

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:17:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549100.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_SRR1549100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:17:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,025,883
Mapped reads	9,393,207 / 85.19%
Unmapped reads	1,632,676 / 14.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	429,707 / 3.9%
Duplication rate	3.22%
Clipped reads	489,296 / 4.44%

2.2. ACGT Content

Number/percentage of A's	113,274,384 / 30.39%
Number/percentage of C's	72,900,379 / 19.56%
Number/percentage of T's	113,814,085 / 30.54%
Number/percentage of G's	72,684,947 / 19.5%
Number/percentage of N's	1,605 / 0%
GC Percentage	39.06%

2.3. Coverage

Mean	0.1204
Standard Deviation	1.0703

2.4. Mapping Quality

Mean Mapping Quality	44.43
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2.5. Mismatches and indels

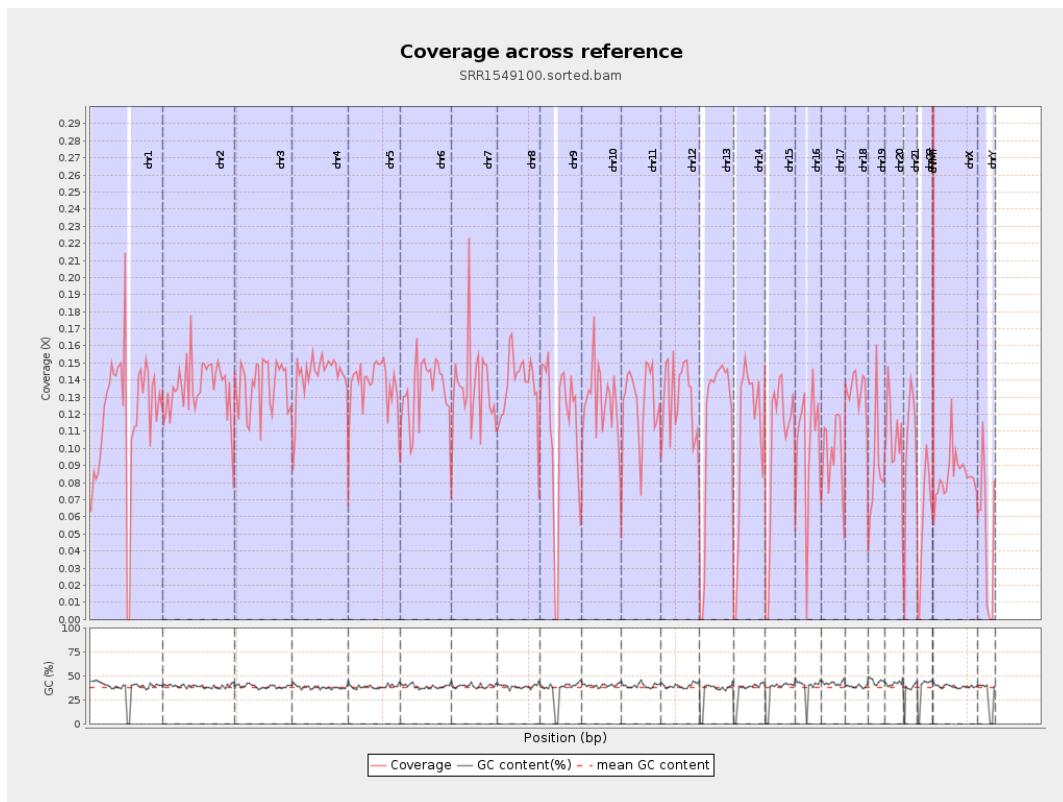
General error rate	0.31%
Mismatches	1,125,622
Insertions	9,419
Mapped reads with at least one insertion	0.1%
Deletions	28,644
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.15%

2.6. Chromosome stats

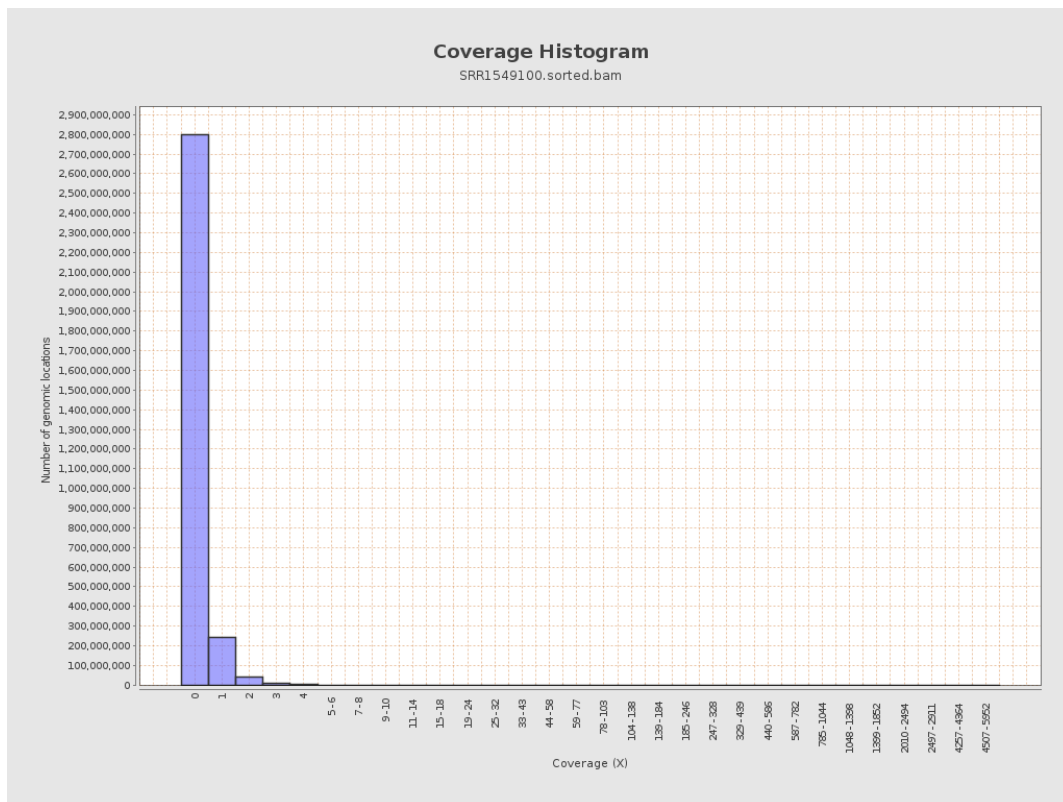
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29573258	0.1186	1.9673
chr2	243199373	32929358	0.1354	0.7186
chr3	198022430	27044003	0.1366	0.4443
chr4	191154276	27311713	0.1429	0.4805
chr5	180915260	24680546	0.1364	0.4554
chr6	171115067	23066979	0.1348	0.5315
chr7	159138663	21450040	0.1348	1.3362
chr8	146364022	20019266	0.1368	2.9454

chr9	141213431	15869123	0.1124	0.6792
chr10	135534747	17290621	0.1276	0.7229
chr11	135006516	17203179	0.1274	0.7084
chr12	133851895	17157336	0.1282	0.4683
chr13	115169878	13244615	0.115	0.4012
chr14	107349540	11595191	0.108	0.5452
chr15	102531392	10444614	0.1019	0.3783
chr16	90354753	9094528	0.1007	0.4692
chr17	81195210	7940889	0.0978	0.4376
chr18	78077248	10504678	0.1345	1.5474
chr19	59128983	5258968	0.0889	1.4826
chr20	63025520	6837233	0.1085	0.4441
chr21	48129895	4918337	0.1022	0.4739
chr22	51304566	3050391	0.0595	0.3152
chrMT	16571	121231	7.3159	9.0327
chrX	155270560	13045947	0.084	0.4995
chrY	59373566	3059536	0.0515	0.448

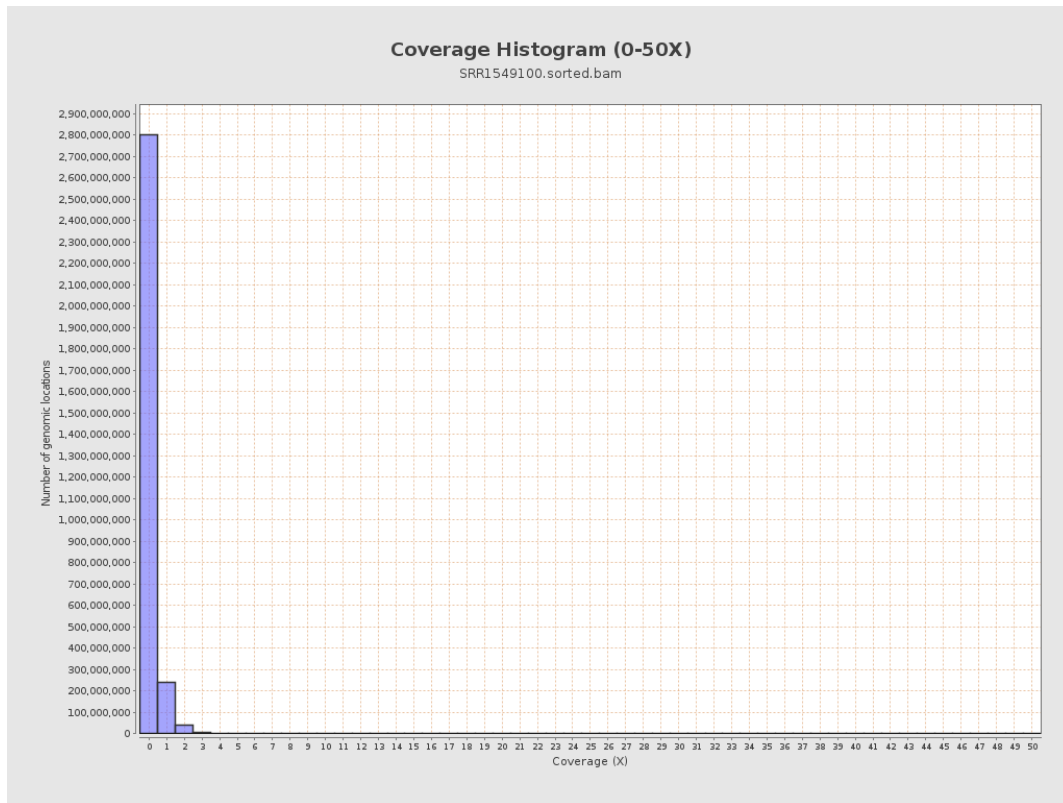
3. Results : Coverage across reference



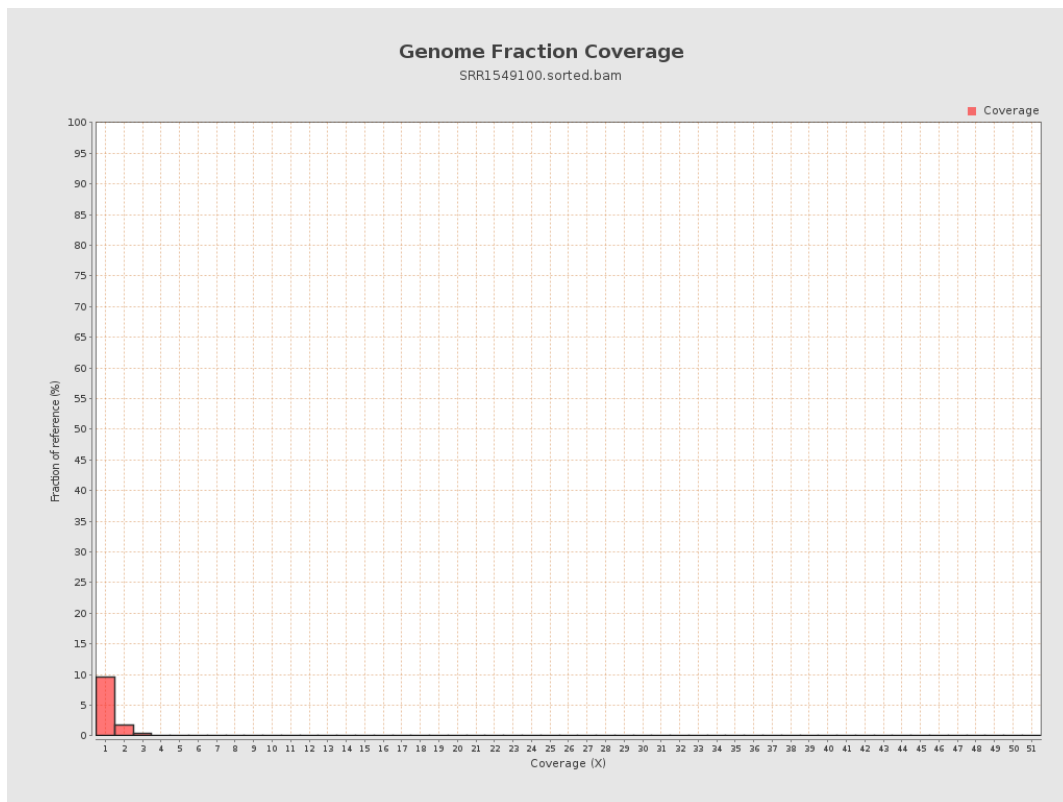
4. Results : Coverage Histogram



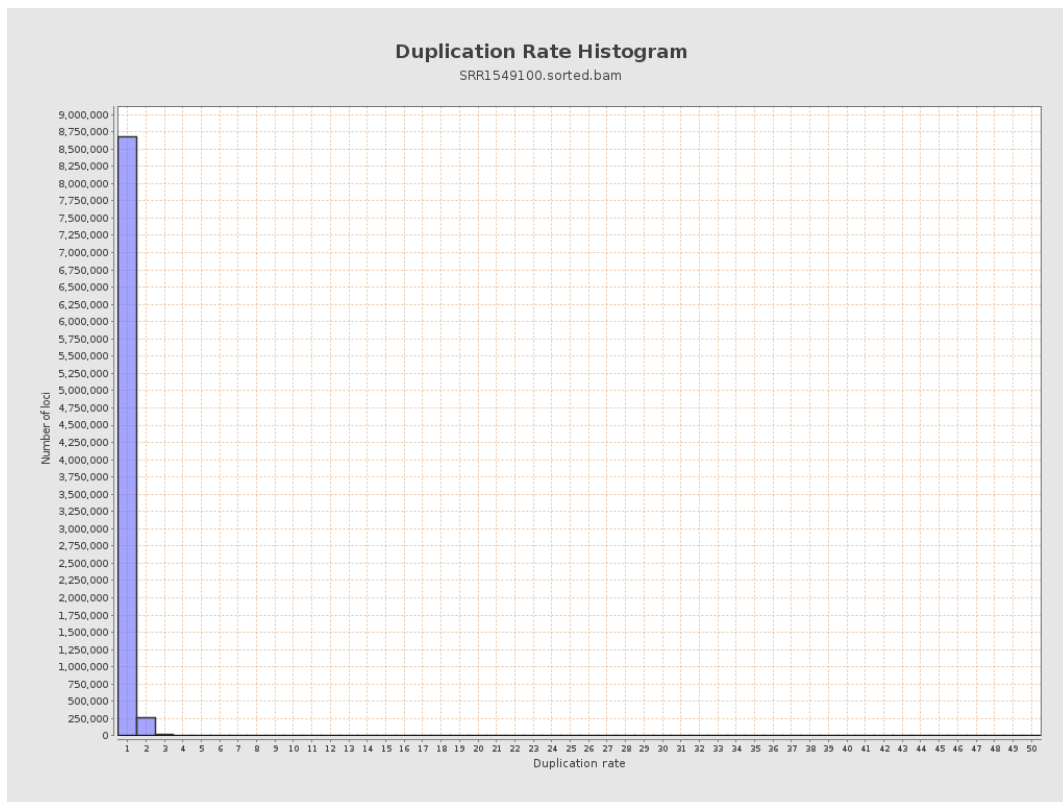
5. Results : Coverage Histogram (0-50X)



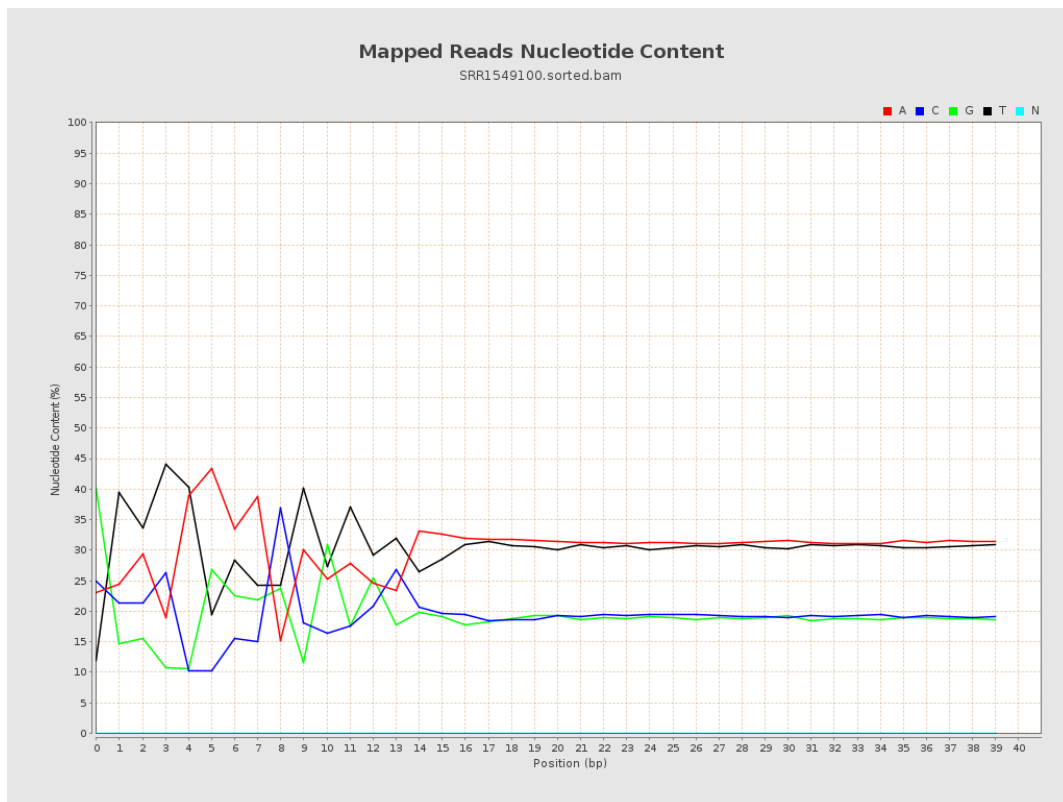
6. Results : Genome Fraction Coverage



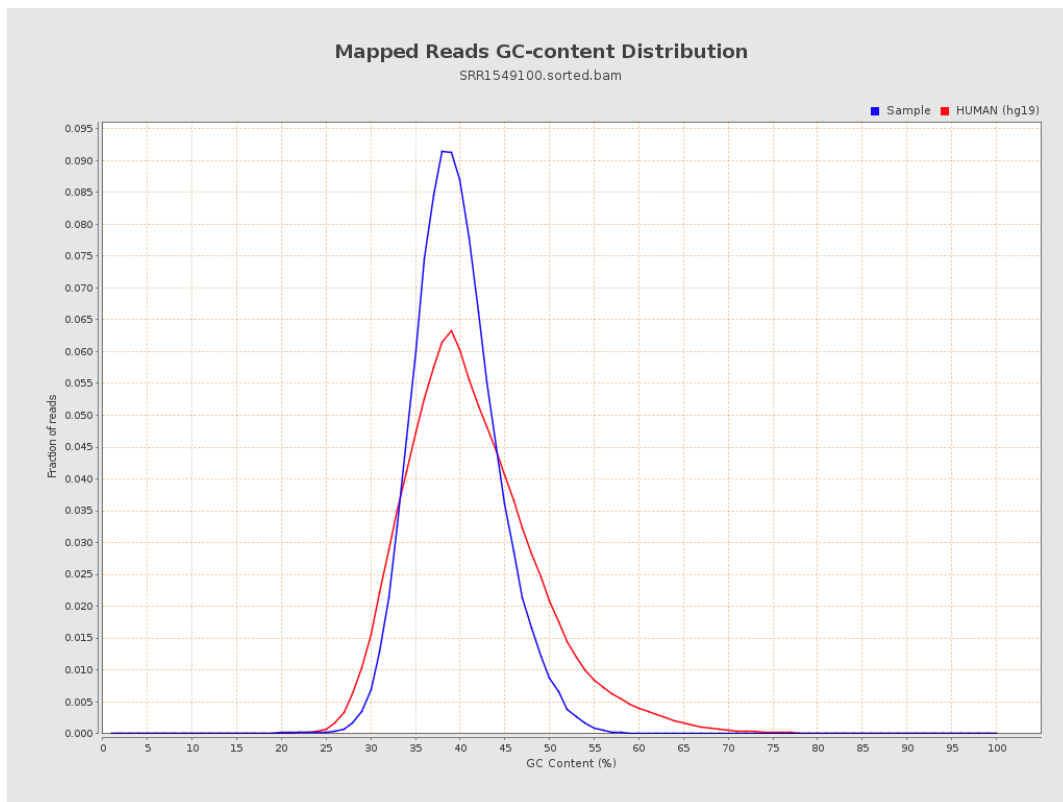
7. Results : Duplication Rate Histogram



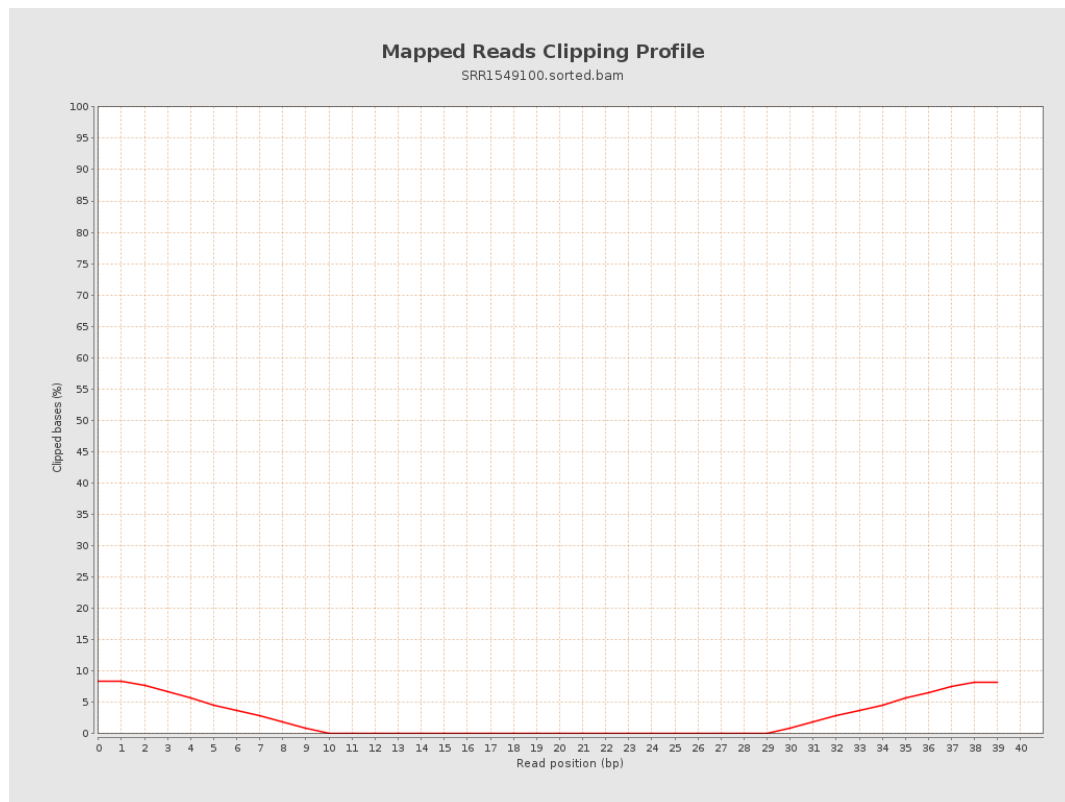
8. Results : Mapped Reads Nucleotide Content



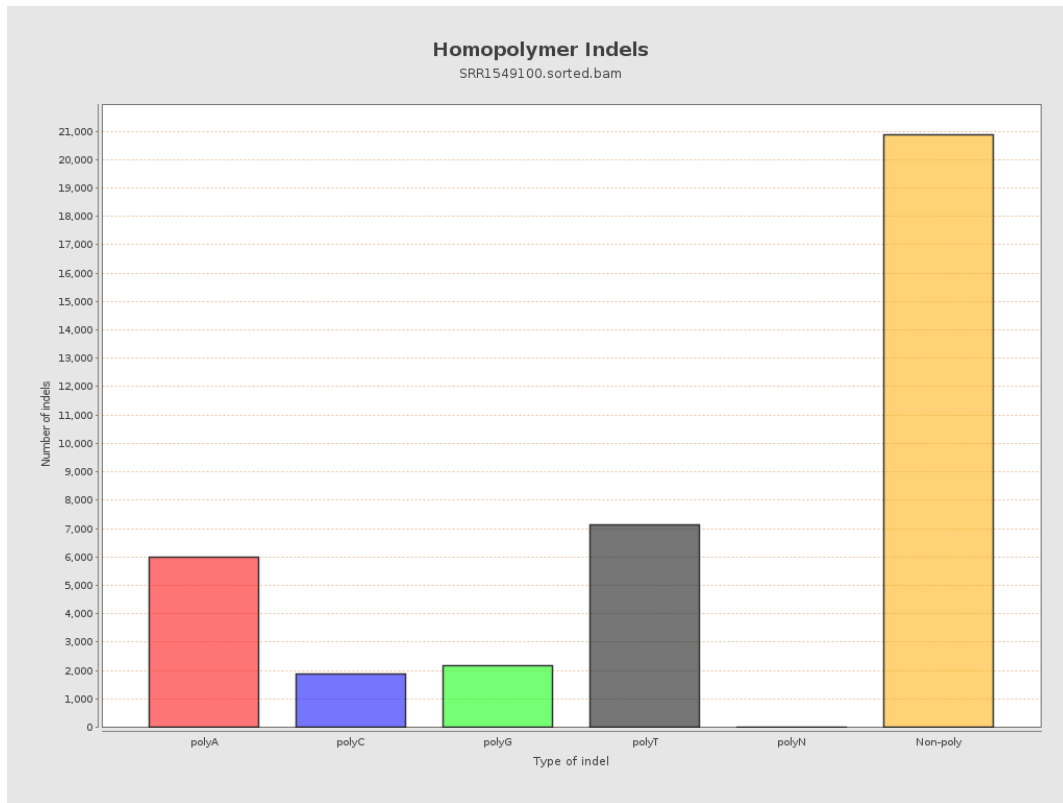
9. Results : Mapped Reads GC-content Distribution



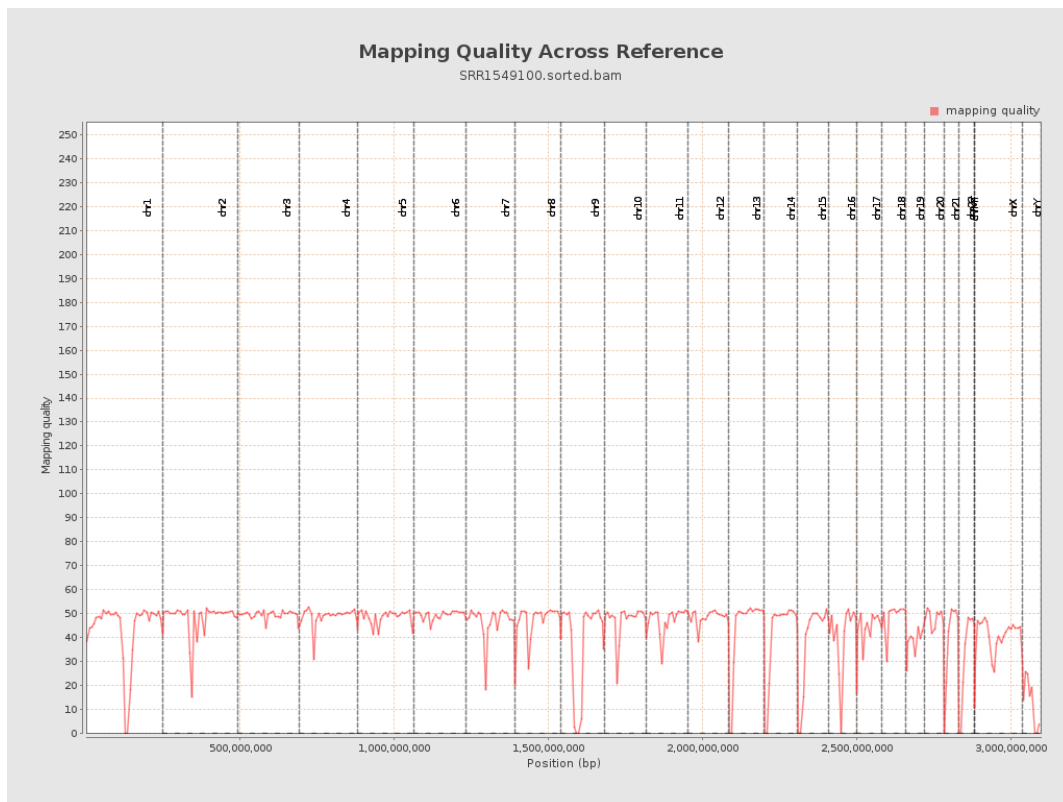
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

