Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:43:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524646.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_SRR10524646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:43:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,675,772
Mapped reads	2,475,816 / 92.53%
Unmapped reads	199,956 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,006 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	195,718 / 7.31%
Duplication rate	6.09%
Clipped reads	2,480,353 / 92.7%

2.2. ACGT Content

Number/percentage of A's	37,899,063 / 26.21%
Number/percentage of C's	27,143,734 / 18.77%
Number/percentage of T's	44,122,744 / 30.51%
Number/percentage of G's	35,454,783 / 24.52%
Number/percentage of N's	1,152 / 0%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0467

Standard Deviation	0.4026

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

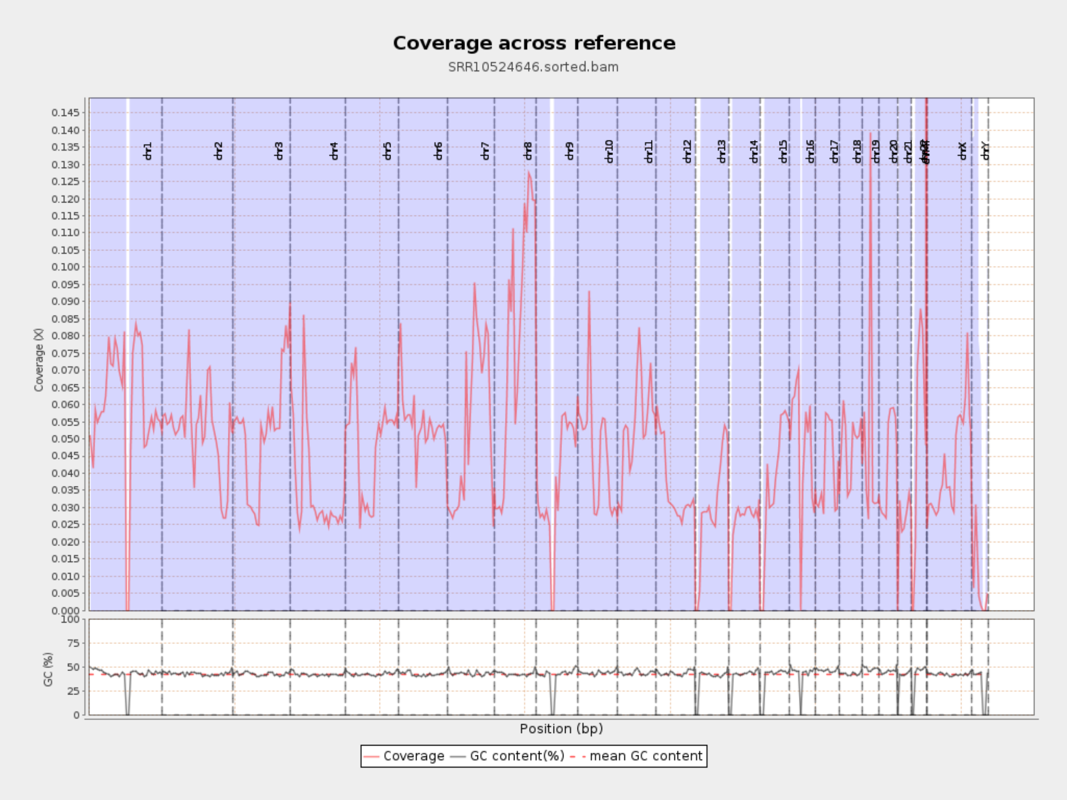
General error rate	0.52%
Mismatches	732,365
Insertions	11,148
Mapped reads with at least one insertion	0.45%
Deletions	27,763
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.2%

2.6. Chromosome stats

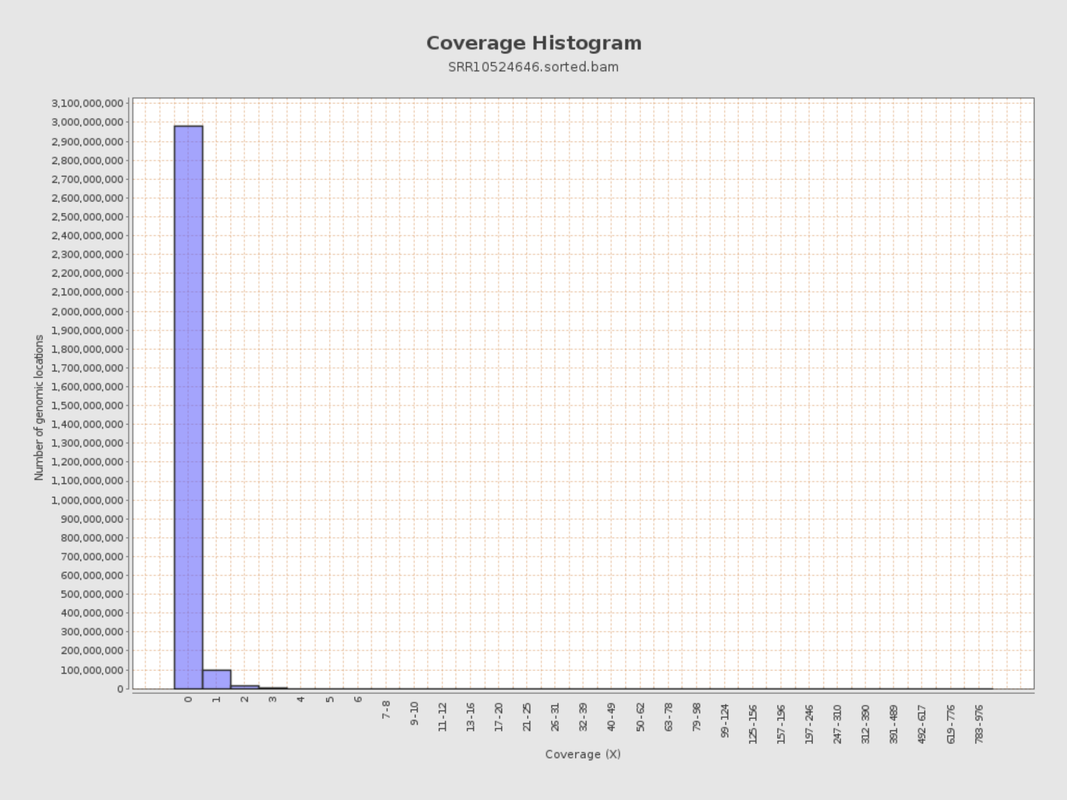
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14830964	0.0595	0.7479
chr2	243199373	12812386	0.0527	0.5108
chr3	198022430	10294533	0.052	0.2729
chr4	191154276	6679398	0.0349	0.3094
chr5	180915260	8854514	0.0489	0.265
chr6	171115067	9411560	0.055	0.3006
chr7	159138663	8726936	0.0548	0.4928

chr8	146364022	11700722	0.0799	0.5391
chr9	141213431	5162107	0.0366	0.3036
chr10	135534747	6222841	0.0459	0.4373
chr11	135006516	7304135	0.0541	0.3468
chr12	133851895	4799420	0.0359	0.2338
chr13	115169878	3429037	0.0298	0.2091
chr14	107349540	2628503	0.0245	0.1996
chr15	102531392	3796344	0.037	0.2324
chr16	90354753	4353375	0.0482	0.2846
chr17	81195210	3331532	0.041	0.261
chr18	78077248	3796238	0.0486	0.5367
chr19	59128983	2925395	0.0495	0.5107
chr20	63025520	2744266	0.0435	0.2631
chr21	48129895	1244644	0.0259	0.2627
chr22	51304566	2564696	0.05	0.2692
chrMT	16571	27611	1.6662	1.6306
chrX	155270560	6591647	0.0425	0.2728
chrY	59373566	435316	0.0073	0.2863

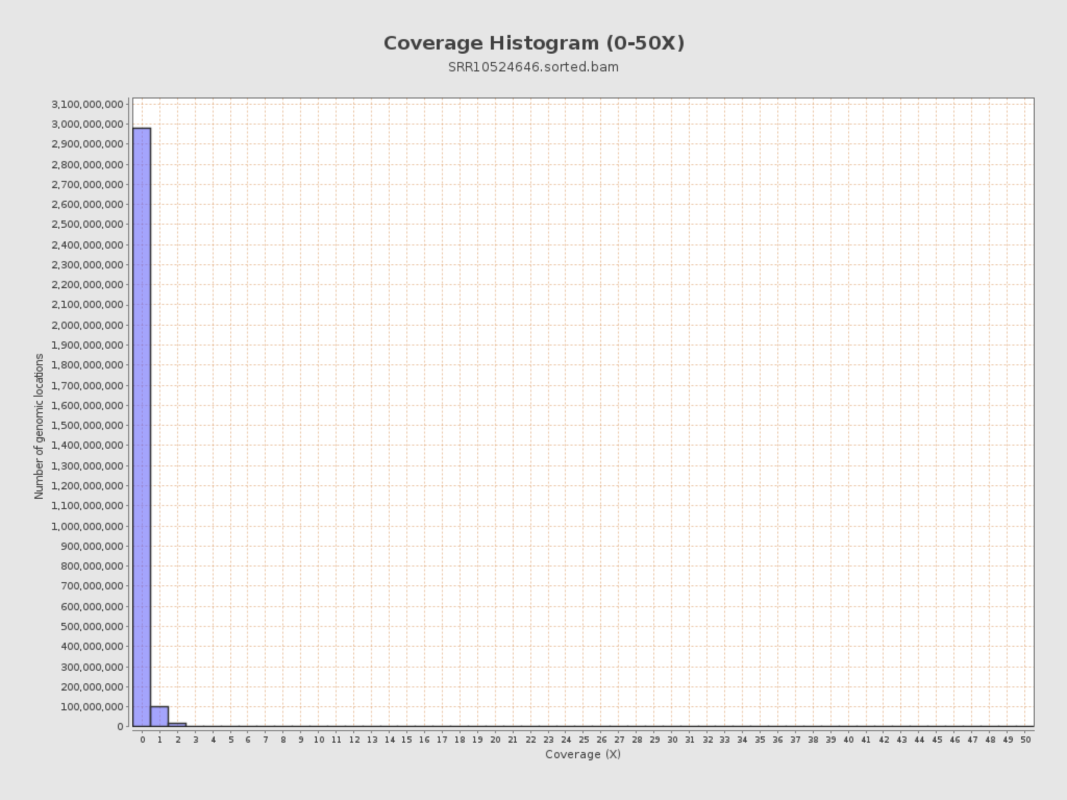
3. Results : Coverage across reference



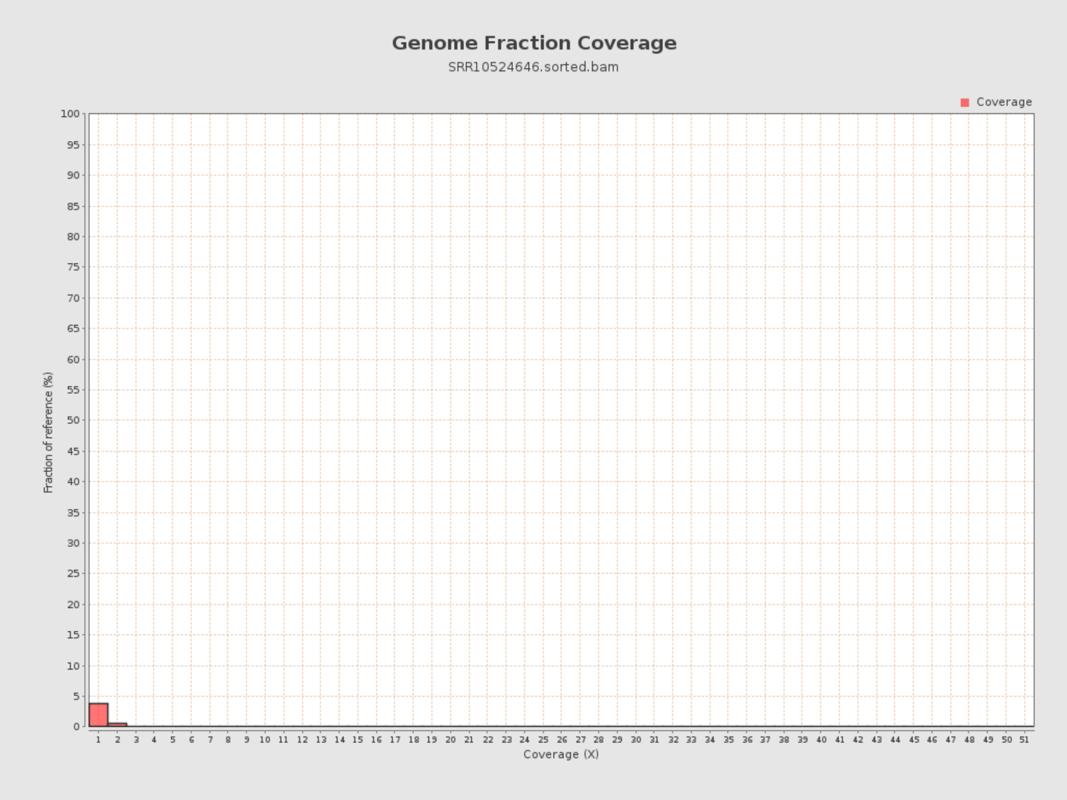
4. Results : Coverage Histogram



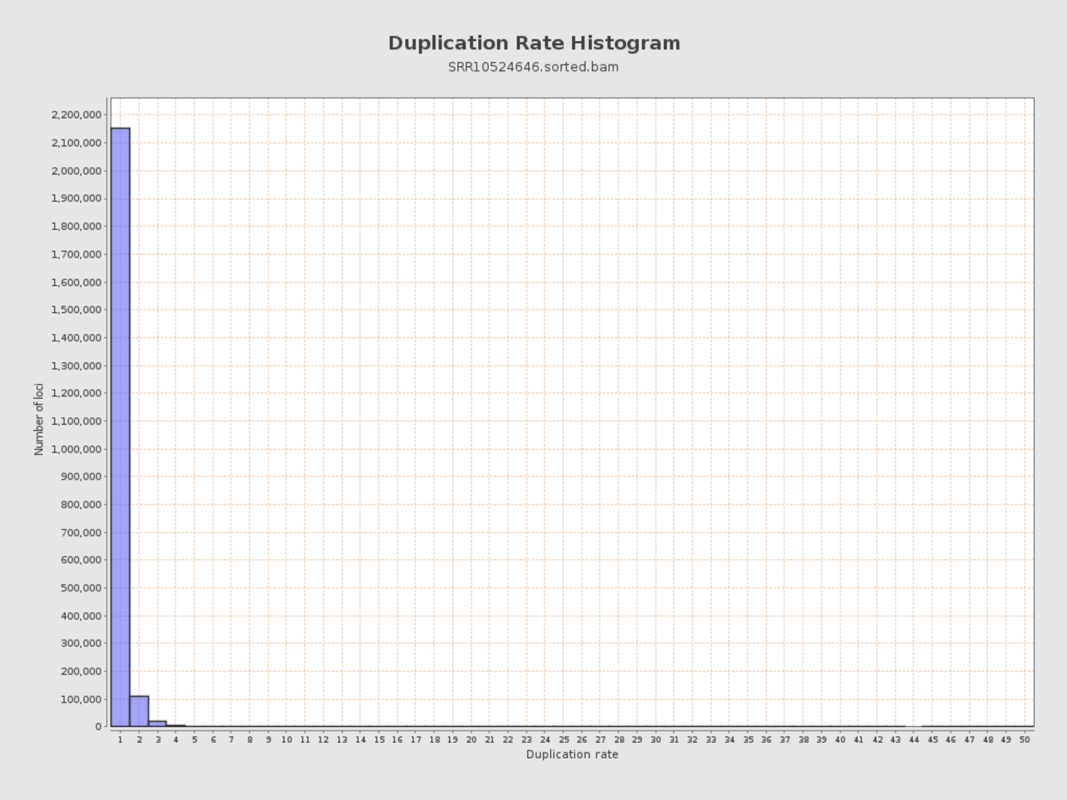
5. Results : Coverage Histogram (0-50X)



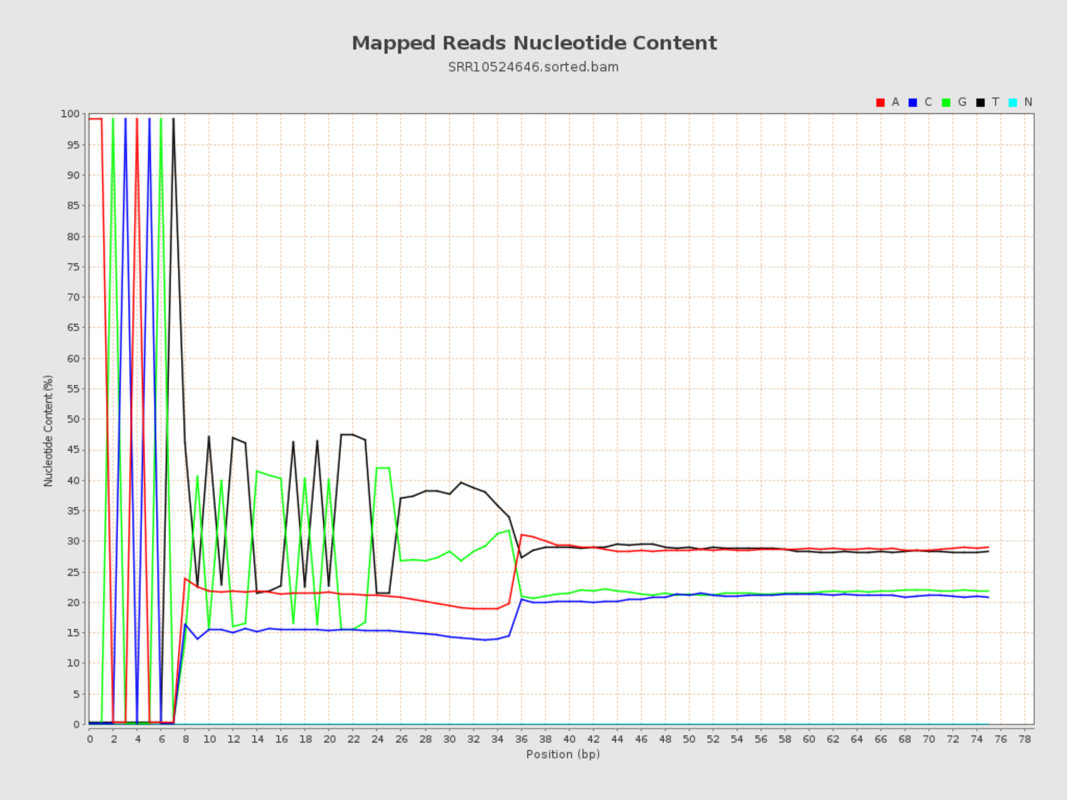
6. Results : Genome Fraction Coverage



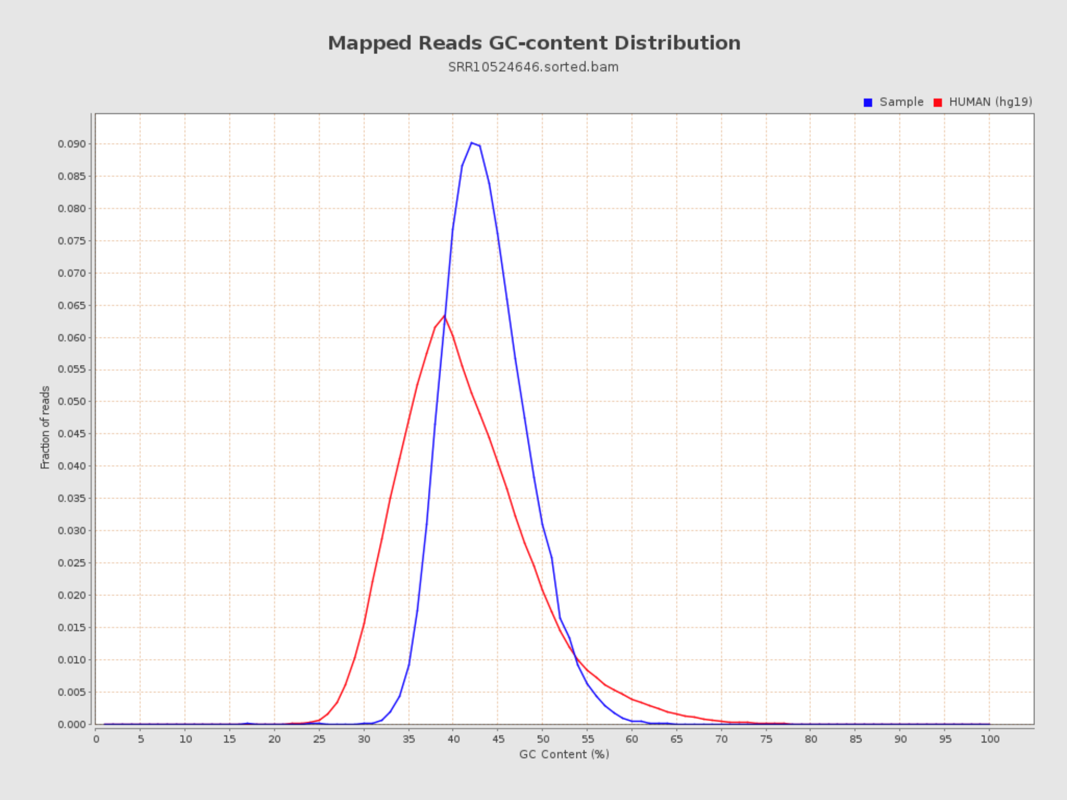
7. Results : Duplication Rate Histogram



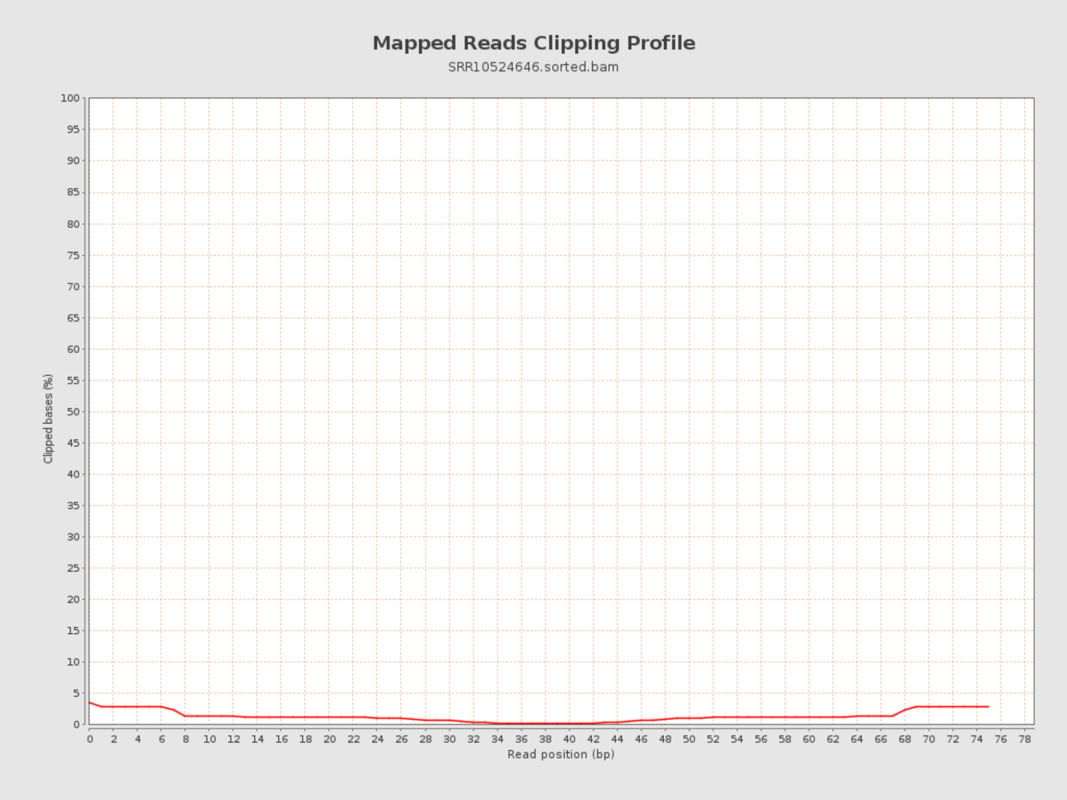
8. Results : Mapped Reads Nucleotide Content



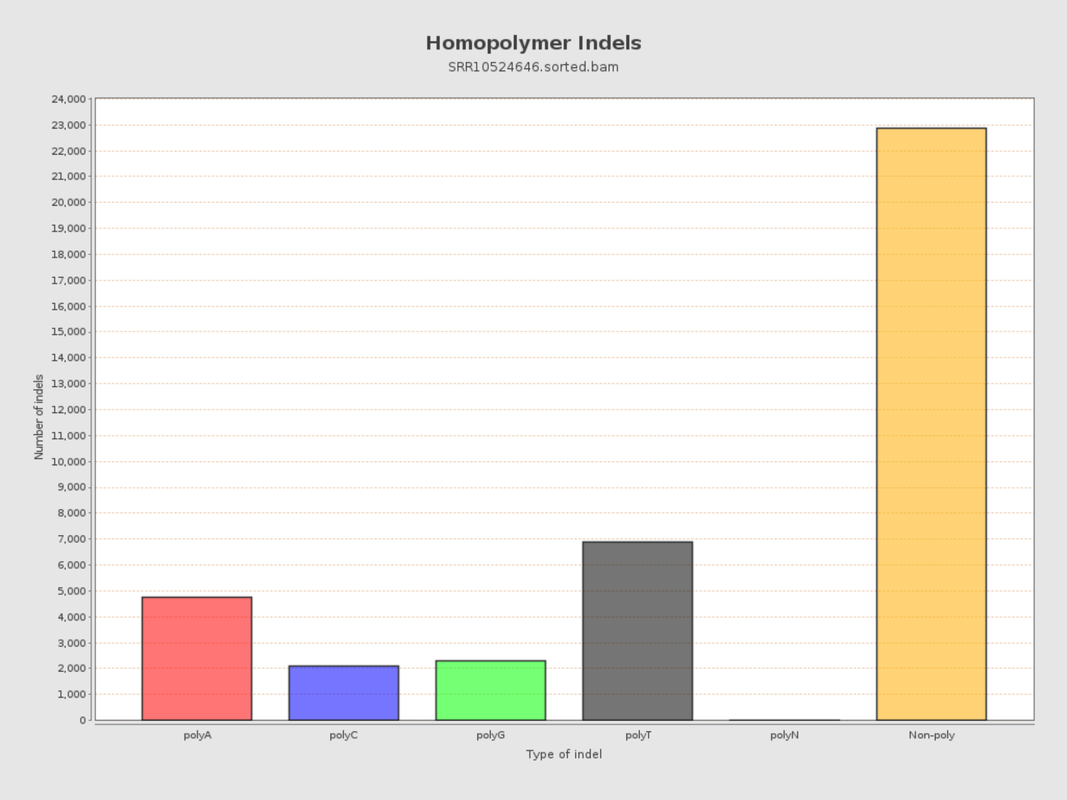
9. Results : Mapped Reads GC-content Distribution



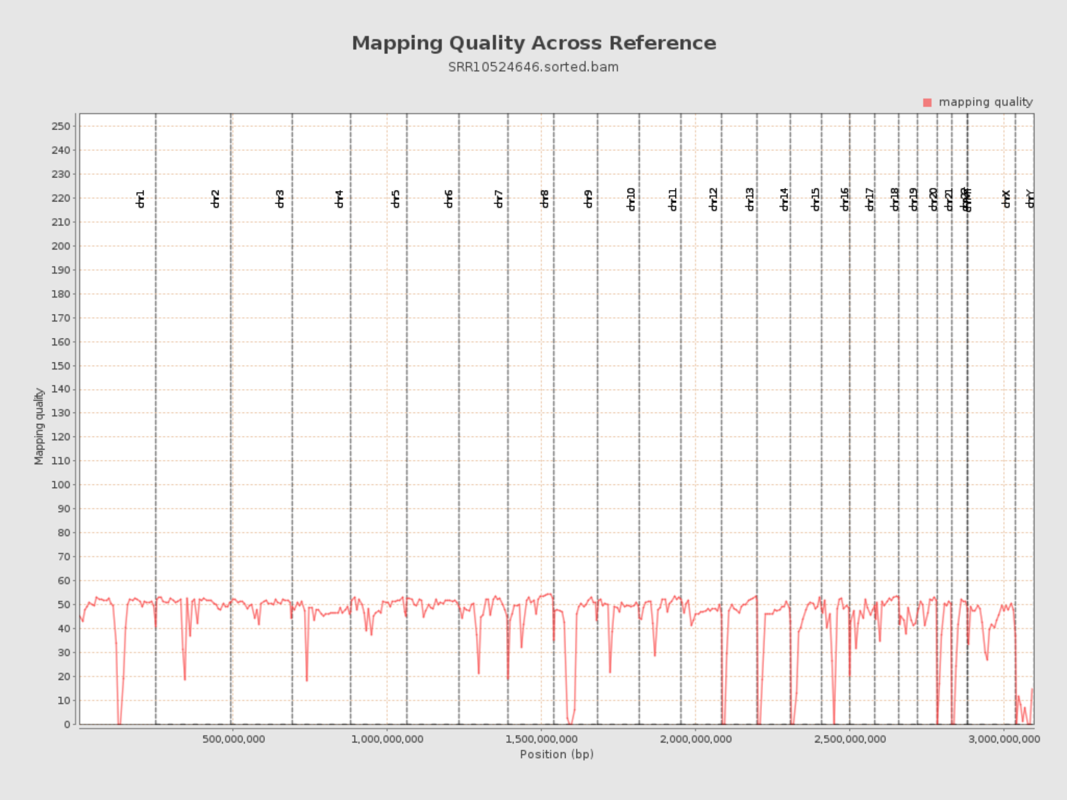
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram