Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 21:56:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514700.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_SRR5514700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514700.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 21:56:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,792,105
Mapped reads	38,312,785 / 98.76%
Unmapped reads	479,320 / 1.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,205,563 / 13.42%
Read min/max/mean length	30 / 100 / 102.69
Duplicated reads (estimated)	37,705,752 / 97.2%
Duplication rate	41.94%
Clipped reads	19,504,884 / 50.28%

2.2. ACGT Content

Number/percentage of A's	966,254,437 / 27.34%
Number/percentage of C's	789,863,244 / 22.35%
Number/percentage of T's	966,704,321 / 27.36%
Number/percentage of G's	808,081,469 / 22.87%
Number/percentage of N's	2,844,750 / 0.08%
GC Percentage	45.22%

2.3. Coverage

Mean	1.1441

Standard Deviation	437.4196

2.4. Mapping Quality

Mean Mapping Quality	48.6

2.5. Mismatches and indels

General error rate	1.22%
Mismatches	37,052,049
Insertions	2,621,567
Mapped reads with at least one insertion	6.46%
Deletions	2,605,688
Mapped reads with at least one deletion	6.23%
Homopolymer indels	21.78%

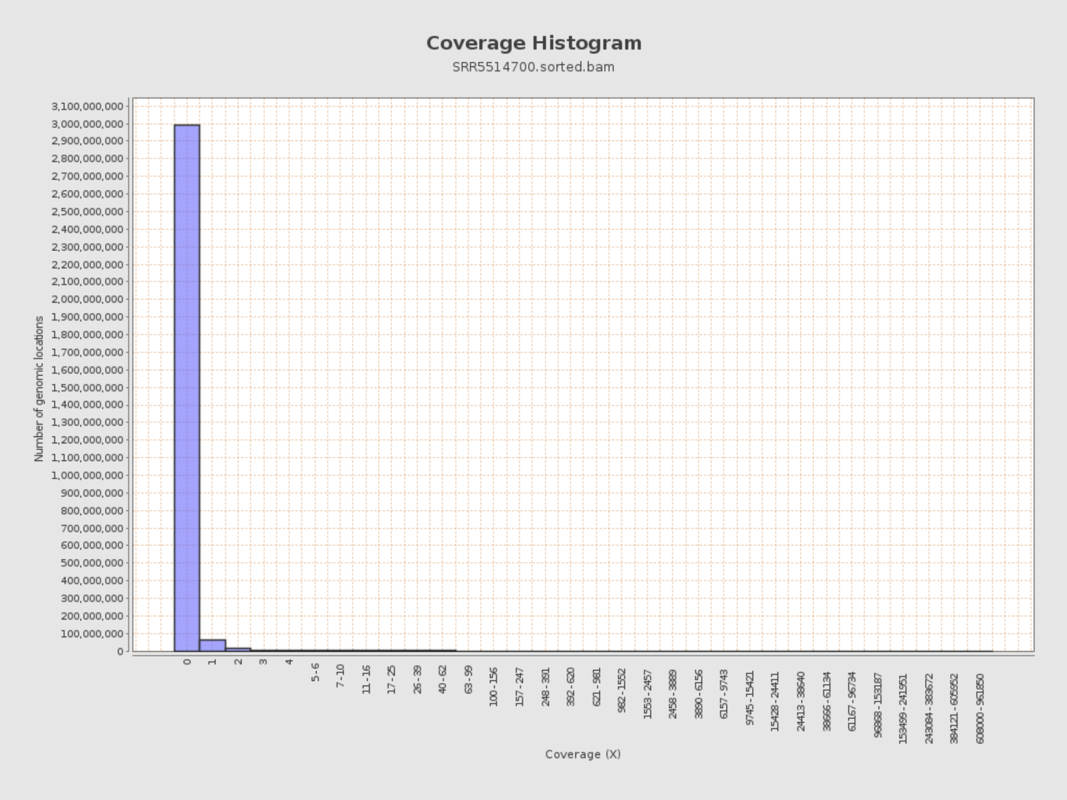
2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	156661395	0.6285	32.5436
chr2	243199373	447195975	1.8388	478.3563
chr3	198022430	116533279	0.5885	21.5587
chr4	191154276	174343689	0.9121	42.6666
chr5	180915260	101692371	0.5621	23.2823
chr6	171115067	145352374	0.8494	47.7227
chr7	159138663	103282788	0.649	32.1391

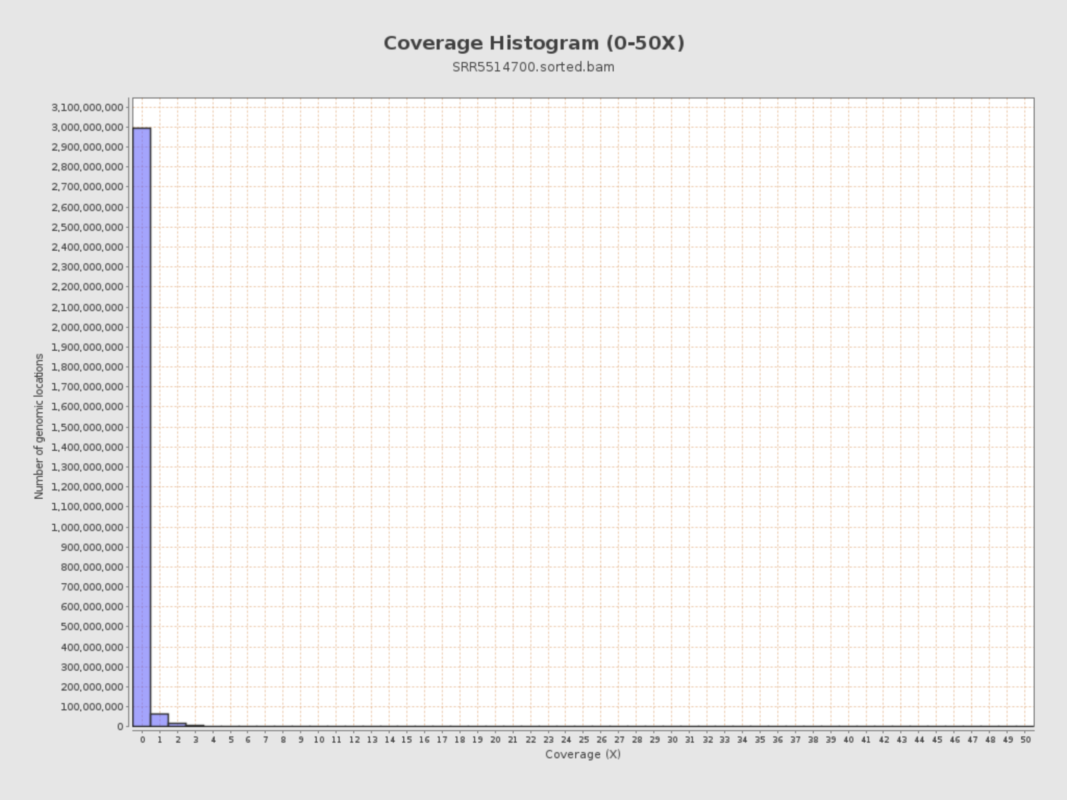
chr8	146364022	147569331	1.0082	97.9135
chr9	141213431	61296728	0.4341	16.0488
chr10	135534747	234231202	1.7282	201.557
chr11	135006516	95814938	0.7097	25.984
chr12	133851895	240629459	1.7977	297.8566
chr13	115169878	398548807	3.4605	997.7536
chr14	107349540	696423854	6.4874	1,930.4779
chr15	102531392	68885077	0.6718	34.7952
chr16	90354753	44501936	0.4925	20.7245
chr17	81195210	24448977	0.3011	11.5561
chr18	78077248	50194889	0.6429	24.1447
chr19	59128983	54016052	0.9135	58.5315
chr20	63025520	37249555	0.591	39.8993
chr21	48129895	33961515	0.7056	35.2097
chr22	51304566	40731820	0.7939	142.1447
chrMT	16571	1254969	75.7328	47.8235
chrX	155270560	56325755	0.3628	19.1623
chrY	59373566	10579912	0.1782	5.1476

3. Results : Coverage across reference

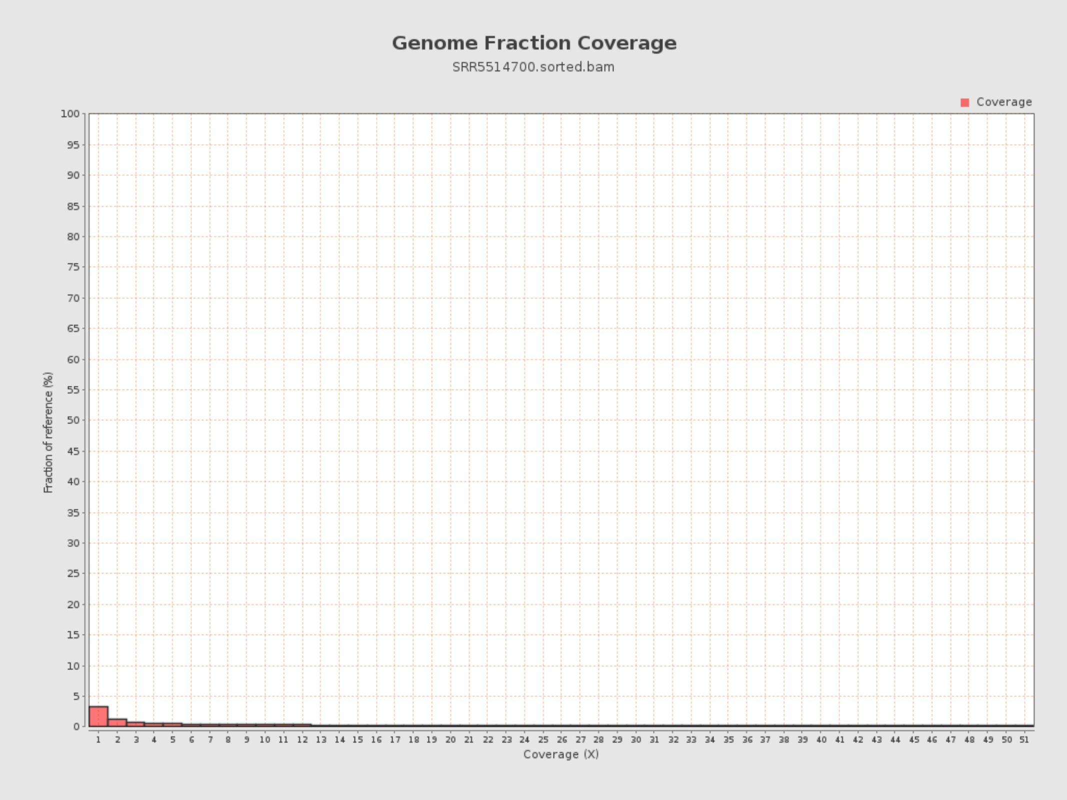
4. Results : Coverage Histogram



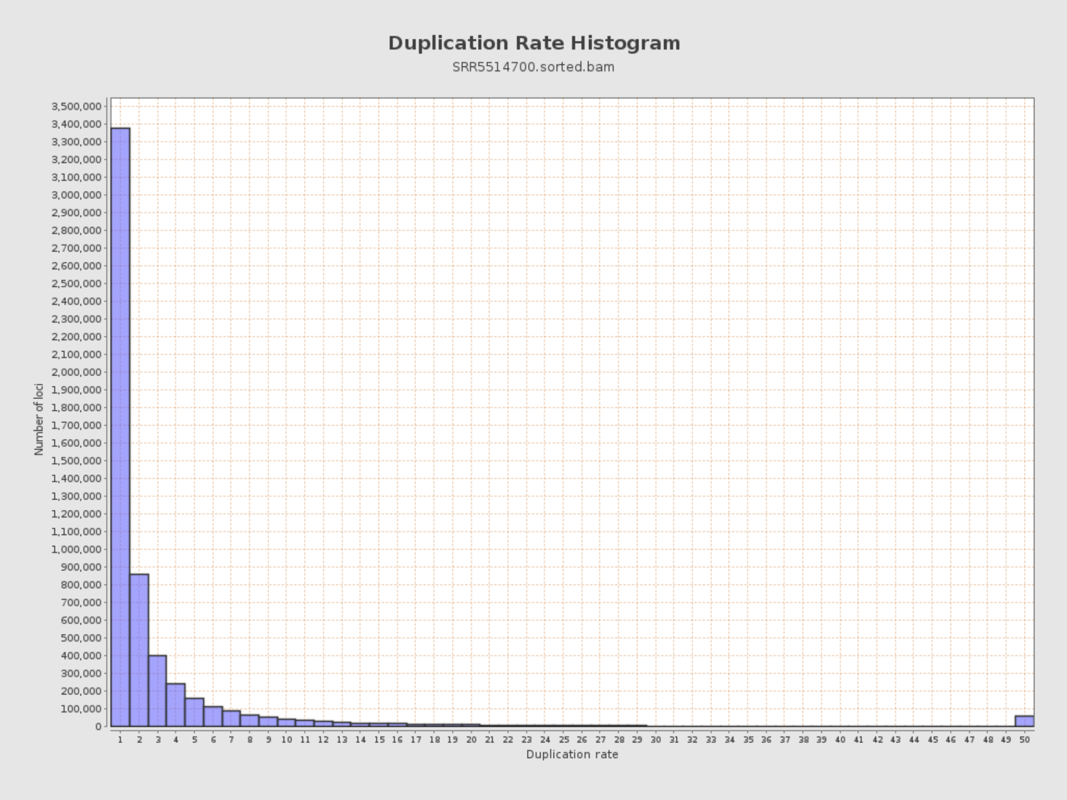
5. Results : Coverage Histogram (0-50X)



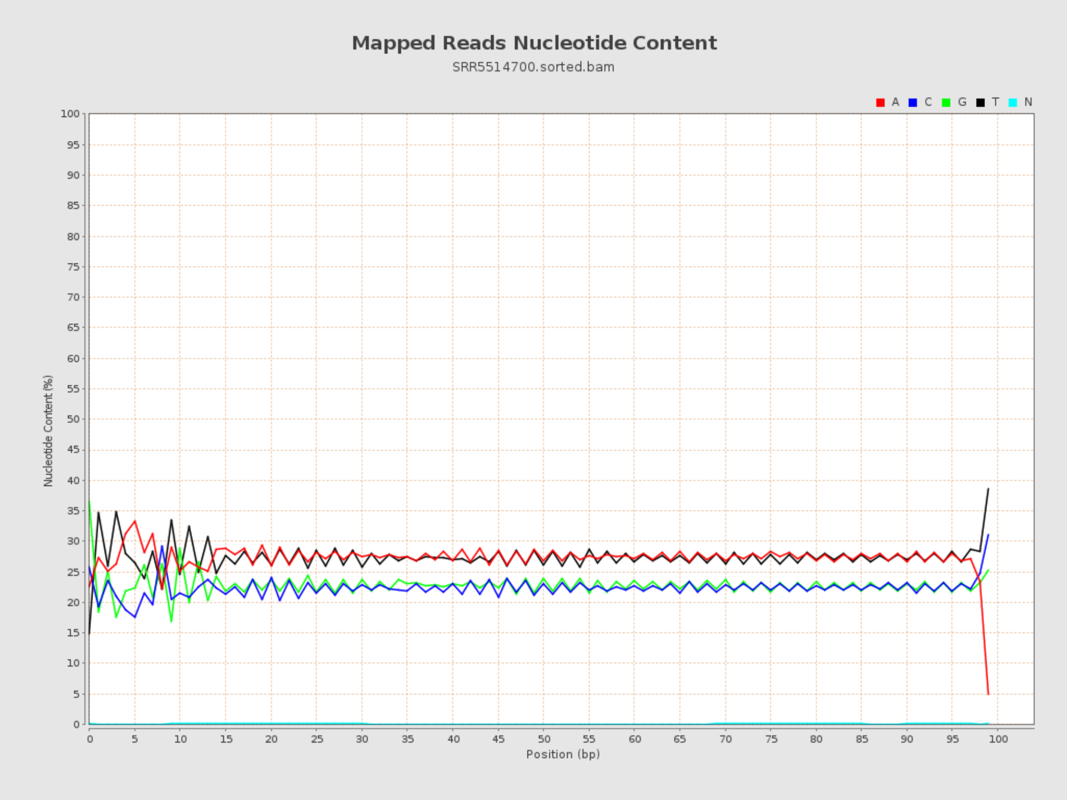
6. Results : Genome Fraction Coverage



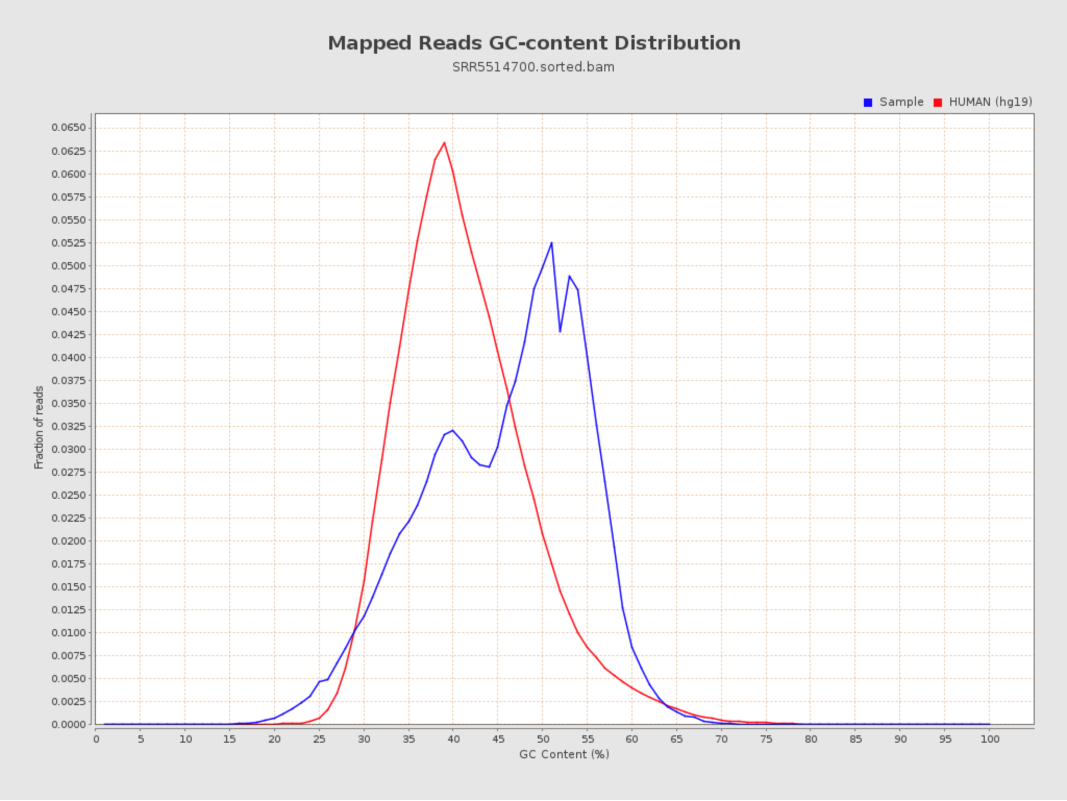
7. Results : Duplication Rate Histogram



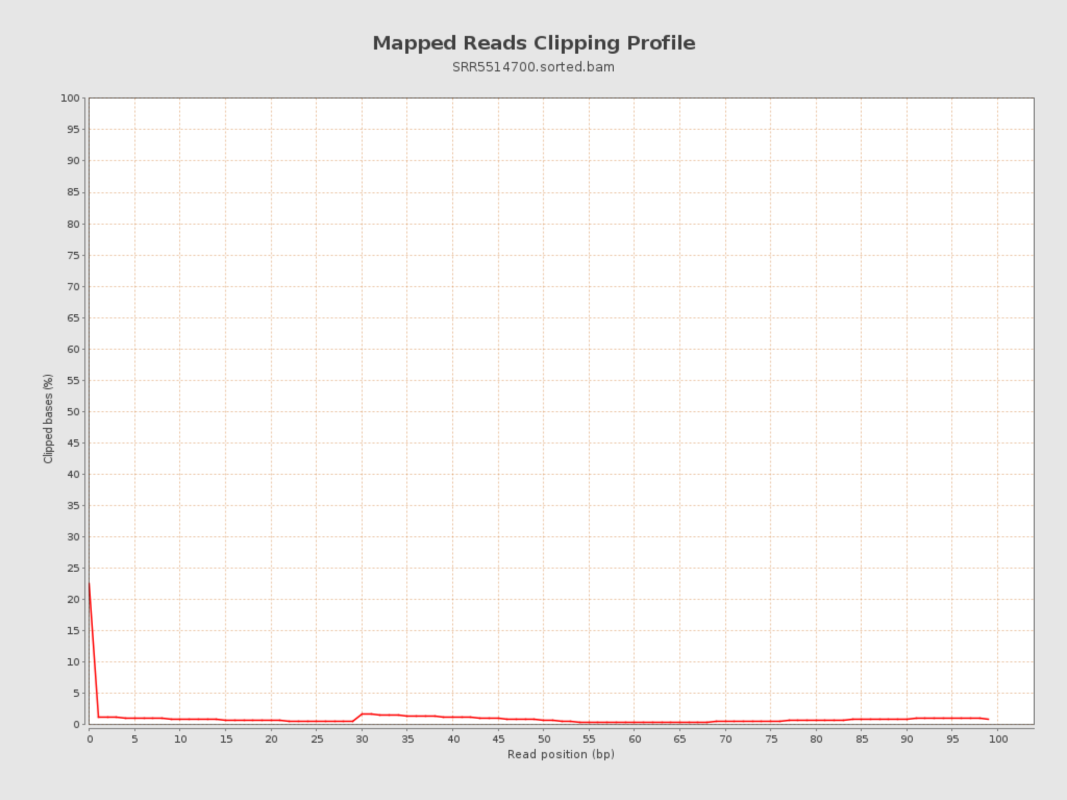
8. Results : Mapped Reads Nucleotide Content



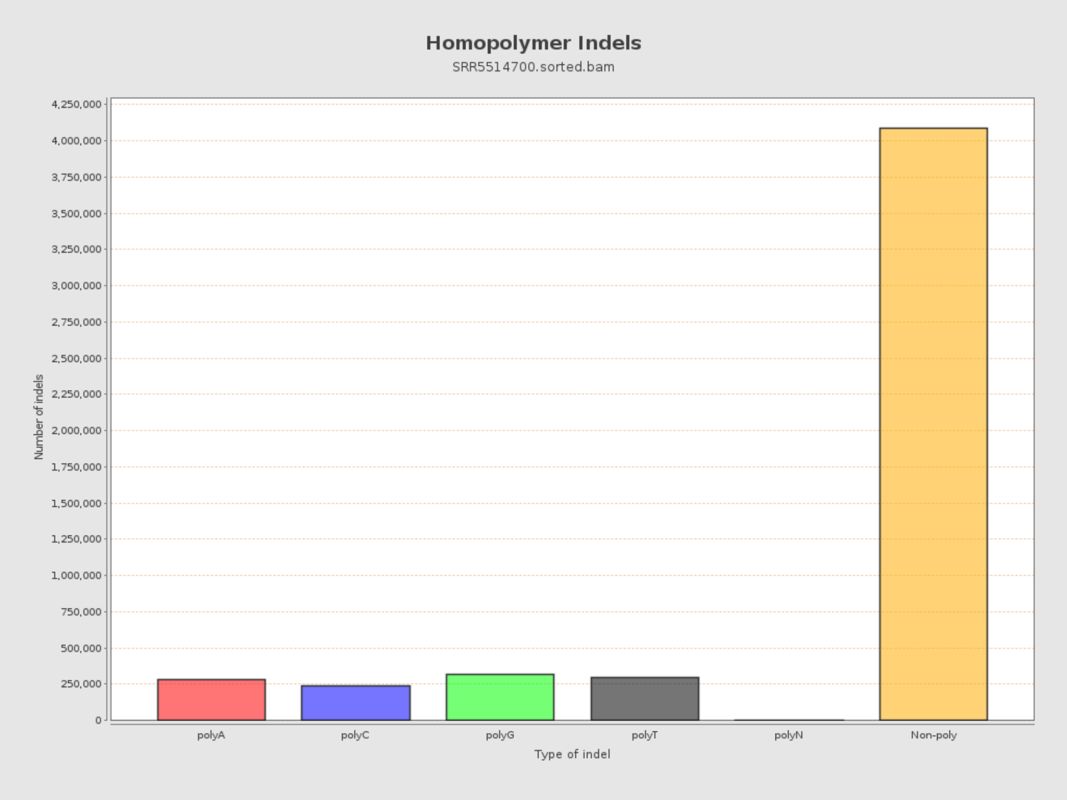
9. Results : Mapped Reads GC-content Distribution



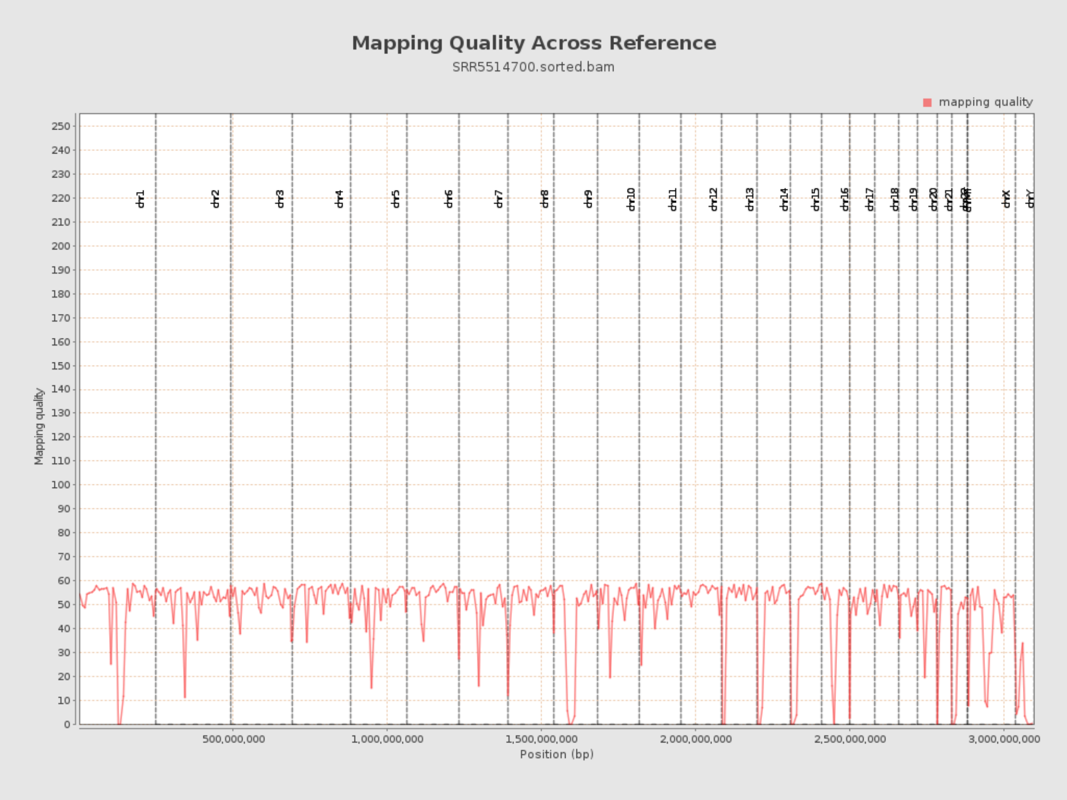
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram