Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:37:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716160.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_SRR9716160 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716160.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:37:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,535,397
Mapped reads	1,247,239 / 81.23%
Unmapped reads	288,158 / 18.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,758 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	31,251 / 2.04%
Duplication rate	1.92%
Clipped reads	1,248,366 / 81.31%

2.2. ACGT Content

Number/percentage of A's	18,035,540 / 25.46%
Number/percentage of C's	12,563,196 / 17.73%
Number/percentage of T's	22,190,820 / 31.32%
Number/percentage of G's	18,057,826 / 25.49%
Number/percentage of N's	1,588 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0229

Standard Deviation	0.1936

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

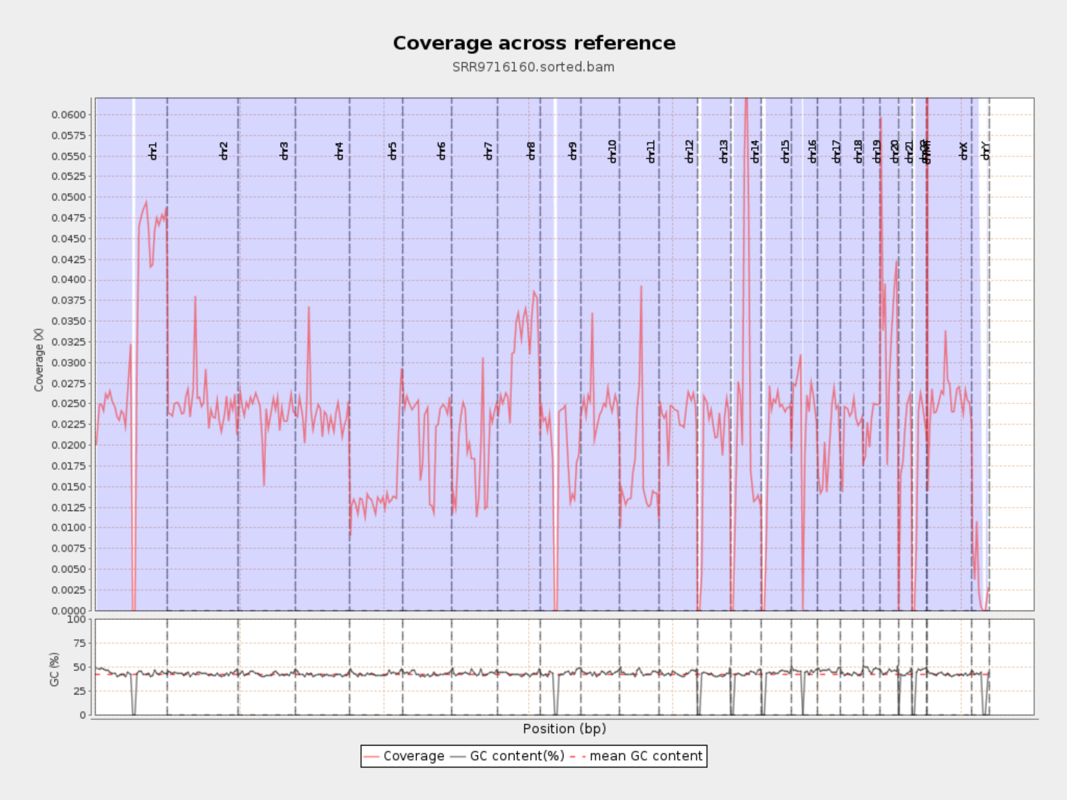
General error rate	0.5%
Mismatches	348,746
Insertions	4,601
Mapped reads with at least one insertion	0.37%
Deletions	11,186
Mapped reads with at least one deletion	0.89%
Homopolymer indels	41.49%

2.6. Chromosome stats

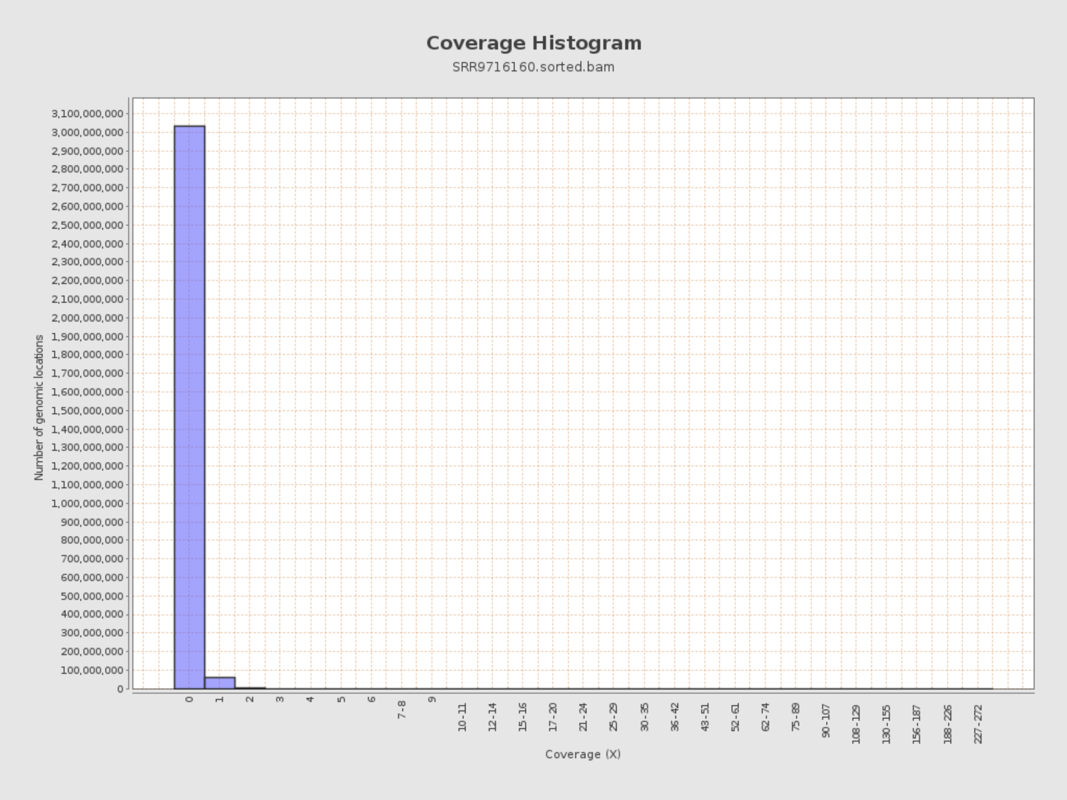
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8071474	0.0324	0.2754
chr2	243199373	6079627	0.025	0.2183
chr3	198022430	4762218	0.024	0.1665
chr4	191154276	4570415	0.0239	0.1763
chr5	180915260	2579421	0.0143	0.1291
chr6	171115067	3795769	0.0222	0.1663
chr7	159138663	3092094	0.0194	0.1737

chr8	146364022	4589774	0.0314	0.2111
chr9	141213431	2576950	0.0182	0.1947
chr10	135534747	3396973	0.0251	0.2034
chr11	135006516	2282194	0.0169	0.1842
chr12	133851895	3192984	0.0239	0.1668
chr13	115169878	2229868	0.0194	0.1483
chr14	107349540	2534718	0.0236	0.1735
chr15	102531392	2084068	0.0203	0.1528
chr16	90354753	2113727	0.0234	0.1734
chr17	81195210	1620312	0.02	0.1557
chr18	78077248	1756306	0.0225	0.3458
chr19	59128983	1338203	0.0226	0.2069
chr20	63025520	2237413	0.0355	0.2072
chr21	48129895	935993	0.0194	0.1617
chr22	51304566	854750	0.0167	0.1377
chrMT	16571	21100	1.2733	1.4077
chrX	155270560	3956186	0.0255	0.189
chrY	59373566	195582	0.0033	0.0823

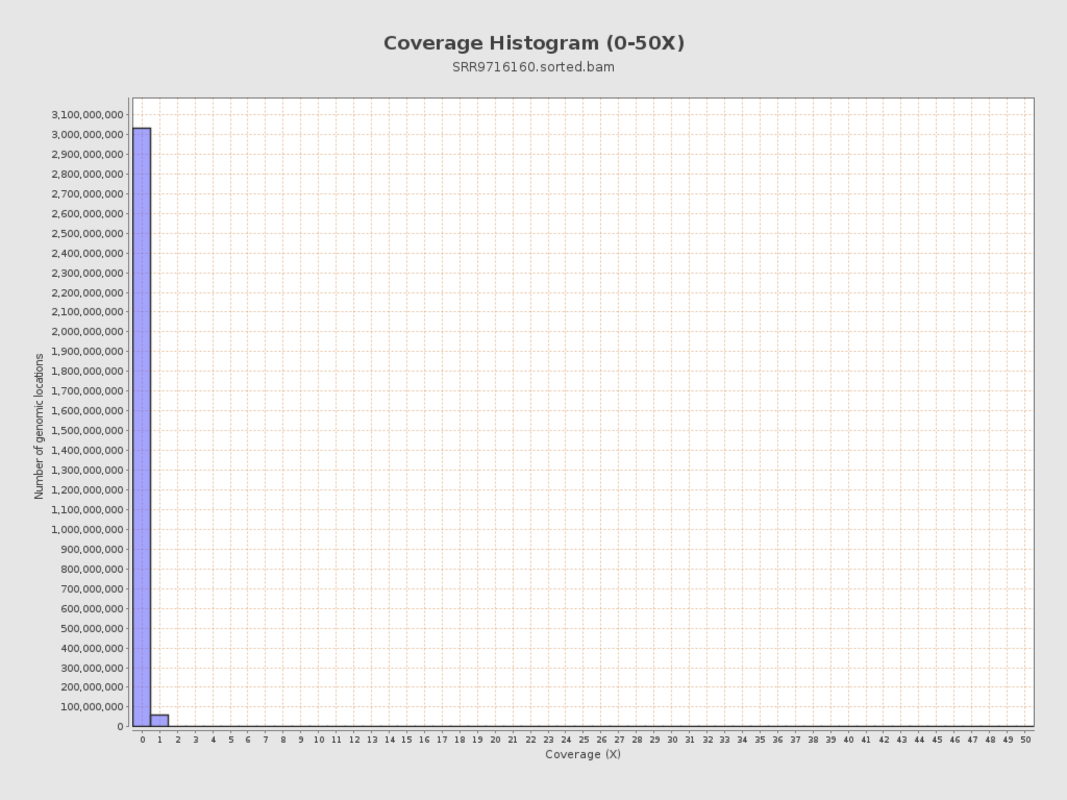
3. Results : Coverage across reference



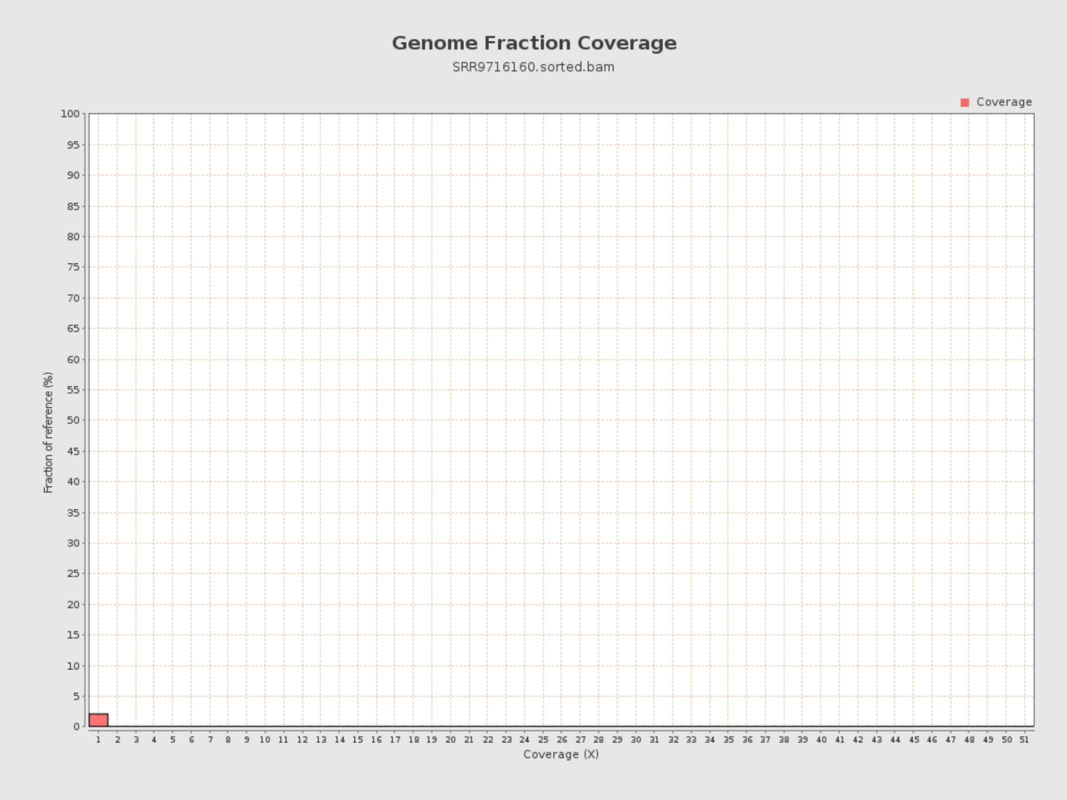
4. Results : Coverage Histogram



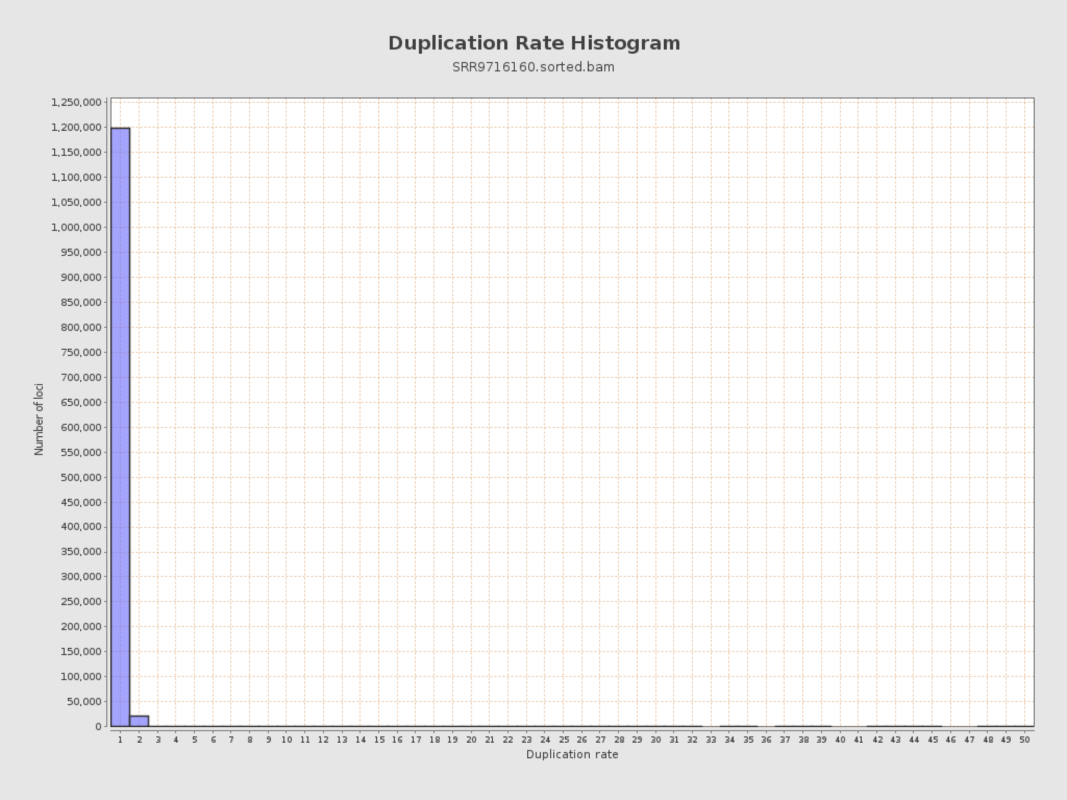
5. Results : Coverage Histogram (0-50X)



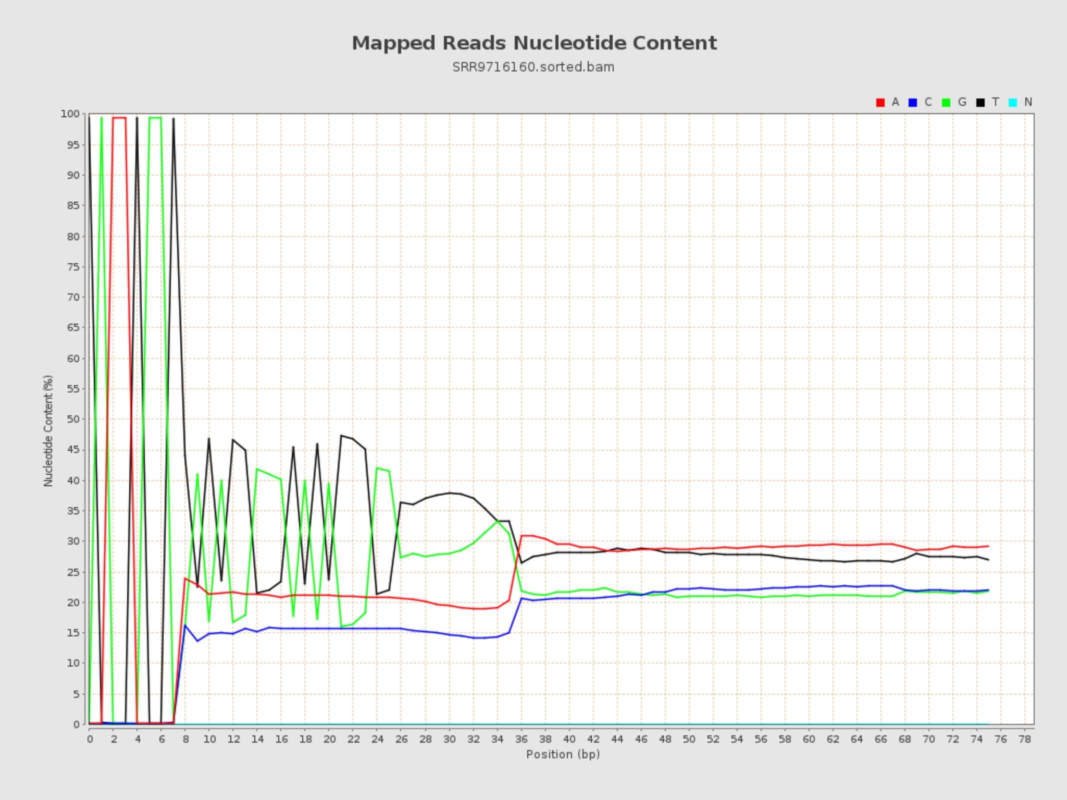
6. Results : Genome Fraction Coverage



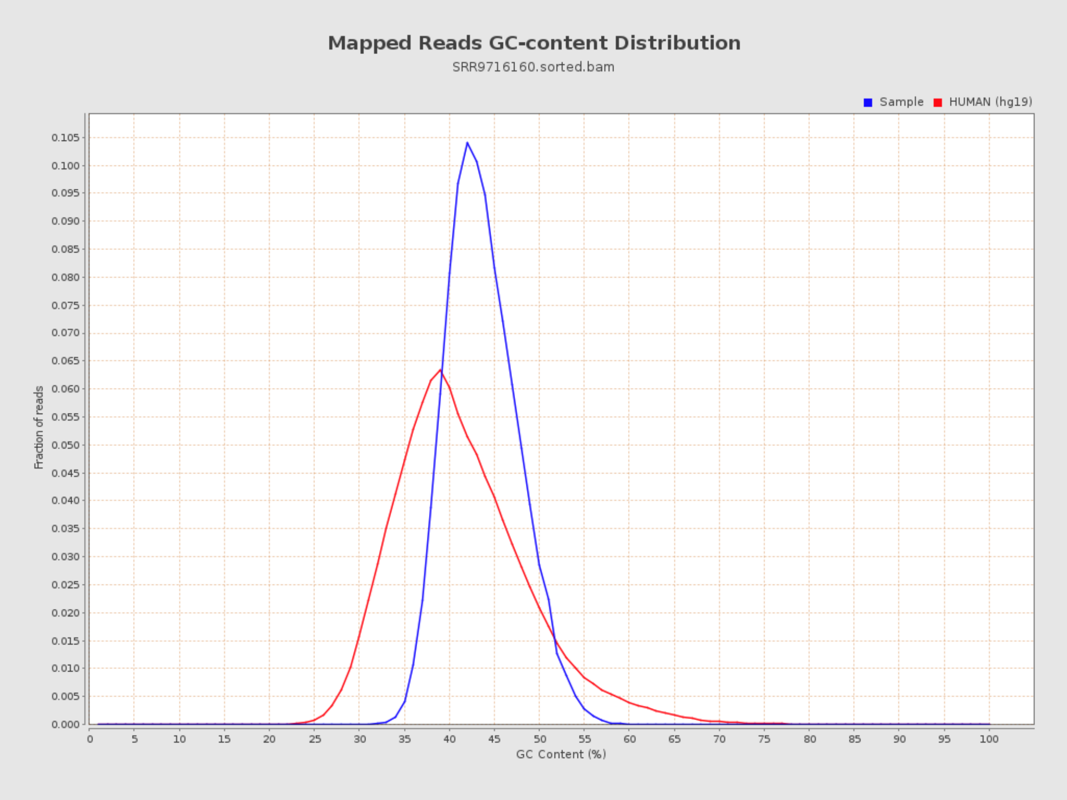
7. Results : Duplication Rate Histogram



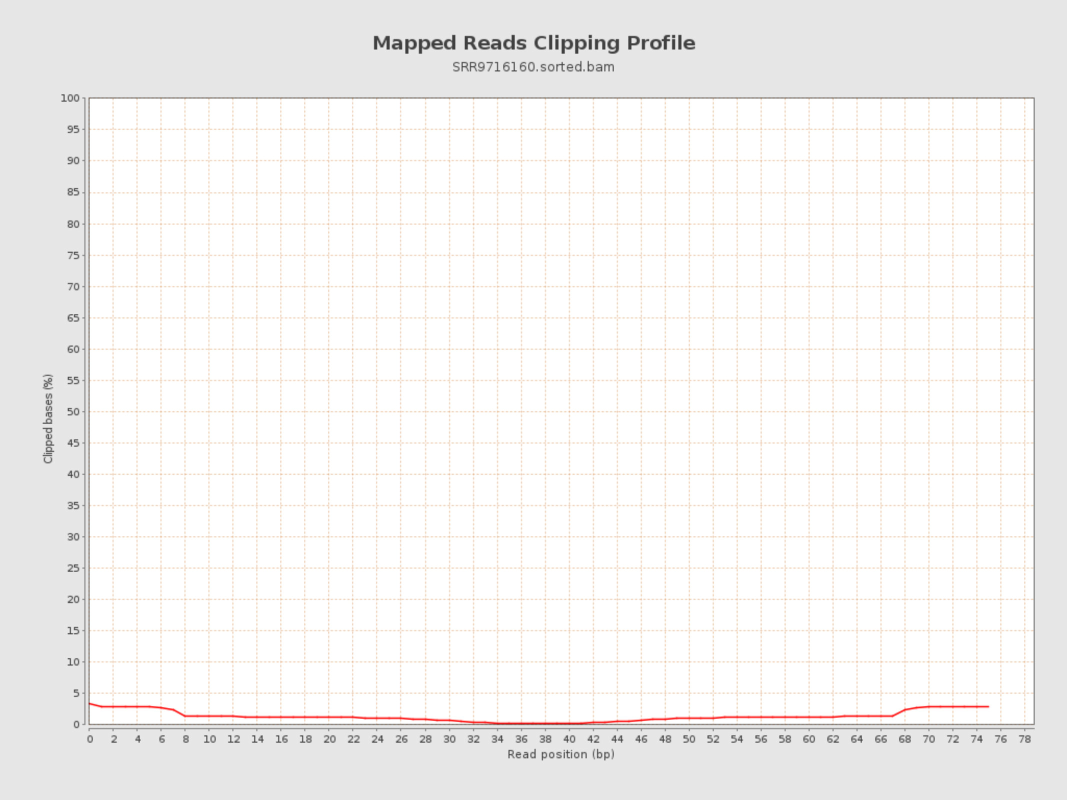
8. Results : Mapped Reads Nucleotide Content



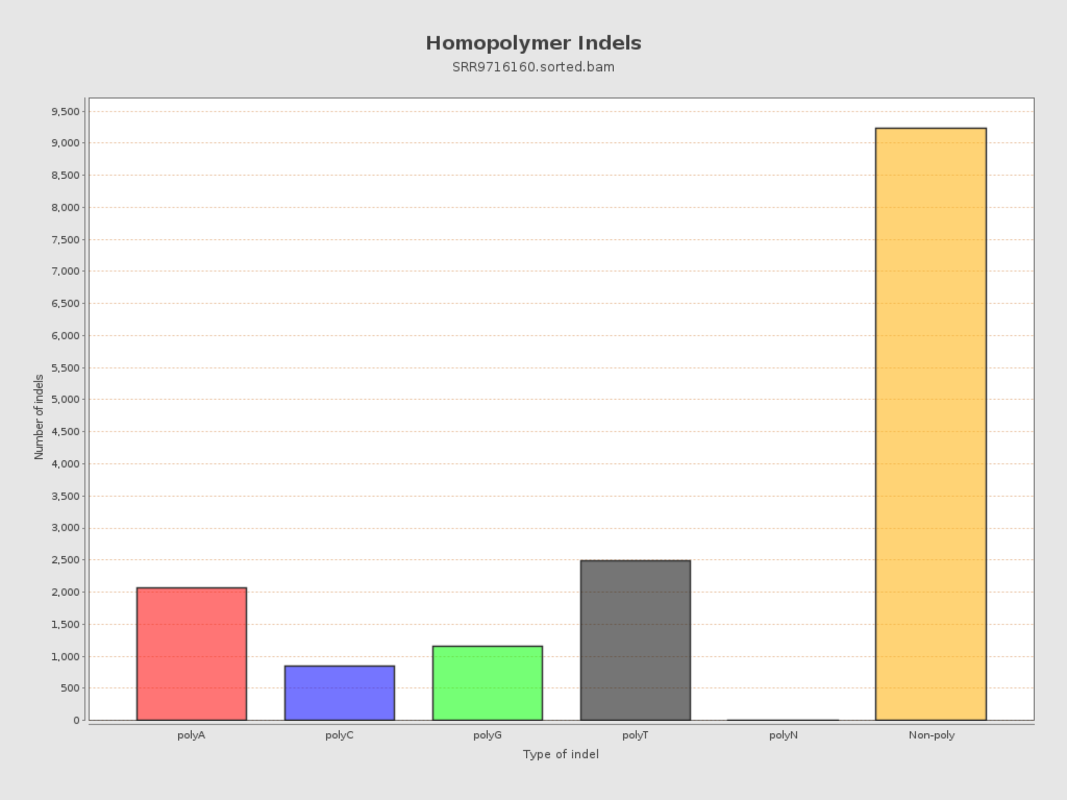
9. Results : Mapped Reads GC-content Distribution



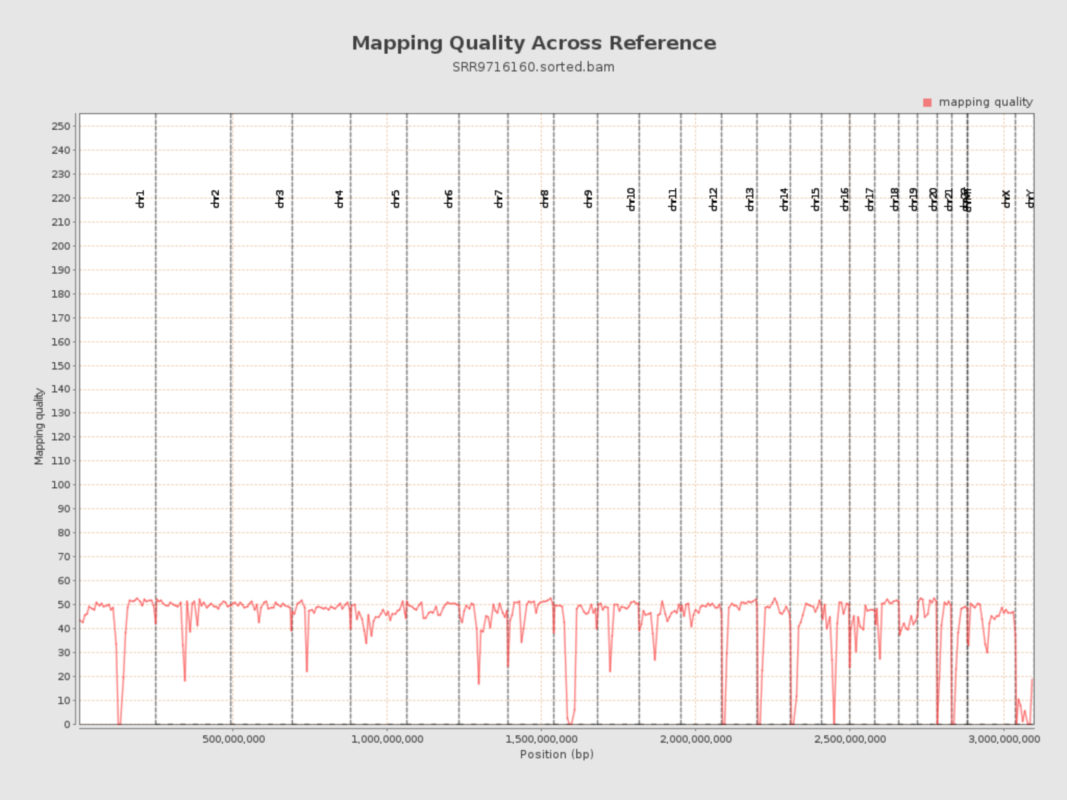
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram