Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:50:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524843.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_SRR10524843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524843.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:50:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,167,431
Mapped reads	1,985,848 / 91.62%
Unmapped reads	181,583 / 8.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,947 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	80,111 / 3.7%
Duplication rate	2.78%
Clipped reads	1,989,994 / 91.81%

2.2. ACGT Content

Number/percentage of A's	29,650,333 / 25.92%
Number/percentage of C's	21,603,978 / 18.89%
Number/percentage of T's	36,468,432 / 31.88%
Number/percentage of G's	26,643,525 / 23.29%
Number/percentage of N's	15,178 / 0.01%
GC Percentage	42.18%

2.3. Coverage

Mean	0.037

Standard Deviation	0.3611

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Mismatches and indels

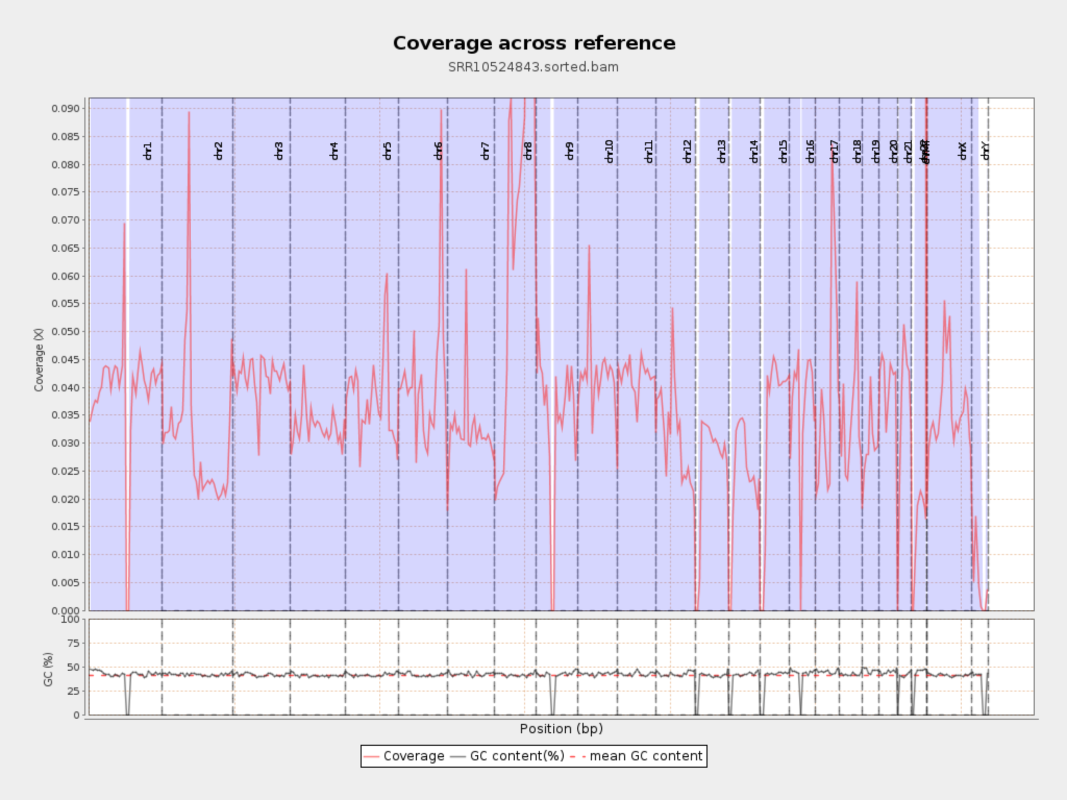
General error rate	0.5%
Mismatches	559,766
Insertions	7,365
Mapped reads with at least one insertion	0.37%
Deletions	21,175
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.88%

2.6. Chromosome stats

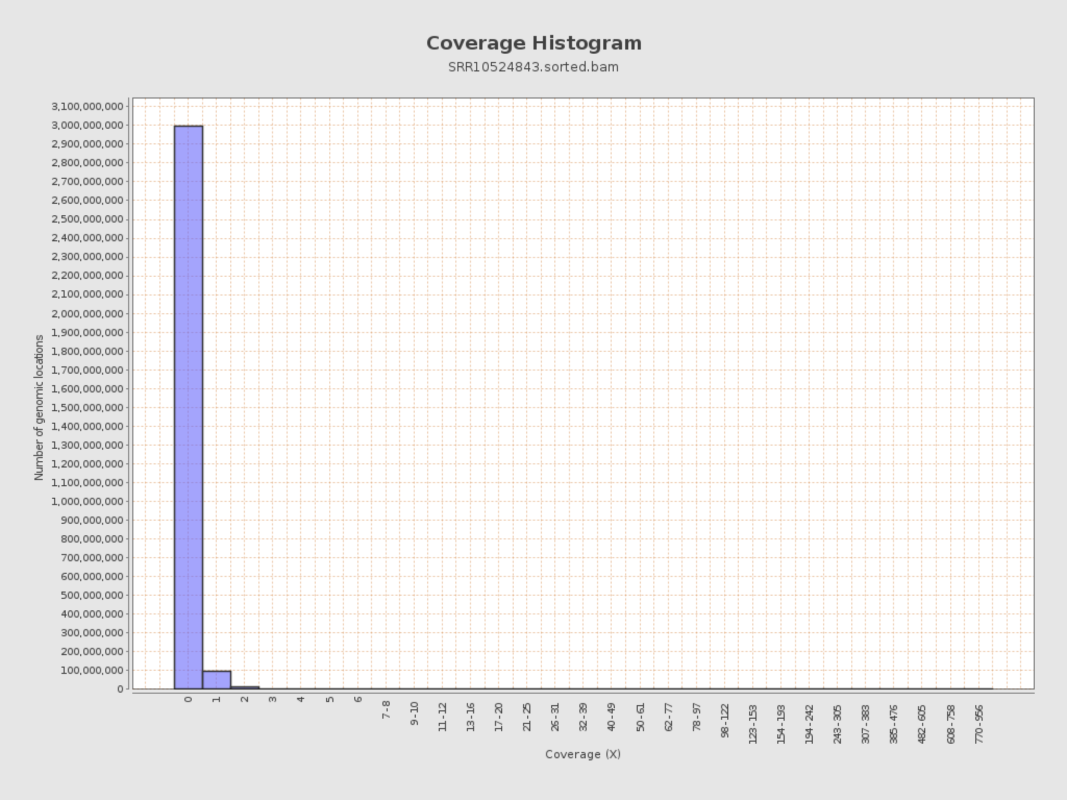
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9789785	0.0393	0.7042
chr2	243199373	7527862	0.031	0.3925
chr3	198022430	8277194	0.0418	0.2252
chr4	191154276	6296657	0.0329	0.2252
chr5	180915260	6962318	0.0385	0.2193
chr6	171115067	6987421	0.0408	0.2605
chr7	159138663	5220734	0.0328	0.4745

chr8	146364022	11661684	0.0797	0.4592
chr9	141213431	4851862	0.0344	0.2983
chr10	135534747	5749519	0.0424	0.3245
chr11	135006516	5637995	0.0418	0.3143
chr12	133851895	4224000	0.0316	0.2039
chr13	115169878	2938663	0.0255	0.177
chr14	107349540	2508386	0.0234	0.1841
chr15	102531392	3447612	0.0336	0.2092
chr16	90354753	3310370	0.0366	0.2322
chr17	81195210	3182431	0.0392	0.2542
chr18	78077248	2744027	0.0351	0.5351
chr19	59128983	1775698	0.03	0.4889
chr20	63025520	2559778	0.0406	0.2254
chr21	48129895	1728458	0.0359	0.2256
chr22	51304566	721370	0.0141	0.1292
chrMT	16571	424529	25.6188	13.9474
chrX	155270560	5588626	0.036	0.2524
chrY	59373566	297495	0.005	0.1254

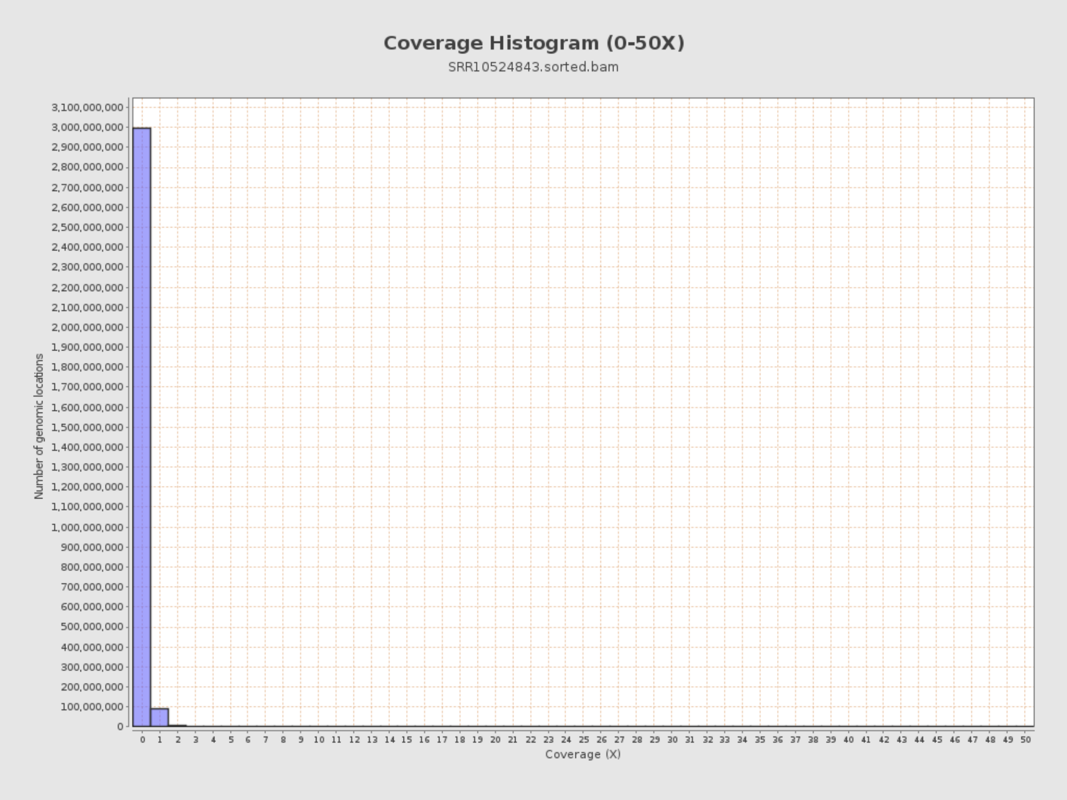
3. Results : Coverage across reference



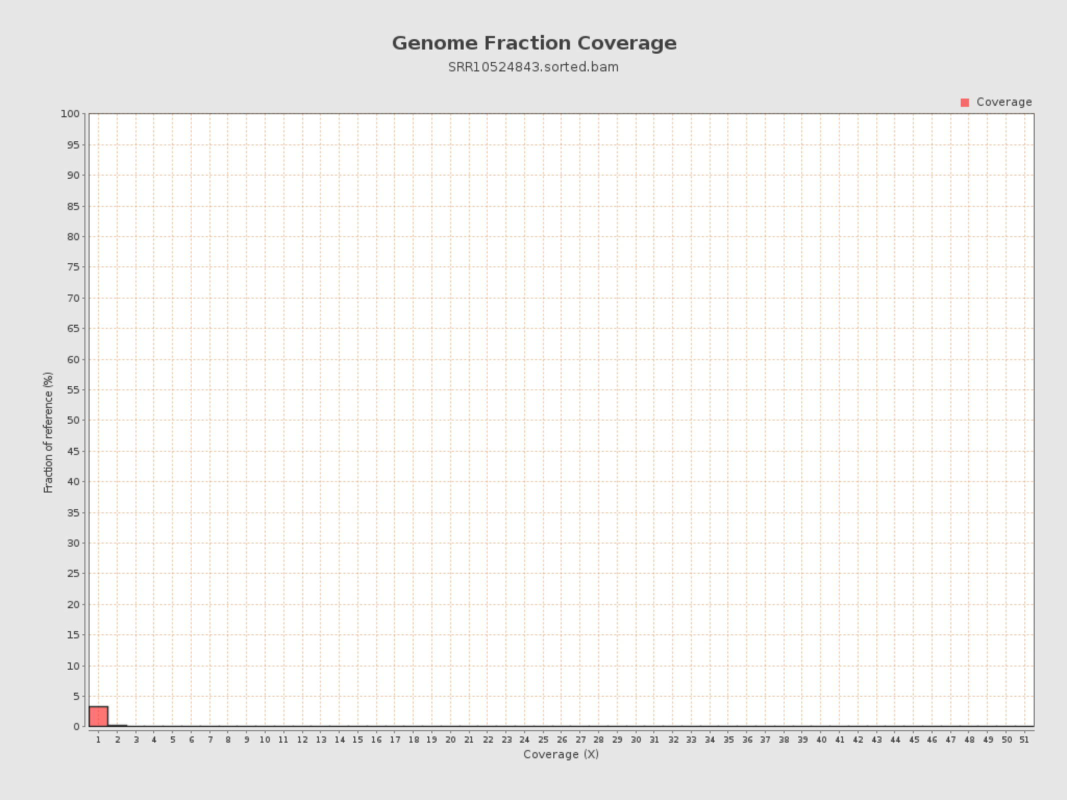
4. Results : Coverage Histogram



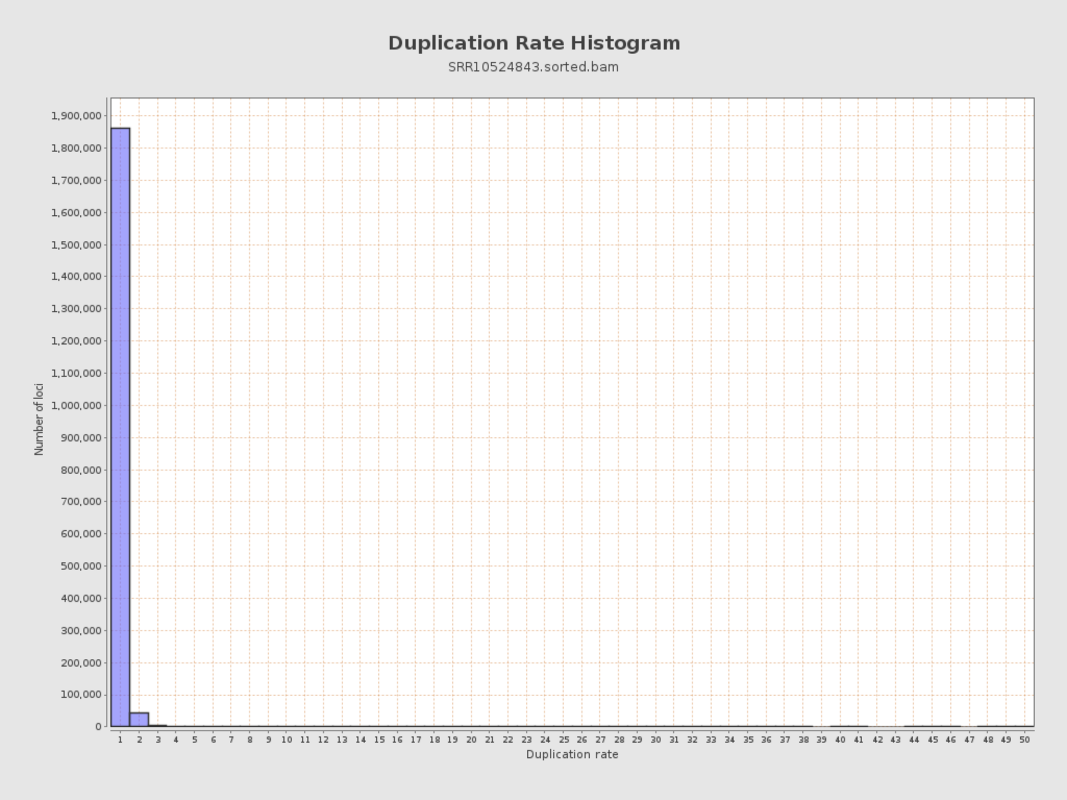
5. Results : Coverage Histogram (0-50X)



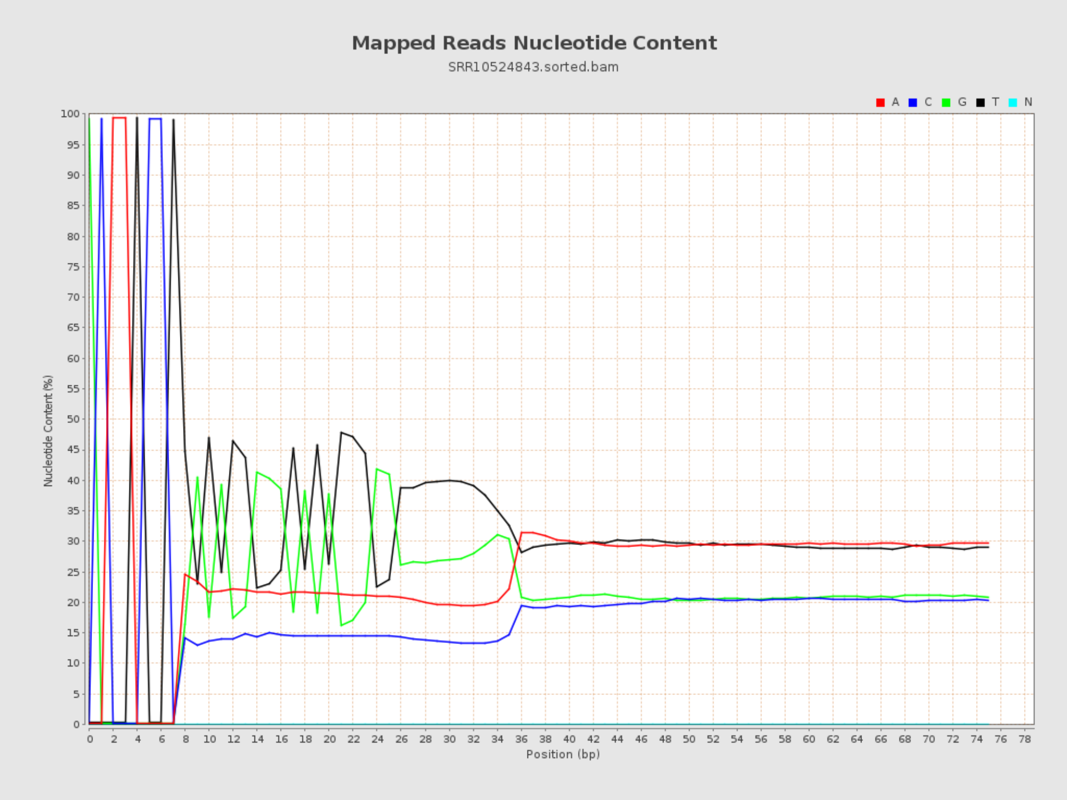
6. Results : Genome Fraction Coverage



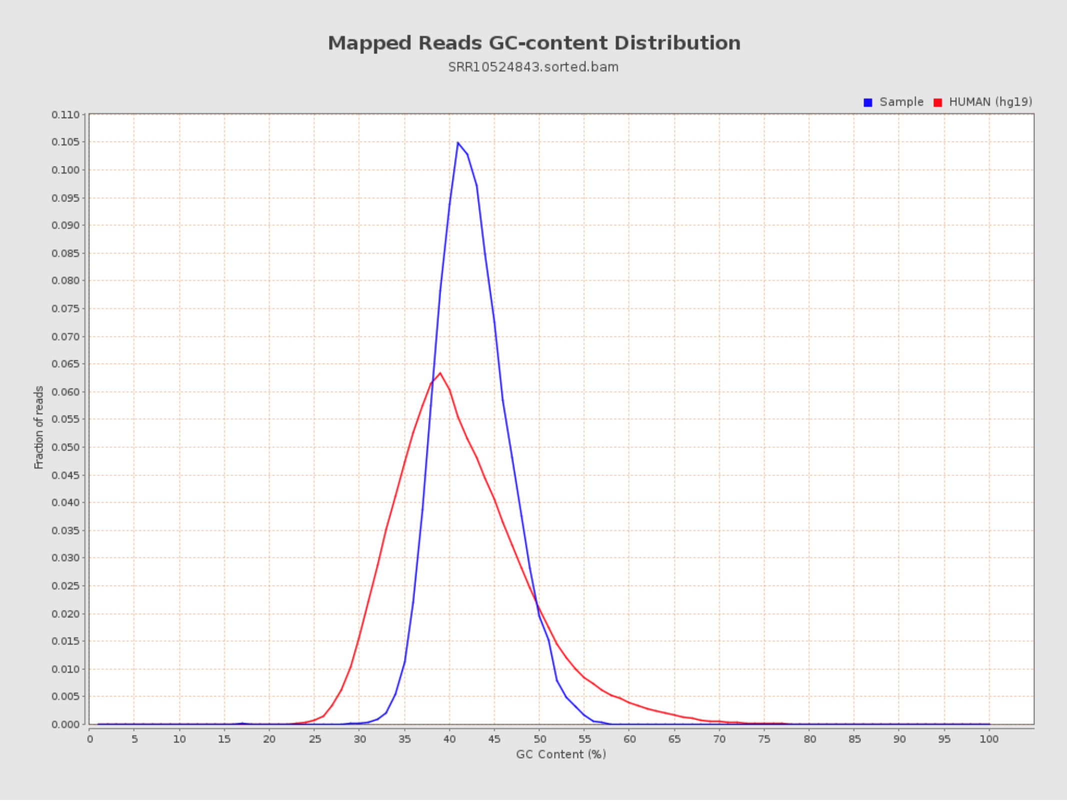
7. Results : Duplication Rate Histogram



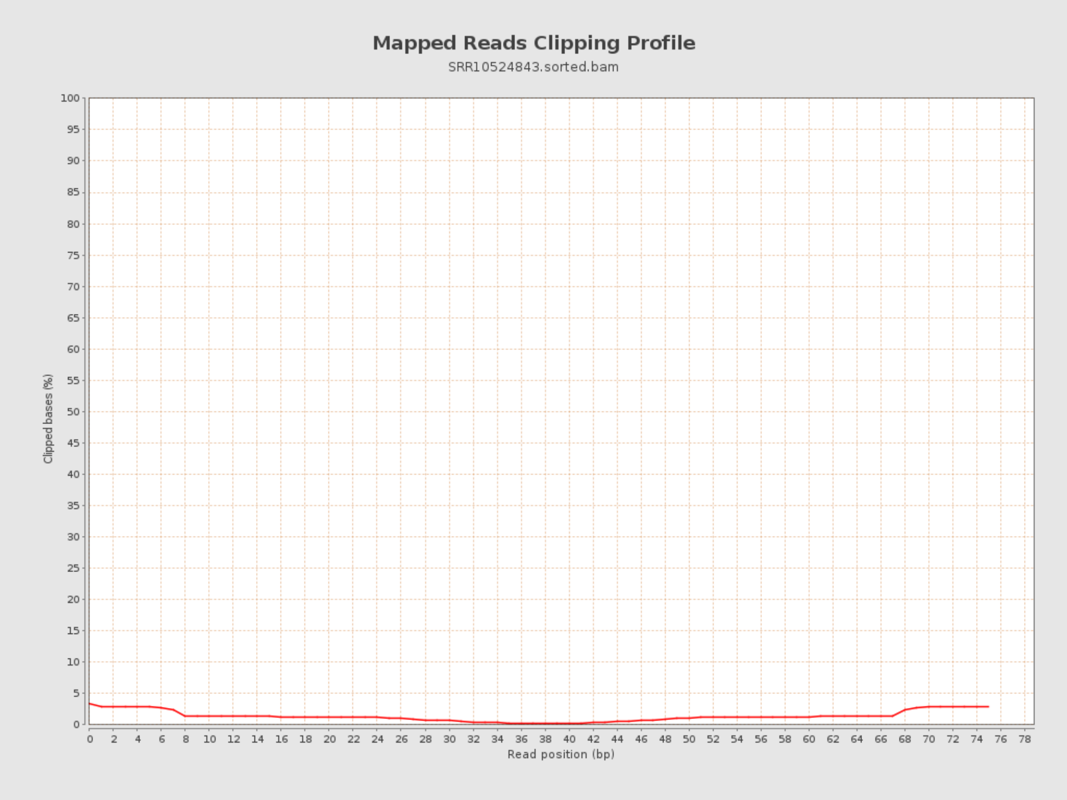
8. Results : Mapped Reads Nucleotide Content



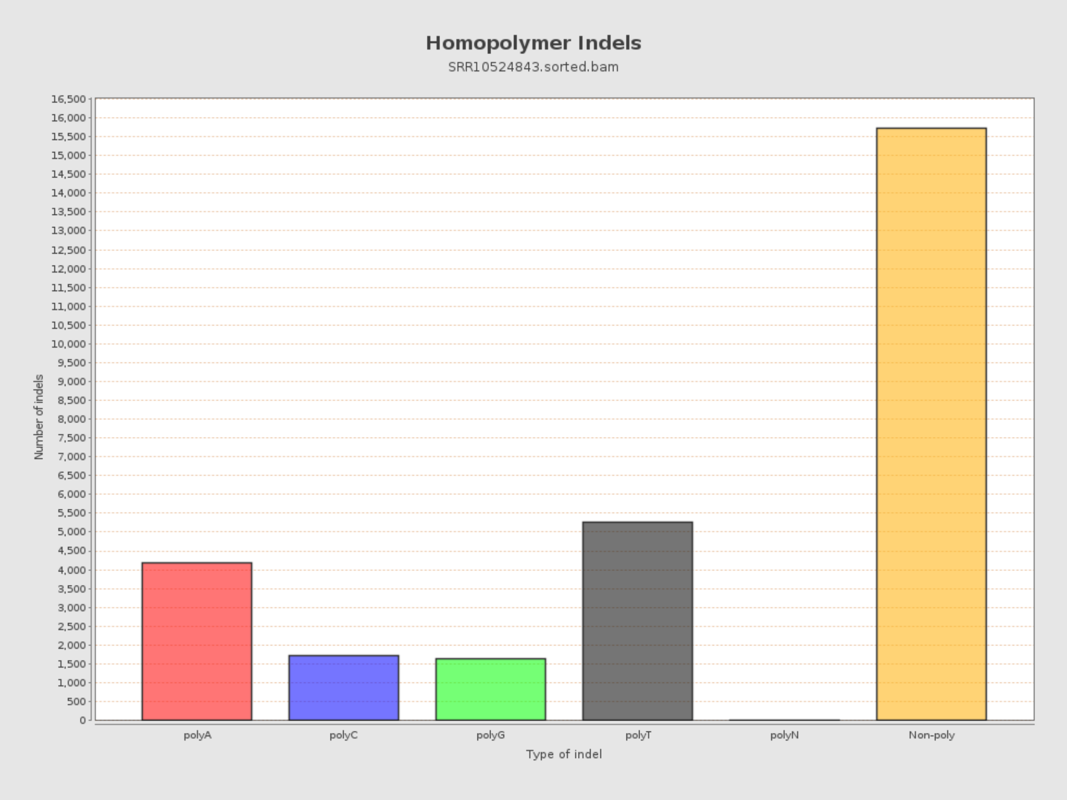
9. Results : Mapped Reads GC-content Distribution



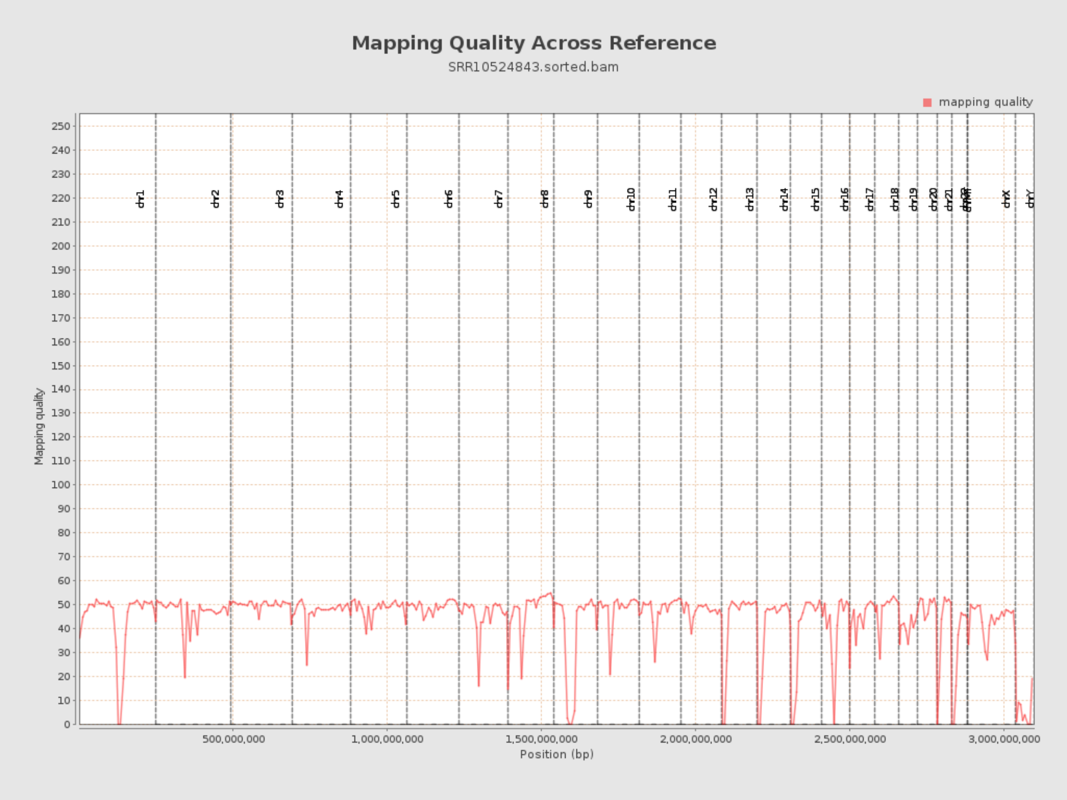
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram