Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:09:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524491.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_SRR10524491 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524491.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:09:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,617,435
Mapped reads	1,487,110 / 91.94%
Unmapped reads	130,325 / 8.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,370 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	66,646 / 4.12%
Duplication rate	3.46%
Clipped reads	1,486,075 / 91.88%

2.2. ACGT Content

Number/percentage of A's	22,013,413 / 25.53%
Number/percentage of C's	15,933,298 / 18.48%
Number/percentage of T's	27,759,334 / 32.19%
Number/percentage of G's	20,525,051 / 23.8%
Number/percentage of N's	1,836 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.2623

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

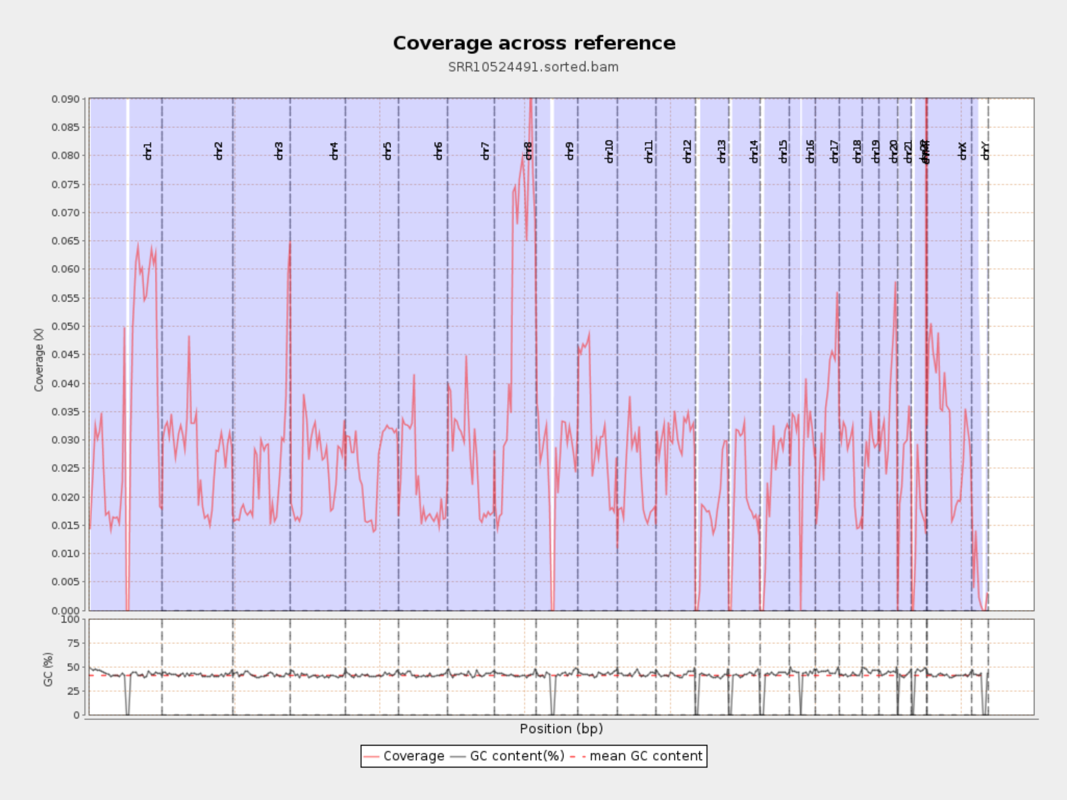
General error rate	0.48%
Mismatches	406,021
Insertions	5,332
Mapped reads with at least one insertion	0.36%
Deletions	16,039
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.66%

2.6. Chromosome stats

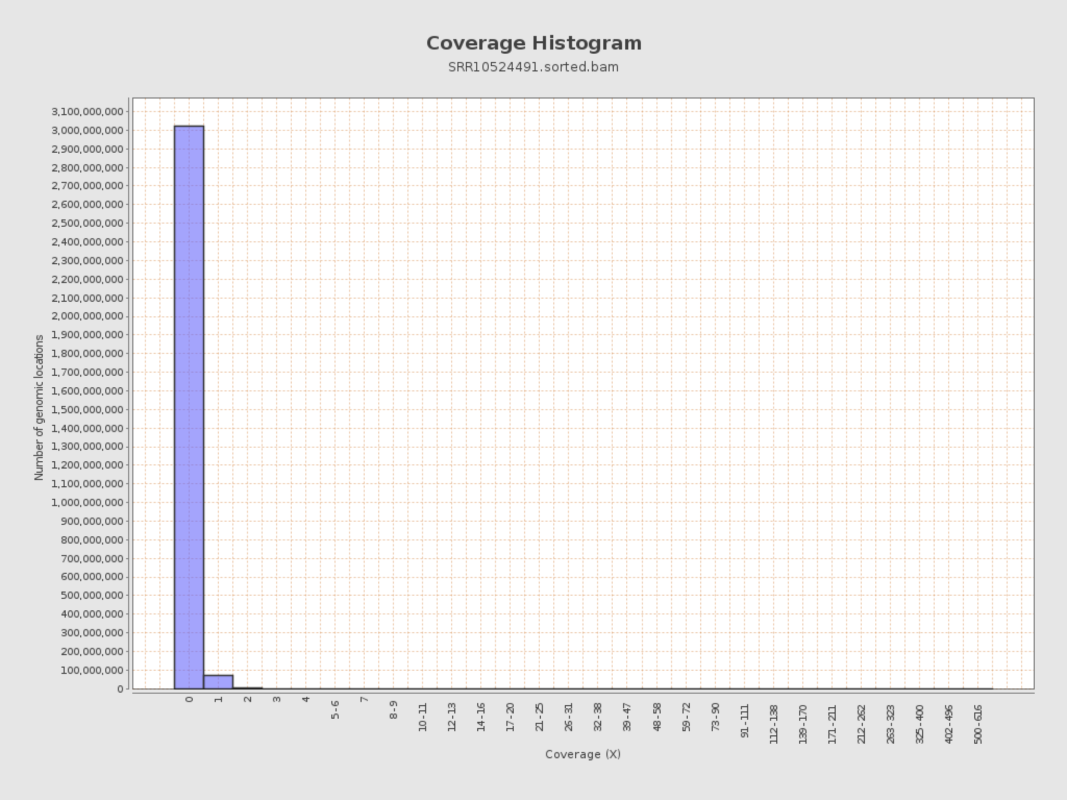
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8664409	0.0348	0.4663
chr2	243199373	6861393	0.0282	0.2981
chr3	198022430	4737260	0.0239	0.1731
chr4	191154276	4877684	0.0255	0.1965
chr5	180915260	4657975	0.0257	0.1785
chr6	171115067	3805862	0.0222	0.2175
chr7	159138663	4289502	0.027	0.3433

chr8	146364022	7918890	0.0541	0.2954
chr9	141213431	3603966	0.0255	0.2305
chr10	135534747	4403244	0.0325	0.2605
chr11	135006516	3072234	0.0228	0.2546
chr12	133851895	4095296	0.0306	0.1948
chr13	115169878	1955258	0.017	0.1453
chr14	107349540	2136458	0.0199	0.1607
chr15	102531392	2268433	0.0221	0.173
chr16	90354753	2647655	0.0293	0.2029
chr17	81195210	2937683	0.0362	0.2205
chr18	78077248	2007281	0.0257	0.388
chr19	59128983	1684233	0.0285	0.3212
chr20	63025520	2335892	0.0371	0.2167
chr21	48129895	1187045	0.0247	0.186
chr22	51304566	710495	0.0138	0.1297
chrMT	16571	8114	0.4897	0.8079
chrX	155270560	5136972	0.0331	0.2223
chrY	59373566	256895	0.0043	0.1164

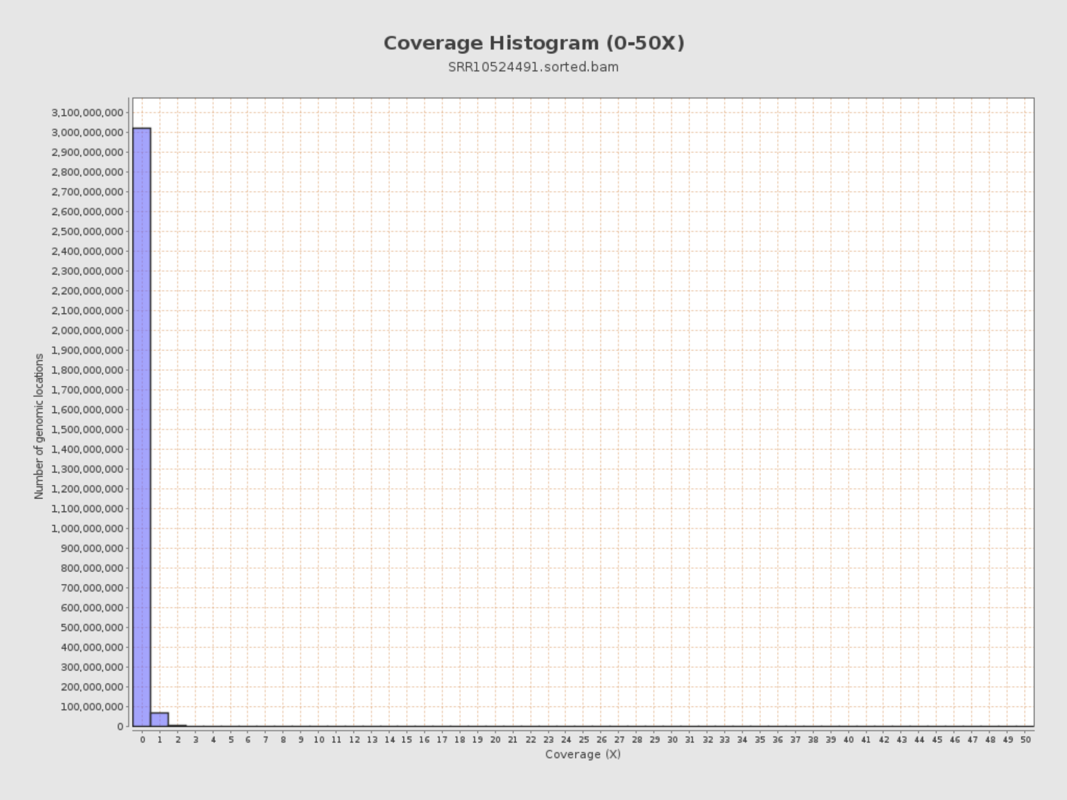
3. Results : Coverage across reference



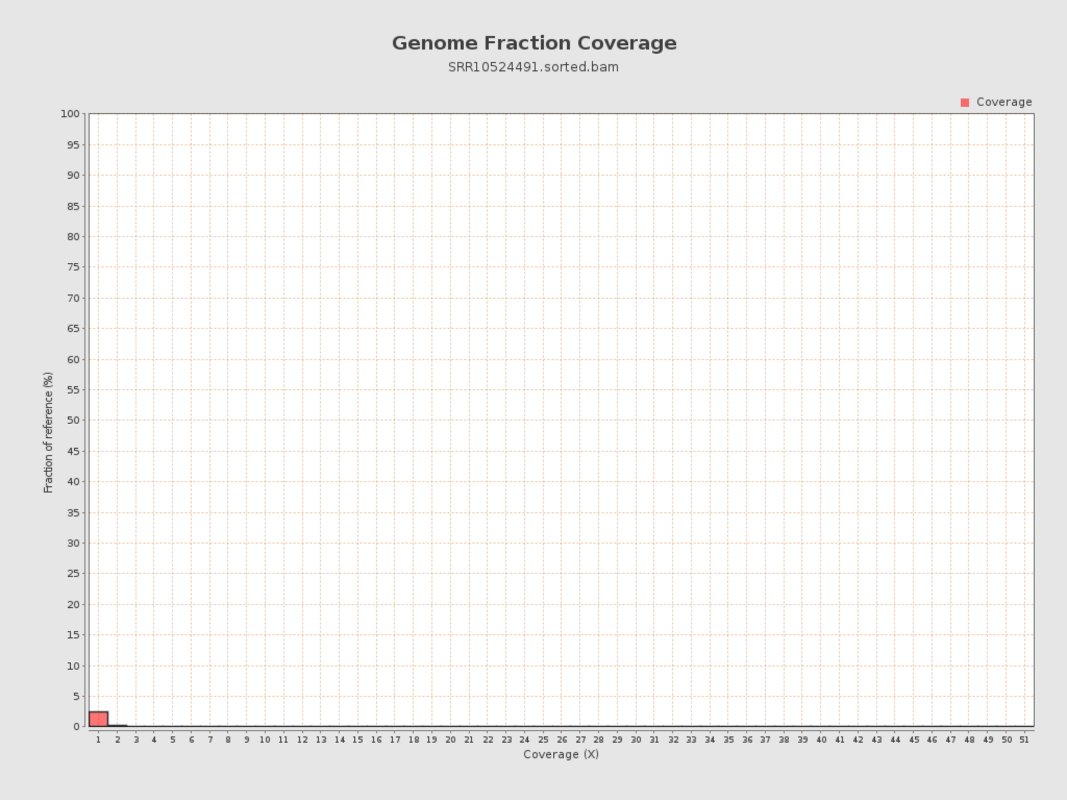
4. Results : Coverage Histogram



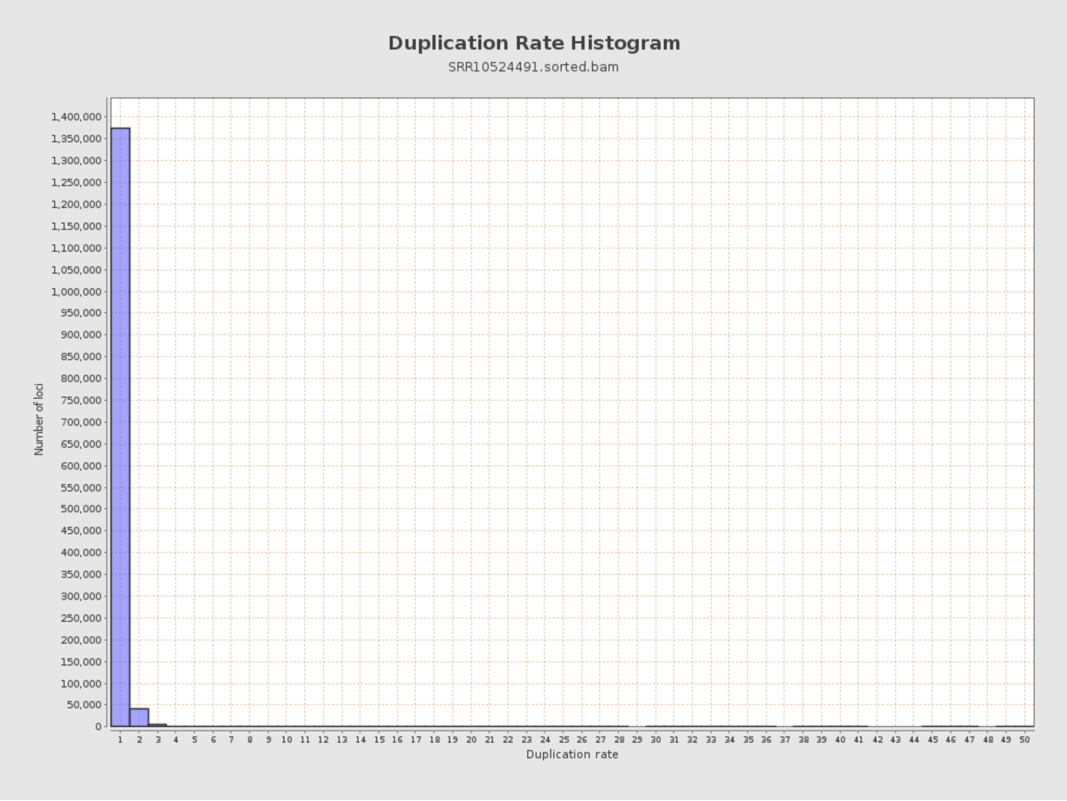
5. Results : Coverage Histogram (0-50X)



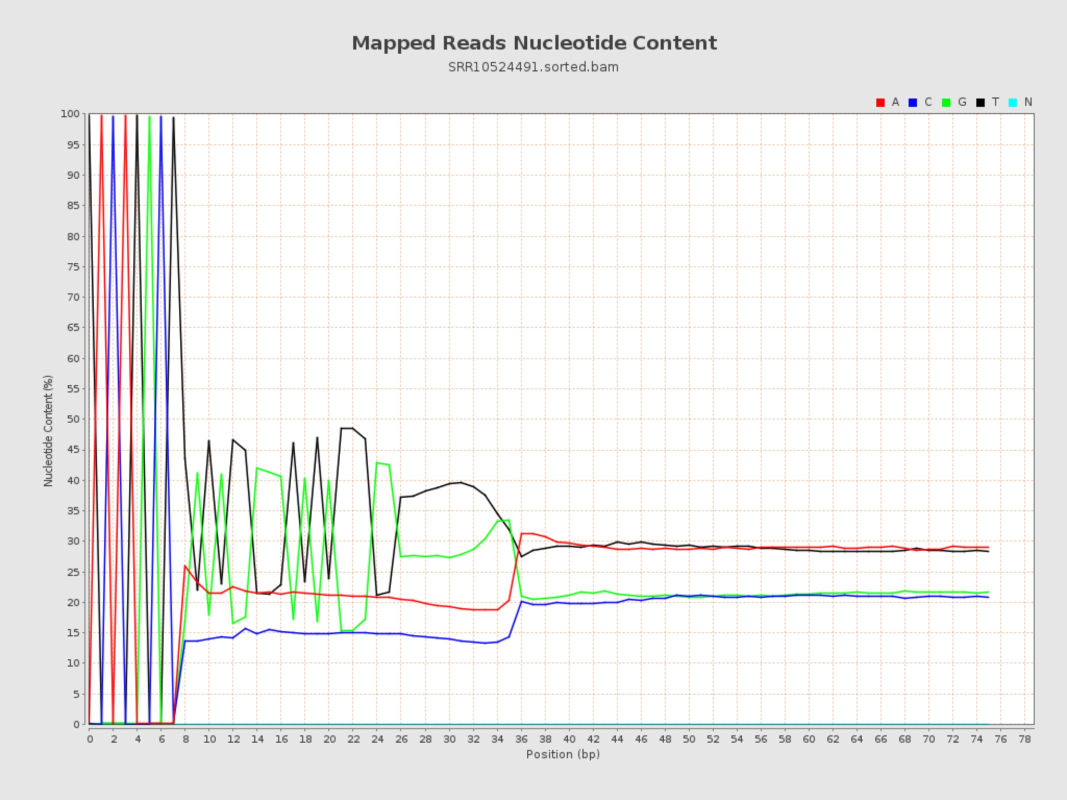
6. Results : Genome Fraction Coverage



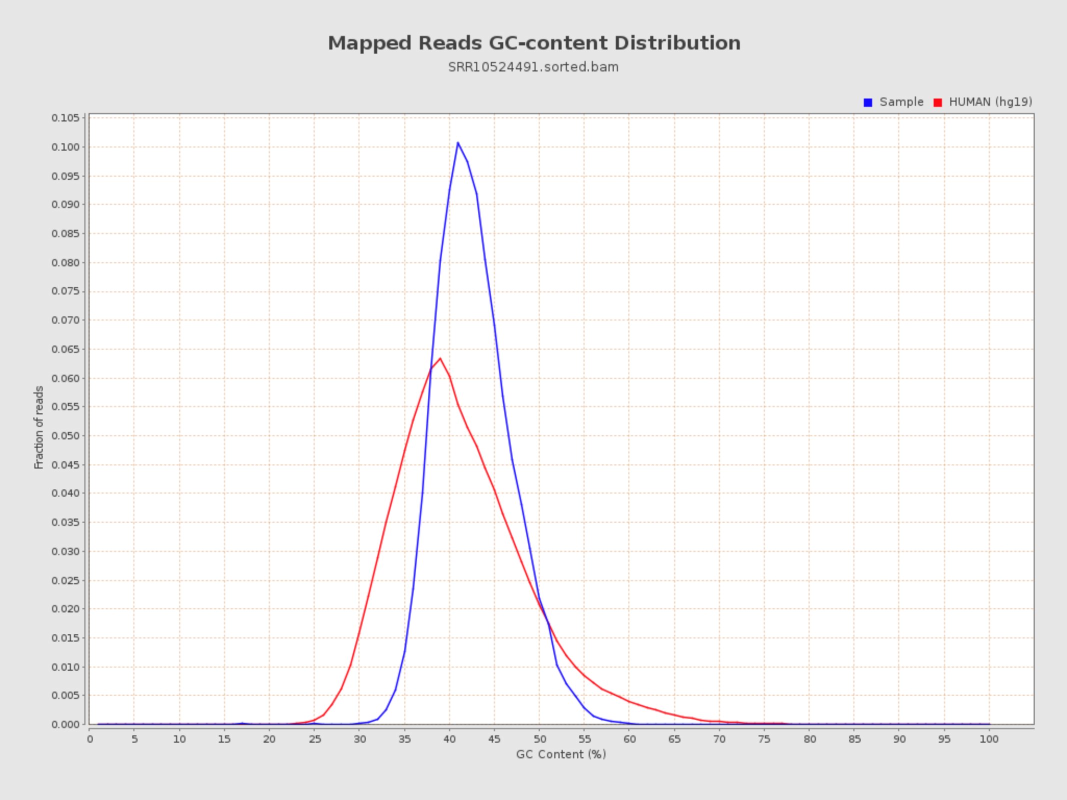
7. Results : Duplication Rate Histogram



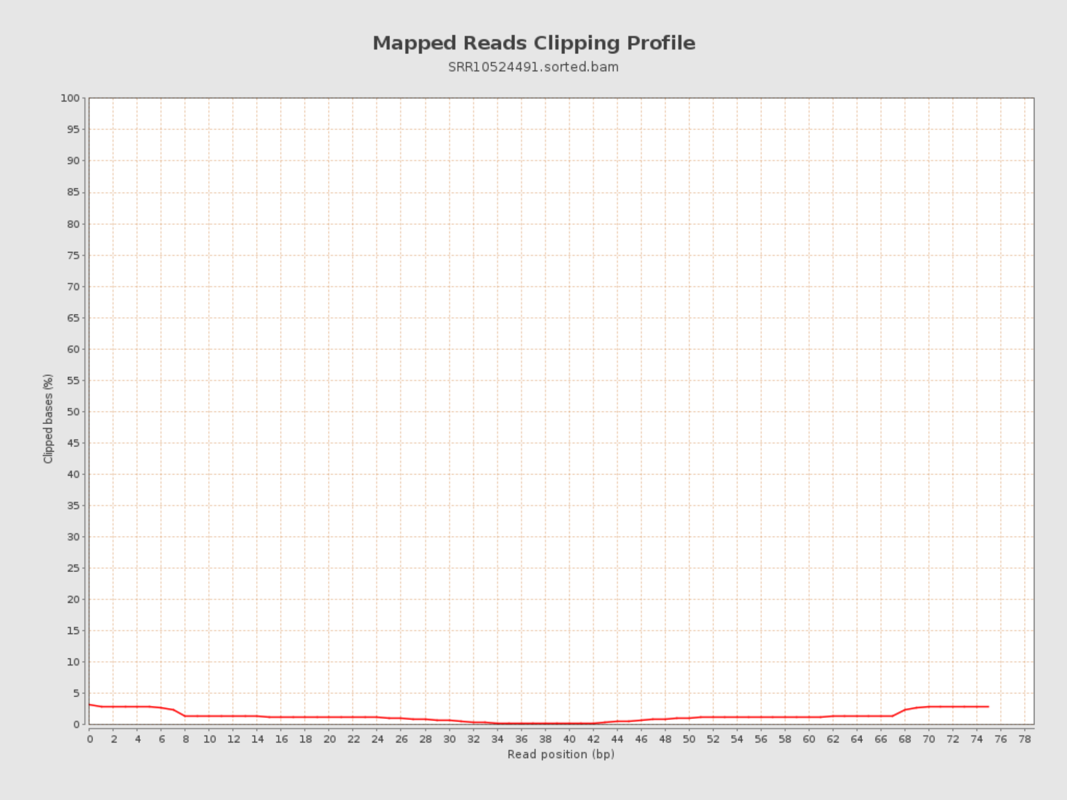
8. Results : Mapped Reads Nucleotide Content



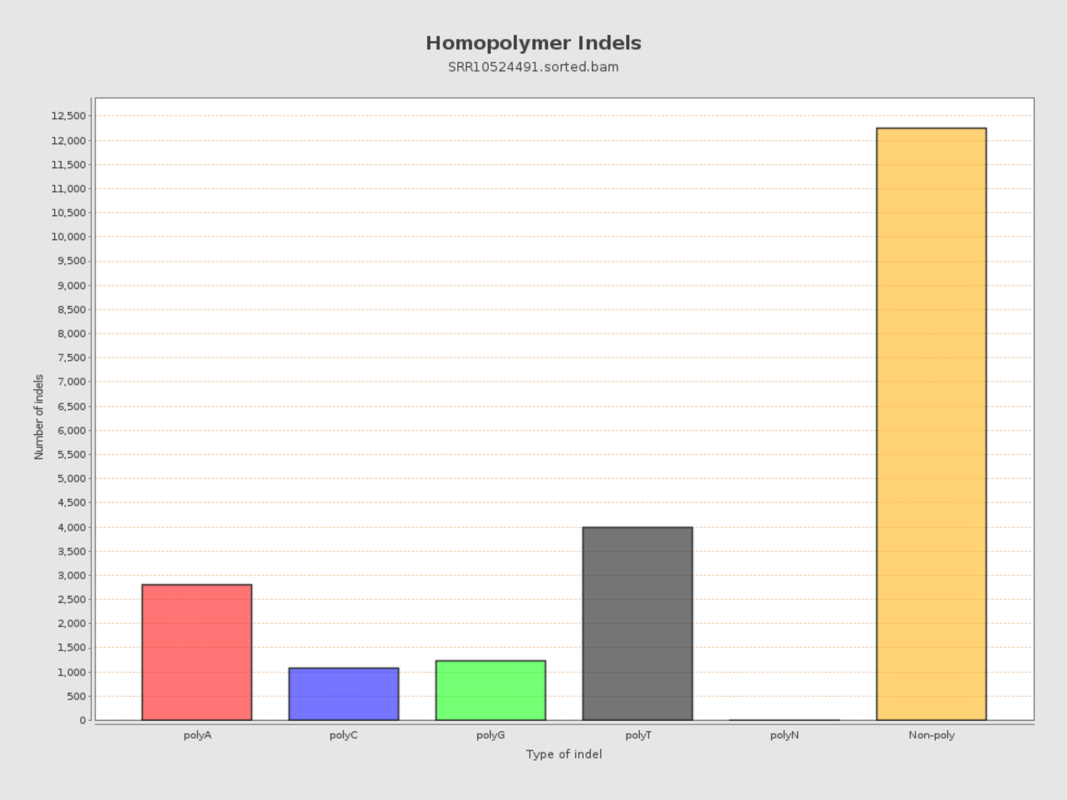
9. Results : Mapped Reads GC-content Distribution



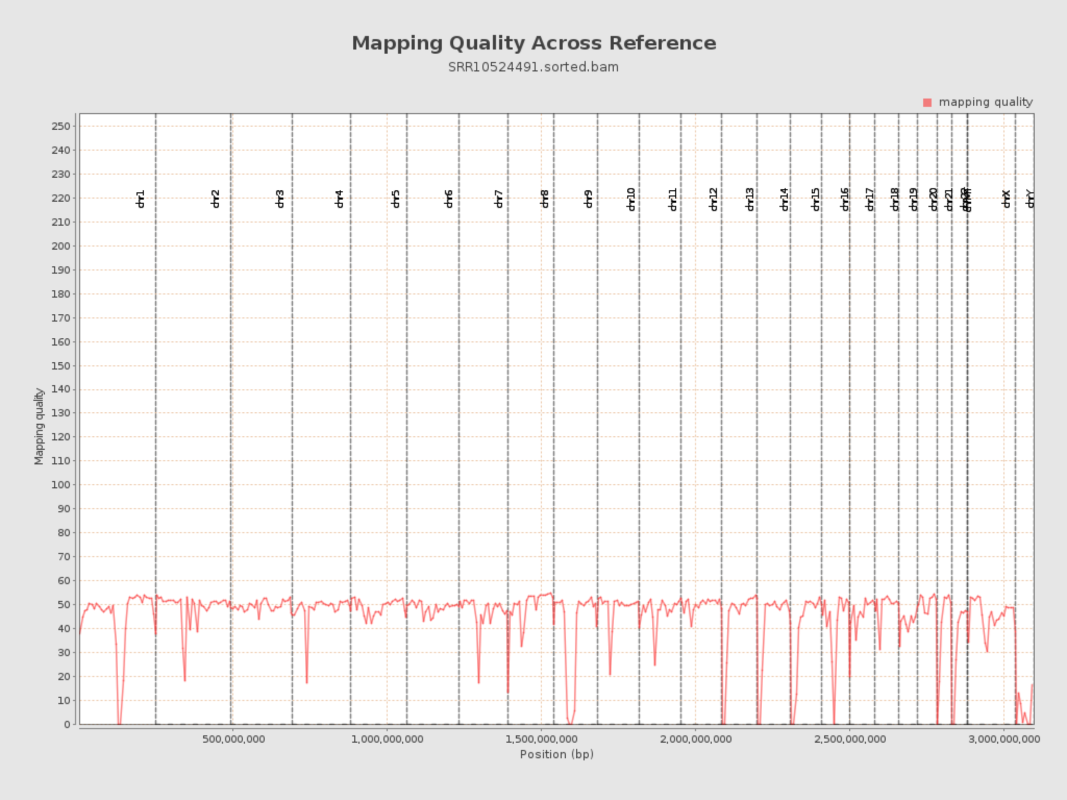
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram