Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:12:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524731.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_SRR10524731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524731.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:12:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,873,804
Mapped reads	1,693,963 / 90.4%
Unmapped reads	179,841 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,961 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	73,108 / 3.9%
Duplication rate	3.25%
Clipped reads	1,695,125 / 90.46%

2.2. ACGT Content

Number/percentage of A's	23,841,070 / 24.81%
Number/percentage of C's	15,895,280 / 16.54%
Number/percentage of T's	31,367,199 / 32.64%
Number/percentage of G's	24,979,316 / 25.99%
Number/percentage of N's	11,374 / 0.01%
GC Percentage	42.54%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.2717

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

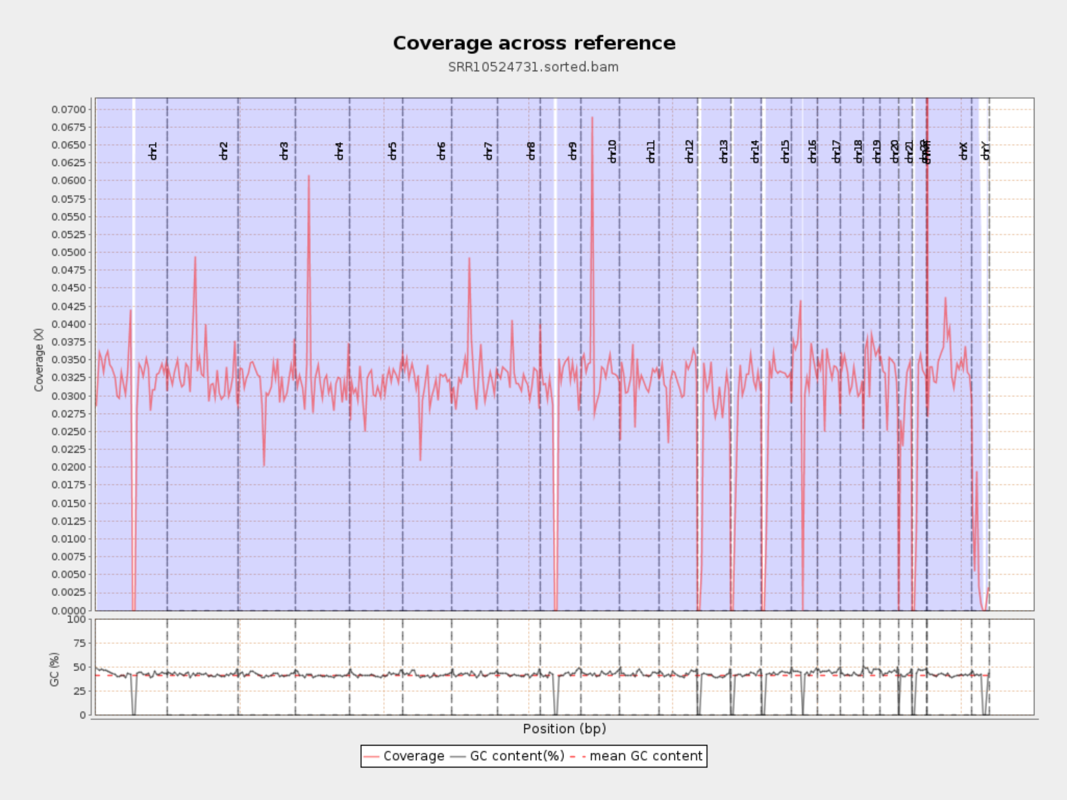
General error rate	0.53%
Mismatches	498,400
Insertions	6,877
Mapped reads with at least one insertion	0.4%
Deletions	19,362
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.84%

2.6. Chromosome stats

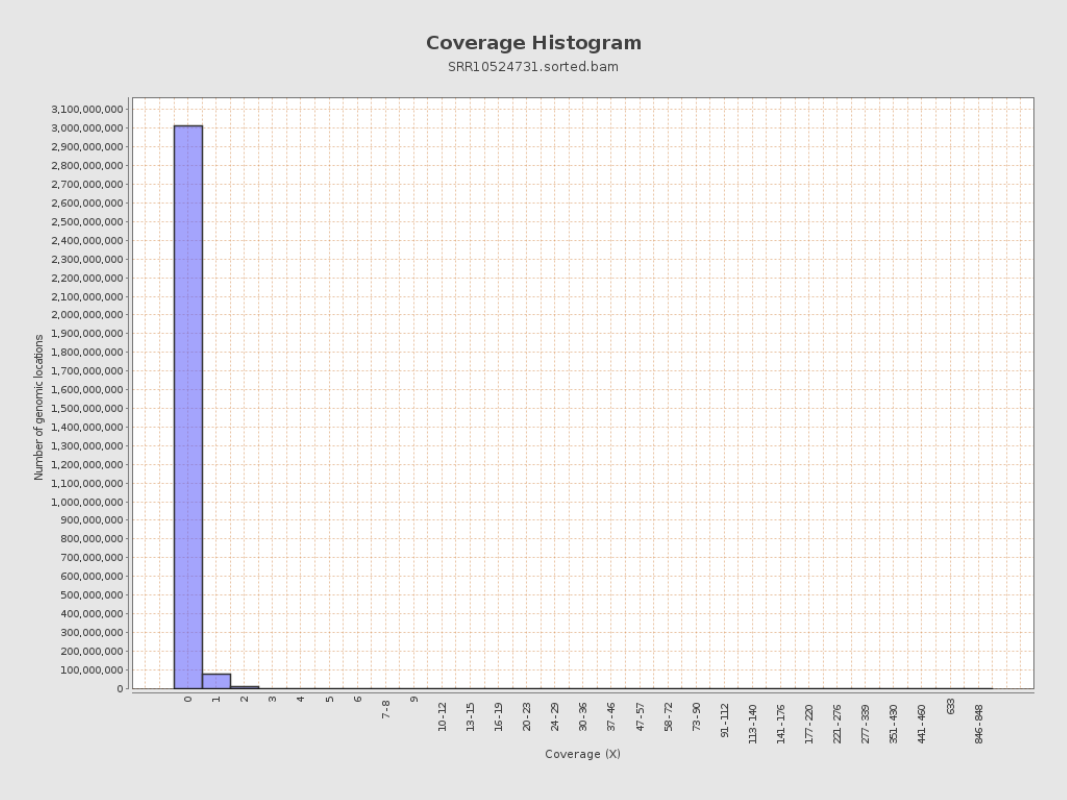
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7721749	0.031	0.3798
chr2	243199373	8107735	0.0333	0.4274
chr3	198022430	6305697	0.0318	0.2024
chr4	191154276	6265026	0.0328	0.2381
chr5	180915260	5718205	0.0316	0.1982
chr6	171115067	5405597	0.0316	0.2164
chr7	159138663	5259372	0.033	0.3307

chr8	146364022	4766146	0.0326	0.2445
chr9	141213431	4090290	0.029	0.2393
chr10	135534747	4752666	0.0351	0.3416
chr11	135006516	4344872	0.0322	0.2347
chr12	133851895	4332511	0.0324	0.2032
chr13	115169878	2948638	0.0256	0.177
chr14	107349540	2873317	0.0268	0.188
chr15	102531392	2770651	0.027	0.1854
chr16	90354753	2892881	0.032	0.2259
chr17	81195210	2695744	0.0332	0.2122
chr18	78077248	2535333	0.0325	0.3641
chr19	59128983	2096304	0.0355	0.3102
chr20	63025520	2056927	0.0326	0.213
chr21	48129895	1280656	0.0266	0.2041
chr22	51304566	1197801	0.0233	0.1703
chrMT	16571	17643	1.0647	1.1873
chrX	155270560	5366932	0.0346	0.2251
chrY	59373566	323015	0.0054	0.1567

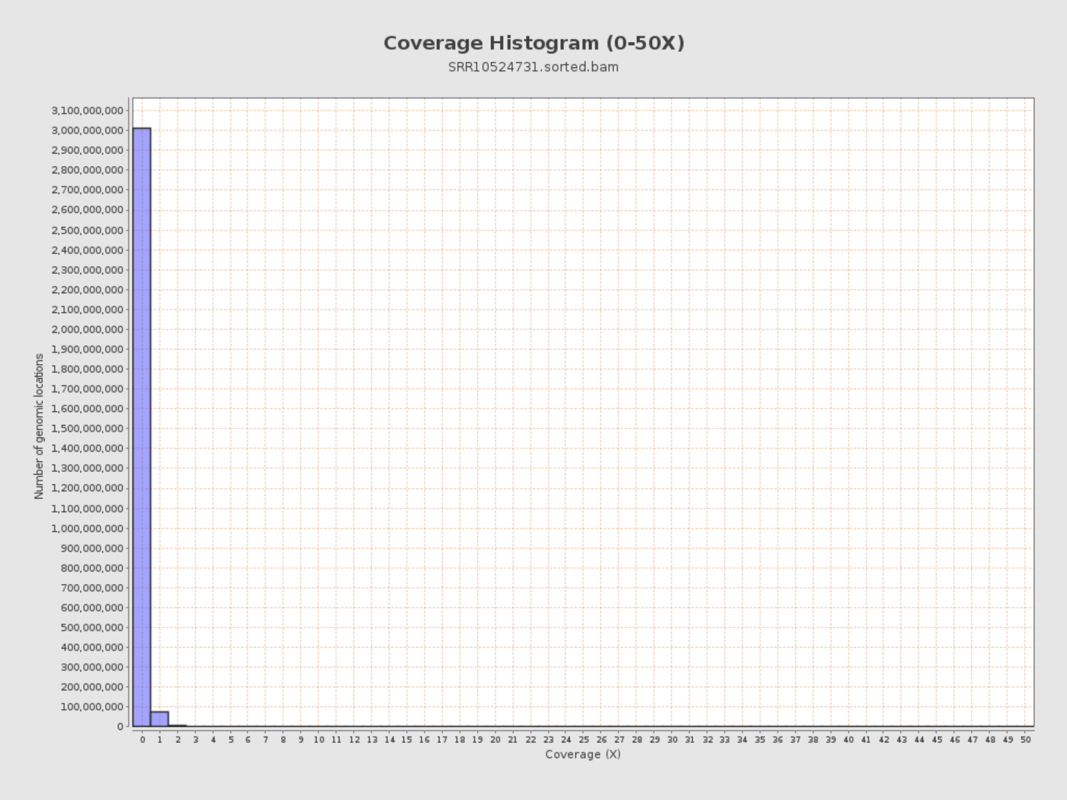
3. Results : Coverage across reference



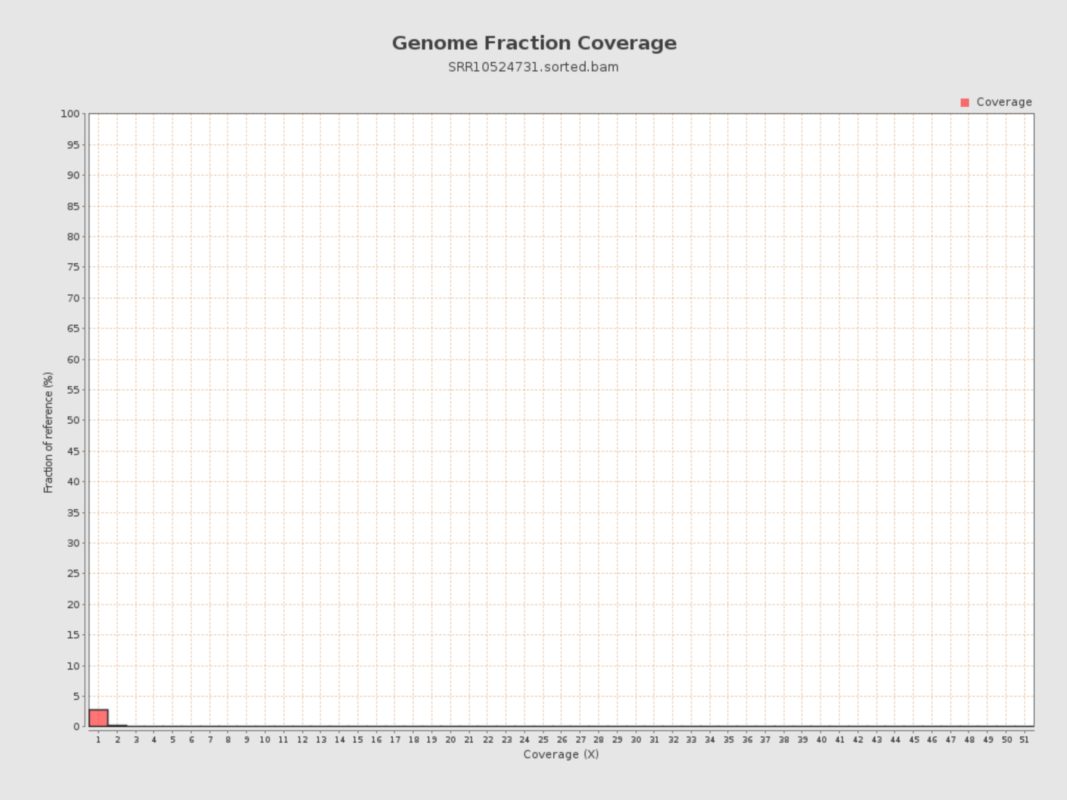
4. Results : Coverage Histogram



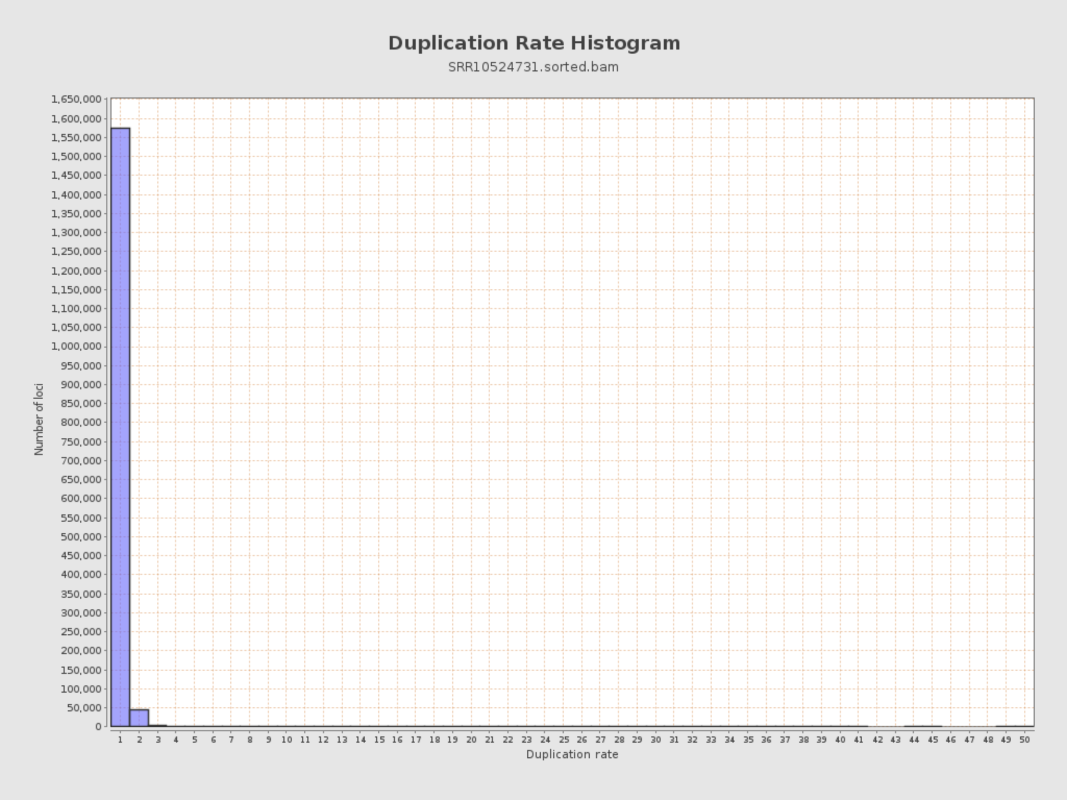
5. Results : Coverage Histogram (0-50X)



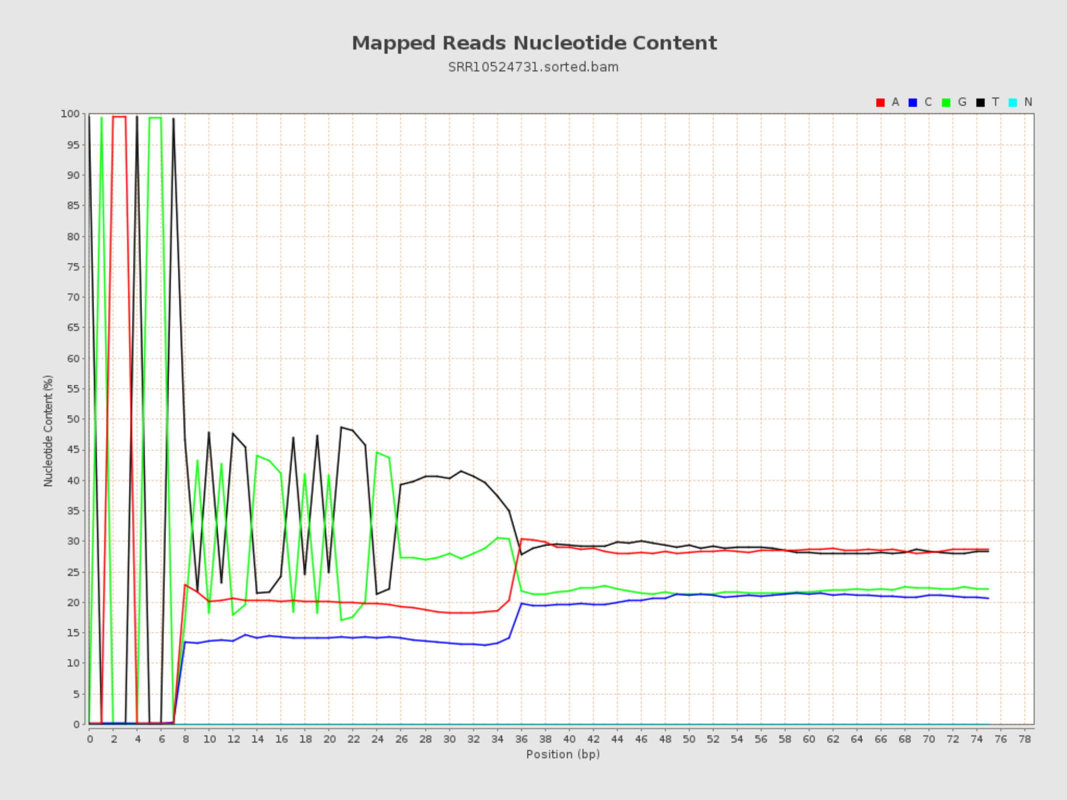
6. Results : Genome Fraction Coverage



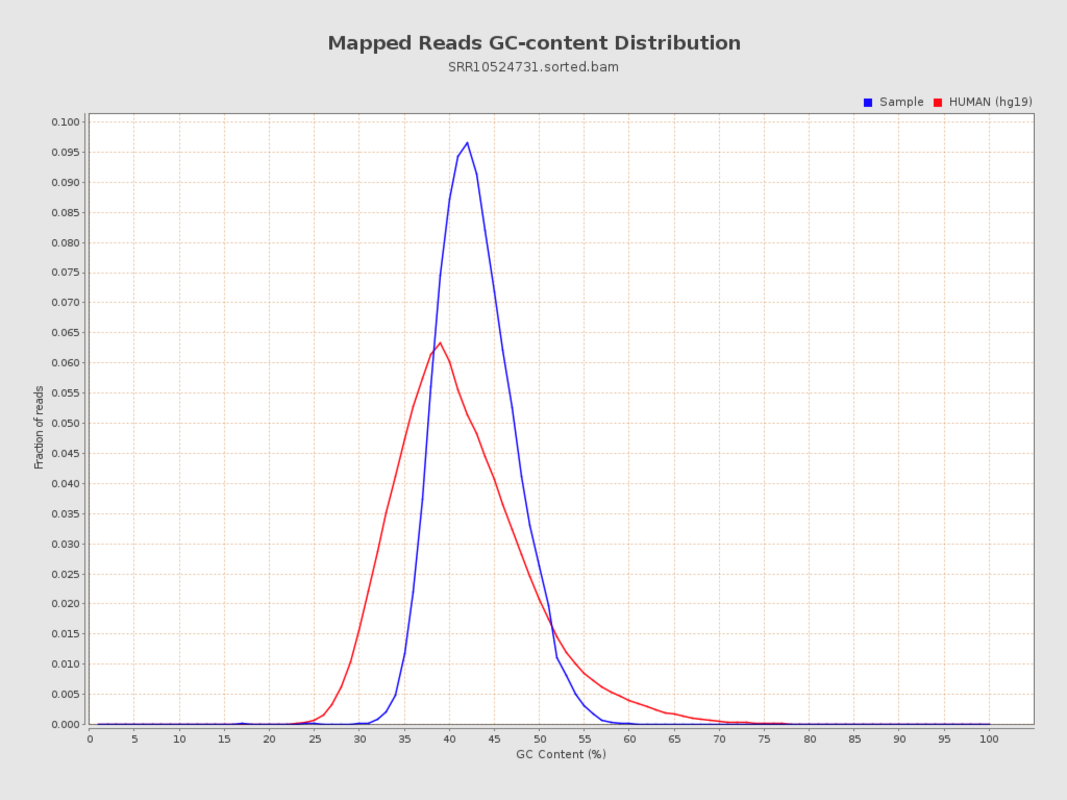
7. Results : Duplication Rate Histogram



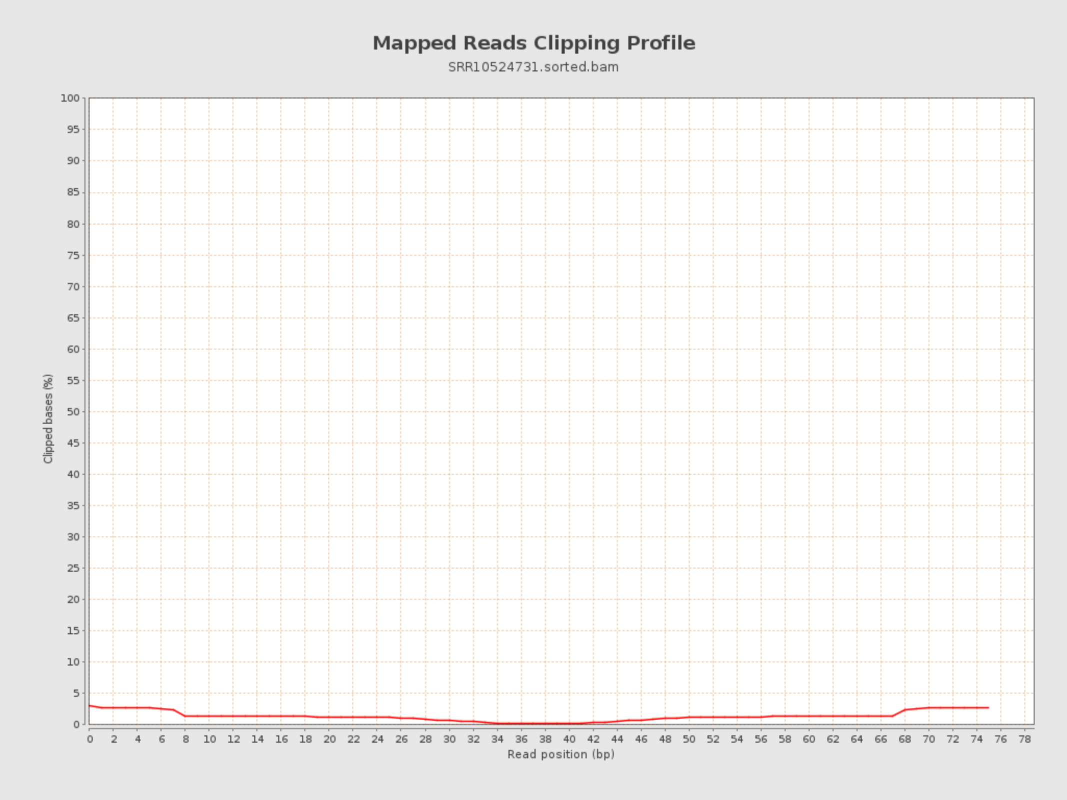
8. Results : Mapped Reads Nucleotide Content



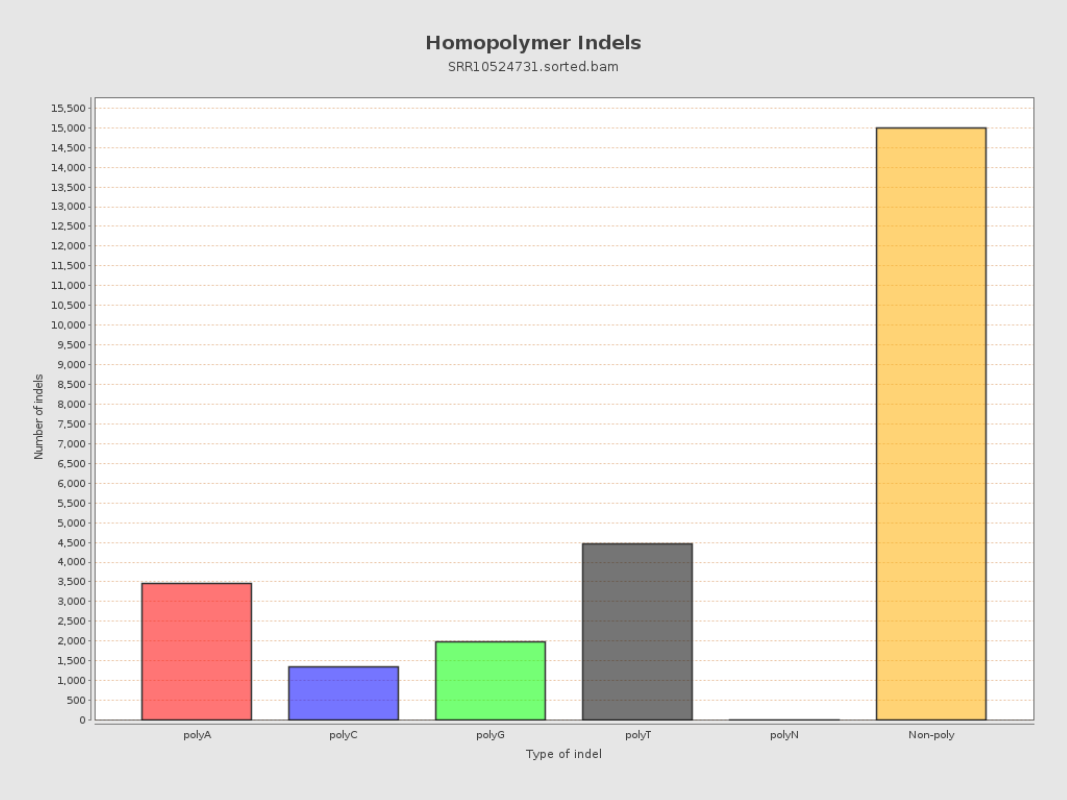
9. Results : Mapped Reads GC-content Distribution



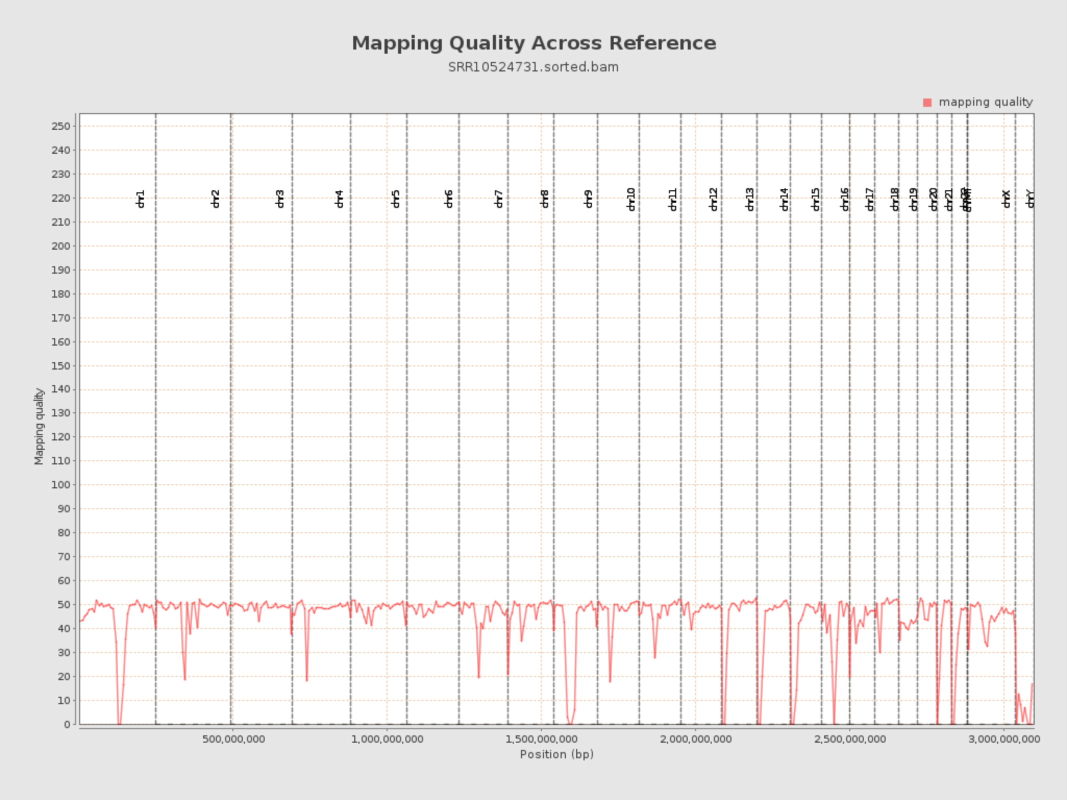
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram