Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 15:34:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514703.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_SRR5514703 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514703.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 15:34:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514703.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	109,525,720
Mapped reads	108,877,240 / 99.41%
Unmapped reads	648,480 / 0.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,379,519 / 4%
Read min/max/mean length	30 / 100 / 99.32
Duplicated reads (estimated)	75,764,321 / 69.17%
Duplication rate	49.16%
Clipped reads	18,154,051 / 16.58%

2.2. ACGT Content

Number/percentage of A's	2,999,627,879 / 28.65%
Number/percentage of C's	2,232,907,705 / 21.33%
Number/percentage of T's	2,970,933,159 / 28.38%
Number/percentage of G's	2,260,936,372 / 21.59%
Number/percentage of N's	5,516,070 / 0.05%
GC Percentage	42.92%

2.3. Coverage

Mean	3.3838

Standard Deviation	54.7963

2.4. Mapping Quality

Mean Mapping Quality	46.8

2.5. Mismatches and indels

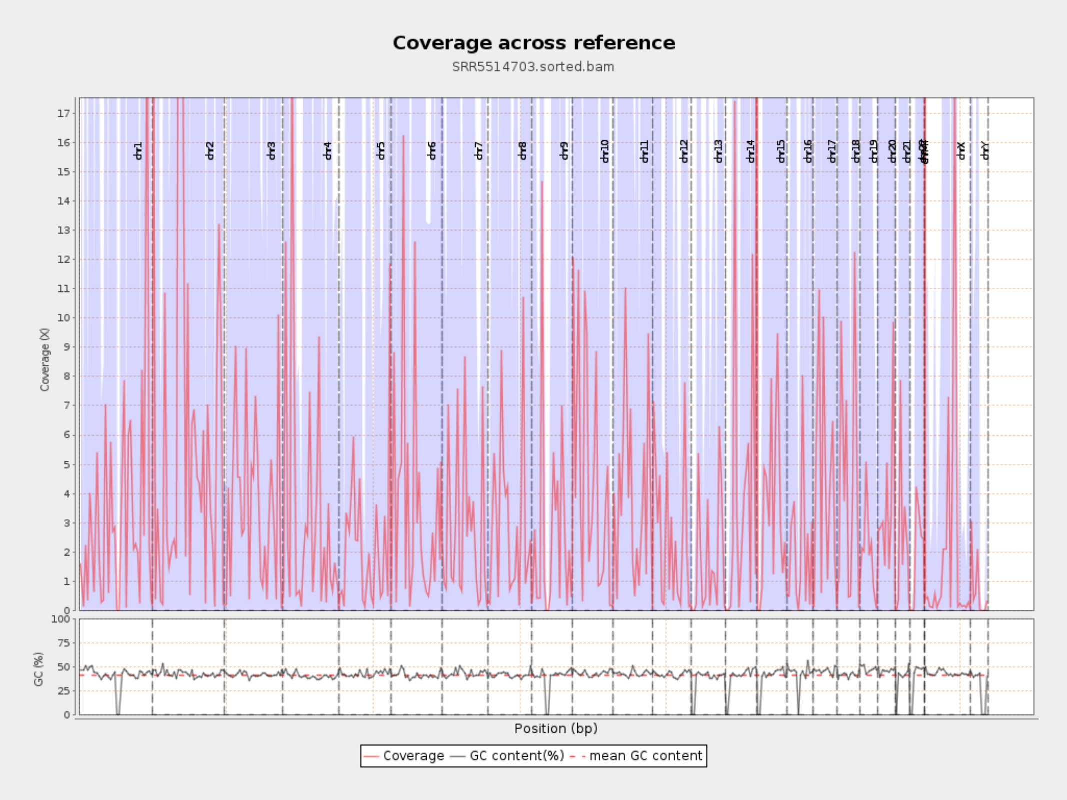
General error rate	0.66%
Mismatches	65,496,058
Insertions	2,817,482
Mapped reads with at least one insertion	2.52%
Deletions	2,824,636
Mapped reads with at least one deletion	2.52%
Homopolymer indels	47.17%

2.6. Chromosome stats

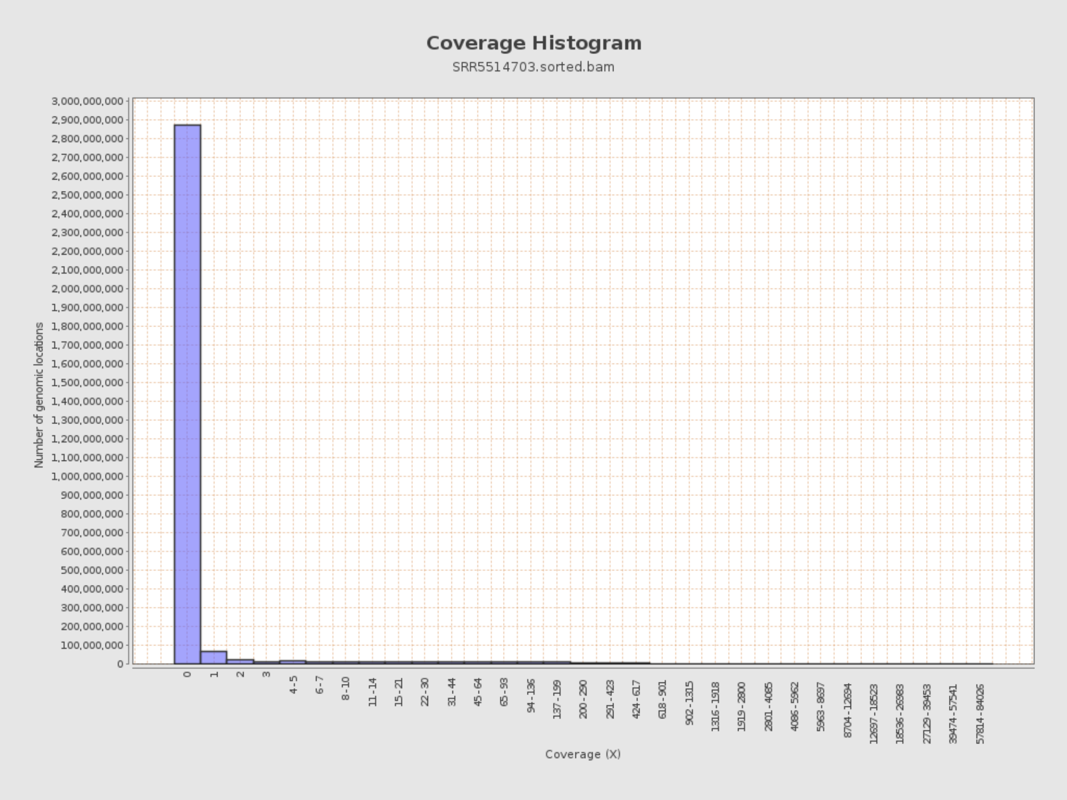
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	811315525	3.255	40.897
chr2	243199373	1658089653	6.8178	97.8918
chr3	198022430	712260877	3.5969	46.3194
chr4	191154276	680634480	3.5607	37.9025
chr5	180915260	411746105	2.2759	28.0601
chr6	171115067	640212920	3.7414	40.43
chr7	159138663	438523323	2.7556	35.8382

chr8	146364022	458014793	3.1293	35.4581
chr9	141213431	359808062	2.548	34.2759
chr10	135534747	626018119	4.6189	42.1512
chr11	135006516	542152678	4.0158	37.5216
chr12	133851895	350727613	2.6203	31.3803
chr13	115169878	214817238	1.8652	24.0762
chr14	107349540	454366786	4.2326	125.0601
chr15	102531392	345920340	3.3738	47.1976
chr16	90354753	180289506	1.9954	110.9083
chr17	81195210	350445772	4.3161	54.9024
chr18	78077248	327128038	4.1898	41.2643
chr19	59128983	115107520	1.9467	71.8654
chr20	63025520	224462075	3.5614	41.1961
chr21	48129895	120032019	2.4939	30.4564
chr22	51304566	99659847	1.9425	32.9747
chrMT	16571	9663714	583.1702	292.8458
chrX	155270560	302065847	1.9454	44.6199
chrY	59373566	41706780	0.7024	14.0869

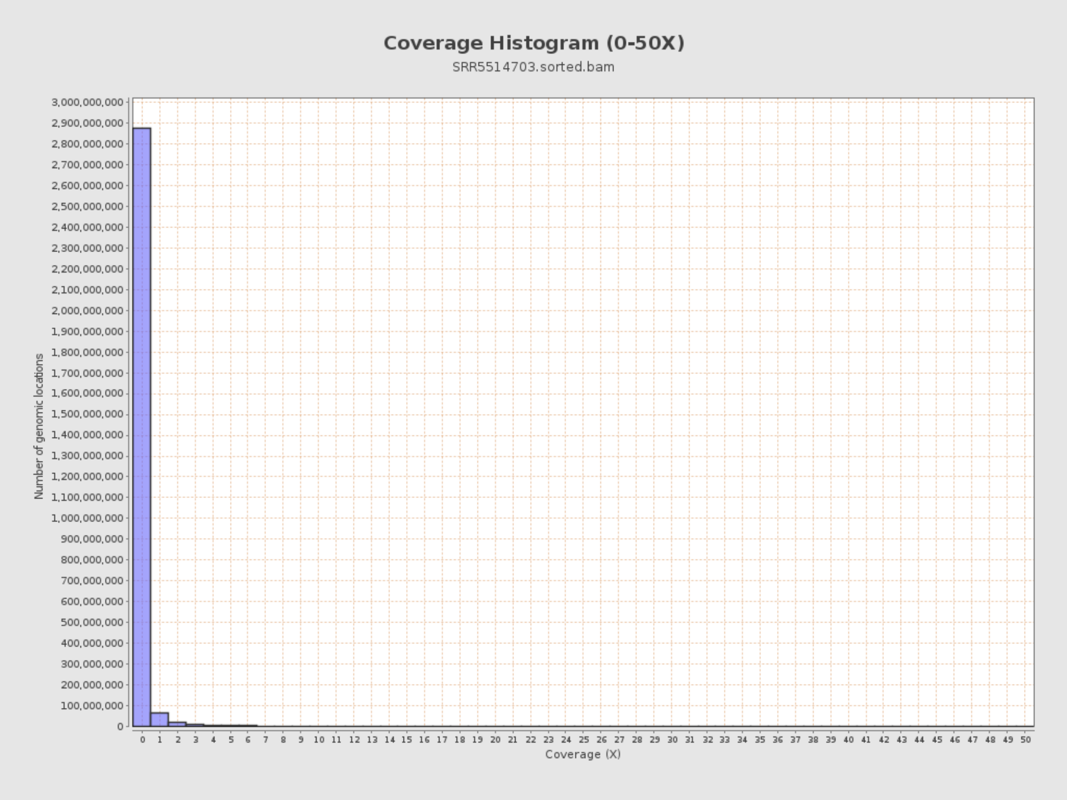
3. Results : Coverage across reference



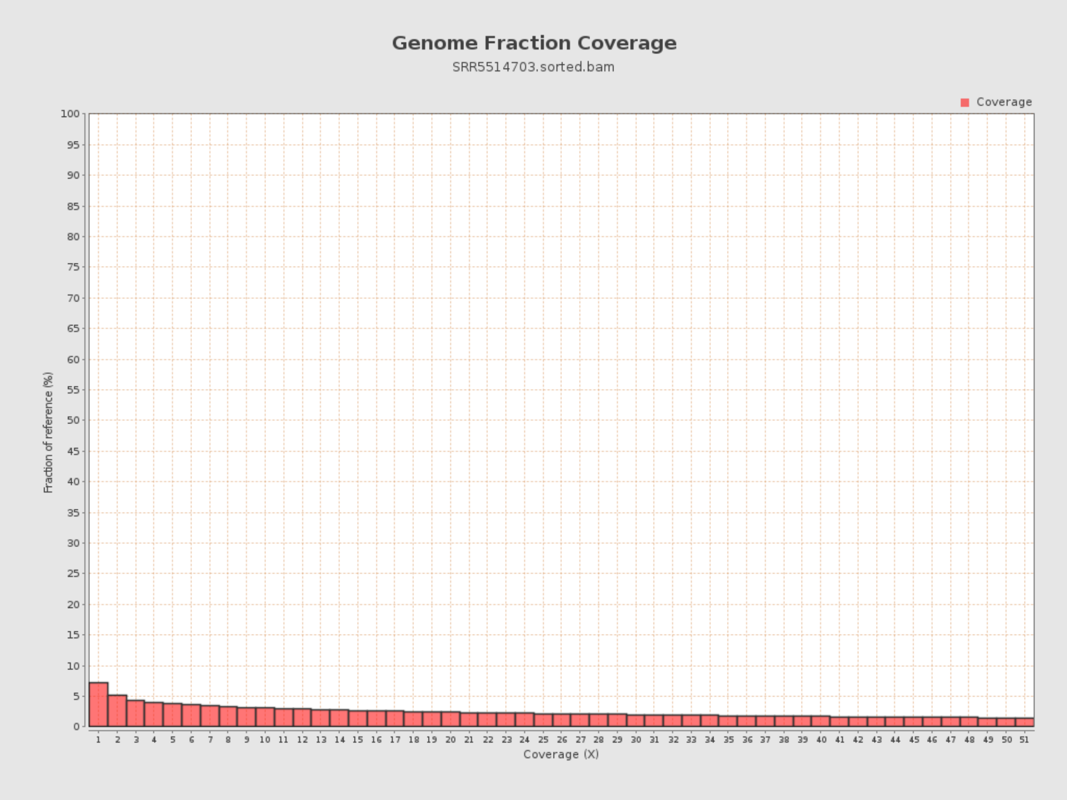
4. Results : Coverage Histogram



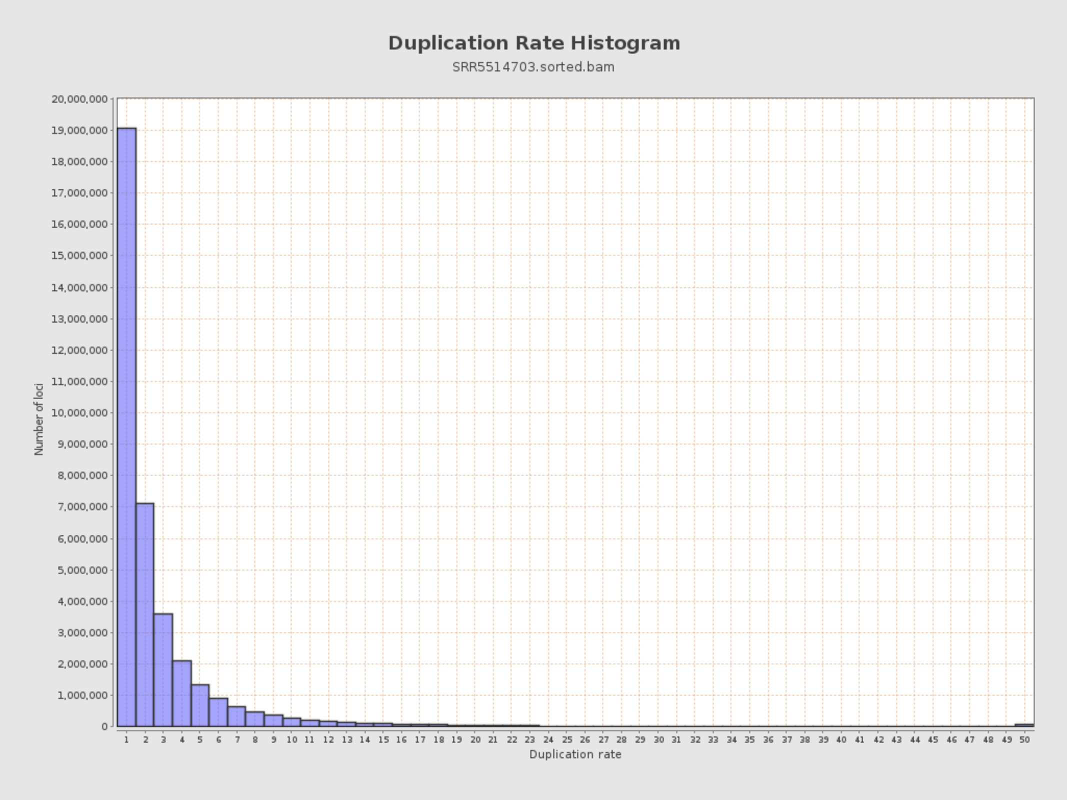
5. Results : Coverage Histogram (0-50X)



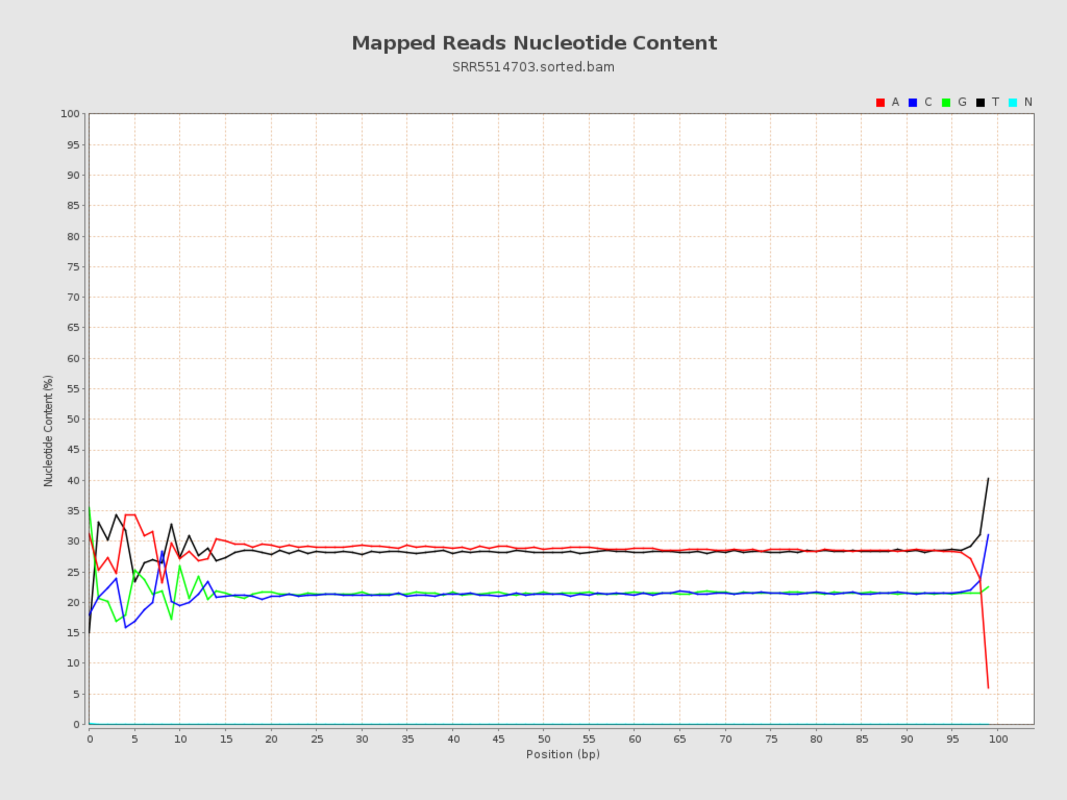
6. Results : Genome Fraction Coverage



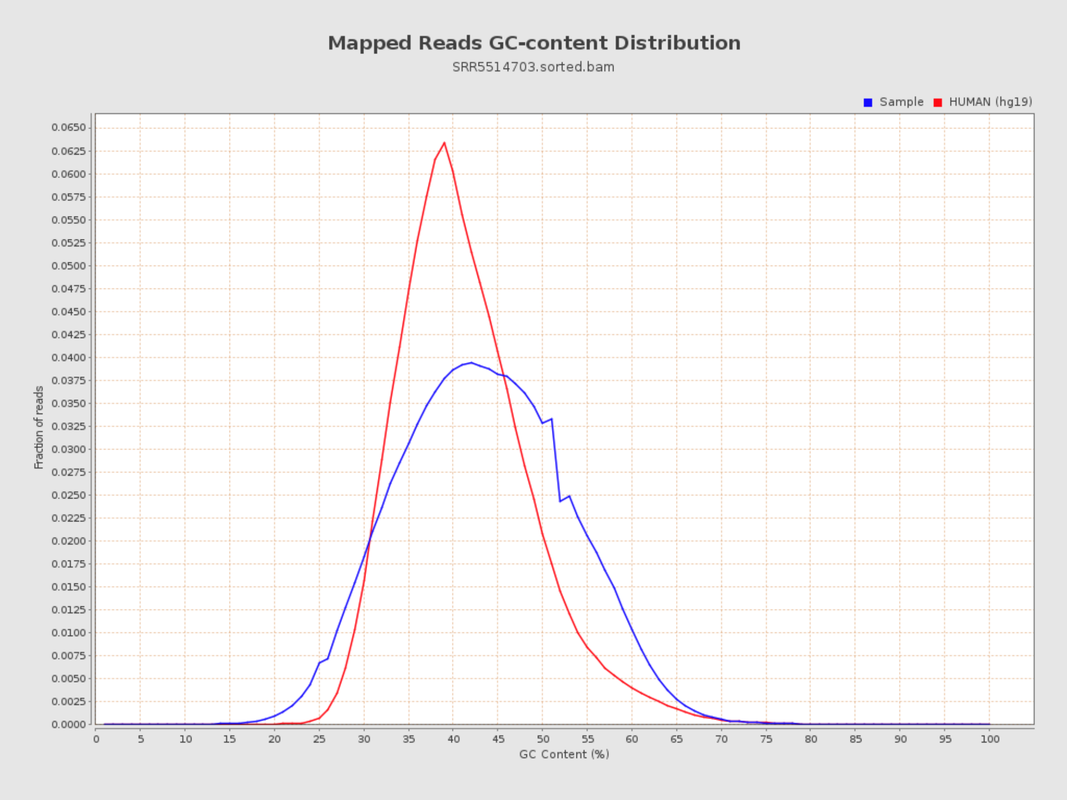
7. Results : Duplication Rate Histogram



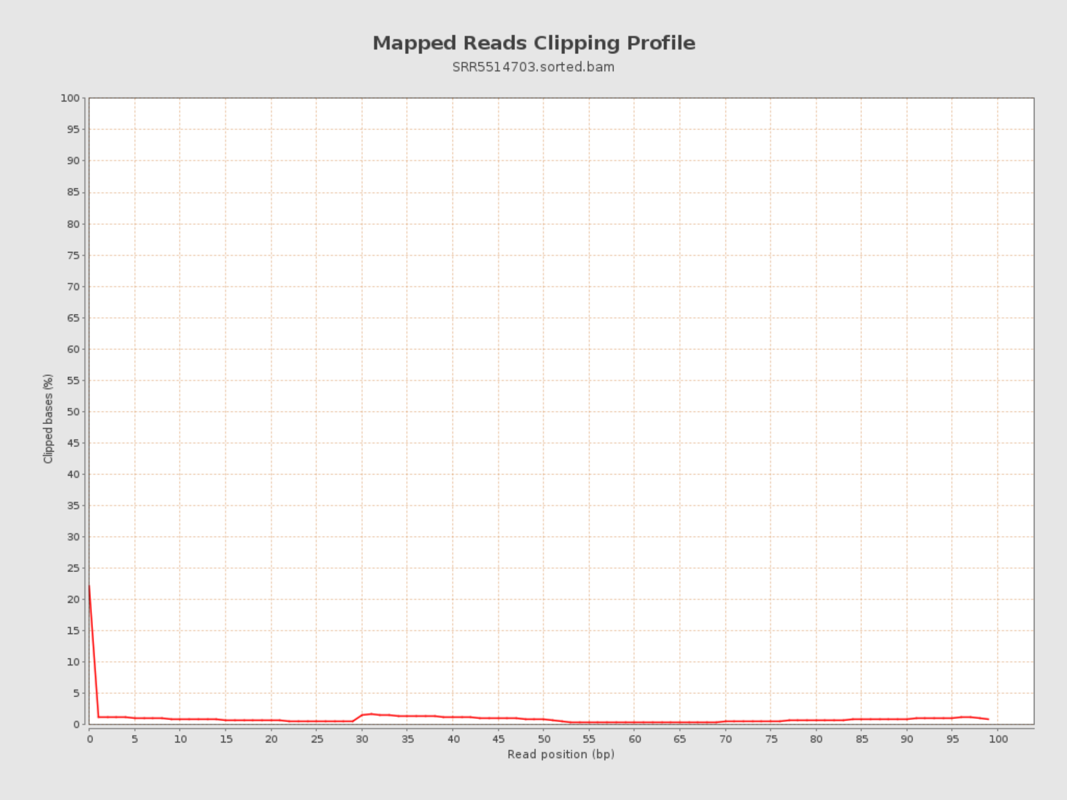
8. Results : Mapped Reads Nucleotide Content



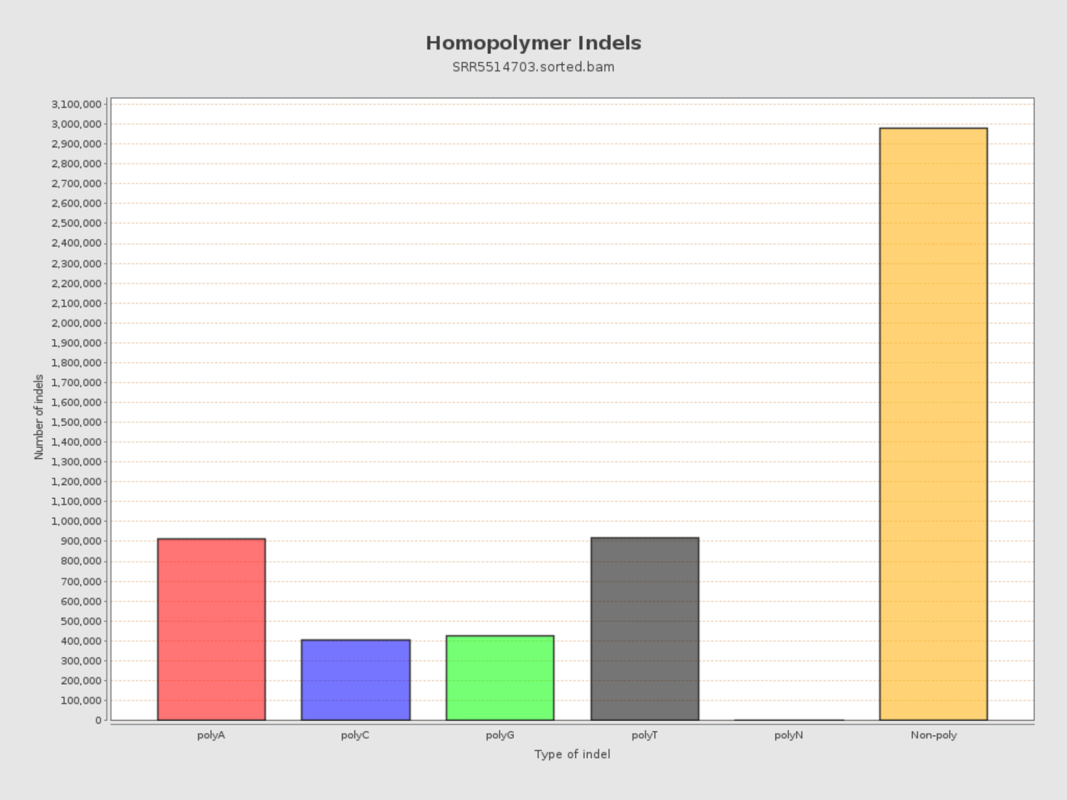
9. Results : Mapped Reads GC-content Distribution



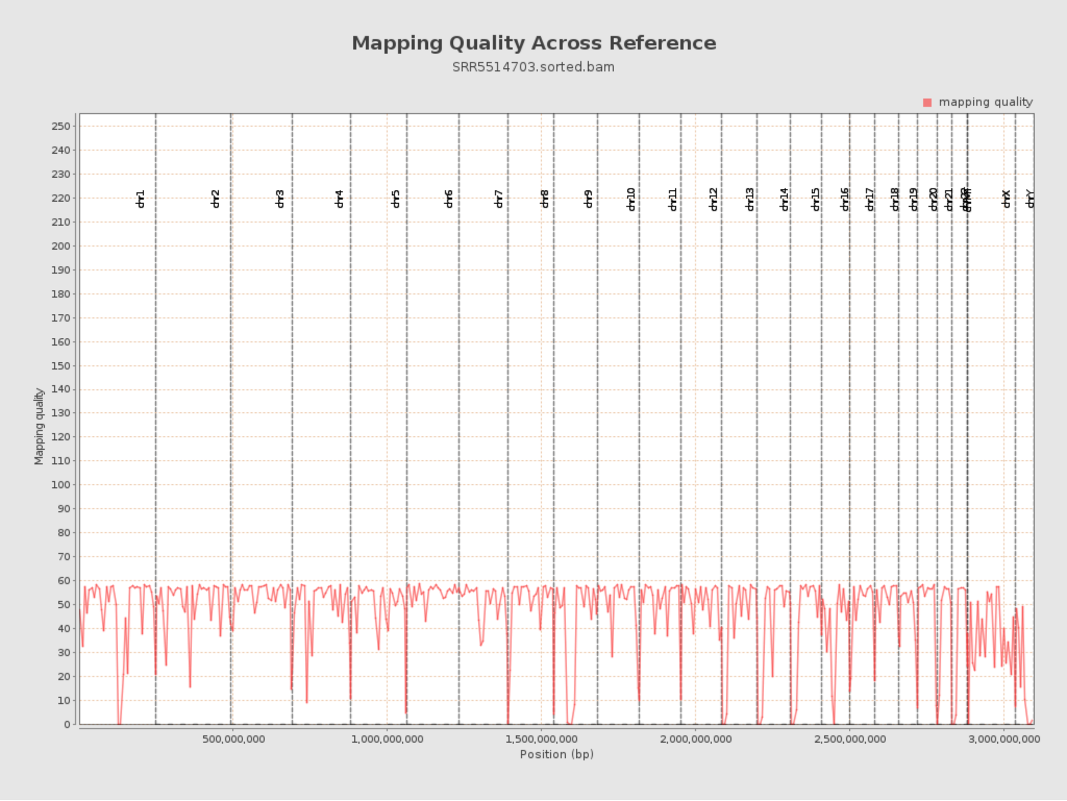
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram