Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 18:08:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514736.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_SRR5514736 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514736.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 18:08:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514736.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	145,705,723
Mapped reads	142,113,014 / 97.53%
Unmapped reads	3,592,709 / 2.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,750,692 / 2.57%
Read min/max/mean length	30 / 100 / 99.88
Duplicated reads (estimated)	114,012,073 / 78.25%
Duplication rate	51.87%
Clipped reads	22,727,951 / 15.6%

2.2. ACGT Content

Number/percentage of A's	3,582,731,567 / 26.29%
Number/percentage of C's	3,176,244,402 / 23.31%
Number/percentage of T's	3,614,903,665 / 26.53%
Number/percentage of G's	3,181,824,274 / 23.35%
Number/percentage of N's	69,557,974 / 0.51%
GC Percentage	46.66%

2.3. Coverage

Mean	4.4037

Standard Deviation	81.9485

2.4. Mapping Quality

Mean Mapping Quality	37.2

2.5. Mismatches and indels

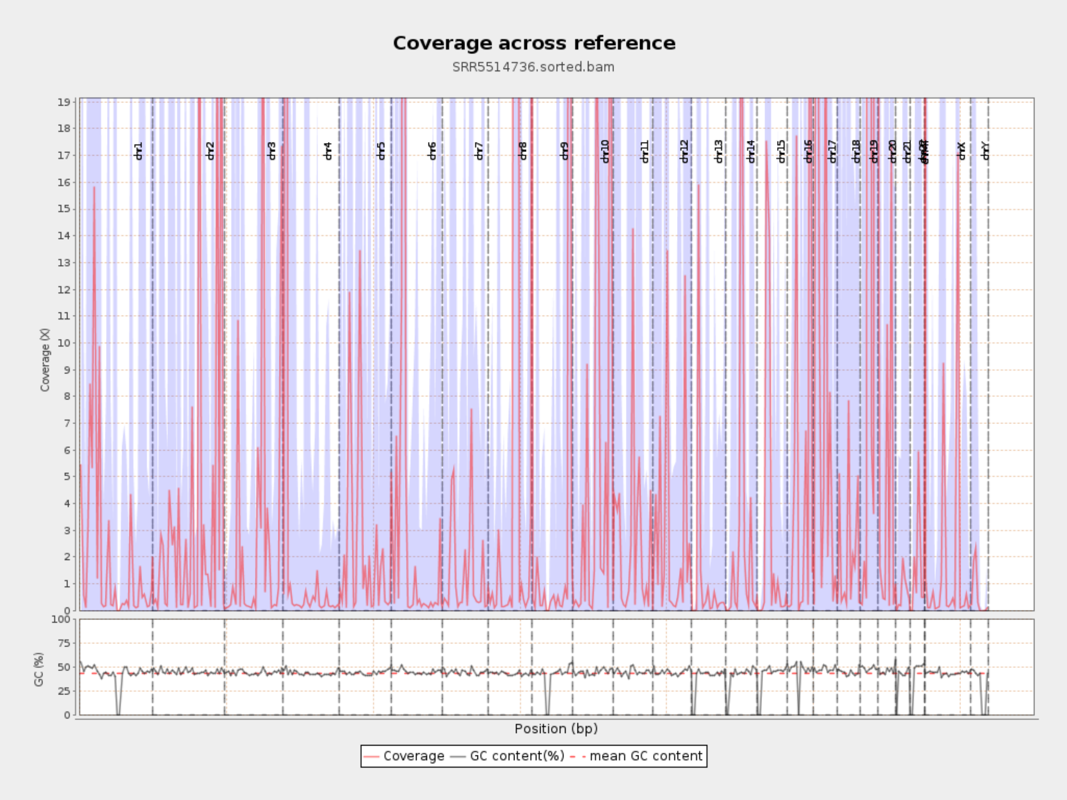
General error rate	0.99%
Mismatches	127,336,299
Insertions	4,330,949
Mapped reads with at least one insertion	2.94%
Deletions	3,513,930
Mapped reads with at least one deletion	2.41%
Homopolymer indels	45.95%

2.6. Chromosome stats

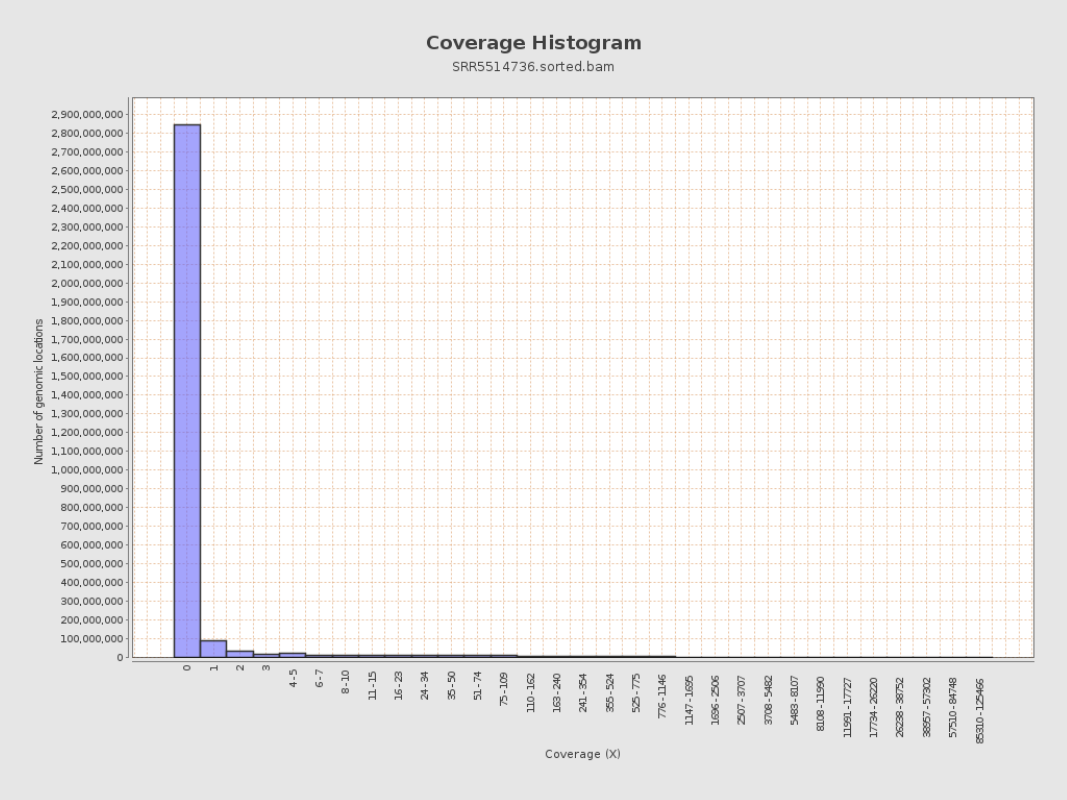
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	504930525	2.0258	39.0705
chr2	243199373	963812558	3.9631	102.1495
chr3	198022430	620218211	3.1321	64.3742
chr4	191154276	489217482	2.5593	44.1663
chr5	180915260	428426909	2.3681	29.5567
chr6	171115067	812885123	4.7505	61.333
chr7	159138663	229570272	1.4426	22.4931

chr8	146364022	1374263930	9.3894	117.5446
chr9	141213431	684143213	4.8447	126.988
chr10	135534747	800273087	5.9046	85.8869
chr11	135006516	365653488	2.7084	35.483
chr12	133851895	378329197	2.8265	32.6248
chr13	115169878	158932469	1.38	55.3689
chr14	107349540	328975616	3.0645	49.9492
chr15	102531392	273824818	2.6706	37.9075
chr16	90354753	530458343	5.8708	102.9054
chr17	81195210	725090203	8.9302	75.8425
chr18	78077248	186292446	2.386	35.014
chr19	59128983	3042284219	51.4517	346.6816
chr20	63025520	314179354	4.985	47.4161
chr21	48129895	34651965	0.72	23.2832
chr22	51304566	87473375	1.705	26.0747
chrMT	16571	14480062	873.8194	356.0044
chrX	155270560	247312252	1.5928	27.9611
chrY	59373566	36768899	0.6193	71.5197

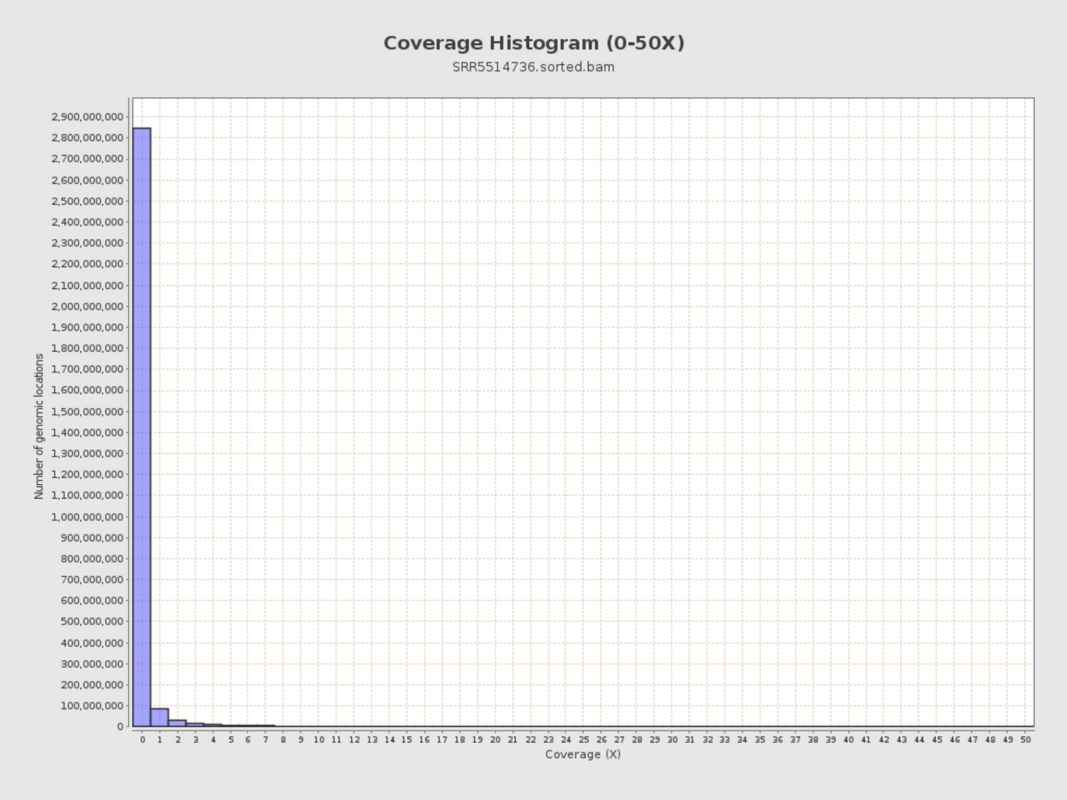
3. Results : Coverage across reference



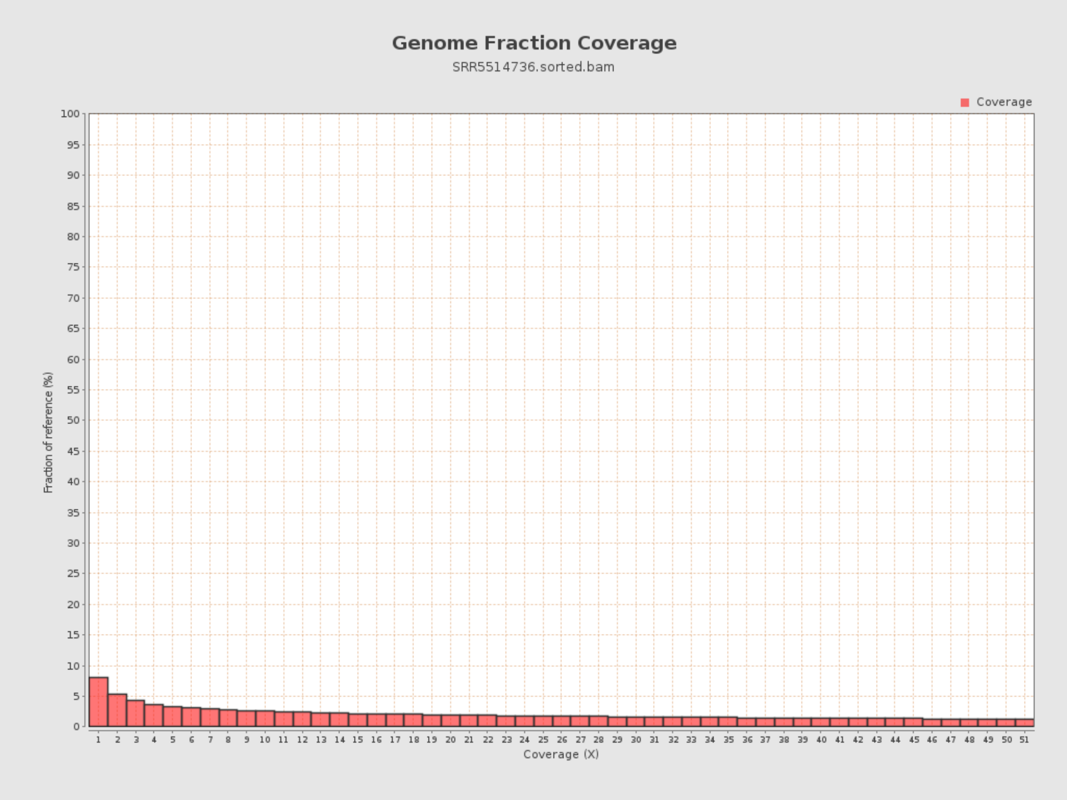
4. Results : Coverage Histogram



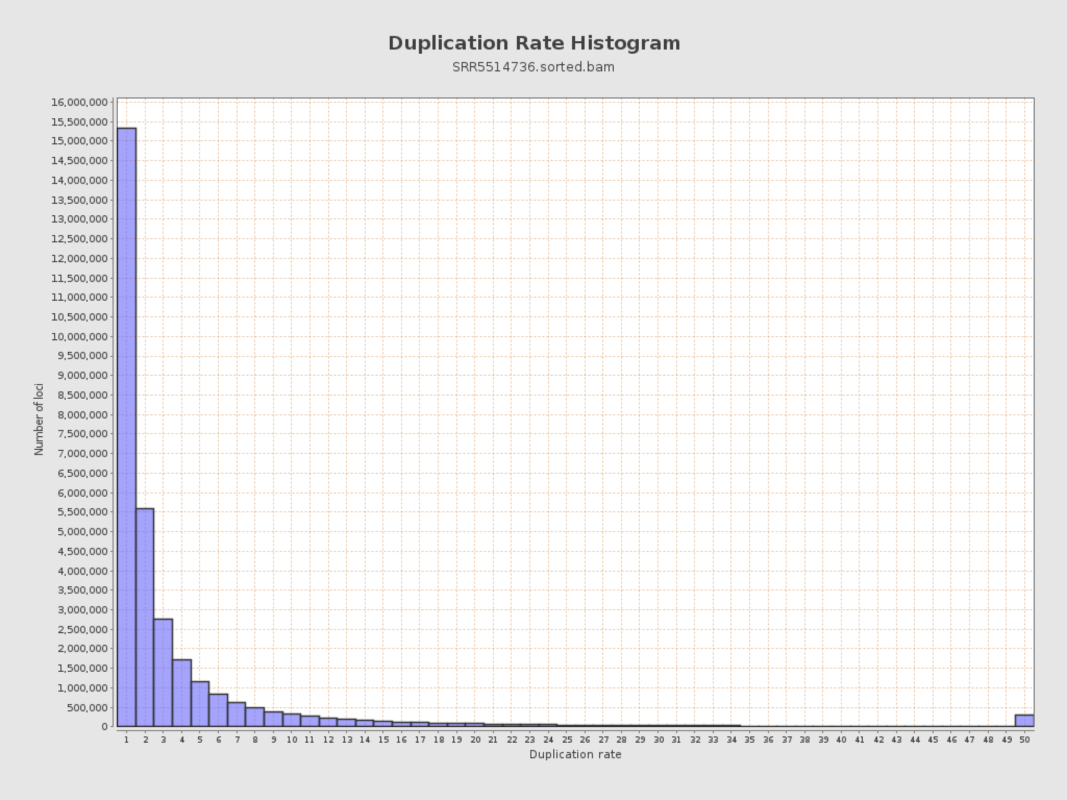
5. Results : Coverage Histogram (0-50X)



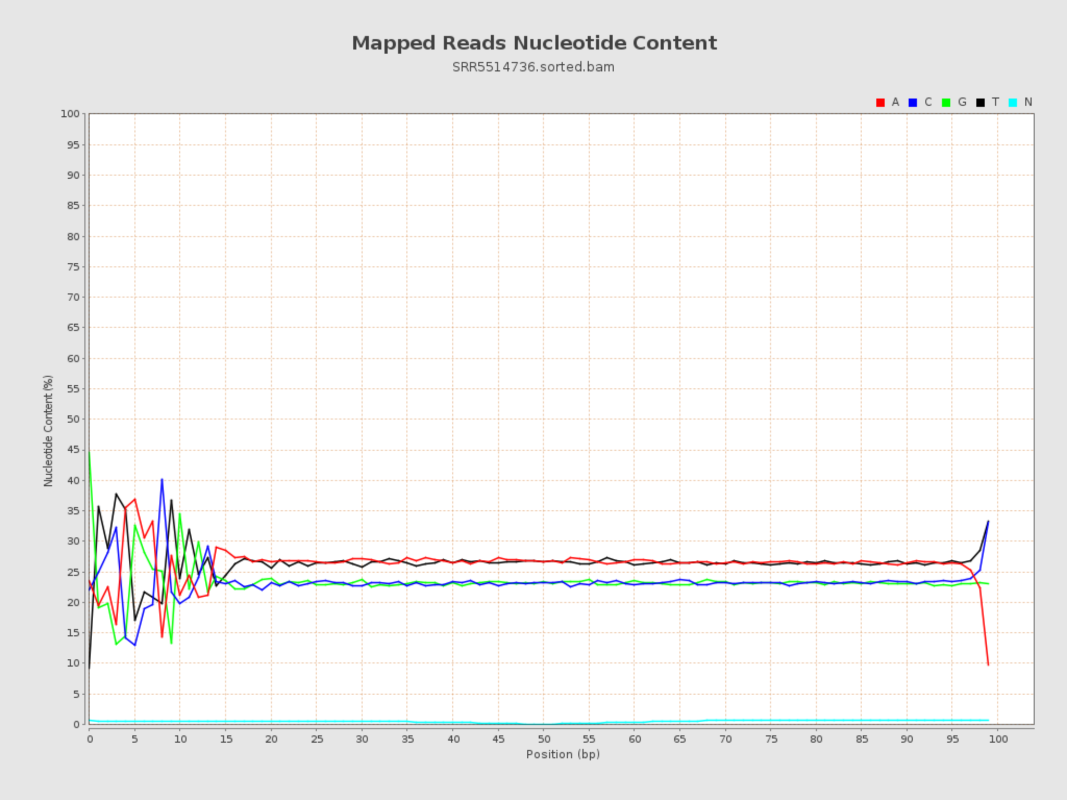
6. Results : Genome Fraction Coverage



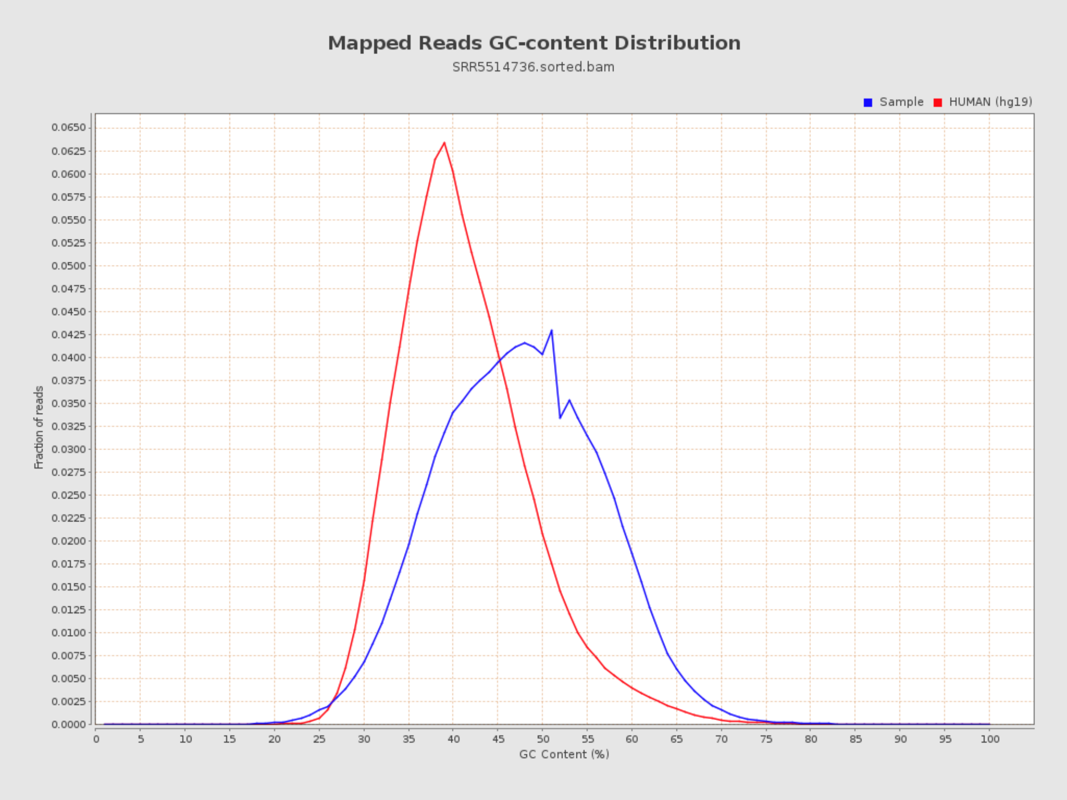
7. Results : Duplication Rate Histogram



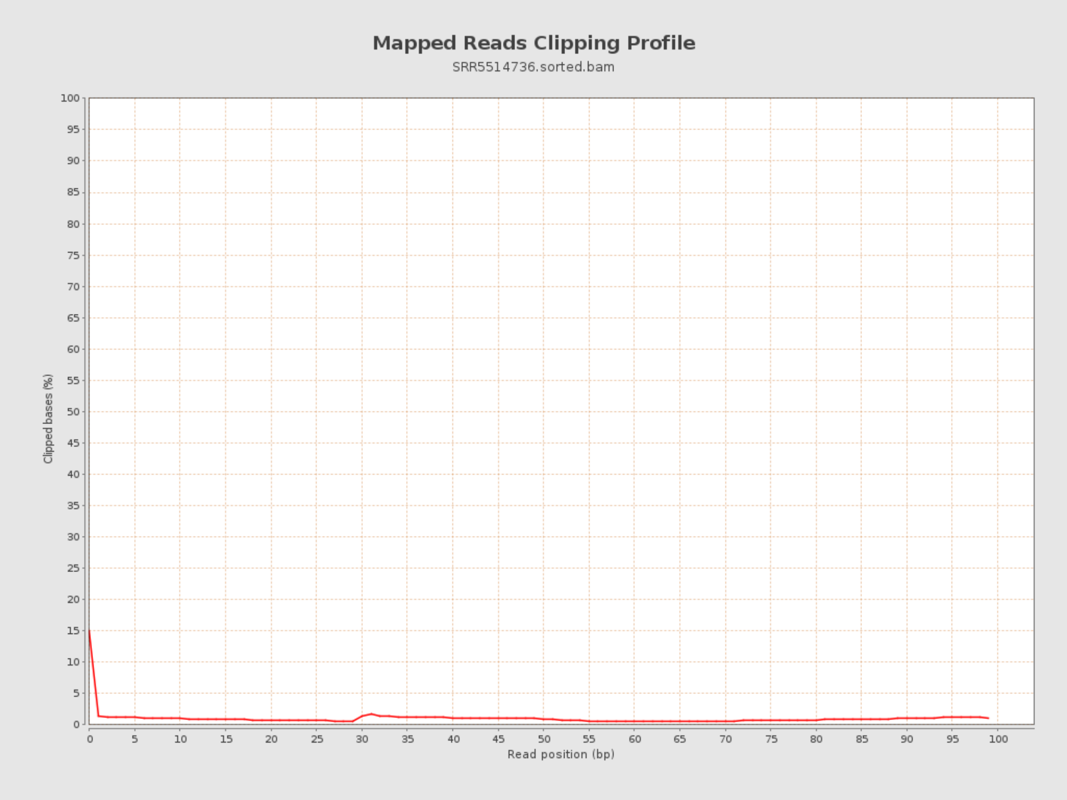
8. Results : Mapped Reads Nucleotide Content



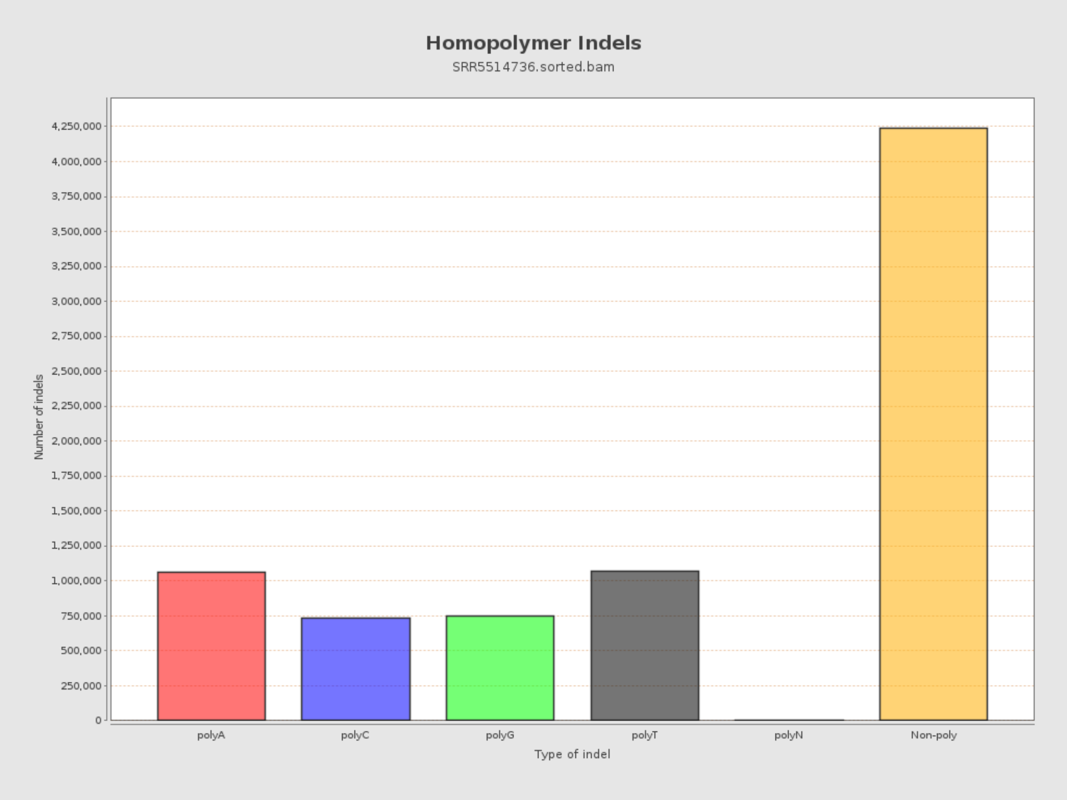
9. Results : Mapped Reads GC-content Distribution



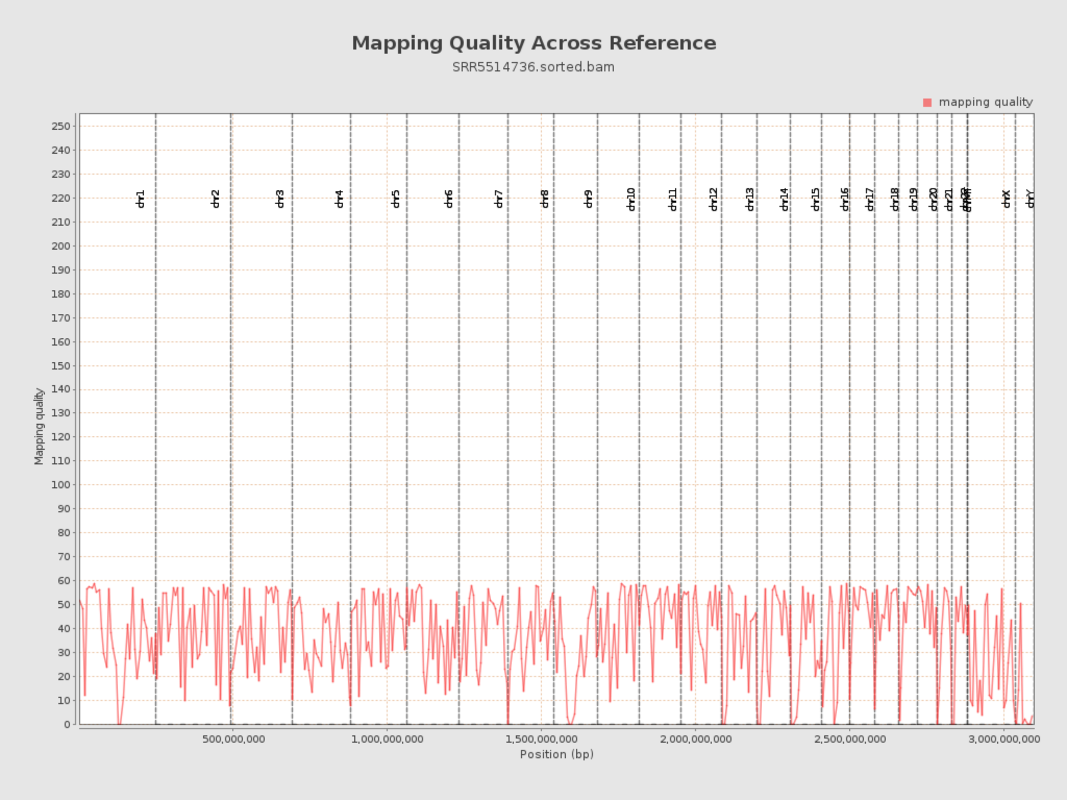
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram