Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:02:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082951.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_SRR3082951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082951.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:02:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,577,017
Mapped reads	1,455,292 / 92.28%
Unmapped reads	121,725 / 7.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,722 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	63,924 / 4.05%
Duplication rate	3.52%
Clipped reads	613,034 / 38.87%

2.2. ACGT Content

Number/percentage of A's	27,294,555 / 27.91%
Number/percentage of C's	17,835,087 / 18.24%
Number/percentage of T's	31,338,836 / 32.05%
Number/percentage of G's	21,313,332 / 21.8%
Number/percentage of N's	5,206 / 0.01%
GC Percentage	40.03%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.3048

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

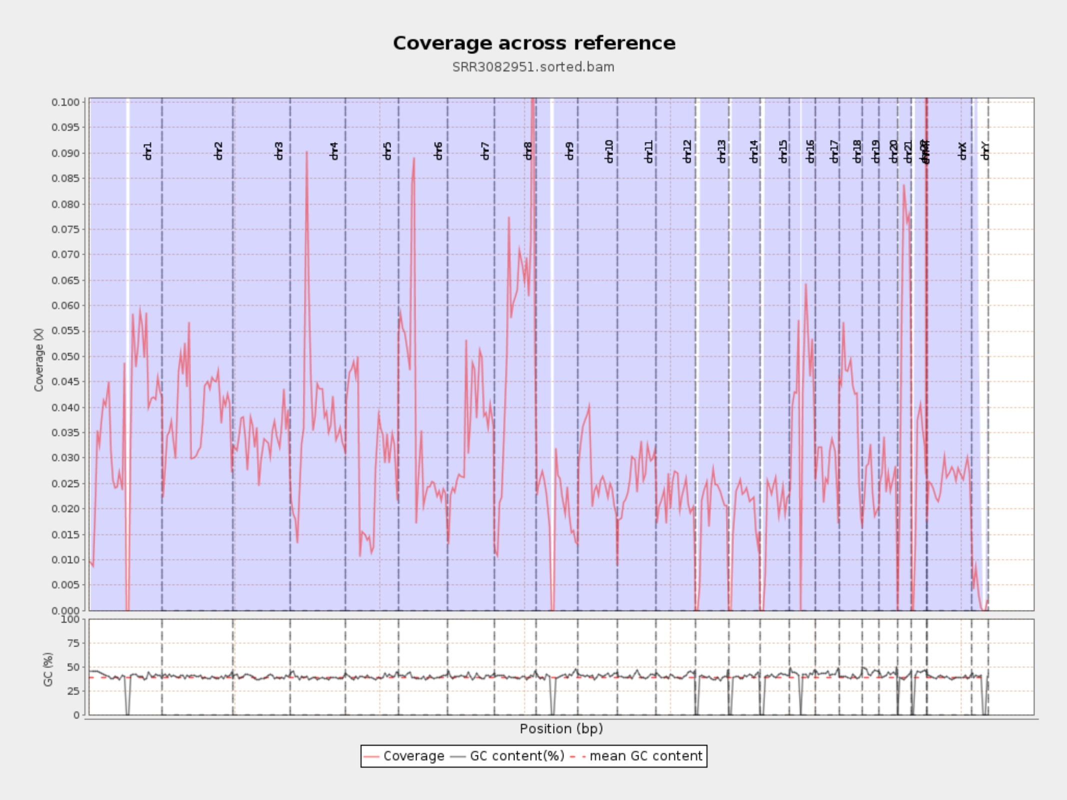
General error rate	0.72%
Mismatches	693,591
Insertions	8,548
Mapped reads with at least one insertion	0.58%
Deletions	23,481
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.62%

2.6. Chromosome stats

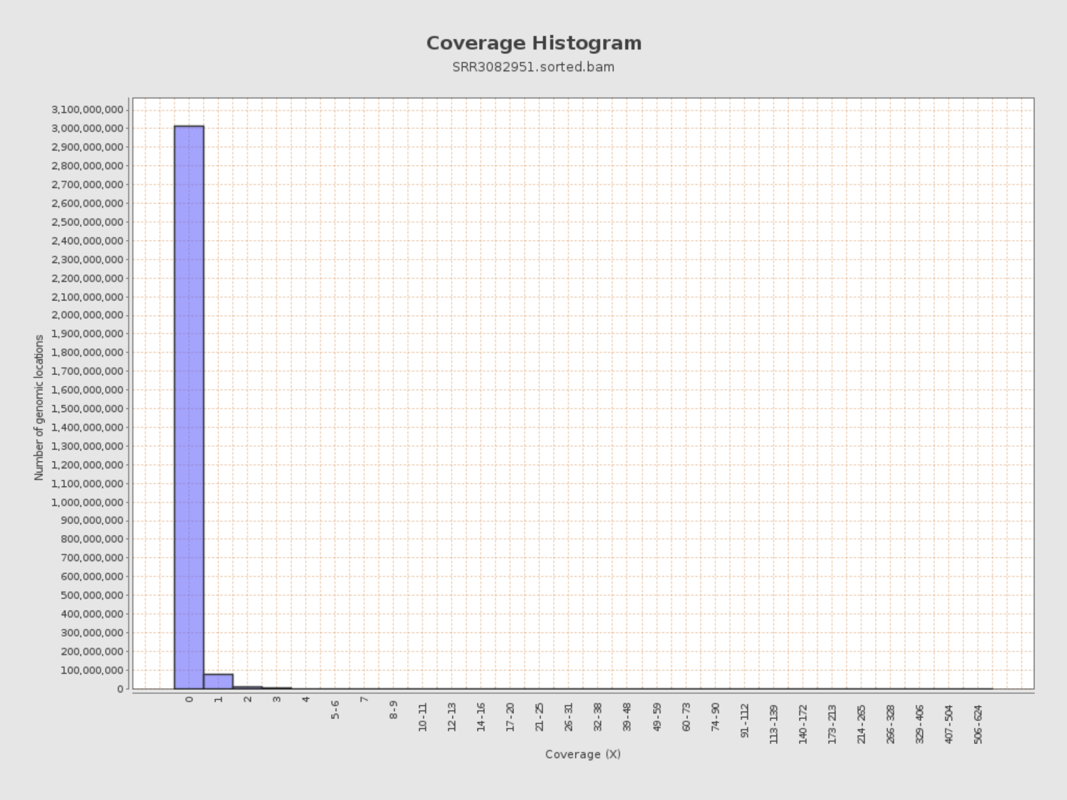
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8936551	0.0359	0.5219
chr2	243199373	9591419	0.0394	0.398
chr3	198022430	6766903	0.0342	0.2074
chr4	191154276	7124407	0.0373	0.2238
chr5	180915260	5460781	0.0302	0.1964
chr6	171115067	6349389	0.0371	0.2665
chr7	159138663	5635231	0.0354	0.3853

chr8	146364022	8118529	0.0555	0.3911
chr9	141213431	2790662	0.0198	0.2567
chr10	135534747	3738707	0.0276	0.2193
chr11	135006516	3525664	0.0261	0.2405
chr12	133851895	2972988	0.0222	0.1713
chr13	115169878	2180148	0.0189	0.1557
chr14	107349540	1975251	0.0184	0.1756
chr15	102531392	1897505	0.0185	0.1588
chr16	90354753	3867177	0.0428	0.2473
chr17	81195210	2257024	0.0278	0.2058
chr18	78077248	3341765	0.0428	0.6304
chr19	59128983	1433693	0.0242	0.3467
chr20	63025520	1659856	0.0263	0.1943
chr21	48129895	2703747	0.0562	0.2725
chr22	51304566	1281337	0.025	0.1765
chrMT	16571	26499	1.5991	1.6056
chrX	155270560	4011176	0.0258	0.2023
chrY	59373566	179061	0.003	0.0696

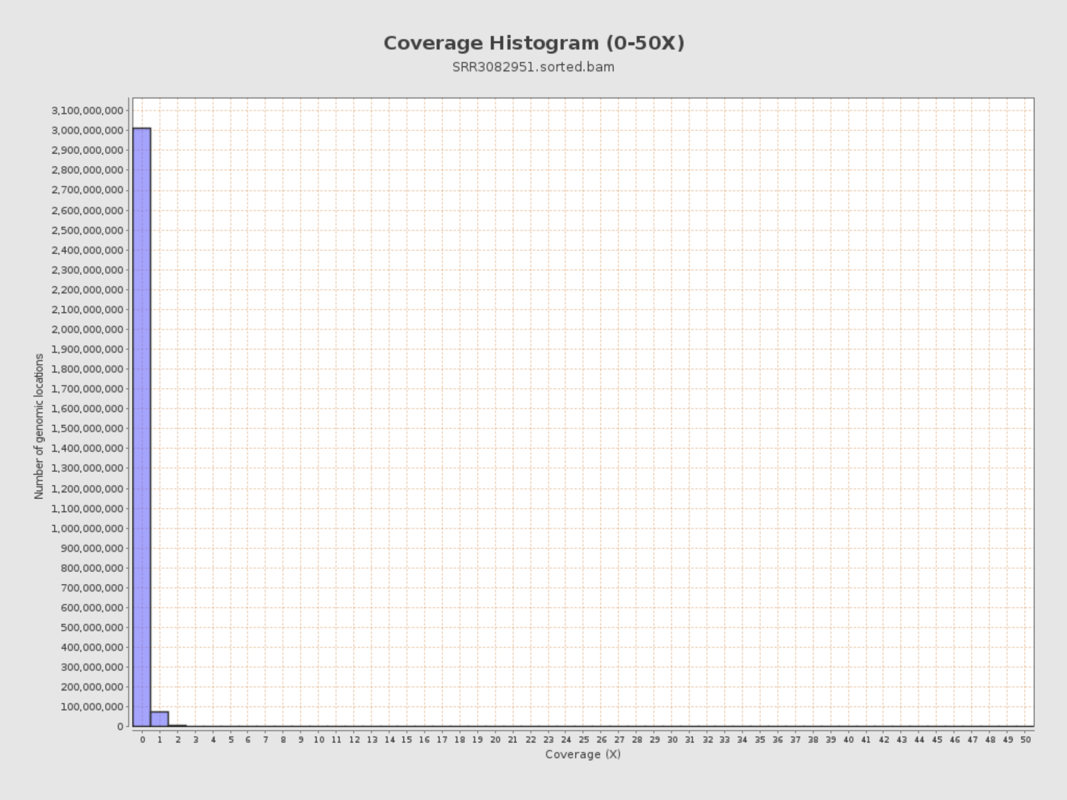
3. Results : Coverage across reference



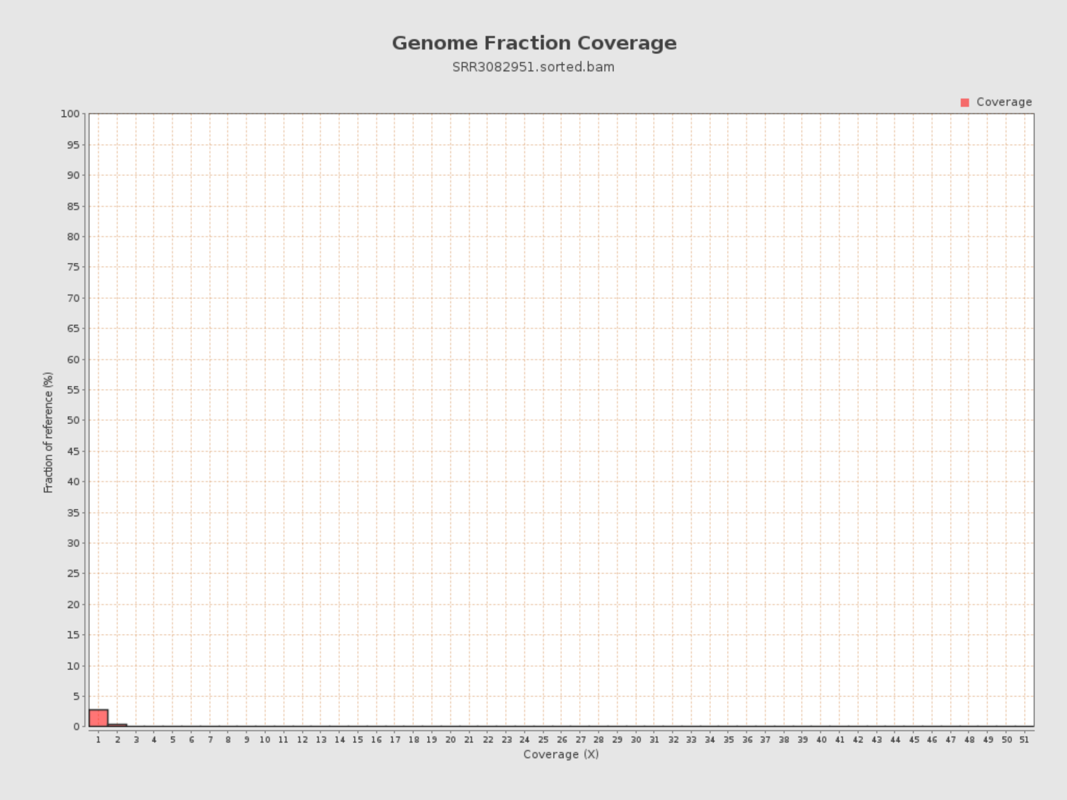
4. Results : Coverage Histogram



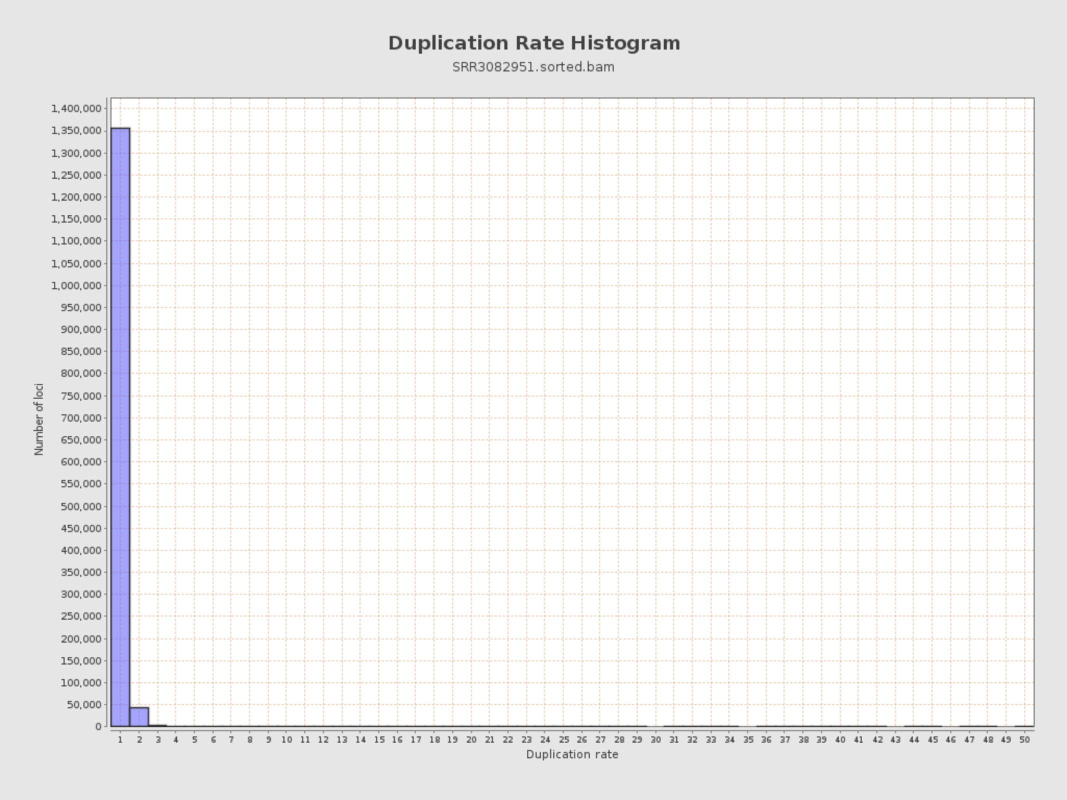
5. Results : Coverage Histogram (0-50X)



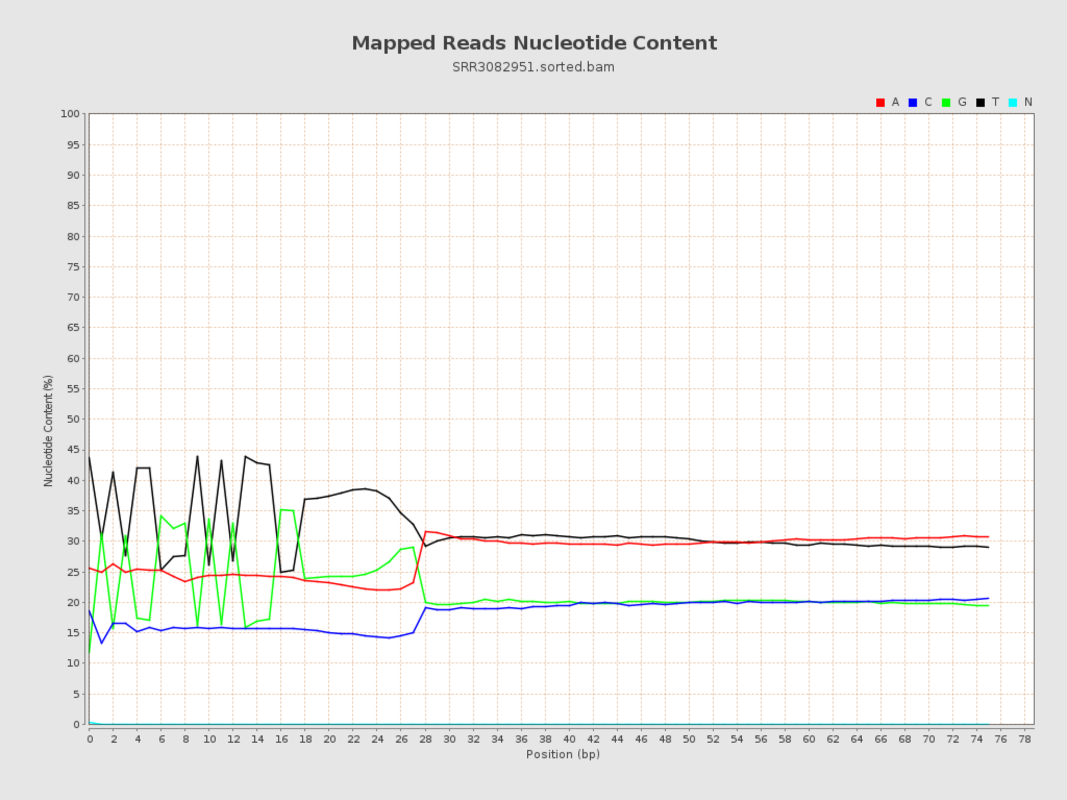
6. Results : Genome Fraction Coverage



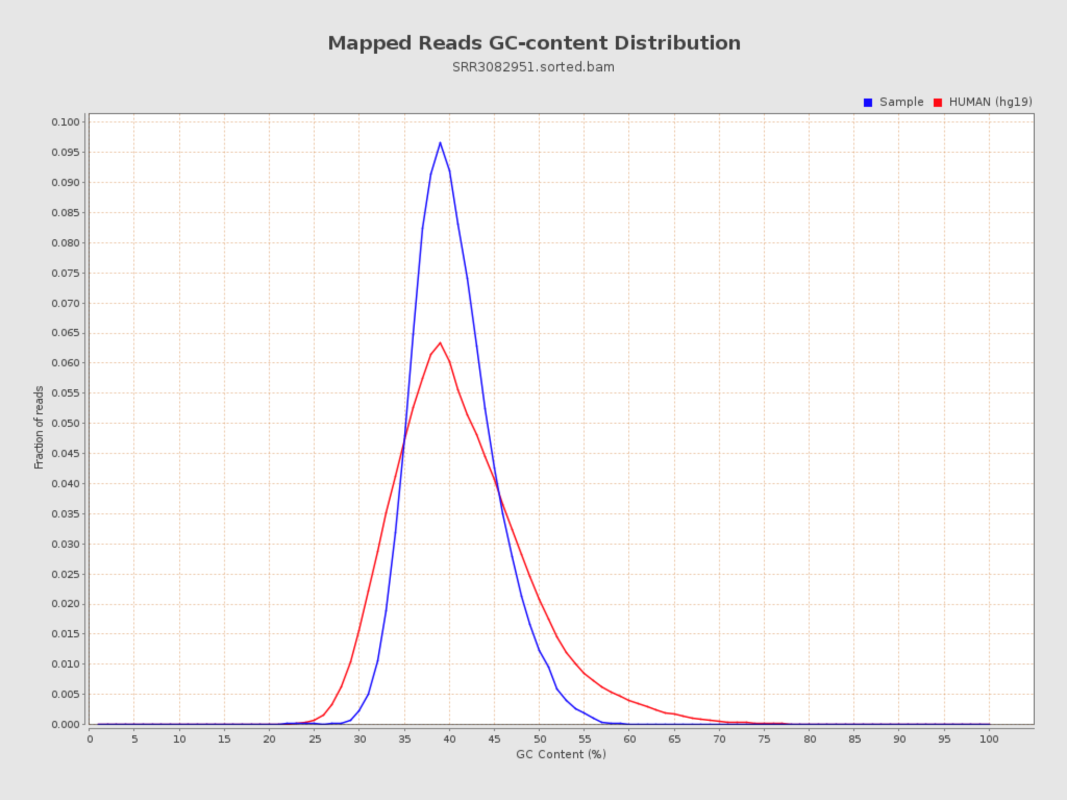
7. Results : Duplication Rate Histogram



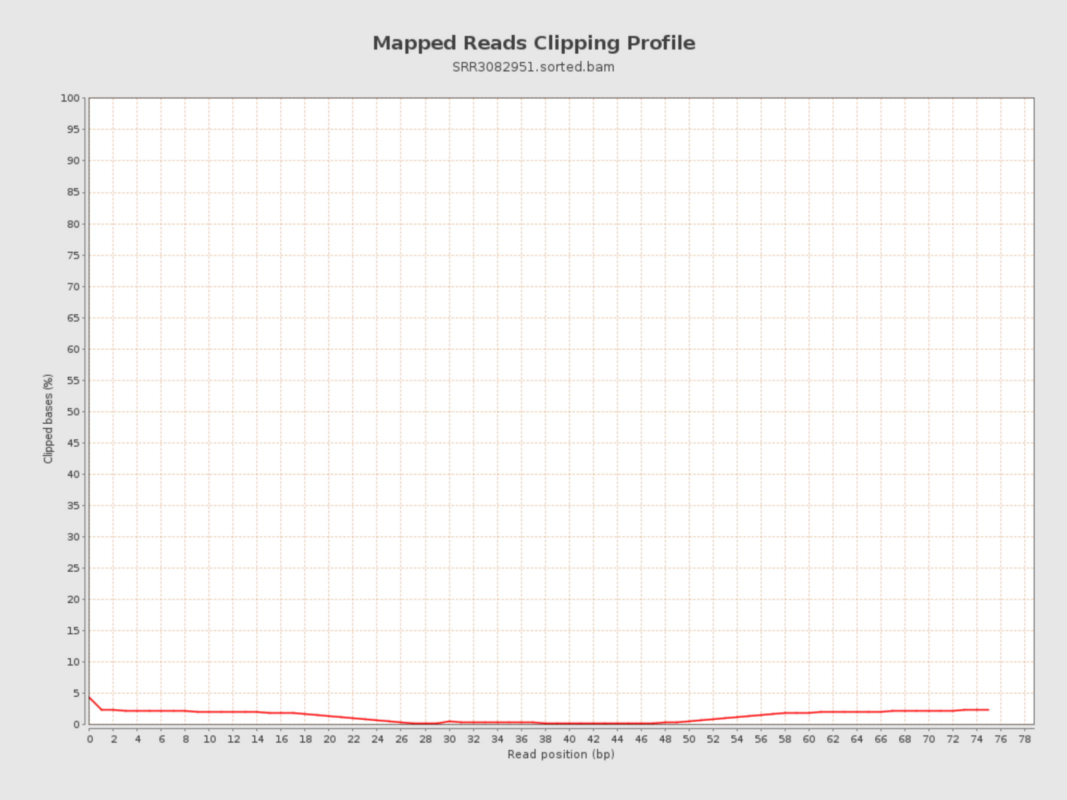
8. Results : Mapped Reads Nucleotide Content



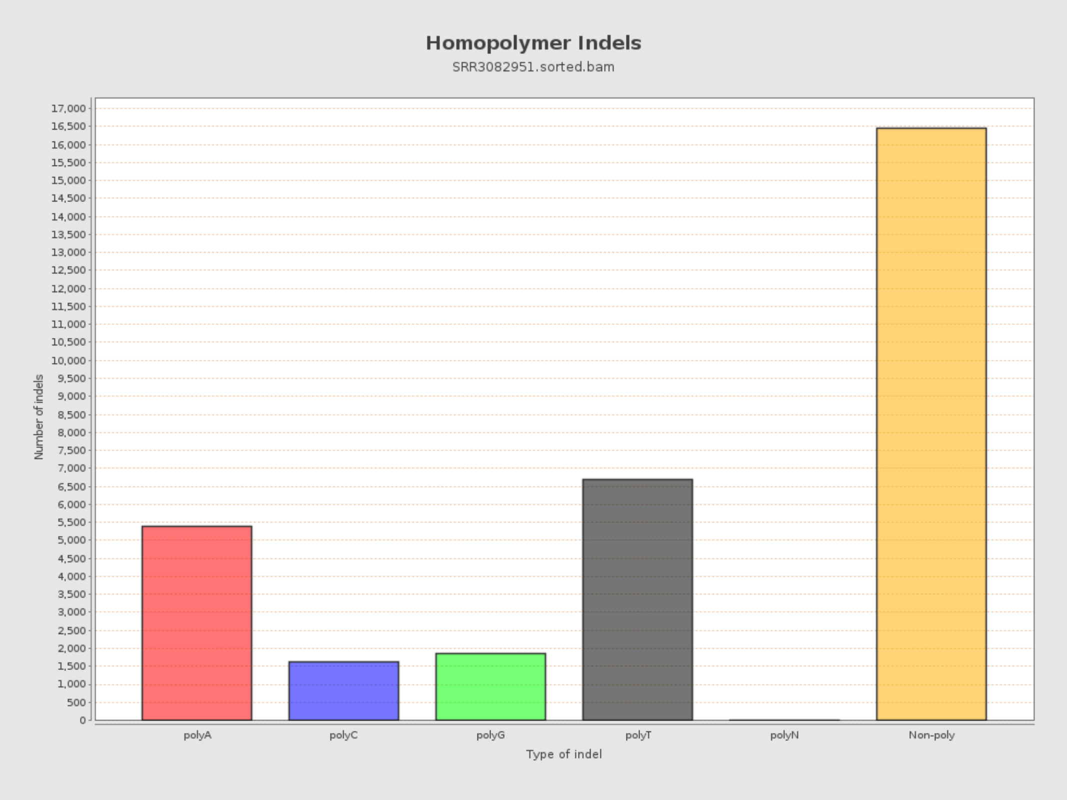
9. Results : Mapped Reads GC-content Distribution



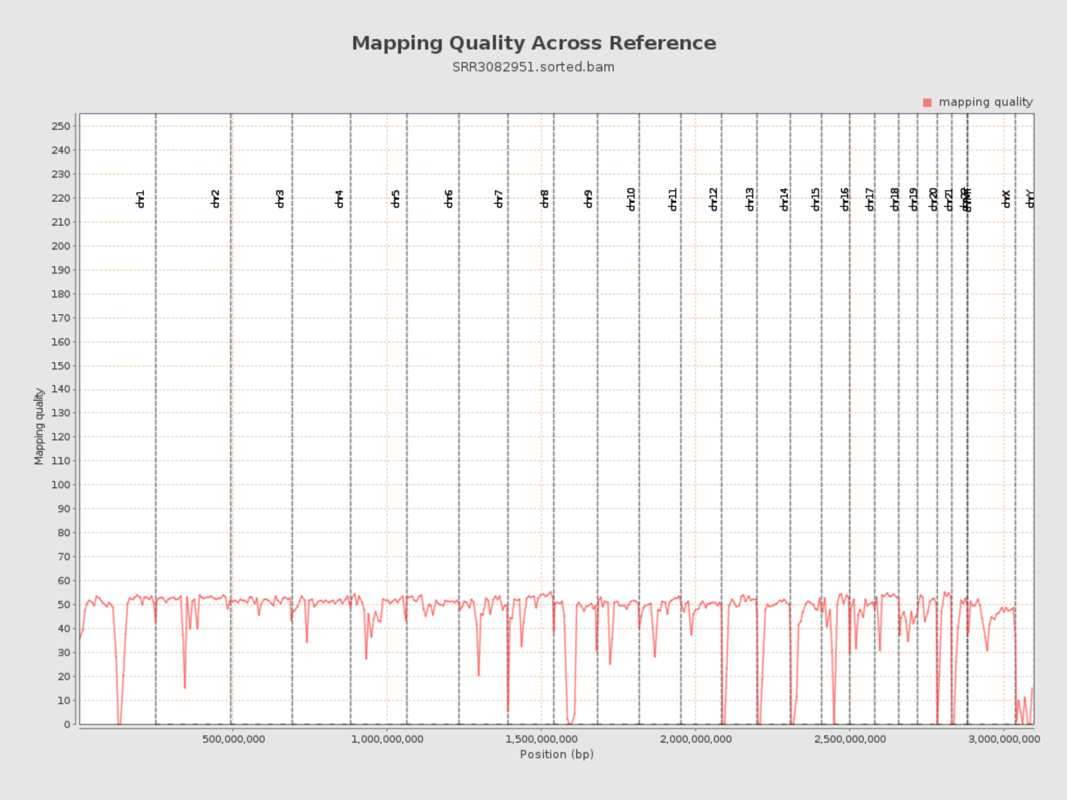
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram