Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 09:15:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524945.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_SRR10524945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 09:15:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,178,886
Mapped reads	2,905,820 / 91.41%
Unmapped reads	273,066 / 8.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,347 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	154,521 / 4.86%
Duplication rate	3.83%
Clipped reads	2,909,467 / 91.52%

2.2. ACGT Content

Number/percentage of A's	41,956,724 / 25.04%
Number/percentage of C's	32,485,472 / 19.39%
Number/percentage of T's	52,908,778 / 31.58%
Number/percentage of G's	40,204,028 / 23.99%
Number/percentage of N's	3,230 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0541

Standard Deviation	0.461

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

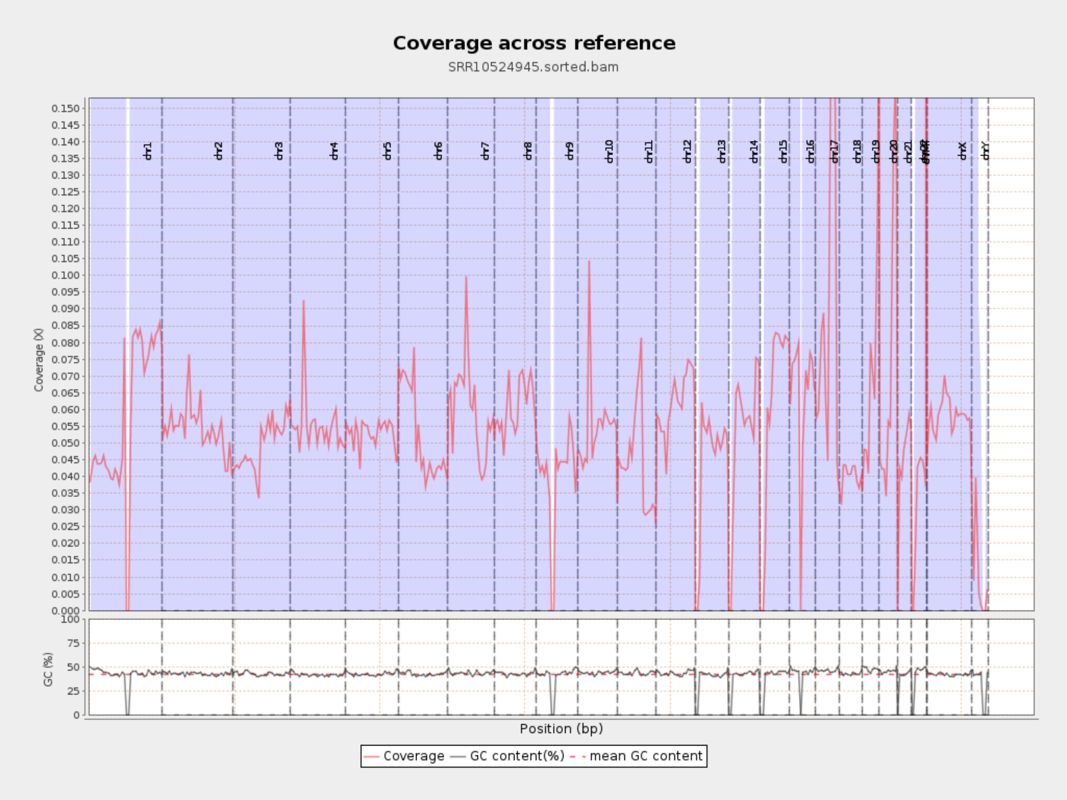
General error rate	0.53%
Mismatches	857,728
Insertions	11,508
Mapped reads with at least one insertion	0.39%
Deletions	33,130
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.99%

2.6. Chromosome stats

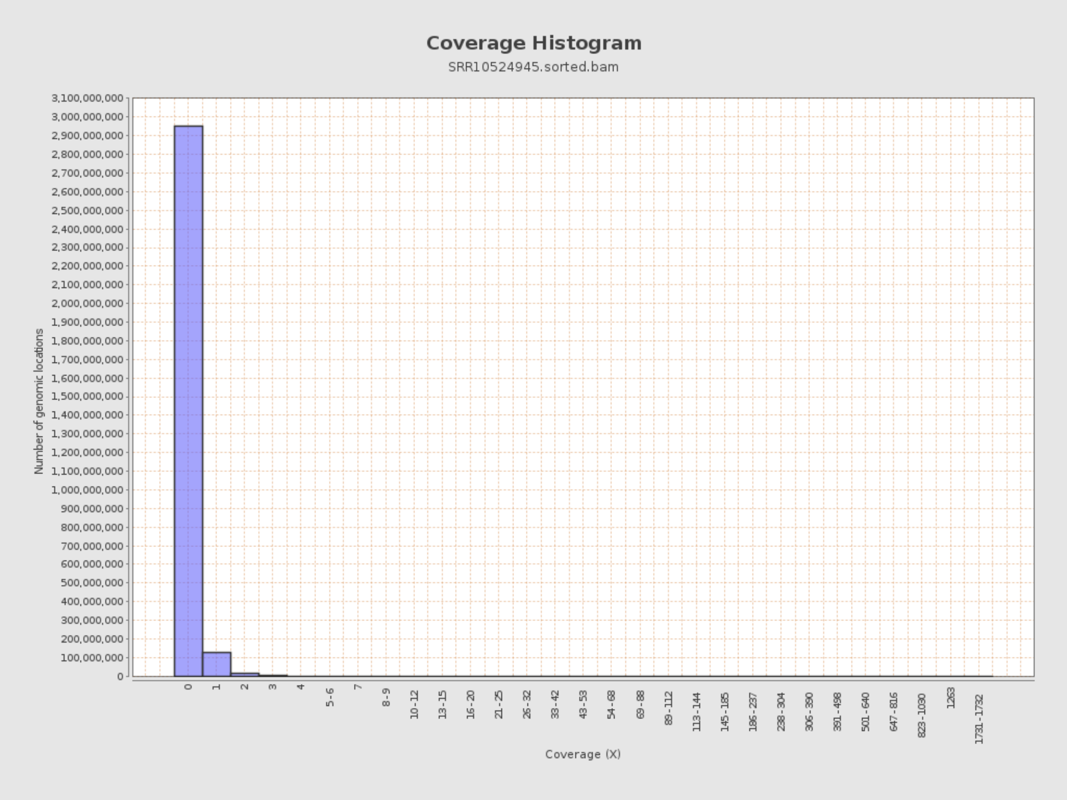
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14196354	0.057	0.7485
chr2	243199373	13249034	0.0545	0.7415
chr3	198022430	9720873	0.0491	0.2584
chr4	191154276	10479802	0.0548	0.3407
chr5	180915260	9549795	0.0528	0.2658
chr6	171115067	9010866	0.0527	0.3473
chr7	159138663	9614077	0.0604	0.644

chr8	146364022	8918250	0.0609	0.5886
chr9	141213431	5594744	0.0396	0.3088
chr10	135534747	7448343	0.055	0.4728
chr11	135006516	6055870	0.0449	0.3505
chr12	133851895	8347387	0.0624	0.292
chr13	115169878	5063395	0.044	0.2424
chr14	107349540	5561064	0.0518	0.2713
chr15	102531392	6157101	0.0601	0.2877
chr16	90354753	5817667	0.0644	0.3166
chr17	81195210	7400225	0.0911	0.3754
chr18	78077248	3119709	0.04	0.5592
chr19	59128983	4202856	0.0711	0.5896
chr20	63025520	4741922	0.0752	0.3336
chr21	48129895	2140195	0.0445	0.3017
chr22	51304566	1562121	0.0304	0.2
chrMT	16571	37838	2.2834	2.2172
chrX	155270560	9025802	0.0581	0.3127
chrY	59373566	596727	0.0101	0.4008

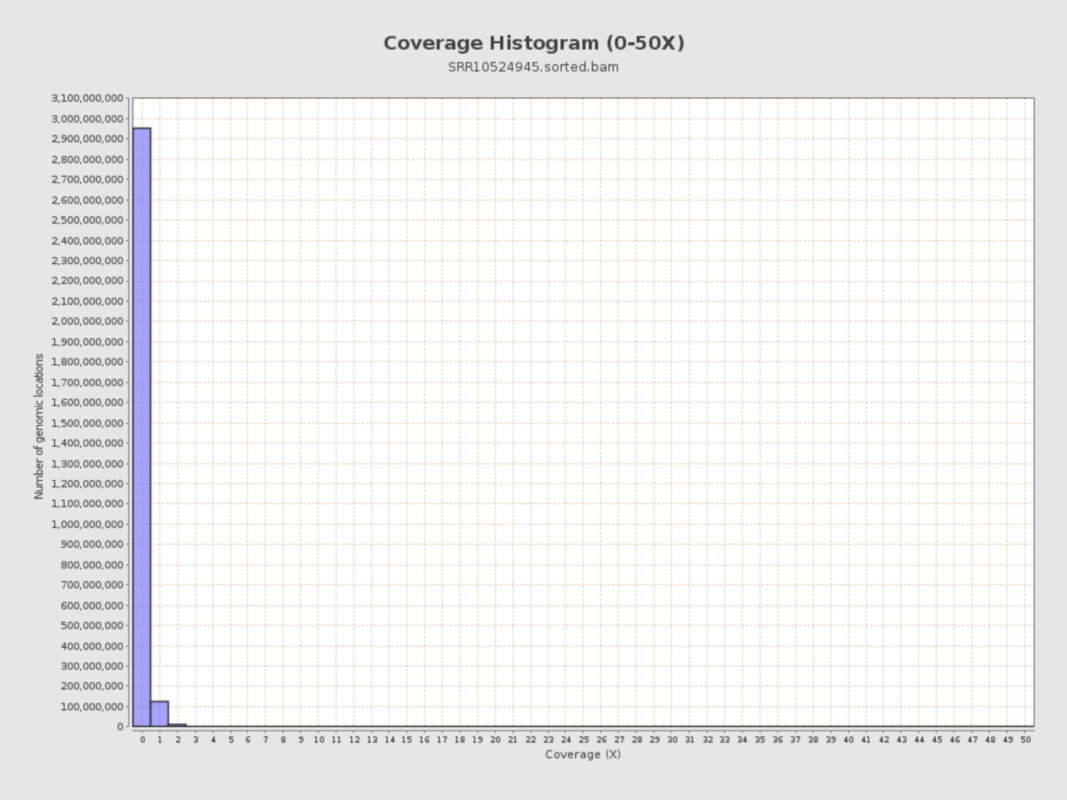
3. Results : Coverage across reference



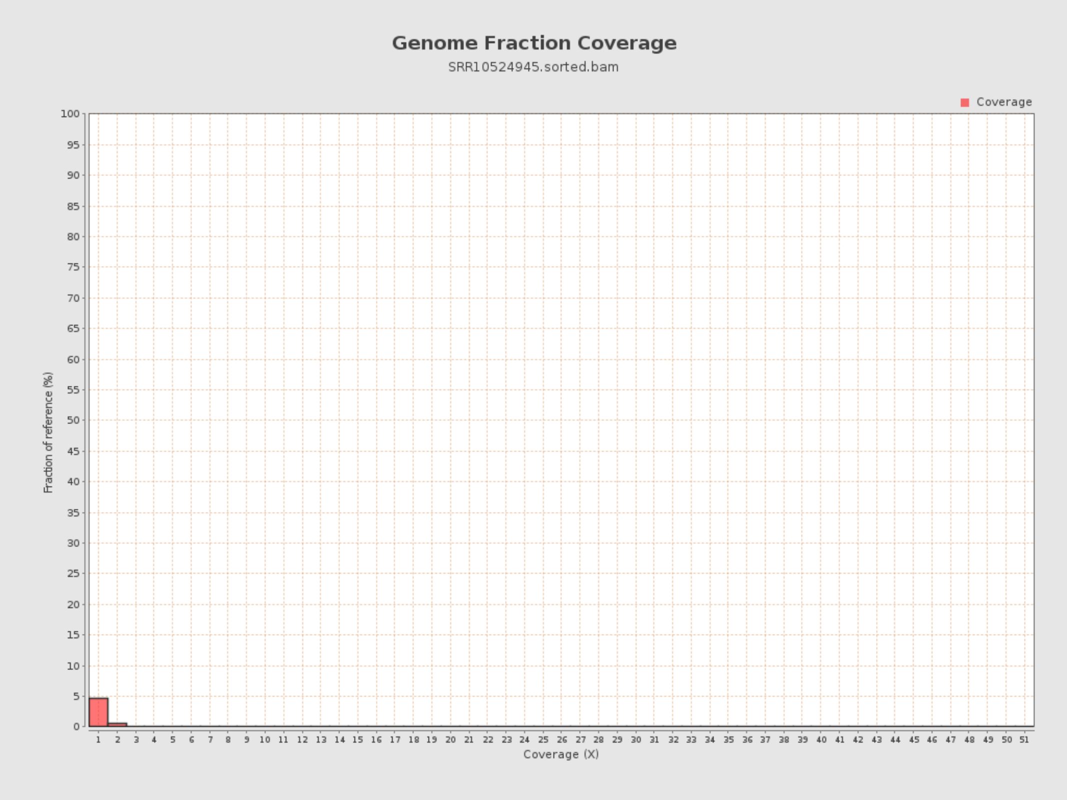
4. Results : Coverage Histogram



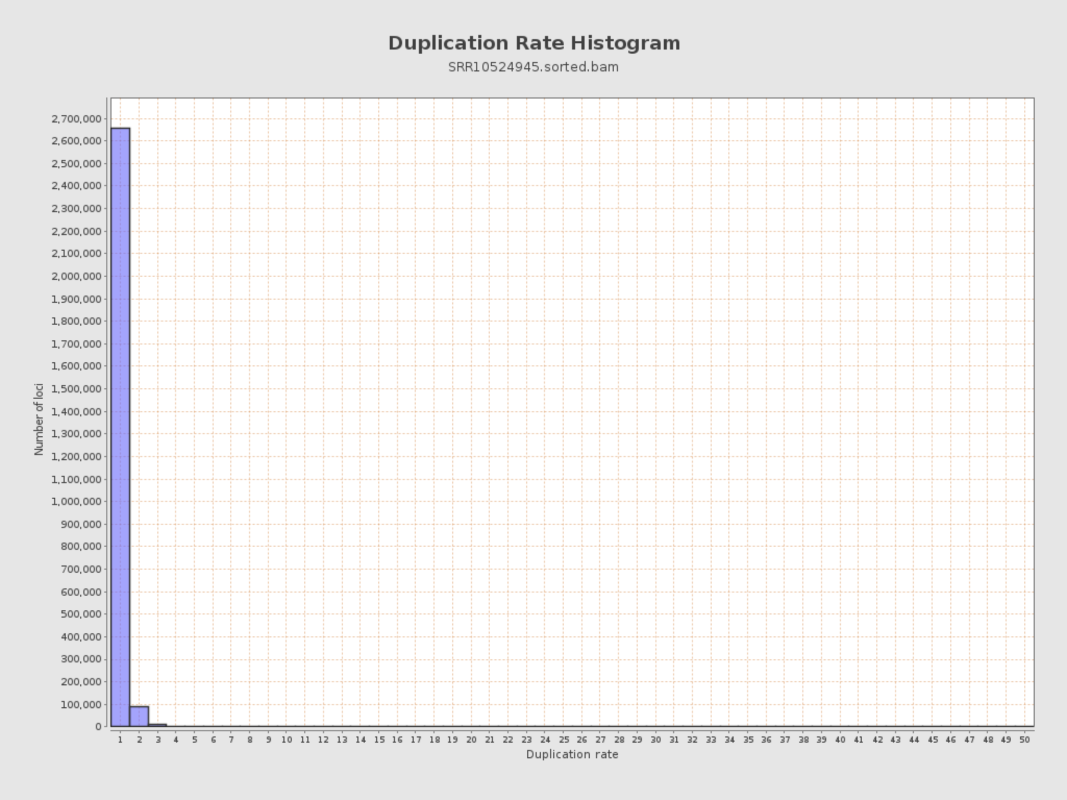
5. Results : Coverage Histogram (0-50X)



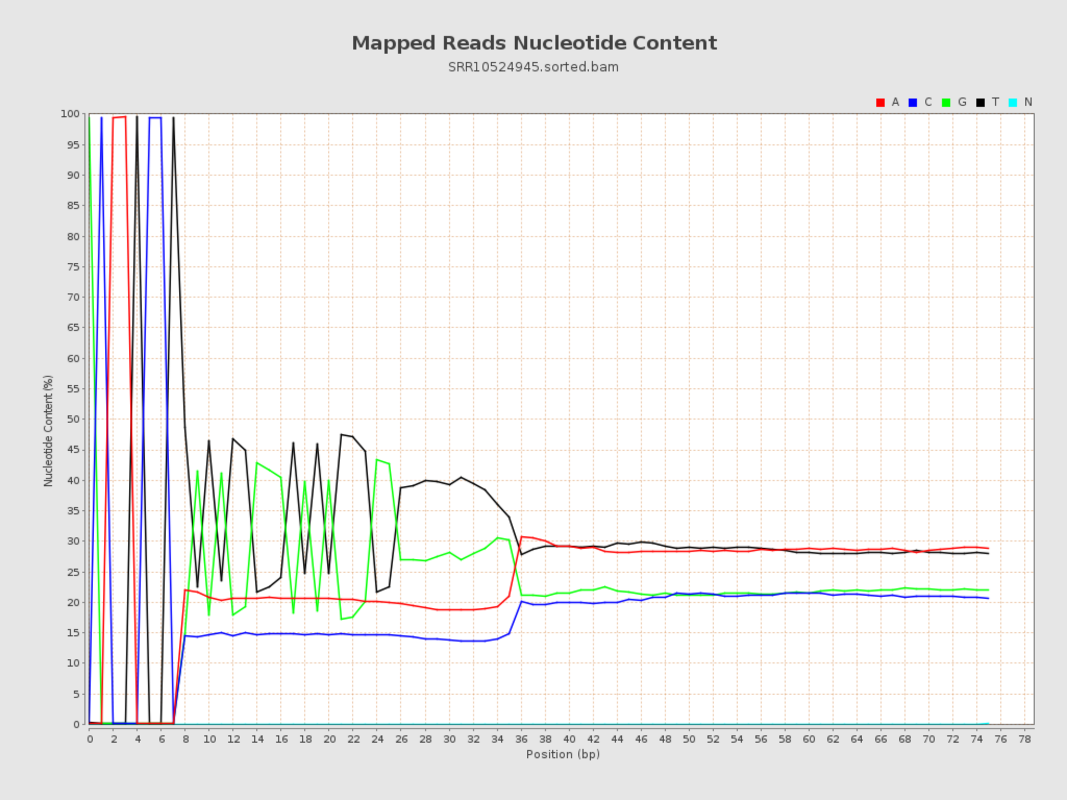
6. Results : Genome Fraction Coverage



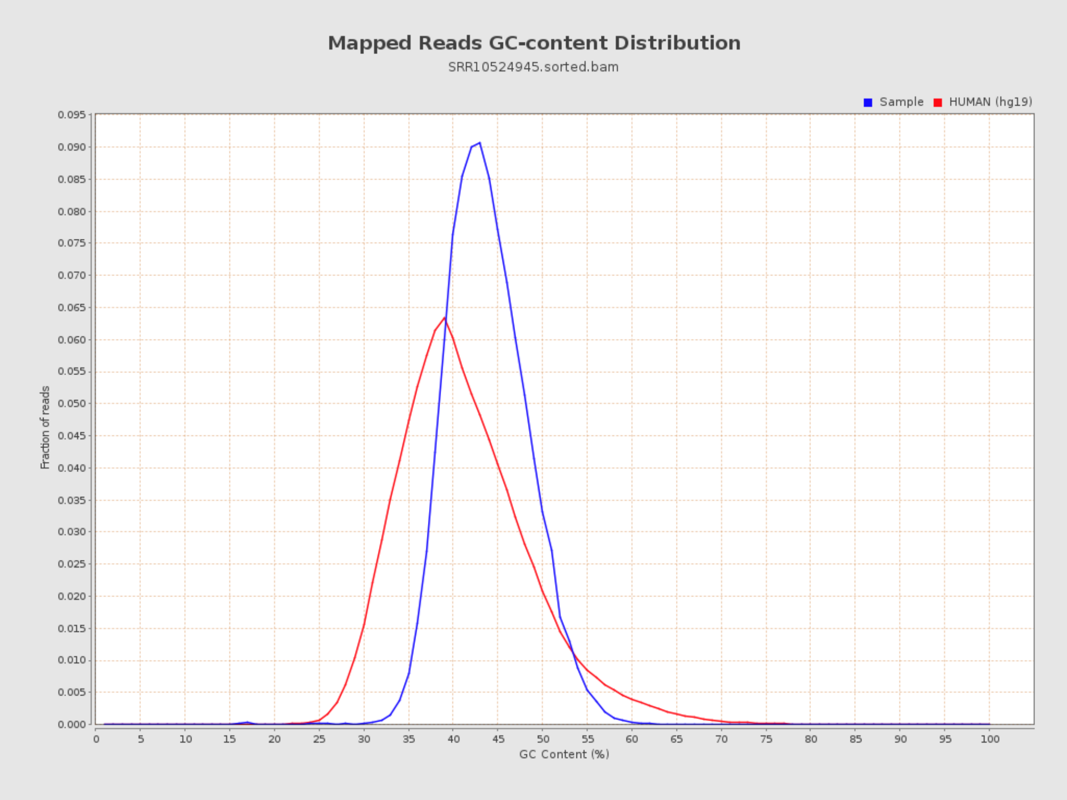
7. Results : Duplication Rate Histogram



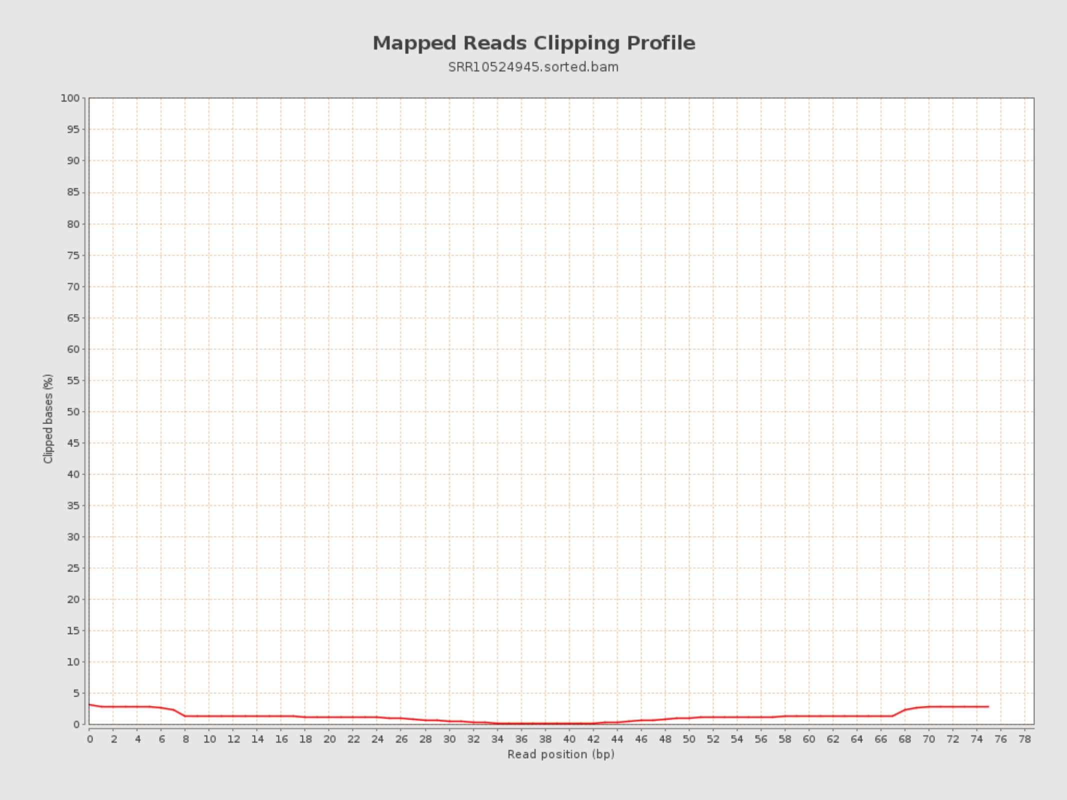
8. Results : Mapped Reads Nucleotide Content



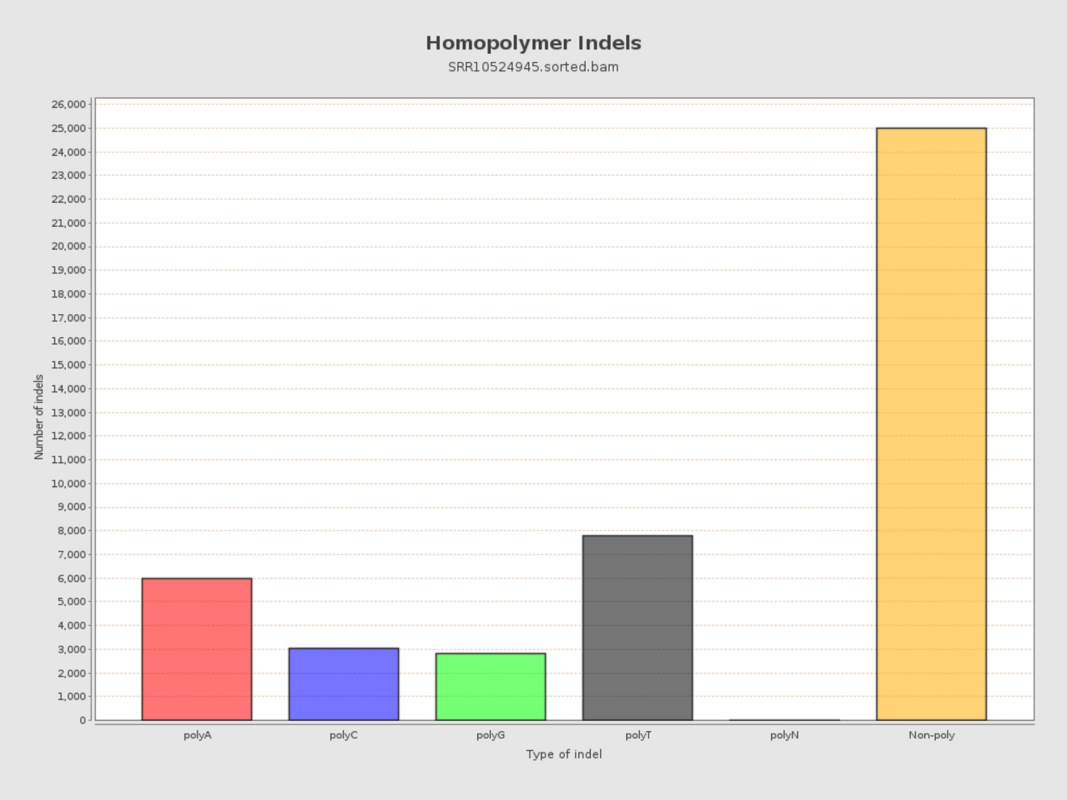
9. Results : Mapped Reads GC-content Distribution



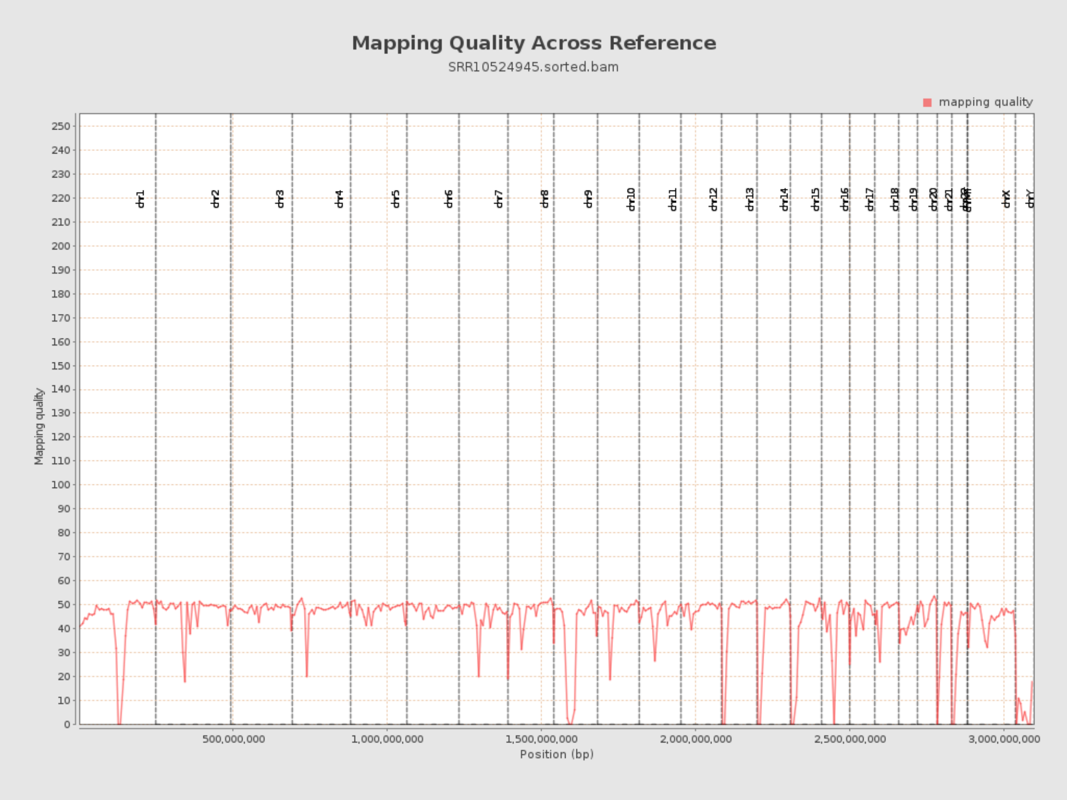
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram