Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:52:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525050.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_SRR10525050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:52:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	596,491
Mapped reads	551,369 / 92.44%
Unmapped reads	45,122 / 7.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,394 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	38,982 / 6.54%
Duplication rate	5.89%
Clipped reads	551,042 / 92.38%

2.2. ACGT Content

Number/percentage of A's	8,492,348 / 26.04%
Number/percentage of C's	6,716,261 / 20.59%
Number/percentage of T's	9,909,395 / 30.38%
Number/percentage of G's	7,497,155 / 22.98%
Number/percentage of N's	3,549 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.1436

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

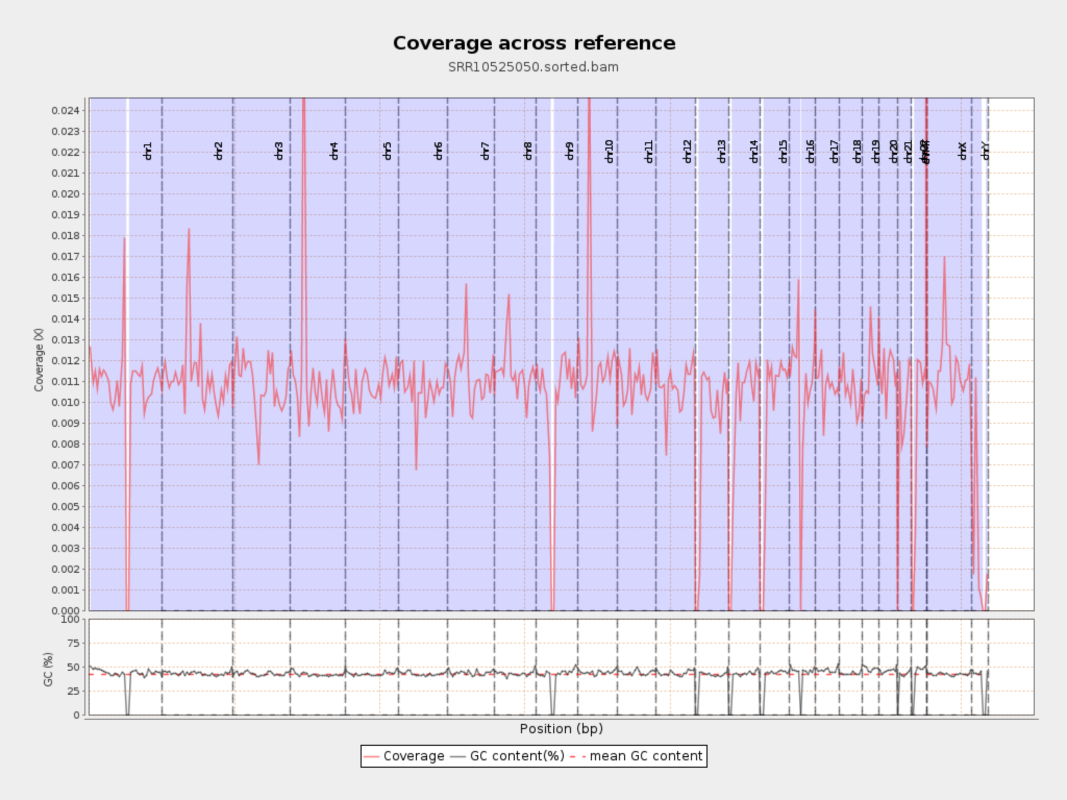
General error rate	0.51%
Mismatches	160,505
Insertions	2,782
Mapped reads with at least one insertion	0.5%
Deletions	6,565
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.05%

2.6. Chromosome stats

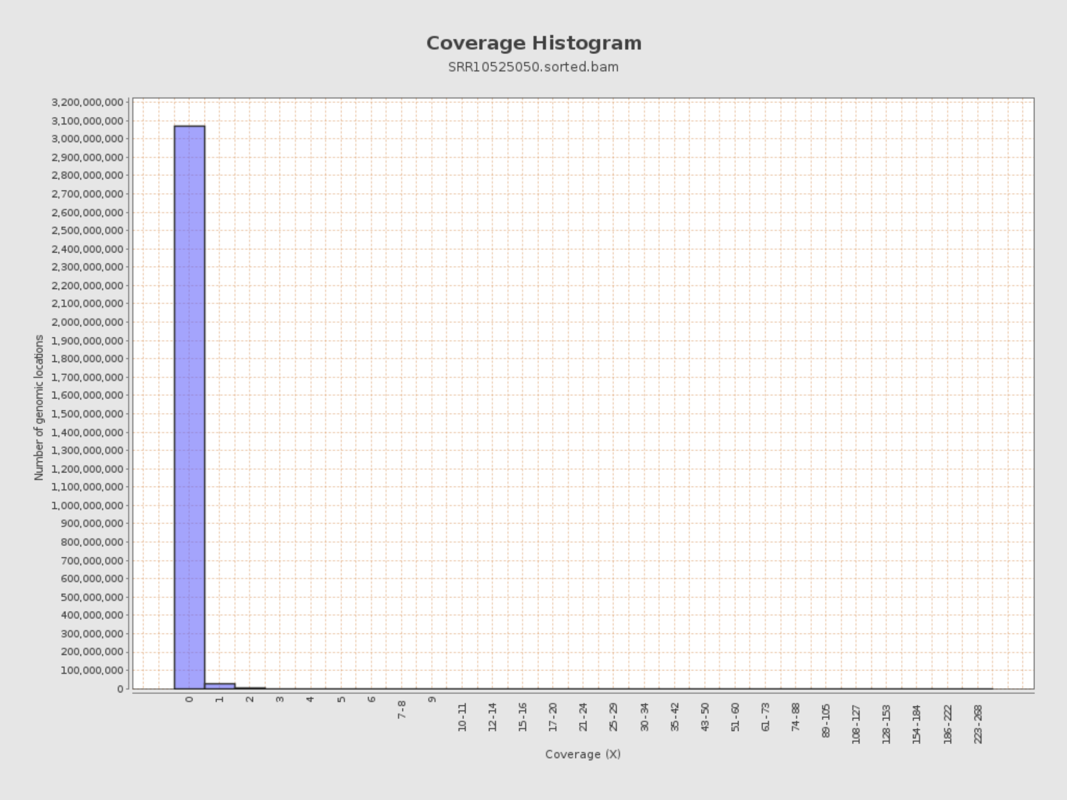
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2620173	0.0105	0.205
chr2	243199373	2762957	0.0114	0.1704
chr3	198022430	2140847	0.0108	0.1172
chr4	191154276	2142436	0.0112	0.1447
chr5	180915260	1972538	0.0109	0.1176
chr6	171115067	1826714	0.0107	0.1188
chr7	159138663	1780656	0.0112	0.1436

chr8	146364022	1680556	0.0115	0.1945
chr9	141213431	1366092	0.0097	0.1209
chr10	135534747	1644042	0.0121	0.1794
chr11	135006516	1475972	0.0109	0.1257
chr12	133851895	1443335	0.0108	0.1184
chr13	115169878	996570	0.0087	0.1041
chr14	107349540	983621	0.0092	0.1081
chr15	102531392	946163	0.0092	0.1075
chr16	90354753	957346	0.0106	0.1193
chr17	81195210	875289	0.0108	0.1212
chr18	78077248	830929	0.0106	0.1652
chr19	59128983	680291	0.0115	0.1615
chr20	63025520	715294	0.0113	0.1236
chr21	48129895	450788	0.0094	0.1309
chr22	51304566	409053	0.008	0.1012
chrMT	16571	7522	0.4539	0.7724
chrX	155270560	1772308	0.0114	0.1249
chrY	59373566	147710	0.0025	0.1196

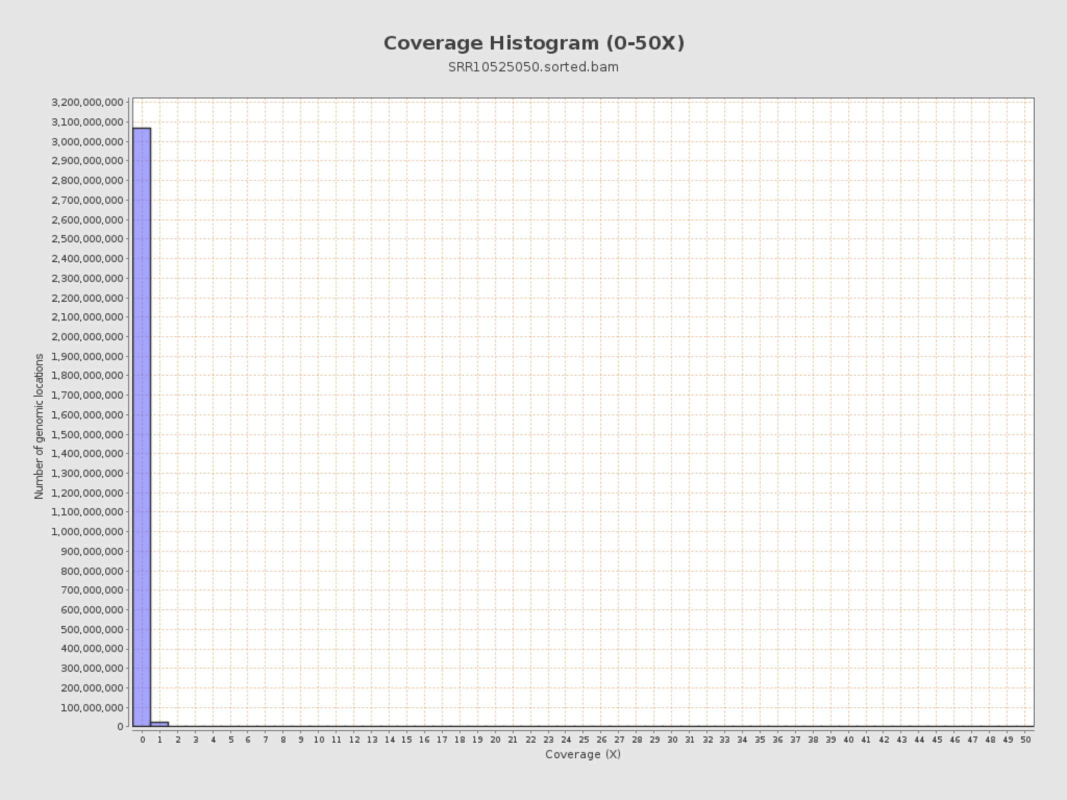
3. Results : Coverage across reference



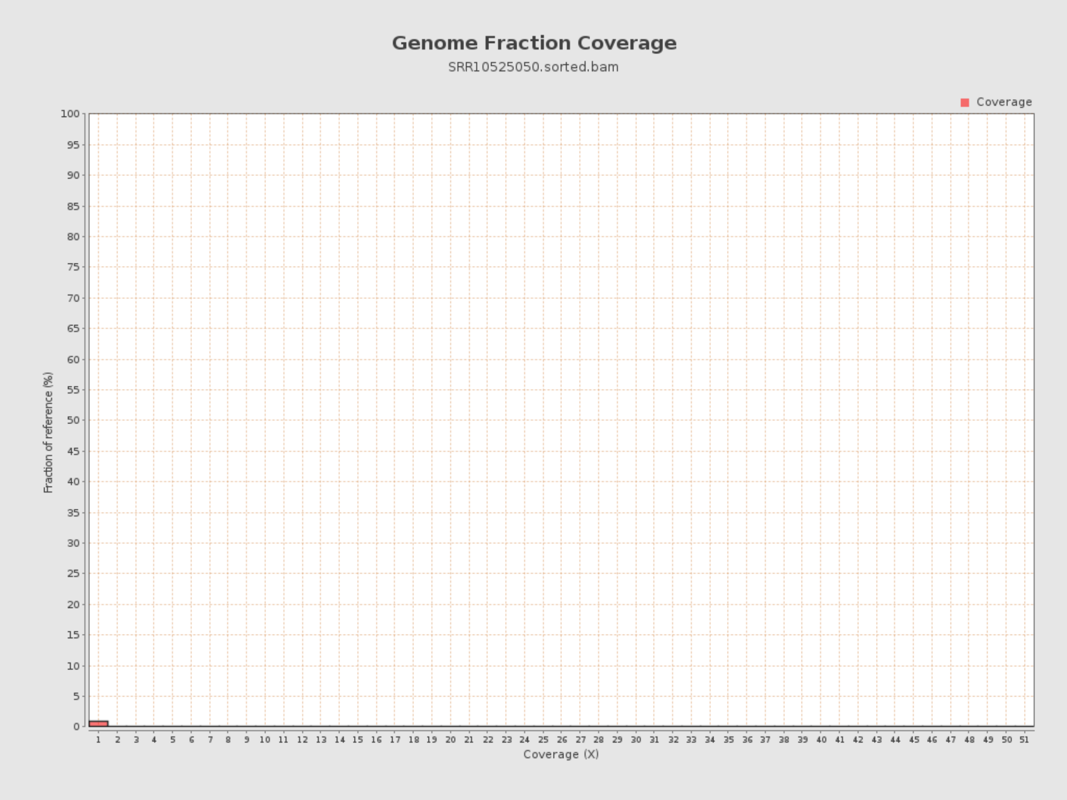
4. Results : Coverage Histogram



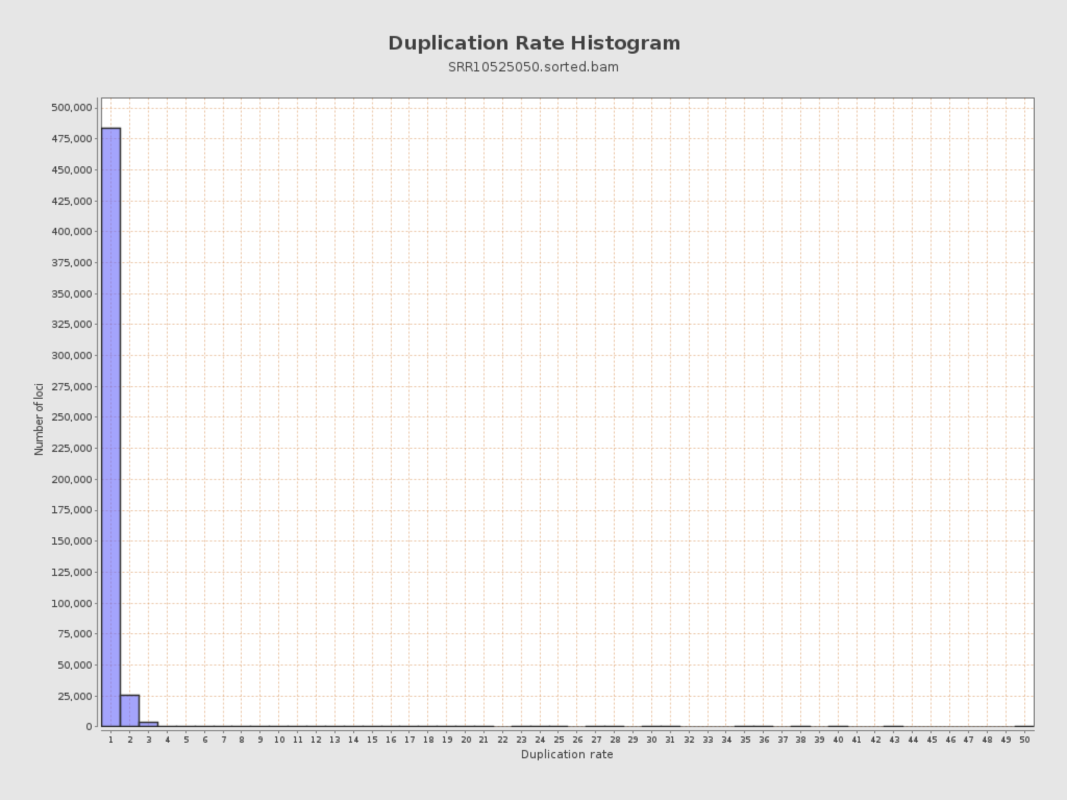
5. Results : Coverage Histogram (0-50X)



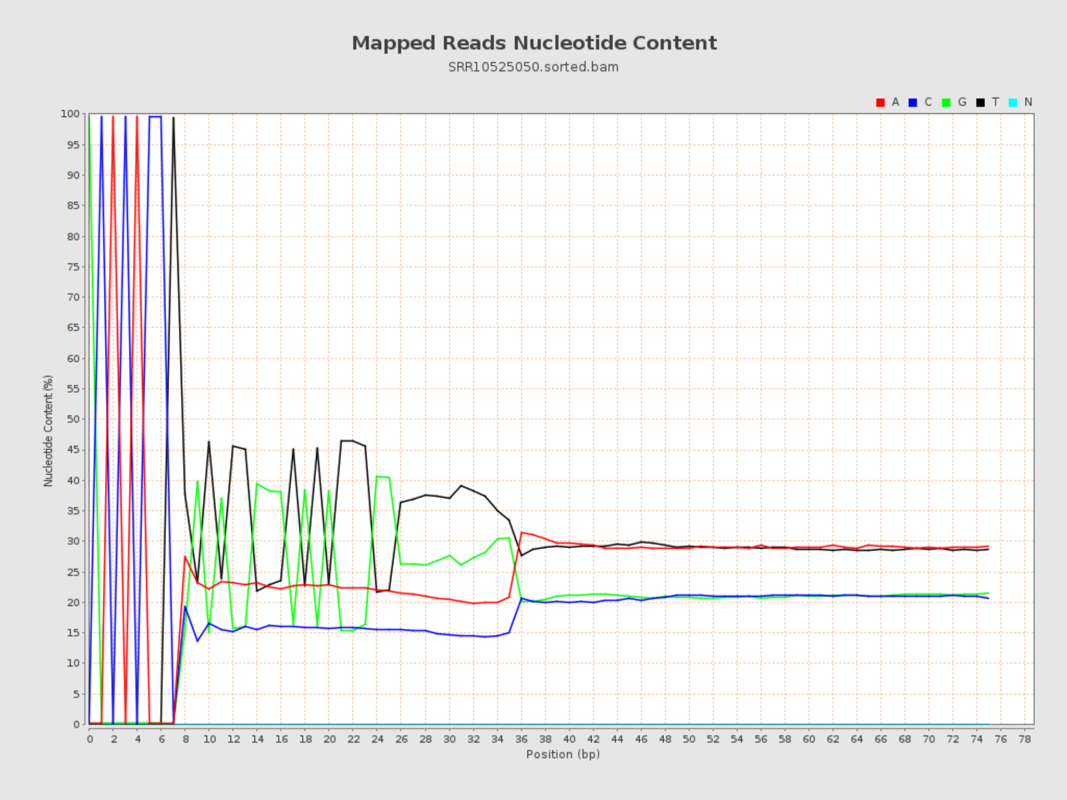
6. Results : Genome Fraction Coverage



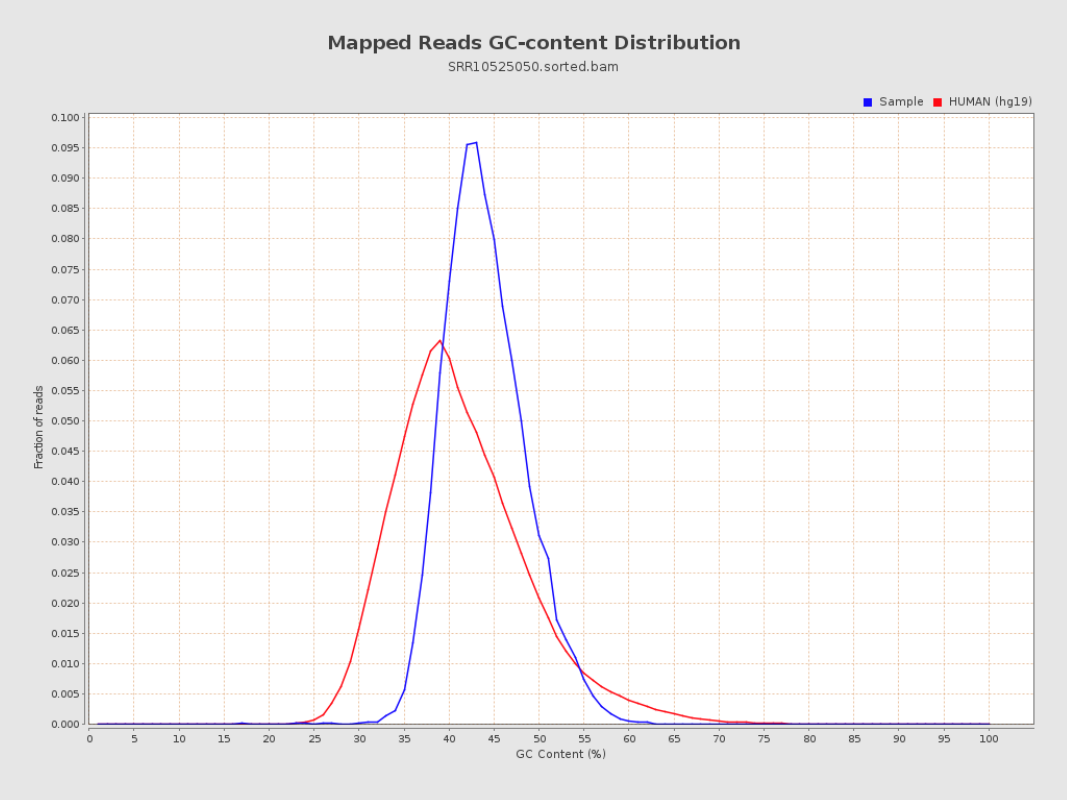
7. Results : Duplication Rate Histogram



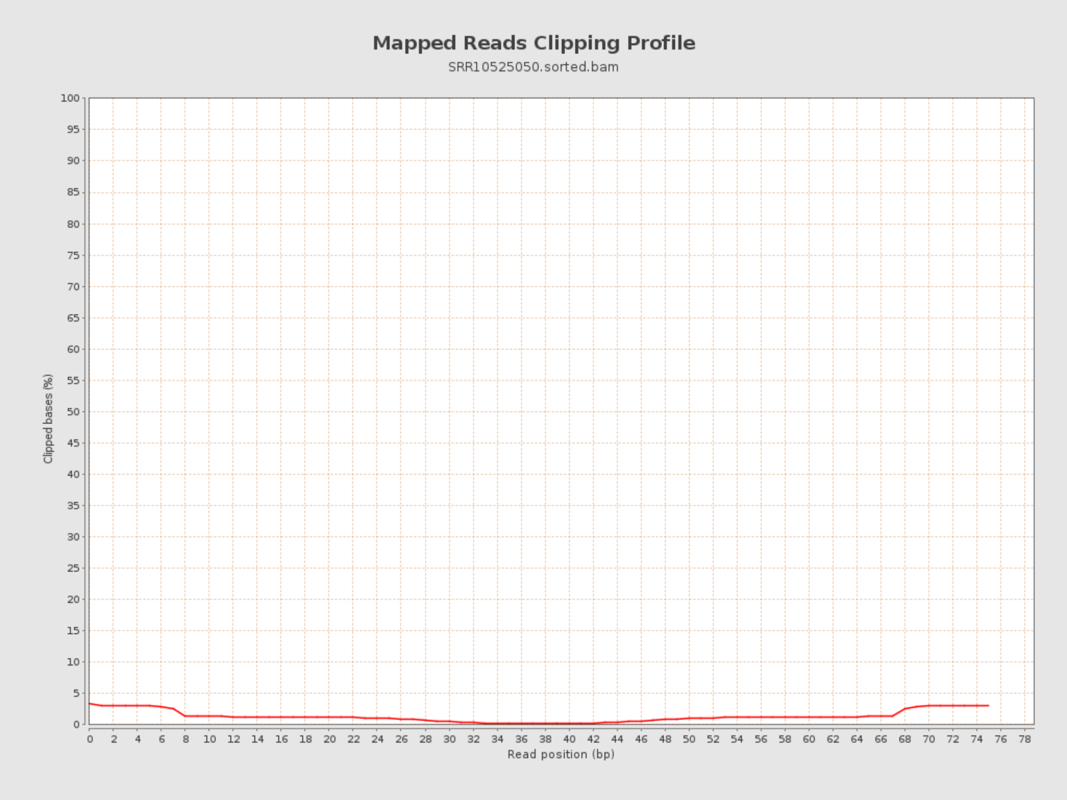
8. Results : Mapped Reads Nucleotide Content



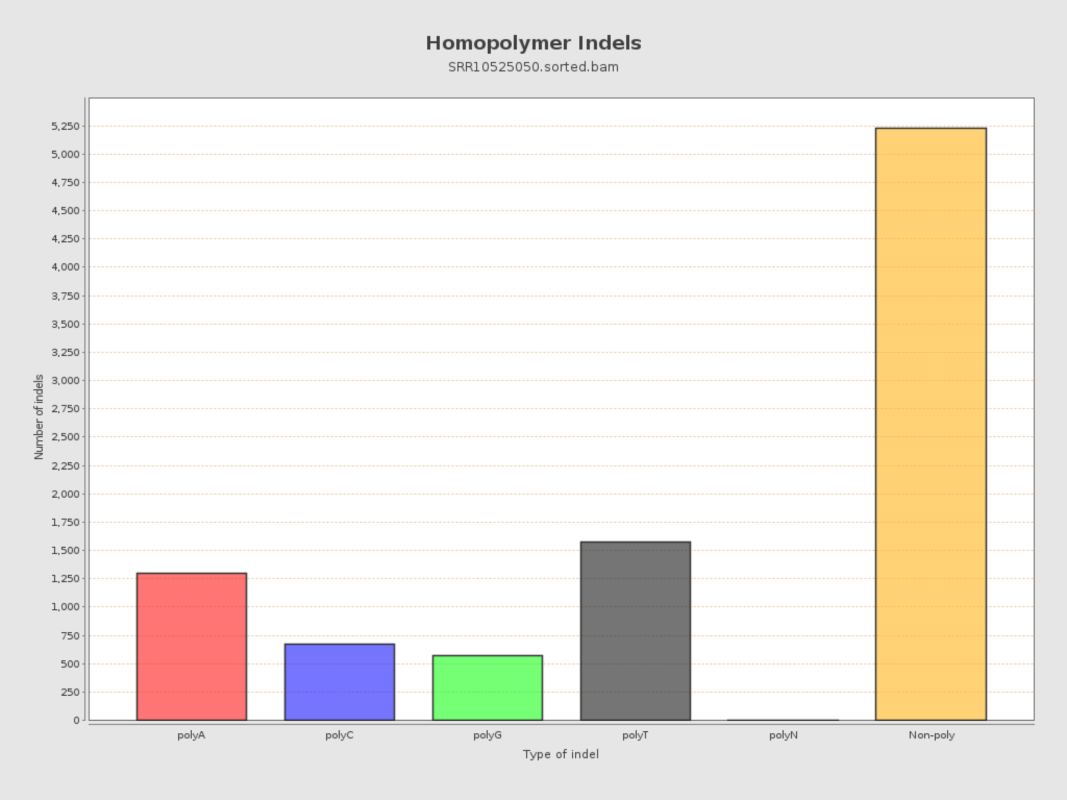
9. Results : Mapped Reads GC-content Distribution



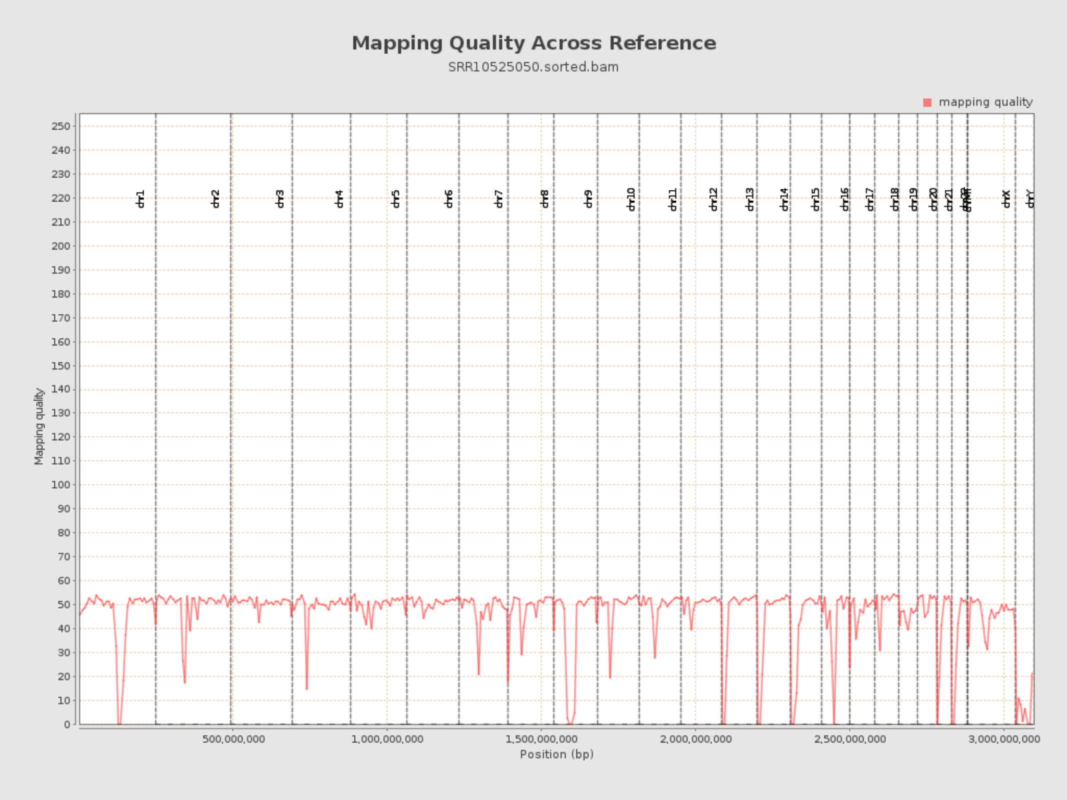
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram