Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:55:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525084.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_SRR10525084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:55:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,016,873
Mapped reads	844,704 / 83.07%
Unmapped reads	172,169 / 16.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,838 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	51,510 / 5.07%
Duplication rate	5.01%
Clipped reads	844,591 / 83.06%

2.2. ACGT Content

Number/percentage of A's	12,172,391 / 24.7%
Number/percentage of C's	9,644,313 / 19.57%
Number/percentage of T's	16,244,977 / 32.96%
Number/percentage of G's	11,215,519 / 22.76%
Number/percentage of N's	5,037 / 0.01%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0159

Standard Deviation	0.1825

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

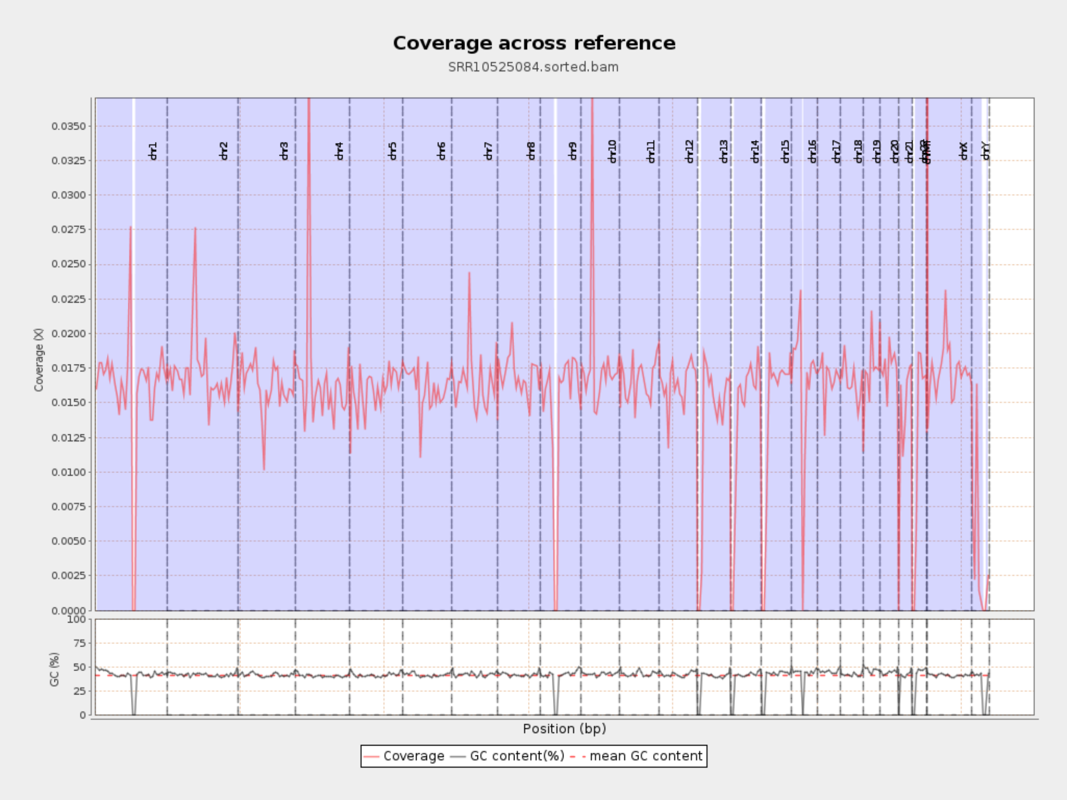
General error rate	0.52%
Mismatches	246,265
Insertions	3,617
Mapped reads with at least one insertion	0.43%
Deletions	10,079
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.68%

2.6. Chromosome stats

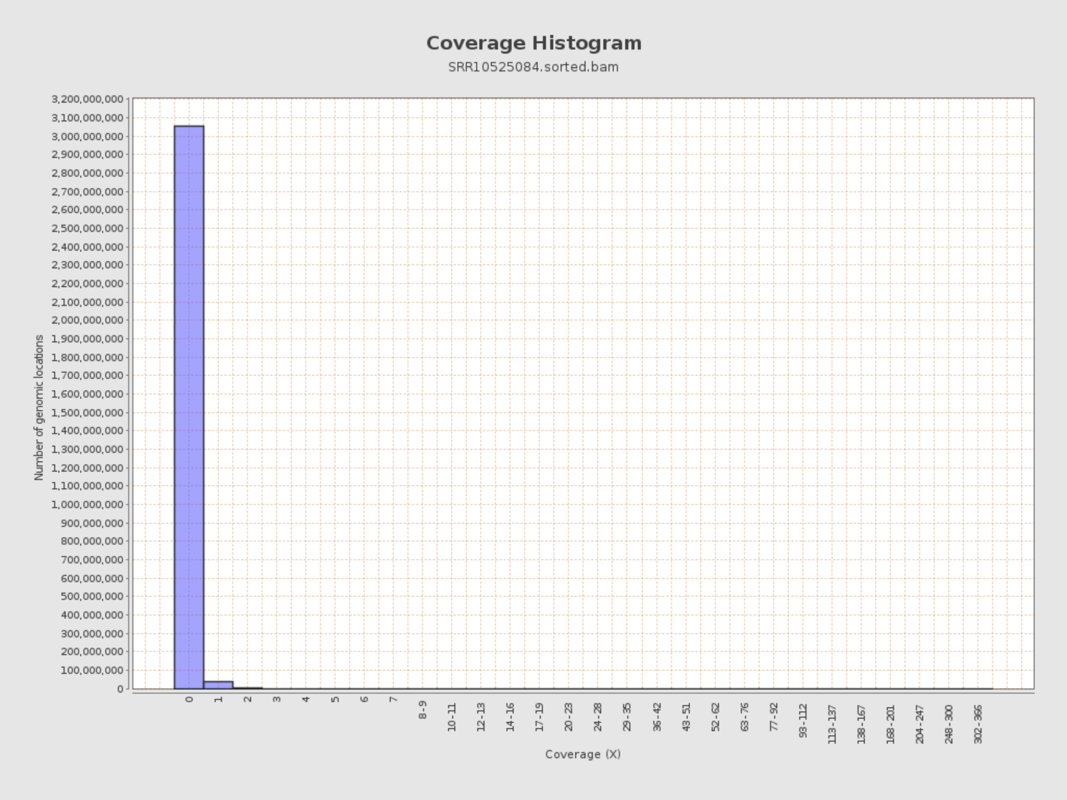
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3969395	0.0159	0.2873
chr2	243199373	4216063	0.0173	0.23
chr3	198022430	3211441	0.0162	0.1406
chr4	191154276	3230618	0.0169	0.1824
chr5	180915260	2913113	0.0161	0.1409
chr6	171115067	2762543	0.0161	0.1458
chr7	159138663	2650939	0.0167	0.1823

chr8	146364022	2494136	0.017	0.2016
chr9	141213431	2079655	0.0147	0.1538
chr10	135534747	2445394	0.018	0.2319
chr11	135006516	2246746	0.0166	0.1569
chr12	133851895	2189263	0.0164	0.1439
chr13	115169878	1532552	0.0133	0.1278
chr14	107349540	1472524	0.0137	0.1304
chr15	102531392	1433344	0.014	0.1312
chr16	90354753	1459773	0.0162	0.1454
chr17	81195210	1362067	0.0168	0.1482
chr18	78077248	1286192	0.0165	0.211
chr19	59128983	1030716	0.0174	0.2059
chr20	63025520	1102632	0.0175	0.1522
chr21	48129895	669146	0.0139	0.1584
chr22	51304566	622642	0.0121	0.1224
chrMT	16571	8696	0.5248	0.8098
chrX	155270560	2690287	0.0173	0.1545
chrY	59373566	218682	0.0037	0.1749

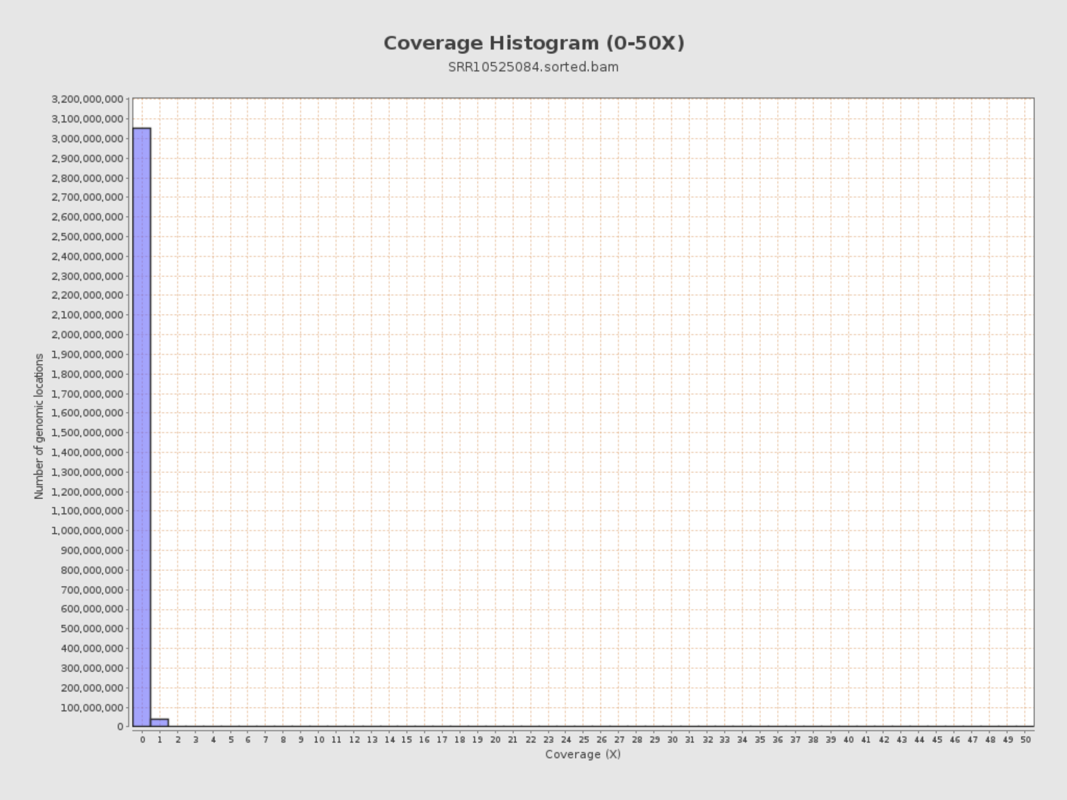
3. Results : Coverage across reference



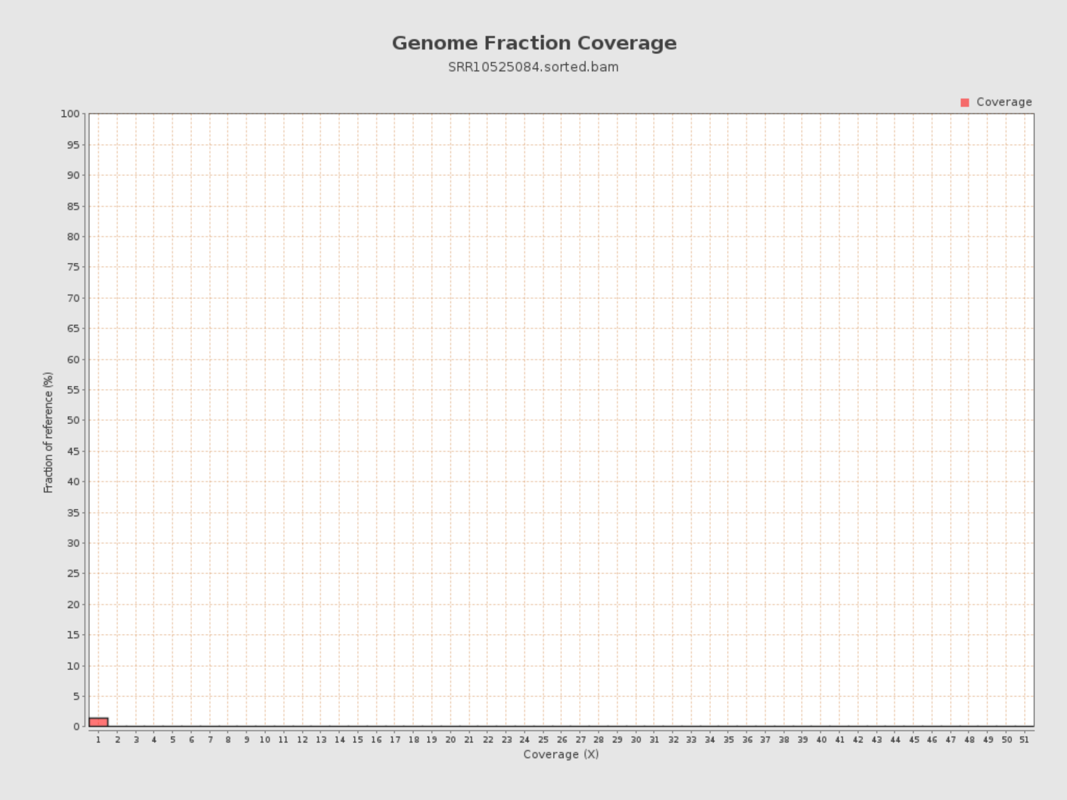
4. Results : Coverage Histogram



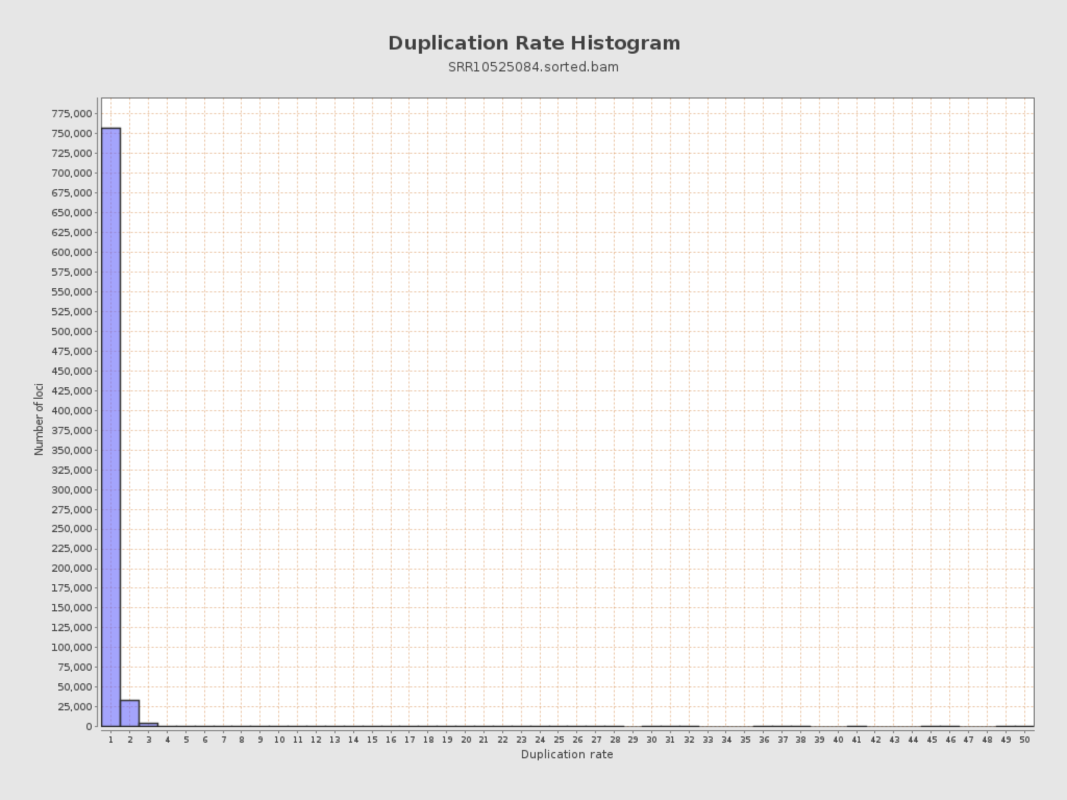
5. Results : Coverage Histogram (0-50X)



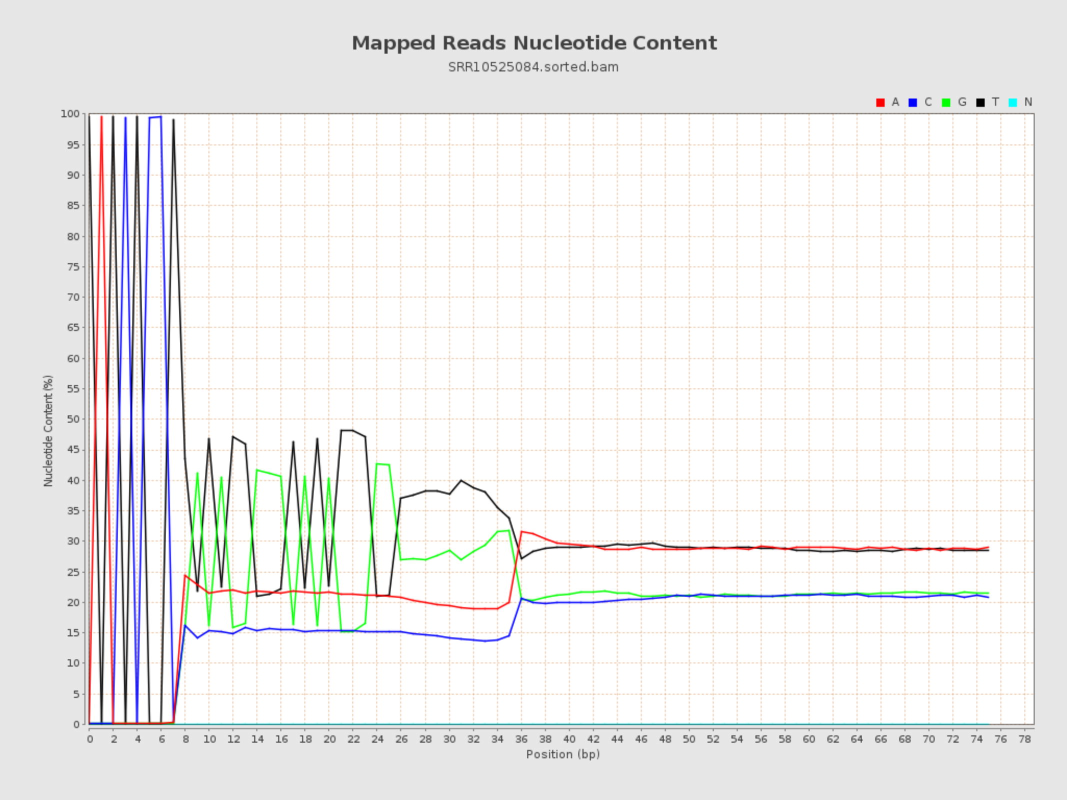
6. Results : Genome Fraction Coverage



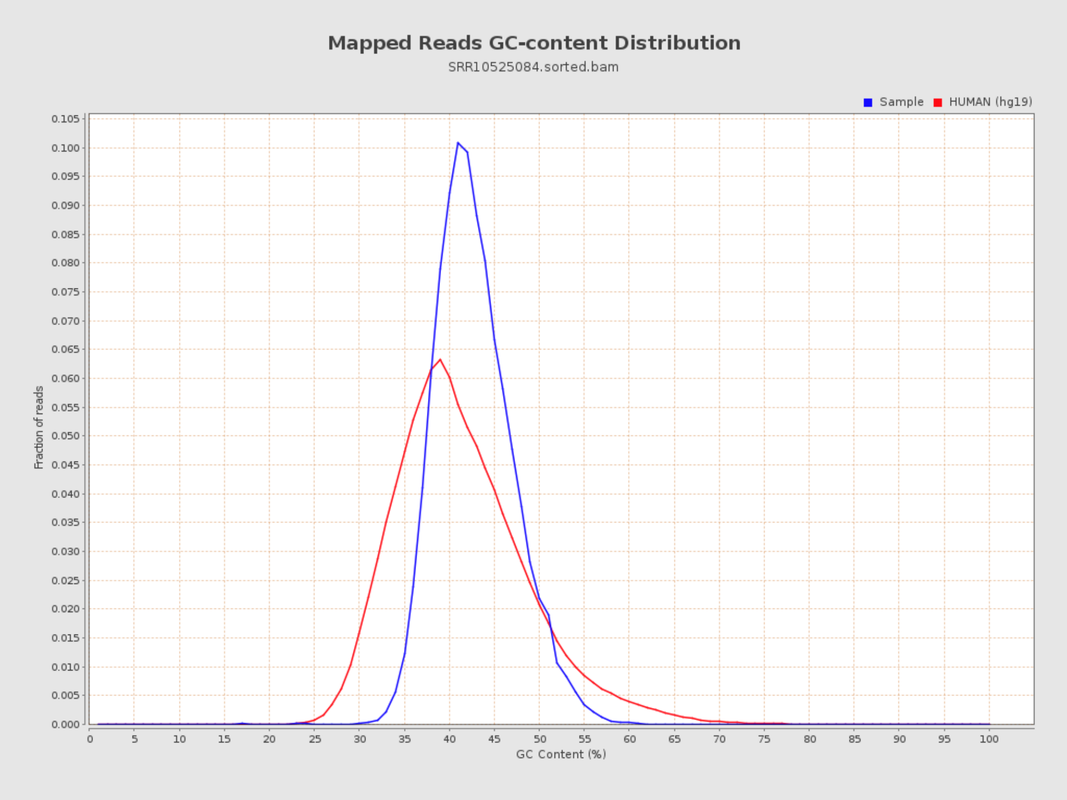
7. Results : Duplication Rate Histogram



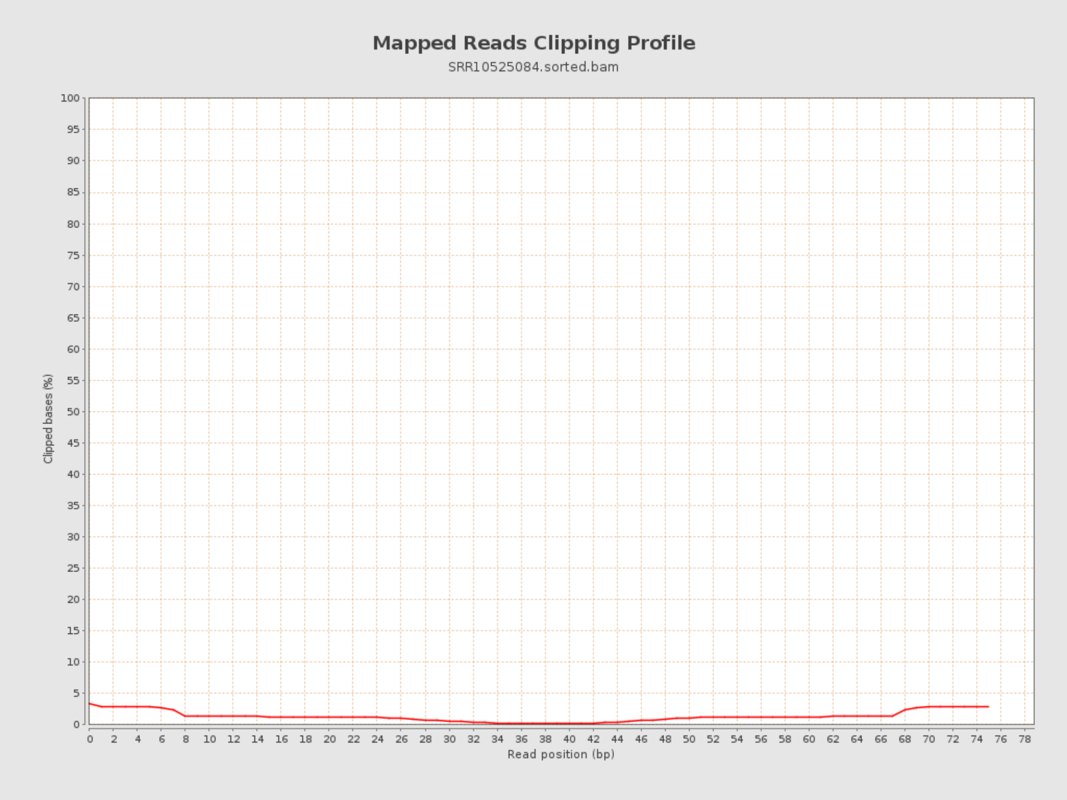
8. Results : Mapped Reads Nucleotide Content



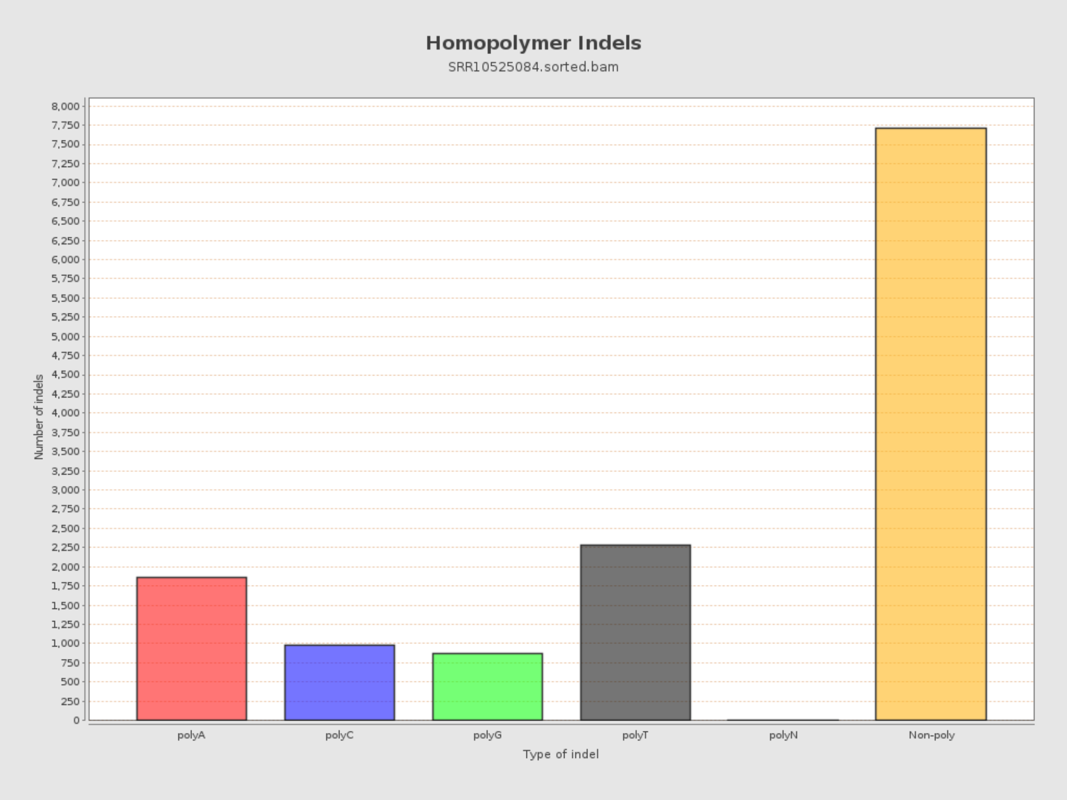
9. Results : Mapped Reads GC-content Distribution



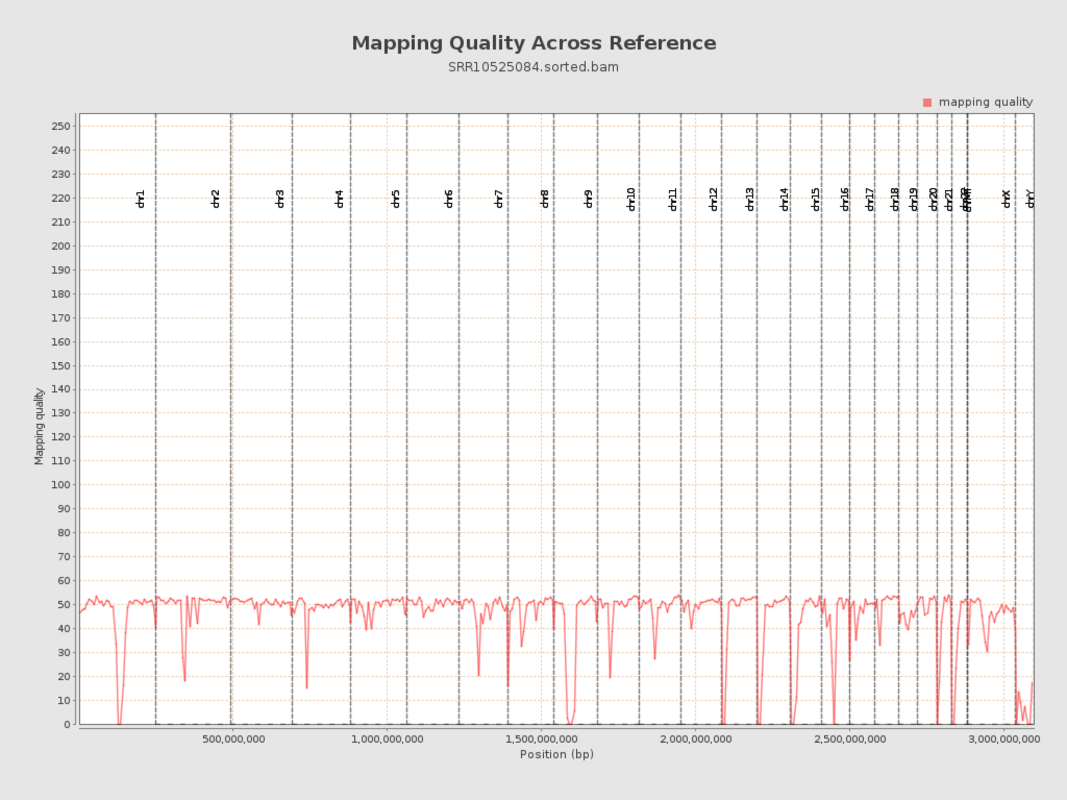
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram