Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:10:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524435.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_SRR10524435 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524435.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:10:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524435.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,359,641
Mapped reads	1,259,640 / 92.65%
Unmapped reads	100,001 / 7.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,540 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	52,555 / 3.87%
Duplication rate	3.09%
Clipped reads	1,261,480 / 92.78%

2.2. ACGT Content

Number/percentage of A's	17,337,769 / 23.47%
Number/percentage of C's	13,640,681 / 18.47%
Number/percentage of T's	23,976,008 / 32.46%
Number/percentage of G's	18,899,613 / 25.59%
Number/percentage of N's	7,764 / 0.01%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.2484

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

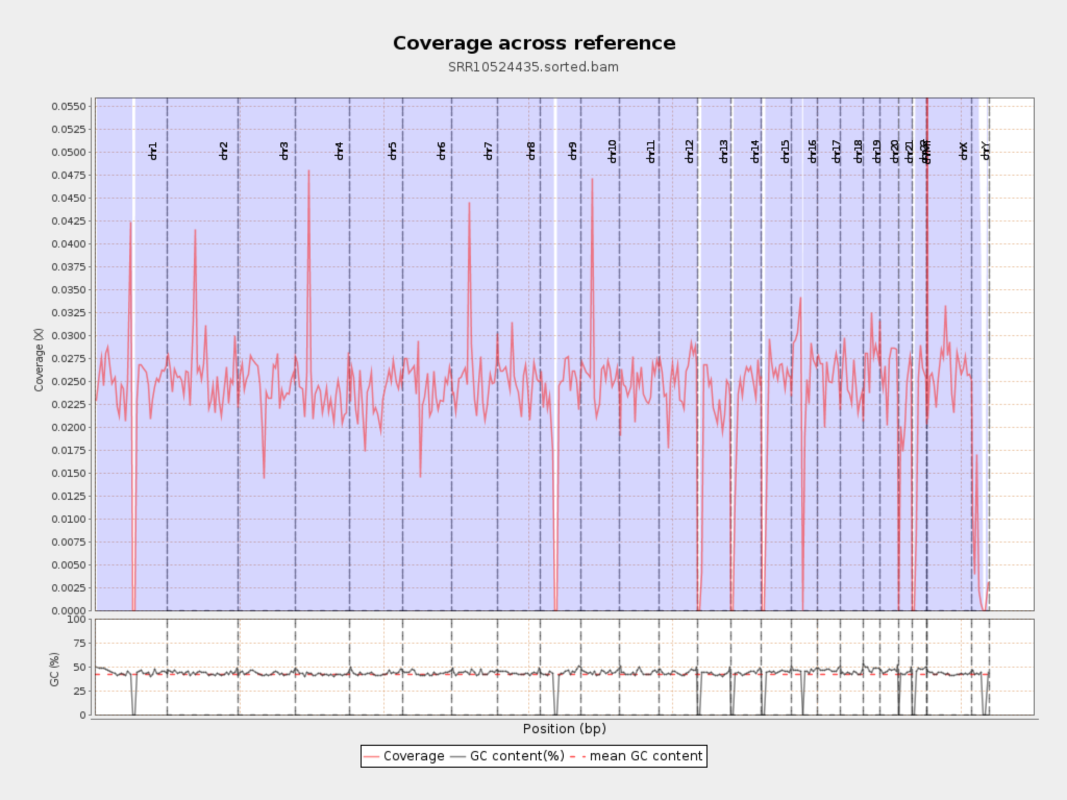
General error rate	0.52%
Mismatches	370,799
Insertions	5,231
Mapped reads with at least one insertion	0.41%
Deletions	12,869
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.19%

2.6. Chromosome stats

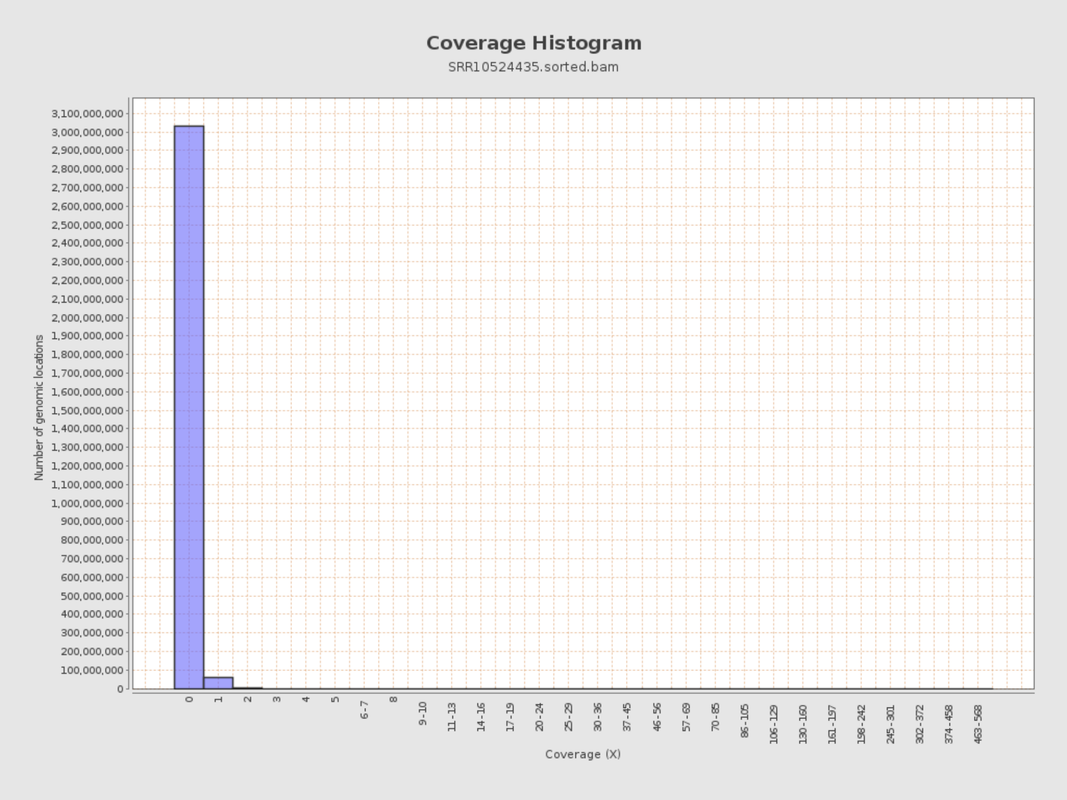
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5972599	0.024	0.4509
chr2	243199373	6281228	0.0258	0.3187
chr3	198022430	4863562	0.0246	0.1717
chr4	191154276	4692674	0.0245	0.2064
chr5	180915260	4290281	0.0237	0.1674
chr6	171115067	4162838	0.0243	0.1844
chr7	159138663	4059826	0.0255	0.3322

chr8	146364022	3703939	0.0253	0.2058
chr9	141213431	3056819	0.0216	0.1976
chr10	135534747	3593315	0.0265	0.2545
chr11	135006516	3325166	0.0246	0.2234
chr12	133851895	3371351	0.0252	0.1766
chr13	115169878	2251348	0.0195	0.1525
chr14	107349540	2260309	0.0211	0.1657
chr15	102531392	2204910	0.0215	0.1599
chr16	90354753	2237944	0.0248	0.1844
chr17	81195210	2093470	0.0258	0.1885
chr18	78077248	1924417	0.0246	0.3481
chr19	59128983	1642953	0.0278	0.3269
chr20	63025520	1649176	0.0262	0.1838
chr21	48129895	981193	0.0204	0.1791
chr22	51304566	932019	0.0182	0.1494
chrMT	16571	2706	0.1633	0.4496
chrX	155270560	4064296	0.0262	0.1927
chrY	59373566	264069	0.0044	0.1462

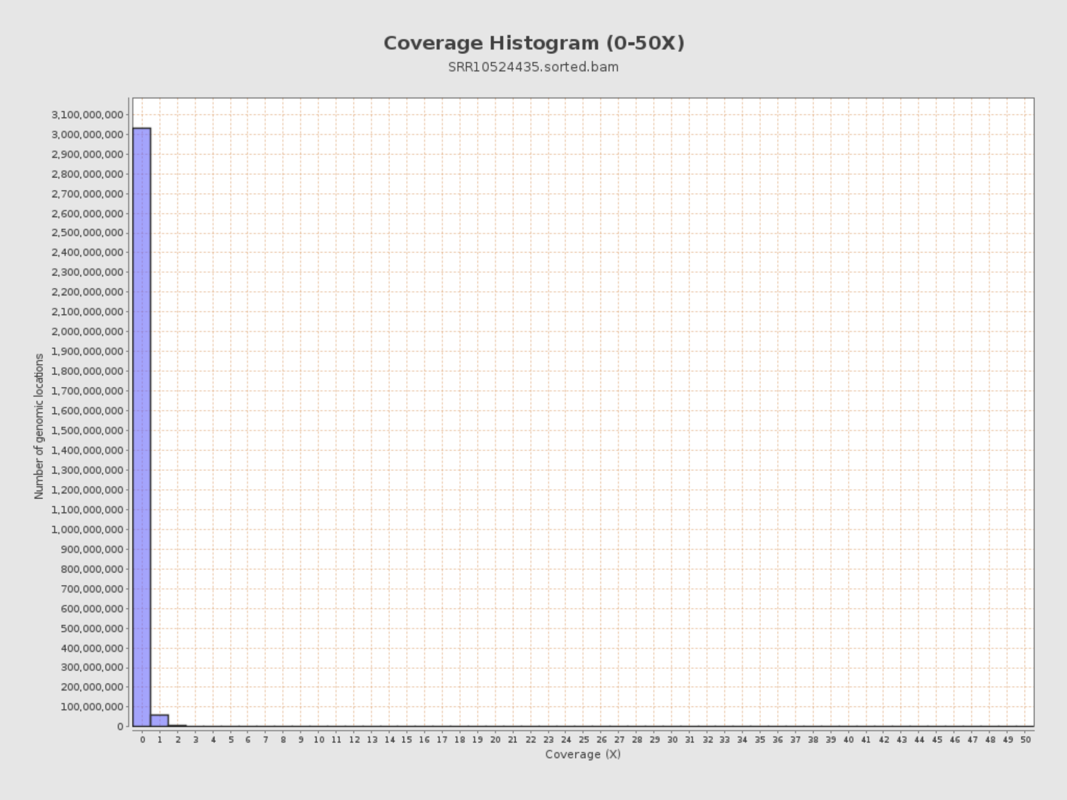
3. Results : Coverage across reference



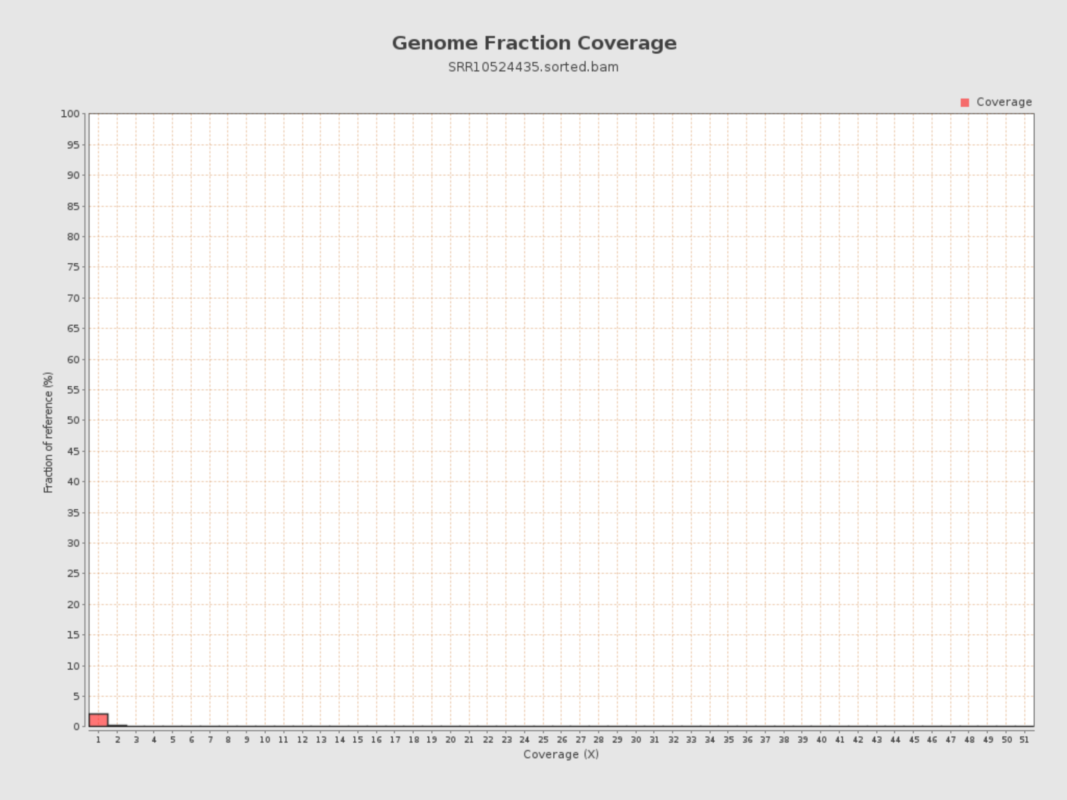
4. Results : Coverage Histogram



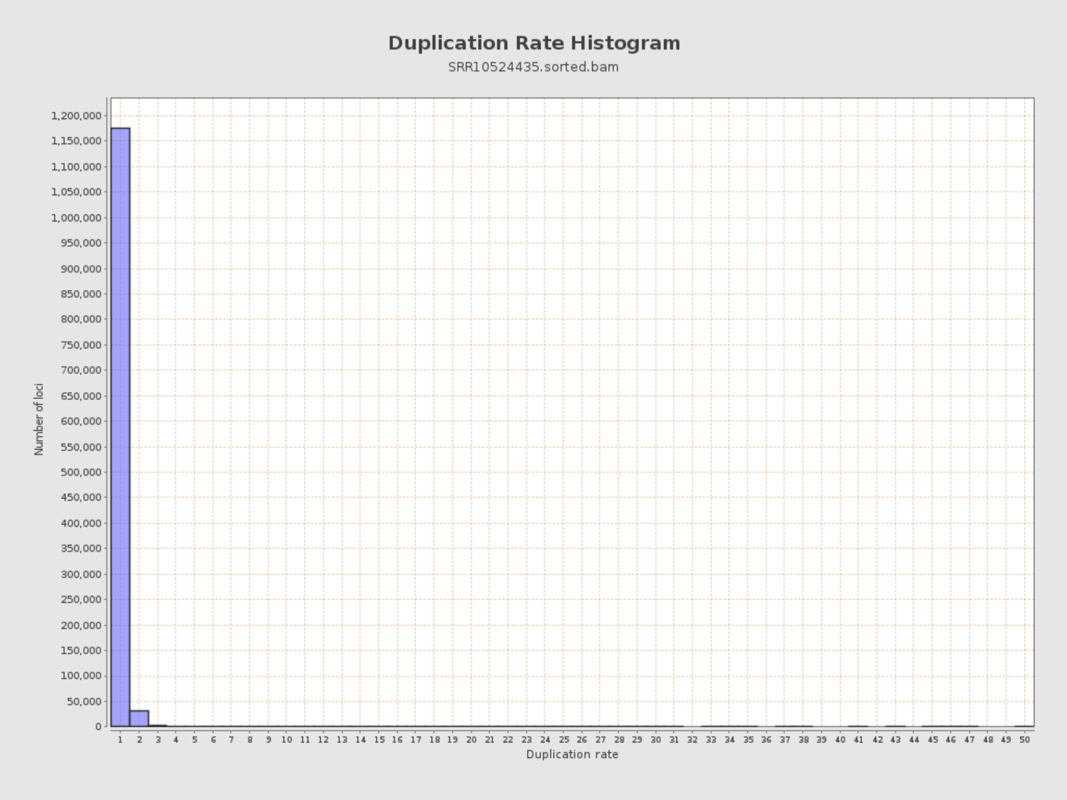
5. Results : Coverage Histogram (0-50X)



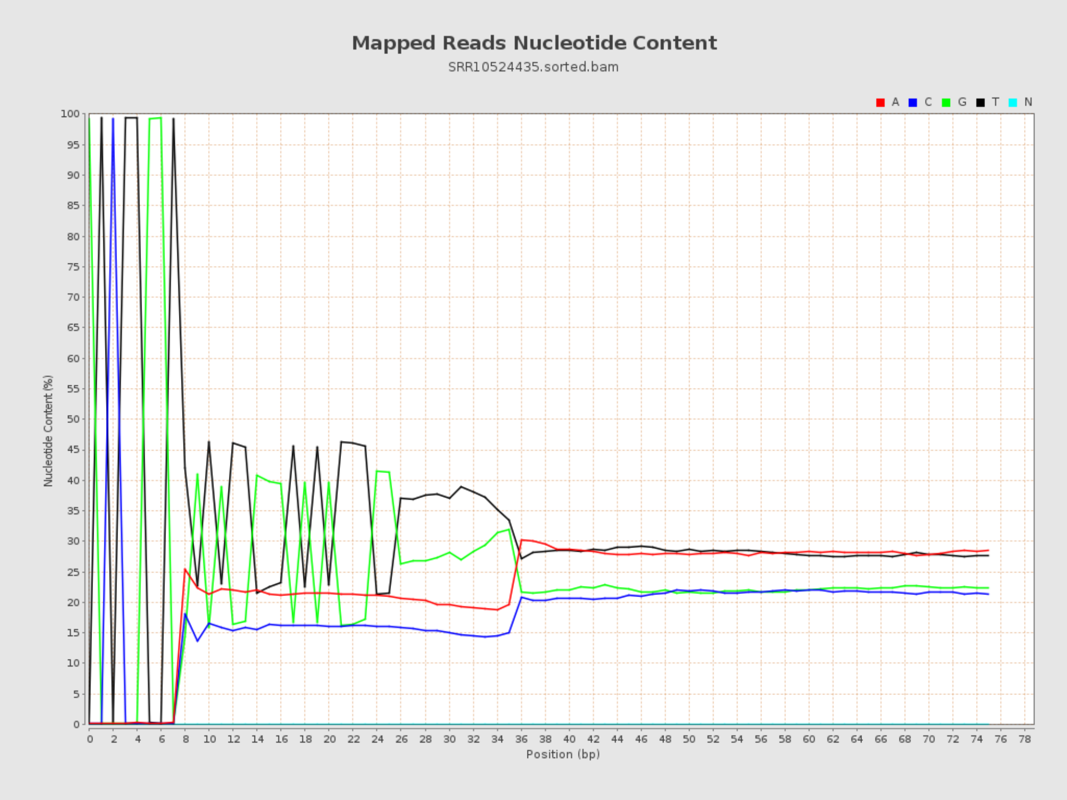
6. Results : Genome Fraction Coverage



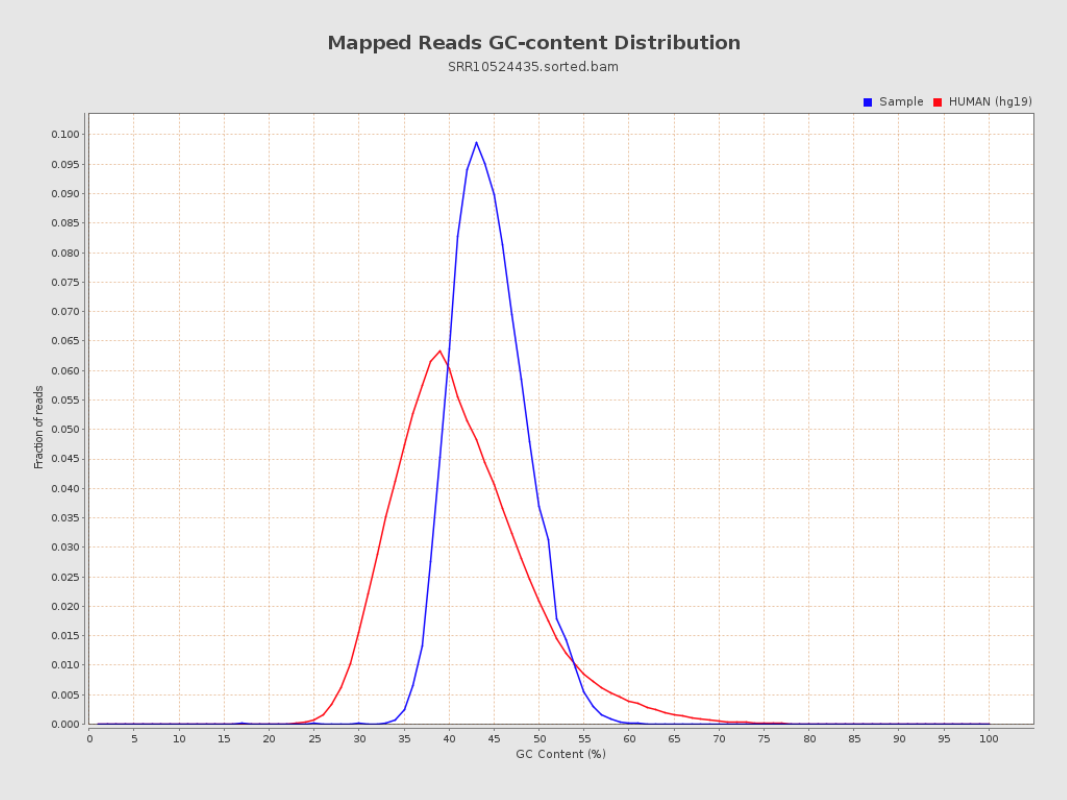
7. Results : Duplication Rate Histogram



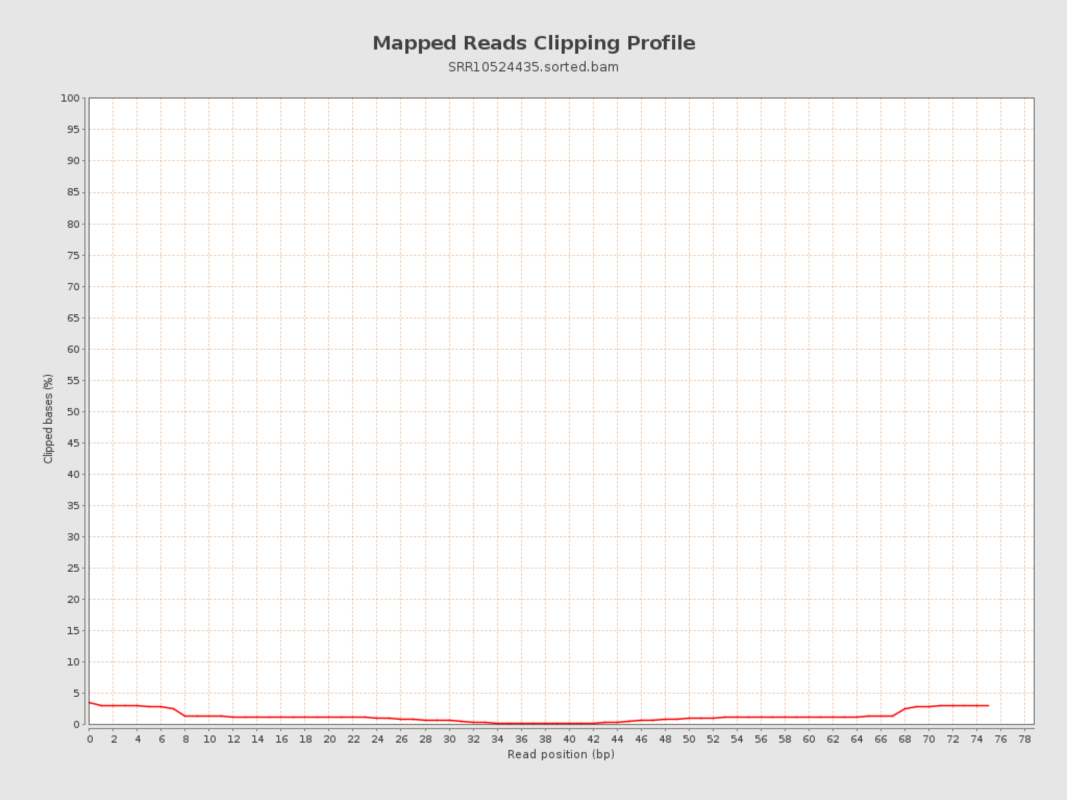
8. Results : Mapped Reads Nucleotide Content



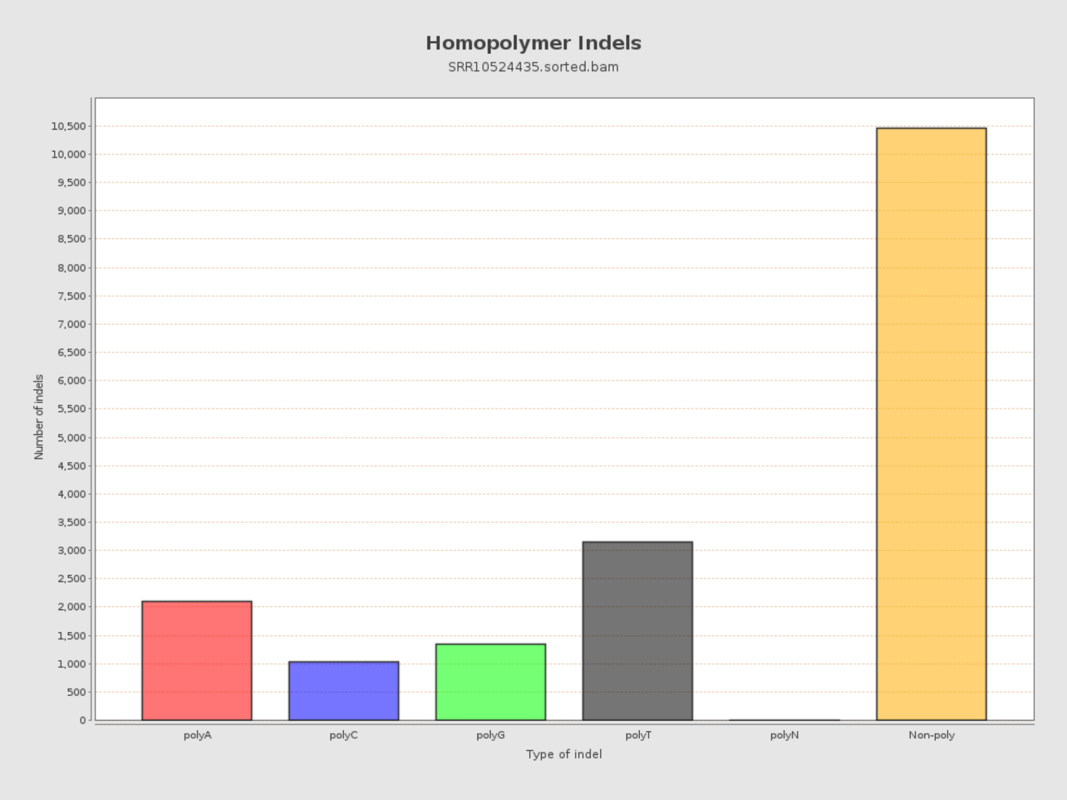
9. Results : Mapped Reads GC-content Distribution



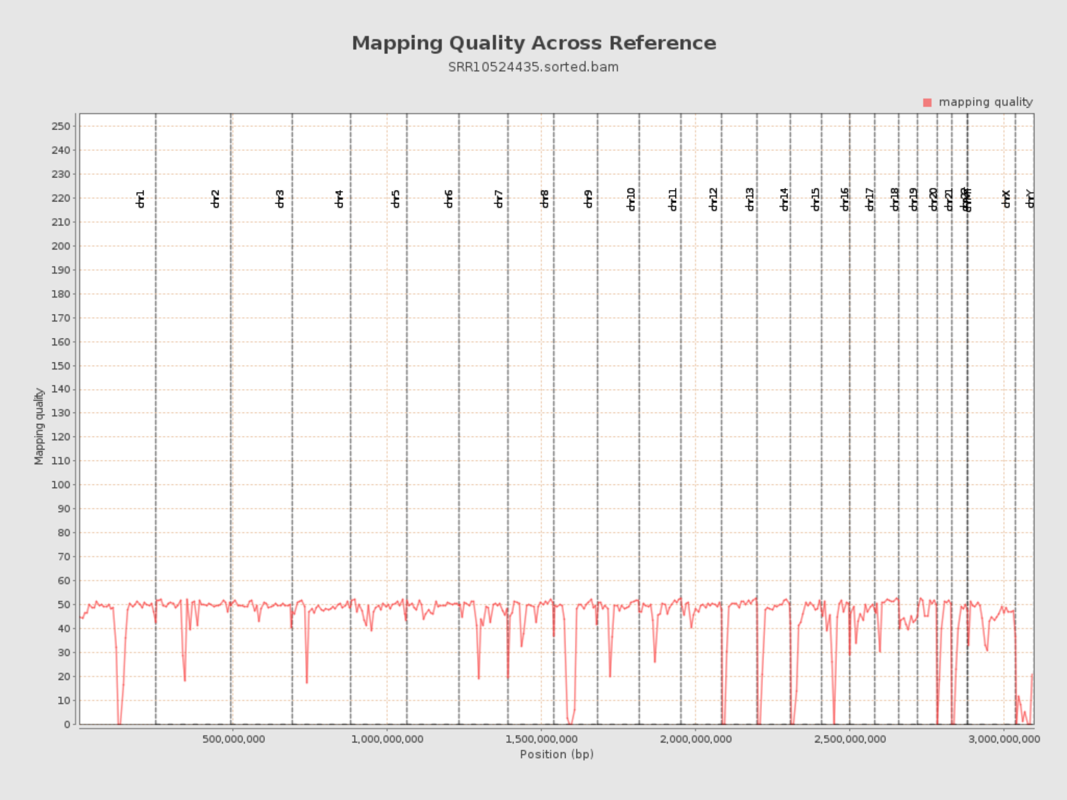
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram