Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:19:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549030.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_SRR1549030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:19:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,943,815
Mapped reads	6,939,508 / 87.36%
Unmapped reads	1,004,307 / 12.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	276,296 / 3.48%
Duplication rate	3.13%
Clipped reads	482,750 / 6.08%

2.2. ACGT Content

Number/percentage of A's	79,097,683 / 28.78%
Number/percentage of C's	57,564,975 / 20.94%
Number/percentage of T's	79,844,267 / 29.05%
Number/percentage of G's	58,335,255 / 21.22%
Number/percentage of N's	2,812 / 0%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0888
Standard Deviation	0.9139

2.4. Mapping Quality

Mean Mapping Quality	42.41

2.5. Mismatches and indels

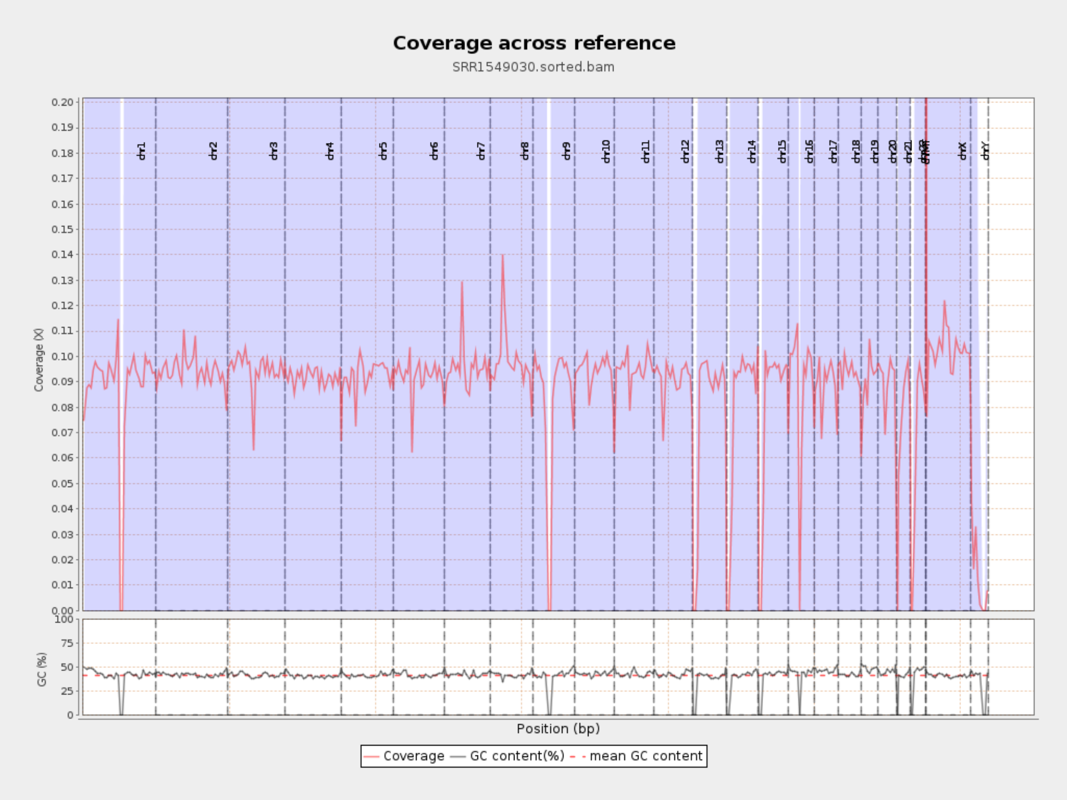
General error rate	0.26%
Mismatches	709,716
Insertions	8,149
Mapped reads with at least one insertion	0.12%
Deletions	21,343
Mapped reads with at least one deletion	0.31%
Homopolymer indels	41.52%

2.6. Chromosome stats

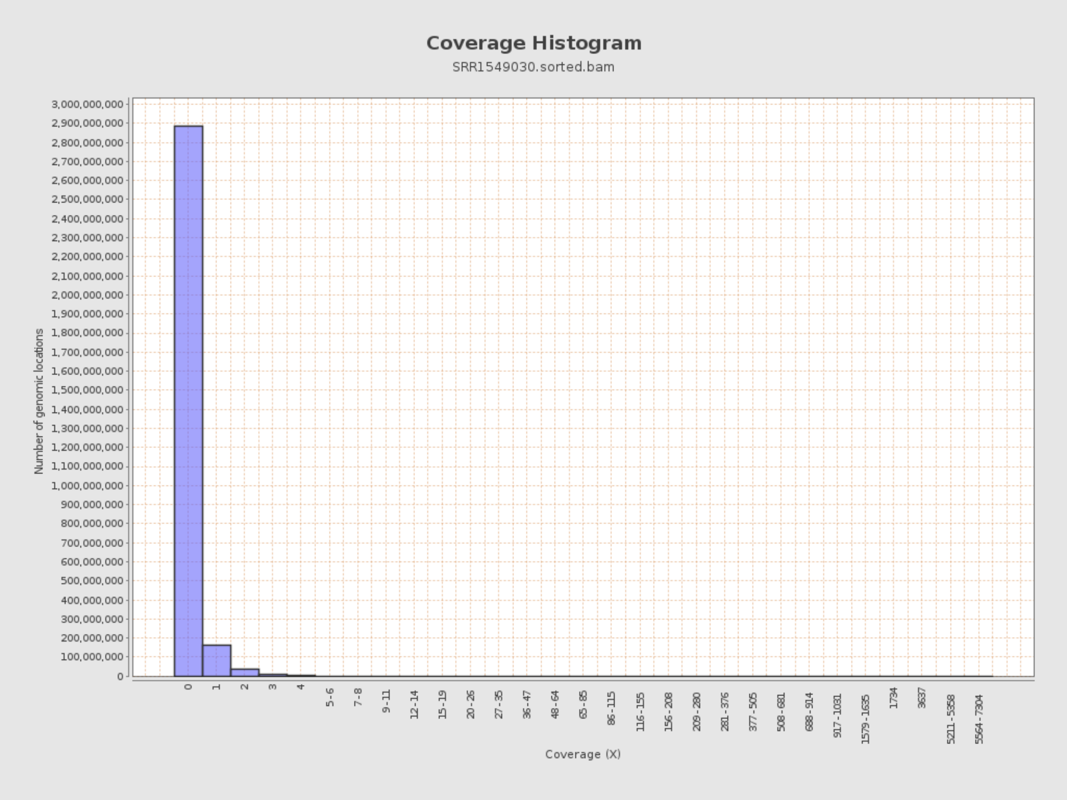
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21755365	0.0873	0.8098
chr2	243199373	22981858	0.0945	0.4861
chr3	198022430	18749602	0.0947	0.3848
chr4	191154276	17557932	0.0919	0.3855
chr5	180915260	16735724	0.0925	0.3848
chr6	171115067	15815697	0.0924	0.4099
chr7	159138663	15258086	0.0959	0.7025
chr8	146364022	14413055	0.0985	3.5467

chr9	141213431	11496241	0.0814	0.4637
chr10	135534747	12839463	0.0947	0.4539
chr11	135006516	12776302	0.0946	0.5848
chr12	133851895	12255402	0.0916	0.3857
chr13	115169878	8903155	0.0773	0.3462
chr14	107349540	8449106	0.0787	0.3906
chr15	102531392	7997686	0.078	0.3482
chr16	90354753	7804149	0.0864	0.3896
chr17	81195210	7274268	0.0896	0.4035
chr18	78077248	7339593	0.094	0.8131
chr19	59128983	5374081	0.0909	0.7175
chr20	63025520	5661749	0.0898	0.3825
chr21	48129895	3521447	0.0732	0.3619
chr22	51304566	3218490	0.0627	0.3466
chrMT	16571	20037	1.2092	1.676
chrX	155270560	15906893	0.1024	0.4507
chrY	59373566	767598	0.0129	0.1722

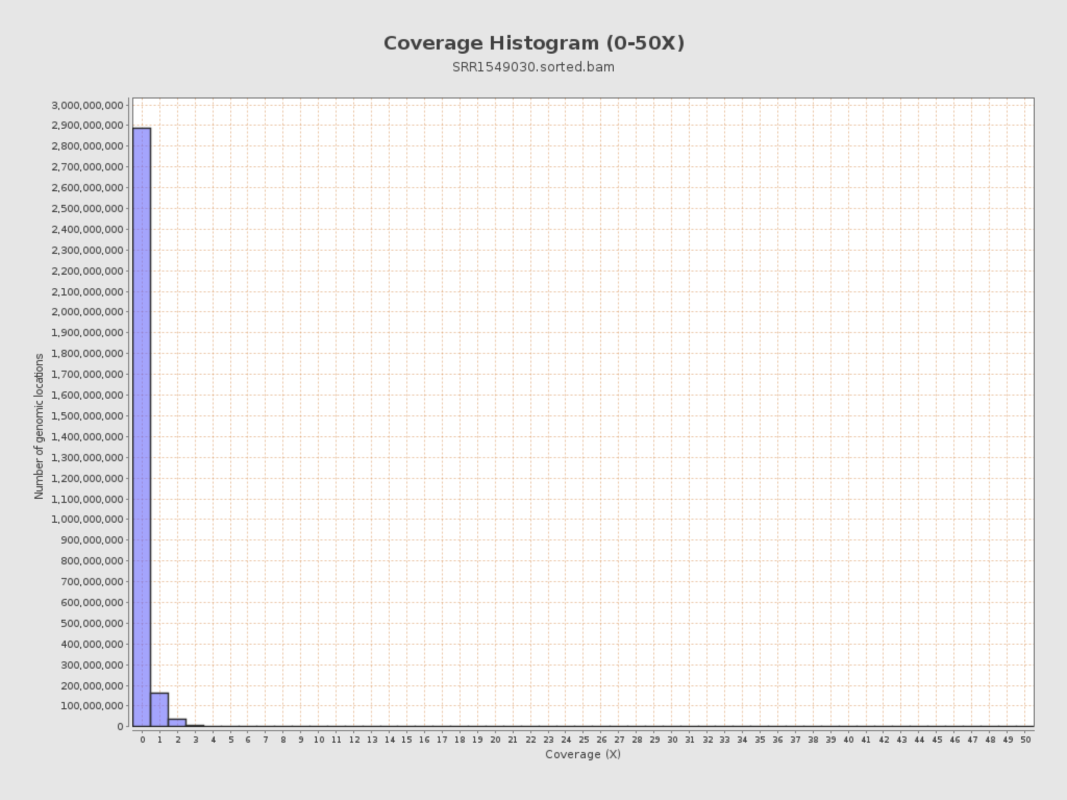
3. Results : Coverage across reference



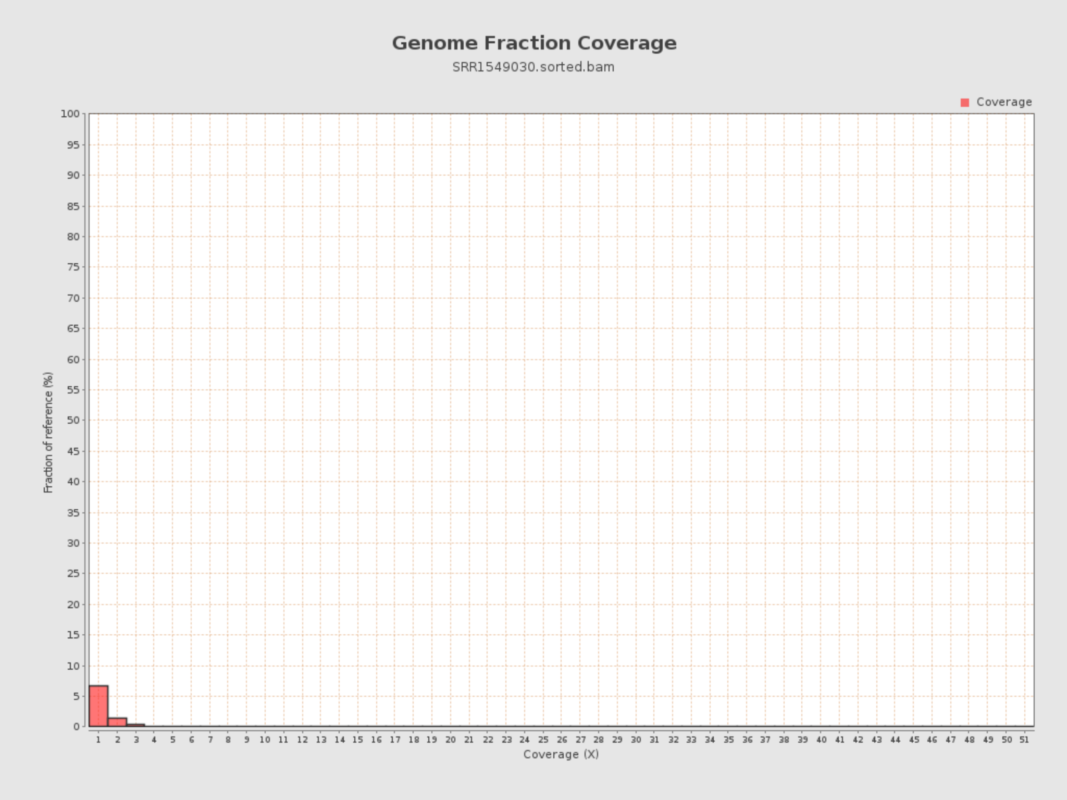
4. Results : Coverage Histogram



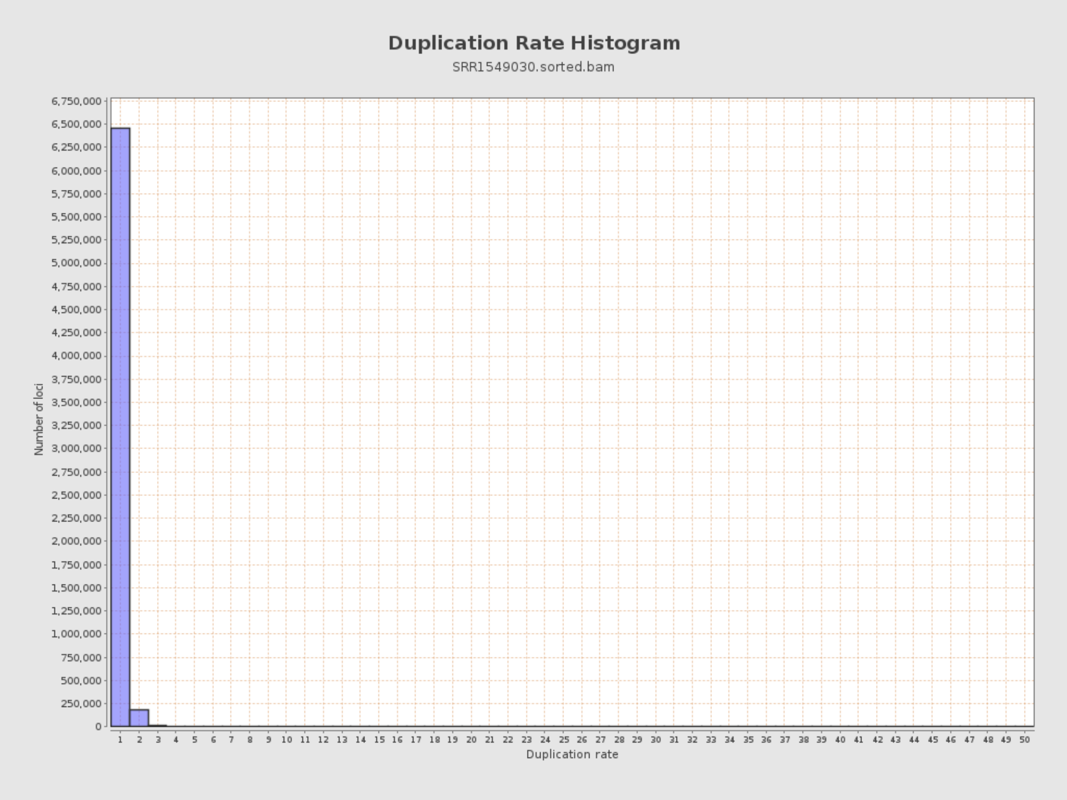
5. Results : Coverage Histogram (0-50X)



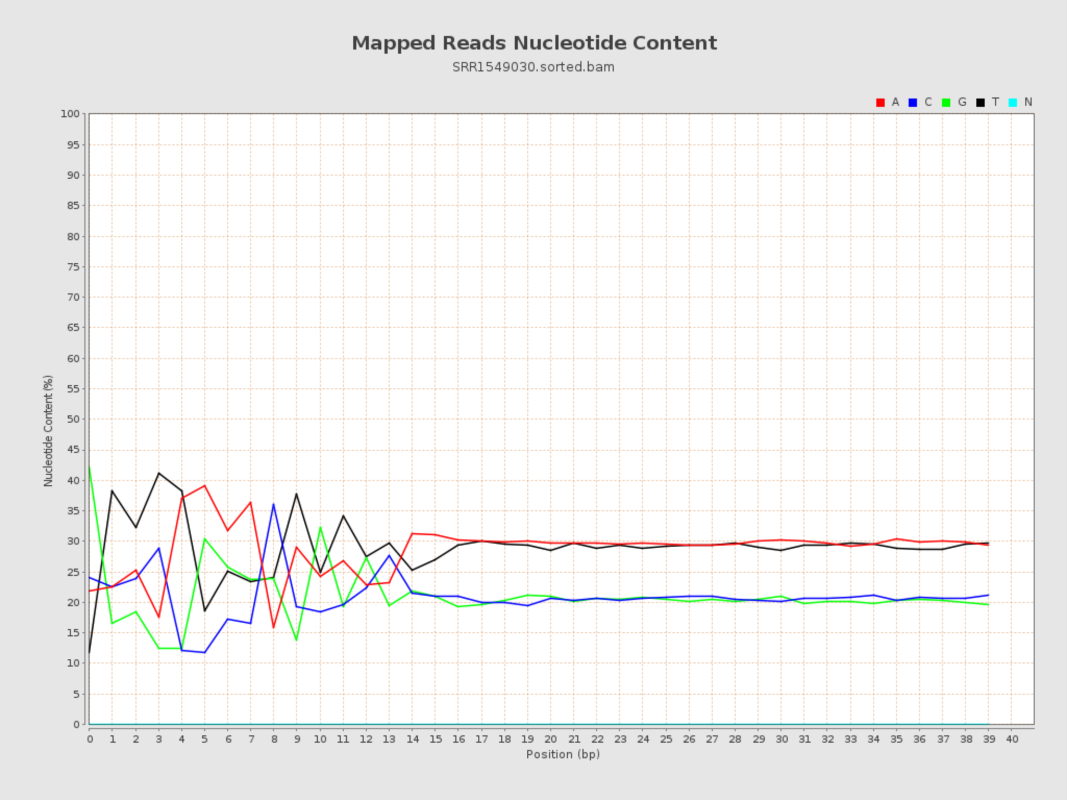
6. Results : Genome Fraction Coverage



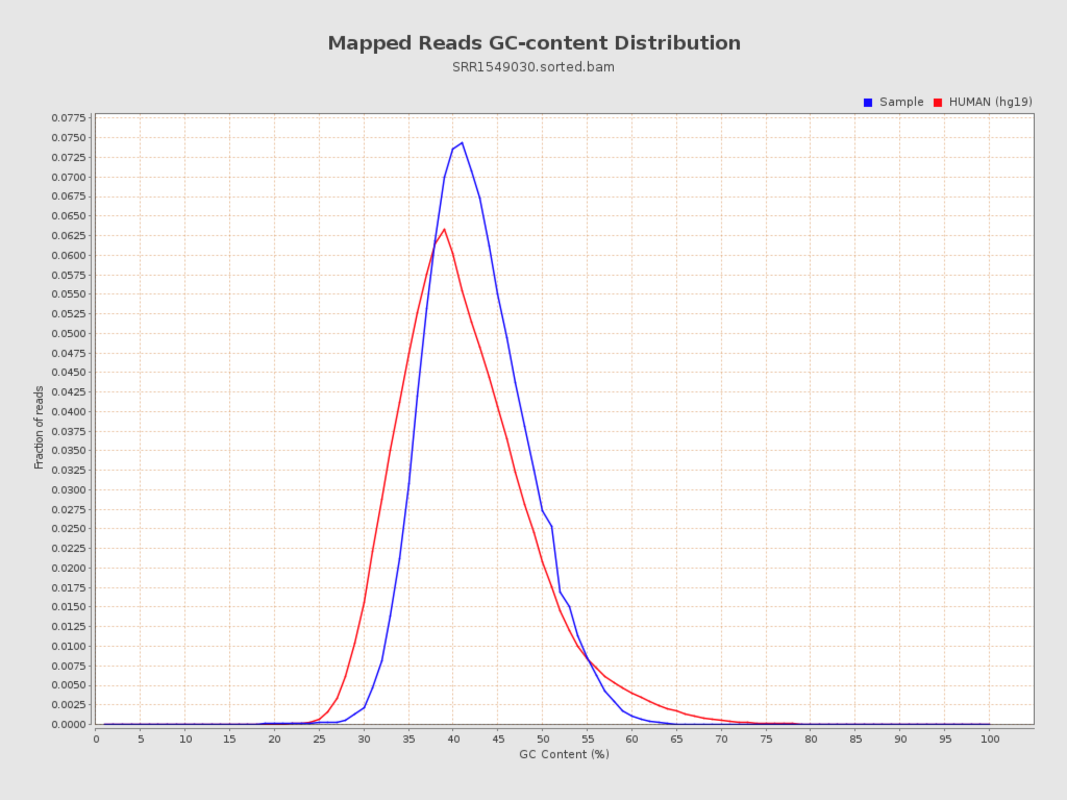
7. Results : Duplication Rate Histogram



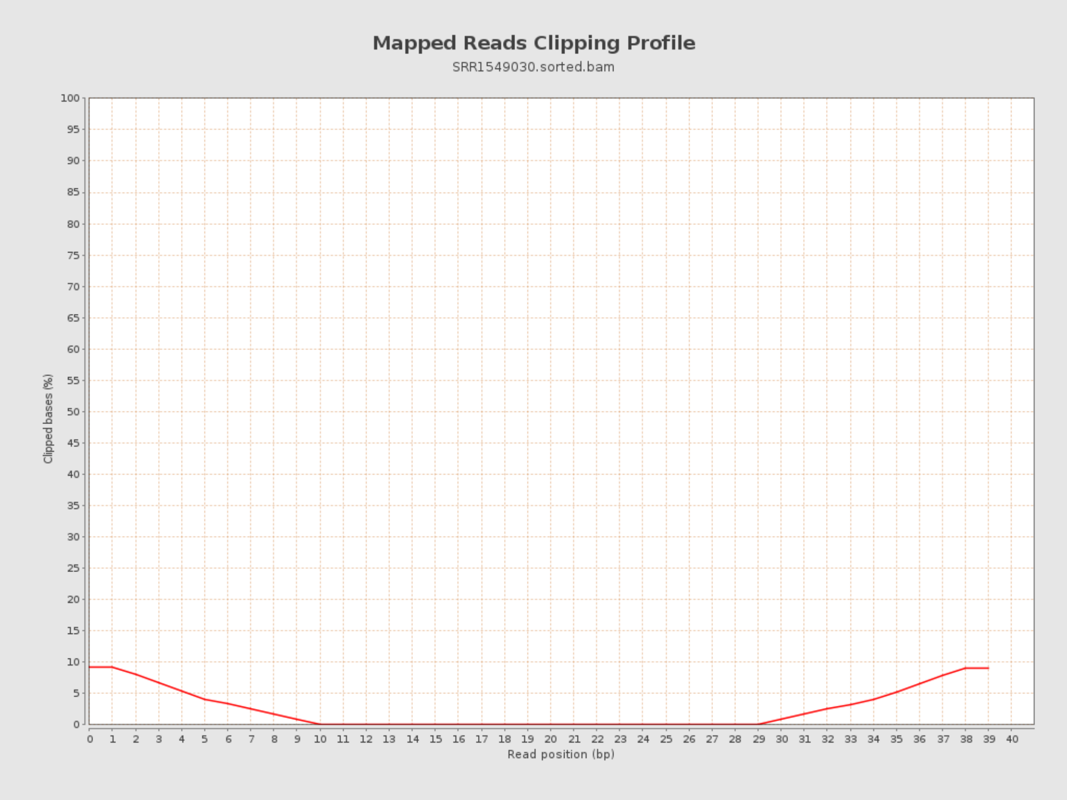
8. Results : Mapped Reads Nucleotide Content



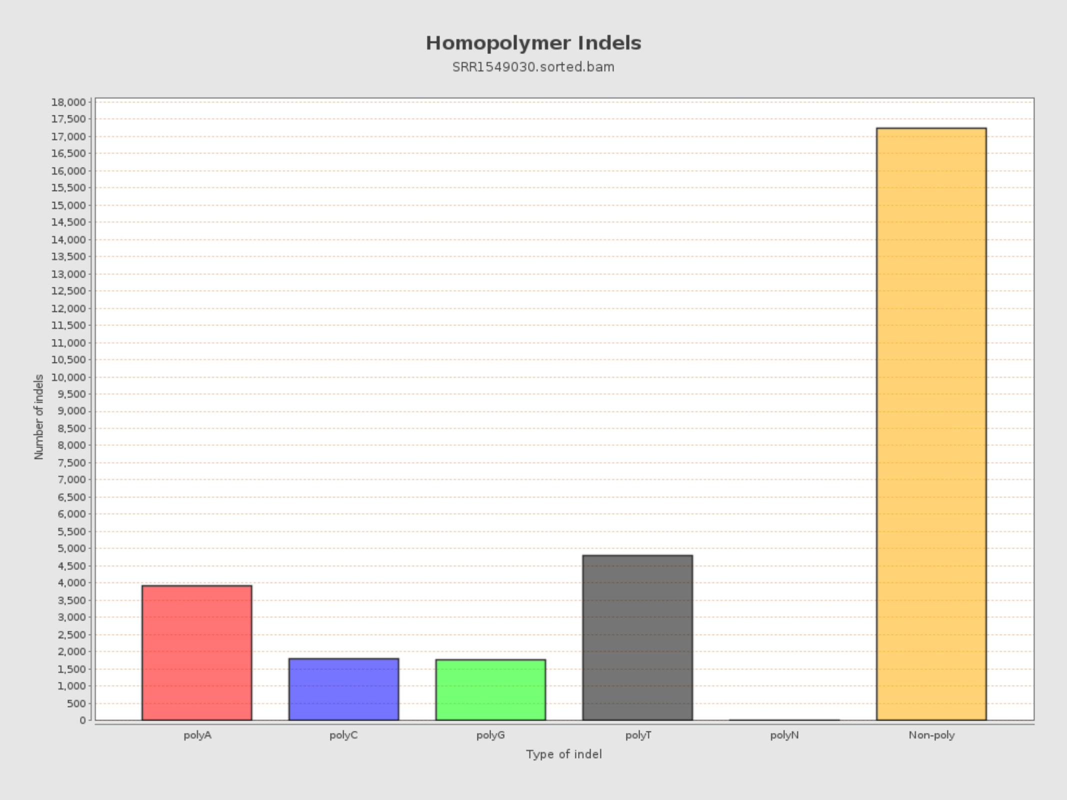
9. Results : Mapped Reads GC-content Distribution



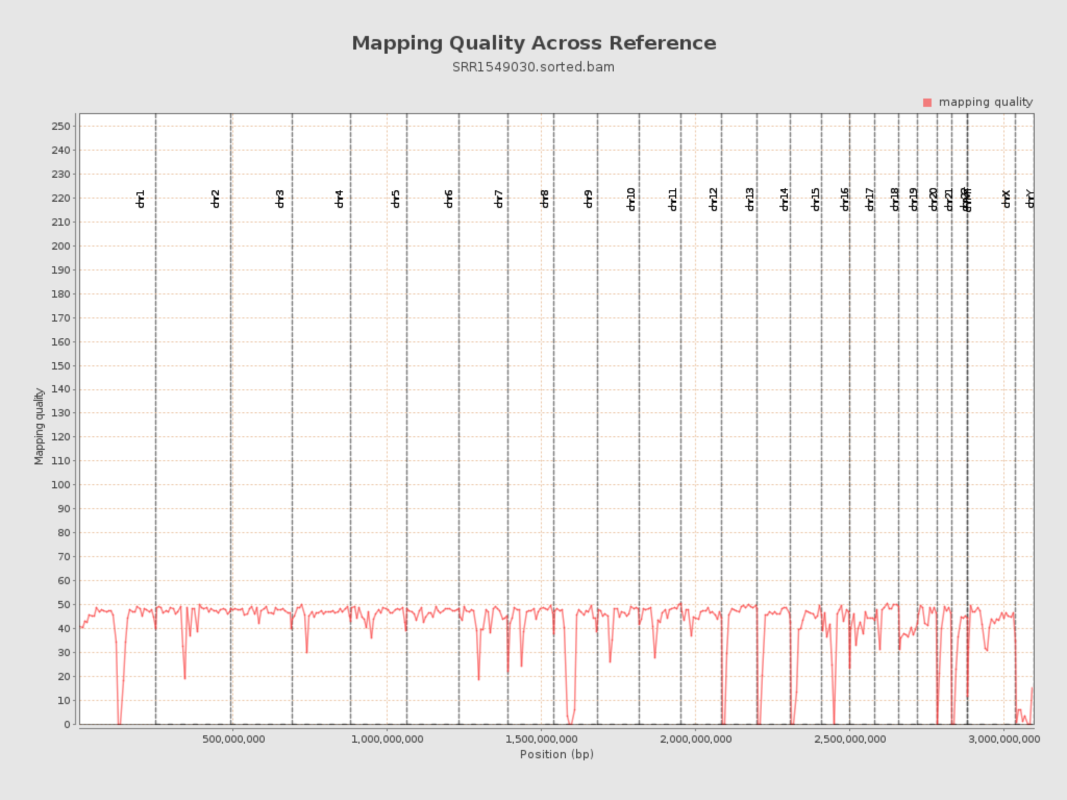
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram