Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:38:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751176.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_SRR8751176 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751176.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:38:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751176.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,833,031
Mapped reads	5,343,659 / 91.61%
Unmapped reads	489,372 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	201,030 / 3.45%
Read min/max/mean length	30 / 101 / 102.43
Duplicated reads (estimated)	159,588 / 2.74%
Duplication rate	1.54%
Clipped reads	980,373 / 16.81%

2.2. ACGT Content

Number/percentage of A's	156,588,707 / 29.7%
Number/percentage of C's	106,754,497 / 20.25%
Number/percentage of T's	157,424,371 / 29.86%
Number/percentage of G's	106,422,412 / 20.19%
Number/percentage of N's	2,856 / 0%
GC Percentage	40.44%

2.3. Coverage

Mean	0.1704

Standard Deviation	1.525

2.4. Mapping Quality

Mean Mapping Quality	51.34

2.5. Mismatches and indels

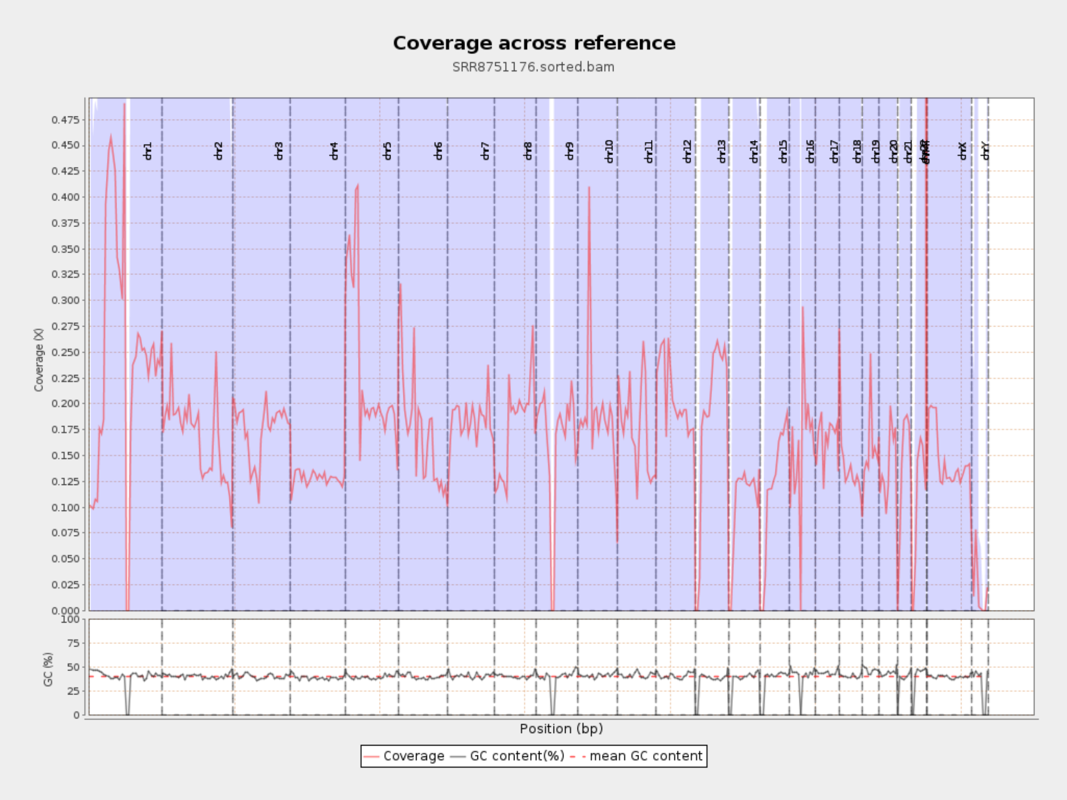
General error rate	0.43%
Mismatches	1,981,752
Insertions	187,140
Mapped reads with at least one insertion	3.41%
Deletions	75,192
Mapped reads with at least one deletion	1.38%
Homopolymer indels	50.69%

2.6. Chromosome stats

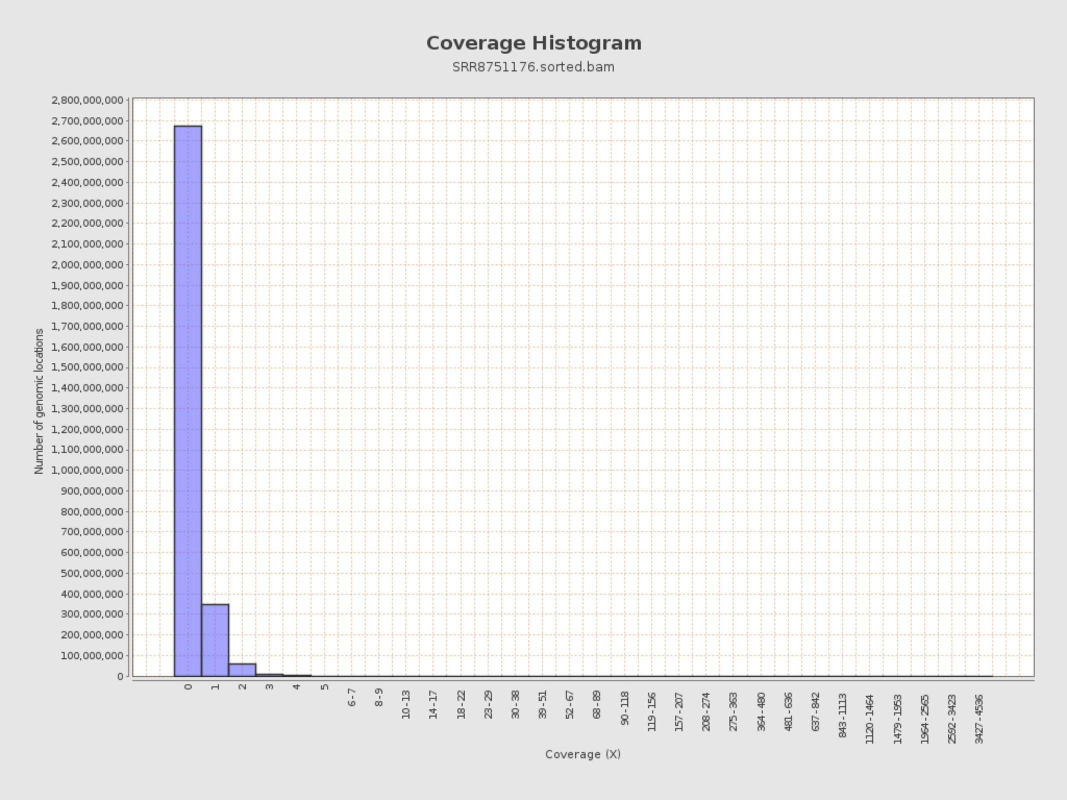
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	62053058	0.249	4.2424
chr2	243199373	41005280	0.1686	0.6725
chr3	198022430	34635726	0.1749	0.5508
chr4	191154276	24444311	0.1279	0.4759
chr5	180915260	41905915	0.2316	0.5514
chr6	171115067	29656253	0.1733	1.0601
chr7	159138663	29358329	0.1845	0.9262

chr8	146364022	26208986	0.1791	0.6246
chr9	141213431	23210670	0.1644	0.8338
chr10	135534747	25974679	0.1916	2.2455
chr11	135006516	23727738	0.1758	0.7847
chr12	133851895	27586230	0.2061	0.5213
chr13	115169878	21463433	0.1864	0.4903
chr14	107349540	10949195	0.102	0.3987
chr15	102531392	12224624	0.1192	0.3889
chr16	90354753	14185498	0.157	1.094
chr17	81195210	13443085	0.1656	0.7825
chr18	78077248	10828271	0.1387	1.6683
chr19	59128983	9252753	0.1565	3.0016
chr20	63025520	8735433	0.1386	0.4424
chr21	48129895	6486634	0.1348	0.4577
chr22	51304566	5269990	0.1027	0.3658
chrMT	16571	1099122	66.328	24.0665
chrX	155270560	22511087	0.145	0.5166
chrY	59373566	1140481	0.0192	0.7257

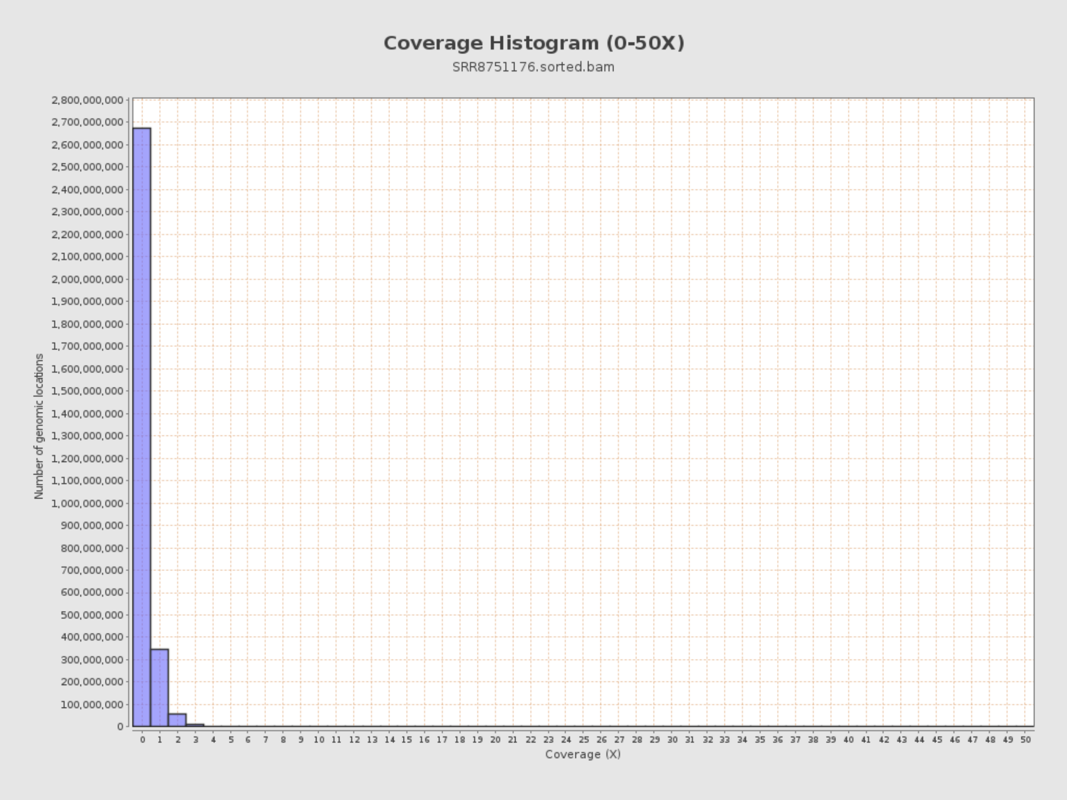
3. Results : Coverage across reference



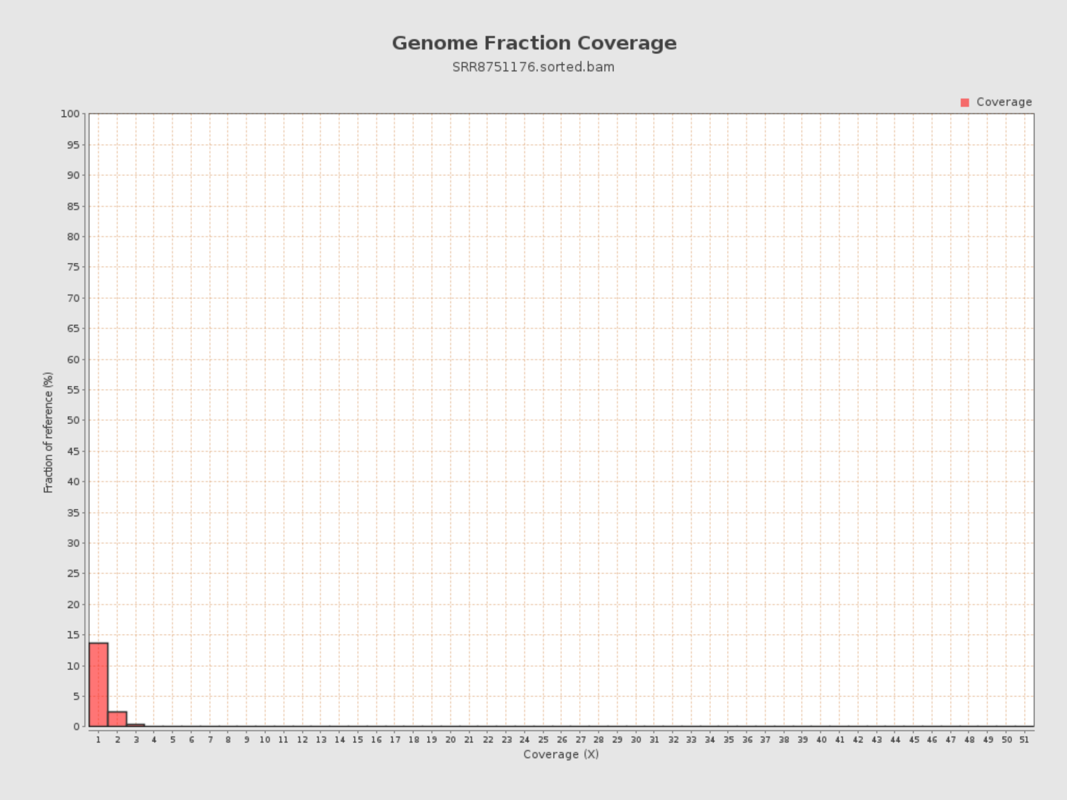
4. Results : Coverage Histogram



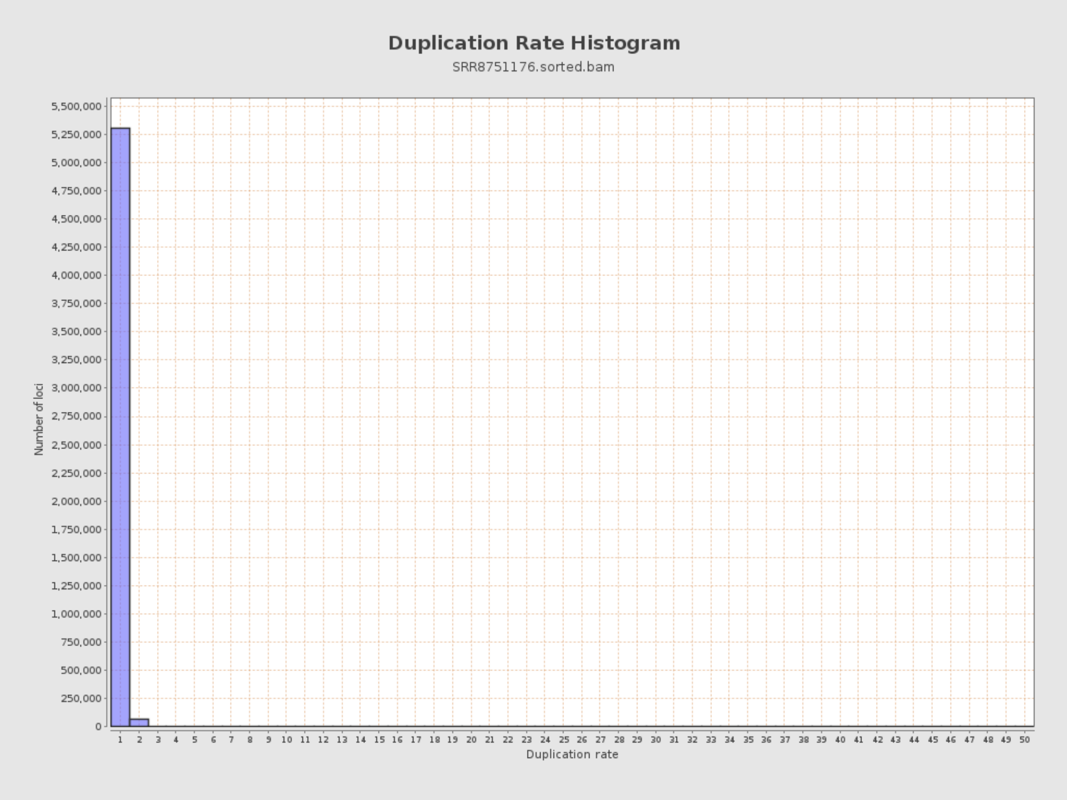
5. Results : Coverage Histogram (0-50X)



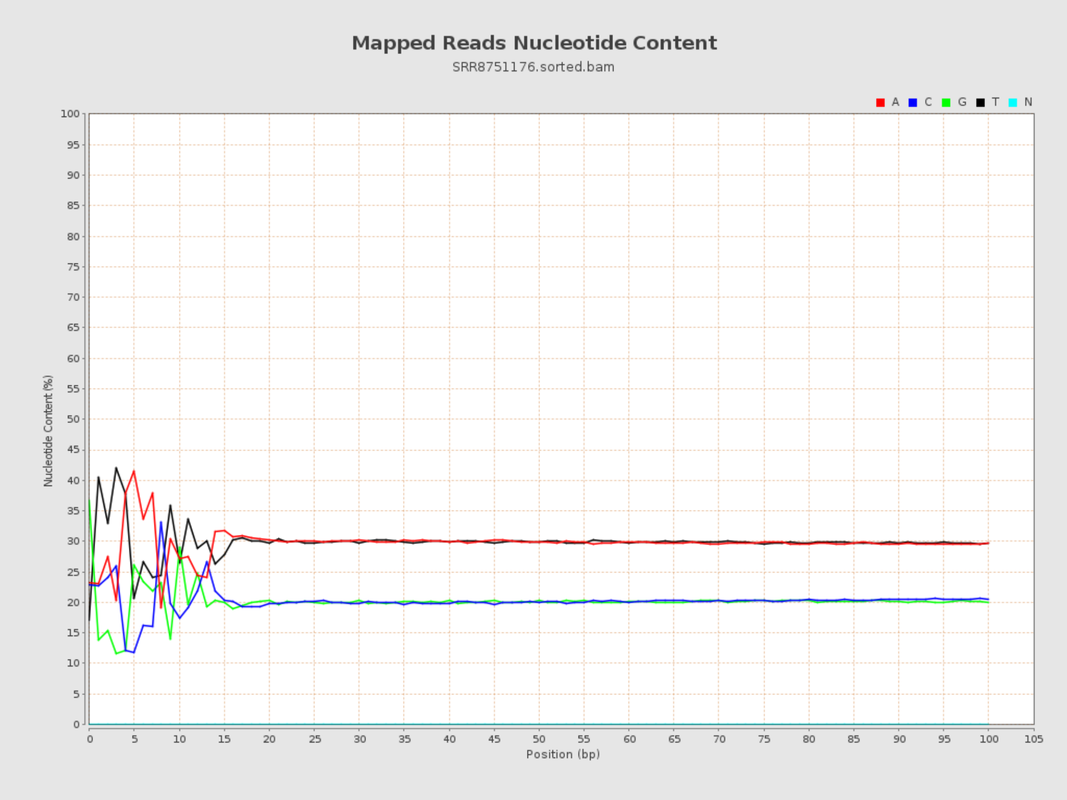
6. Results : Genome Fraction Coverage



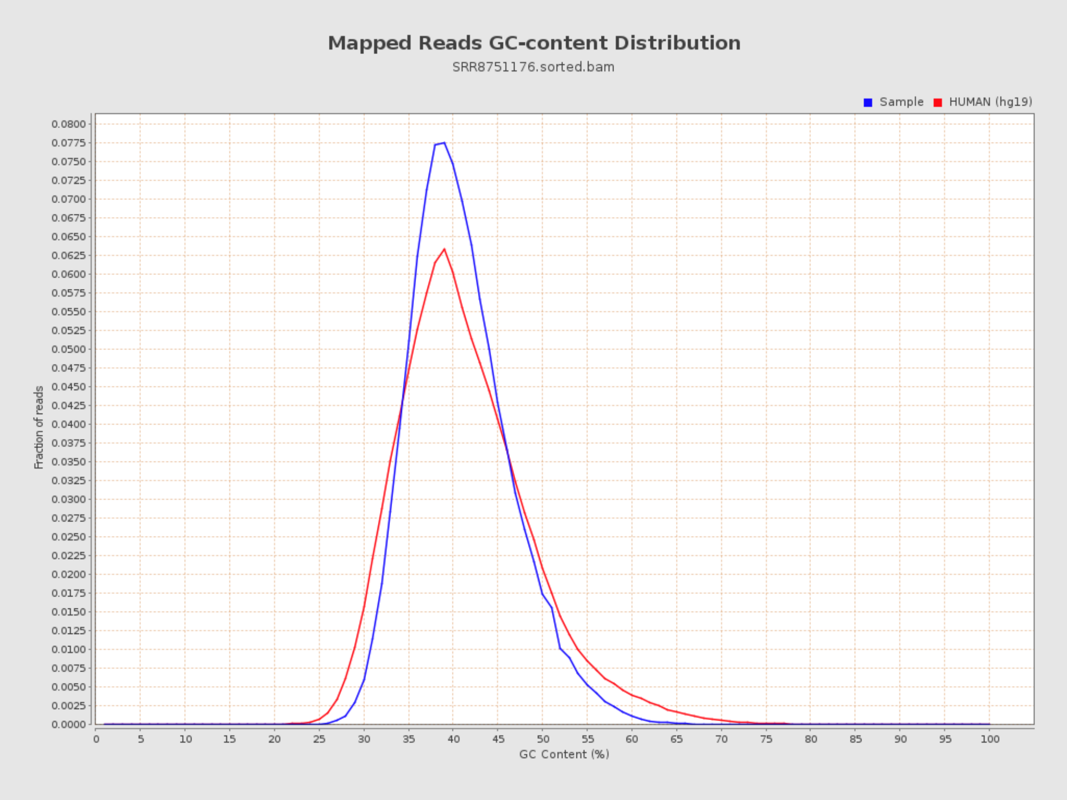
7. Results : Duplication Rate Histogram



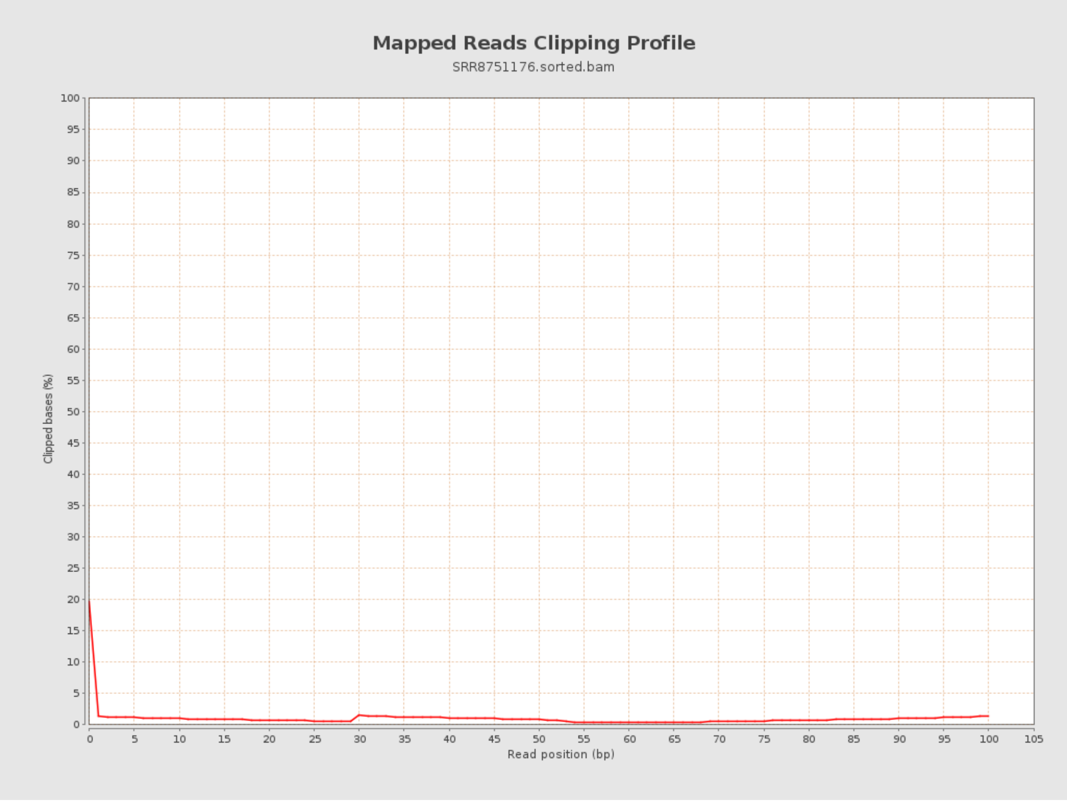
8. Results : Mapped Reads Nucleotide Content



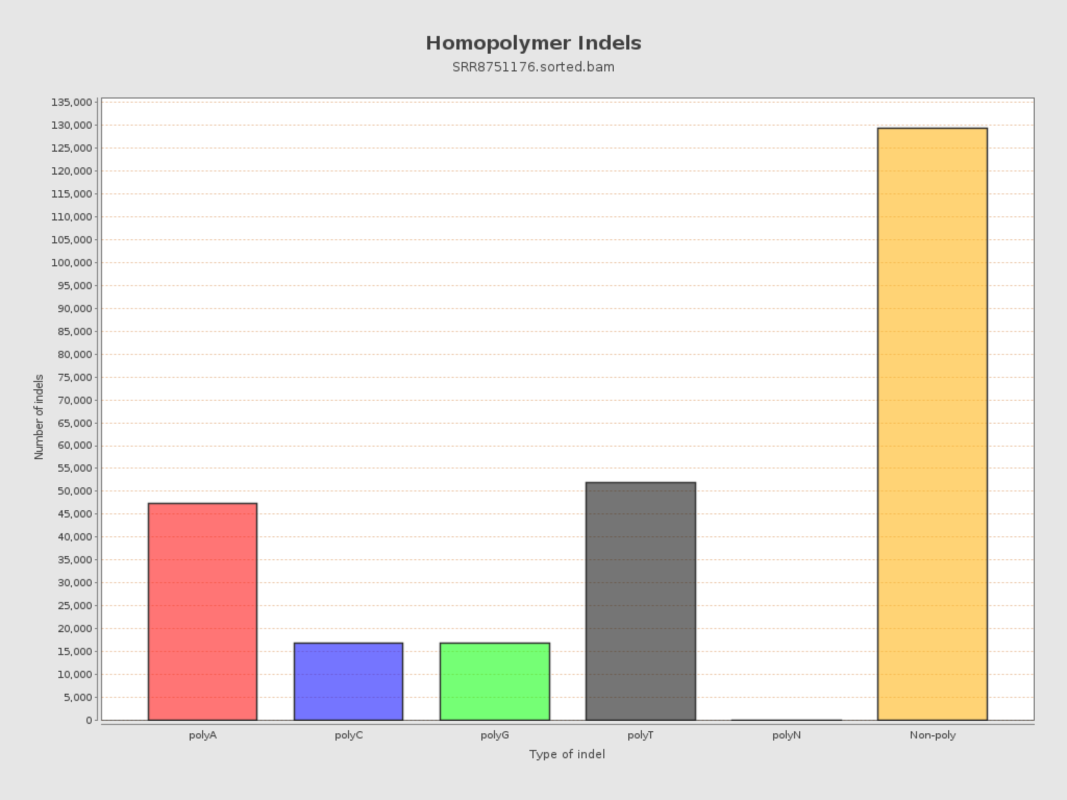
9. Results : Mapped Reads GC-content Distribution



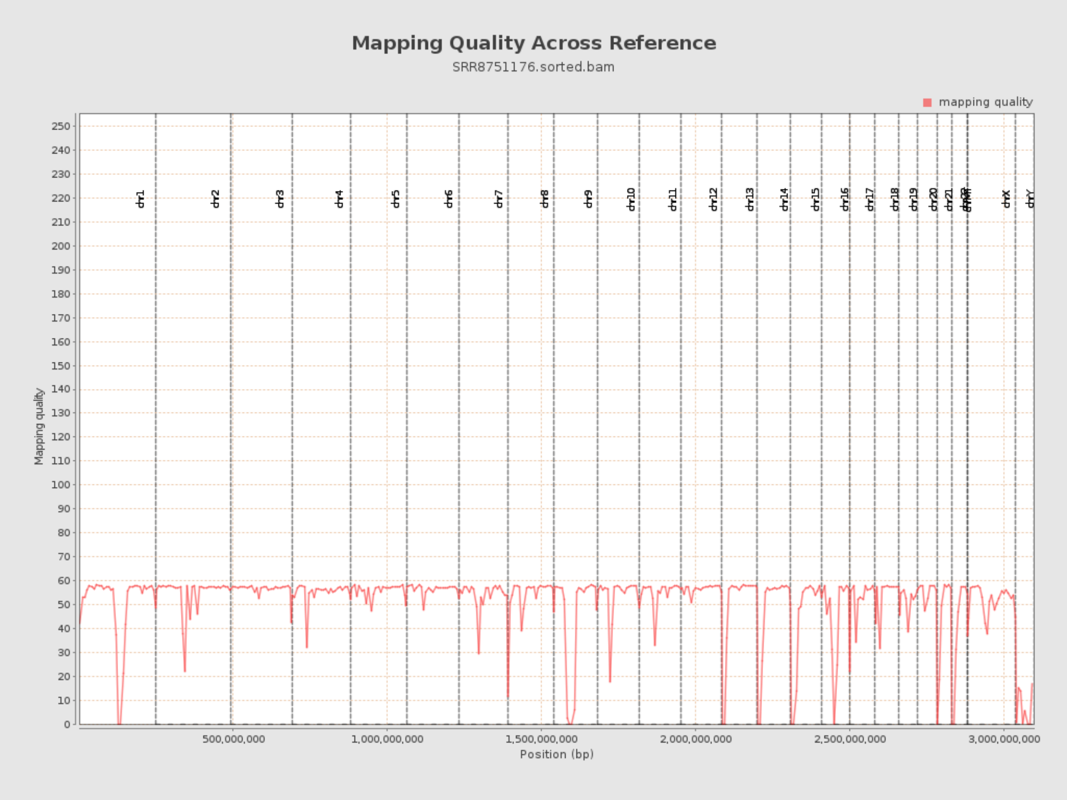
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram