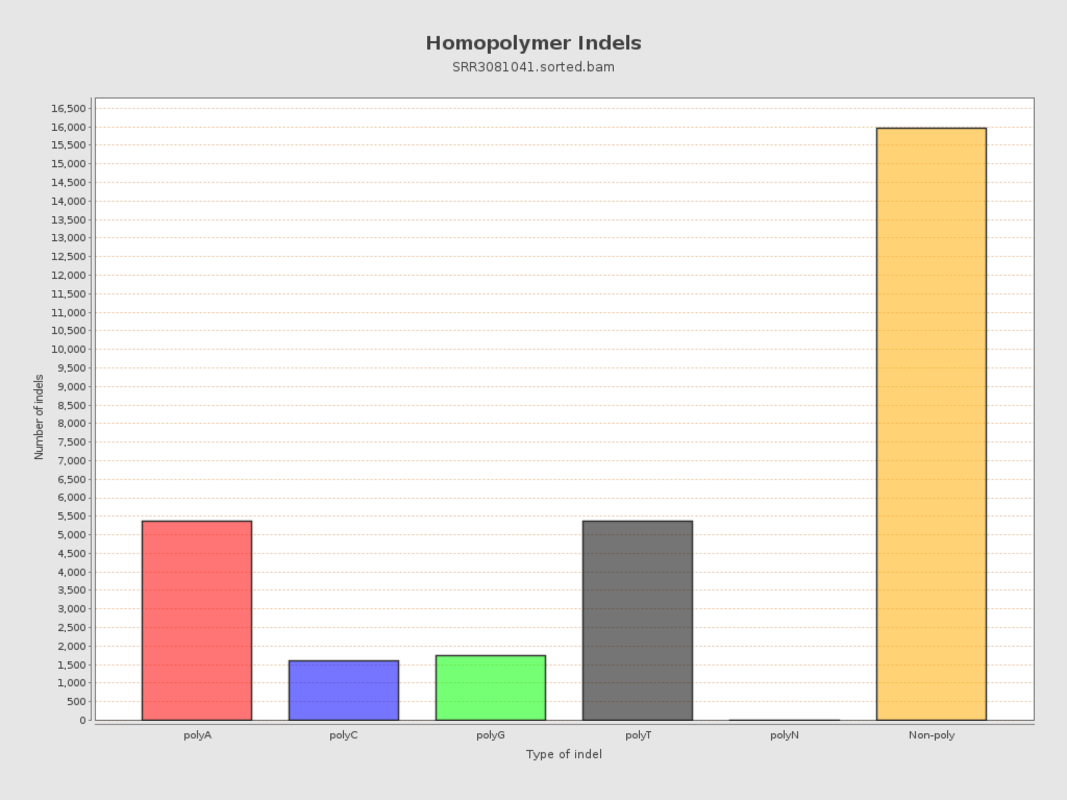
9. Results : Mapped Reads GC-content Distribution



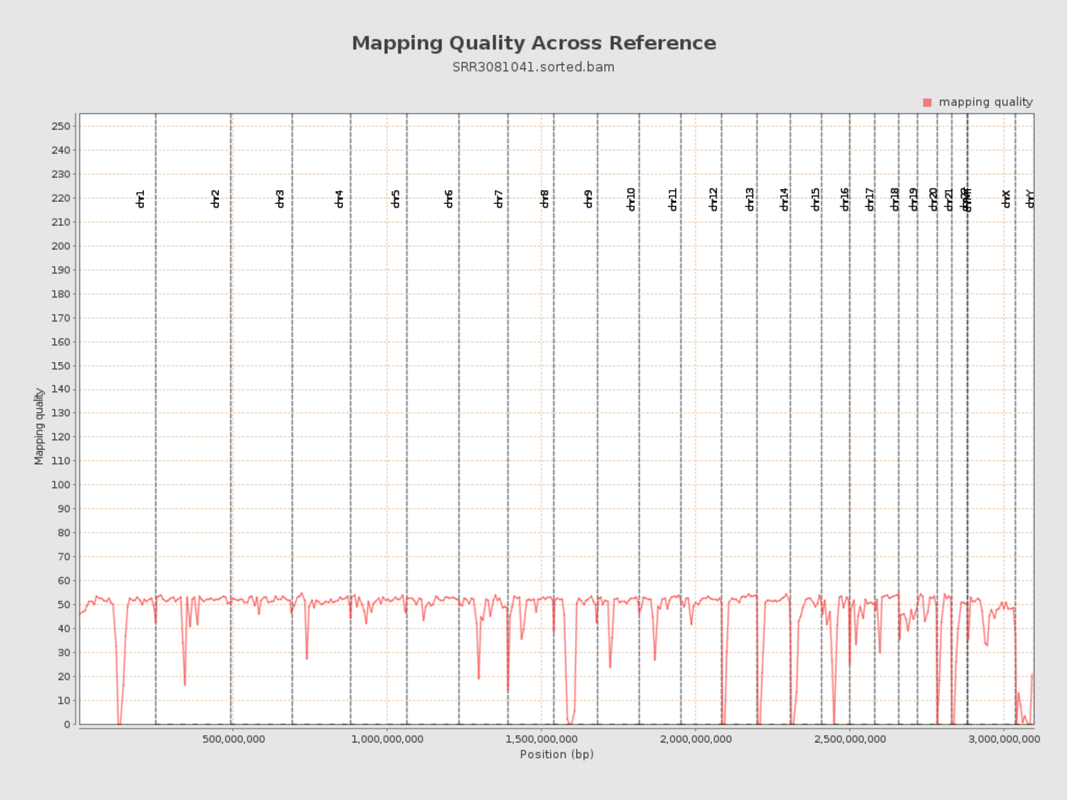
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram