Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 07:17:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524511.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_SRR10524511 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524511.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 07:17:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524511.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,389,317
Mapped reads	1,261,442 / 90.8%
Unmapped reads	127,875 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,087 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	29,382 / 2.11%
Duplication rate	1.59%
Clipped reads	1,263,849 / 90.97%

2.2. ACGT Content

Number/percentage of A's	19,095,400 / 25.88%
Number/percentage of C's	12,928,949 / 17.52%
Number/percentage of T's	23,225,526 / 31.47%
Number/percentage of G's	18,540,712 / 25.13%
Number/percentage of N's	2,153 / 0%
GC Percentage	42.65%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.2226

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

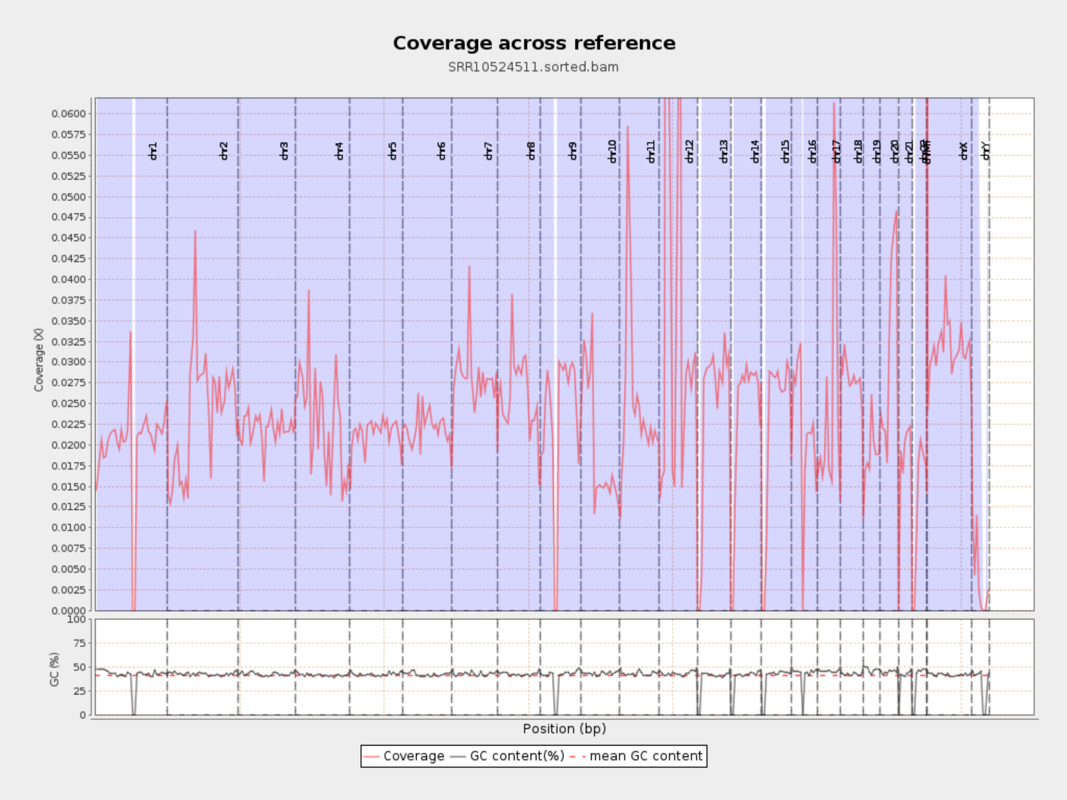
General error rate	0.48%
Mismatches	346,854
Insertions	4,976
Mapped reads with at least one insertion	0.39%
Deletions	11,658
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.36%

2.6. Chromosome stats

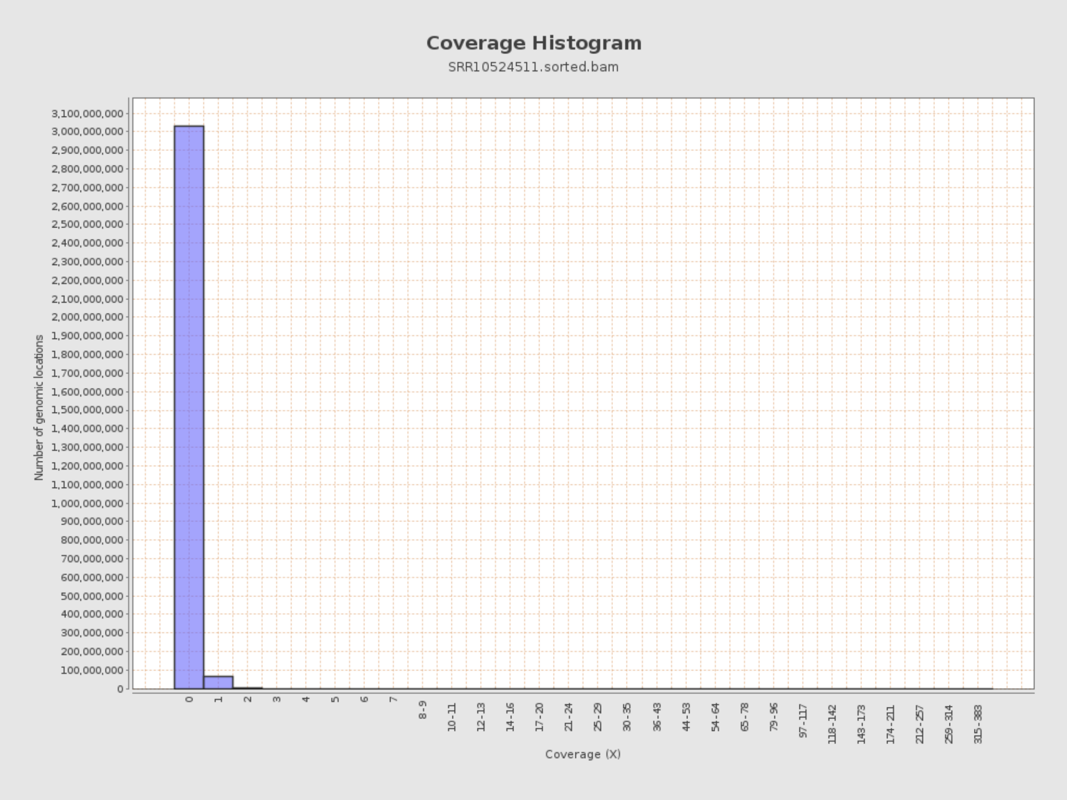
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4988727	0.02	0.3403
chr2	243199373	5819519	0.0239	0.2422
chr3	198022430	4349781	0.022	0.1566
chr4	191154276	4378987	0.0229	0.1742
chr5	180915260	3914186	0.0216	0.1572
chr6	171115067	3792005	0.0222	0.1674
chr7	159138663	4503066	0.0283	0.292

chr8	146364022	3837806	0.0262	0.2294
chr9	141213431	3255137	0.0231	0.2208
chr10	135534747	2684453	0.0198	0.2121
chr11	135006516	3405560	0.0252	0.214
chr12	133851895	5248480	0.0392	0.2287
chr13	115169878	2787729	0.0242	0.1642
chr14	107349540	2486854	0.0232	0.1728
chr15	102531392	2315433	0.0226	0.1605
chr16	90354753	1926681	0.0213	0.1672
chr17	81195210	2073602	0.0255	0.1748
chr18	78077248	2204335	0.0282	0.4076
chr19	59128983	1133616	0.0192	0.2608
chr20	63025520	2017406	0.032	0.1957
chr21	48129895	861462	0.0179	0.1638
chr22	51304566	676160	0.0132	0.1204
chrMT	16571	4255	0.2568	0.5062
chrX	155270560	4924836	0.0317	0.2113
chrY	59373566	221882	0.0037	0.0943

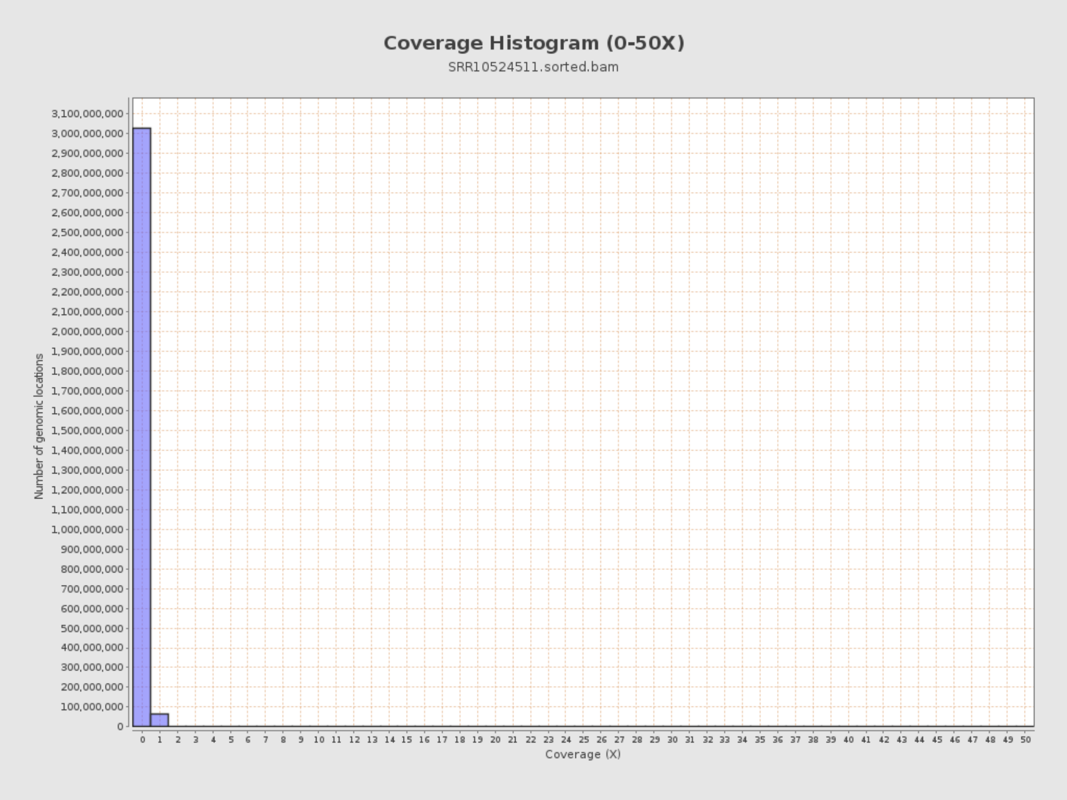
3. Results : Coverage across reference



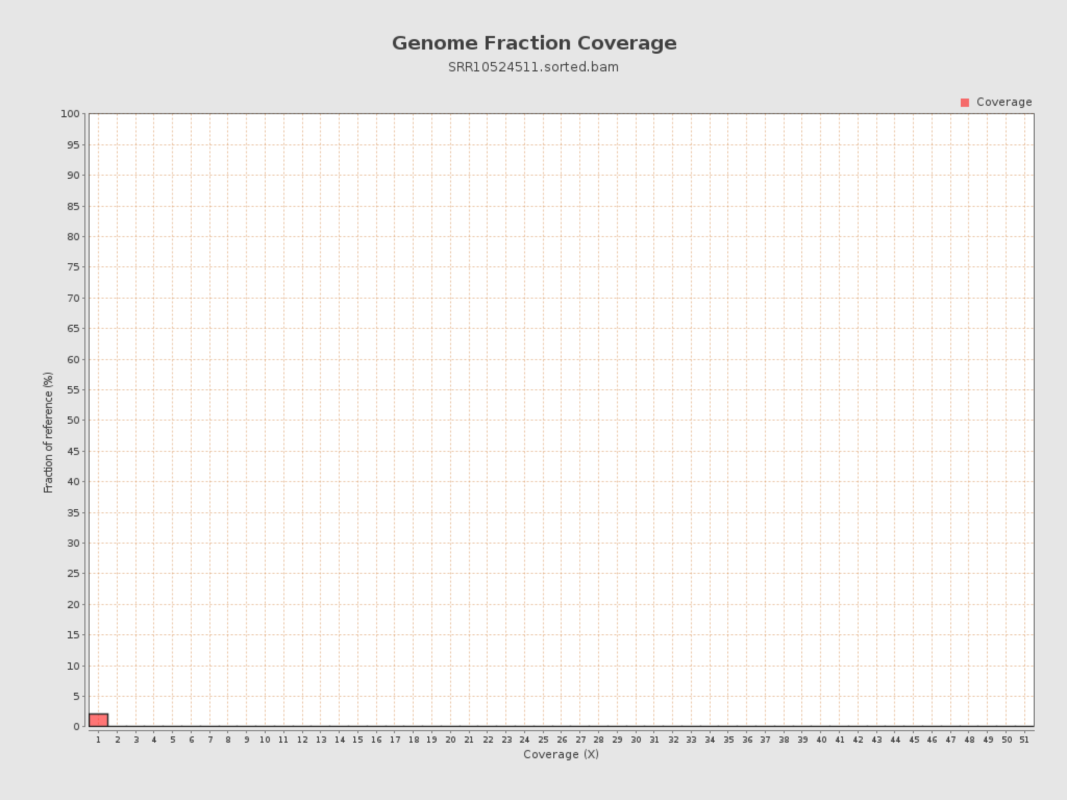
4. Results : Coverage Histogram



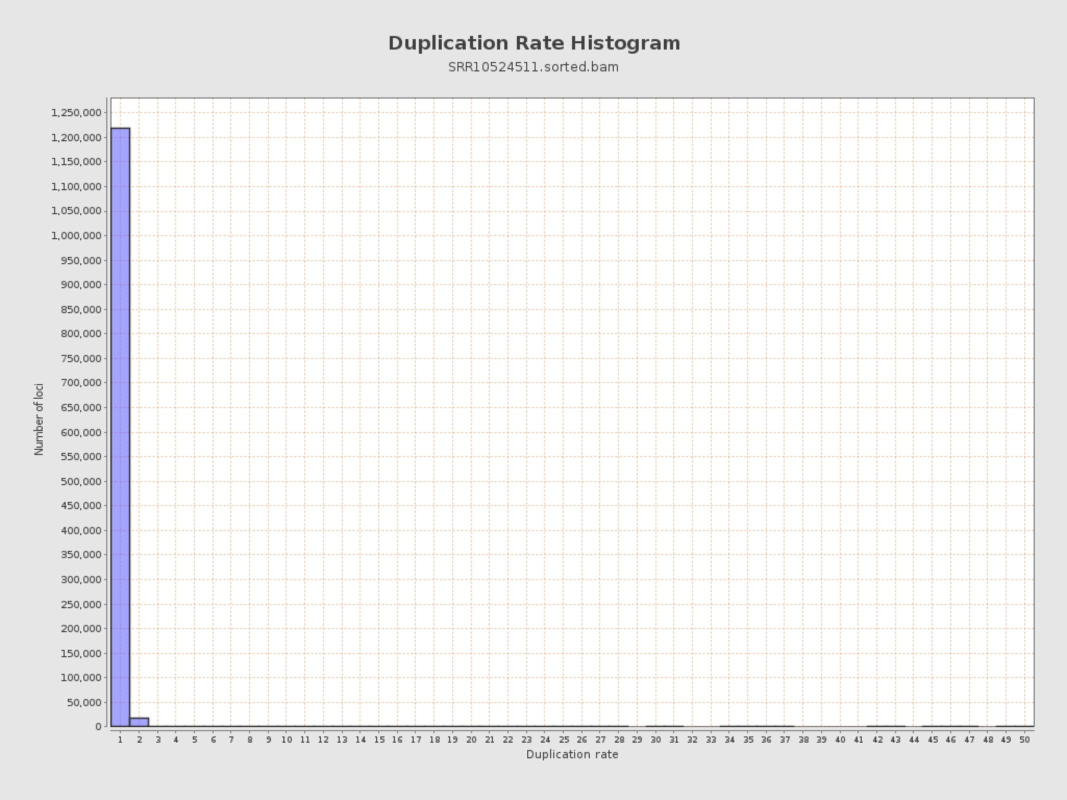
5. Results : Coverage Histogram (0-50X)



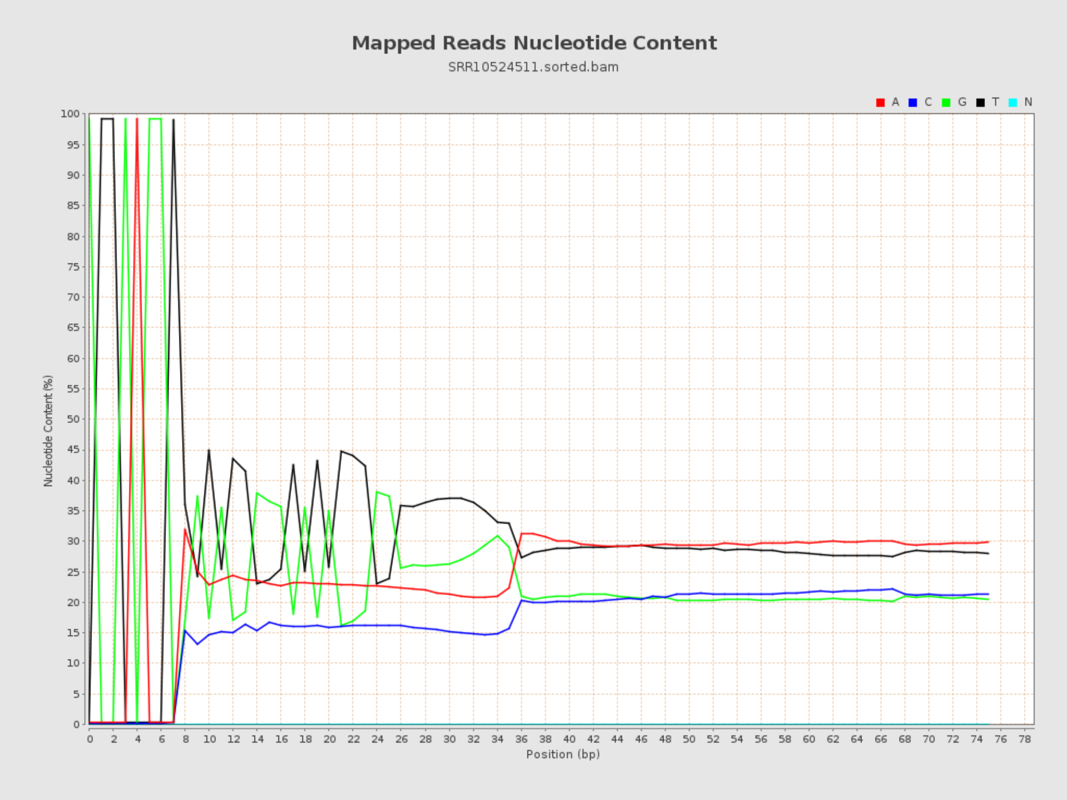
6. Results : Genome Fraction Coverage



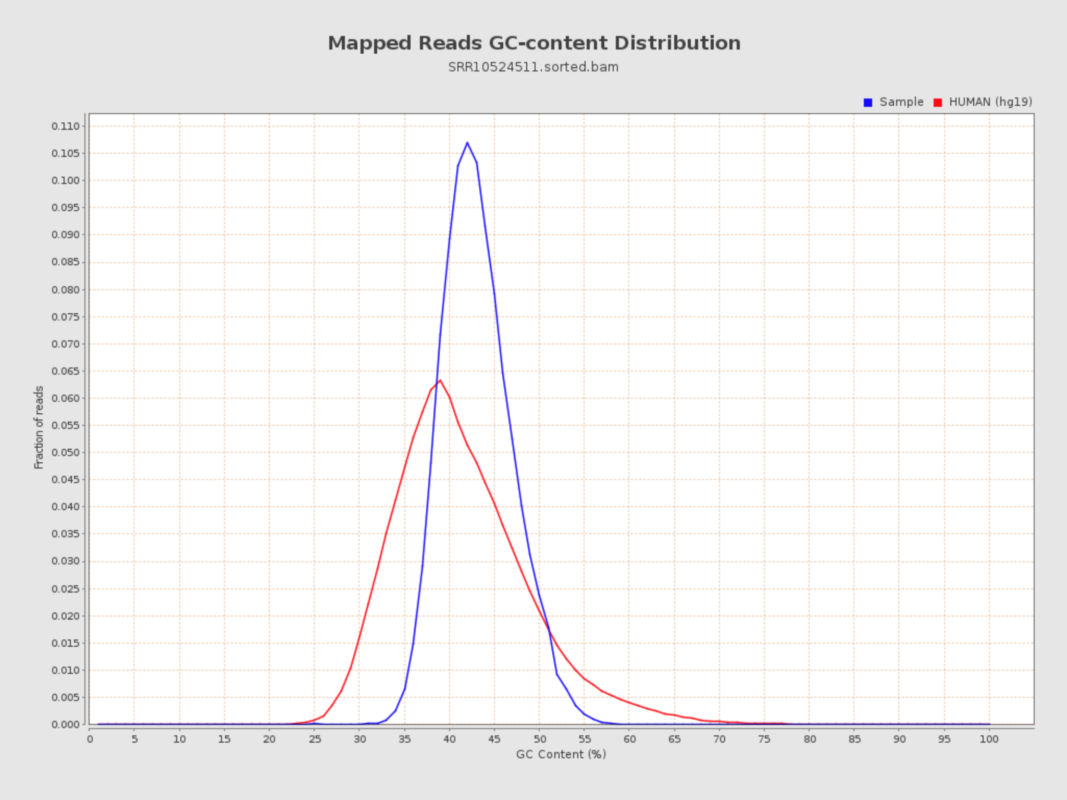
7. Results : Duplication Rate Histogram



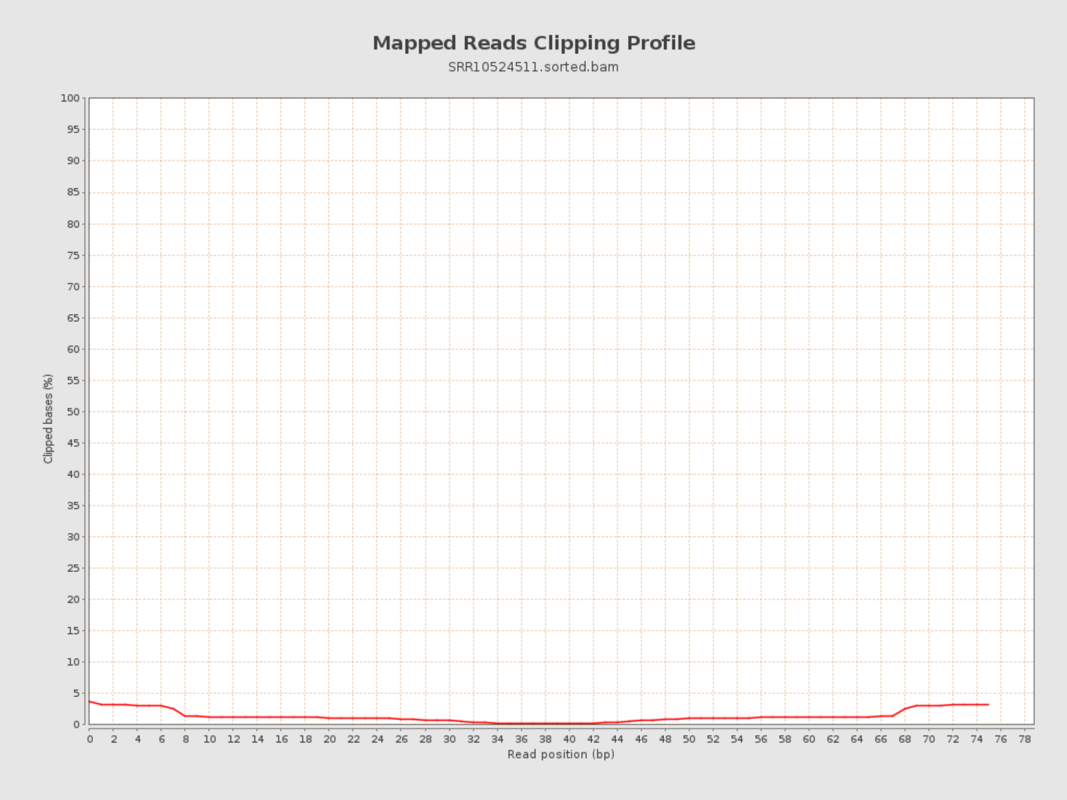
8. Results : Mapped Reads Nucleotide Content



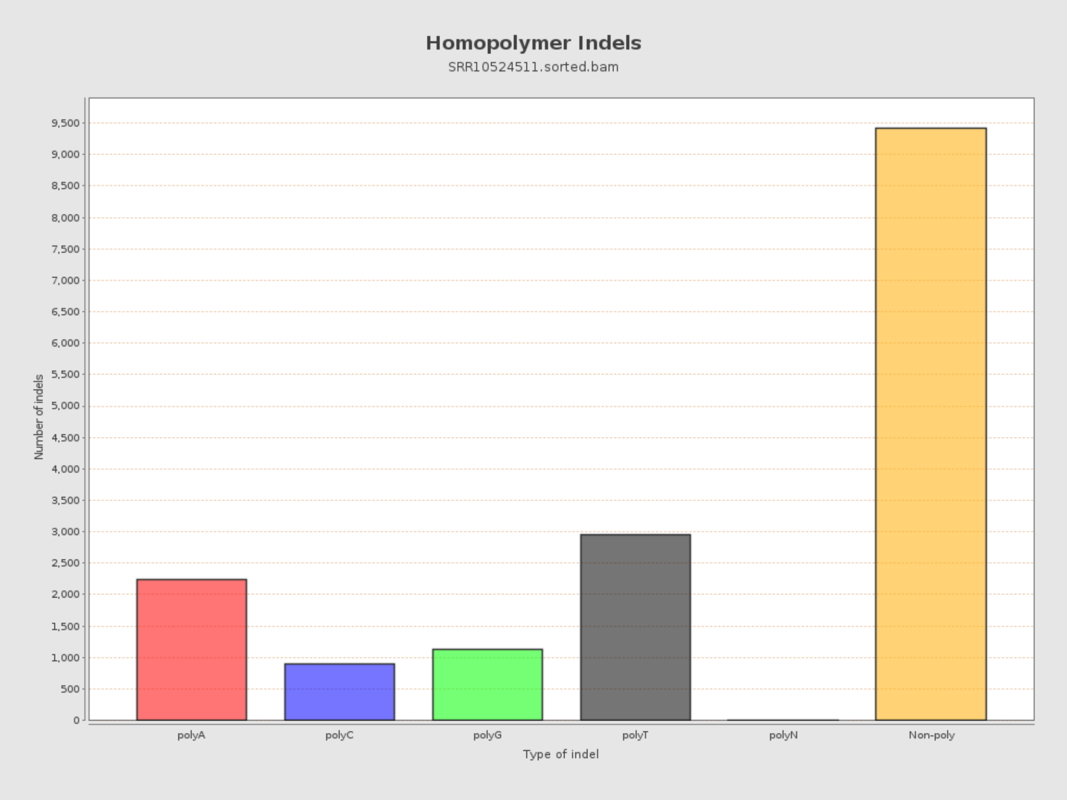
9. Results : Mapped Reads GC-content Distribution



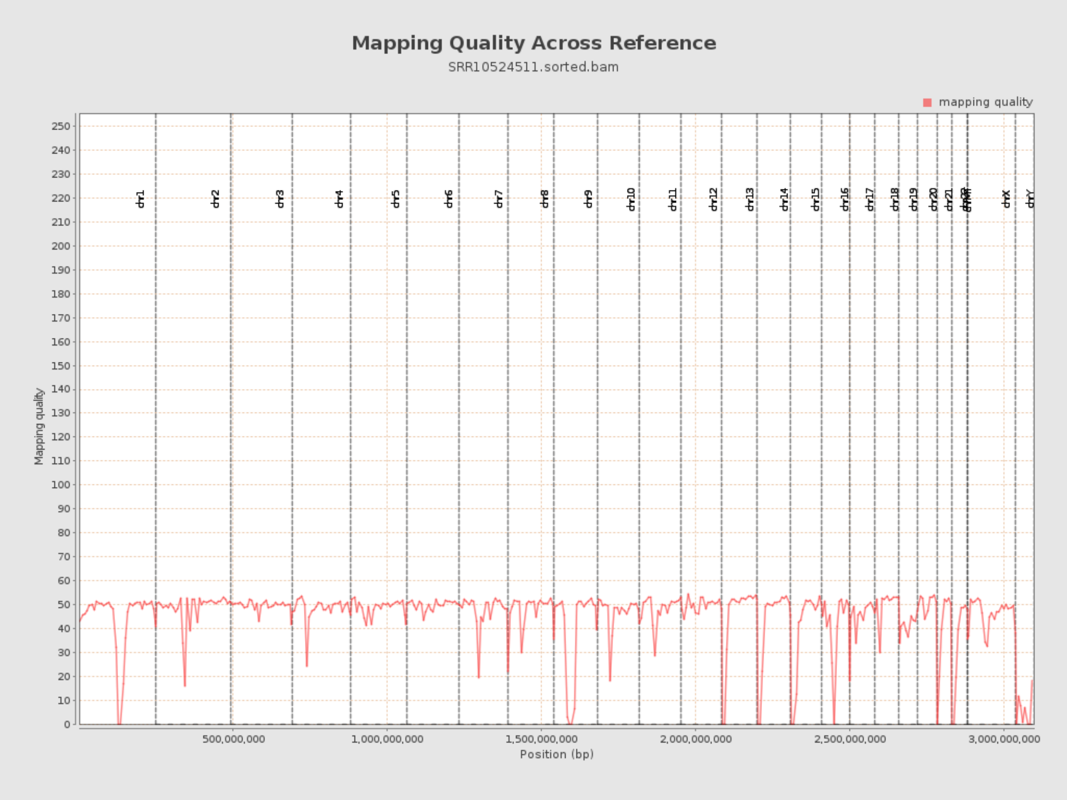
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram