Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:02:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081895.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_SRR3081895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081895.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:02:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,046,096
Mapped reads	1,799,547 / 87.95%
Unmapped reads	246,549 / 12.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,729 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	56,113 / 2.74%
Duplication rate	2.33%
Clipped reads	655,015 / 32.01%

2.2. ACGT Content

Number/percentage of A's	35,891,778 / 29%
Number/percentage of C's	23,215,224 / 18.76%
Number/percentage of T's	38,596,796 / 31.18%
Number/percentage of G's	26,075,464 / 21.07%
Number/percentage of N's	1,369 / 0%
GC Percentage	39.82%

2.3. Coverage

Mean	0.04

Standard Deviation	0.3528

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

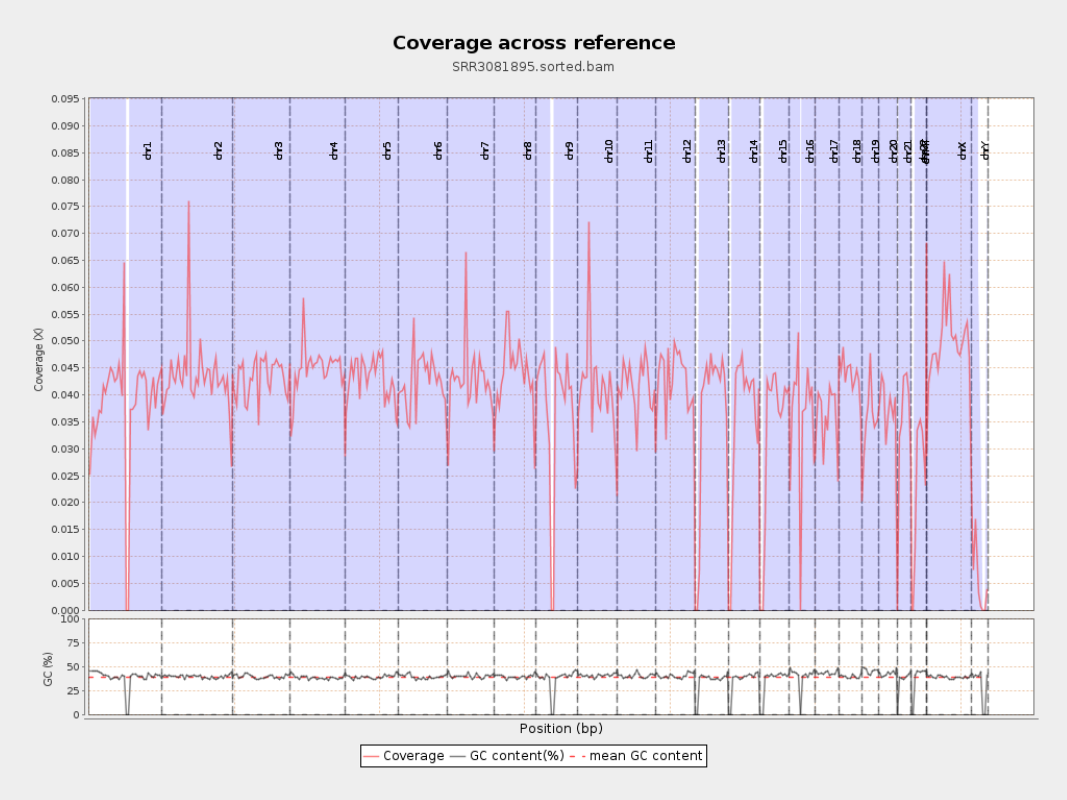
General error rate	0.86%
Mismatches	1,050,119
Insertions	9,692
Mapped reads with at least one insertion	0.53%
Deletions	26,084
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.05%

2.6. Chromosome stats

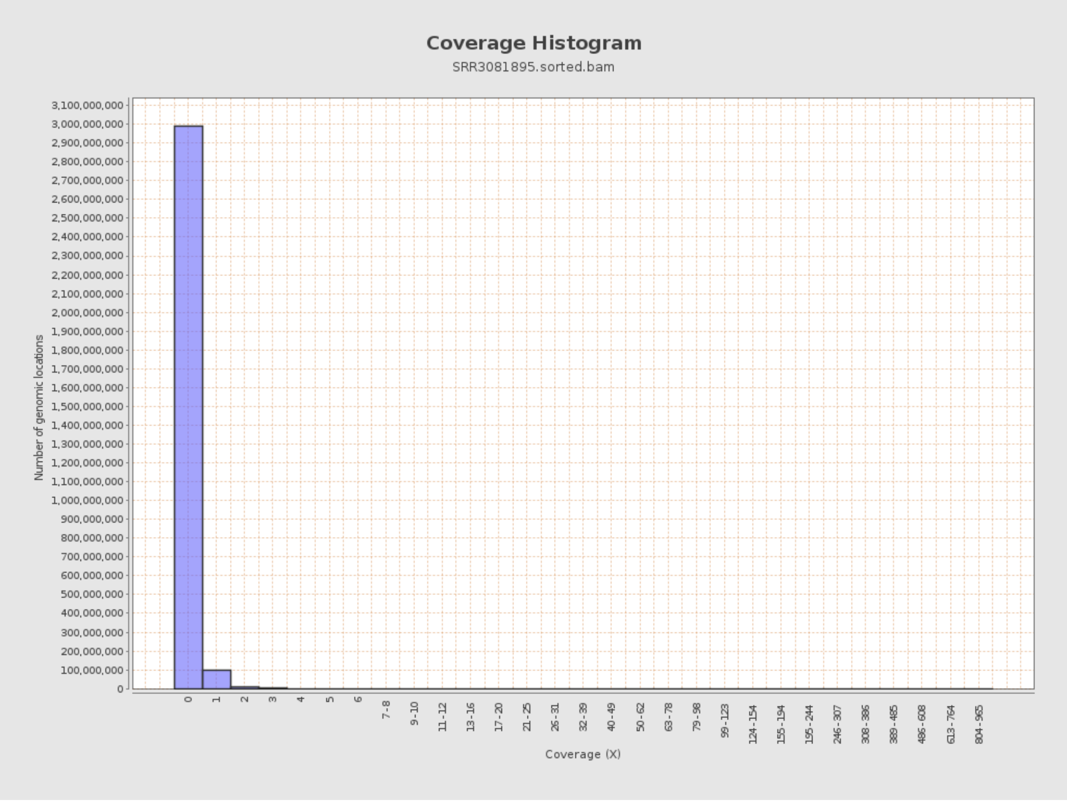
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9542547	0.0383	0.5818
chr2	243199373	10603056	0.0436	0.3973
chr3	198022430	8559324	0.0432	0.2327
chr4	191154276	8576150	0.0449	0.2522
chr5	180915260	7799624	0.0431	0.2312
chr6	171115067	7282552	0.0426	0.2565
chr7	159138663	6868321	0.0432	0.4282

chr8	146364022	6411858	0.0438	0.632
chr9	141213431	5162371	0.0366	0.3167
chr10	135534747	5672569	0.0419	0.3646
chr11	135006516	5597450	0.0415	0.2957
chr12	133851895	5720009	0.0427	0.2304
chr13	115169878	4135536	0.0359	0.2097
chr14	107349540	3750996	0.0349	0.2237
chr15	102531392	3369232	0.0329	0.2023
chr16	90354753	3228018	0.0357	0.2378
chr17	81195210	2886140	0.0355	0.2285
chr18	78077248	3418027	0.0438	0.5713
chr19	59128983	2121941	0.0359	0.4308
chr20	63025520	2348572	0.0373	0.225
chr21	48129895	1640557	0.0341	0.2209
chr22	51304566	1136478	0.0222	0.1627
chrMT	16571	1133	0.0684	0.2826
chrX	155270560	7673922	0.0494	0.2705
chrY	59373566	320998	0.0054	0.1408

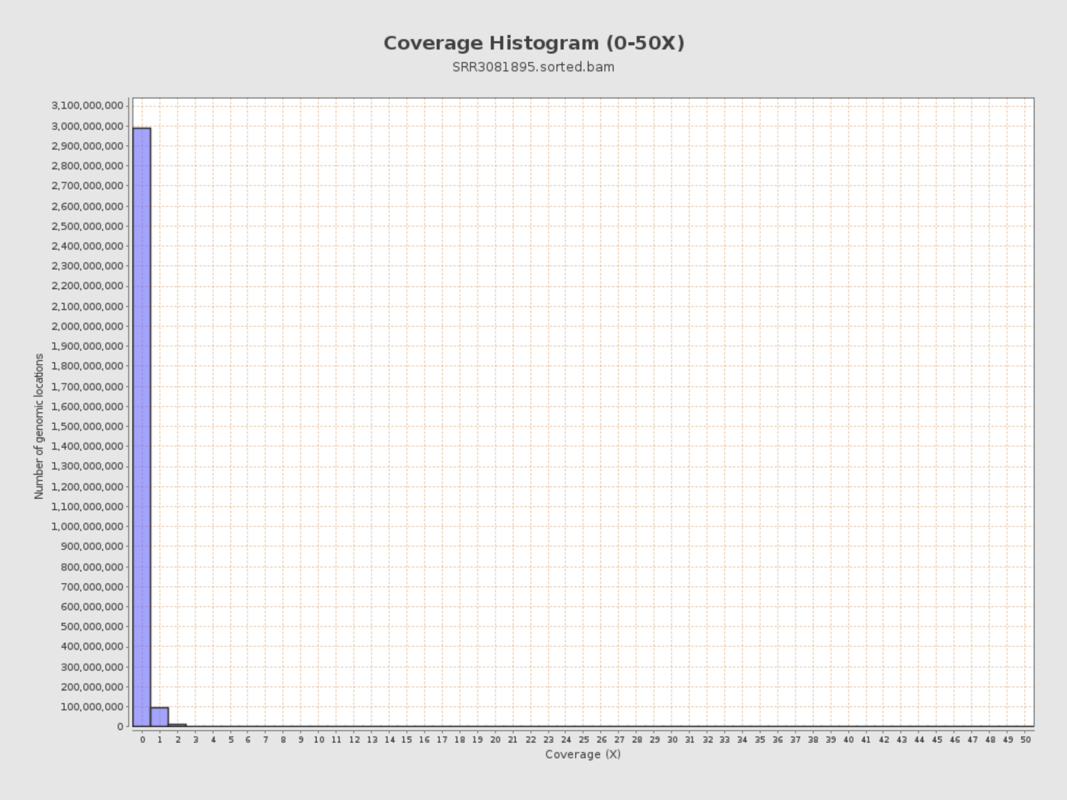
3. Results : Coverage across reference



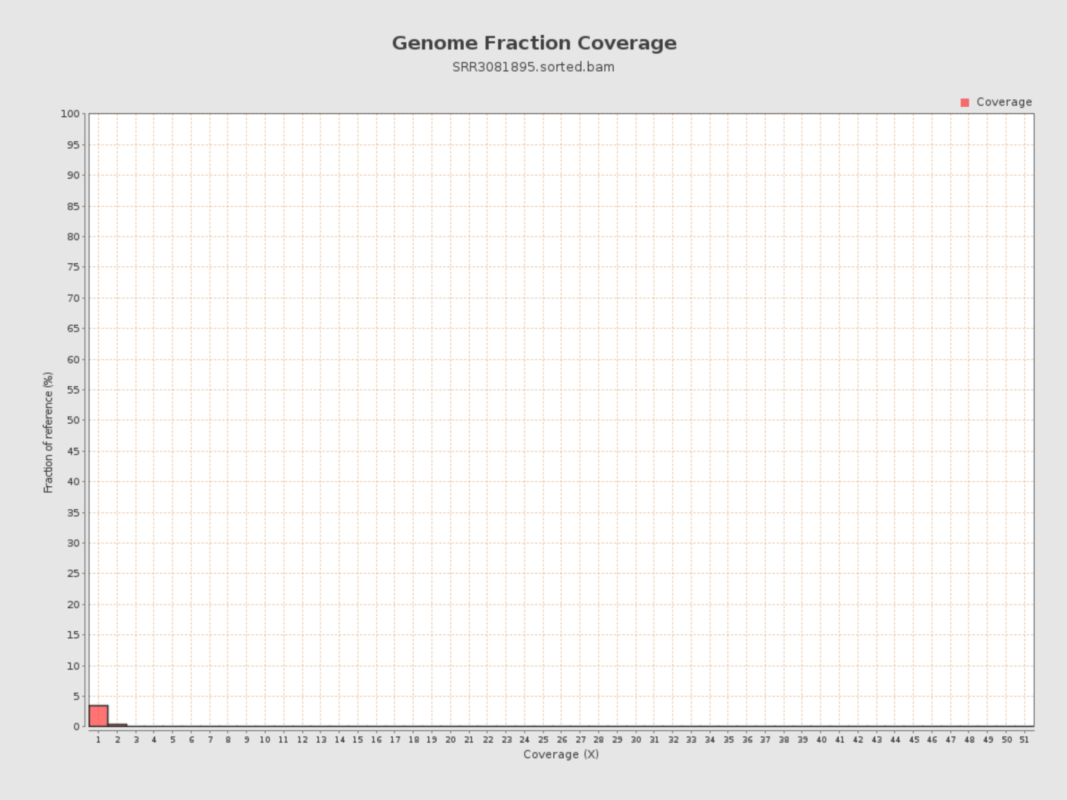
4. Results : Coverage Histogram



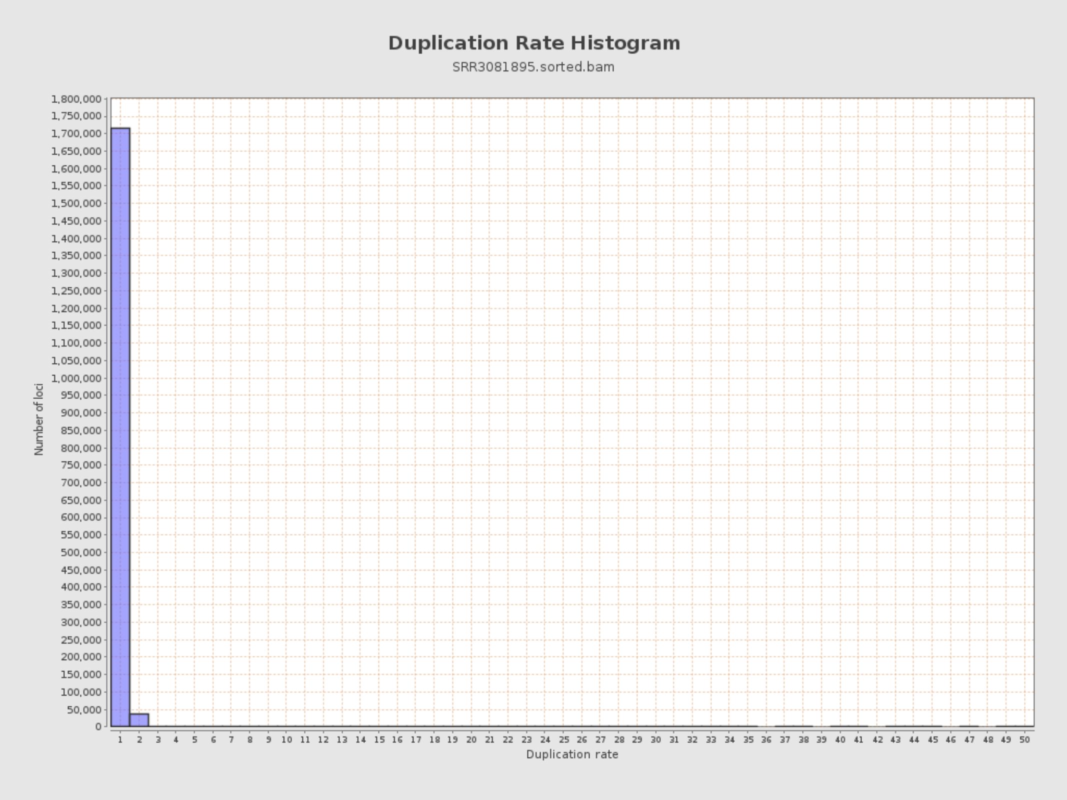
5. Results : Coverage Histogram (0-50X)



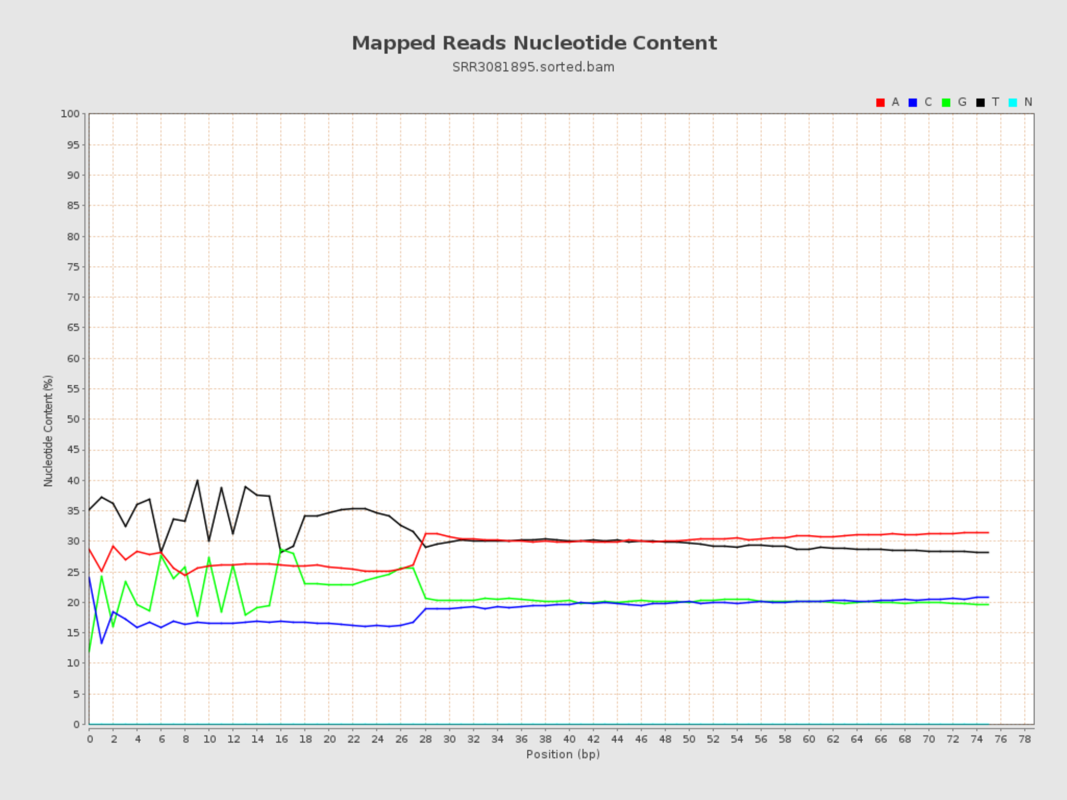
6. Results : Genome Fraction Coverage



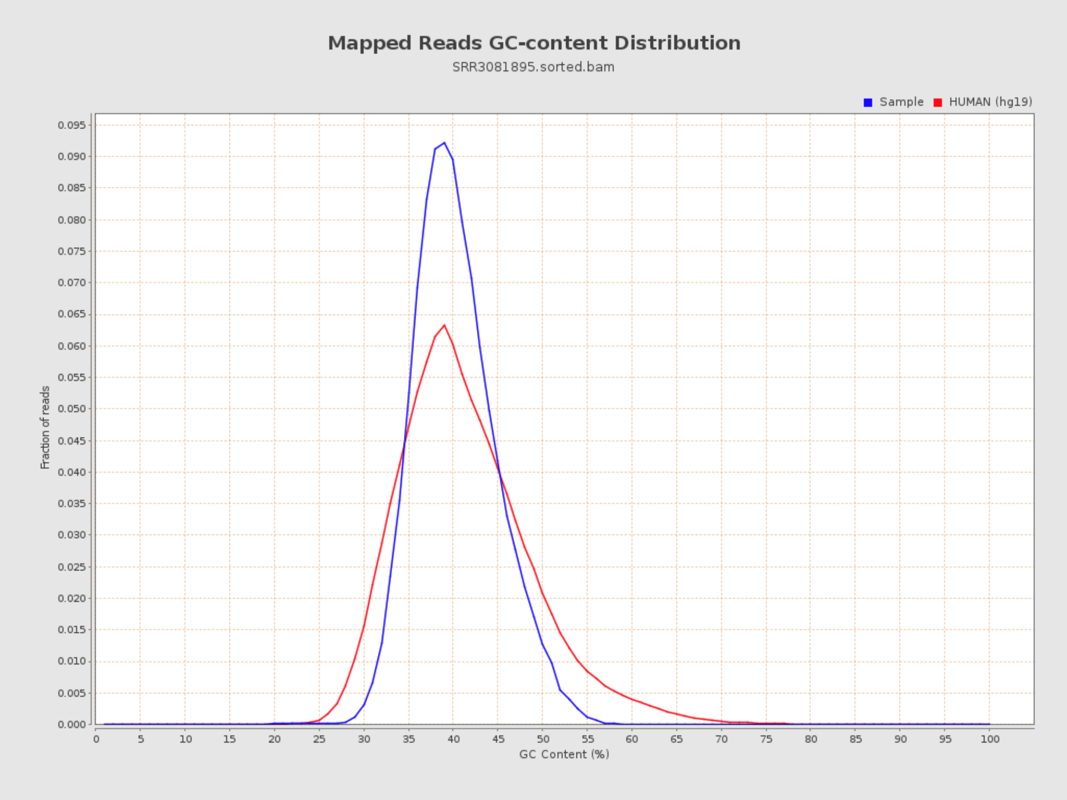
7. Results : Duplication Rate Histogram



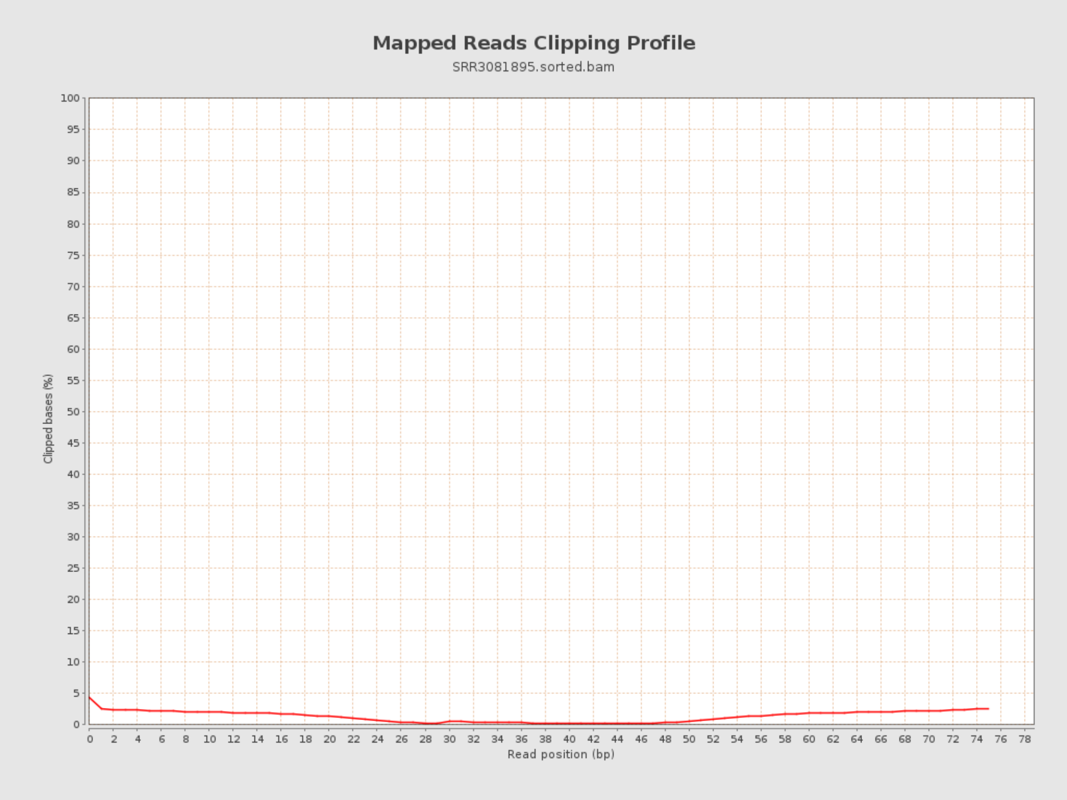
8. Results : Mapped Reads Nucleotide Content



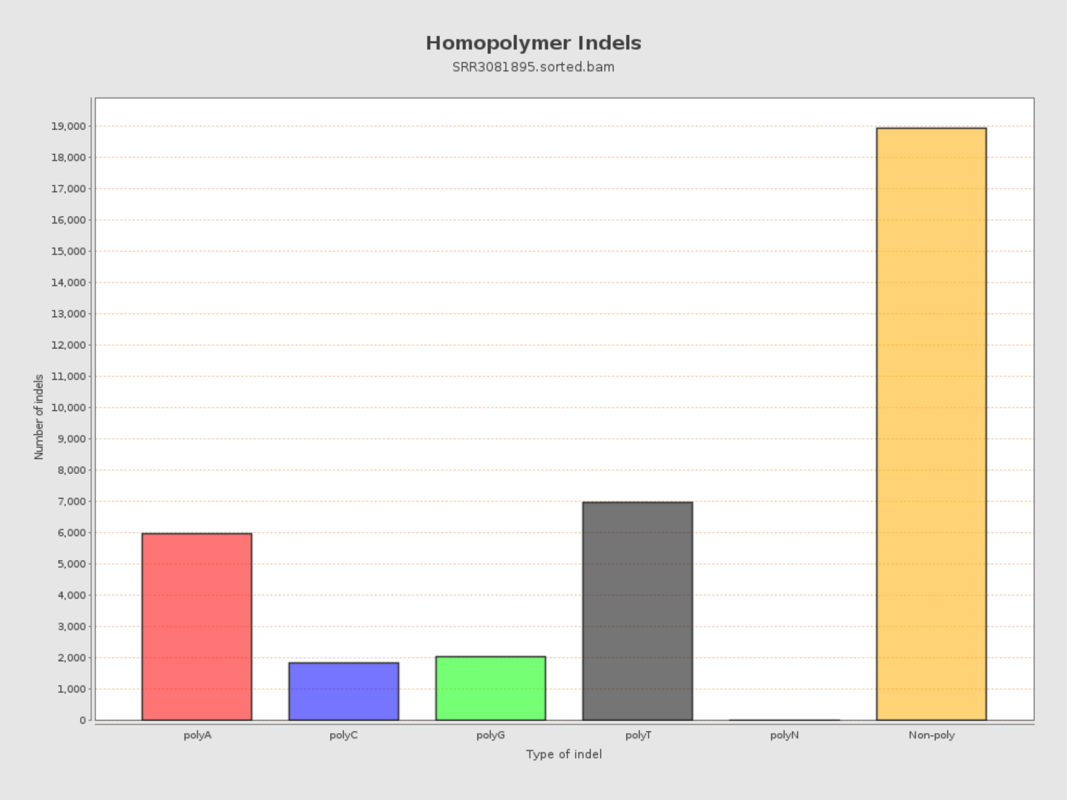
9. Results : Mapped Reads GC-content Distribution



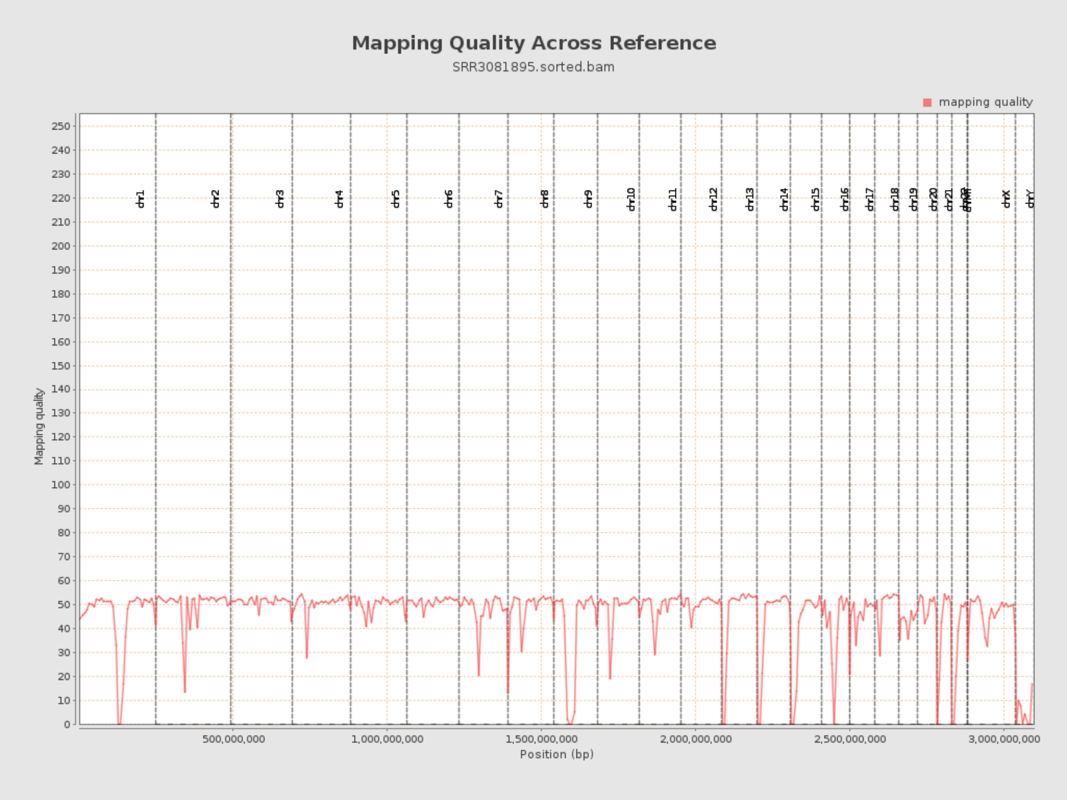
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram