Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:19:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524806.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_SRR10524806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:19:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,489,162
Mapped reads	1,330,997 / 89.38%
Unmapped reads	158,165 / 10.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,675 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	49,296 / 3.31%
Duplication rate	2.83%
Clipped reads	1,331,351 / 89.4%

2.2. ACGT Content

Number/percentage of A's	19,161,874 / 25.53%
Number/percentage of C's	12,935,004 / 17.23%
Number/percentage of T's	23,976,022 / 31.95%
Number/percentage of G's	18,969,968 / 25.28%
Number/percentage of N's	8,800 / 0.01%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2243

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Mismatches and indels

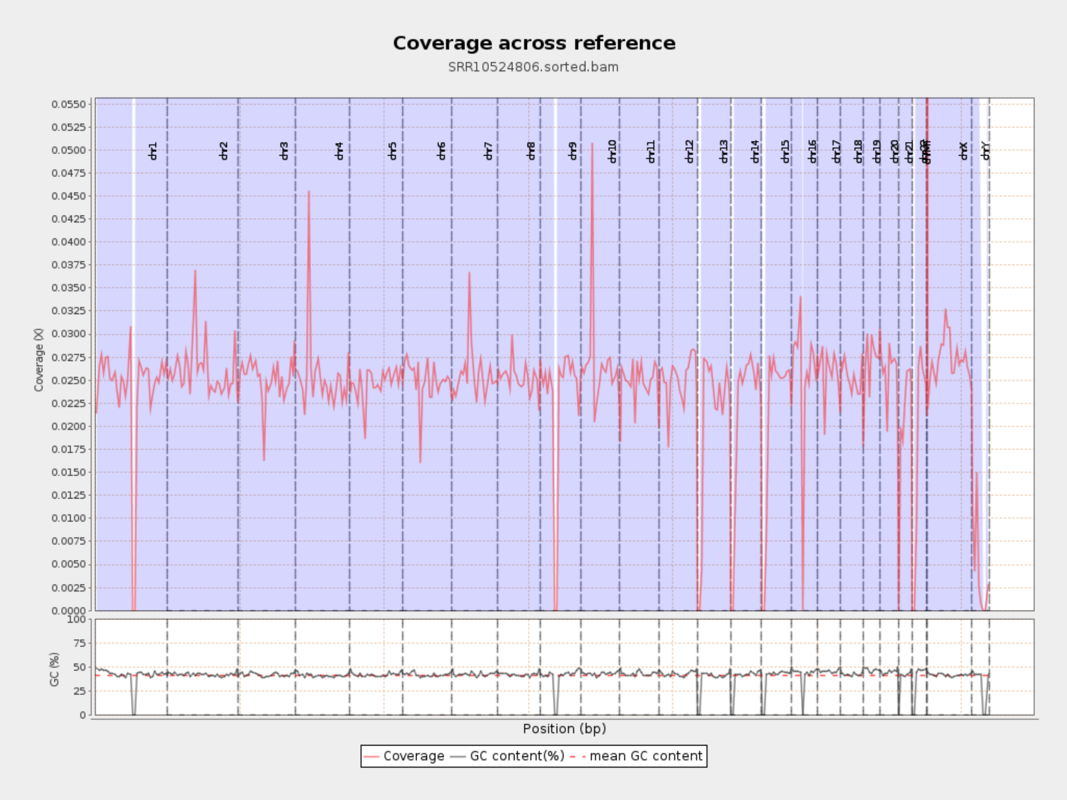
General error rate	0.53%
Mismatches	388,867
Insertions	5,829
Mapped reads with at least one insertion	0.44%
Deletions	14,486
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.98%

2.6. Chromosome stats

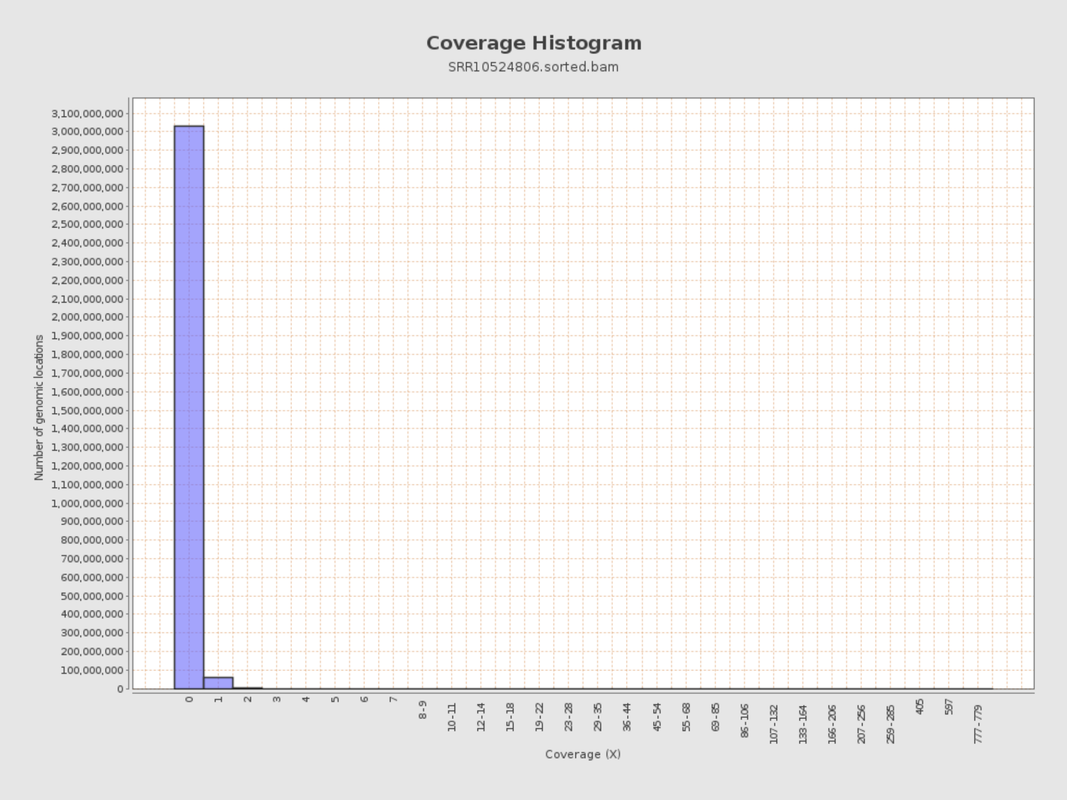
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5932327	0.0238	0.2781
chr2	243199373	6349744	0.0261	0.3739
chr3	198022430	4968352	0.0251	0.1748
chr4	191154276	4866369	0.0255	0.1971
chr5	180915260	4482641	0.0248	0.1717
chr6	171115067	4264349	0.0249	0.1891
chr7	159138663	4082275	0.0257	0.2598

chr8	146364022	3698952	0.0253	0.2112
chr9	141213431	3198816	0.0227	0.1959
chr10	135534747	3654292	0.027	0.2615
chr11	135006516	3386238	0.0251	0.2082
chr12	133851895	3370688	0.0252	0.1746
chr13	115169878	2368512	0.0206	0.1564
chr14	107349540	2295560	0.0214	0.1626
chr15	102531392	2150953	0.021	0.1599
chr16	90354753	2263432	0.0251	0.1894
chr17	81195210	2094995	0.0258	0.1827
chr18	78077248	1970903	0.0252	0.2877
chr19	59128983	1610400	0.0272	0.243
chr20	63025520	1628740	0.0258	0.1842
chr21	48129895	996385	0.0207	0.1727
chr22	51304566	928035	0.0181	0.1469
chrMT	16571	27871	1.6819	1.5524
chrX	155270560	4229718	0.0272	0.1914
chrY	59373566	254617	0.0043	0.1246

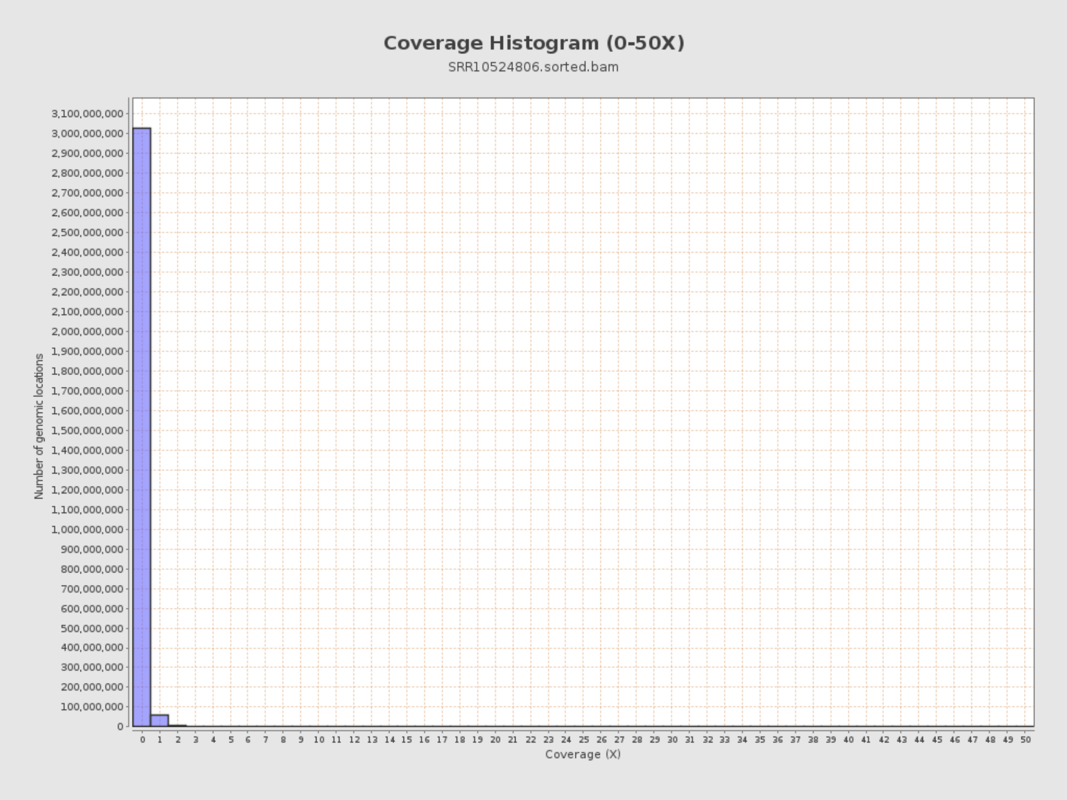
3. Results : Coverage across reference



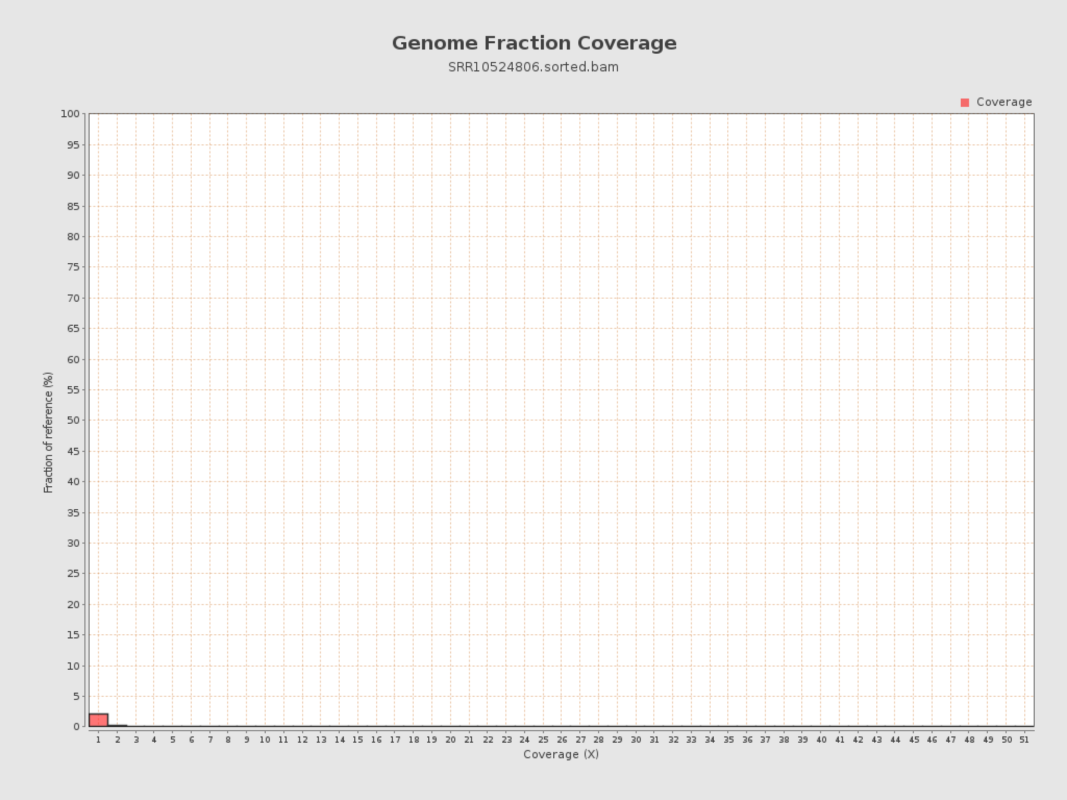
4. Results : Coverage Histogram



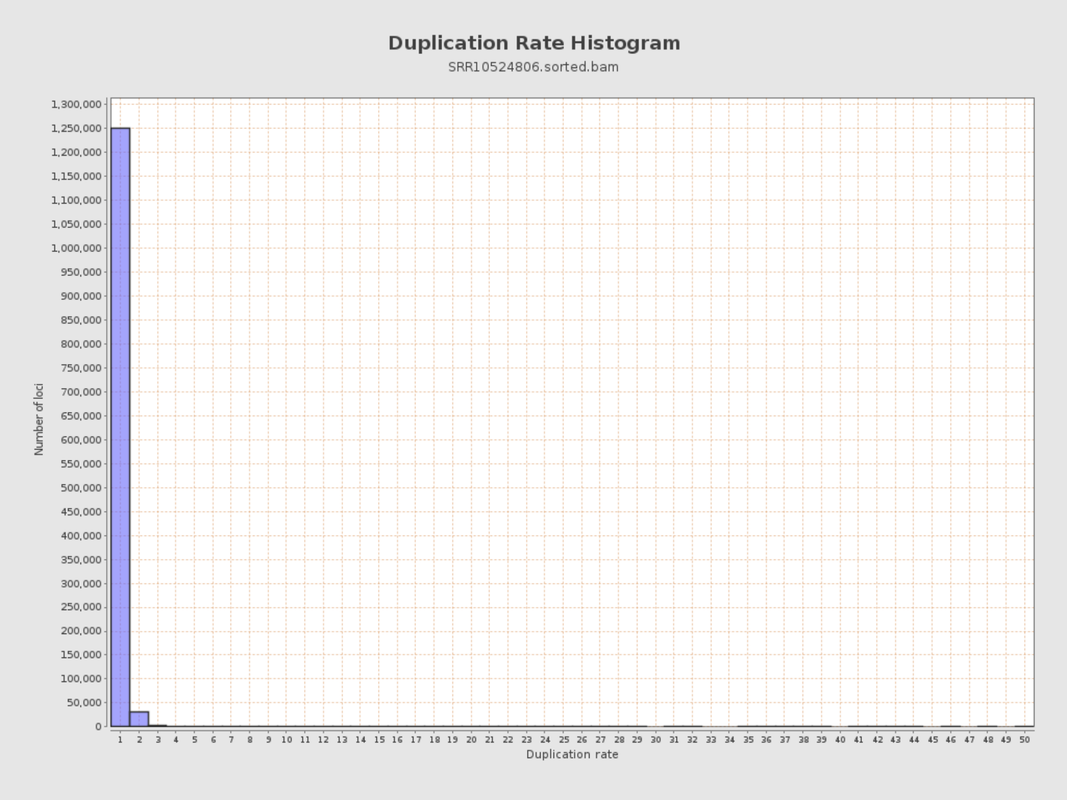
5. Results : Coverage Histogram (0-50X)



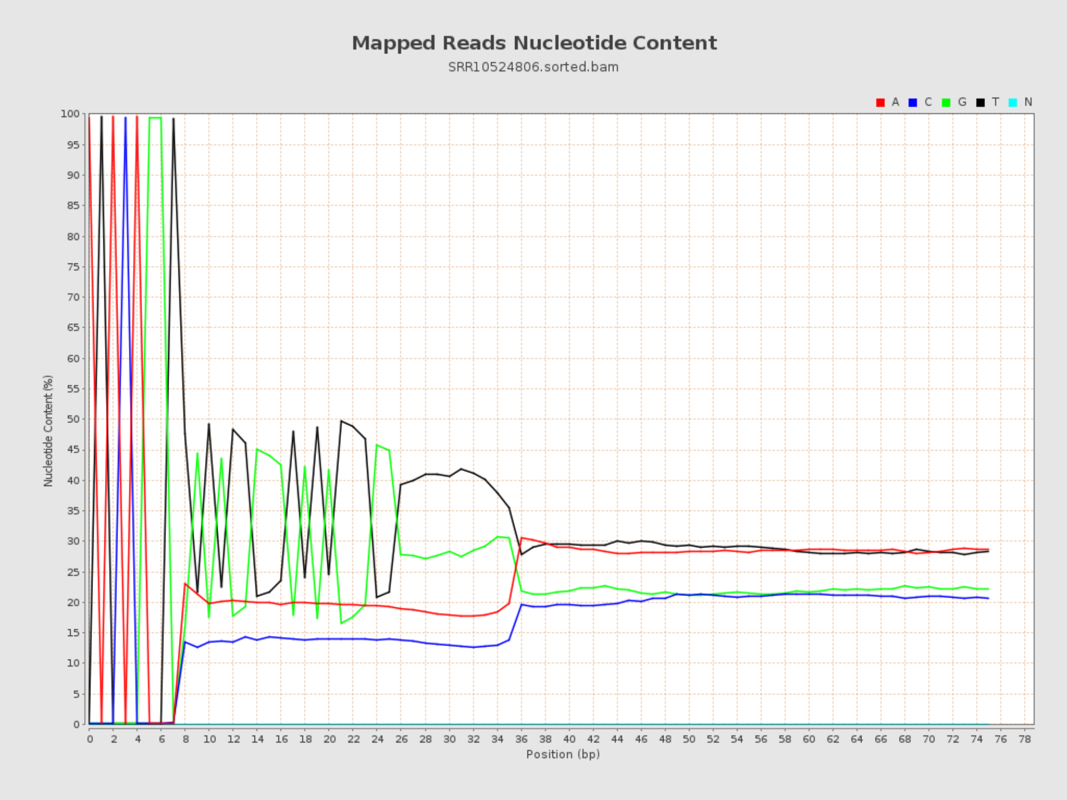
6. Results : Genome Fraction Coverage



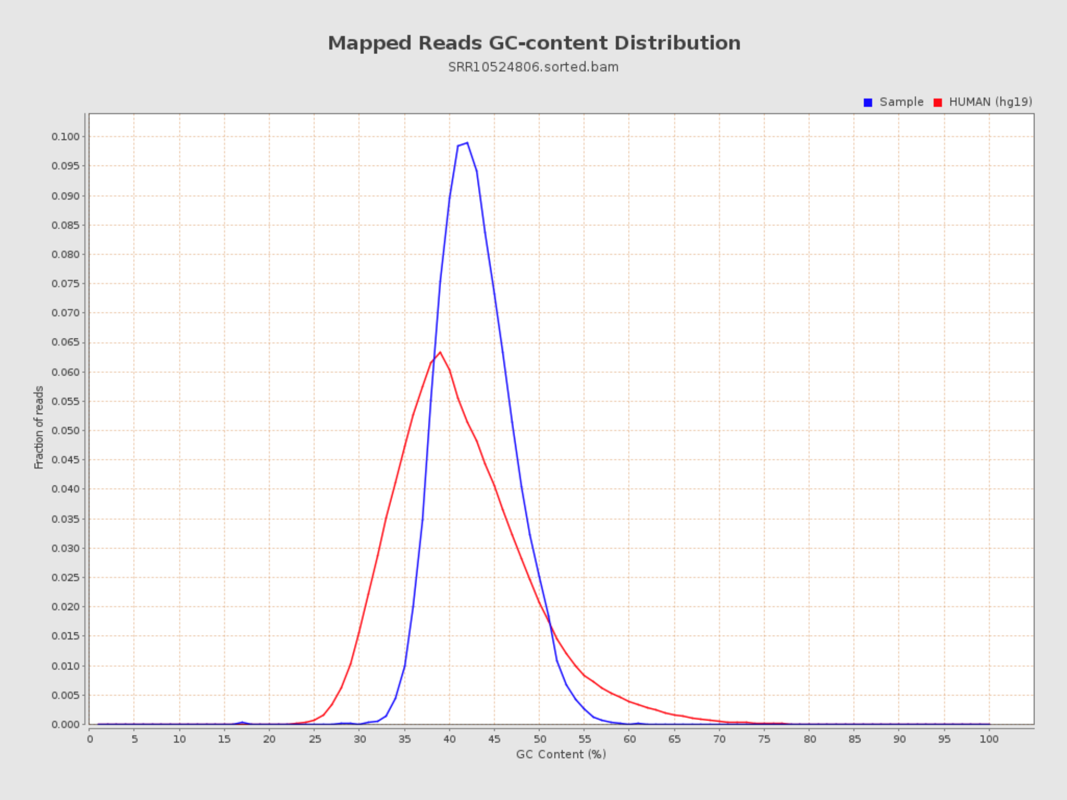
7. Results : Duplication Rate Histogram



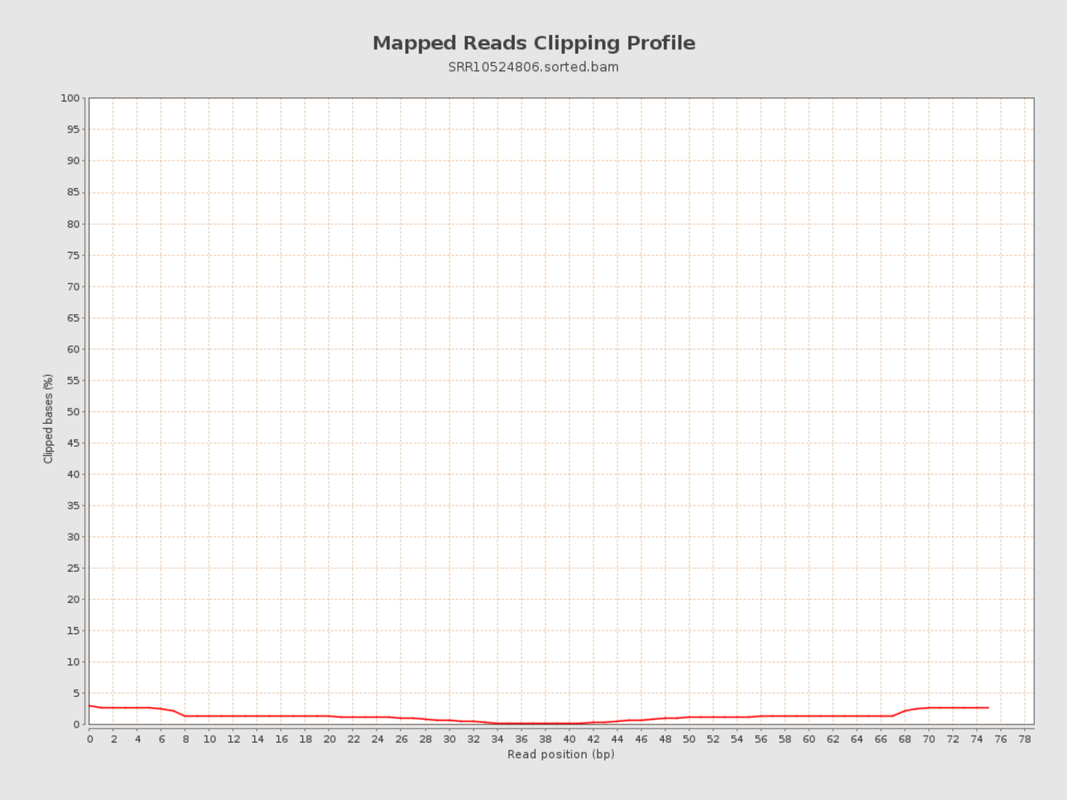
8. Results : Mapped Reads Nucleotide Content



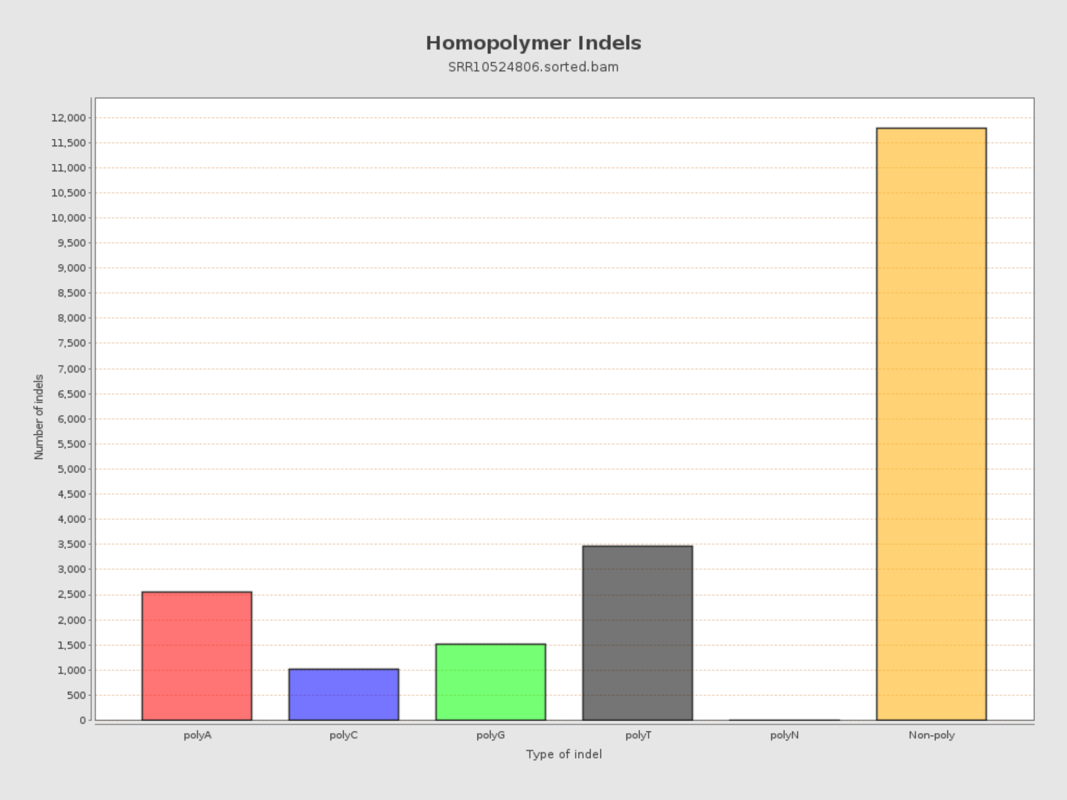
9. Results : Mapped Reads GC-content Distribution



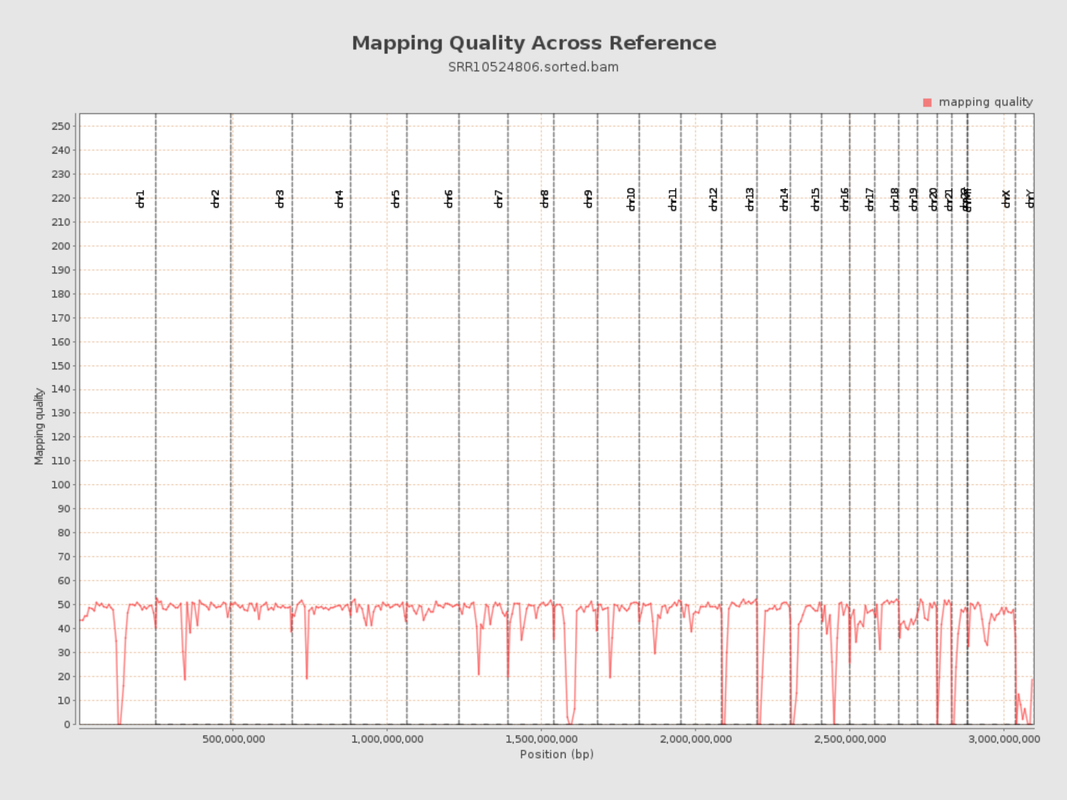
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram