Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:22:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080920.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_SRR3080920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:22:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,935,006
Mapped reads	4,489,595 / 90.97%
Unmapped reads	445,411 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	50,589 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	241,710 / 4.9%
Duplication rate	4.22%
Clipped reads	1,601,696 / 32.46%

2.2. ACGT Content

Number/percentage of A's	89,548,844 / 29%
Number/percentage of C's	54,627,691 / 17.69%
Number/percentage of T's	99,309,072 / 32.16%
Number/percentage of G's	63,861,402 / 20.68%
Number/percentage of N's	1,489,228 / 0.48%
GC Percentage	38.37%

2.3. Coverage

Mean	0.0998

Standard Deviation	0.6819

2.4. Mapping Quality

Mean Mapping Quality	47.9

2.5. Mismatches and indels

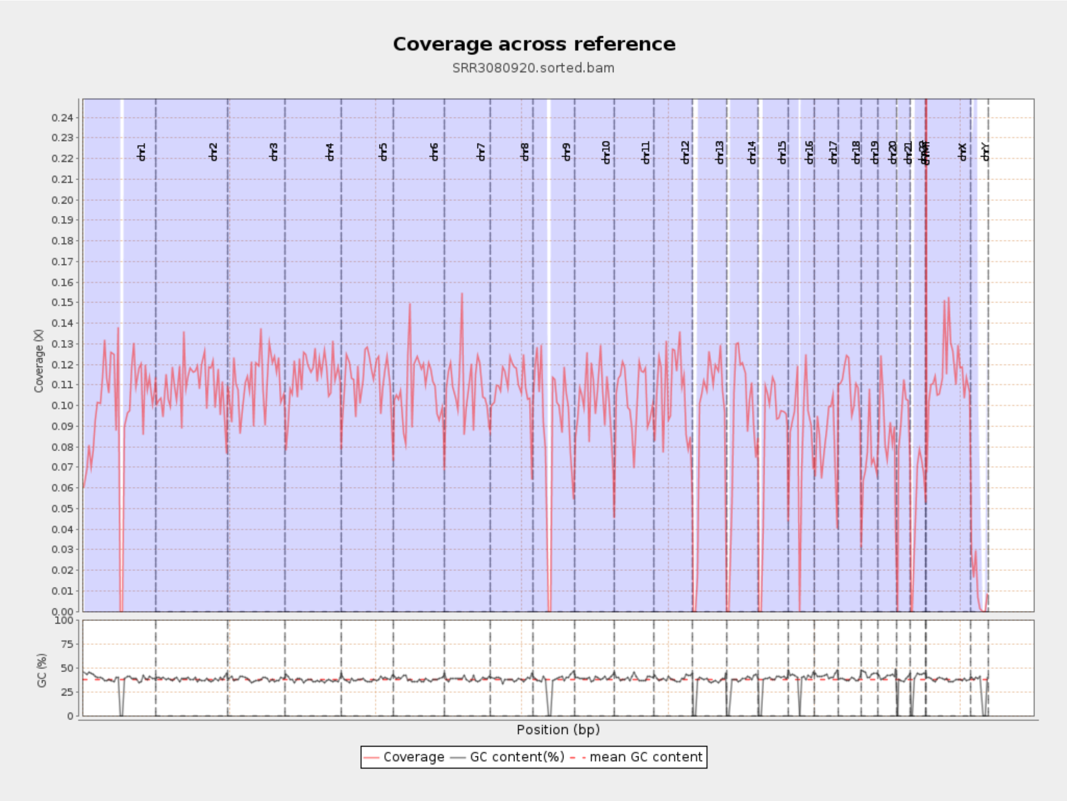
General error rate	1.18%
Mismatches	3,607,298
Insertions	23,612
Mapped reads with at least one insertion	0.52%
Deletions	68,995
Mapped reads with at least one deletion	1.52%
Homopolymer indels	50.26%

2.6. Chromosome stats

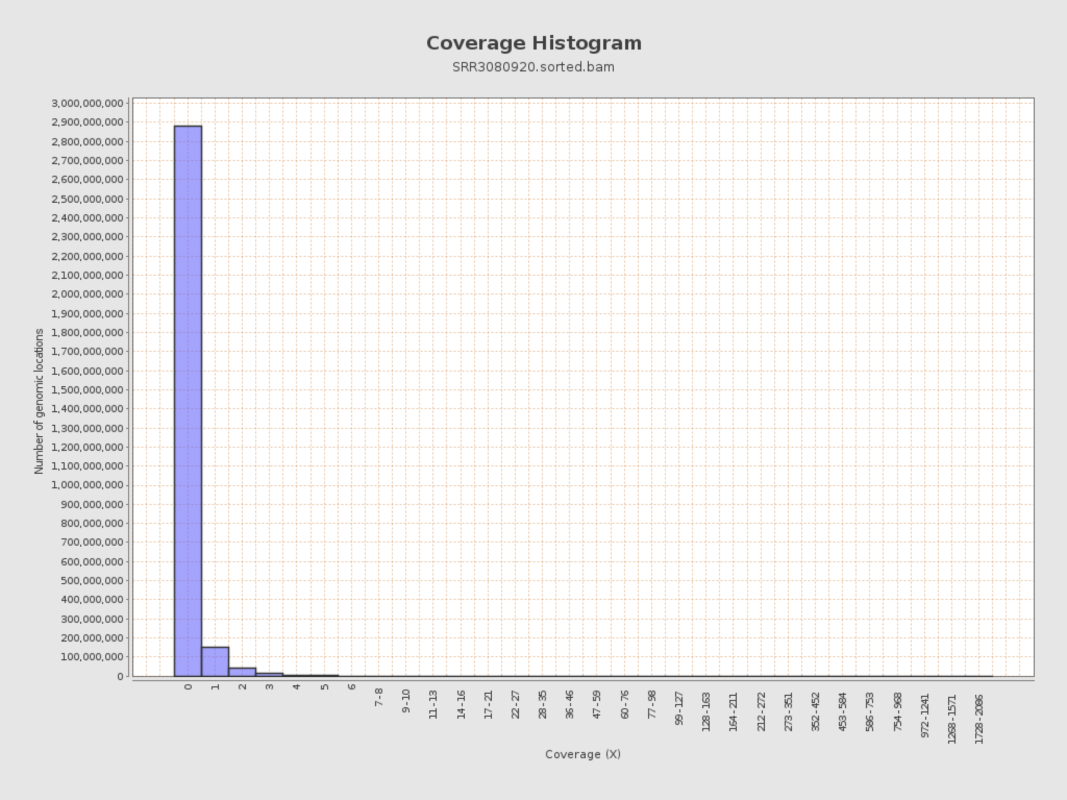
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24287576	0.0974	1.0915
chr2	243199373	26681412	0.1097	0.6377
chr3	198022430	21976918	0.111	0.4488
chr4	191154276	21883755	0.1145	0.469
chr5	180915260	20291612	0.1122	0.4529
chr6	171115067	18719691	0.1094	0.6066
chr7	159138663	17296937	0.1087	1.0142

chr8	146364022	16026647	0.1095	1.3324
chr9	141213431	12744889	0.0903	0.5838
chr10	135534747	13929842	0.1028	0.5895
chr11	135006516	13936904	0.1032	0.5417
chr12	133851895	14124091	0.1055	0.4418
chr13	115169878	10682330	0.0928	0.4107
chr14	107349540	9692002	0.0903	0.4327
chr15	102531392	8465831	0.0826	0.3867
chr16	90354753	7578881	0.0839	0.4205
chr17	81195210	6757212	0.0832	0.4367
chr18	78077248	8618489	0.1104	1.0841
chr19	59128983	4358516	0.0737	0.7473
chr20	63025520	5636284	0.0894	0.4236
chr21	48129895	4122423	0.0857	0.4226
chr22	51304566	2587082	0.0504	0.2948
chrMT	16571	14537	0.8773	1.321
chrX	155270560	17903431	0.1153	0.5
chrY	59373566	631630	0.0106	0.182

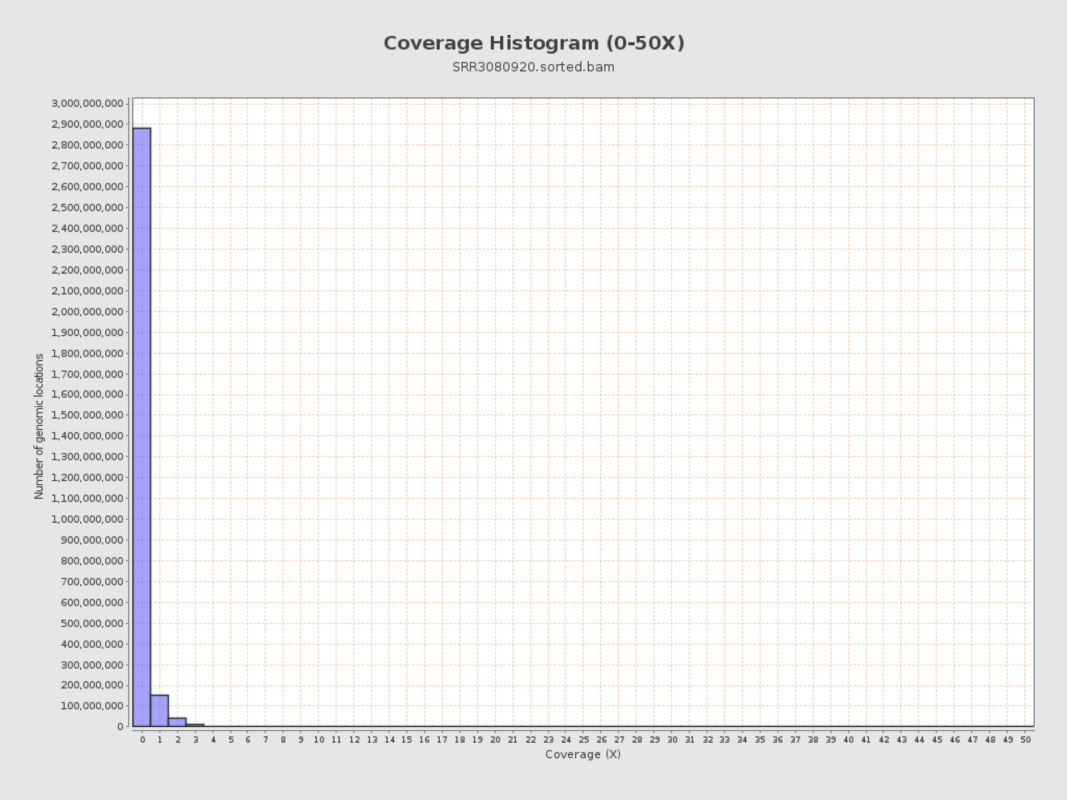
3. Results : Coverage across reference



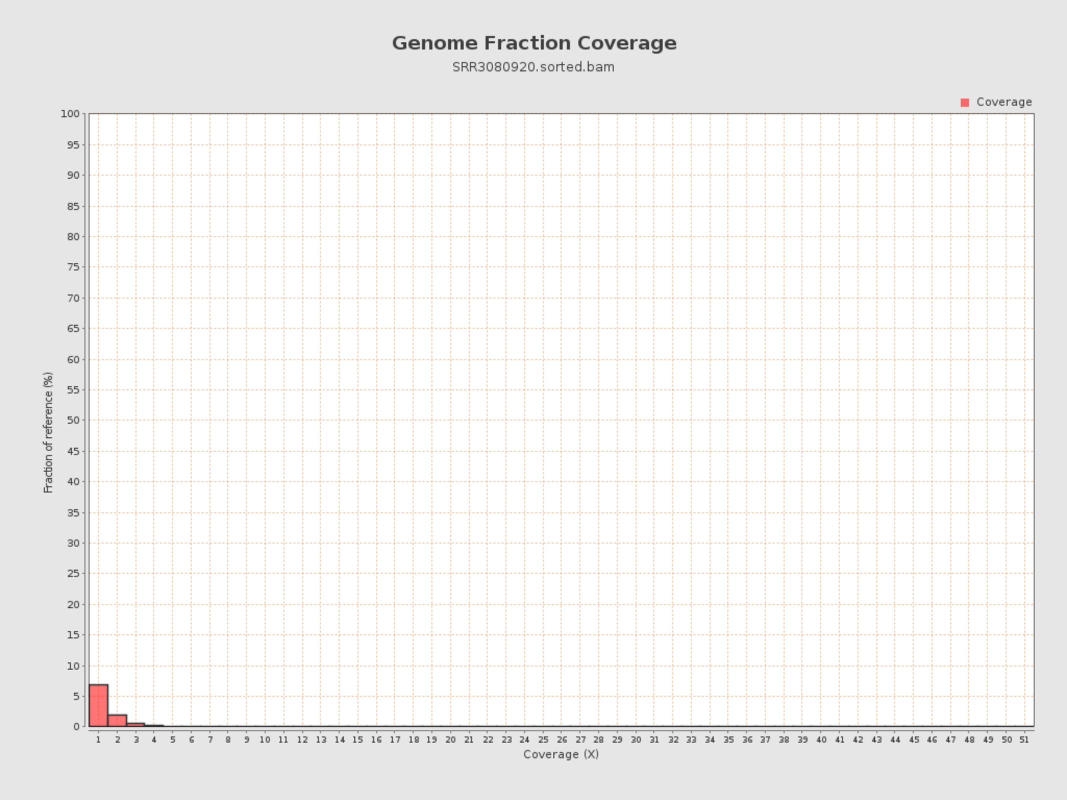
4. Results : Coverage Histogram



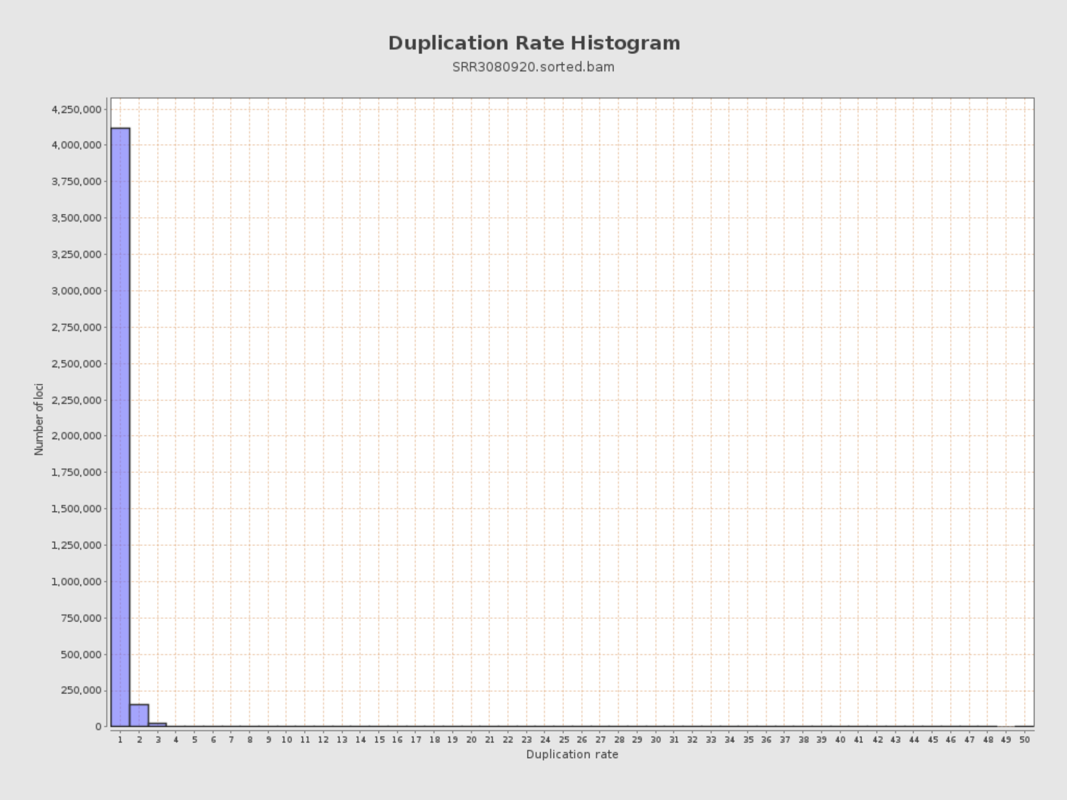
5. Results : Coverage Histogram (0-50X)



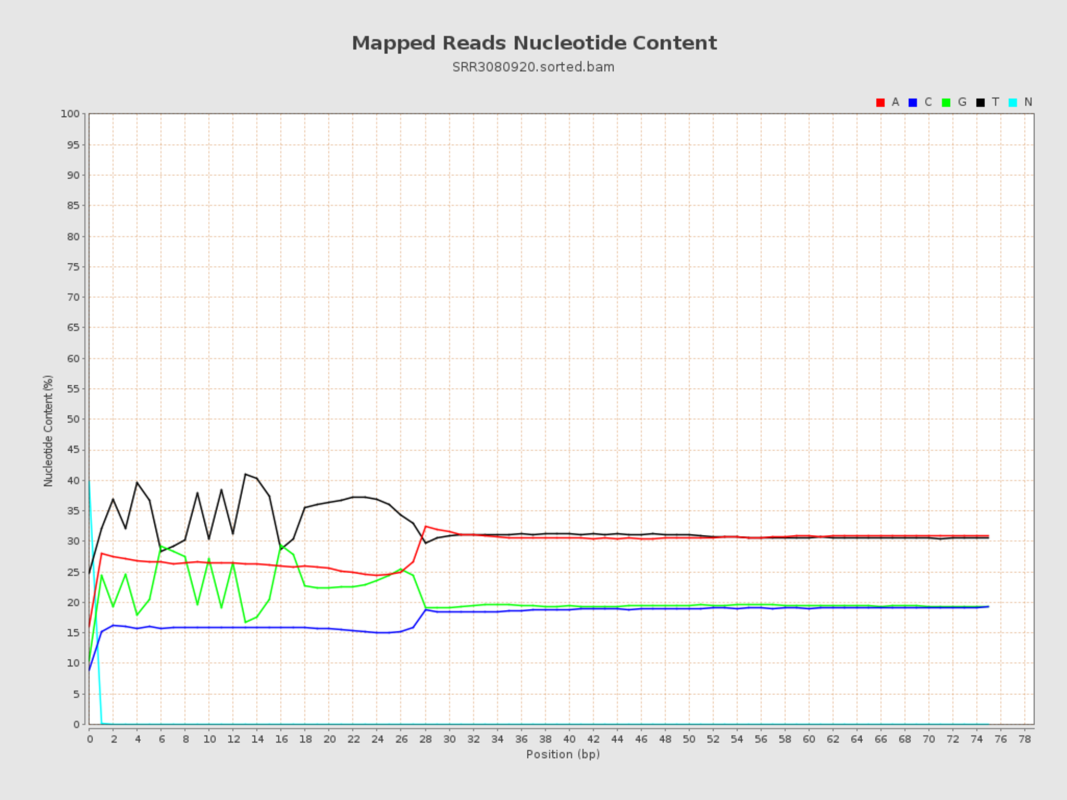
6. Results : Genome Fraction Coverage



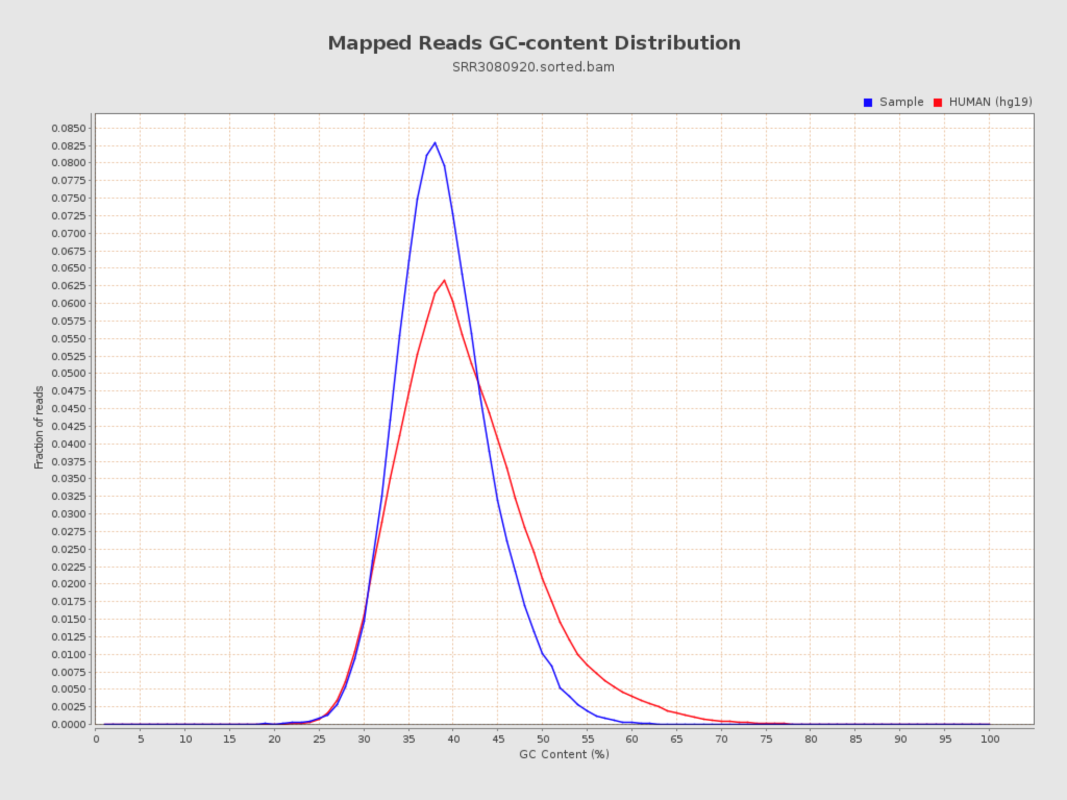
7. Results : Duplication Rate Histogram



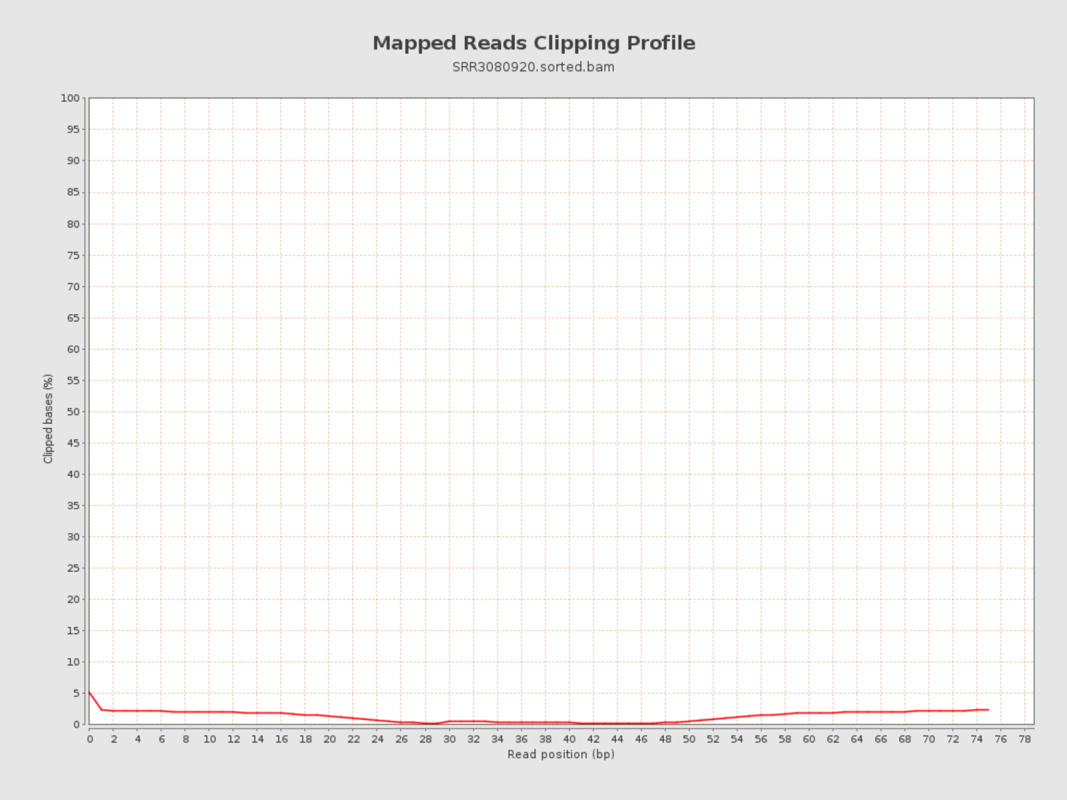
8. Results : Mapped Reads Nucleotide Content



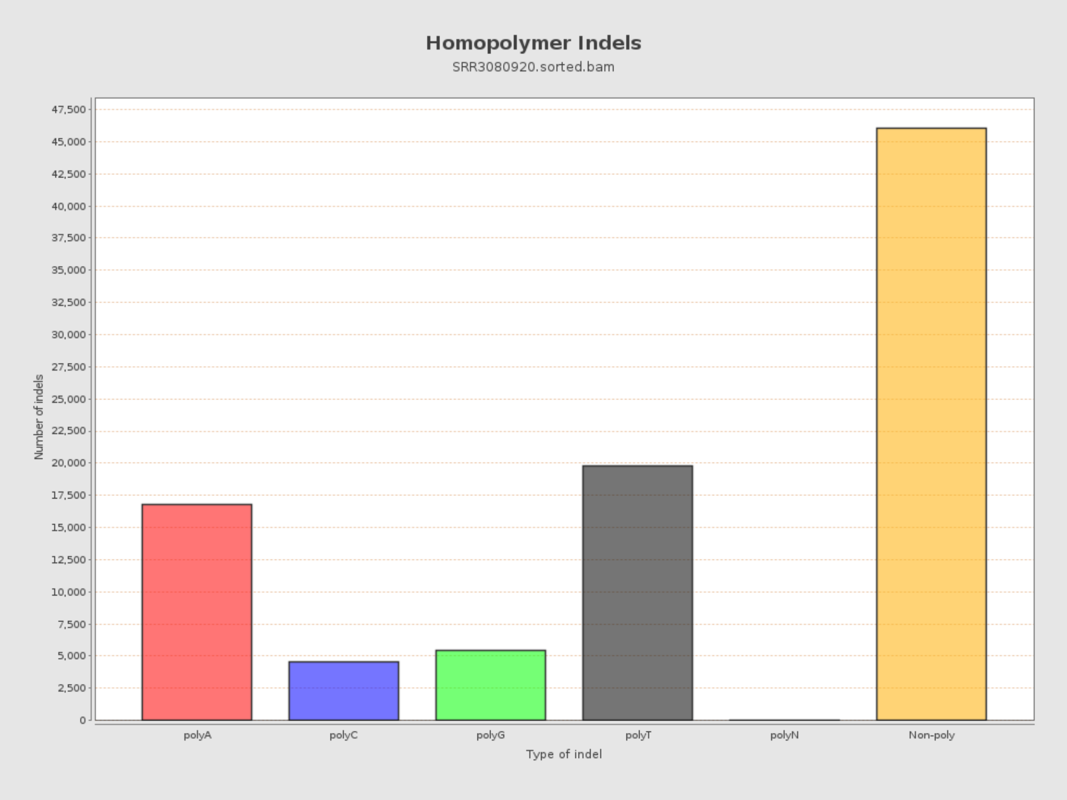
9. Results : Mapped Reads GC-content Distribution



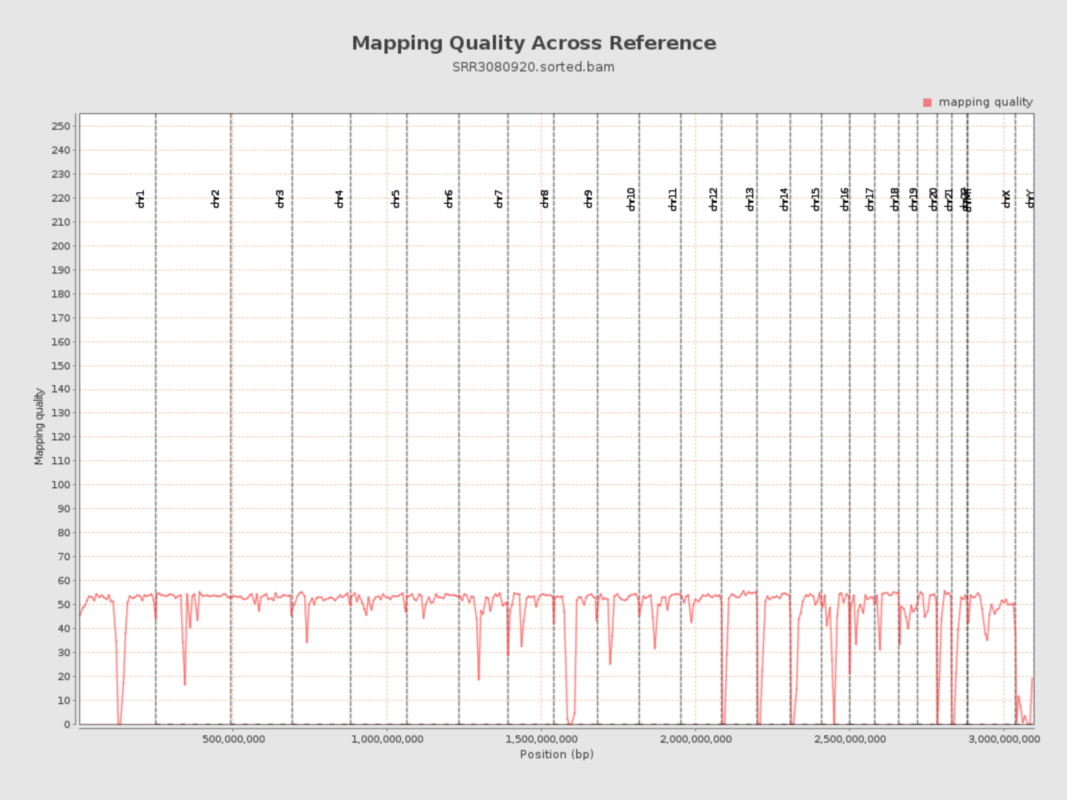
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram