Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:02:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524400.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_SRR10524400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524400.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:02:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	377,706
Mapped reads	332,598 / 88.06%
Unmapped reads	45,108 / 11.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,104 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	5,736 / 1.52%
Duplication rate	1.33%
Clipped reads	332,887 / 88.13%

2.2. ACGT Content

Number/percentage of A's	4,749,853 / 24.9%
Number/percentage of C's	3,254,712 / 17.06%
Number/percentage of T's	6,442,109 / 33.77%
Number/percentage of G's	4,626,754 / 24.26%
Number/percentage of N's	405 / 0%
GC Percentage	41.32%

2.3. Coverage

Mean	0.0062

Standard Deviation	0.093

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

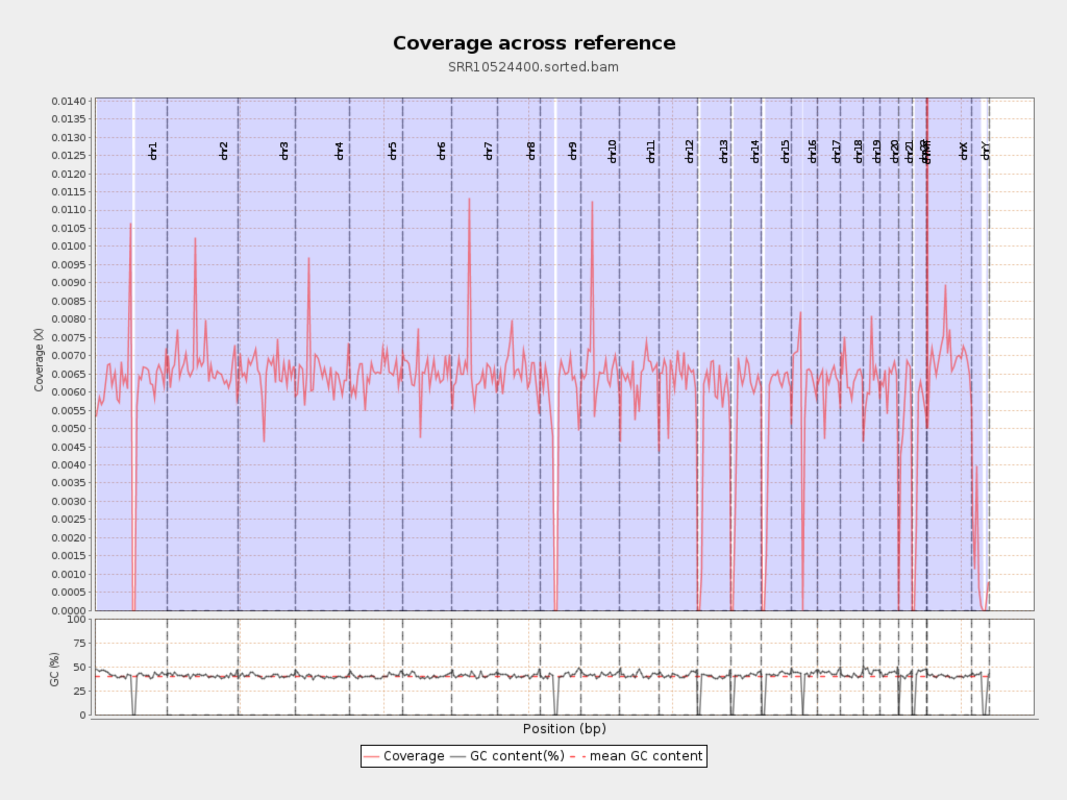
General error rate	0.53%
Mismatches	98,956
Insertions	1,301
Mapped reads with at least one insertion	0.39%
Deletions	4,052
Mapped reads with at least one deletion	1.21%
Homopolymer indels	44.39%

2.6. Chromosome stats

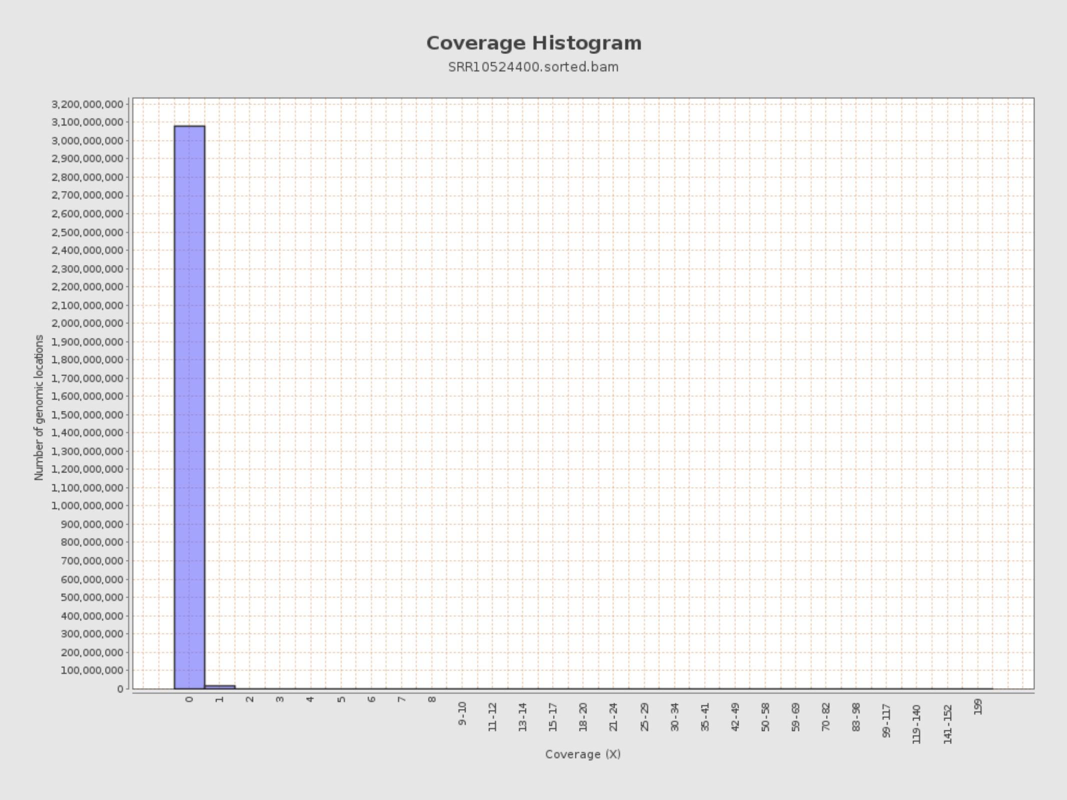
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1502676	0.006	0.1291
chr2	243199373	1647574	0.0068	0.117
chr3	198022430	1297597	0.0066	0.083
chr4	191154276	1246956	0.0065	0.0842
chr5	180915260	1174313	0.0065	0.0827
chr6	171115067	1121617	0.0066	0.0861
chr7	159138663	1052456	0.0066	0.11

chr8	146364022	965622	0.0066	0.0983
chr9	141213431	786326	0.0056	0.0809
chr10	135534747	916012	0.0068	0.0927
chr11	135006516	867720	0.0064	0.086
chr12	133851895	862973	0.0064	0.0824
chr13	115169878	599387	0.0052	0.0741
chr14	107349540	574327	0.0054	0.0752
chr15	102531392	523793	0.0051	0.0731
chr16	90354753	543513	0.006	0.0817
chr17	81195210	506559	0.0062	0.0814
chr18	78077248	505414	0.0065	0.1077
chr19	59128983	372027	0.0063	0.1039
chr20	63025520	396134	0.0063	0.0815
chr21	48129895	247131	0.0051	0.074
chr22	51304566	210821	0.0041	0.0659
chrMT	16571	10140	0.6119	0.8852
chrX	155270560	1084117	0.007	0.0878
chrY	59373566	64978	0.0011	0.044

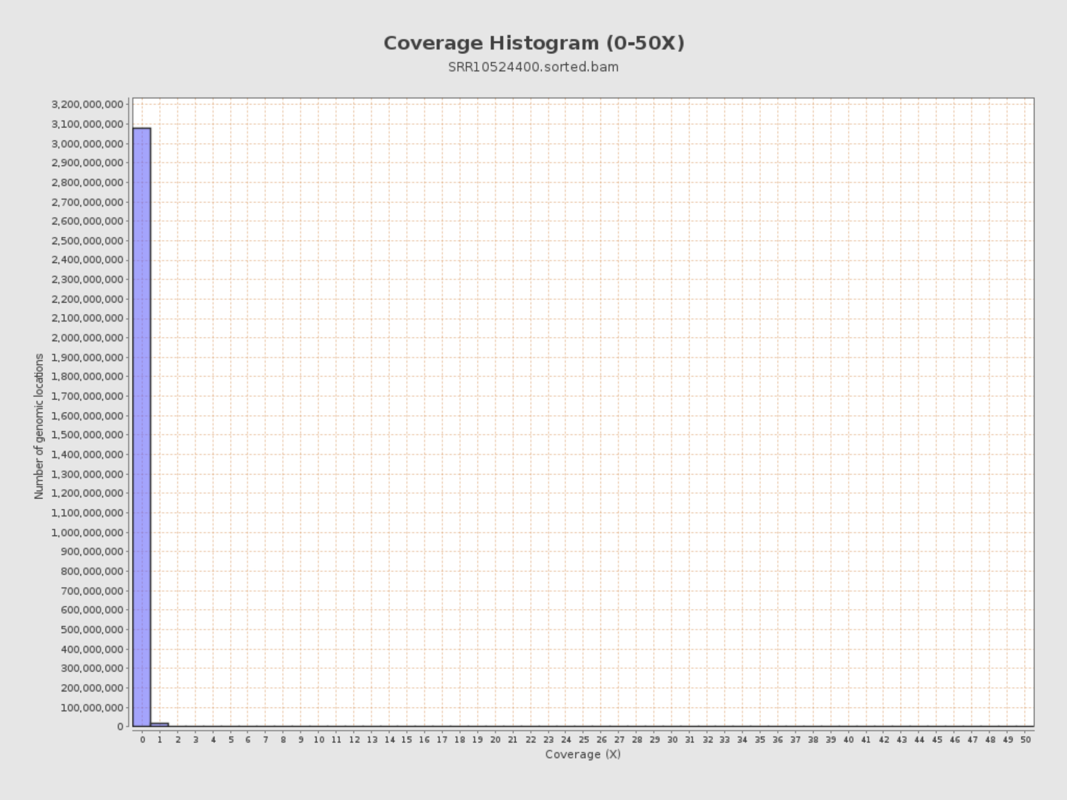
3. Results : Coverage across reference



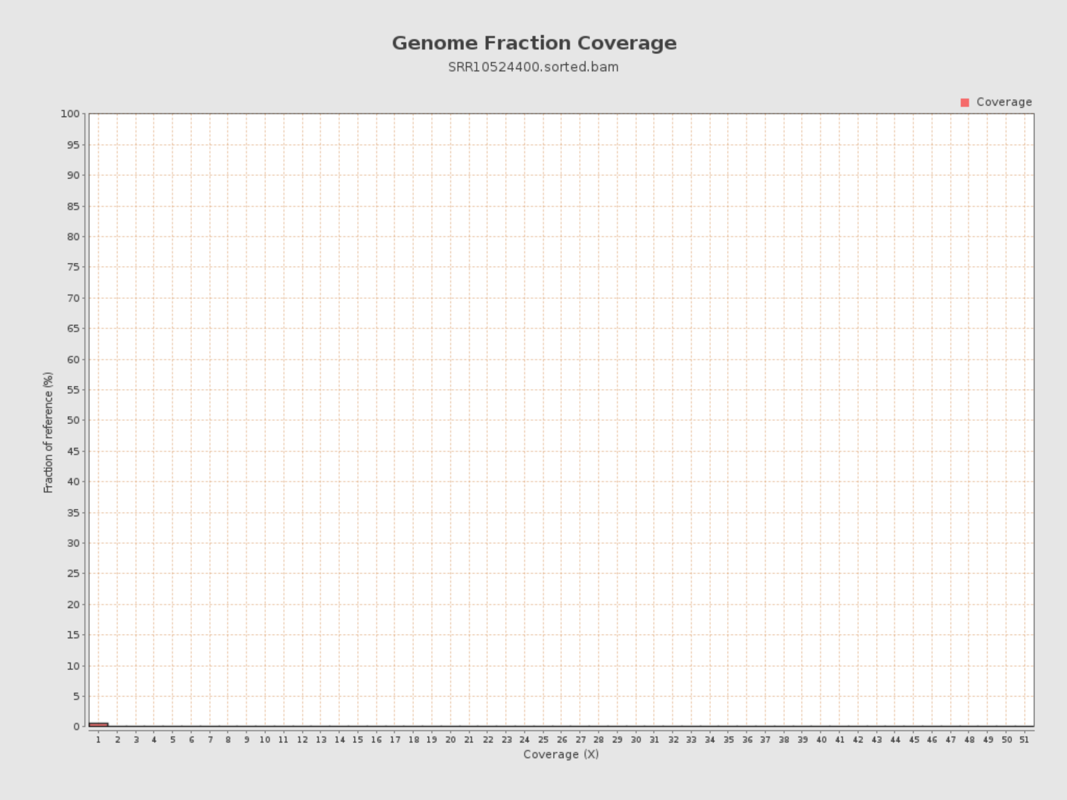
4. Results : Coverage Histogram



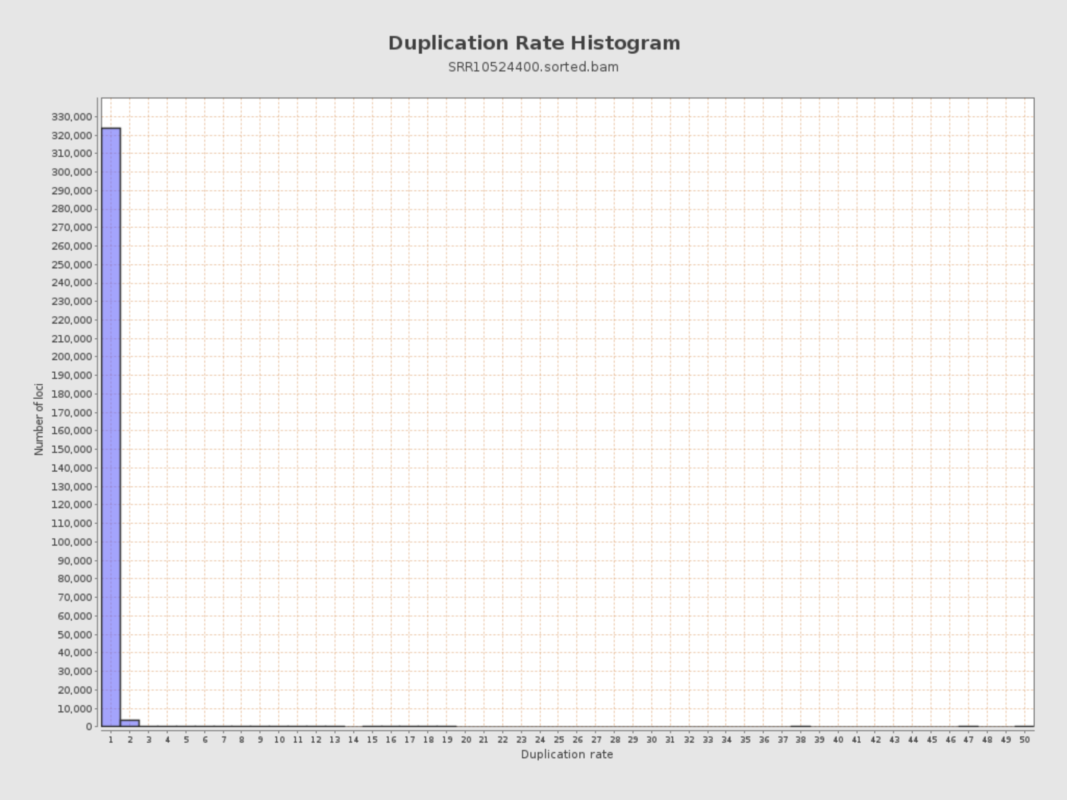
5. Results : Coverage Histogram (0-50X)



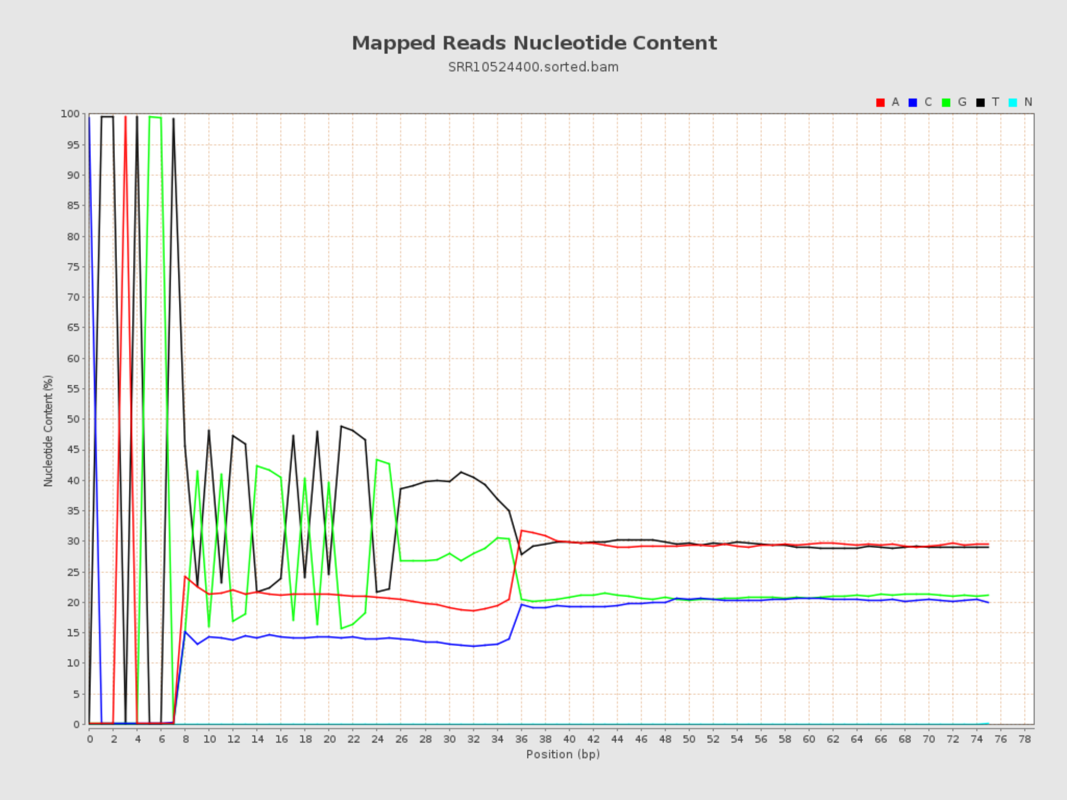
6. Results : Genome Fraction Coverage



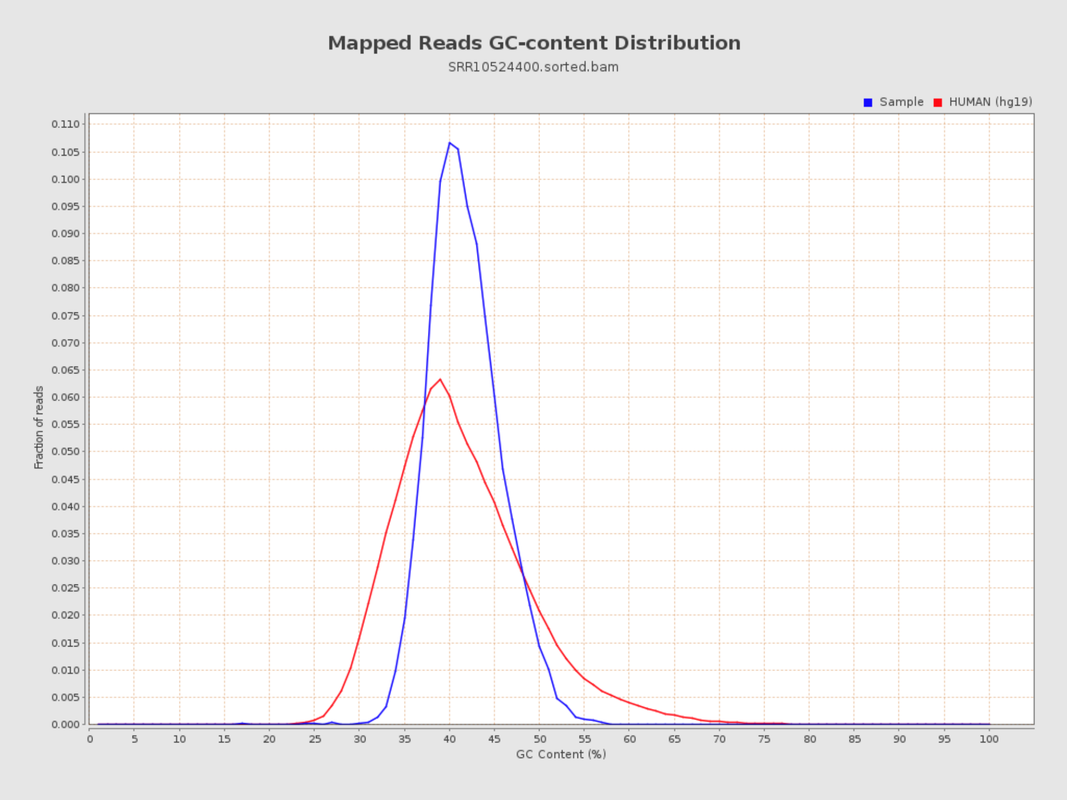
7. Results : Duplication Rate Histogram



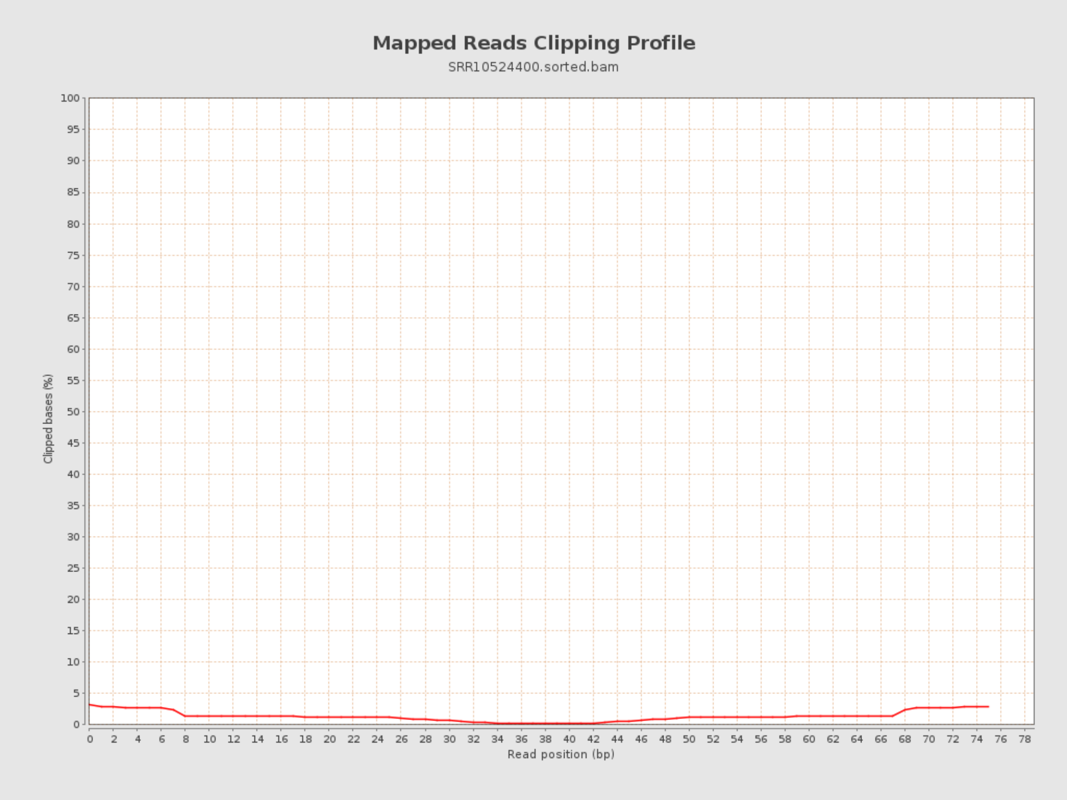
8. Results : Mapped Reads Nucleotide Content



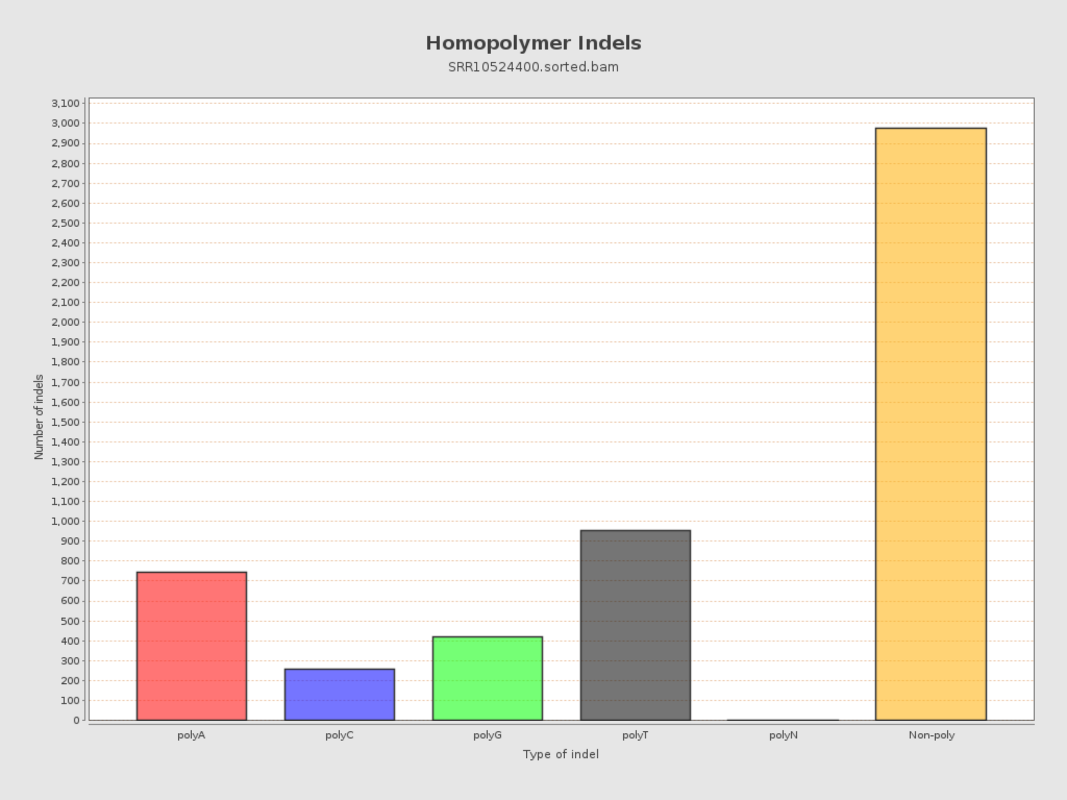
9. Results : Mapped Reads GC-content Distribution



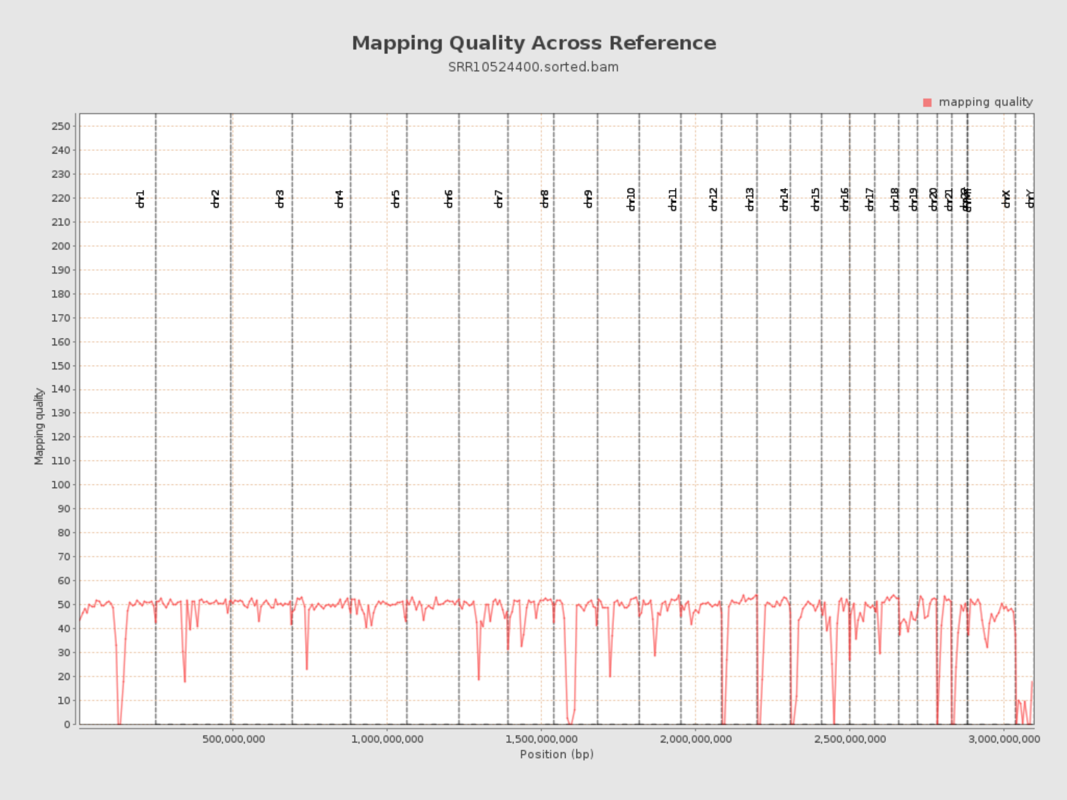
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram