Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:36:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081951.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_SRR3081951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081951.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:36:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,005,636
Mapped reads	2,798,514 / 93.11%
Unmapped reads	207,122 / 6.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,873 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	129,883 / 4.32%
Duplication rate	3.6%
Clipped reads	966,838 / 32.17%

2.2. ACGT Content

Number/percentage of A's	55,274,598 / 28.67%
Number/percentage of C's	35,774,696 / 18.56%
Number/percentage of T's	60,968,889 / 31.62%
Number/percentage of G's	40,752,601 / 21.14%
Number/percentage of N's	25,411 / 0.01%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0623

Standard Deviation	0.5199

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Mismatches and indels

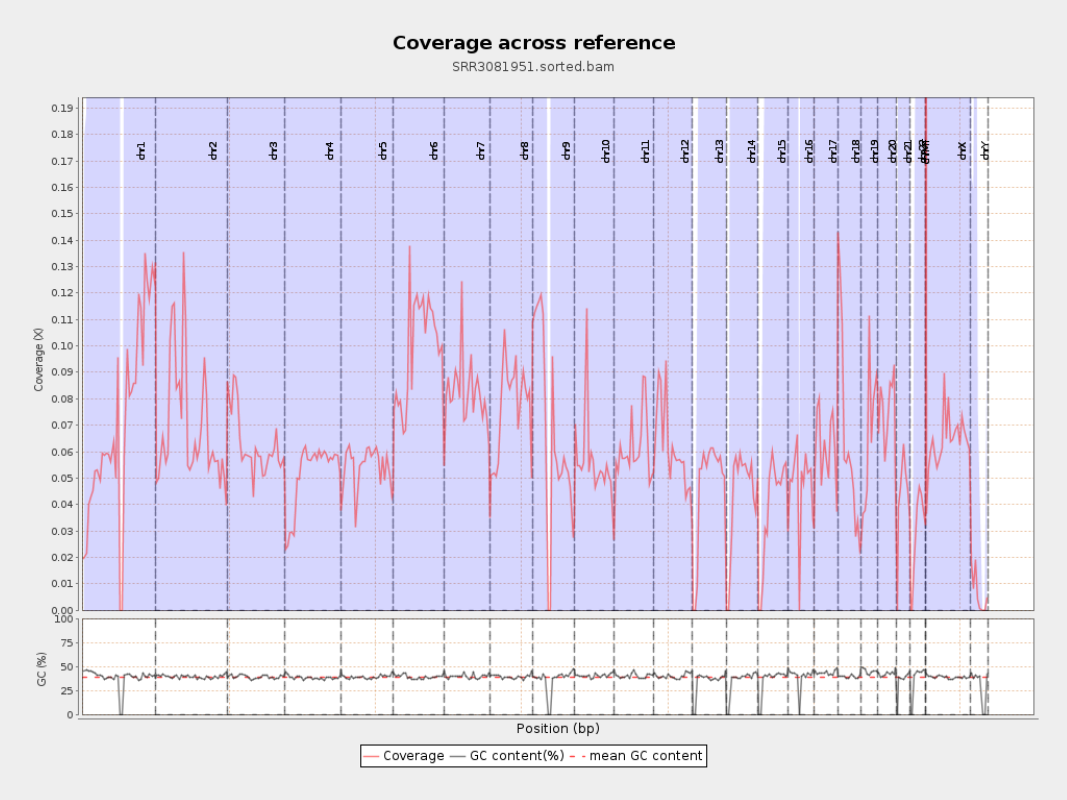
General error rate	0.76%
Mismatches	1,431,698
Insertions	13,504
Mapped reads with at least one insertion	0.48%
Deletions	39,223
Mapped reads with at least one deletion	1.39%
Homopolymer indels	48.22%

2.6. Chromosome stats

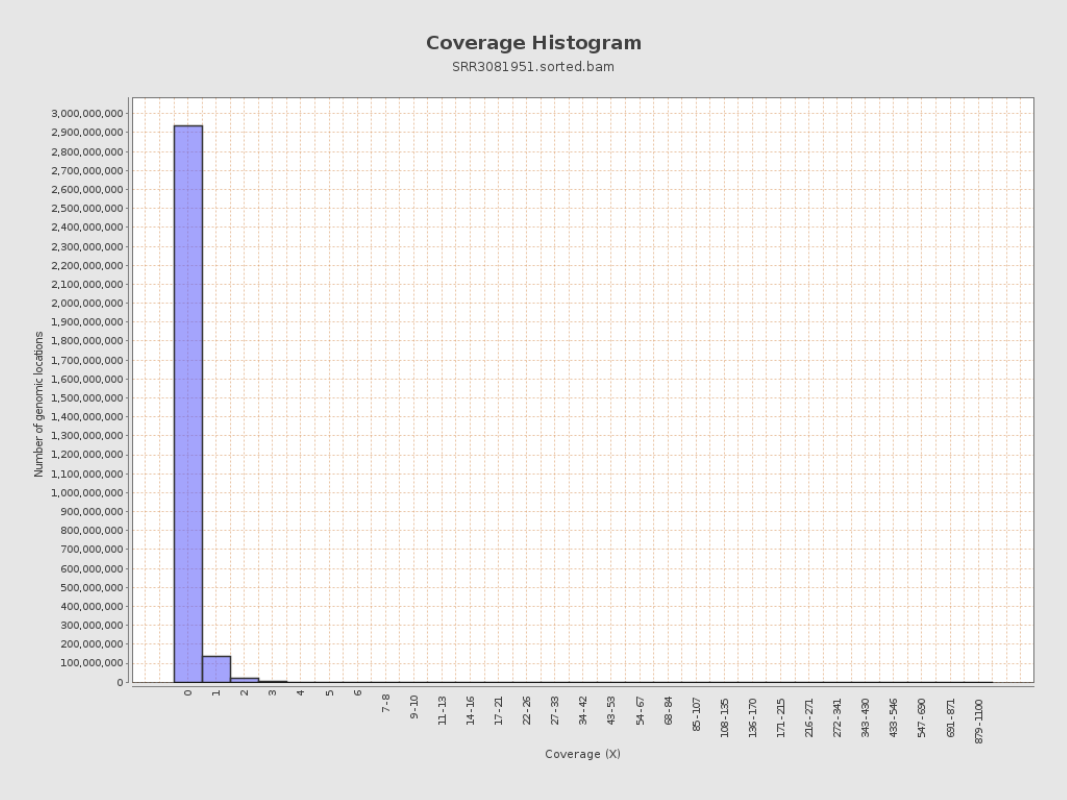
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17851578	0.0716	0.9605
chr2	243199373	17059870	0.0701	0.6347
chr3	198022430	12439889	0.0628	0.2911
chr4	191154276	9842609	0.0515	0.2746
chr5	180915260	9731526	0.0538	0.2692
chr6	171115067	17083448	0.0998	0.505
chr7	159138663	13054609	0.082	0.7517

chr8	146364022	11273848	0.077	0.7608
chr9	141213431	9483619	0.0672	0.5122
chr10	135534747	7662172	0.0565	0.4953
chr11	135006516	8293928	0.0614	0.3706
chr12	133851895	8224342	0.0614	0.2953
chr13	115169878	5376094	0.0467	0.2469
chr14	107349540	4708883	0.0439	0.2758
chr15	102531392	3922386	0.0383	0.2252
chr16	90354753	4184943	0.0463	0.2973
chr17	81195210	5080171	0.0626	0.321
chr18	78077248	5029116	0.0644	0.7882
chr19	59128983	3839280	0.0649	0.6926
chr20	63025520	4796873	0.0761	0.3233
chr21	48129895	2068820	0.043	0.2655
chr22	51304566	1504200	0.0293	0.1924
chrMT	16571	20600	1.2431	1.3828
chrX	155270560	9947351	0.0641	0.3408
chrY	59373566	385236	0.0065	0.1474

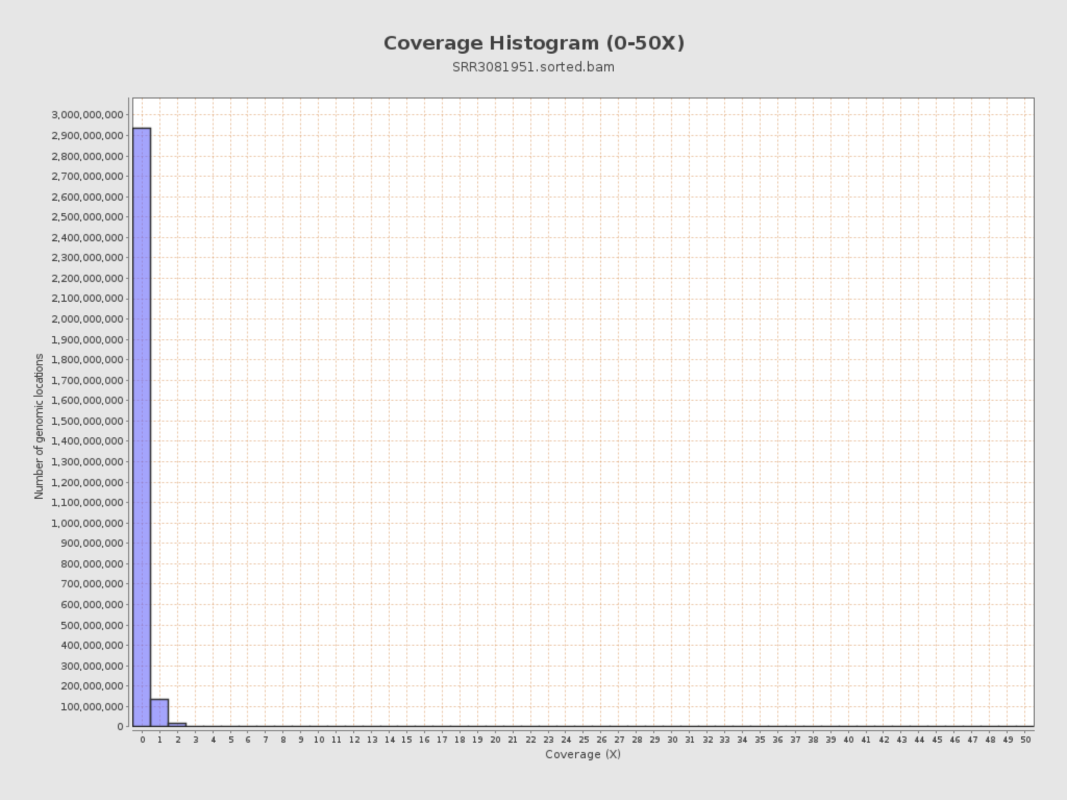
3. Results : Coverage across reference



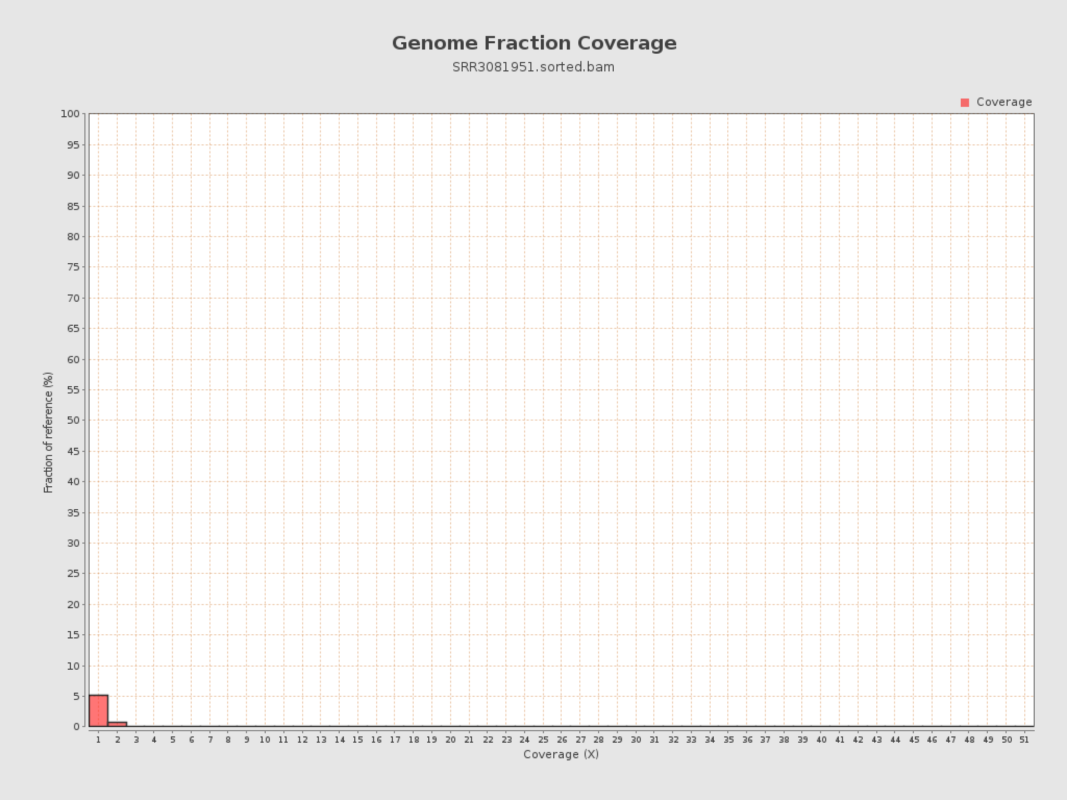
4. Results : Coverage Histogram



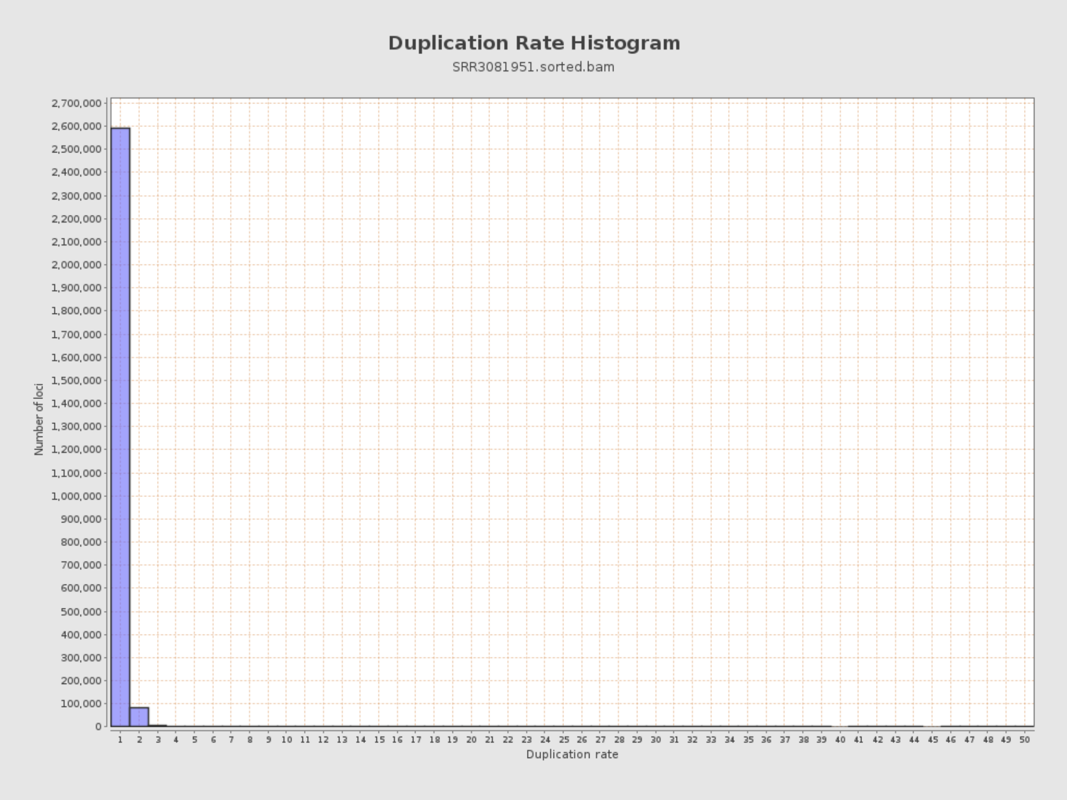
5. Results : Coverage Histogram (0-50X)



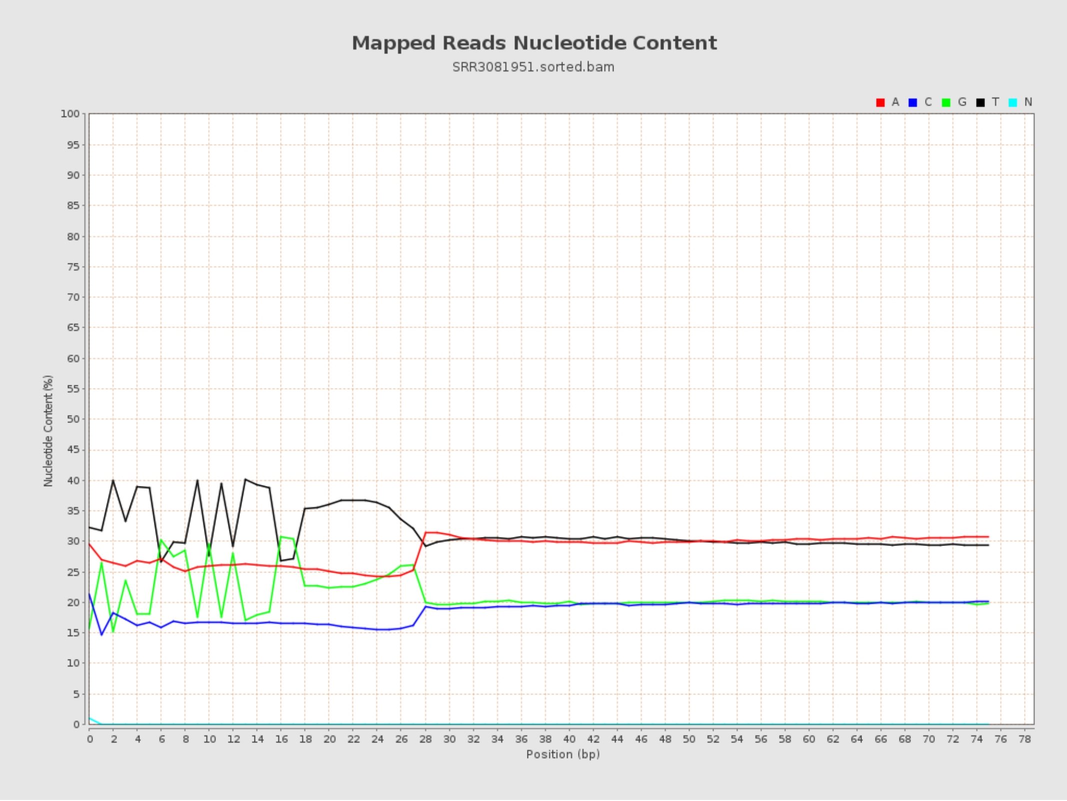
6. Results : Genome Fraction Coverage



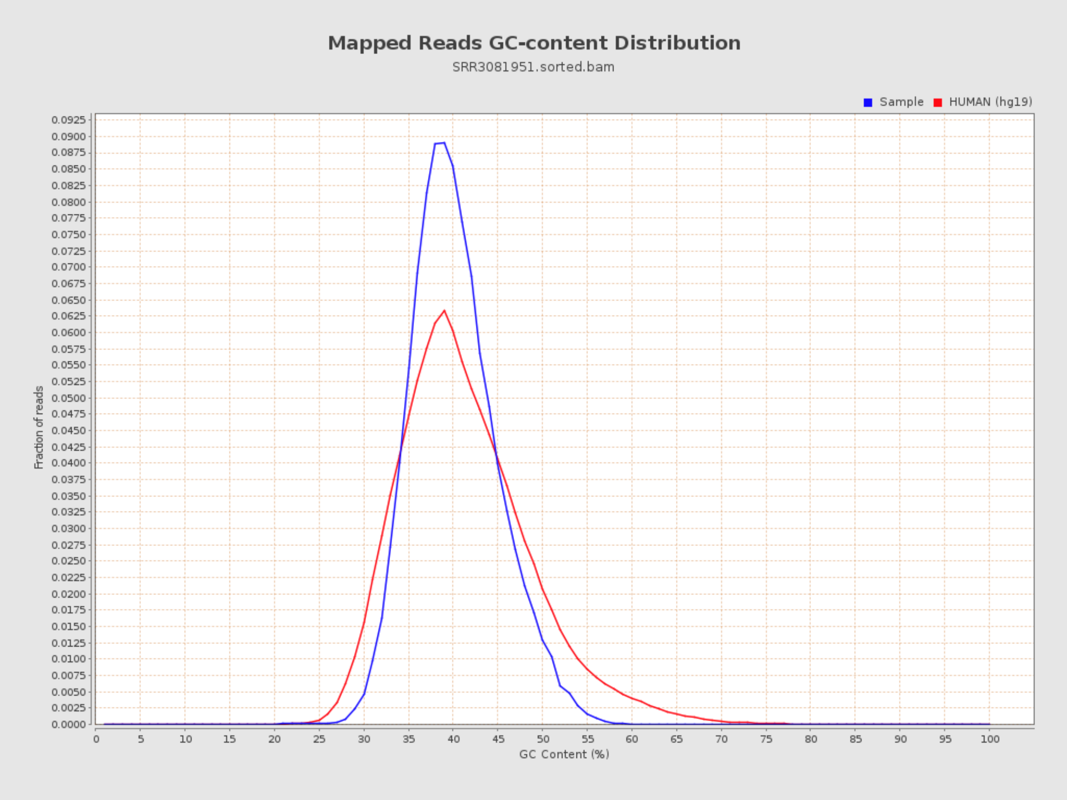
7. Results : Duplication Rate Histogram



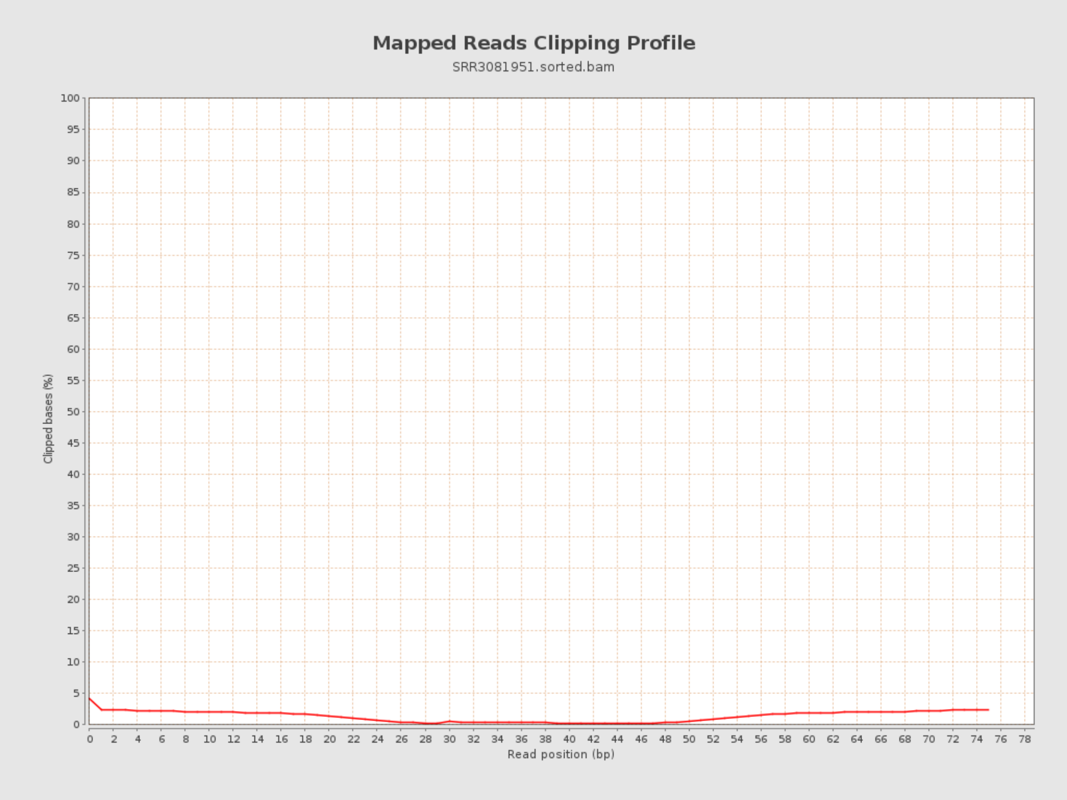
8. Results : Mapped Reads Nucleotide Content



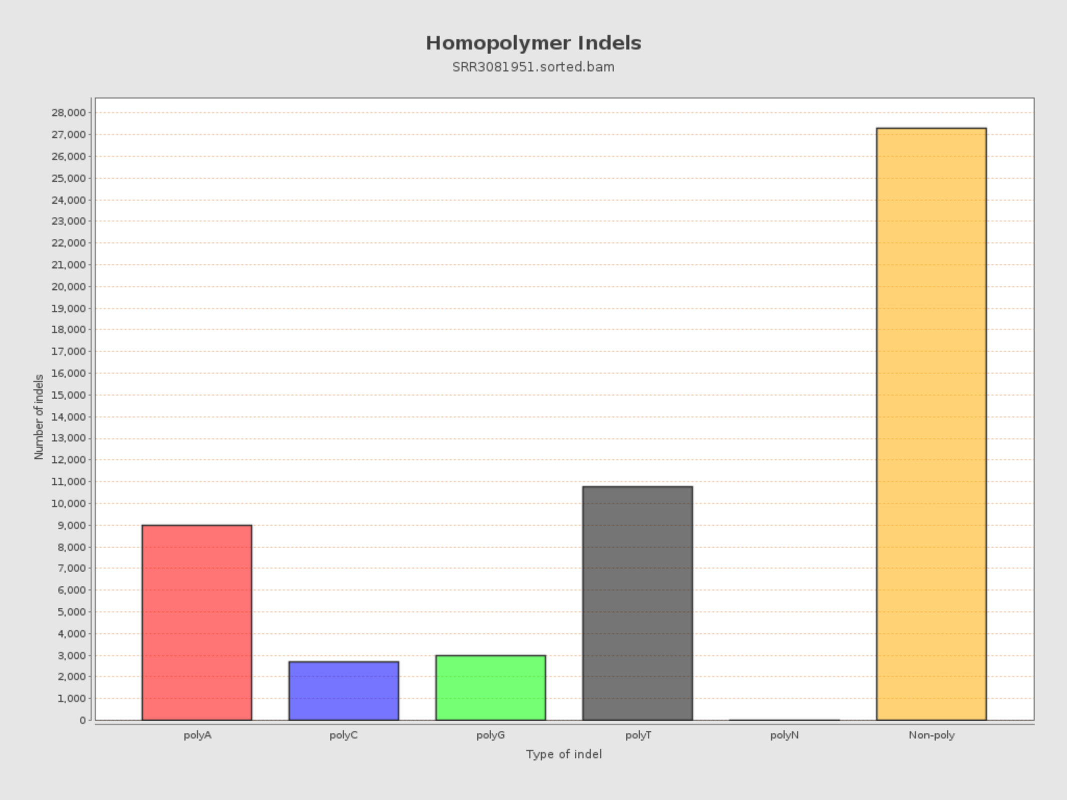
9. Results : Mapped Reads GC-content Distribution



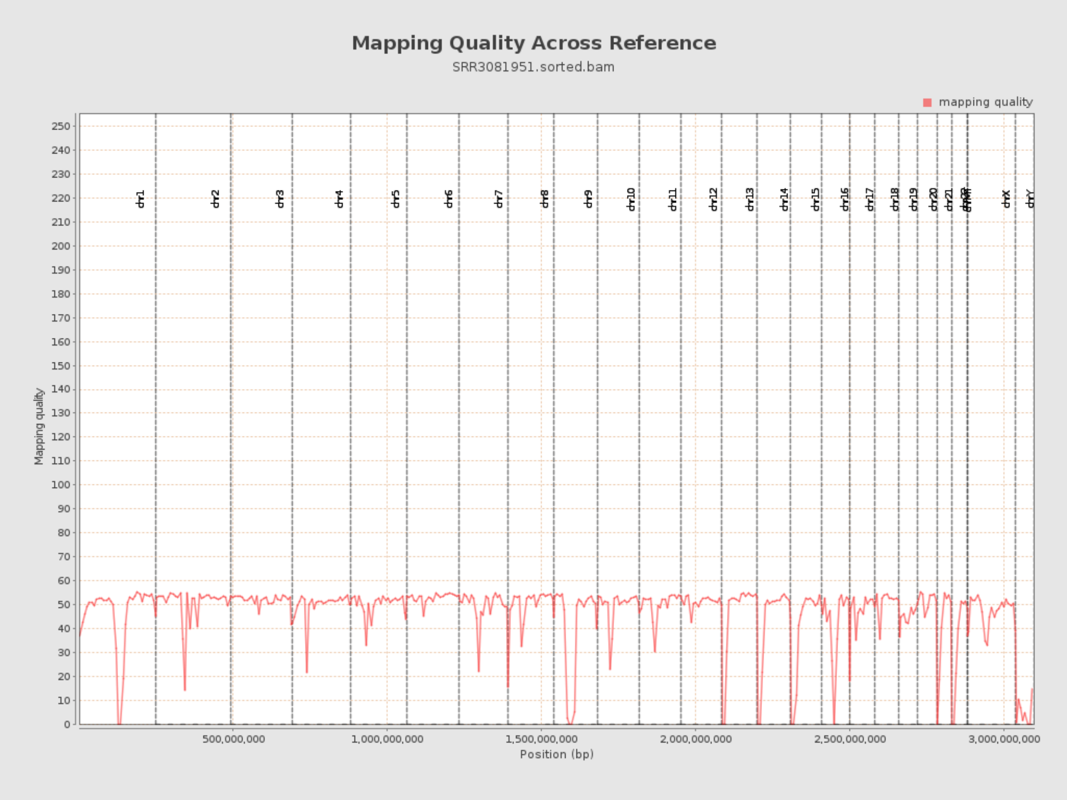
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram