Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 19:09:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514710.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_SRR5514710 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514710.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 19:09:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514710.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,642,158
Mapped reads	38,403,152 / 99.38%
Unmapped reads	239,006 / 0.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,568,445 / 4.06%
Read min/max/mean length	30 / 100 / 99.43
Duplicated reads (estimated)	16,280,150 / 42.13%
Duplication rate	31.44%
Clipped reads	6,408,915 / 16.59%

2.2. ACGT Content

Number/percentage of A's	1,122,668,974 / 30.34%
Number/percentage of C's	734,470,260 / 19.85%
Number/percentage of T's	1,094,665,926 / 29.58%
Number/percentage of G's	748,127,852 / 20.22%
Number/percentage of N's	531,616 / 0.01%
GC Percentage	40.07%

2.3. Coverage

Mean	1.1961

Standard Deviation	42.7011

2.4. Mapping Quality

Mean Mapping Quality	50.01

2.5. Mismatches and indels

General error rate	0.59%
Mismatches	20,033,007
Insertions	1,209,481
Mapped reads with at least one insertion	3.05%
Deletions	1,179,768
Mapped reads with at least one deletion	2.96%
Homopolymer indels	45.68%

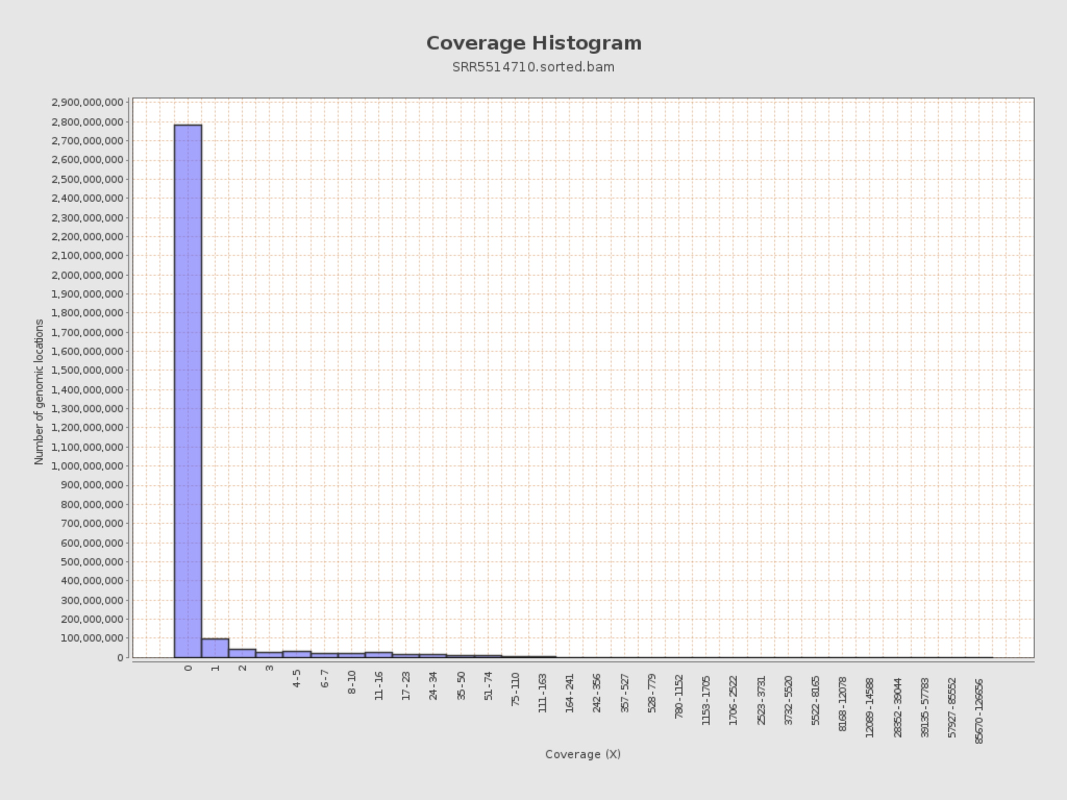
2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	267864021	1.0747	11.2972
chr2	243199373	402349455	1.6544	147.2957
chr3	198022430	182278284	0.9205	7.3028
chr4	191154276	274402000	1.4355	10.1235
chr5	180915260	291701303	1.6124	12.4416
chr6	171115067	249120274	1.4559	10.1008
chr7	159138663	235865755	1.4821	12.691

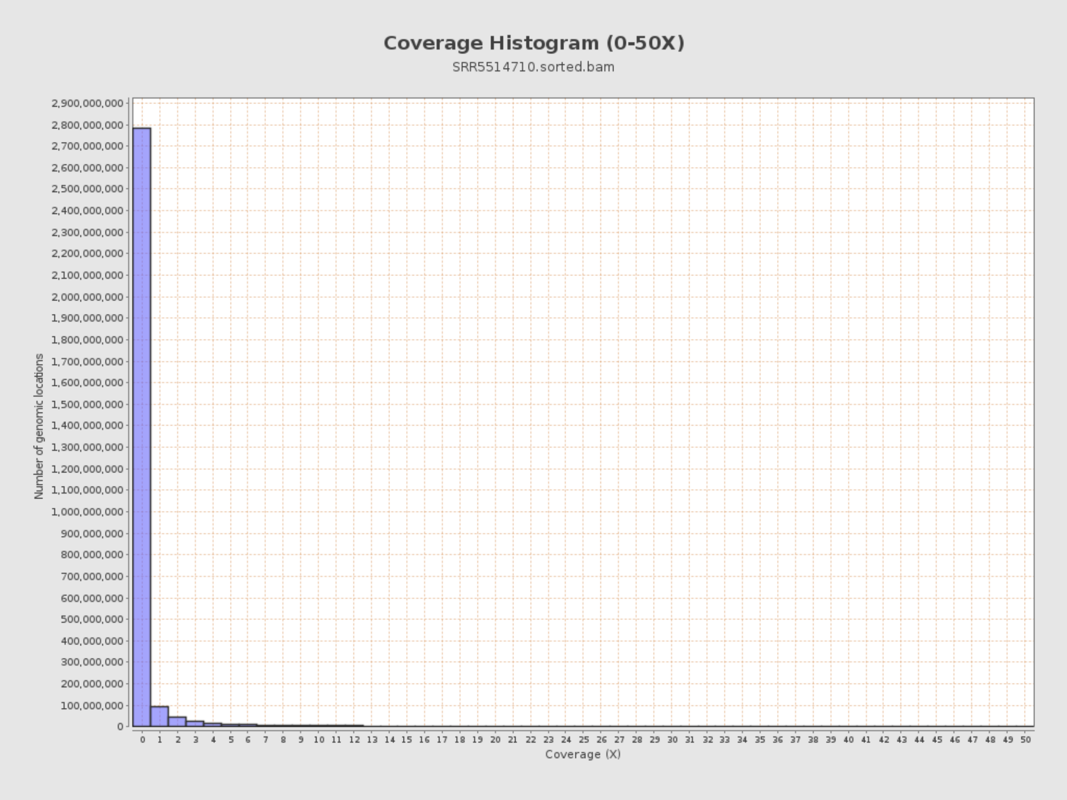
chr8	146364022	171546893	1.1721	10.458
chr9	141213431	151230907	1.0709	11.4716
chr10	135534747	154139941	1.1373	8.581
chr11	135006516	201960609	1.4959	11.8544
chr12	133851895	182511115	1.3635	15.0035
chr13	115169878	93140684	0.8087	7.3139
chr14	107349540	165782427	1.5443	27.8316
chr15	102531392	174490609	1.7018	11.9317
chr16	90354753	78235258	0.8659	7.526
chr17	81195210	51798760	0.638	5.7946
chr18	78077248	69526369	0.8905	6.9795
chr19	59128983	104909234	1.7742	12.6306
chr20	63025520	31727257	0.5034	5.2724
chr21	48129895	43532836	0.9045	11.4251
chr22	51304566	24316976	0.474	4.607
chrMT	16571	1794227	108.2751	53.3228
chrX	155270560	83870556	0.5402	6.1728
chrY	59373566	14708500	0.2477	3.4917

3. Results : Coverage across reference

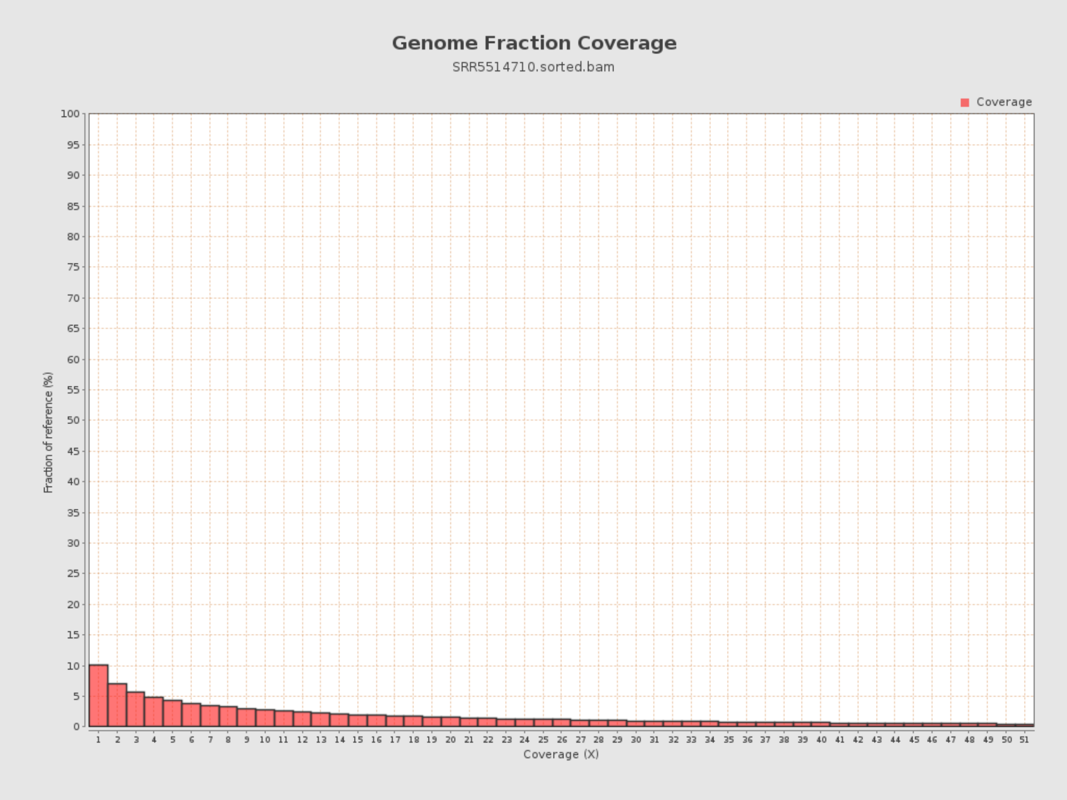
4. Results : Coverage Histogram



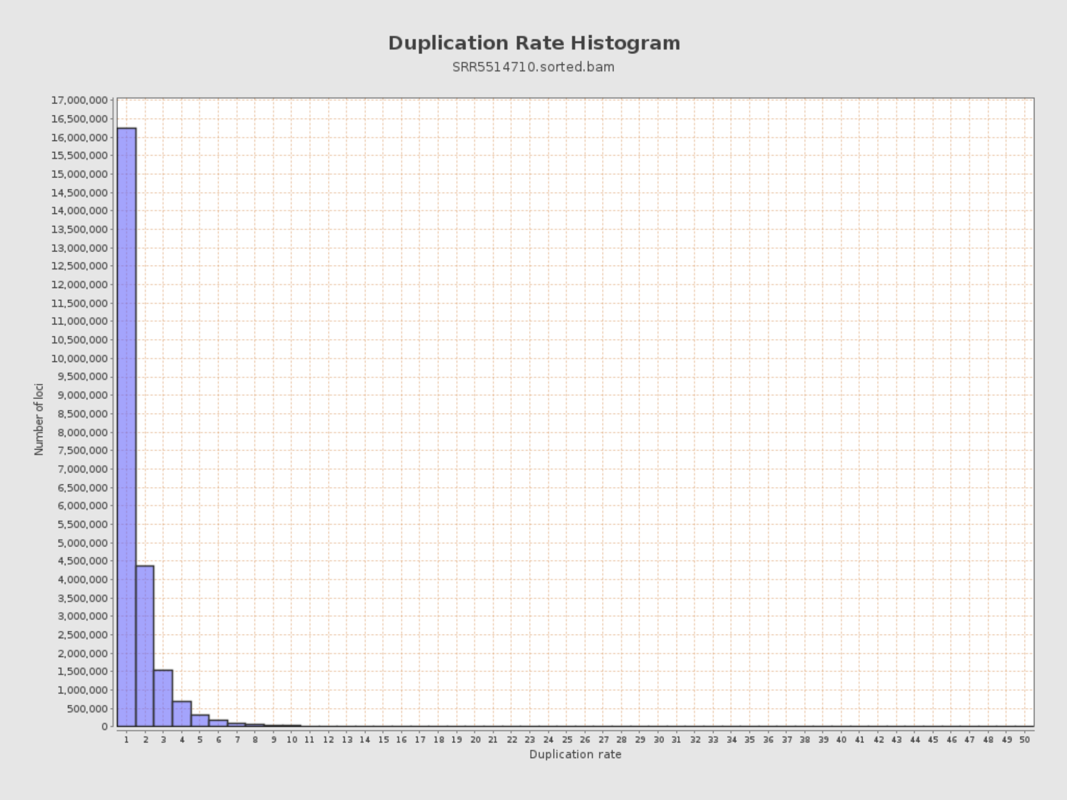
5. Results : Coverage Histogram (0-50X)



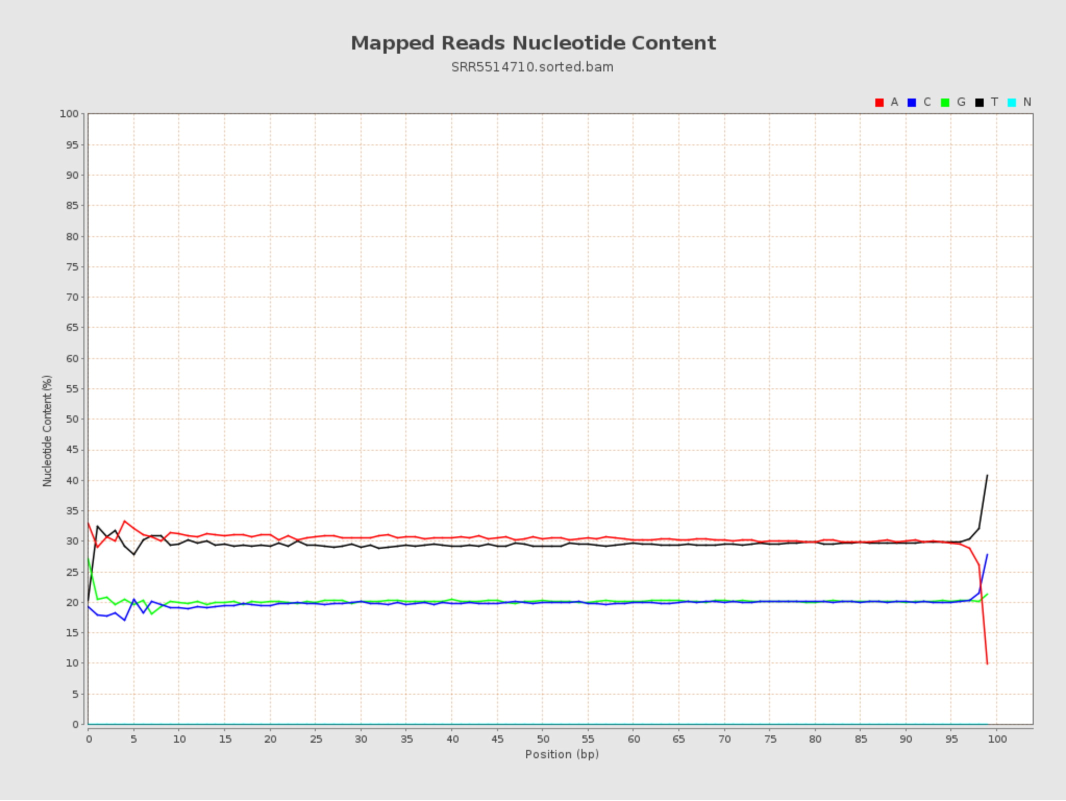
6. Results : Genome Fraction Coverage



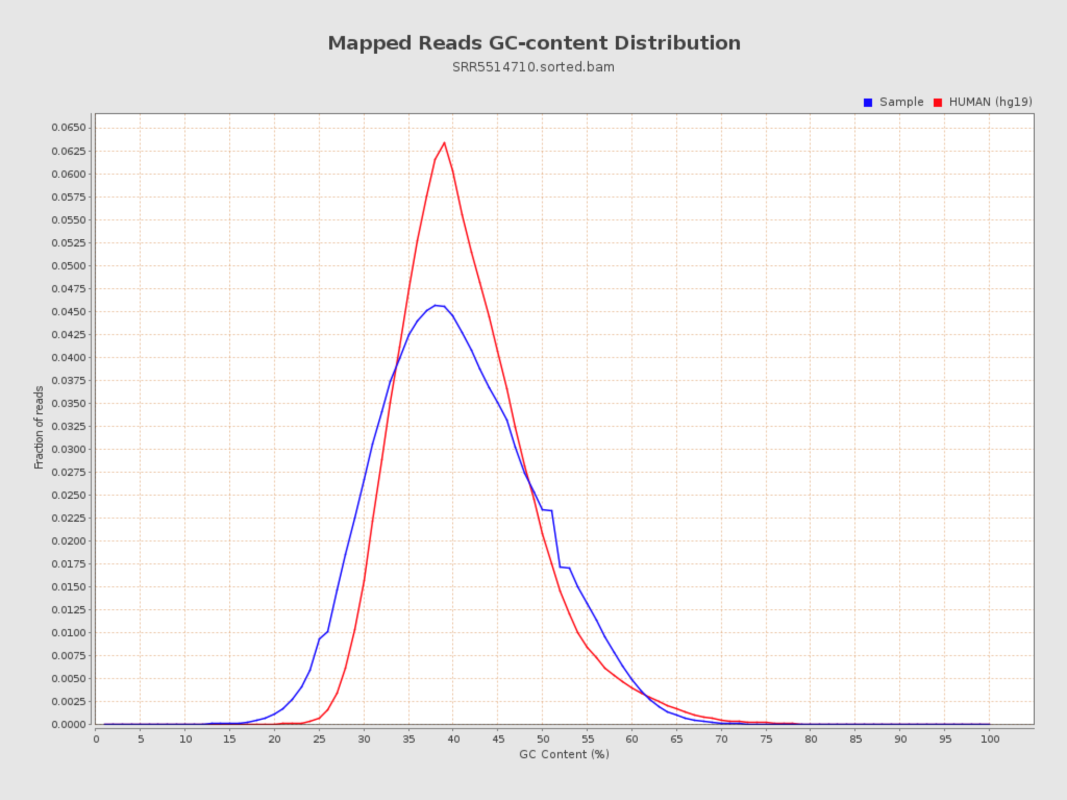
7. Results : Duplication Rate Histogram



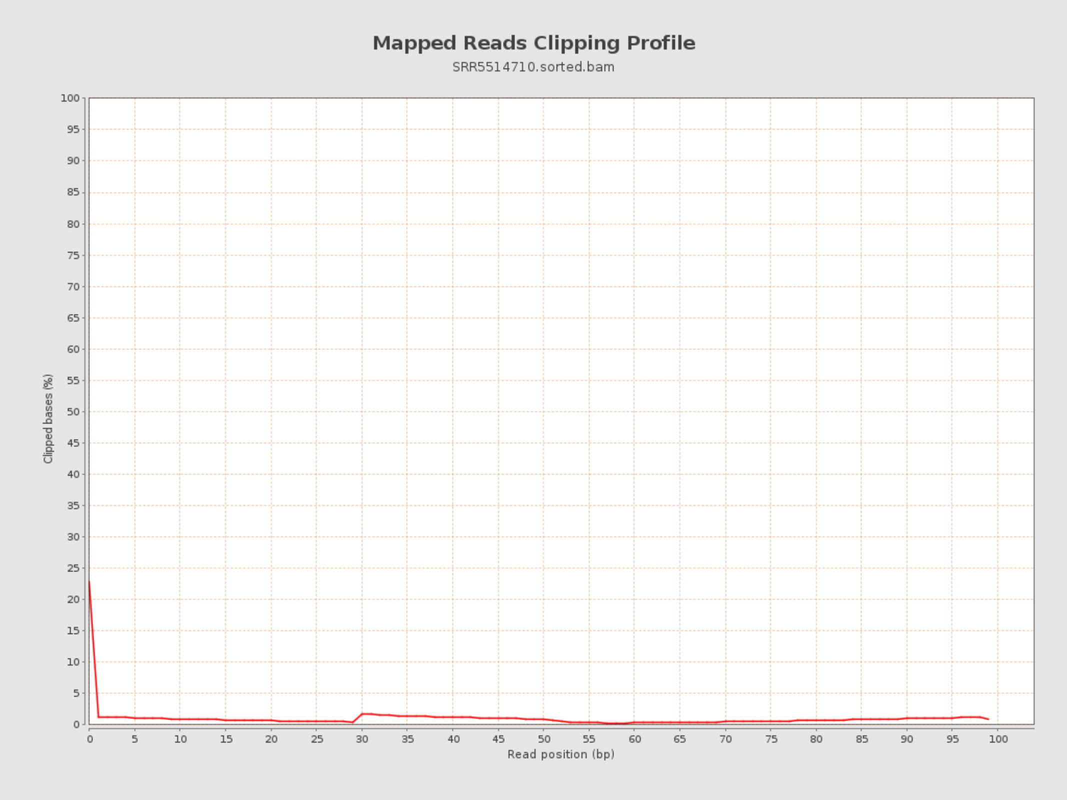
8. Results : Mapped Reads Nucleotide Content



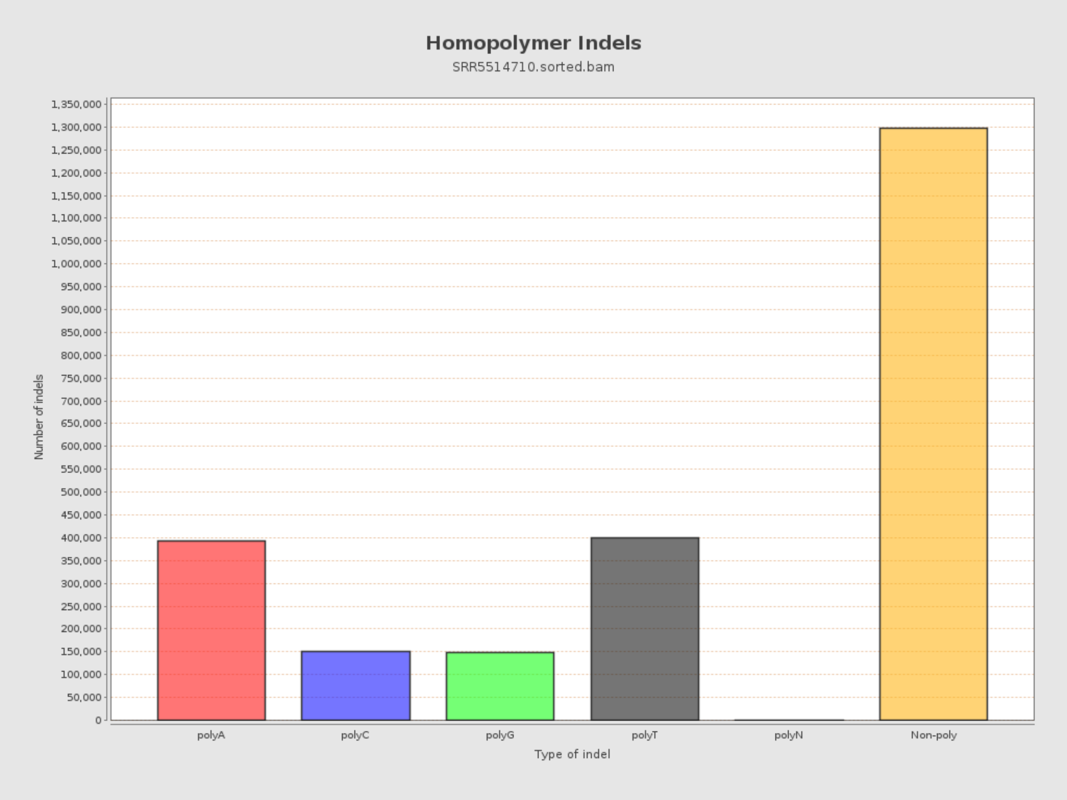
9. Results : Mapped Reads GC-content Distribution



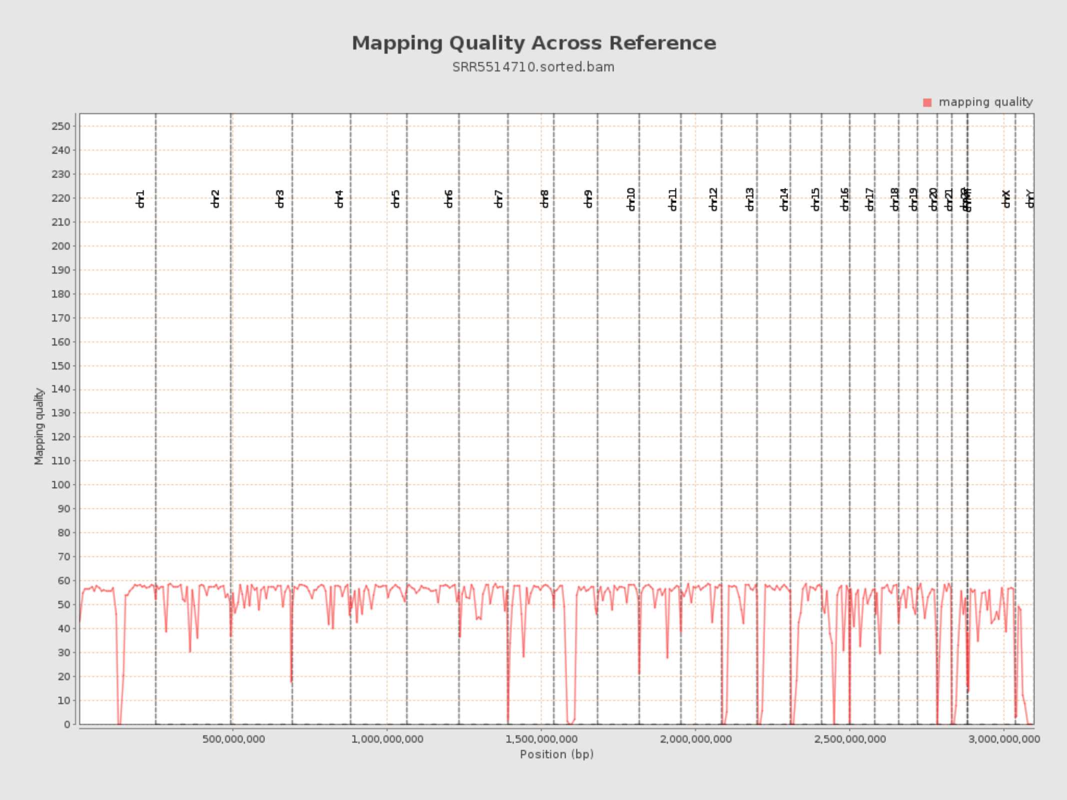
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram