Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:25:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716841.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_SRR9716841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:25:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	506,084
Mapped reads	415,598 / 82.12%
Unmapped reads	90,486 / 17.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,037 / 1.19%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	9,931 / 1.96%
Duplication rate	1.47%
Clipped reads	420,868 / 83.16%

2.2. ACGT Content

Number/percentage of A's	8,533,128 / 25.65%
Number/percentage of C's	6,205,011 / 18.65%
Number/percentage of T's	10,234,615 / 30.77%
Number/percentage of G's	8,287,412 / 24.92%
Number/percentage of N's	2,166 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1532

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

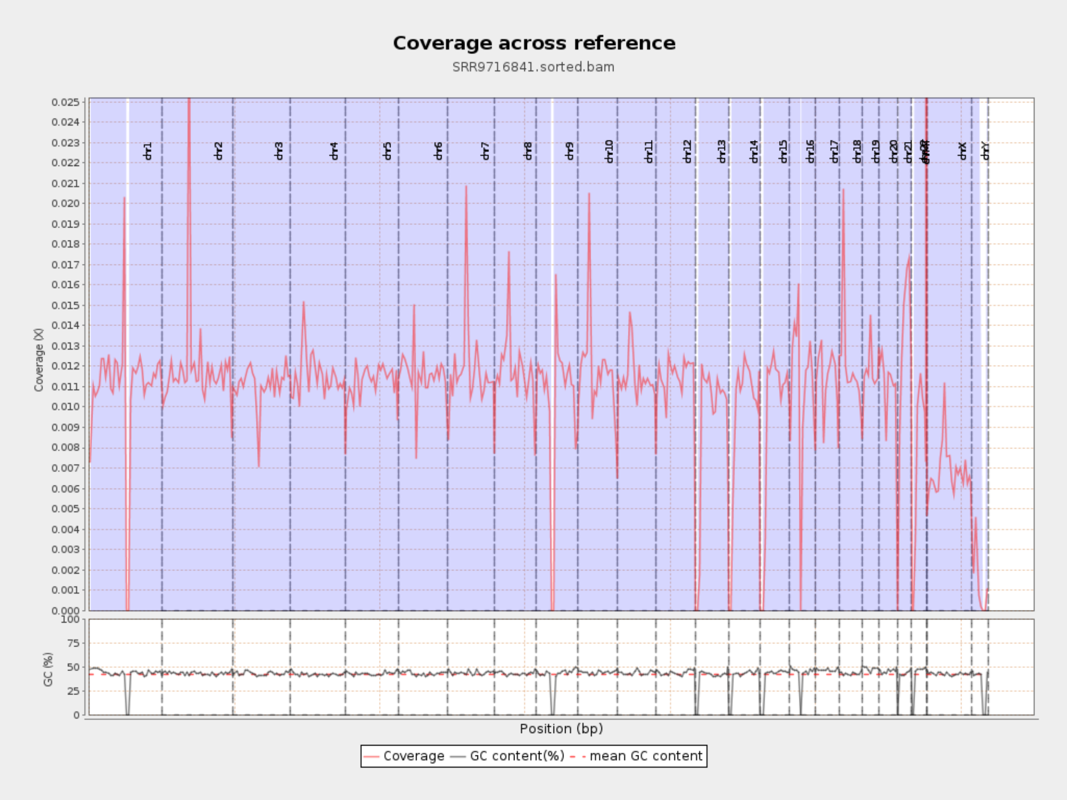
General error rate	0.83%
Mismatches	269,097
Insertions	3,049
Mapped reads with at least one insertion	0.72%
Deletions	8,166
Mapped reads with at least one deletion	1.93%
Homopolymer indels	43.2%

2.6. Chromosome stats

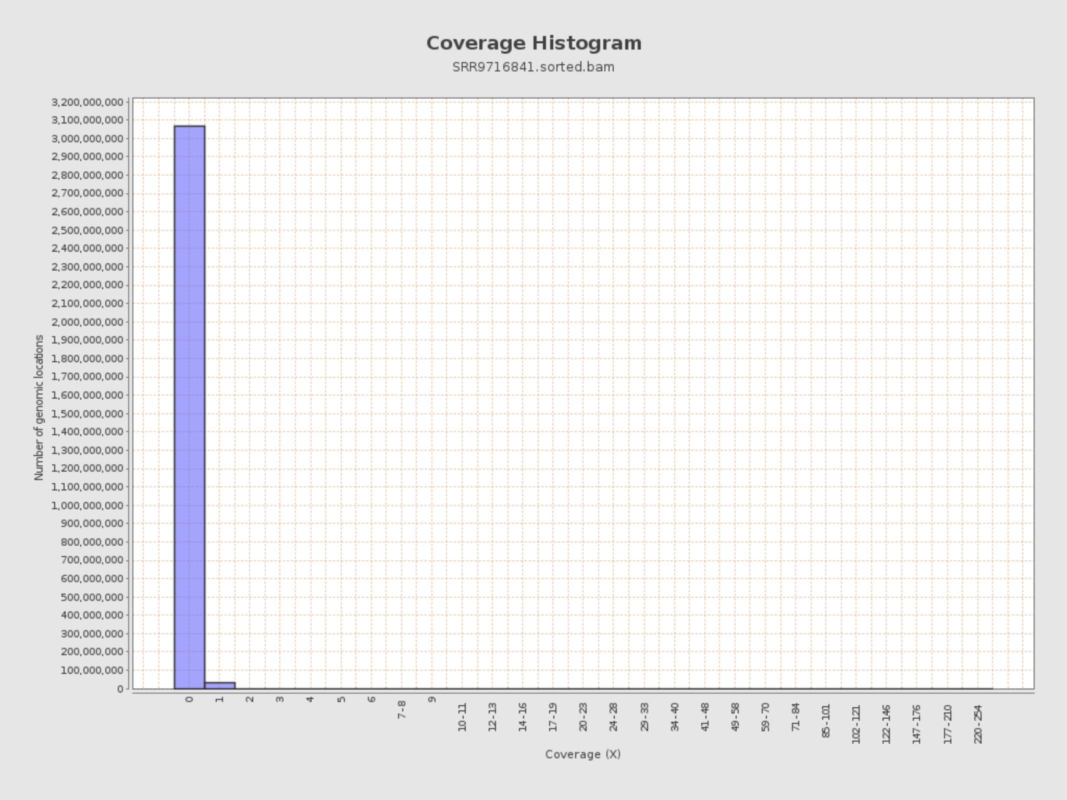
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2733793	0.011	0.2259
chr2	243199373	2929465	0.012	0.2008
chr3	198022430	2197065	0.0111	0.109
chr4	191154276	2210237	0.0116	0.1156
chr5	180915260	2046895	0.0113	0.1111
chr6	171115067	1981644	0.0116	0.1197
chr7	159138663	1896912	0.0119	0.1842

chr8	146364022	1728037	0.0118	0.1968
chr9	141213431	1460797	0.0103	0.1618
chr10	135534747	1613982	0.0119	0.1476
chr11	135006516	1536791	0.0114	0.1508
chr12	133851895	1542706	0.0115	0.1127
chr13	115169878	1038500	0.009	0.0978
chr14	107349540	1005235	0.0094	0.1115
chr15	102531392	957576	0.0093	0.1011
chr16	90354753	997932	0.011	0.1186
chr17	81195210	919863	0.0113	0.116
chr18	78077248	963957	0.0123	0.2923
chr19	59128983	696942	0.0118	0.1763
chr20	63025520	692987	0.011	0.1136
chr21	48129895	605712	0.0126	0.1187
chr22	51304566	365379	0.0071	0.0874
chrMT	16571	9892	0.5969	0.8897
chrX	155270560	1065267	0.0069	0.1022
chrY	59373566	78614	0.0013	0.0528

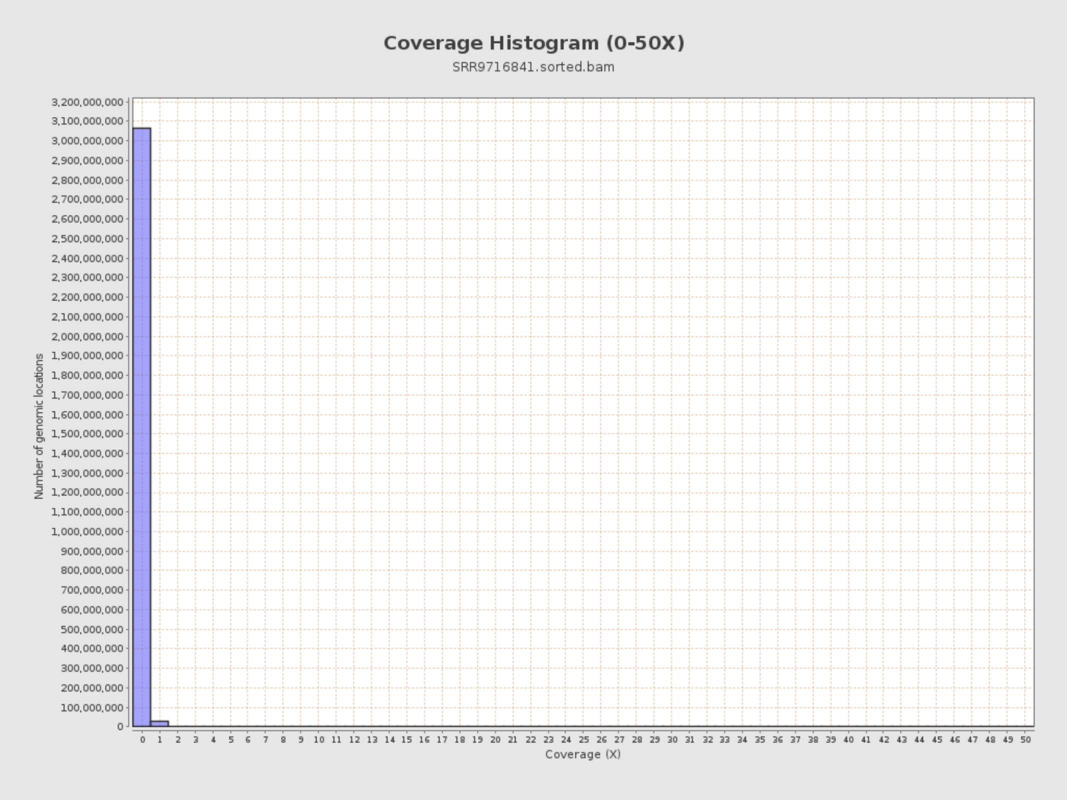
3. Results : Coverage across reference



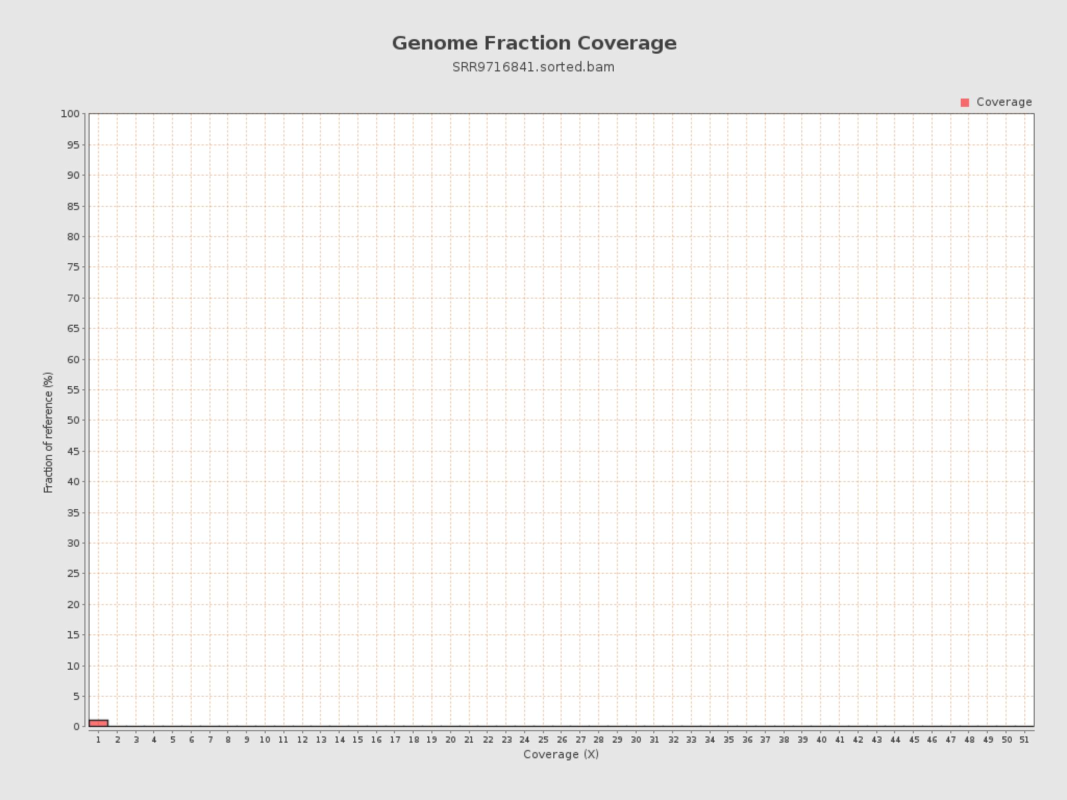
4. Results : Coverage Histogram



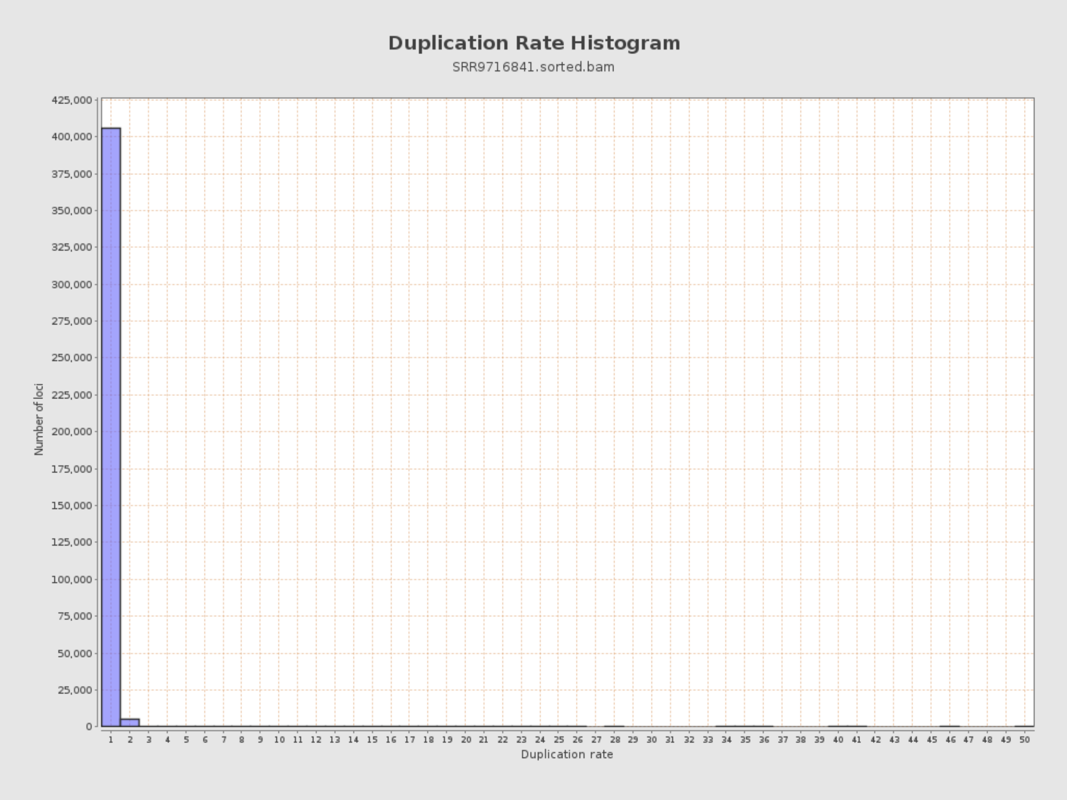
5. Results : Coverage Histogram (0-50X)



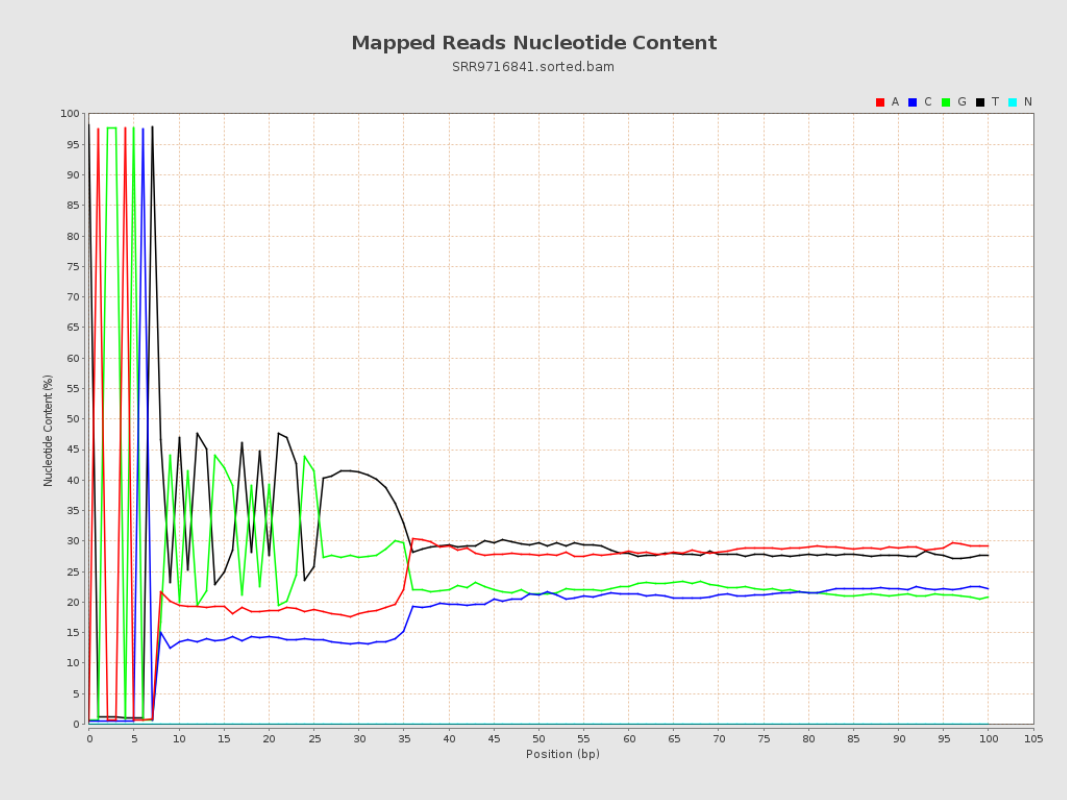
6. Results : Genome Fraction Coverage



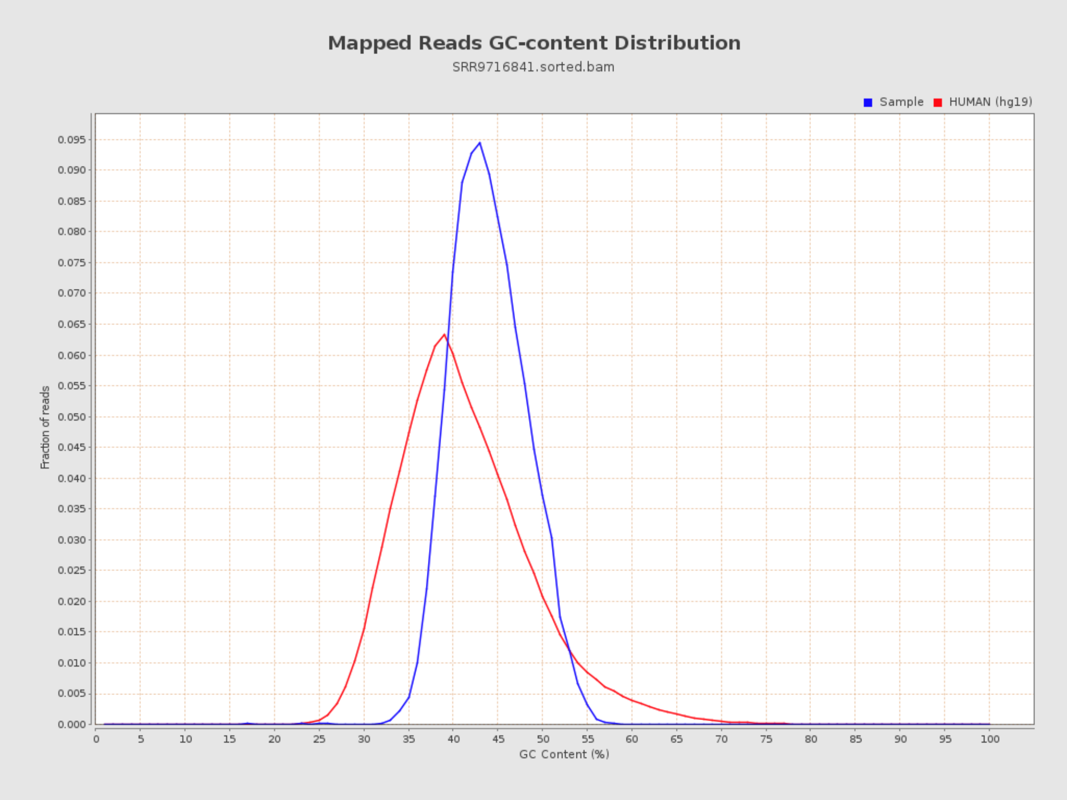
7. Results : Duplication Rate Histogram



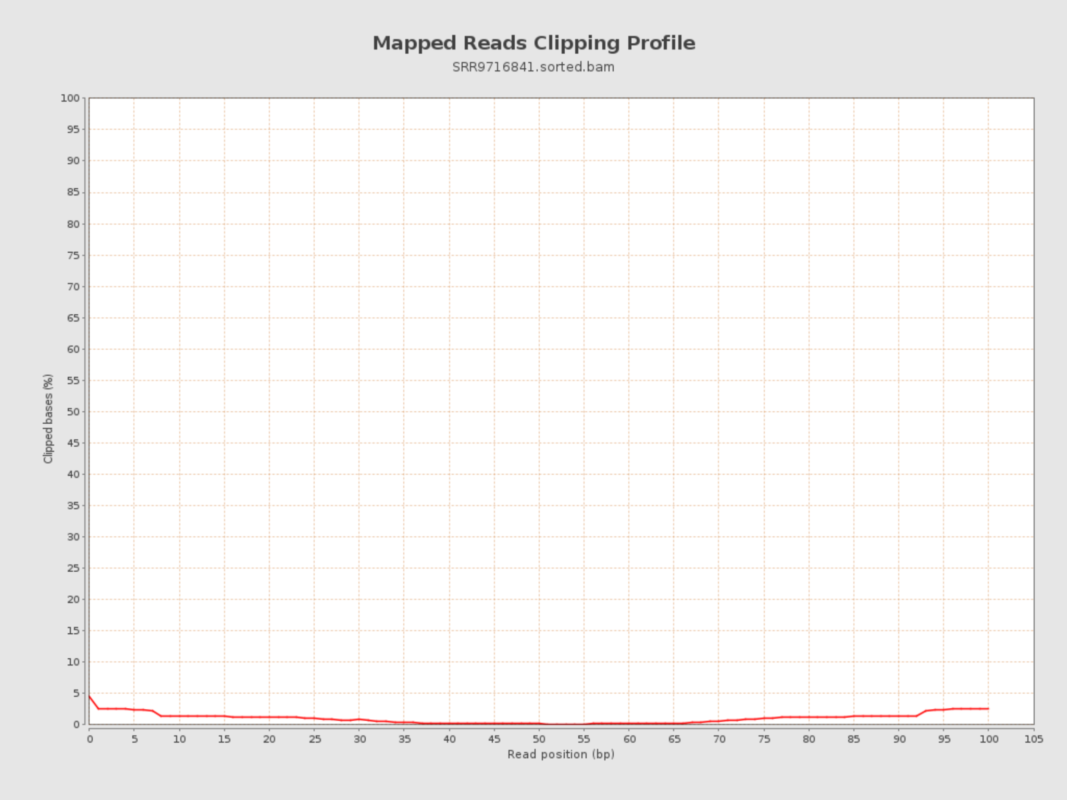
8. Results : Mapped Reads Nucleotide Content



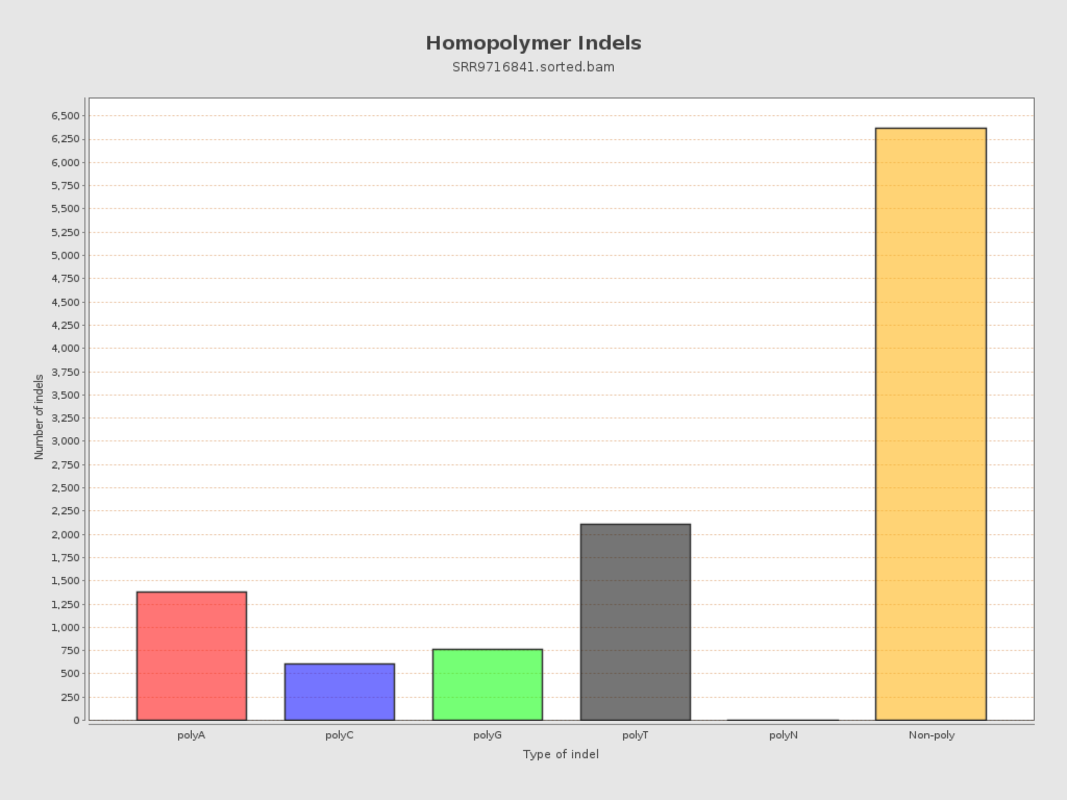
9. Results : Mapped Reads GC-content Distribution



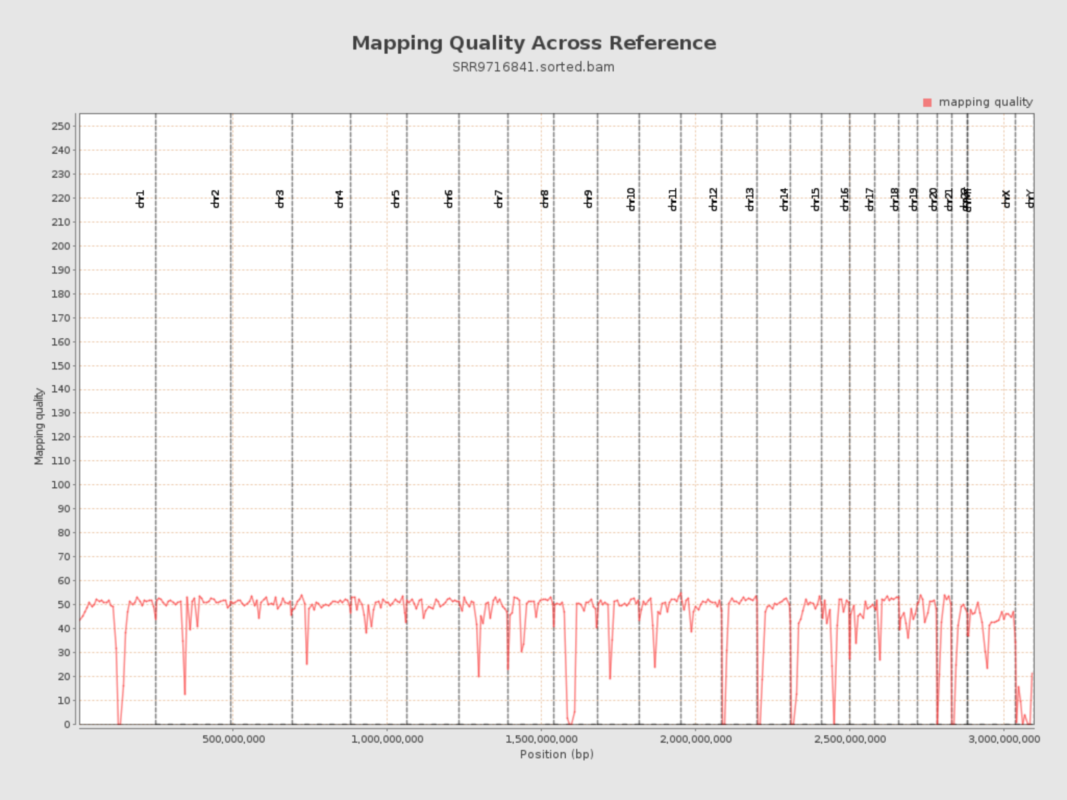
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram