Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:23:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524404.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_SRR10524404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524404.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:23:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524404.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,164,540
Mapped reads	1,081,901 / 92.9%
Unmapped reads	82,639 / 7.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,095 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	31,830 / 2.73%
Duplication rate	2.2%
Clipped reads	1,082,639 / 92.97%

2.2. ACGT Content

Number/percentage of A's	15,915,213 / 25.03%
Number/percentage of C's	11,955,654 / 18.8%
Number/percentage of T's	20,238,501 / 31.83%
Number/percentage of G's	15,467,775 / 24.33%
Number/percentage of N's	8,800 / 0.01%
GC Percentage	43.13%

2.3. Coverage

Mean	0.0205

Standard Deviation	0.2161

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

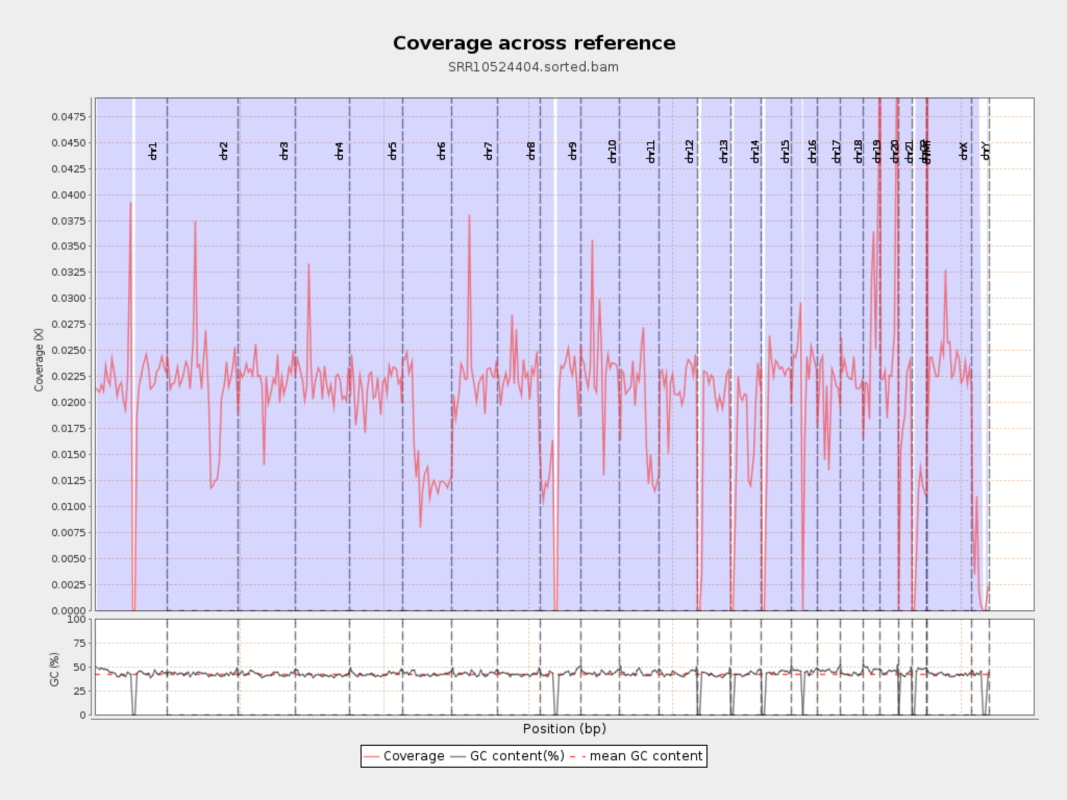
General error rate	0.49%
Mismatches	303,843
Insertions	4,348
Mapped reads with at least one insertion	0.4%
Deletions	11,533
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.79%

2.6. Chromosome stats

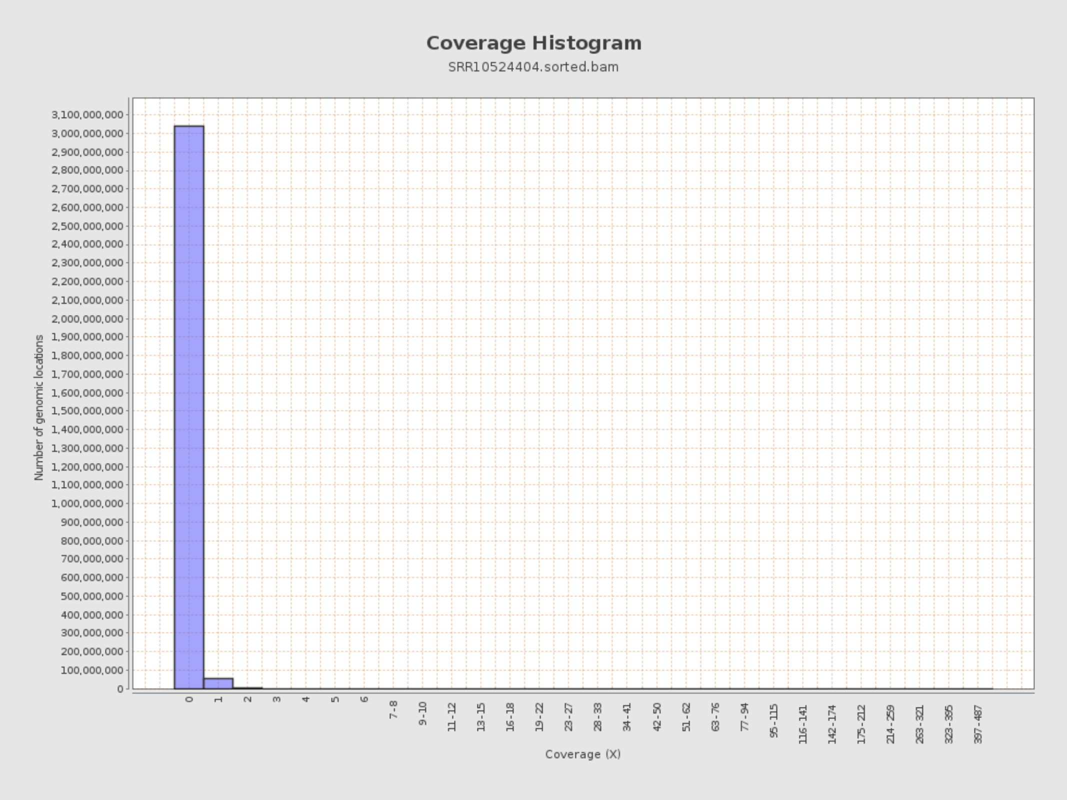
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5305944	0.0213	0.4226
chr2	243199373	5270224	0.0217	0.2389
chr3	198022430	4398043	0.0222	0.1581
chr4	191154276	4274457	0.0224	0.1722
chr5	180915260	3901104	0.0216	0.1558
chr6	171115067	2538551	0.0148	0.1371
chr7	159138663	3601967	0.0226	0.2957

chr8	146364022	3298999	0.0225	0.2017
chr9	141213431	2399519	0.017	0.1694
chr10	135534747	3192185	0.0236	0.202
chr11	135006516	2601653	0.0193	0.1756
chr12	133851895	2925659	0.0219	0.1592
chr13	115169878	2069494	0.018	0.1426
chr14	107349540	1710453	0.0159	0.1369
chr15	102531392	1983197	0.0193	0.1476
chr16	90354753	1964496	0.0217	0.1609
chr17	81195210	1670306	0.0206	0.1641
chr18	78077248	1768513	0.0227	0.2644
chr19	59128983	1750316	0.0296	0.29
chr20	63025520	1733449	0.0275	0.1794
chr21	48129895	859372	0.0179	0.1536
chr22	51304566	435297	0.0085	0.097
chrMT	16571	45442	2.7423	2.1965
chrX	155270560	3711439	0.0239	0.1783
chrY	59373566	194074	0.0033	0.0939

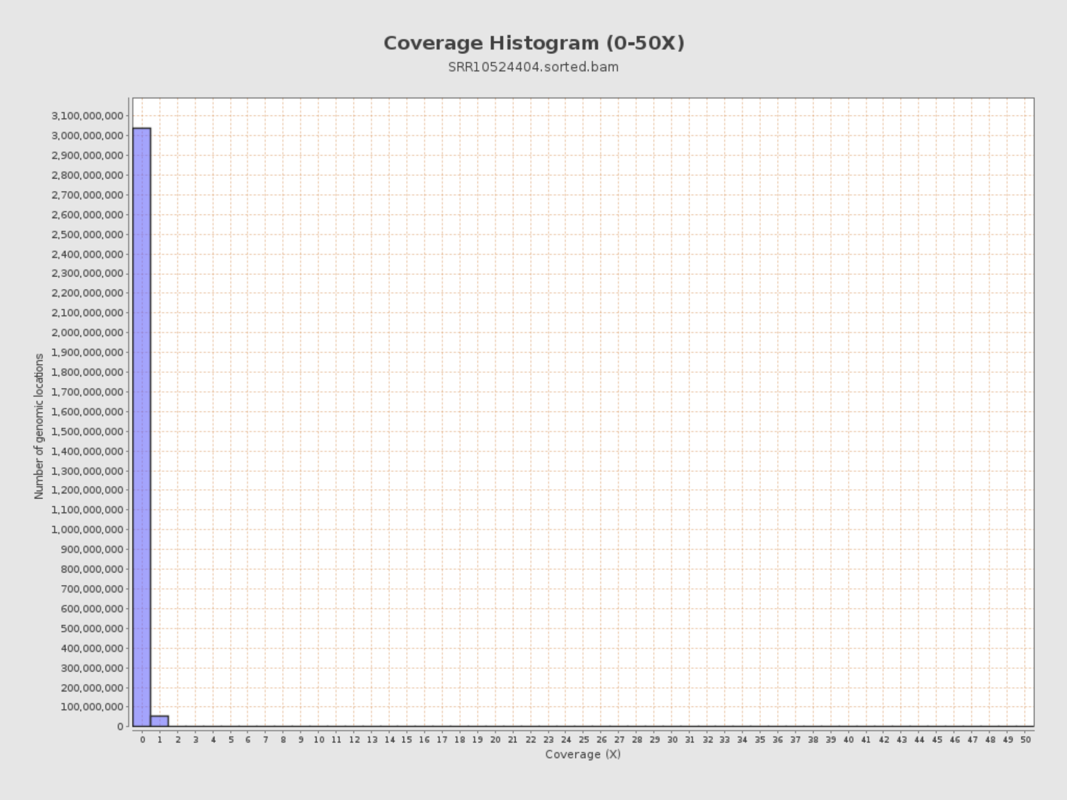
3. Results : Coverage across reference



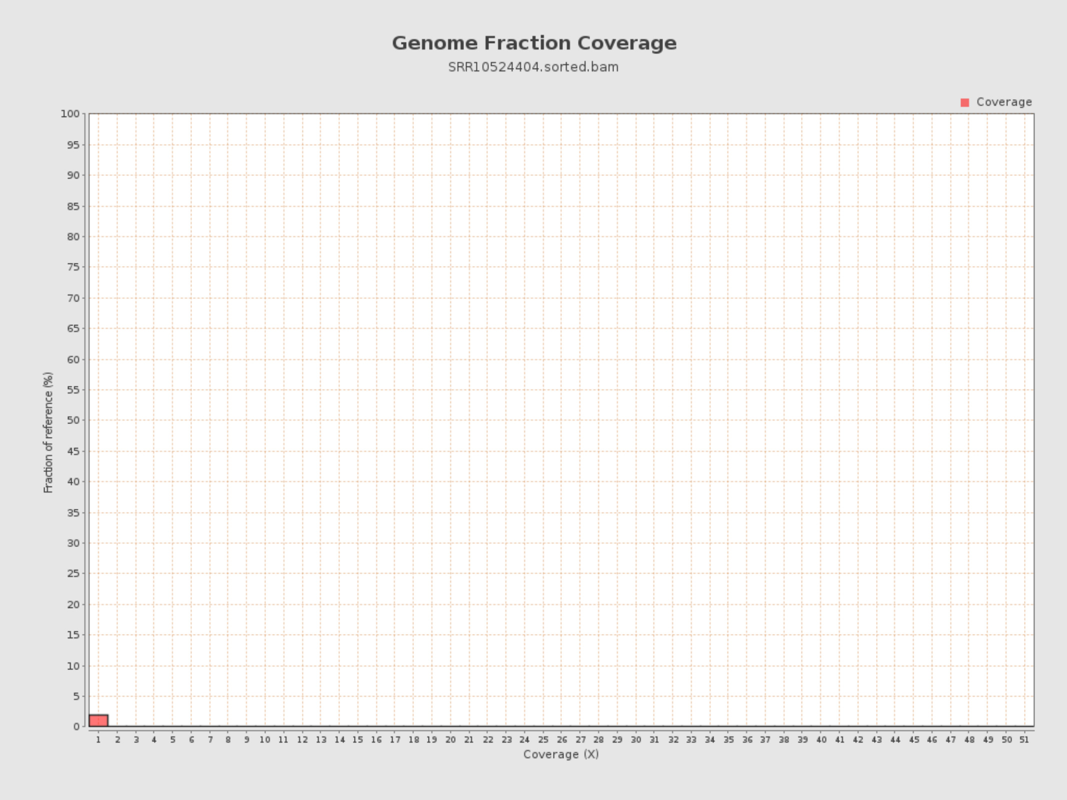
4. Results : Coverage Histogram



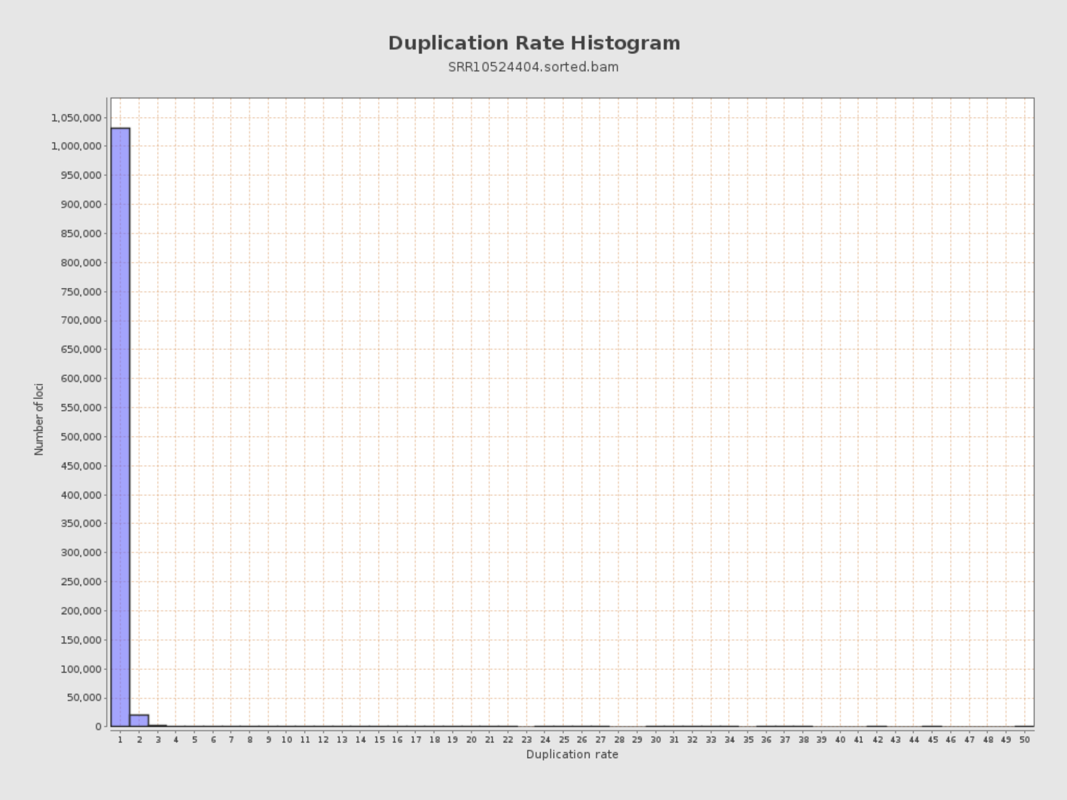
5. Results : Coverage Histogram (0-50X)



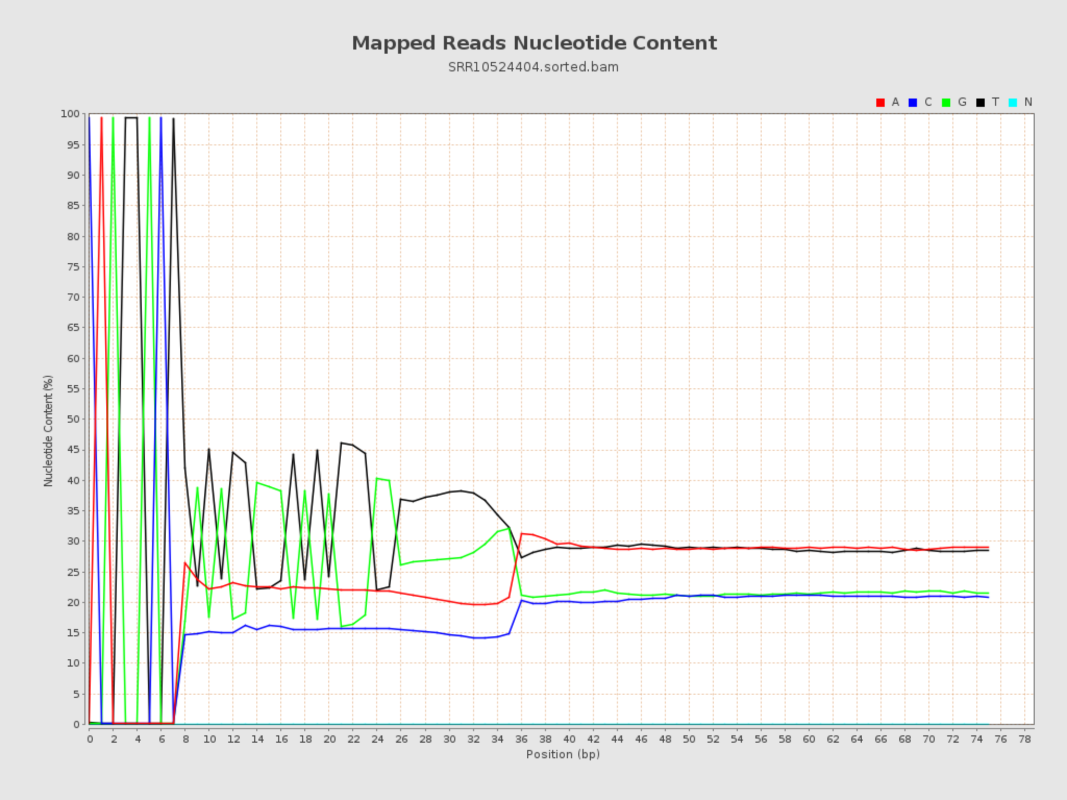
6. Results : Genome Fraction Coverage



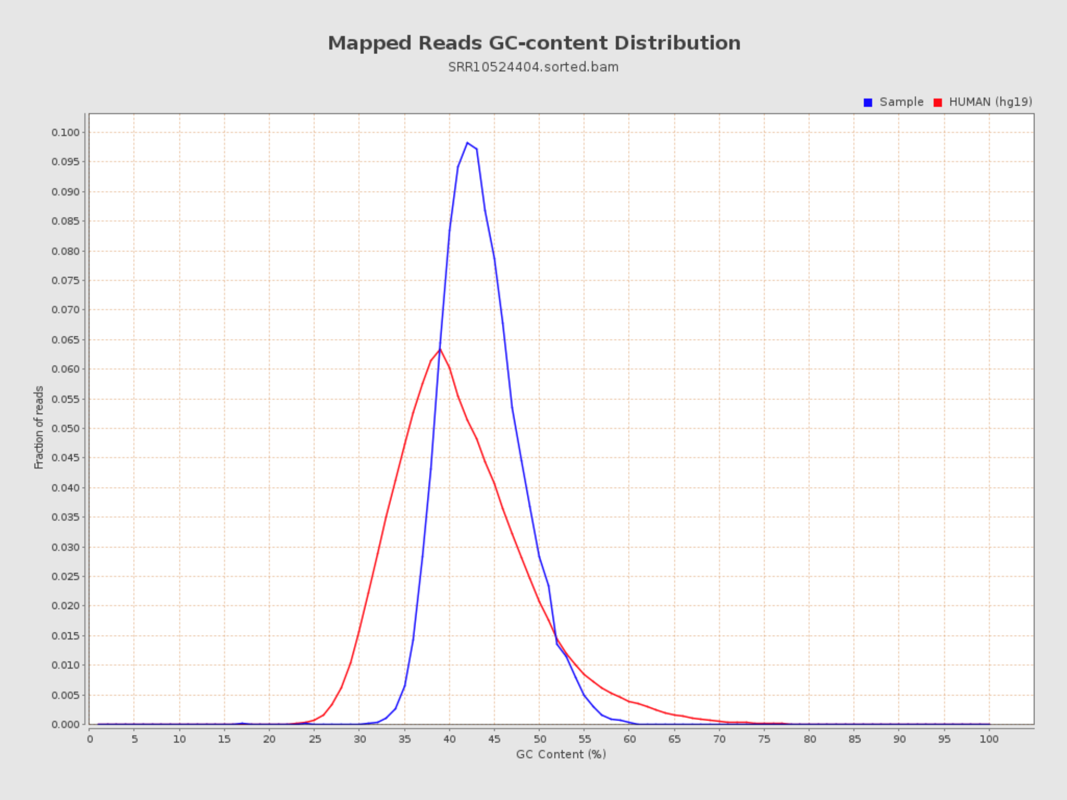
7. Results : Duplication Rate Histogram



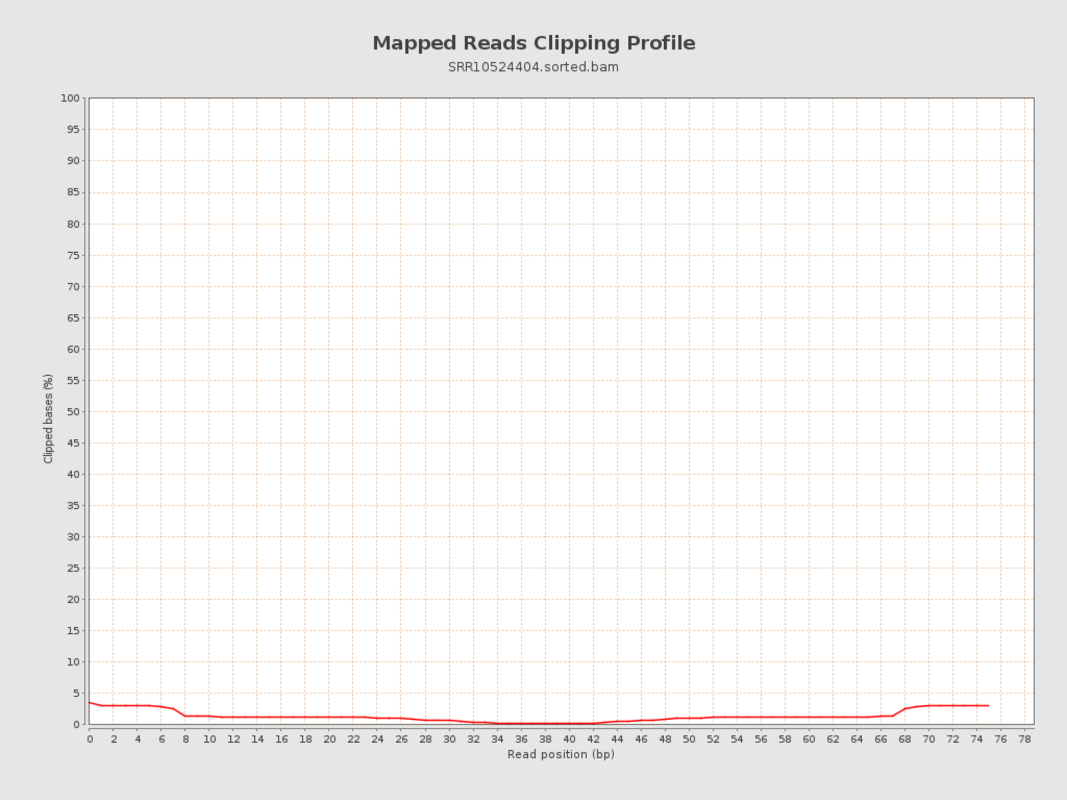
8. Results : Mapped Reads Nucleotide Content



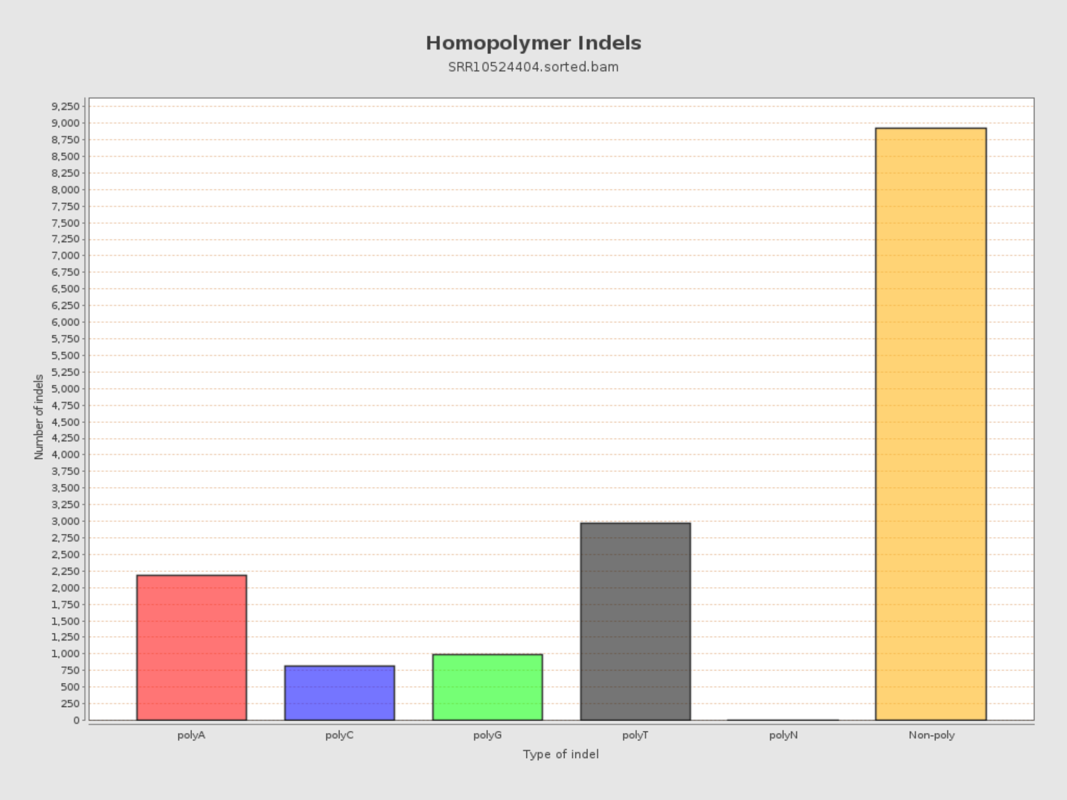
9. Results : Mapped Reads GC-content Distribution



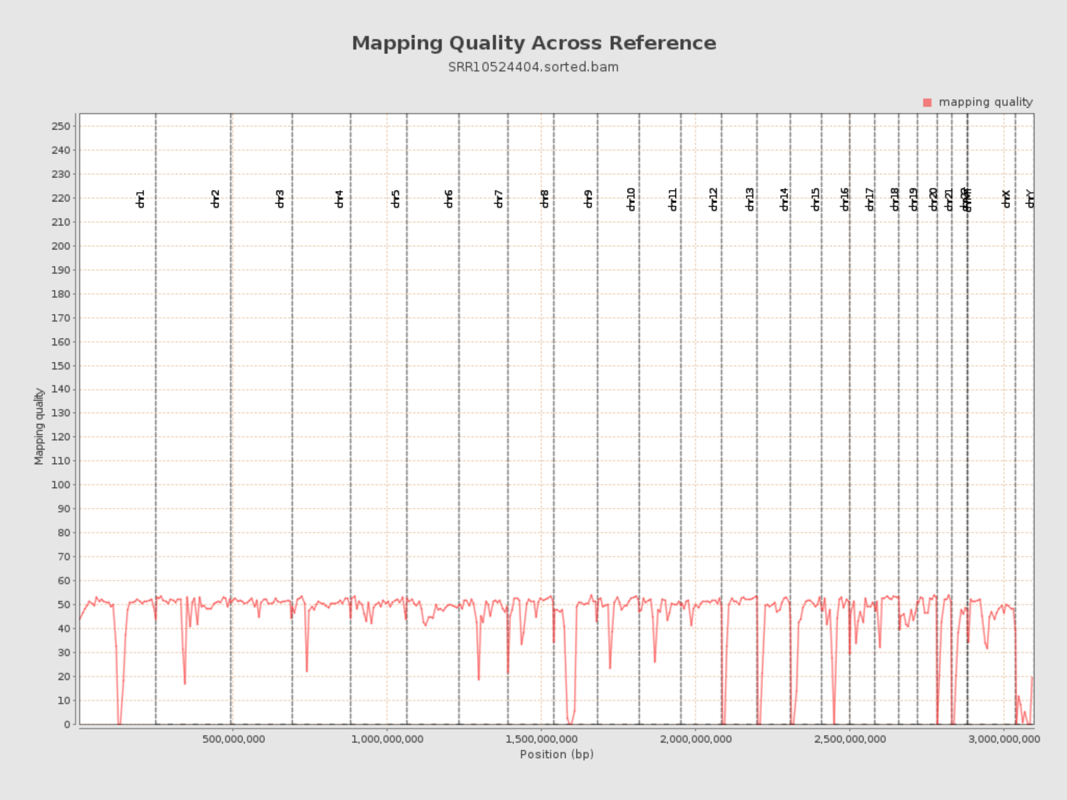
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram