Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:04:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716333.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_SRR9716333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716333.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:04:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,012,094
Mapped reads	925,585 / 91.45%
Unmapped reads	86,509 / 8.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,986 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	27,373 / 2.7%
Duplication rate	2.36%
Clipped reads	926,824 / 91.57%

2.2. ACGT Content

Number/percentage of A's	13,719,033 / 25.52%
Number/percentage of C's	9,942,569 / 18.5%
Number/percentage of T's	17,260,010 / 32.11%
Number/percentage of G's	12,833,488 / 23.87%
Number/percentage of N's	787 / 0%
GC Percentage	42.37%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.1798

2.4. Mapping Quality

Mean Mapping Quality	46.28

2.5. Mismatches and indels

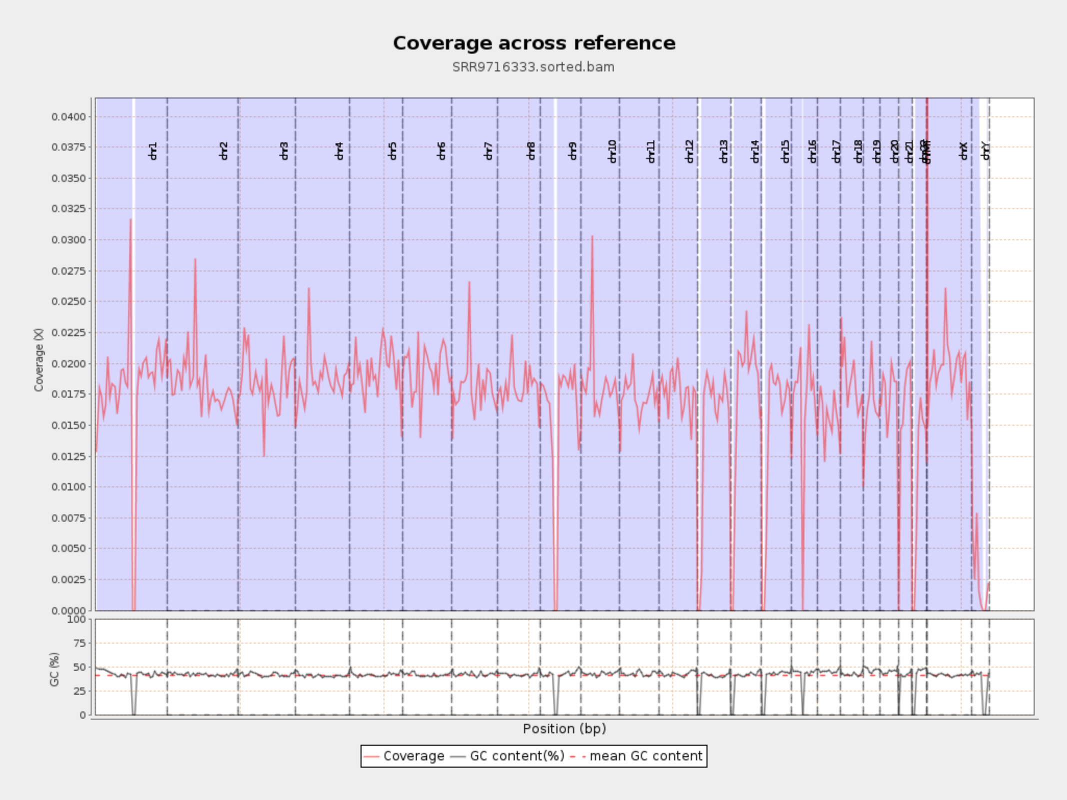
General error rate	0.52%
Mismatches	274,296
Insertions	3,389
Mapped reads with at least one insertion	0.37%
Deletions	8,557
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.92%

2.6. Chromosome stats

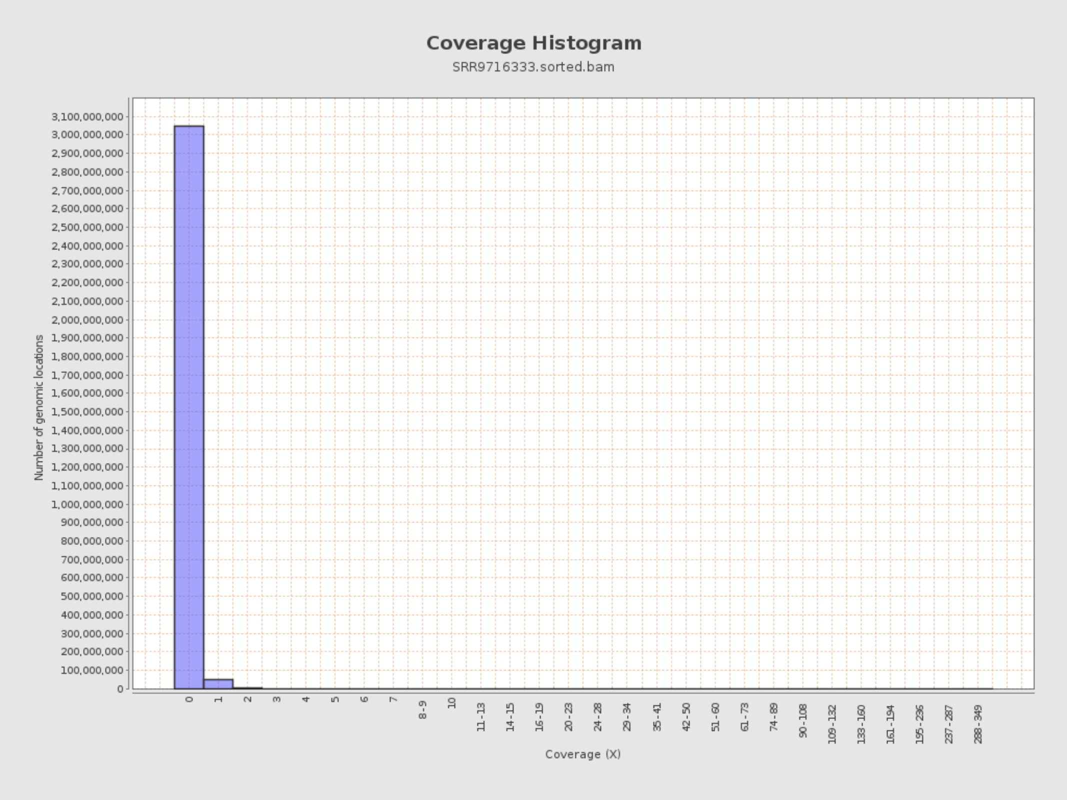
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4457213	0.0179	0.3126
chr2	243199373	4484684	0.0184	0.1775
chr3	198022430	3682017	0.0186	0.1436
chr4	191154276	3573590	0.0187	0.1514
chr5	180915260	3522755	0.0195	0.1484
chr6	171115067	3317413	0.0194	0.1548
chr7	159138663	2888324	0.0181	0.1932

chr8	146364022	2656595	0.0182	0.209
chr9	141213431	2199151	0.0156	0.1625
chr10	135534747	2493326	0.0184	0.1775
chr11	135006516	2350129	0.0174	0.1645
chr12	133851895	2364487	0.0177	0.1435
chr13	115169878	1676907	0.0146	0.127
chr14	107349540	1812033	0.0169	0.1418
chr15	102531392	1508248	0.0147	0.1282
chr16	90354753	1491859	0.0165	0.1407
chr17	81195210	1272263	0.0157	0.1349
chr18	78077248	1453139	0.0186	0.2704
chr19	59128983	985286	0.0167	0.2301
chr20	63025520	1096529	0.0174	0.1418
chr21	48129895	753016	0.0156	0.1381
chr22	51304566	552072	0.0108	0.1092
chrMT	16571	2797	0.1688	0.4196
chrX	155270560	3029259	0.0195	0.1571
chrY	59373566	147044	0.0025	0.0705

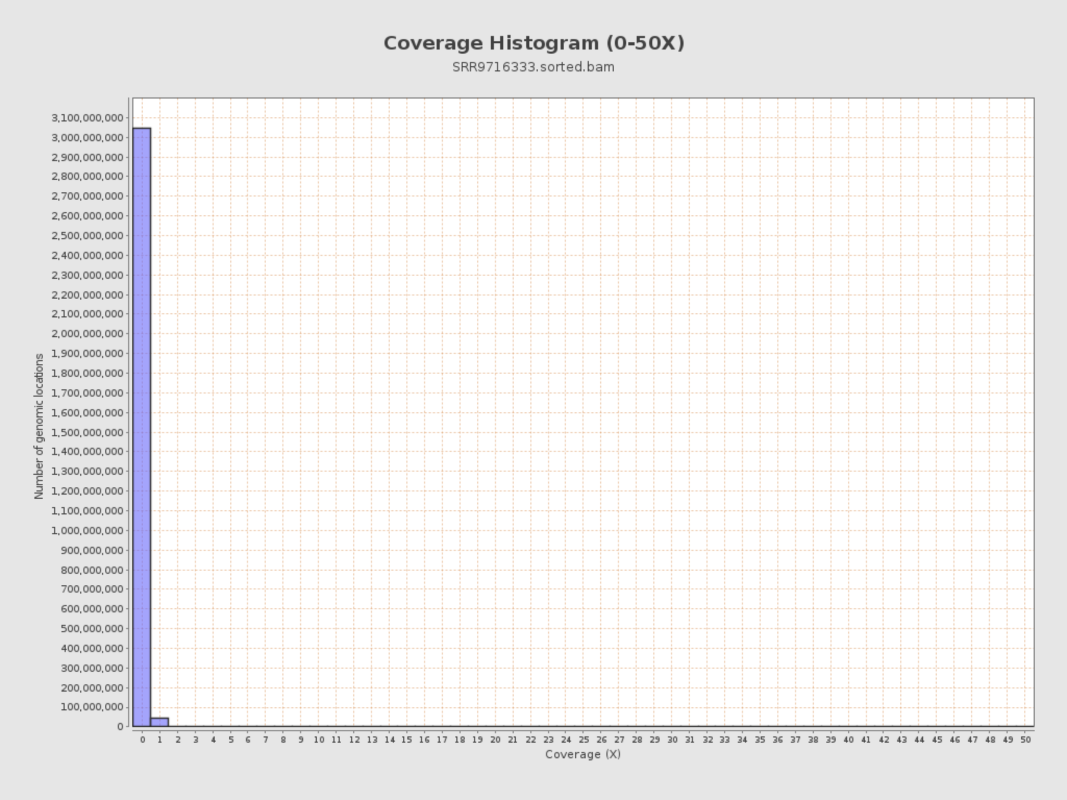
3. Results : Coverage across reference



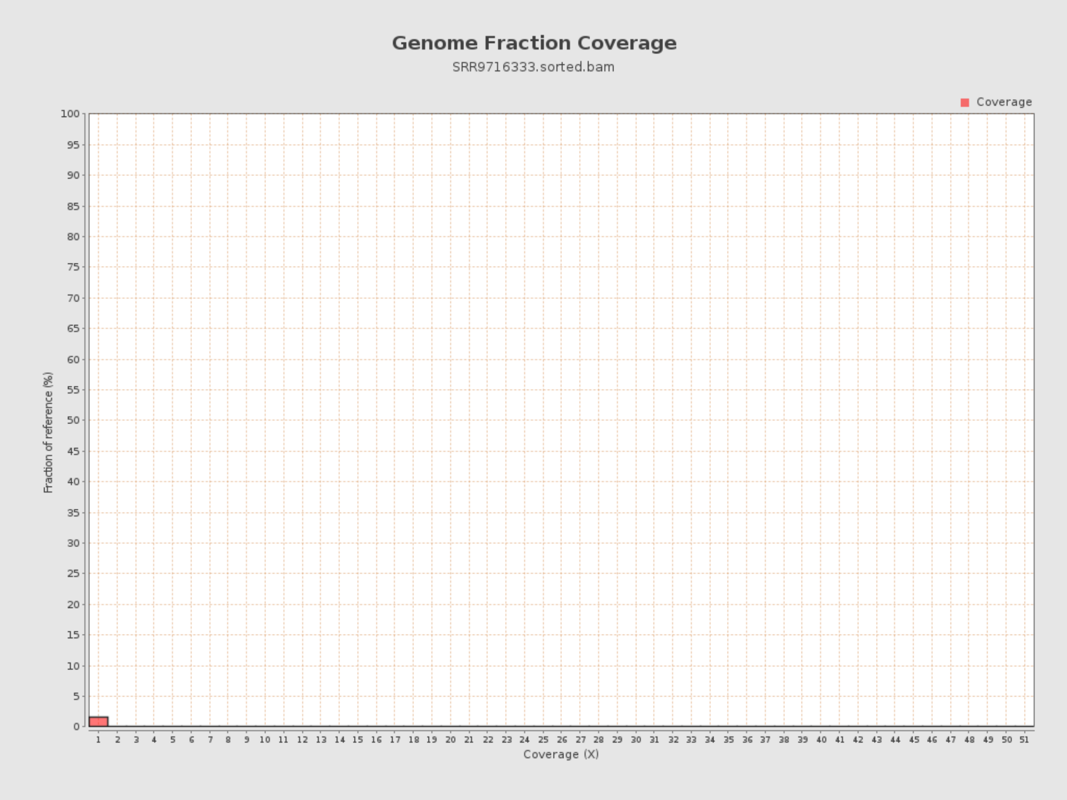
4. Results : Coverage Histogram



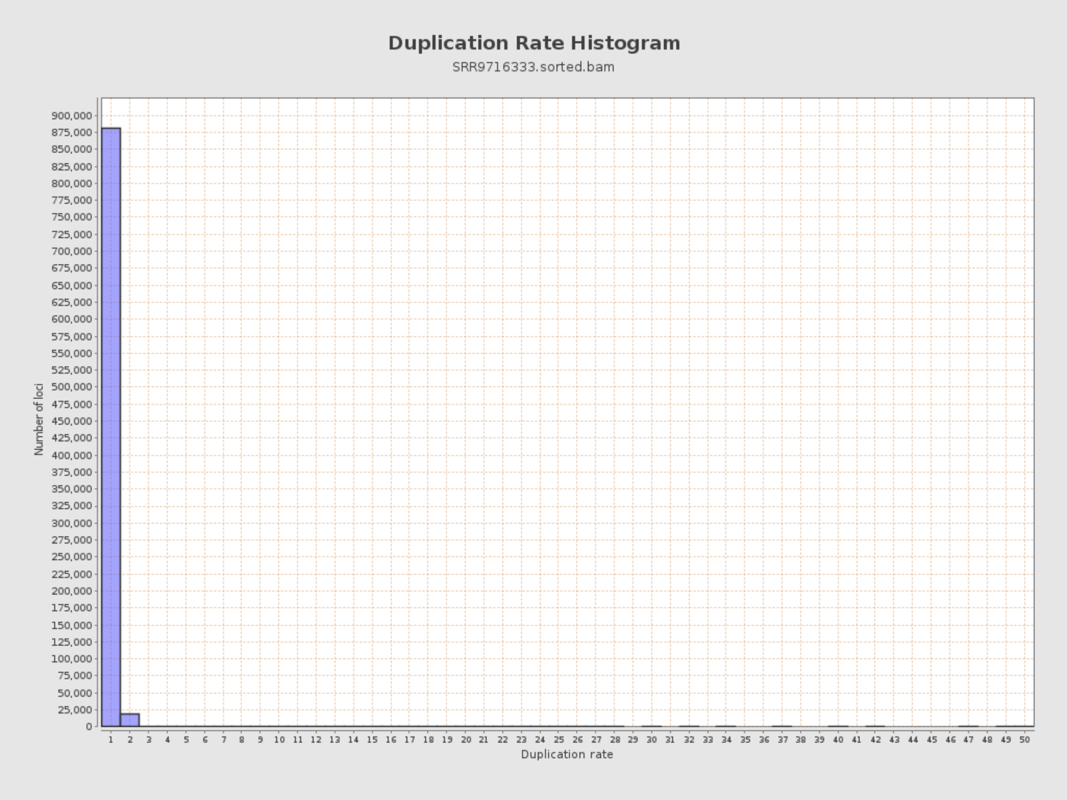
5. Results : Coverage Histogram (0-50X)



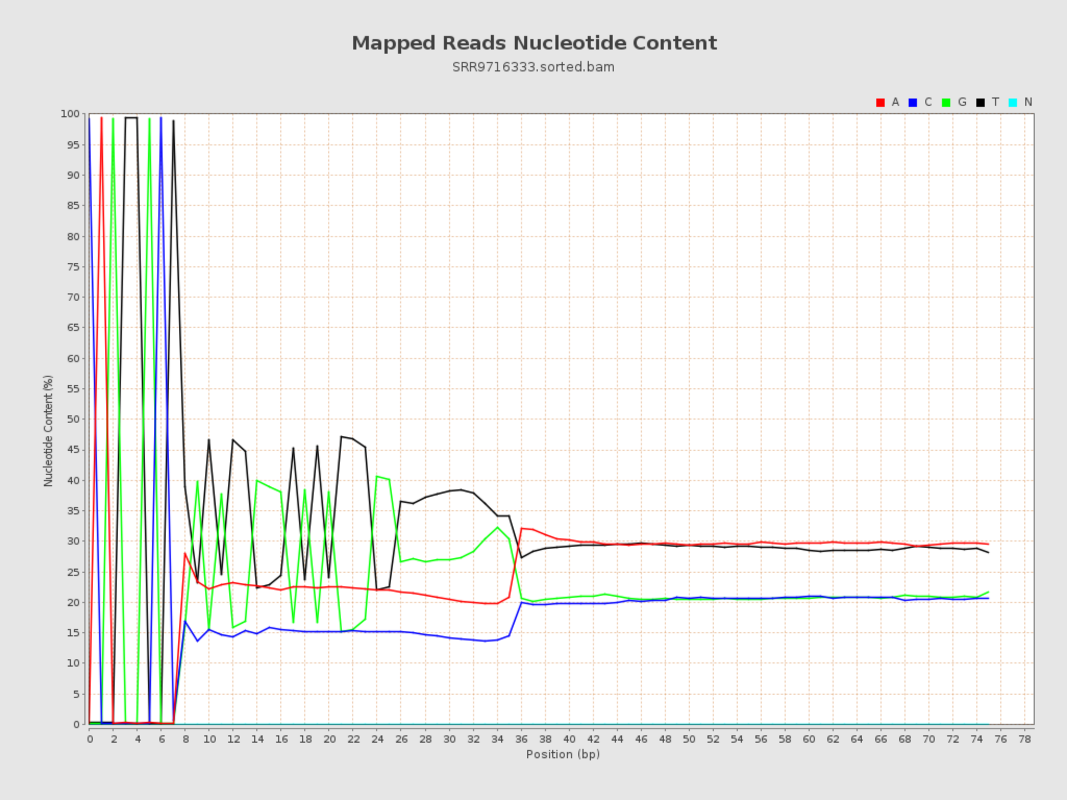
6. Results : Genome Fraction Coverage



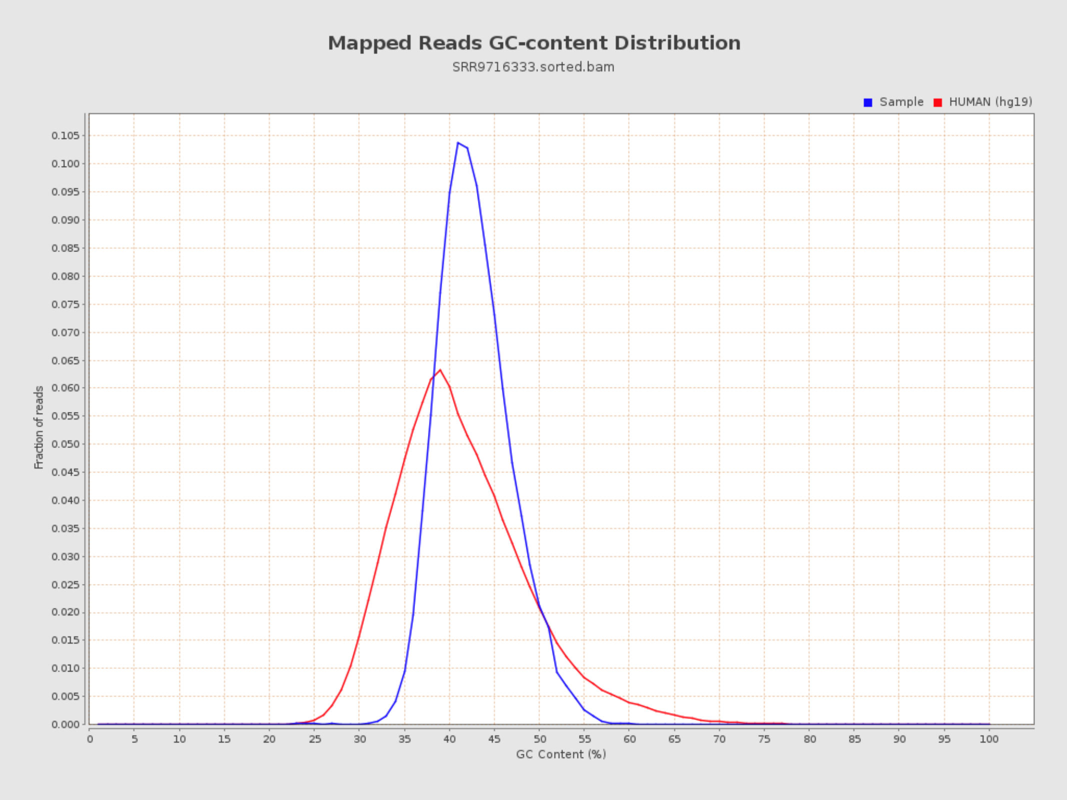
7. Results : Duplication Rate Histogram



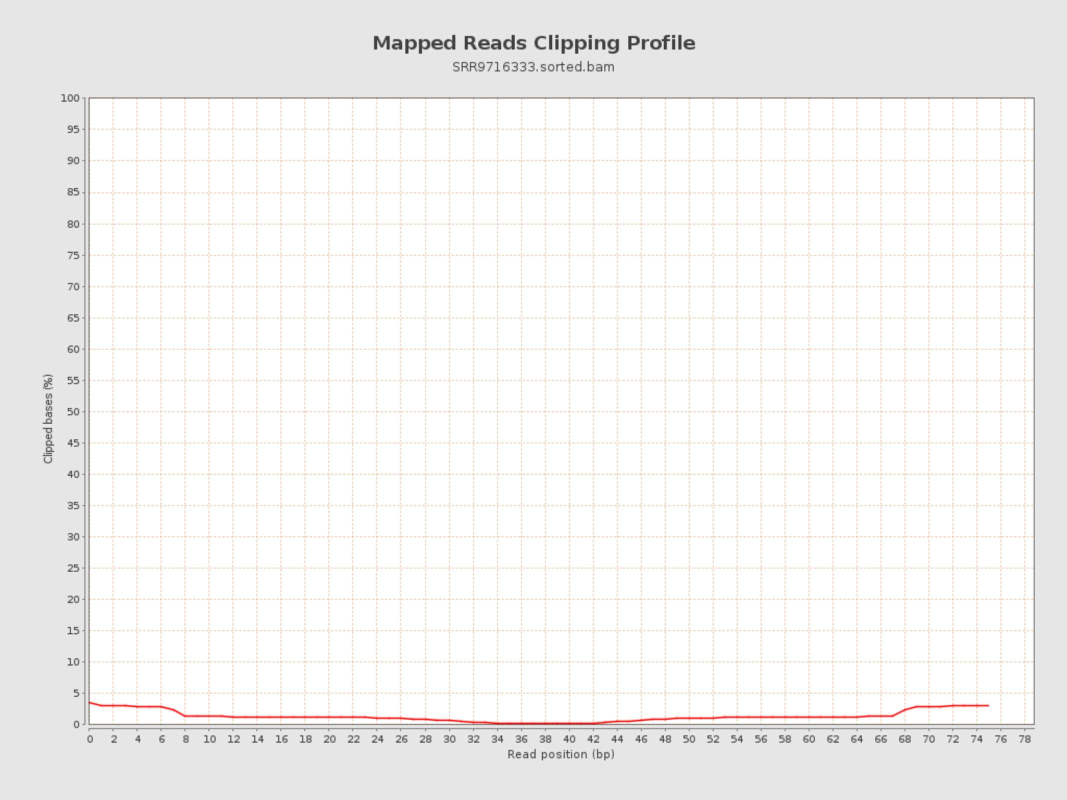
8. Results : Mapped Reads Nucleotide Content



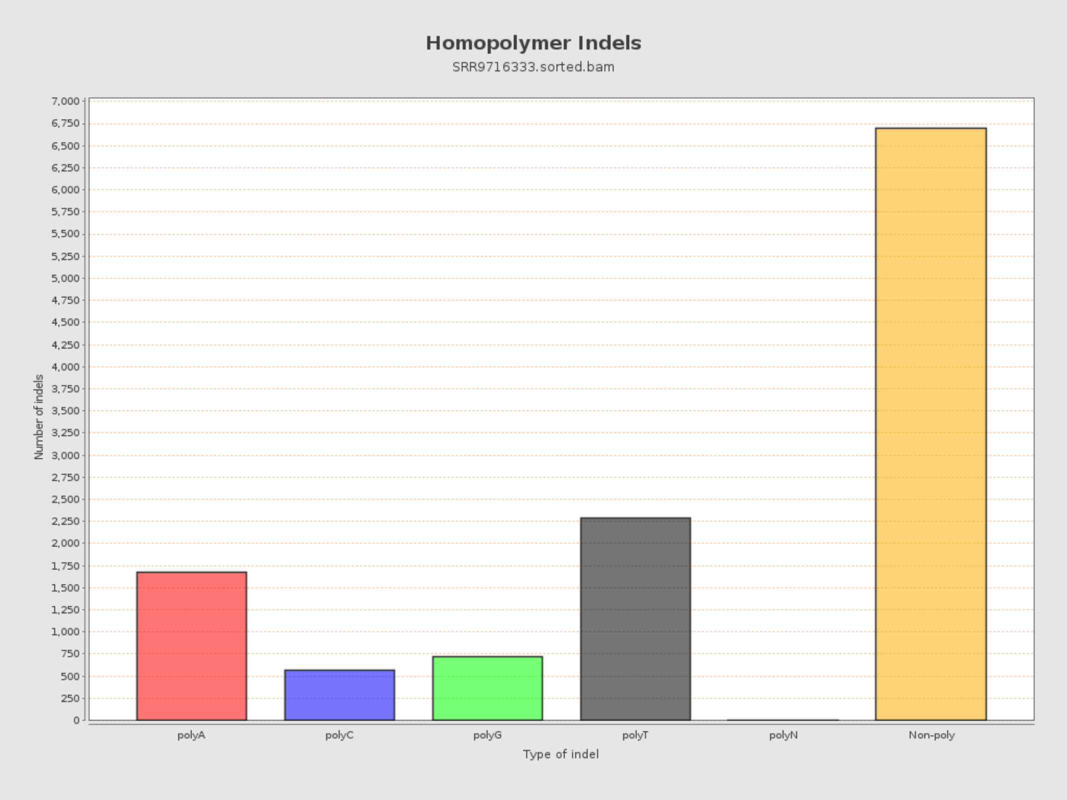
9. Results : Mapped Reads GC-content Distribution



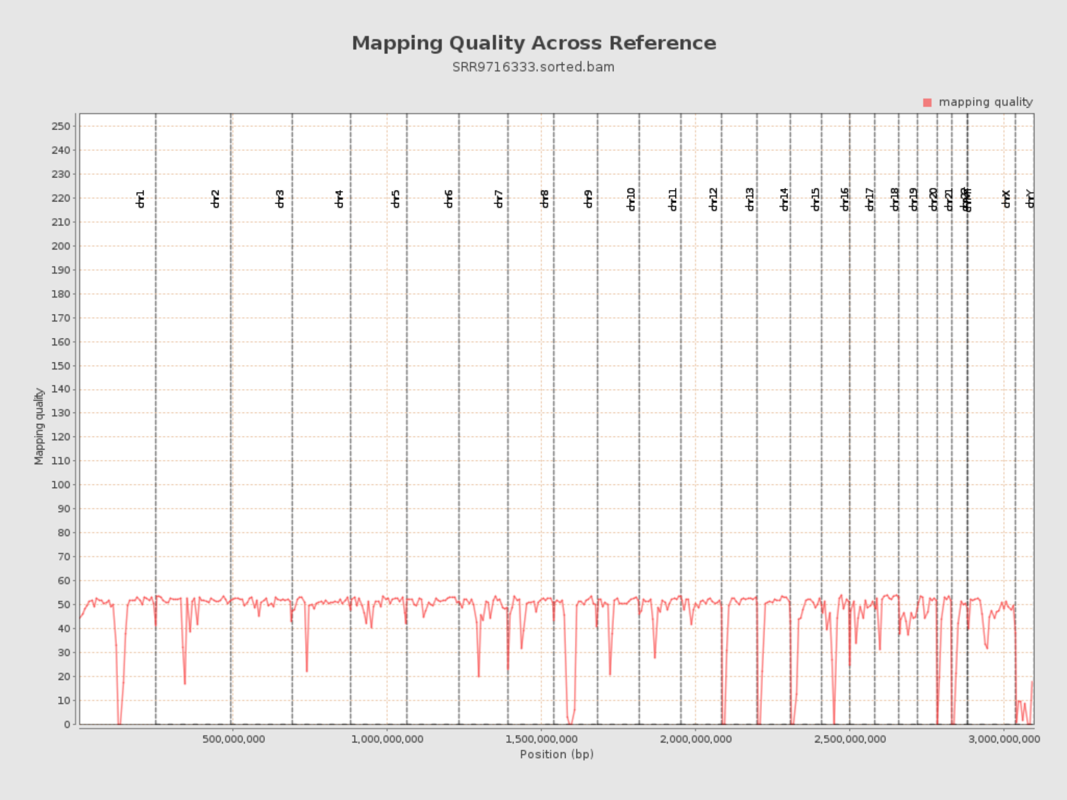
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram