Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:01:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081736.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_SRR3081736 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081736.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:01:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081736.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,642,489
Mapped reads	2,413,751 / 91.34%
Unmapped reads	228,738 / 8.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,988 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	90,784 / 3.44%
Duplication rate	3%
Clipped reads	987,920 / 37.39%

2.2. ACGT Content

Number/percentage of A's	44,972,217 / 27.59%
Number/percentage of C's	31,431,165 / 19.28%
Number/percentage of T's	49,879,507 / 30.6%
Number/percentage of G's	36,739,653 / 22.54%
Number/percentage of N's	1,881 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.3737

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

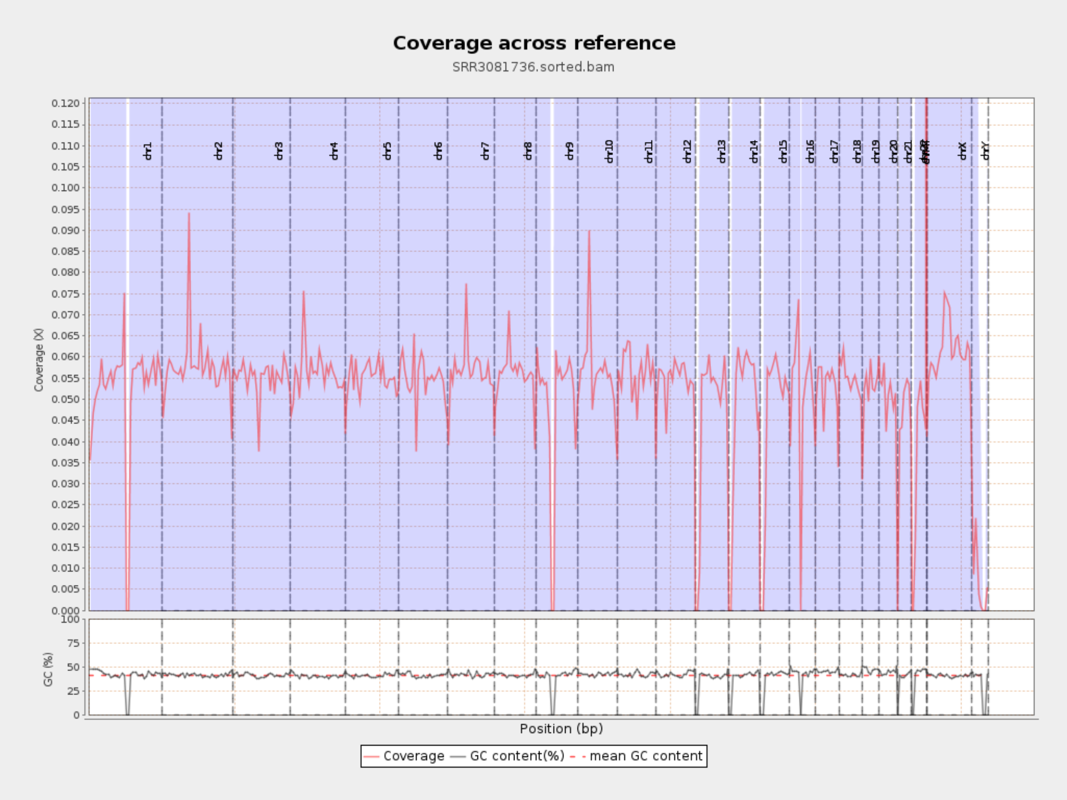
General error rate	0.8%
Mismatches	1,278,210
Insertions	11,583
Mapped reads with at least one insertion	0.47%
Deletions	32,486
Mapped reads with at least one deletion	1.33%
Homopolymer indels	46.47%

2.6. Chromosome stats

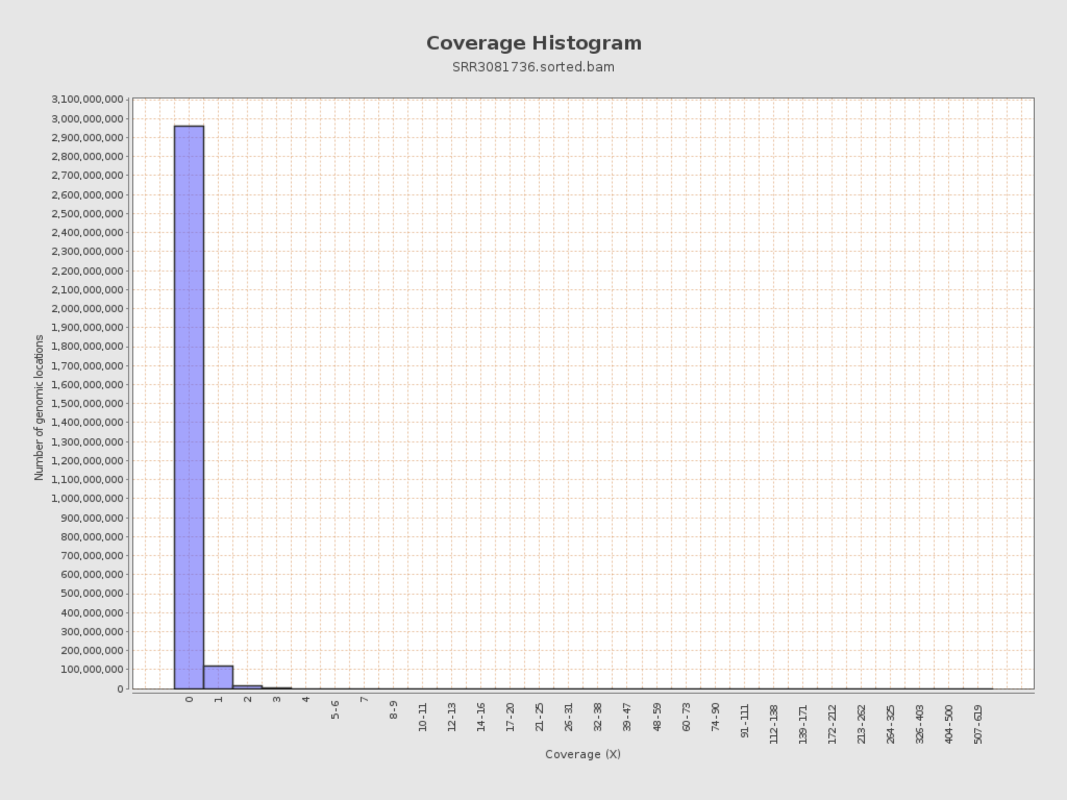
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12970435	0.052	0.5824
chr2	243199373	14084666	0.0579	0.4731
chr3	198022430	10938110	0.0552	0.2711
chr4	191154276	10735928	0.0562	0.2999
chr5	180915260	10013938	0.0554	0.2689
chr6	171115067	9398149	0.0549	0.2939
chr7	159138663	9086217	0.0571	0.4483

chr8	146364022	8167667	0.0558	0.4122
chr9	141213431	6807654	0.0482	0.3605
chr10	135534747	7712866	0.0569	0.4373
chr11	135006516	7590858	0.0562	0.3383
chr12	133851895	7319940	0.0547	0.2693
chr13	115169878	5225027	0.0454	0.243
chr14	107349540	5060164	0.0471	0.2613
chr15	102531392	4611037	0.045	0.2473
chr16	90354753	4662022	0.0516	0.3024
chr17	81195210	4256209	0.0524	0.2888
chr18	78077248	4311122	0.0552	0.6207
chr19	59128983	3141758	0.0531	0.4955
chr20	63025520	3178645	0.0504	0.2684
chr21	48129895	2108164	0.0438	0.2636
chr22	51304566	1733733	0.0338	0.2105
chrMT	16571	29655	1.7896	1.6624
chrX	155270560	9520385	0.0613	0.3123
chrY	59373566	418174	0.007	0.1778

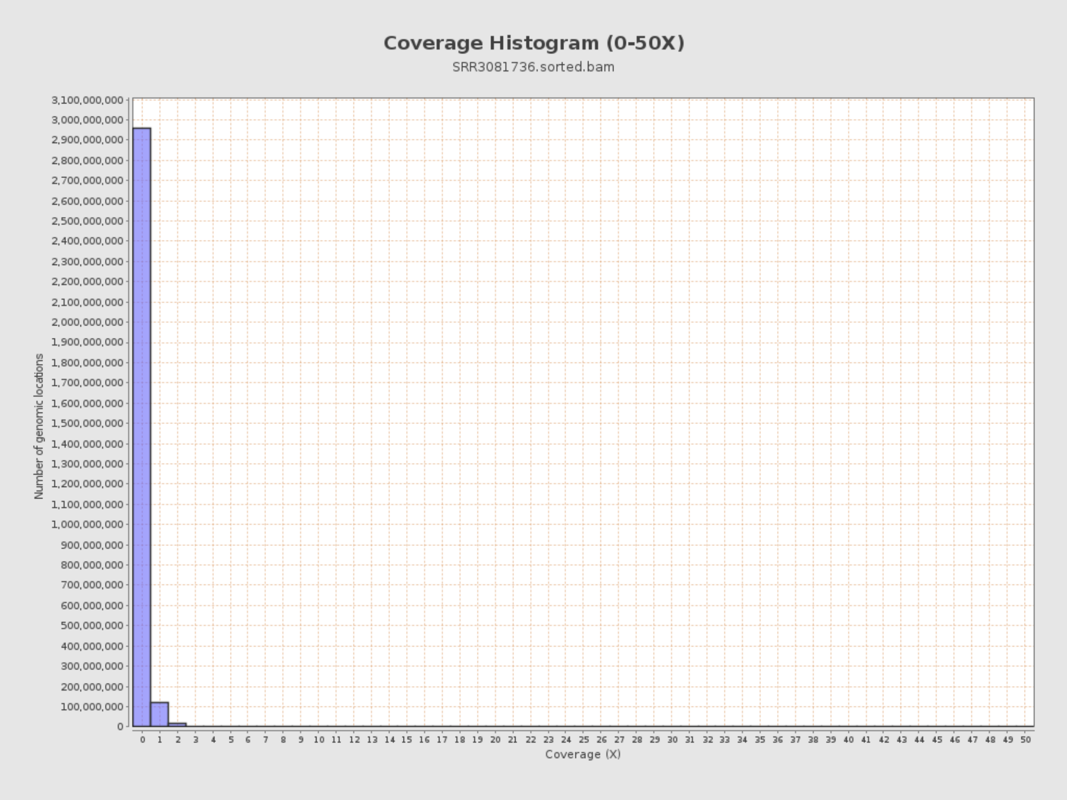
3. Results : Coverage across reference



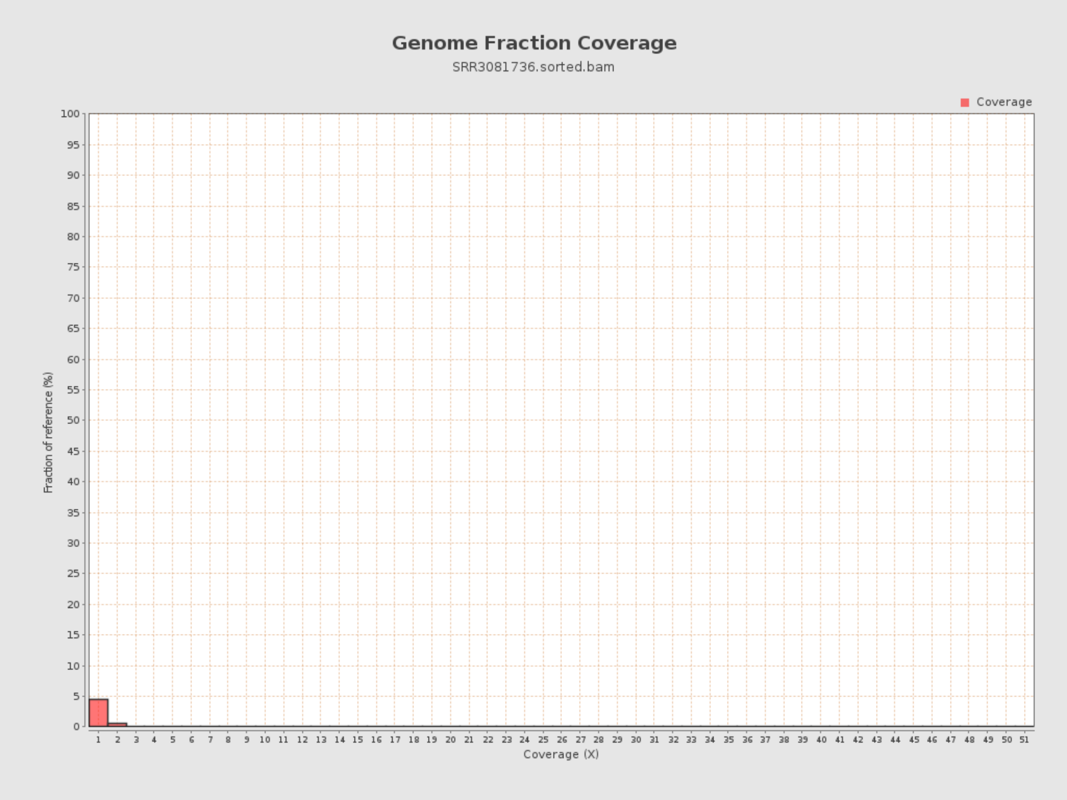
4. Results : Coverage Histogram



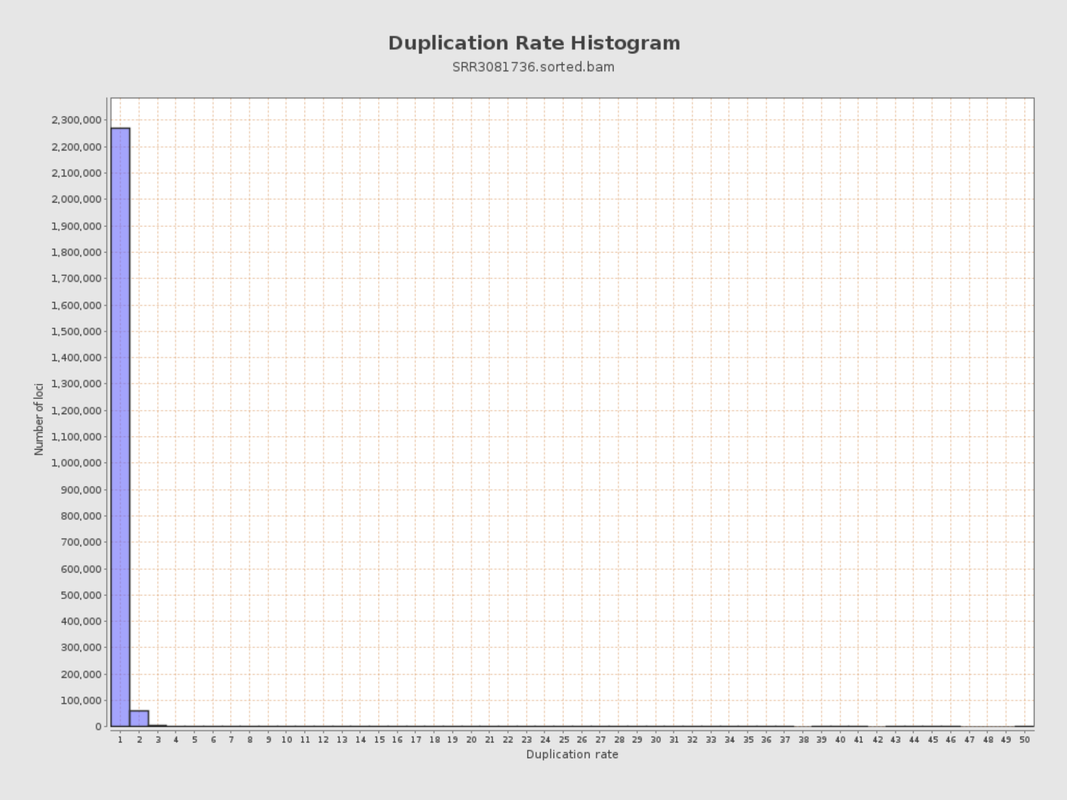
5. Results : Coverage Histogram (0-50X)



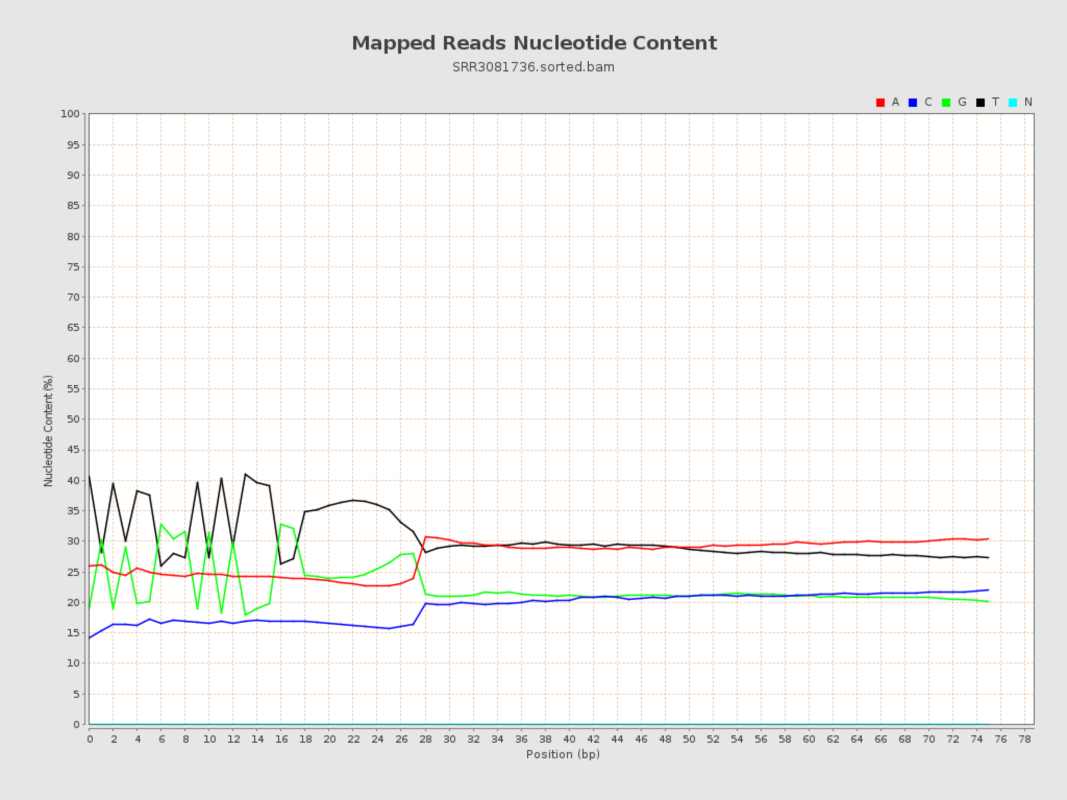
6. Results : Genome Fraction Coverage



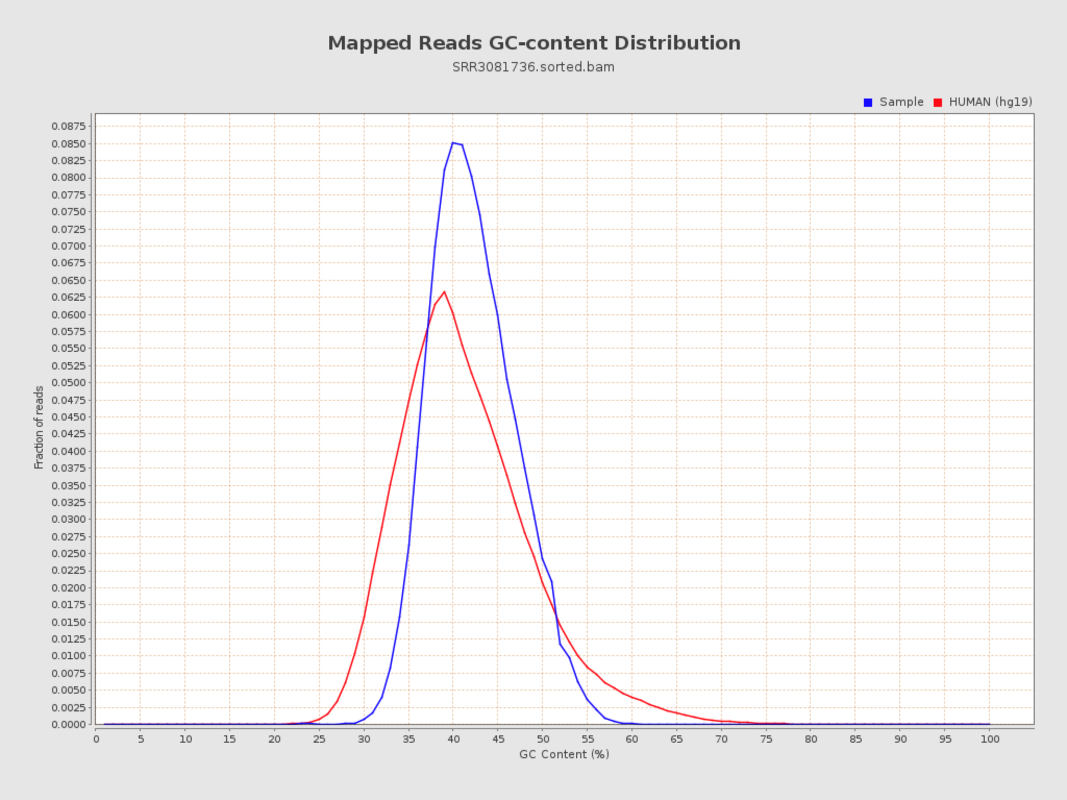
7. Results : Duplication Rate Histogram



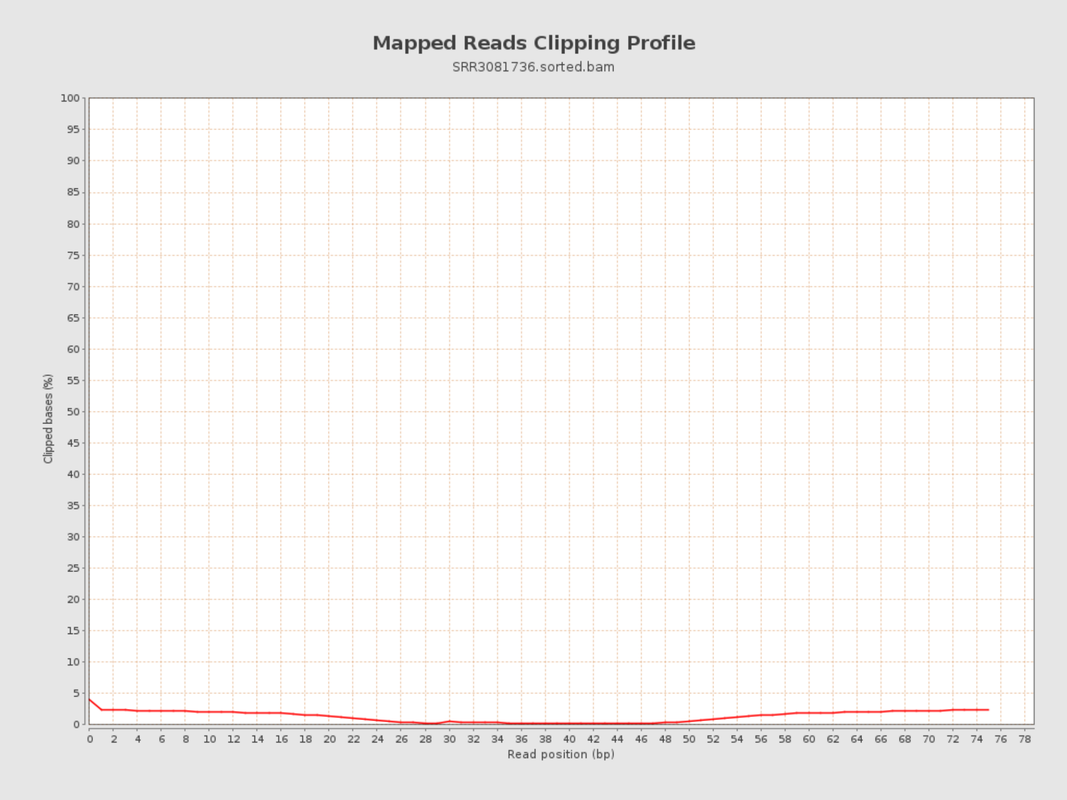
8. Results : Mapped Reads Nucleotide Content



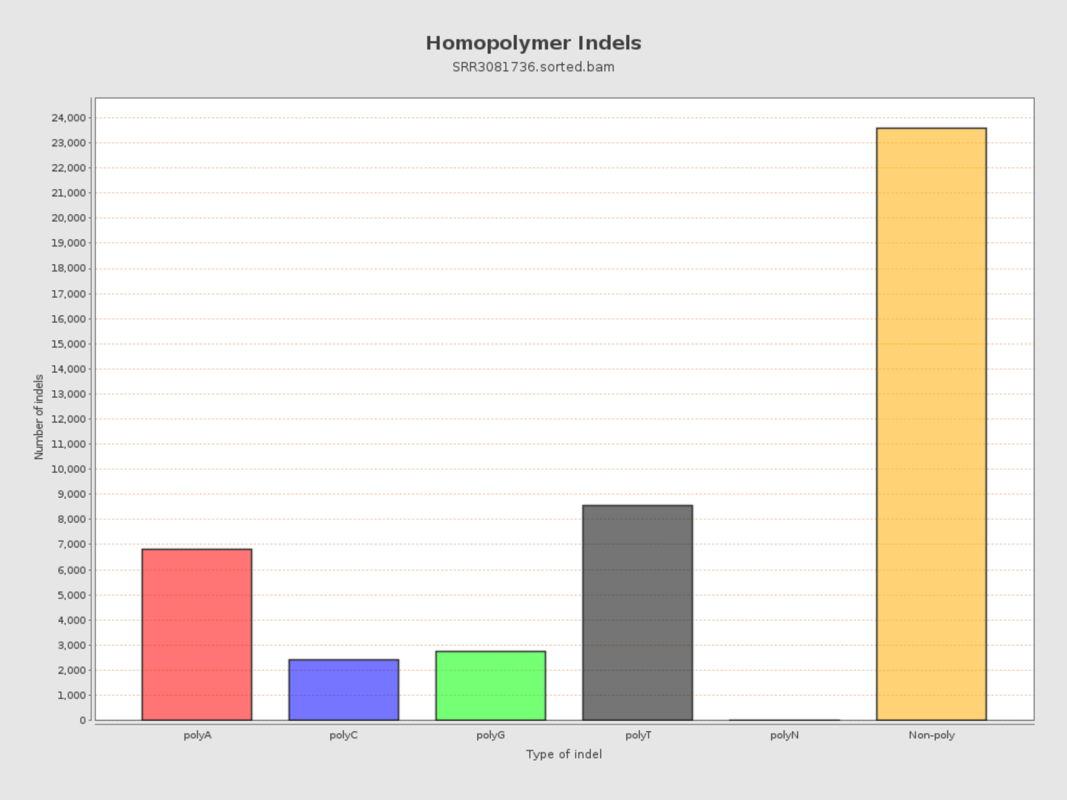
9. Results : Mapped Reads GC-content Distribution



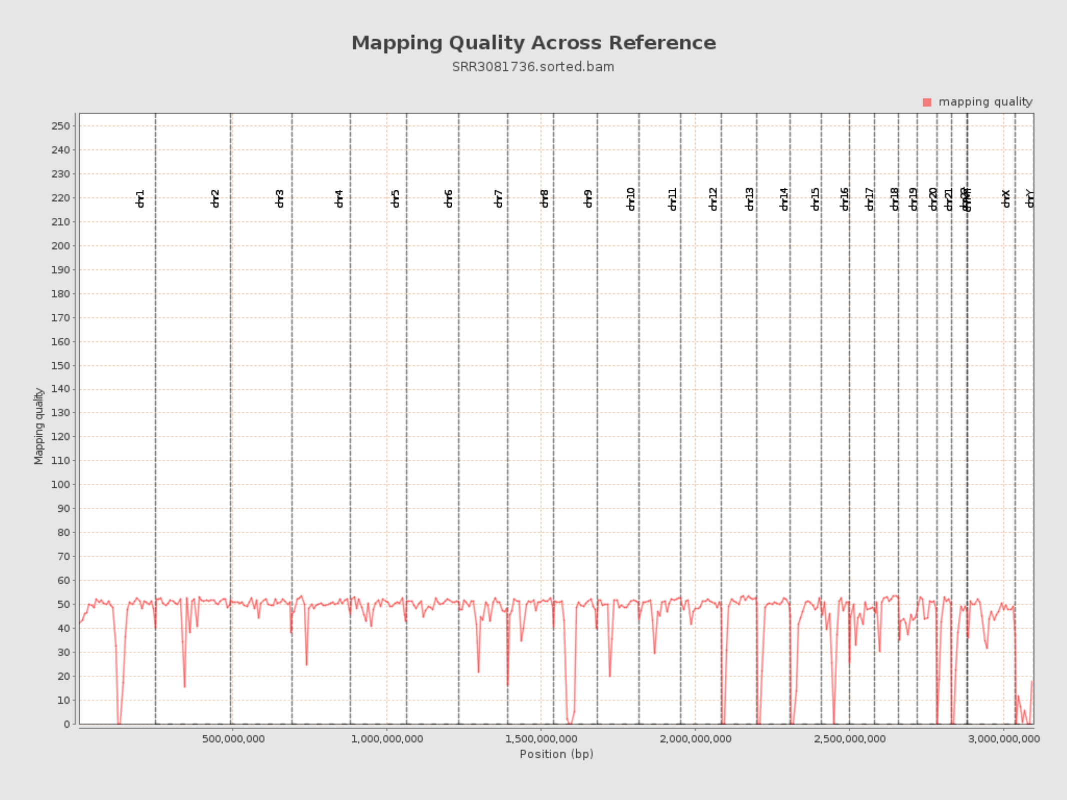
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram