Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:14:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716460.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_SRR9716460 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716460.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:14:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716460.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,395,338
Mapped reads	1,264,878 / 90.65%
Unmapped reads	130,460 / 9.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,368 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	33,852 / 2.43%
Duplication rate	1.99%
Clipped reads	1,267,734 / 90.85%

2.2. ACGT Content

Number/percentage of A's	18,345,924 / 24.9%
Number/percentage of C's	13,840,133 / 18.78%
Number/percentage of T's	22,471,406 / 30.5%
Number/percentage of G's	19,021,929 / 25.82%
Number/percentage of N's	676 / 0%
GC Percentage	44.6%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.207

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

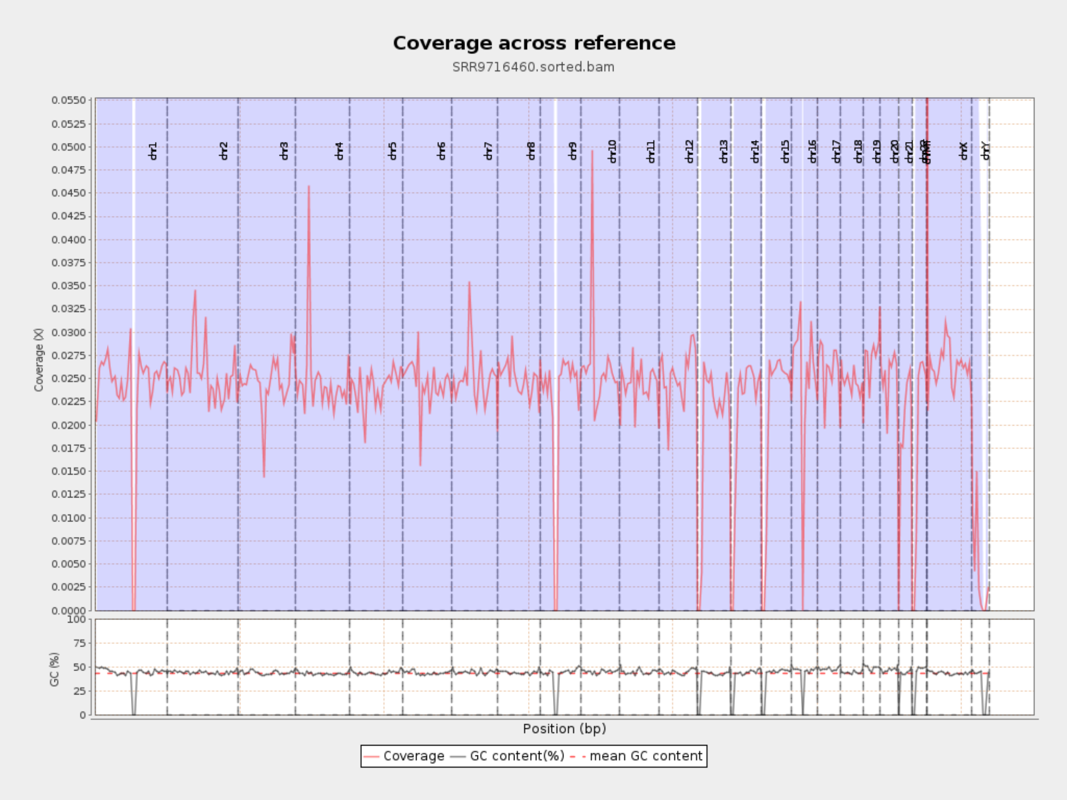
General error rate	0.53%
Mismatches	382,696
Insertions	4,385
Mapped reads with at least one insertion	0.34%
Deletions	14,046
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.26%

2.6. Chromosome stats

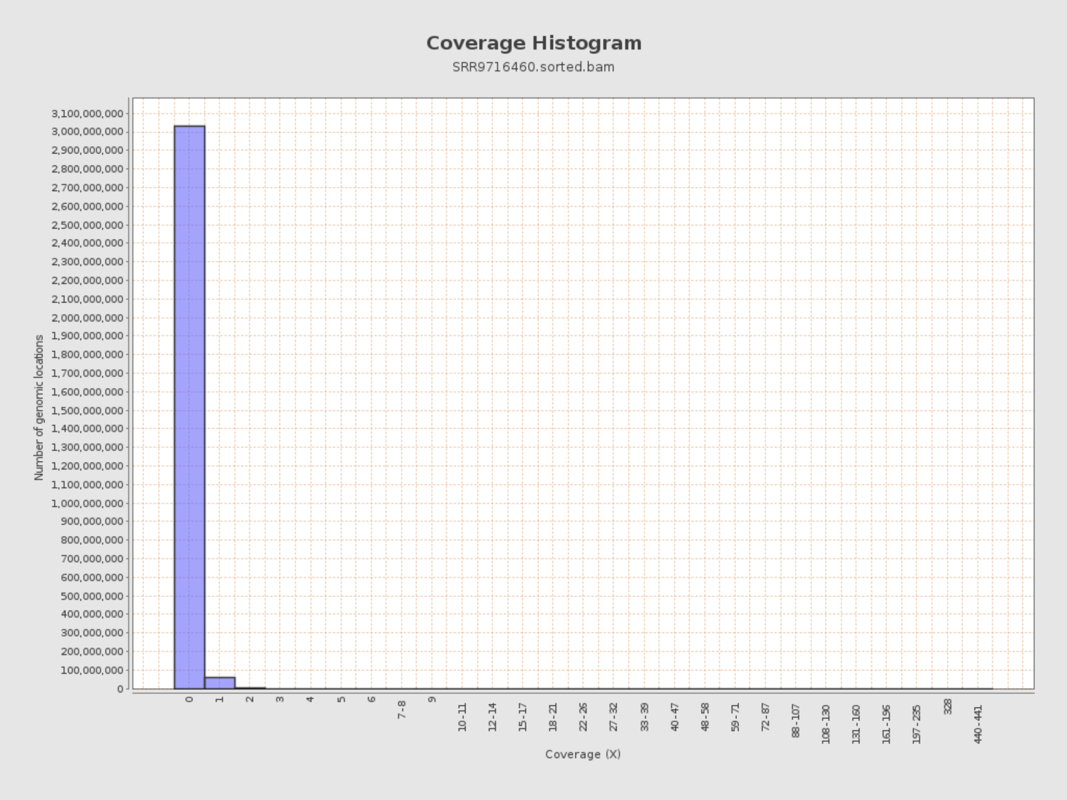
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5913433	0.0237	0.2533
chr2	243199373	6150518	0.0253	0.281
chr3	198022430	4888945	0.0247	0.1711
chr4	191154276	4751539	0.0249	0.1935
chr5	180915260	4373043	0.0242	0.1673
chr6	171115067	4192156	0.0245	0.1871
chr7	159138663	4026385	0.0253	0.2537

chr8	146364022	3663984	0.025	0.2063
chr9	141213431	3140557	0.0222	0.1821
chr10	135534747	3568481	0.0263	0.2707
chr11	135006516	3325865	0.0246	0.1944
chr12	133851895	3389474	0.0253	0.1733
chr13	115169878	2265733	0.0197	0.1507
chr14	107349540	2224027	0.0207	0.1613
chr15	102531392	2146999	0.0209	0.1576
chr16	90354753	2228925	0.0247	0.184
chr17	81195210	2117377	0.0261	0.1803
chr18	78077248	1925514	0.0247	0.2611
chr19	59128983	1607545	0.0272	0.2359
chr20	63025520	1583334	0.0251	0.1777
chr21	48129895	947668	0.0197	0.1697
chr22	51304566	916108	0.0179	0.1464
chrMT	16571	6312	0.3809	0.6182
chrX	155270560	4102645	0.0264	0.1853
chrY	59373566	246006	0.0041	0.1391

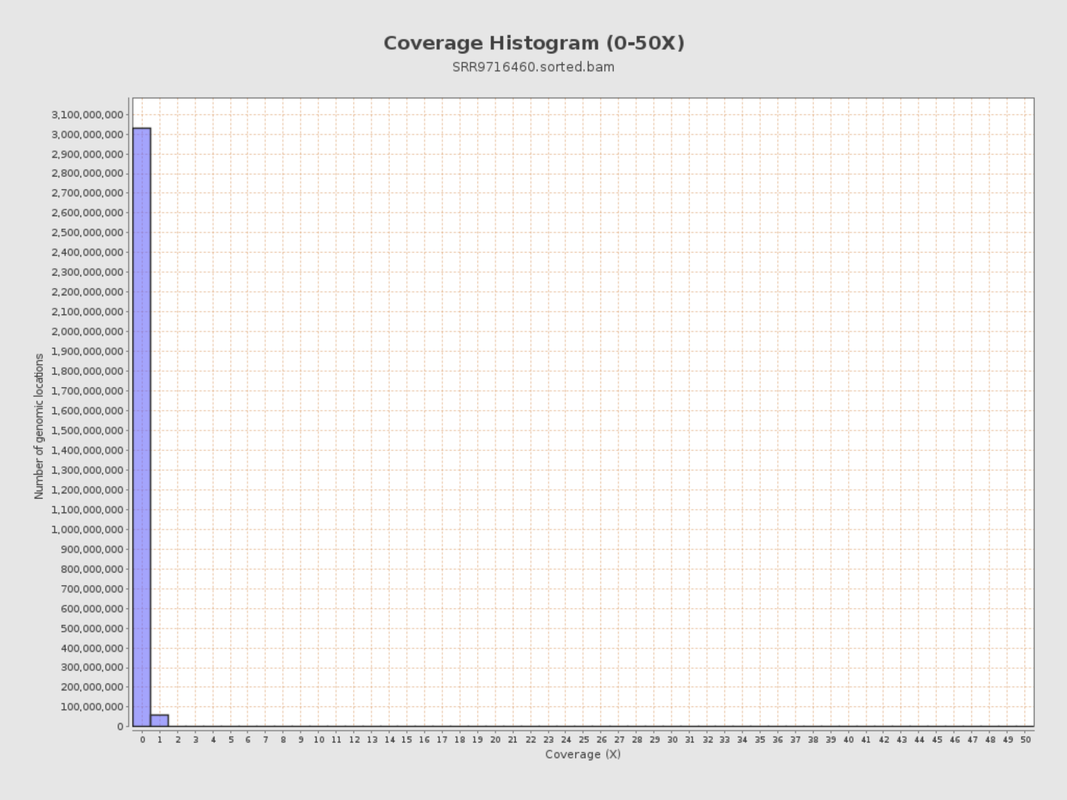
3. Results : Coverage across reference



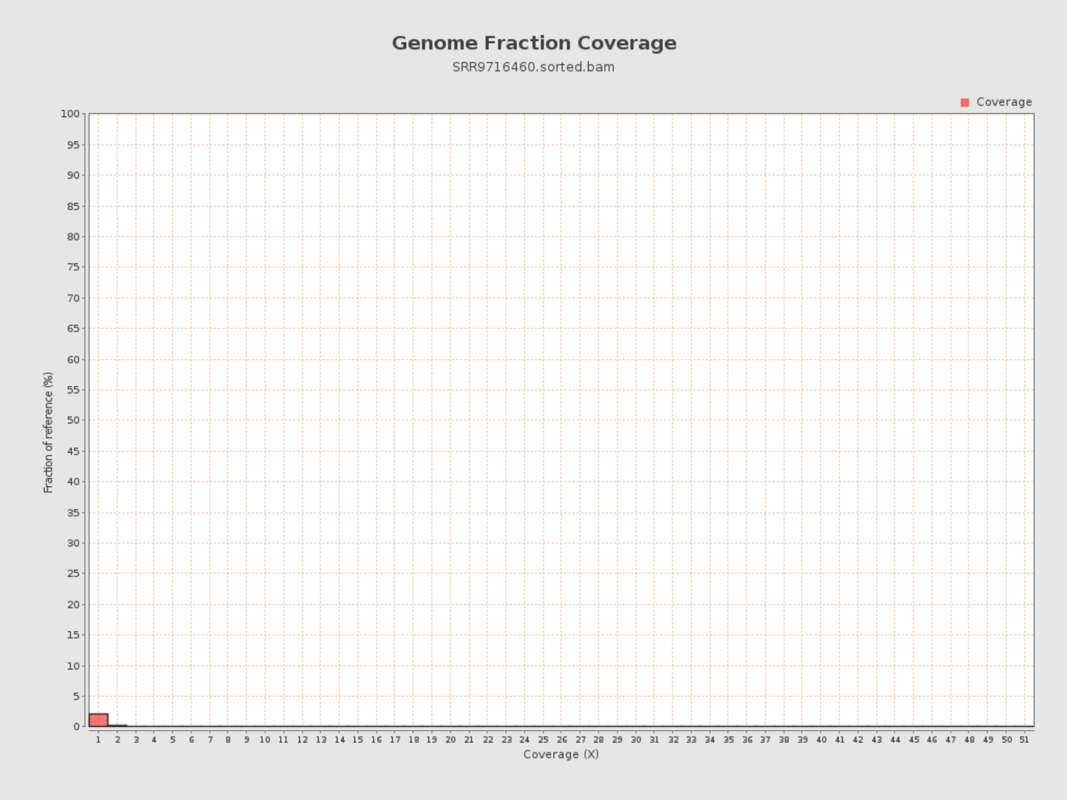
4. Results : Coverage Histogram



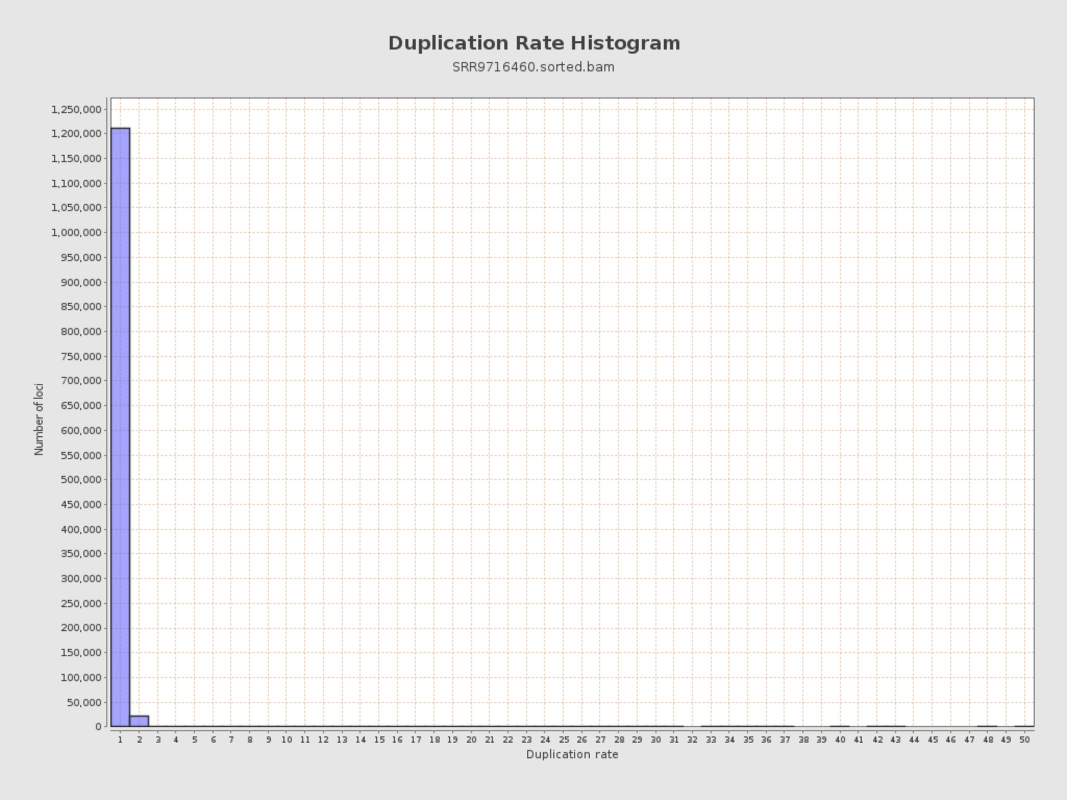
5. Results : Coverage Histogram (0-50X)



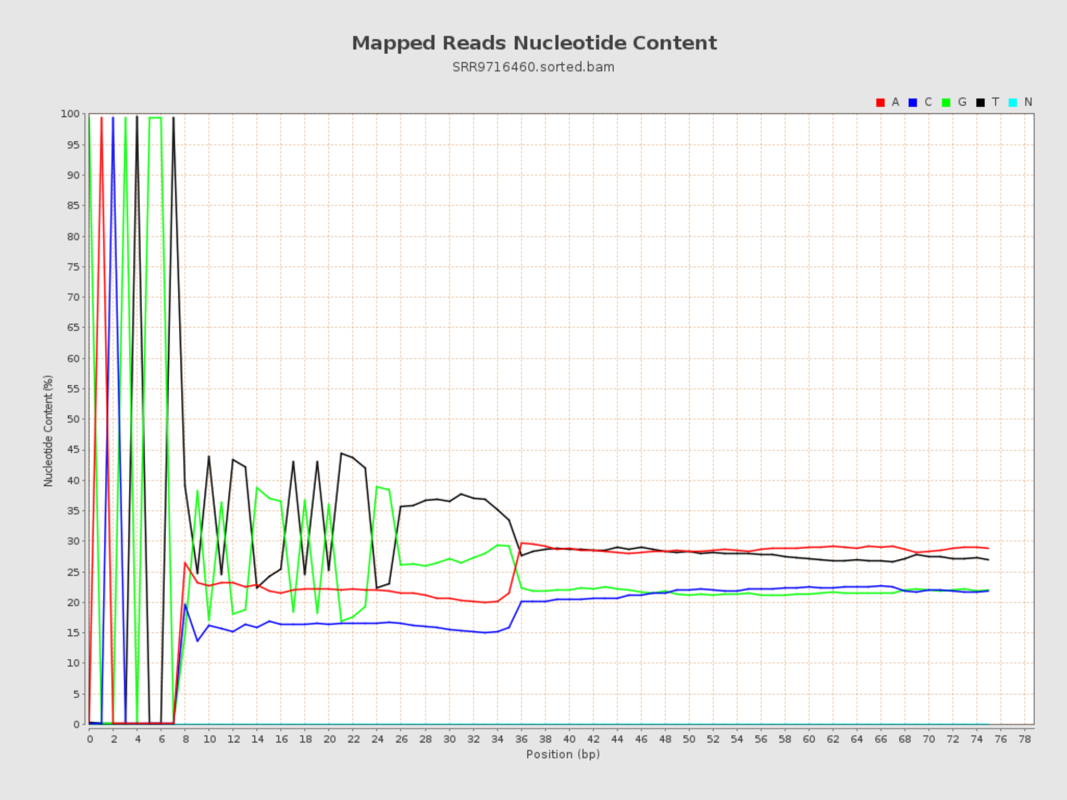
6. Results : Genome Fraction Coverage



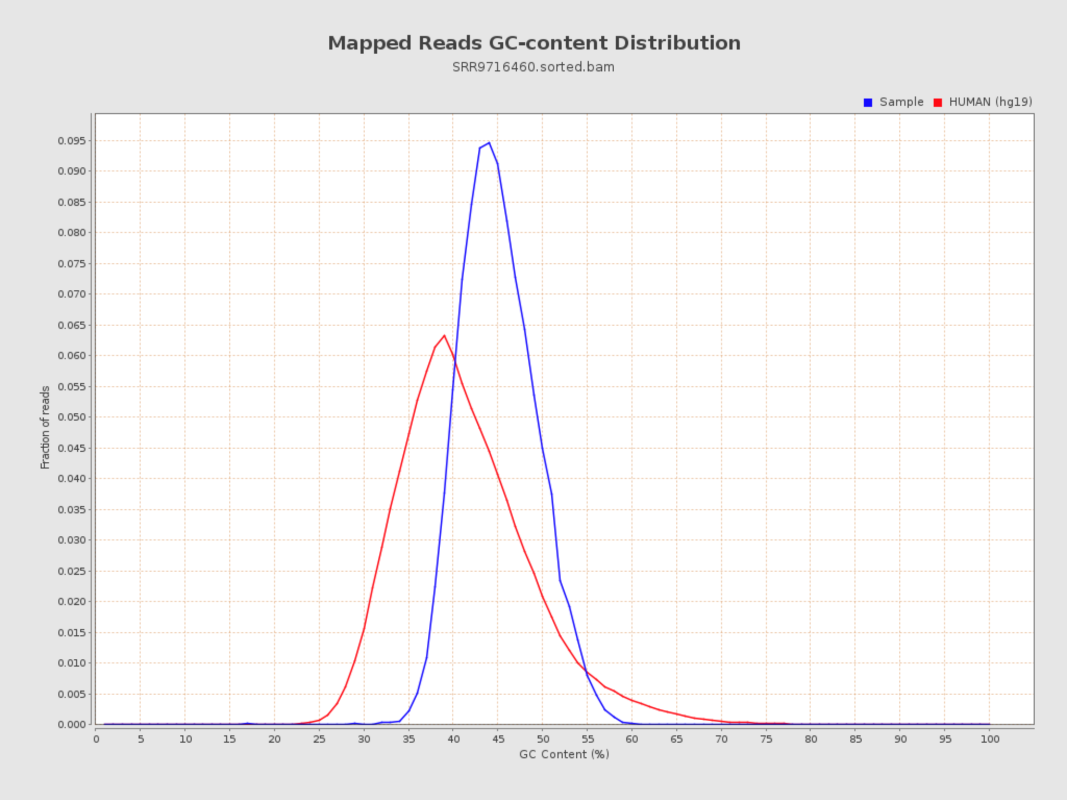
7. Results : Duplication Rate Histogram



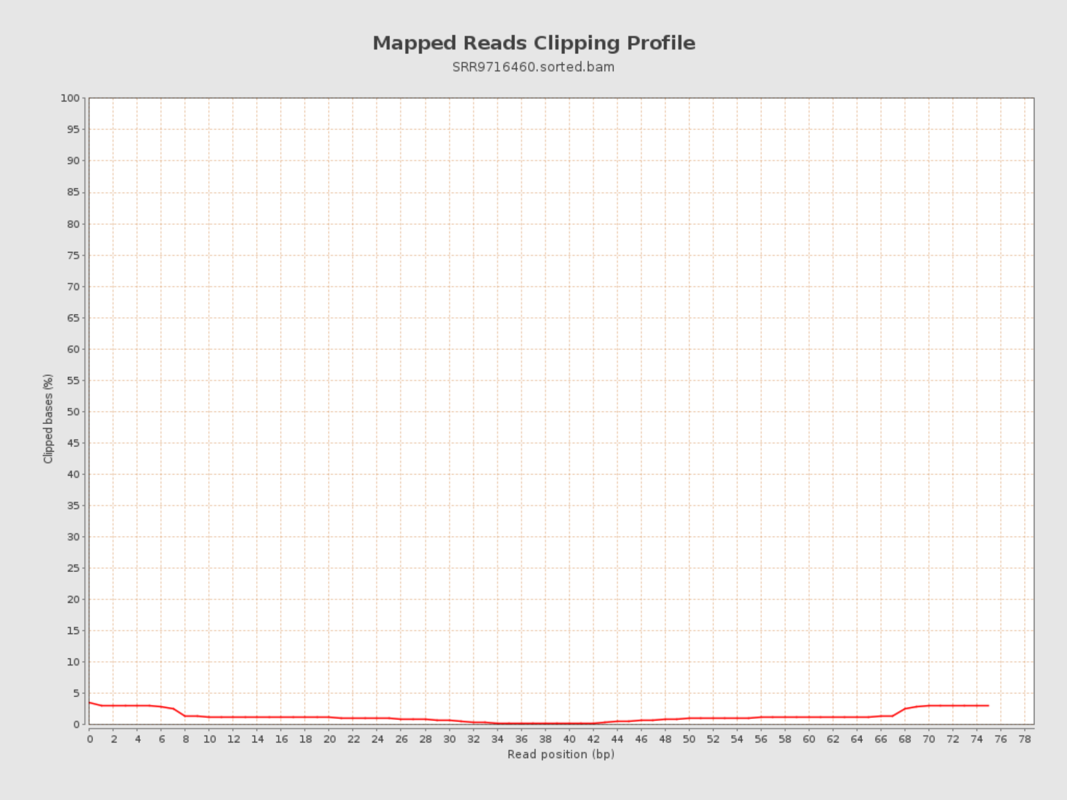
8. Results : Mapped Reads Nucleotide Content



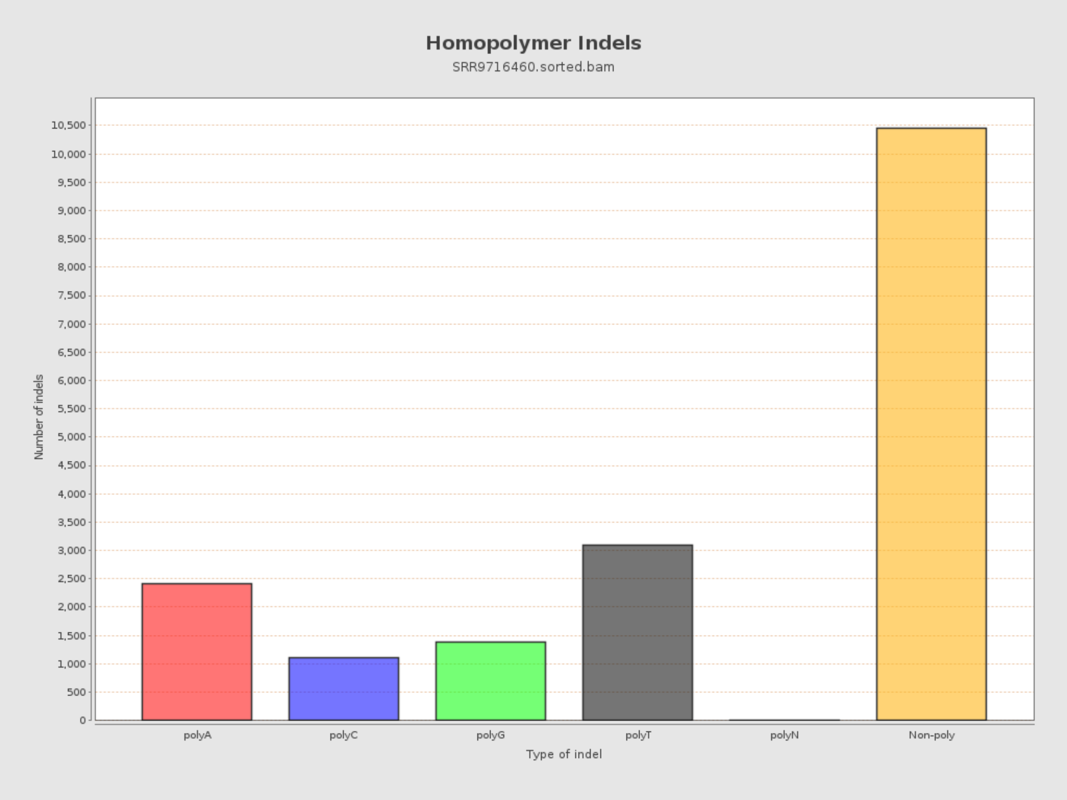
9. Results : Mapped Reads GC-content Distribution



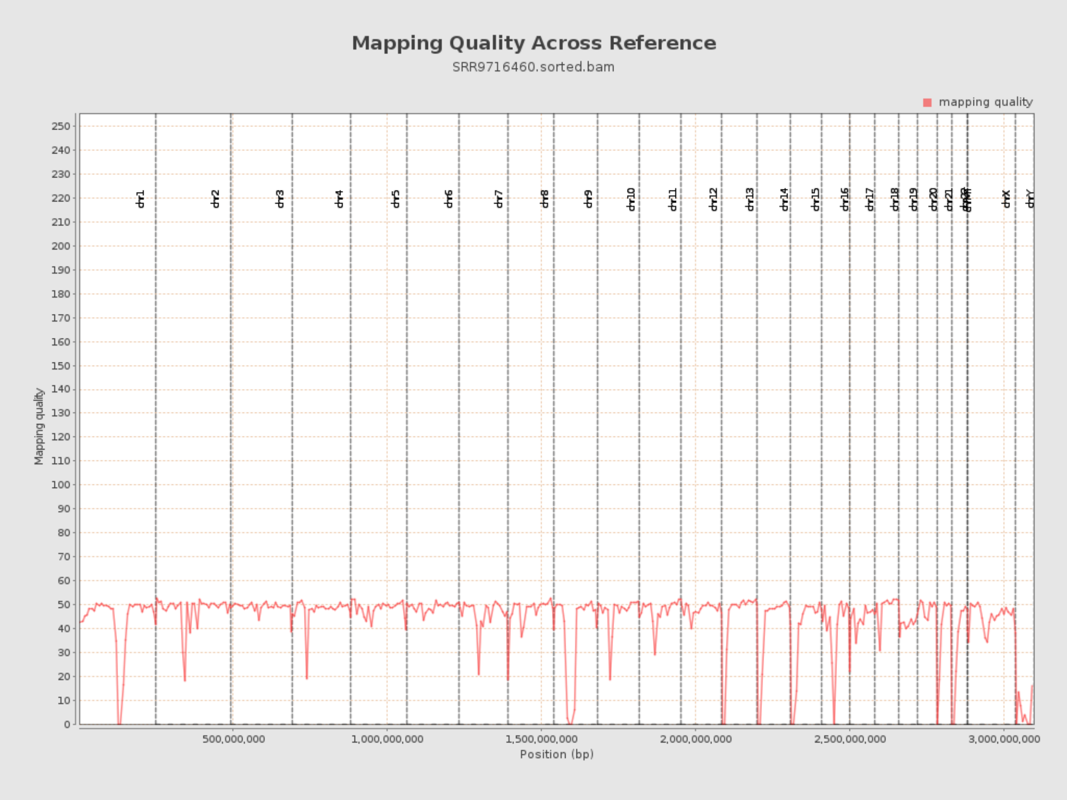
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram