Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:26:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716761.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_SRR9716761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:26:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,155,183
Mapped reads	979,132 / 84.76%
Unmapped reads	176,051 / 15.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,786 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	18,495 / 1.6%
Duplication rate	1.33%
Clipped reads	979,595 / 84.8%

2.2. ACGT Content

Number/percentage of A's	13,167,093 / 24.04%
Number/percentage of C's	11,429,827 / 20.87%
Number/percentage of T's	16,501,150 / 30.13%
Number/percentage of G's	13,671,293 / 24.96%
Number/percentage of N's	1,443 / 0%
GC Percentage	45.83%

2.3. Coverage

Mean	0.0177

Standard Deviation	0.1655

2.4. Mapping Quality

Mean Mapping Quality	39.82

2.5. Mismatches and indels

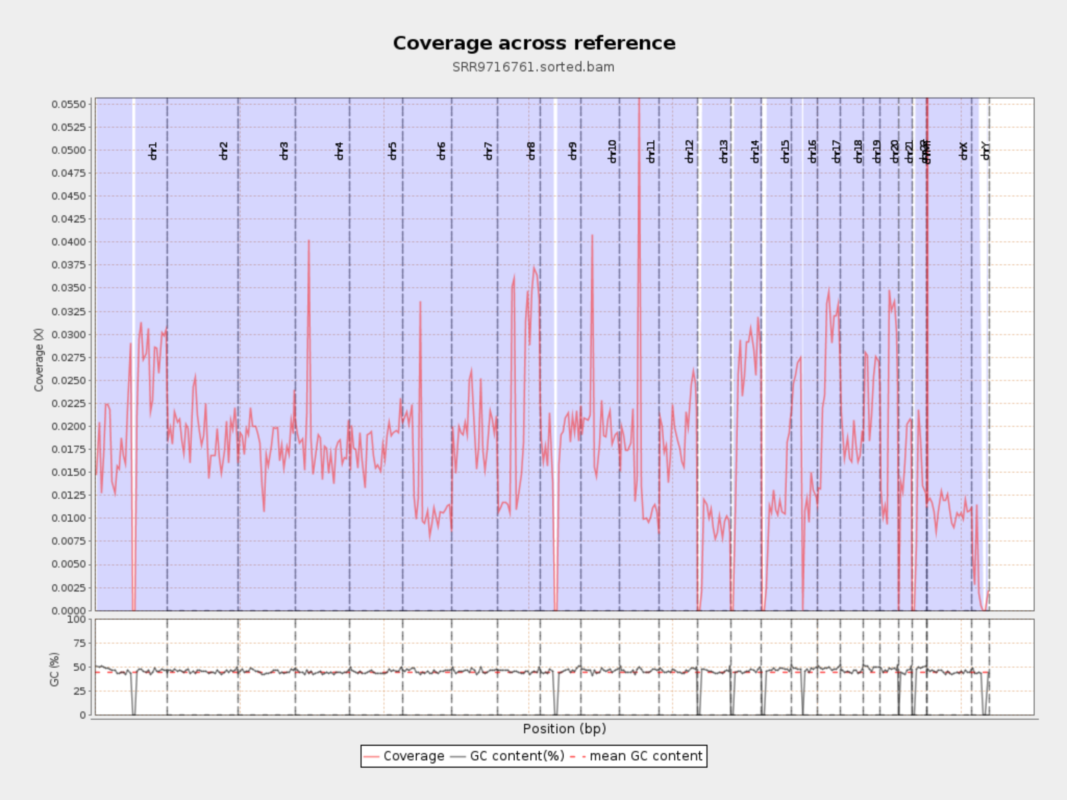
General error rate	0.54%
Mismatches	288,632
Insertions	4,262
Mapped reads with at least one insertion	0.43%
Deletions	9,097
Mapped reads with at least one deletion	0.92%
Homopolymer indels	37.73%

2.6. Chromosome stats

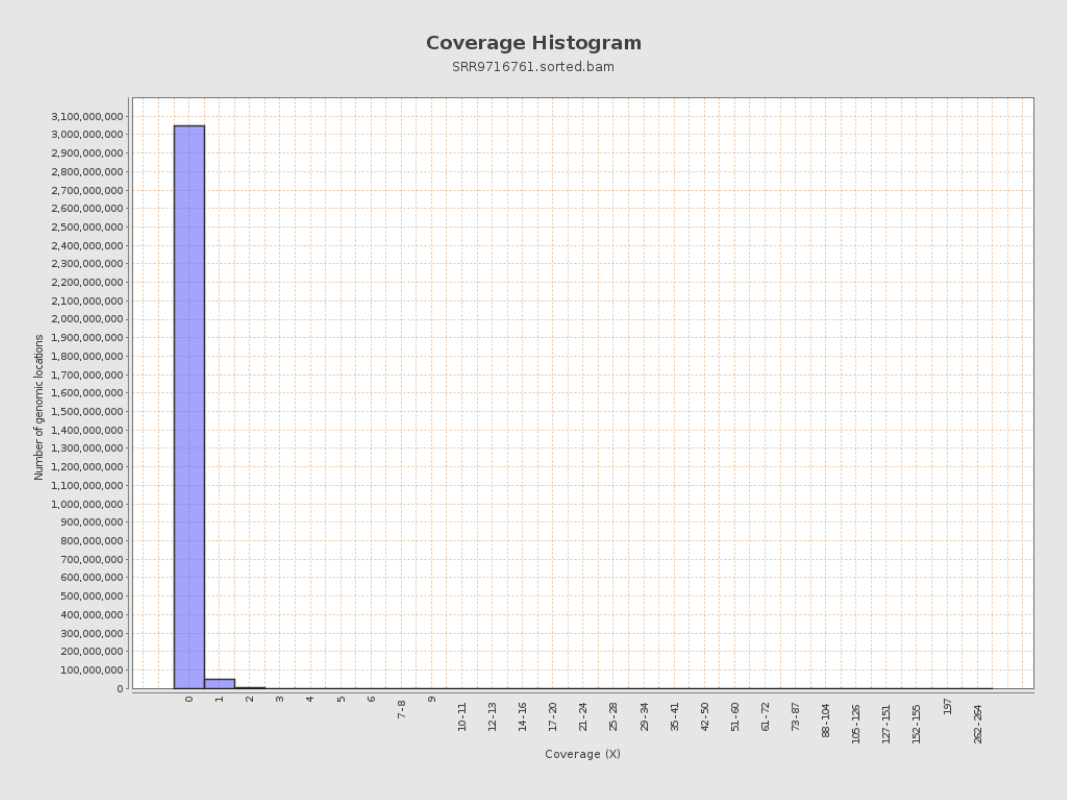
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5277837	0.0212	0.199
chr2	243199373	4657899	0.0192	0.2037
chr3	198022430	3588407	0.0181	0.1455
chr4	191154276	3520661	0.0184	0.1682
chr5	180915260	3268182	0.0181	0.1442
chr6	171115067	2355930	0.0138	0.128
chr7	159138663	3125652	0.0196	0.1858

chr8	146364022	3317532	0.0227	0.1703
chr9	141213431	2360389	0.0167	0.1523
chr10	135534747	2784865	0.0205	0.2395
chr11	135006516	2239773	0.0166	0.1601
chr12	133851895	2631981	0.0197	0.1509
chr13	115169878	945056	0.0082	0.096
chr14	107349540	2480675	0.0231	0.1657
chr15	102531392	1066288	0.0104	0.1119
chr16	90354753	1483834	0.0164	0.1469
chr17	81195210	2164480	0.0267	0.1827
chr18	78077248	1404771	0.018	0.188
chr19	59128983	1460654	0.0247	0.1925
chr20	63025520	1409119	0.0224	0.1651
chr21	48129895	749802	0.0156	0.1493
chr22	51304566	592672	0.0116	0.116
chrMT	16571	17121	1.0332	1.3753
chrX	155270560	1705271	0.011	0.1212
chrY	59373566	176718	0.003	0.0991

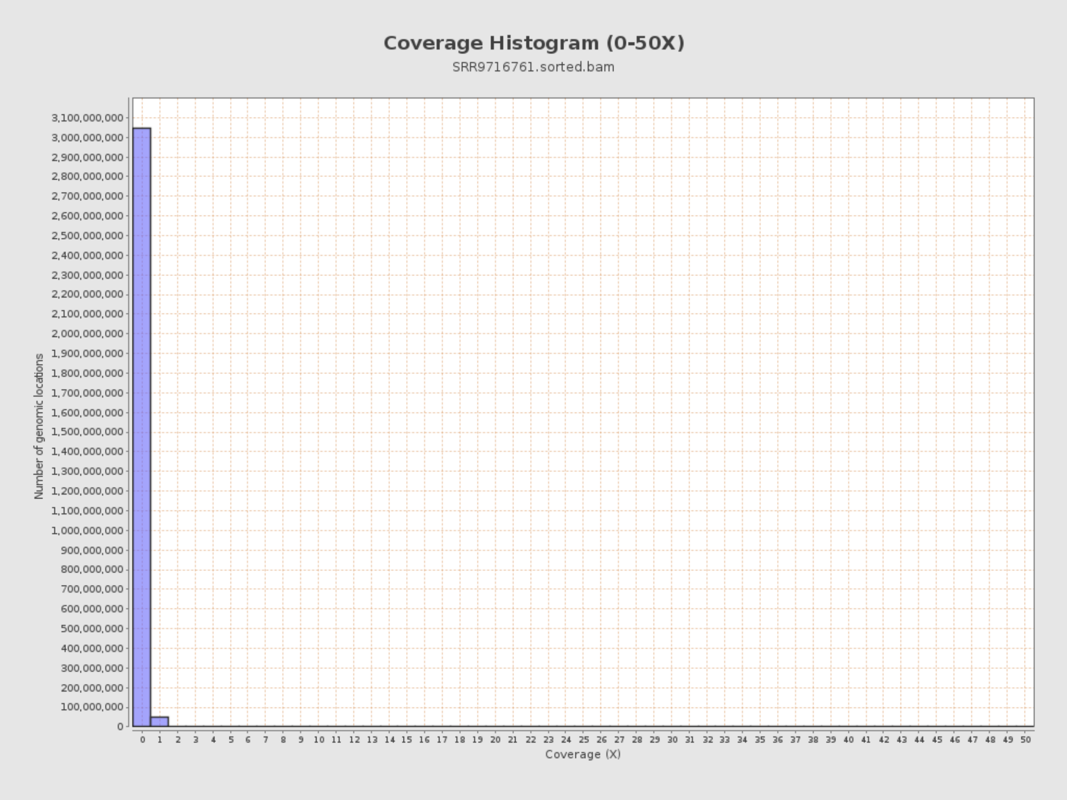
3. Results : Coverage across reference



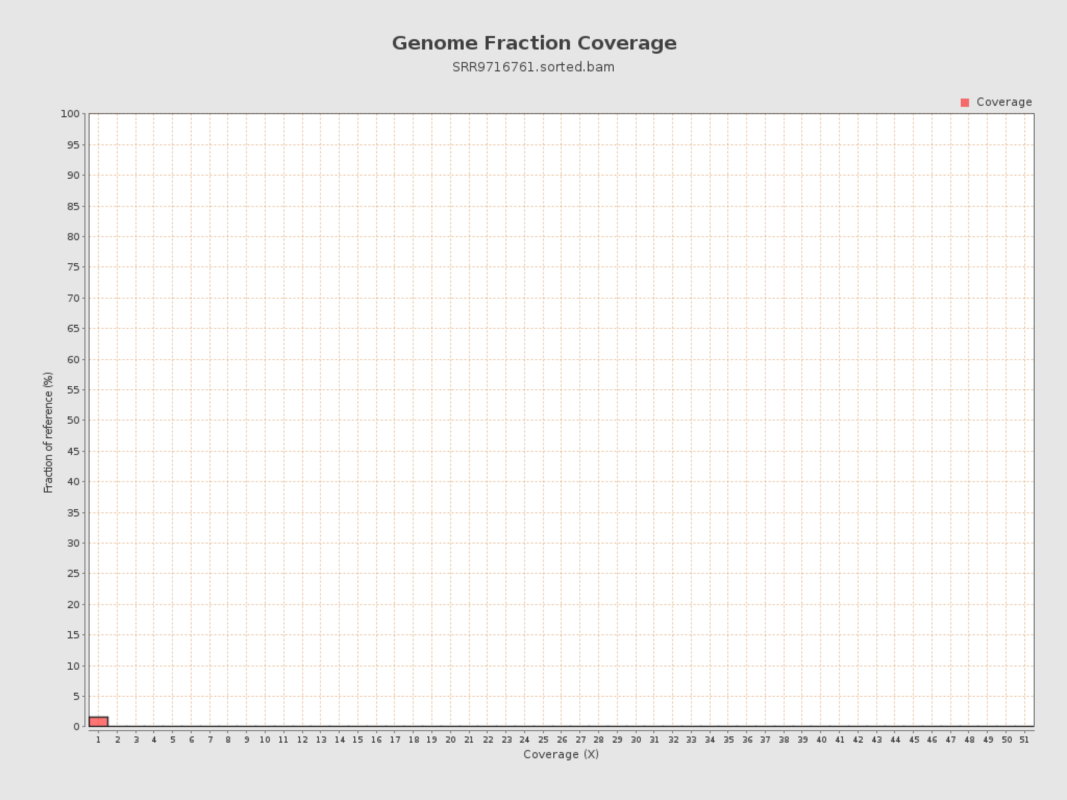
4. Results : Coverage Histogram



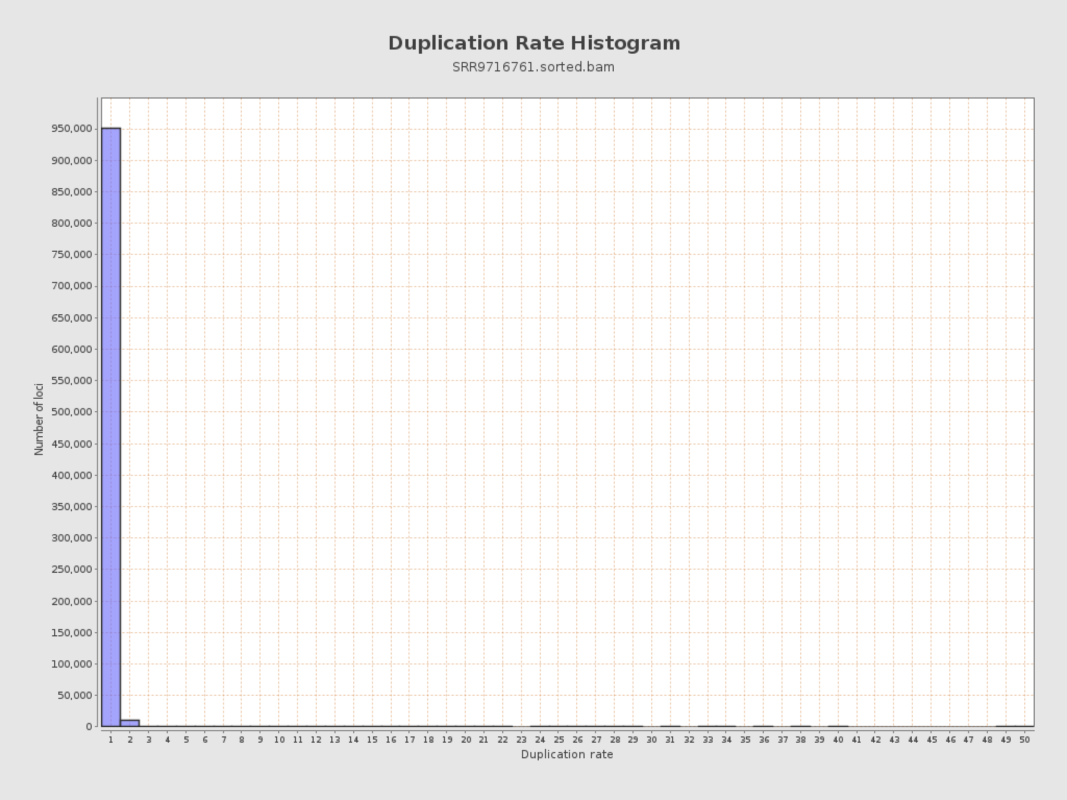
5. Results : Coverage Histogram (0-50X)



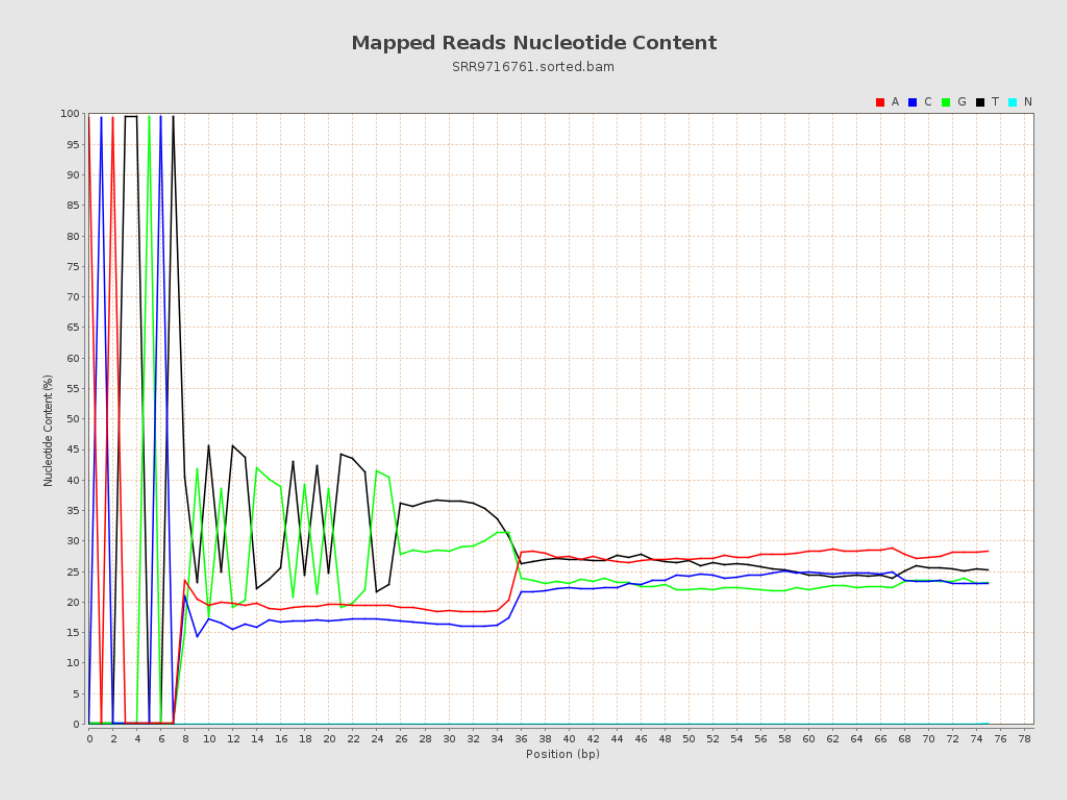
6. Results : Genome Fraction Coverage



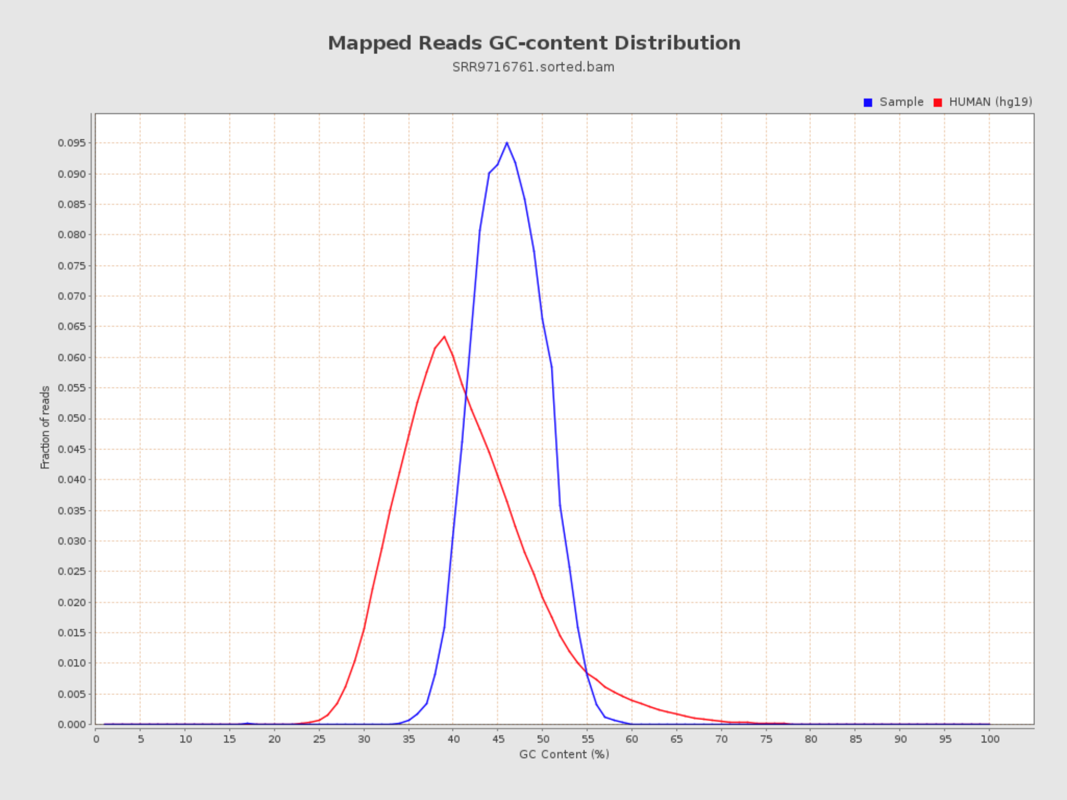
7. Results : Duplication Rate Histogram



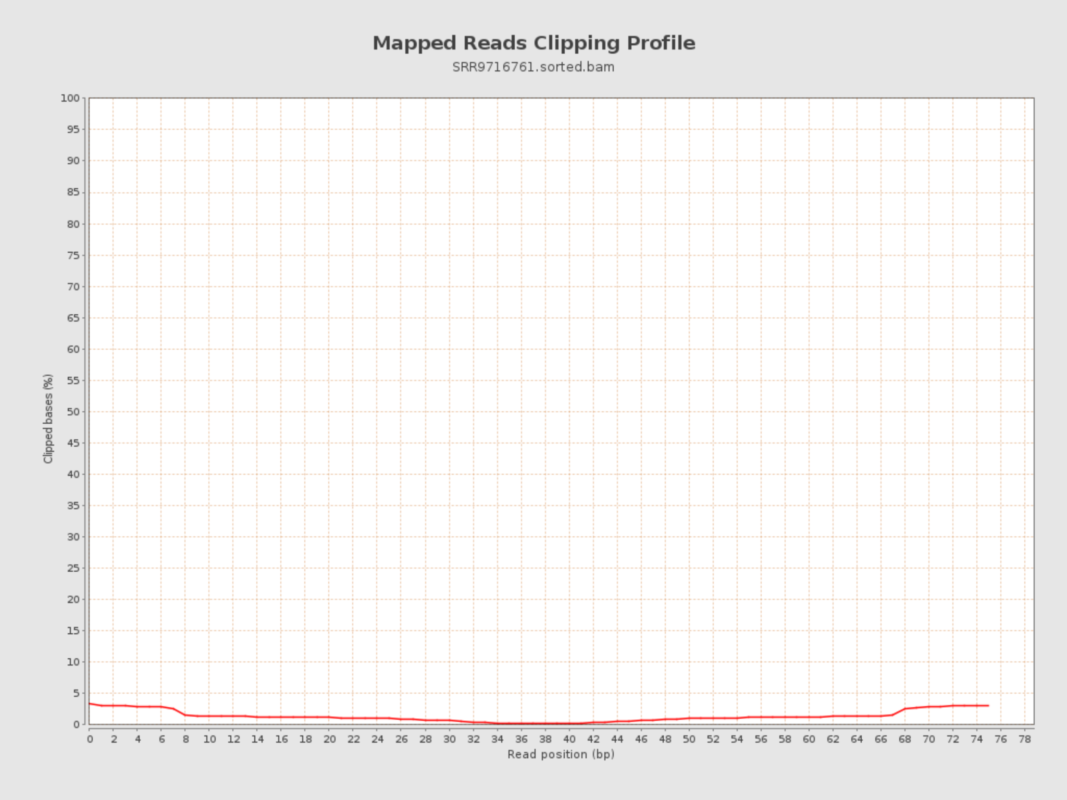
8. Results : Mapped Reads Nucleotide Content



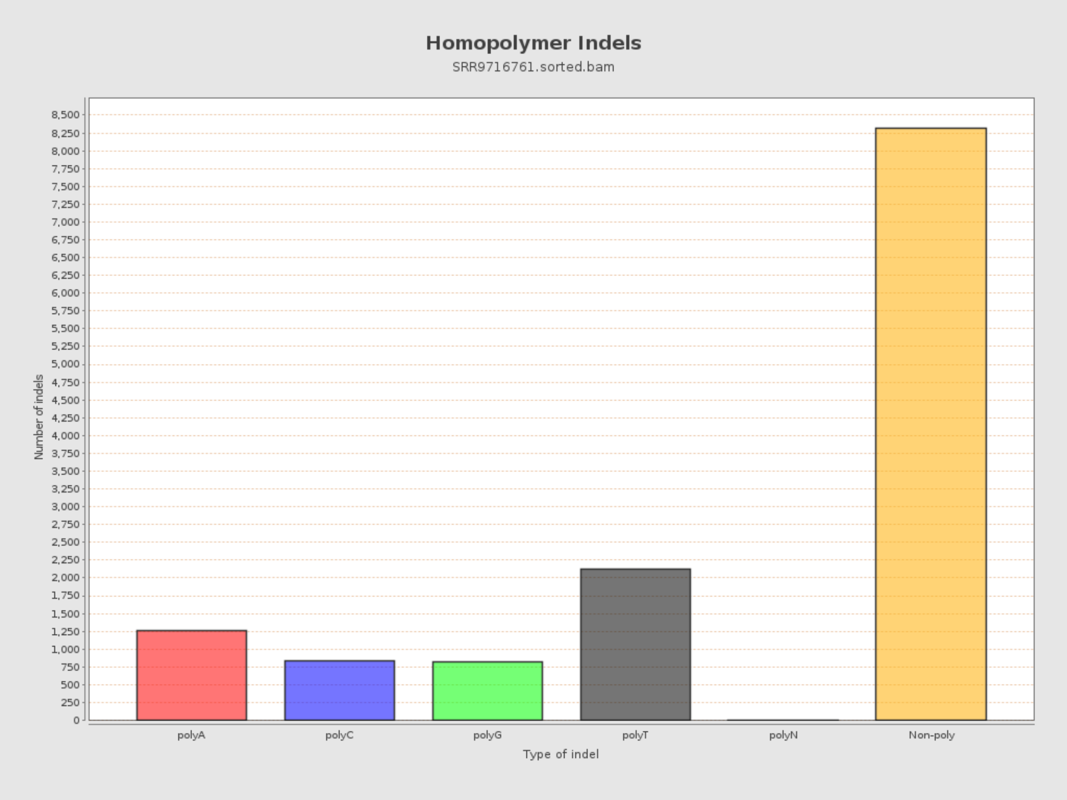
9. Results : Mapped Reads GC-content Distribution



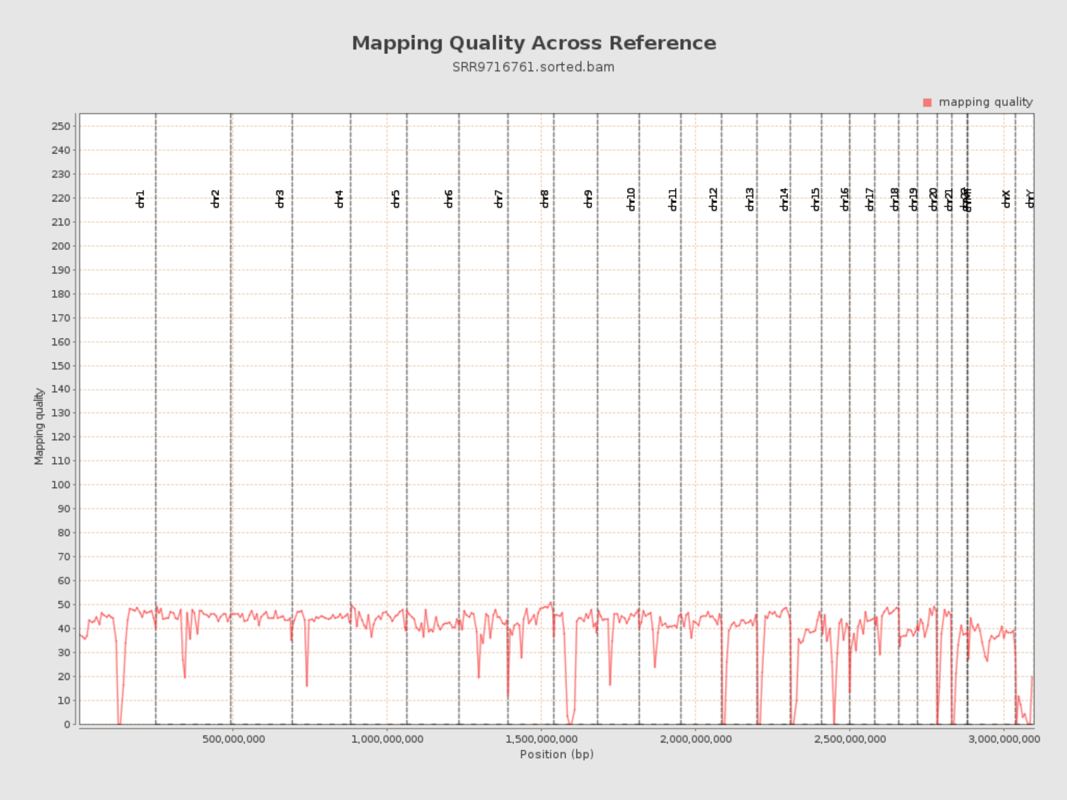
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram