Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:31:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080796.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_SRR3080796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080796.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:31:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,565,970
Mapped reads	2,353,265 / 91.71%
Unmapped reads	212,705 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,070 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	156,642 / 6.1%
Duplication rate	5.71%
Clipped reads	901,814 / 35.15%

2.2. ACGT Content

Number/percentage of A's	45,633,877 / 28.43%
Number/percentage of C's	29,760,809 / 18.54%
Number/percentage of T's	50,953,983 / 31.74%
Number/percentage of G's	34,164,220 / 21.28%
Number/percentage of N's	23,001 / 0.01%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0519

Standard Deviation	0.3682

2.4. Mapping Quality

Mean Mapping Quality	47.15

2.5. Mismatches and indels

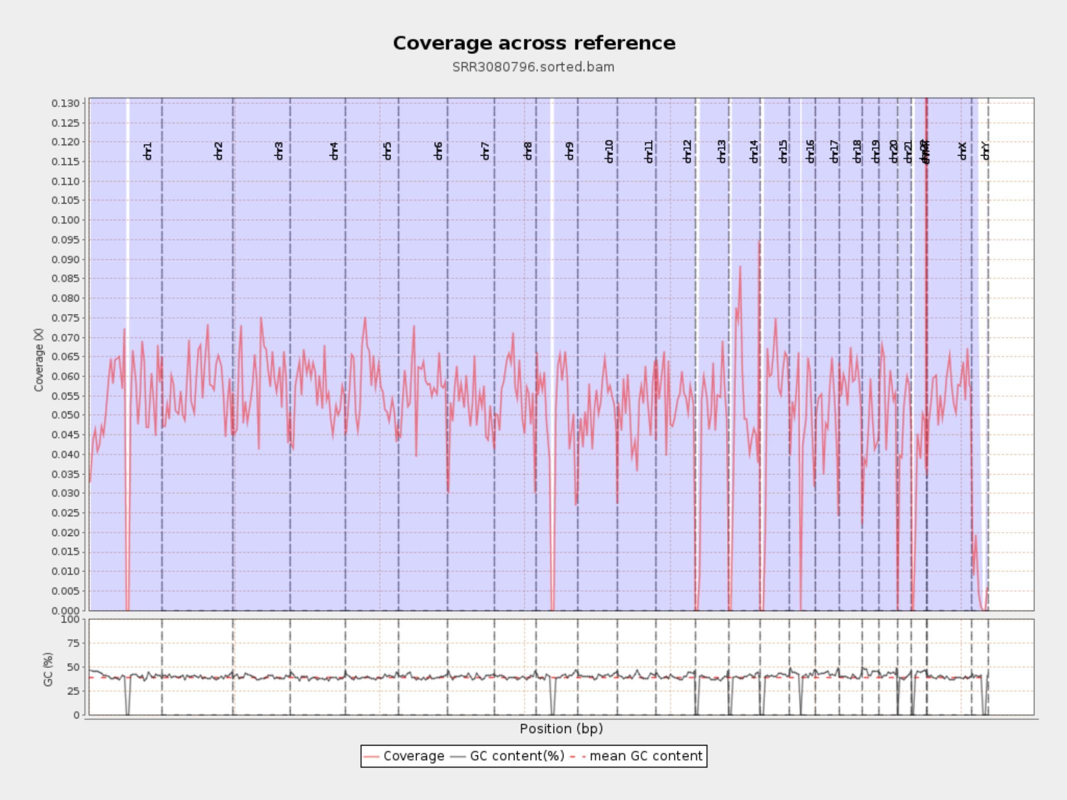
General error rate	0.8%
Mismatches	1,267,776
Insertions	11,973
Mapped reads with at least one insertion	0.5%
Deletions	32,934
Mapped reads with at least one deletion	1.39%
Homopolymer indels	48.72%

2.6. Chromosome stats

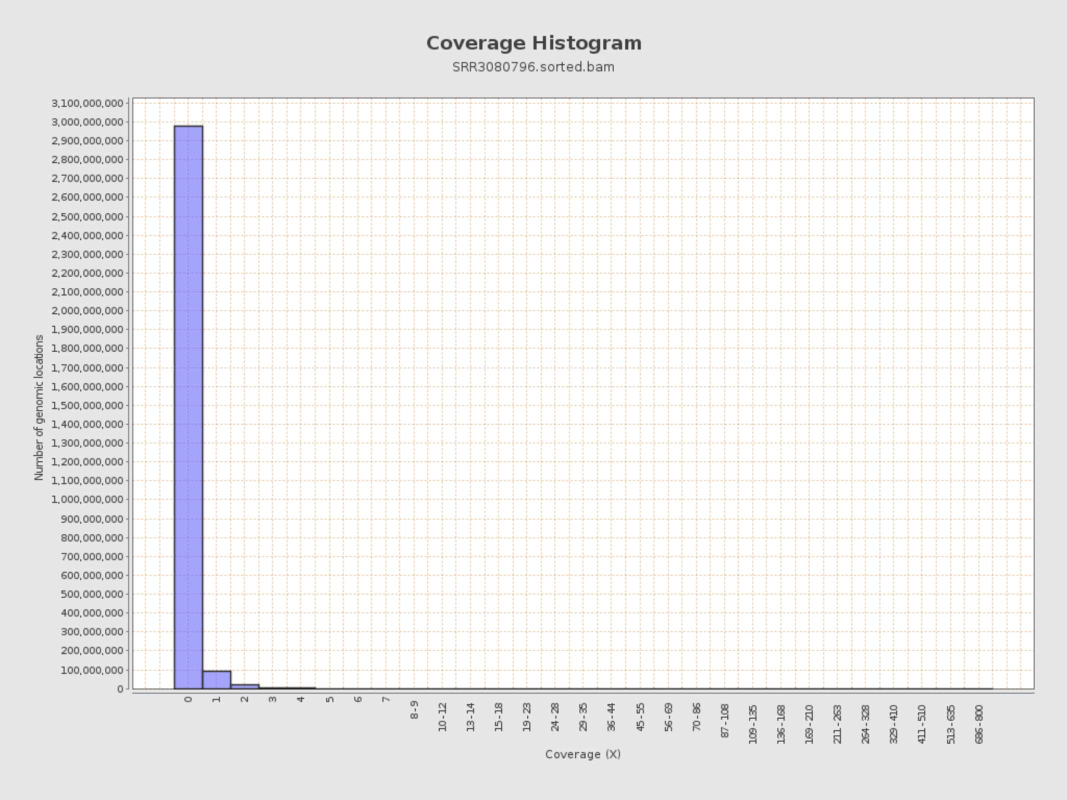
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12848209	0.0515	0.554
chr2	243199373	13806263	0.0568	0.4219
chr3	198022430	11480208	0.058	0.3064
chr4	191154276	10733132	0.0561	0.3094
chr5	180915260	10306926	0.057	0.3032
chr6	171115067	9727978	0.0569	0.341
chr7	159138663	8336903	0.0524	0.3518

chr8	146364022	8055589	0.055	0.5668
chr9	141213431	6667344	0.0472	0.3281
chr10	135534747	7049009	0.052	0.3457
chr11	135006516	6979247	0.0517	0.307
chr12	133851895	7274953	0.0544	0.2986
chr13	115169878	5239803	0.0455	0.2723
chr14	107349540	5058896	0.0471	0.2887
chr15	102531392	5215132	0.0509	0.2874
chr16	90354753	4240121	0.0469	0.2957
chr17	81195210	3970298	0.0489	0.2968
chr18	78077248	4615677	0.0591	0.545
chr19	59128983	2606009	0.0441	0.4216
chr20	63025520	3516106	0.0558	0.3053
chr21	48129895	2157054	0.0448	0.2833
chr22	51304566	1635073	0.0319	0.2256
chrMT	16571	64038	3.8645	2.941
chrX	155270560	8622188	0.0555	0.307
chrY	59373566	387927	0.0065	0.1551

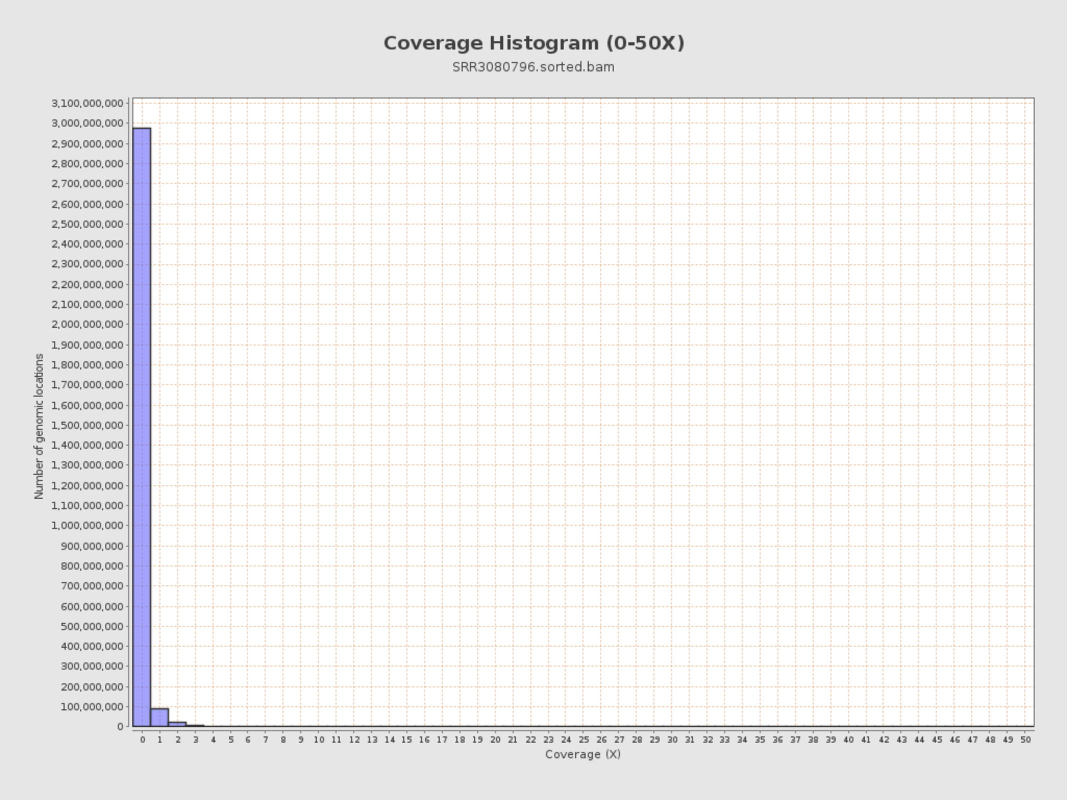
3. Results : Coverage across reference



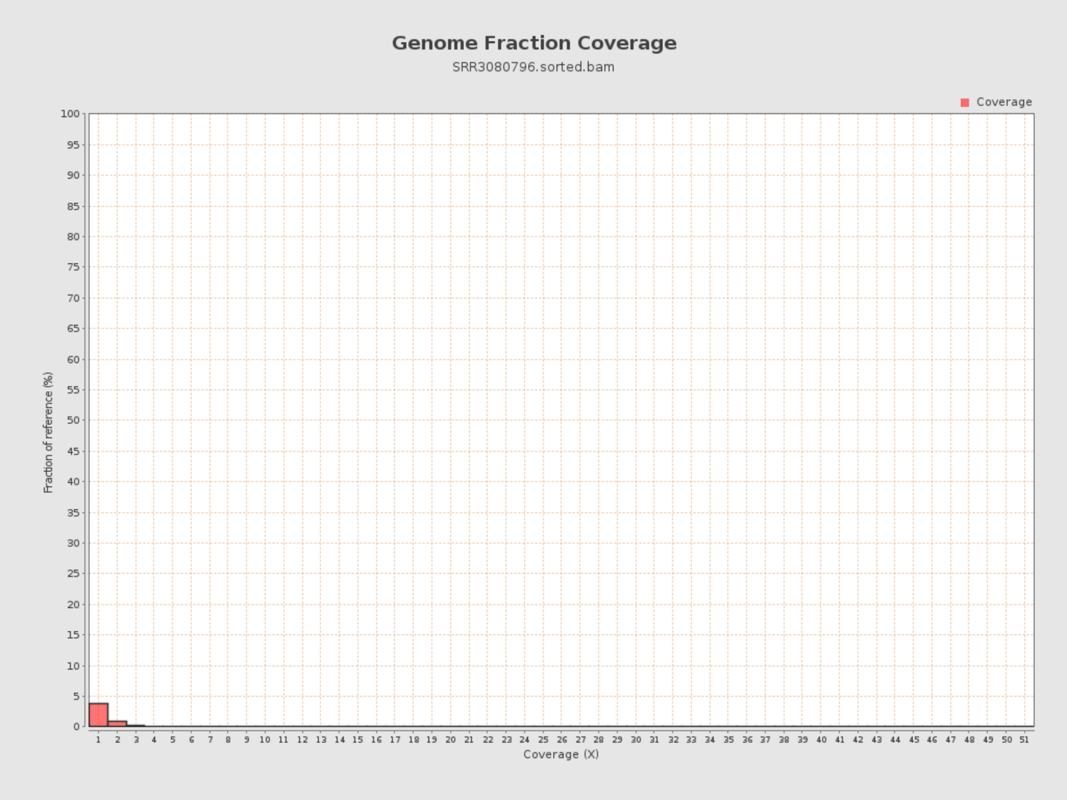
4. Results : Coverage Histogram



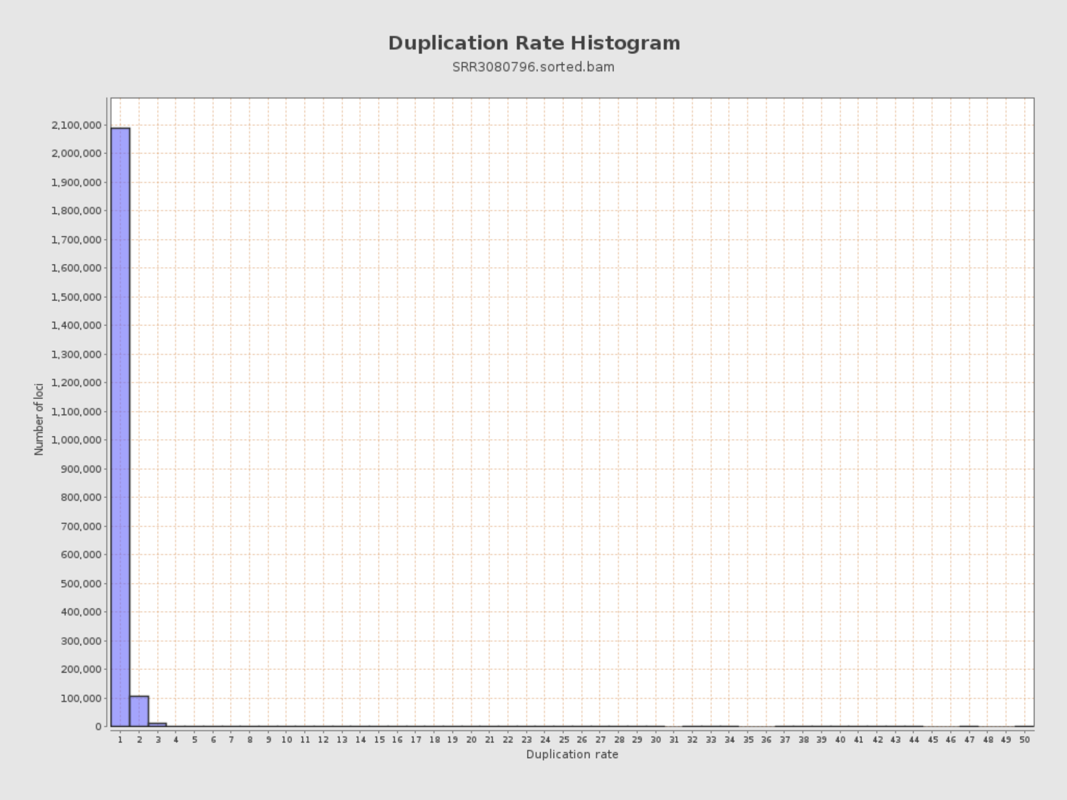
5. Results : Coverage Histogram (0-50X)



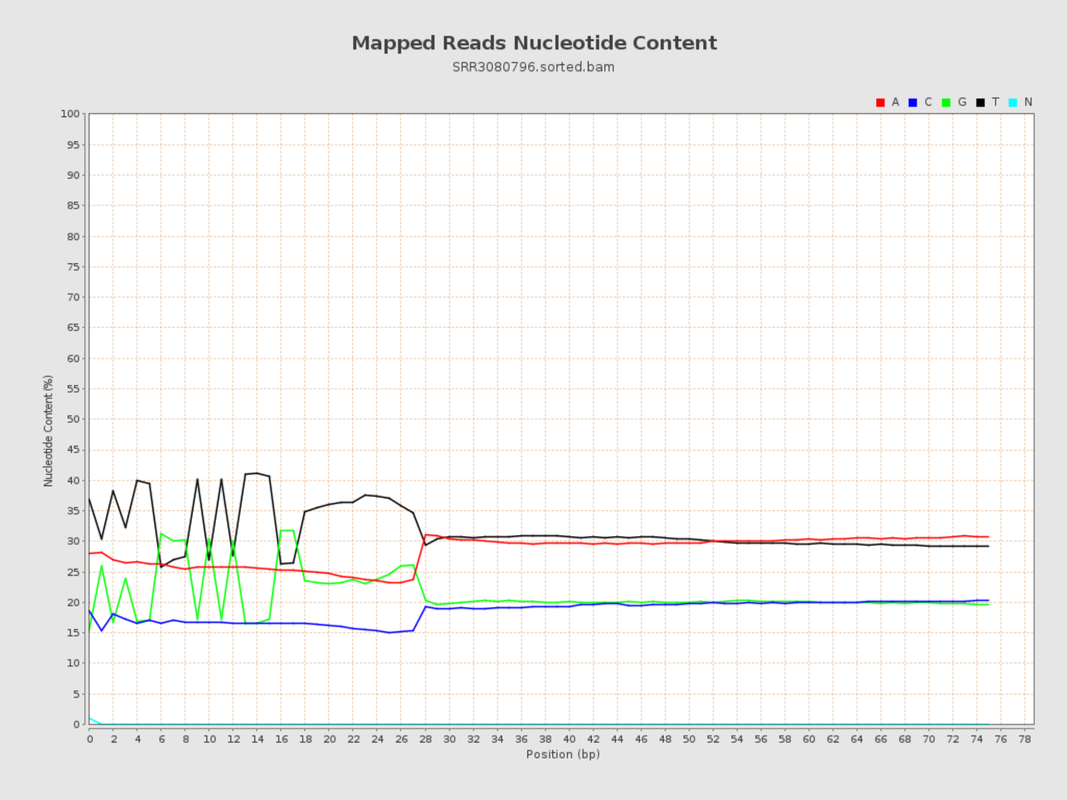
6. Results : Genome Fraction Coverage



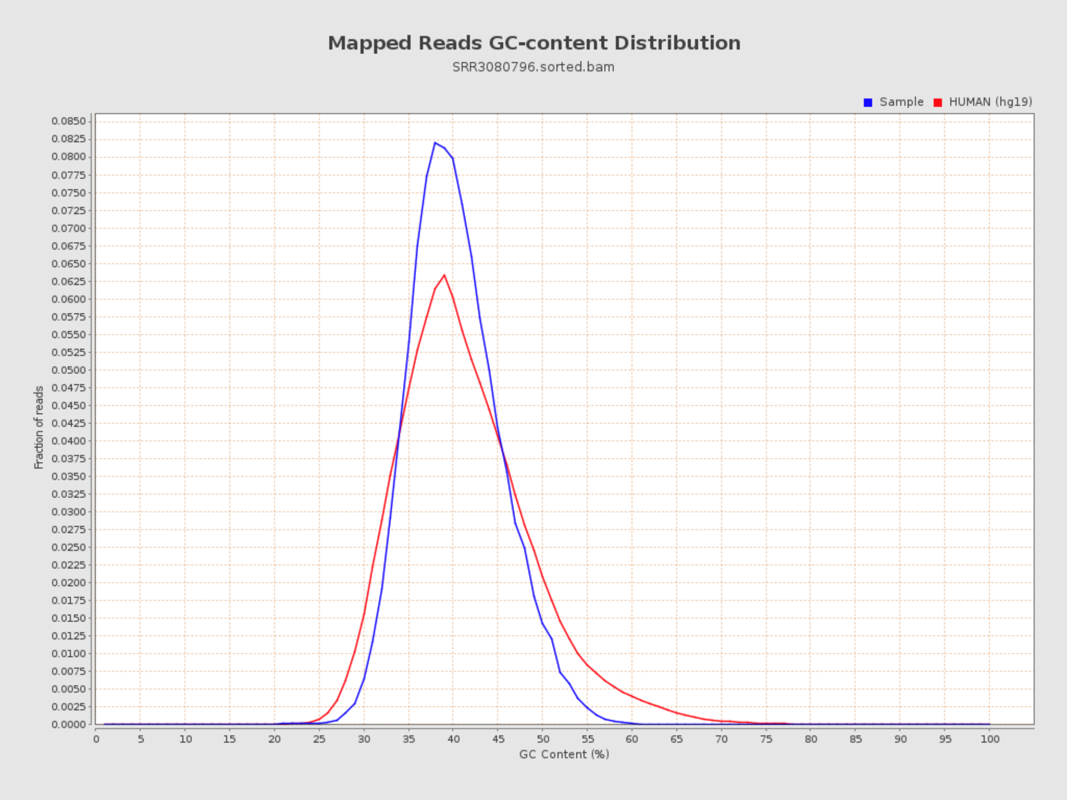
7. Results : Duplication Rate Histogram



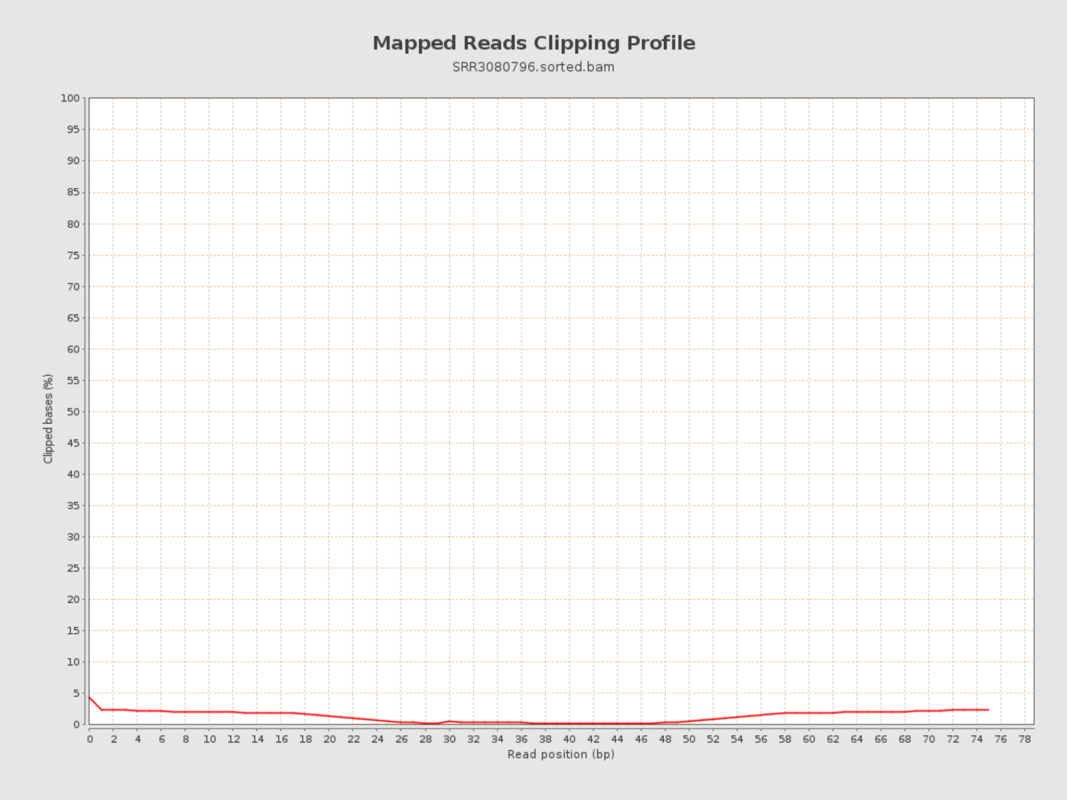
8. Results : Mapped Reads Nucleotide Content



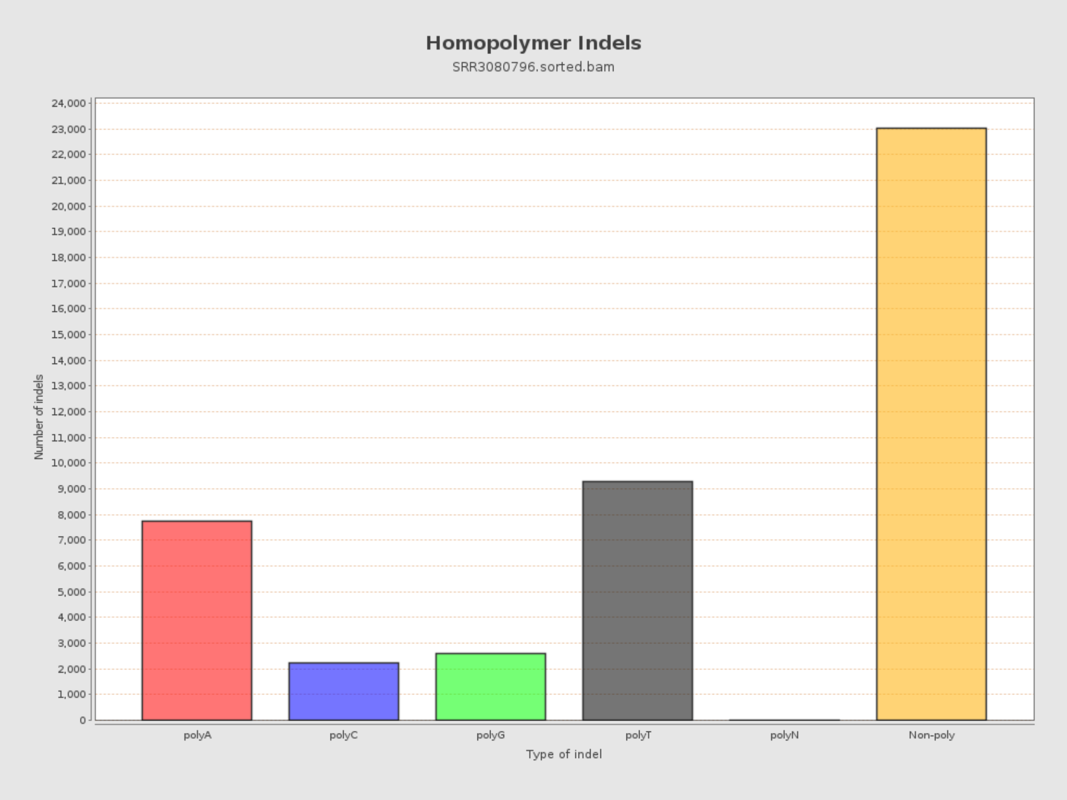
9. Results : Mapped Reads GC-content Distribution



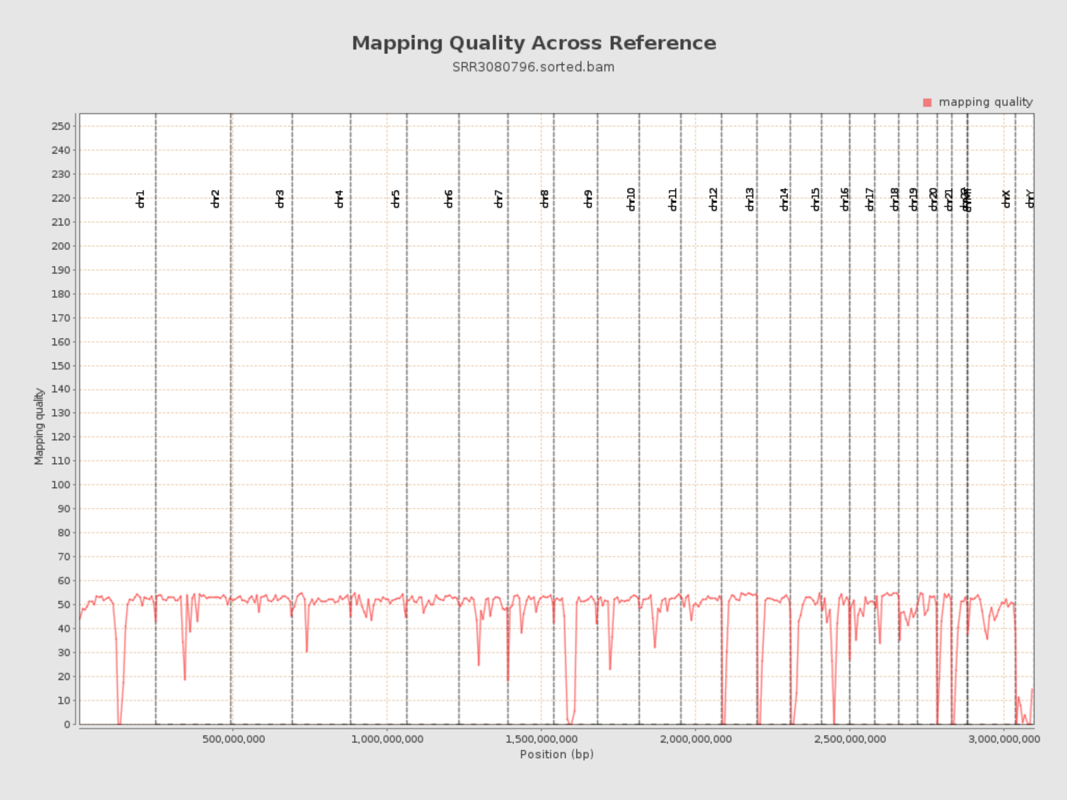
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram