Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:20:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716437.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_SRR9716437 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716437.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:20:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716437.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,258,976
Mapped reads	1,088,165 / 86.43%
Unmapped reads	170,811 / 13.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,128 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	24,512 / 1.95%
Duplication rate	1.58%
Clipped reads	1,088,668 / 86.47%

2.2. ACGT Content

Number/percentage of A's	16,063,132 / 26.07%
Number/percentage of C's	12,359,003 / 20.06%
Number/percentage of T's	18,942,152 / 30.75%
Number/percentage of G's	14,239,251 / 23.11%
Number/percentage of N's	856 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.2022

2.4. Mapping Quality

Mean Mapping Quality	42.95

2.5. Mismatches and indels

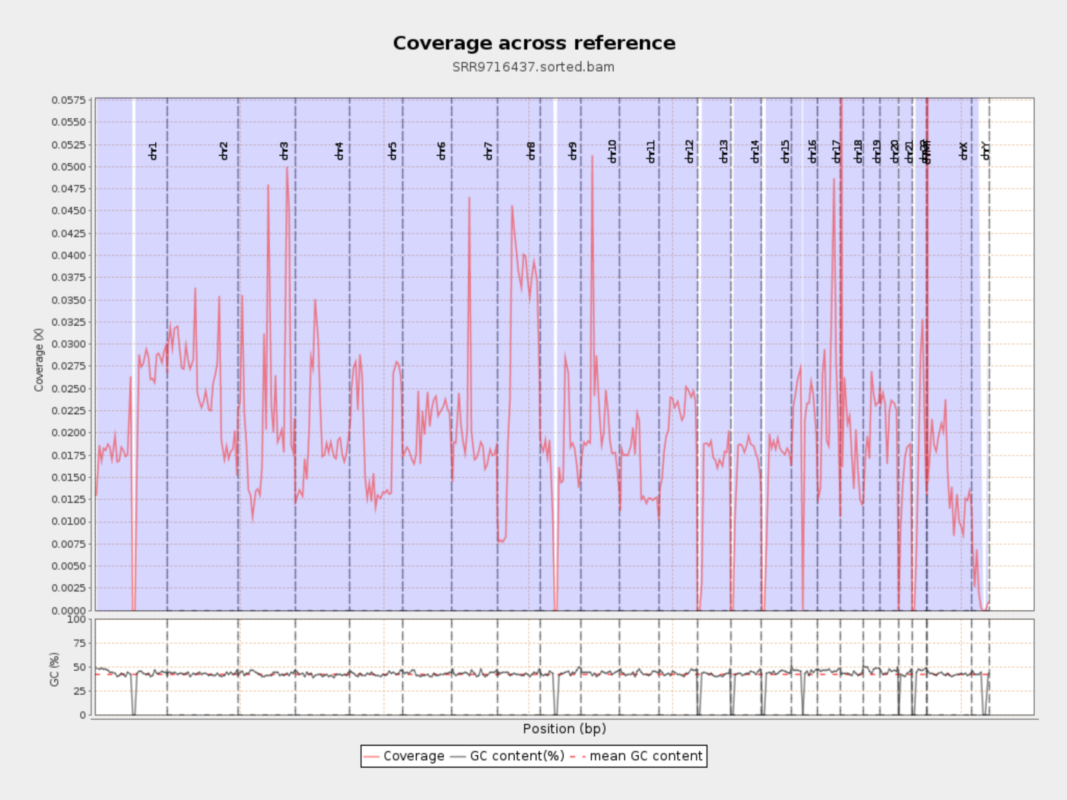
General error rate	0.53%
Mismatches	317,941
Insertions	4,986
Mapped reads with at least one insertion	0.46%
Deletions	11,912
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.66%

2.6. Chromosome stats

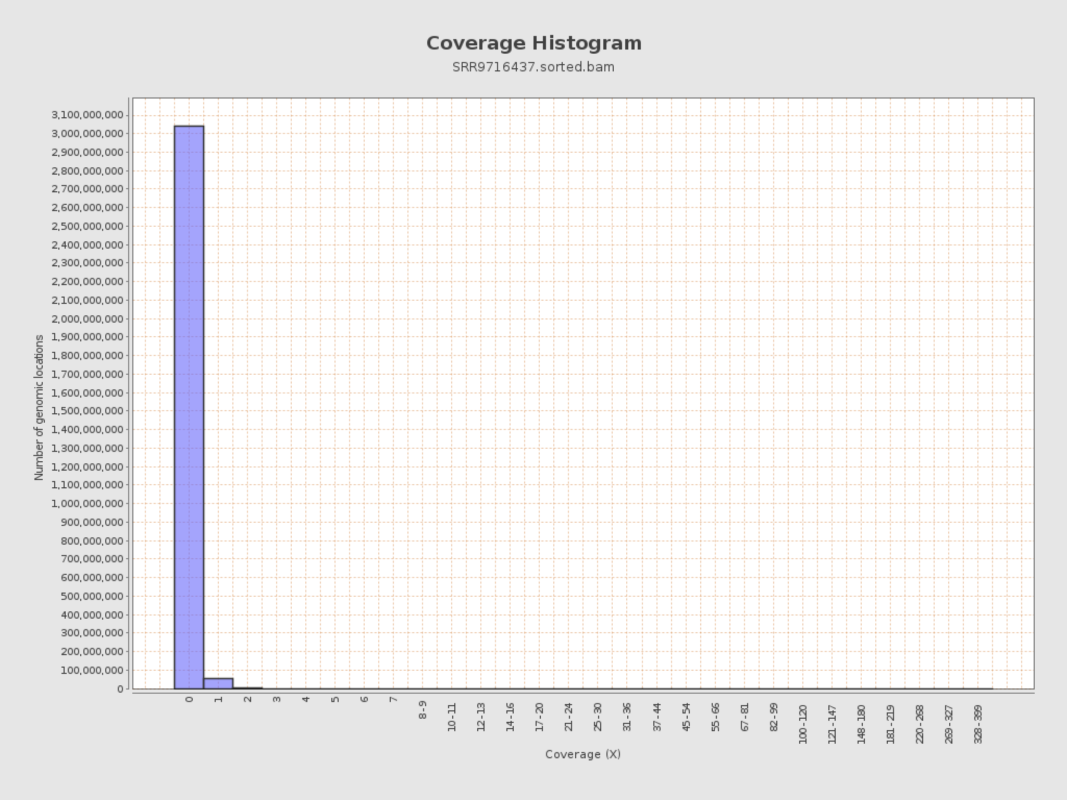
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5234178	0.021	0.2664
chr2	243199373	6191822	0.0255	0.2485
chr3	198022430	4523256	0.0228	0.1649
chr4	191154276	3697011	0.0193	0.1508
chr5	180915260	3484826	0.0193	0.1464
chr6	171115067	3563343	0.0208	0.1621
chr7	159138663	3164315	0.0199	0.393

chr8	146364022	4404599	0.0301	0.2186
chr9	141213431	2274895	0.0161	0.1533
chr10	135534747	2955239	0.0218	0.2594
chr11	135006516	2141054	0.0159	0.1531
chr12	133851895	2901919	0.0217	0.161
chr13	115169878	1714916	0.0149	0.1284
chr14	107349540	1637383	0.0153	0.1369
chr15	102531392	1533283	0.015	0.1311
chr16	90354753	1933802	0.0214	0.1629
chr17	81195210	2008183	0.0247	0.169
chr18	78077248	1625827	0.0208	0.2405
chr19	59128983	1264671	0.0214	0.2375
chr20	63025520	1383269	0.0219	0.16
chr21	48129895	672865	0.014	0.1281
chr22	51304566	799465	0.0156	0.1325
chrMT	16571	22374	1.3502	1.4643
chrX	155270560	2354503	0.0152	0.1437
chrY	59373566	135933	0.0023	0.0614

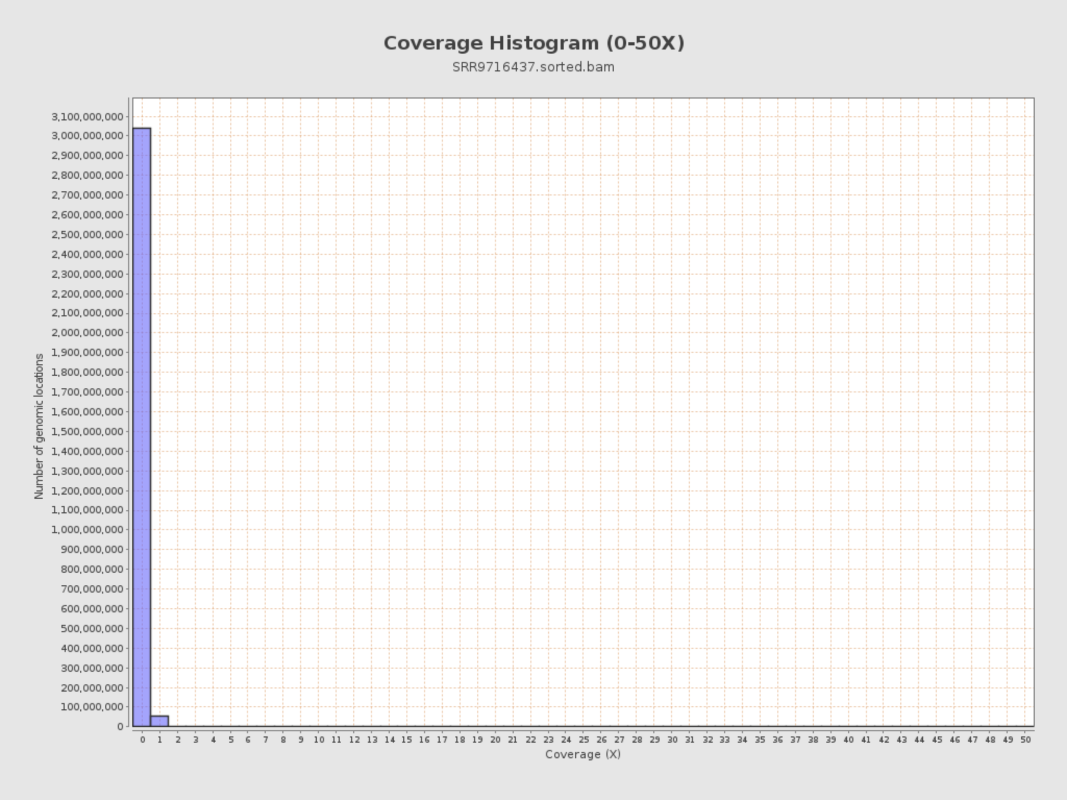
3. Results : Coverage across reference



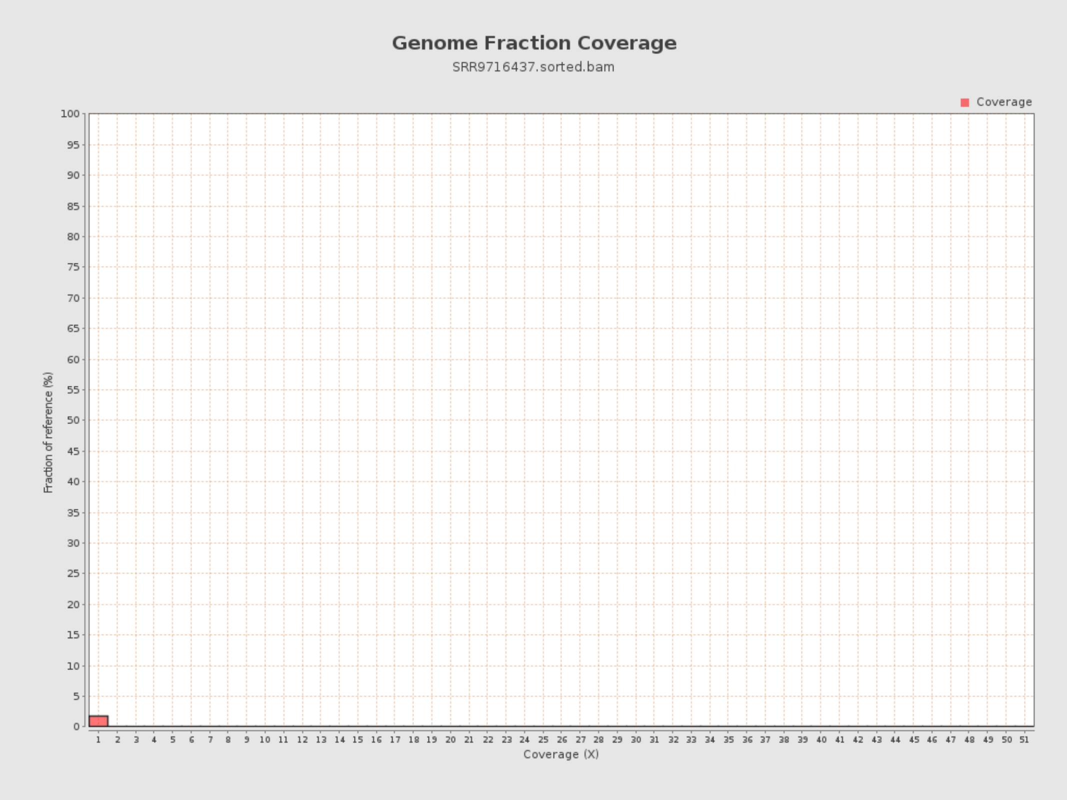
4. Results : Coverage Histogram



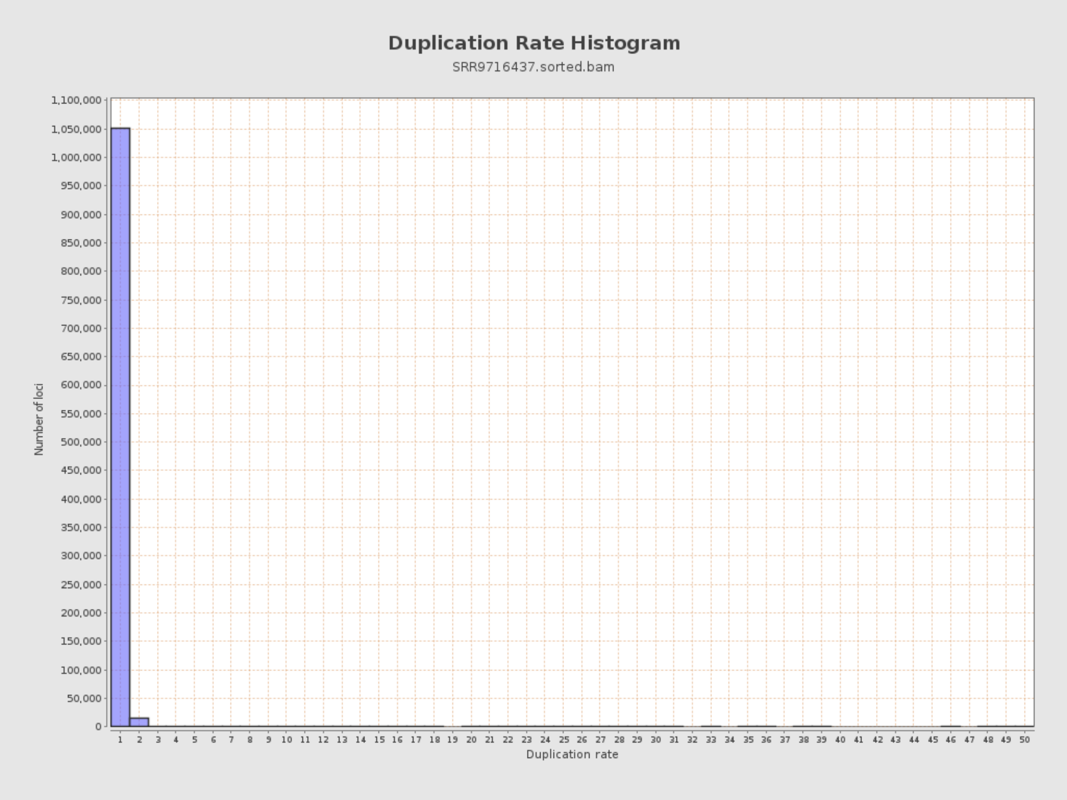
5. Results : Coverage Histogram (0-50X)



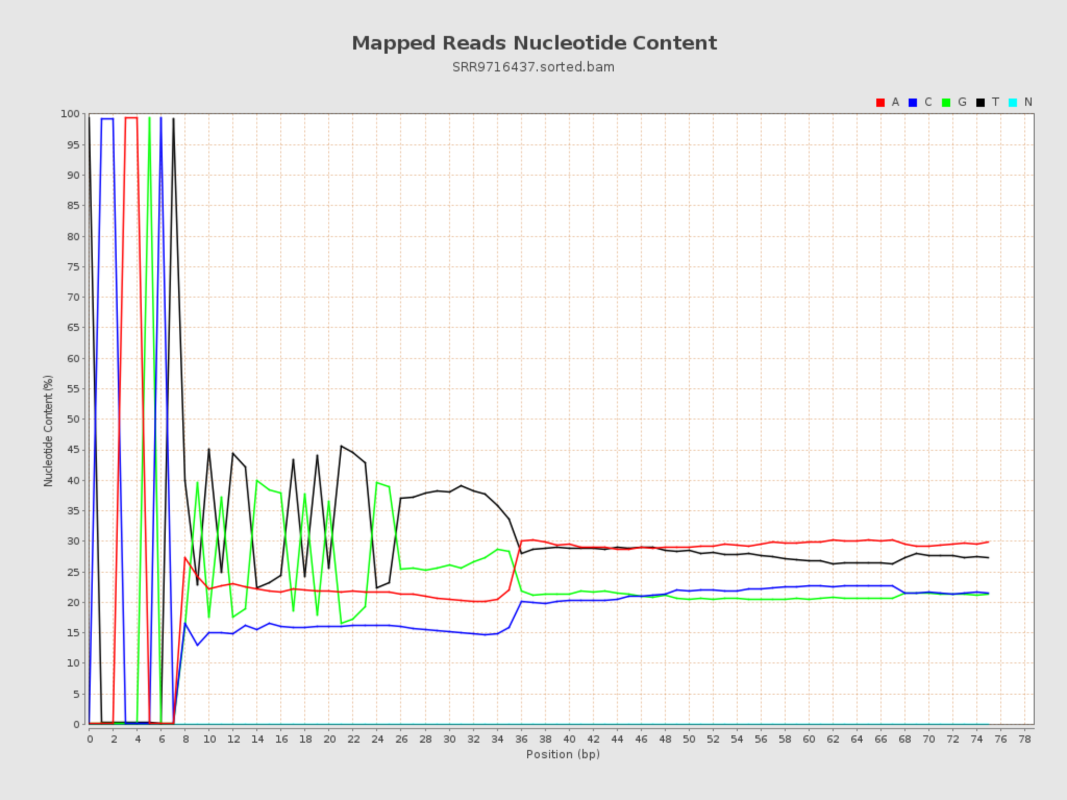
6. Results : Genome Fraction Coverage



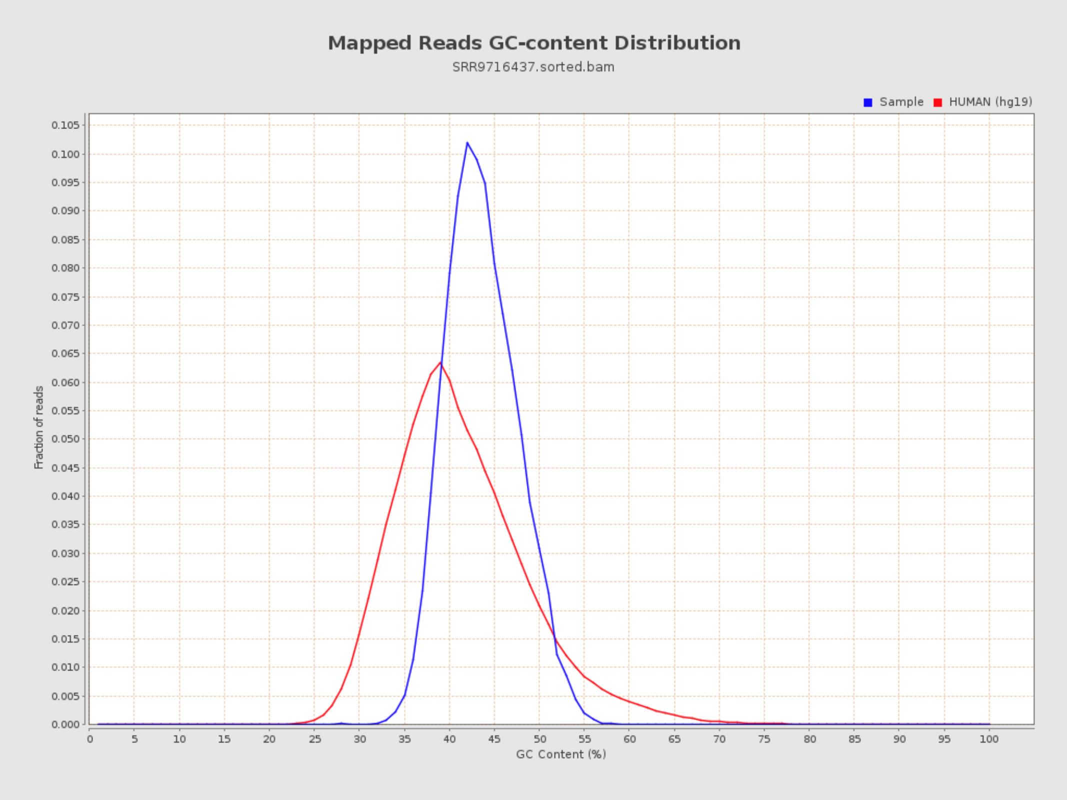
7. Results : Duplication Rate Histogram



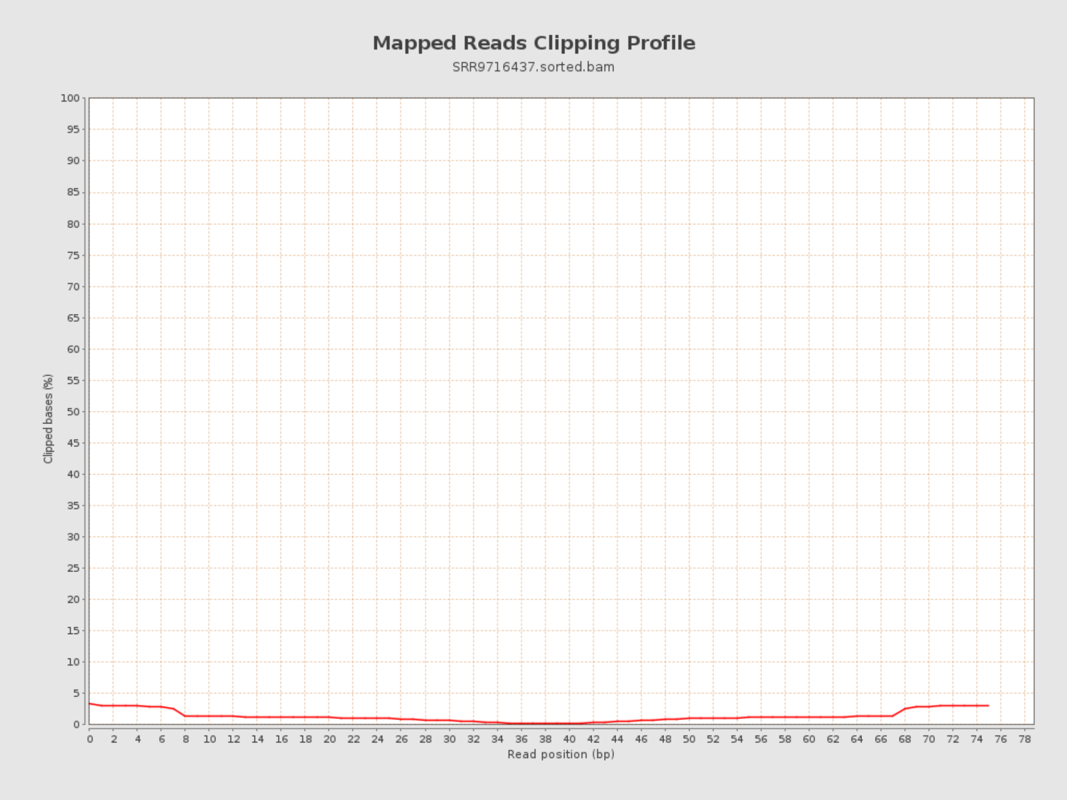
8. Results : Mapped Reads Nucleotide Content



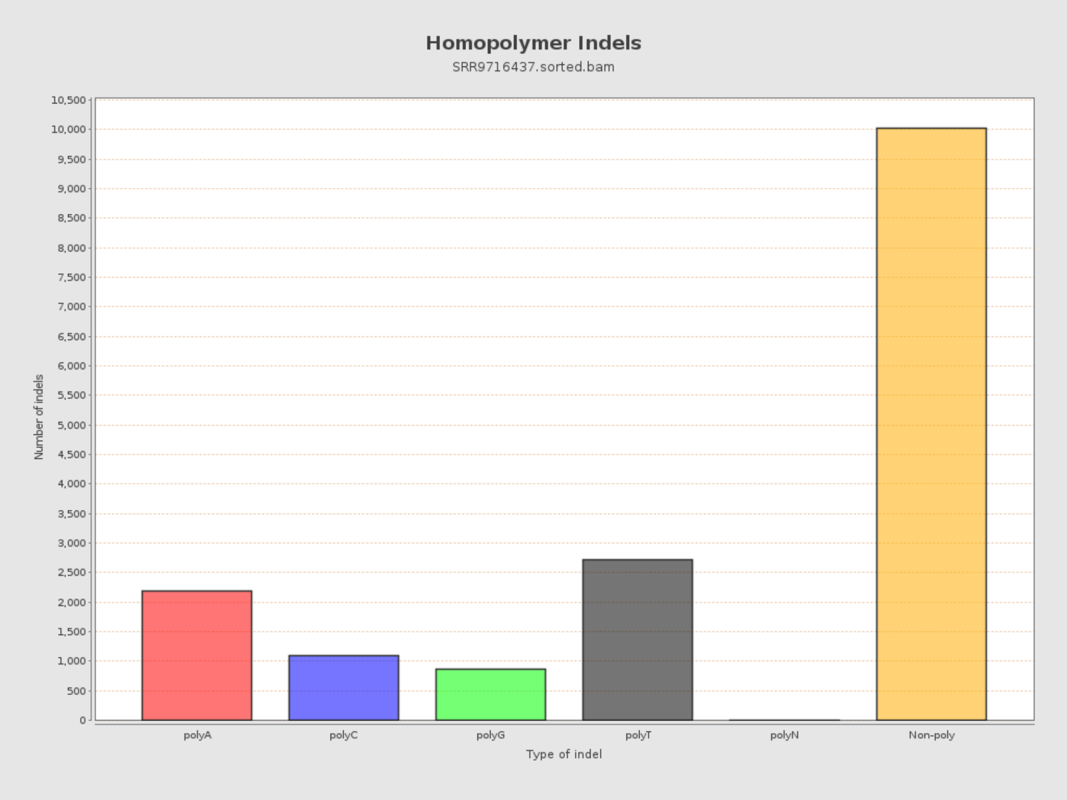
9. Results : Mapped Reads GC-content Distribution



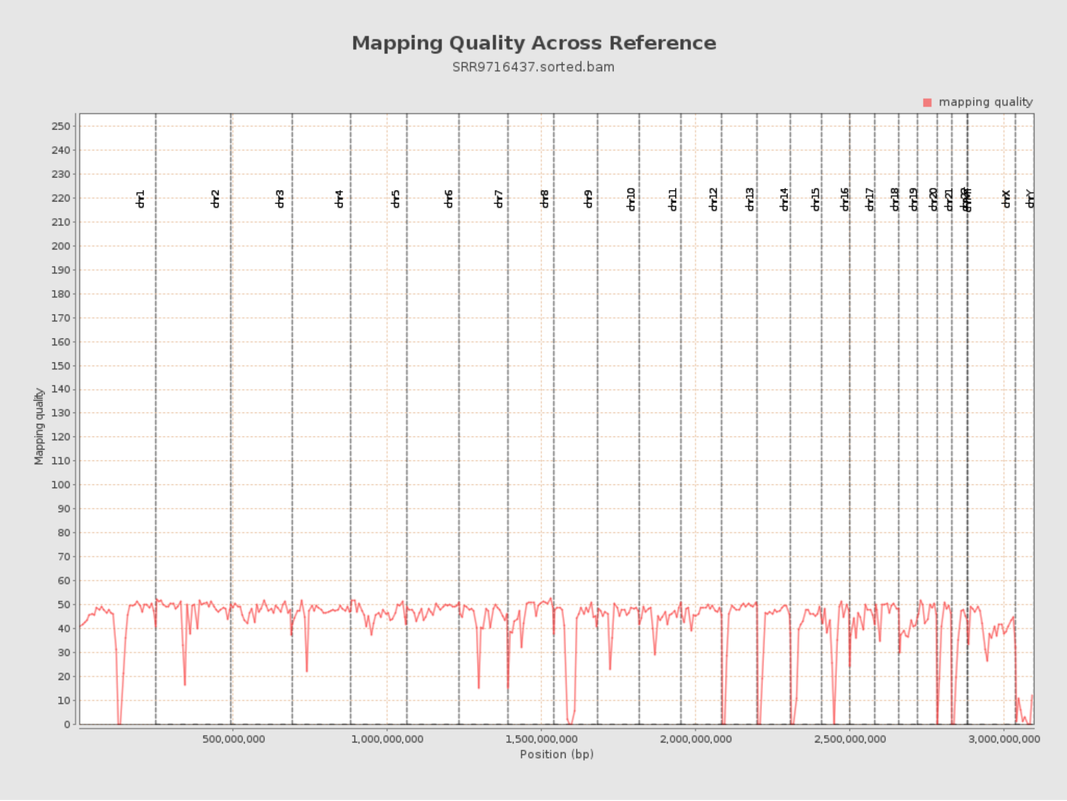
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram