Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:12:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081959.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_SRR3081959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:12:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,258,173
Mapped reads	2,983,572 / 91.57%
Unmapped reads	274,601 / 8.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,295 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	130,404 / 4%
Duplication rate	3.28%
Clipped reads	936,346 / 28.74%

2.2. ACGT Content

Number/percentage of A's	60,411,194 / 29.07%
Number/percentage of C's	38,765,411 / 18.65%
Number/percentage of T's	65,505,749 / 31.52%
Number/percentage of G's	43,128,491 / 20.75%
Number/percentage of N's	27,224 / 0.01%
GC Percentage	39.4%

2.3. Coverage

Mean	0.0672

Standard Deviation	0.5608

2.4. Mapping Quality

Mean Mapping Quality	46.79

2.5. Mismatches and indels

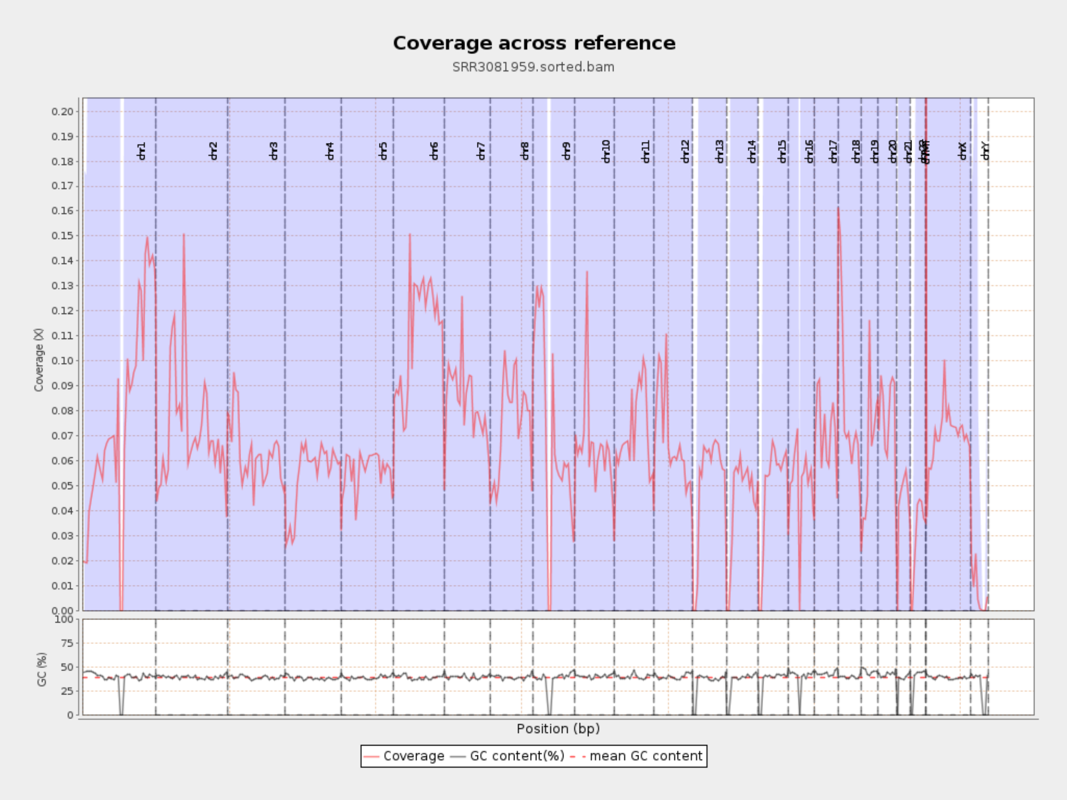
General error rate	0.78%
Mismatches	1,600,060
Insertions	15,208
Mapped reads with at least one insertion	0.5%
Deletions	47,100
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.05%

2.6. Chromosome stats

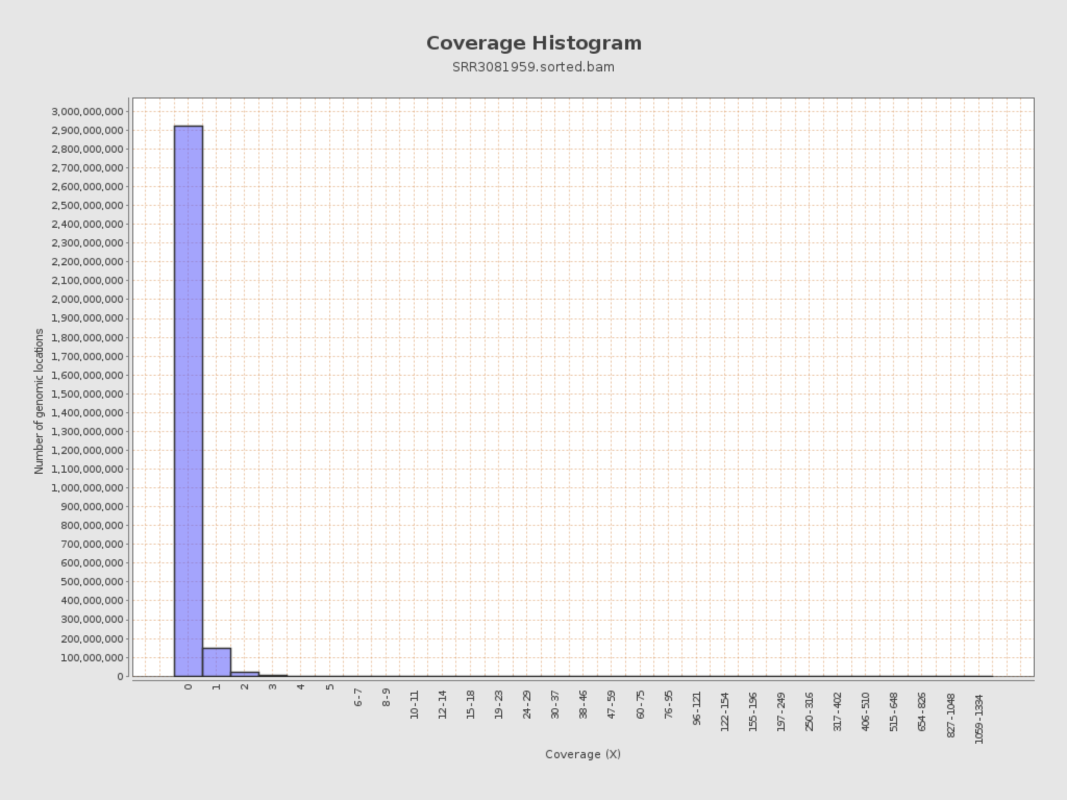
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19477836	0.0781	0.9529
chr2	243199373	17833627	0.0733	0.7664
chr3	198022430	12540728	0.0633	0.2919
chr4	191154276	10427759	0.0546	0.294
chr5	180915260	10099892	0.0558	0.2735
chr6	171115067	19193069	0.1122	0.5179
chr7	159138663	13286686	0.0835	0.7919

chr8	146364022	11013048	0.0752	0.9034
chr9	141213431	10069577	0.0713	0.5615
chr10	135534747	8970399	0.0662	0.6002
chr11	135006516	9678499	0.0717	0.3979
chr12	133851895	9169729	0.0685	0.3147
chr13	115169878	5862048	0.0509	0.2579
chr14	107349540	4763981	0.0444	0.2674
chr15	102531392	4921698	0.048	0.249
chr16	90354753	4466186	0.0494	0.3129
chr17	81195210	5887129	0.0725	0.3754
chr18	78077248	6550568	0.0839	0.8506
chr19	59128983	3772500	0.0638	0.7161
chr20	63025520	5054377	0.0802	0.3336
chr21	48129895	2065451	0.0429	0.269
chr22	51304566	1504595	0.0293	0.1932
chrMT	16571	7603	0.4588	0.6617
chrX	155270560	10872114	0.07	0.3615
chrY	59373566	433122	0.0073	0.1813

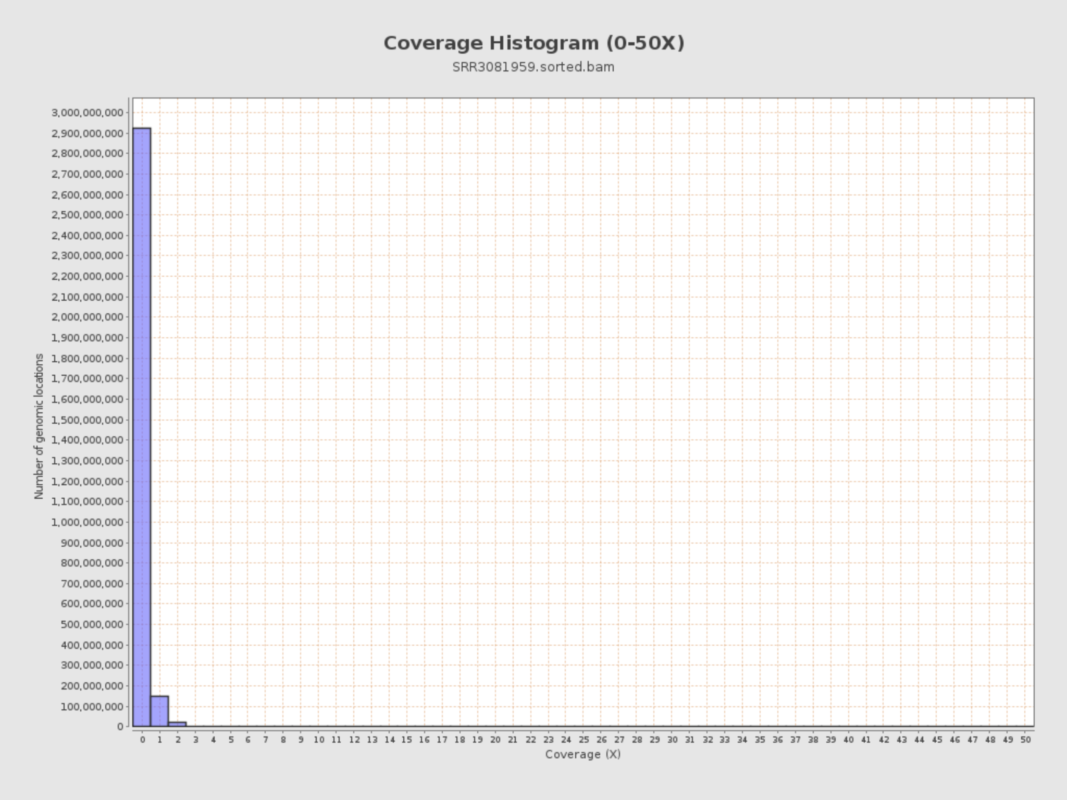
3. Results : Coverage across reference



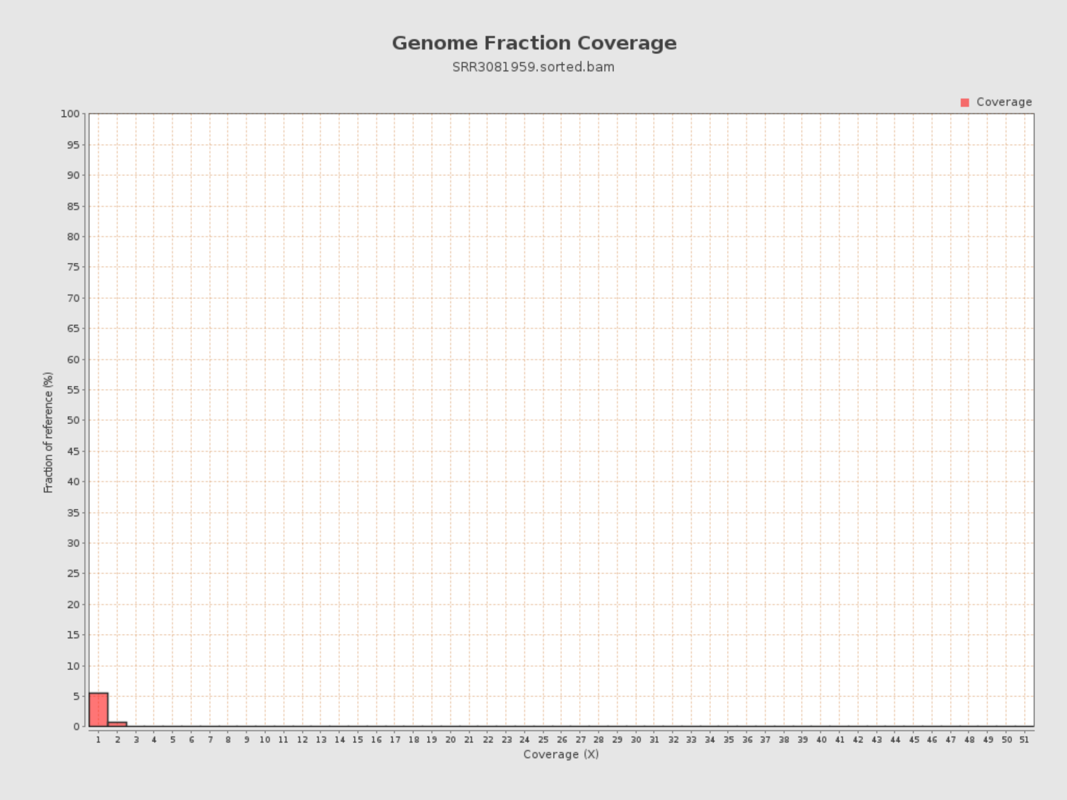
4. Results : Coverage Histogram



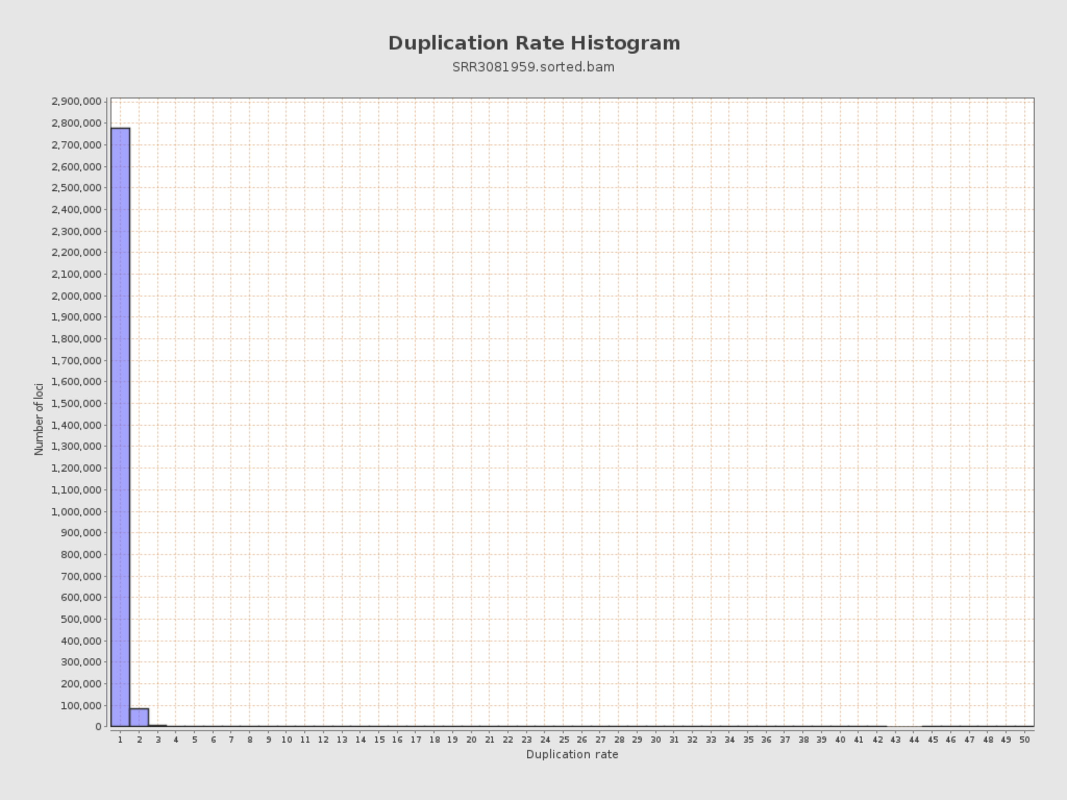
5. Results : Coverage Histogram (0-50X)



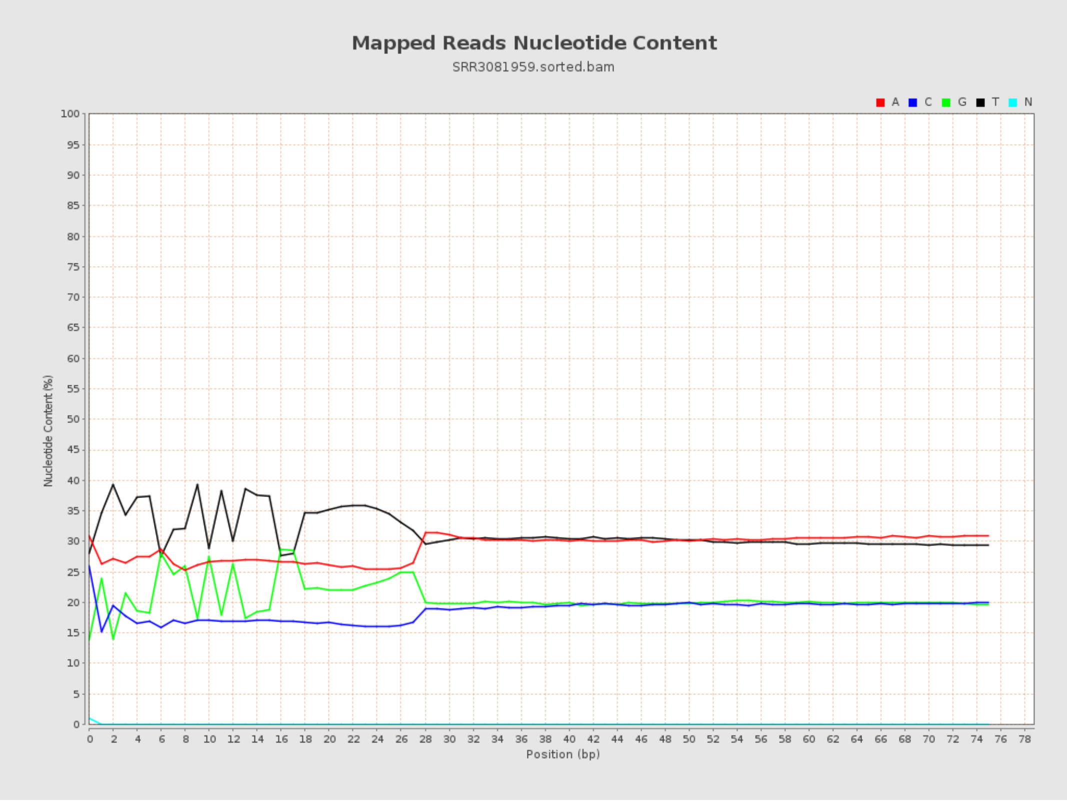
6. Results : Genome Fraction Coverage



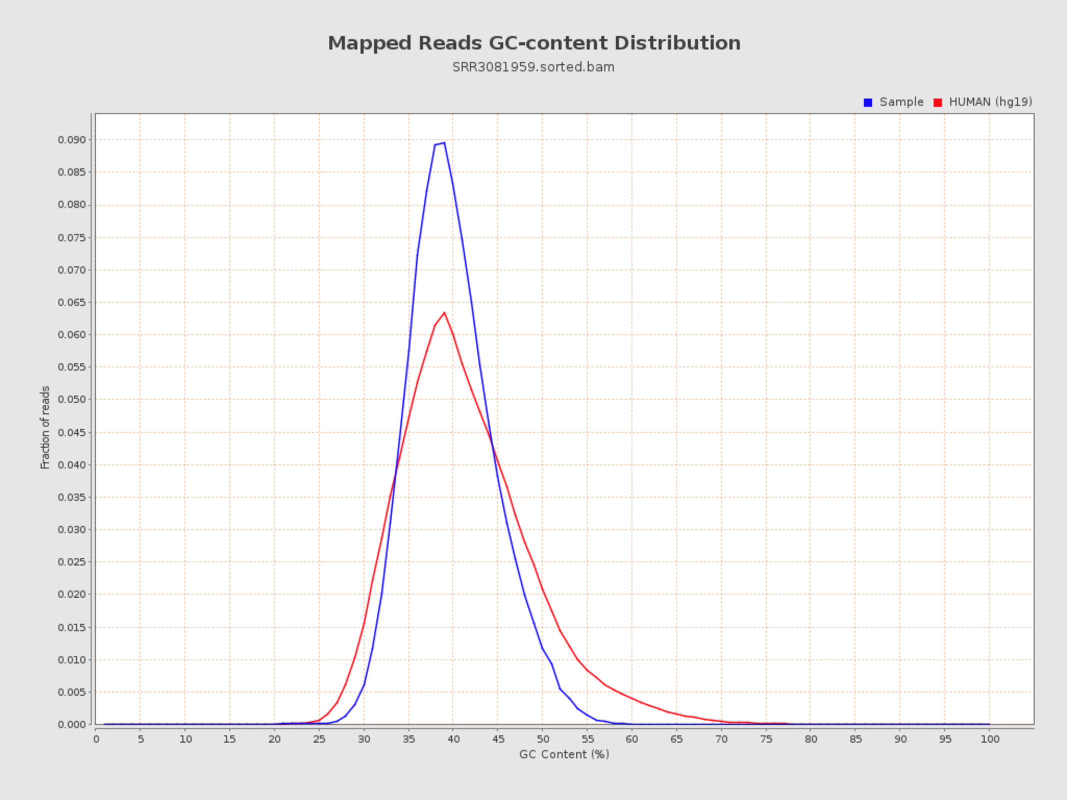
7. Results : Duplication Rate Histogram



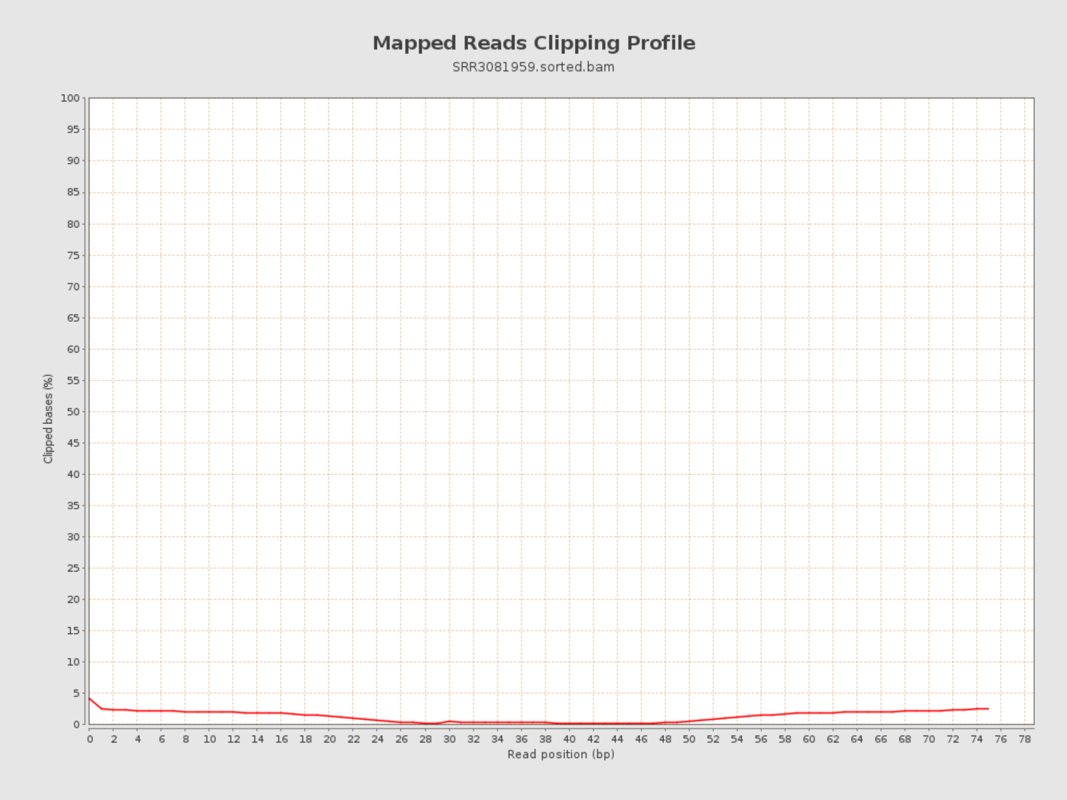
8. Results : Mapped Reads Nucleotide Content



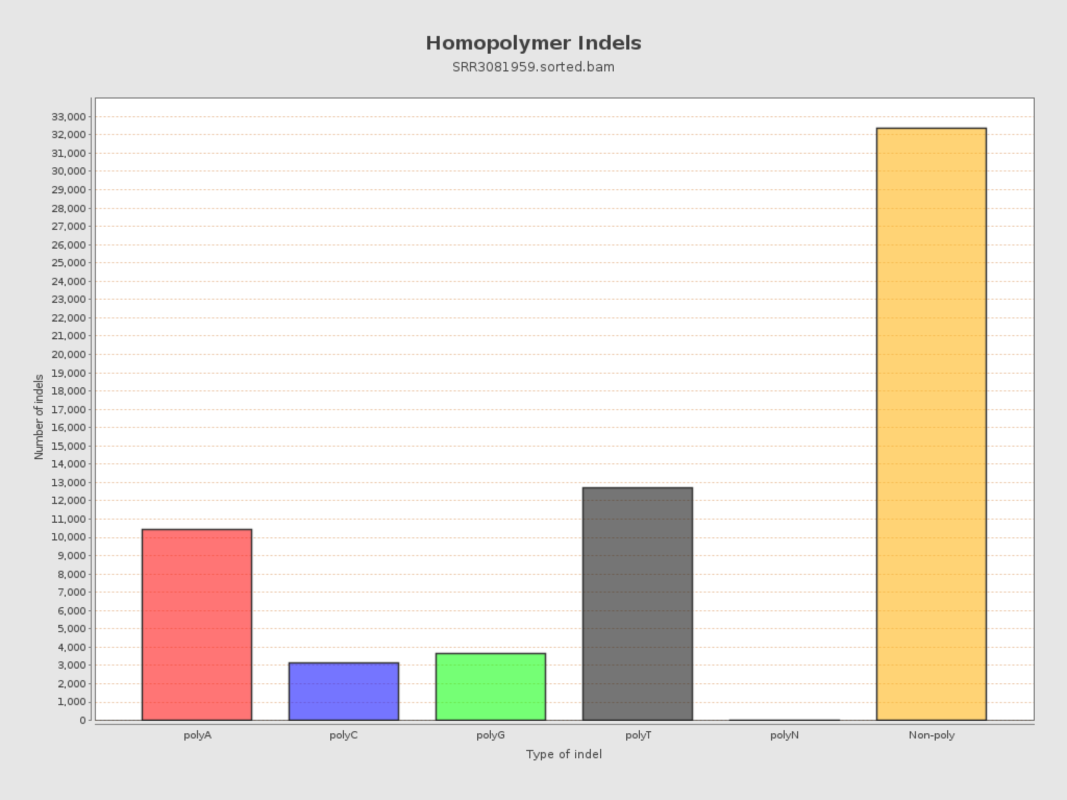
9. Results : Mapped Reads GC-content Distribution



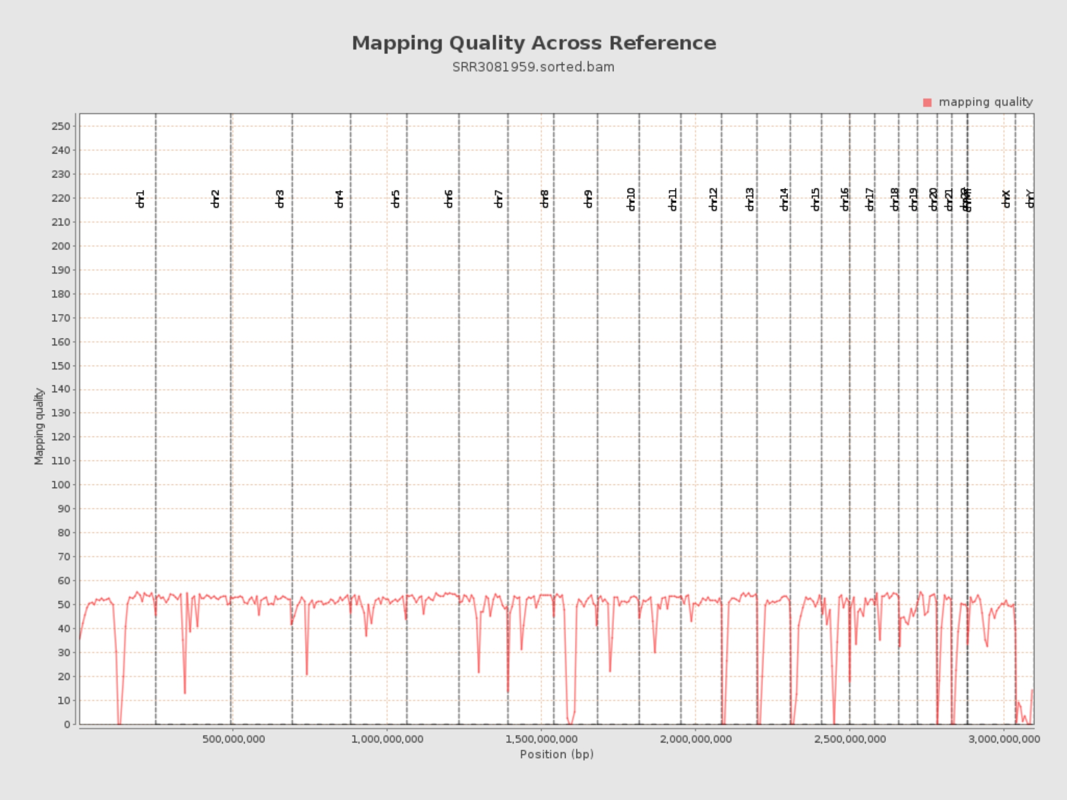
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram