Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:49:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716440.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_SRR9716440 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716440.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:49:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716440.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,222,694
Mapped reads	1,119,881 / 91.59%
Unmapped reads	102,813 / 8.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,468 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	32,618 / 2.67%
Duplication rate	1.99%
Clipped reads	1,121,061 / 91.69%

2.2. ACGT Content

Number/percentage of A's	15,573,783 / 24.21%
Number/percentage of C's	11,755,996 / 18.27%
Number/percentage of T's	21,035,928 / 32.7%
Number/percentage of G's	15,970,633 / 24.82%
Number/percentage of N's	1,232 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0208

Standard Deviation	0.2121

2.4. Mapping Quality

Mean Mapping Quality	43.76

2.5. Mismatches and indels

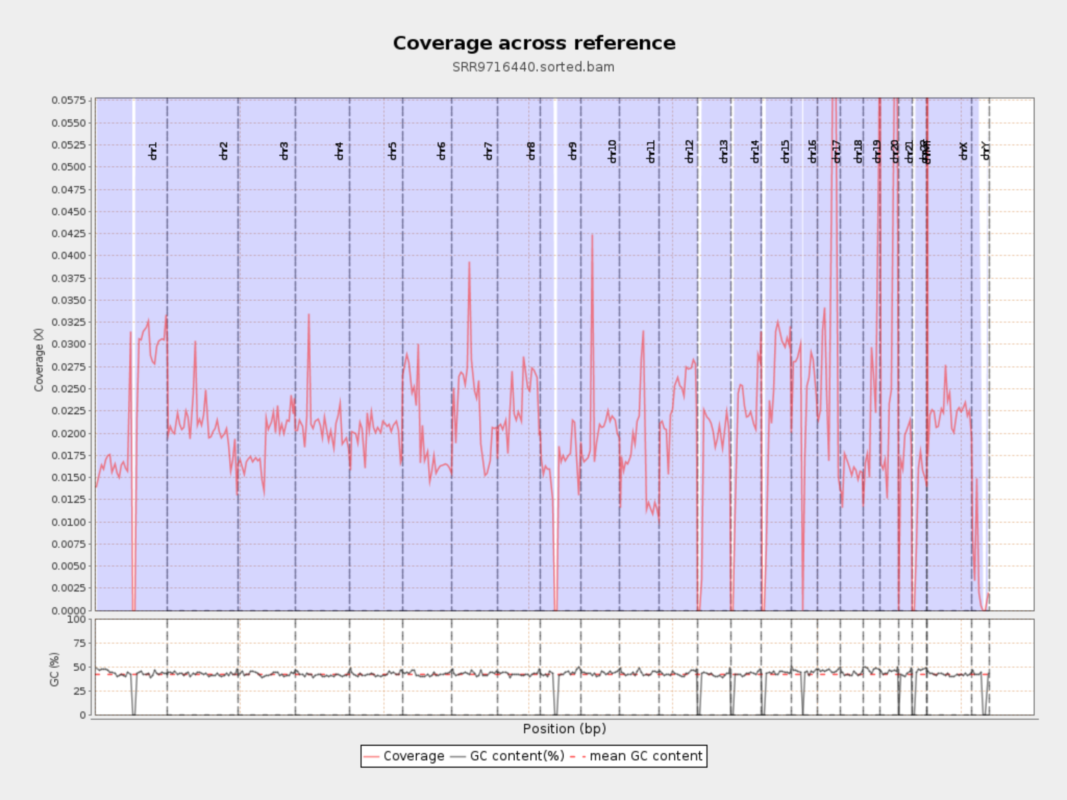
General error rate	0.53%
Mismatches	329,621
Insertions	4,384
Mapped reads with at least one insertion	0.39%
Deletions	12,181
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.56%

2.6. Chromosome stats

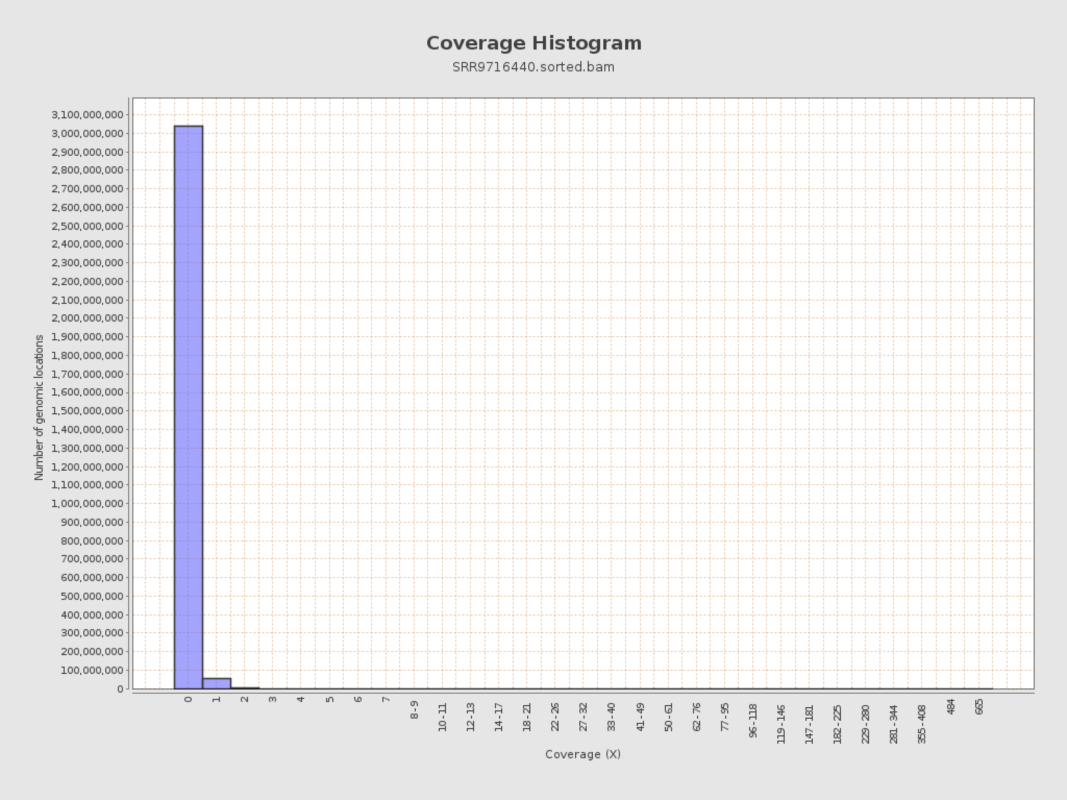
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5398267	0.0217	0.3063
chr2	243199373	5031459	0.0207	0.3095
chr3	198022430	3763819	0.019	0.1499
chr4	191154276	4005936	0.021	0.1703
chr5	180915260	3663219	0.0202	0.1513
chr6	171115067	3450640	0.0202	0.1711
chr7	159138663	3690800	0.0232	0.284

chr8	146364022	3426563	0.0234	0.2535
chr9	141213431	2132671	0.0151	0.1566
chr10	135534747	2832801	0.0209	0.2243
chr11	135006516	2326133	0.0172	0.1728
chr12	133851895	3208517	0.024	0.1662
chr13	115169878	1977296	0.0172	0.1408
chr14	107349540	2149177	0.02	0.1535
chr15	102531392	2359886	0.023	0.1628
chr16	90354753	2157339	0.0239	0.1746
chr17	81195210	2787995	0.0343	0.2026
chr18	78077248	1205616	0.0154	0.2462
chr19	59128983	1602997	0.0271	0.2649
chr20	63025520	2044772	0.0324	0.1968
chr21	48129895	823559	0.0171	0.1594
chr22	51304566	581249	0.0113	0.1123
chrMT	16571	52968	3.1964	2.4182
chrX	155270560	3463600	0.0223	0.1718
chrY	59373566	219722	0.0037	0.1597

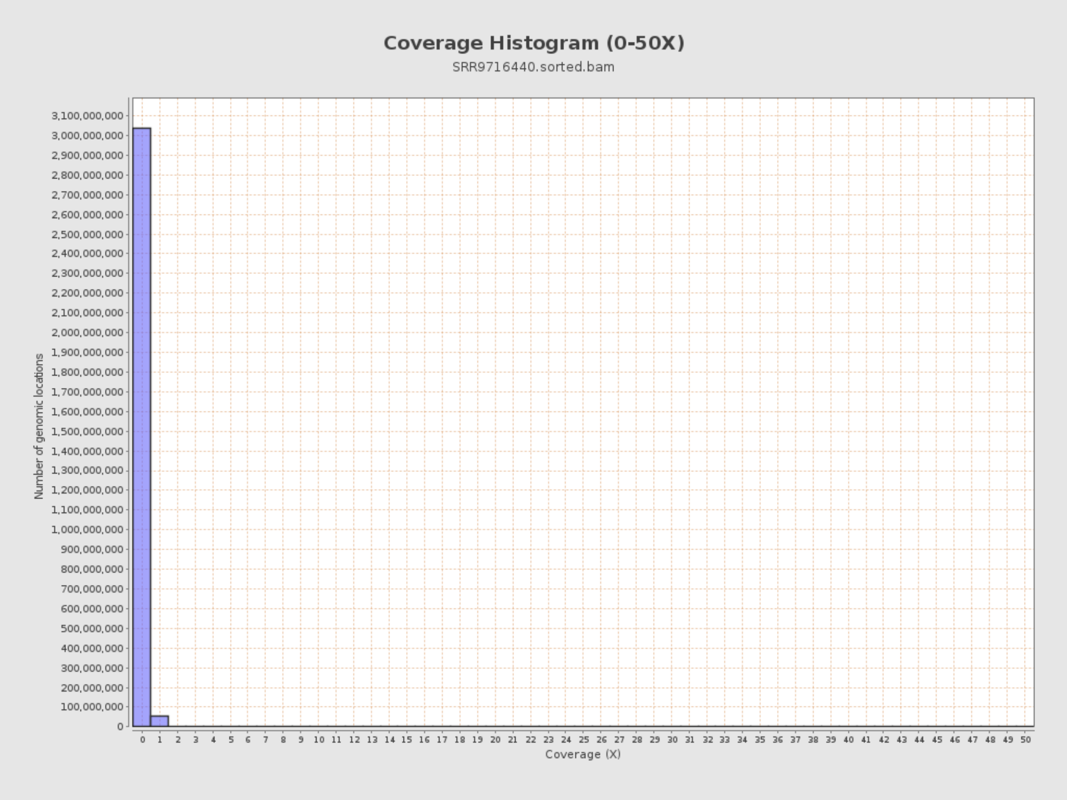
3. Results : Coverage across reference



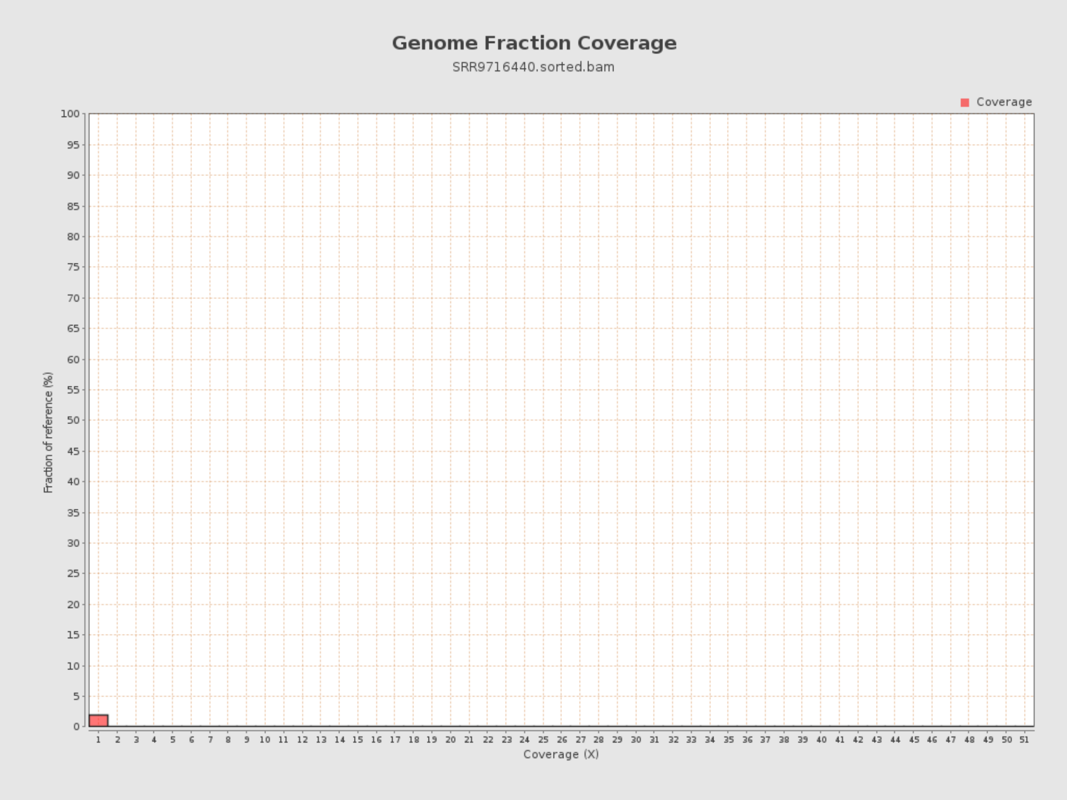
4. Results : Coverage Histogram



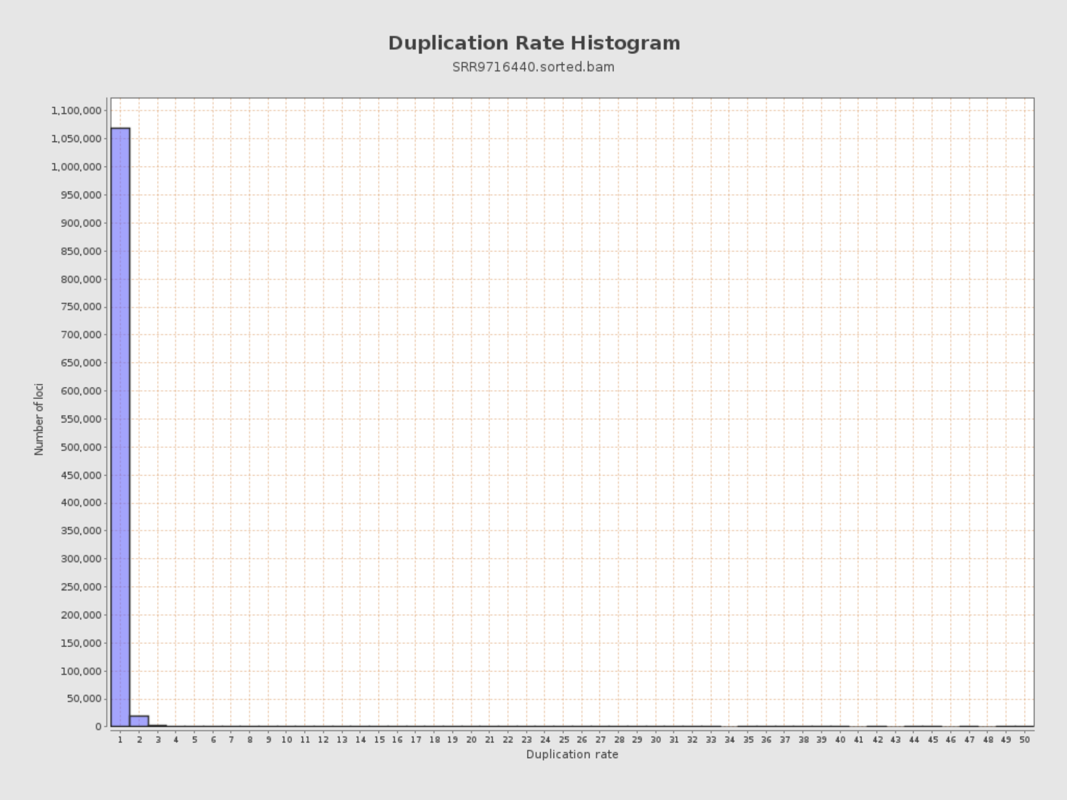
5. Results : Coverage Histogram (0-50X)



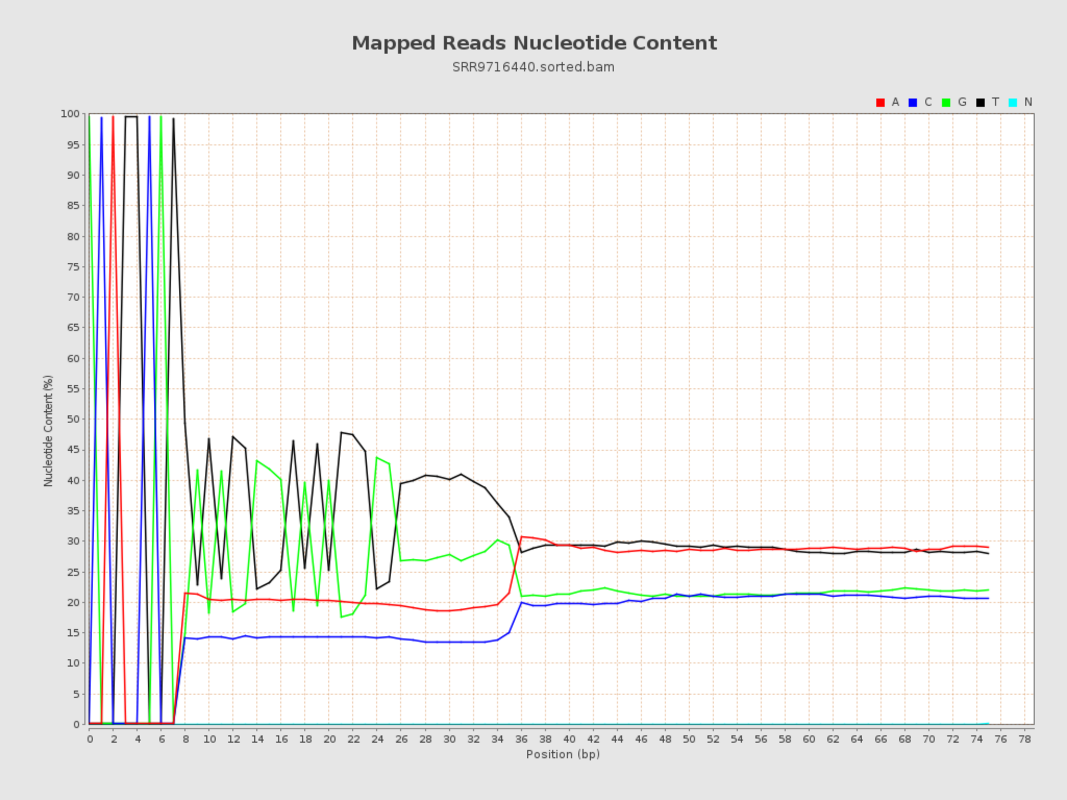
6. Results : Genome Fraction Coverage



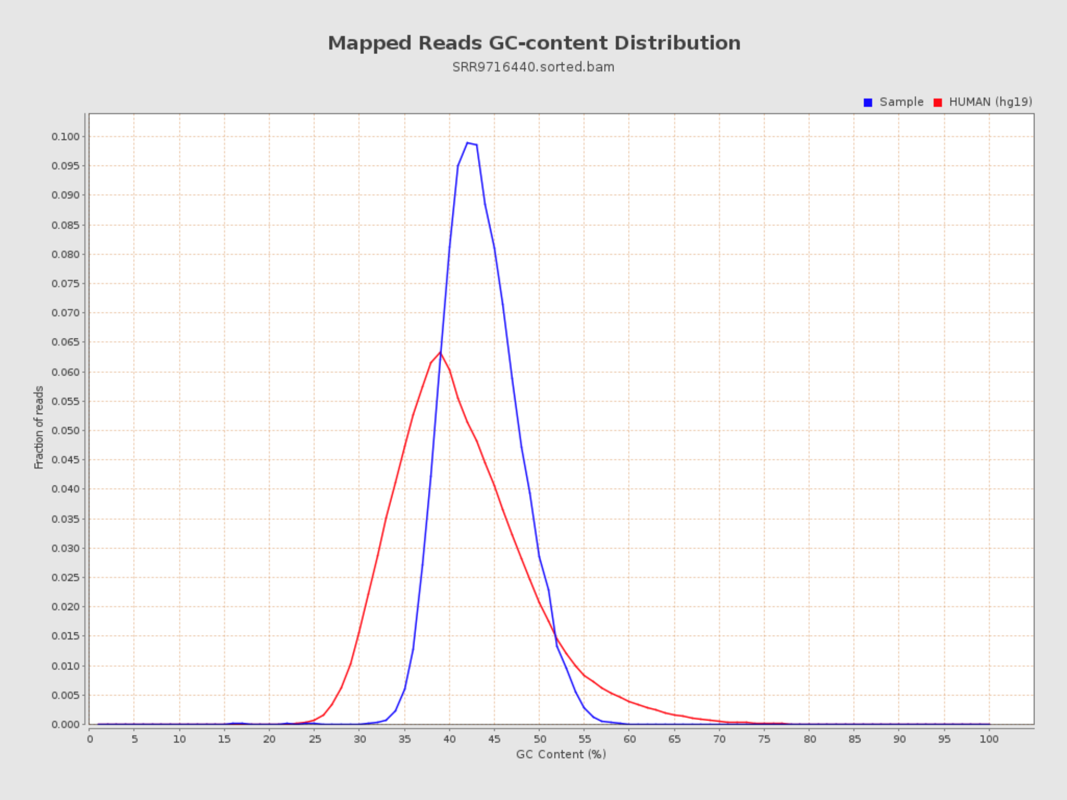
7. Results : Duplication Rate Histogram



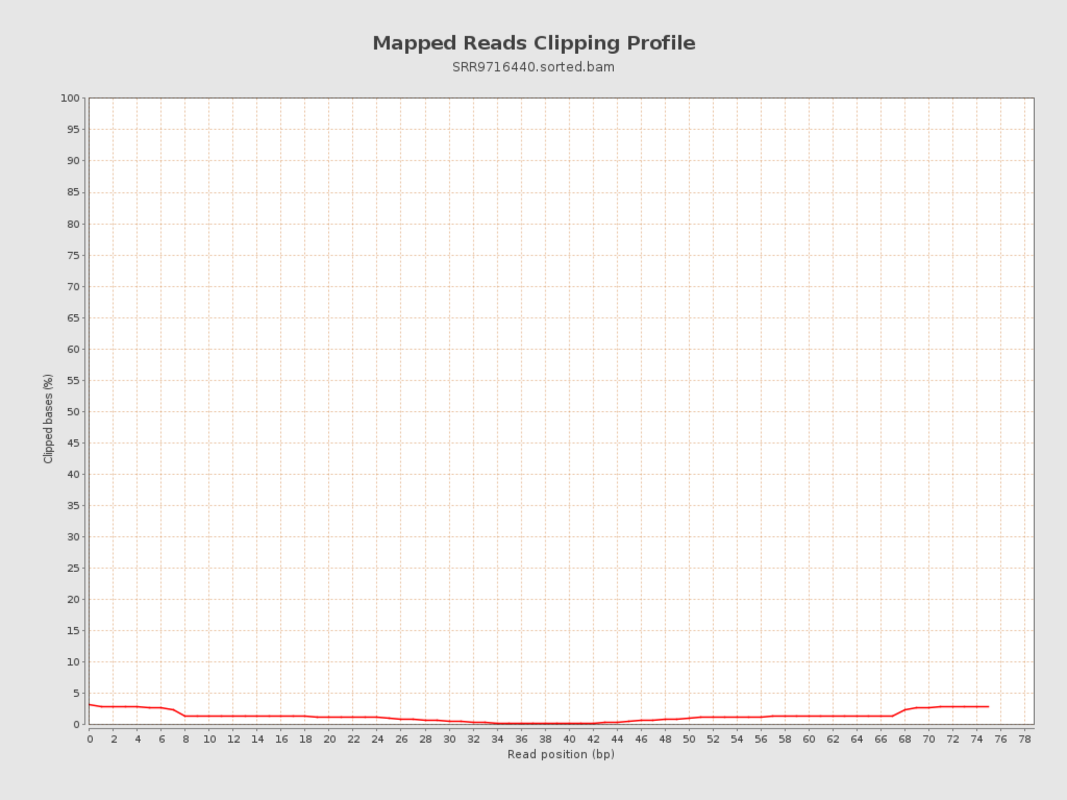
8. Results : Mapped Reads Nucleotide Content



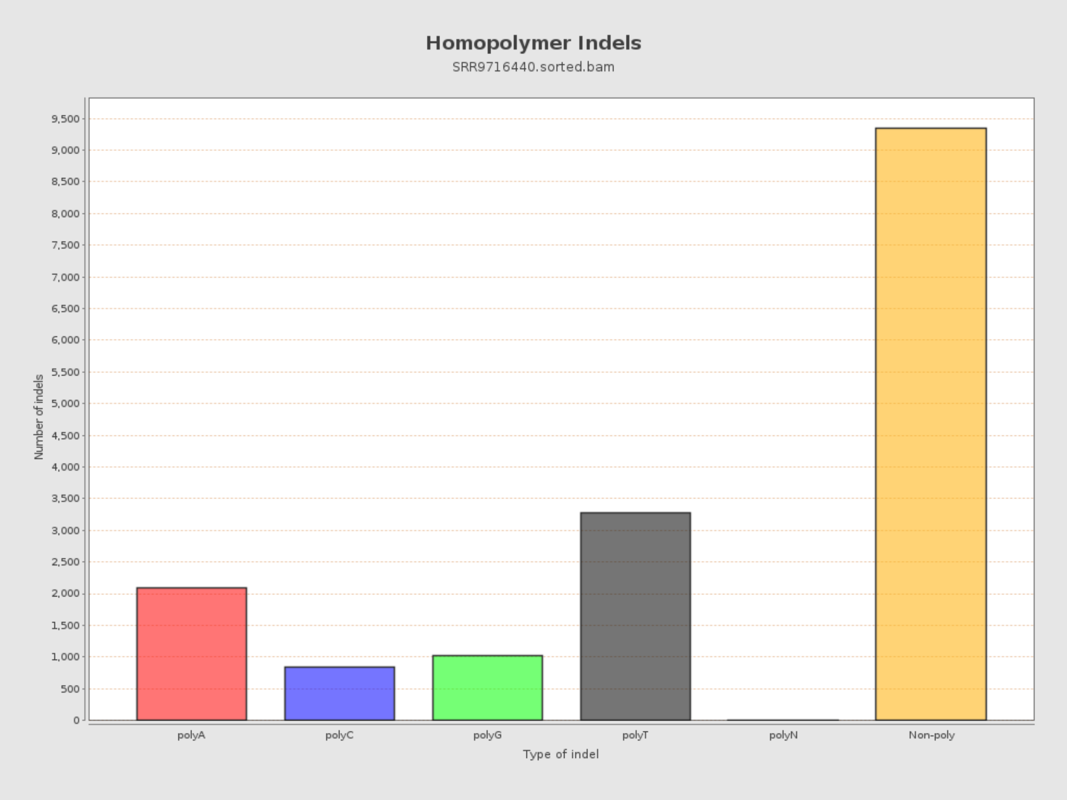
9. Results : Mapped Reads GC-content Distribution



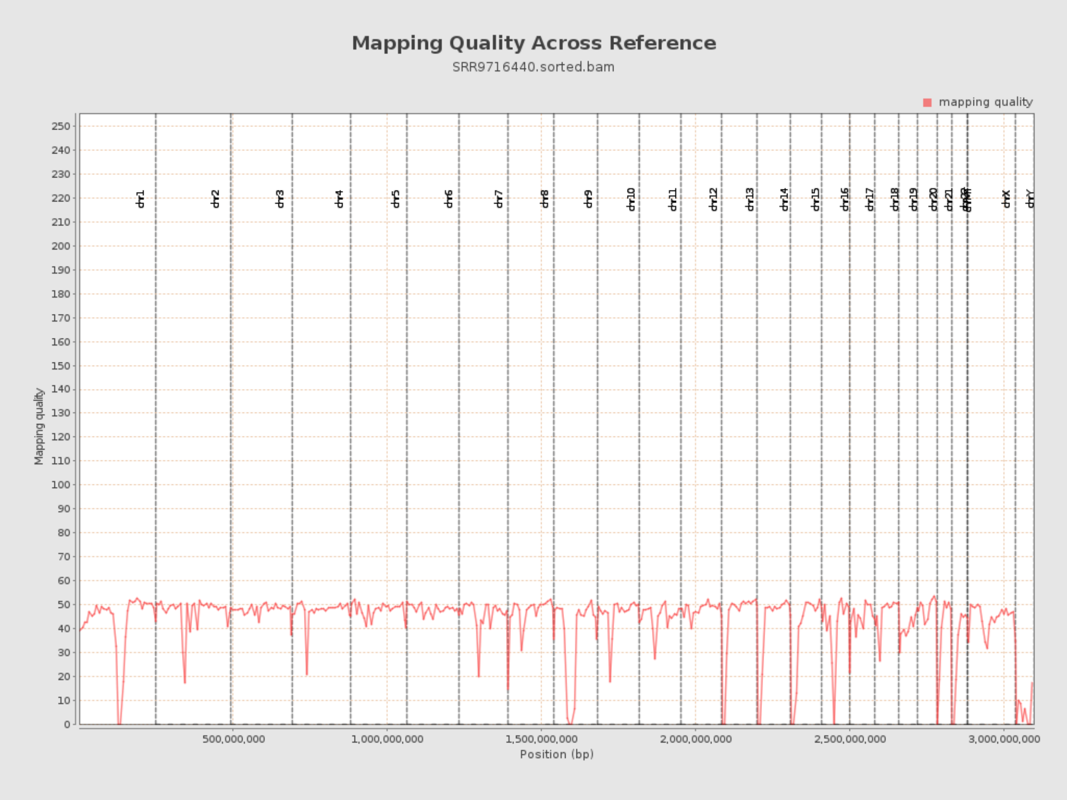
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram