Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:24:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716110.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_SRR9716110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:24:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	988,652
Mapped reads	886,952 / 89.71%
Unmapped reads	101,700 / 10.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,136 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	15,705 / 1.59%
Duplication rate	1.28%
Clipped reads	887,871 / 89.81%

2.2. ACGT Content

Number/percentage of A's	12,662,149 / 24.87%
Number/percentage of C's	9,974,465 / 19.59%
Number/percentage of T's	15,973,374 / 31.37%
Number/percentage of G's	12,306,631 / 24.17%
Number/percentage of N's	343 / 0%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0165

Standard Deviation	0.16

2.4. Mapping Quality

Mean Mapping Quality	42.95

2.5. Mismatches and indels

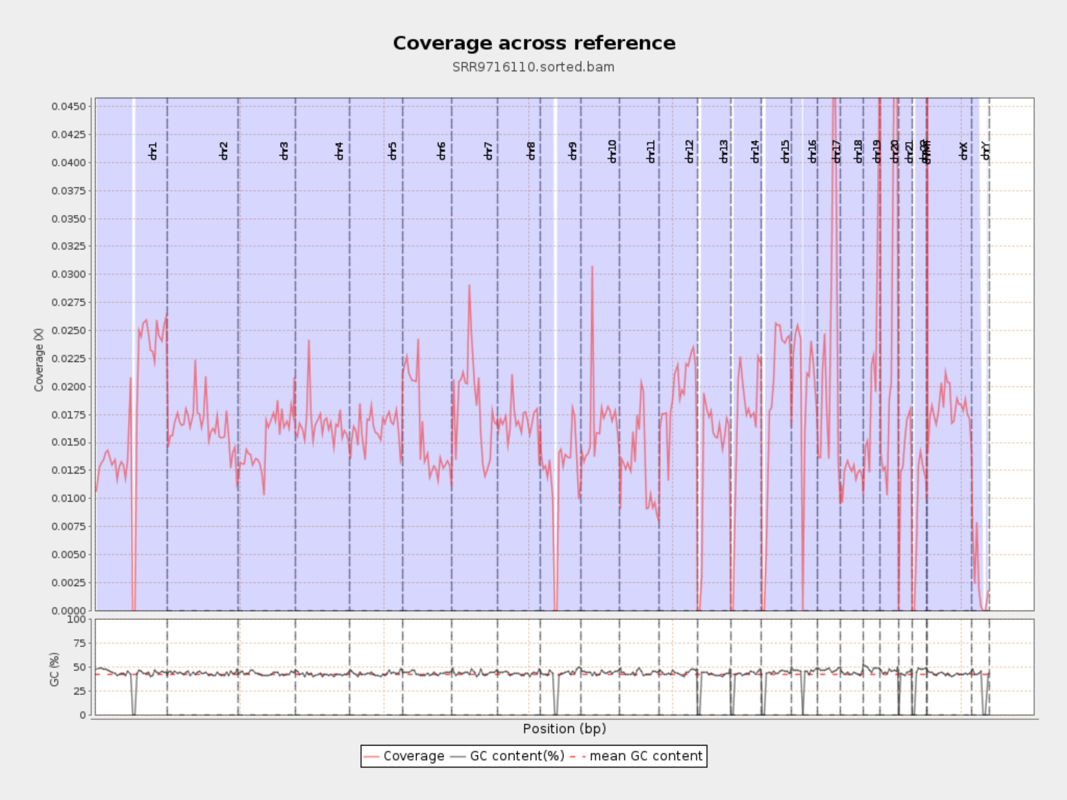
General error rate	0.54%
Mismatches	266,036
Insertions	3,672
Mapped reads with at least one insertion	0.41%
Deletions	9,699
Mapped reads with at least one deletion	1.08%
Homopolymer indels	39.34%

2.6. Chromosome stats

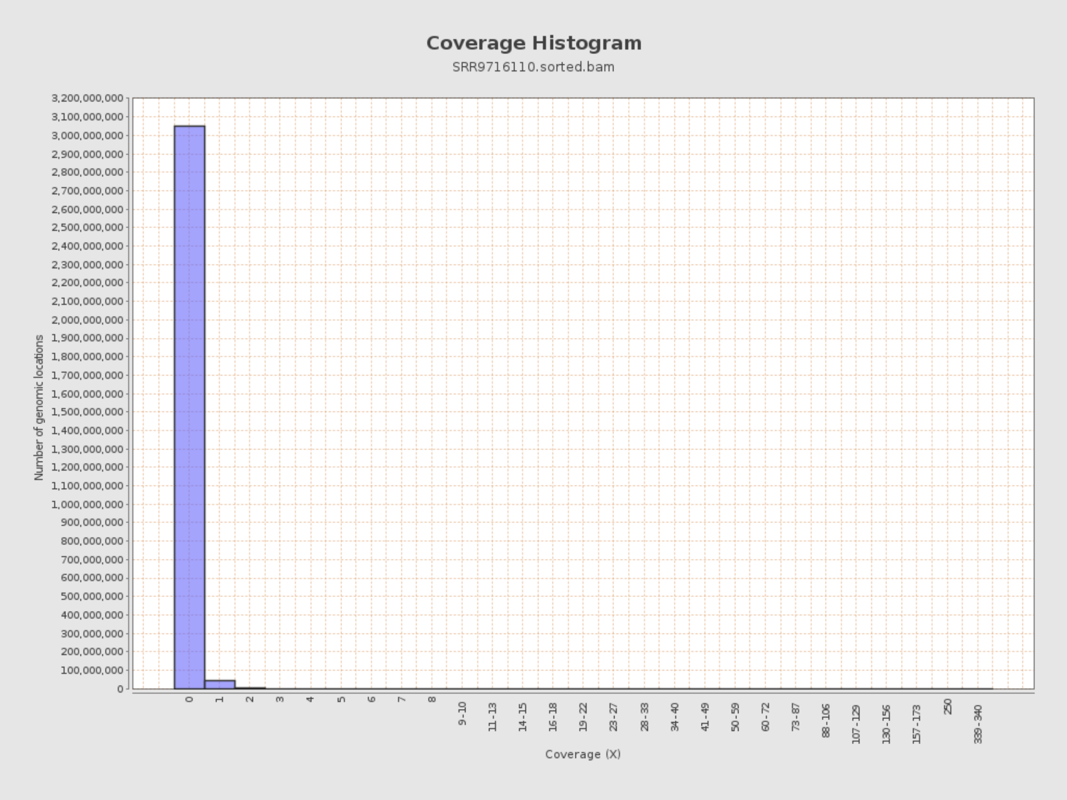
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4322591	0.0173	0.1908
chr2	243199373	4007642	0.0165	0.1992
chr3	198022430	3009891	0.0152	0.1313
chr4	191154276	3183701	0.0167	0.1417
chr5	180915260	2947855	0.0163	0.1332
chr6	171115067	2755247	0.0161	0.1446
chr7	159138663	2924251	0.0184	0.2201

chr8	146364022	2466820	0.0169	0.1704
chr9	141213431	1705369	0.0121	0.1263
chr10	135534747	2269955	0.0167	0.1879
chr11	135006516	1764522	0.0131	0.1378
chr12	133851895	2594097	0.0194	0.1469
chr13	115169878	1589817	0.0138	0.1229
chr14	107349540	1752694	0.0163	0.1375
chr15	102531392	1887787	0.0184	0.1439
chr16	90354753	1789406	0.0198	0.1522
chr17	81195210	1940289	0.0239	0.1664
chr18	78077248	952251	0.0122	0.1826
chr19	59128983	1332016	0.0225	0.1976
chr20	63025520	1649688	0.0262	0.1749
chr21	48129895	654225	0.0136	0.1276
chr22	51304566	465043	0.0091	0.1002
chrMT	16571	3505	0.2115	0.4967
chrX	155270560	2814067	0.0181	0.1457
chrY	59373566	149788	0.0025	0.0758

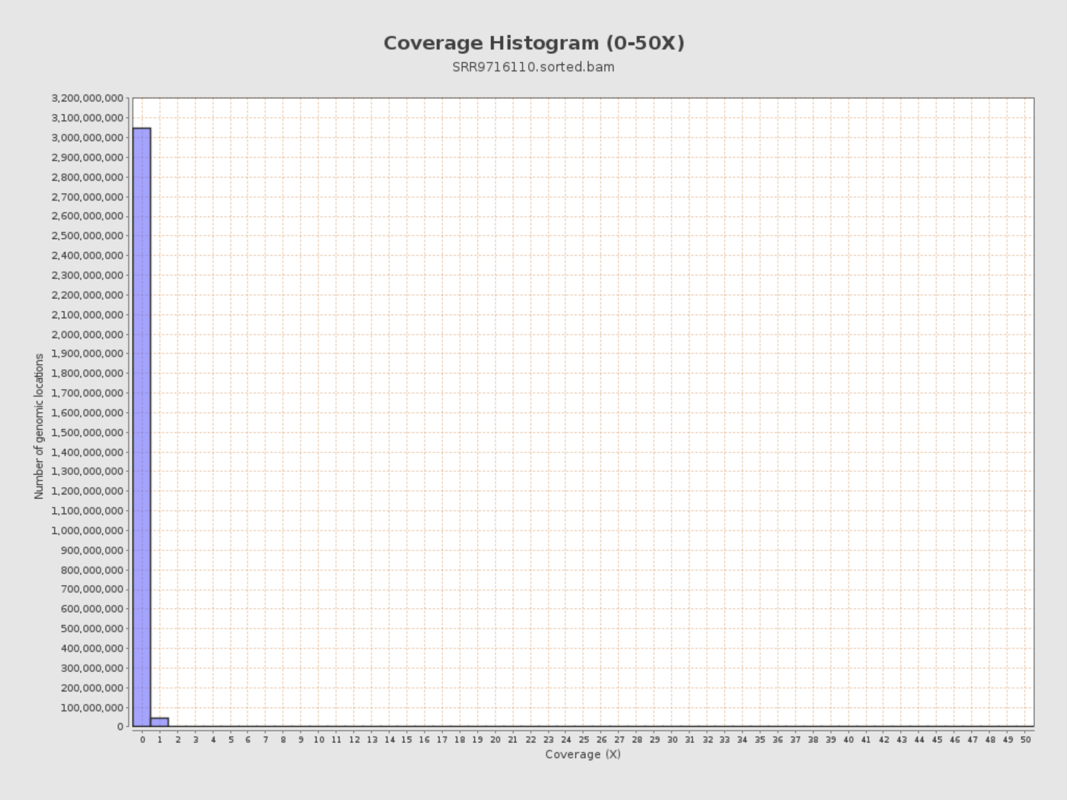
3. Results : Coverage across reference



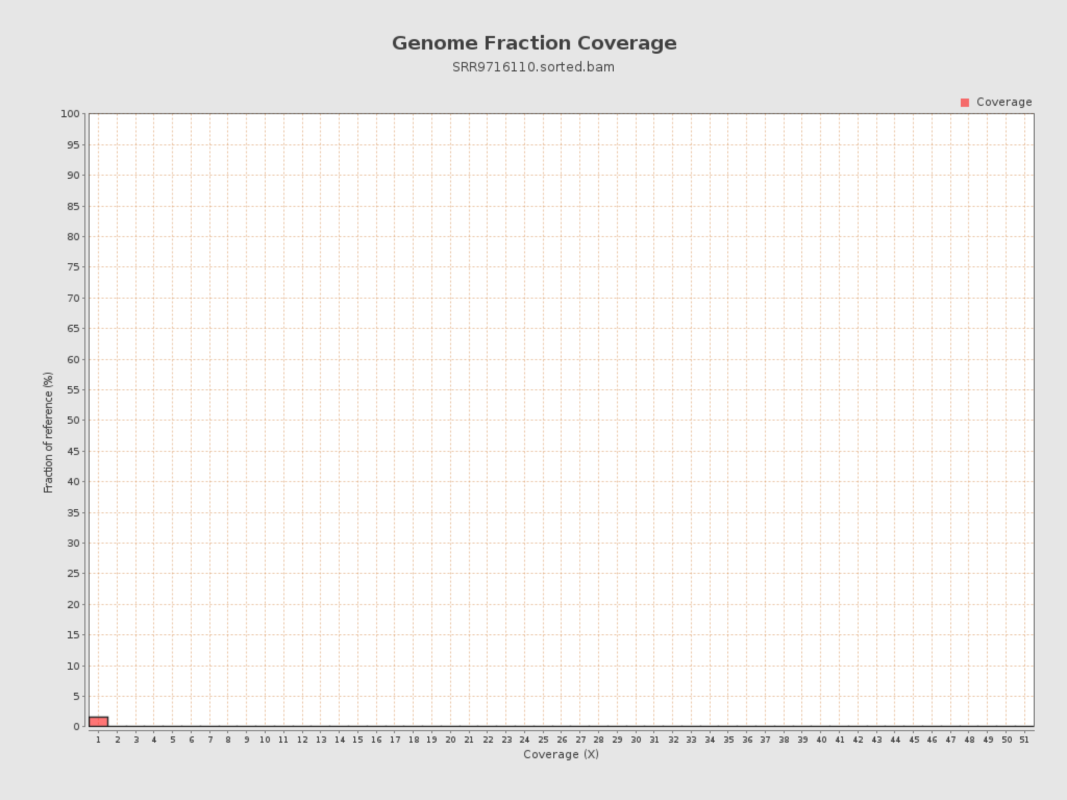
4. Results : Coverage Histogram



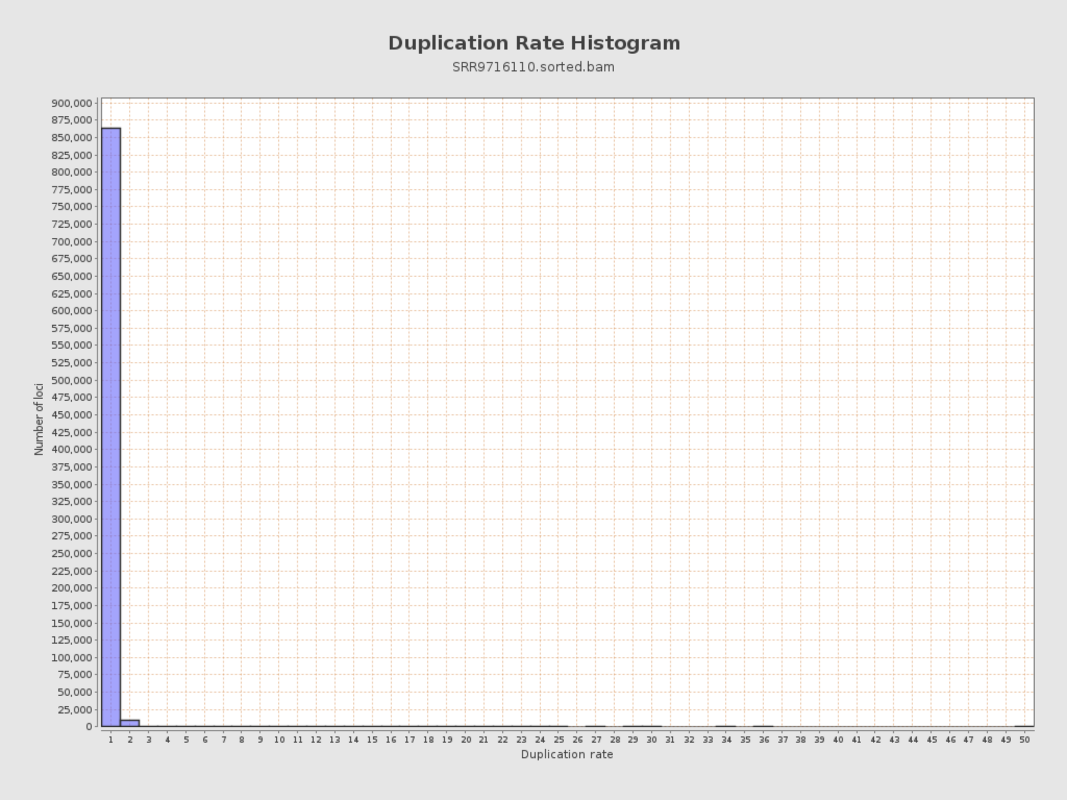
5. Results : Coverage Histogram (0-50X)



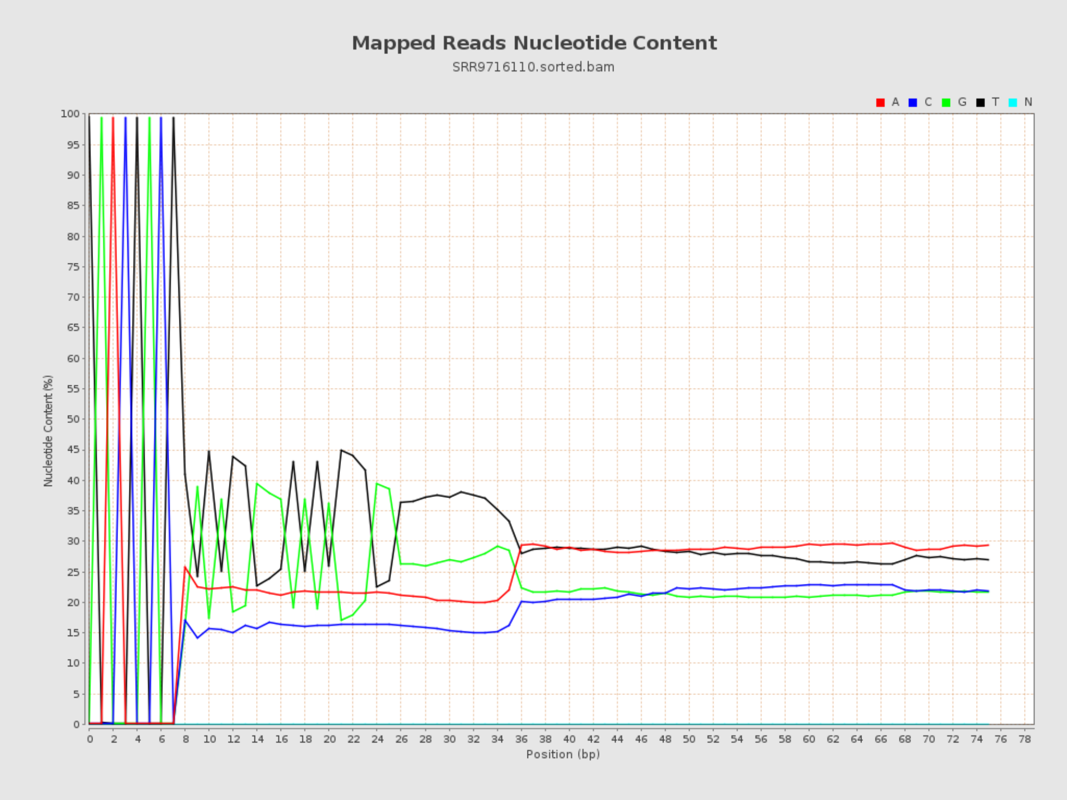
6. Results : Genome Fraction Coverage



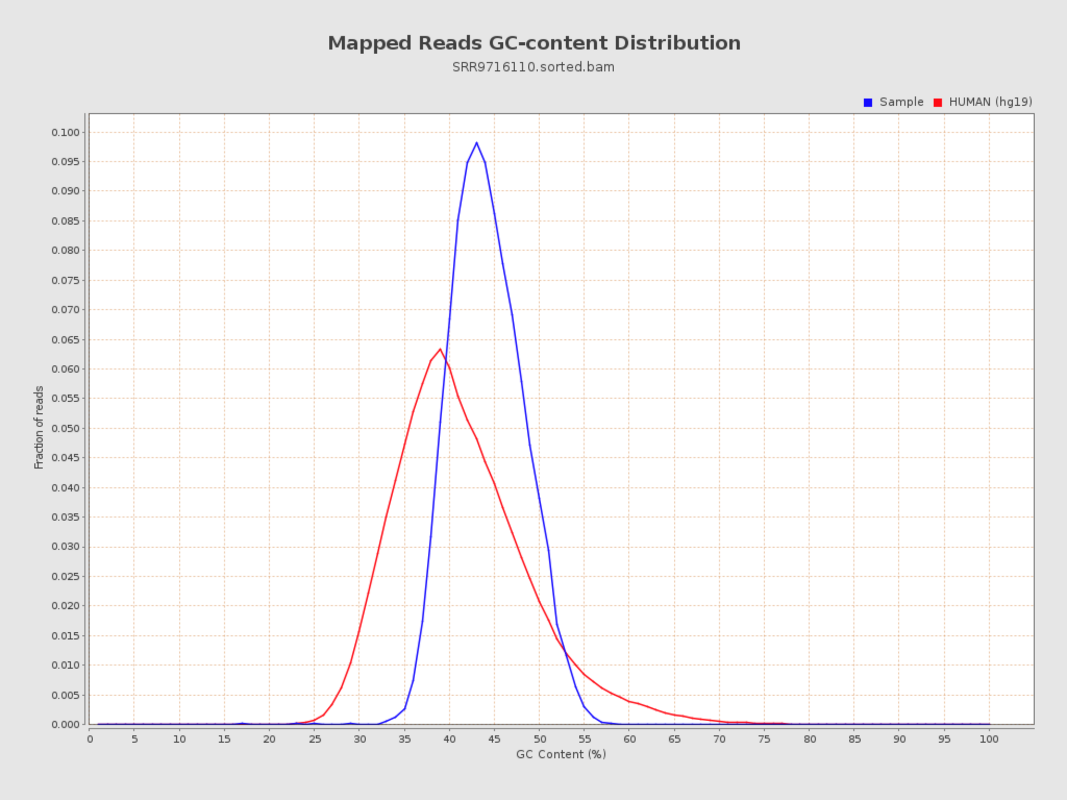
7. Results : Duplication Rate Histogram



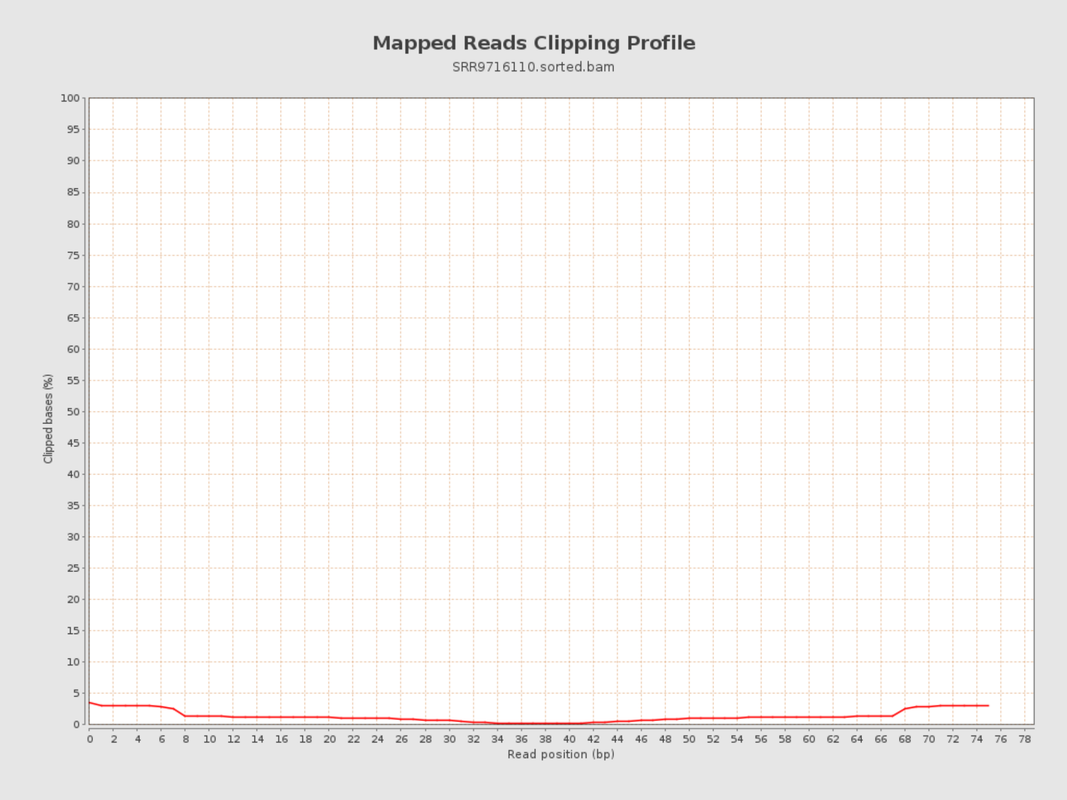
8. Results : Mapped Reads Nucleotide Content



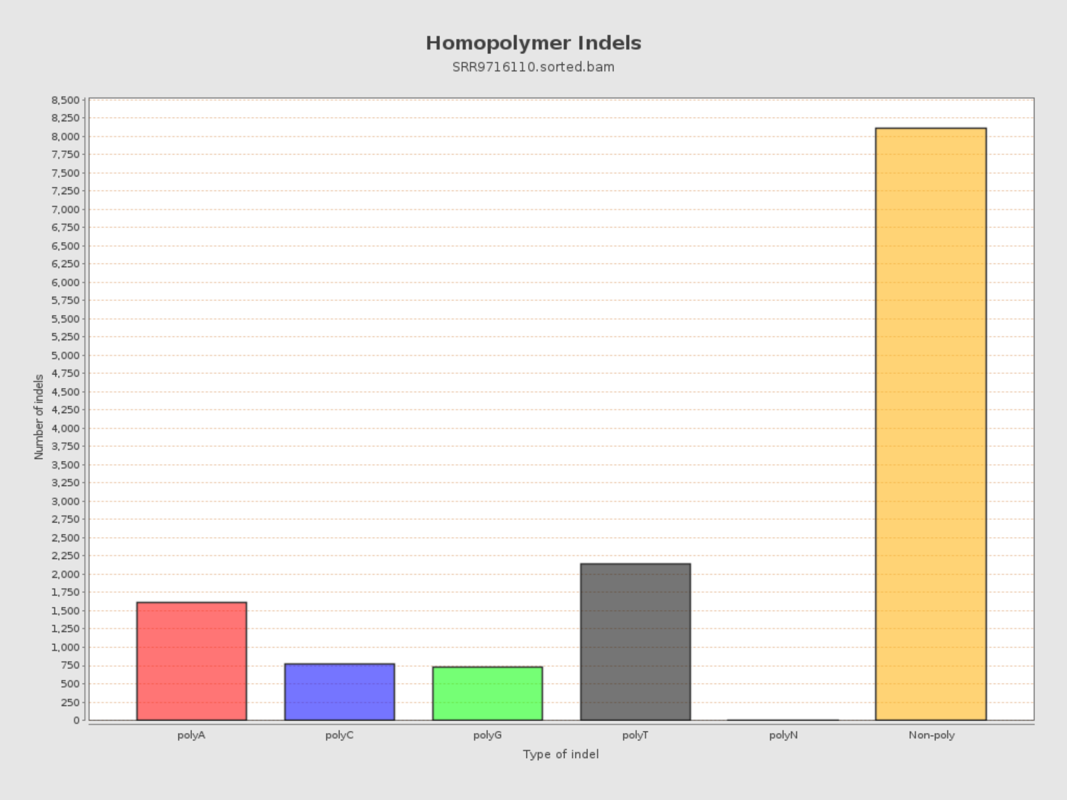
9. Results : Mapped Reads GC-content Distribution



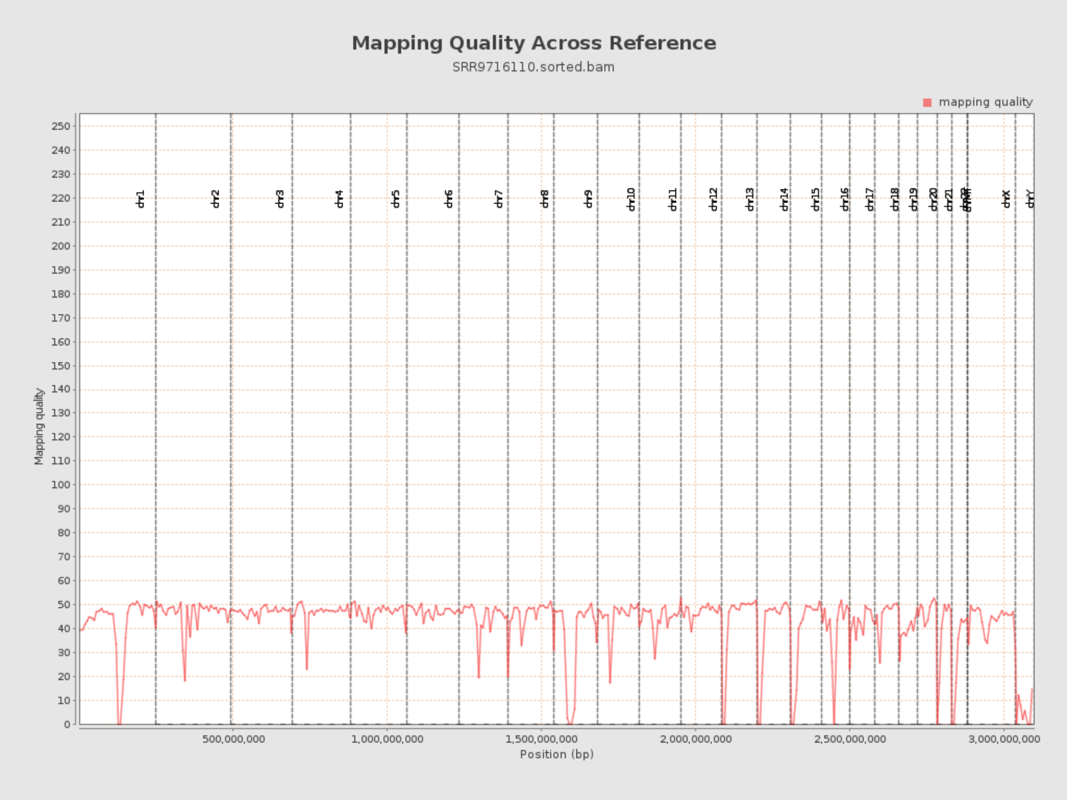
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram