Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:34:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524836.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_SRR10524836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524836.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:34:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	475,709
Mapped reads	440,482 / 92.59%
Unmapped reads	35,227 / 7.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,366 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	7,112 / 1.5%
Duplication rate	1.14%
Clipped reads	441,035 / 92.71%

2.2. ACGT Content

Number/percentage of A's	6,812,233 / 26.17%
Number/percentage of C's	4,722,718 / 18.14%
Number/percentage of T's	8,484,538 / 32.6%
Number/percentage of G's	6,005,686 / 23.07%
Number/percentage of N's	3,722 / 0.01%
GC Percentage	41.22%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1171

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

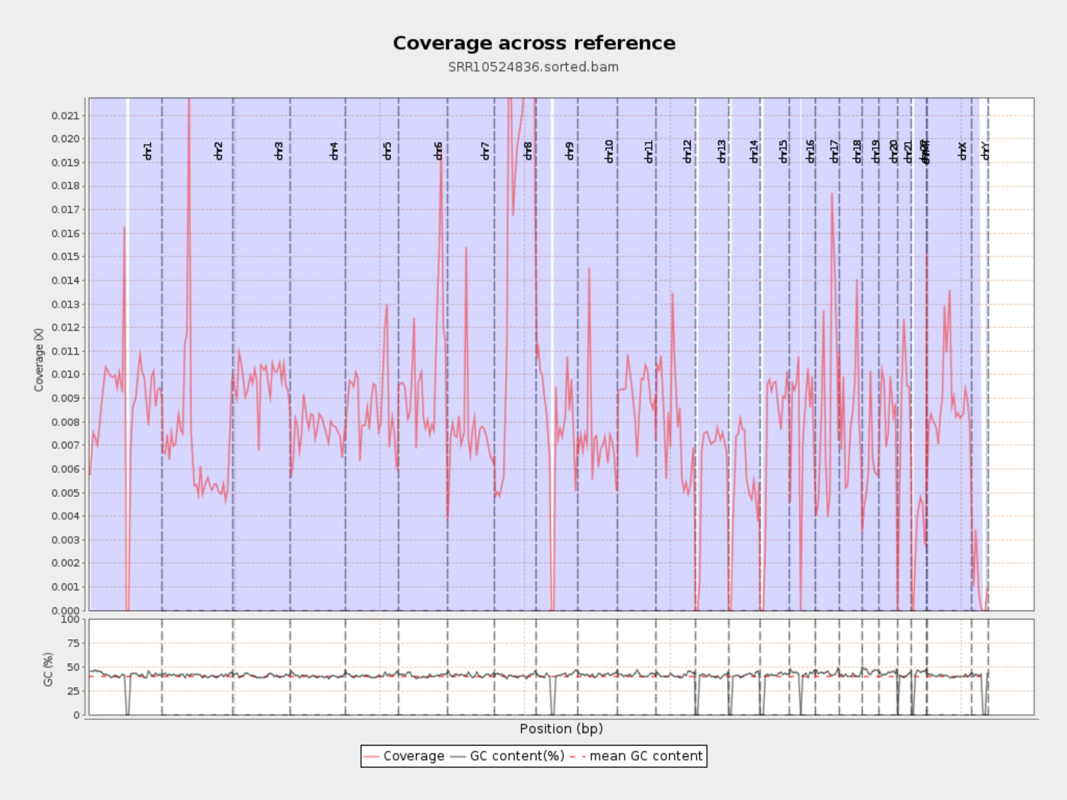
General error rate	0.5%
Mismatches	124,918
Insertions	2,196
Mapped reads with at least one insertion	0.5%
Deletions	5,010
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.7%

2.6. Chromosome stats

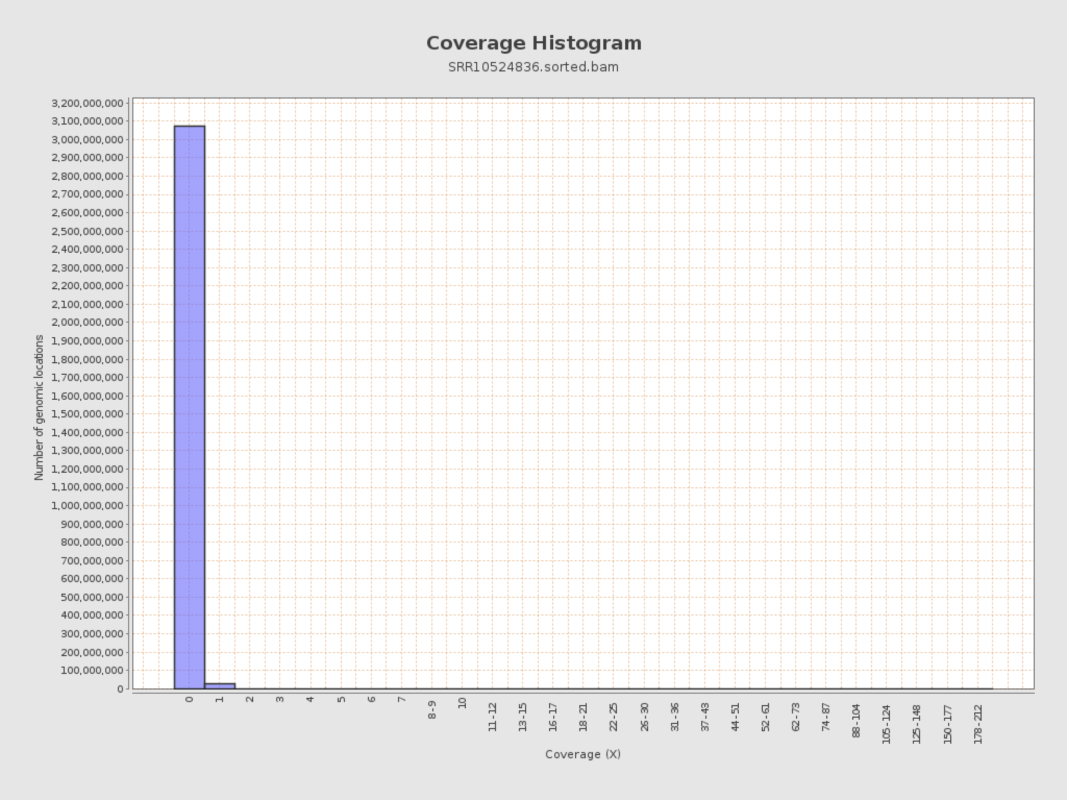
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2171648	0.0087	0.1937
chr2	243199373	1712447	0.007	0.1076
chr3	198022430	1935464	0.0098	0.1009
chr4	191154276	1458912	0.0076	0.0912
chr5	180915260	1587674	0.0088	0.0963
chr6	171115067	1707426	0.01	0.1054
chr7	159138663	1219929	0.0077	0.1436

chr8	146364022	2933209	0.02	0.1735
chr9	141213431	1078244	0.0076	0.1021
chr10	135534747	988550	0.0073	0.101
chr11	135006516	1239206	0.0092	0.1121
chr12	133851895	1044969	0.0078	0.0917
chr13	115169878	689690	0.006	0.0802
chr14	107349540	557382	0.0052	0.0758
chr15	102531392	760426	0.0074	0.0883
chr16	90354753	725589	0.008	0.0945
chr17	81195210	705315	0.0087	0.0989
chr18	78077248	652471	0.0084	0.1625
chr19	59128983	360553	0.0061	0.1357
chr20	63025520	536200	0.0085	0.0949
chr21	48129895	389933	0.0081	0.0944
chr22	51304566	149349	0.0029	0.0551
chrMT	16571	251	0.0151	0.1221
chrX	155270560	1370554	0.0088	0.1007
chrY	59373566	61348	0.001	0.0386

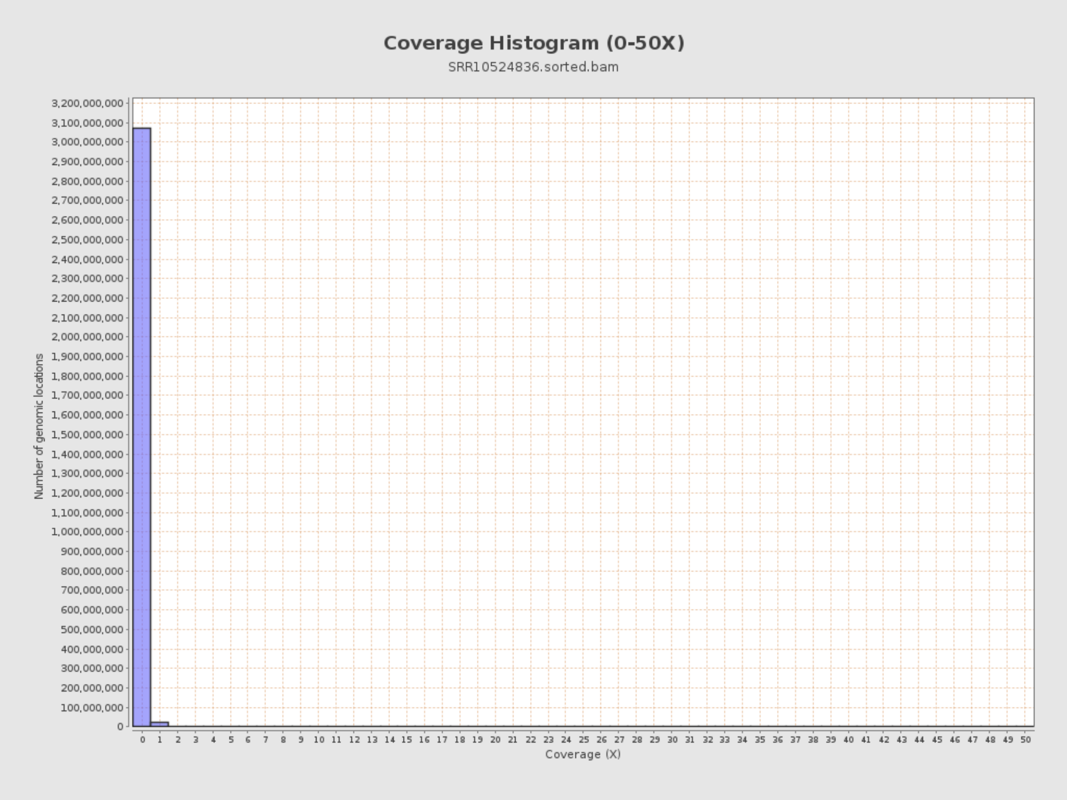
3. Results : Coverage across reference



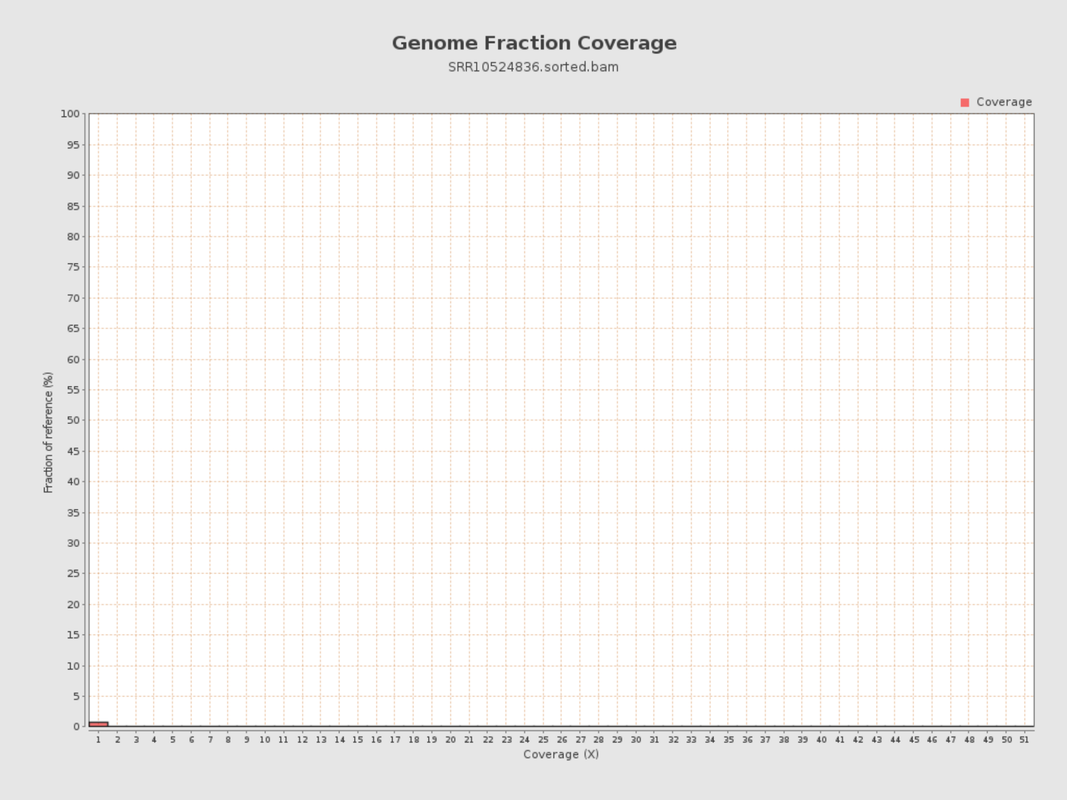
4. Results : Coverage Histogram



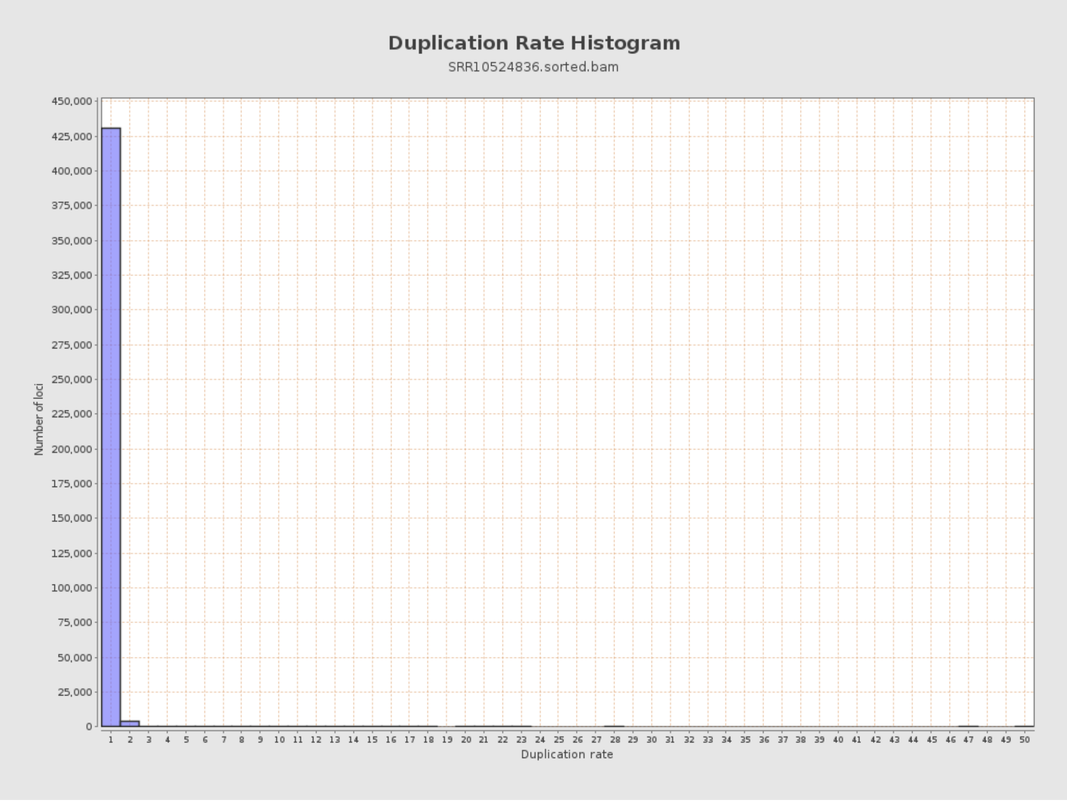
5. Results : Coverage Histogram (0-50X)



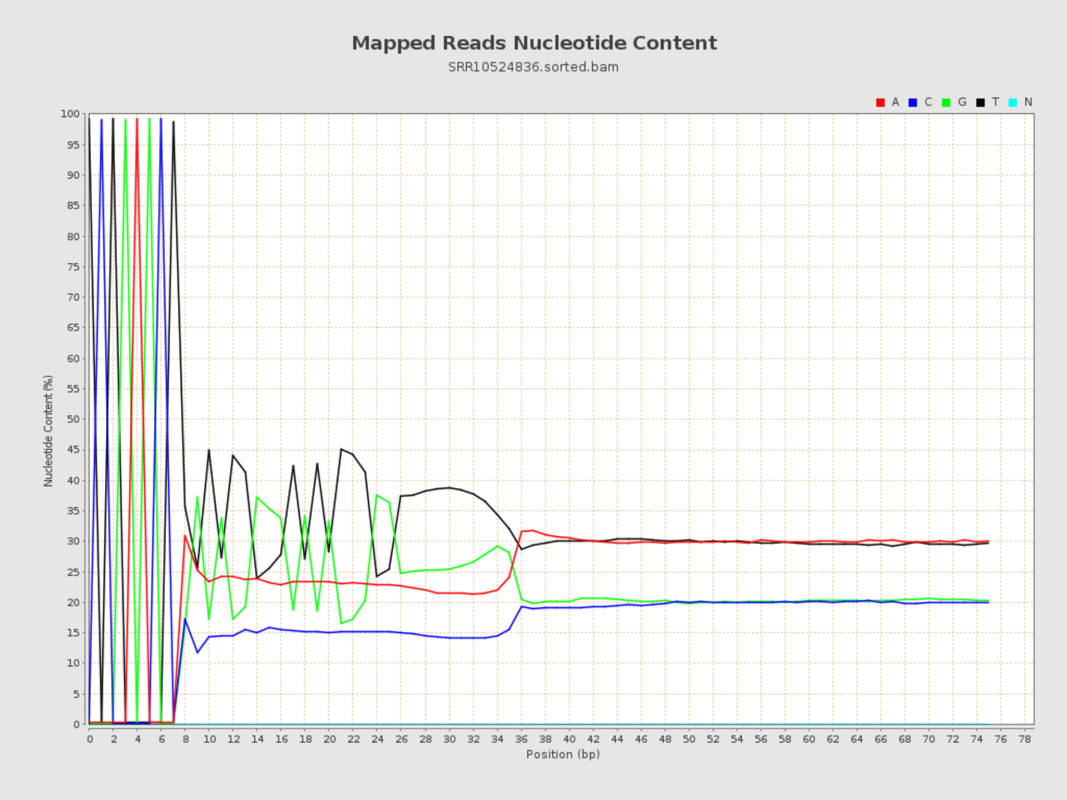
6. Results : Genome Fraction Coverage



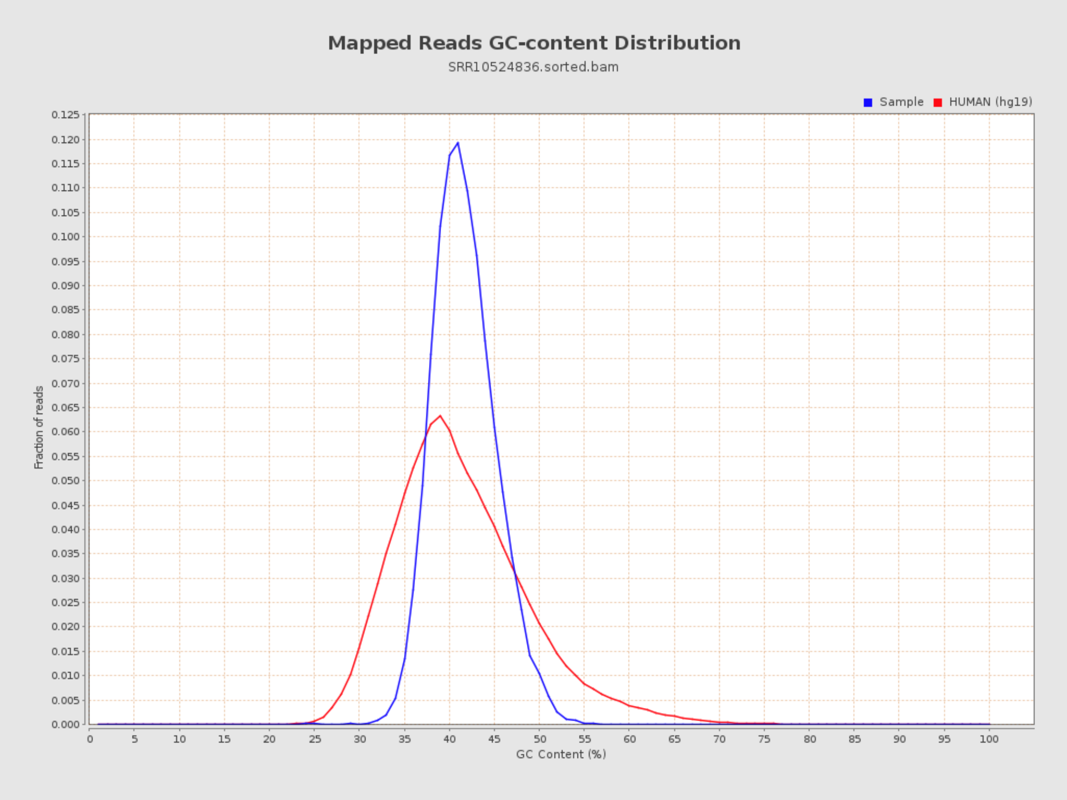
7. Results : Duplication Rate Histogram



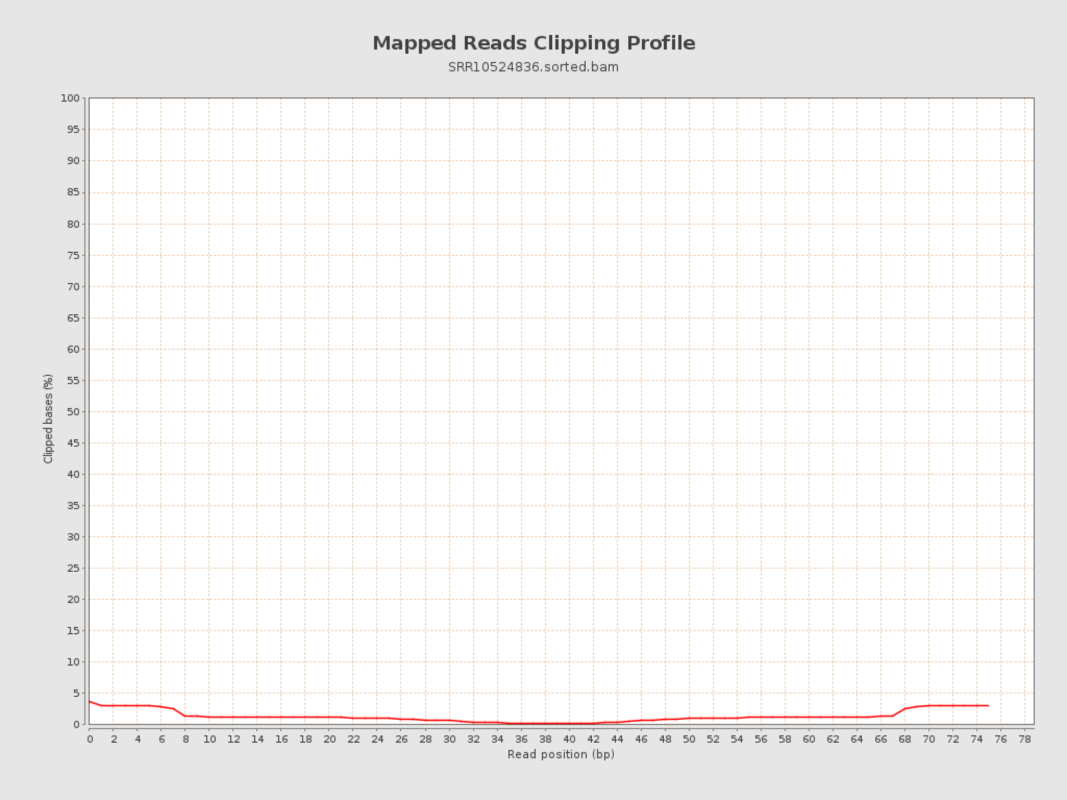
8. Results : Mapped Reads Nucleotide Content



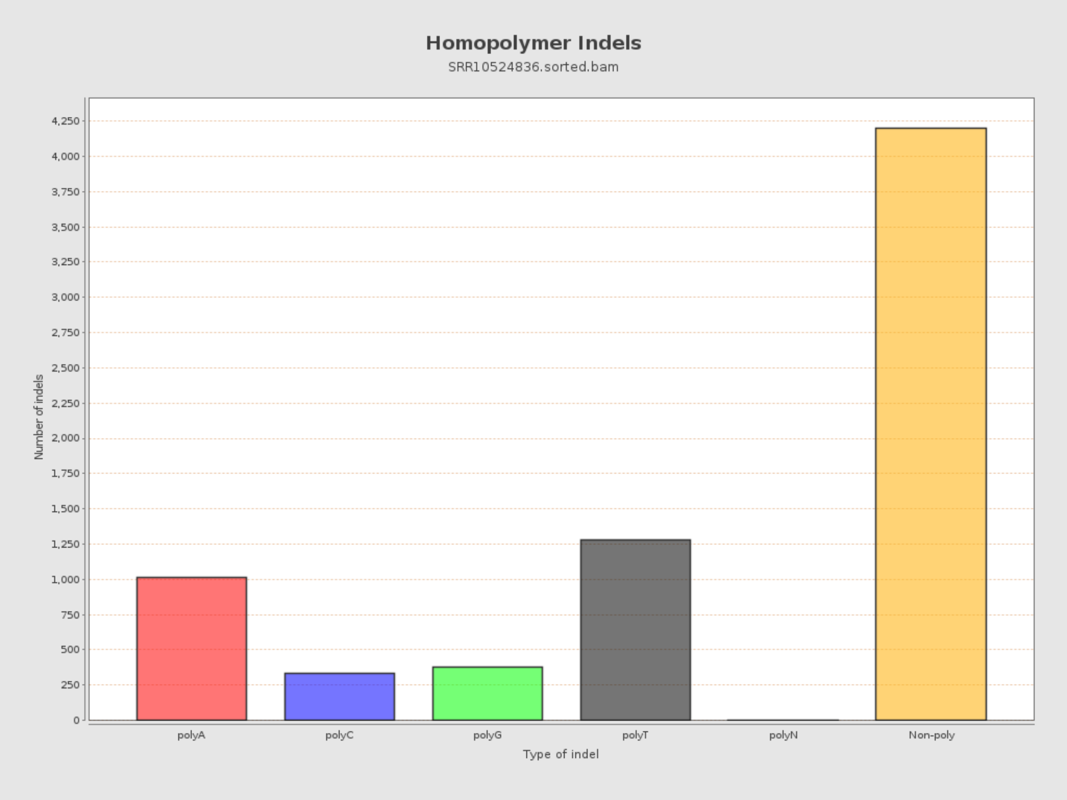
9. Results : Mapped Reads GC-content Distribution



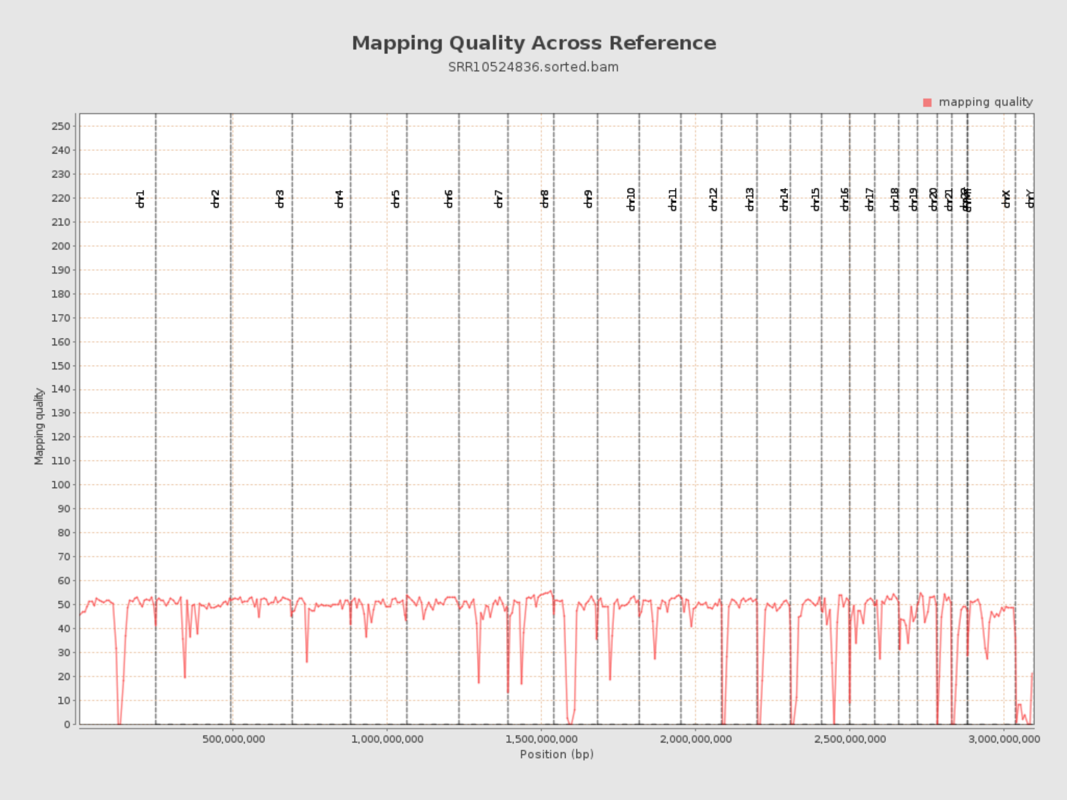
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram