Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:04:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716446.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_SRR9716446 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716446.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:04:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716446.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	743,370
Mapped reads	711,642 / 95.73%
Unmapped reads	31,728 / 4.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,331 / 1.93%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	25,855 / 3.48%
Duplication rate	2.55%
Clipped reads	725,824 / 97.64%

2.2. ACGT Content

Number/percentage of A's	14,913,586 / 25.33%
Number/percentage of C's	11,753,748 / 19.96%
Number/percentage of T's	18,063,360 / 30.67%
Number/percentage of G's	14,151,542 / 24.03%
Number/percentage of N's	4,280 / 0.01%
GC Percentage	43.99%

2.3. Coverage

Mean	0.019

Standard Deviation	0.221

2.4. Mapping Quality

Mean Mapping Quality	48.82

2.5. Mismatches and indels

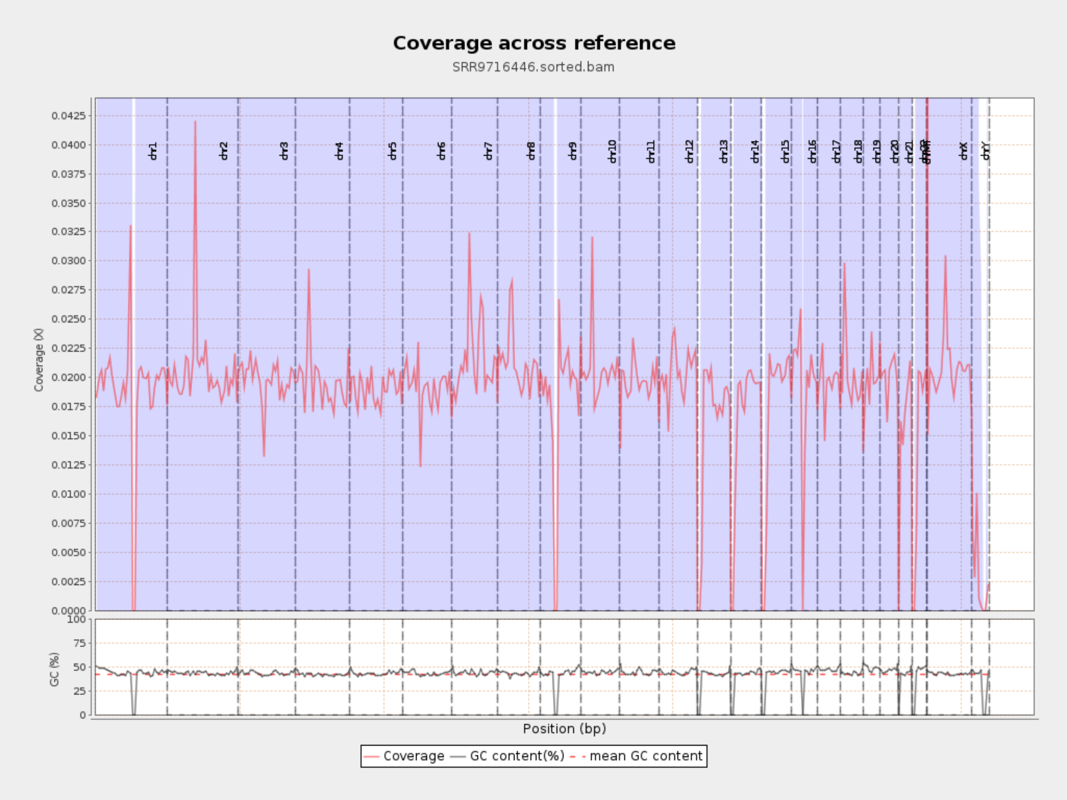
General error rate	0.72%
Mismatches	414,360
Insertions	4,982
Mapped reads with at least one insertion	0.69%
Deletions	14,217
Mapped reads with at least one deletion	1.97%
Homopolymer indels	44.7%

2.6. Chromosome stats

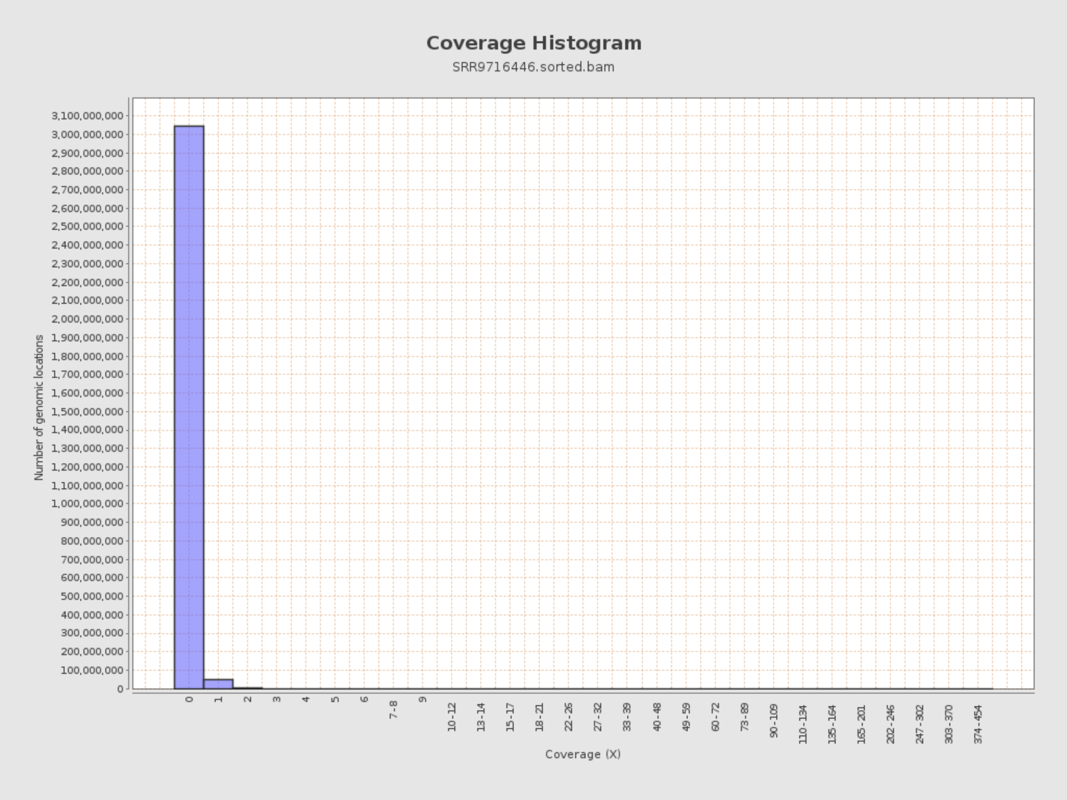
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4669642	0.0187	0.3446
chr2	243199373	5040234	0.0207	0.2489
chr3	198022430	3922055	0.0198	0.1494
chr4	191154276	3766240	0.0197	0.162
chr5	180915260	3457606	0.0191	0.1485
chr6	171115067	3278089	0.0192	0.1588
chr7	159138663	3450103	0.0217	0.253

chr8	146364022	3117366	0.0213	0.3548
chr9	141213431	2512636	0.0178	0.2337
chr10	135534747	2805855	0.0207	0.2001
chr11	135006516	2680137	0.0199	0.226
chr12	133851895	2734131	0.0204	0.1544
chr13	115169878	1805064	0.0157	0.1327
chr14	107349540	1739367	0.0162	0.1556
chr15	102531392	1721694	0.0168	0.1379
chr16	90354753	1704213	0.0189	0.1592
chr17	81195210	1586749	0.0195	0.161
chr18	78077248	1578886	0.0202	0.4105
chr19	59128983	1175189	0.0199	0.254
chr20	63025520	1265952	0.0201	0.1558
chr21	48129895	771288	0.016	0.1441
chr22	51304566	707940	0.0138	0.1248
chrMT	16571	11835	0.7142	1.0624
chrX	155270560	3246782	0.0209	0.1795
chrY	59373566	162394	0.0027	0.1054

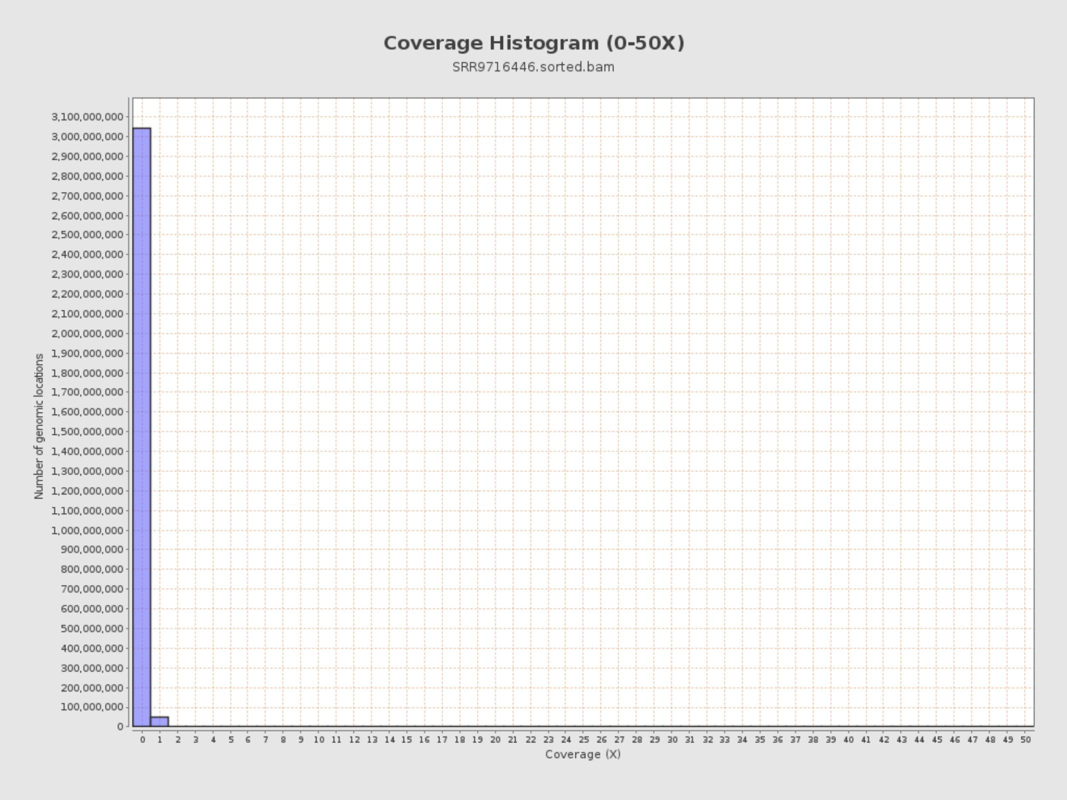
3. Results : Coverage across reference



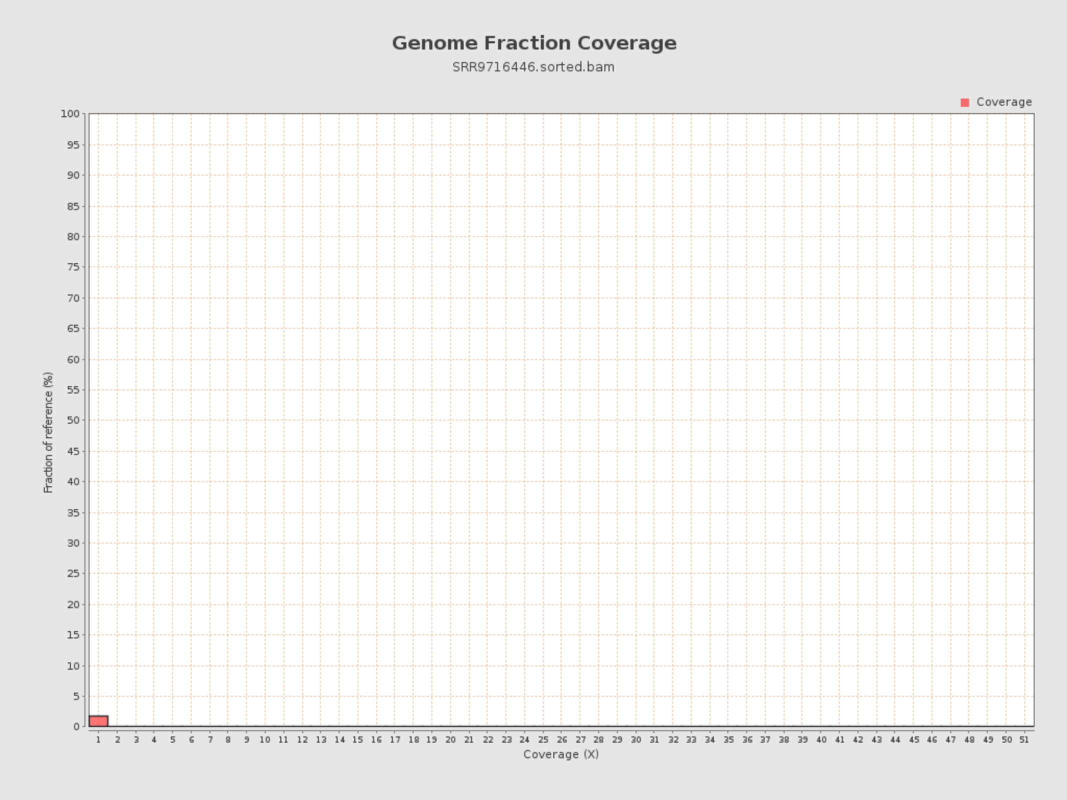
4. Results : Coverage Histogram



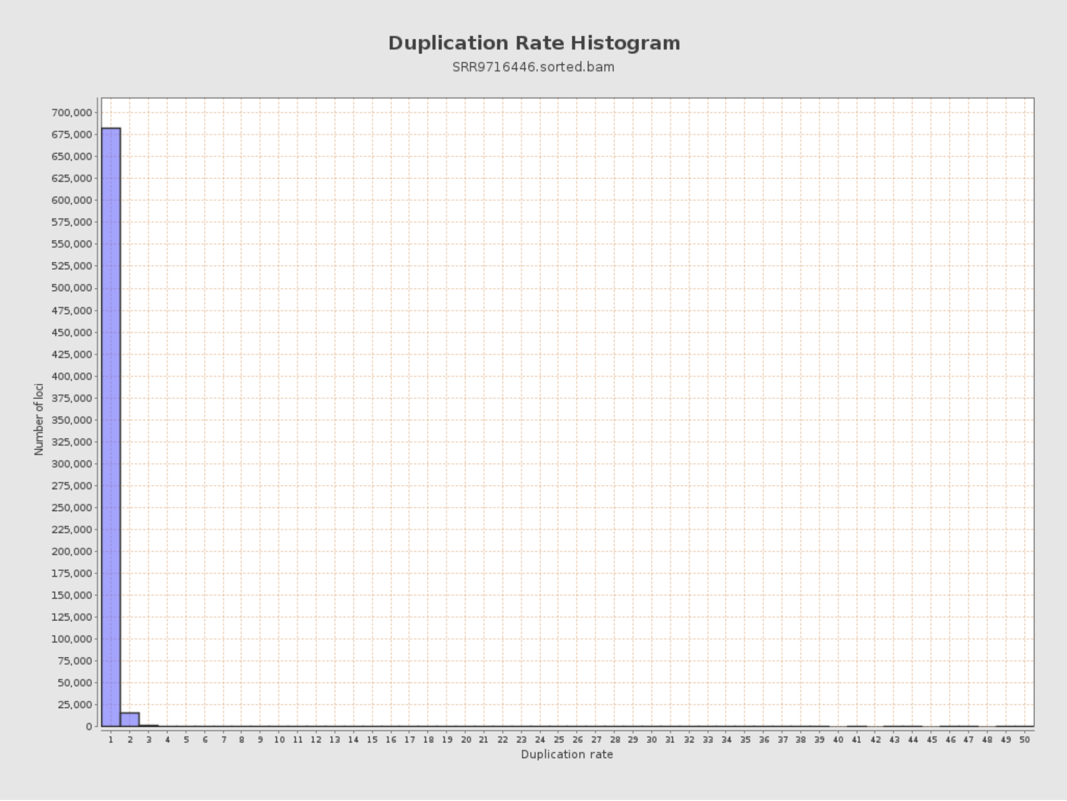
5. Results : Coverage Histogram (0-50X)



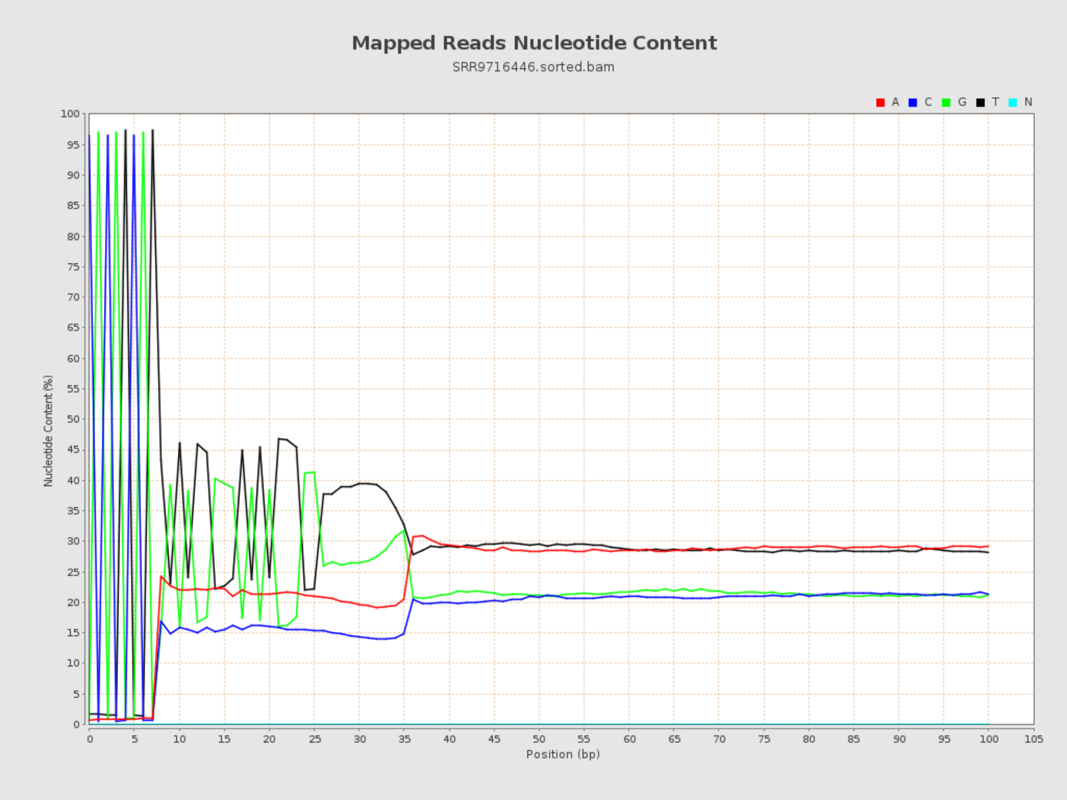
6. Results : Genome Fraction Coverage



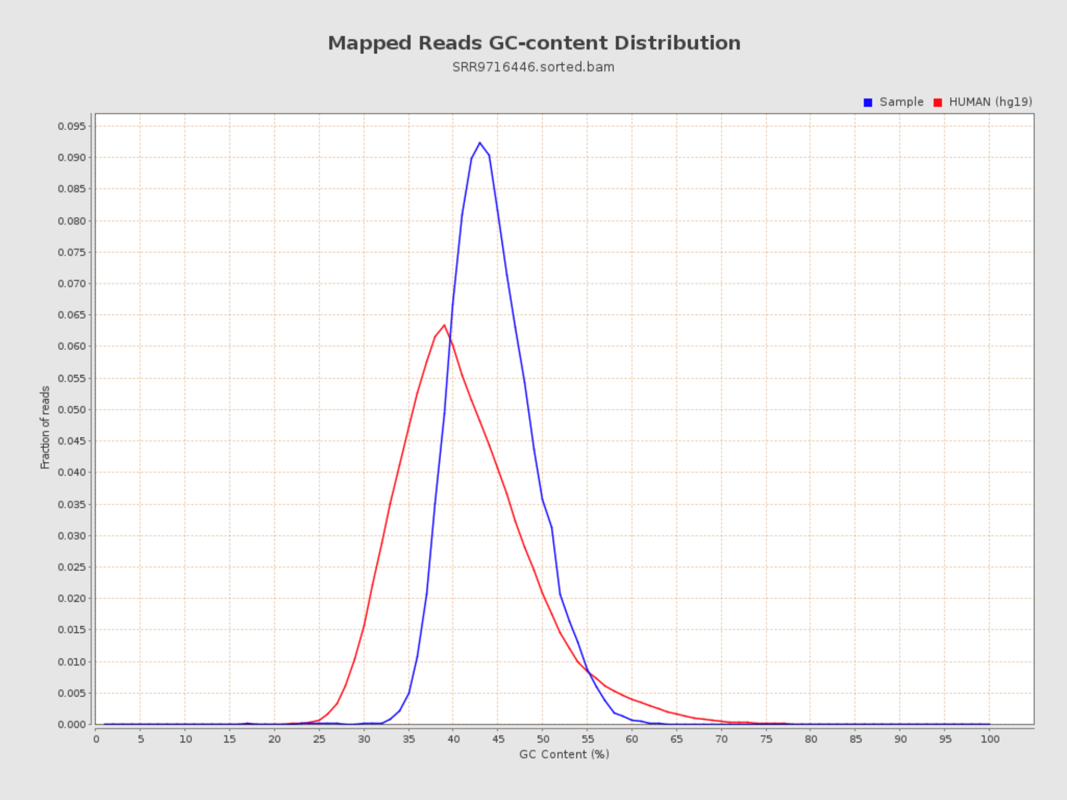
7. Results : Duplication Rate Histogram



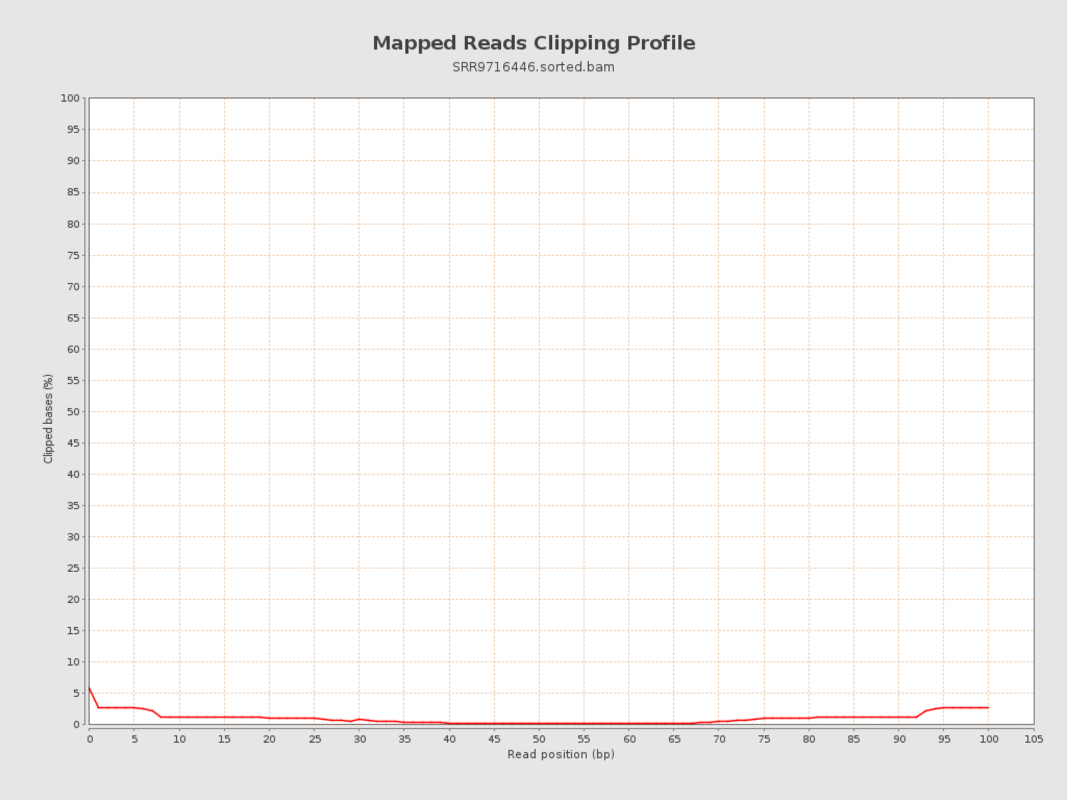
8. Results : Mapped Reads Nucleotide Content



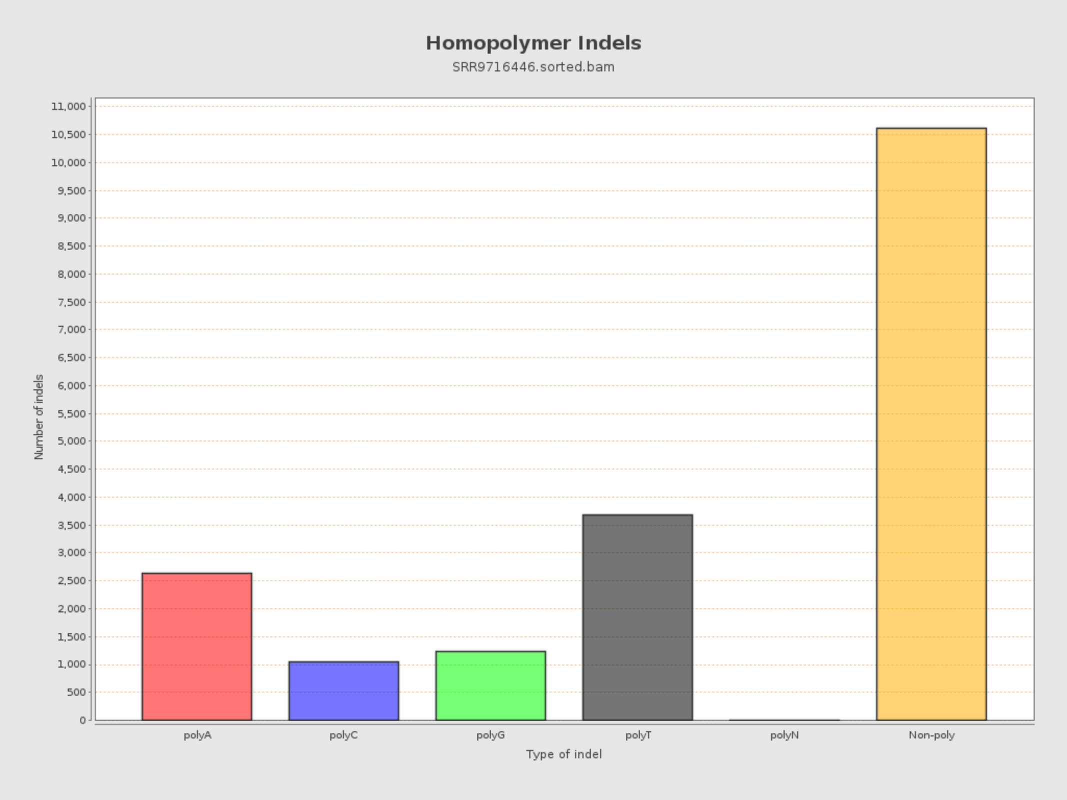
9. Results : Mapped Reads GC-content Distribution



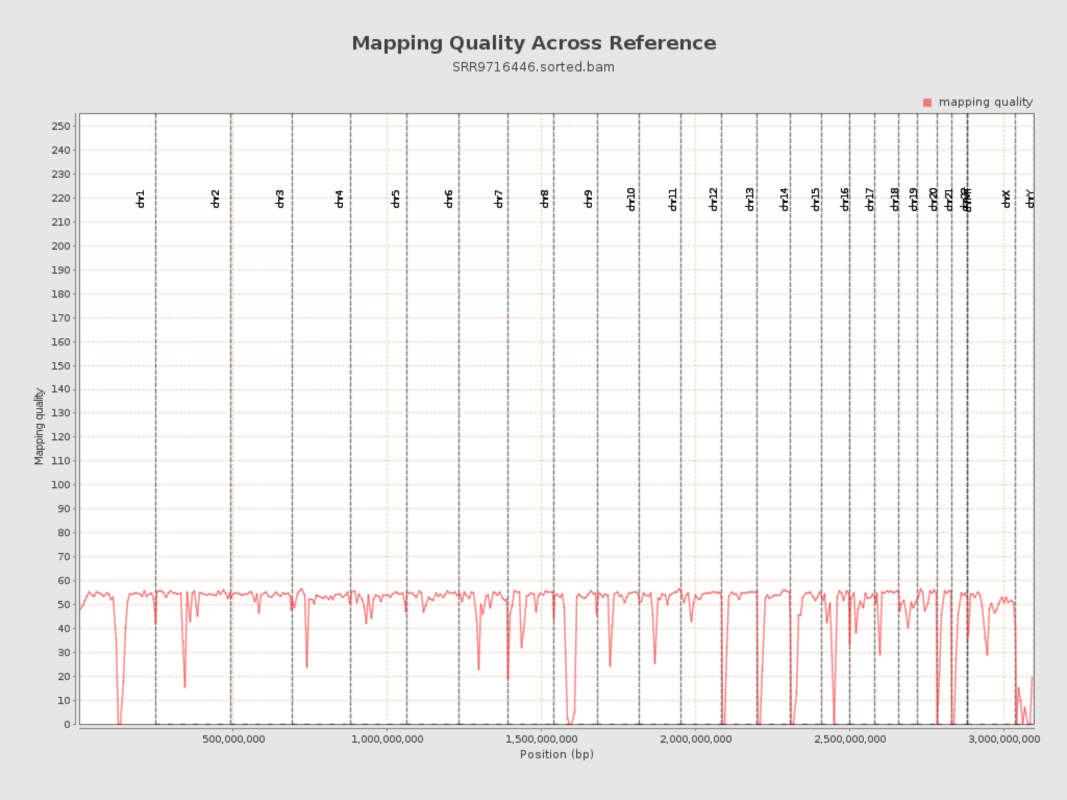
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram