Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:32:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081928.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_SRR3081928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081928.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:32:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,840,838
Mapped reads	2,591,417 / 91.22%
Unmapped reads	249,421 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,779 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	123,148 / 4.33%
Duplication rate	3.38%
Clipped reads	947,269 / 33.34%

2.2. ACGT Content

Number/percentage of A's	50,417,838 / 28.43%
Number/percentage of C's	32,918,001 / 18.56%
Number/percentage of T's	55,726,041 / 31.43%
Number/percentage of G's	38,239,575 / 21.56%
Number/percentage of N's	22,915 / 0.01%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0573

Standard Deviation	0.5826

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

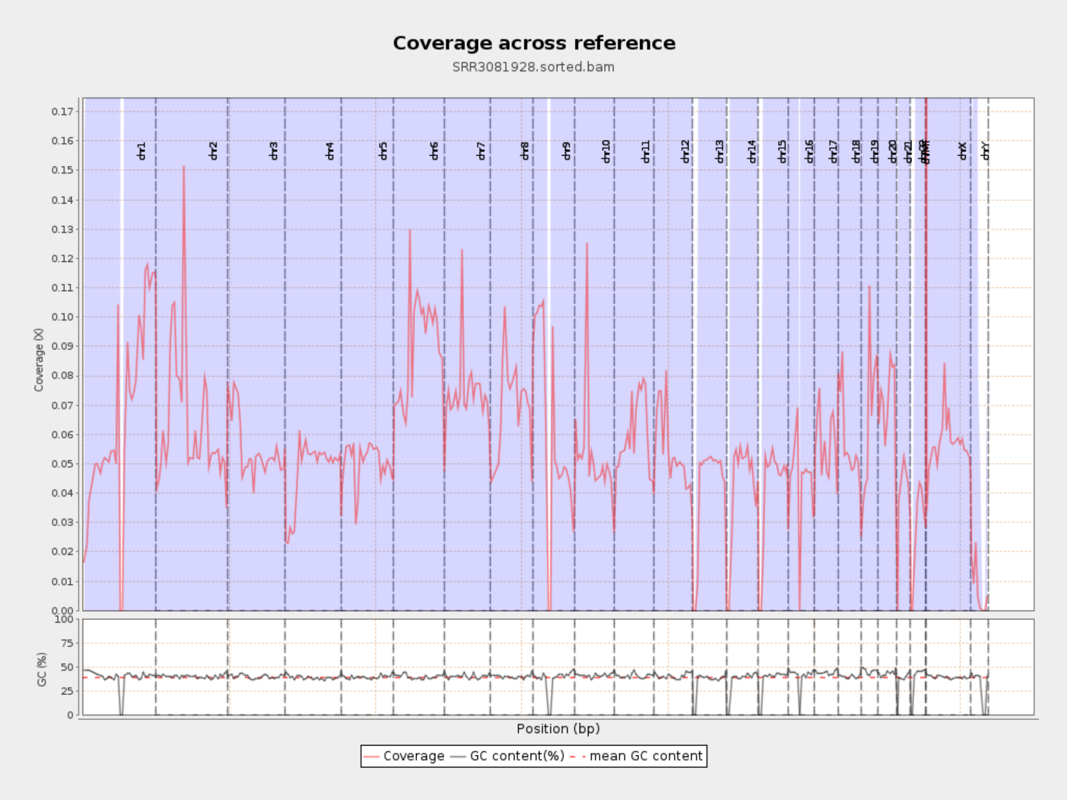
General error rate	0.81%
Mismatches	1,406,038
Insertions	13,169
Mapped reads with at least one insertion	0.5%
Deletions	40,062
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.28%

2.6. Chromosome stats

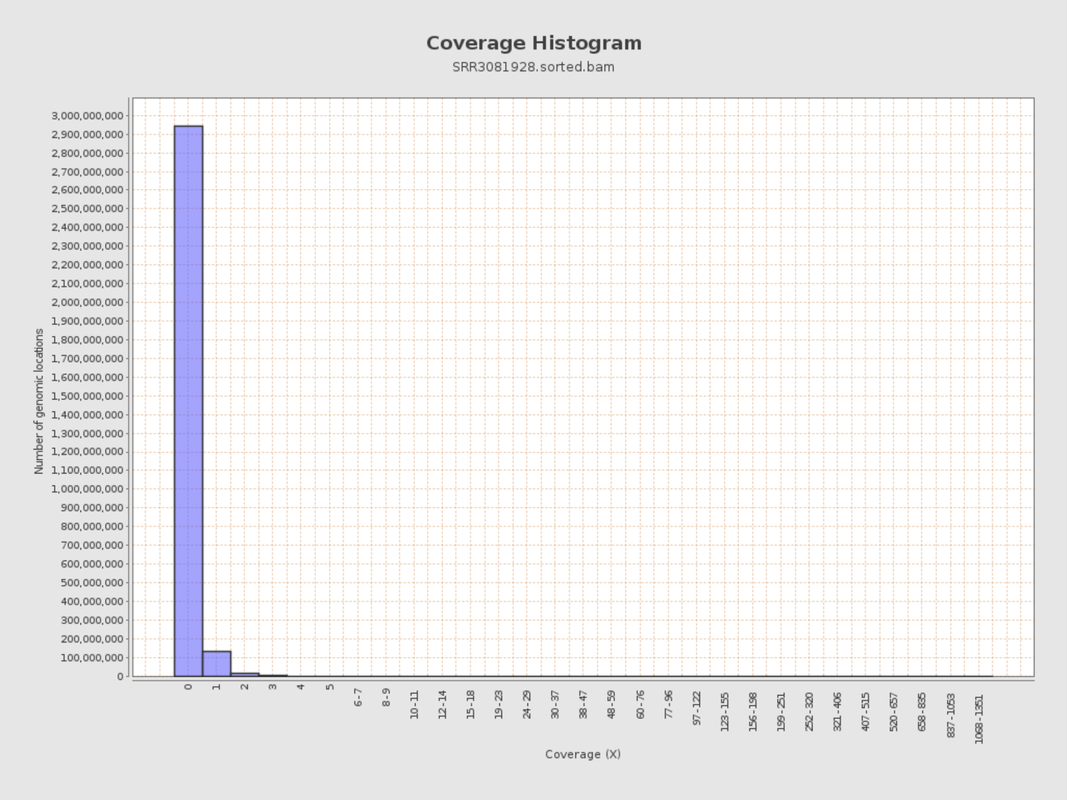
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16282477	0.0653	1.161
chr2	243199373	15844646	0.0652	0.7244
chr3	198022430	11014469	0.0556	0.2689
chr4	191154276	9123685	0.0477	0.2847
chr5	180915260	9099308	0.0503	0.2568
chr6	171115067	15453801	0.0903	0.4919
chr7	159138663	11827370	0.0743	0.8534

chr8	146364022	10082503	0.0689	0.6933
chr9	141213431	8526878	0.0604	0.61
chr10	135534747	7248697	0.0535	0.5873
chr11	135006516	8077571	0.0598	0.3978
chr12	133851895	7271169	0.0543	0.2757
chr13	115169878	4769084	0.0414	0.2276
chr14	107349540	4509374	0.042	0.2898
chr15	102531392	4134246	0.0403	0.2291
chr16	90354753	3925474	0.0434	0.3124
chr17	81195210	4687823	0.0577	0.3063
chr18	78077248	4530528	0.058	1.011
chr19	59128983	3855474	0.0652	0.8133
chr20	63025520	4545929	0.0721	0.3171
chr21	48129895	1901370	0.0395	0.2727
chr22	51304566	1392118	0.0271	0.1802
chrMT	16571	19476	1.1753	1.3257
chrX	155270560	8847384	0.057	0.3273
chrY	59373566	424179	0.0071	0.1924

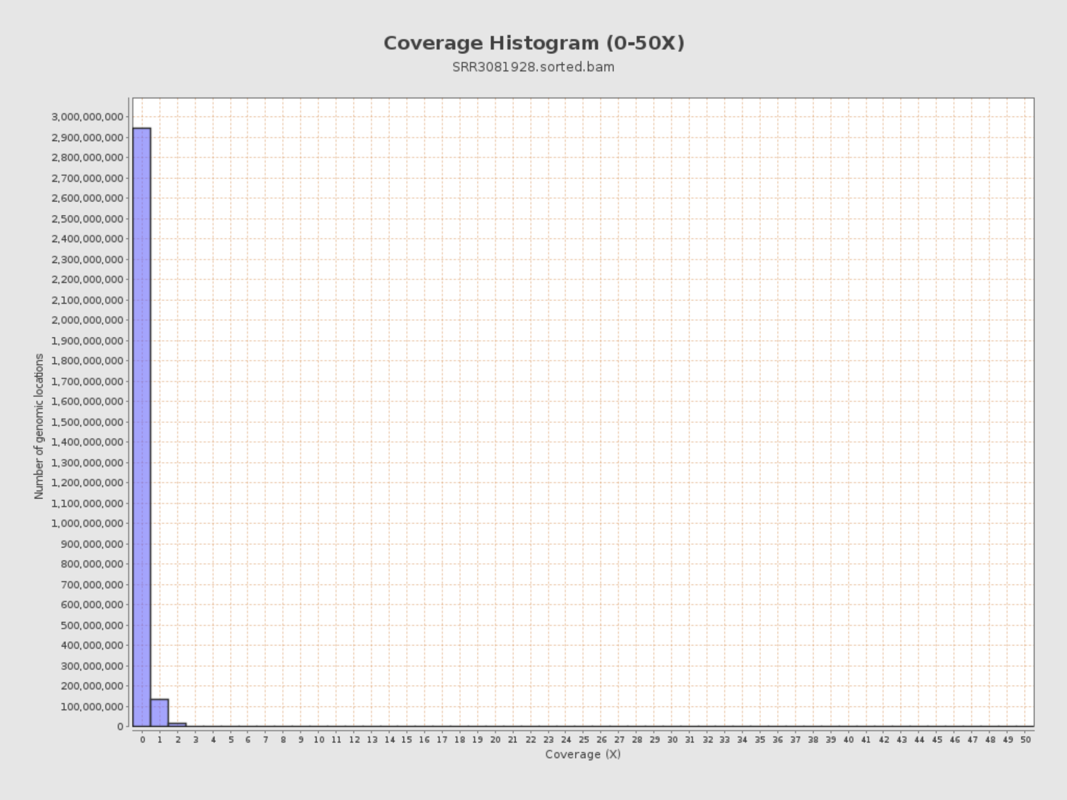
3. Results : Coverage across reference



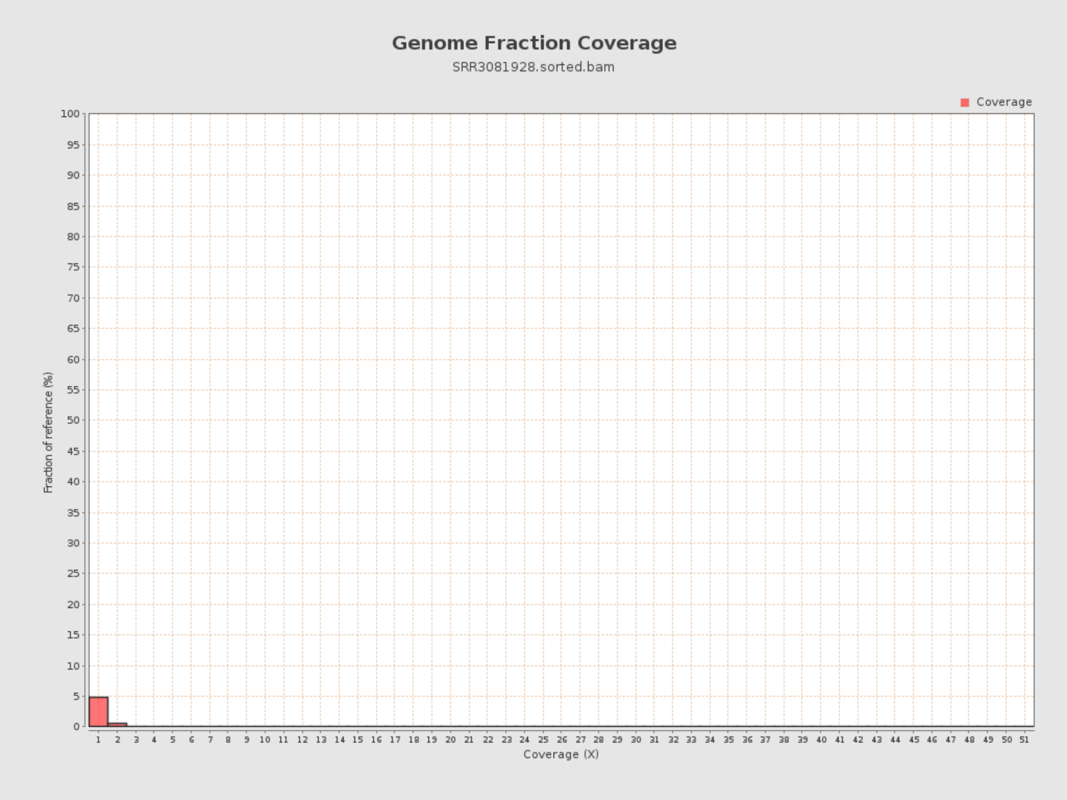
4. Results : Coverage Histogram



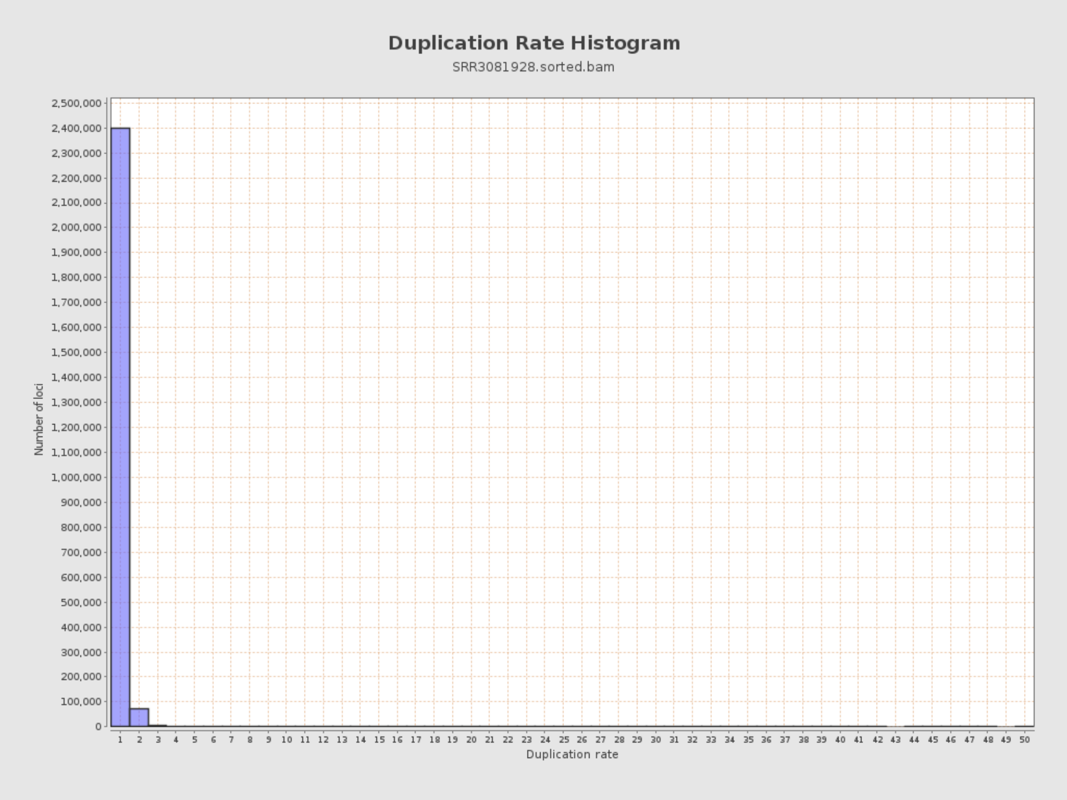
5. Results : Coverage Histogram (0-50X)



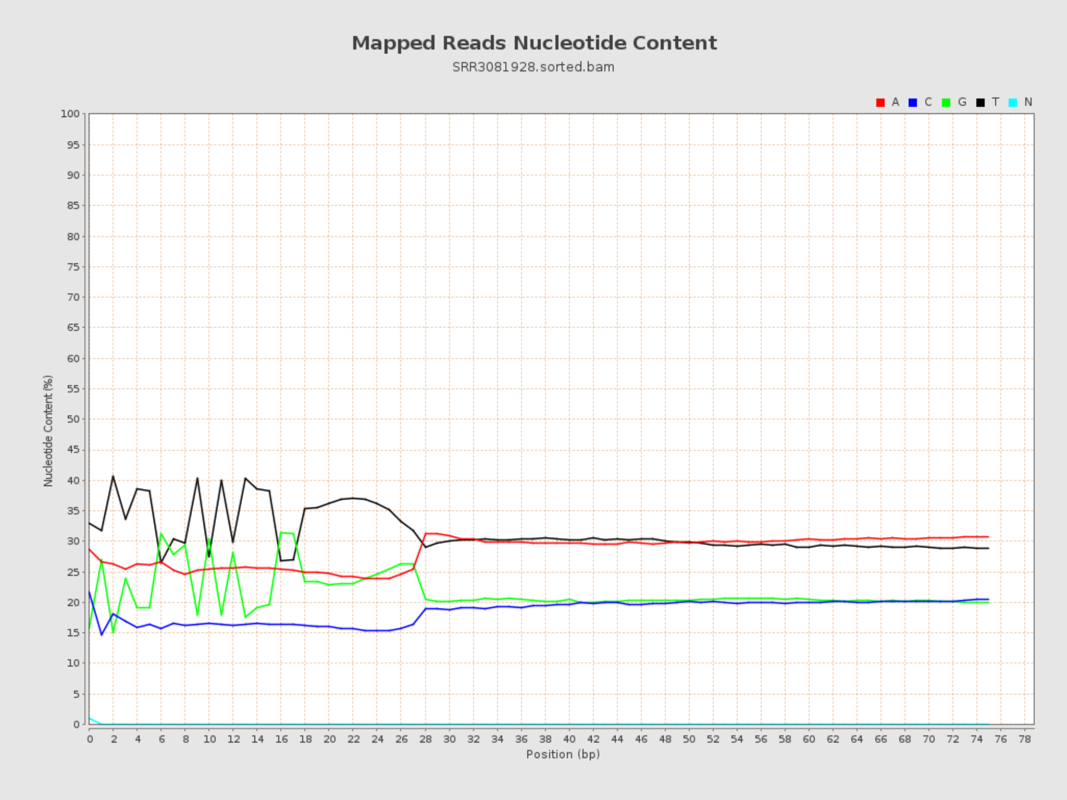
6. Results : Genome Fraction Coverage



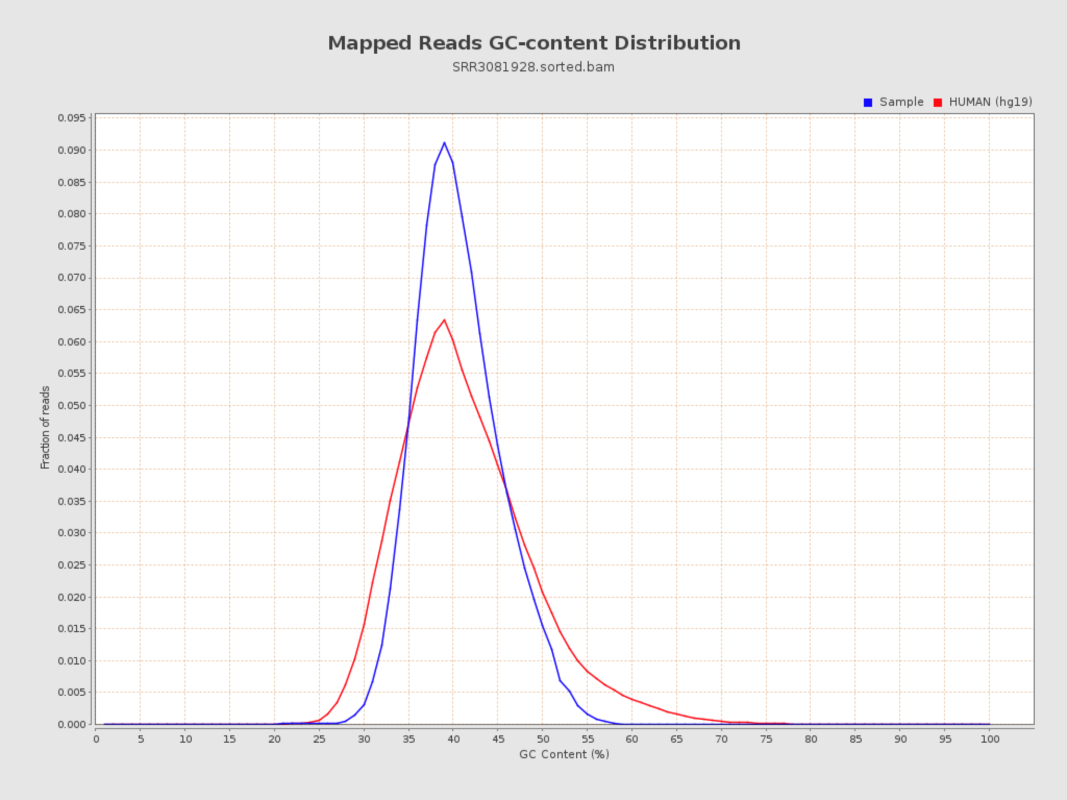
7. Results : Duplication Rate Histogram



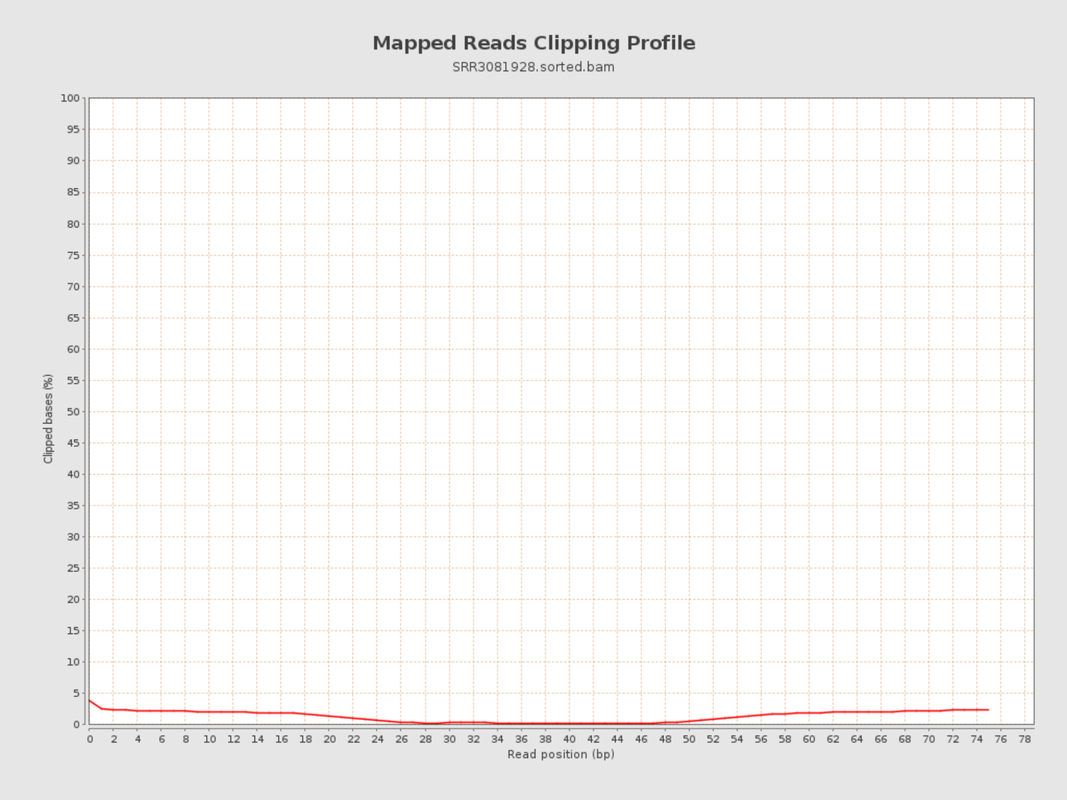
8. Results : Mapped Reads Nucleotide Content



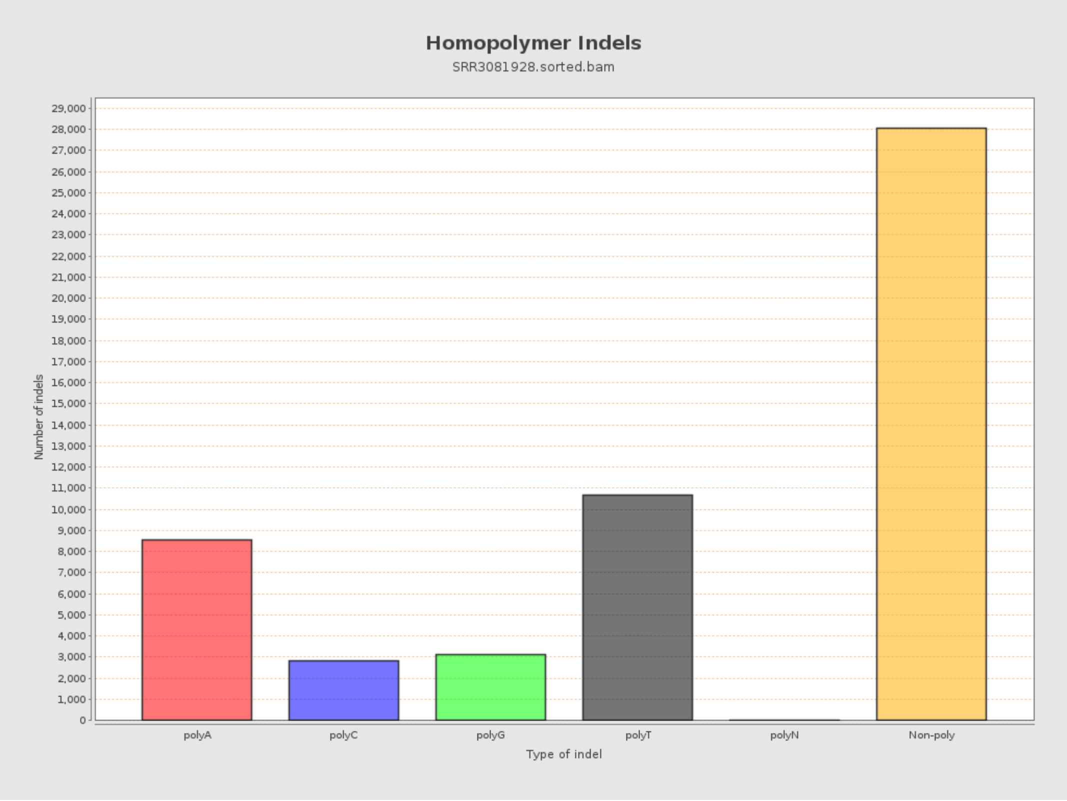
9. Results : Mapped Reads GC-content Distribution



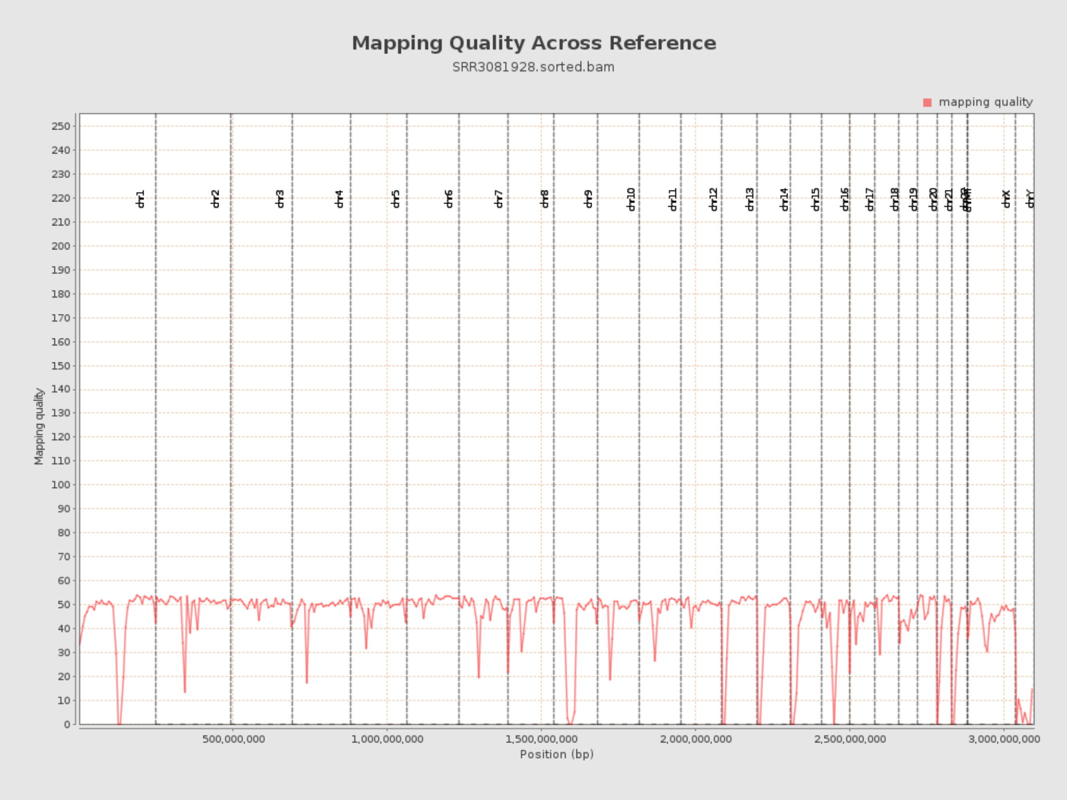
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram