Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:41:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716864.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_SRR9716864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716864.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:41:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,636,794
Mapped reads	1,515,676 / 92.6%
Unmapped reads	121,118 / 7.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,074 / 1.78%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	70,033 / 4.28%
Duplication rate	3.66%
Clipped reads	1,542,776 / 94.26%

2.2. ACGT Content

Number/percentage of A's	29,369,380 / 25.49%
Number/percentage of C's	23,267,005 / 20.19%
Number/percentage of T's	34,726,999 / 30.14%
Number/percentage of G's	27,851,220 / 24.17%
Number/percentage of N's	4,468 / 0%
GC Percentage	44.37%

2.3. Coverage

Mean	0.0372

Standard Deviation	0.3208

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

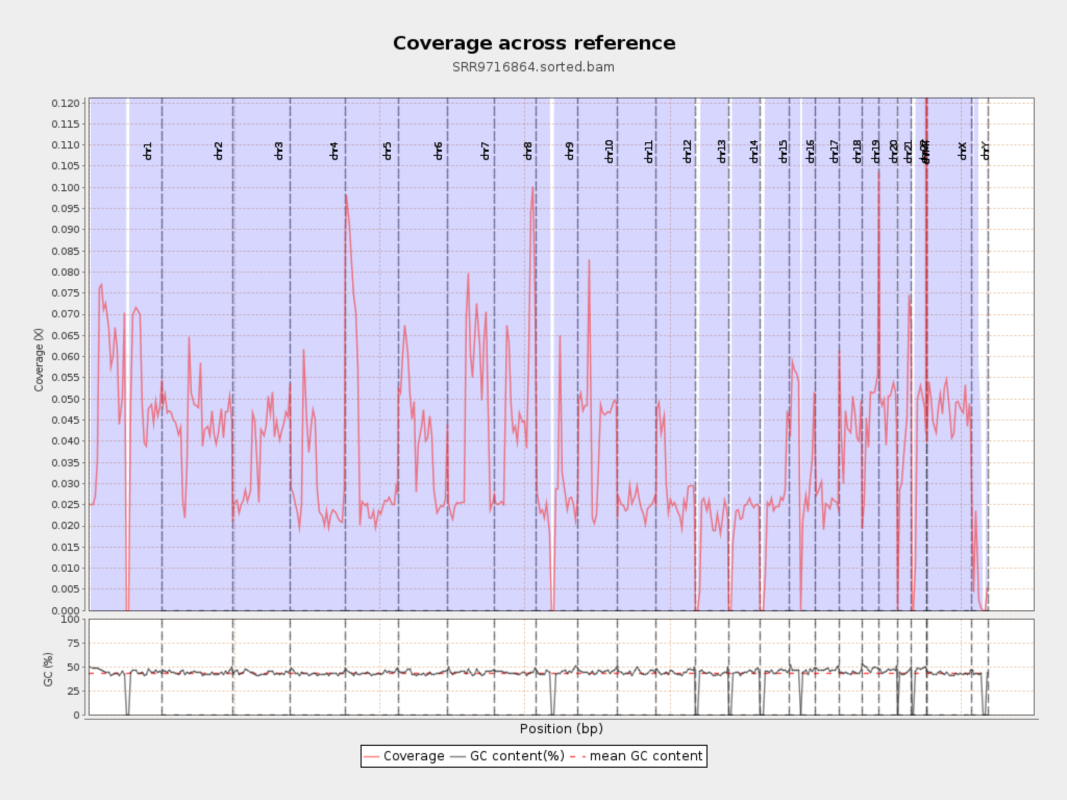
General error rate	0.67%
Mismatches	746,409
Insertions	8,985
Mapped reads with at least one insertion	0.58%
Deletions	21,599
Mapped reads with at least one deletion	1.4%
Homopolymer indels	39.2%

2.6. Chromosome stats

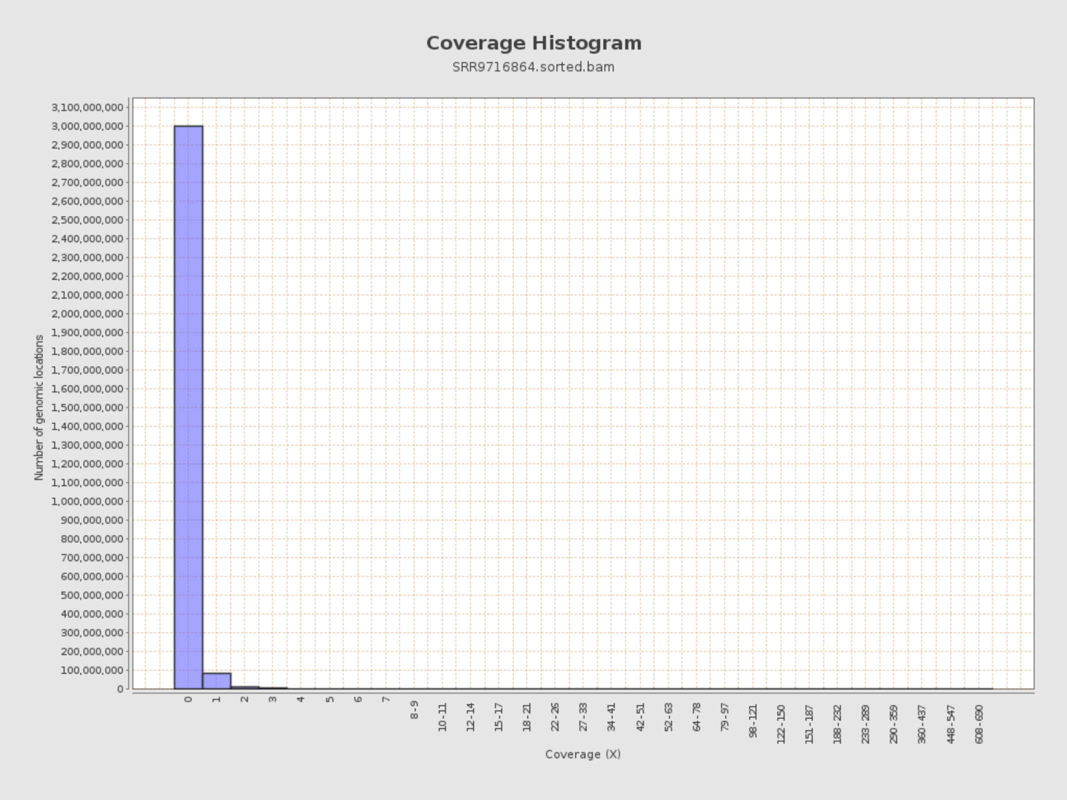
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12707631	0.051	0.6237
chr2	243199373	10875378	0.0447	0.3389
chr3	198022430	7457878	0.0377	0.2241
chr4	191154276	5575459	0.0292	0.2589
chr5	180915260	6984797	0.0386	0.2302
chr6	171115067	7102264	0.0415	0.245
chr7	159138663	7213734	0.0453	0.4095

chr8	146364022	7170160	0.049	0.3444
chr9	141213431	3493801	0.0247	0.2264
chr10	135534747	6083979	0.0449	0.3976
chr11	135006516	3410043	0.0253	0.2496
chr12	133851895	4046987	0.0302	0.1993
chr13	115169878	2203466	0.0191	0.1558
chr14	107349540	2215312	0.0206	0.1774
chr15	102531392	2347234	0.0229	0.1732
chr16	90354753	3428587	0.0379	0.2365
chr17	81195210	2082385	0.0256	0.2049
chr18	78077248	3416656	0.0438	0.3398
chr19	59128983	2757826	0.0466	0.4534
chr20	63025520	3088674	0.049	0.2687
chr21	48129895	2004988	0.0417	0.2658
chr22	51304566	1721776	0.0336	0.2141
chrMT	16571	111650	6.7377	5.5546
chrX	155270560	7400002	0.0477	0.2659
chrY	59373566	361815	0.0061	0.2197

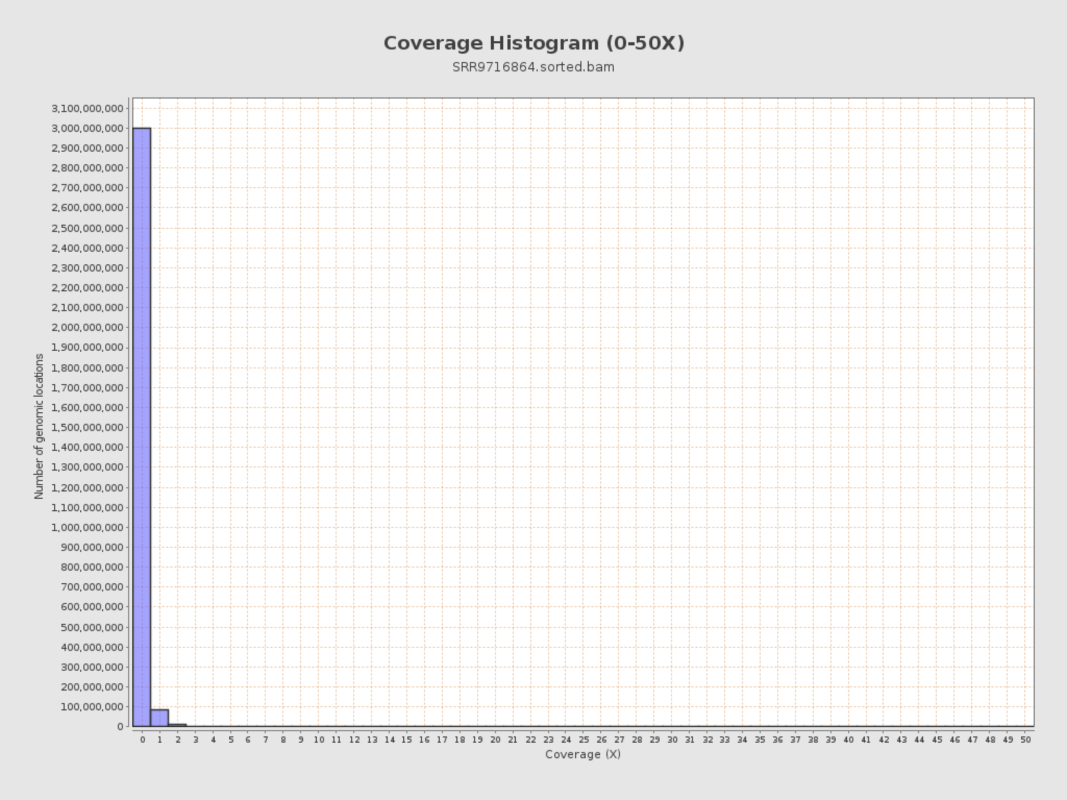
3. Results : Coverage across reference



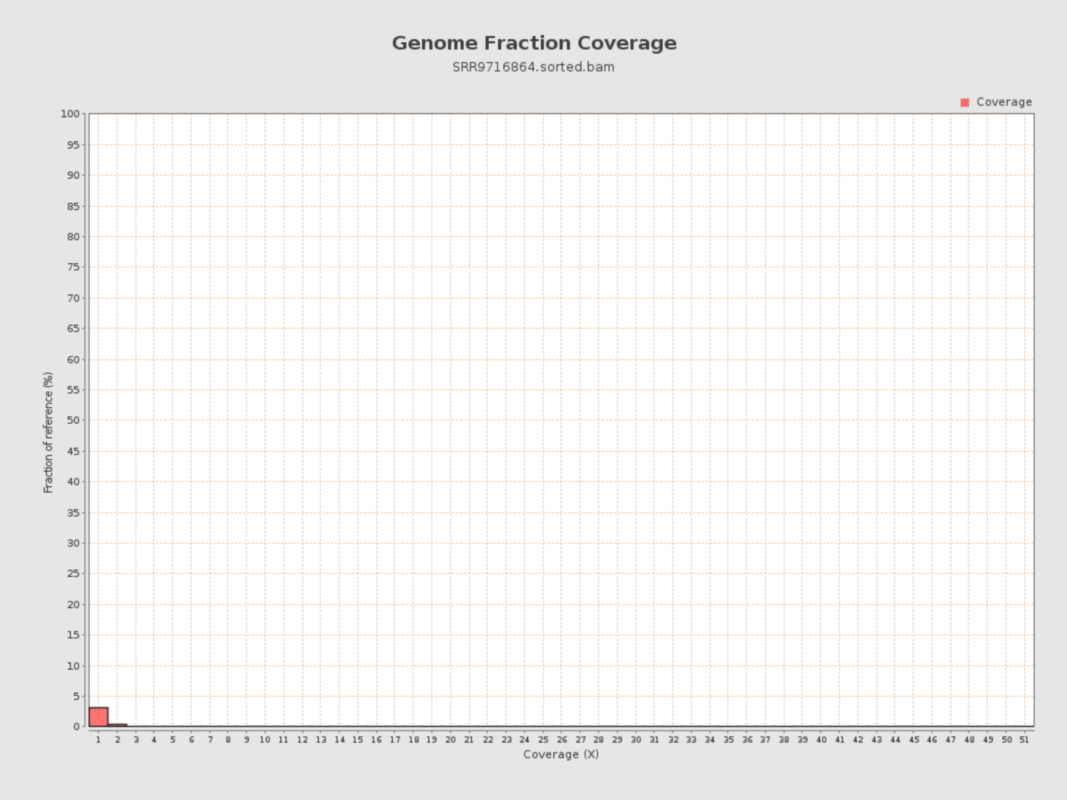
4. Results : Coverage Histogram



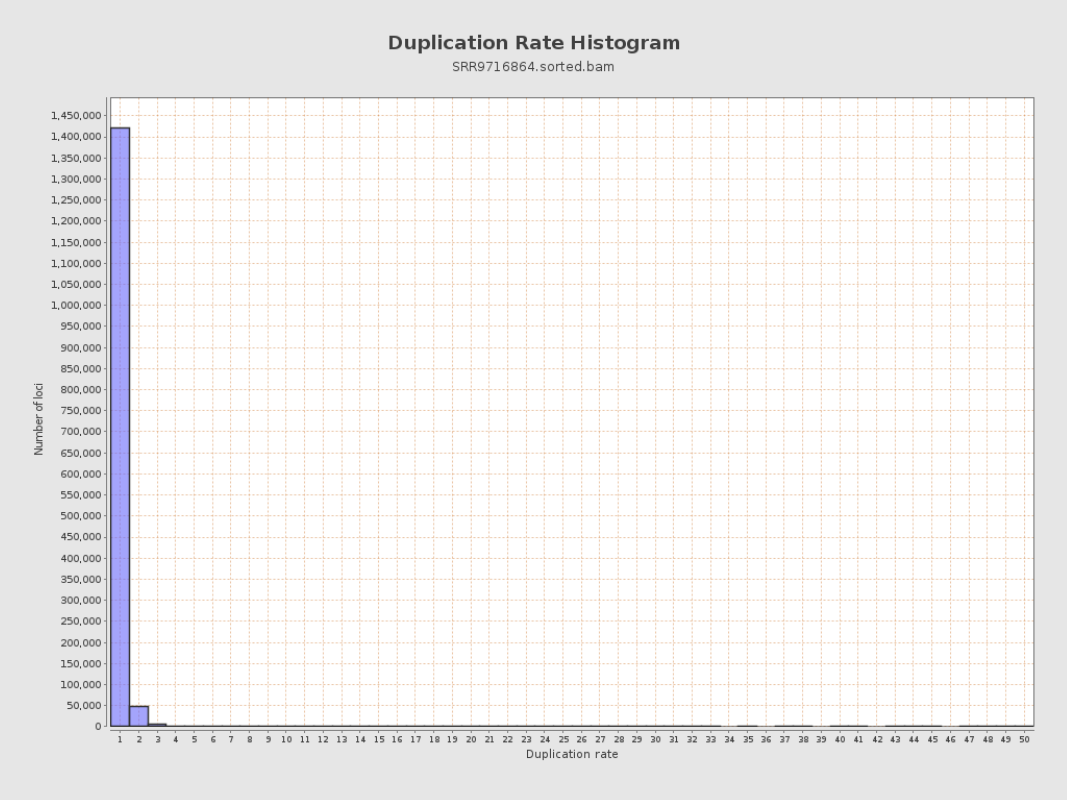
5. Results : Coverage Histogram (0-50X)



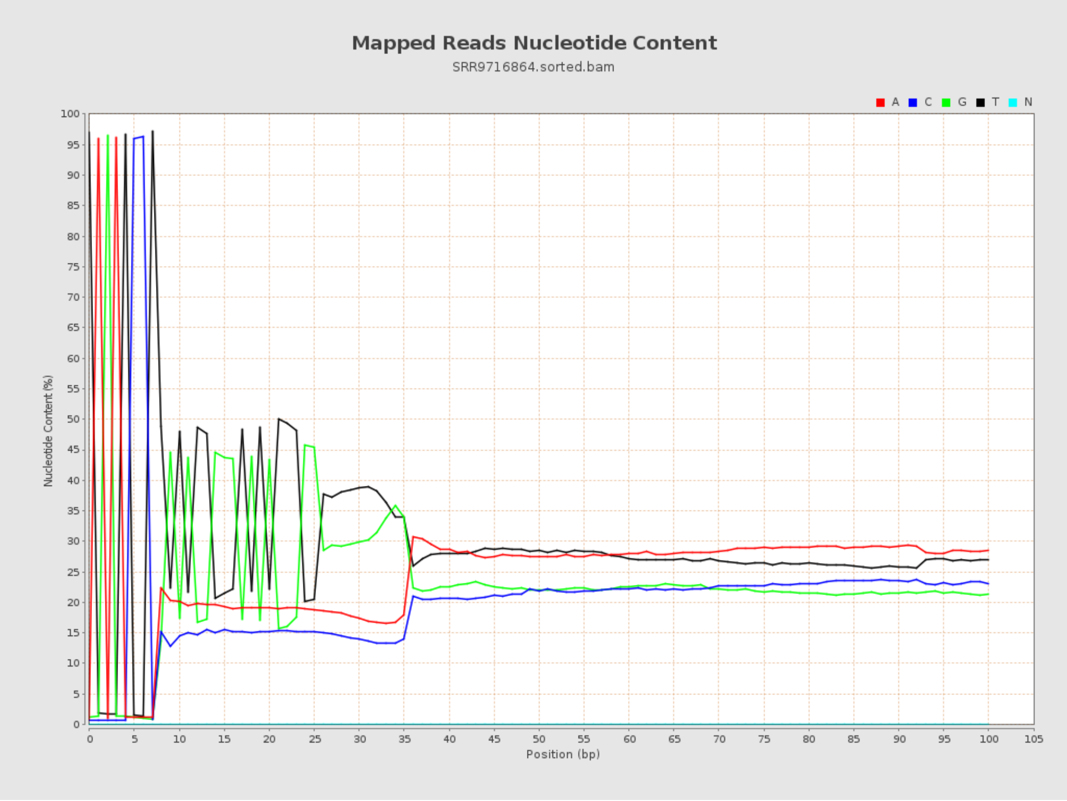
6. Results : Genome Fraction Coverage



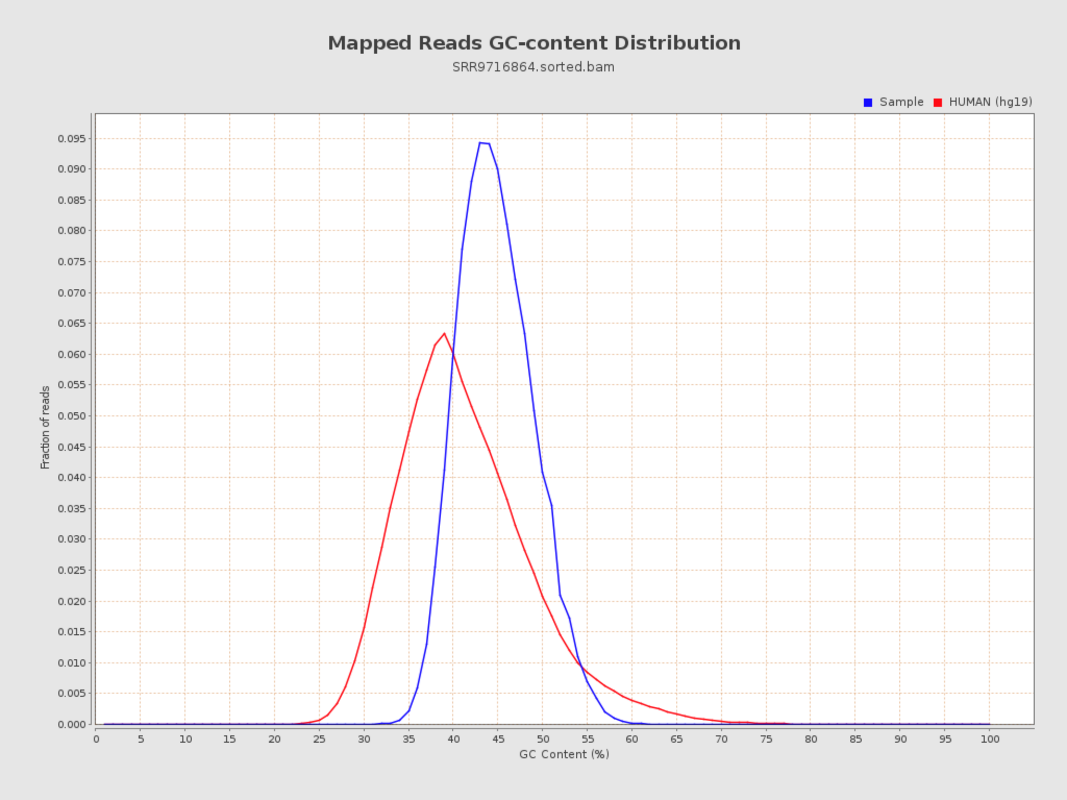
7. Results : Duplication Rate Histogram



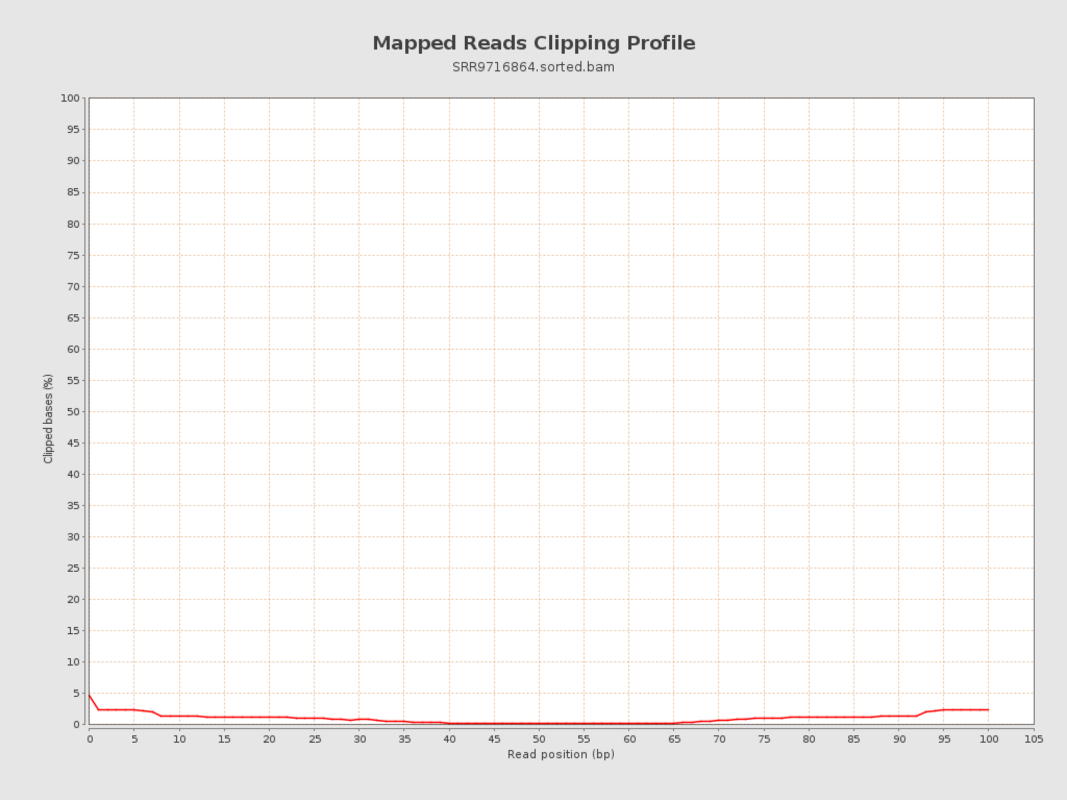
8. Results : Mapped Reads Nucleotide Content



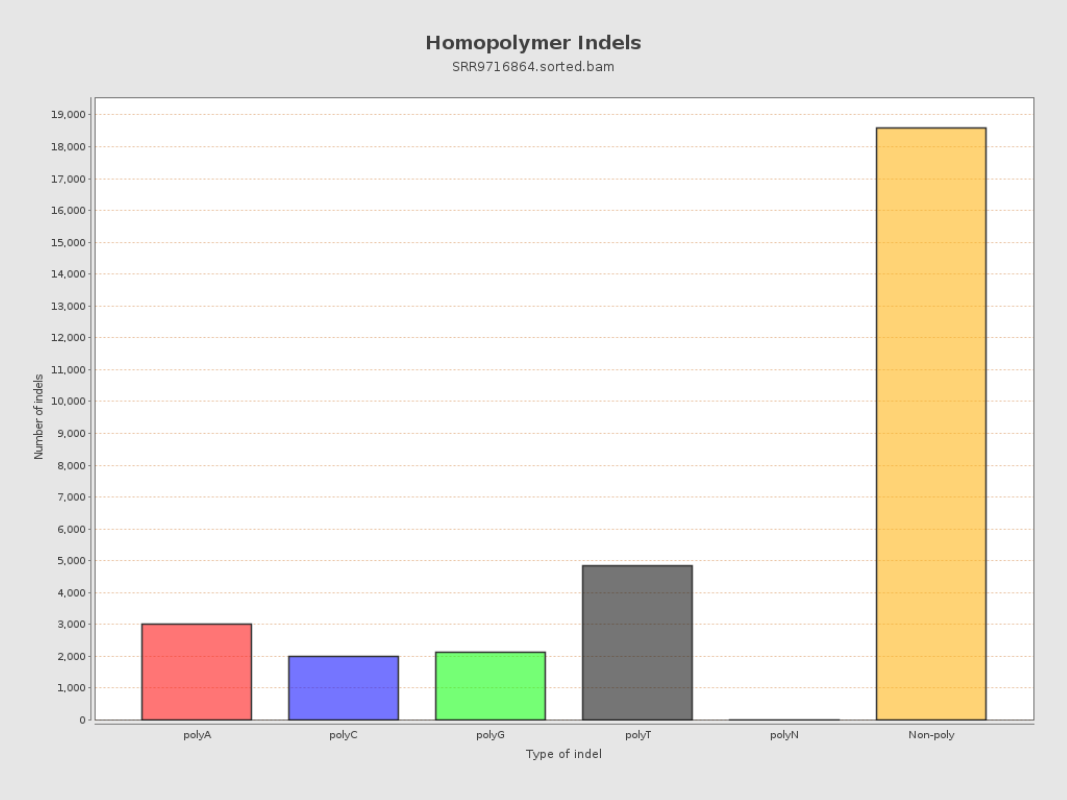
9. Results : Mapped Reads GC-content Distribution



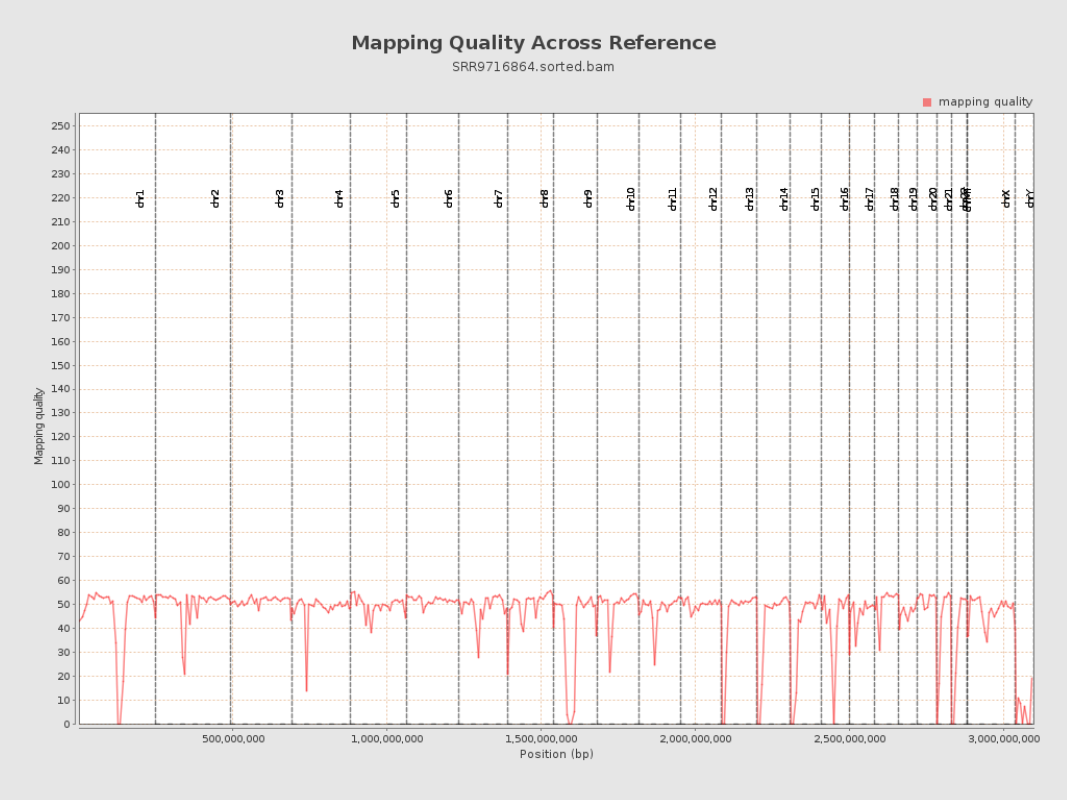
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram