Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:46:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081732.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_SRR3081732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081732.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:46:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,730,705
Mapped reads	2,490,233 / 91.19%
Unmapped reads	240,472 / 8.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,184 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	99,090 / 3.63%
Duplication rate	3.09%
Clipped reads	1,066,874 / 39.07%

2.2. ACGT Content

Number/percentage of A's	45,562,124 / 27.26%
Number/percentage of C's	32,619,938 / 19.52%
Number/percentage of T's	50,670,317 / 30.32%
Number/percentage of G's	38,269,680 / 22.9%
Number/percentage of N's	1,755 / 0%
GC Percentage	42.42%

2.3. Coverage

Mean	0.054

Standard Deviation	0.4022

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

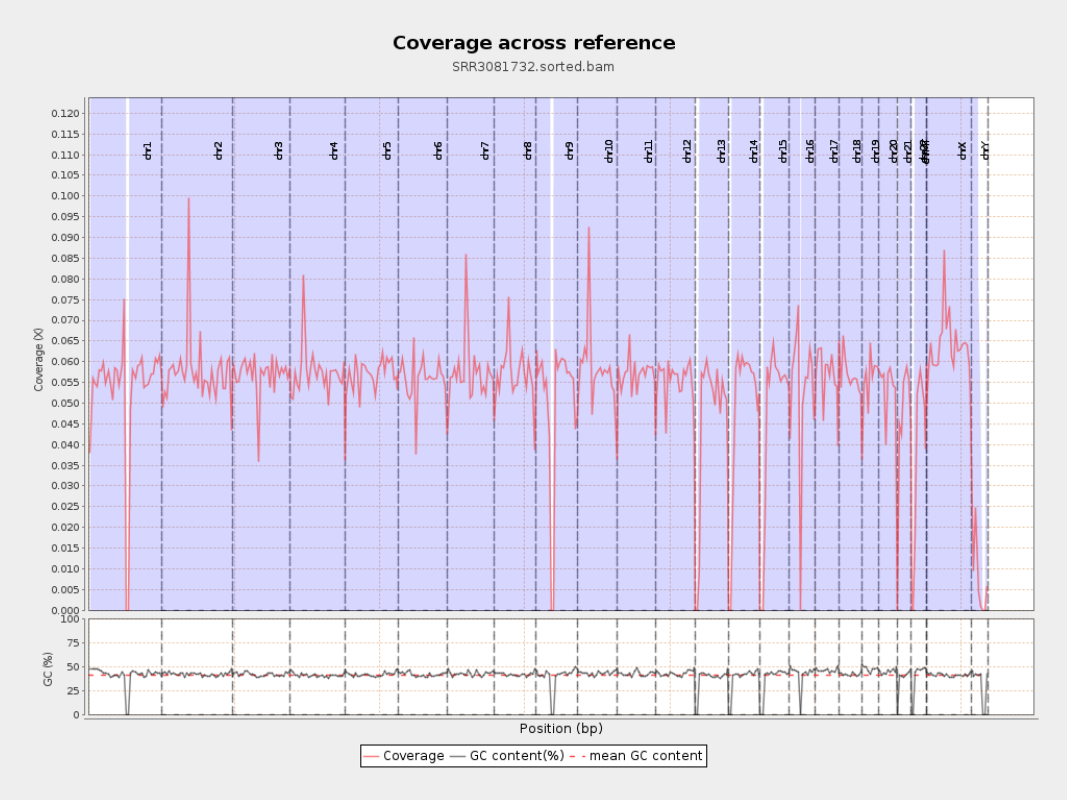
General error rate	0.82%
Mismatches	1,354,845
Insertions	12,209
Mapped reads with at least one insertion	0.49%
Deletions	32,116
Mapped reads with at least one deletion	1.28%
Homopolymer indels	46.37%

2.6. Chromosome stats

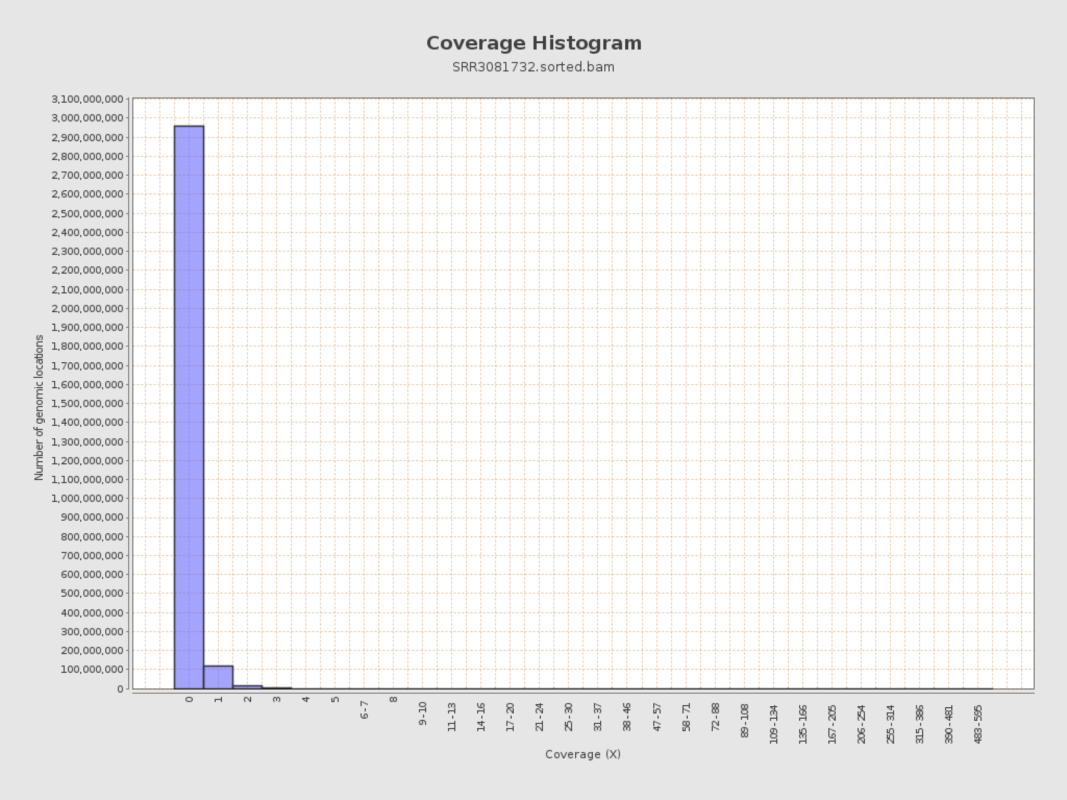
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13266752	0.0532	0.5882
chr2	243199373	14013870	0.0576	0.5476
chr3	198022430	11256946	0.0568	0.2784
chr4	191154276	10979085	0.0574	0.3111
chr5	180915260	10322776	0.0571	0.2779
chr6	171115067	9547226	0.0558	0.3131
chr7	159138663	9222865	0.058	0.524

chr8	146364022	8312646	0.0568	0.4604
chr9	141213431	7076527	0.0501	0.4028
chr10	135534747	7931431	0.0585	0.456
chr11	135006516	7672635	0.0568	0.3663
chr12	133851895	7433586	0.0555	0.276
chr13	115169878	5213324	0.0453	0.2477
chr14	107349540	5159162	0.0481	0.2729
chr15	102531392	4808274	0.0469	0.2567
chr16	90354753	4793879	0.0531	0.3193
chr17	81195210	4601126	0.0567	0.295
chr18	78077248	4459014	0.0571	0.7052
chr19	59128983	3312626	0.056	0.5054
chr20	63025520	3339670	0.053	0.276
chr21	48129895	2210100	0.0459	0.2816
chr22	51304566	1873868	0.0365	0.2207
chrMT	16571	988	0.0596	0.2426
chrX	155270560	9903383	0.0638	0.3335
chrY	59373566	469558	0.0079	0.2001

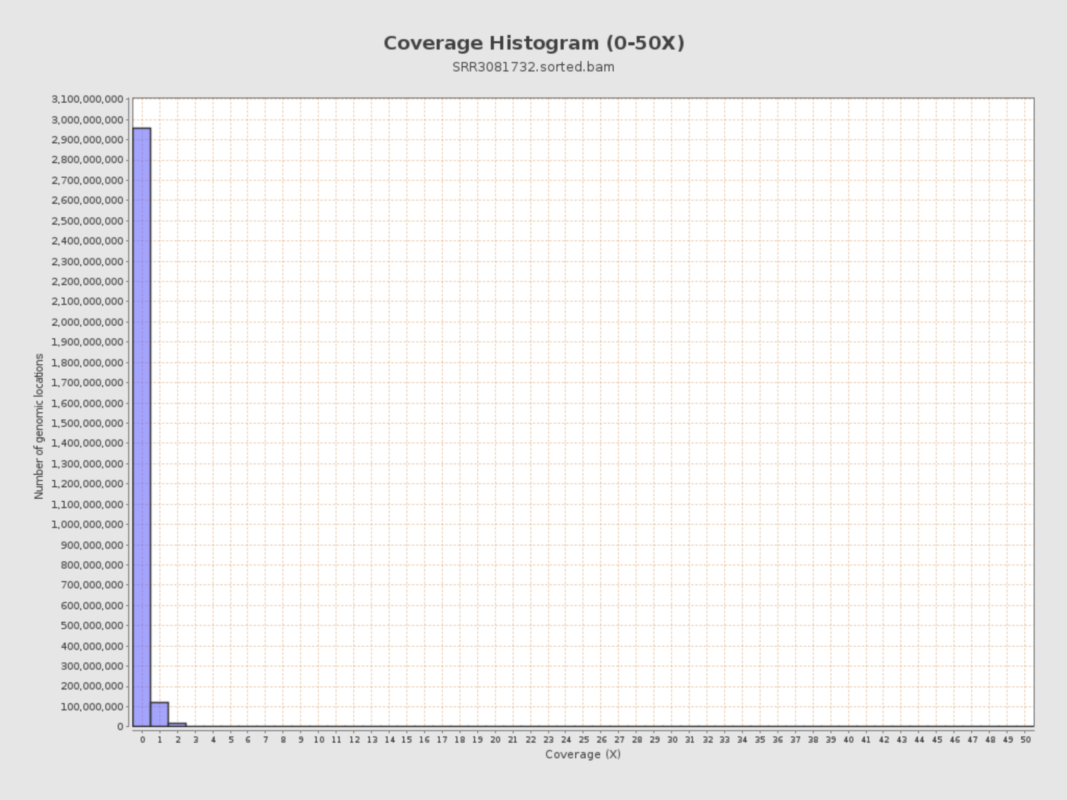
3. Results : Coverage across reference



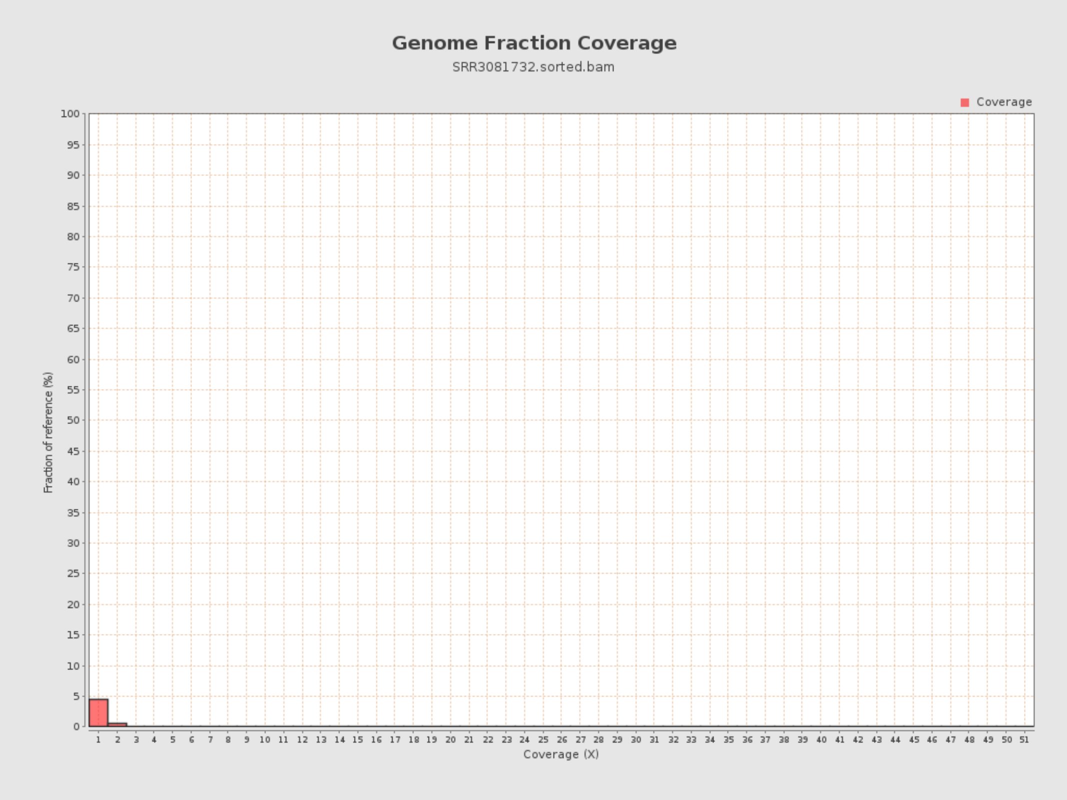
4. Results : Coverage Histogram



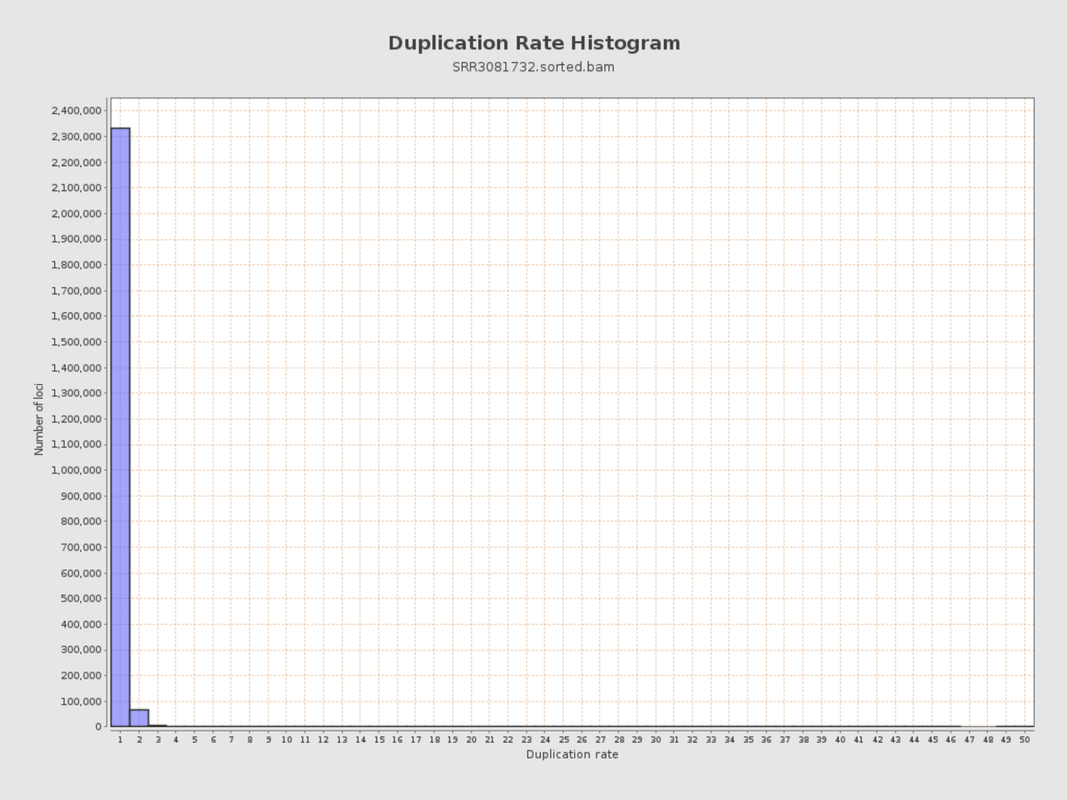
5. Results : Coverage Histogram (0-50X)



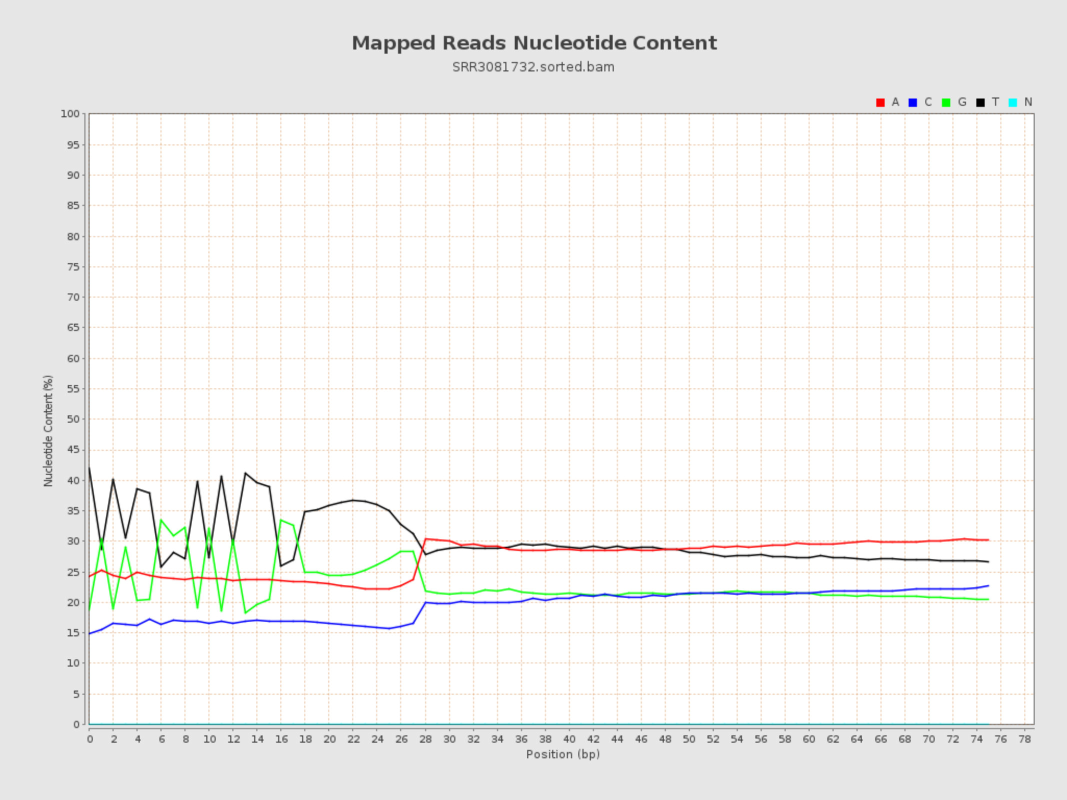
6. Results : Genome Fraction Coverage



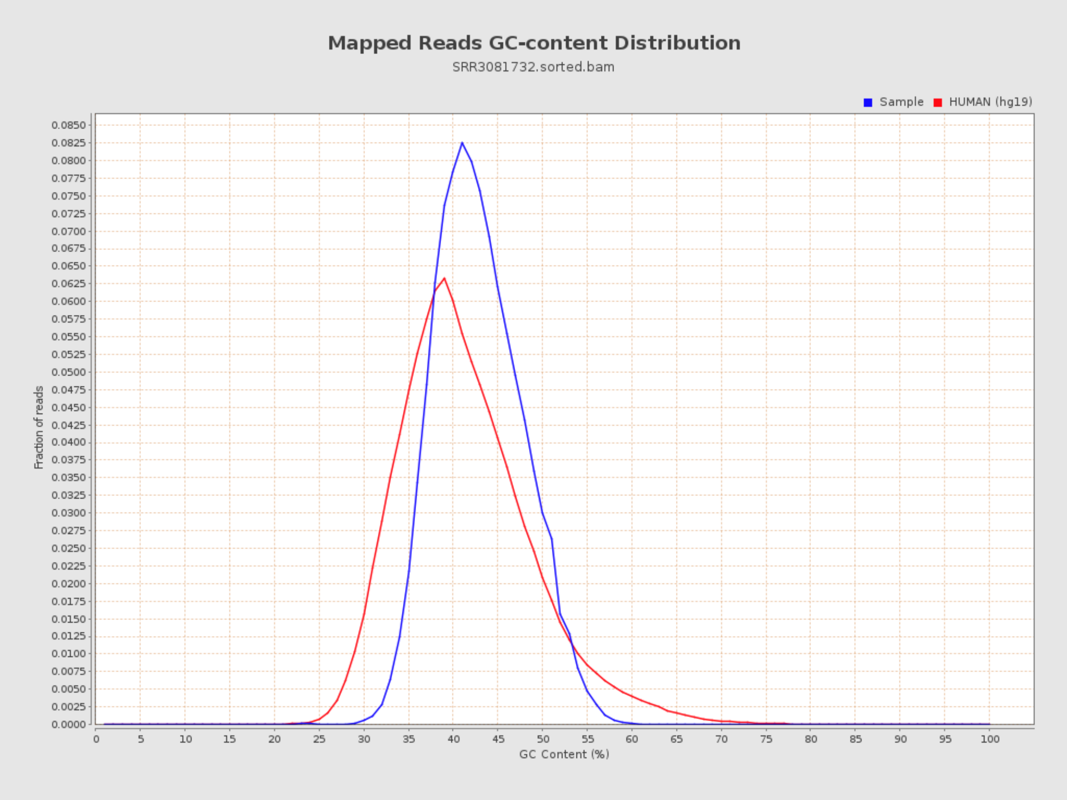
7. Results : Duplication Rate Histogram



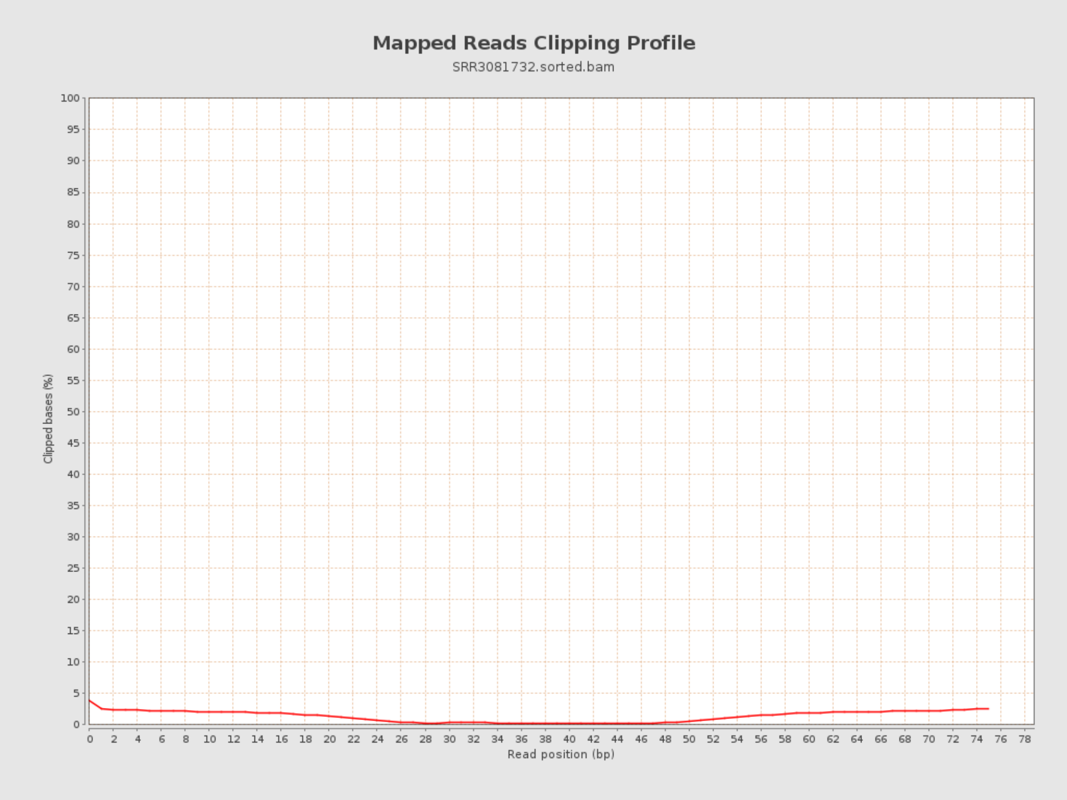
8. Results : Mapped Reads Nucleotide Content



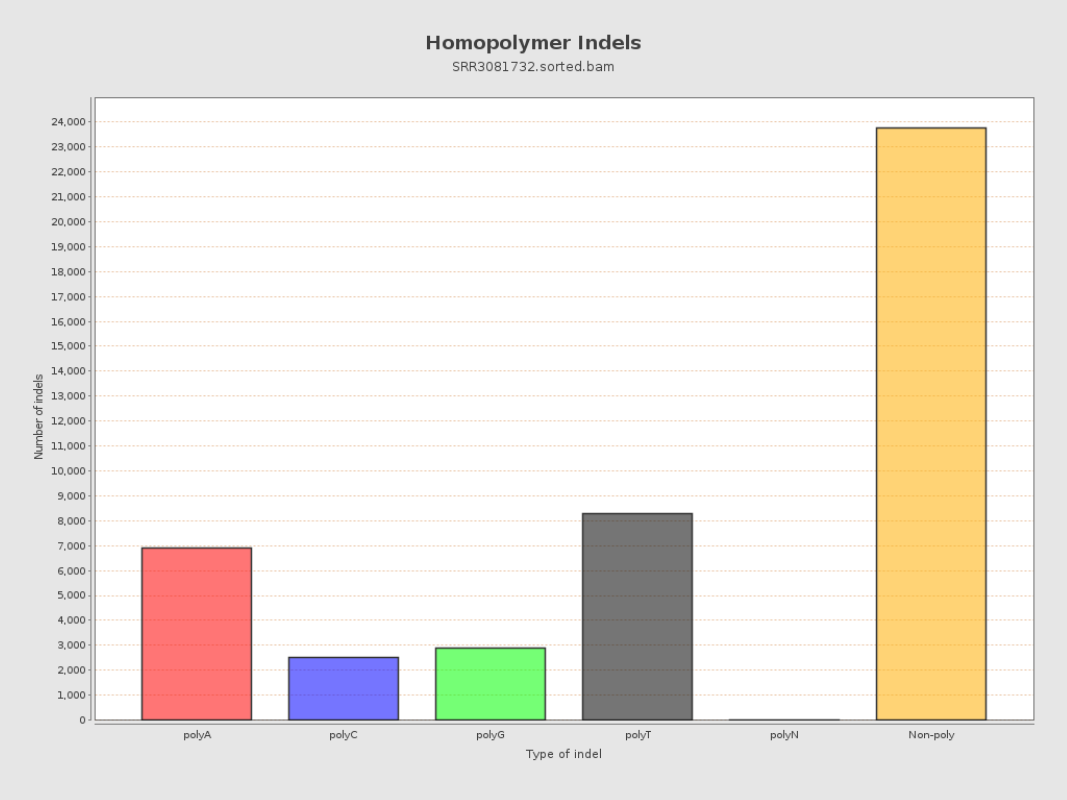
9. Results : Mapped Reads GC-content Distribution



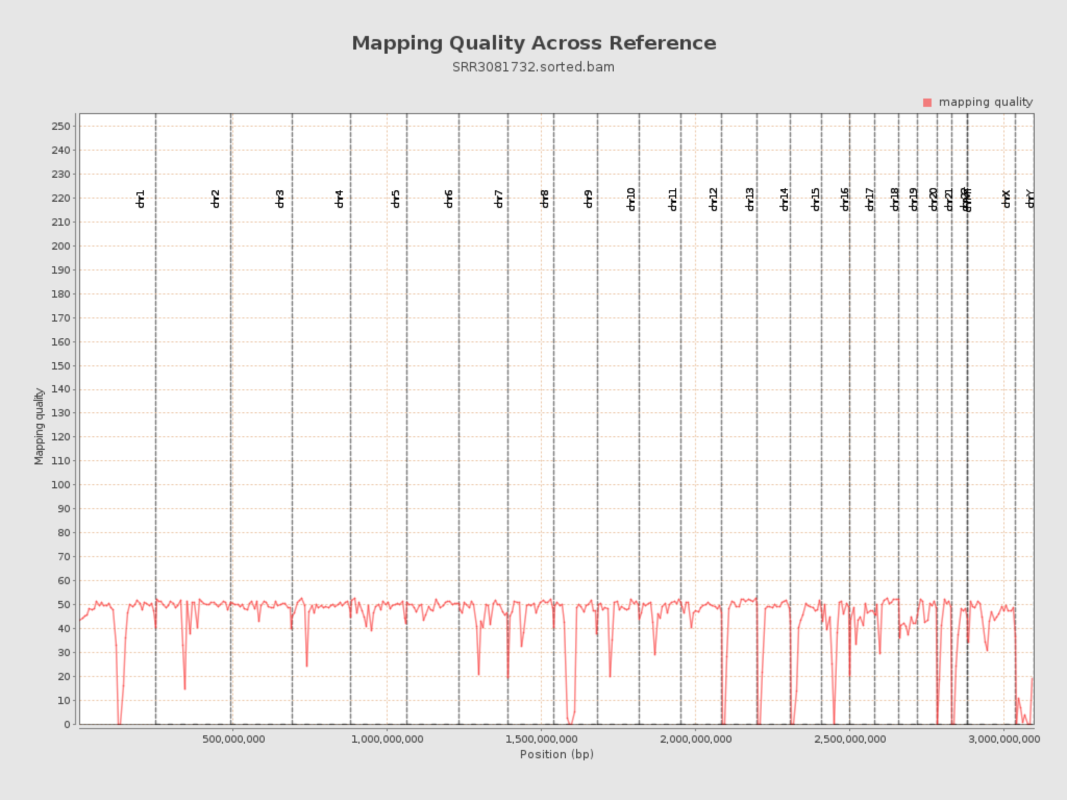
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram