Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:45:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525200.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_SRR10525200 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525200.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:45:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,271,906
Mapped reads	1,166,892 / 91.74%
Unmapped reads	105,014 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,001 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	29,955 / 2.36%
Duplication rate	1.76%
Clipped reads	1,166,556 / 91.72%

2.2. ACGT Content

Number/percentage of A's	17,915,177 / 25.76%
Number/percentage of C's	14,212,661 / 20.44%
Number/percentage of T's	22,060,050 / 31.72%
Number/percentage of G's	15,352,926 / 22.08%
Number/percentage of N's	1,696 / 0%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2263

2.4. Mapping Quality

Mean Mapping Quality	45.03

2.5. Mismatches and indels

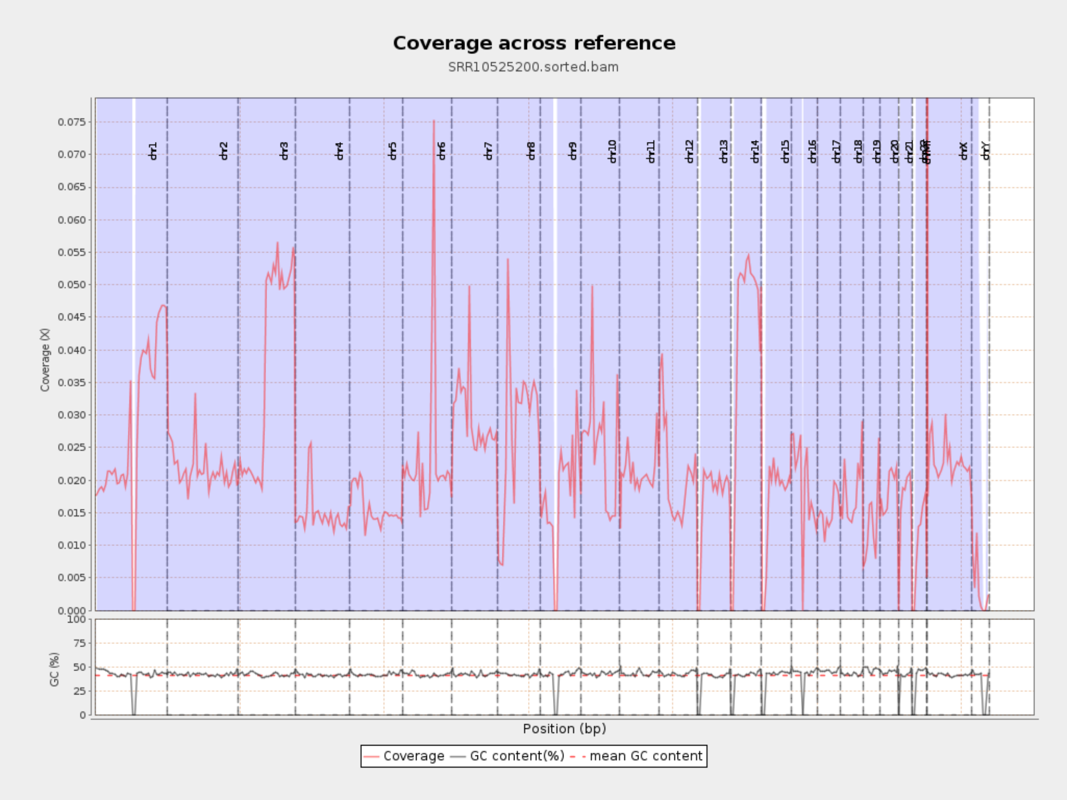
General error rate	0.51%
Mismatches	345,352
Insertions	5,683
Mapped reads with at least one insertion	0.49%
Deletions	14,762
Mapped reads with at least one deletion	1.26%
Homopolymer indels	42.81%

2.6. Chromosome stats

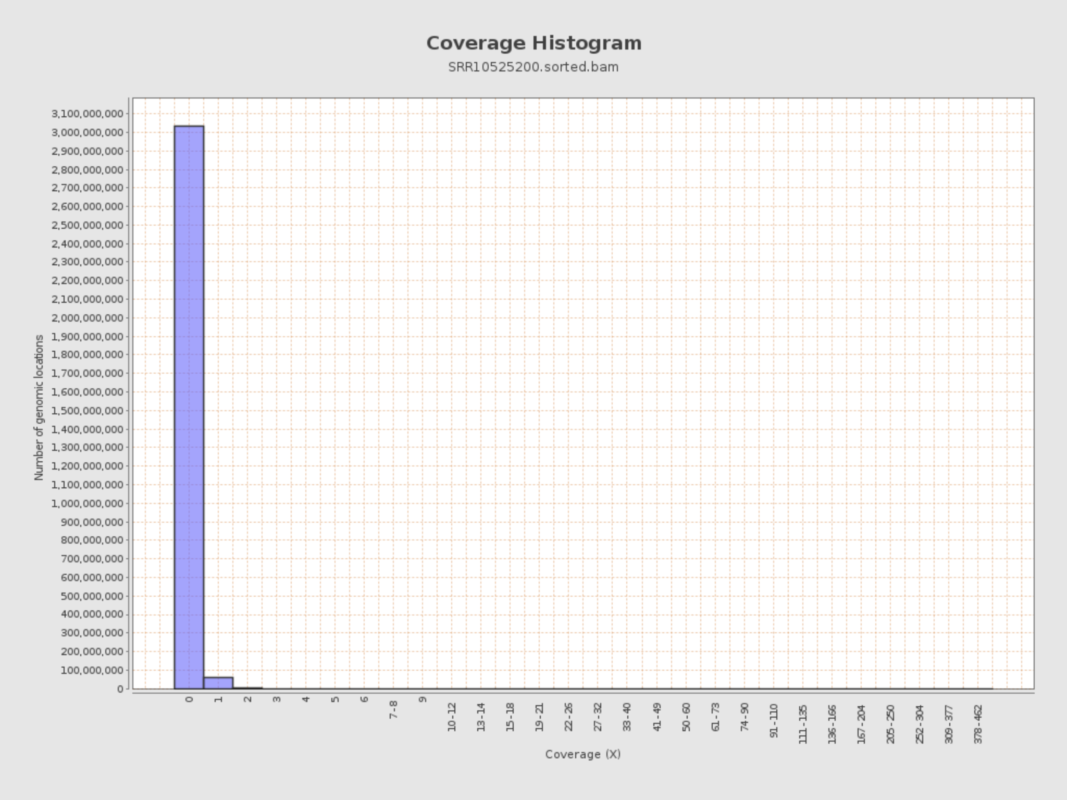
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6986576	0.028	0.3395
chr2	243199373	5316383	0.0219	0.2646
chr3	198022430	7353871	0.0371	0.2045
chr4	191154276	2848050	0.0149	0.1372
chr5	180915260	2856121	0.0158	0.1325
chr6	171115067	4057960	0.0237	0.1751
chr7	159138663	4739688	0.0298	0.403

chr8	146364022	4140825	0.0283	0.2323
chr9	141213431	2502229	0.0177	0.1769
chr10	135534747	3451628	0.0255	0.2545
chr11	135006516	2856987	0.0212	0.2104
chr12	133851895	2823591	0.0211	0.1554
chr13	115169878	1977142	0.0172	0.1377
chr14	107349540	4495598	0.0419	0.2185
chr15	102531392	1678631	0.0164	0.1374
chr16	90354753	1716365	0.019	0.1613
chr17	81195210	1241248	0.0153	0.1334
chr18	78077248	1381046	0.0177	0.3659
chr19	59128983	792598	0.0134	0.2523
chr20	63025520	1157513	0.0184	0.1451
chr21	48129895	816936	0.017	0.1459
chr22	51304566	533791	0.0104	0.1072
chrMT	16571	80951	4.8851	3.4389
chrX	155270560	3555249	0.0229	0.1712
chrY	59373566	205063	0.0035	0.1178

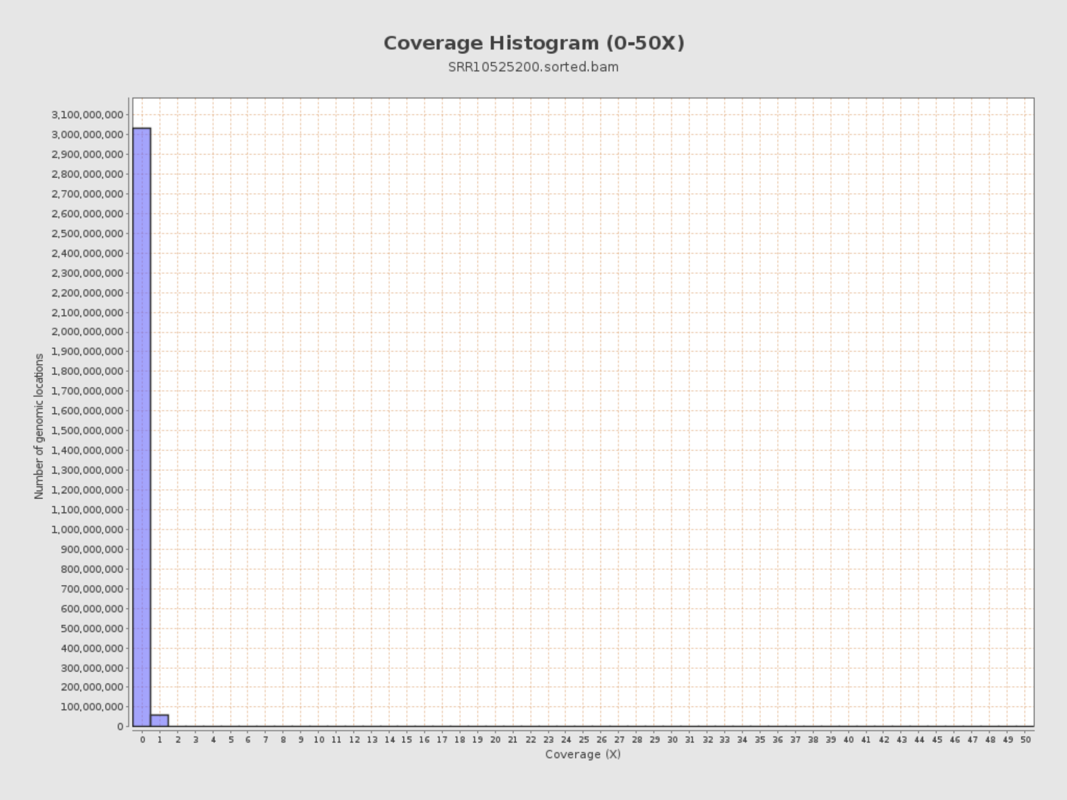
3. Results : Coverage across reference



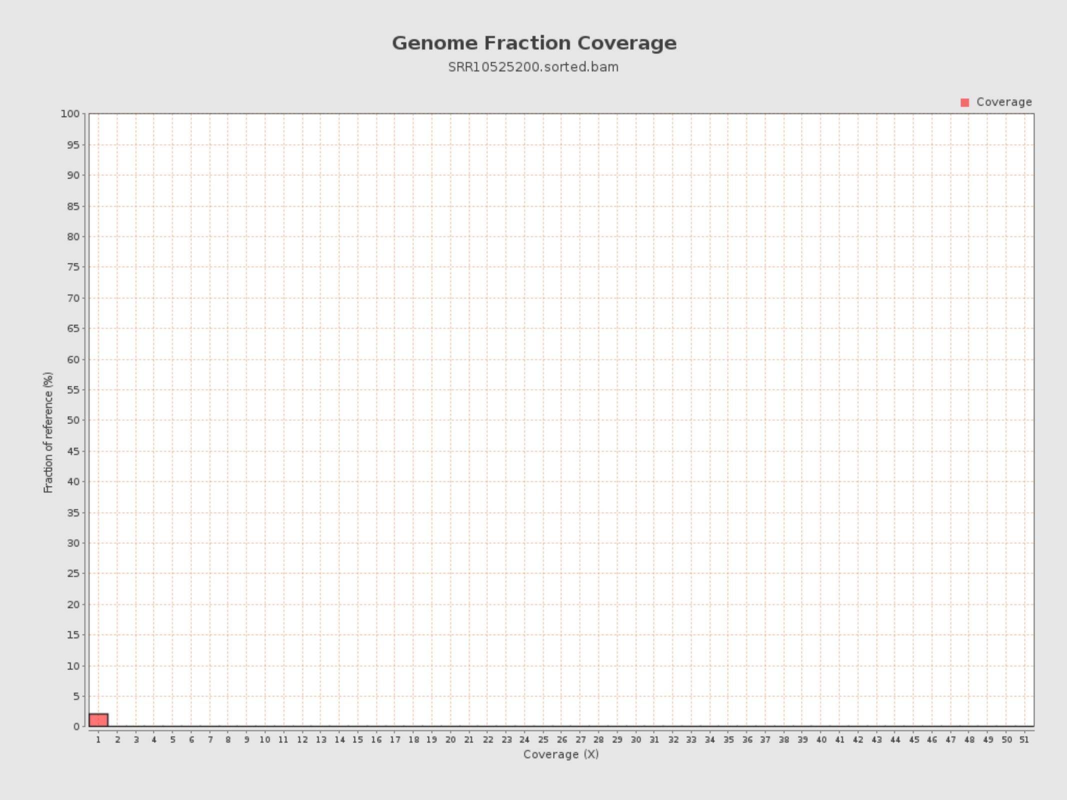
4. Results : Coverage Histogram



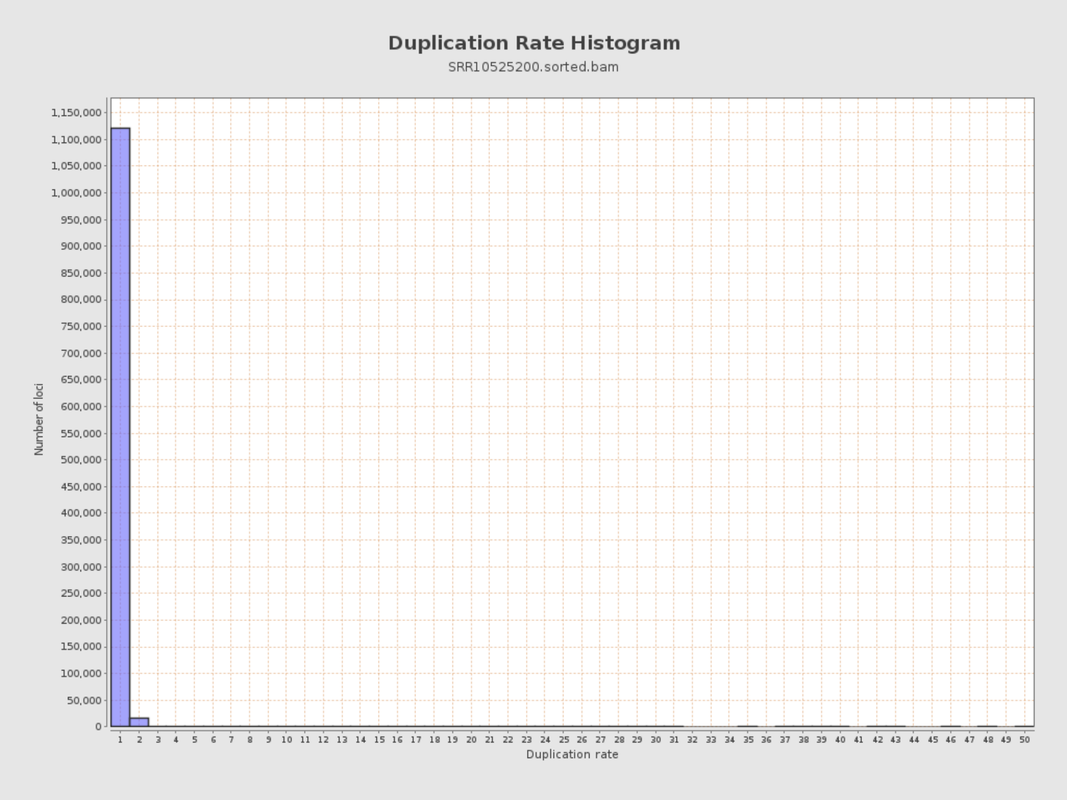
5. Results : Coverage Histogram (0-50X)



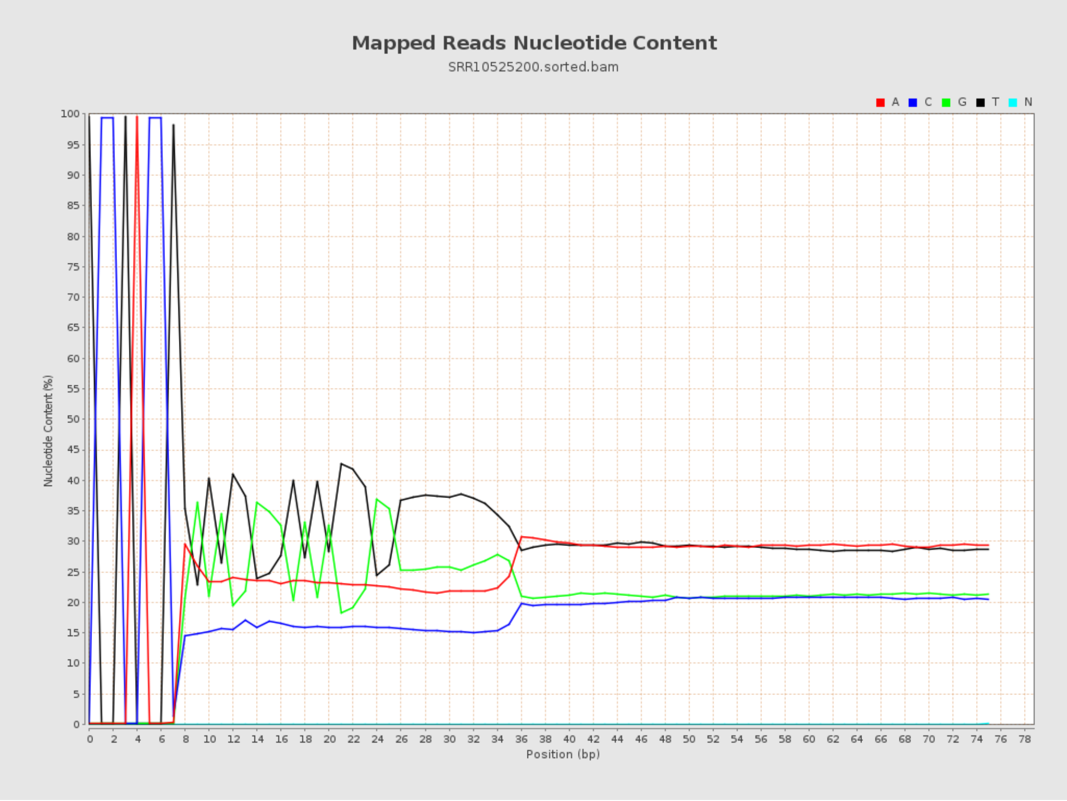
6. Results : Genome Fraction Coverage



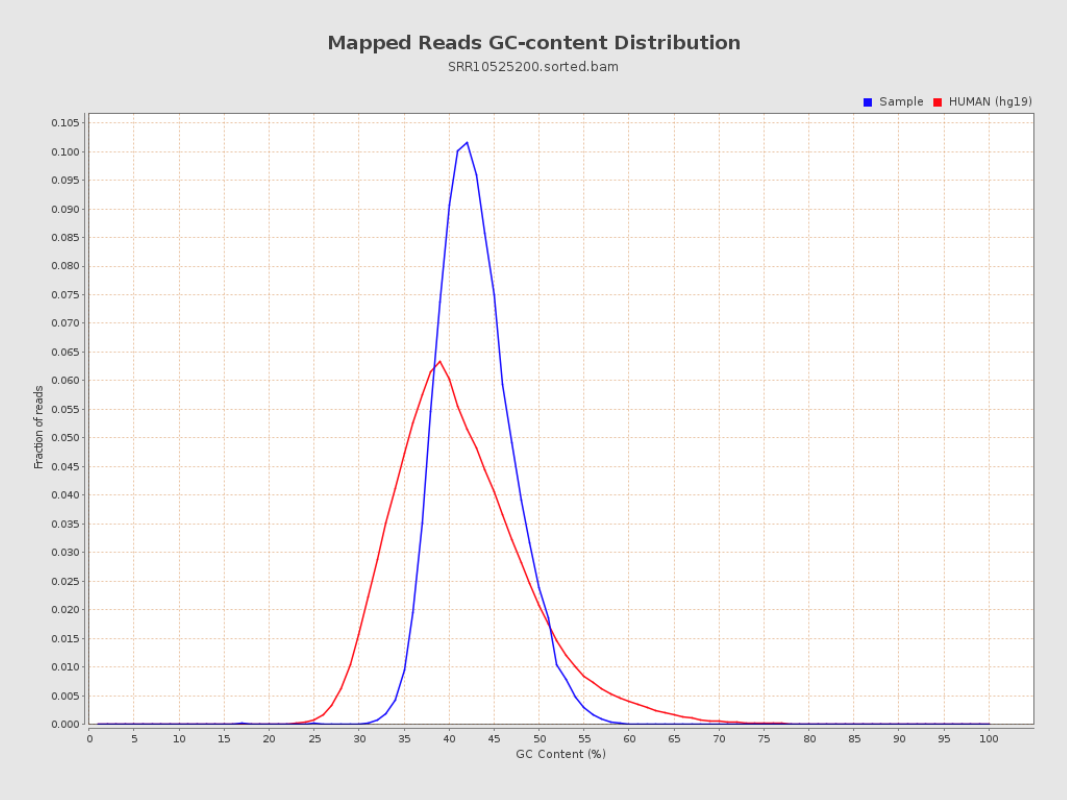
7. Results : Duplication Rate Histogram



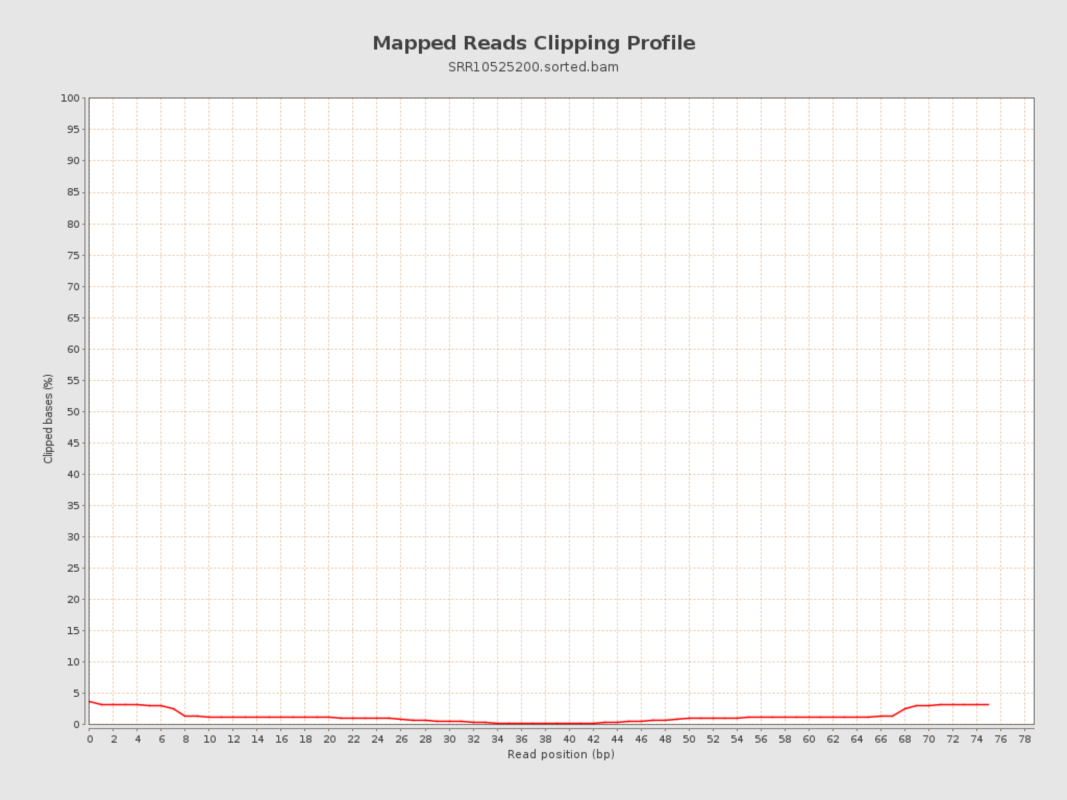
8. Results : Mapped Reads Nucleotide Content



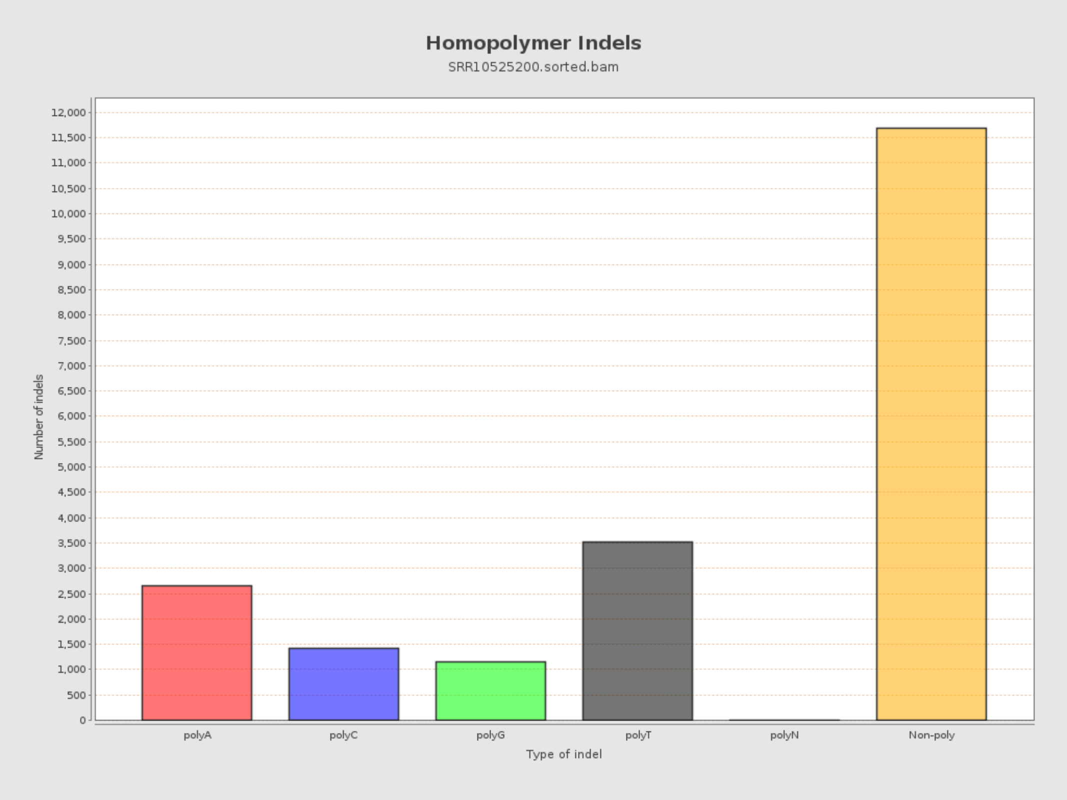
9. Results : Mapped Reads GC-content Distribution



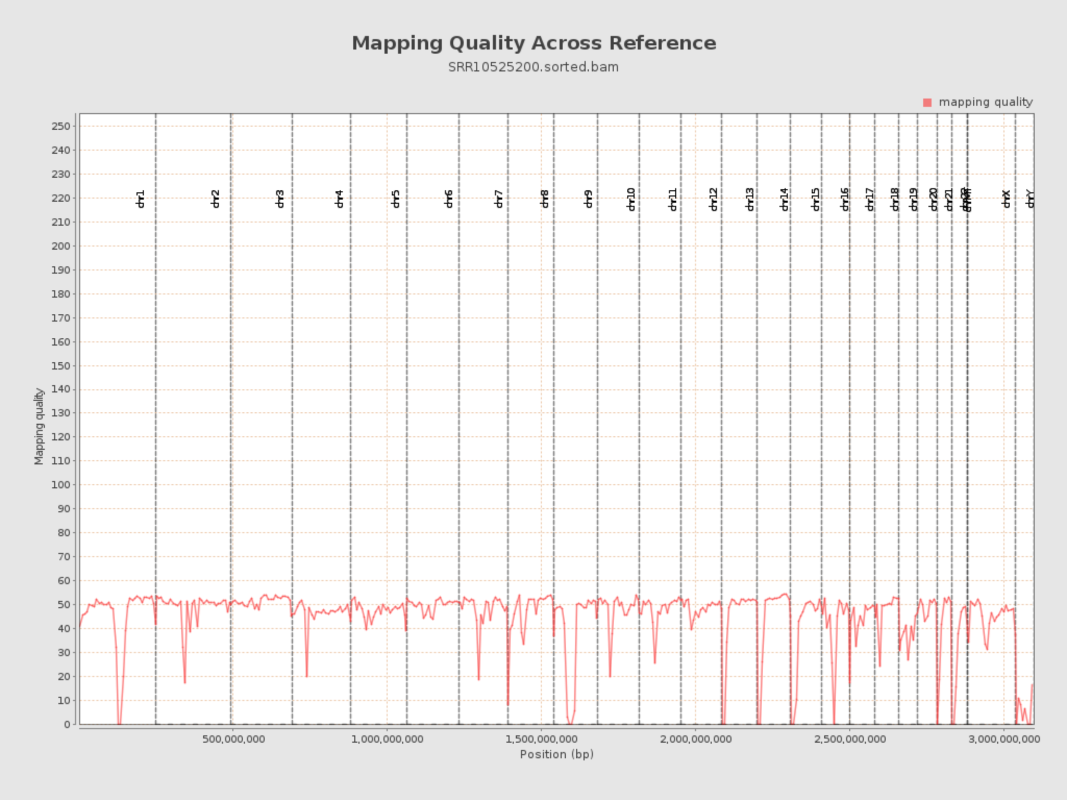
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram