

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:34:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549025.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_SRR1549025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549025.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:34:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,714,080
Mapped reads	7,669,292 / 88.01%
Unmapped reads	1,044,788 / 11.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	311,686 / 3.58%
Duplication rate	3.21%
Clipped reads	537,594 / 6.17%

2.2. ACGT Content

Number/percentage of A's	87,397,877 / 28.78%
Number/percentage of C's	63,881,254 / 21.03%
Number/percentage of T's	87,848,272 / 28.93%
Number/percentage of G's	64,579,494 / 21.26%
Number/percentage of N's	3,130 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0981
Standard Deviation	0.8112

2.4. Mapping Quality

Mean Mapping Quality	41.18
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2.5. Mismatches and indels

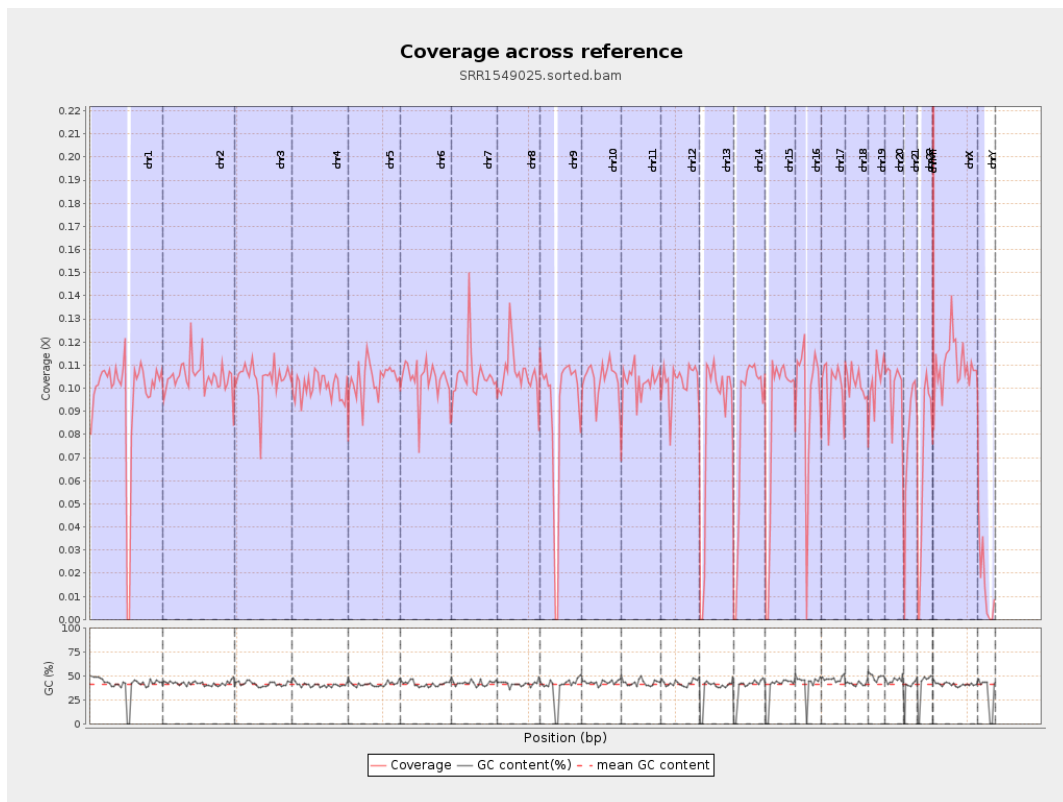
General error rate	0.28%
Mismatches	824,622
Insertions	9,246
Mapped reads with at least one insertion	0.12%
Deletions	23,677
Mapped reads with at least one deletion	0.31%
Homopolymer indels	41.58%

2.6. Chromosome stats

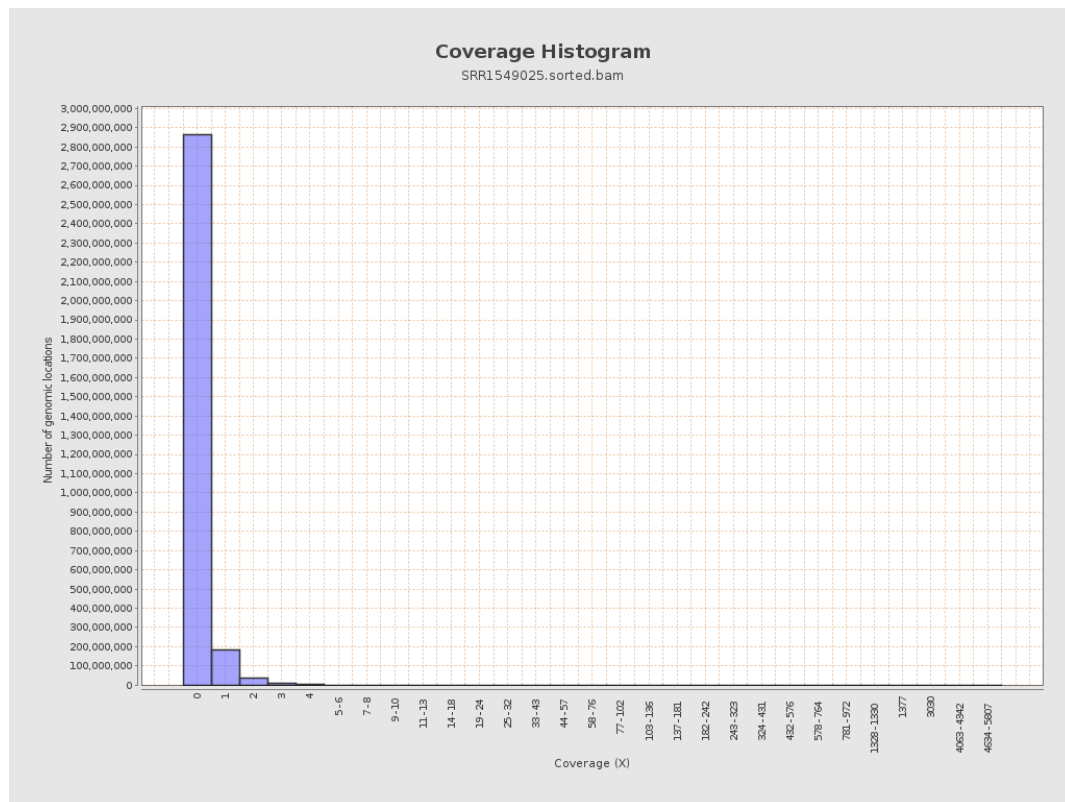
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24072226	0.0966	0.7908
chr2	243199373	25548716	0.1051	0.5535
chr3	198022430	20658210	0.1043	0.4035
chr4	191154276	19224654	0.1006	0.4051
chr5	180915260	18793238	0.1039	0.4049
chr6	171115067	17771574	0.1039	0.4278
chr7	159138663	16825417	0.1057	0.7988
chr8	146364022	15566877	0.1064	2.8404

chr9	141213431	12834500	0.0909	0.5448
chr10	135534747	14139879	0.1043	0.4743
chr11	135006516	13876976	0.1028	0.6555
chr12	133851895	13828036	0.1033	0.412
chr13	115169878	9859531	0.0856	0.3646
chr14	107349540	9368522	0.0873	0.427
chr15	102531392	8851260	0.0863	0.366
chr16	90354753	8571293	0.0949	0.4211
chr17	81195210	8276301	0.1019	0.4387
chr18	78077248	7994532	0.1024	0.9307
chr19	59128983	6097542	0.1031	0.7709
chr20	63025520	6348955	0.1007	0.4085
chr21	48129895	3776852	0.0785	0.3838
chr22	51304566	3502735	0.0683	0.3614
chrMT	16571	32343	1.9518	2.496
chrX	155270560	17059144	0.1099	0.4872
chrY	59373566	861546	0.0145	0.1733

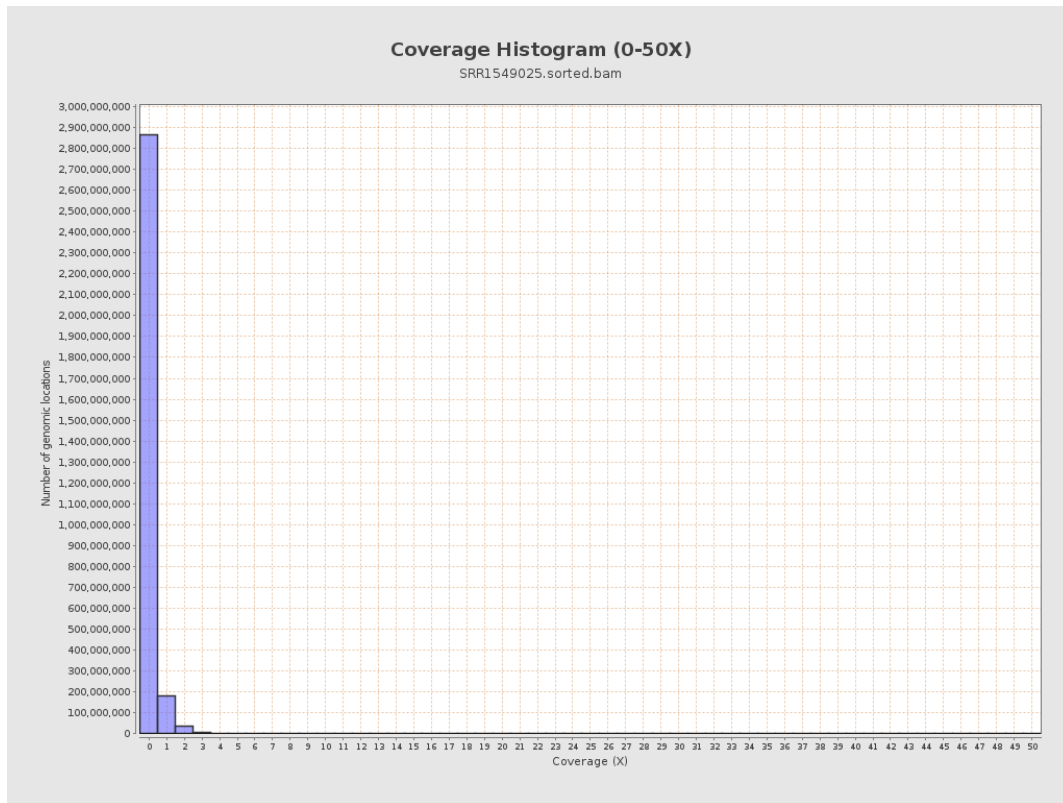
3. Results : Coverage across reference



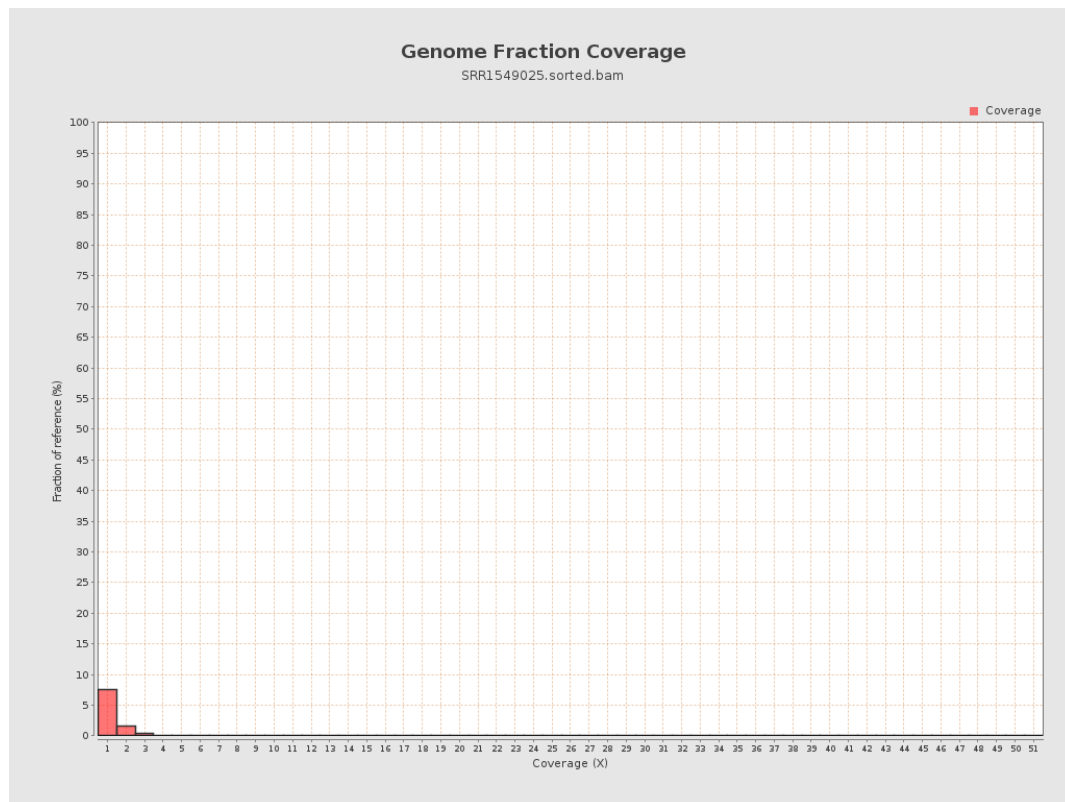
4. Results : Coverage Histogram



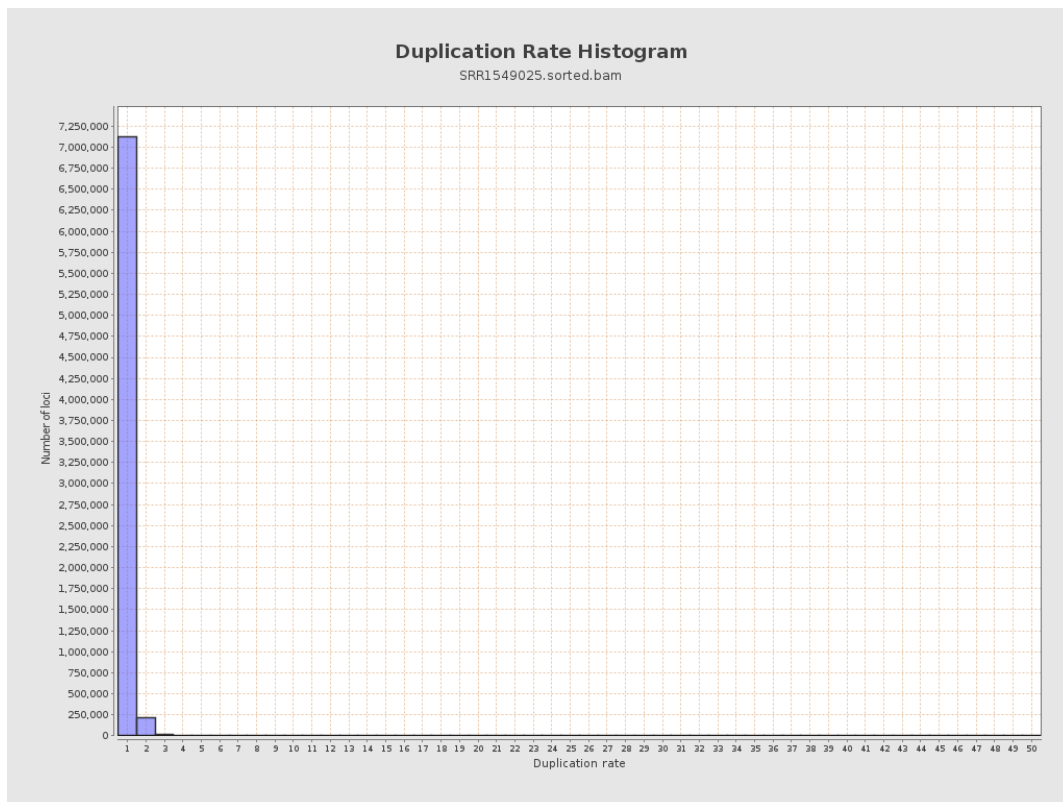
5. Results : Coverage Histogram (0-50X)



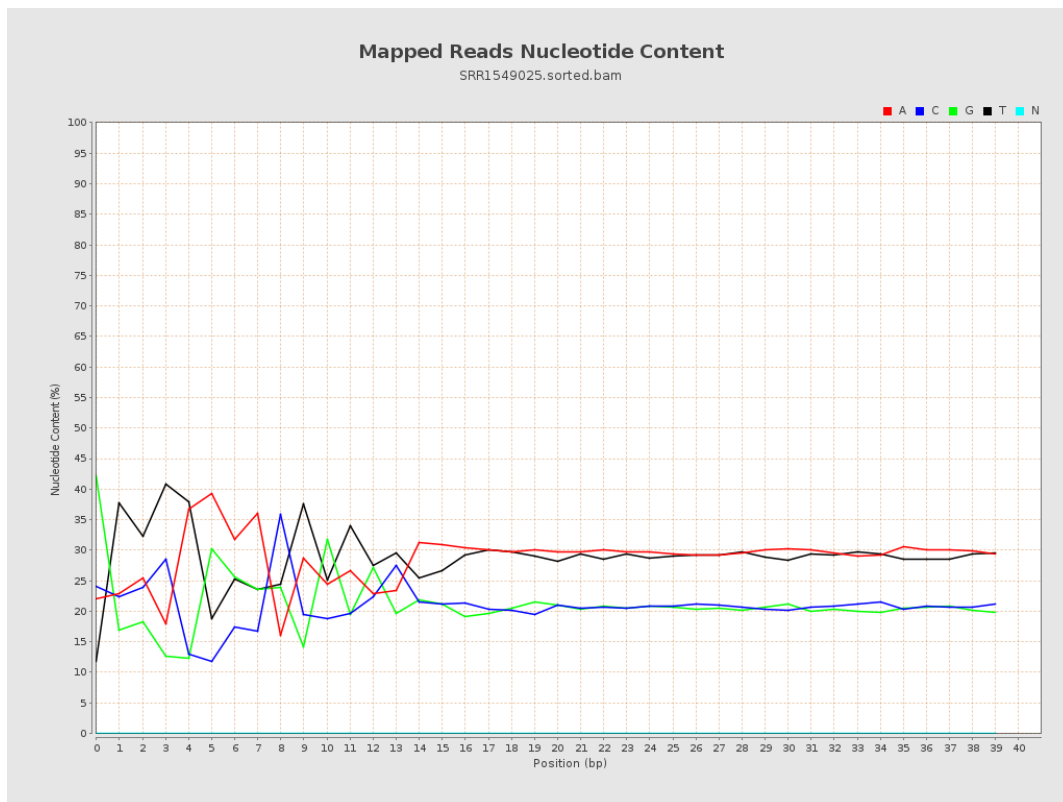
6. Results : Genome Fraction Coverage



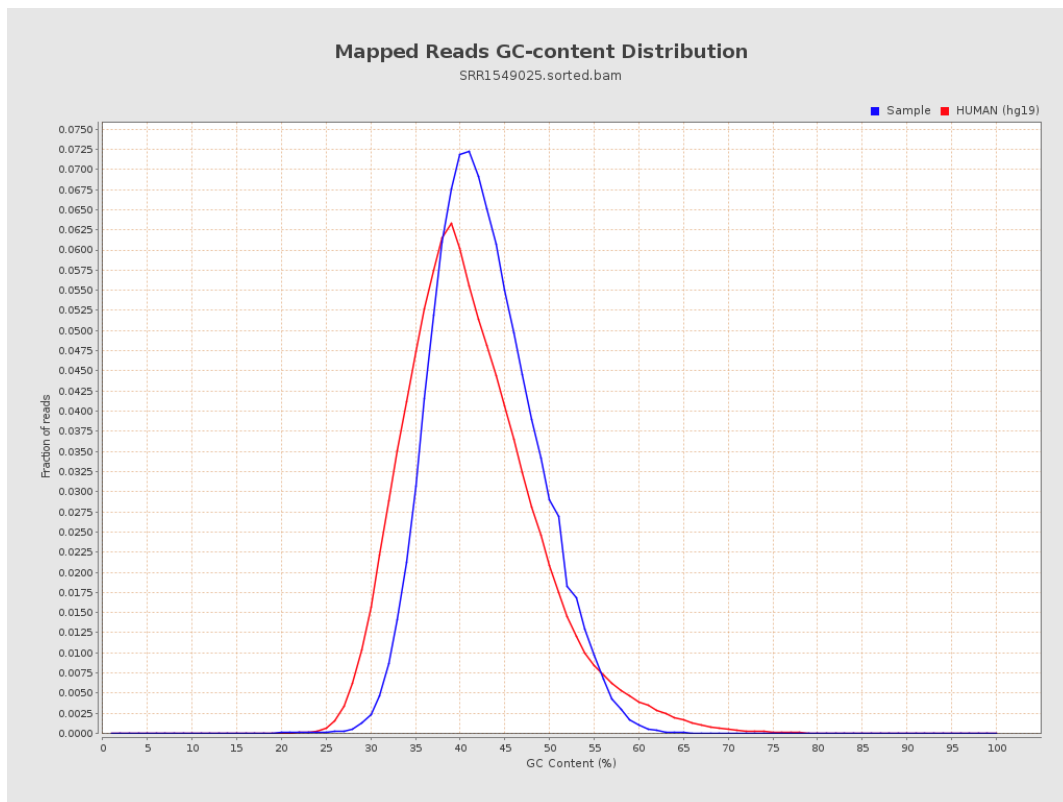
7. Results : Duplication Rate Histogram



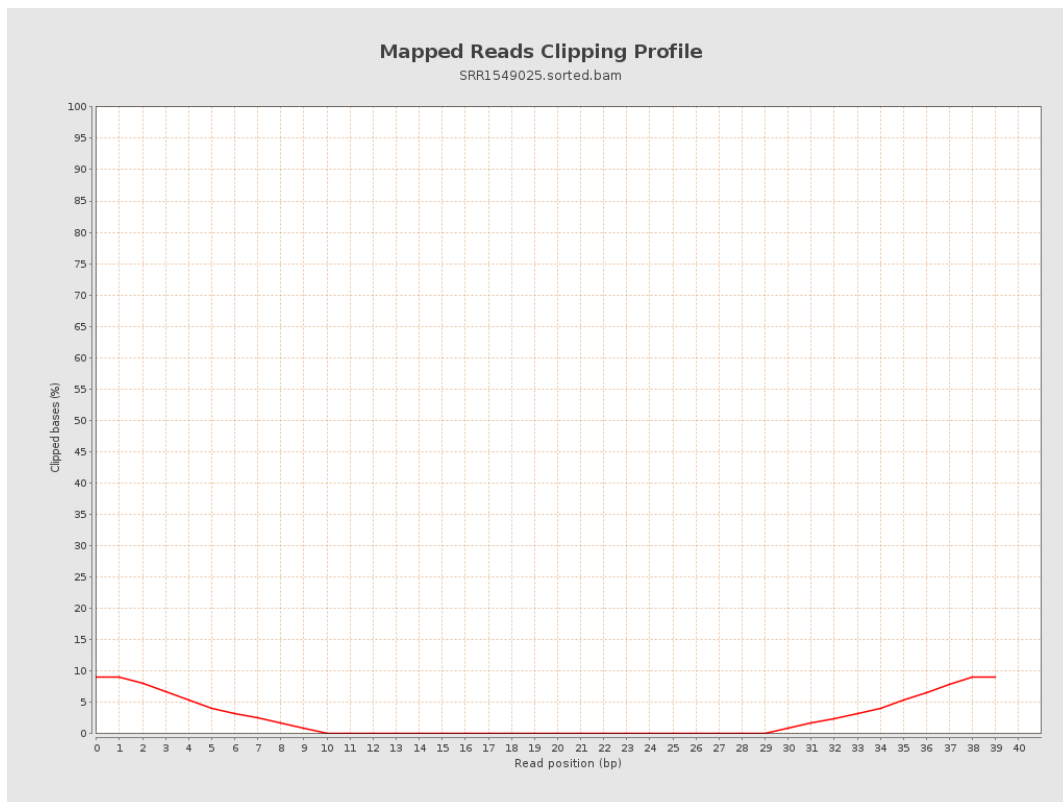
8. Results : Mapped Reads Nucleotide Content



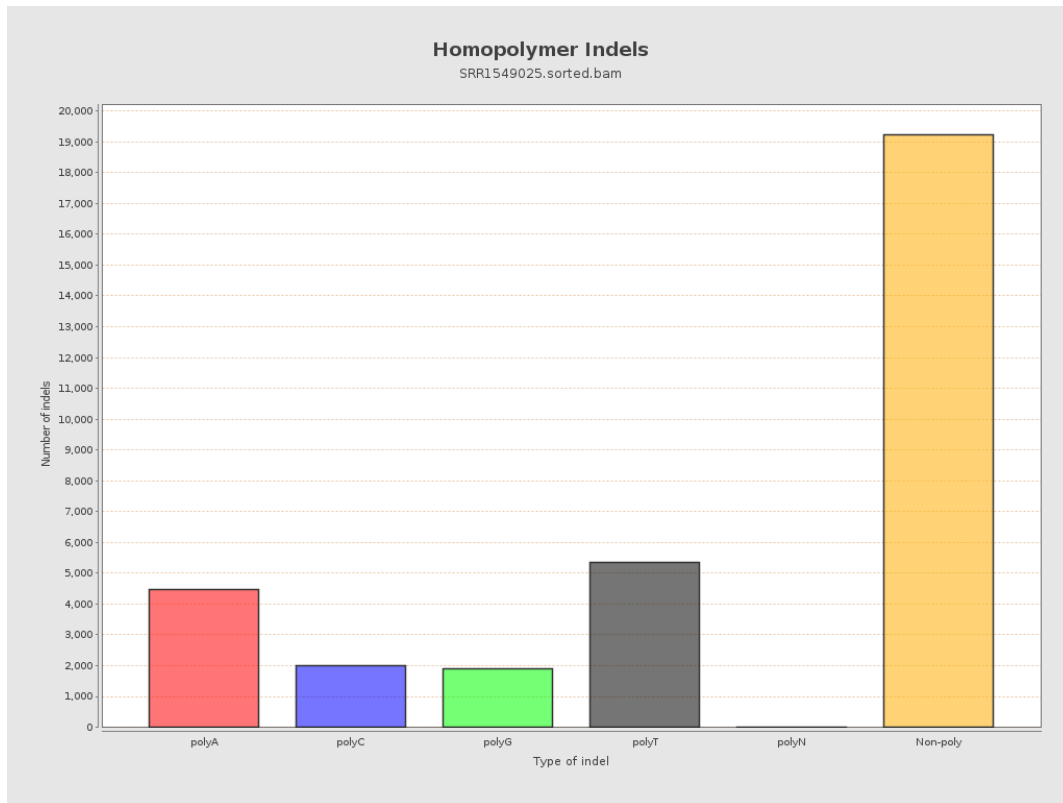
9. Results : Mapped Reads GC-content Distribution



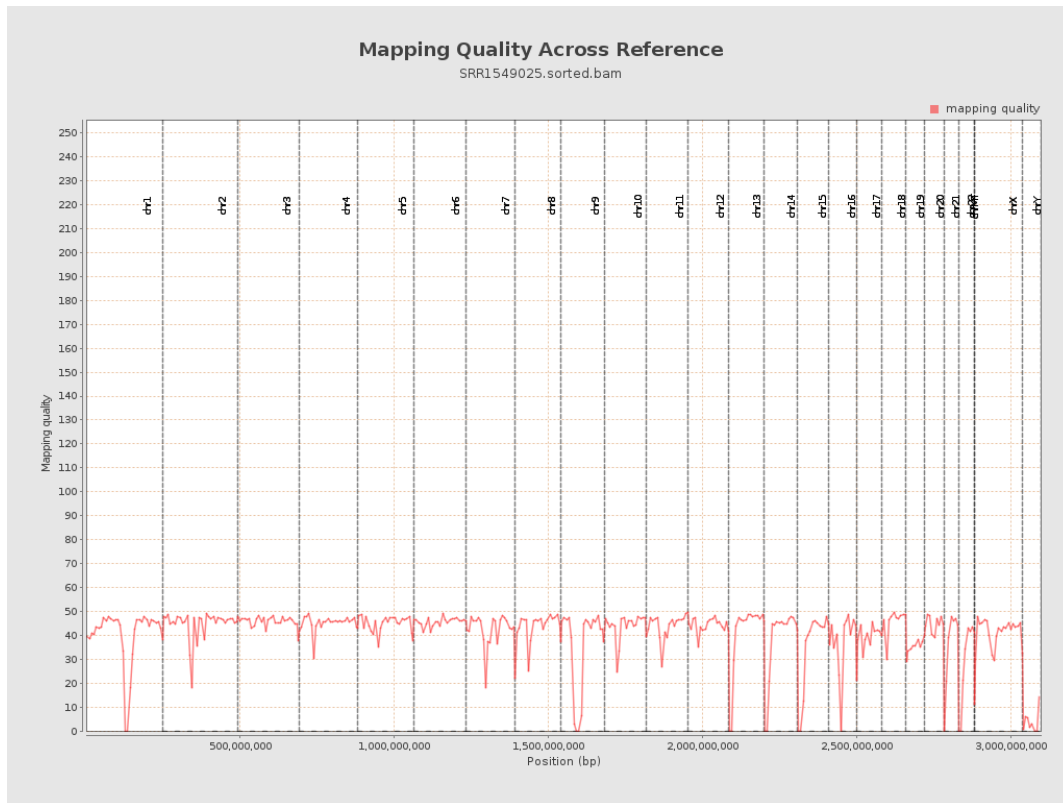
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

