Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:45:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081953.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_SRR3081953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081953.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:45:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,668,611
Mapped reads	2,441,294 / 91.48%
Unmapped reads	227,317 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,782 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	108,999 / 4.08%
Duplication rate	3.6%
Clipped reads	978,326 / 36.66%

2.2. ACGT Content

Number/percentage of A's	46,047,795 / 27.81%
Number/percentage of C's	31,042,667 / 18.75%
Number/percentage of T's	51,555,419 / 31.14%
Number/percentage of G's	36,886,960 / 22.28%
Number/percentage of N's	21,021 / 0.01%
GC Percentage	41.03%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.4097

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

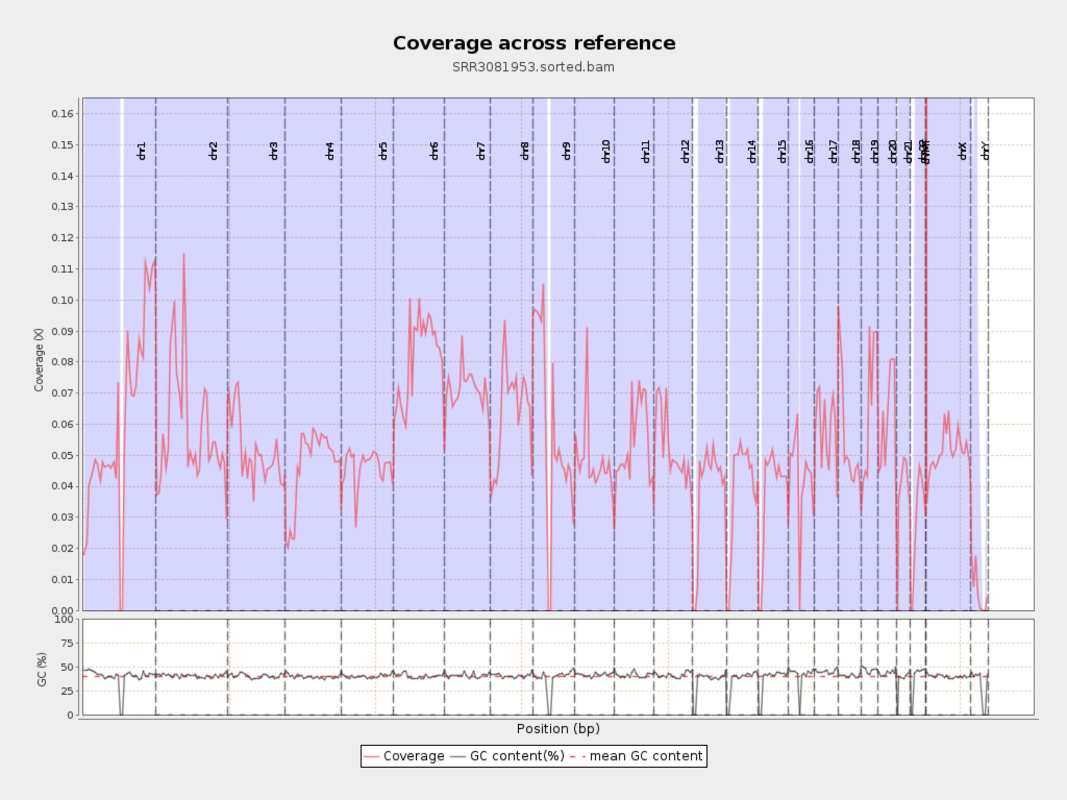
General error rate	0.78%
Mismatches	1,262,838
Insertions	11,919
Mapped reads with at least one insertion	0.48%
Deletions	36,451
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.25%

2.6. Chromosome stats

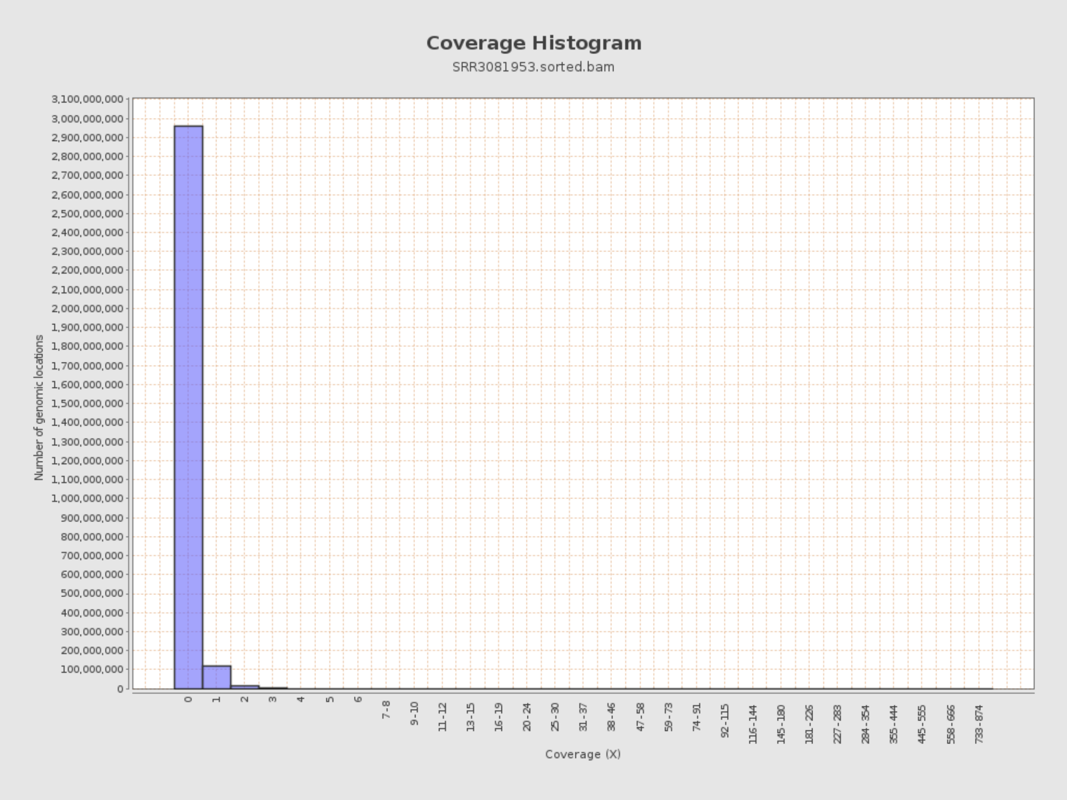
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15149070	0.0608	0.6043
chr2	243199373	14368216	0.0591	0.575
chr3	198022430	10223969	0.0516	0.2624
chr4	191154276	8989373	0.047	0.2639
chr5	180915260	8329801	0.046	0.2479
chr6	171115067	13977077	0.0817	0.3833
chr7	159138663	11304114	0.071	0.5139

chr8	146364022	9370636	0.064	0.6492
chr9	141213431	8135889	0.0576	0.4463
chr10	135534747	6520635	0.0481	0.4004
chr11	135006516	7342554	0.0544	0.3299
chr12	133851895	6980002	0.0521	0.2687
chr13	115169878	4431159	0.0385	0.2256
chr14	107349540	4263954	0.0397	0.249
chr15	102531392	3820576	0.0373	0.2287
chr16	90354753	3751002	0.0415	0.2644
chr17	81195210	4822922	0.0594	0.2974
chr18	78077248	4325808	0.0554	0.6559
chr19	59128983	3848919	0.0651	0.5222
chr20	63025520	3959819	0.0628	0.2953
chr21	48129895	1819935	0.0378	0.2499
chr22	51304566	1473325	0.0287	0.1943
chrMT	16571	101287	6.1123	3.8441
chrX	155270560	7941798	0.0511	0.2894
chrY	59373566	367561	0.0062	0.1342

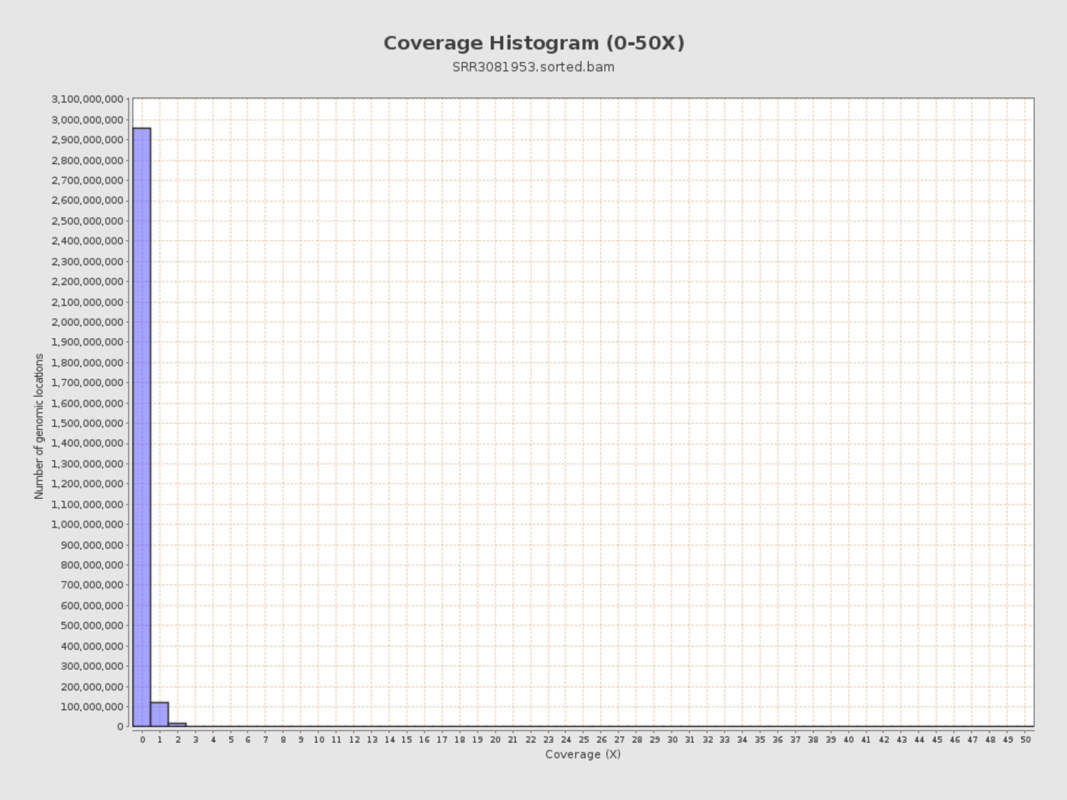
3. Results : Coverage across reference



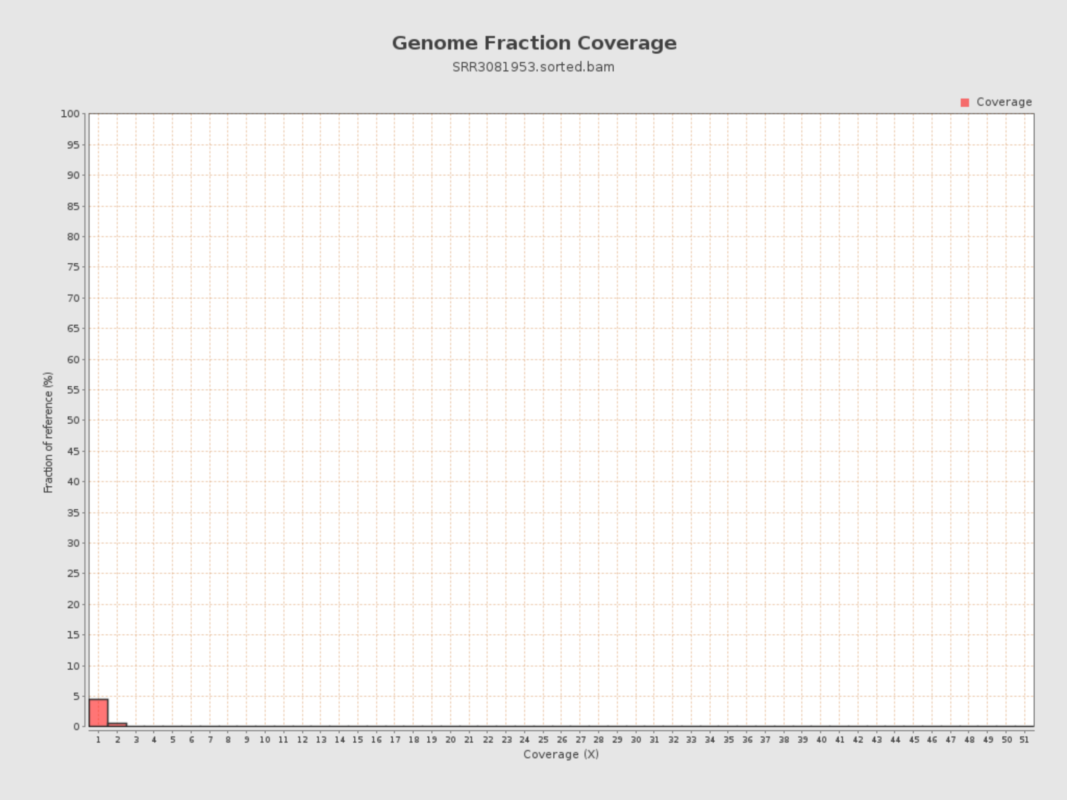
4. Results : Coverage Histogram



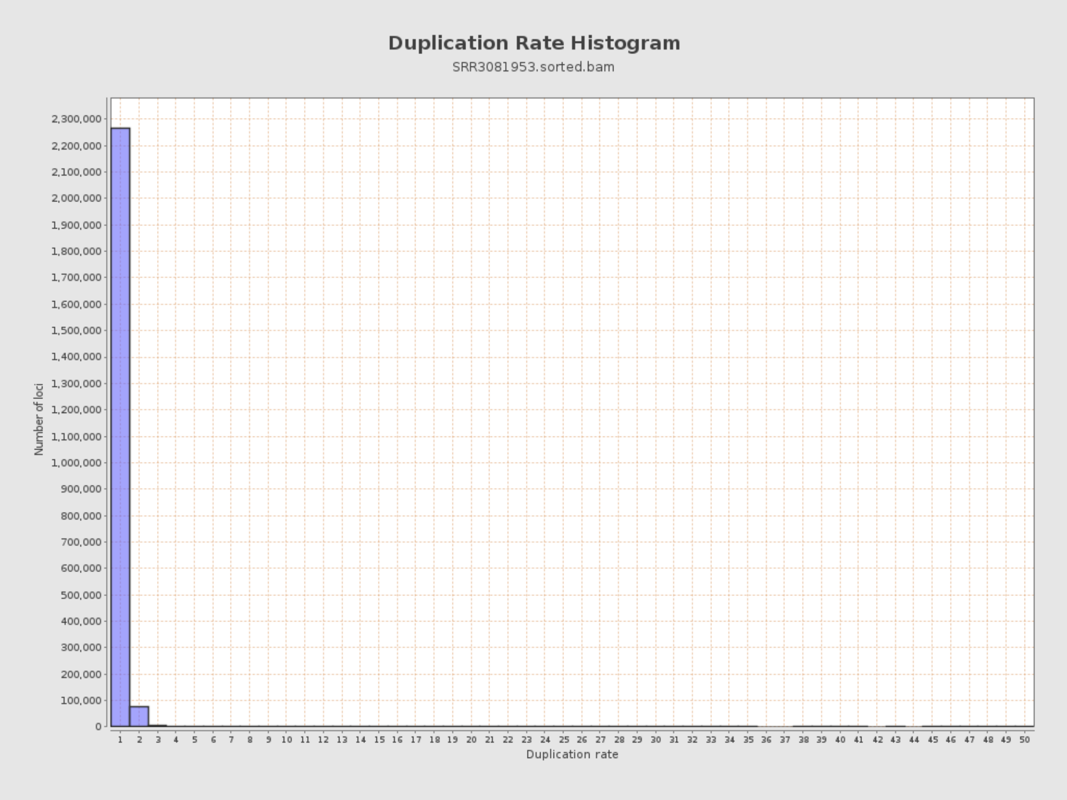
5. Results : Coverage Histogram (0-50X)



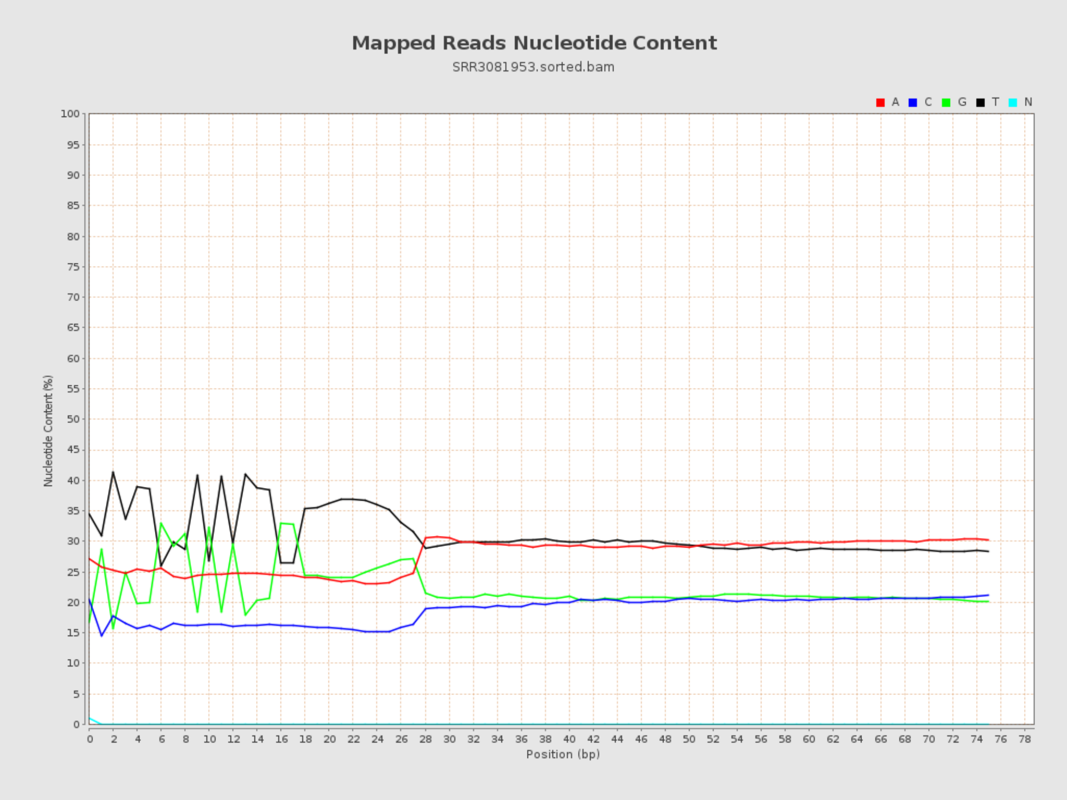
6. Results : Genome Fraction Coverage



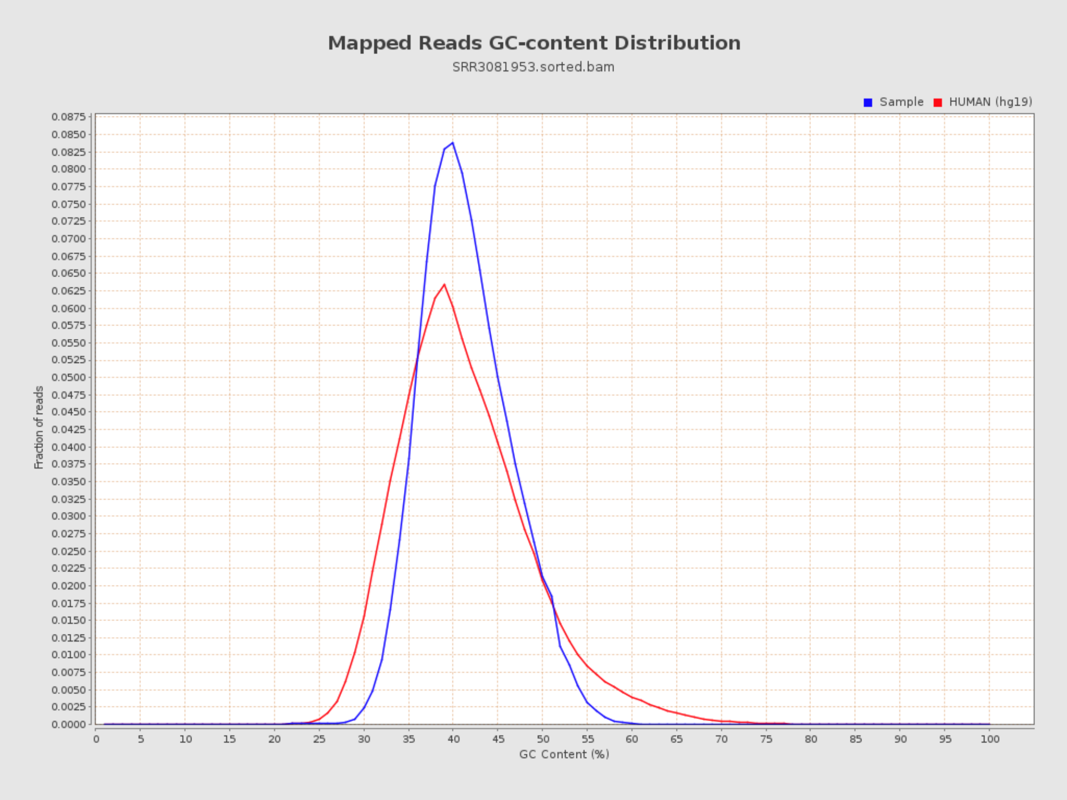
7. Results : Duplication Rate Histogram



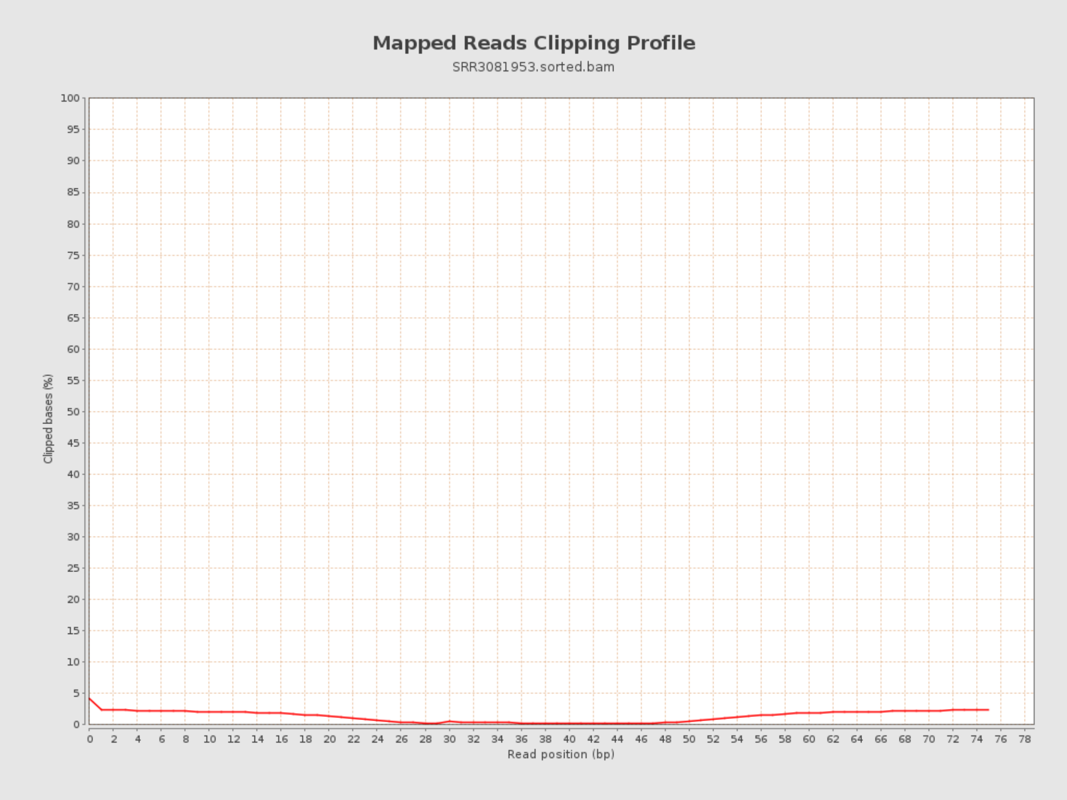
8. Results : Mapped Reads Nucleotide Content



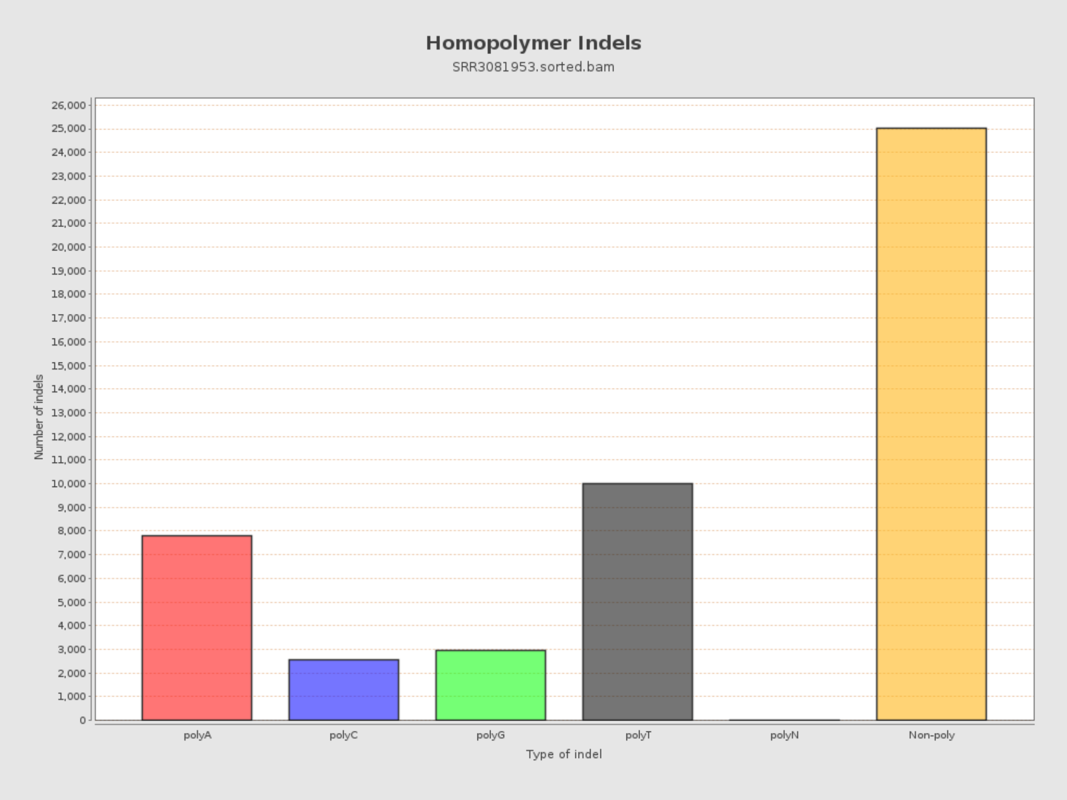
9. Results : Mapped Reads GC-content Distribution



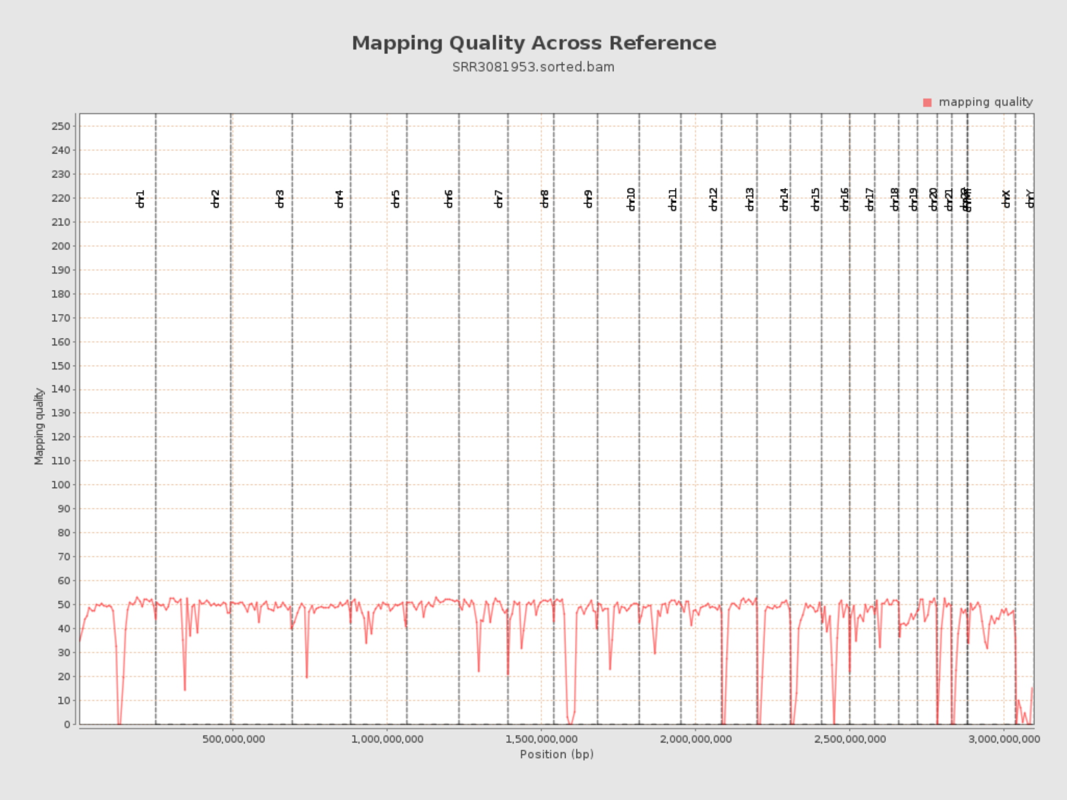
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram