Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:32:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716113.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_SRR9716113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:32:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,652,861
Mapped reads	1,233,907 / 74.65%
Unmapped reads	418,954 / 25.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,108 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	24,596 / 1.49%
Duplication rate	1.51%
Clipped reads	1,235,166 / 74.73%

2.2. ACGT Content

Number/percentage of A's	15,981,296 / 23.75%
Number/percentage of C's	14,566,199 / 21.65%
Number/percentage of T's	19,583,264 / 29.11%
Number/percentage of G's	17,145,880 / 25.48%
Number/percentage of N's	1,756 / 0%
GC Percentage	47.14%

2.3. Coverage

Mean	0.0217

Standard Deviation	0.1776

2.4. Mapping Quality

Mean Mapping Quality	40.16

2.5. Mismatches and indels

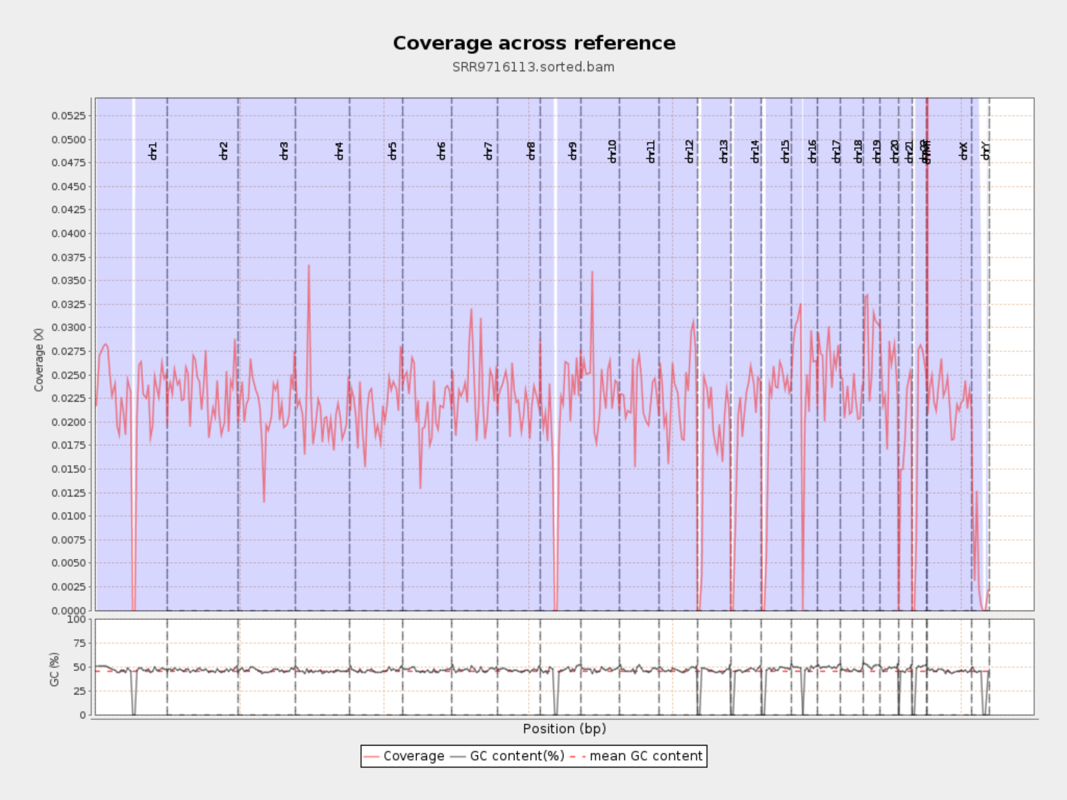
General error rate	0.52%
Mismatches	342,698
Insertions	5,006
Mapped reads with at least one insertion	0.4%
Deletions	10,672
Mapped reads with at least one deletion	0.86%
Homopolymer indels	36.04%

2.6. Chromosome stats

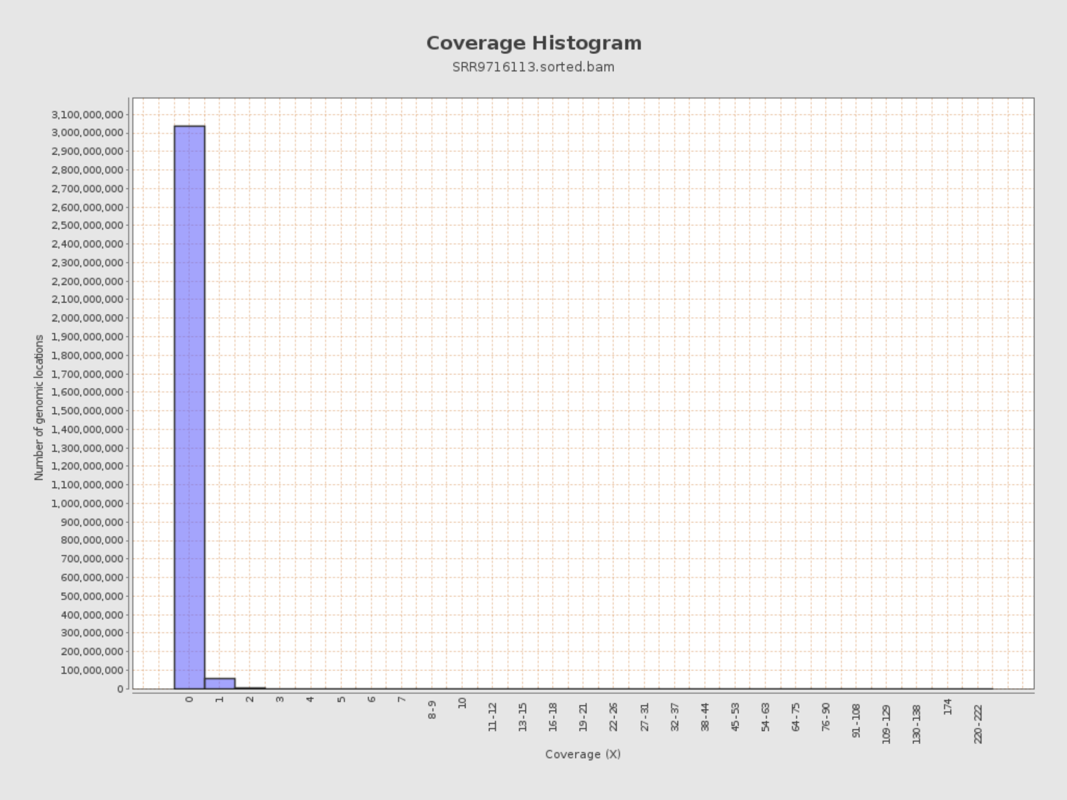
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5513015	0.0221	0.1929
chr2	243199373	5649853	0.0232	0.2051
chr3	198022430	4291409	0.0217	0.1625
chr4	191154276	4045483	0.0212	0.1759
chr5	180915260	3924369	0.0217	0.1603
chr6	171115067	3726093	0.0218	0.1637
chr7	159138663	3750902	0.0236	0.2106

chr8	146364022	3275915	0.0224	0.1694
chr9	141213431	2789834	0.0198	0.1614
chr10	135534747	3271264	0.0241	0.2087
chr11	135006516	3036537	0.0225	0.1866
chr12	133851895	3095198	0.0231	0.1662
chr13	115169878	1992010	0.0173	0.1434
chr14	107349540	2021151	0.0188	0.1525
chr15	102531392	1997611	0.0195	0.1538
chr16	90354753	2224731	0.0246	0.1819
chr17	81195210	2152927	0.0265	0.1816
chr18	78077248	1744151	0.0223	0.2079
chr19	59128983	1726948	0.0292	0.2077
chr20	63025520	1533689	0.0243	0.1737
chr21	48129895	868265	0.018	0.1608
chr22	51304566	950736	0.0185	0.1496
chrMT	16571	8243	0.4974	0.7882
chrX	155270560	3483125	0.0224	0.1712
chrY	59373566	222194	0.0037	0.1084

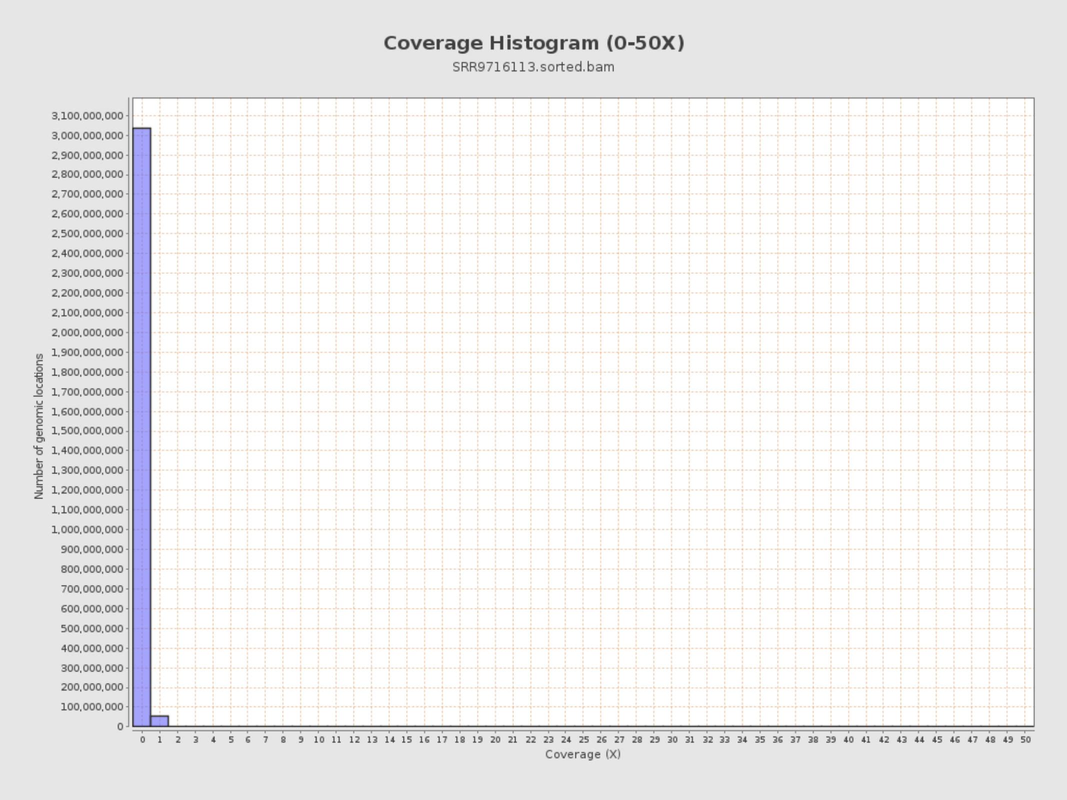
3. Results : Coverage across reference



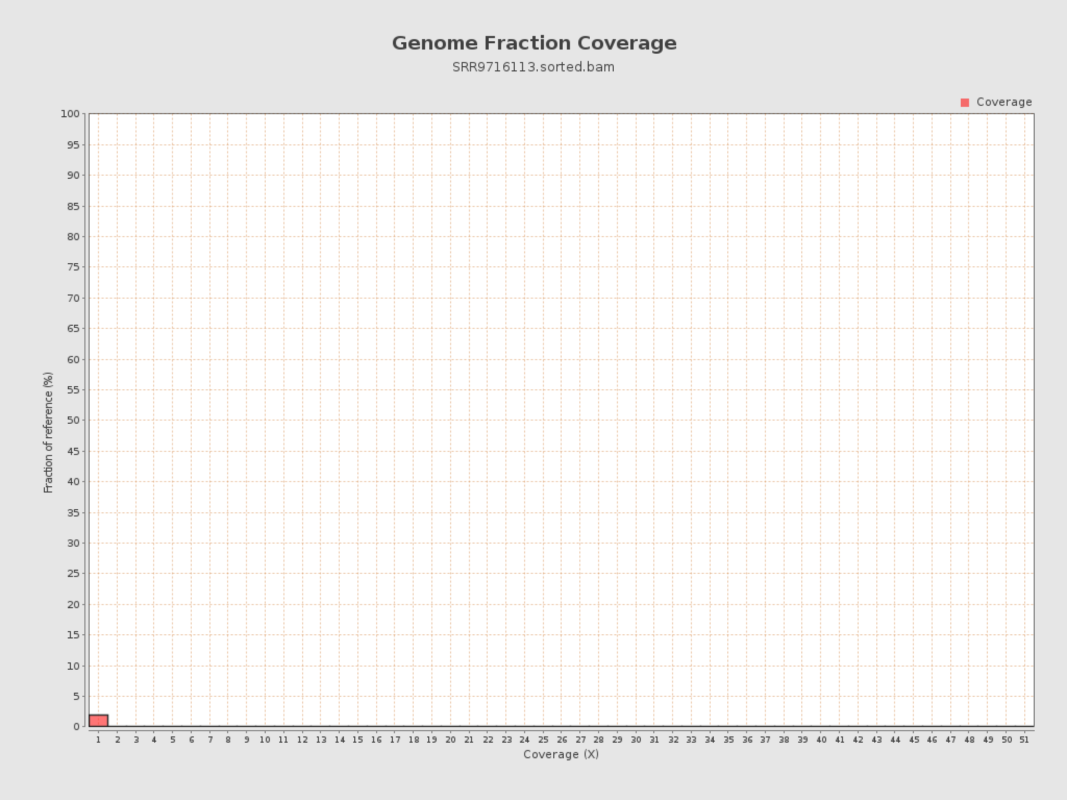
4. Results : Coverage Histogram



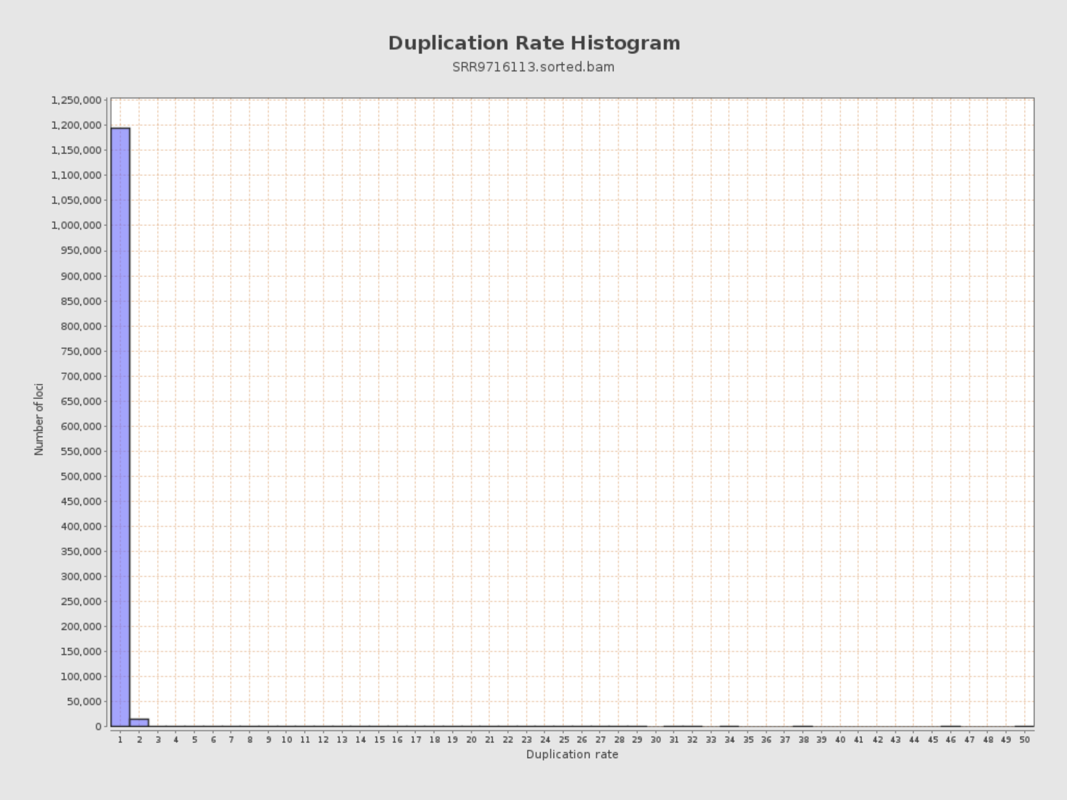
5. Results : Coverage Histogram (0-50X)



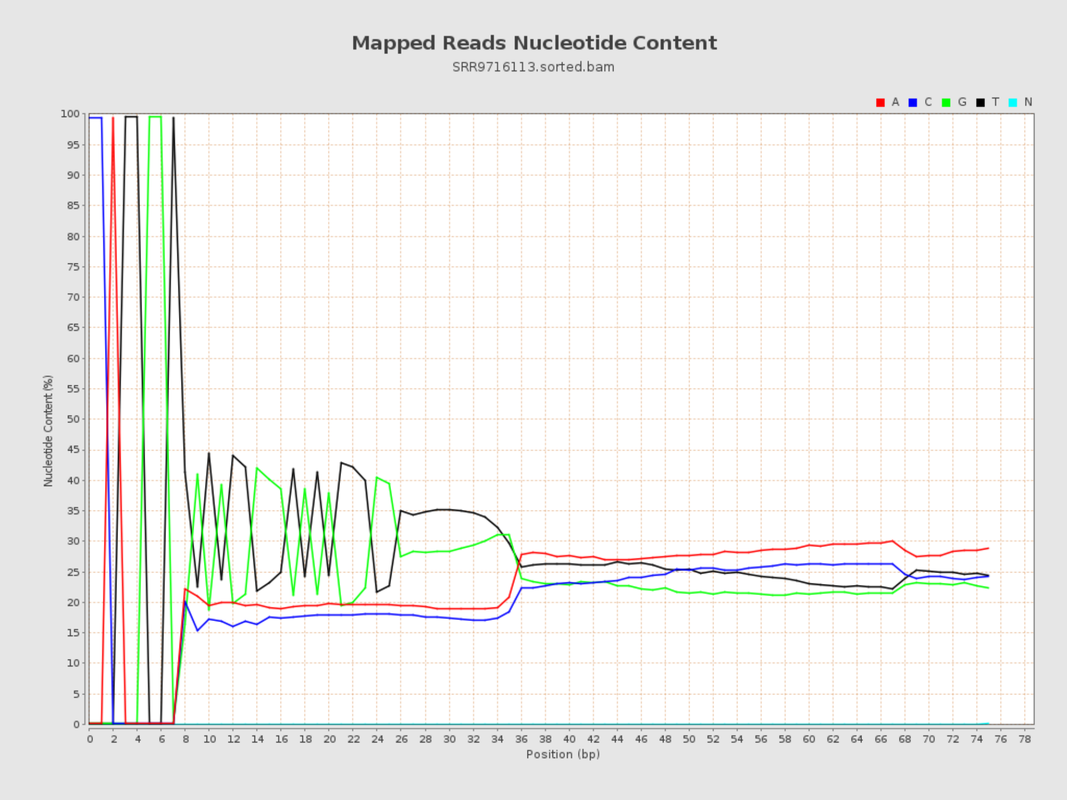
6. Results : Genome Fraction Coverage



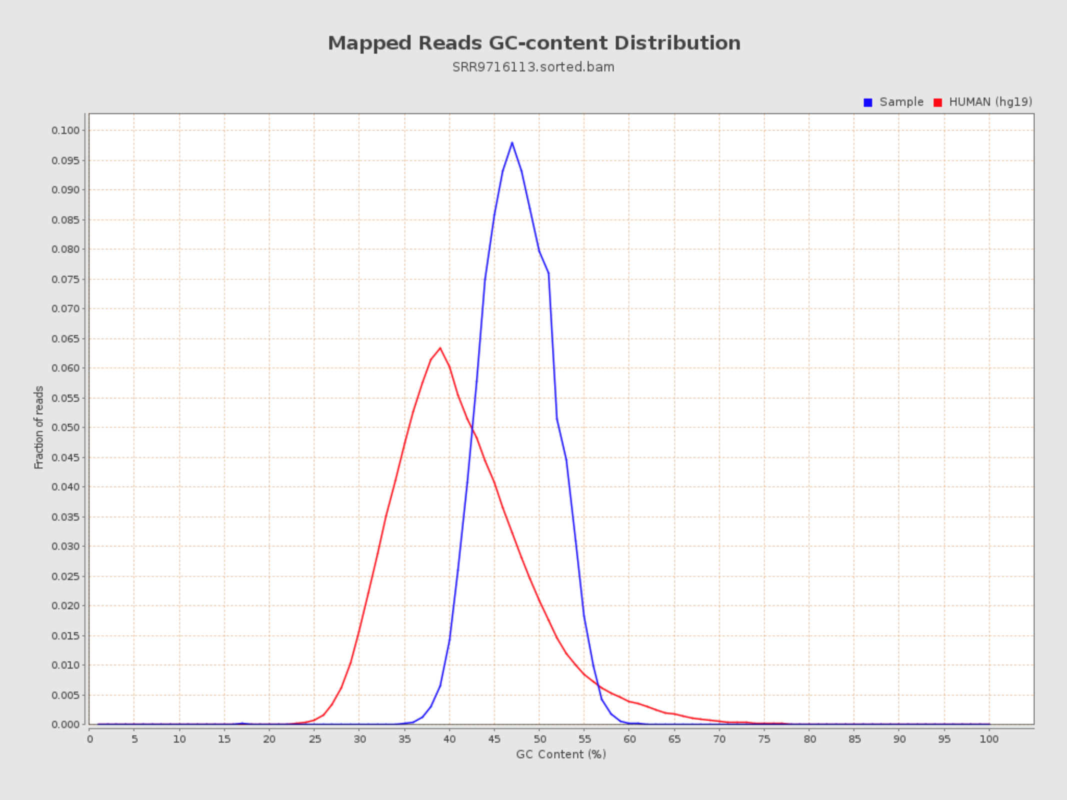
7. Results : Duplication Rate Histogram



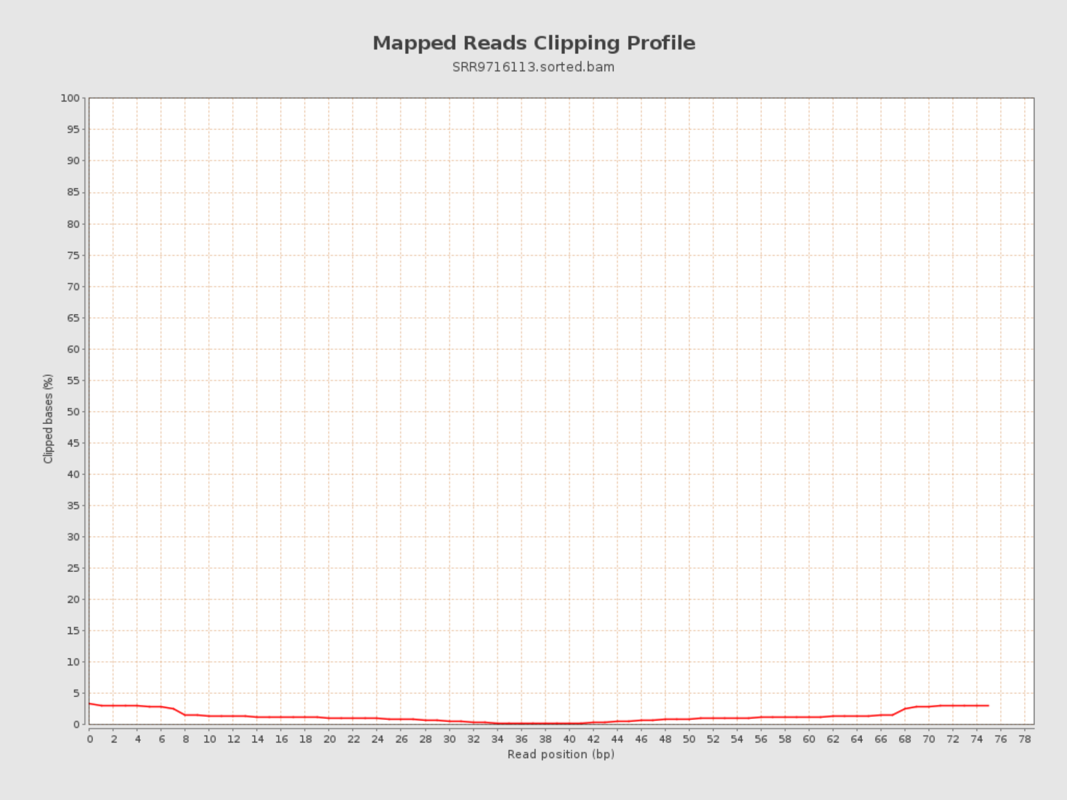
8. Results : Mapped Reads Nucleotide Content



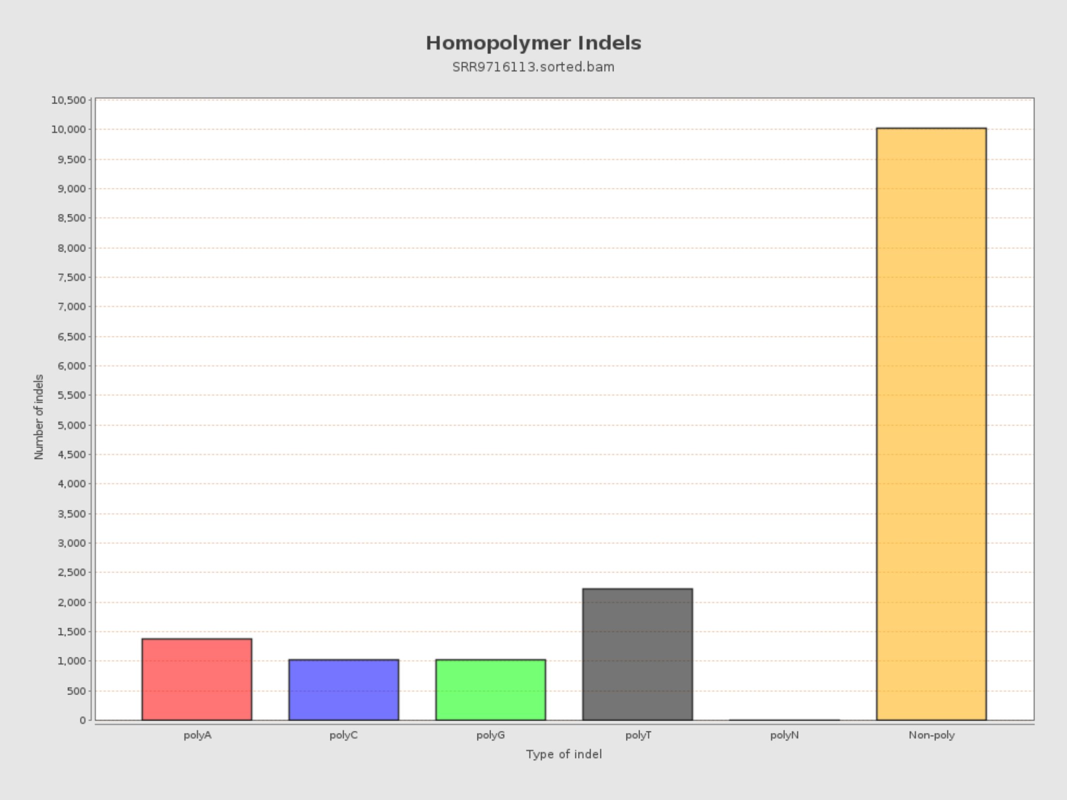
9. Results : Mapped Reads GC-content Distribution



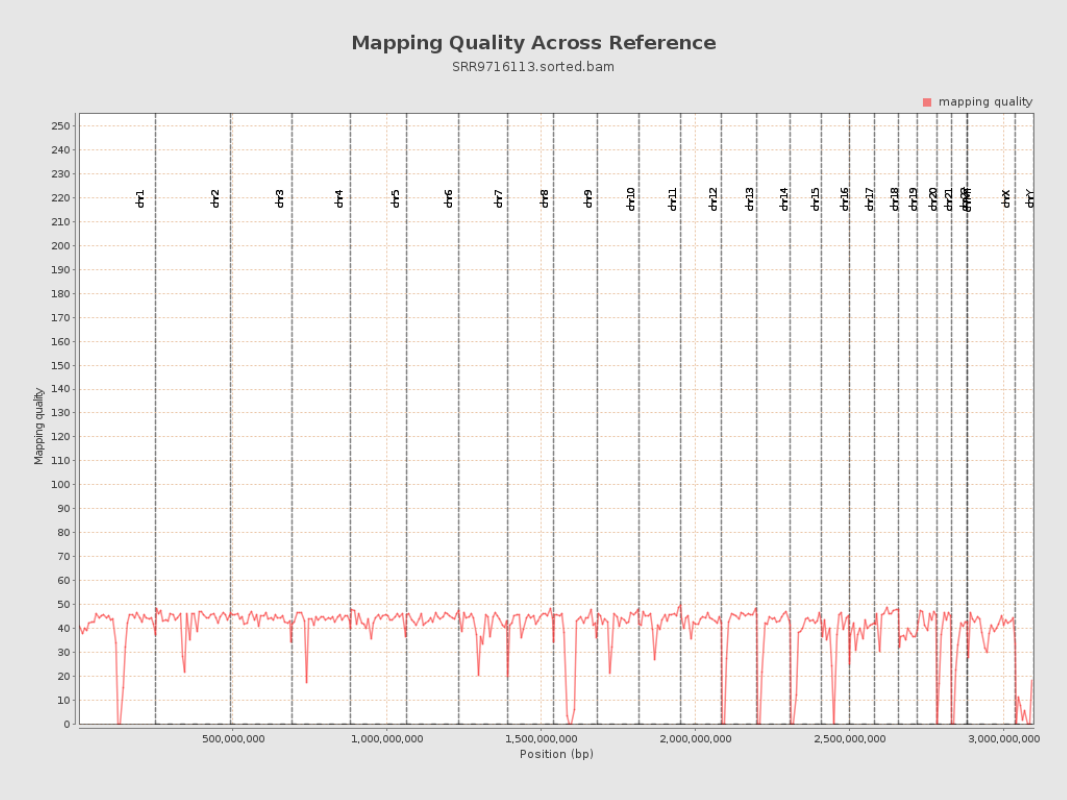
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram