Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:57:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525204.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_SRR10525204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525204.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:57:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	965,547
Mapped reads	874,881 / 90.61%
Unmapped reads	90,666 / 9.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,277 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	16,529 / 1.71%
Duplication rate	1.28%
Clipped reads	875,786 / 90.7%

2.2. ACGT Content

Number/percentage of A's	13,208,063 / 26.32%
Number/percentage of C's	9,501,697 / 18.93%
Number/percentage of T's	15,164,694 / 30.22%
Number/percentage of G's	12,311,304 / 24.53%
Number/percentage of N's	1,480 / 0%
GC Percentage	43.46%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.171

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

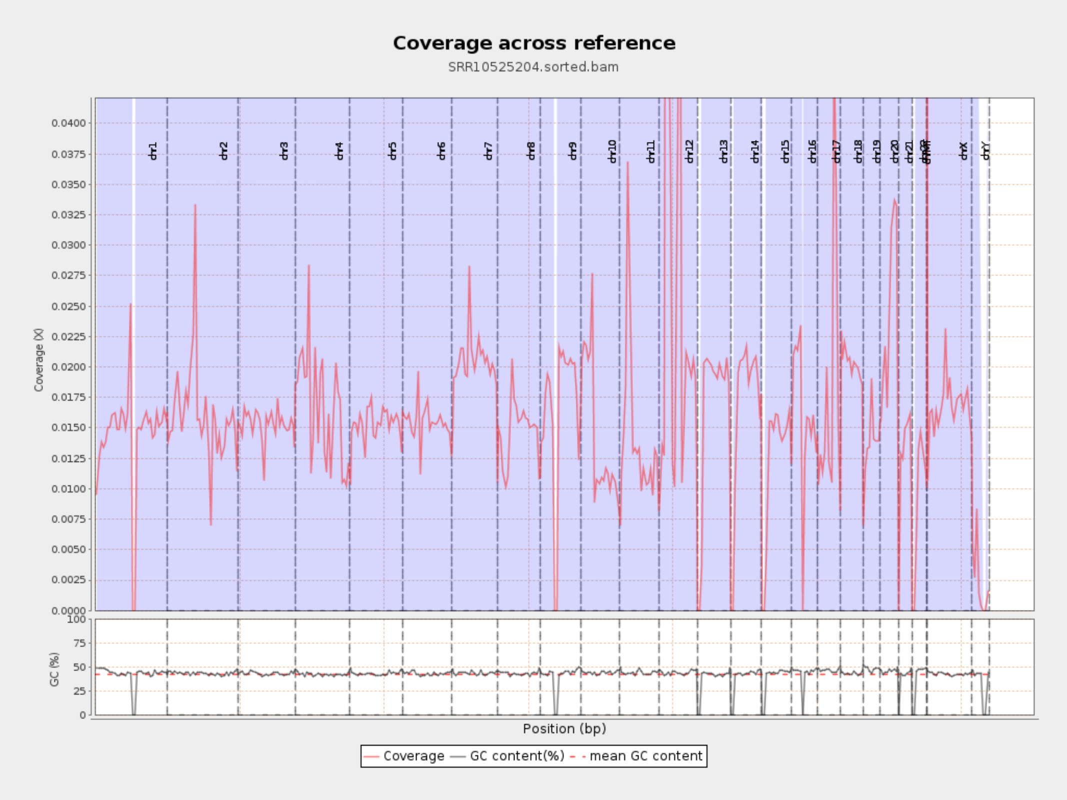
General error rate	0.5%
Mismatches	244,194
Insertions	3,581
Mapped reads with at least one insertion	0.41%
Deletions	7,952
Mapped reads with at least one deletion	0.9%
Homopolymer indels	40.88%

2.6. Chromosome stats

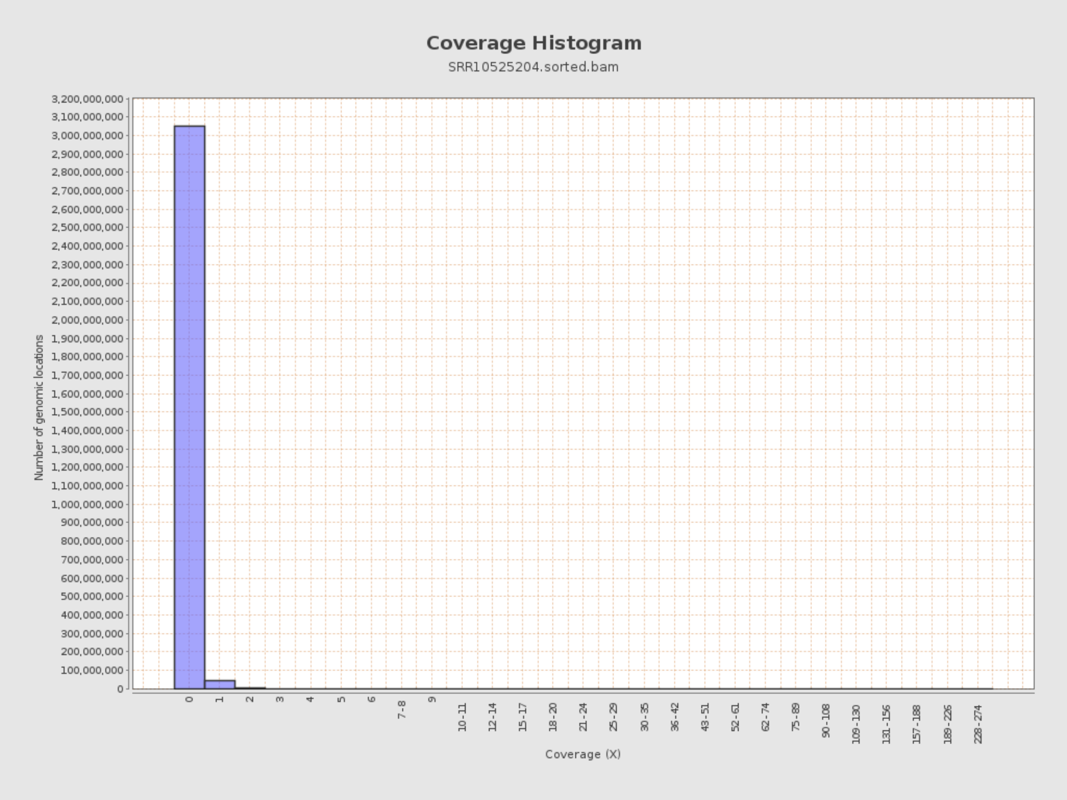
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3588755	0.0144	0.2596
chr2	243199373	3914617	0.0161	0.1839
chr3	198022430	3036072	0.0153	0.1287
chr4	191154276	3169628	0.0166	0.1425
chr5	180915260	2795206	0.0155	0.1301
chr6	171115067	2646077	0.0155	0.1364
chr7	159138663	3275463	0.0206	0.215

chr8	146364022	2180917	0.0149	0.1692
chr9	141213431	2311413	0.0164	0.1748
chr10	135534747	1952898	0.0144	0.1727
chr11	135006516	1923266	0.0142	0.1489
chr12	133851895	3774609	0.0282	0.1881
chr13	115169878	1892202	0.0164	0.1332
chr14	107349540	1782224	0.0166	0.1437
chr15	102531392	1262656	0.0123	0.1162
chr16	90354753	1419845	0.0157	0.1397
chr17	81195210	1478853	0.0182	0.1439
chr18	78077248	1588641	0.0203	0.2842
chr19	59128983	821677	0.0139	0.1971
chr20	63025520	1545131	0.0245	0.1662
chr21	48129895	605851	0.0126	0.1256
chr22	51304566	473607	0.0092	0.0996
chrMT	16571	1226	0.074	0.273
chrX	155270560	2619538	0.0169	0.1494
chrY	59373566	140029	0.0024	0.0703

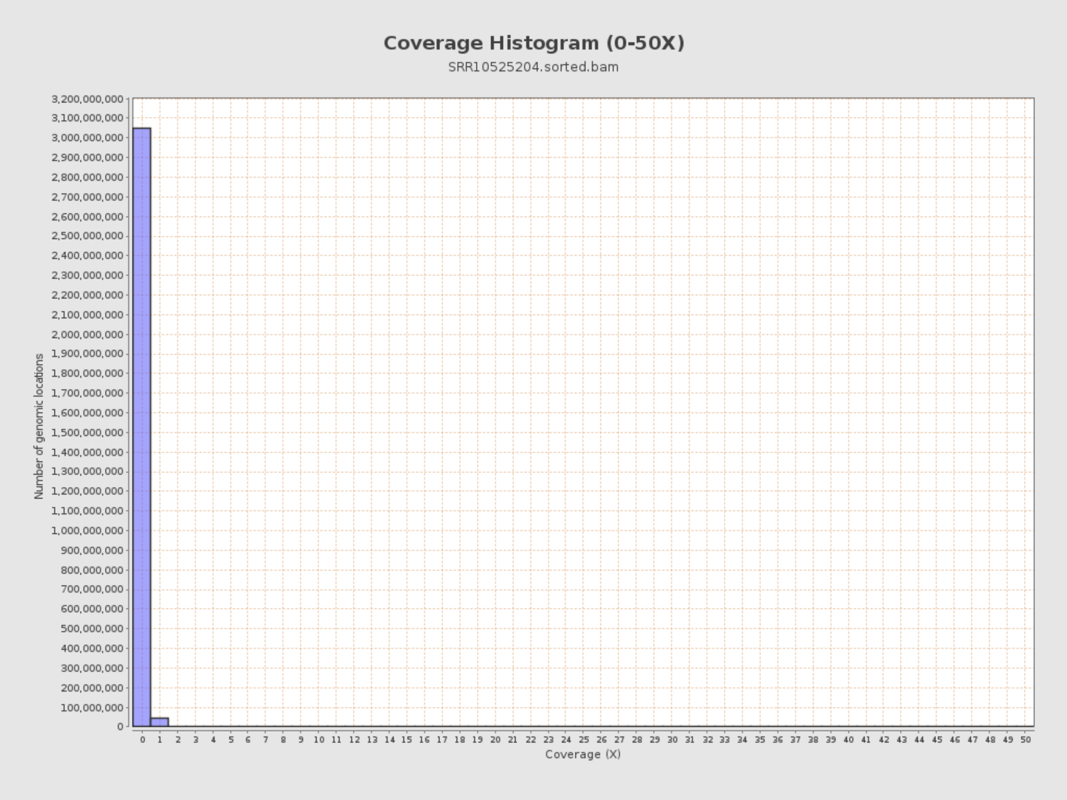
3. Results : Coverage across reference



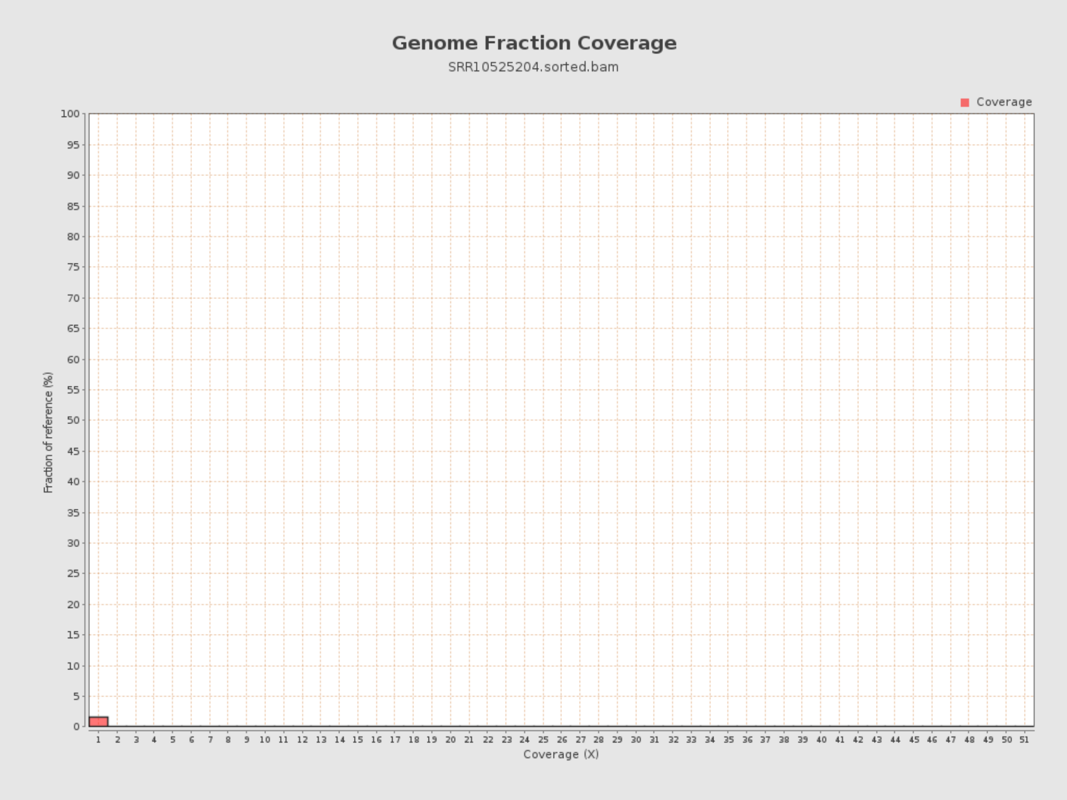
4. Results : Coverage Histogram



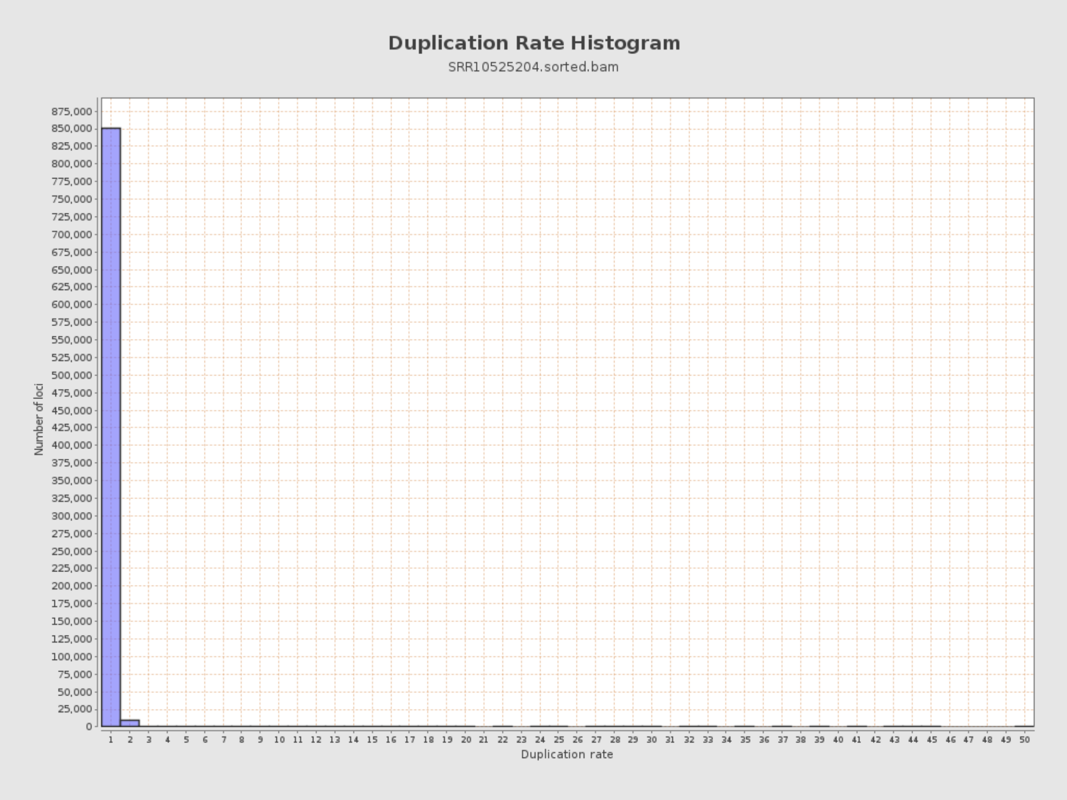
5. Results : Coverage Histogram (0-50X)



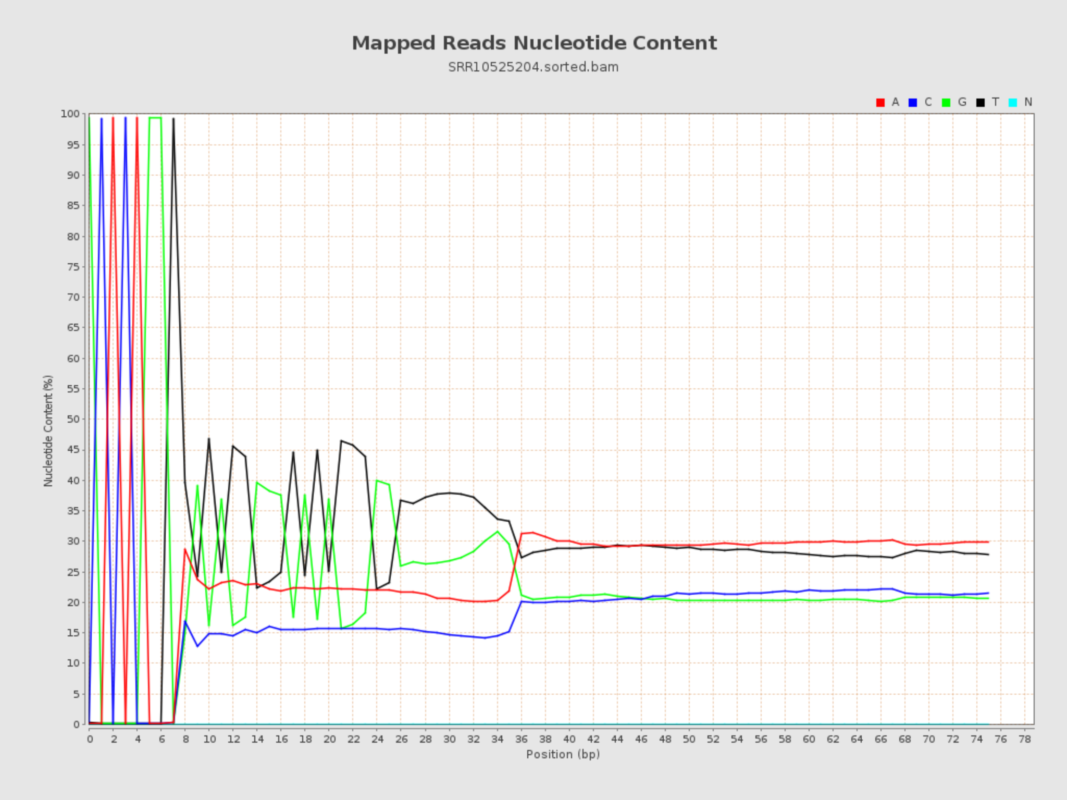
6. Results : Genome Fraction Coverage



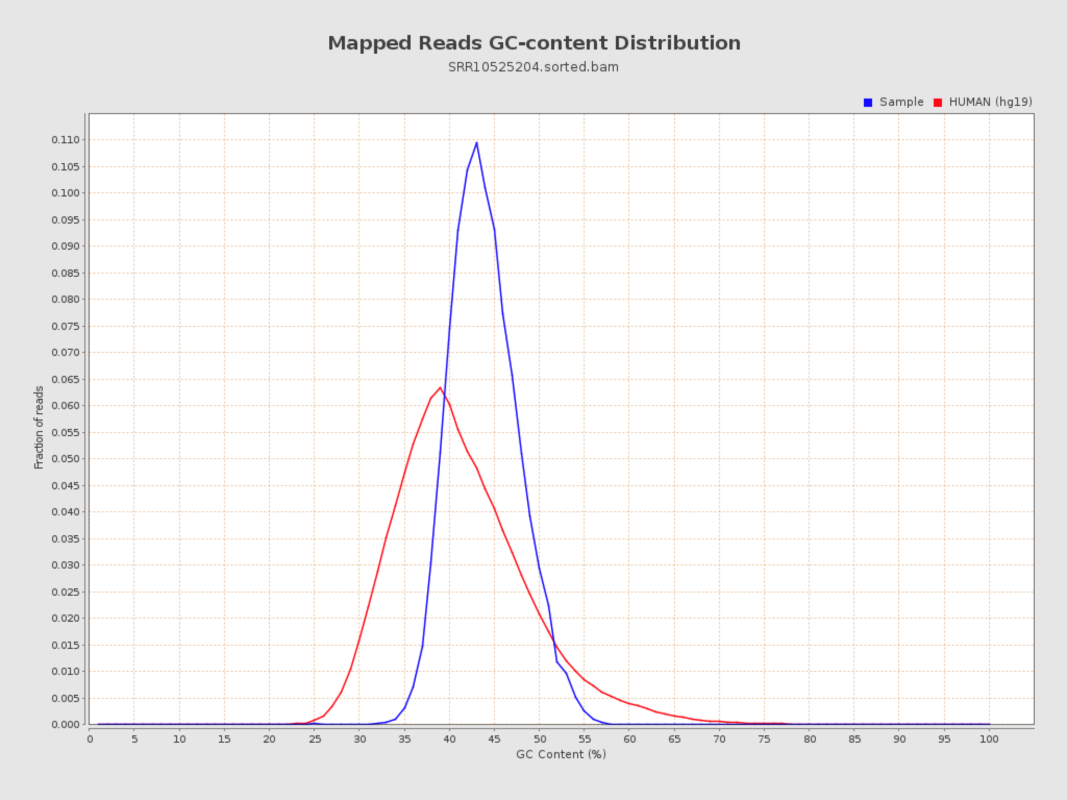
7. Results : Duplication Rate Histogram



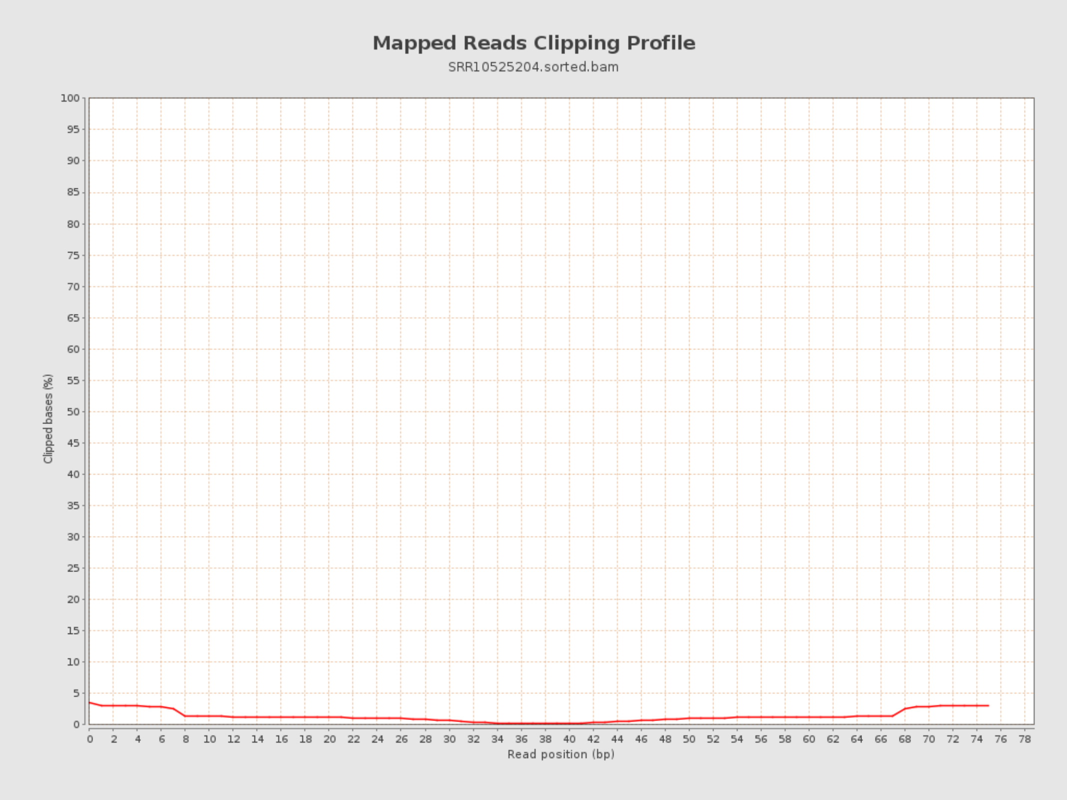
8. Results : Mapped Reads Nucleotide Content



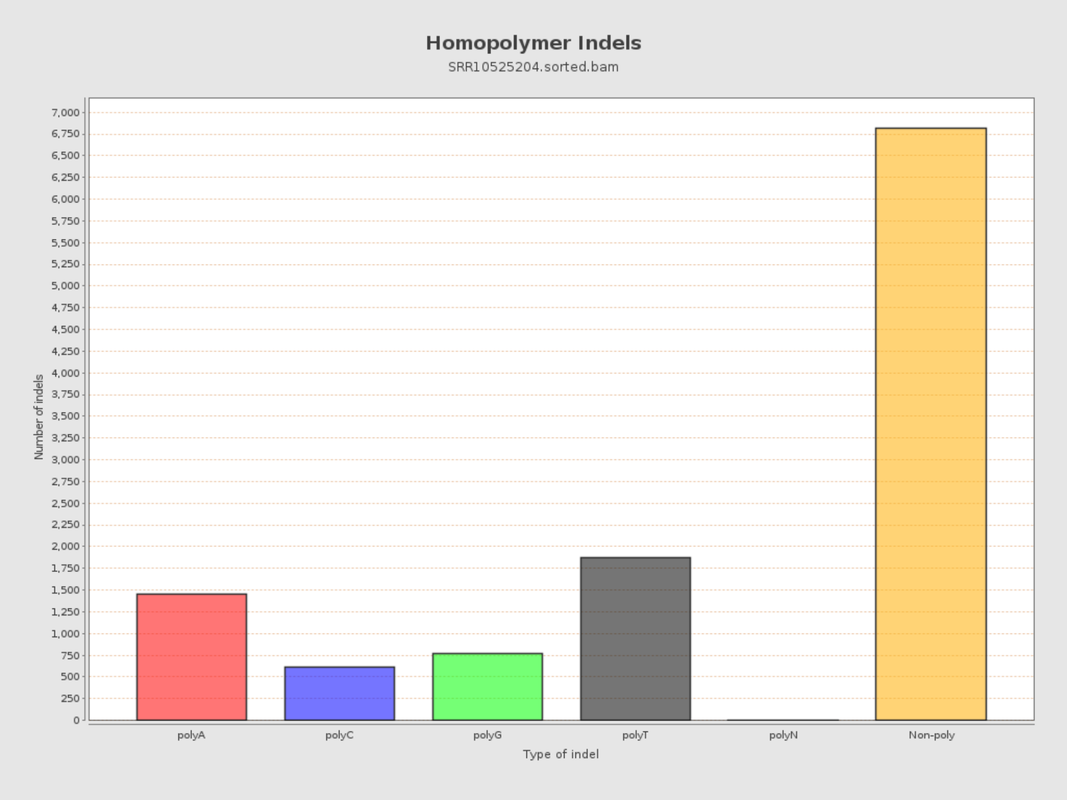
9. Results : Mapped Reads GC-content Distribution



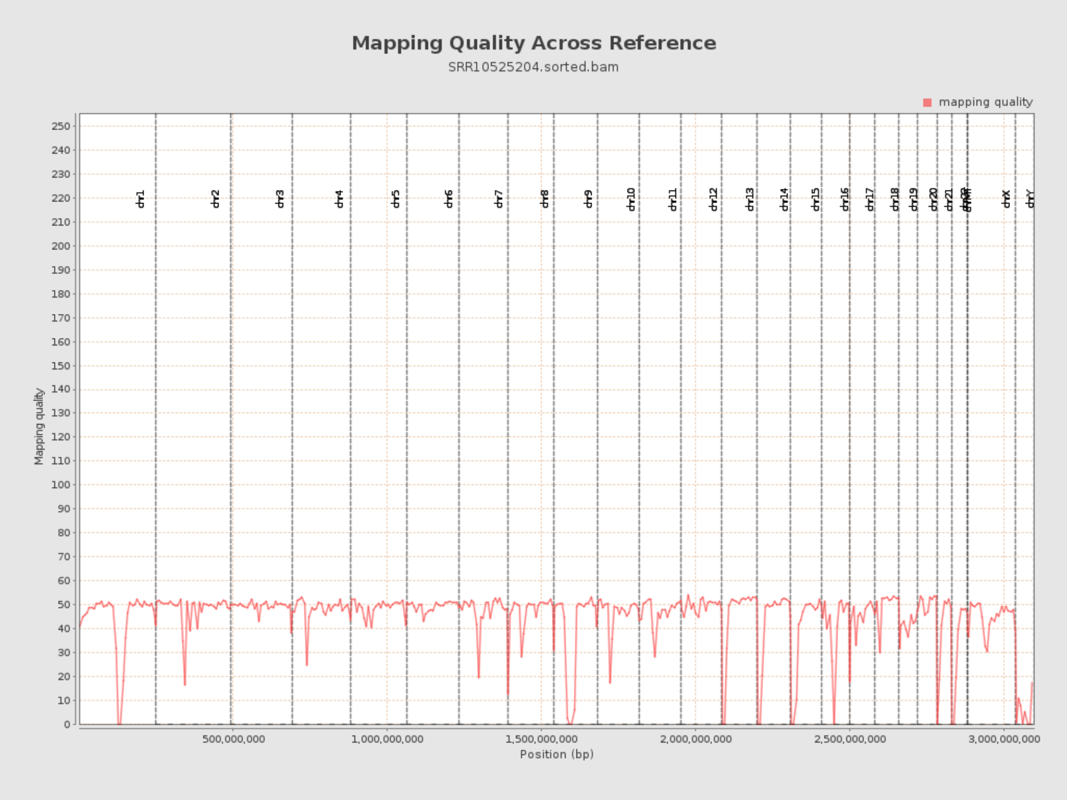
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram