Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:24:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524996.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_SRR10524996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524996.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:24:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,150,052
Mapped reads	3,720,791 / 89.66%
Unmapped reads	429,261 / 10.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,418 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	217,684 / 5.25%
Duplication rate	4.28%
Clipped reads	3,722,222 / 89.69%

2.2. ACGT Content

Number/percentage of A's	54,483,618 / 25.75%
Number/percentage of C's	36,799,752 / 17.39%
Number/percentage of T's	66,992,760 / 31.66%
Number/percentage of G's	53,319,873 / 25.2%
Number/percentage of N's	2,046 / 0%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0684

Standard Deviation	0.5417

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

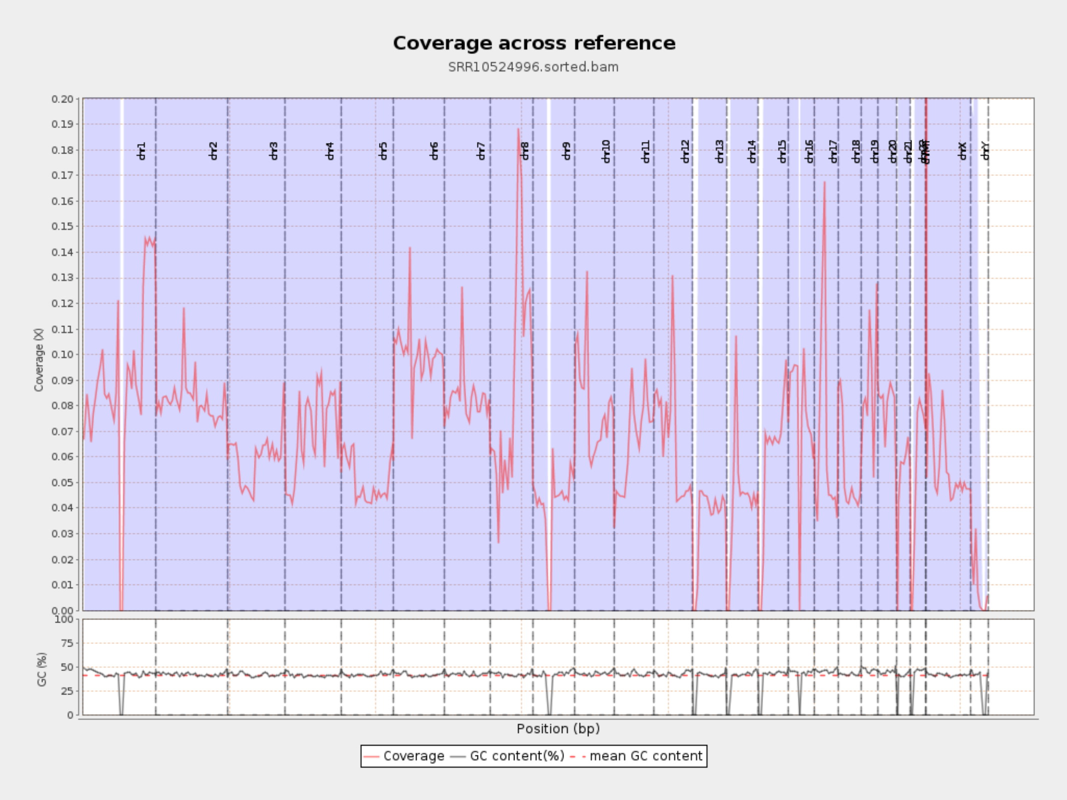
General error rate	0.51%
Mismatches	1,046,998
Insertions	14,814
Mapped reads with at least one insertion	0.4%
Deletions	40,206
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.28%

2.6. Chromosome stats

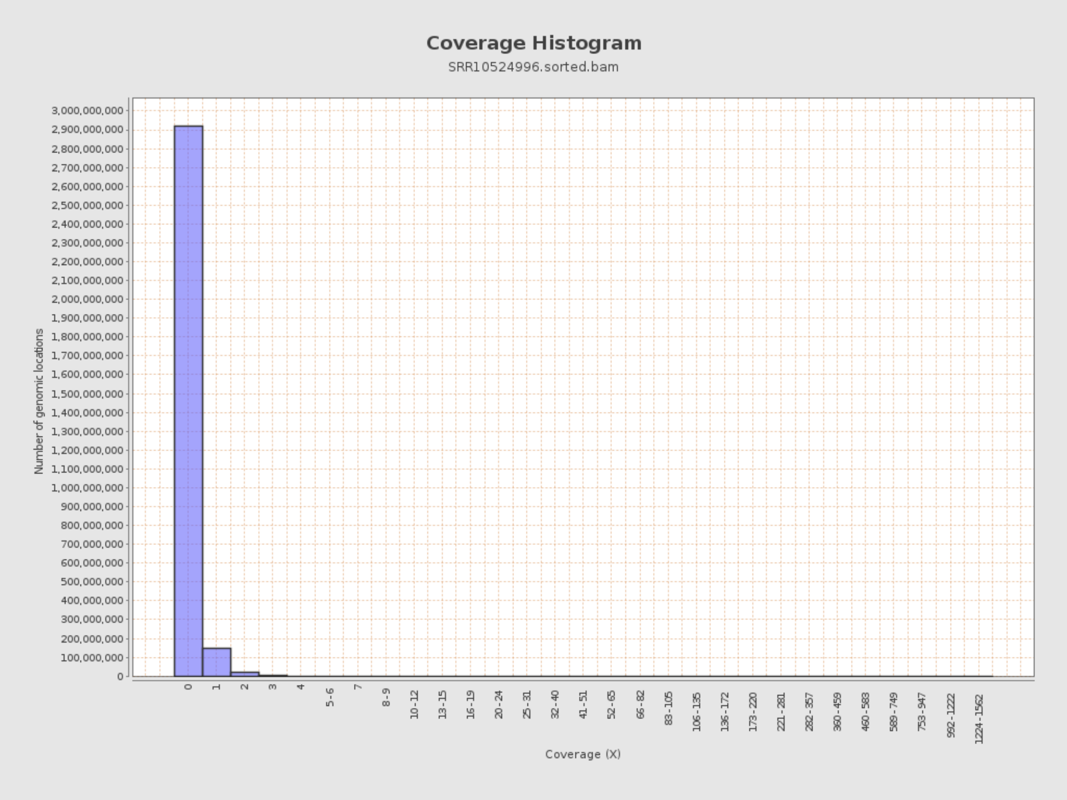
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22584269	0.0906	1.0838
chr2	243199373	19985952	0.0822	0.6614
chr3	198022430	11741210	0.0593	0.2955
chr4	191154276	13430591	0.0703	0.3696
chr5	180915260	9157030	0.0506	0.2762
chr6	171115067	17239752	0.1007	0.6113
chr7	159138663	13347458	0.0839	0.7599

chr8	146364022	13105926	0.0895	0.5083
chr9	141213431	5796968	0.0411	0.4076
chr10	135534747	10840577	0.08	0.518
chr11	135006516	9016546	0.0668	0.4631
chr12	133851895	9086739	0.0679	0.3158
chr13	115169878	4071386	0.0354	0.2289
chr14	107349540	4734562	0.0441	0.2634
chr15	102531392	5972255	0.0582	0.3324
chr16	90354753	6843732	0.0757	0.3564
chr17	81195210	5348981	0.0659	0.4677
chr18	78077248	4234931	0.0542	0.6857
chr19	59128983	5273826	0.0892	0.6399
chr20	63025520	5097337	0.0809	0.342
chr21	48129895	2495928	0.0519	0.3011
chr22	51304566	2779355	0.0542	0.2711
chrMT	16571	51543	3.1104	2.555
chrX	155270560	8876323	0.0572	0.3728
chrY	59373566	551123	0.0093	0.2222

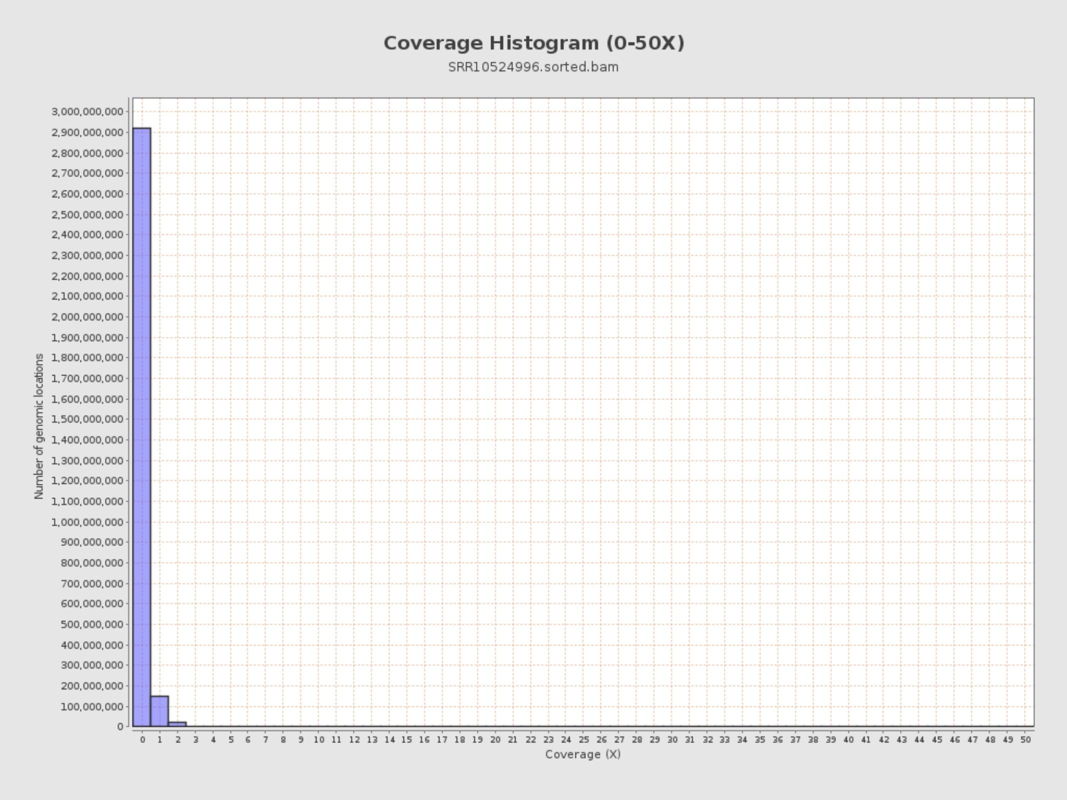
3. Results : Coverage across reference



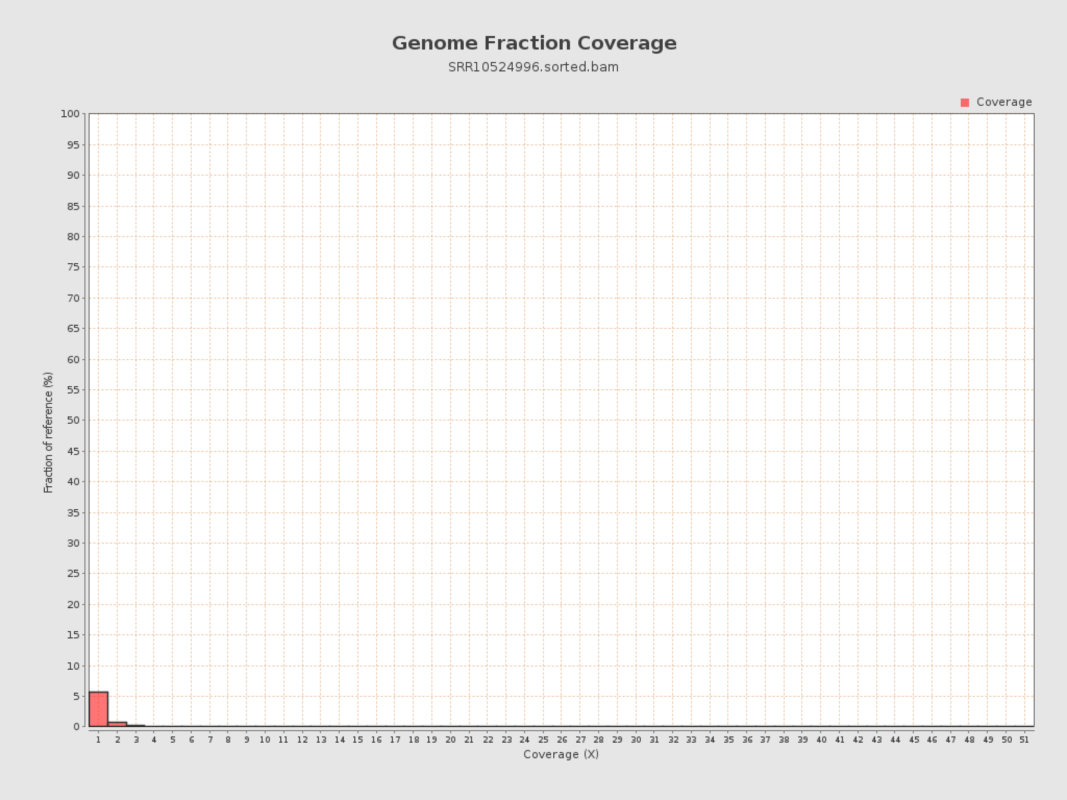
4. Results : Coverage Histogram



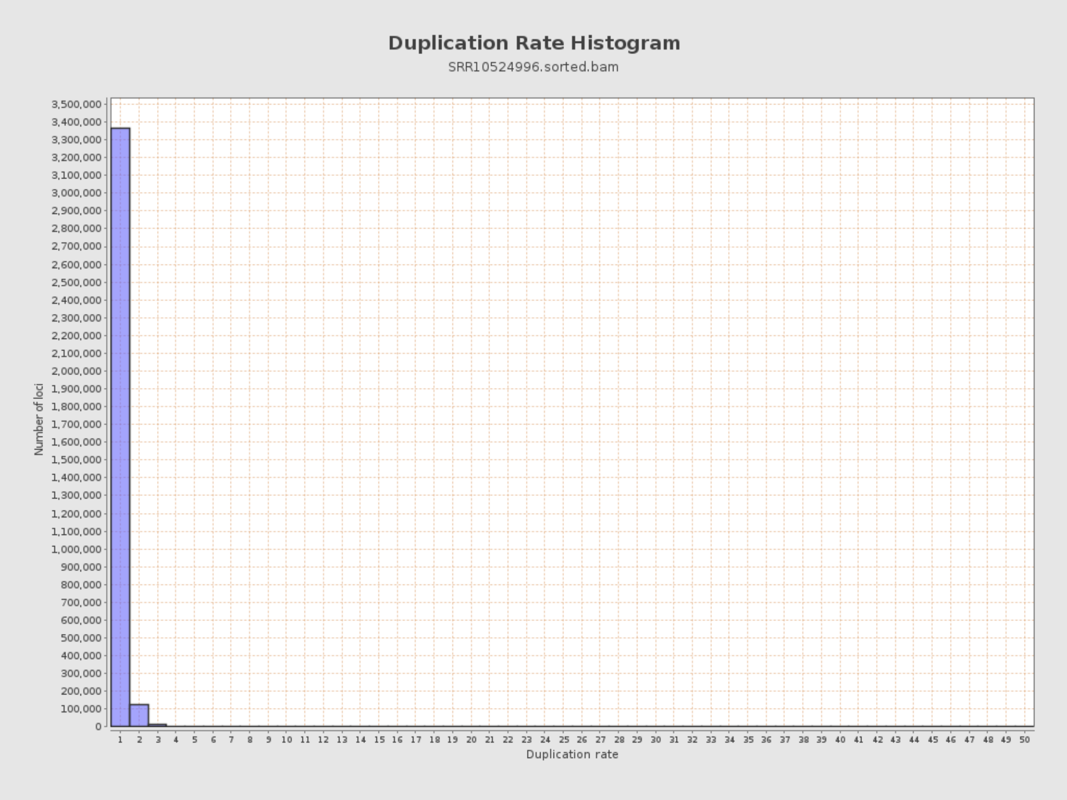
5. Results : Coverage Histogram (0-50X)



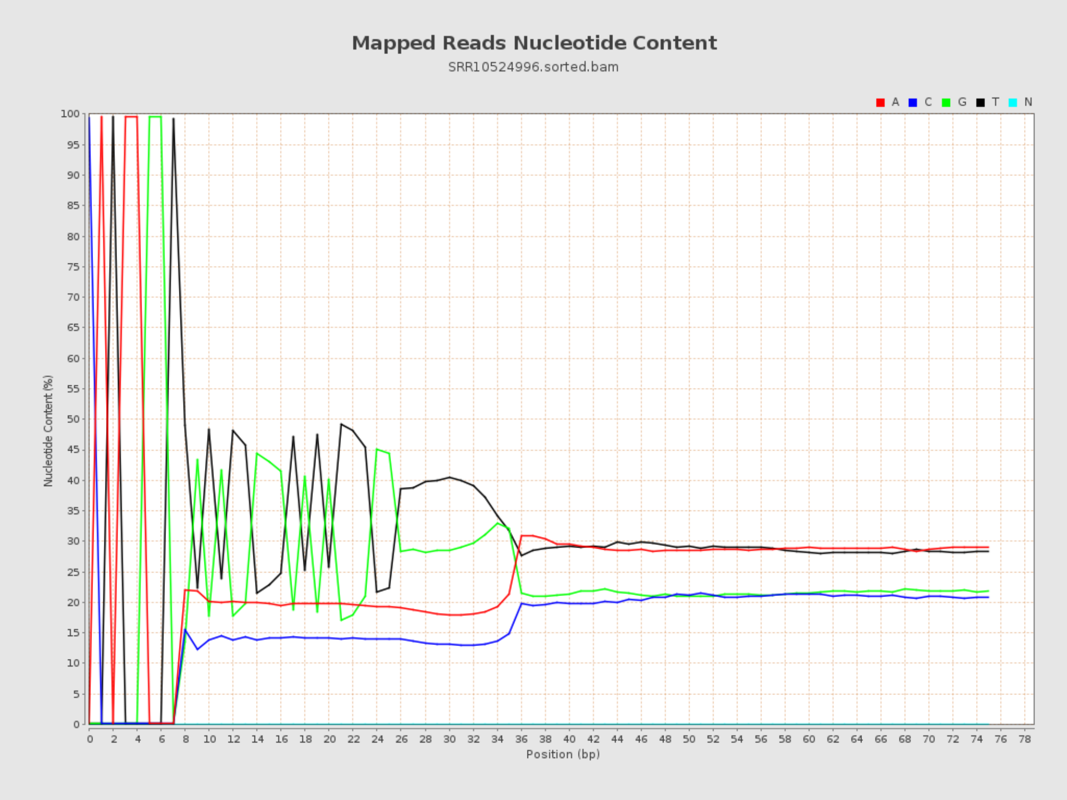
6. Results : Genome Fraction Coverage



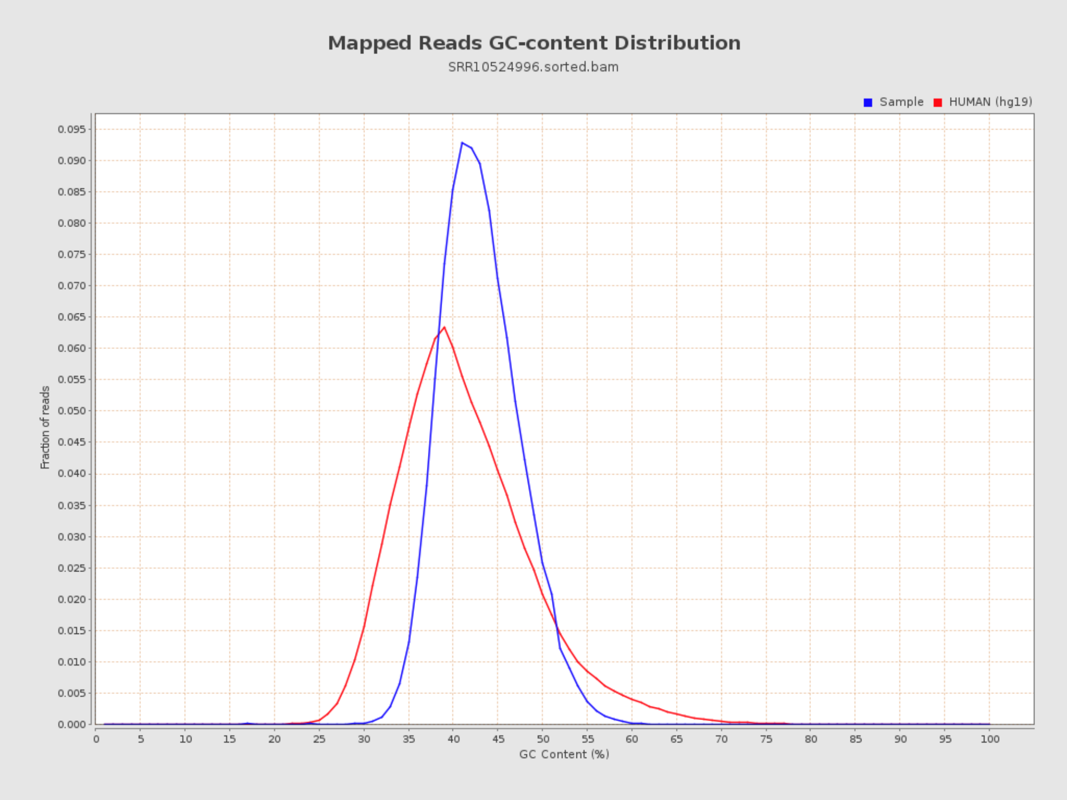
7. Results : Duplication Rate Histogram



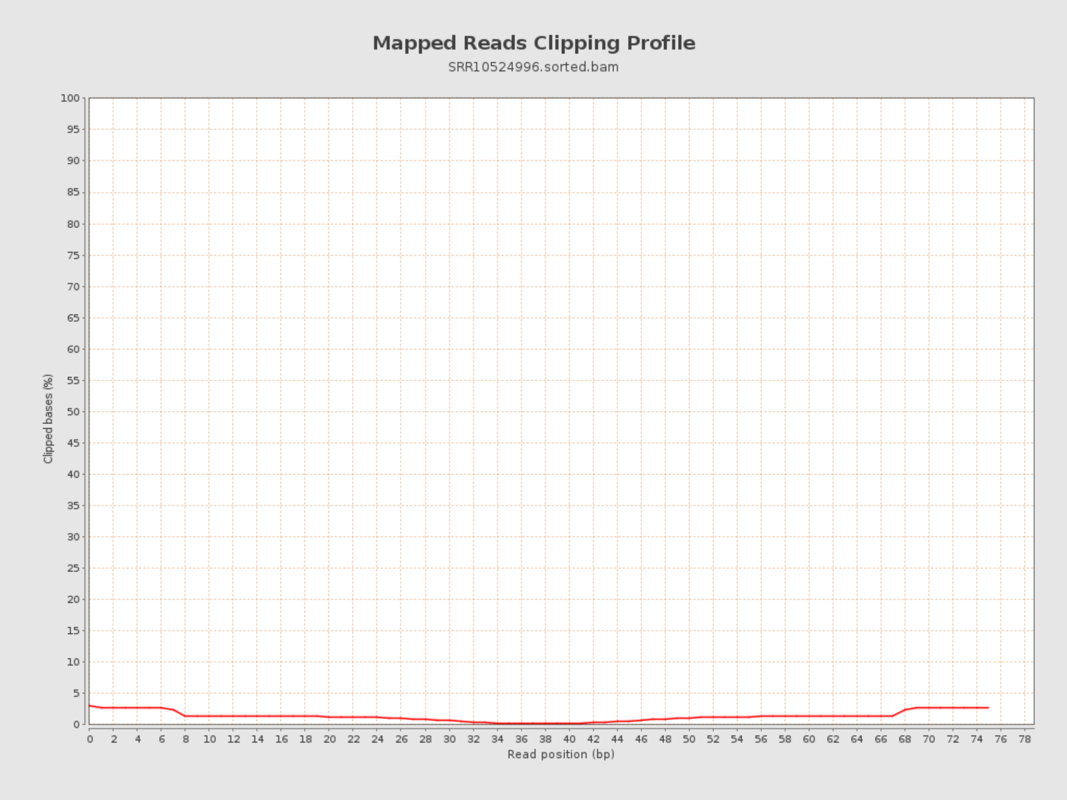
8. Results : Mapped Reads Nucleotide Content



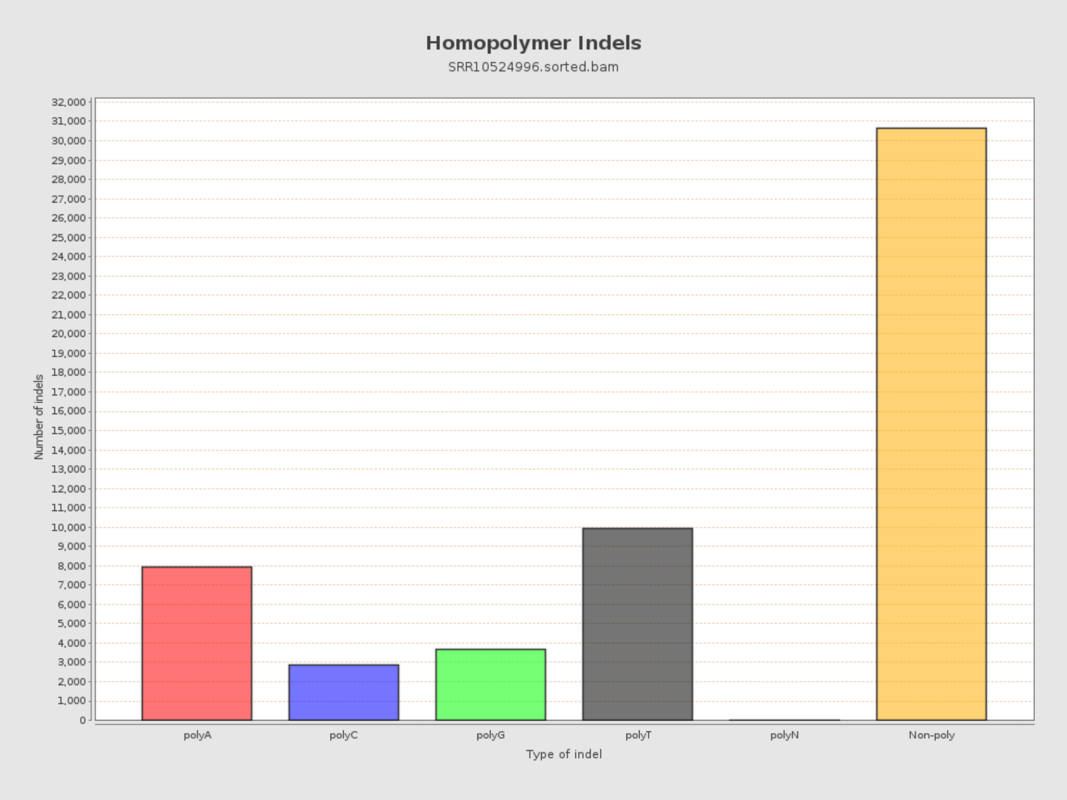
9. Results : Mapped Reads GC-content Distribution



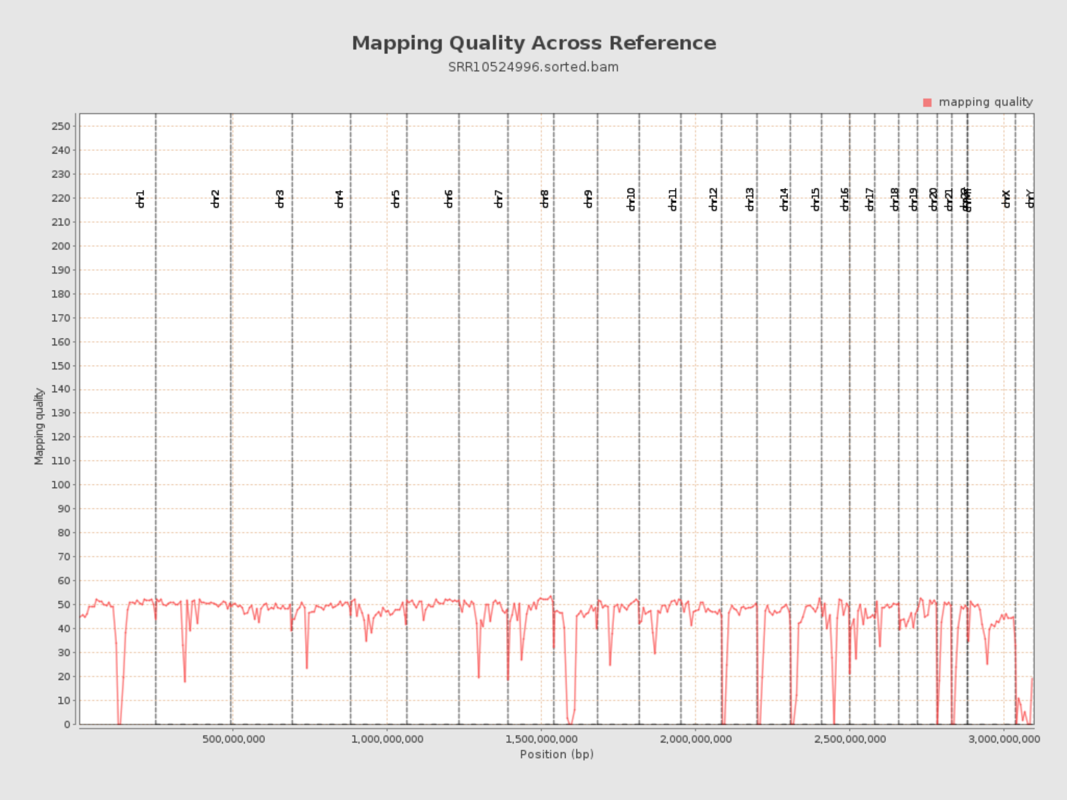
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram