Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:55:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081008.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_SRR3081008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081008.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:54:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,525,209
Mapped reads	2,941,949 / 83.45%
Unmapped reads	583,260 / 16.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,898 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	119,810 / 3.4%
Duplication rate	3.15%
Clipped reads	1,645,890 / 46.69%

2.2. ACGT Content

Number/percentage of A's	52,791,620 / 28.2%
Number/percentage of C's	37,766,582 / 20.18%
Number/percentage of T's	55,008,276 / 29.39%
Number/percentage of G's	41,623,096 / 22.24%
Number/percentage of N's	2,432 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0605

Standard Deviation	0.4504

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

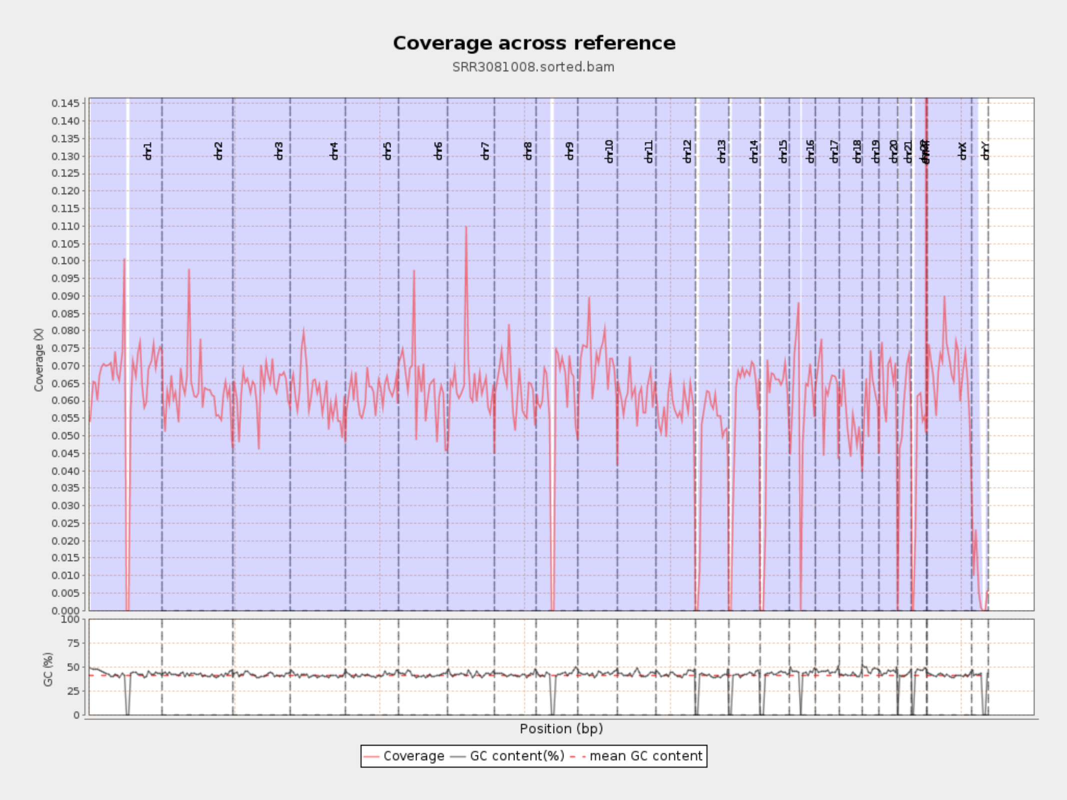
General error rate	0.78%
Mismatches	1,437,086
Insertions	13,025
Mapped reads with at least one insertion	0.44%
Deletions	38,803
Mapped reads with at least one deletion	1.31%
Homopolymer indels	45.64%

2.6. Chromosome stats

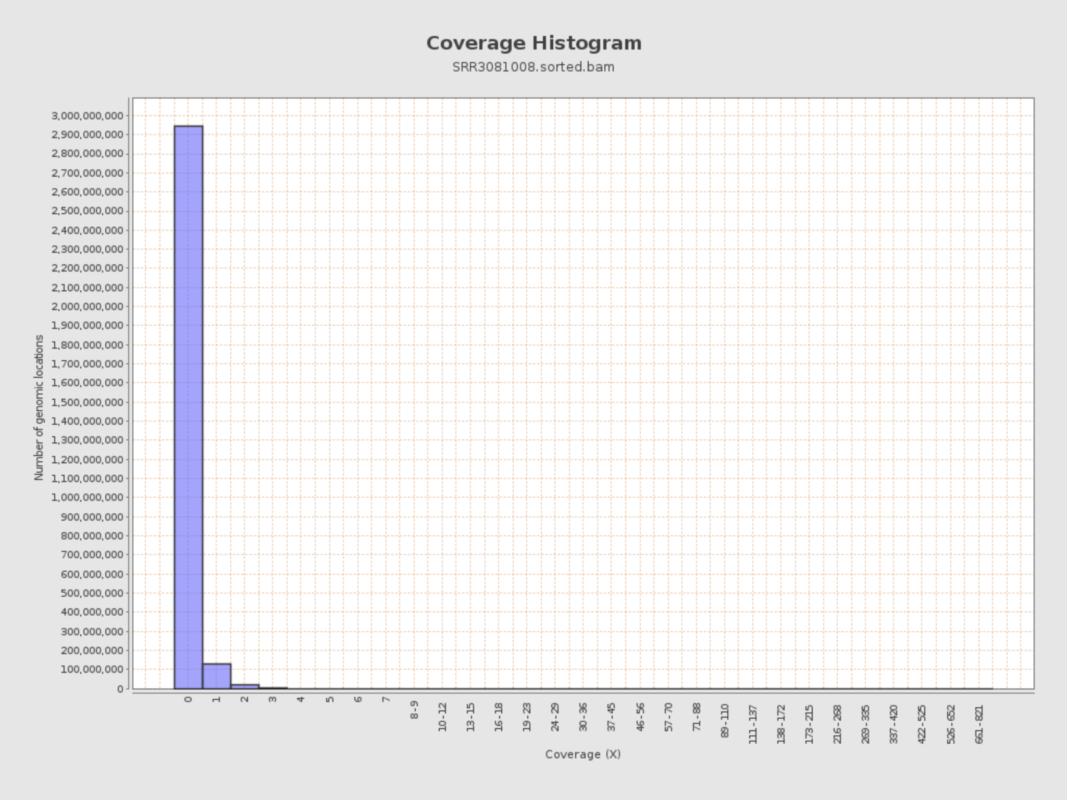
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16176347	0.0649	0.7504
chr2	243199373	15272776	0.0628	0.4581
chr3	198022430	12610327	0.0637	0.2955
chr4	191154276	11803605	0.0617	0.3081
chr5	180915260	11284839	0.0624	0.2957
chr6	171115067	11064557	0.0647	0.4394
chr7	159138663	10416670	0.0655	0.7485

chr8	146364022	9300788	0.0635	0.4402
chr9	141213431	8205658	0.0581	0.4331
chr10	135534747	9753340	0.072	0.4029
chr11	135006516	8277944	0.0613	0.4183
chr12	133851895	7743288	0.0578	0.293
chr13	115169878	5431564	0.0472	0.2558
chr14	107349540	5993619	0.0558	0.3032
chr15	102531392	5469729	0.0533	0.2845
chr16	90354753	5403141	0.0598	0.3232
chr17	81195210	5171690	0.0637	0.3573
chr18	78077248	4247269	0.0544	0.8023
chr19	59128983	3569410	0.0604	0.5798
chr20	63025520	4178235	0.0663	0.3154
chr21	48129895	2580975	0.0536	0.2993
chr22	51304566	2069854	0.0403	0.2376
chrMT	16571	59453	3.5878	3.5791
chrX	155270560	10703678	0.0689	0.3597
chrY	59373566	470574	0.0079	0.1558

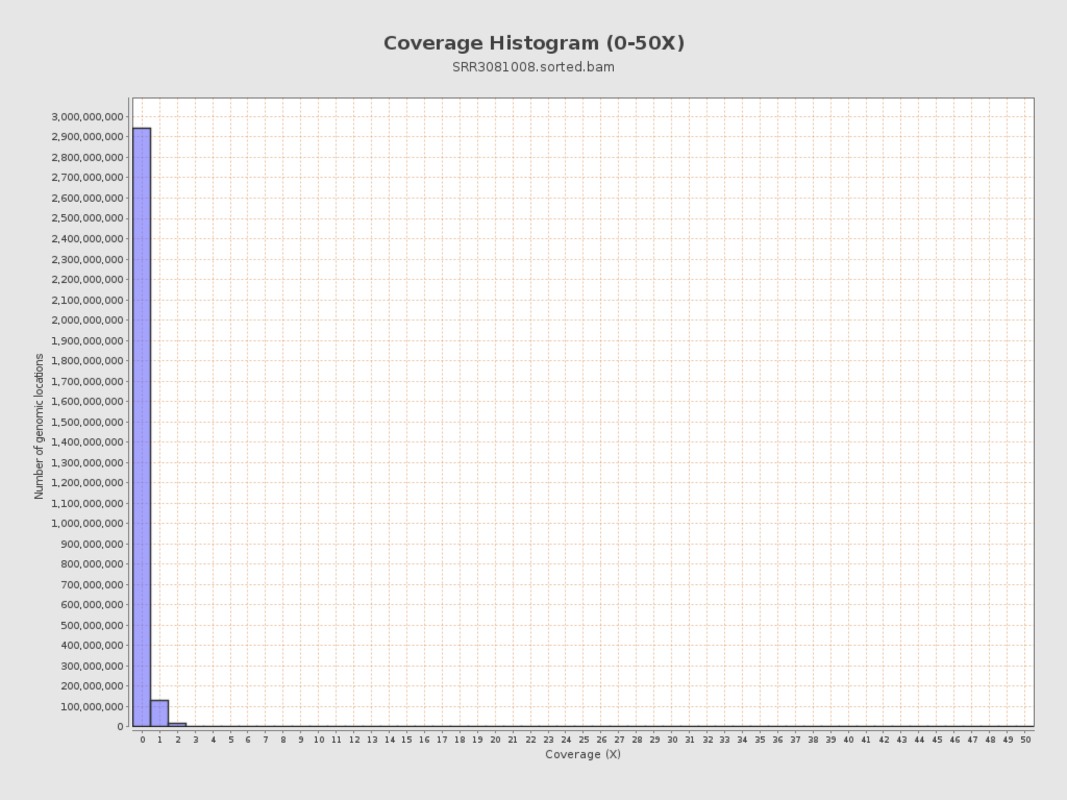
3. Results : Coverage across reference



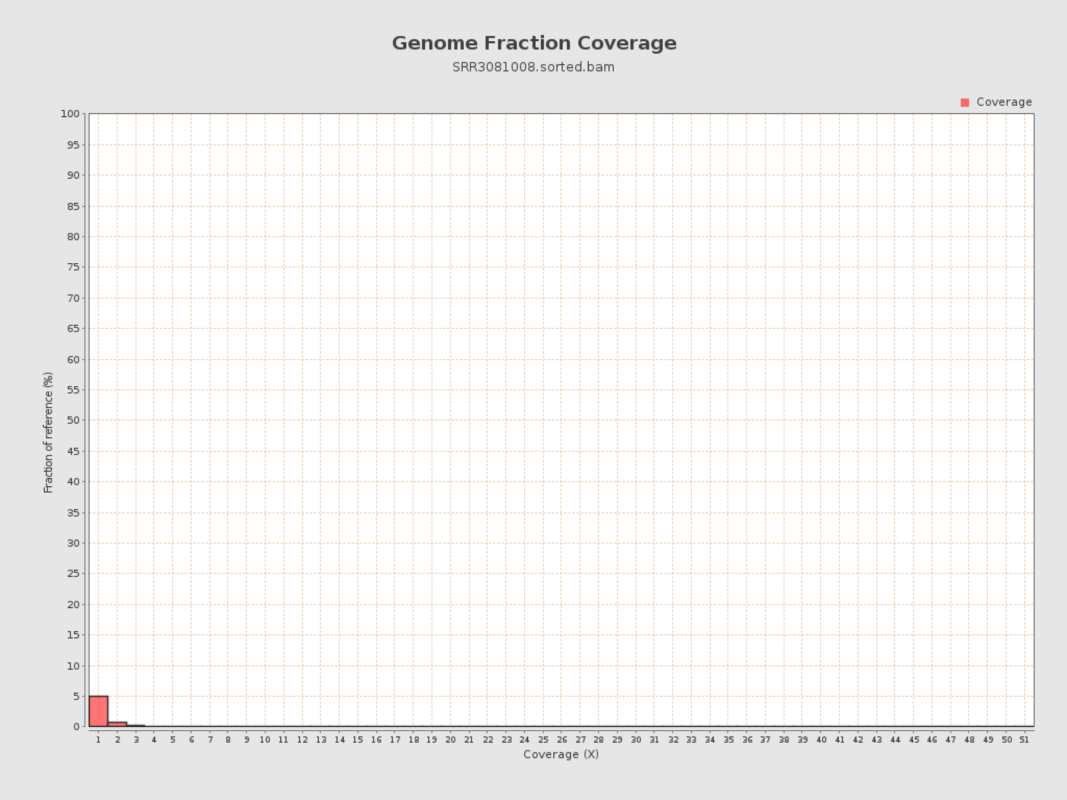
4. Results : Coverage Histogram



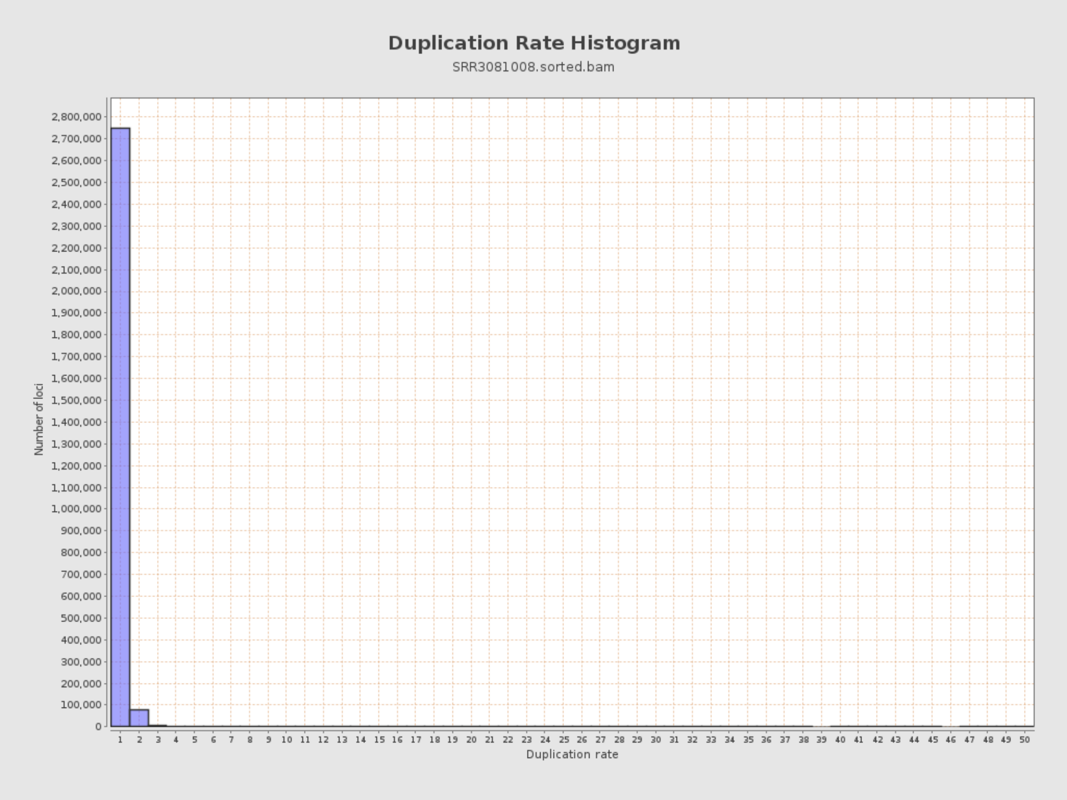
5. Results : Coverage Histogram (0-50X)



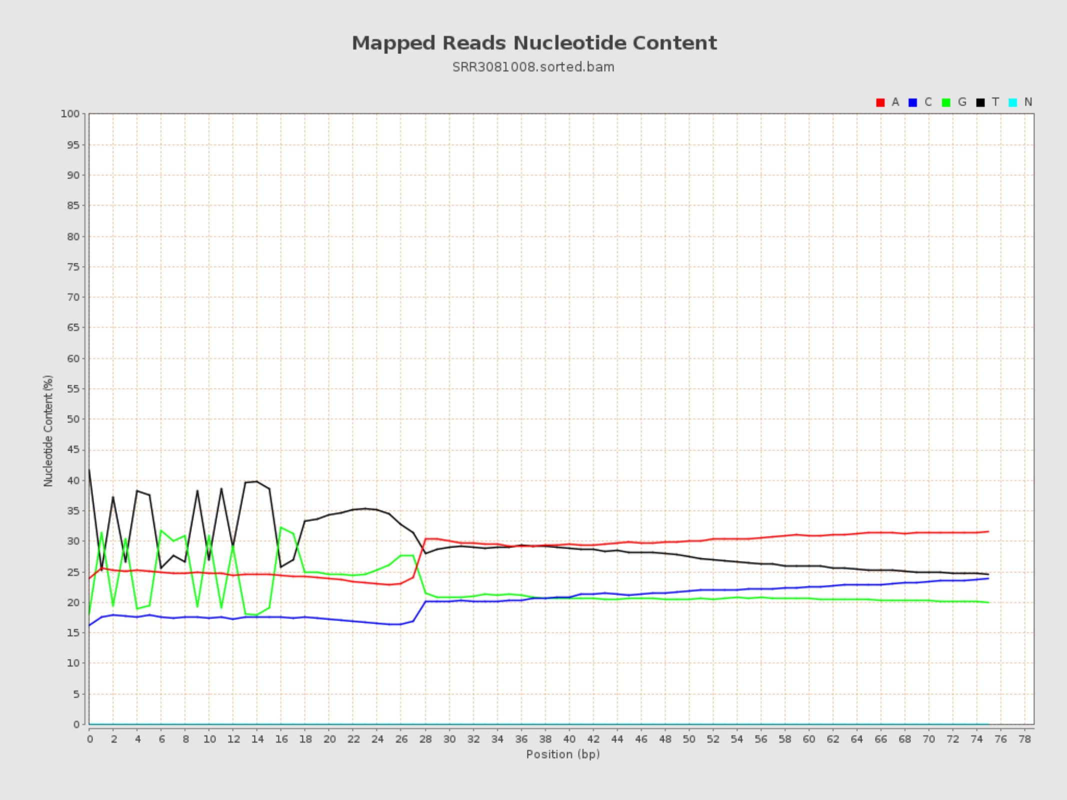
6. Results : Genome Fraction Coverage



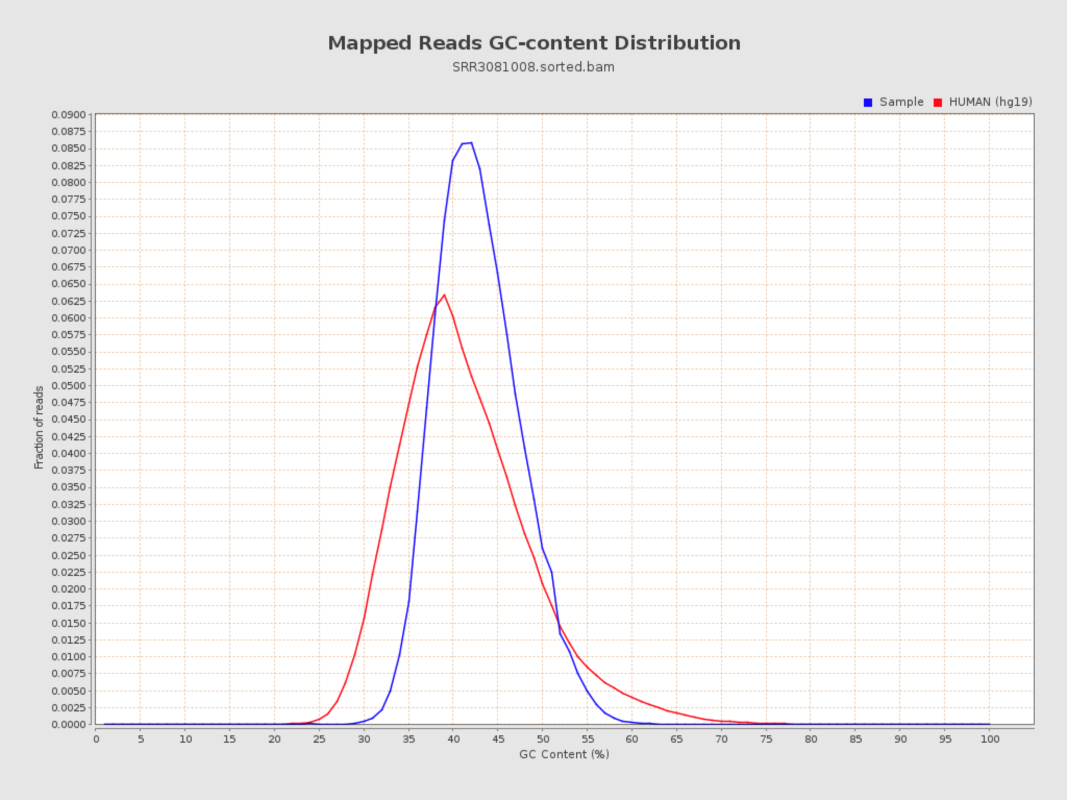
7. Results : Duplication Rate Histogram



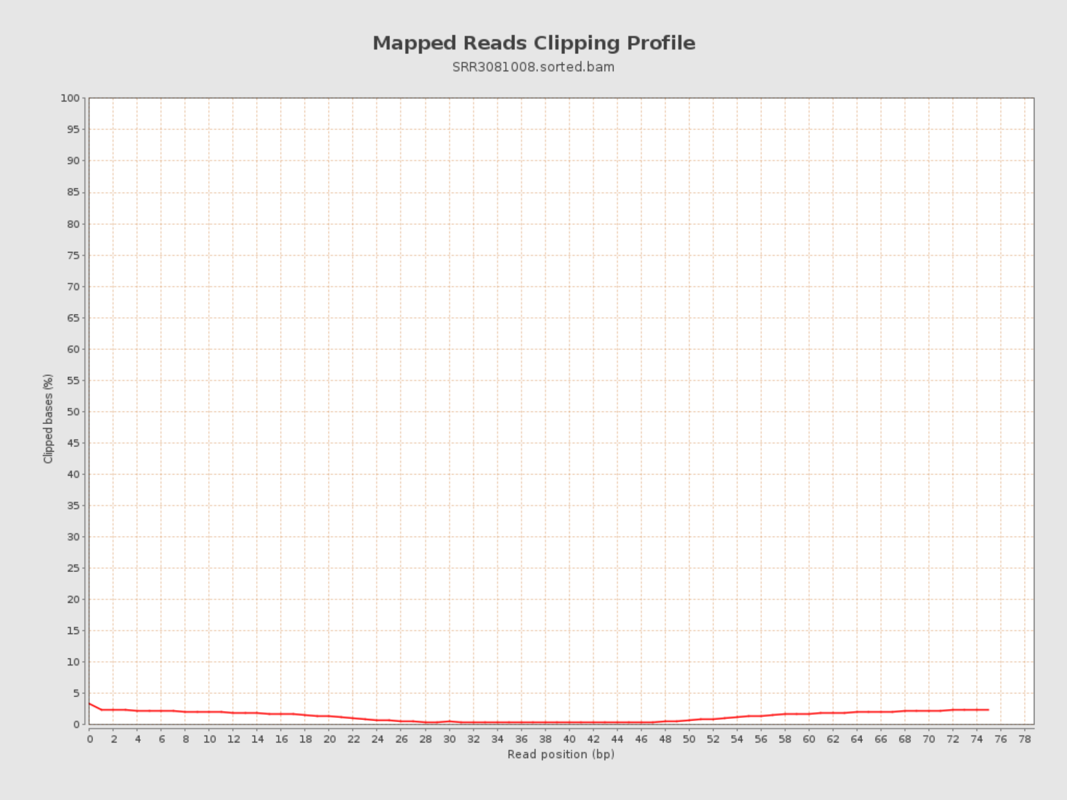
8. Results : Mapped Reads Nucleotide Content



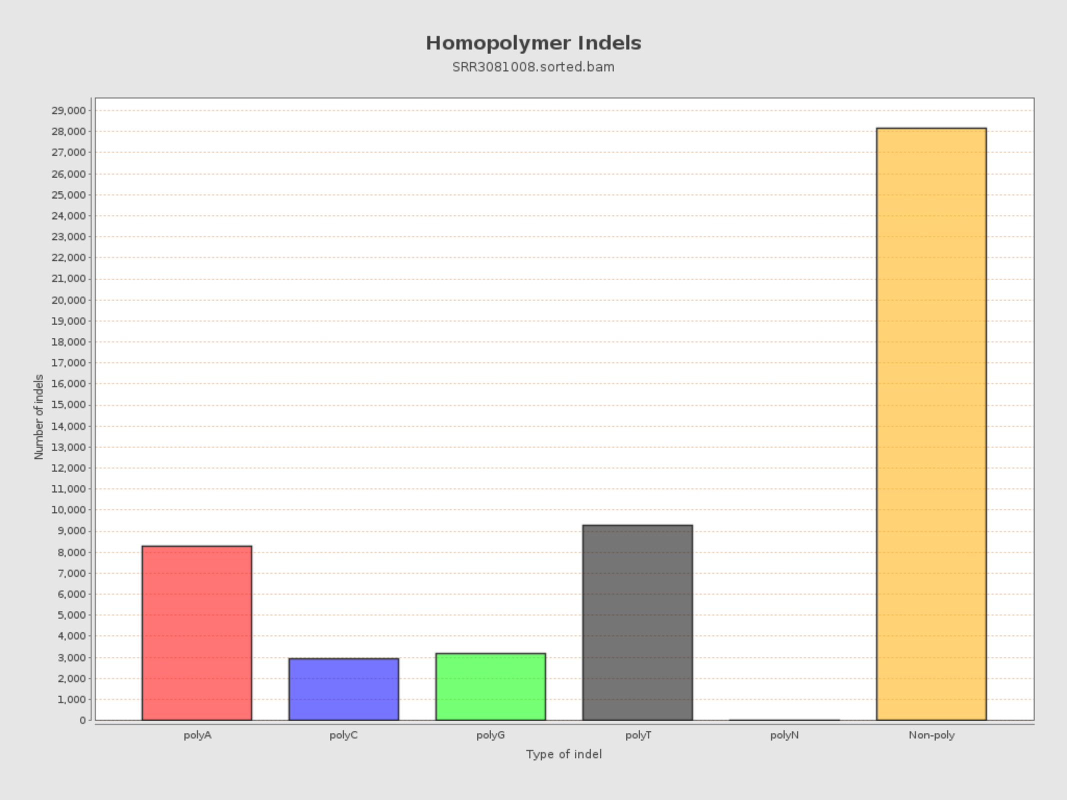
9. Results : Mapped Reads GC-content Distribution



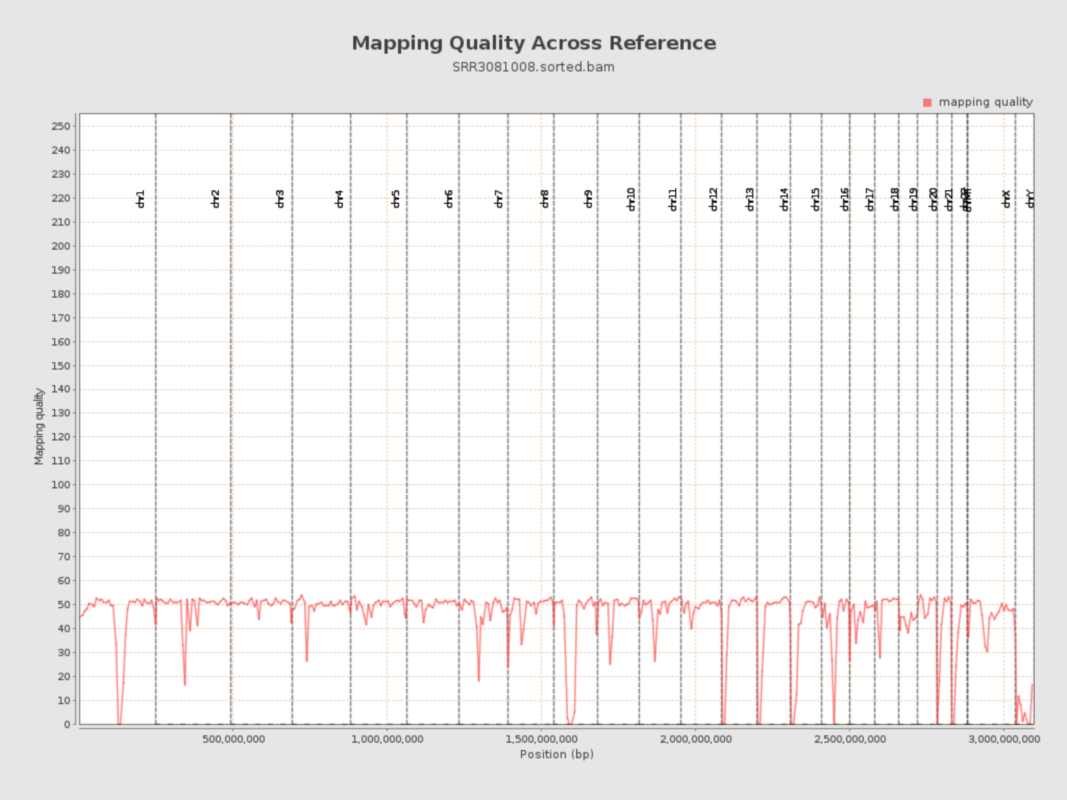
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram