Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:10:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751181.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_SRR8751181 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751181.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:10:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751181.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,411,779
Mapped reads	4,402,225 / 99.78%
Unmapped reads	9,554 / 0.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,326 / 0.85%
Read min/max/mean length	30 / 101 / 101.35
Duplicated reads (estimated)	461,689 / 10.46%
Duplication rate	7.71%
Clipped reads	411,032 / 9.32%

2.2. ACGT Content

Number/percentage of A's	134,358,687 / 30.77%
Number/percentage of C's	84,182,840 / 19.28%
Number/percentage of T's	134,913,285 / 30.9%
Number/percentage of G's	83,204,789 / 19.05%
Number/percentage of N's	3,289 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	0.1411

Standard Deviation	1.333

2.4. Mapping Quality

Mean Mapping Quality	50.8

2.5. Mismatches and indels

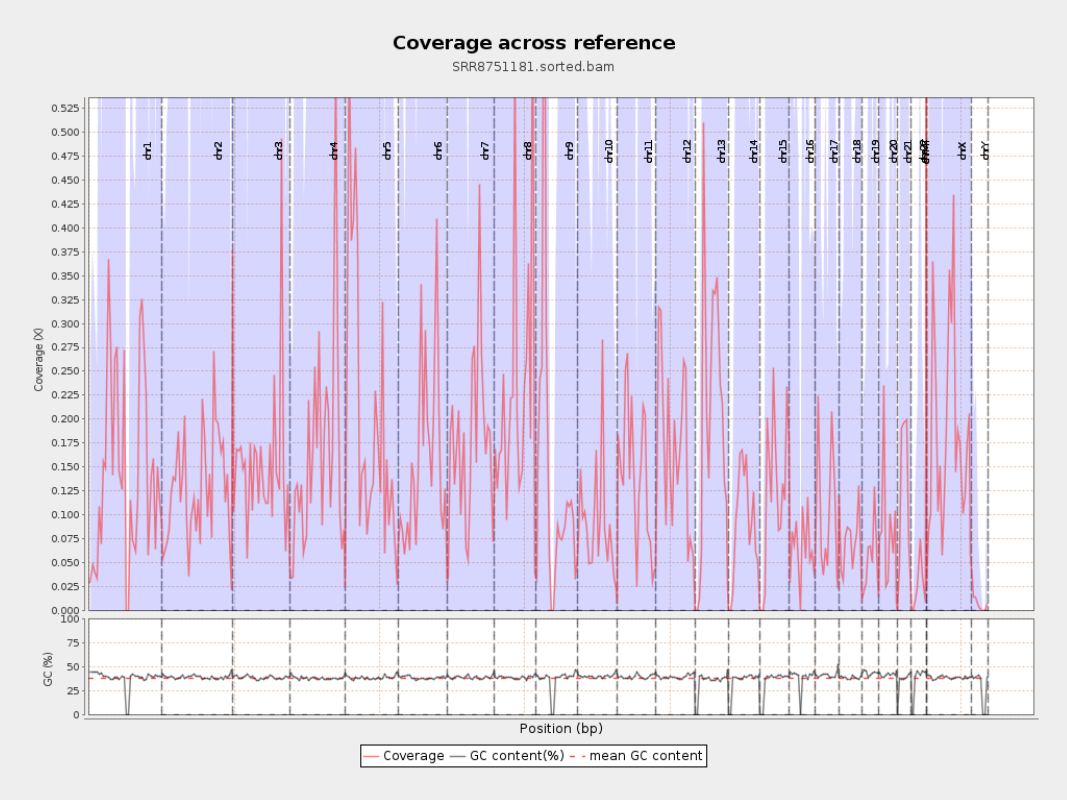
General error rate	0.24%
Mismatches	991,067
Insertions	40,381
Mapped reads with at least one insertion	0.91%
Deletions	44,608
Mapped reads with at least one deletion	1%
Homopolymer indels	47.29%

2.6. Chromosome stats

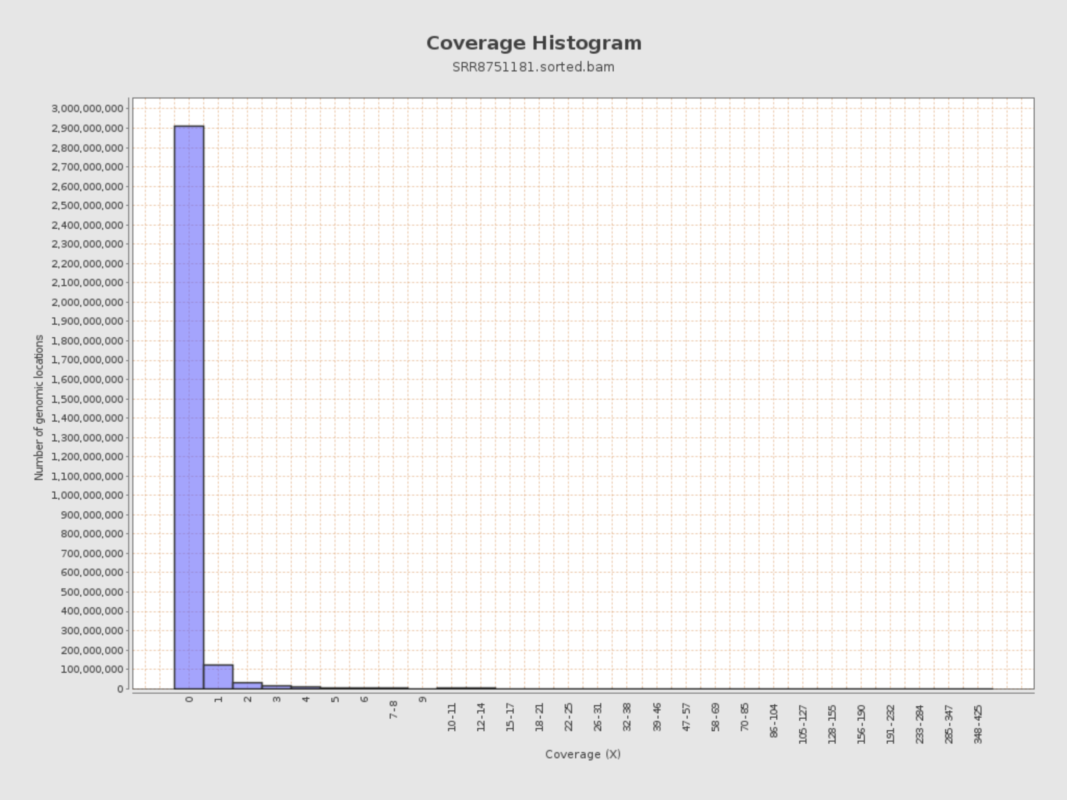
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36512405	0.1465	1.048
chr2	243199373	30878593	0.127	0.8552
chr3	198022430	30714254	0.1551	1.2961
chr4	191154276	30824444	0.1613	1.6234
chr5	180915260	36157041	0.1999	1.6203
chr6	171115067	26331877	0.1539	1.1635
chr7	159138663	28557576	0.1795	1.2244

chr8	146364022	34121537	0.2331	2.041
chr9	141213431	20903603	0.148	2.1656
chr10	135534747	12749357	0.0941	0.7596
chr11	135006516	18583336	0.1376	1.0721
chr12	133851895	22212858	0.166	1.7991
chr13	115169878	22409142	0.1946	1.8234
chr14	107349540	9790372	0.0912	0.6092
chr15	102531392	12662827	0.1235	1.0134
chr16	90354753	5780046	0.064	0.5208
chr17	81195210	7903552	0.0973	0.8907
chr18	78077248	5645416	0.0723	0.591
chr19	59128983	3121747	0.0528	0.5297
chr20	63025520	5419450	0.086	1.6051
chr21	48129895	5513054	0.1145	0.9734
chr22	51304566	1265983	0.0247	0.252
chrMT	16571	21918	1.3227	1.3463
chrX	155270560	28200760	0.1816	1.6994
chrY	59373566	477727	0.008	0.1533

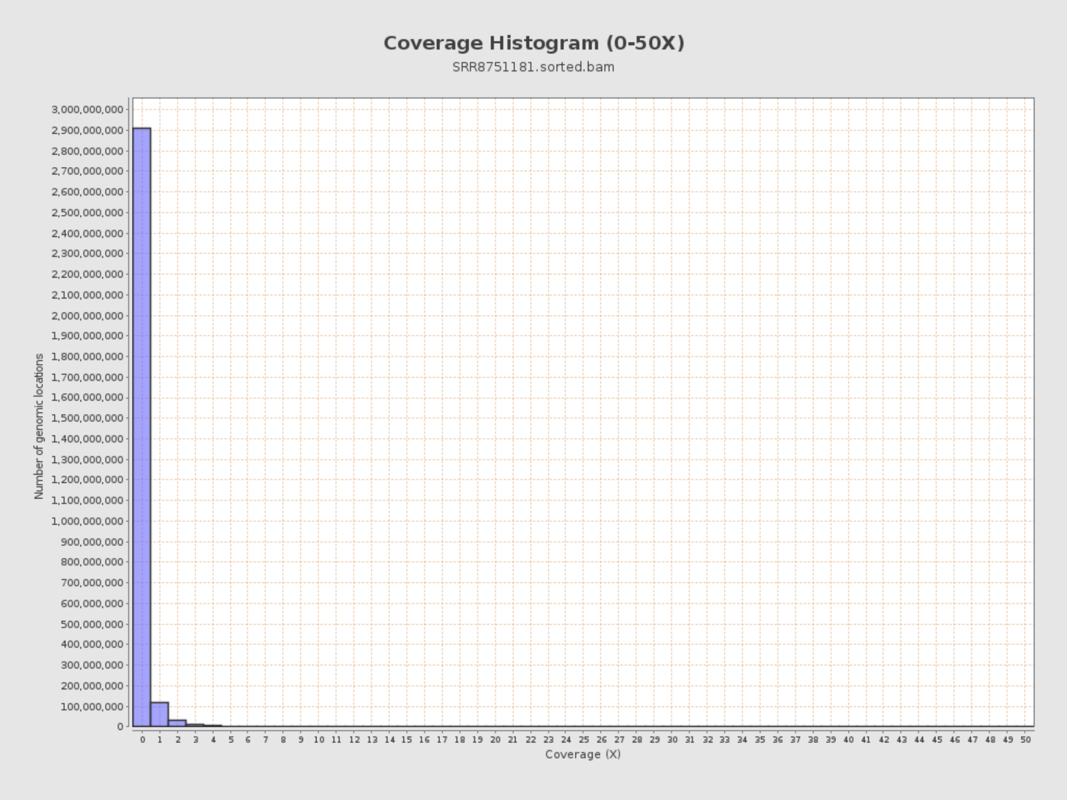
3. Results : Coverage across reference



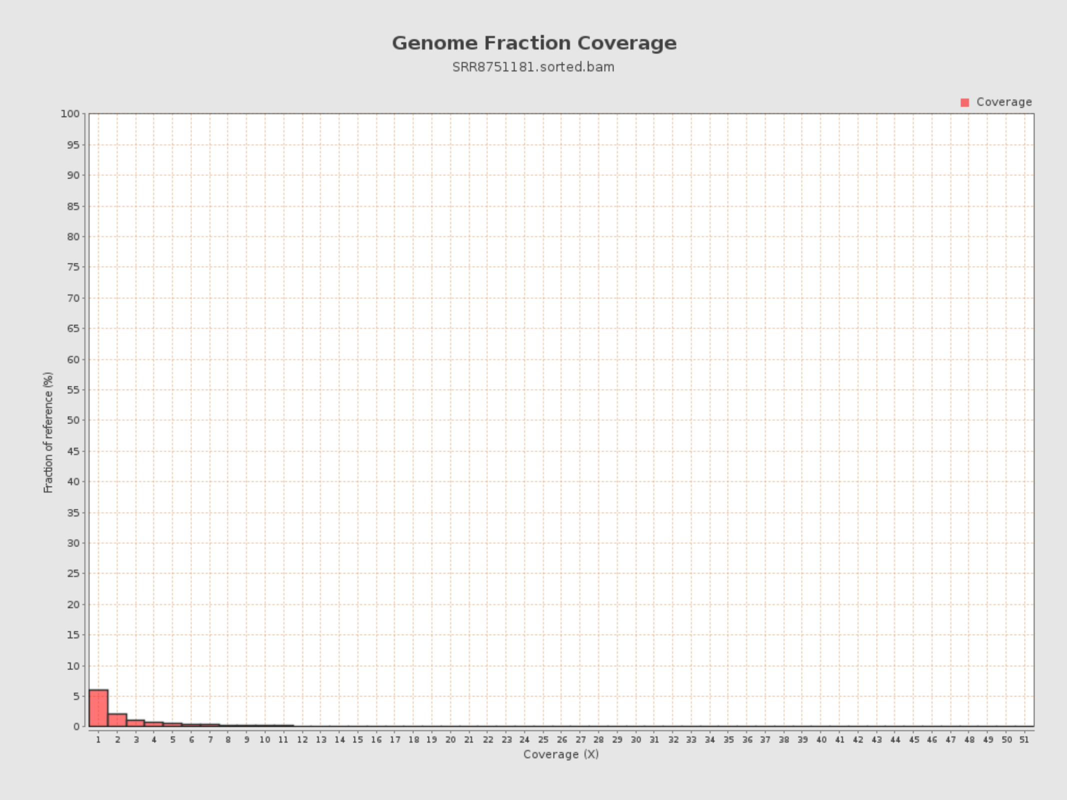
4. Results : Coverage Histogram



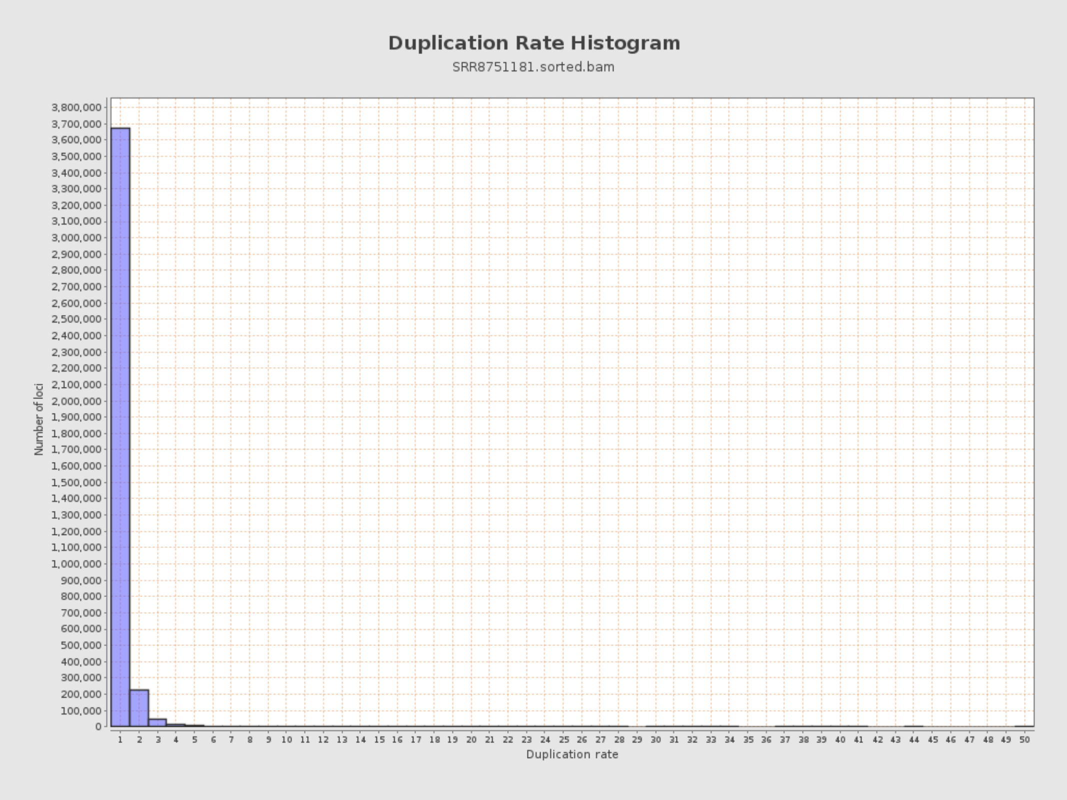
5. Results : Coverage Histogram (0-50X)



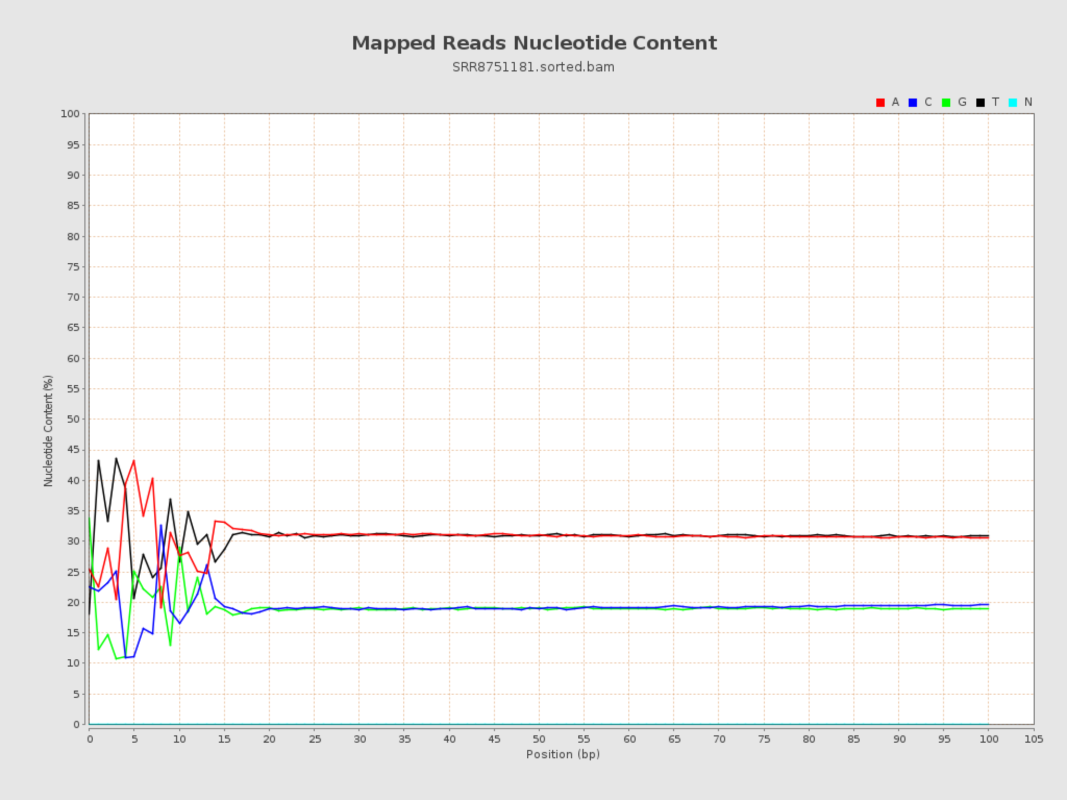
6. Results : Genome Fraction Coverage



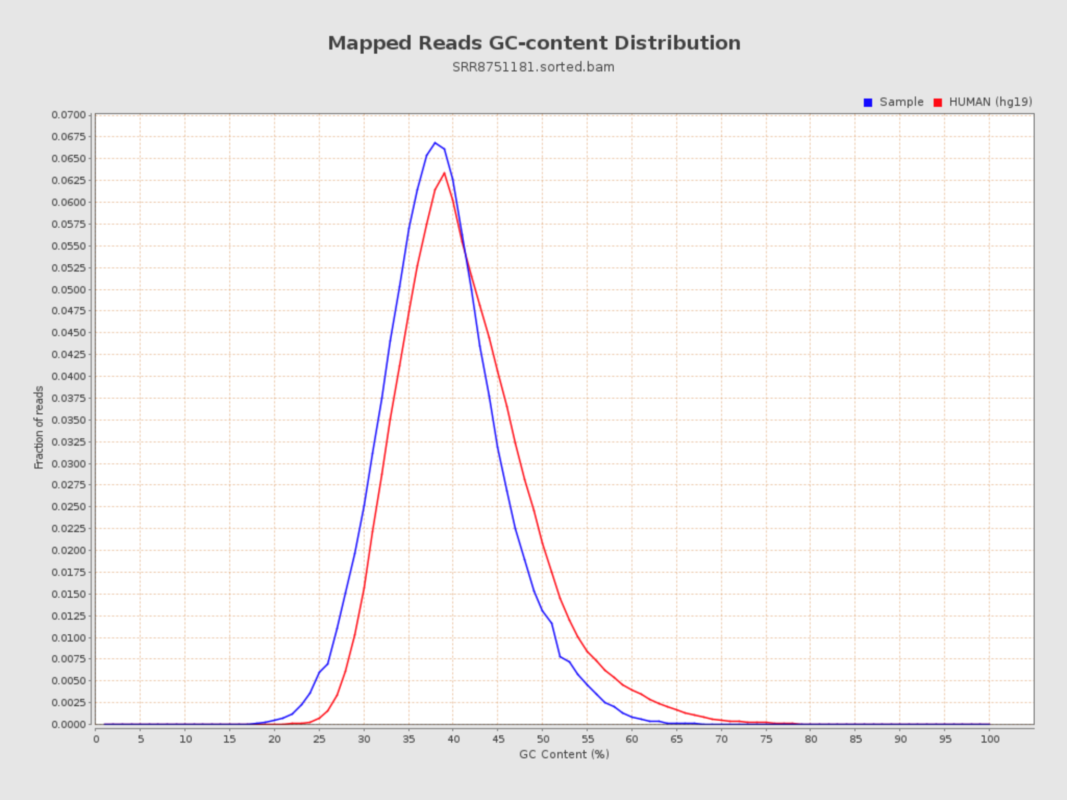
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

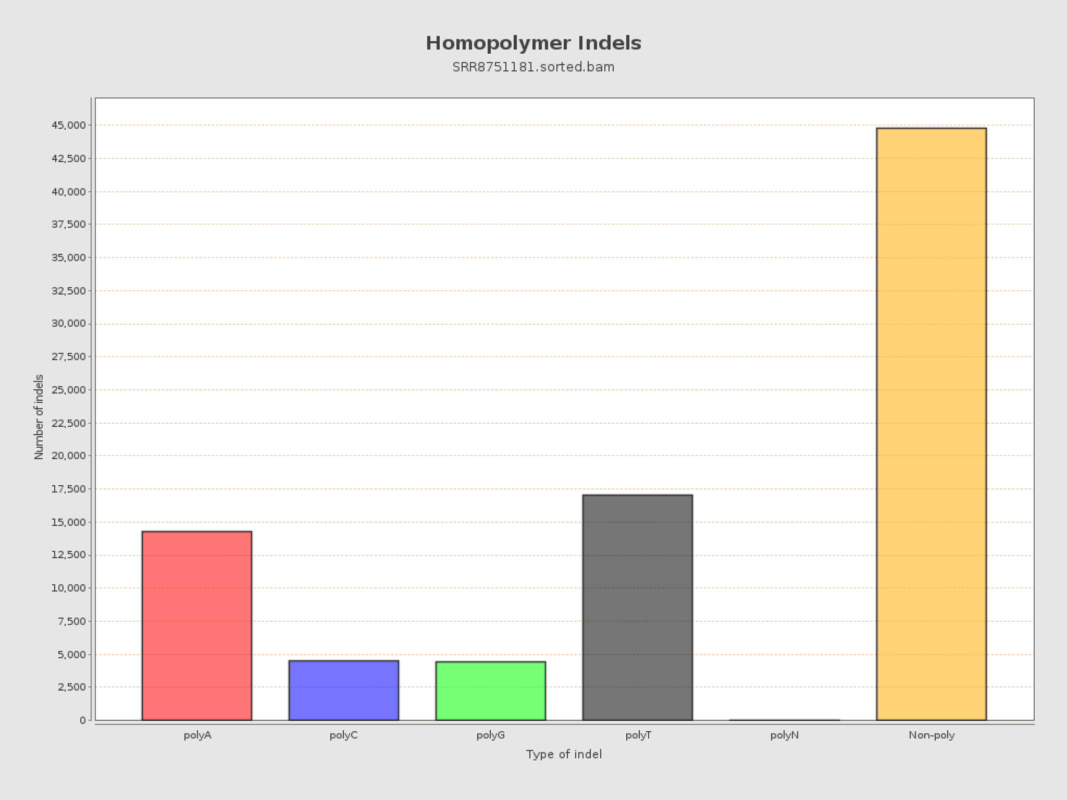


9. Results : Mapped Reads GC-content Distribution

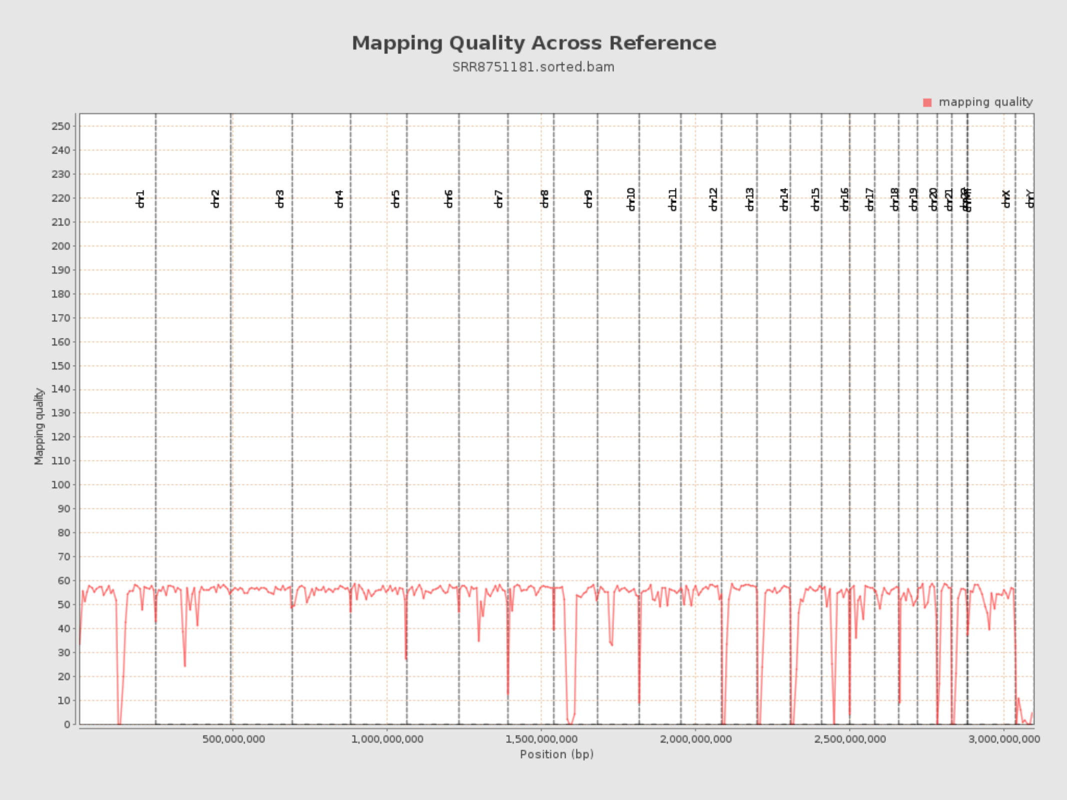


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram