Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:35:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524391.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_SRR10524391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524391.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:35:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,604,772
Mapped reads	1,482,283 / 92.37%
Unmapped reads	122,489 / 7.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,661 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	49,911 / 3.11%
Duplication rate	2.47%
Clipped reads	1,487,077 / 92.67%

2.2. ACGT Content

Number/percentage of A's	21,826,170 / 25.03%
Number/percentage of C's	17,171,903 / 19.69%
Number/percentage of T's	26,934,910 / 30.88%
Number/percentage of G's	21,271,521 / 24.39%
Number/percentage of N's	11,579 / 0.01%
GC Percentage	44.08%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2819

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

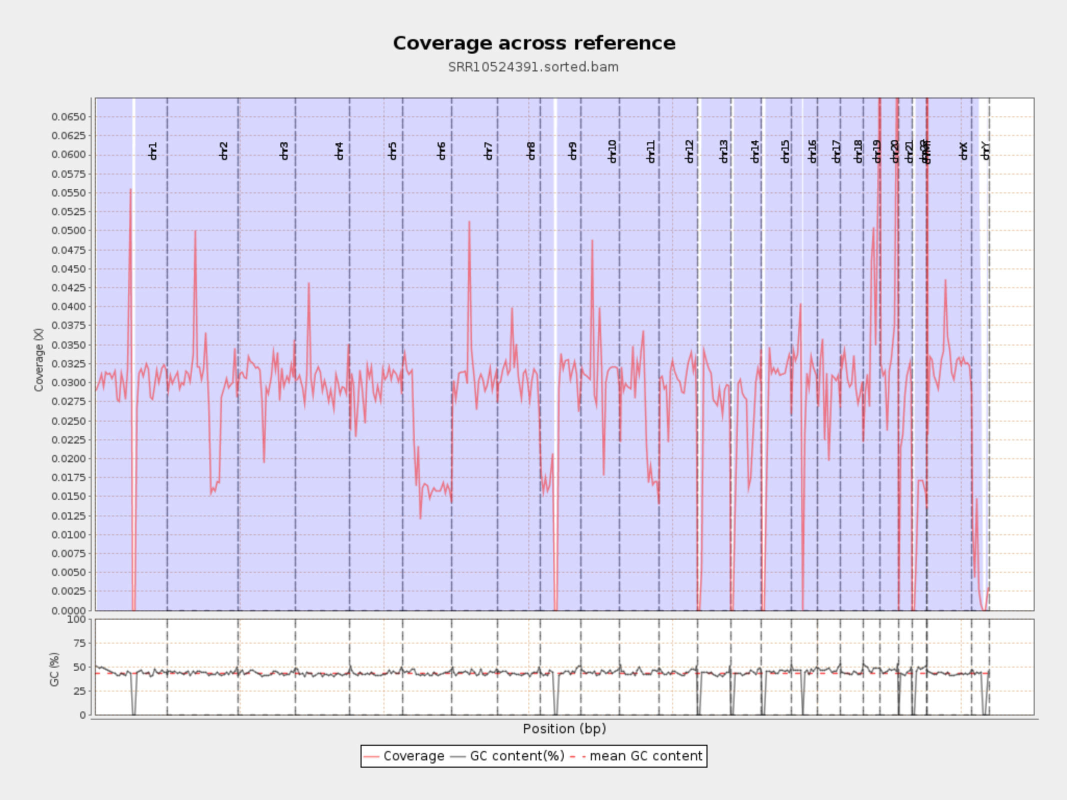
General error rate	0.49%
Mismatches	413,796
Insertions	4,993
Mapped reads with at least one insertion	0.33%
Deletions	15,091
Mapped reads with at least one deletion	1.01%
Homopolymer indels	43.69%

2.6. Chromosome stats

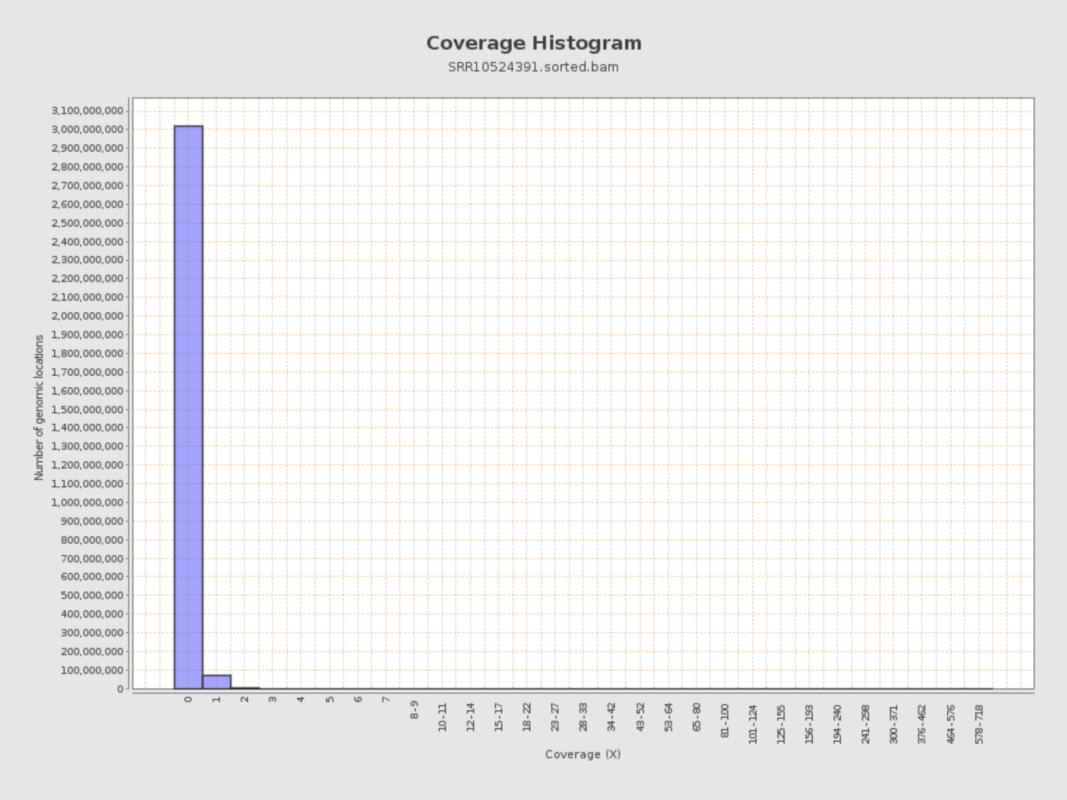
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7287042	0.0292	0.5959
chr2	243199373	7063735	0.029	0.3009
chr3	198022430	6083011	0.0307	0.1877
chr4	191154276	5804172	0.0304	0.2027
chr5	180915260	5383233	0.0298	0.1855
chr6	171115067	3381412	0.0198	0.1627
chr7	159138663	4987158	0.0313	0.3786

chr8	146364022	4572448	0.0312	0.2489
chr9	141213431	3277504	0.0232	0.21
chr10	135534747	4286532	0.0316	0.2502
chr11	135006516	3597916	0.0266	0.2229
chr12	133851895	4069176	0.0304	0.1914
chr13	115169878	2841235	0.0247	0.1687
chr14	107349540	2425005	0.0226	0.1664
chr15	102531392	2697444	0.0263	0.1749
chr16	90354753	2627085	0.0291	0.1918
chr17	81195210	2363014	0.0291	0.2016
chr18	78077248	2394537	0.0307	0.3698
chr19	59128983	2442204	0.0413	0.4305
chr20	63025520	2417161	0.0384	0.2168
chr21	48129895	1202681	0.025	0.1826
chr22	51304566	603753	0.0118	0.1159
chrMT	16571	103932	6.2719	3.885
chrX	155270560	5072531	0.0327	0.2121
chrY	59373566	256312	0.0043	0.12

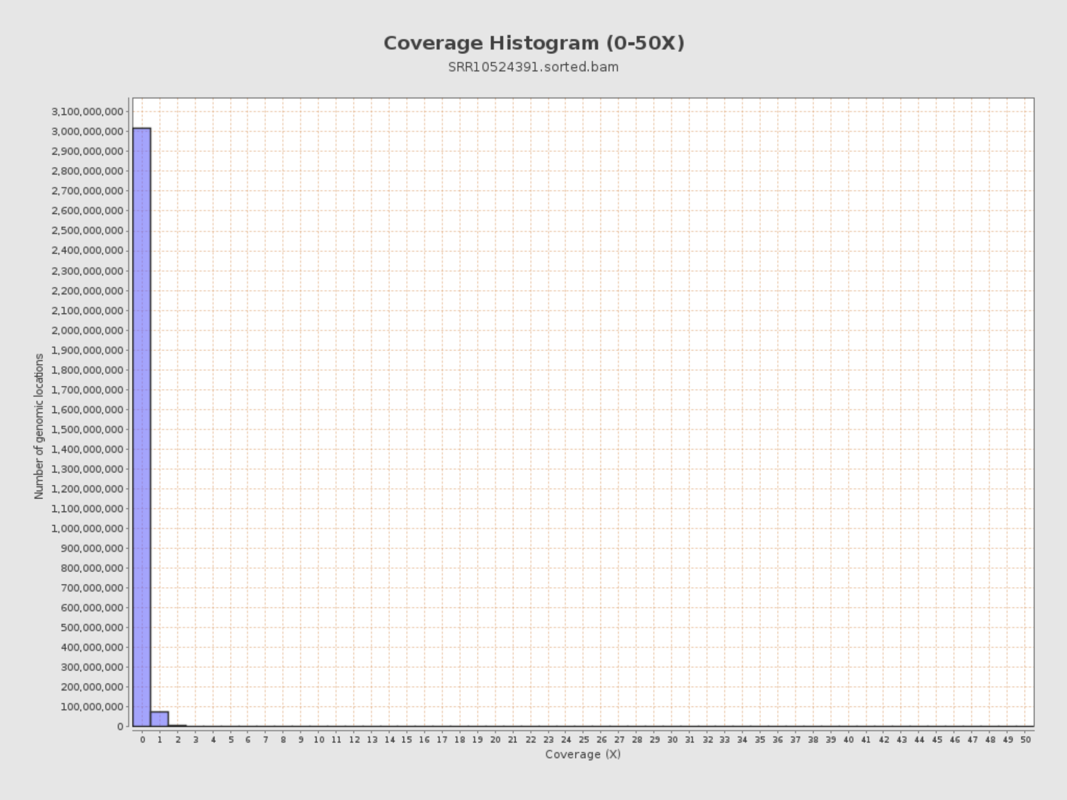
3. Results : Coverage across reference



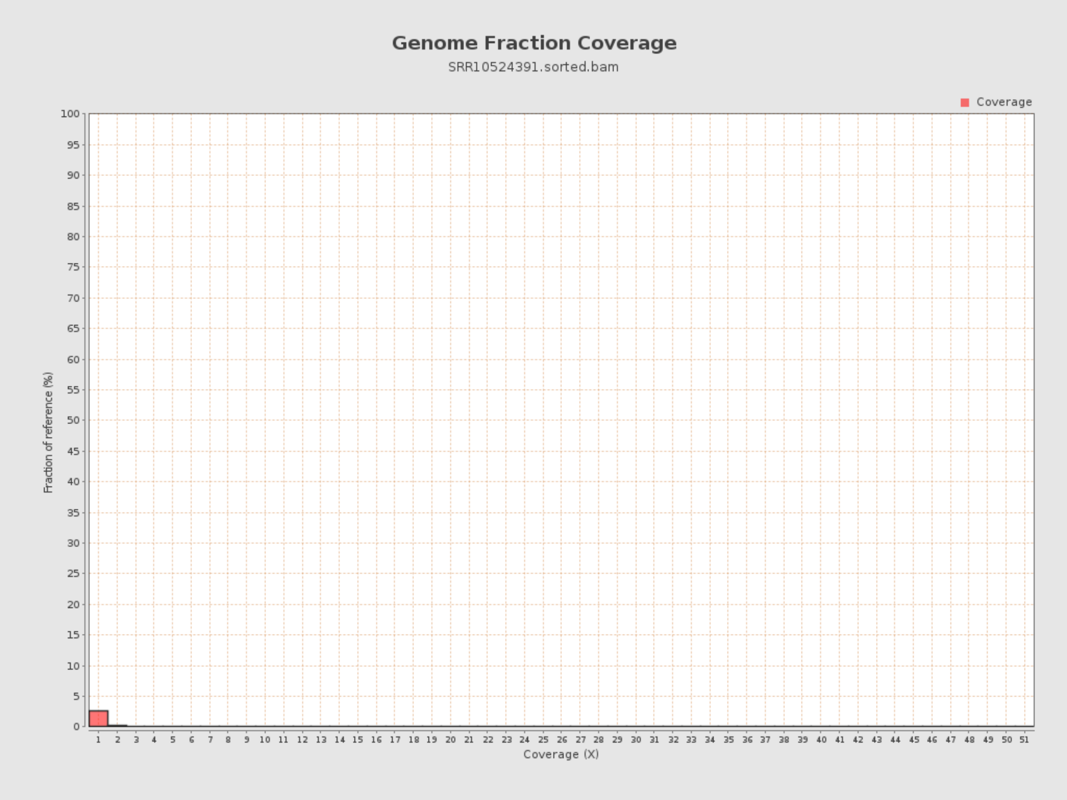
4. Results : Coverage Histogram



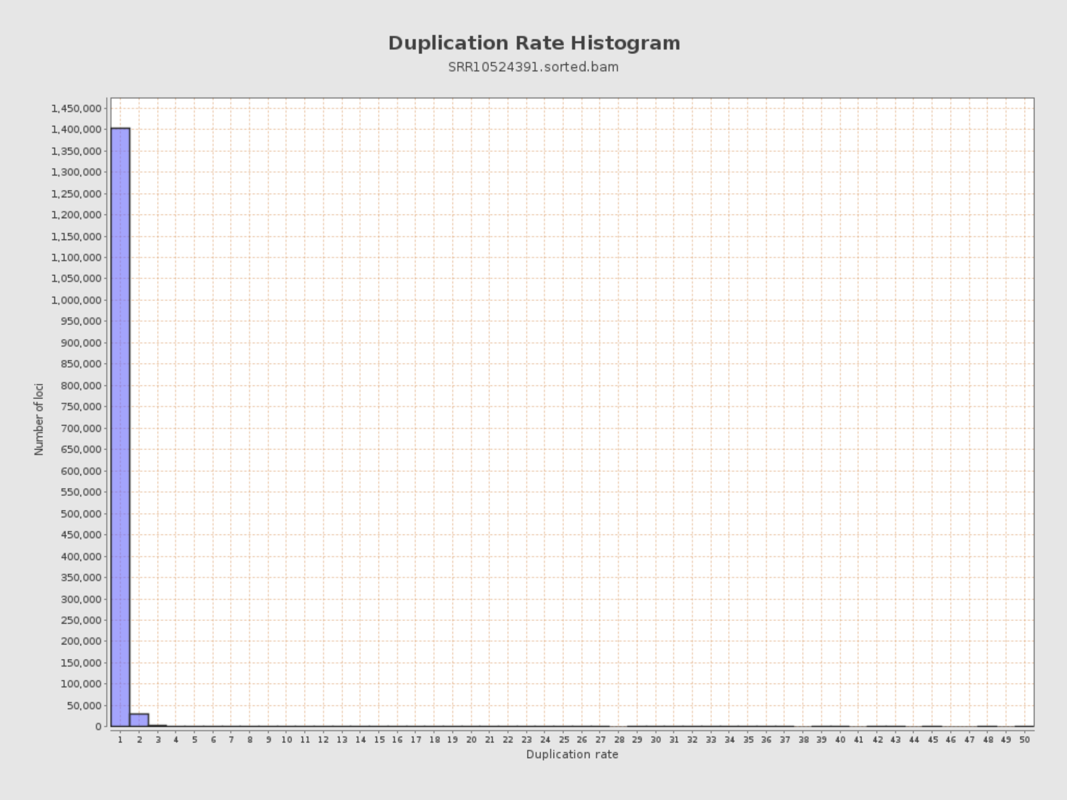
5. Results : Coverage Histogram (0-50X)



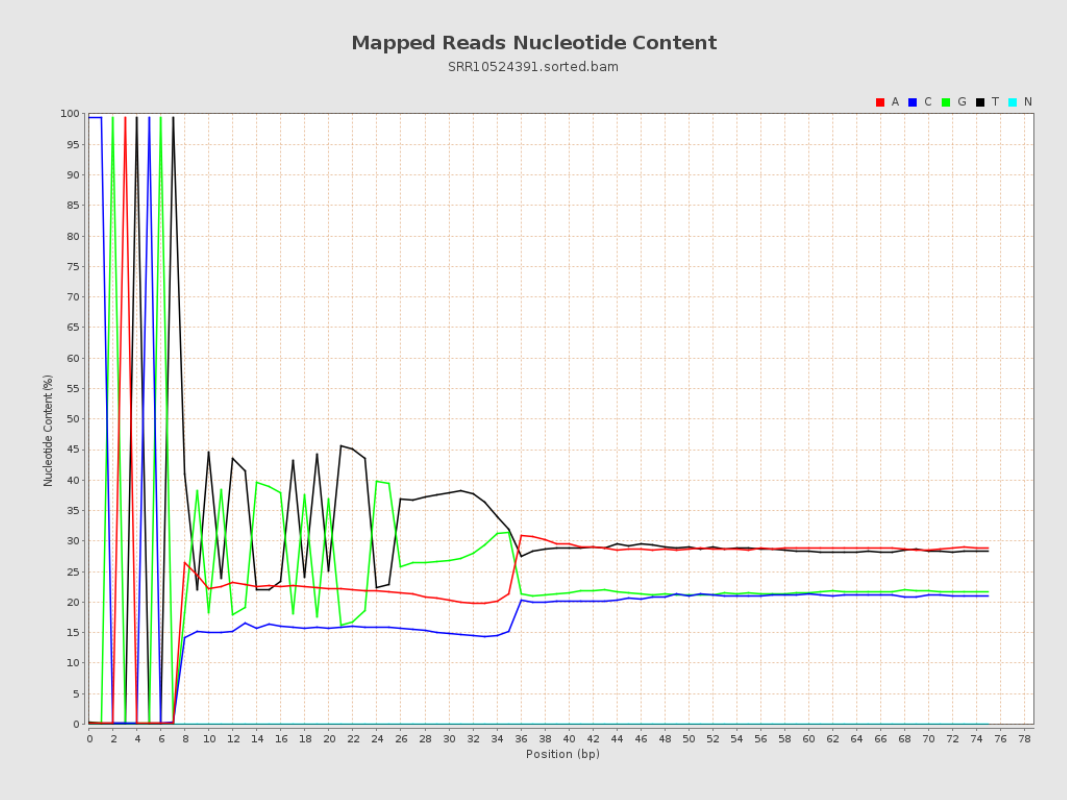
6. Results : Genome Fraction Coverage



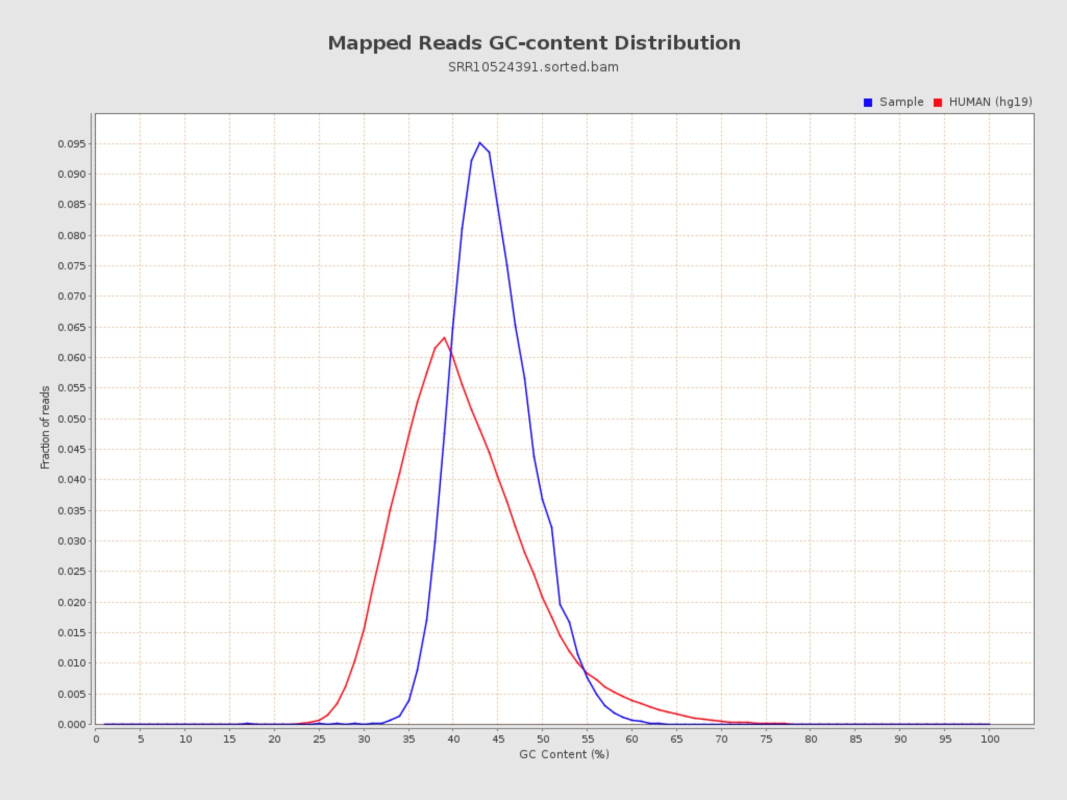
7. Results : Duplication Rate Histogram



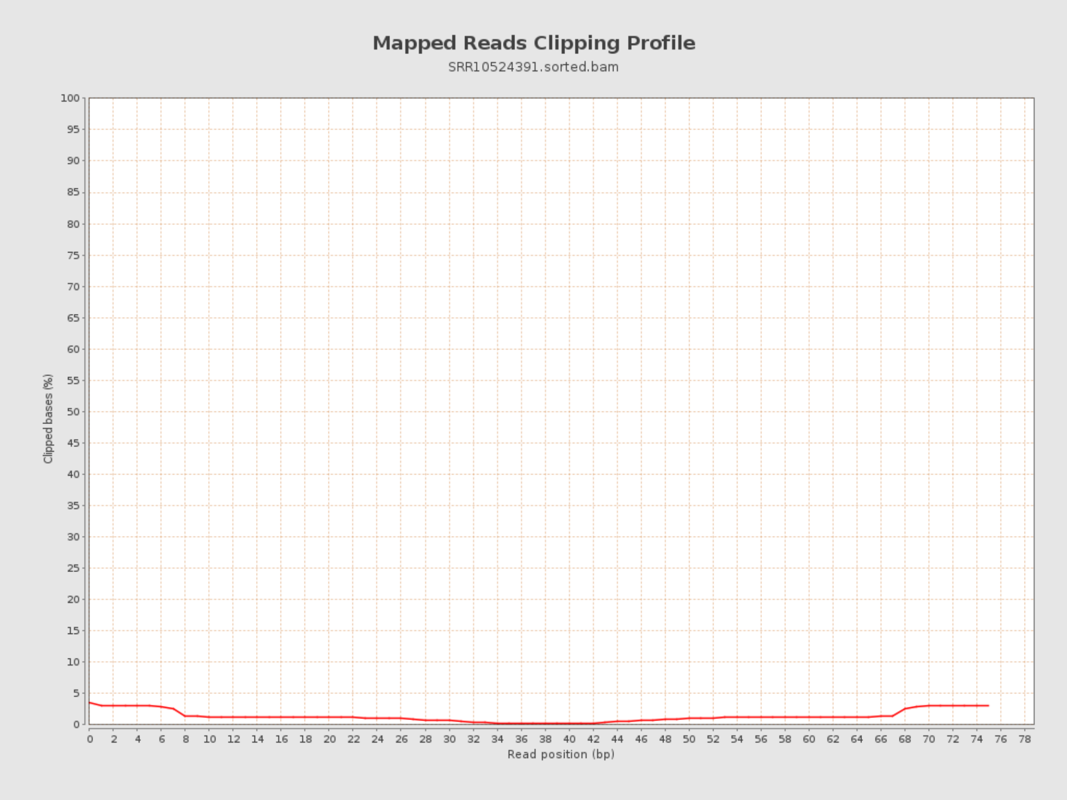
8. Results : Mapped Reads Nucleotide Content



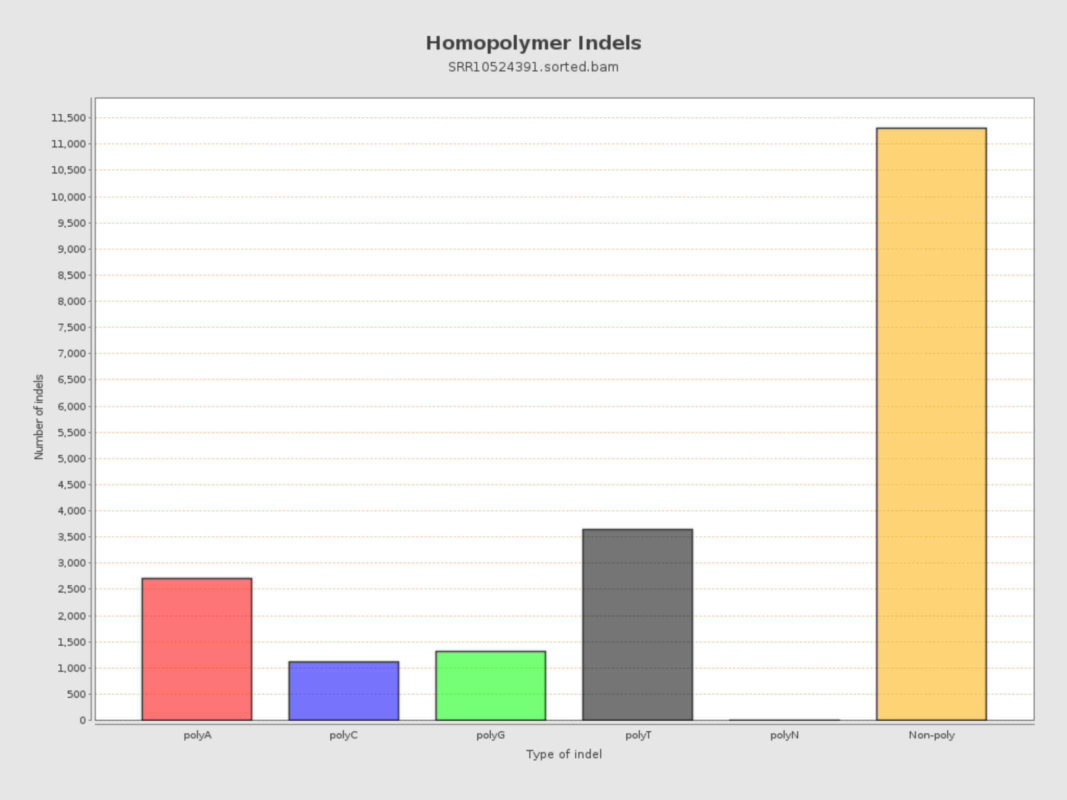
9. Results : Mapped Reads GC-content Distribution



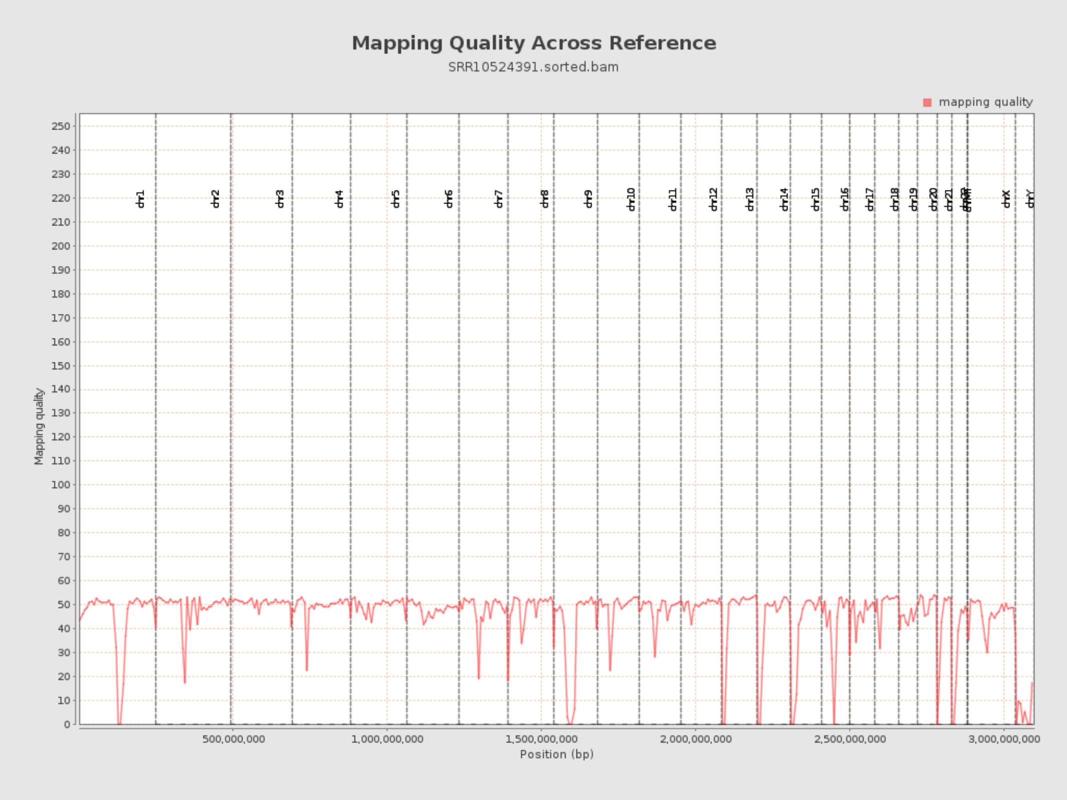
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram