Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:46:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524558.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_SRR10524558 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524558.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:46:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524558.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,003,948
Mapped reads	1,832,291 / 91.43%
Unmapped reads	171,657 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,433 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	84,490 / 4.22%
Duplication rate	3.47%
Clipped reads	1,836,784 / 91.66%

2.2. ACGT Content

Number/percentage of A's	27,122,887 / 25.41%
Number/percentage of C's	20,097,670 / 18.83%
Number/percentage of T's	32,378,877 / 30.34%
Number/percentage of G's	27,129,612 / 25.42%
Number/percentage of N's	1,546 / 0%
GC Percentage	44.25%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.3132

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

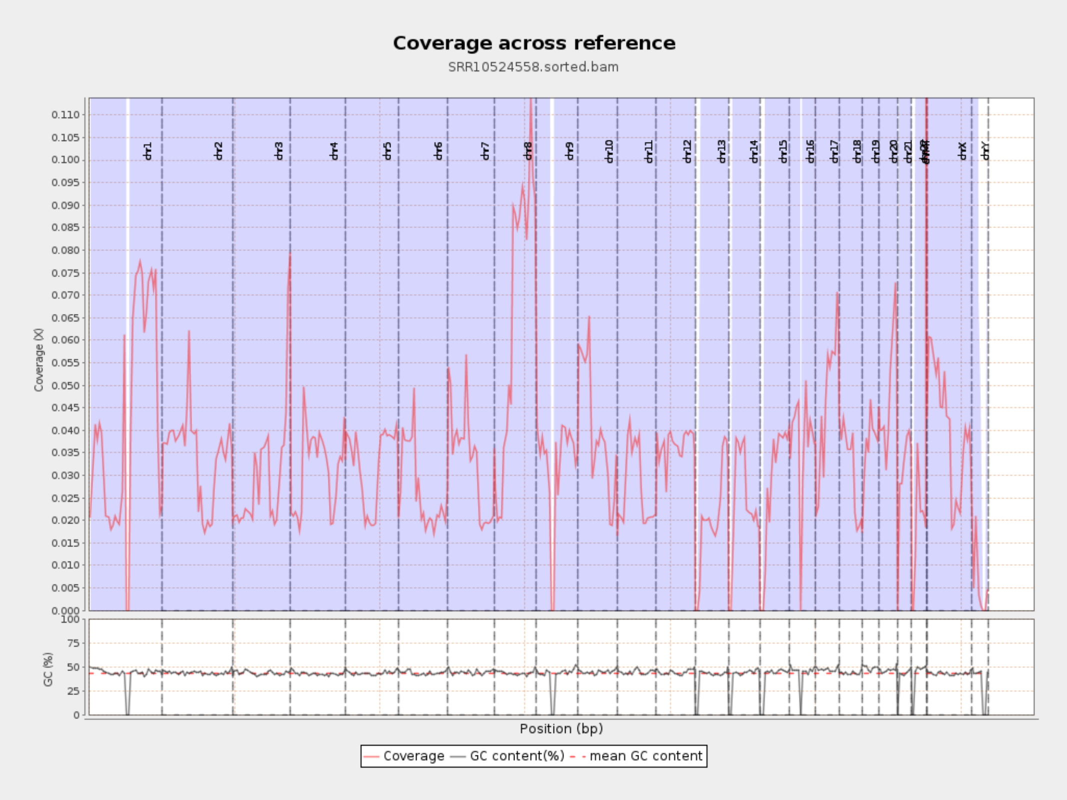
General error rate	0.52%
Mismatches	539,868
Insertions	6,142
Mapped reads with at least one insertion	0.33%
Deletions	19,826
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.02%

2.6. Chromosome stats

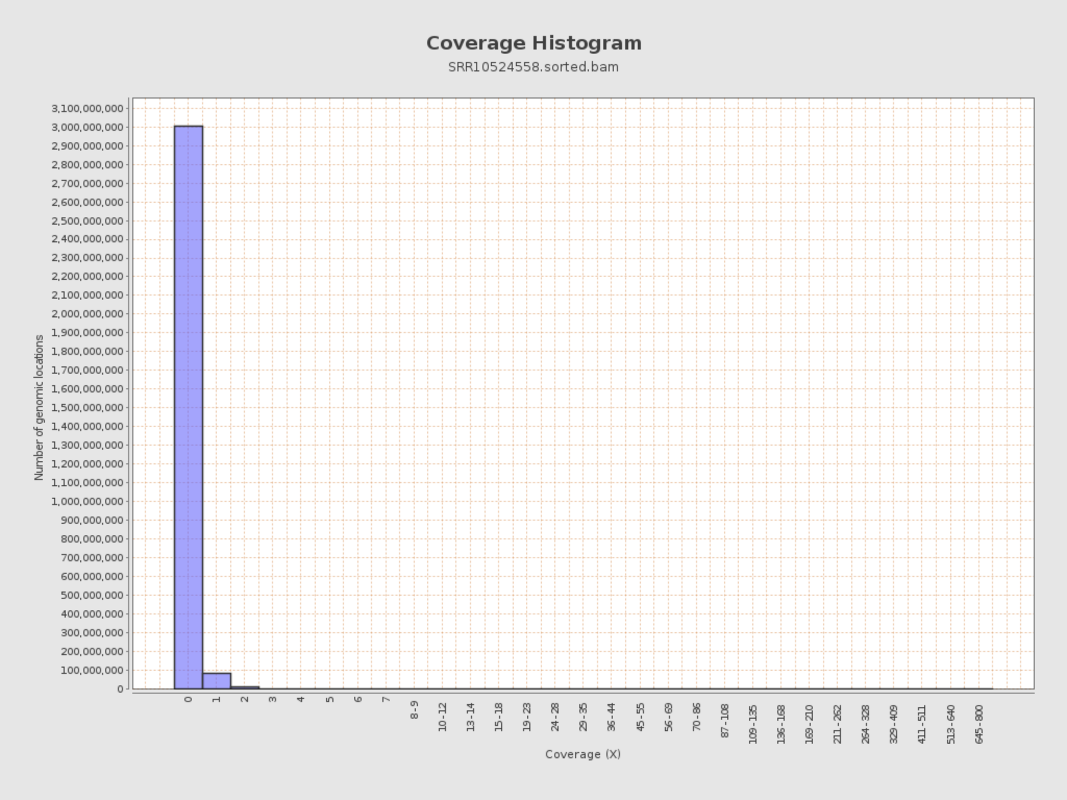
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10579157	0.0424	0.6002
chr2	243199373	8453862	0.0348	0.3663
chr3	198022430	5824657	0.0294	0.1913
chr4	191154276	5991593	0.0313	0.2252
chr5	180915260	5858072	0.0324	0.2002
chr6	171115067	4574271	0.0267	0.2343
chr7	159138663	5280846	0.0332	0.3687

chr8	146364022	9758268	0.0667	0.3418
chr9	141213431	4497254	0.0318	0.2578
chr10	135534747	5503727	0.0406	0.3198
chr11	135006516	3696413	0.0274	0.2987
chr12	133851895	4931398	0.0368	0.2148
chr13	115169878	2350280	0.0204	0.1589
chr14	107349540	2548630	0.0237	0.1765
chr15	102531392	2834304	0.0276	0.1906
chr16	90354753	3368694	0.0373	0.2306
chr17	81195210	3833538	0.0472	0.2574
chr18	78077248	2487959	0.0319	0.4716
chr19	59128983	2218113	0.0375	0.4125
chr20	63025520	3075133	0.0488	0.2495
chr21	48129895	1479332	0.0307	0.2204
chr22	51304566	917131	0.0179	0.1489
chrMT	16571	8748	0.5279	0.8734
chrX	155270560	6338574	0.0408	0.2545
chrY	59373566	353312	0.006	0.1817

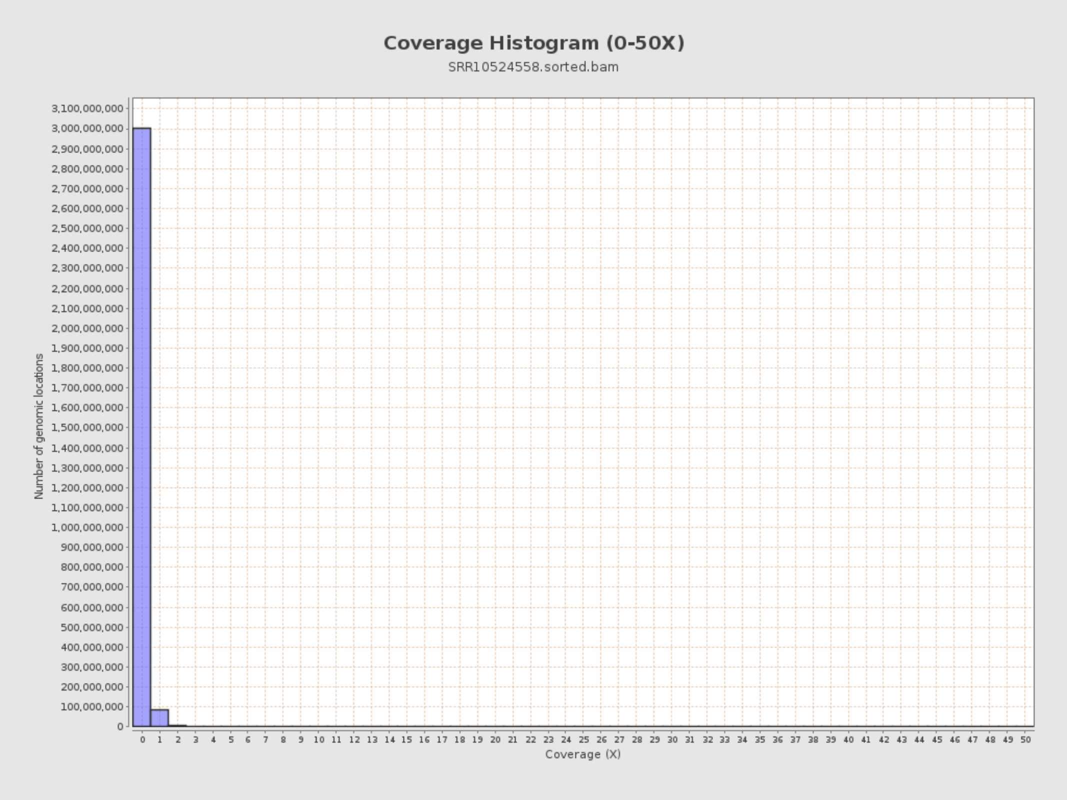
3. Results : Coverage across reference



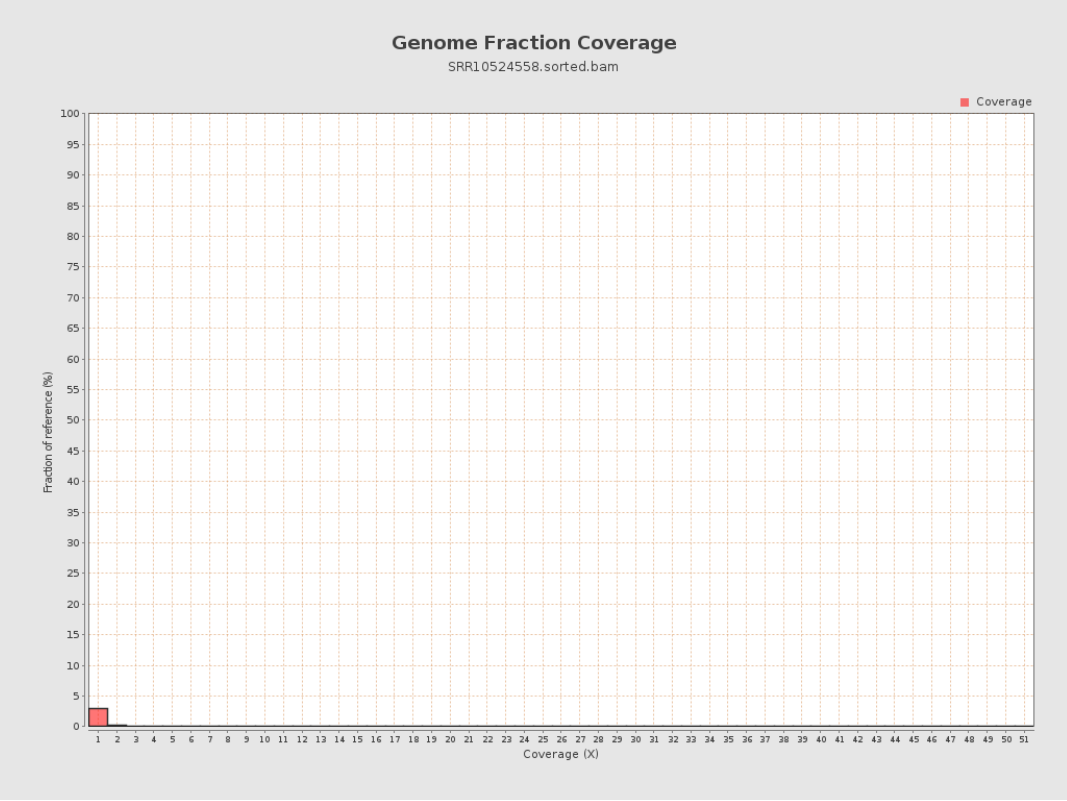
4. Results : Coverage Histogram



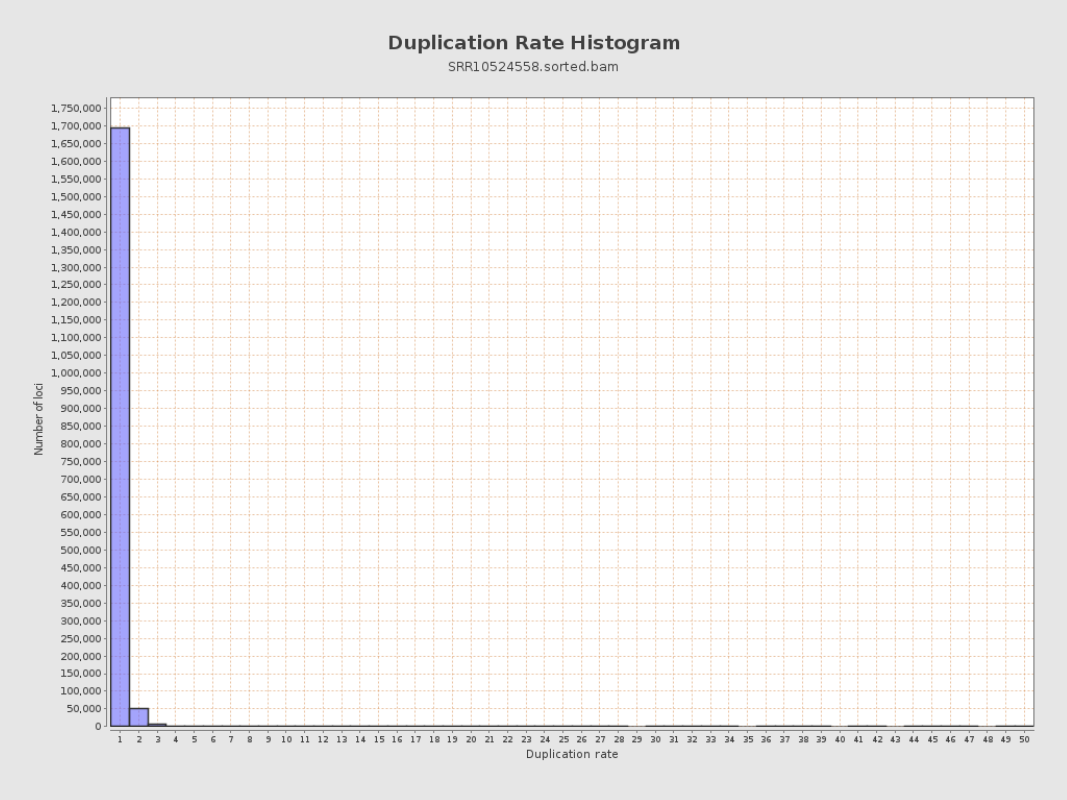
5. Results : Coverage Histogram (0-50X)



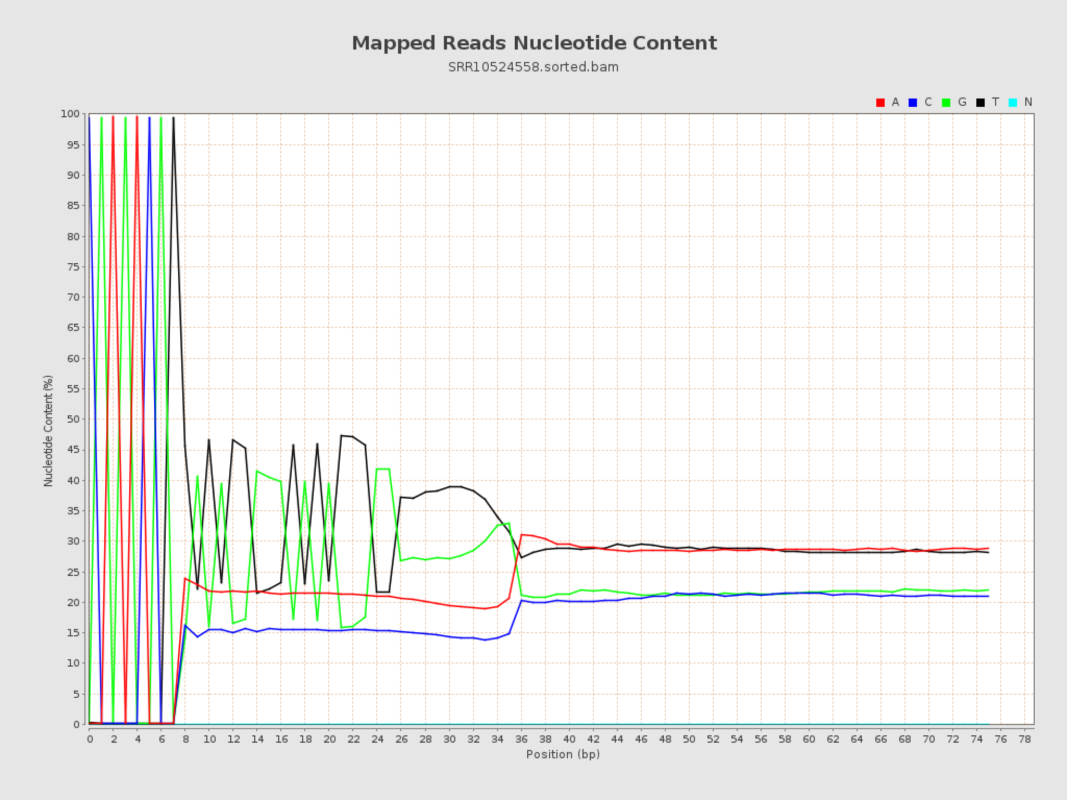
6. Results : Genome Fraction Coverage



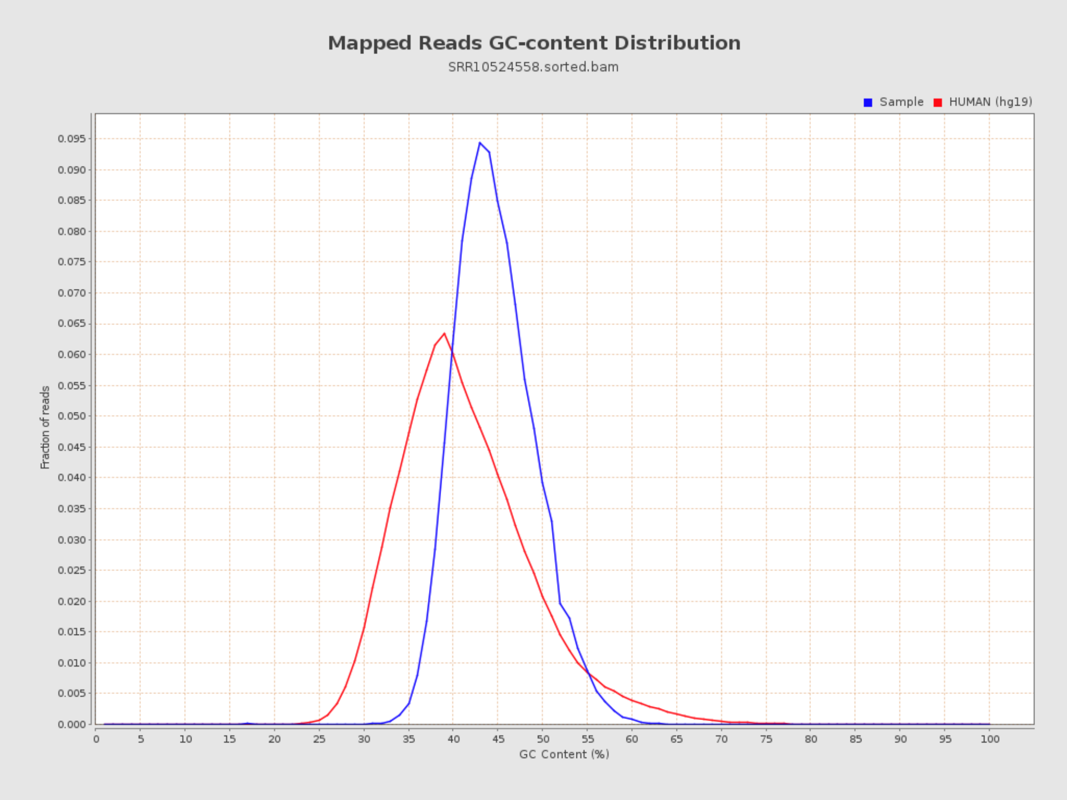
7. Results : Duplication Rate Histogram



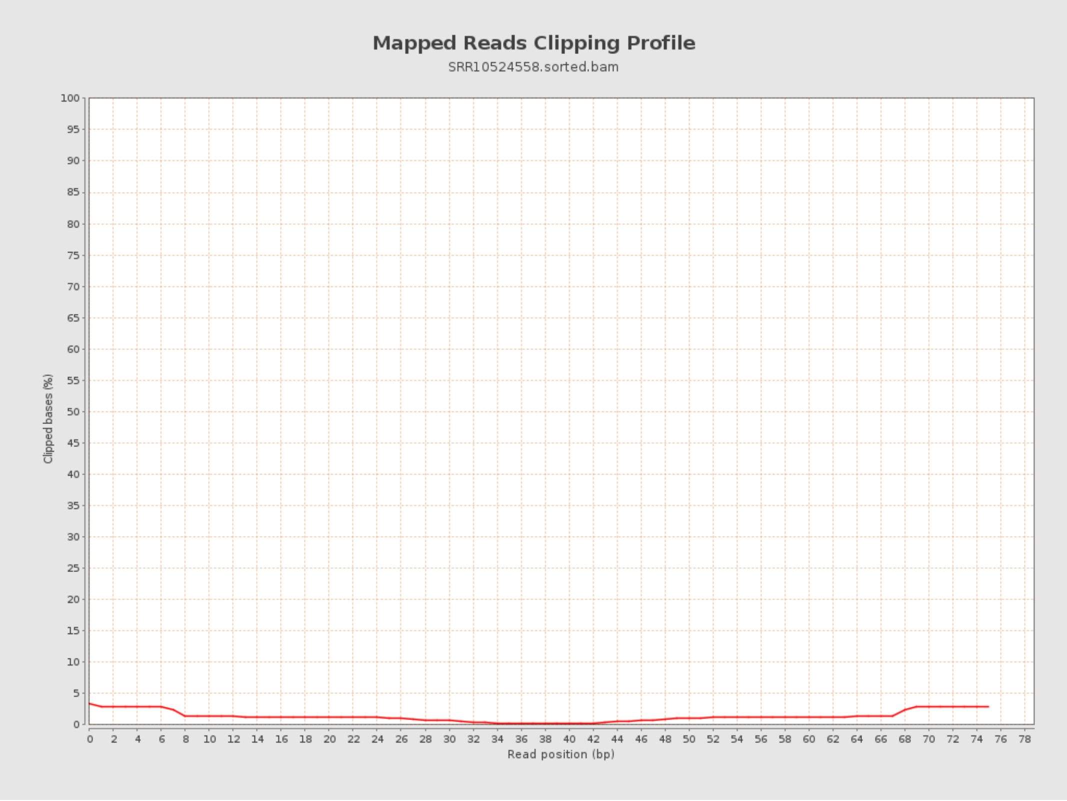
8. Results : Mapped Reads Nucleotide Content



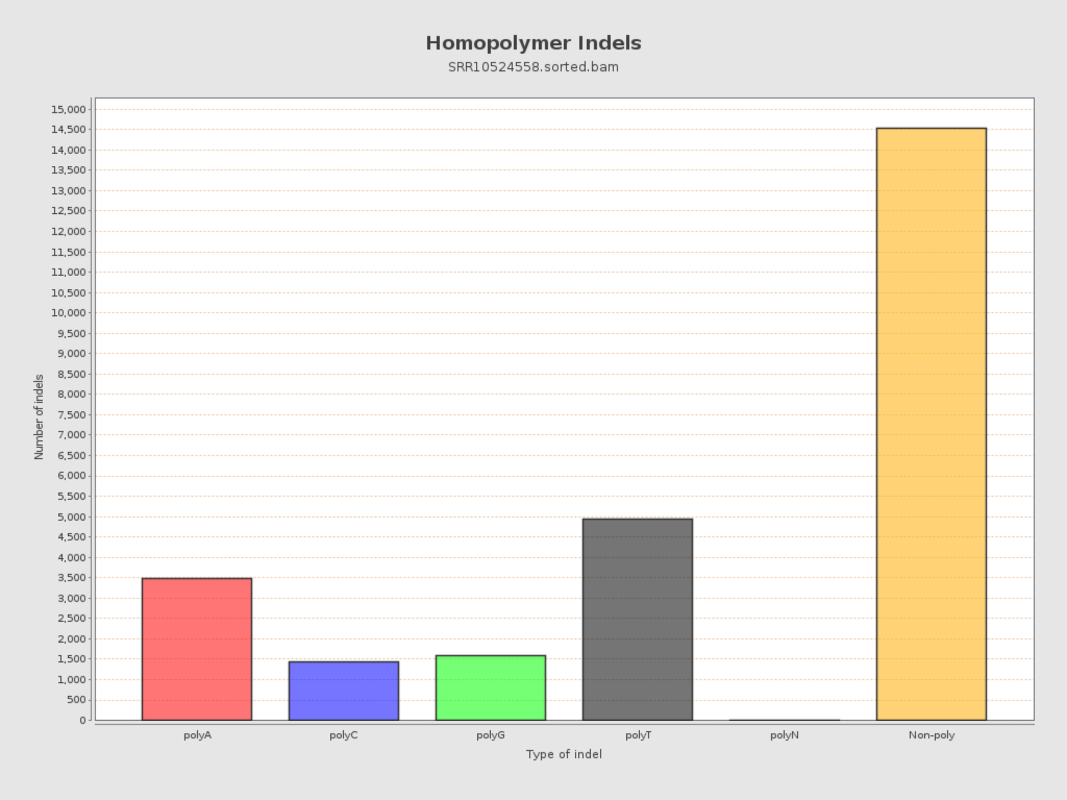
9. Results : Mapped Reads GC-content Distribution



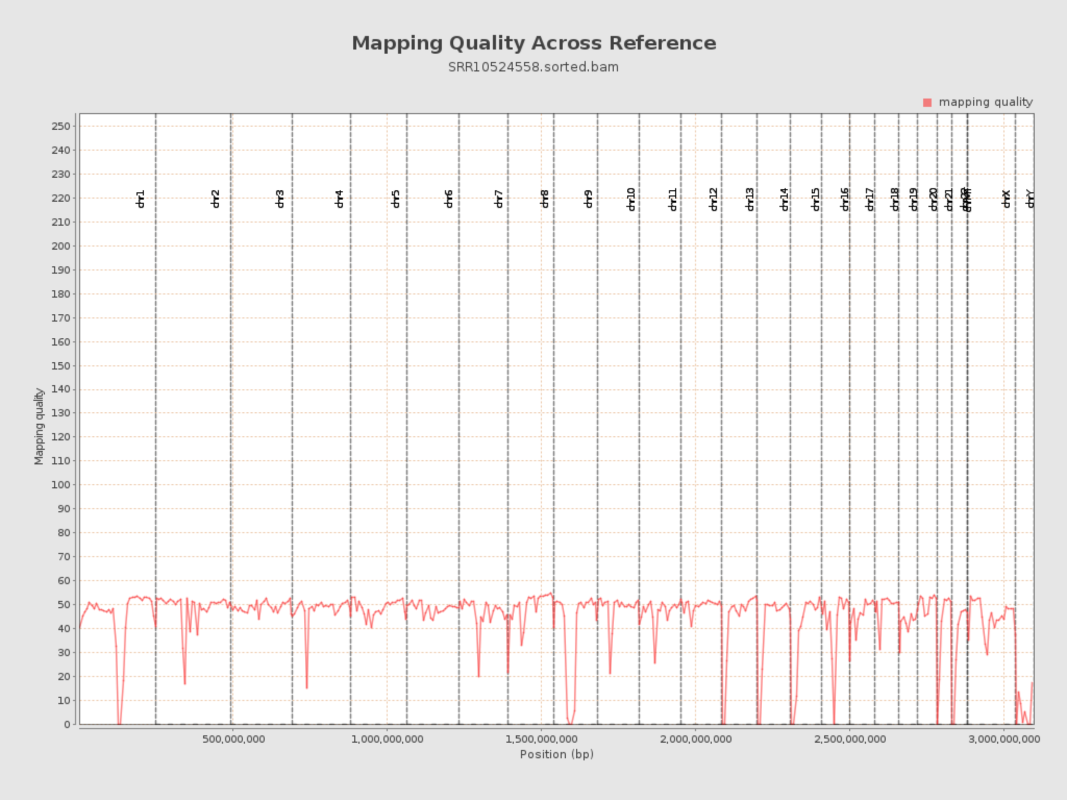
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram