

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:16:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082421.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_SRR3082421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082421.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:16:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,476,644
Mapped reads	3,126,221 / 89.92%
Unmapped reads	350,423 / 10.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,482 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	137,937 / 3.97%
Duplication rate	3.48%
Clipped reads	1,339,118 / 38.52%

2.2. ACGT Content

Number/percentage of A's	58,994,193 / 27.99%
Number/percentage of C's	39,117,574 / 18.56%
Number/percentage of T's	66,194,241 / 31.4%
Number/percentage of G's	46,472,957 / 22.05%
Number/percentage of N's	4,302 / 0%
GC Percentage	40.61%

2.3. Coverage

Mean	0.0681

Standard Deviation	0.4989
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2.4. Mapping Quality

Mean Mapping Quality	46.37
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2.5. Mismatches and indels

General error rate	0.82%
Mismatches	1,708,961
Insertions	16,587
Mapped reads with at least one insertion	0.53%
Deletions	45,642
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.68%

2.6. Chromosome stats

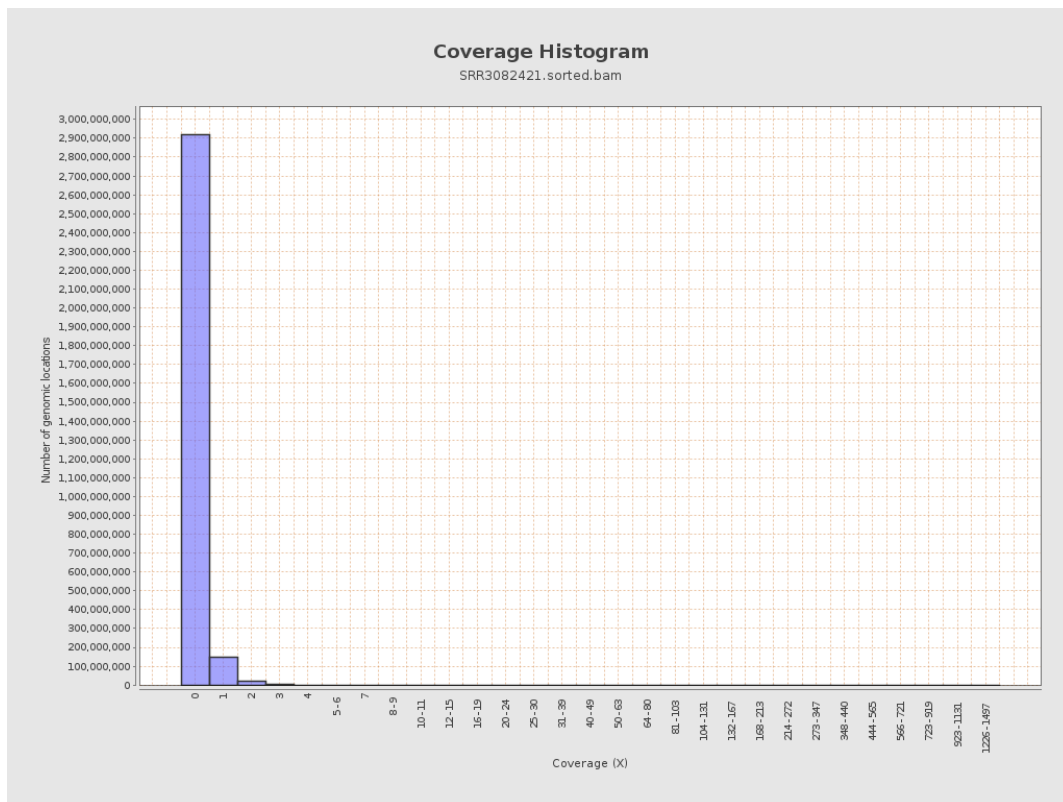
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16448124	0.066	0.766
chr2	243199373	18225434	0.0749	0.6474
chr3	198022430	14686004	0.0742	0.3142
chr4	191154276	14155442	0.0741	0.3251
chr5	180915260	13299556	0.0735	0.3149
chr6	171115067	12163277	0.0711	0.3702
chr7	159138663	11555677	0.0726	0.6274

chr8	146364022	10899540	0.0745	0.9461
chr9	141213431	8822270	0.0625	0.4466
chr10	135534747	9900408	0.073	0.4249
chr11	135006516	9620767	0.0713	0.4219
chr12	133851895	9570830	0.0715	0.3144
chr13	115169878	6732026	0.0585	0.2791
chr14	107349540	6386084	0.0595	0.2986
chr15	102531392	6093338	0.0594	0.295
chr16	90354753	5771004	0.0639	0.3228
chr17	81195210	5220934	0.0643	0.3268
chr18	78077248	5842660	0.0748	0.831
chr19	59128983	3773382	0.0638	0.6223
chr20	63025520	3995785	0.0634	0.3013
chr21	48129895	2788448	0.0579	0.2949
chr22	51304566	2069802	0.0403	0.23
chrMT	16571	3145	0.1898	0.4547
chrX	155270560	12346586	0.0795	0.3653
chrY	59373566	485862	0.0082	0.1559

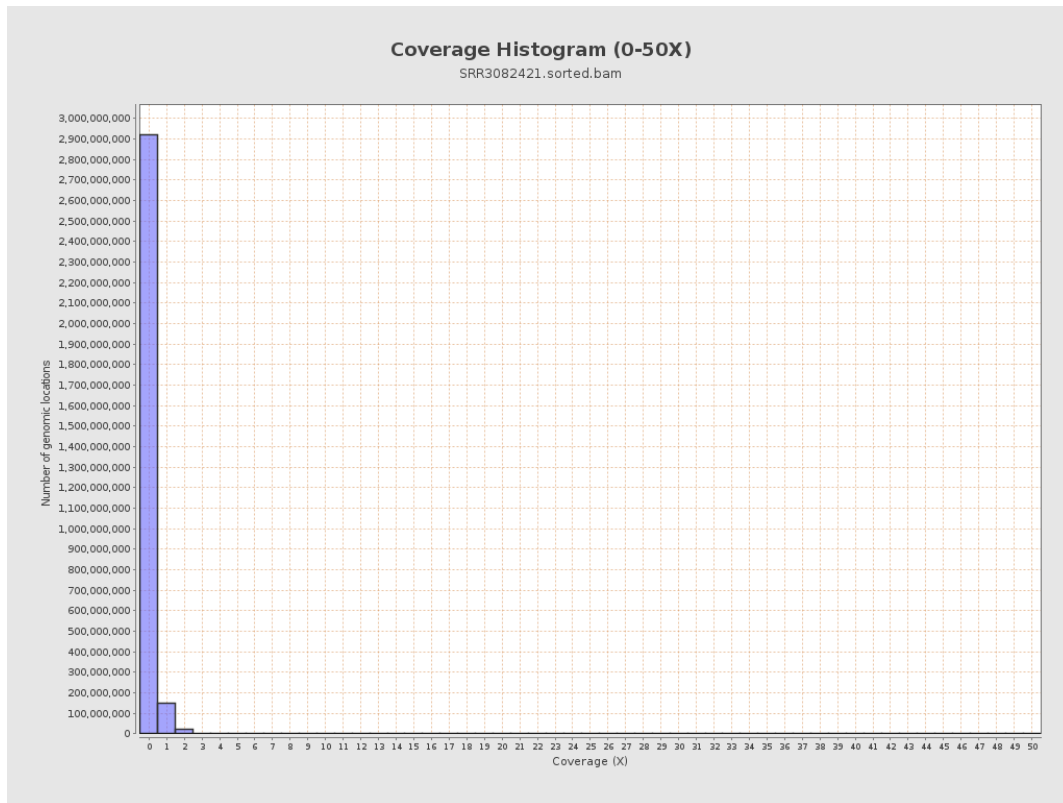
3. Results : Coverage across reference



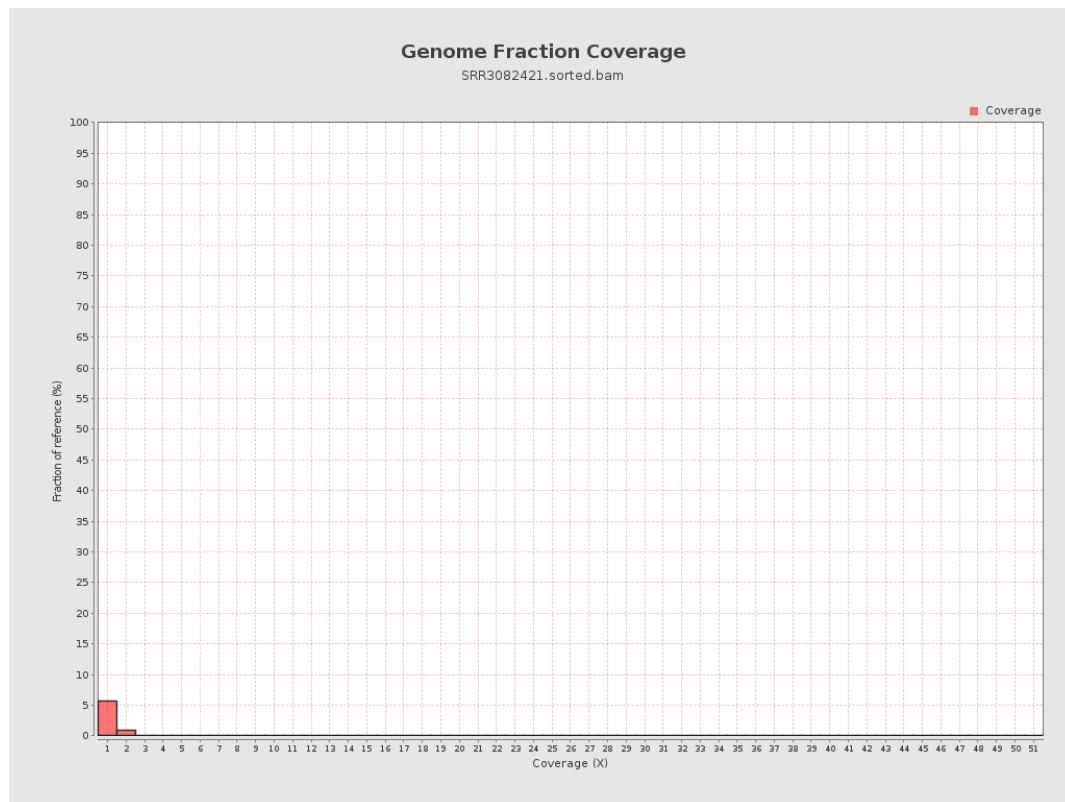
4. Results : Coverage Histogram



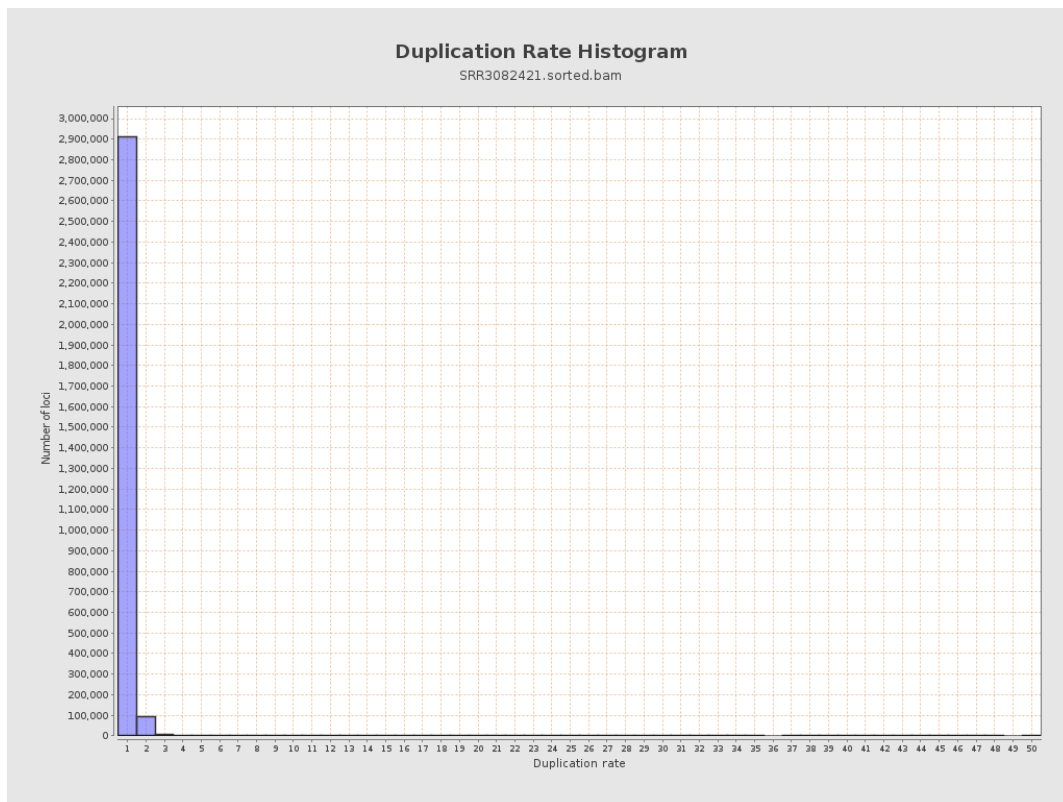
5. Results : Coverage Histogram (0-50X)



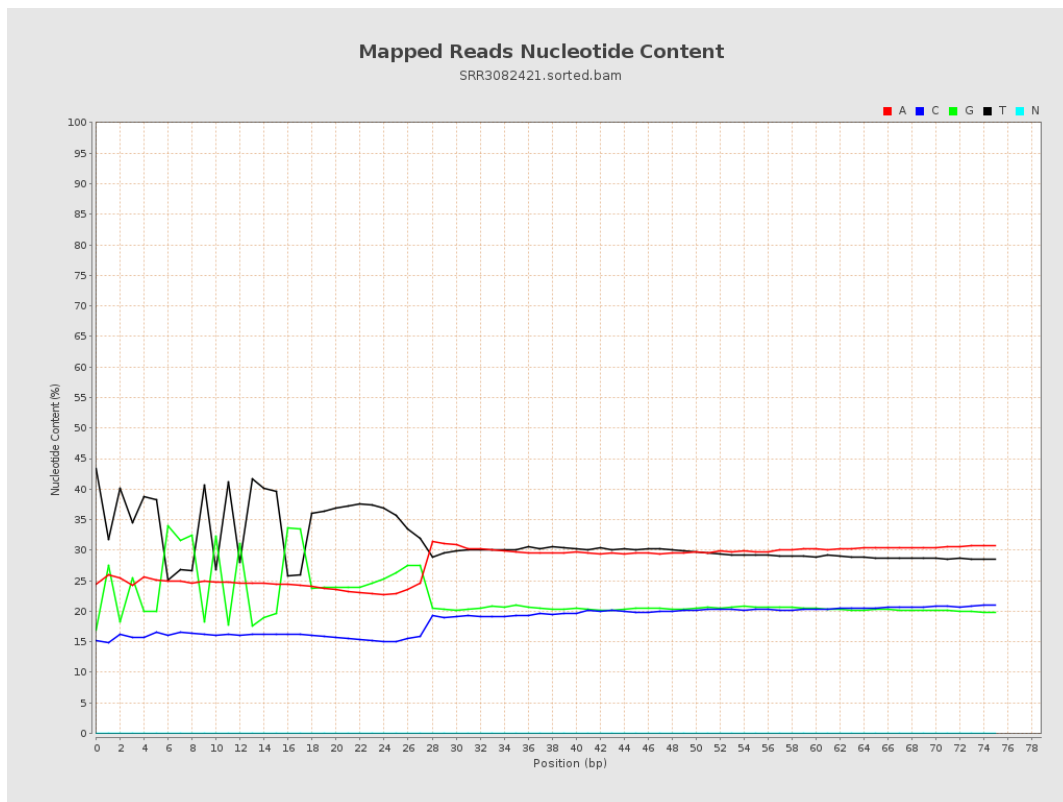
6. Results : Genome Fraction Coverage



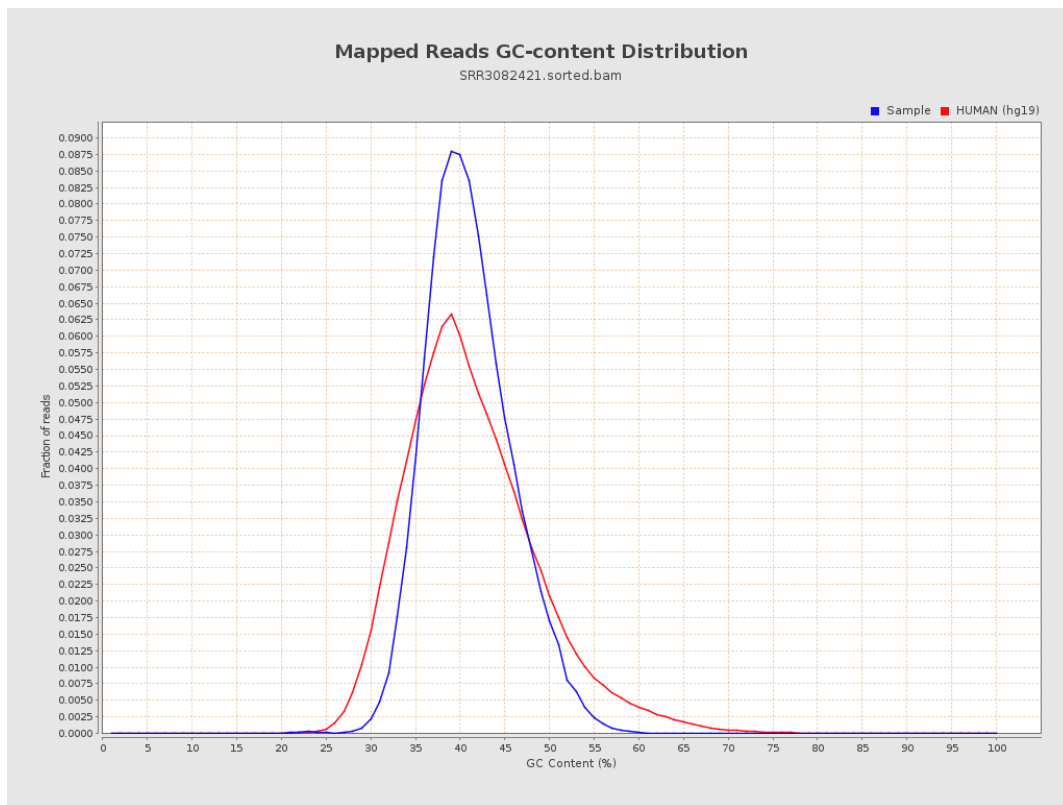
7. Results : Duplication Rate Histogram



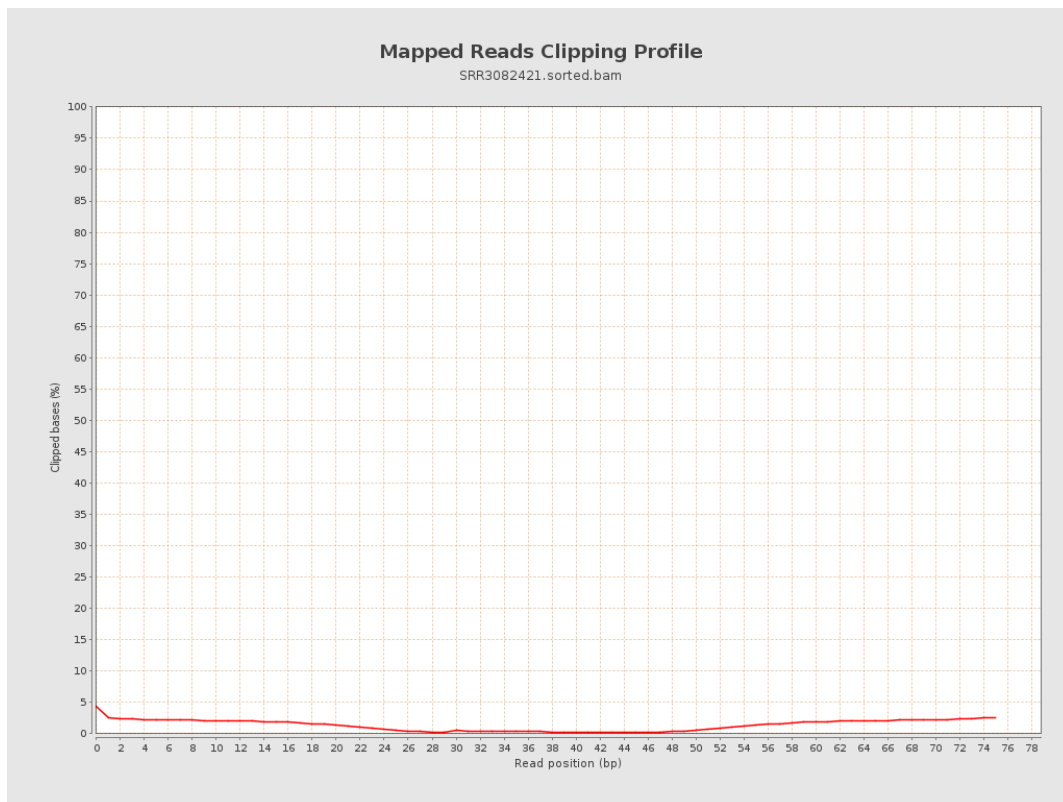
8. Results : Mapped Reads Nucleotide Content



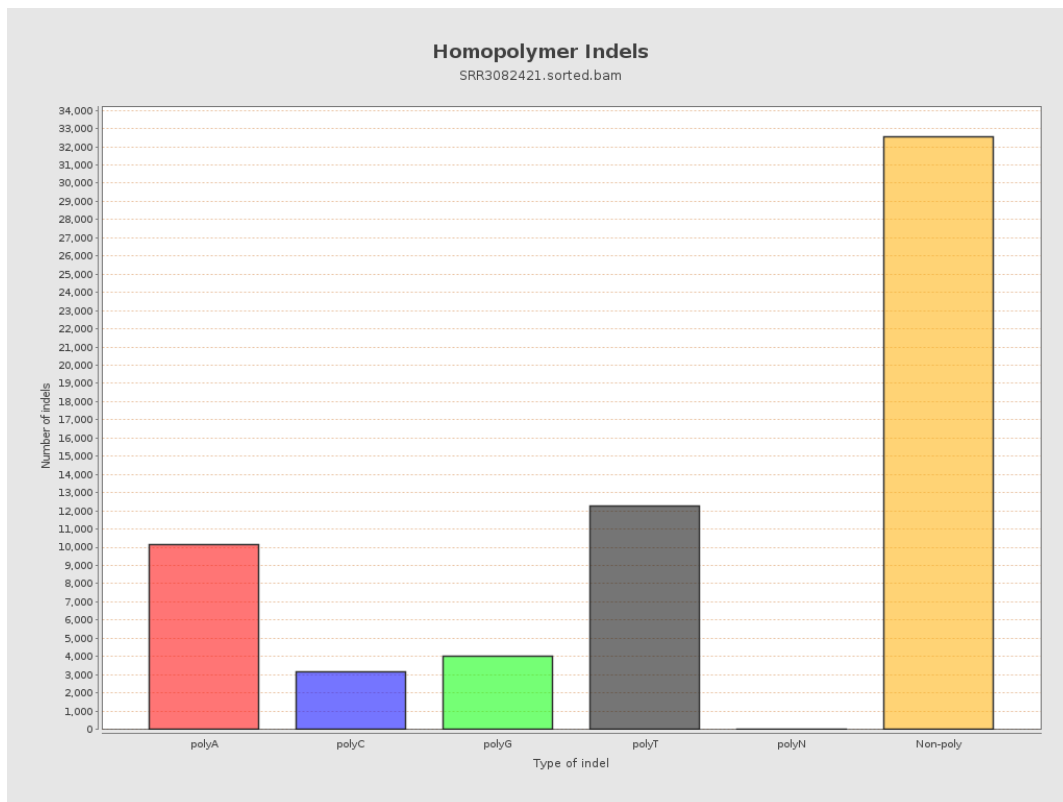
9. Results : Mapped Reads GC-content Distribution



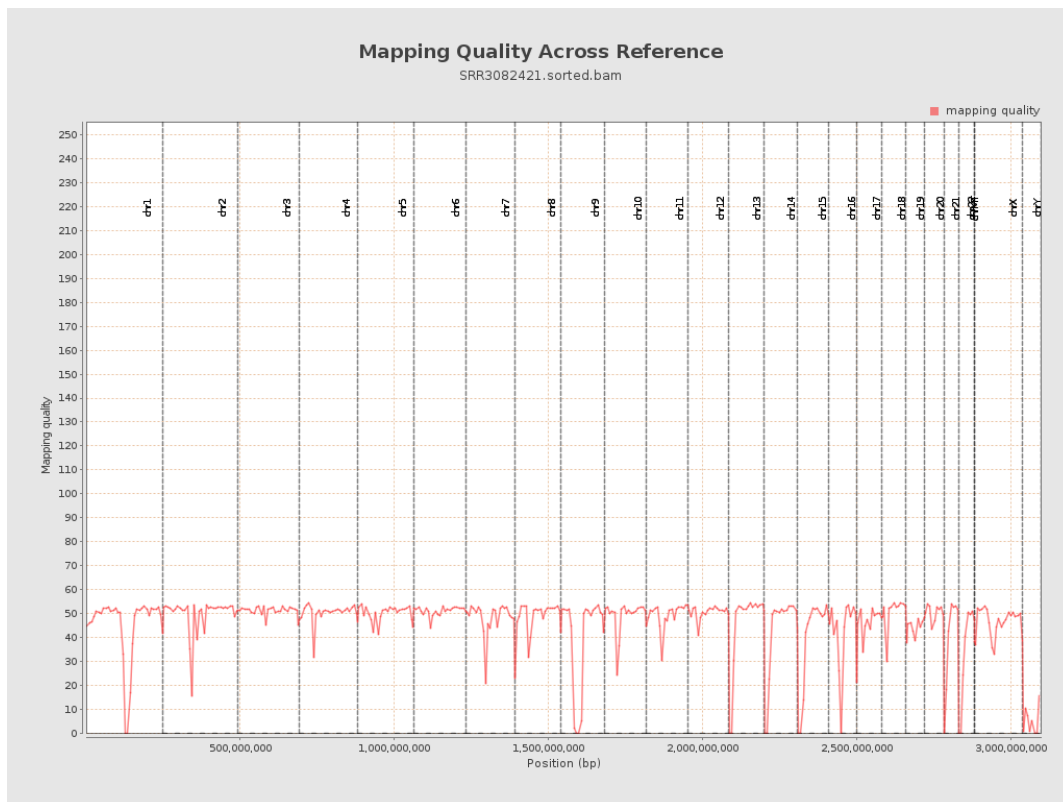
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

