Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:41:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524716.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_SRR10524716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524716.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:41:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	832,031
Mapped reads	761,260 / 91.49%
Unmapped reads	70,771 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,645 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	21,845 / 2.63%
Duplication rate	2.13%
Clipped reads	761,822 / 91.56%

2.2. ACGT Content

Number/percentage of A's	11,870,852 / 26.62%
Number/percentage of C's	7,919,576 / 17.76%
Number/percentage of T's	13,981,943 / 31.36%
Number/percentage of G's	10,806,870 / 24.24%
Number/percentage of N's	6,128 / 0.01%
GC Percentage	42%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1644

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

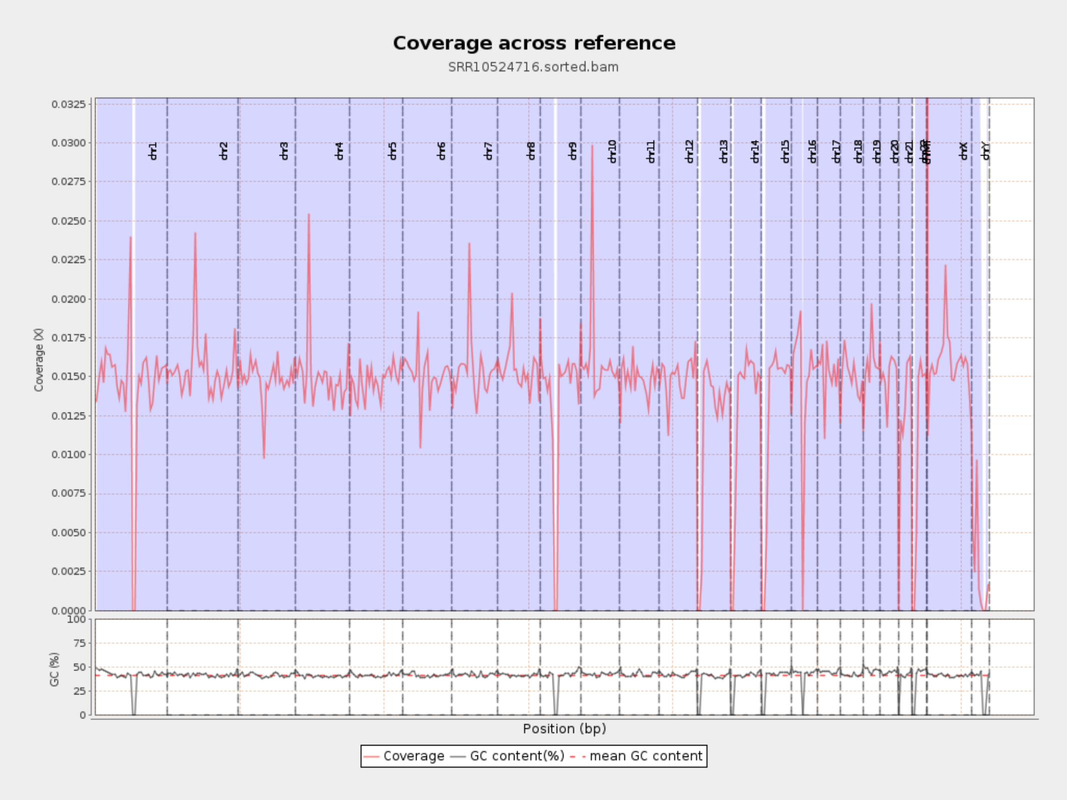
General error rate	0.52%
Mismatches	227,932
Insertions	3,219
Mapped reads with at least one insertion	0.42%
Deletions	8,545
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43%

2.6. Chromosome stats

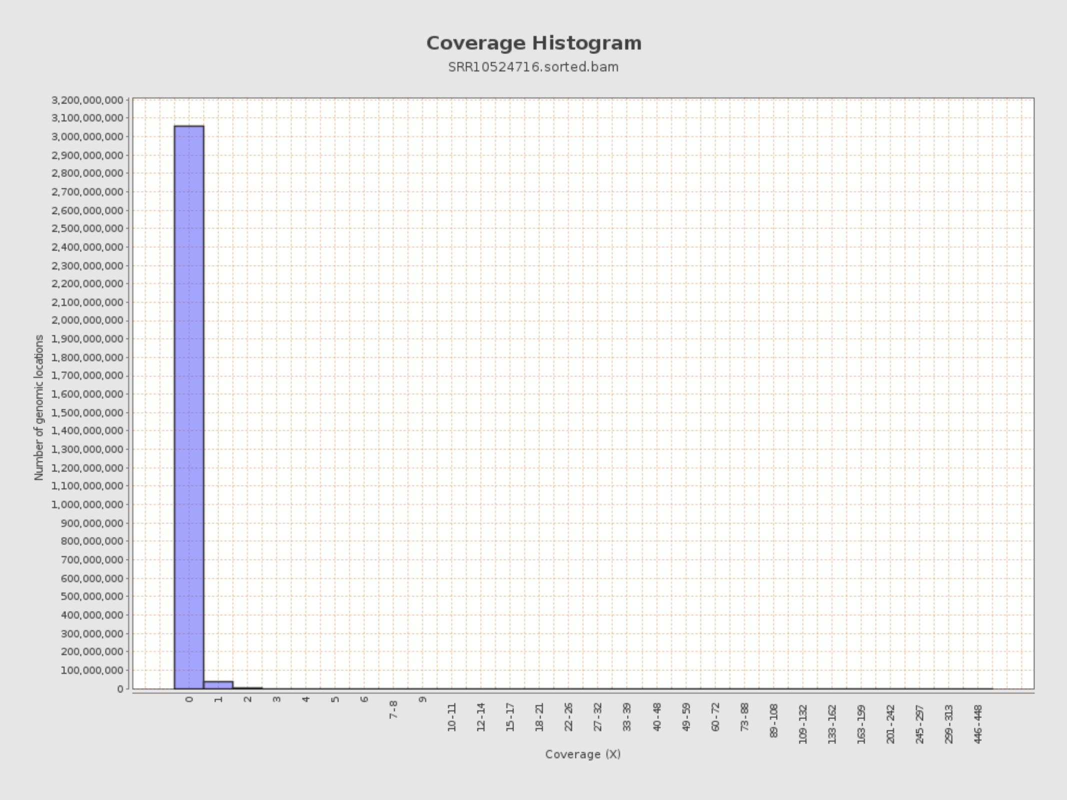
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3576218	0.0143	0.2517
chr2	243199373	3773058	0.0155	0.2279
chr3	198022430	2932505	0.0148	0.128
chr4	191154276	2888520	0.0151	0.1391
chr5	180915260	2675248	0.0148	0.1279
chr6	171115067	2581390	0.0151	0.141
chr7	159138663	2463798	0.0155	0.1872

chr8	146364022	2269493	0.0155	0.1679
chr9	141213431	1876998	0.0133	0.1458
chr10	135534747	2180765	0.0161	0.175
chr11	135006516	2012795	0.0149	0.1496
chr12	133851895	1995504	0.0149	0.1293
chr13	115169878	1361767	0.0118	0.115
chr14	107349540	1357786	0.0126	0.1205
chr15	102531392	1293168	0.0126	0.12
chr16	90354753	1306846	0.0145	0.1322
chr17	81195210	1233071	0.0152	0.1324
chr18	78077248	1175764	0.0151	0.2136
chr19	59128983	942227	0.0159	0.2061
chr20	63025520	936231	0.0149	0.1294
chr21	48129895	597679	0.0124	0.1303
chr22	51304566	535048	0.0104	0.1073
chrMT	16571	10168	0.6136	0.8582
chrX	155270560	2474229	0.0159	0.1412
chrY	59373566	148844	0.0025	0.0984

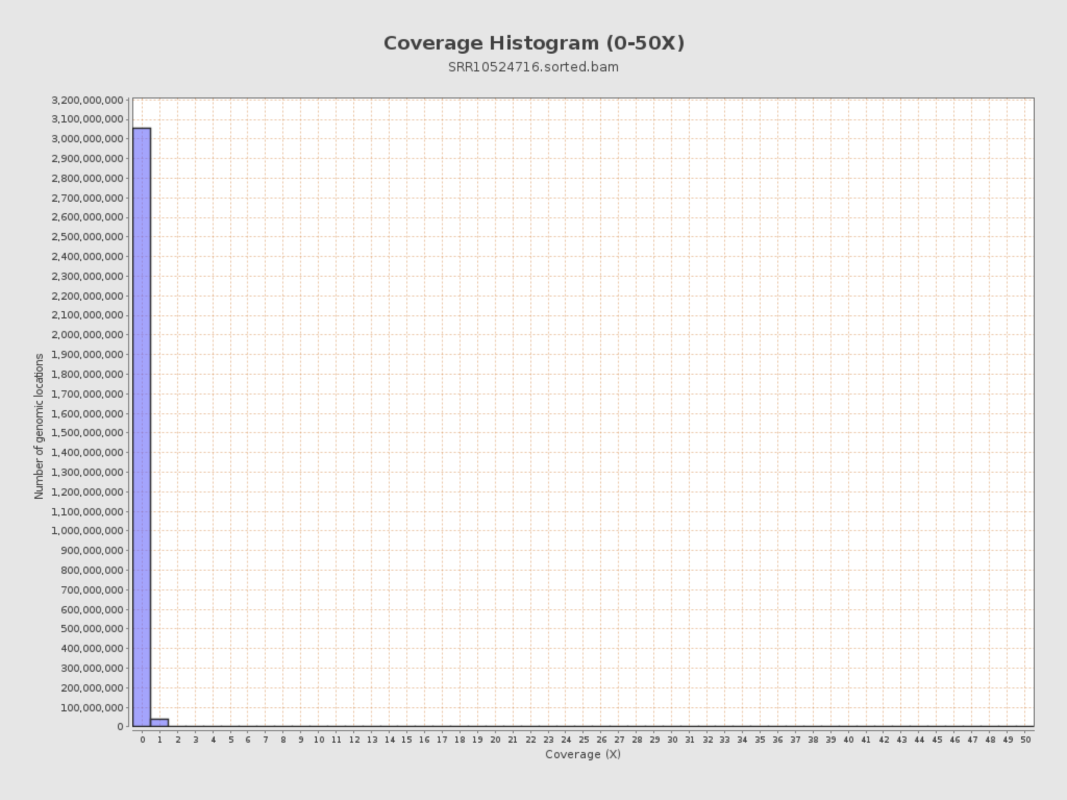
3. Results : Coverage across reference



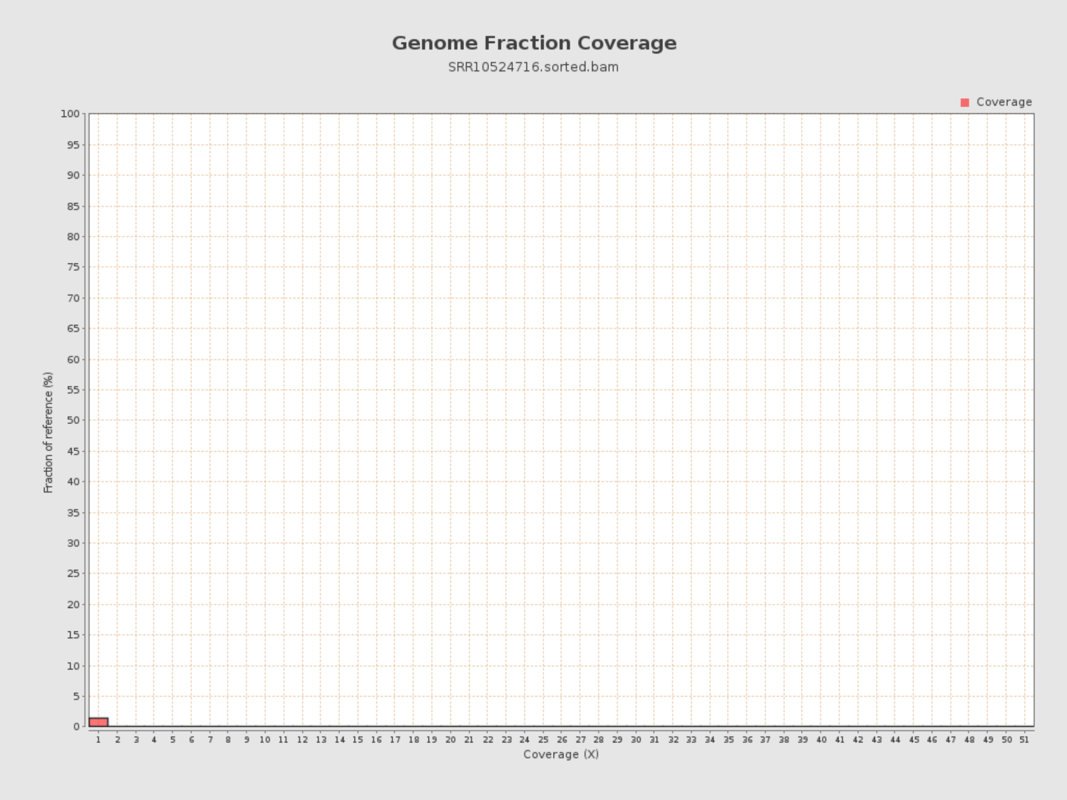
4. Results : Coverage Histogram



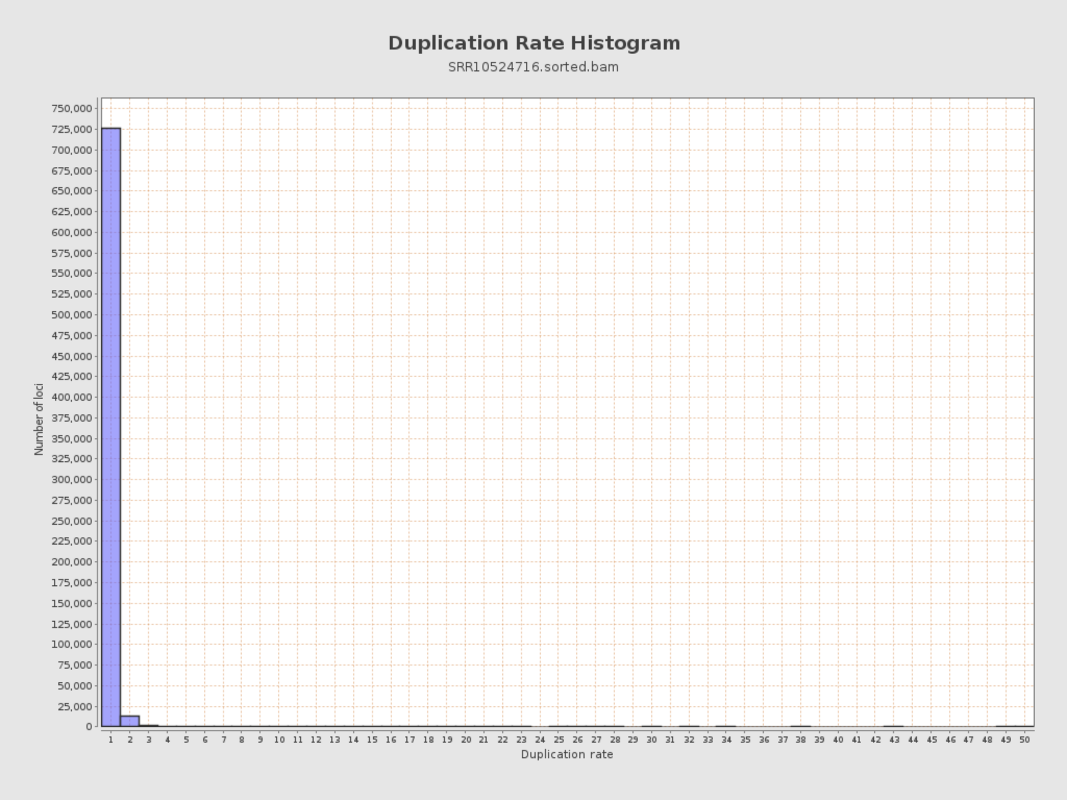
5. Results : Coverage Histogram (0-50X)



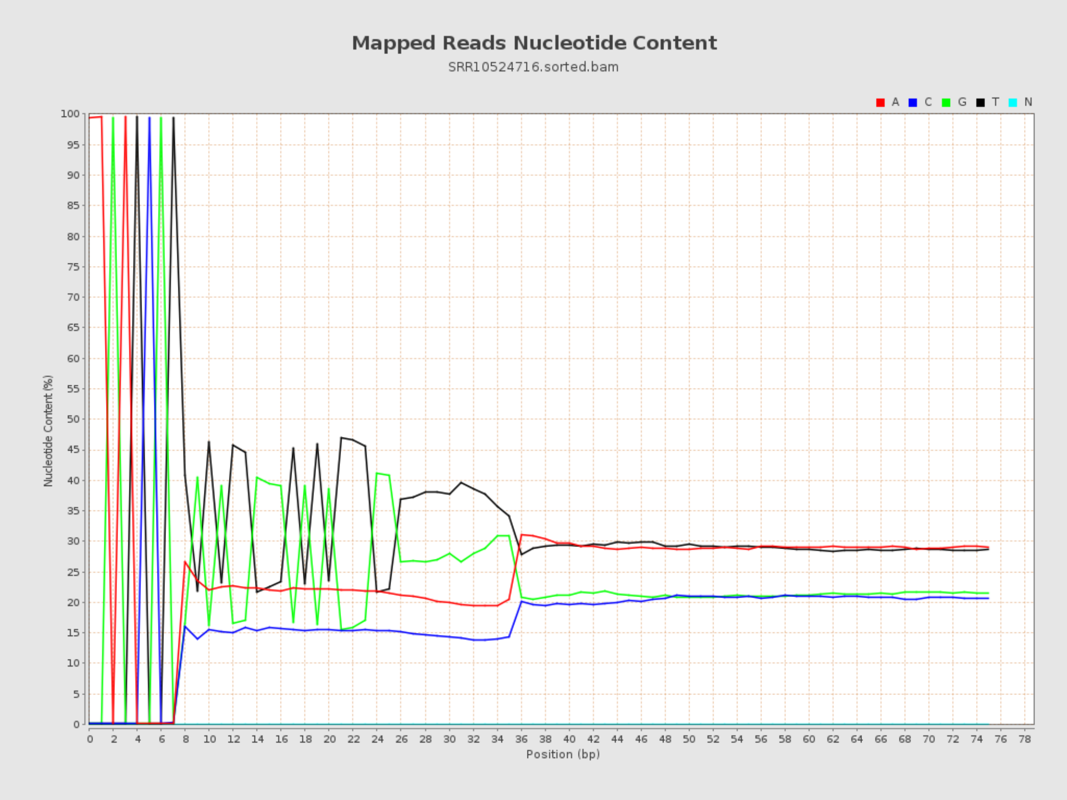
6. Results : Genome Fraction Coverage



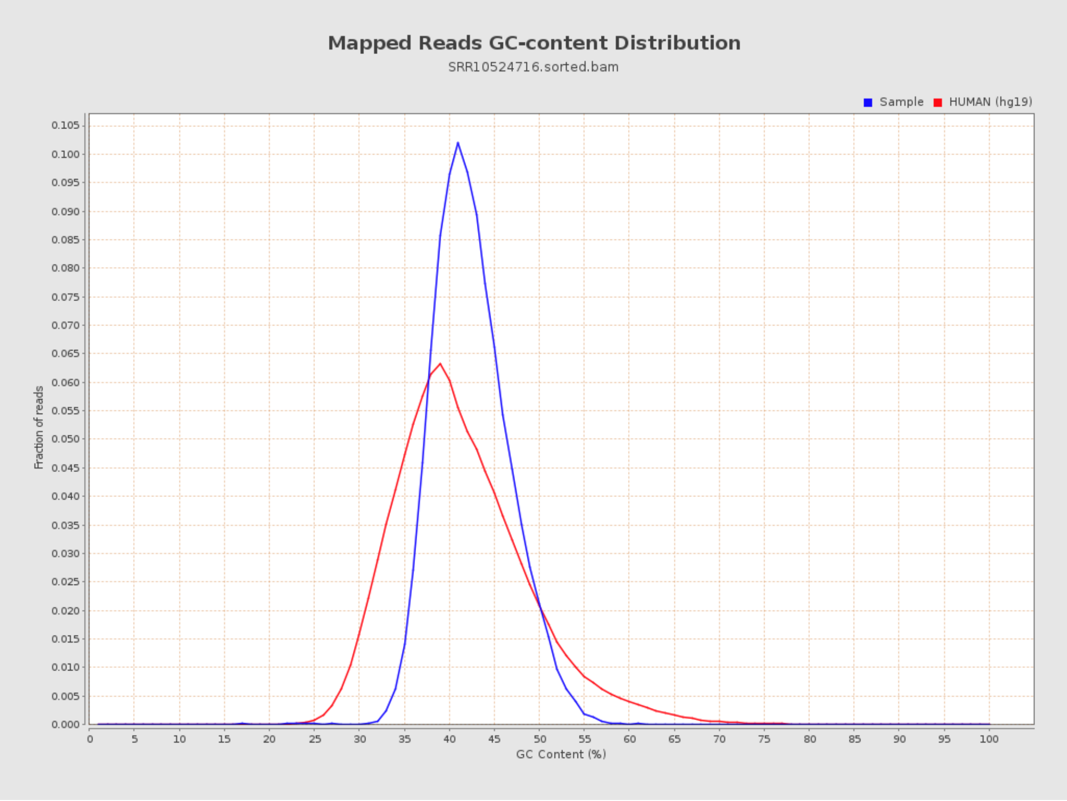
7. Results : Duplication Rate Histogram



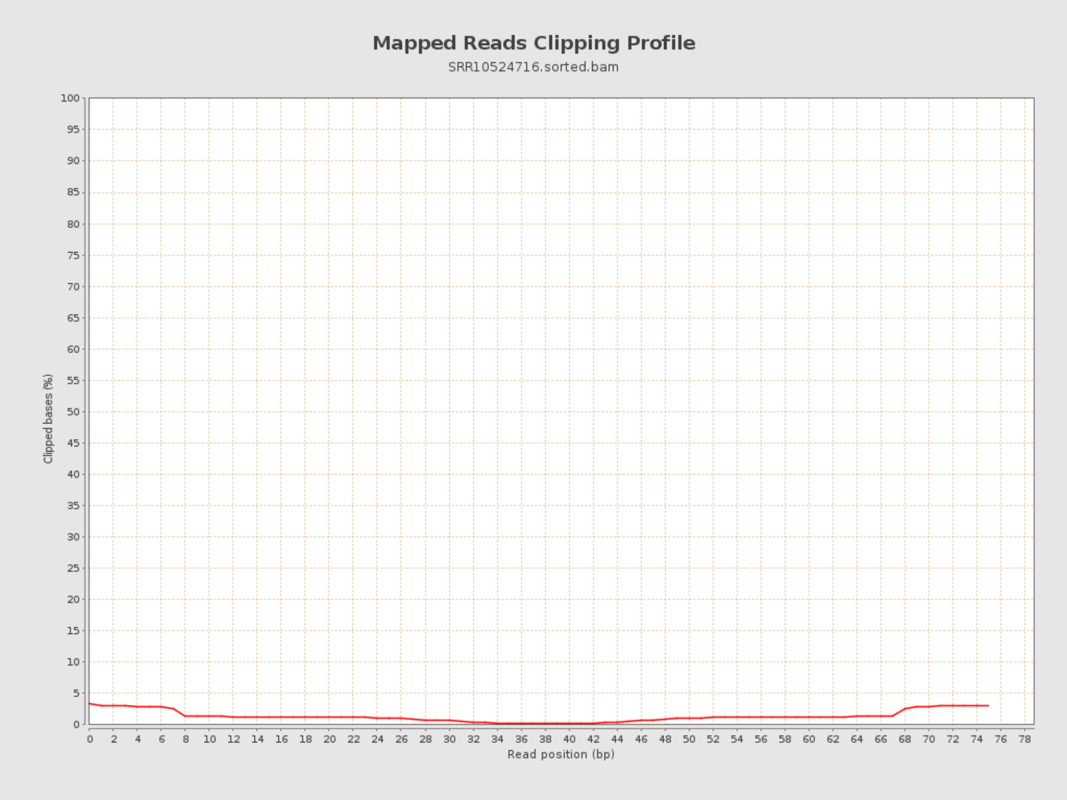
8. Results : Mapped Reads Nucleotide Content



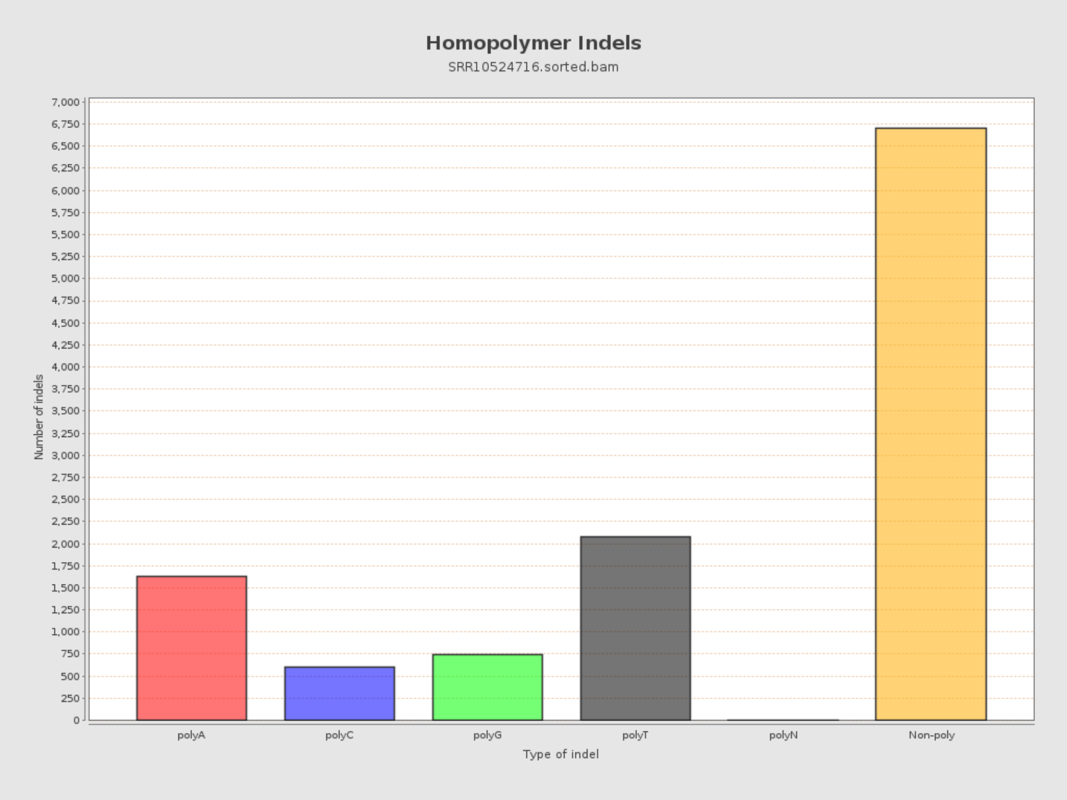
9. Results : Mapped Reads GC-content Distribution



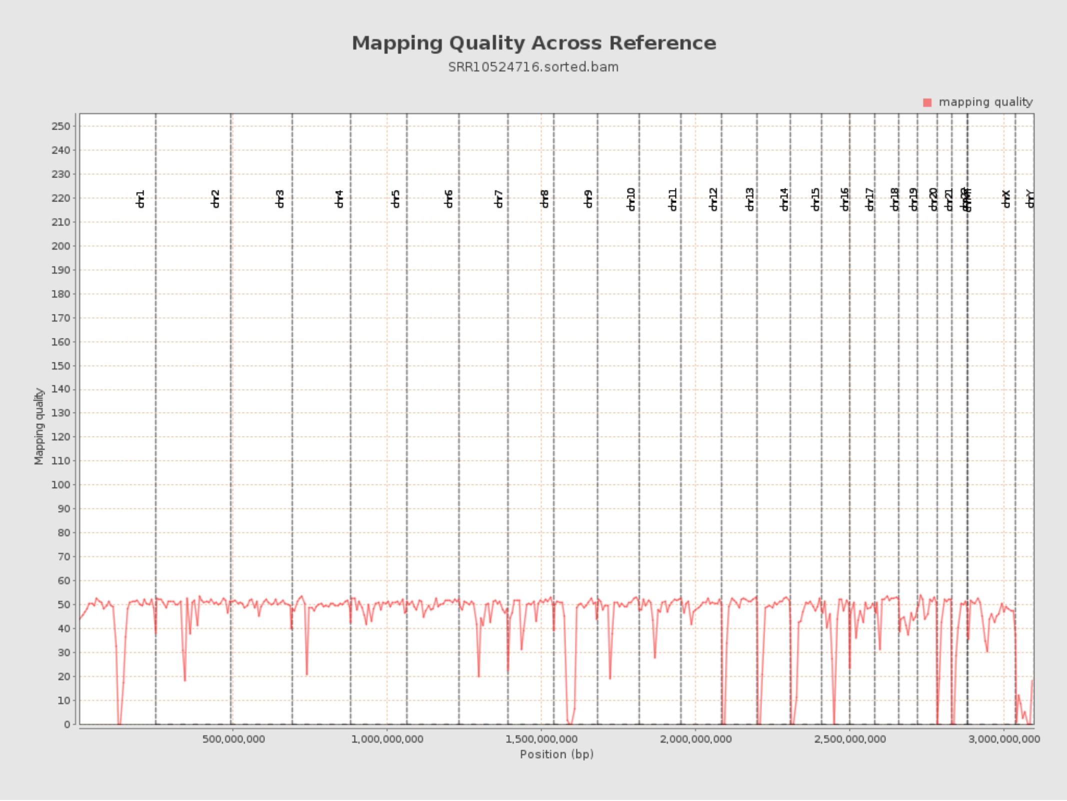
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram