Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:53:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549082.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_SRR1549082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:53:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,875,802
Mapped reads	6,953,951 / 88.3%
Unmapped reads	921,851 / 11.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	236,865 / 3.01%
Duplication rate	2.44%
Clipped reads	303,403 / 3.85%

2.2. ACGT Content

Number/percentage of A's	82,236,328 / 29.76%
Number/percentage of C's	55,632,448 / 20.13%
Number/percentage of T's	83,659,900 / 30.27%
Number/percentage of G's	54,750,643 / 19.81%
Number/percentage of N's	66,821 / 0.02%
GC Percentage	39.94%

2.3. Coverage

Mean	0.0893
Standard Deviation	0.6388

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Mismatches and indels

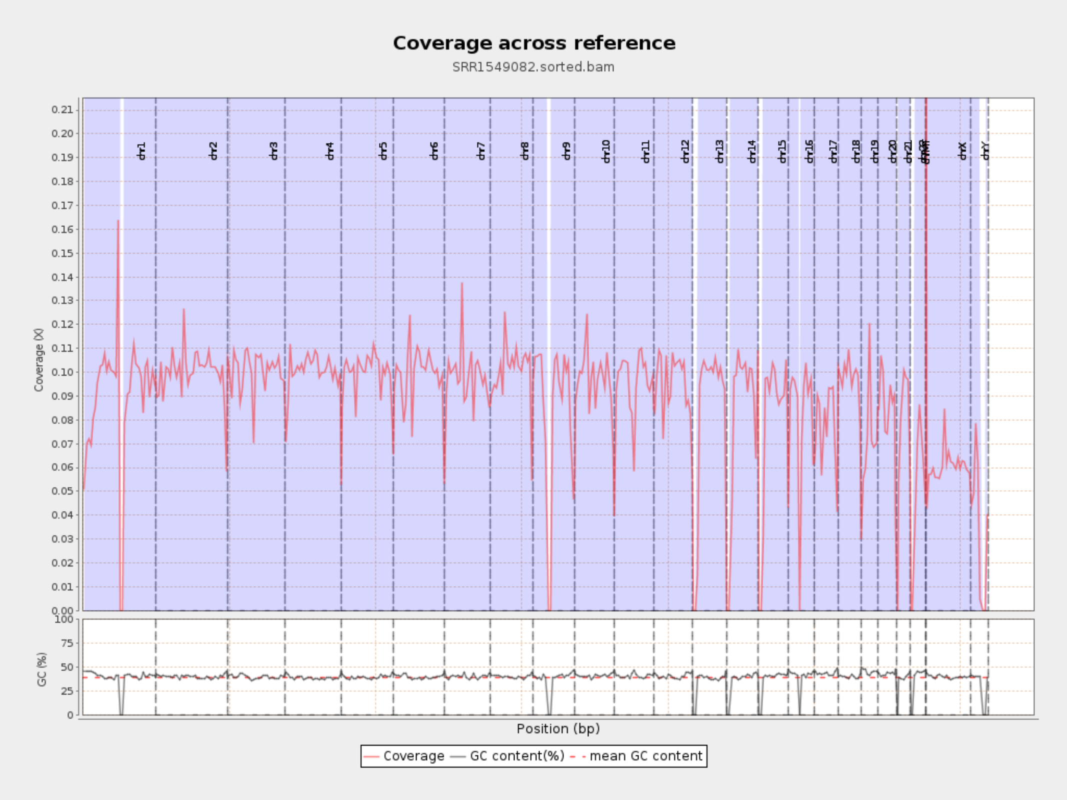
General error rate	0.39%
Mismatches	1,056,826
Insertions	6,176
Mapped reads with at least one insertion	0.09%
Deletions	19,663
Mapped reads with at least one deletion	0.28%
Homopolymer indels	45.81%

2.6. Chromosome stats

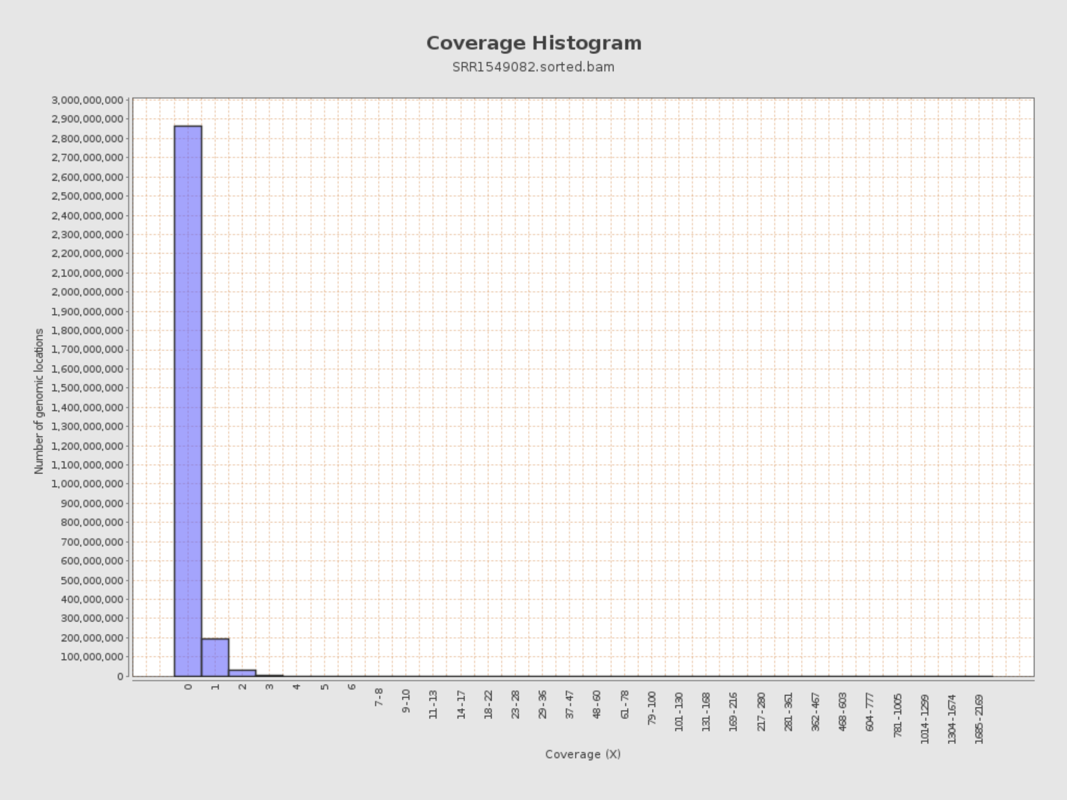
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22302828	0.0895	1.4894
chr2	243199373	24375674	0.1002	0.5161
chr3	198022430	19884315	0.1004	0.3681
chr4	191154276	19254977	0.1007	0.3716
chr5	180915260	17972723	0.0993	0.372
chr6	171115067	17070356	0.0998	0.4454
chr7	159138663	15522310	0.0975	0.7223
chr8	146364022	14707804	0.1005	0.5663

chr9	141213431	11830835	0.0838	0.5111
chr10	135534747	13182635	0.0973	0.5424
chr11	135006516	12837322	0.0951	0.5434
chr12	133851895	12779378	0.0955	0.3742
chr13	115169878	9517426	0.0826	0.3264
chr14	107349540	8668860	0.0808	0.381
chr15	102531392	7866196	0.0767	0.3164
chr16	90354753	7178625	0.0794	0.3749
chr17	81195210	6387953	0.0787	0.3734
chr18	78077248	7687563	0.0985	1.0722
chr19	59128983	4280501	0.0724	1.1192
chr20	63025520	5469907	0.0868	0.3486
chr21	48129895	3609657	0.075	0.3686
chr22	51304566	2551678	0.0497	0.2899
chrMT	16571	10220	0.6167	1.0607
chrX	155270560	9374333	0.0604	0.3461
chrY	59373566	2046658	0.0345	0.2693

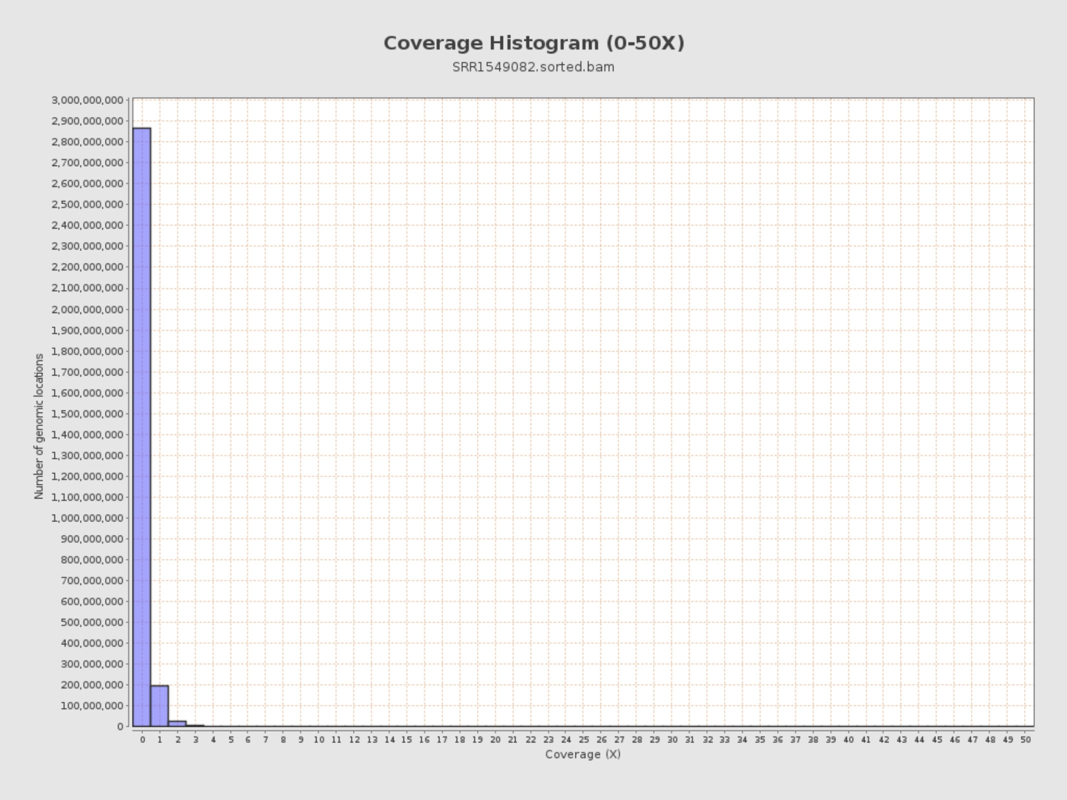
3. Results : Coverage across reference



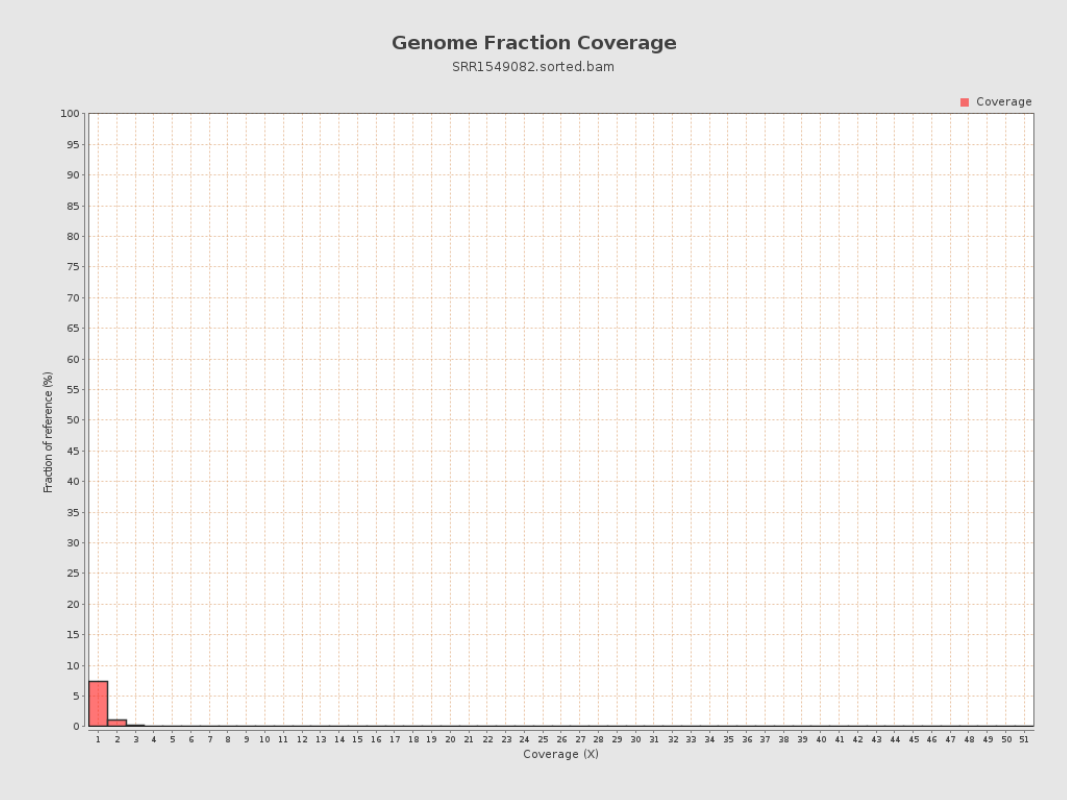
4. Results : Coverage Histogram



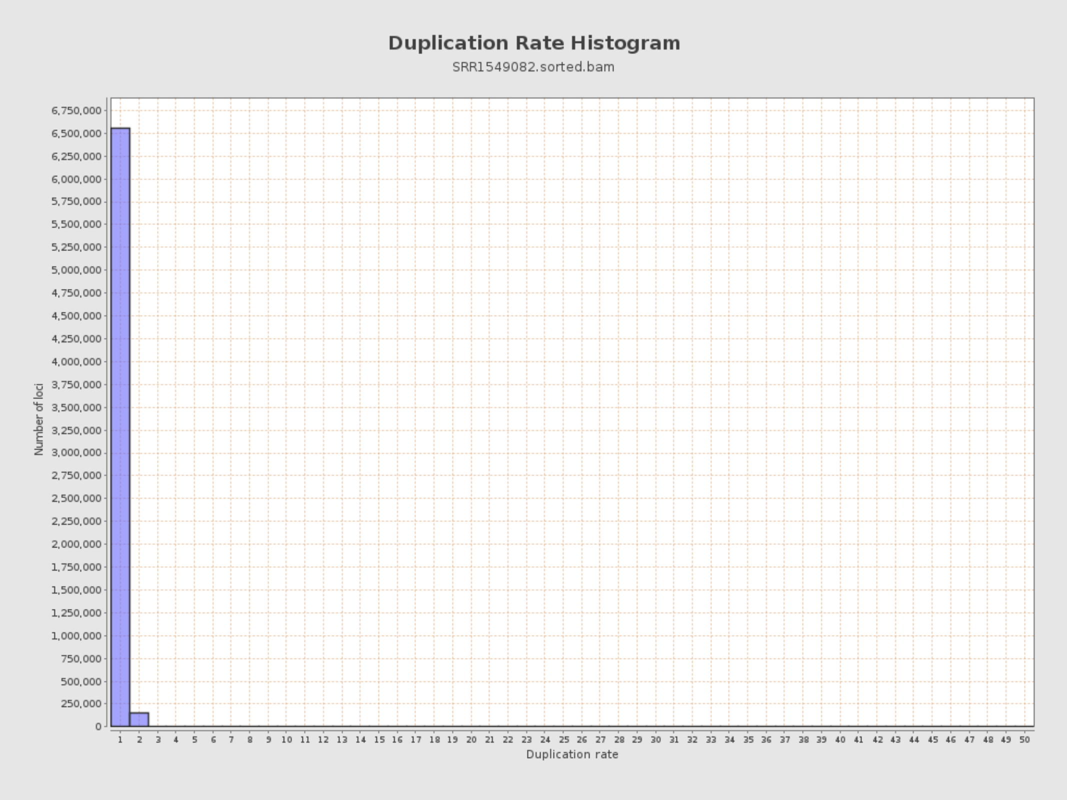
5. Results : Coverage Histogram (0-50X)



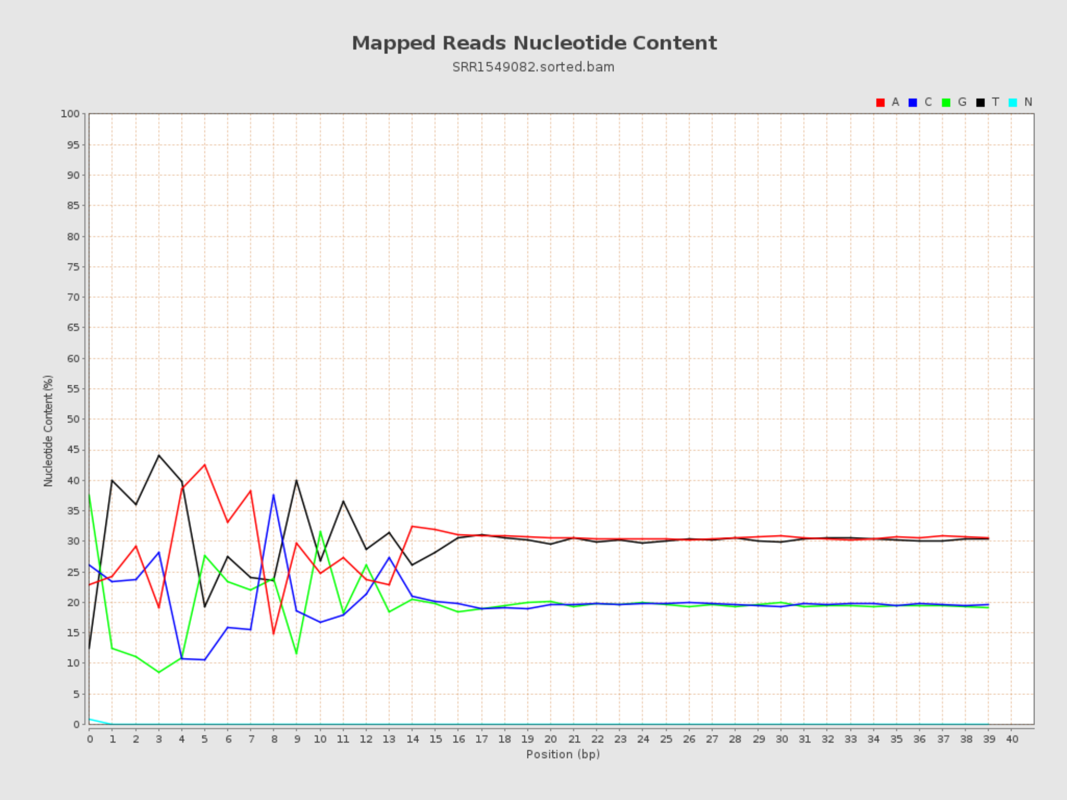
6. Results : Genome Fraction Coverage



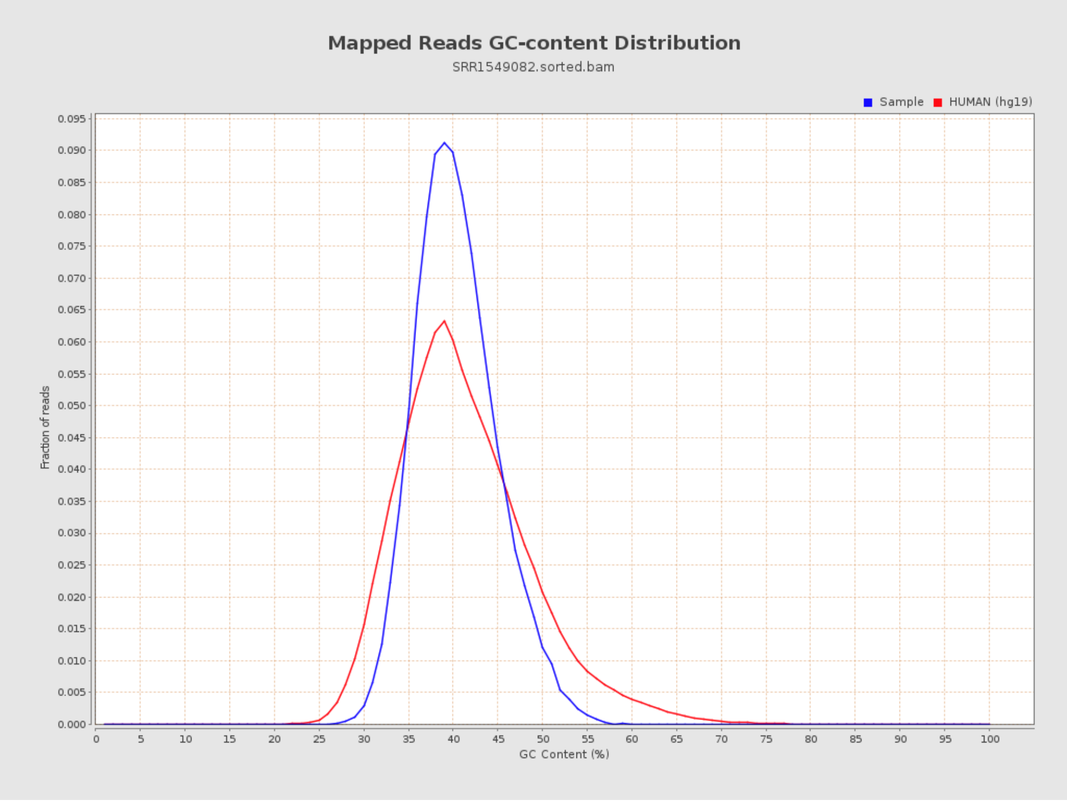
7. Results : Duplication Rate Histogram



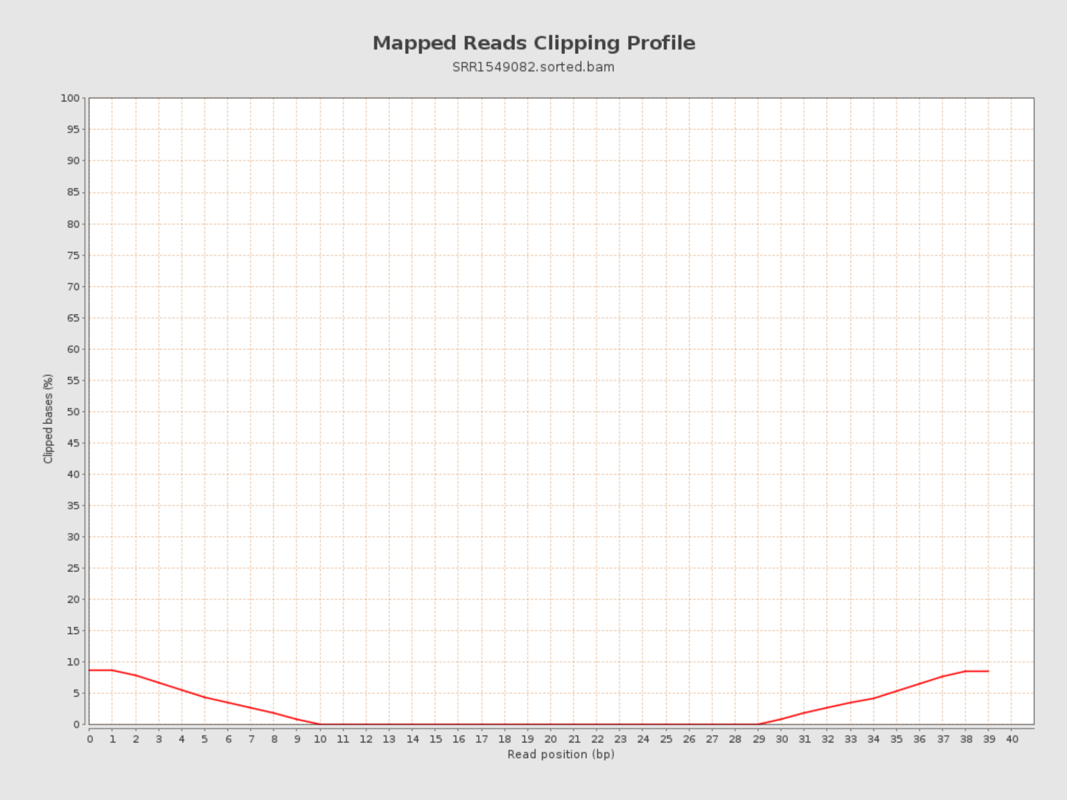
8. Results : Mapped Reads Nucleotide Content



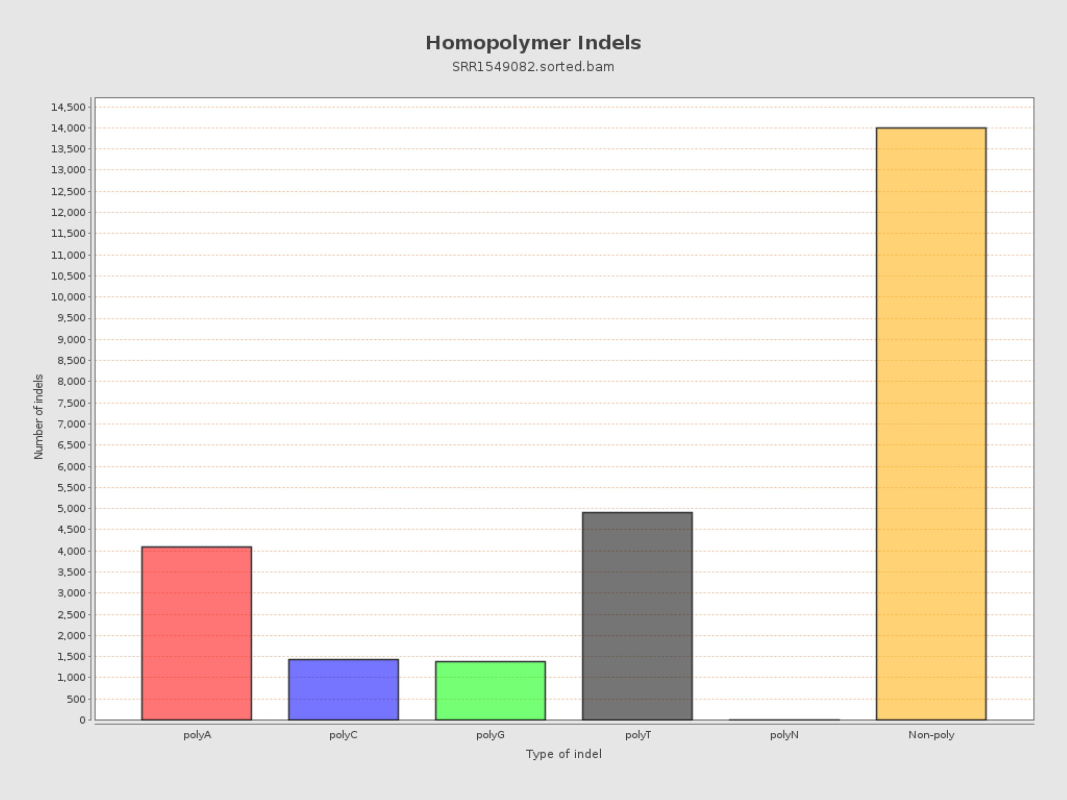
9. Results : Mapped Reads GC-content Distribution



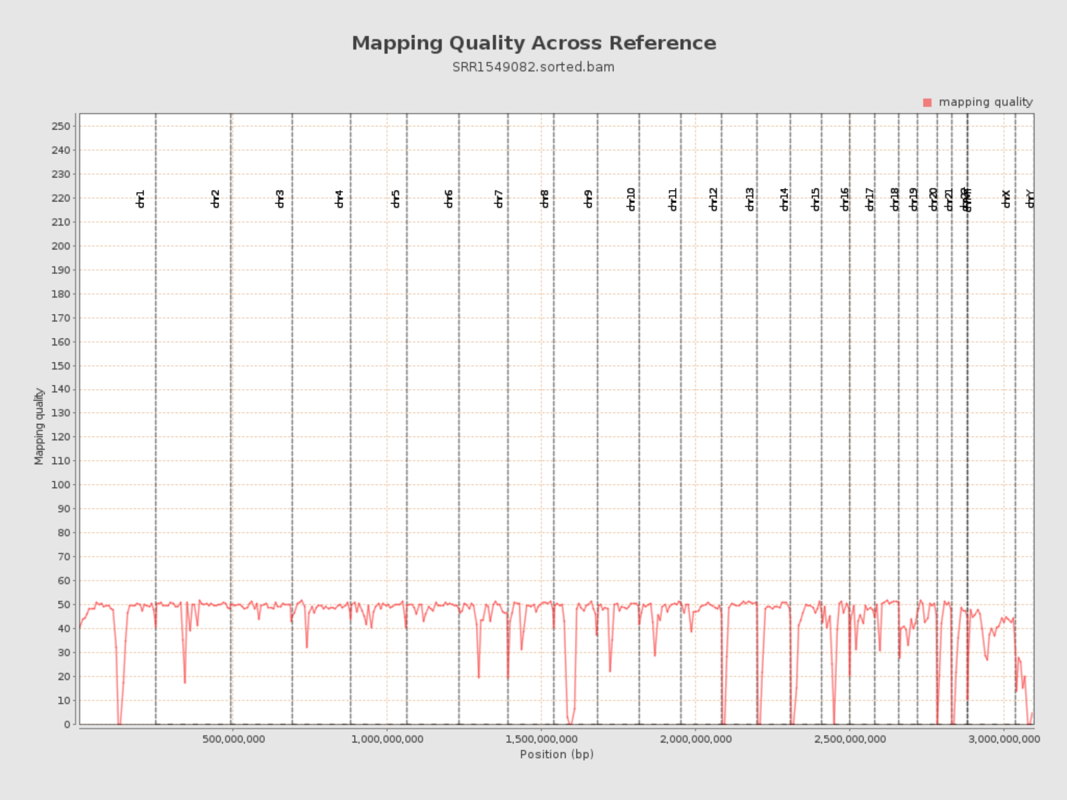
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram