Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:29:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819040.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_SRR1819040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:29:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	979,944
Mapped reads	878,051 / 89.6%
Unmapped reads	101,893 / 10.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,787 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	17,690 / 1.81%
Duplication rate	1.53%
Clipped reads	880,407 / 89.84%

2.2. ACGT Content

Number/percentage of A's	12,672,576 / 25.29%
Number/percentage of C's	9,618,271 / 19.2%
Number/percentage of T's	15,823,208 / 31.58%
Number/percentage of G's	11,989,242 / 23.93%
Number/percentage of N's	1,111 / 0%
GC Percentage	43.12%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.155

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

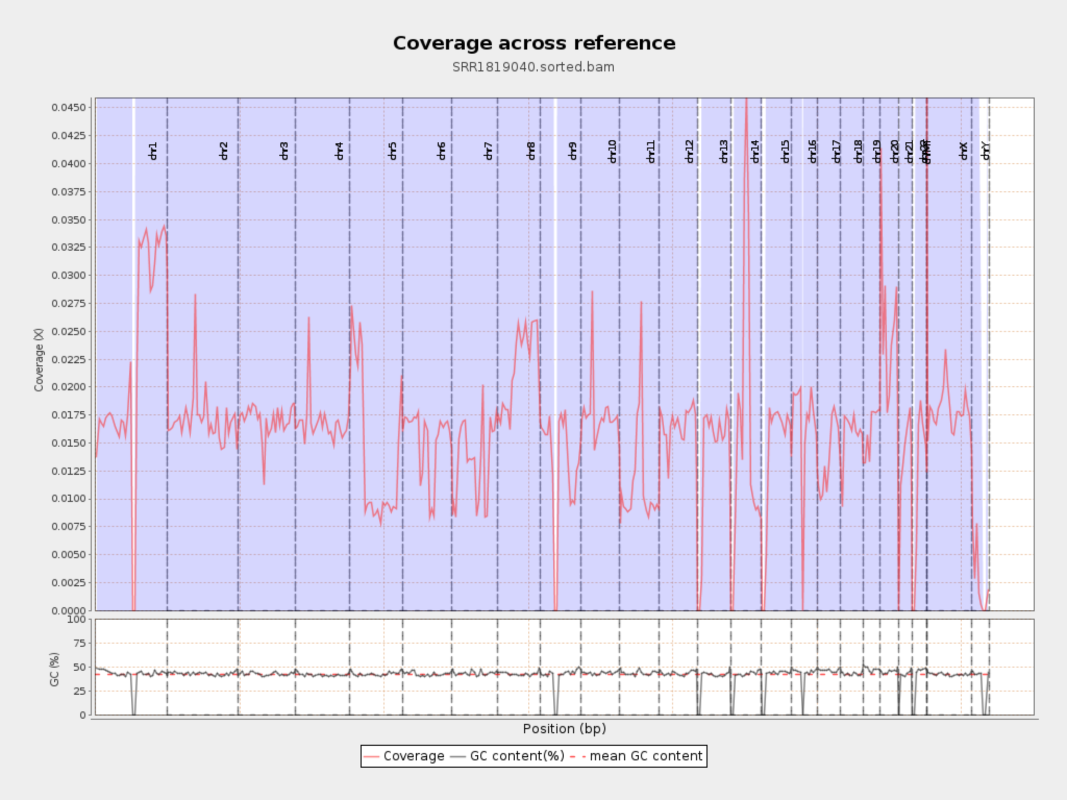
General error rate	0.5%
Mismatches	245,695
Insertions	3,288
Mapped reads with at least one insertion	0.37%
Deletions	8,077
Mapped reads with at least one deletion	0.91%
Homopolymer indels	40.21%

2.6. Chromosome stats

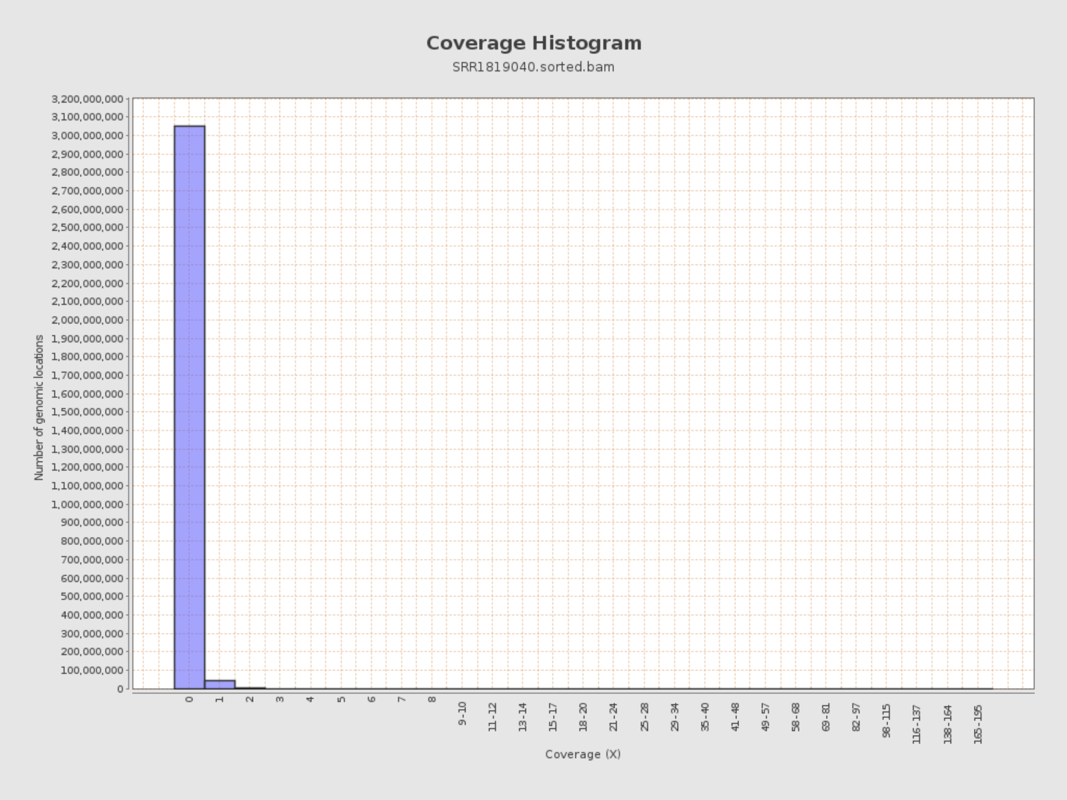
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5590076	0.0224	0.2176
chr2	243199373	4177687	0.0172	0.1738
chr3	198022430	3369852	0.017	0.1378
chr4	191154276	3223837	0.0169	0.1439
chr5	180915260	2524693	0.014	0.1249
chr6	171115067	2589571	0.0151	0.1341
chr7	159138663	2157516	0.0136	0.1378

chr8	146364022	3195410	0.0218	0.168
chr9	141213431	1812540	0.0128	0.1497
chr10	135534747	2388095	0.0176	0.1727
chr11	135006516	1575048	0.0117	0.1361
chr12	133851895	2217025	0.0166	0.1366
chr13	115169878	1578765	0.0137	0.1227
chr14	107349540	1757426	0.0164	0.14
chr15	102531392	1421788	0.0139	0.1243
chr16	90354753	1474474	0.0163	0.1435
chr17	81195210	1116497	0.0138	0.1248
chr18	78077248	1216615	0.0156	0.2453
chr19	59128983	955052	0.0162	0.1772
chr20	63025520	1590272	0.0252	0.1701
chr21	48129895	642509	0.0133	0.1283
chr22	51304566	587841	0.0115	0.1129
chrMT	16571	840	0.0507	0.2221
chrX	155270560	2803475	0.0181	0.1516
chrY	59373566	151210	0.0025	0.0674

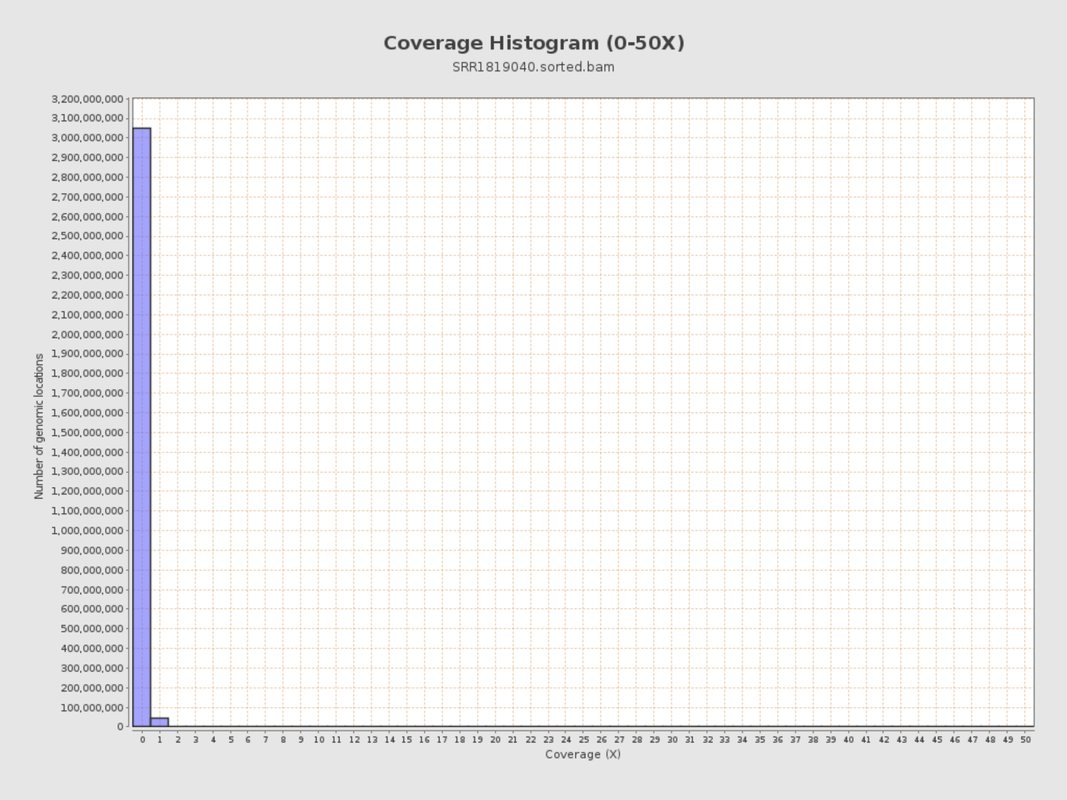
3. Results : Coverage across reference



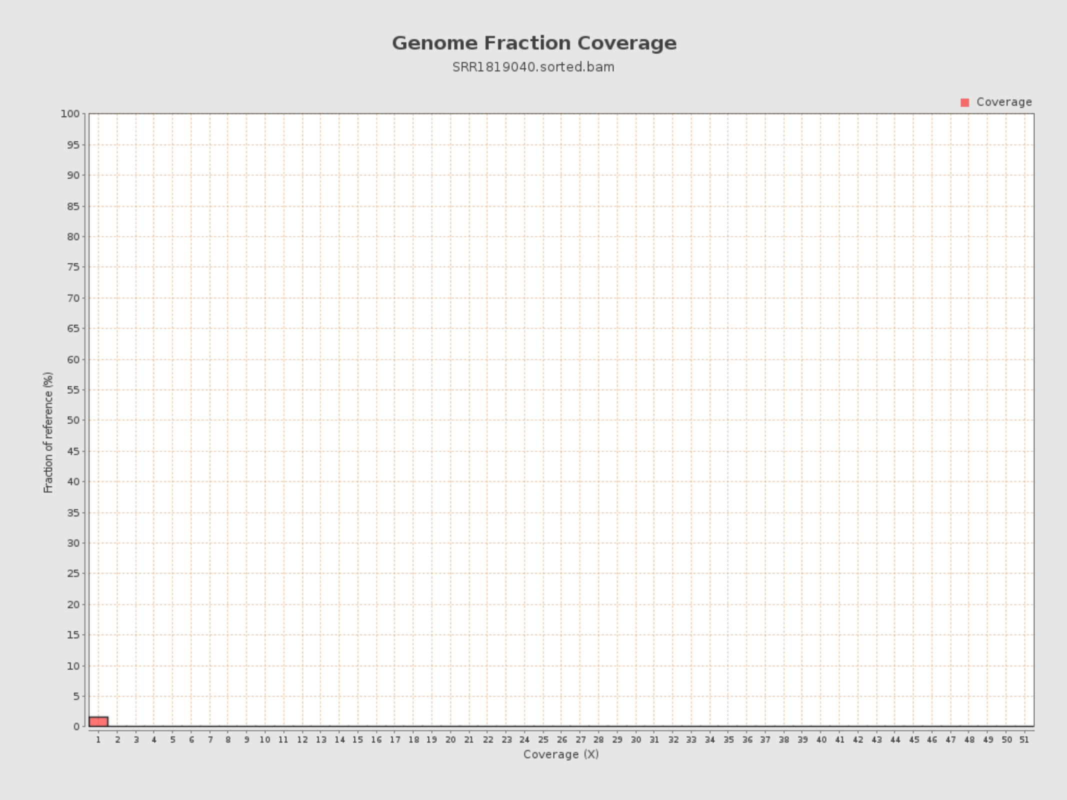
4. Results : Coverage Histogram



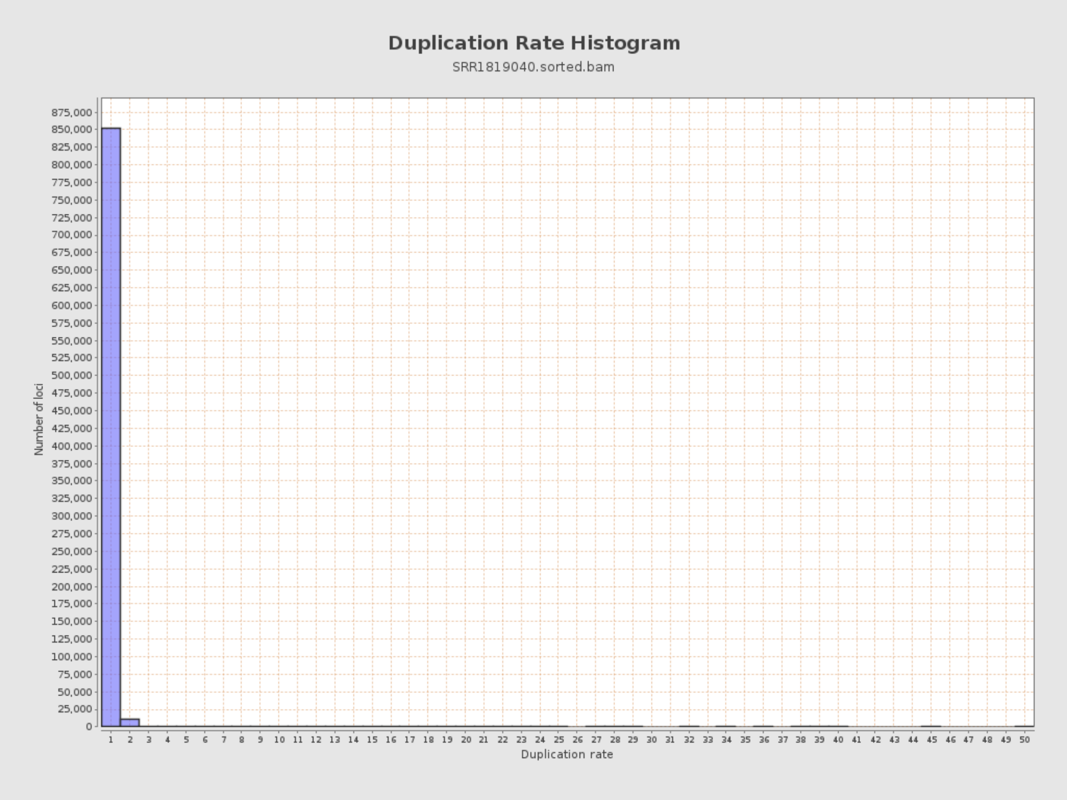
5. Results : Coverage Histogram (0-50X)



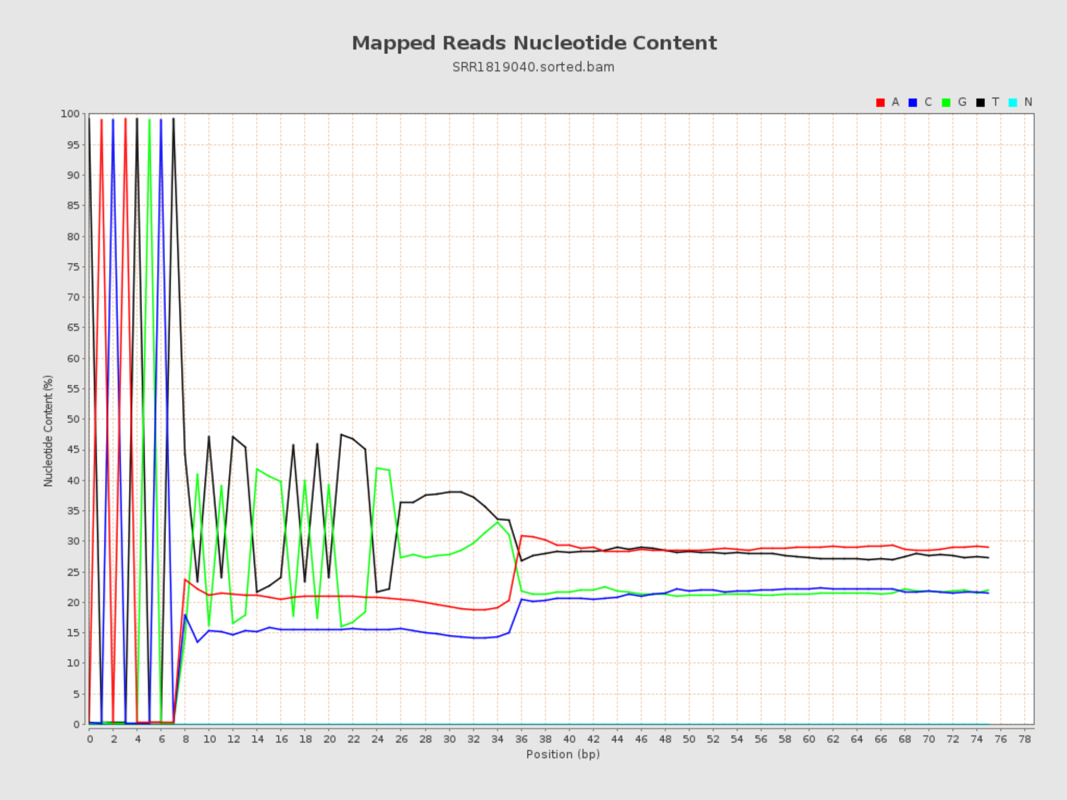
6. Results : Genome Fraction Coverage



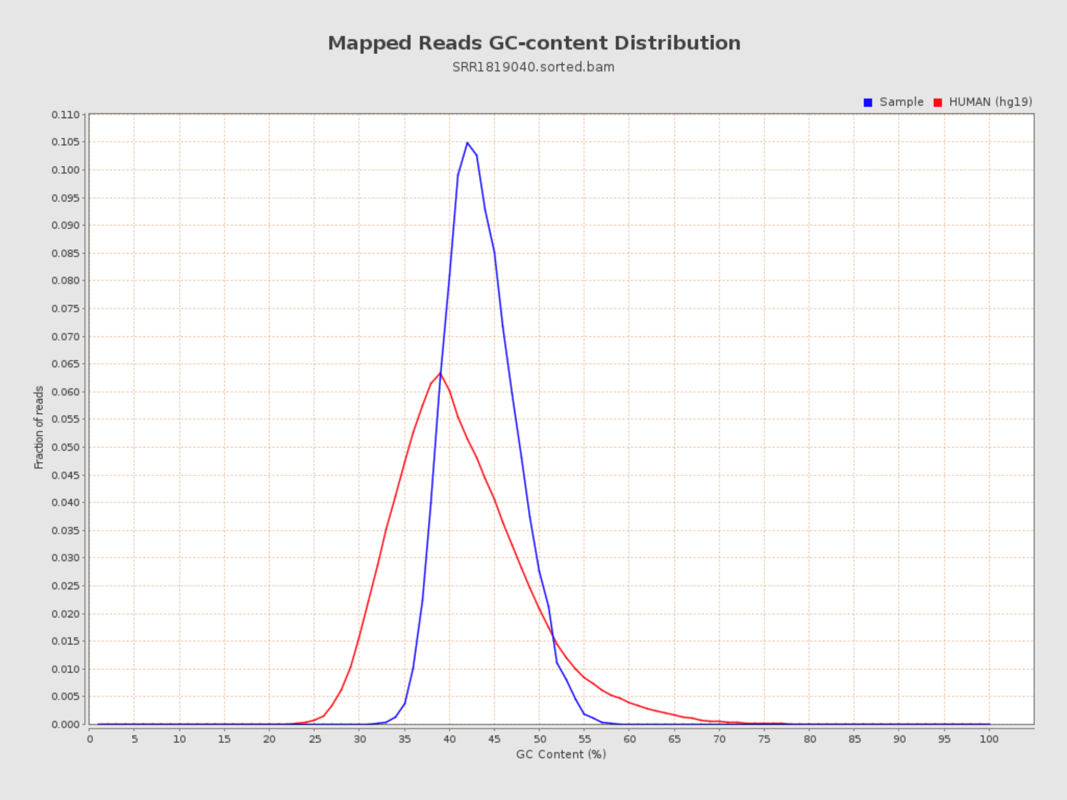
7. Results : Duplication Rate Histogram



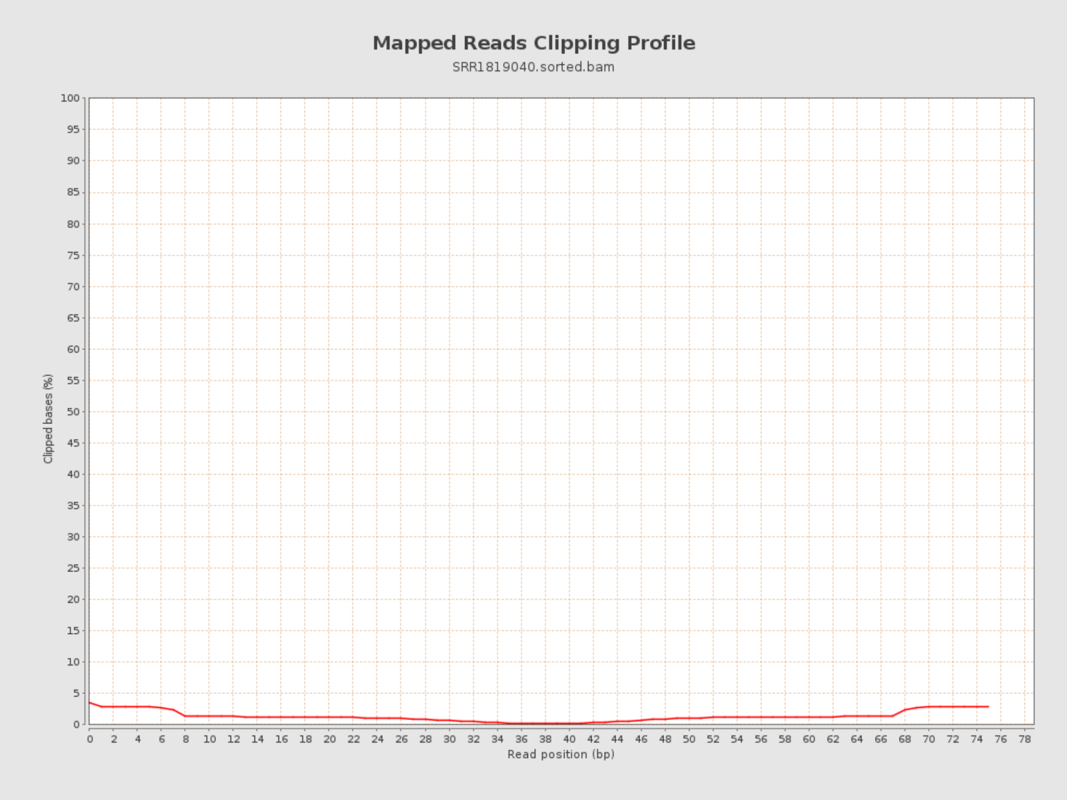
8. Results : Mapped Reads Nucleotide Content



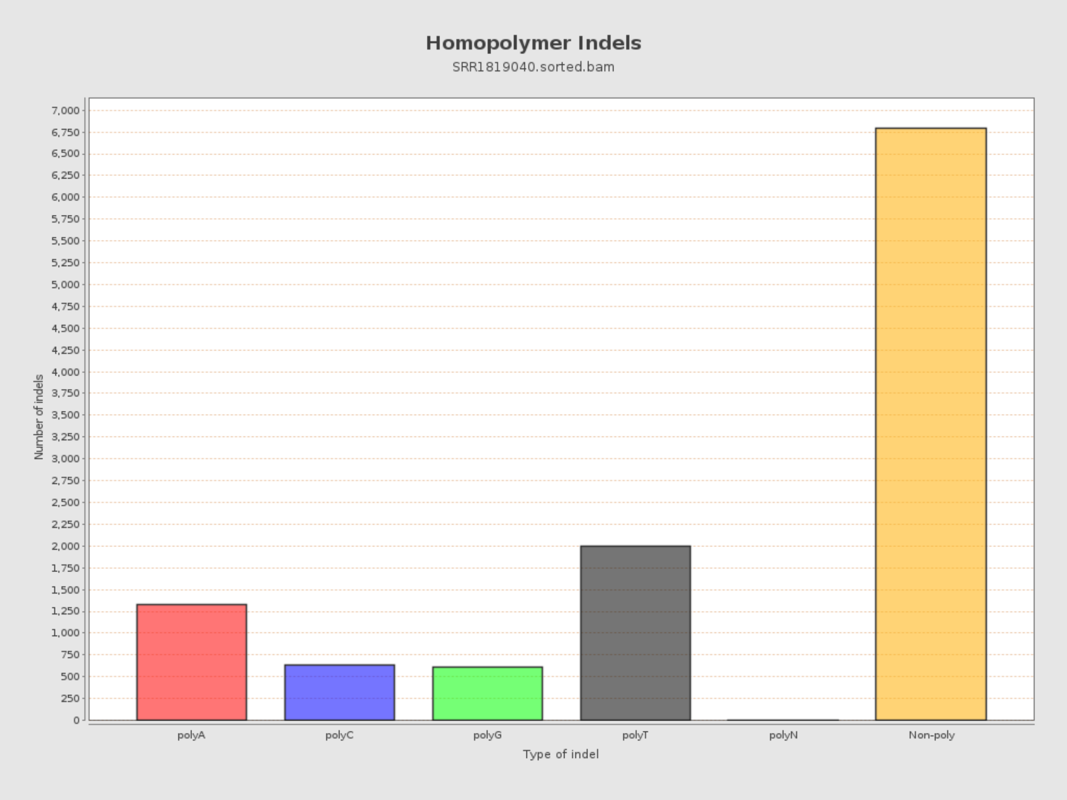
9. Results : Mapped Reads GC-content Distribution



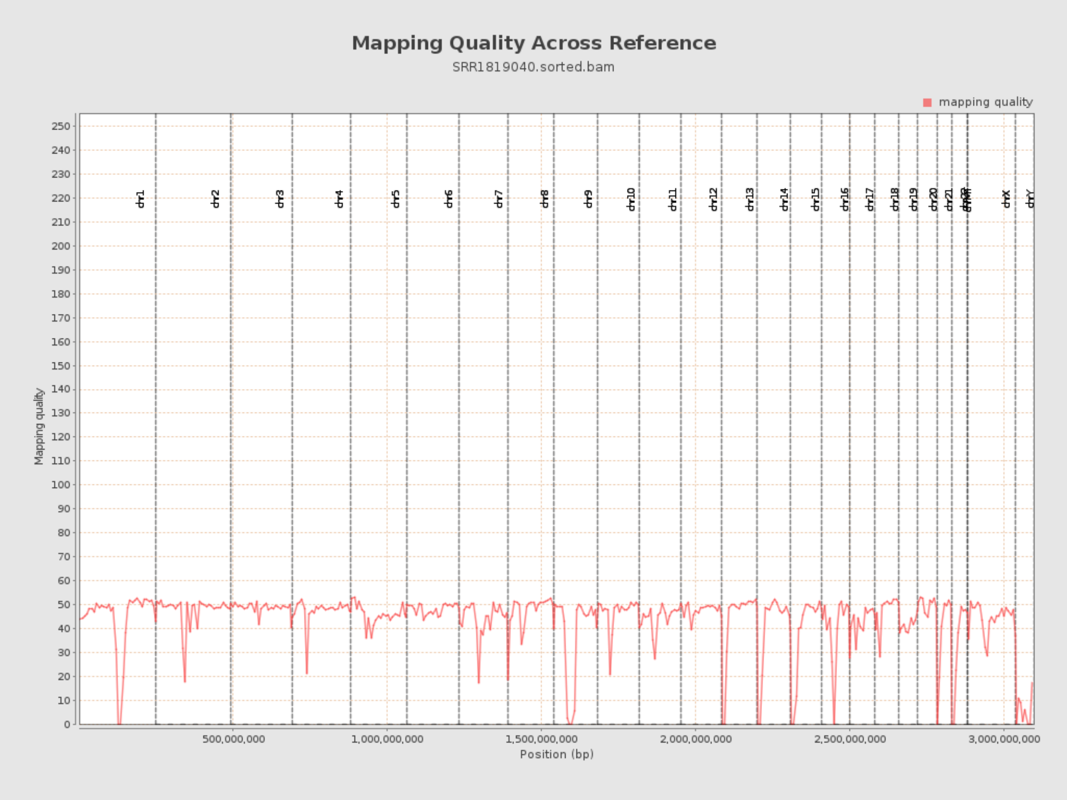
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram