

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:21:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549047.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_SRR1549047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:21:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,304,547
Mapped reads	3,729,580 / 86.64%
Unmapped reads	574,967 / 13.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	118,050 / 2.74%
Duplication rate	2.17%
Clipped reads	288,688 / 6.71%

2.2. ACGT Content

Number/percentage of A's	41,654,856 / 28.23%
Number/percentage of C's	31,714,080 / 21.49%
Number/percentage of T's	42,433,621 / 28.76%
Number/percentage of G's	31,738,868 / 21.51%
Number/percentage of N's	1,196 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0477
Standard Deviation	0.4647

2.4. Mapping Quality

Mean Mapping Quality	39.62
----------------------	-------

2.5. Mismatches and indels

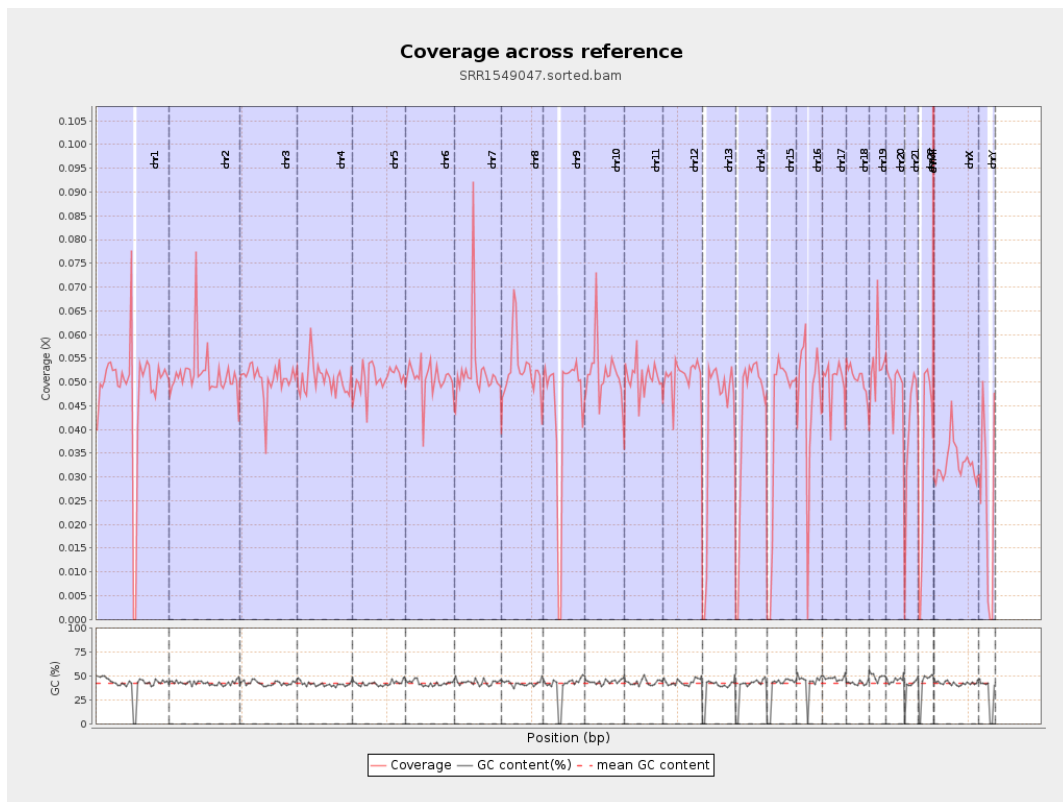
General error rate	0.28%
Mismatches	402,754
Insertions	4,601
Mapped reads with at least one insertion	0.12%
Deletions	11,583
Mapped reads with at least one deletion	0.31%
Homopolymer indels	40.92%

2.6. Chromosome stats

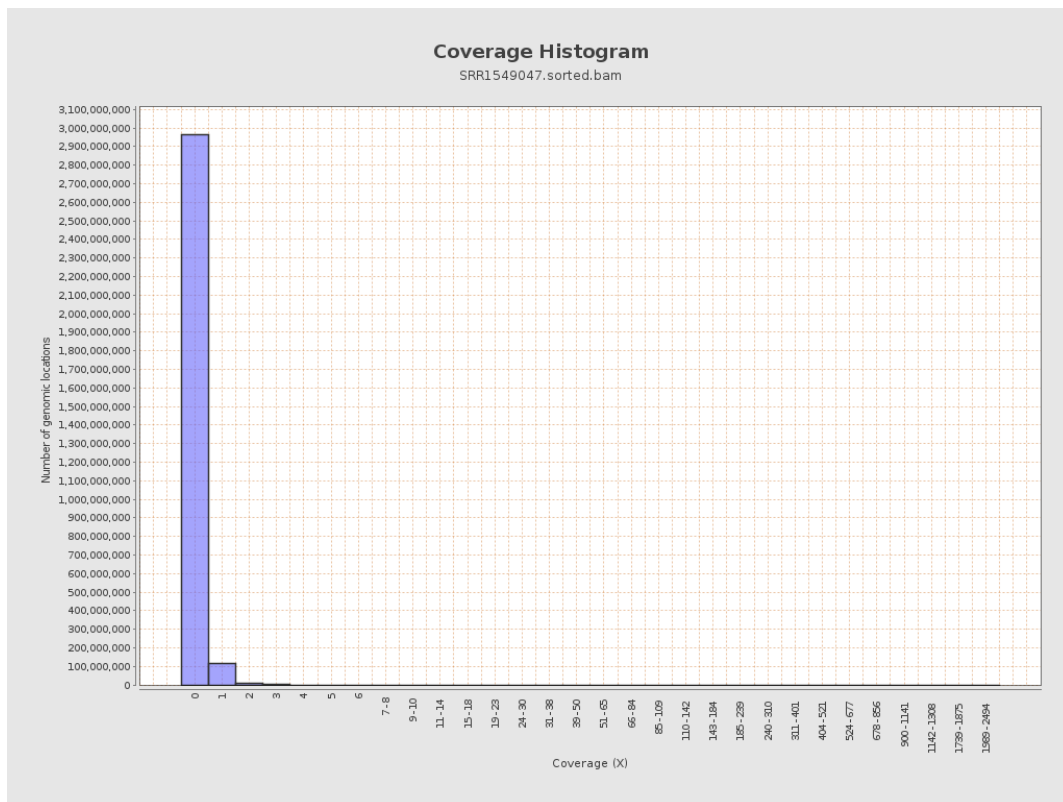
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12023204	0.0482	0.7634
chr2	243199373	12550161	0.0516	0.3623
chr3	198022430	10014209	0.0506	0.2459
chr4	191154276	9664764	0.0506	0.2594
chr5	180915260	9182151	0.0508	0.2491
chr6	171115067	8662254	0.0506	0.2579
chr7	159138663	8390491	0.0527	0.5694
chr8	146364022	7689693	0.0525	1.2438

chr9	141213431	6304766	0.0446	0.3459
chr10	135534747	7027724	0.0519	0.3469
chr11	135006516	6851114	0.0507	0.3011
chr12	133851895	6864370	0.0513	0.256
chr13	115169878	4787524	0.0416	0.2206
chr14	107349540	4585137	0.0427	0.2561
chr15	102531392	4257183	0.0415	0.2226
chr16	90354753	4227890	0.0468	0.2554
chr17	81195210	4049096	0.0499	0.2527
chr18	78077248	3965778	0.0508	0.6118
chr19	59128983	3204678	0.0542	0.7017
chr20	63025520	3074808	0.0488	0.2491
chr21	48129895	1917557	0.0398	0.2562
chr22	51304566	1748767	0.0341	0.2642
chrMT	16571	5441	0.3283	0.6425
chrX	155270560	5118656	0.033	0.2502
chrY	59373566	1390522	0.0234	0.2613

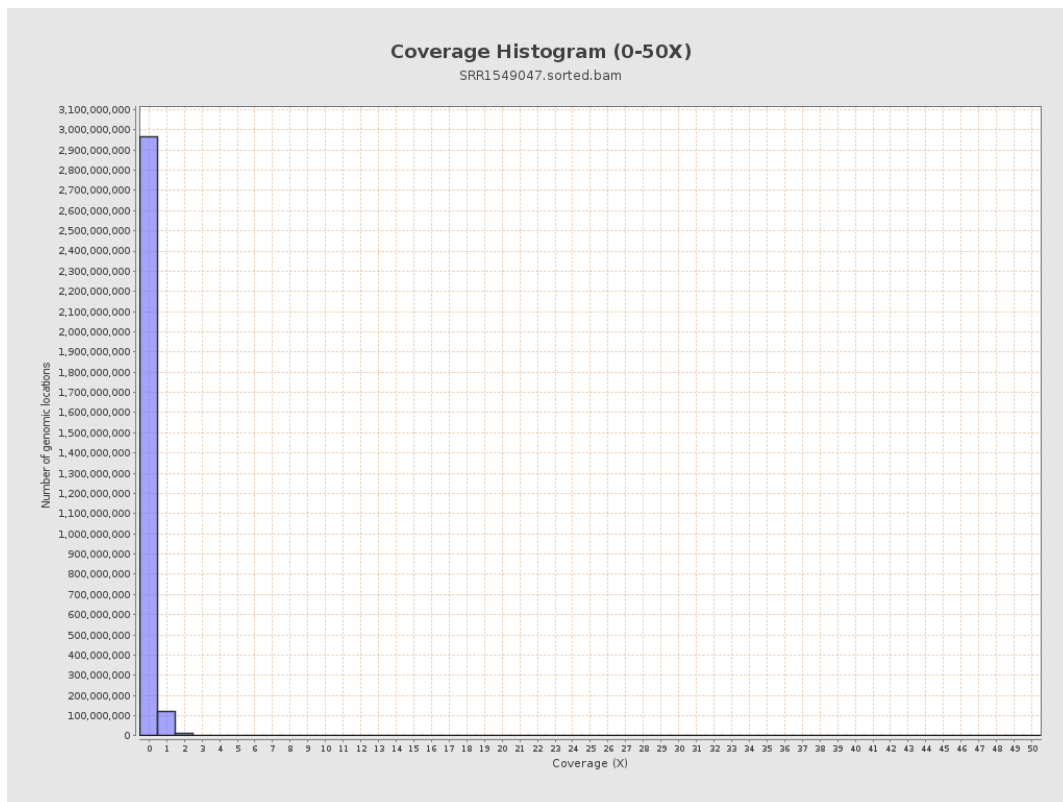
3. Results : Coverage across reference



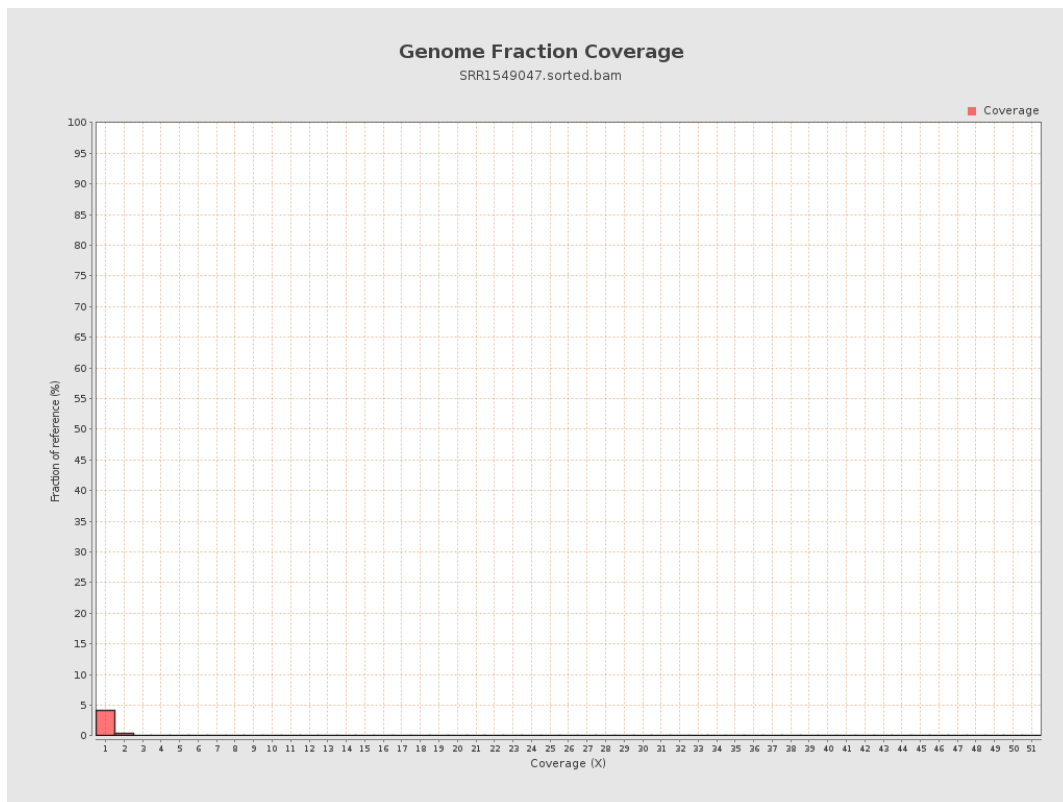
4. Results : Coverage Histogram



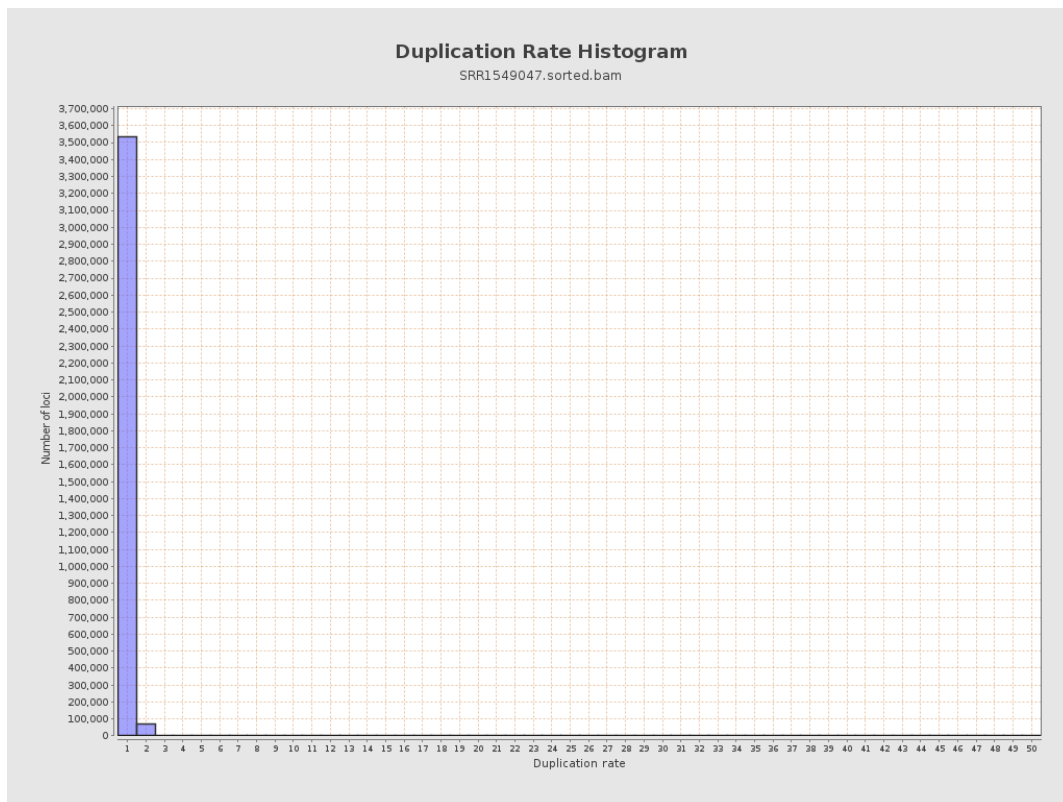
5. Results : Coverage Histogram (0-50X)



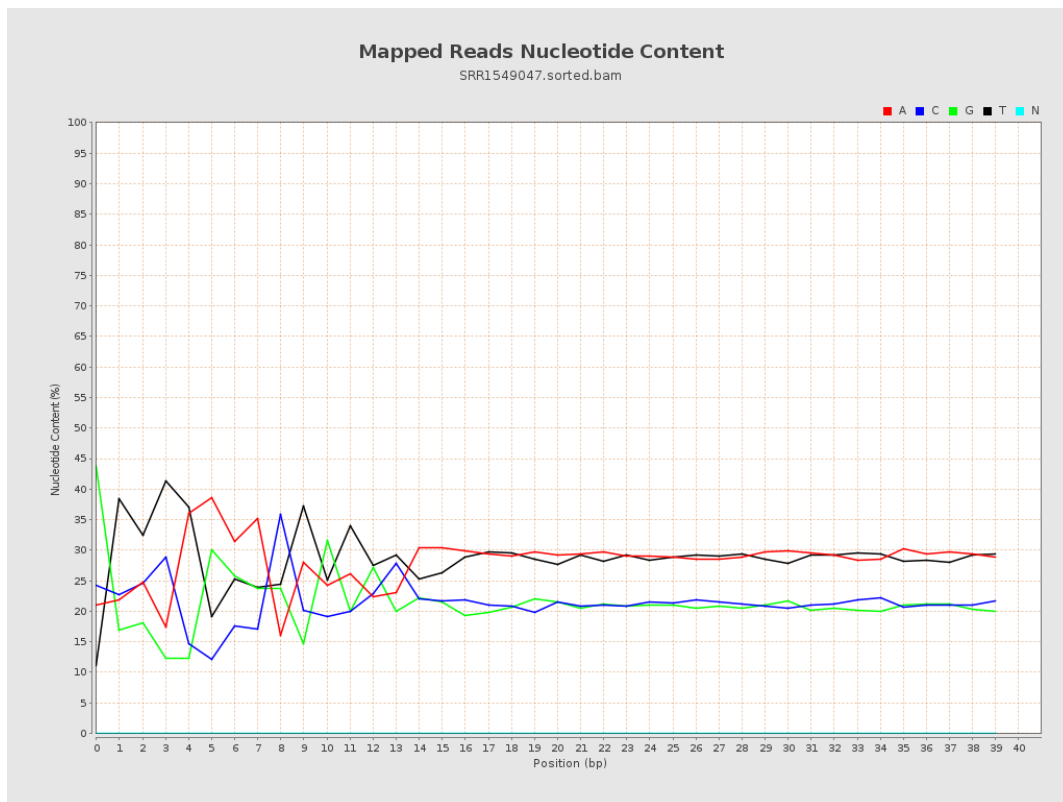
6. Results : Genome Fraction Coverage



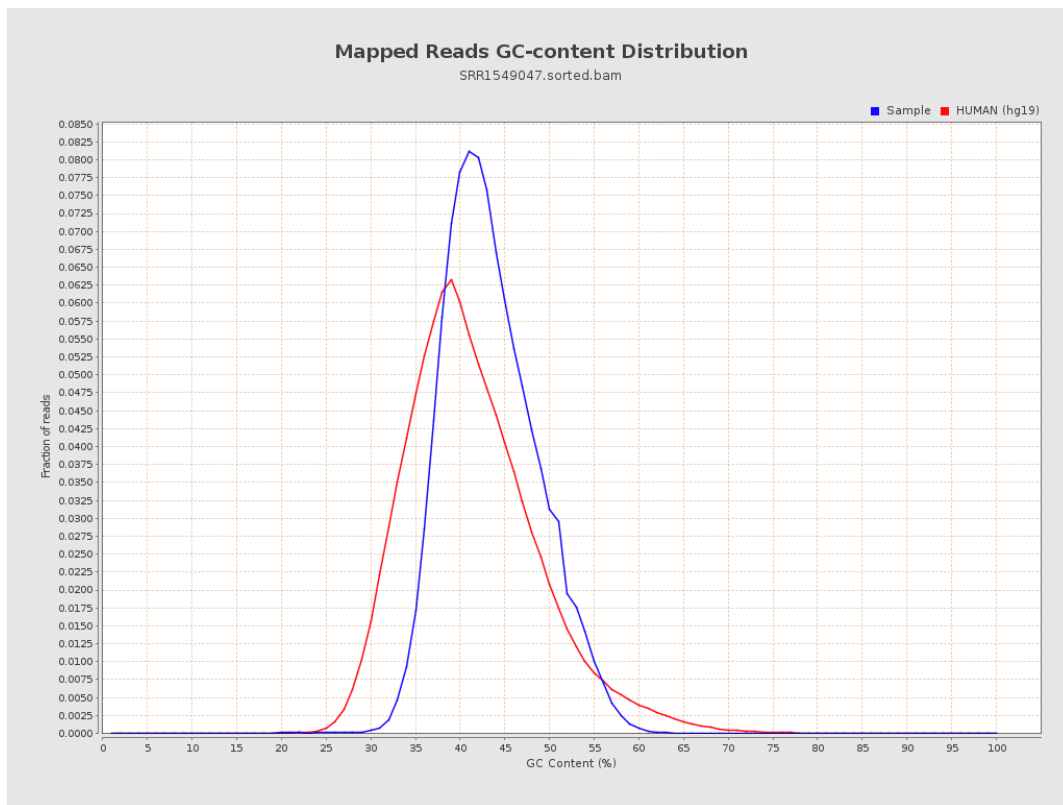
7. Results : Duplication Rate Histogram



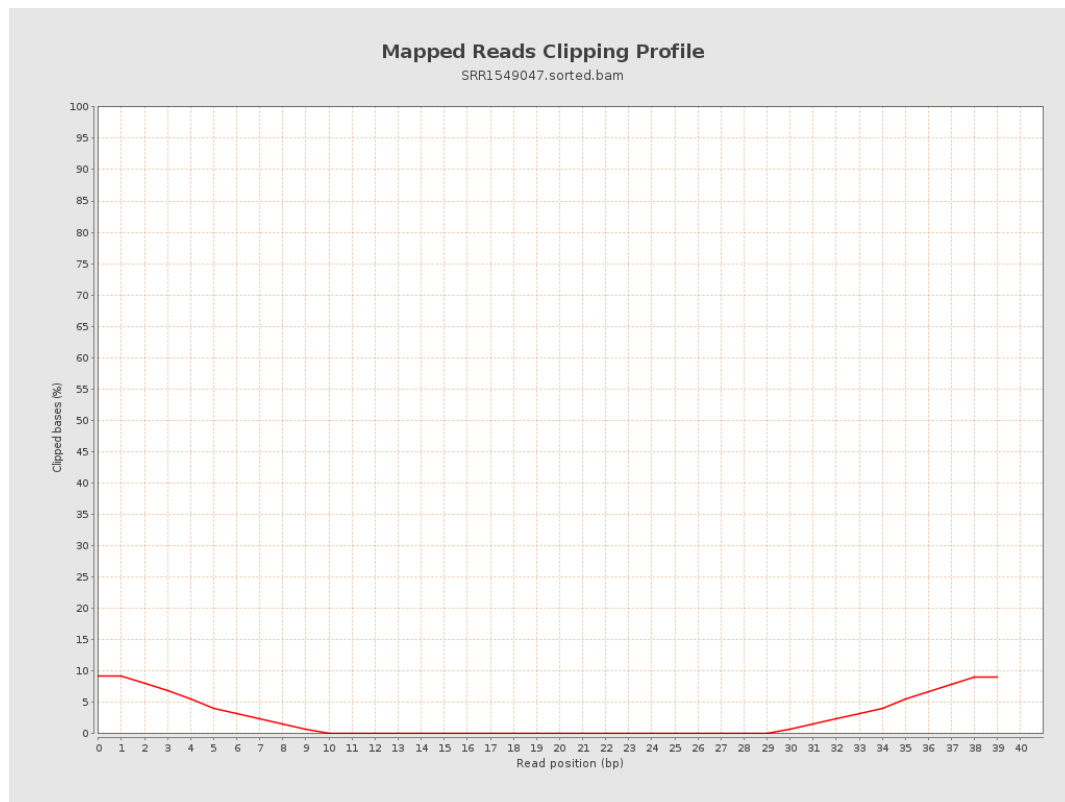
8. Results : Mapped Reads Nucleotide Content



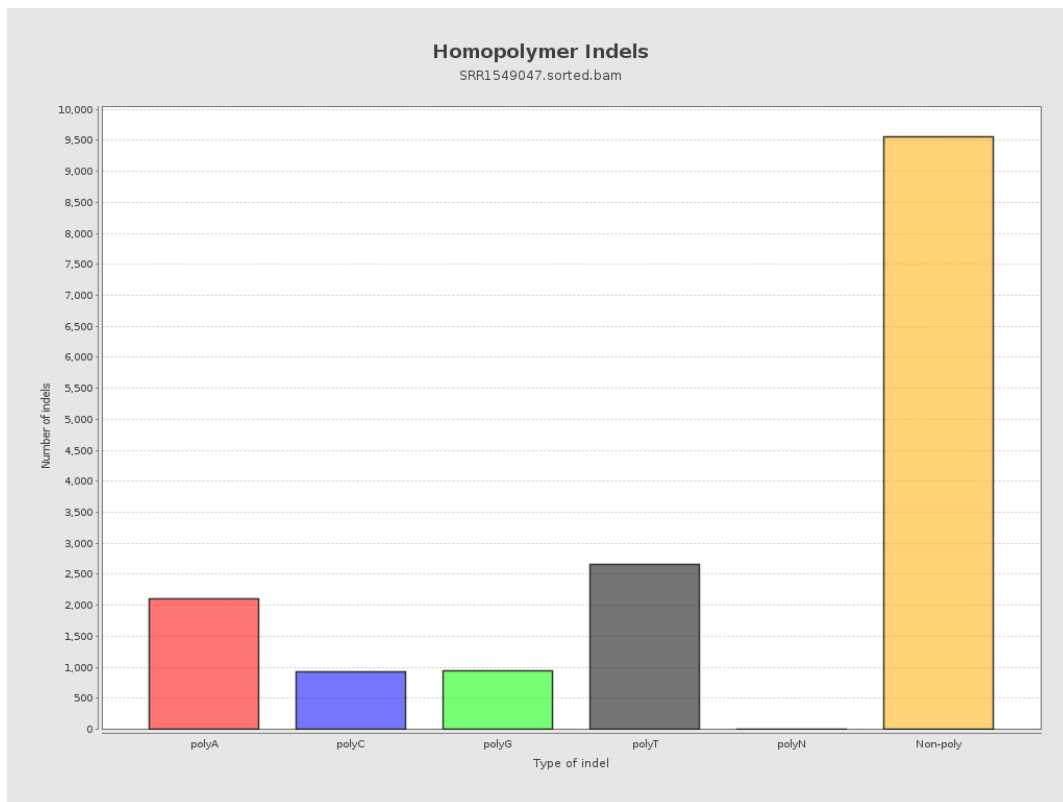
9. Results : Mapped Reads GC-content Distribution



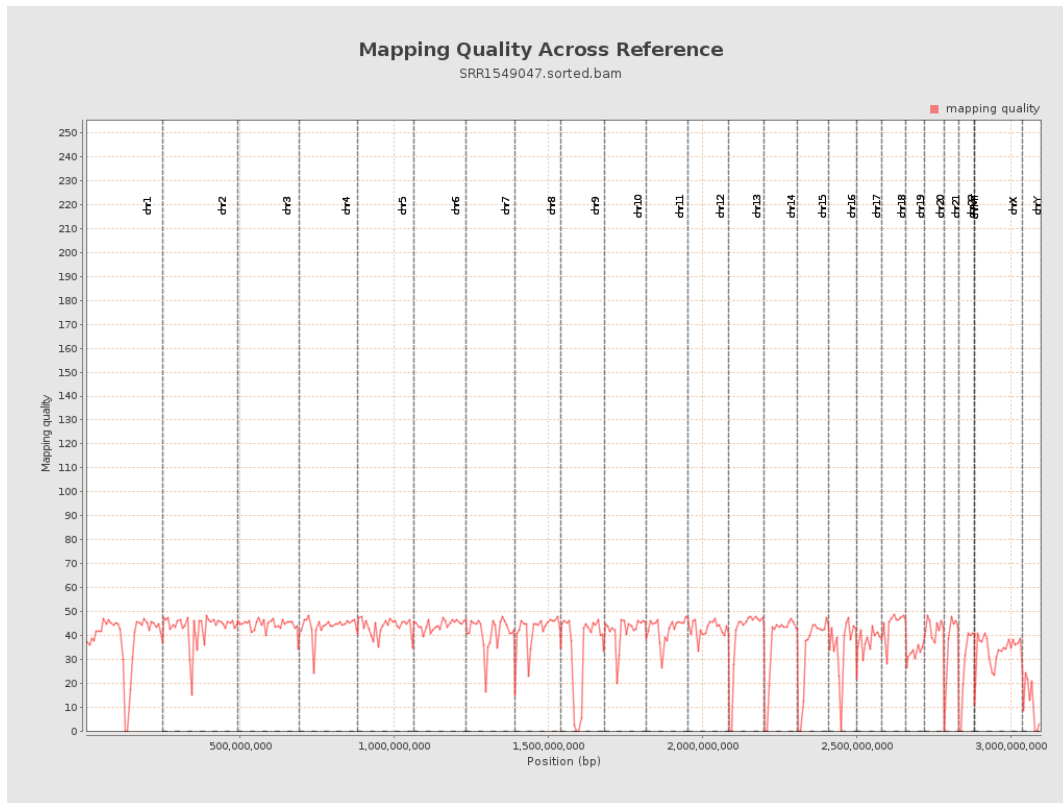
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

