Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:55:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716276.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_SRR9716276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716276.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:55:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,517,148
Mapped reads	1,352,743 / 89.16%
Unmapped reads	164,405 / 10.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,659 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	54,144 / 3.57%
Duplication rate	3.2%
Clipped reads	1,355,005 / 89.31%

2.2. ACGT Content

Number/percentage of A's	20,311,935 / 25.83%
Number/percentage of C's	14,723,703 / 18.73%
Number/percentage of T's	25,230,320 / 32.09%
Number/percentage of G's	18,360,726 / 23.35%
Number/percentage of N's	2,293 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2351

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

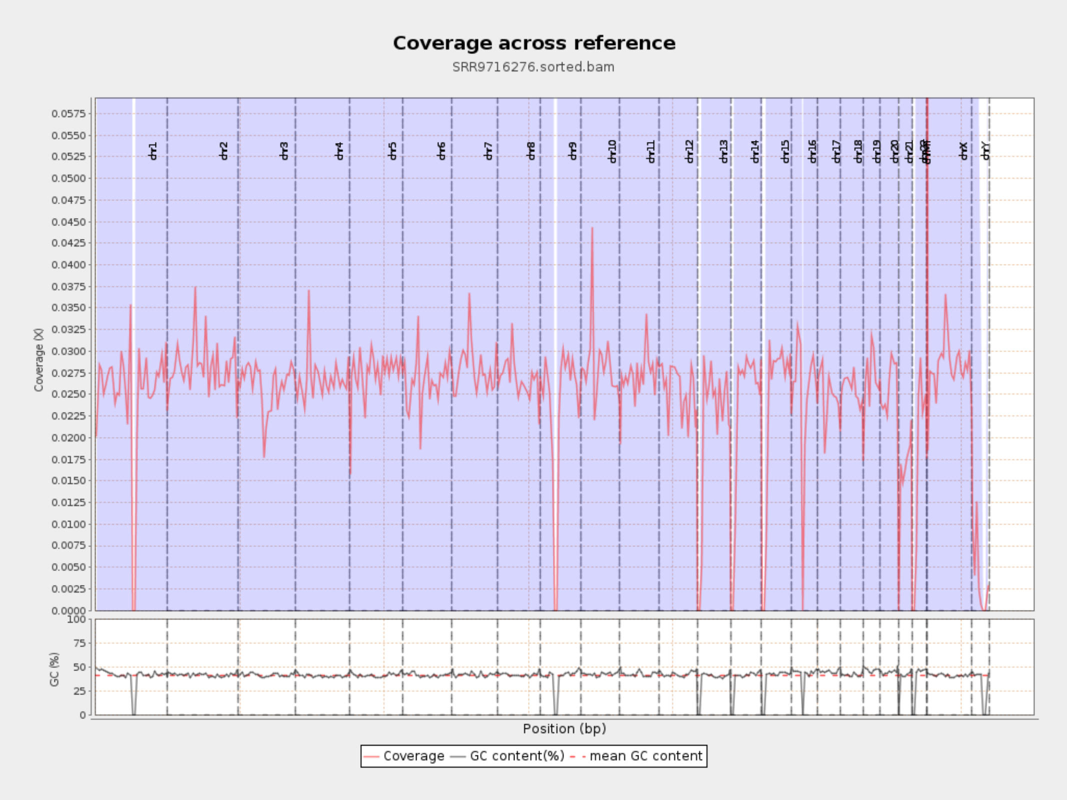
General error rate	0.5%
Mismatches	384,168
Insertions	5,256
Mapped reads with at least one insertion	0.39%
Deletions	13,489
Mapped reads with at least one deletion	0.99%
Homopolymer indels	42.29%

2.6. Chromosome stats

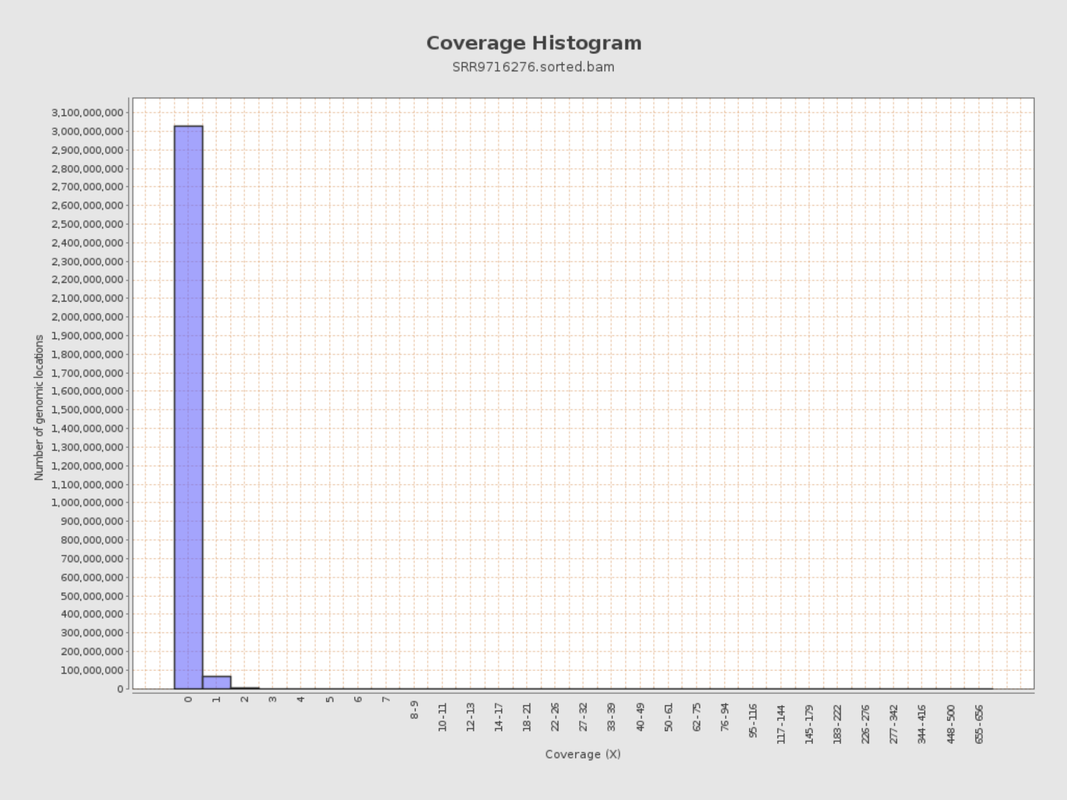
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6215388	0.0249	0.4032
chr2	243199373	6880415	0.0283	0.3292
chr3	198022430	5169422	0.0261	0.1773
chr4	191154276	5128292	0.0268	0.1883
chr5	180915260	5040152	0.0279	0.1833
chr6	171115067	4555357	0.0266	0.2058
chr7	159138663	4462960	0.028	0.2537

chr8	146364022	3933938	0.0269	0.2246
chr9	141213431	3304985	0.0234	0.1944
chr10	135534747	3856923	0.0285	0.2371
chr11	135006516	3685038	0.0273	0.2169
chr12	133851895	3421102	0.0256	0.1773
chr13	115169878	2426771	0.0211	0.1595
chr14	107349540	2442859	0.0228	0.1697
chr15	102531392	2381456	0.0232	0.1674
chr16	90354753	2215348	0.0245	0.1793
chr17	81195210	2011282	0.0248	0.1794
chr18	78077248	2007525	0.0257	0.2869
chr19	59128983	1603124	0.0271	0.2903
chr20	63025520	1621913	0.0257	0.1775
chr21	48129895	763799	0.0159	0.1513
chr22	51304566	878454	0.0171	0.1443
chrMT	16571	13201	0.7966	1.0071
chrX	155270560	4404303	0.0284	0.199
chrY	59373566	226518	0.0038	0.1028

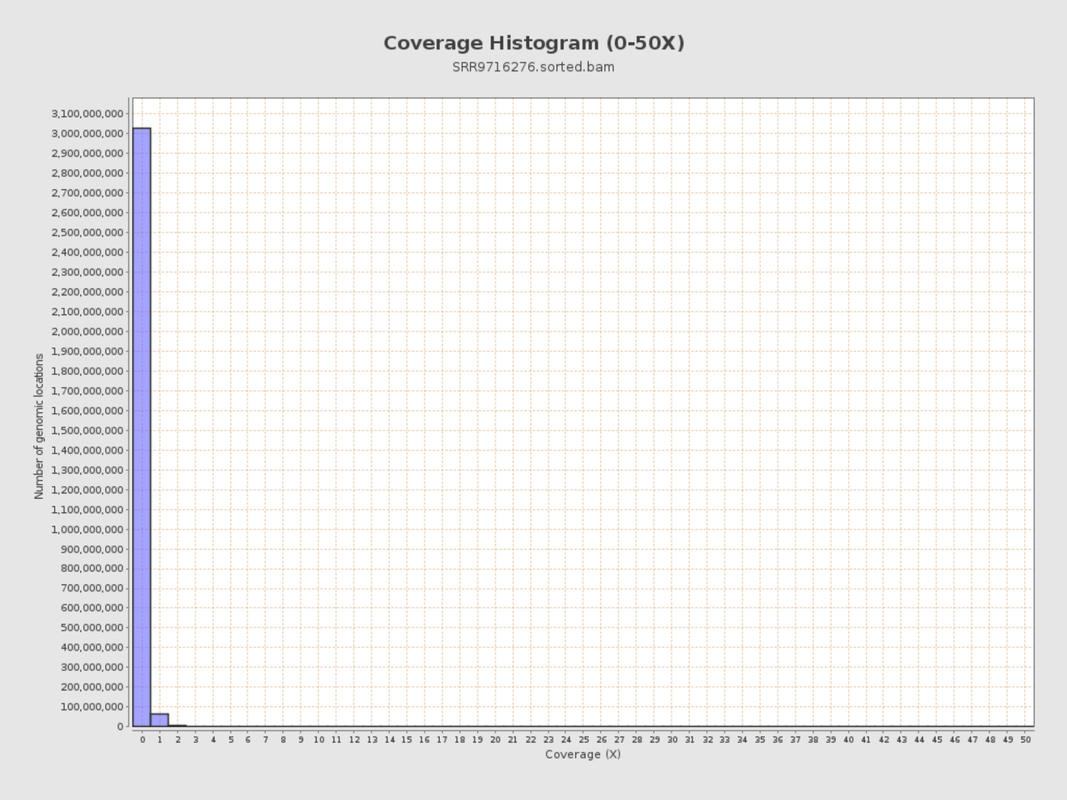
3. Results : Coverage across reference



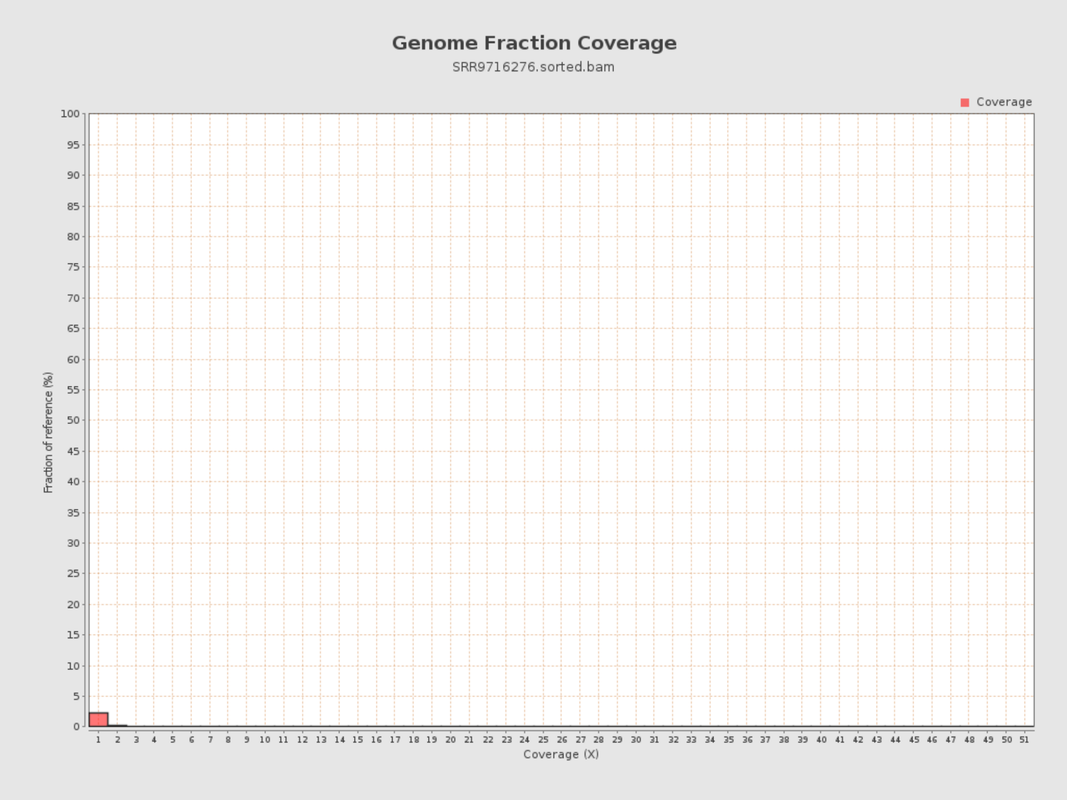
4. Results : Coverage Histogram



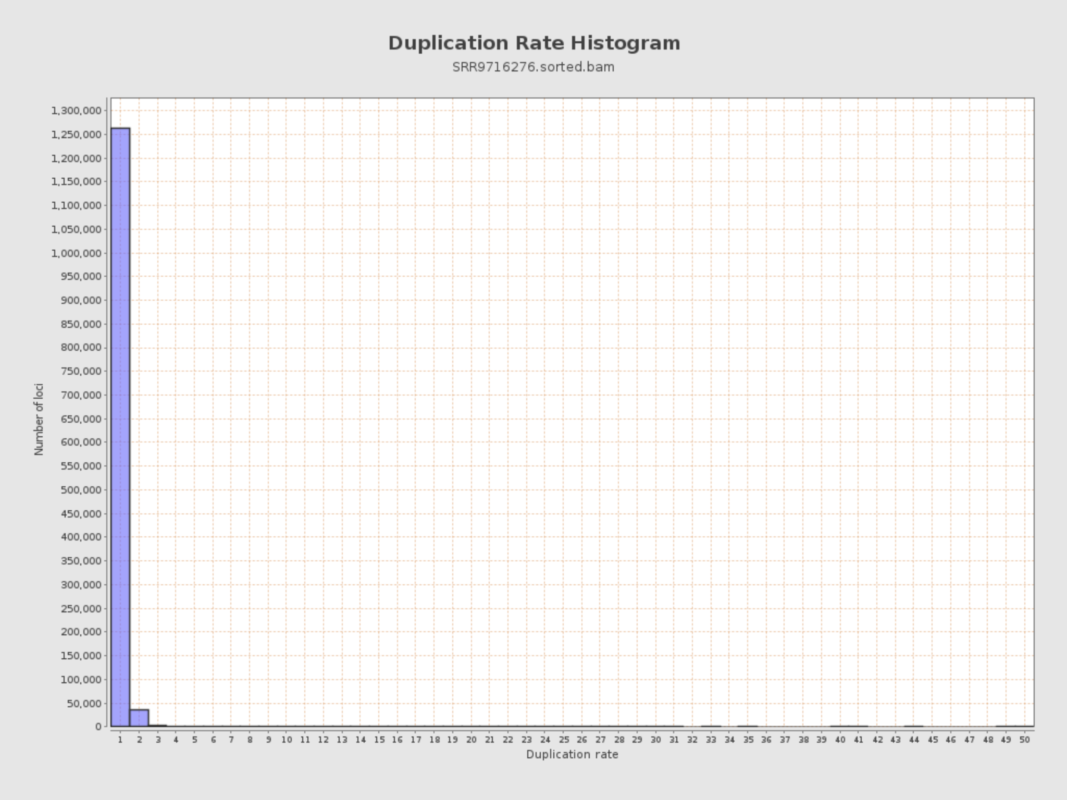
5. Results : Coverage Histogram (0-50X)



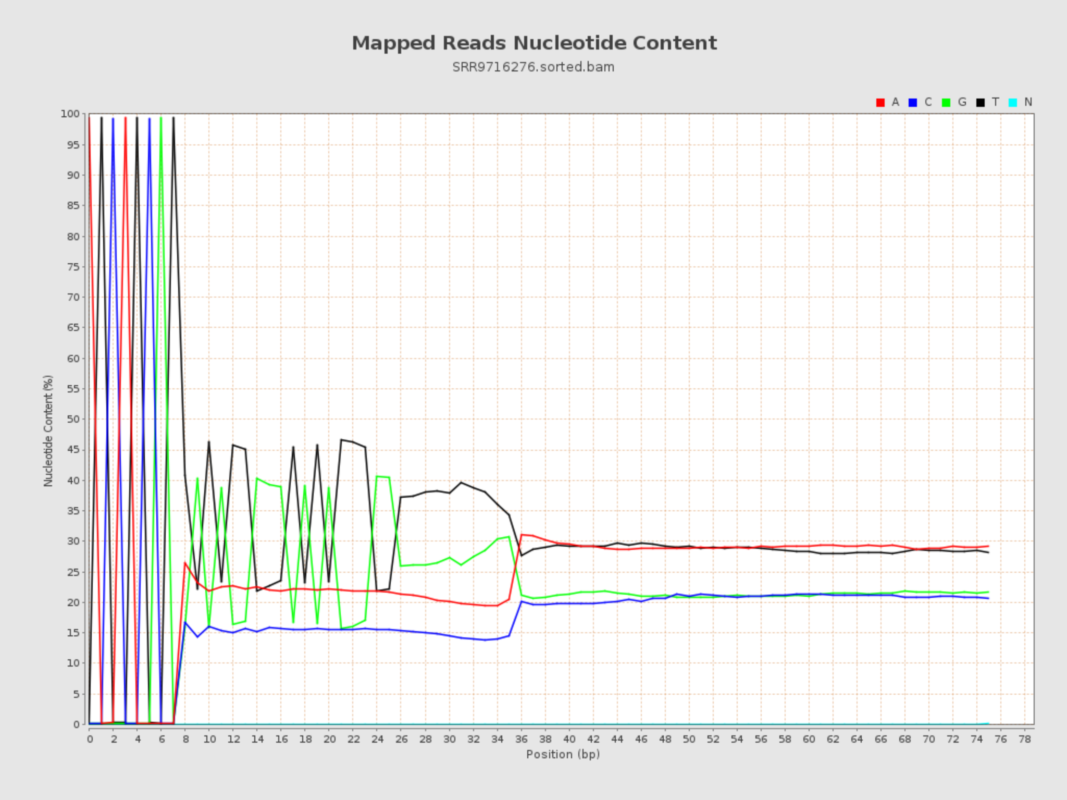
6. Results : Genome Fraction Coverage



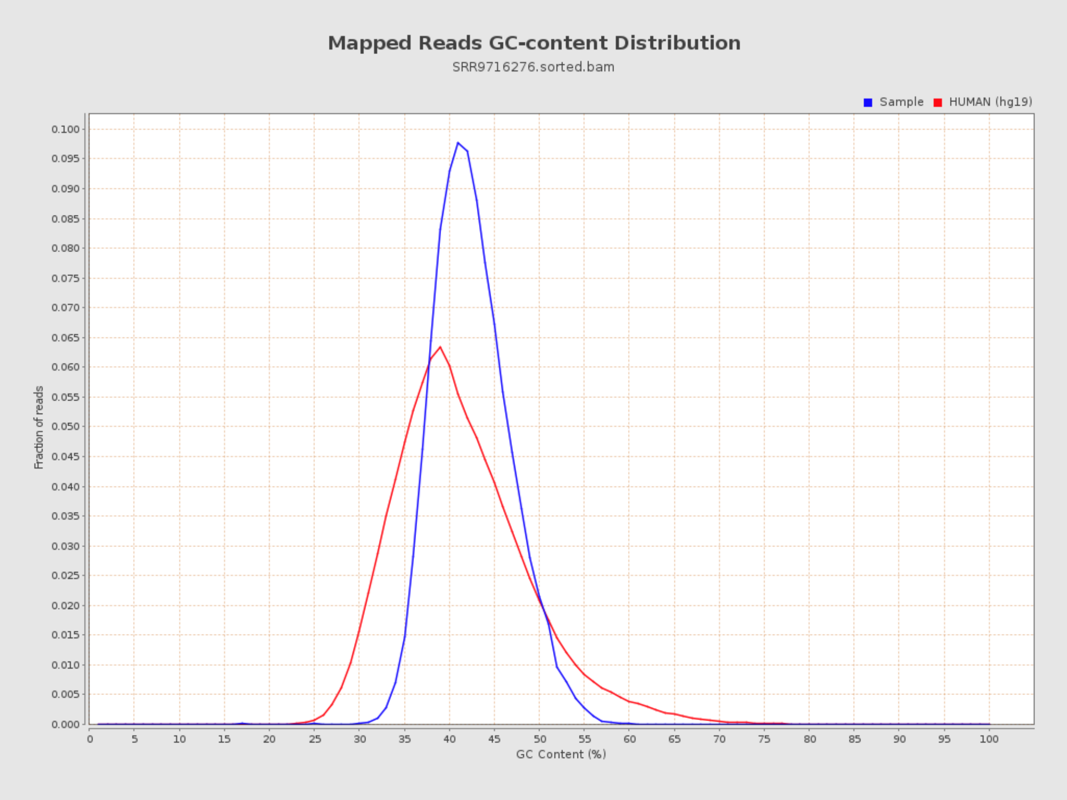
7. Results : Duplication Rate Histogram



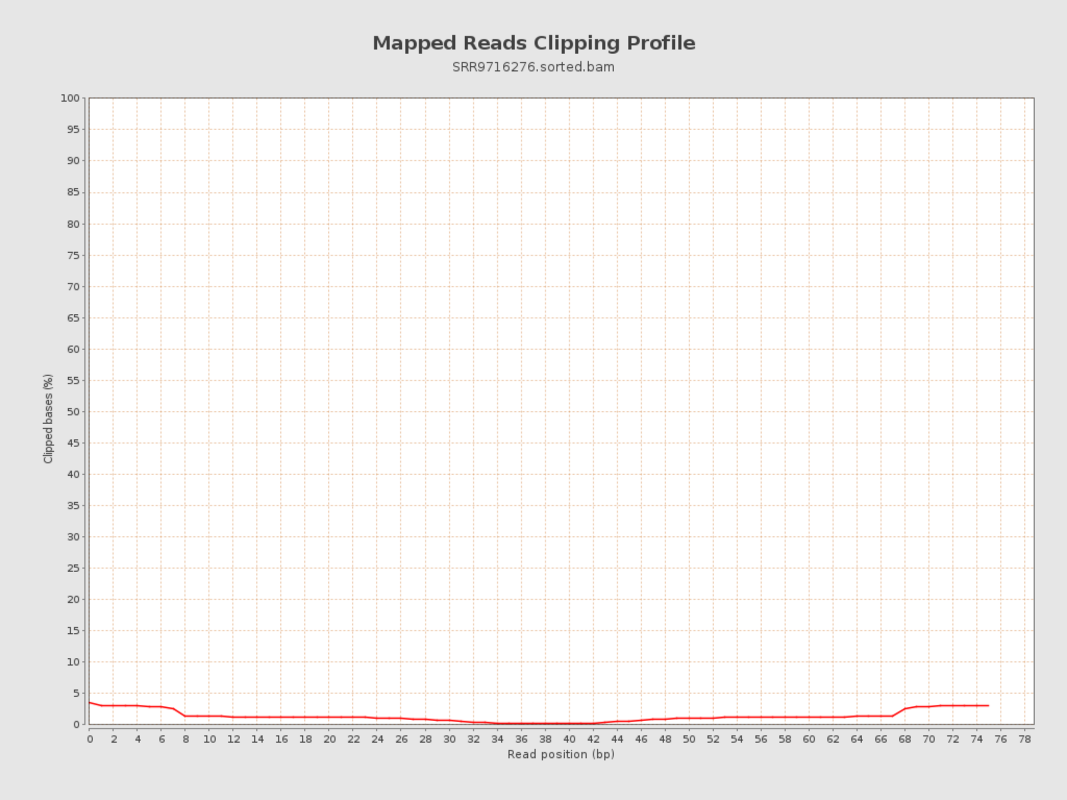
8. Results : Mapped Reads Nucleotide Content



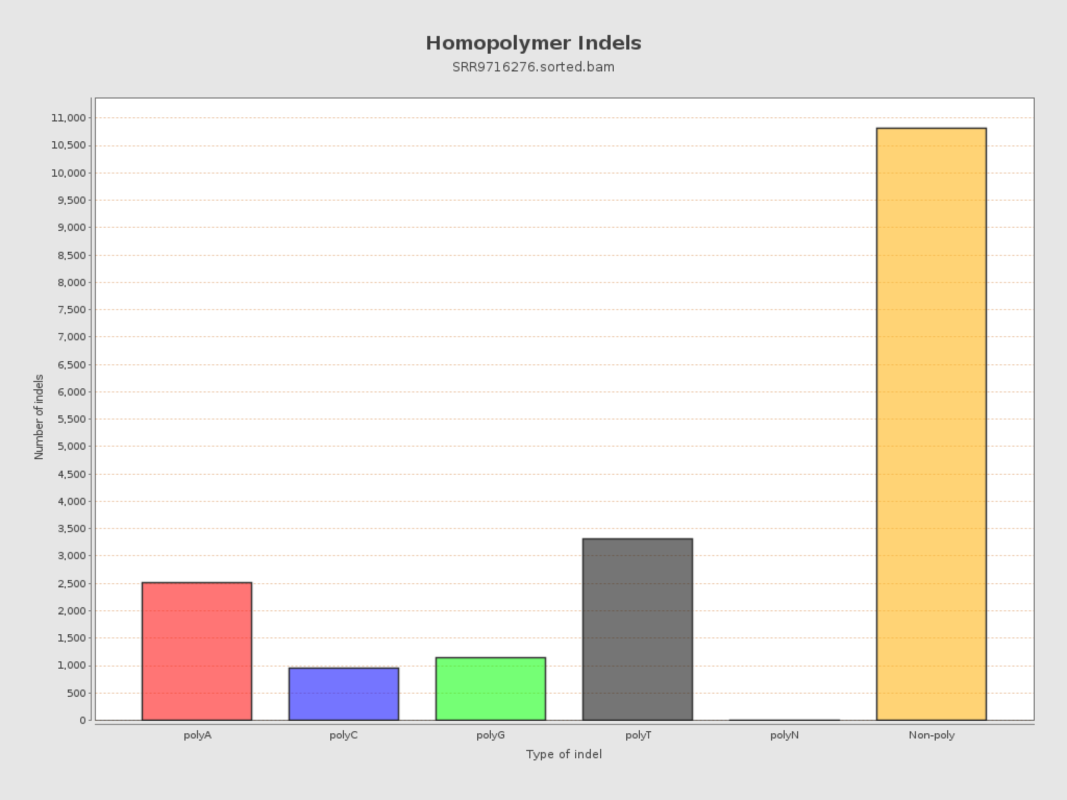
9. Results : Mapped Reads GC-content Distribution



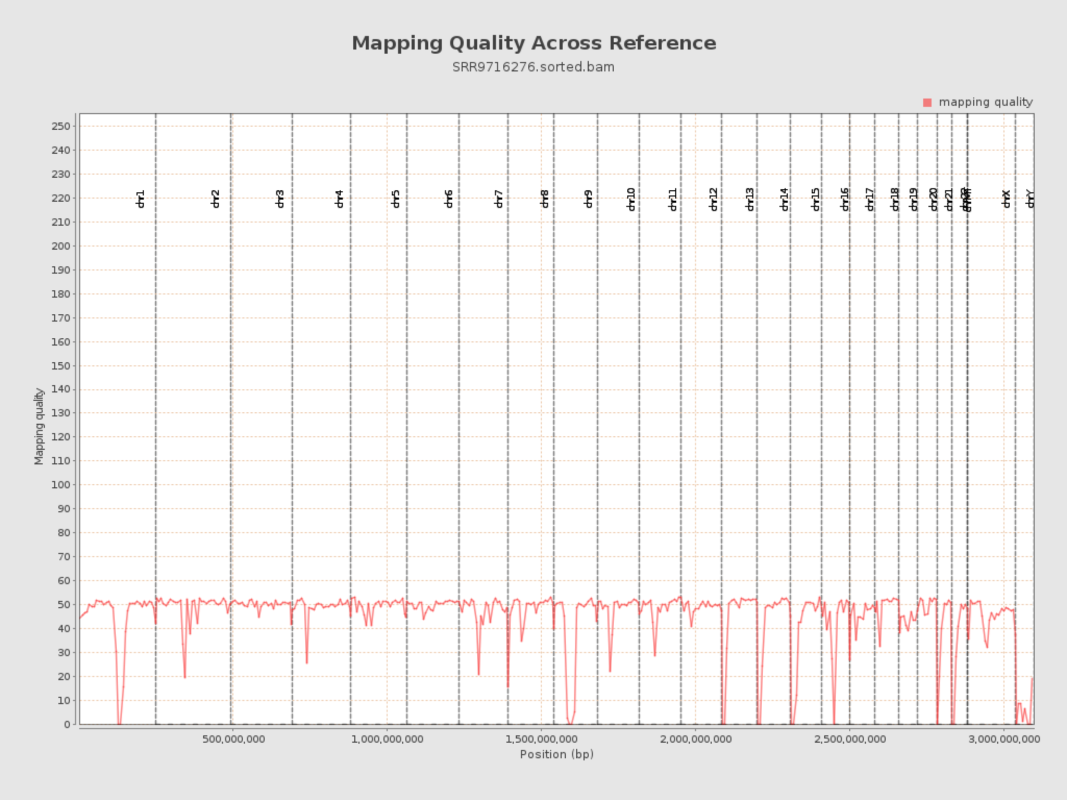
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram