Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:06:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081029.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_SRR3081029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081029.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:06:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,390,197
Mapped reads	2,619,616 / 77.27%
Unmapped reads	770,581 / 22.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,951 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	91,254 / 2.69%
Duplication rate	2.84%
Clipped reads	1,544,181 / 45.55%

2.2. ACGT Content

Number/percentage of A's	46,360,361 / 28.24%
Number/percentage of C's	33,105,603 / 20.17%
Number/percentage of T's	47,939,781 / 29.21%
Number/percentage of G's	36,731,175 / 22.38%
Number/percentage of N's	2,071 / 0%
GC Percentage	42.55%

2.3. Coverage

Mean	0.053

Standard Deviation	0.3611

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

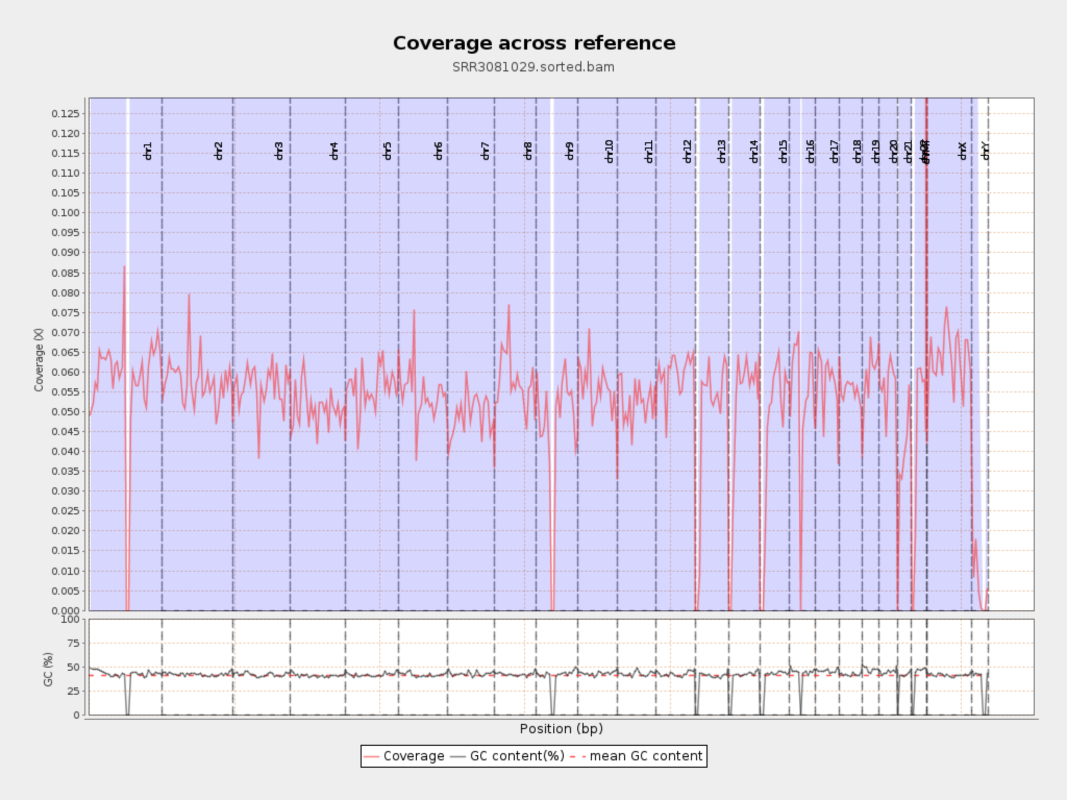
General error rate	0.77%
Mismatches	1,242,573
Insertions	10,895
Mapped reads with at least one insertion	0.41%
Deletions	32,792
Mapped reads with at least one deletion	1.24%
Homopolymer indels	45.99%

2.6. Chromosome stats

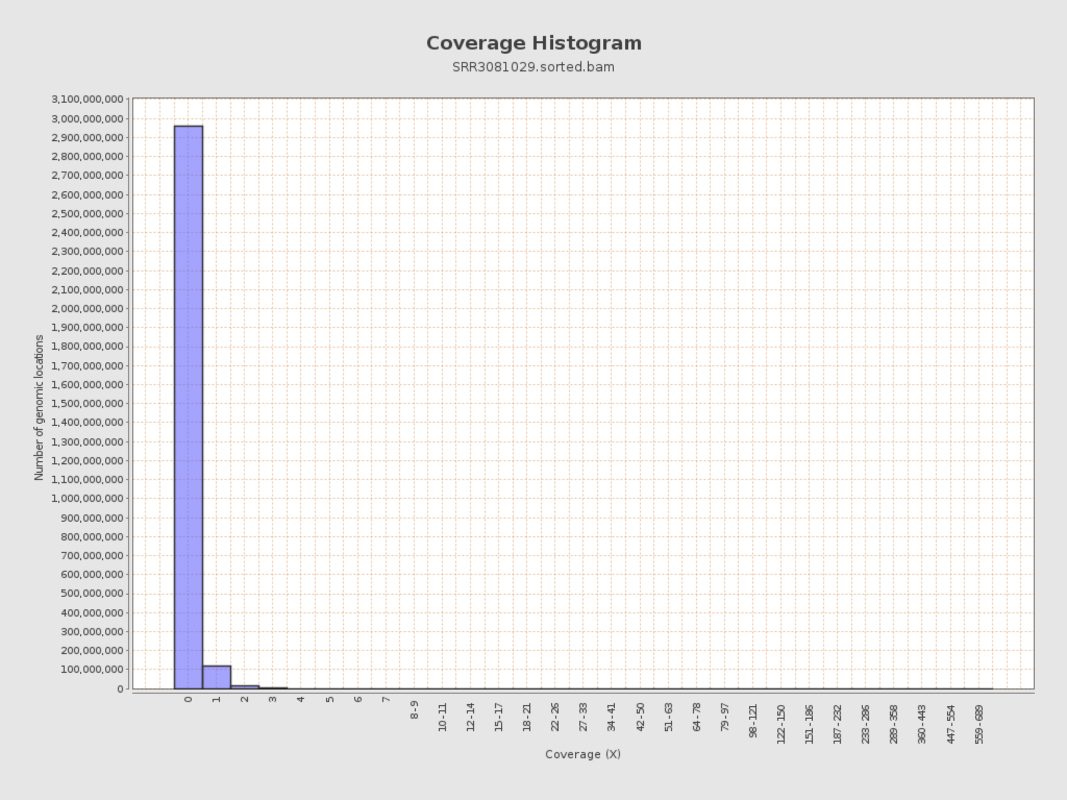
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14245755	0.0572	0.6243
chr2	243199373	14065031	0.0578	0.3957
chr3	198022430	11107268	0.0561	0.2719
chr4	191154276	9721605	0.0509	0.2709
chr5	180915260	10121736	0.0559	0.2751
chr6	171115067	9387896	0.0549	0.3492
chr7	159138663	7872548	0.0495	0.3843

chr8	146364022	8437142	0.0576	0.3779
chr9	141213431	6370728	0.0451	0.327
chr10	135534747	7602951	0.0561	0.3521
chr11	135006516	7028139	0.0521	0.3249
chr12	133851895	7957820	0.0595	0.2839
chr13	115169878	5441681	0.0472	0.2502
chr14	107349540	5255337	0.049	0.2691
chr15	102531392	4578737	0.0447	0.2611
chr16	90354753	4875673	0.054	0.286
chr17	81195210	4602258	0.0567	0.2903
chr18	78077248	4333750	0.0555	0.5905
chr19	59128983	3527795	0.0597	0.4693
chr20	63025520	3540400	0.0562	0.2782
chr21	48129895	1794893	0.0373	0.2333
chr22	51304566	2071260	0.0404	0.2306
chrMT	16571	53132	3.2063	2.5748
chrX	155270560	9824210	0.0633	0.3182
chrY	59373566	378494	0.0064	0.1225

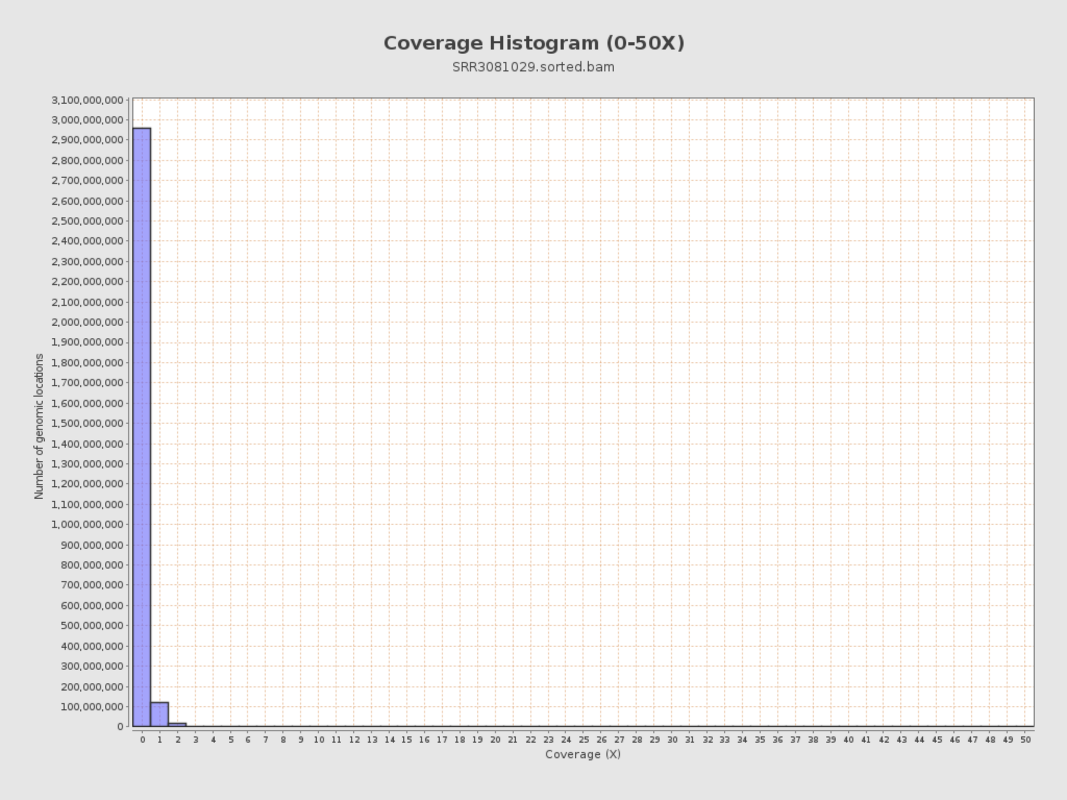
3. Results : Coverage across reference



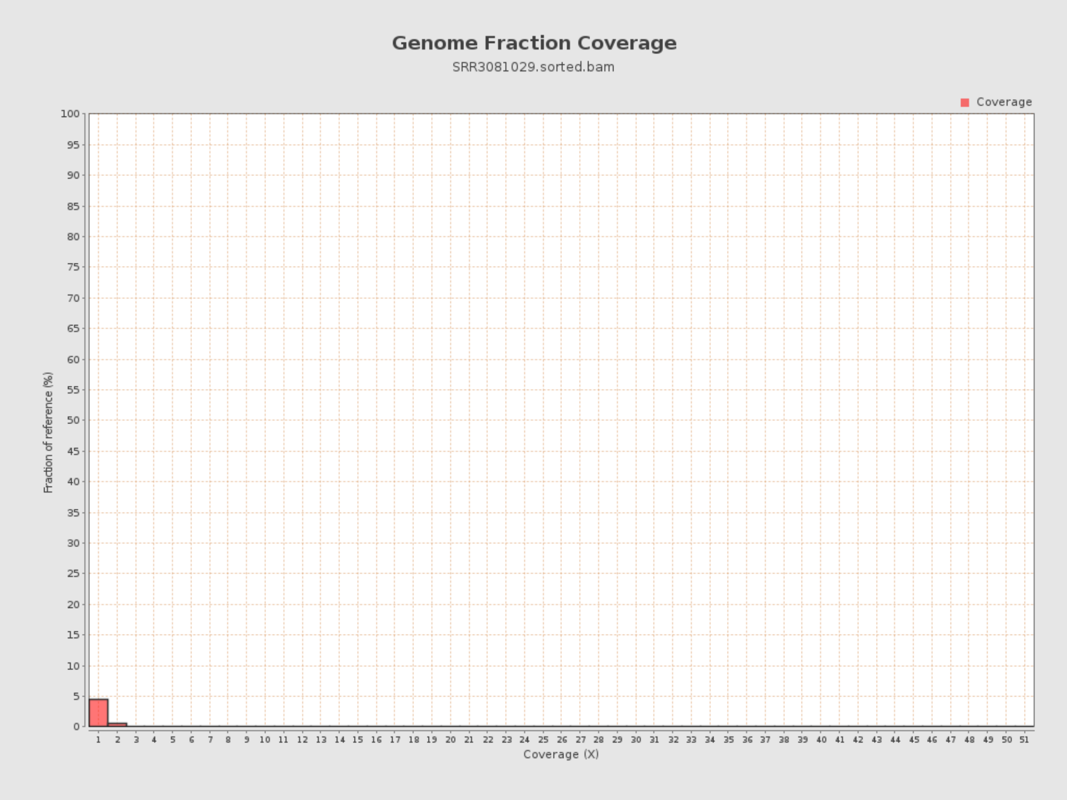
4. Results : Coverage Histogram



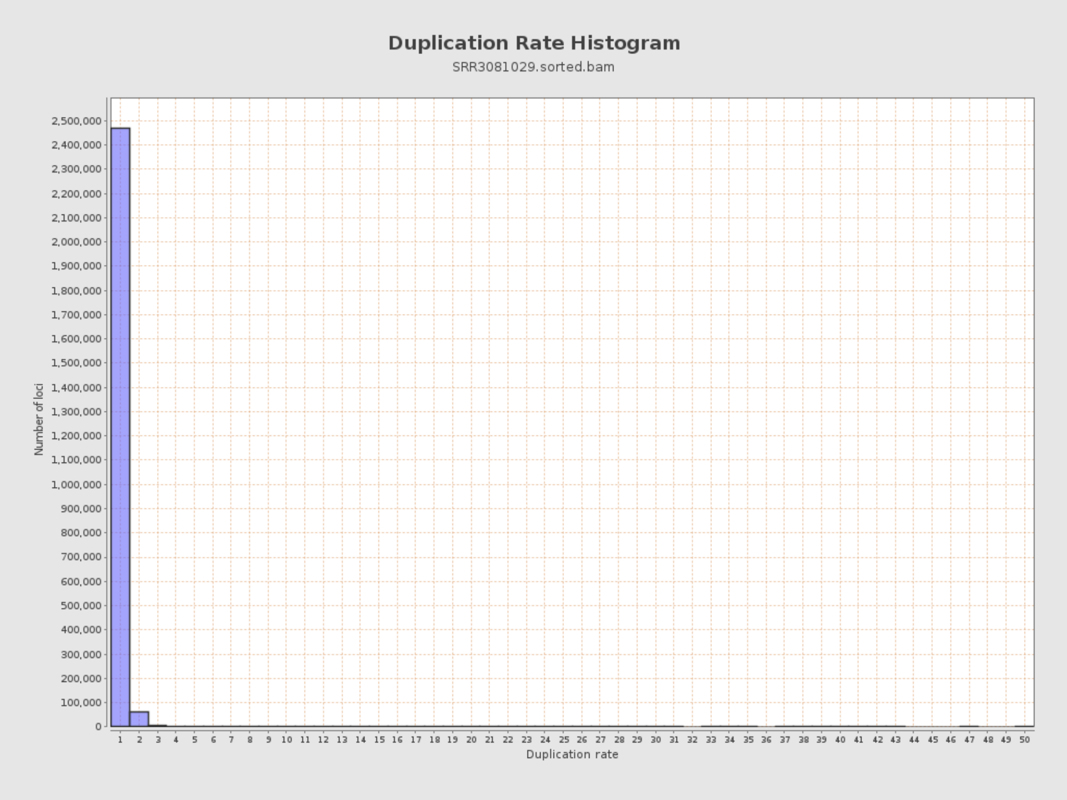
5. Results : Coverage Histogram (0-50X)



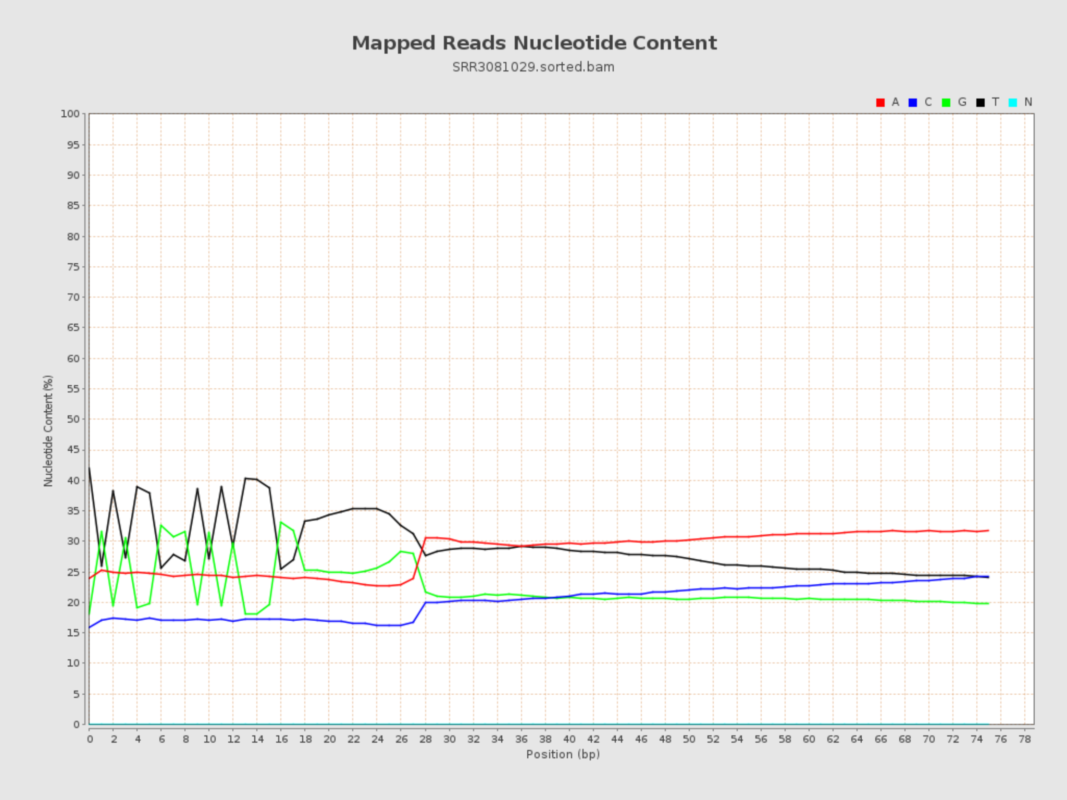
6. Results : Genome Fraction Coverage



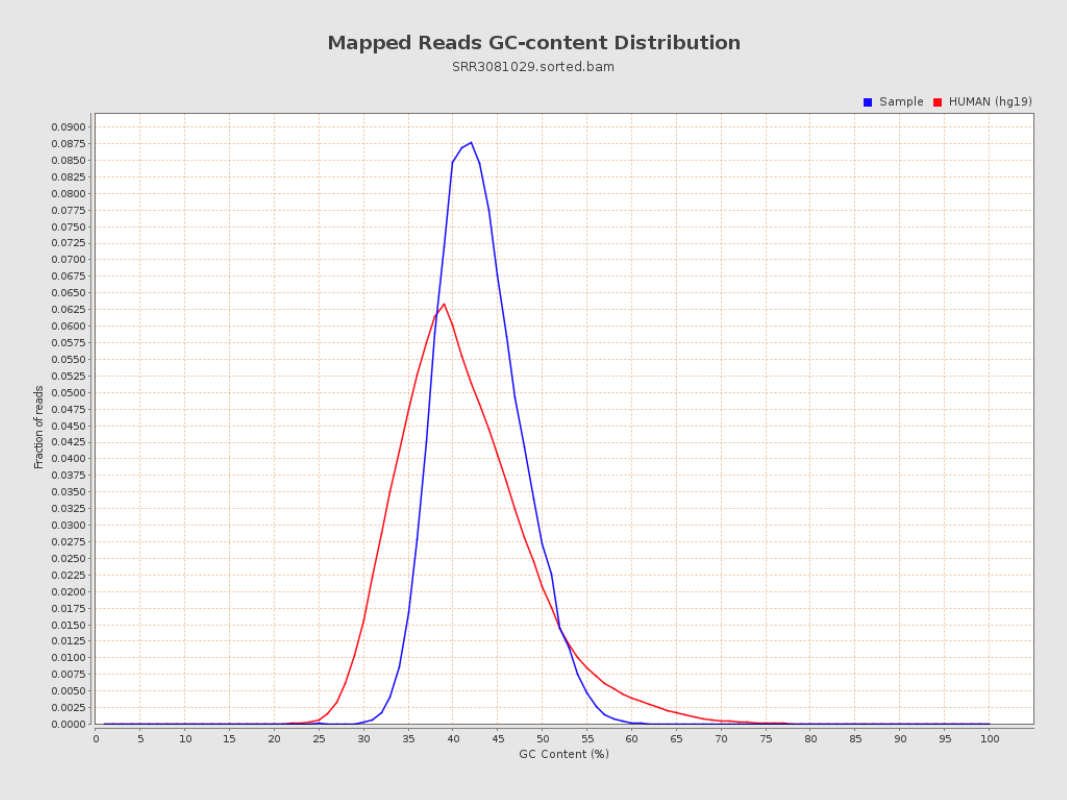
7. Results : Duplication Rate Histogram



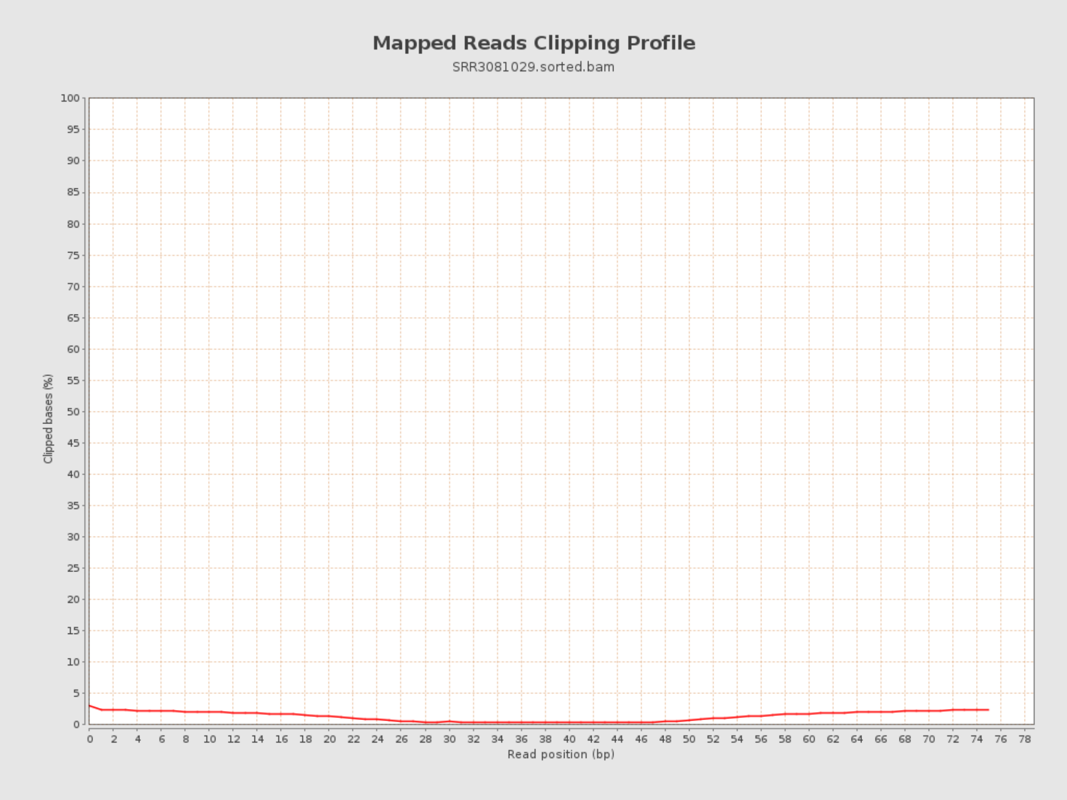
8. Results : Mapped Reads Nucleotide Content



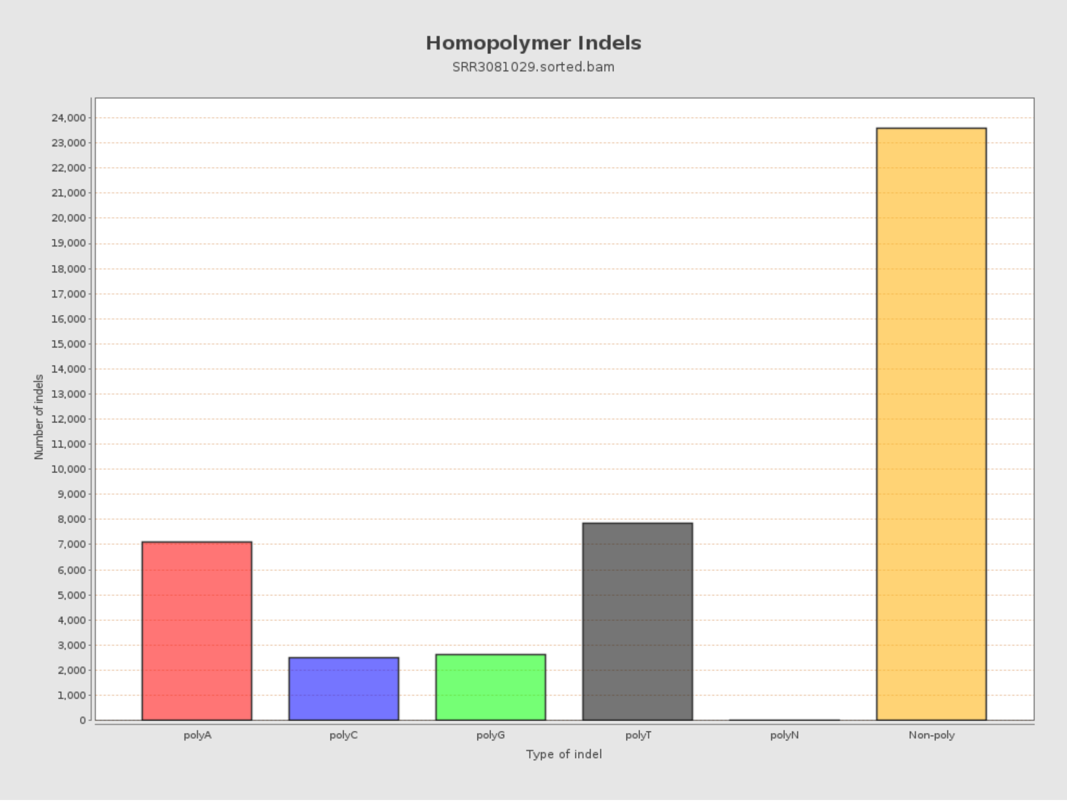
9. Results : Mapped Reads GC-content Distribution



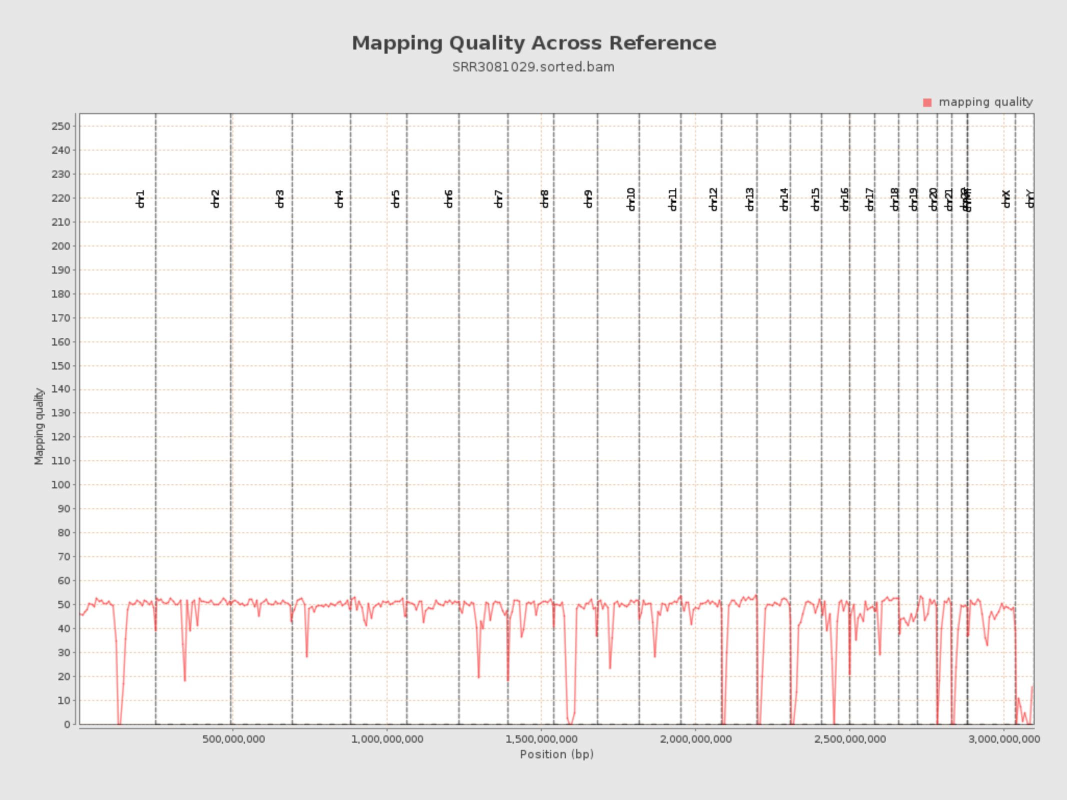
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram