Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:11:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525032.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_SRR10525032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:11:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,095,937
Mapped reads	1,006,261 / 91.82%
Unmapped reads	89,676 / 8.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,520 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	28,148 / 2.57%
Duplication rate	2.07%
Clipped reads	1,008,432 / 92.02%

2.2. ACGT Content

Number/percentage of A's	14,605,372 / 24.87%
Number/percentage of C's	11,523,232 / 19.63%
Number/percentage of T's	19,264,976 / 32.81%
Number/percentage of G's	13,322,191 / 22.69%
Number/percentage of N's	675 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.019

Standard Deviation	0.1908

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

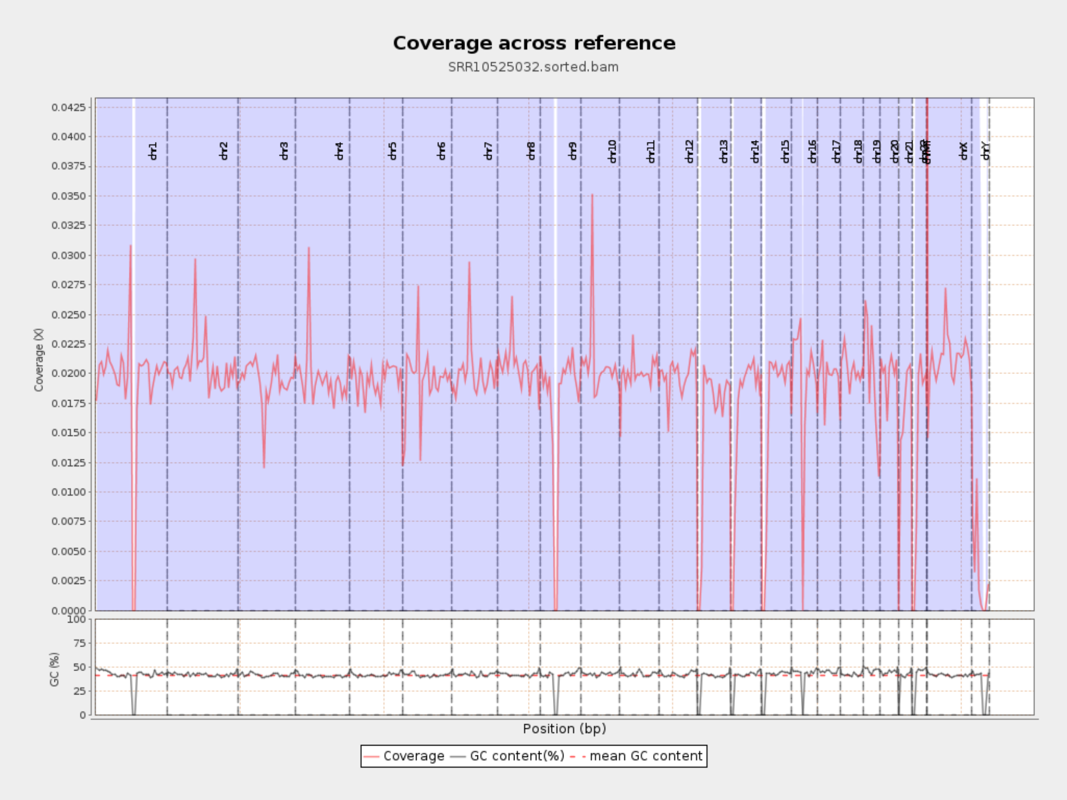
General error rate	0.52%
Mismatches	296,311
Insertions	3,794
Mapped reads with at least one insertion	0.38%
Deletions	11,979
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.95%

2.6. Chromosome stats

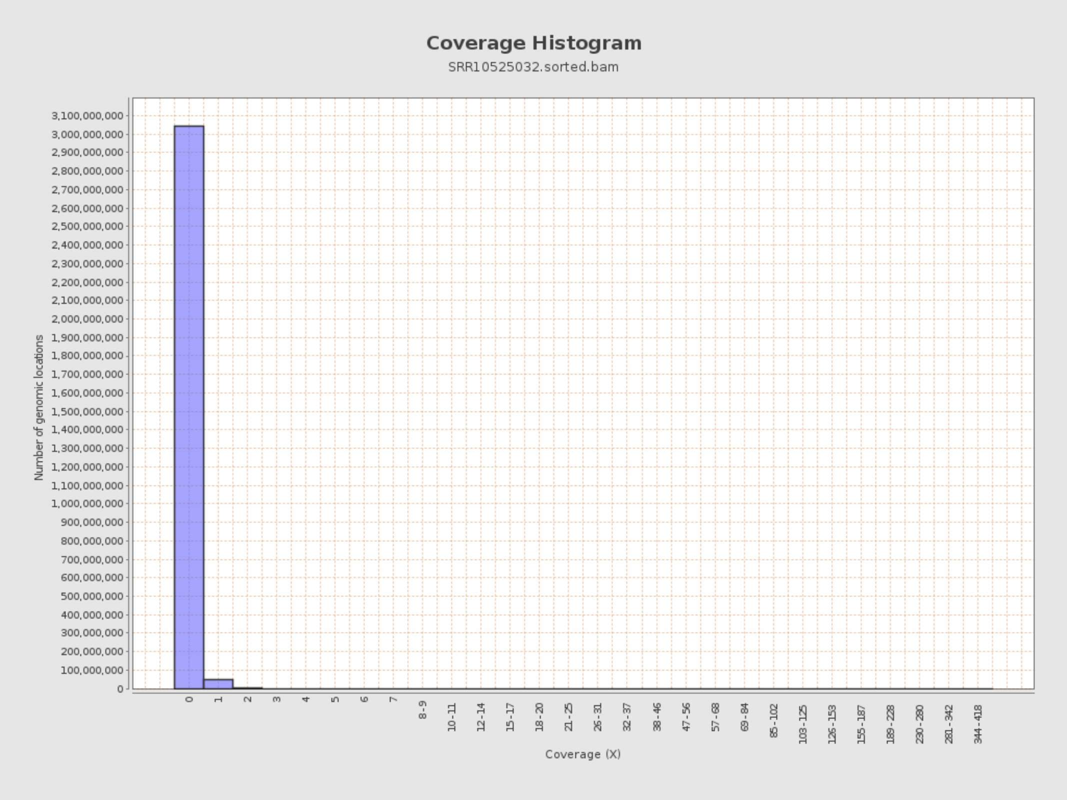
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4773311	0.0192	0.3197
chr2	243199373	4994836	0.0205	0.217
chr3	198022430	3838404	0.0194	0.1474
chr4	191154276	3783229	0.0198	0.164
chr5	180915260	3548115	0.0196	0.1485
chr6	171115067	3313247	0.0194	0.1756
chr7	159138663	3217421	0.0202	0.2181

chr8	146364022	3028291	0.0207	0.1974
chr9	141213431	2447710	0.0173	0.1638
chr10	135534747	2842616	0.021	0.1971
chr11	135006516	2711725	0.0201	0.1863
chr12	133851895	2661770	0.0199	0.1504
chr13	115169878	1798567	0.0156	0.1333
chr14	107349540	1756944	0.0164	0.1387
chr15	102531392	1686762	0.0165	0.1397
chr16	90354753	1721049	0.019	0.1517
chr17	81195210	1608931	0.0198	0.1619
chr18	78077248	1592443	0.0204	0.273
chr19	59128983	1168880	0.0198	0.2241
chr20	63025520	1253398	0.0199	0.1516
chr21	48129895	778345	0.0162	0.1441
chr22	51304566	712937	0.0139	0.1245
chrMT	16571	3507	0.2116	0.4712
chrX	155270560	3306859	0.0213	0.163
chrY	59373566	186974	0.0031	0.0995

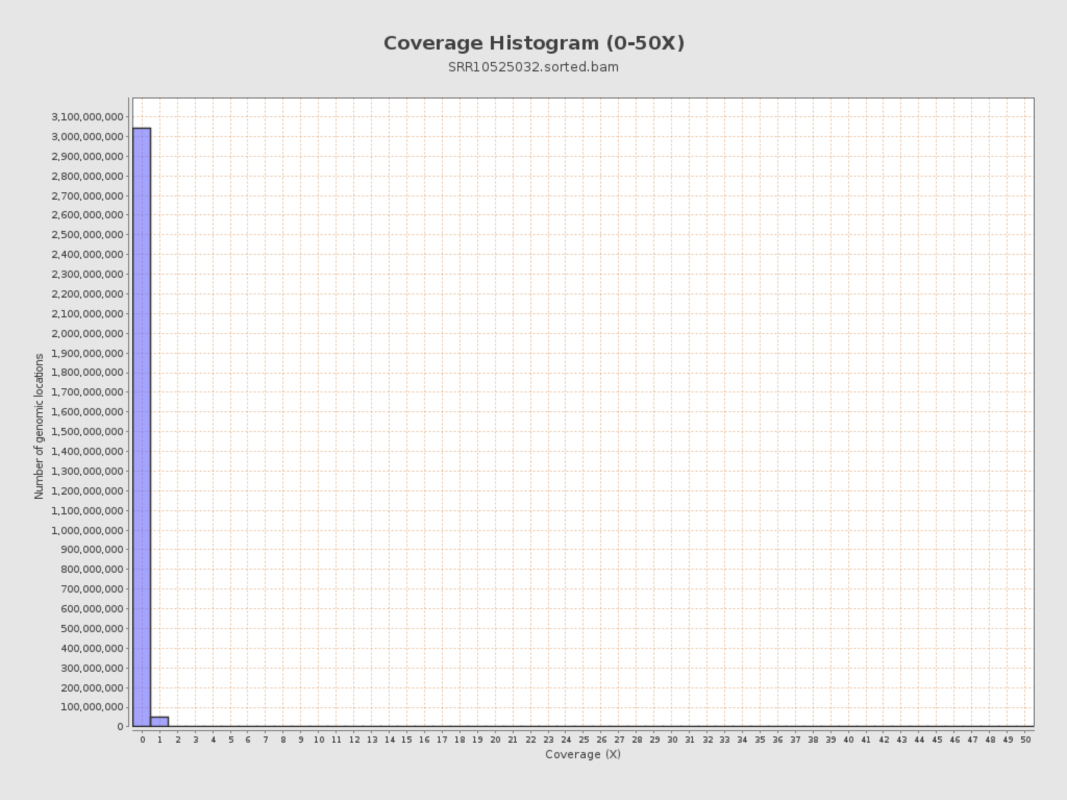
3. Results : Coverage across reference



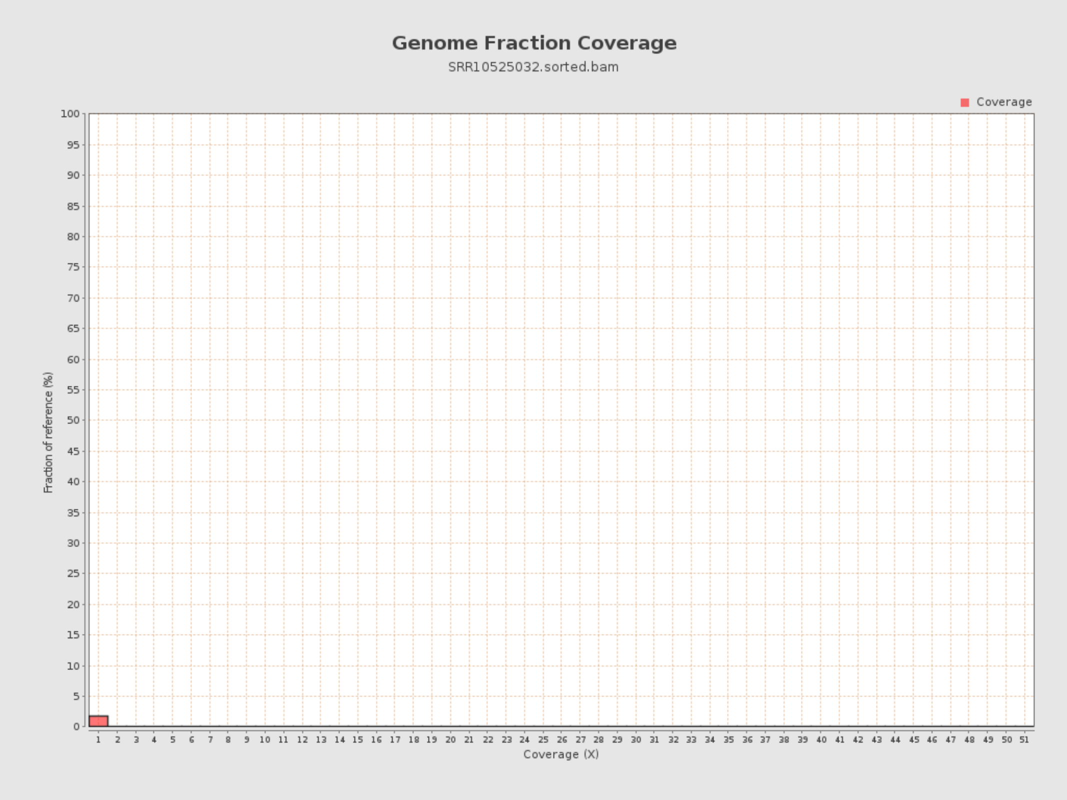
4. Results : Coverage Histogram



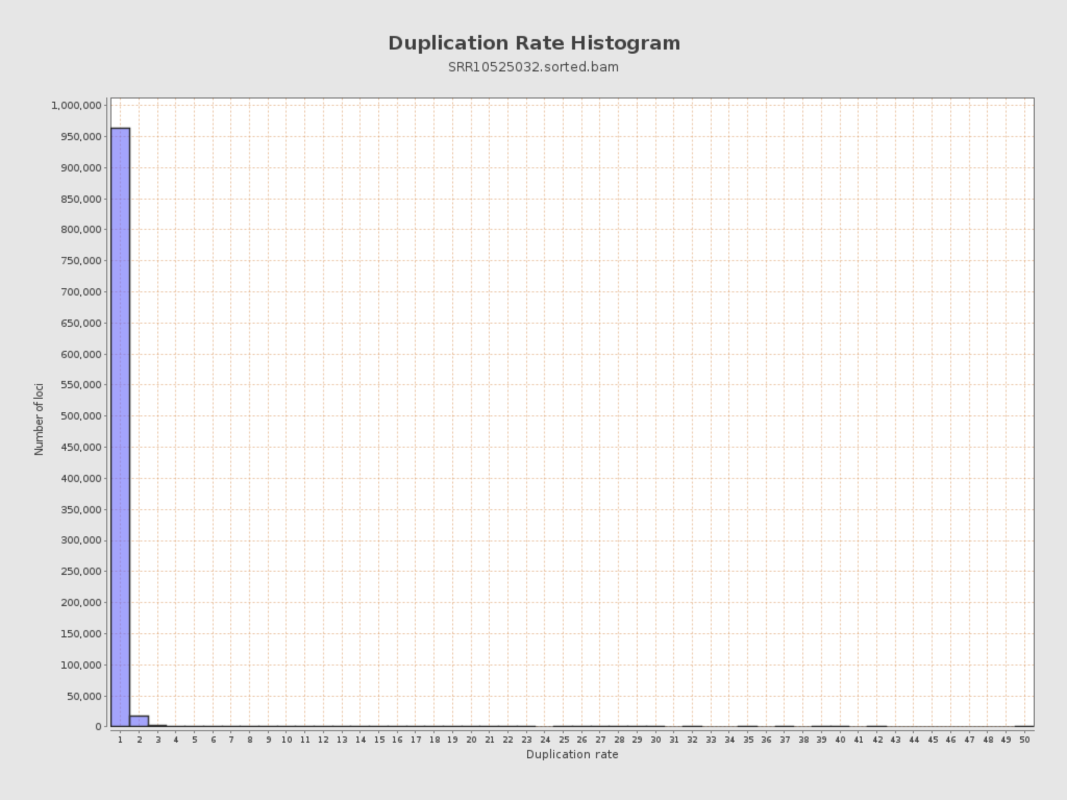
5. Results : Coverage Histogram (0-50X)



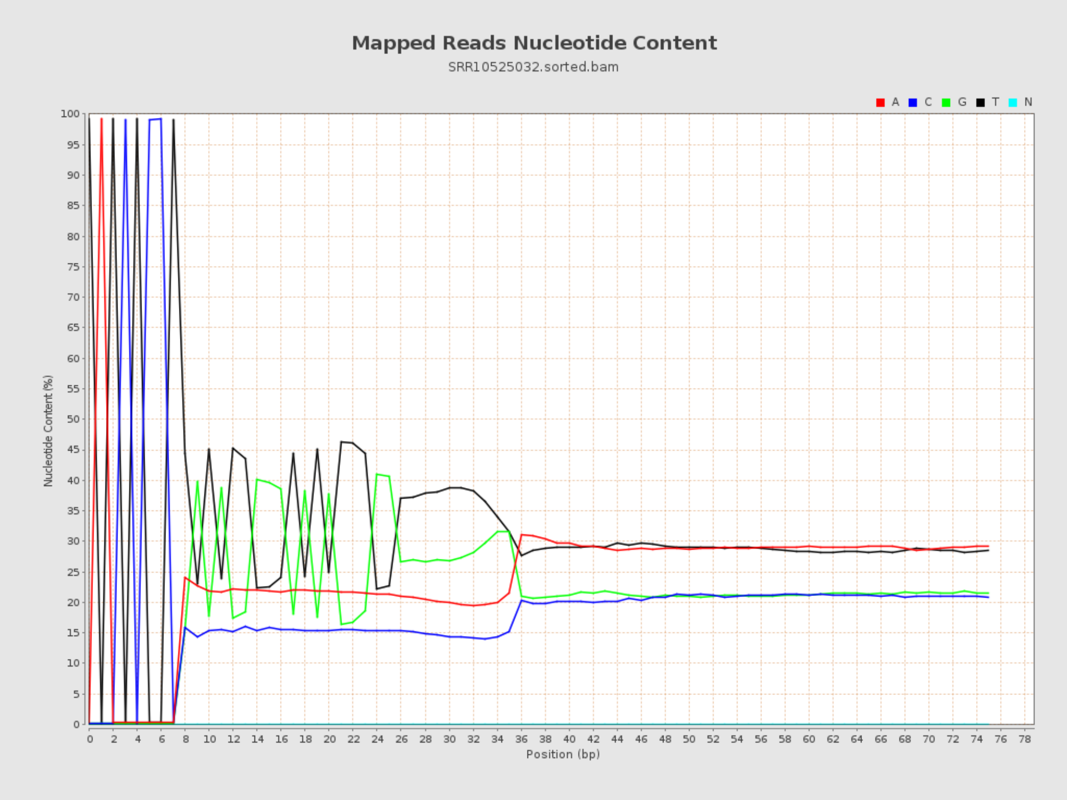
6. Results : Genome Fraction Coverage



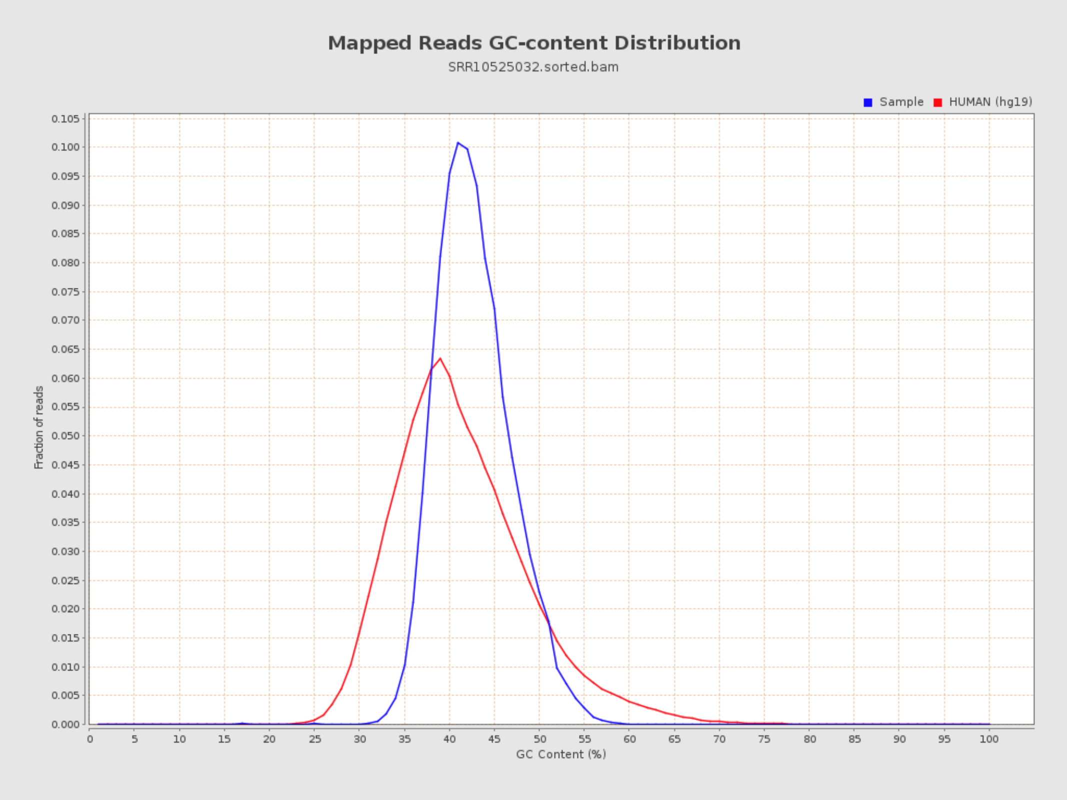
7. Results : Duplication Rate Histogram



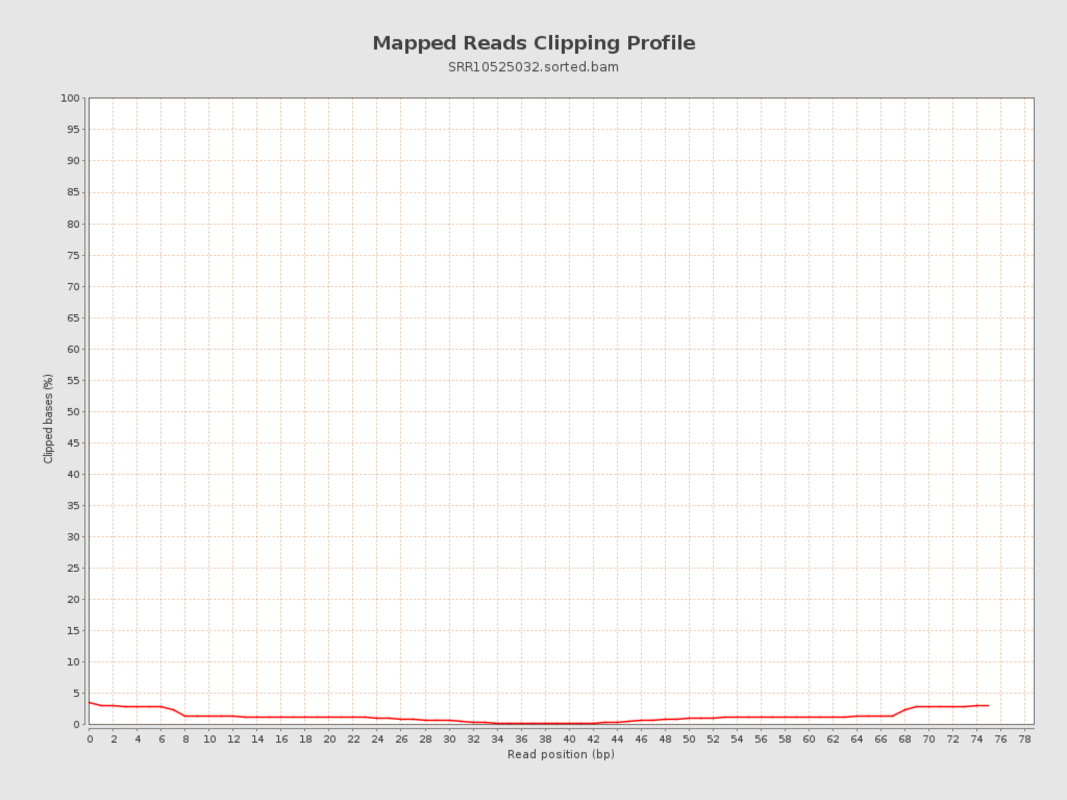
8. Results : Mapped Reads Nucleotide Content



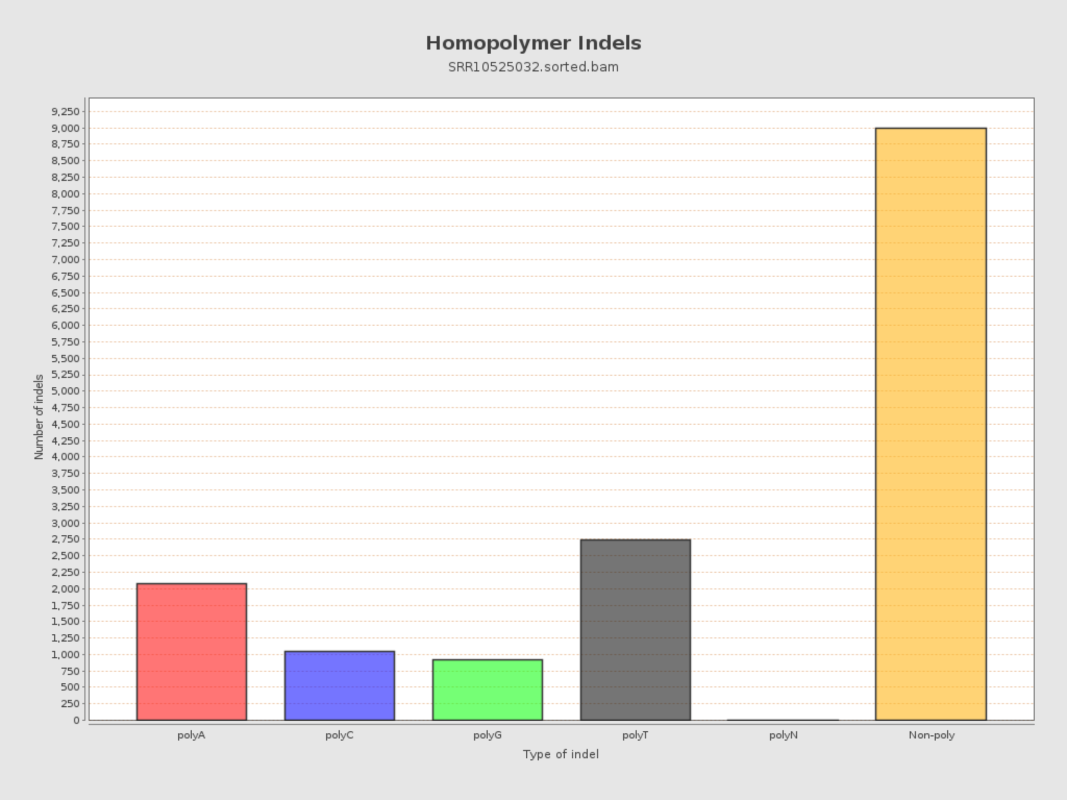
9. Results : Mapped Reads GC-content Distribution



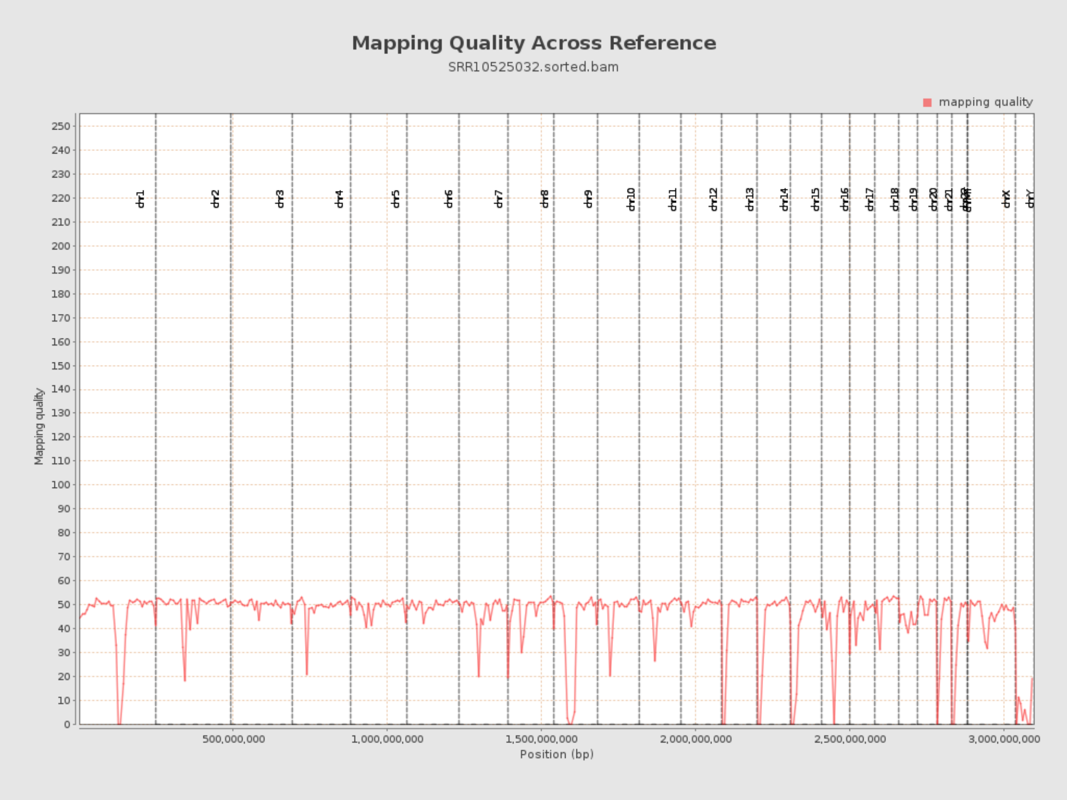
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram