Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:11:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716337.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_SRR9716337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716337.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:11:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	532,536
Mapped reads	468,275 / 87.93%
Unmapped reads	64,261 / 12.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,103 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	10,142 / 1.9%
Duplication rate	1.73%
Clipped reads	468,754 / 88.02%

2.2. ACGT Content

Number/percentage of A's	7,221,859 / 27.02%
Number/percentage of C's	4,737,626 / 17.73%
Number/percentage of T's	8,357,602 / 31.27%
Number/percentage of G's	6,409,589 / 23.98%
Number/percentage of N's	397 / 0%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0086

Standard Deviation	0.1136

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

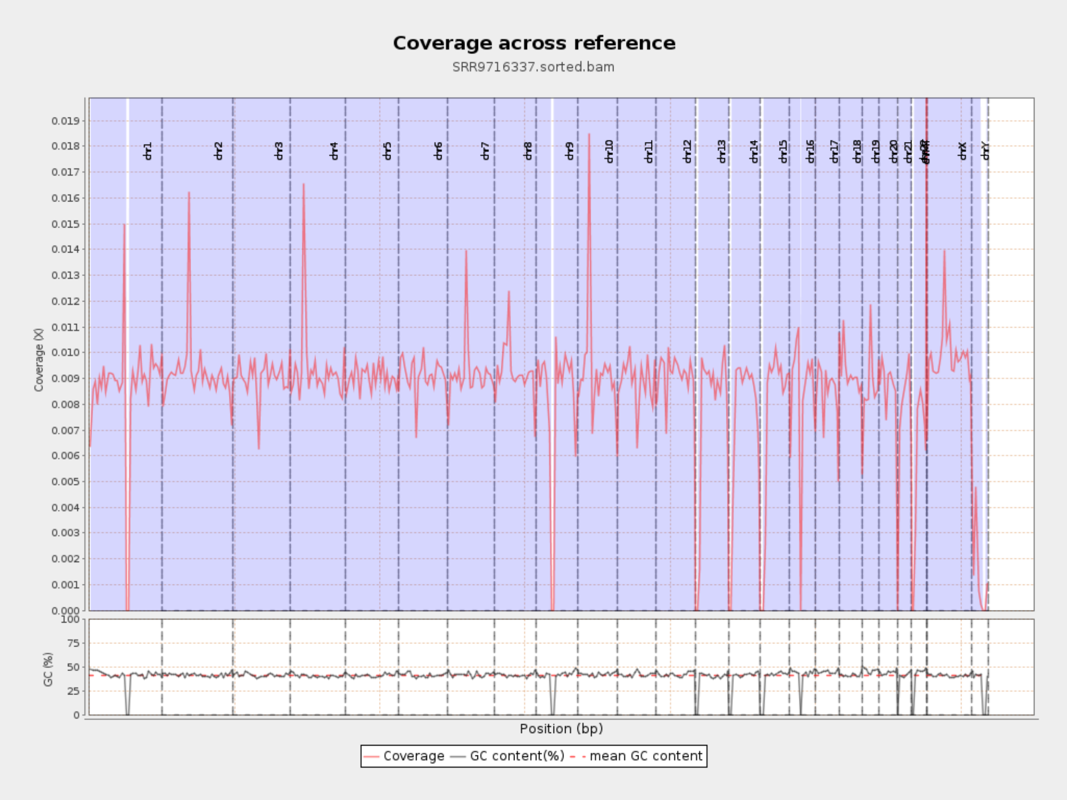
General error rate	0.58%
Mismatches	149,842
Insertions	2,229
Mapped reads with at least one insertion	0.47%
Deletions	4,485
Mapped reads with at least one deletion	0.95%
Homopolymer indels	41.67%

2.6. Chromosome stats

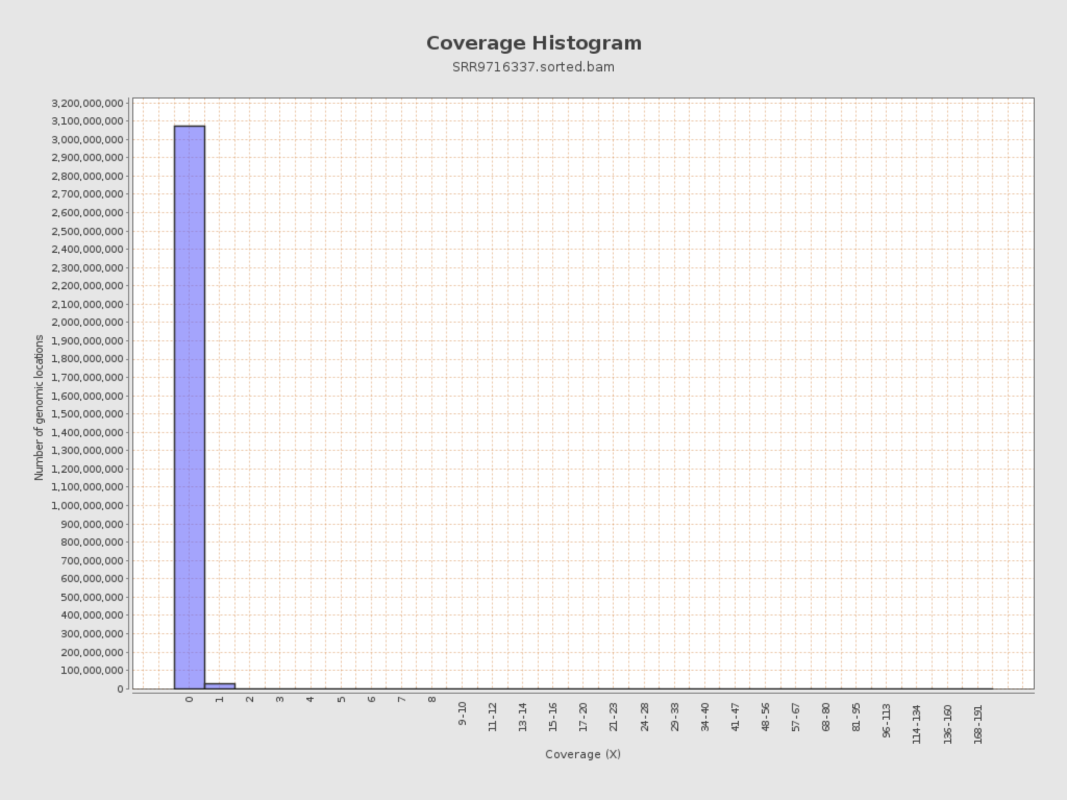
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2134018	0.0086	0.1681
chr2	243199373	2251584	0.0093	0.121
chr3	198022430	1786572	0.009	0.0978
chr4	191154276	1789293	0.0094	0.1047
chr5	180915260	1636943	0.009	0.0982
chr6	171115067	1563074	0.0091	0.1015
chr7	159138663	1475010	0.0093	0.1194

chr8	146364022	1354955	0.0093	0.1217
chr9	141213431	1133533	0.008	0.1122
chr10	135534747	1278431	0.0094	0.1206
chr11	135006516	1193867	0.0088	0.1091
chr12	133851895	1220266	0.0091	0.1
chr13	115169878	871123	0.0076	0.0893
chr14	107349540	794006	0.0074	0.091
chr15	102531392	760281	0.0074	0.0887
chr16	90354753	758274	0.0084	0.0987
chr17	81195210	683449	0.0084	0.0971
chr18	78077248	725443	0.0093	0.1661
chr19	59128983	518299	0.0088	0.1307
chr20	63025520	546776	0.0087	0.0974
chr21	48129895	363165	0.0075	0.0919
chr22	51304566	279986	0.0055	0.076
chrMT	16571	464	0.028	0.1756
chrX	155270560	1533420	0.0099	0.1089
chrY	59373566	82350	0.0014	0.0484

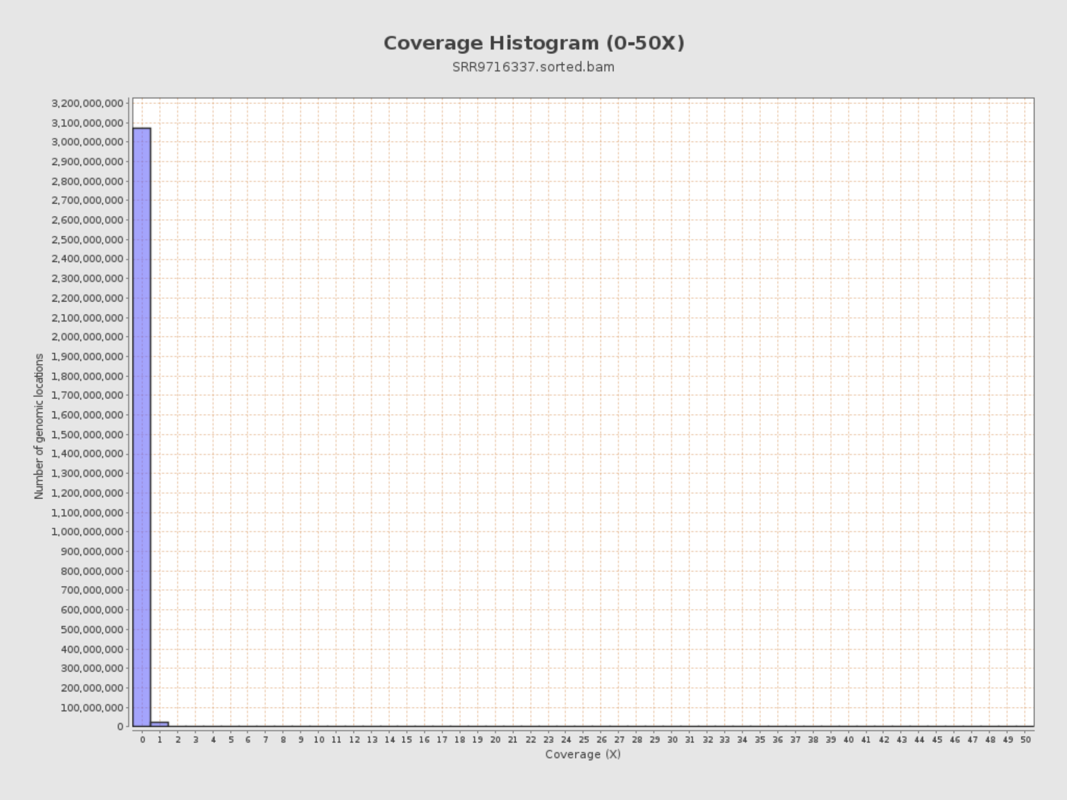
3. Results : Coverage across reference



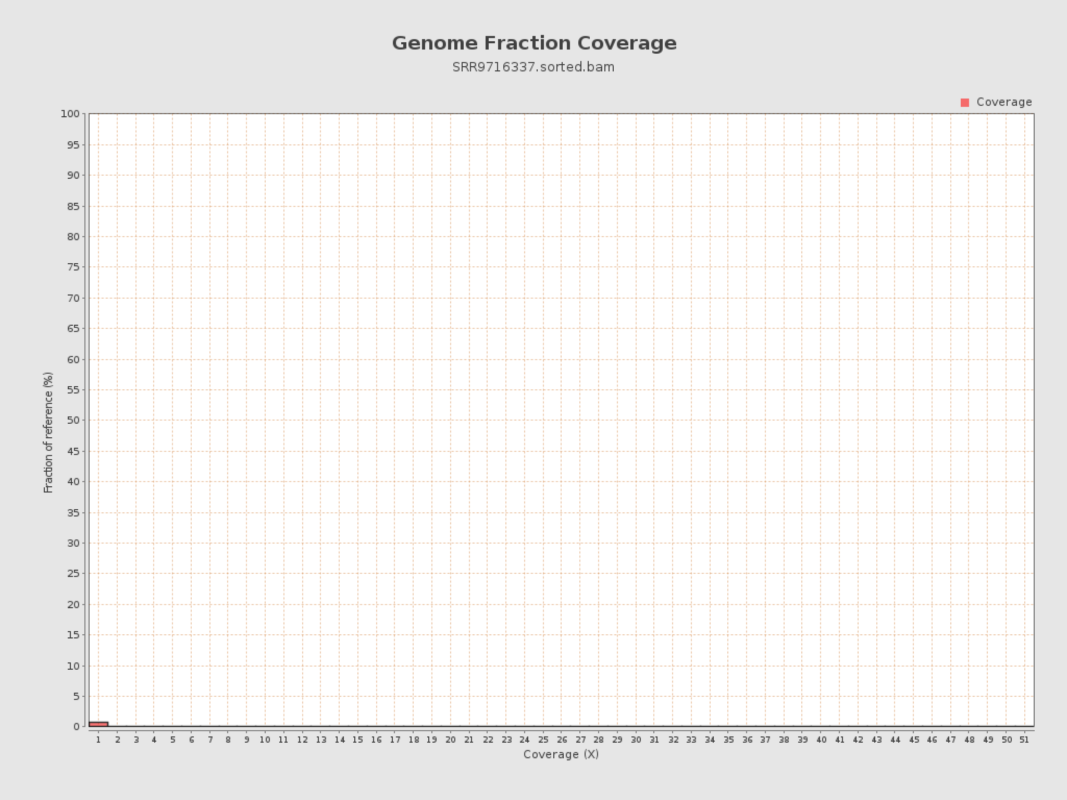
4. Results : Coverage Histogram



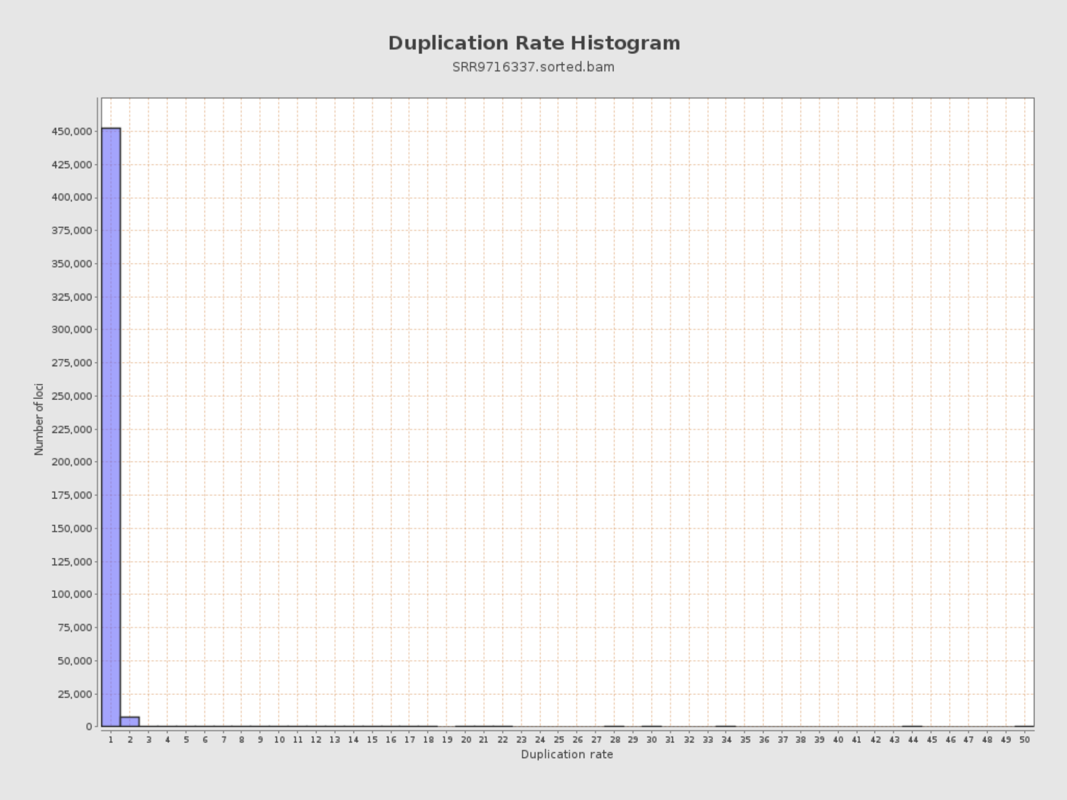
5. Results : Coverage Histogram (0-50X)



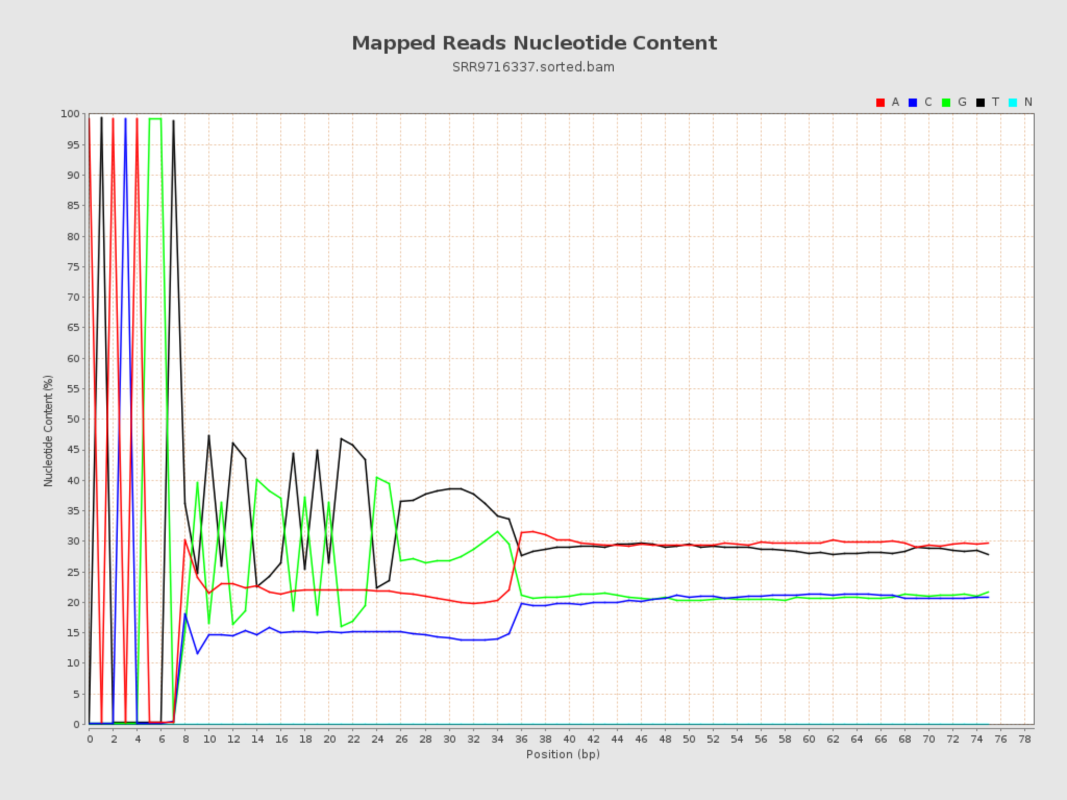
6. Results : Genome Fraction Coverage



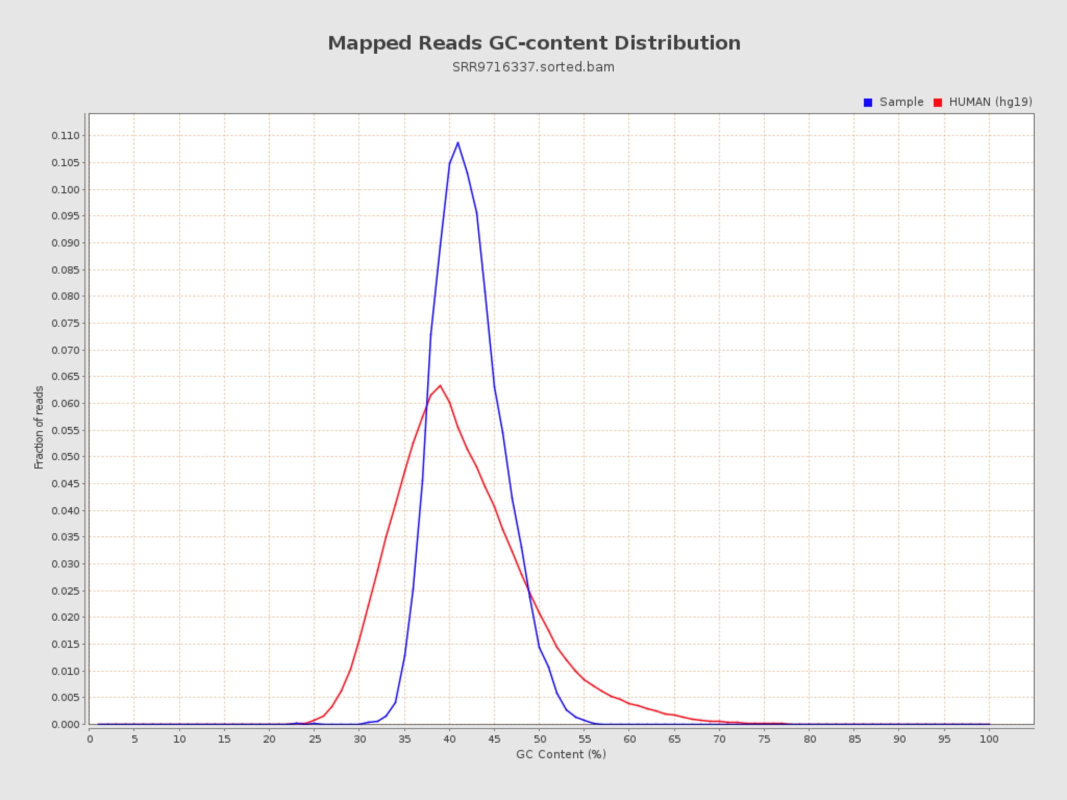
7. Results : Duplication Rate Histogram



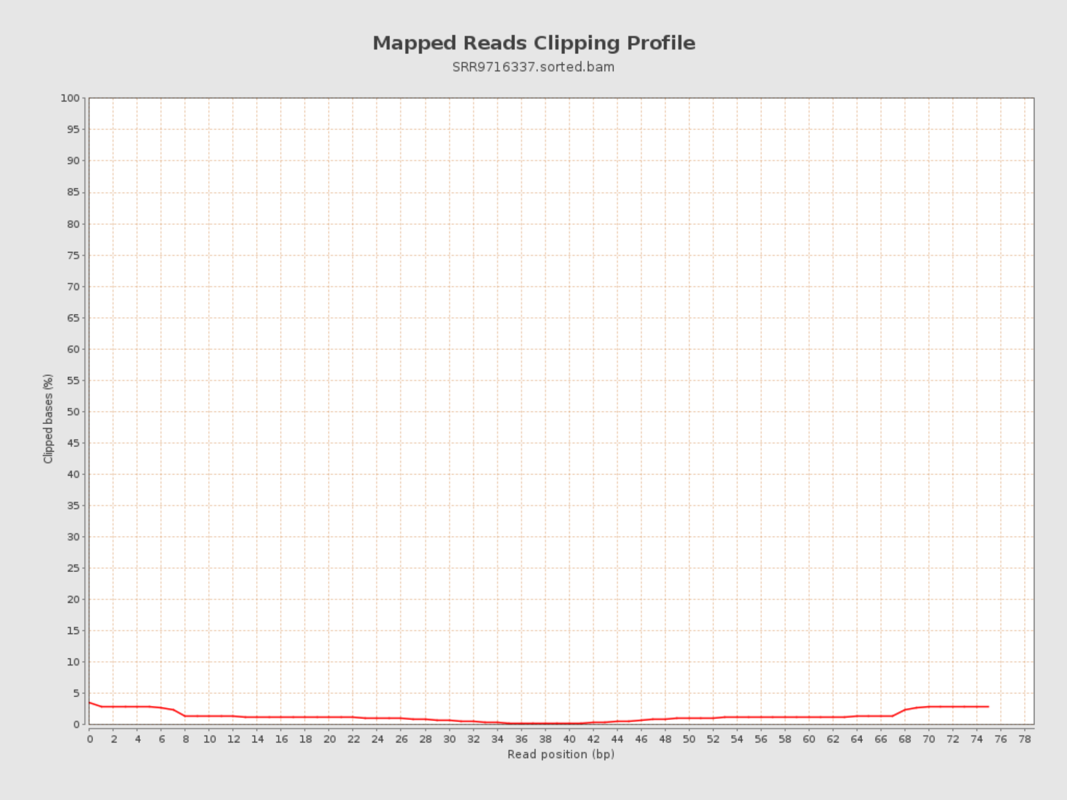
8. Results : Mapped Reads Nucleotide Content



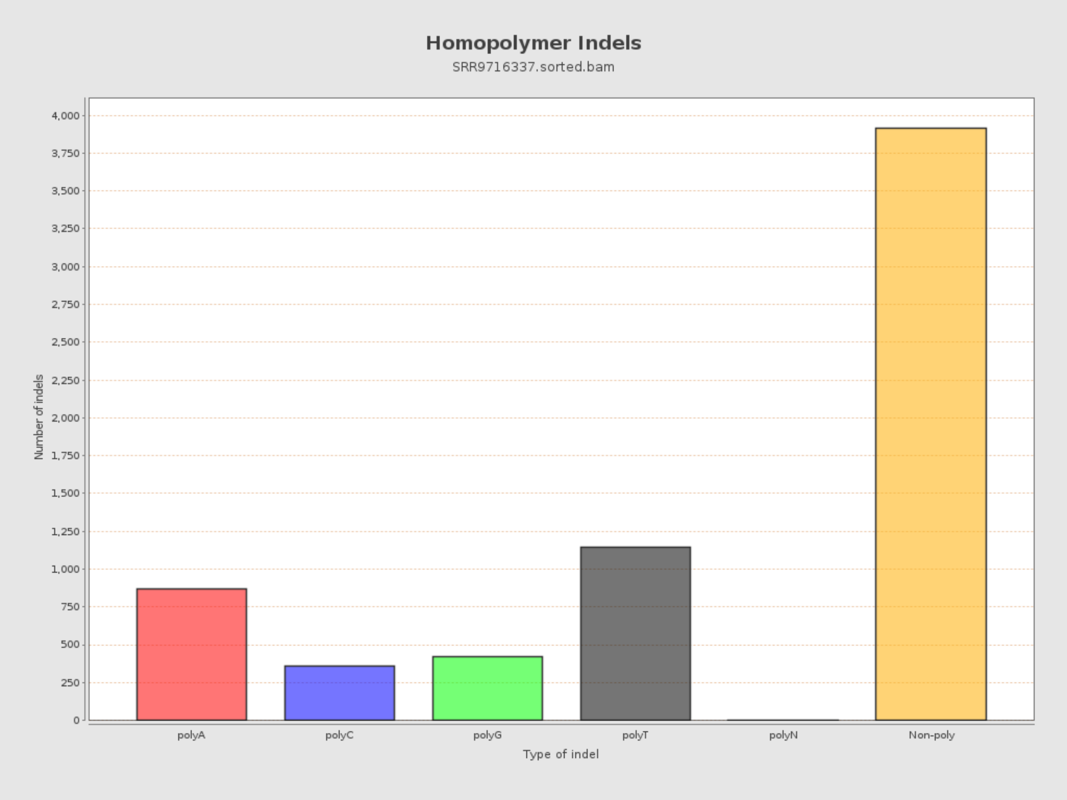
9. Results : Mapped Reads GC-content Distribution



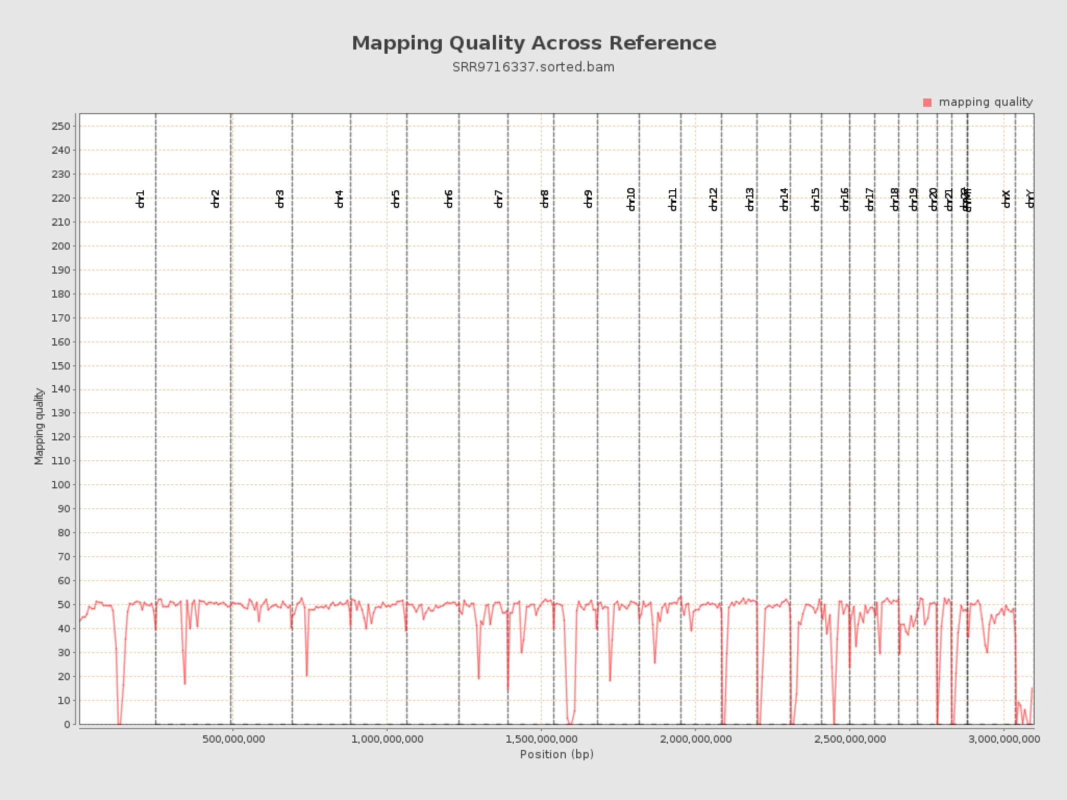
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram