

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:36:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549050.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_SRR1549050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:36:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,781,649
Mapped reads	3,282,295 / 86.8%
Unmapped reads	499,354 / 13.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	96,905 / 2.56%
Duplication rate	2.2%
Clipped reads	242,183 / 6.4%

2.2. ACGT Content

Number/percentage of A's	36,902,699 / 28.41%
Number/percentage of C's	27,558,266 / 21.21%
Number/percentage of T's	37,605,090 / 28.95%
Number/percentage of G's	27,835,347 / 21.43%
Number/percentage of N's	1,125 / 0%
GC Percentage	42.64%

2.3. Coverage

Mean	0.042
Standard Deviation	0.3815

2.4. Mapping Quality

Mean Mapping Quality	41.64
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2.5. Mismatches and indels

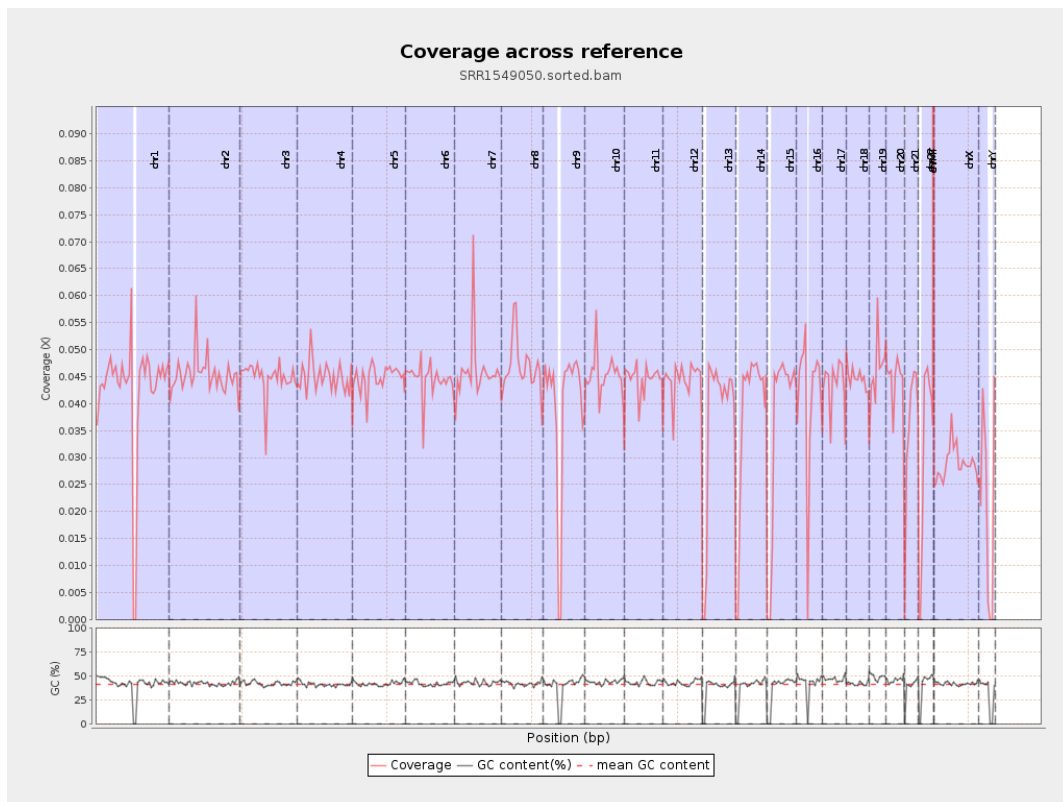
General error rate	0.26%
Mismatches	328,686
Insertions	3,682
Mapped reads with at least one insertion	0.11%
Deletions	10,287
Mapped reads with at least one deletion	0.31%
Homopolymer indels	41.53%

2.6. Chromosome stats

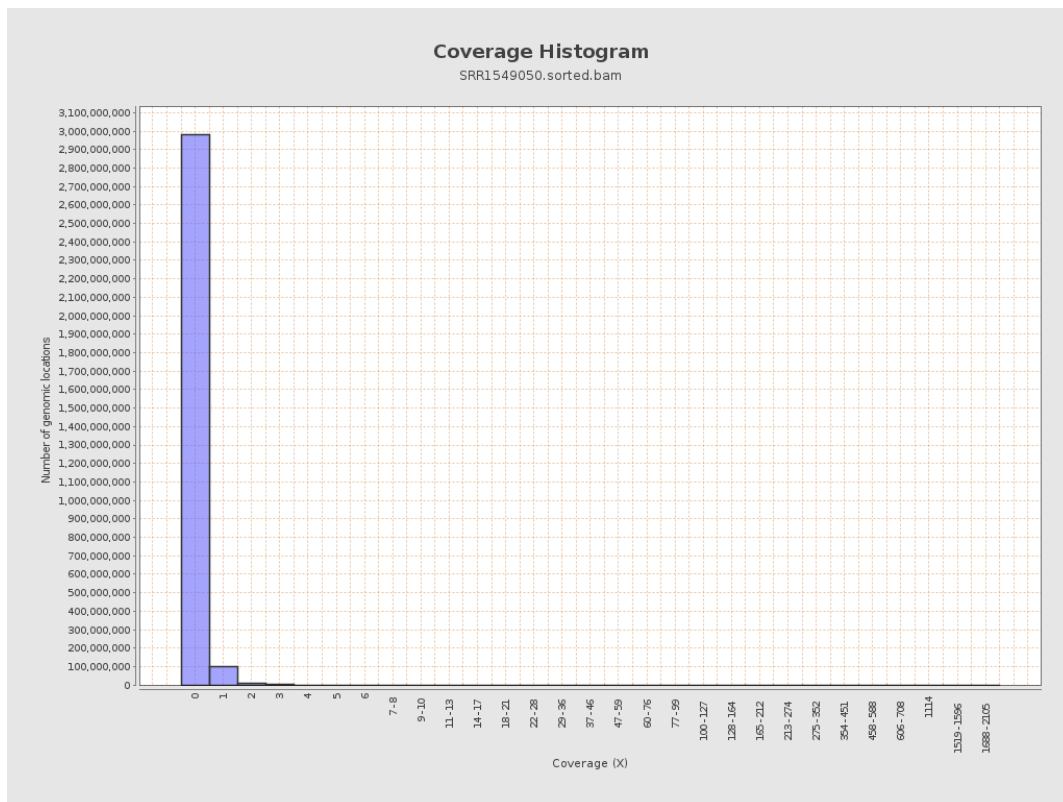
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10584425	0.0425	0.5614
chr2	243199373	11044927	0.0454	0.2937
chr3	198022430	8872083	0.0448	0.2341
chr4	191154276	8581021	0.0449	0.2436
chr5	180915260	8105309	0.0448	0.2356
chr6	171115067	7614430	0.0445	0.2425
chr7	159138663	7341717	0.0461	0.4379
chr8	146364022	6837995	0.0467	1.0502

chr9	141213431	5559961	0.0394	0.2796
chr10	135534747	6154422	0.0454	0.2874
chr11	135006516	5994396	0.0444	0.2761
chr12	133851895	5947714	0.0444	0.2358
chr13	115169878	4206886	0.0365	0.2105
chr14	107349540	4043440	0.0377	0.2345
chr15	102531392	3742340	0.0365	0.2109
chr16	90354753	3735686	0.0413	0.2361
chr17	81195210	3514757	0.0433	0.2378
chr18	78077248	3494911	0.0448	0.4491
chr19	59128983	2754404	0.0466	0.5163
chr20	63025520	2766115	0.0439	0.2384
chr21	48129895	1719741	0.0357	0.2369
chr22	51304566	1557953	0.0304	0.2394
chrMT	16571	10878	0.6564	1.0926
chrX	155270560	4483820	0.0289	0.2143
chrY	59373566	1247096	0.021	0.2477

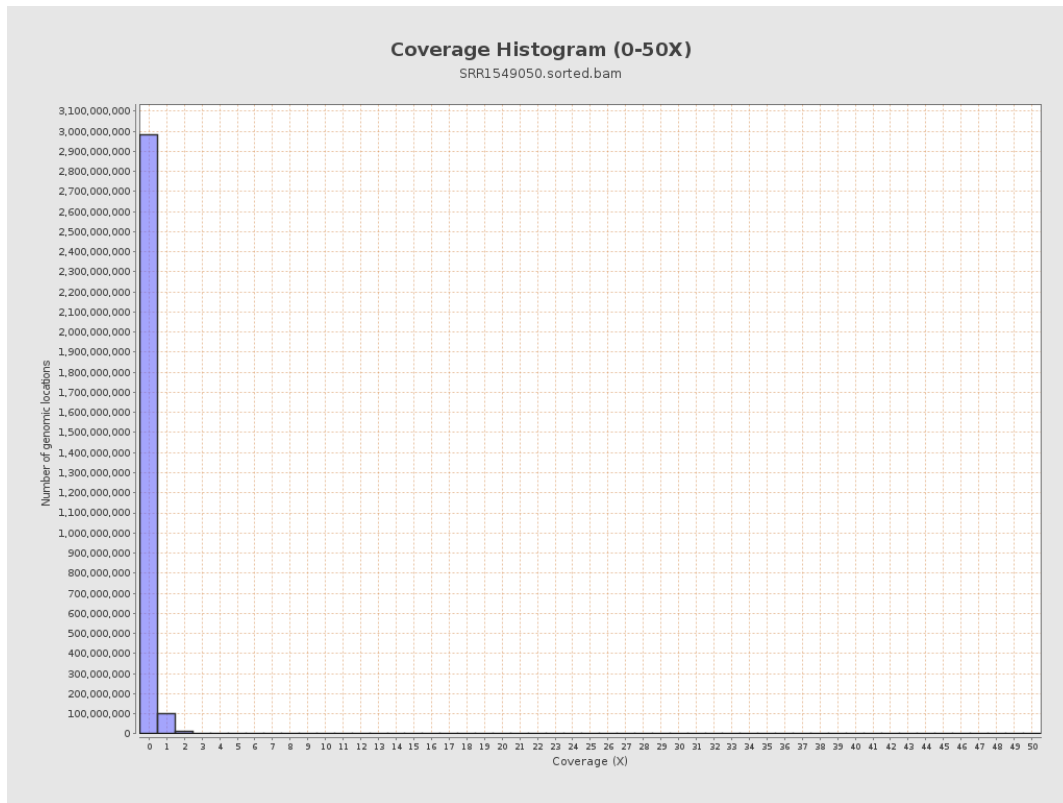
3. Results : Coverage across reference



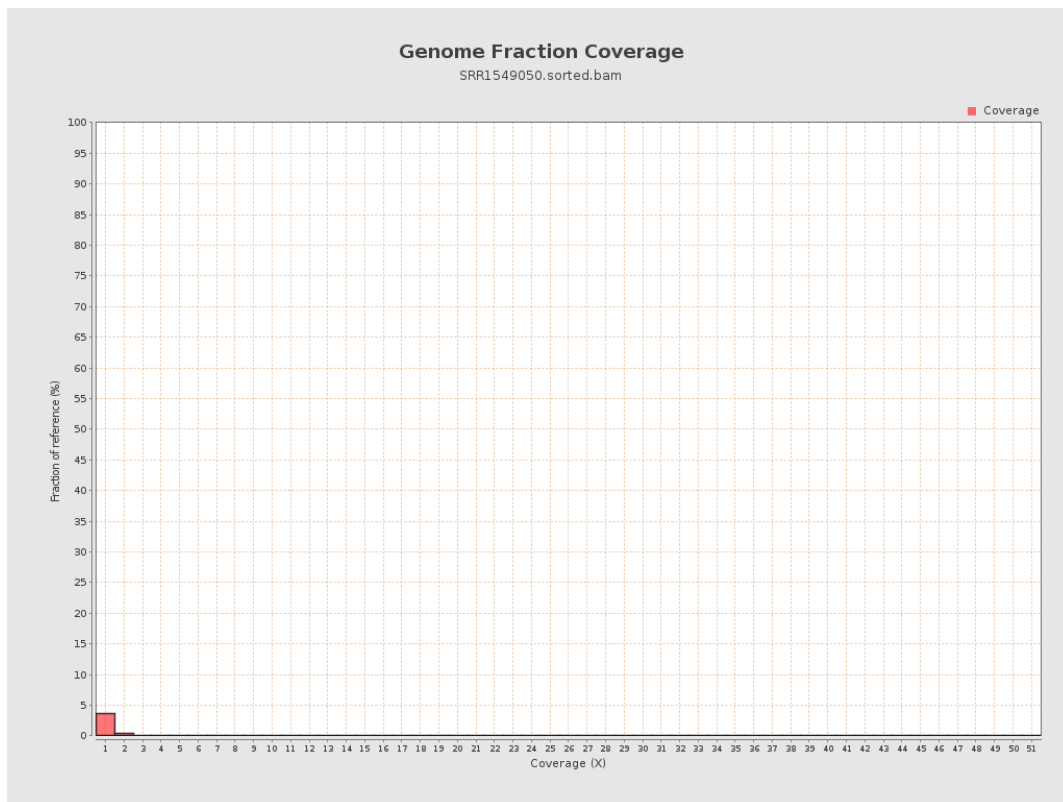
4. Results : Coverage Histogram



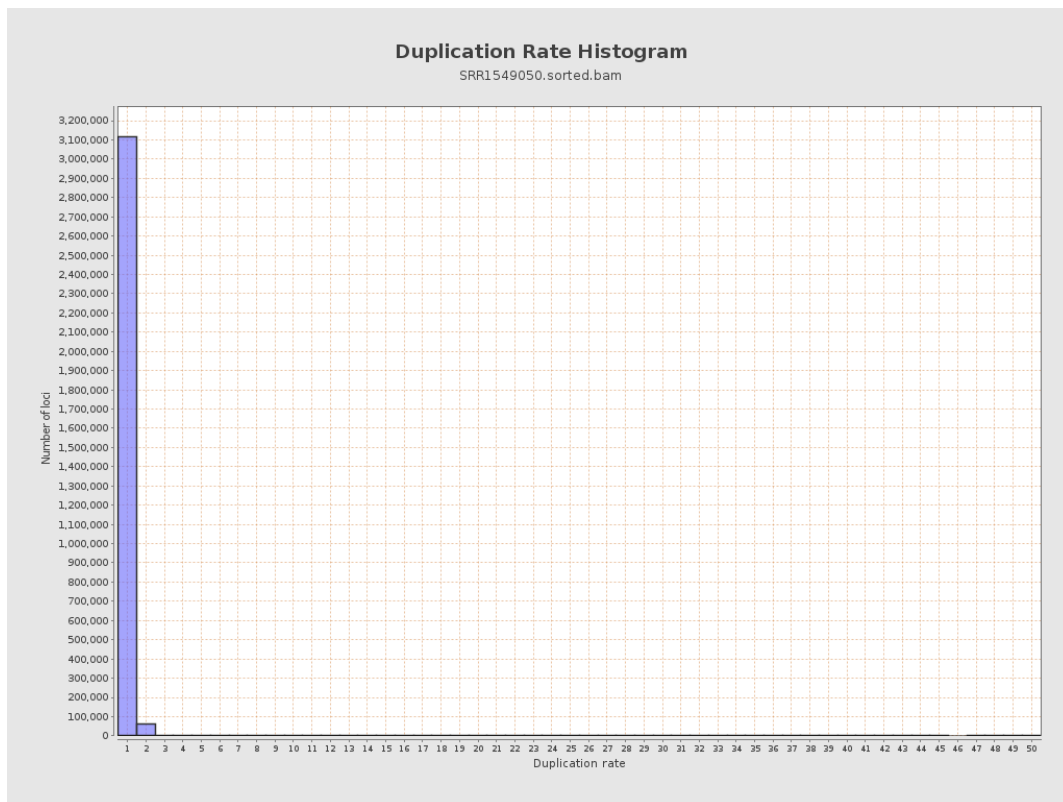
5. Results : Coverage Histogram (0-50X)



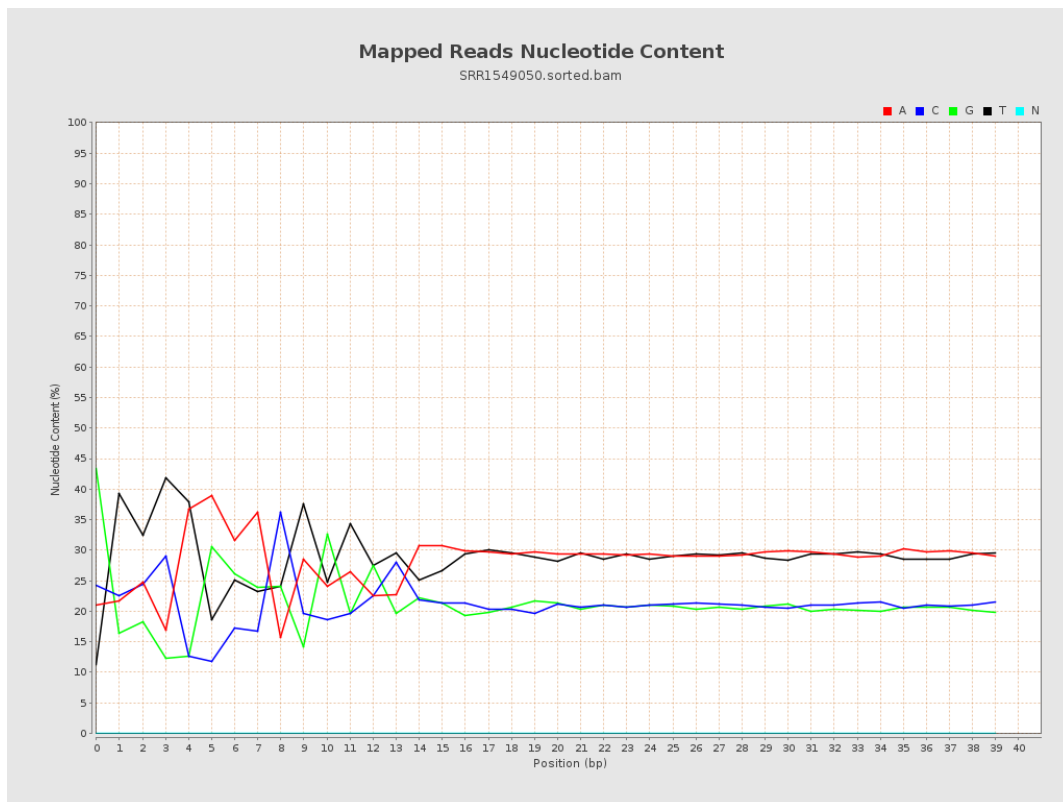
6. Results : Genome Fraction Coverage



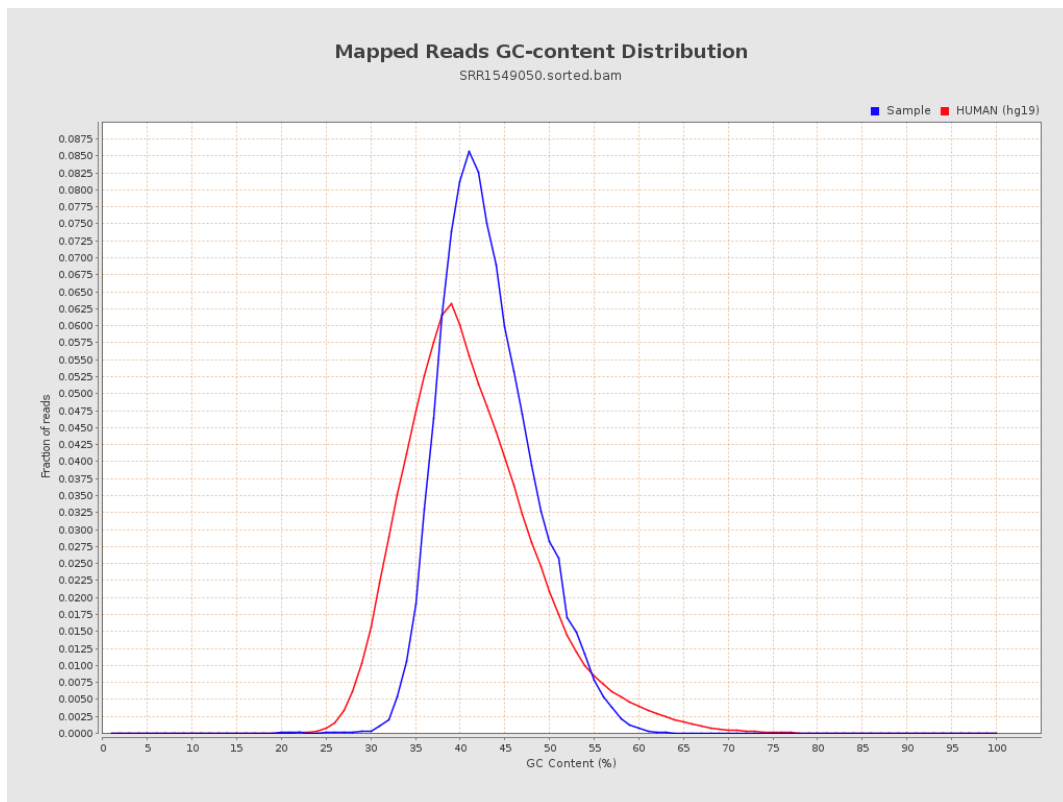
7. Results : Duplication Rate Histogram



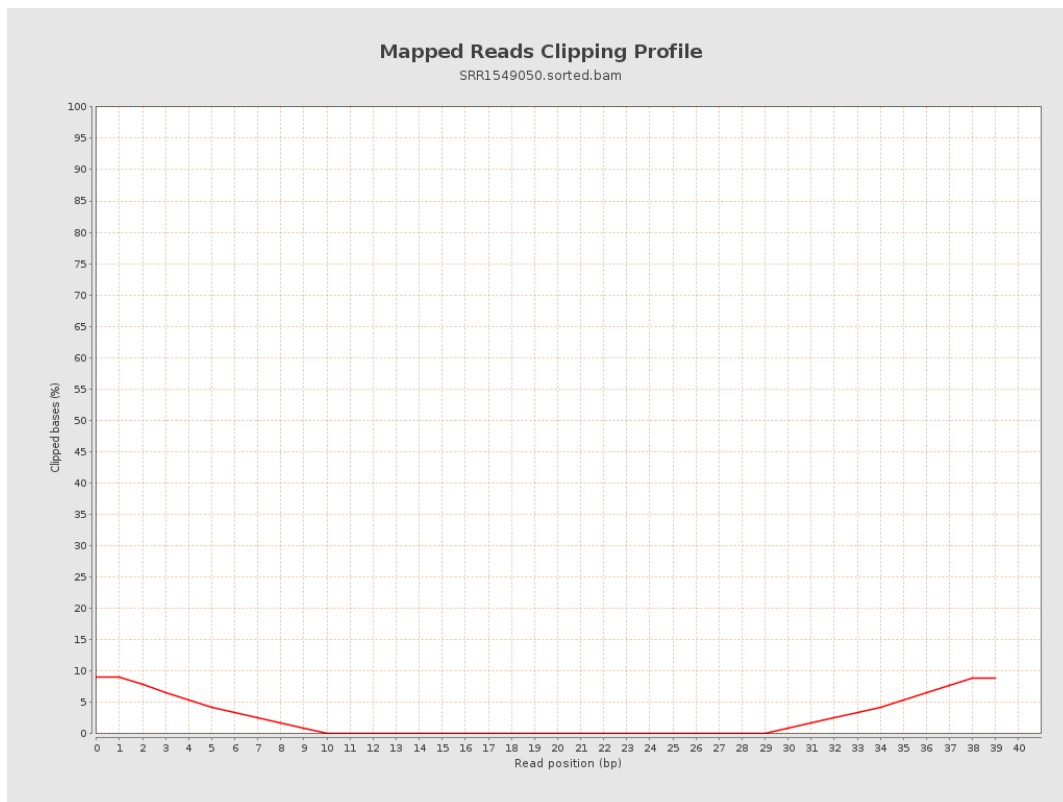
8. Results : Mapped Reads Nucleotide Content



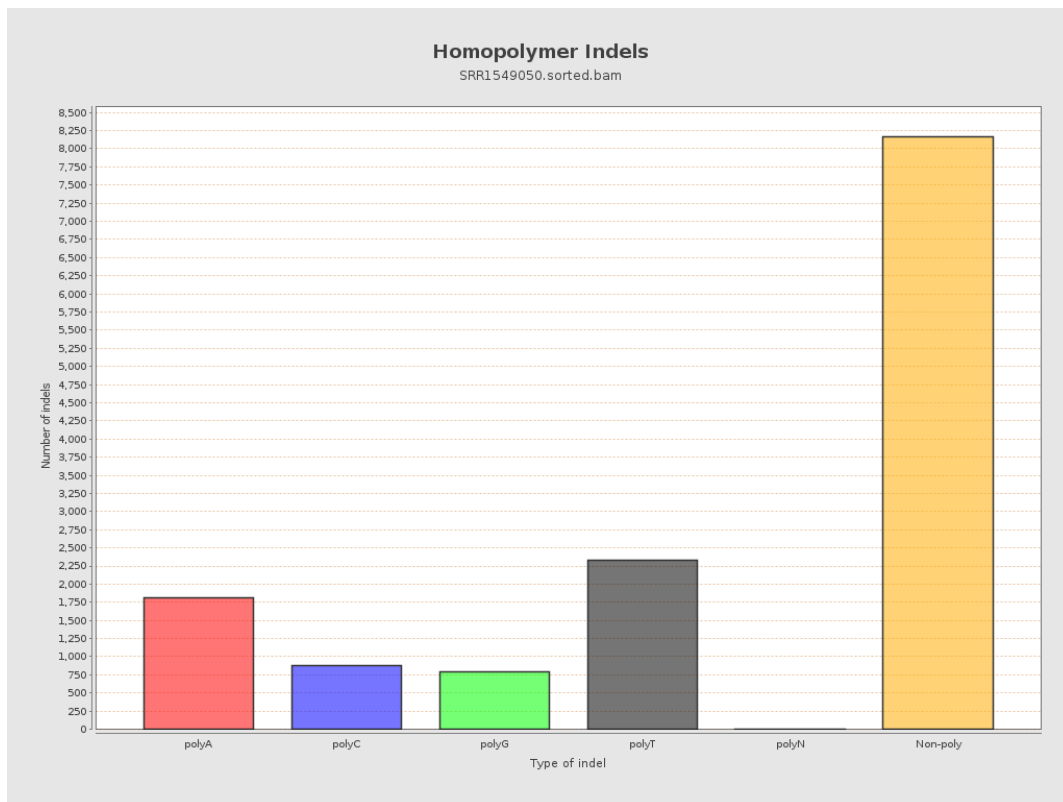
9. Results : Mapped Reads GC-content Distribution



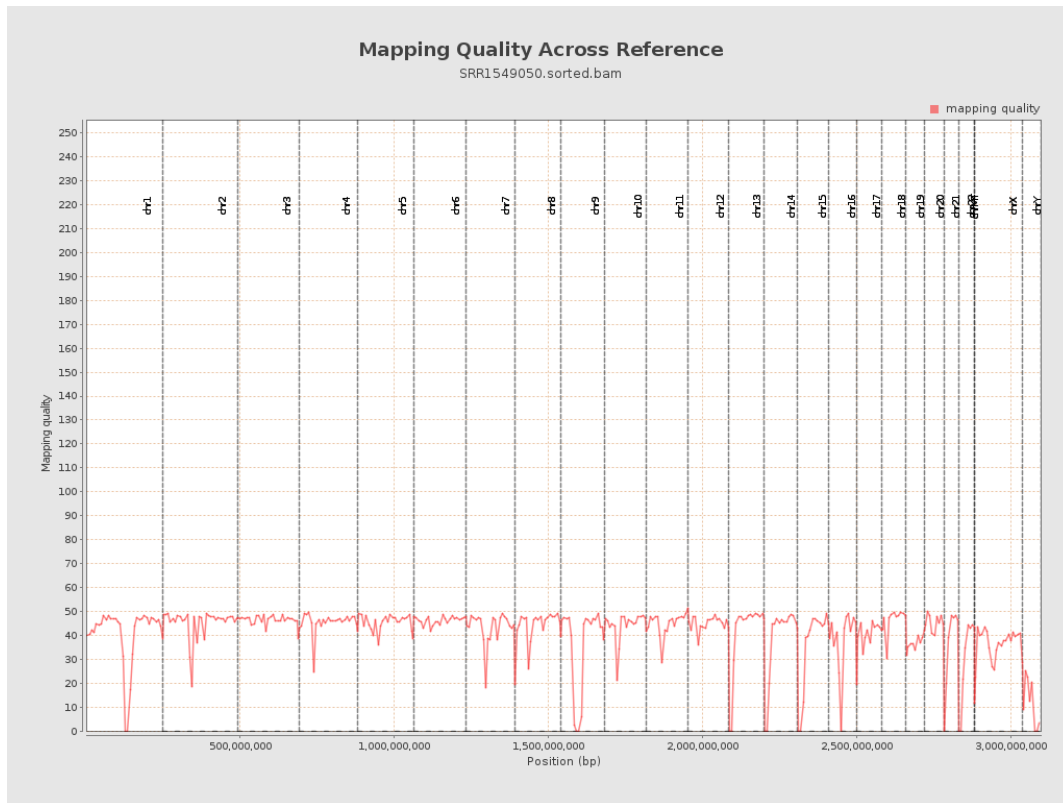
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

