

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081952.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_SRR3081952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:40:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,649,298
Mapped reads	2,465,007 / 93.04%
Unmapped reads	184,291 / 6.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,094 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	110,705 / 4.18%
Duplication rate	3.58%
Clipped reads	859,022 / 32.42%

2.2. ACGT Content

Number/percentage of A's	48,513,542 / 28.62%
Number/percentage of C's	31,422,637 / 18.54%
Number/percentage of T's	53,643,050 / 31.64%
Number/percentage of G's	35,916,910 / 21.19%
Number/percentage of N's	22,183 / 0.01%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0548

Standard Deviation	0.4371
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2.4. Mapping Quality

Mean Mapping Quality	46.91
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2.5. Mismatches and indels

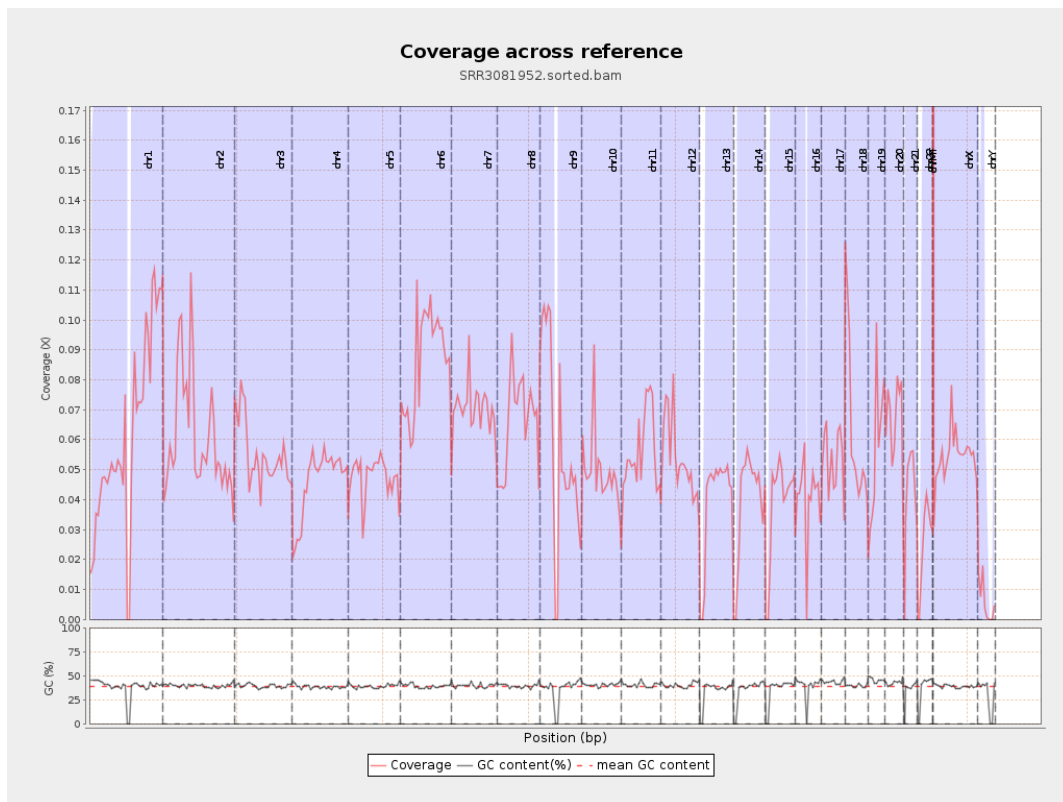
General error rate	0.75%
Mismatches	1,246,698
Insertions	11,924
Mapped reads with at least one insertion	0.48%
Deletions	35,130
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.75%

2.6. Chromosome stats

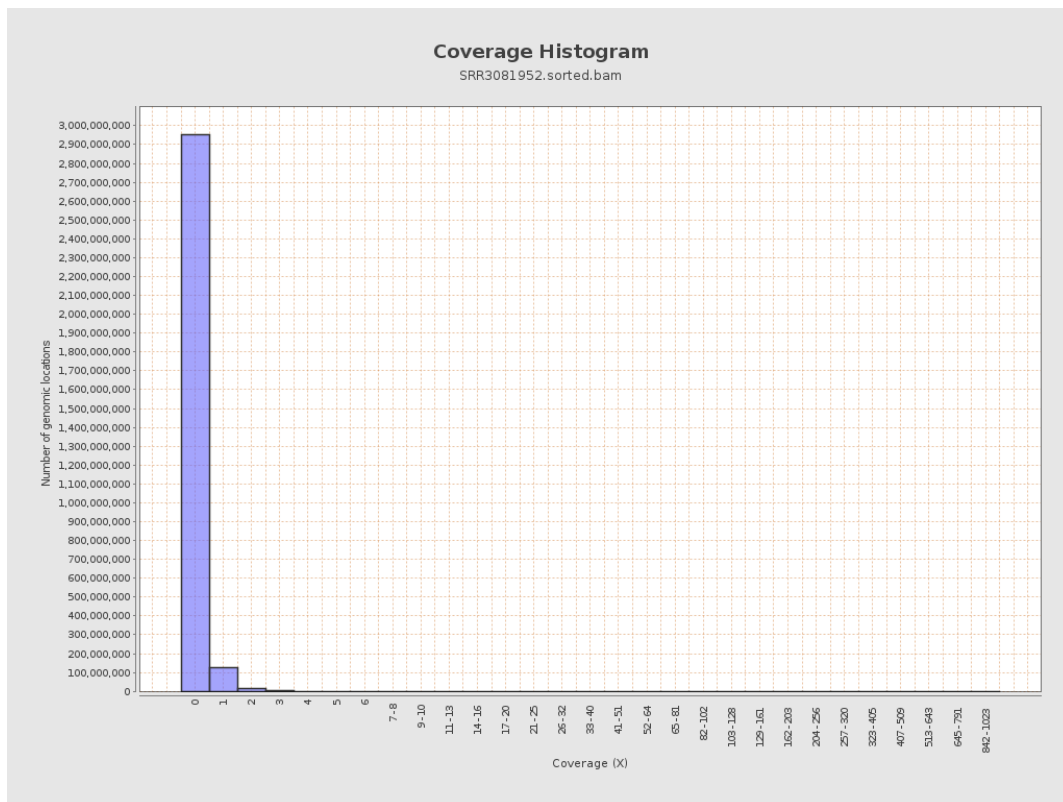
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15440360	0.0619	0.7387
chr2	243199373	14876881	0.0612	0.5397
chr3	198022430	10963247	0.0554	0.2664
chr4	191154276	8844601	0.0463	0.2556
chr5	180915260	8531253	0.0472	0.248
chr6	171115067	14889531	0.087	0.4106
chr7	159138663	11164364	0.0702	0.5613

chr8	146364022	9695979	0.0662	0.7147
chr9	141213431	8279487	0.0586	0.4557
chr10	135534747	6732014	0.0497	0.4113
chr11	135006516	7605029	0.0563	0.3362
chr12	133851895	7180833	0.0536	0.2705
chr13	115169878	4557585	0.0396	0.2237
chr14	107349540	4280524	0.0399	0.2522
chr15	102531392	3872923	0.0378	0.2203
chr16	90354753	3563198	0.0394	0.2675
chr17	81195210	4371882	0.0538	0.2886
chr18	78077248	4883423	0.0625	0.7211
chr19	59128983	3370813	0.057	0.5454
chr20	63025520	4305531	0.0683	0.3009
chr21	48129895	1992281	0.0414	0.2524
chr22	51304566	1299909	0.0253	0.1771
chrMT	16571	74898	4.5198	3.1604
chrX	155270560	8454382	0.0544	0.3032
chrY	59373566	349394	0.0059	0.1375

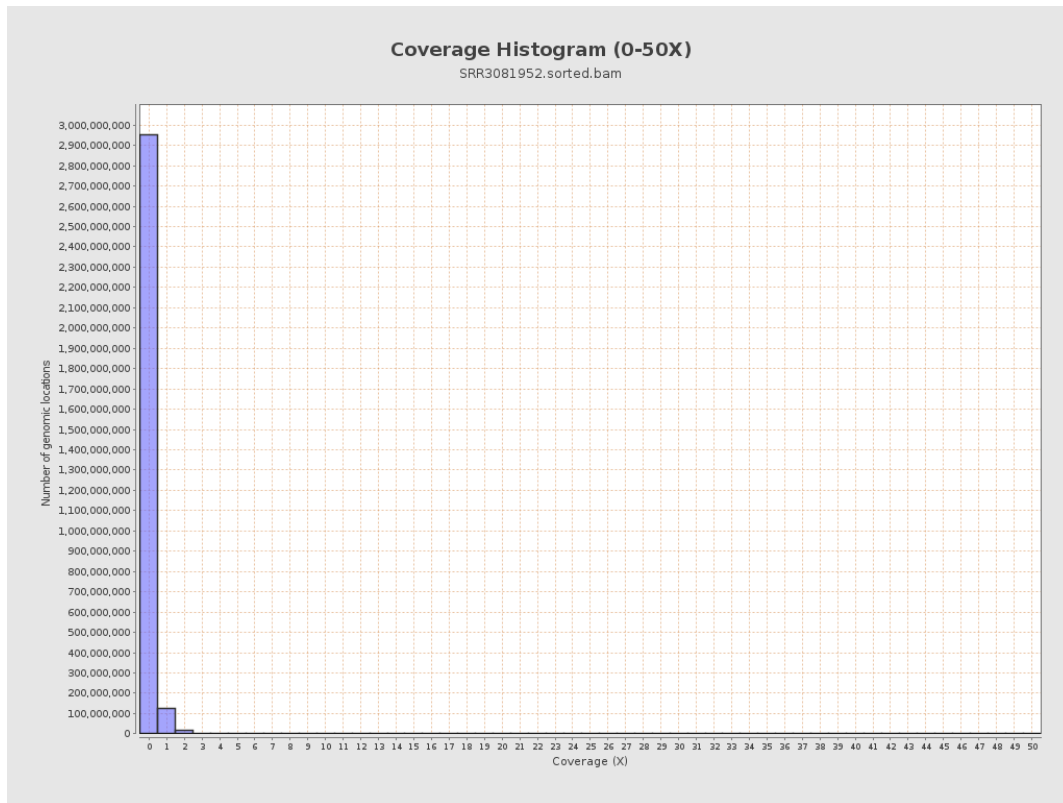
3. Results : Coverage across reference



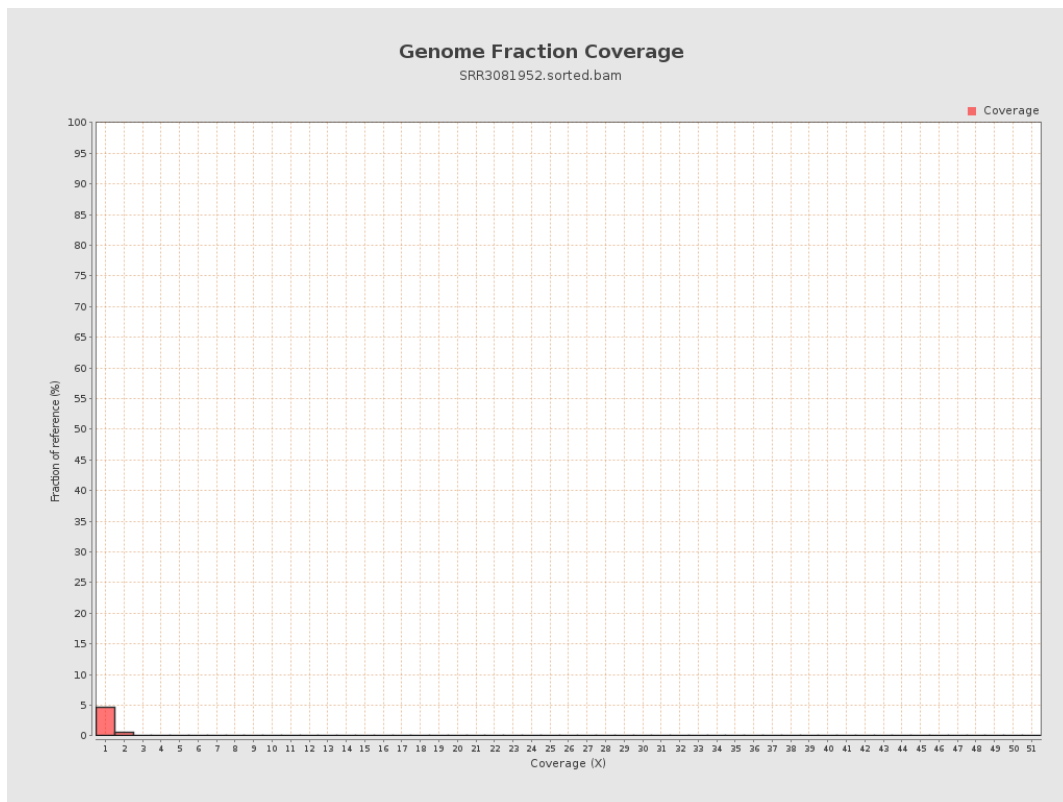
4. Results : Coverage Histogram



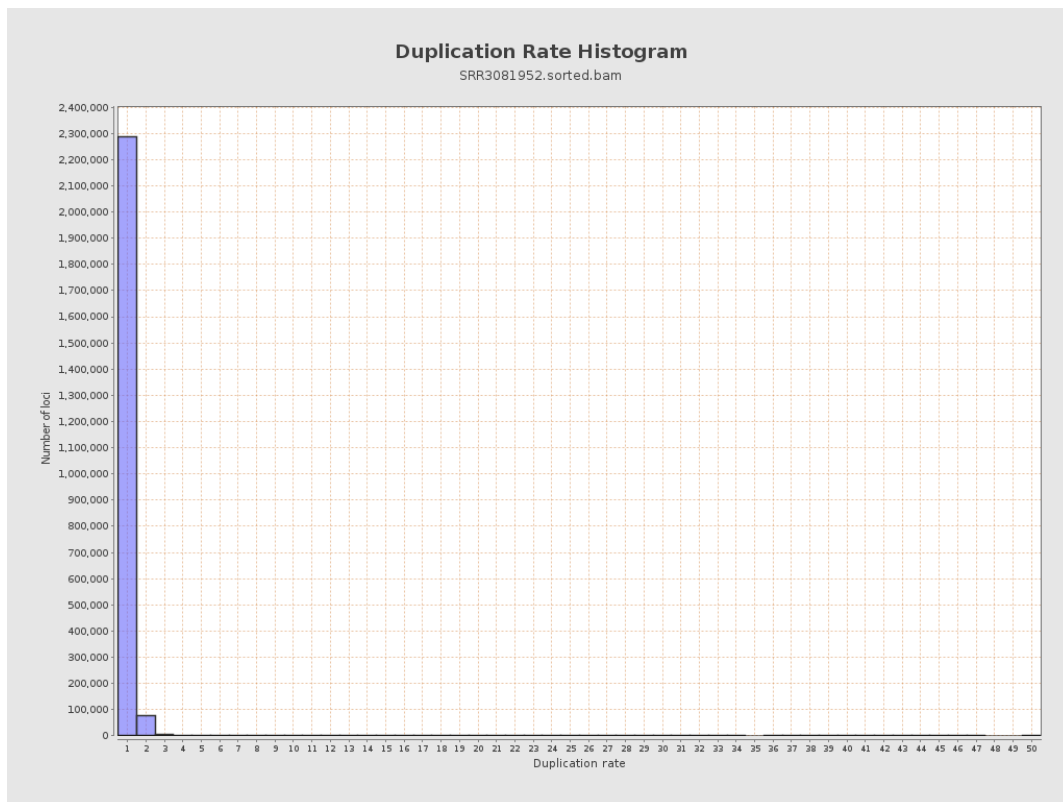
5. Results : Coverage Histogram (0-50X)



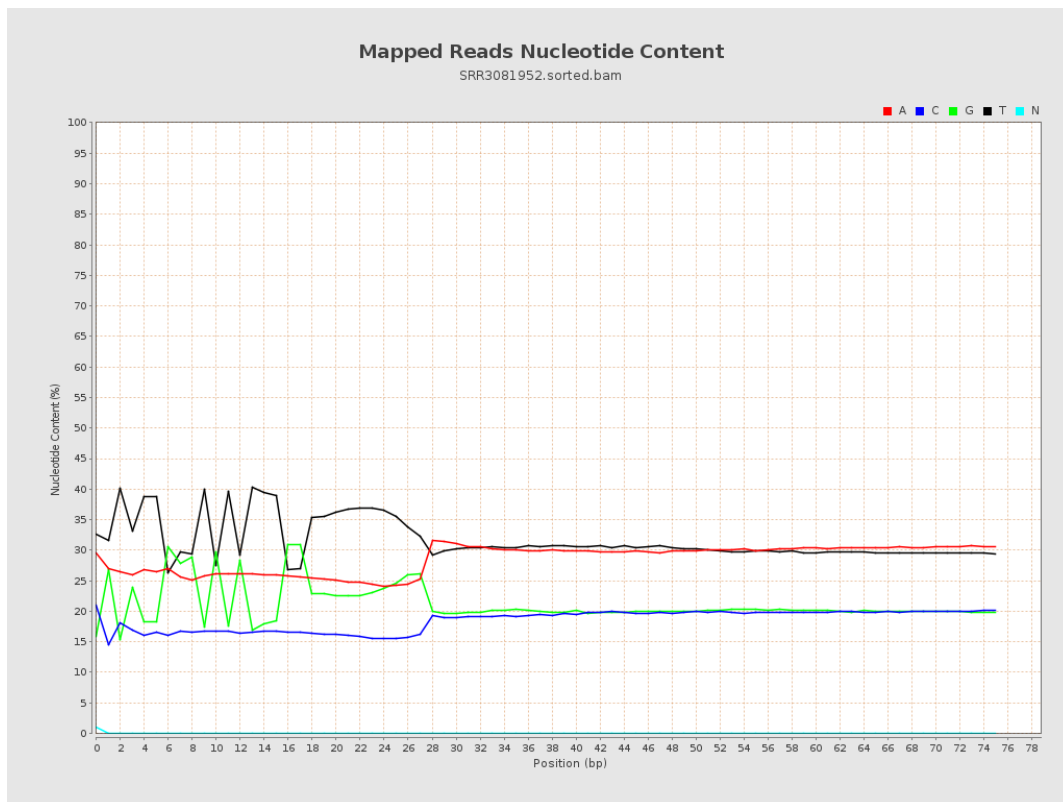
6. Results : Genome Fraction Coverage



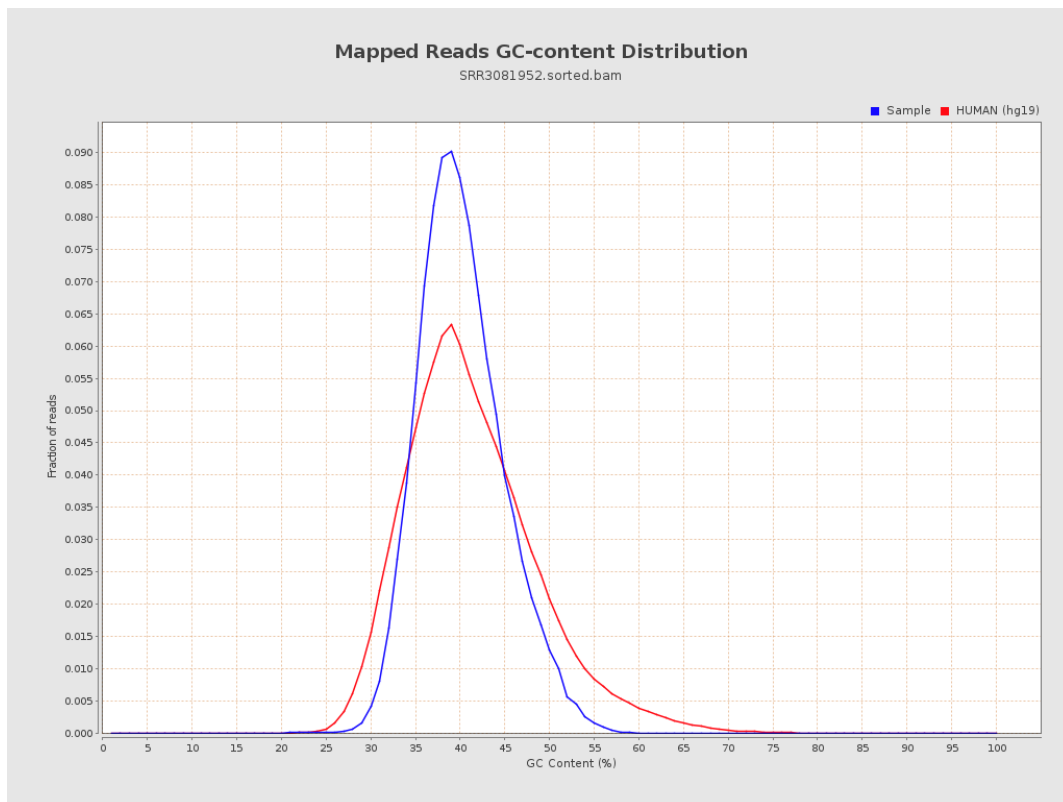
7. Results : Duplication Rate Histogram



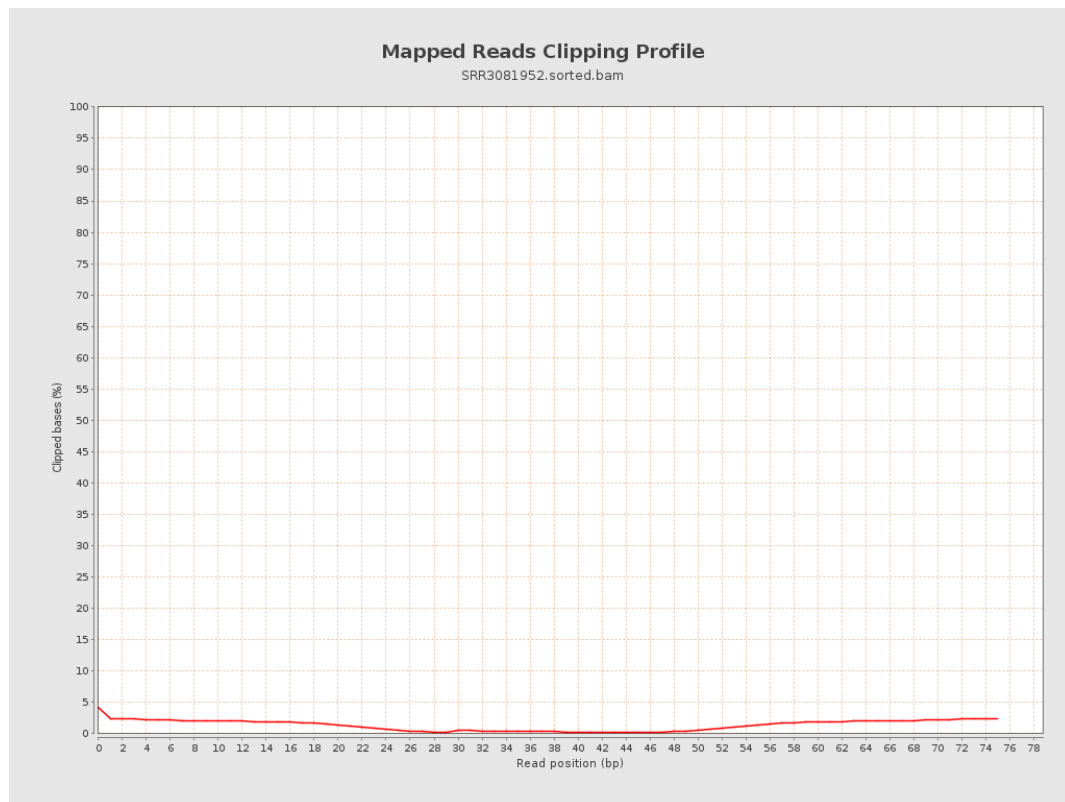
8. Results : Mapped Reads Nucleotide Content



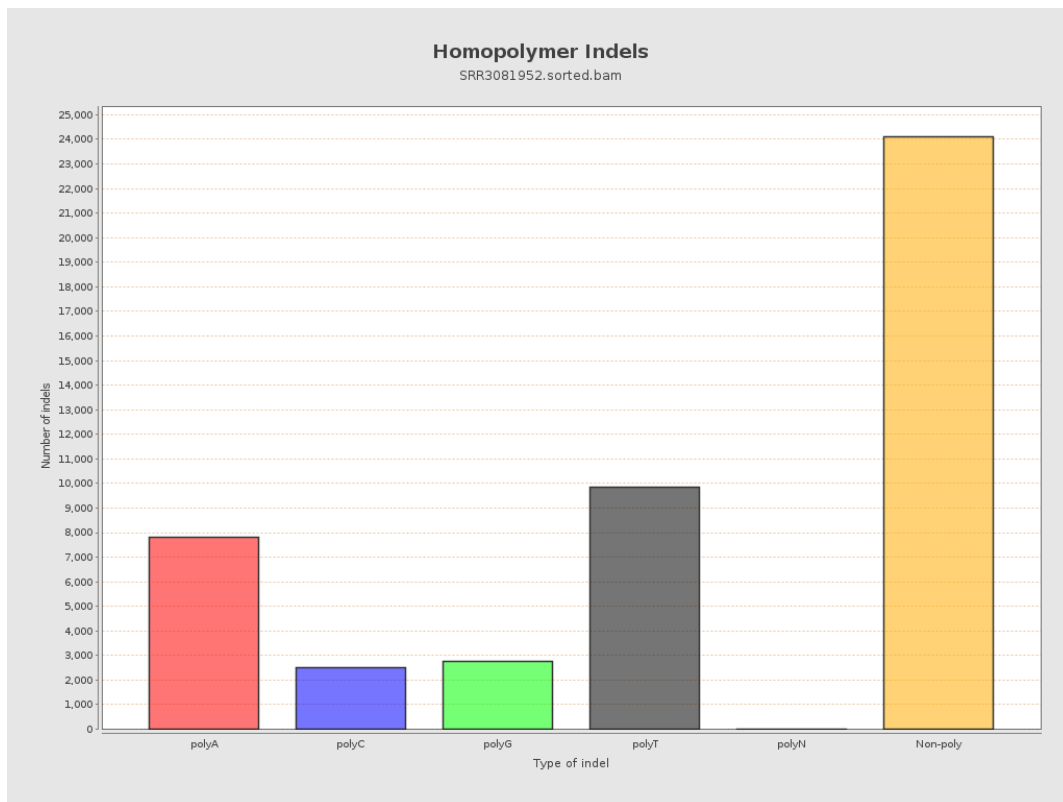
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

