

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:23:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549130.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_SRR1549130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549130.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:23:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,044,686
Mapped reads	13,234,544 / 87.97%
Unmapped reads	1,810,142 / 12.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	799,340 / 5.31%
Duplication rate	4.88%
Clipped reads	646,550 / 4.3%

2.2. ACGT Content

Number/percentage of A's	152,239,153 / 28.97%
Number/percentage of C's	109,573,942 / 20.85%
Number/percentage of T's	154,066,312 / 29.32%
Number/percentage of G's	109,518,382 / 20.84%
Number/percentage of N's	125,722 / 0.02%
GC Percentage	41.69%

2.3. Coverage

Mean	0.1698
Standard Deviation	0.9666

2.4. Mapping Quality

Mean Mapping Quality	43.6
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2.5. Mismatches and indels

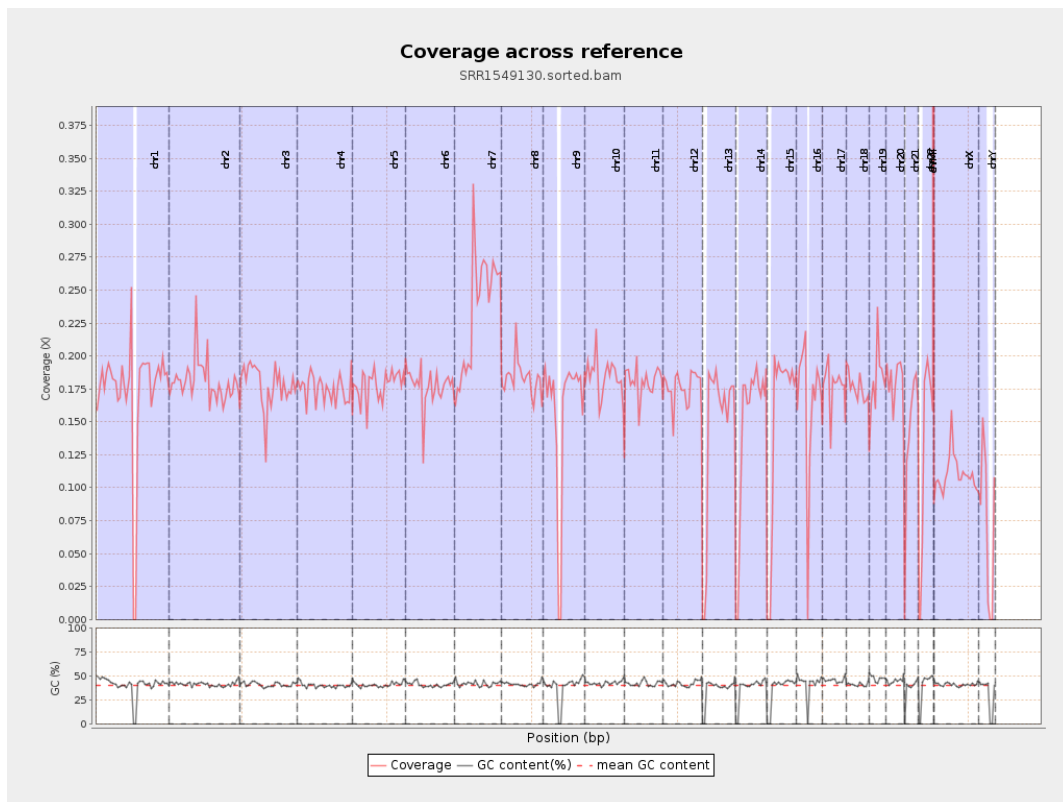
General error rate	0.32%
Mismatches	1,678,484
Insertions	13,047
Mapped reads with at least one insertion	0.1%
Deletions	39,258
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.69%

2.6. Chromosome stats

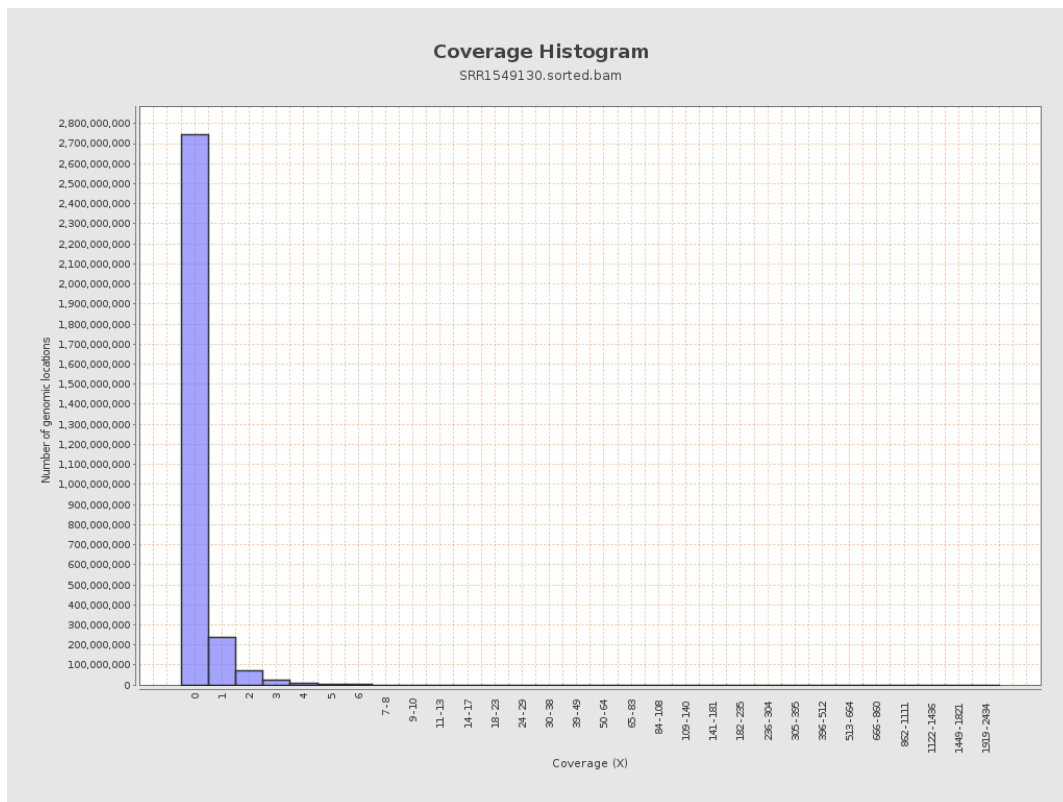
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	43069899	0.1728	1.8686
chr2	243199373	44003506	0.1809	0.9084
chr3	198022430	35166612	0.1776	0.586
chr4	191154276	33390336	0.1747	0.6027
chr5	180915260	32193967	0.178	0.6002
chr6	171115067	30365766	0.1775	0.6716
chr7	159138663	37589559	0.2362	1.5388
chr8	146364022	26774797	0.1829	0.8811

chr9	141213431	22196873	0.1572	0.8449
chr10	135534747	24980458	0.1843	0.8626
chr11	135006516	24271037	0.1798	0.8272
chr12	133851895	23571495	0.1761	0.6178
chr13	115169878	16654156	0.1446	0.5164
chr14	107349540	15731537	0.1465	0.7249
chr15	102531392	15667995	0.1528	0.5342
chr16	90354753	14946359	0.1654	0.634
chr17	81195210	14343369	0.1767	0.6379
chr18	78077248	13767015	0.1763	1.737
chr19	59128983	10833108	0.1832	1.5728
chr20	63025520	11335517	0.1799	0.6385
chr21	48129895	6856886	0.1425	0.6213
chr22	51304566	6453899	0.1258	0.5243
chrMT	16571	114663	6.9195	9.693
chrX	155270560	17099233	0.1101	0.6047
chrY	59373566	4194785	0.0707	0.5593

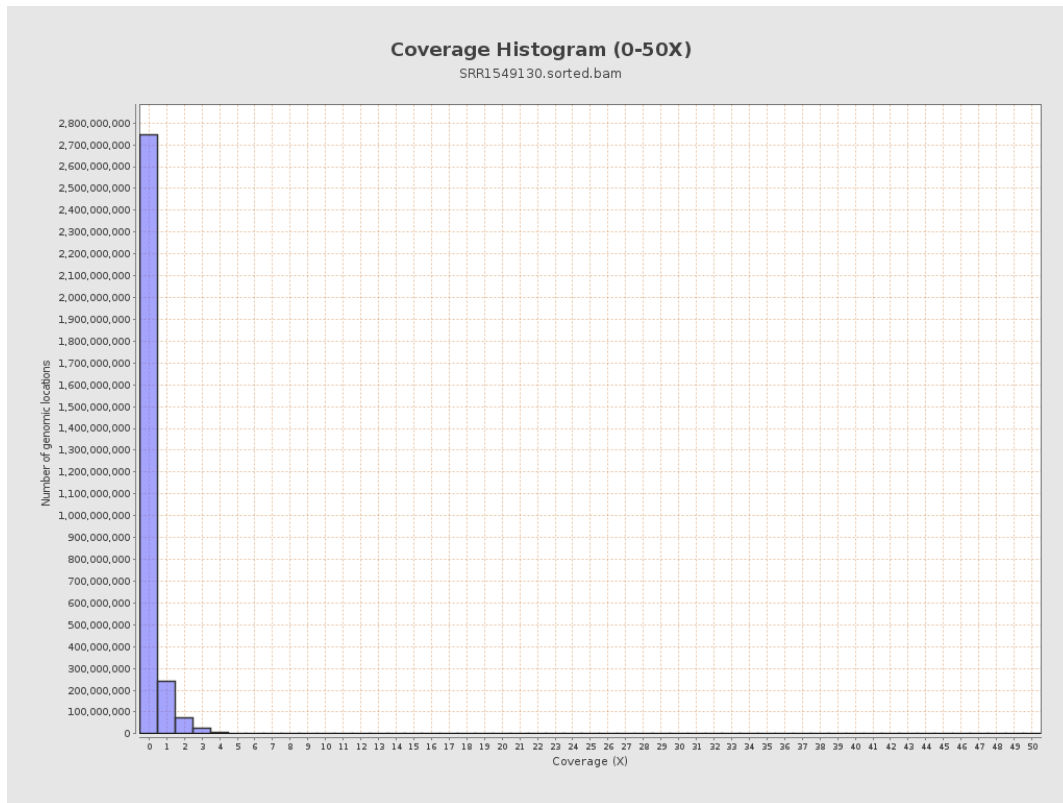
3. Results : Coverage across reference



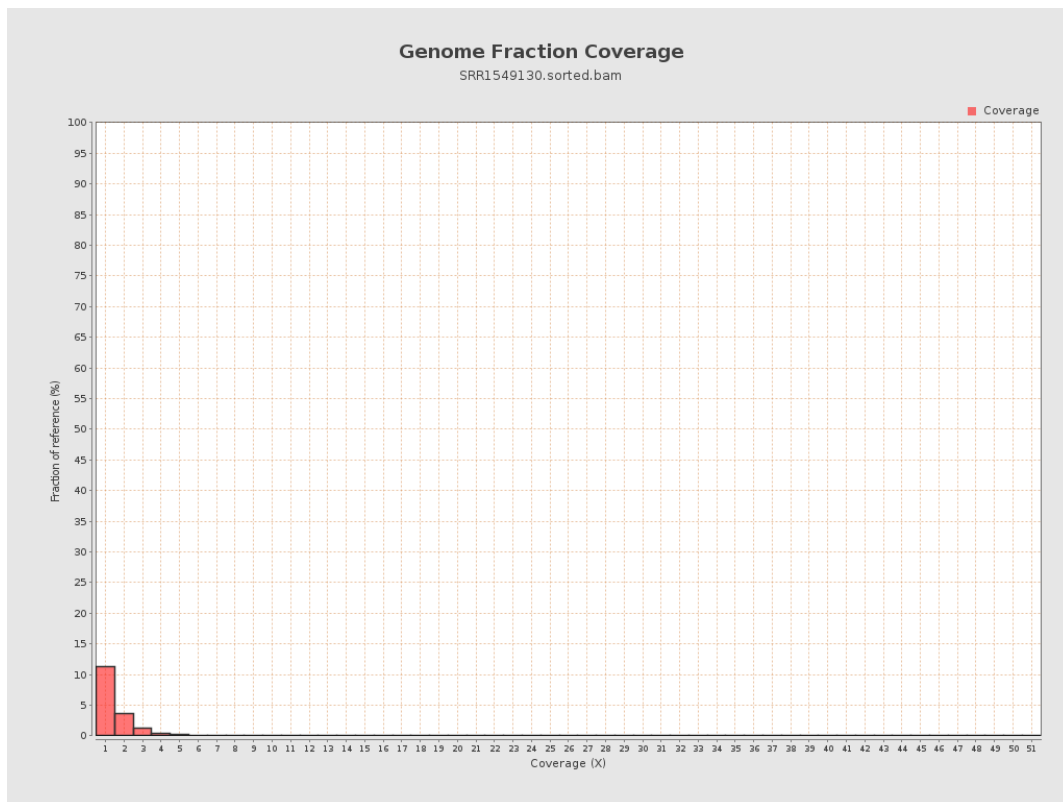
4. Results : Coverage Histogram



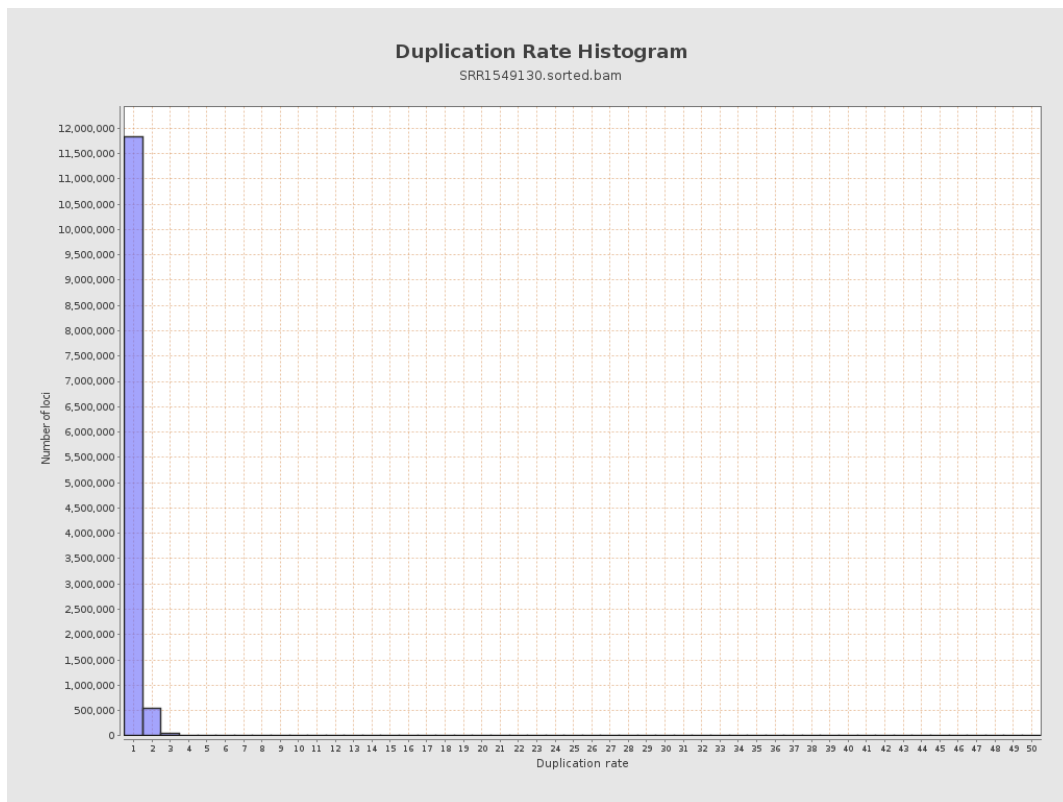
5. Results : Coverage Histogram (0-50X)



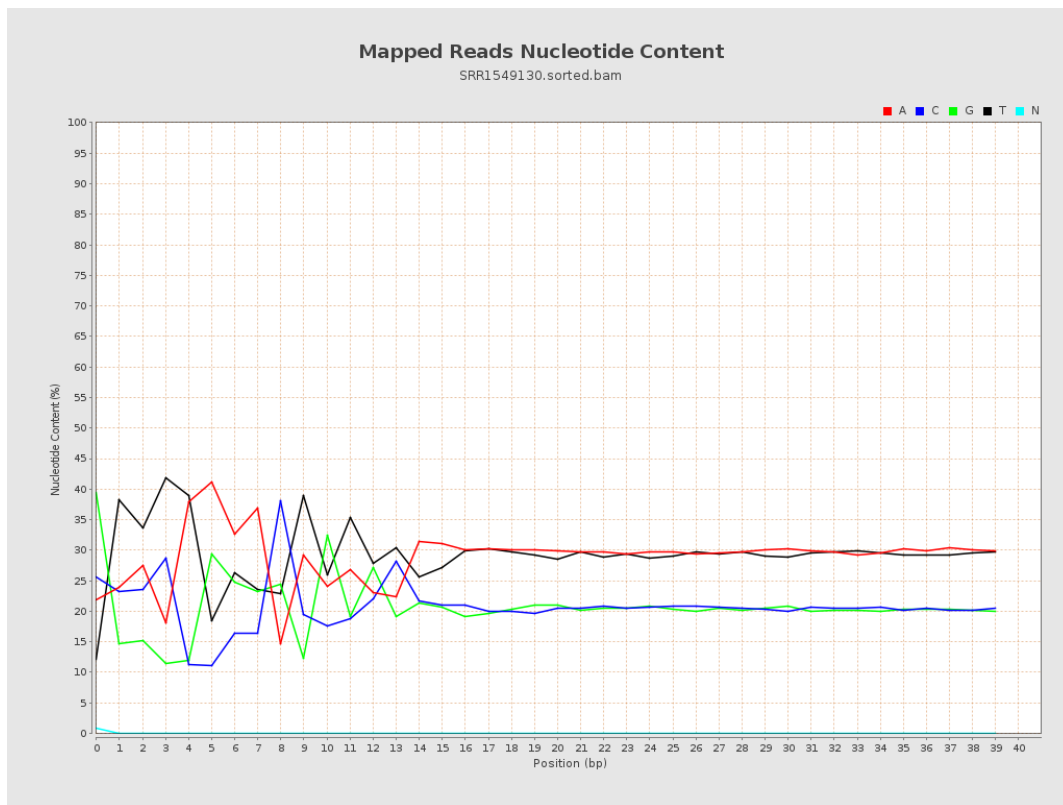
6. Results : Genome Fraction Coverage



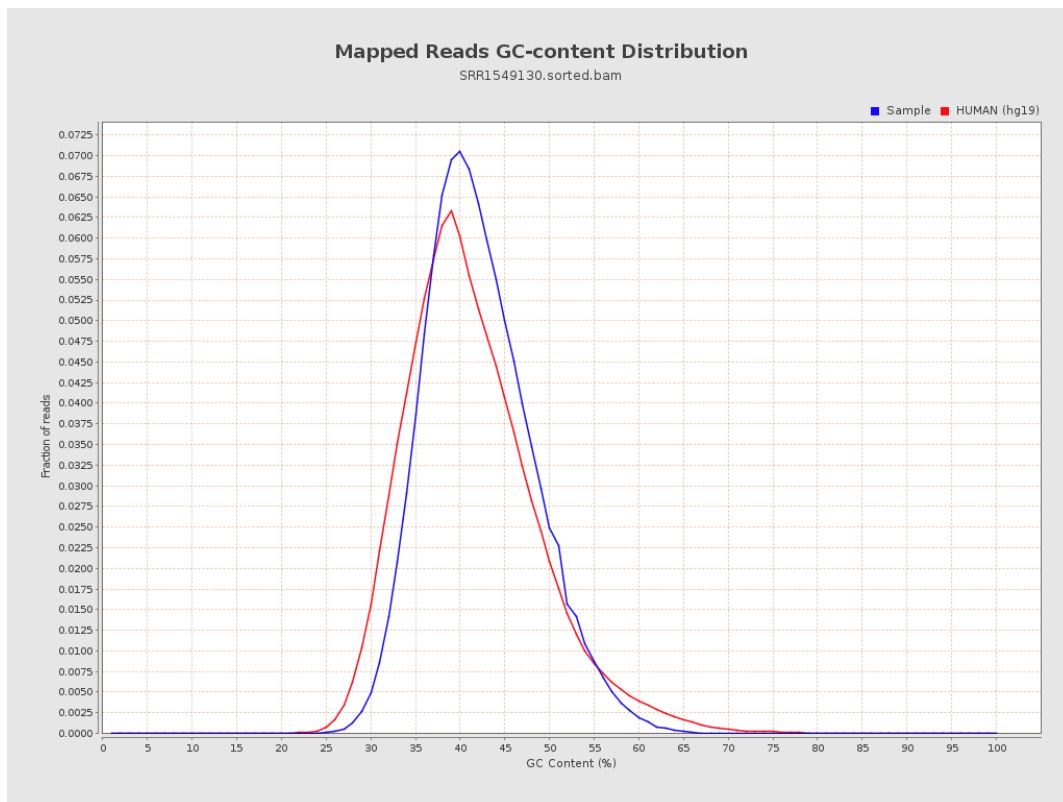
7. Results : Duplication Rate Histogram



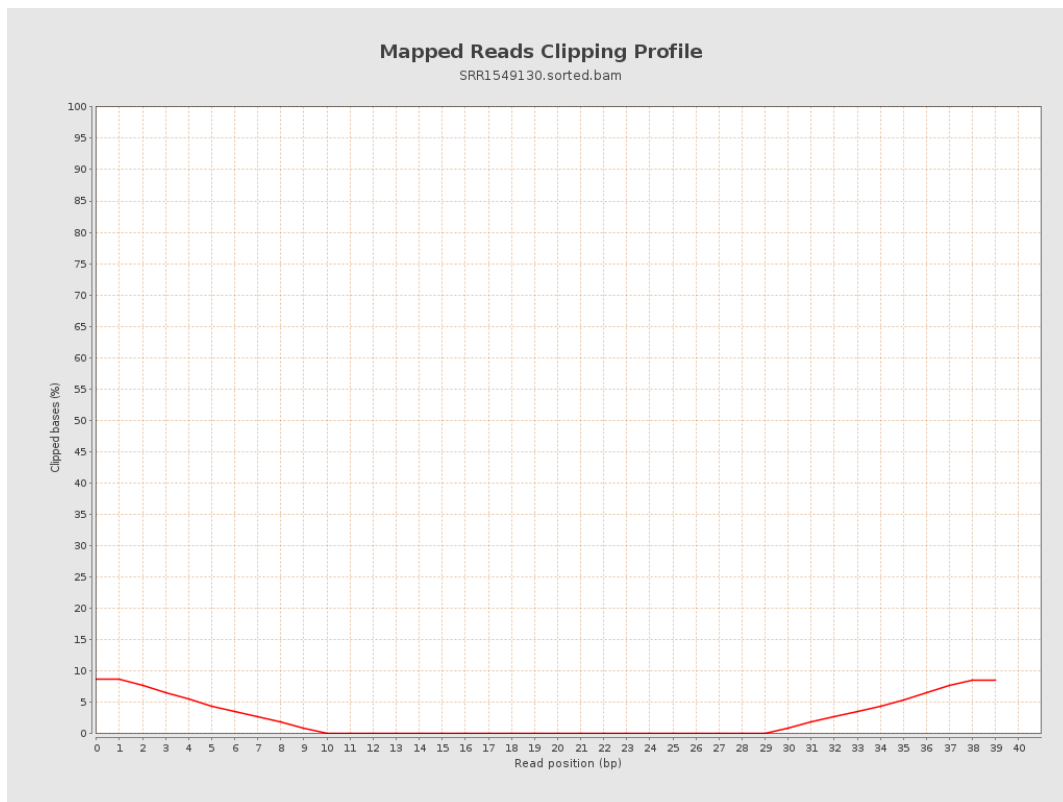
8. Results : Mapped Reads Nucleotide Content



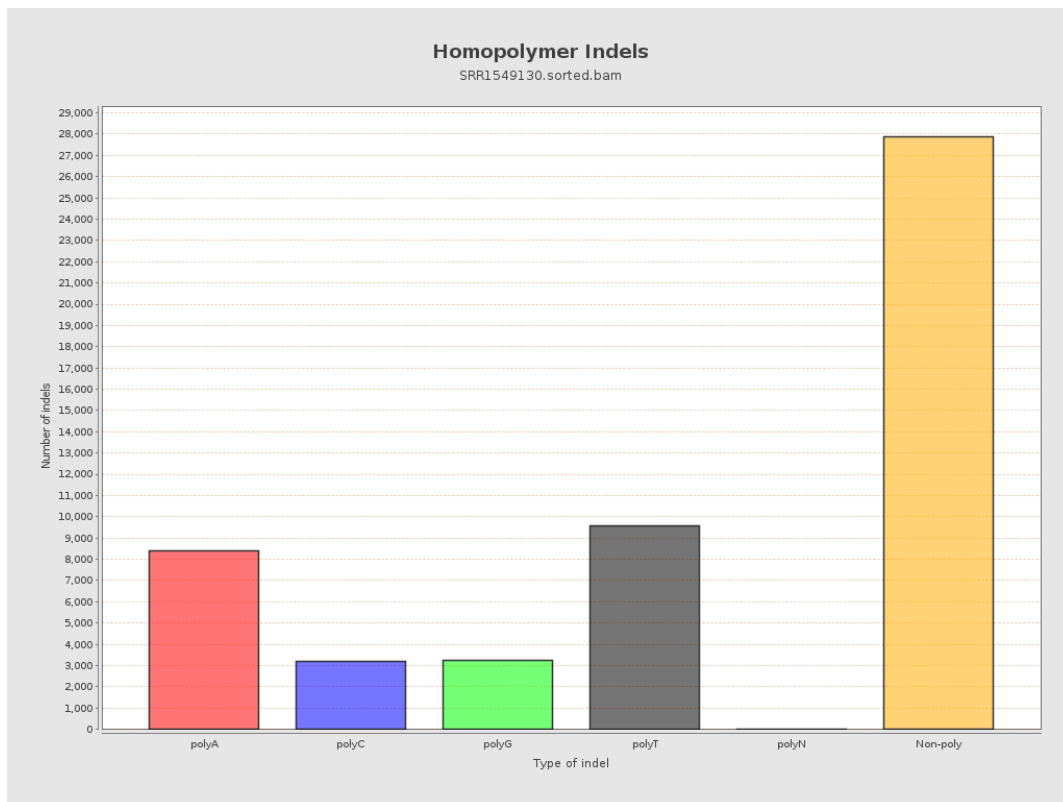
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

