Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:02:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525010.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_SRR10525010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525010.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:02:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	893,690
Mapped reads	820,434 / 91.8%
Unmapped reads	73,256 / 8.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,162 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	15,811 / 1.77%
Duplication rate	1.33%
Clipped reads	822,964 / 92.09%

2.2. ACGT Content

Number/percentage of A's	11,185,720 / 23.6%
Number/percentage of C's	9,305,901 / 19.63%
Number/percentage of T's	14,696,739 / 31%
Number/percentage of G's	12,215,141 / 25.77%
Number/percentage of N's	447 / 0%
GC Percentage	45.4%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1617

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Mismatches and indels

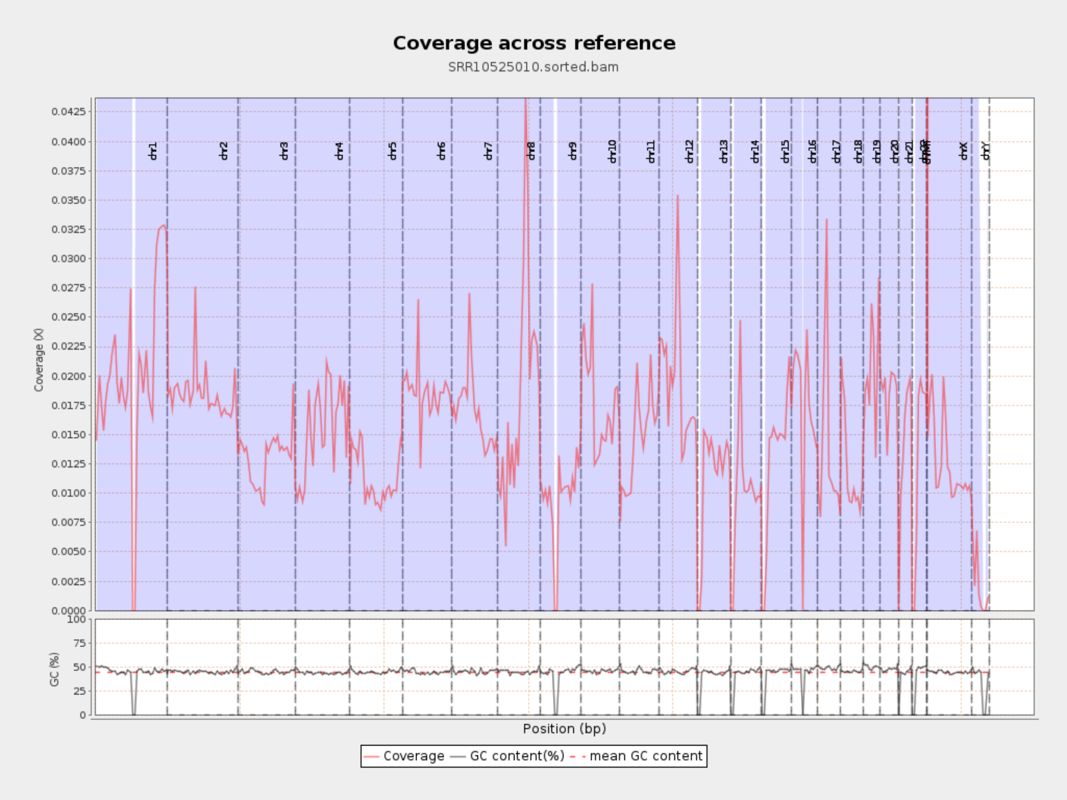
General error rate	0.5%
Mismatches	230,070
Insertions	2,664
Mapped reads with at least one insertion	0.32%
Deletions	8,916
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.55%

2.6. Chromosome stats

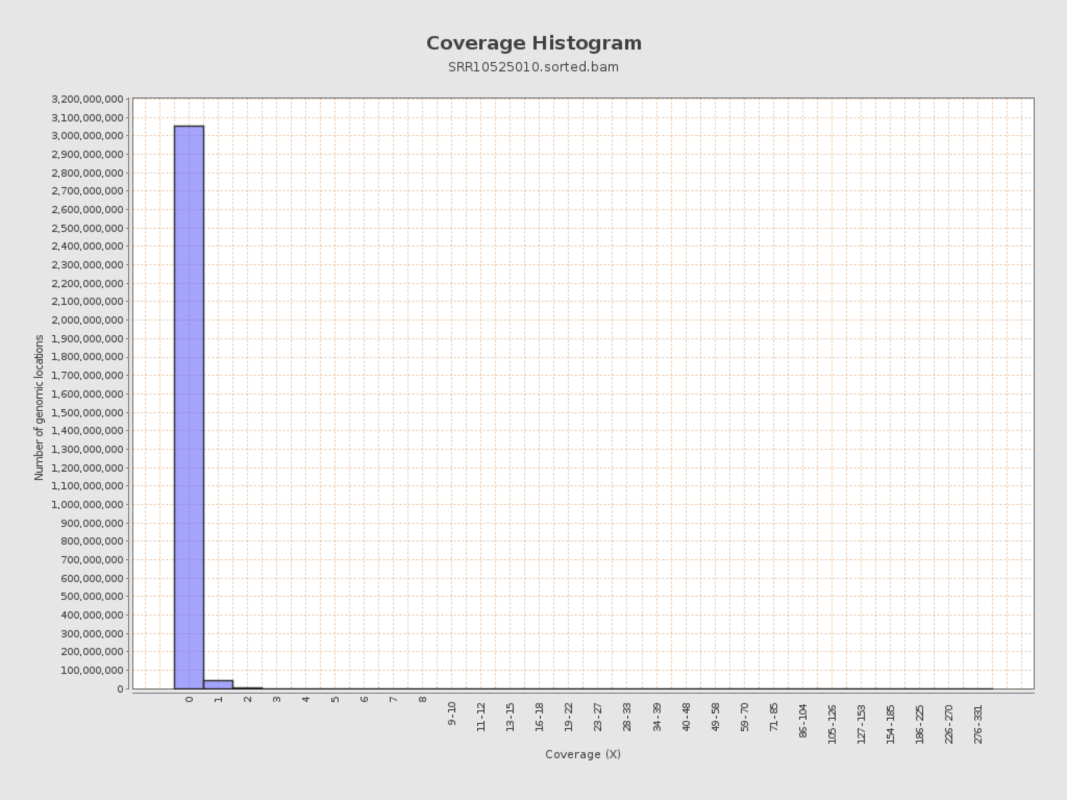
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5072491	0.0204	0.2742
chr2	243199373	4484228	0.0184	0.1863
chr3	198022430	2592984	0.0131	0.1195
chr4	191154276	2989443	0.0156	0.1344
chr5	180915260	2047574	0.0113	0.1118
chr6	171115067	3185729	0.0186	0.1694
chr7	159138663	2705540	0.017	0.1982

chr8	146364022	2764622	0.0189	0.1655
chr9	141213431	1337145	0.0095	0.1244
chr10	135534747	2417470	0.0178	0.1652
chr11	135006516	1990053	0.0147	0.1529
chr12	133851895	2614574	0.0195	0.1465
chr13	115169878	1299905	0.0113	0.1115
chr14	107349540	1088399	0.0101	0.1066
chr15	102531392	1328453	0.013	0.1231
chr16	90354753	1566883	0.0173	0.1414
chr17	81195210	1139415	0.014	0.1438
chr18	78077248	938759	0.012	0.1836
chr19	59128983	1222683	0.0207	0.194
chr20	63025520	1162889	0.0185	0.1423
chr21	48129895	687168	0.0143	0.1288
chr22	51304566	658307	0.0128	0.1174
chrMT	16571	13594	0.8203	1.019
chrX	155270560	1984863	0.0128	0.1281
chrY	59373566	125739	0.0021	0.0608

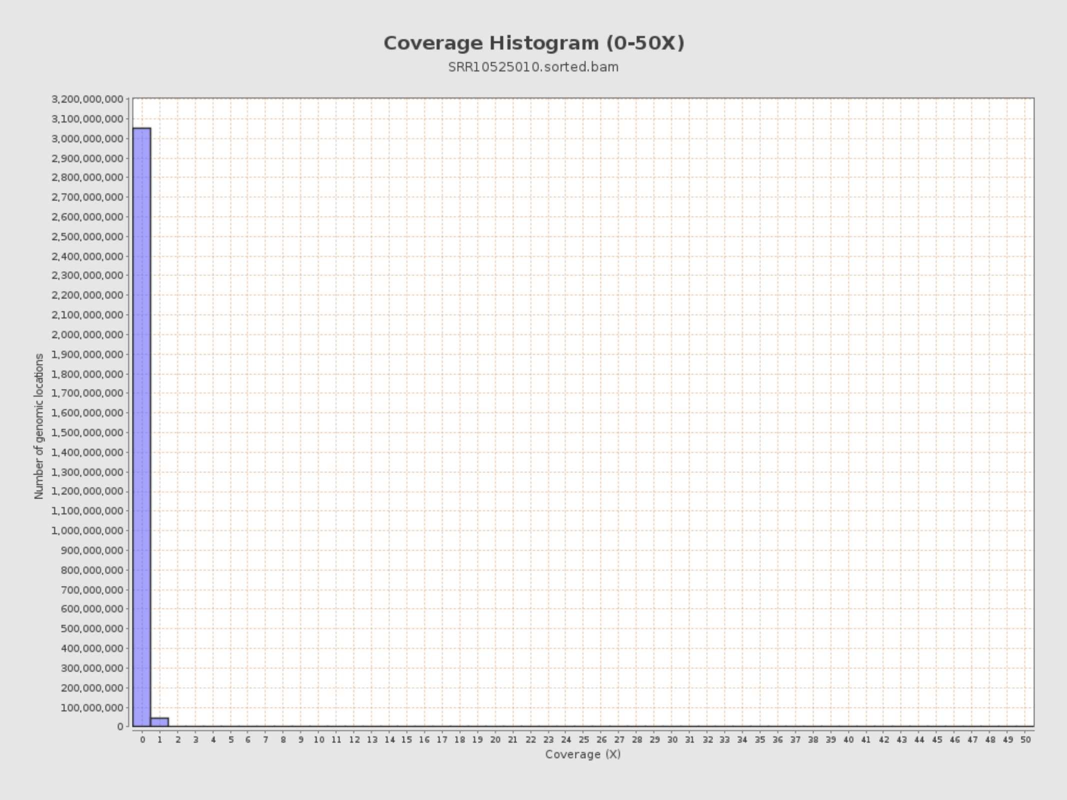
3. Results : Coverage across reference



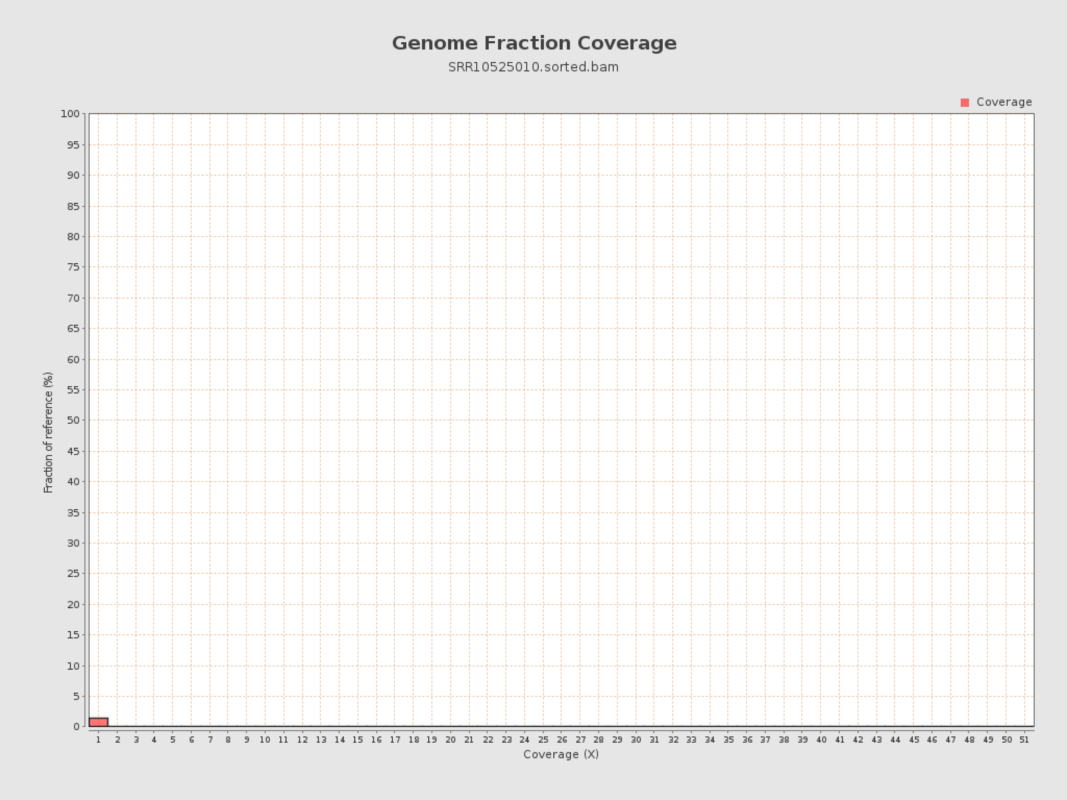
4. Results : Coverage Histogram



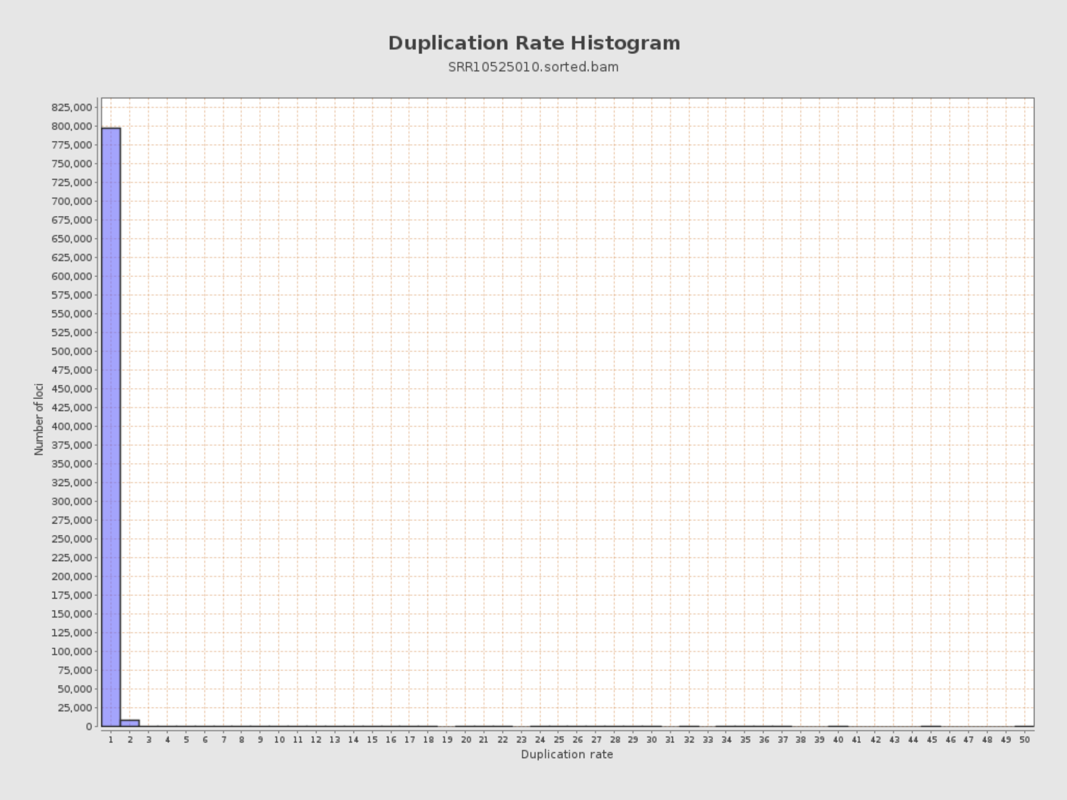
5. Results : Coverage Histogram (0-50X)



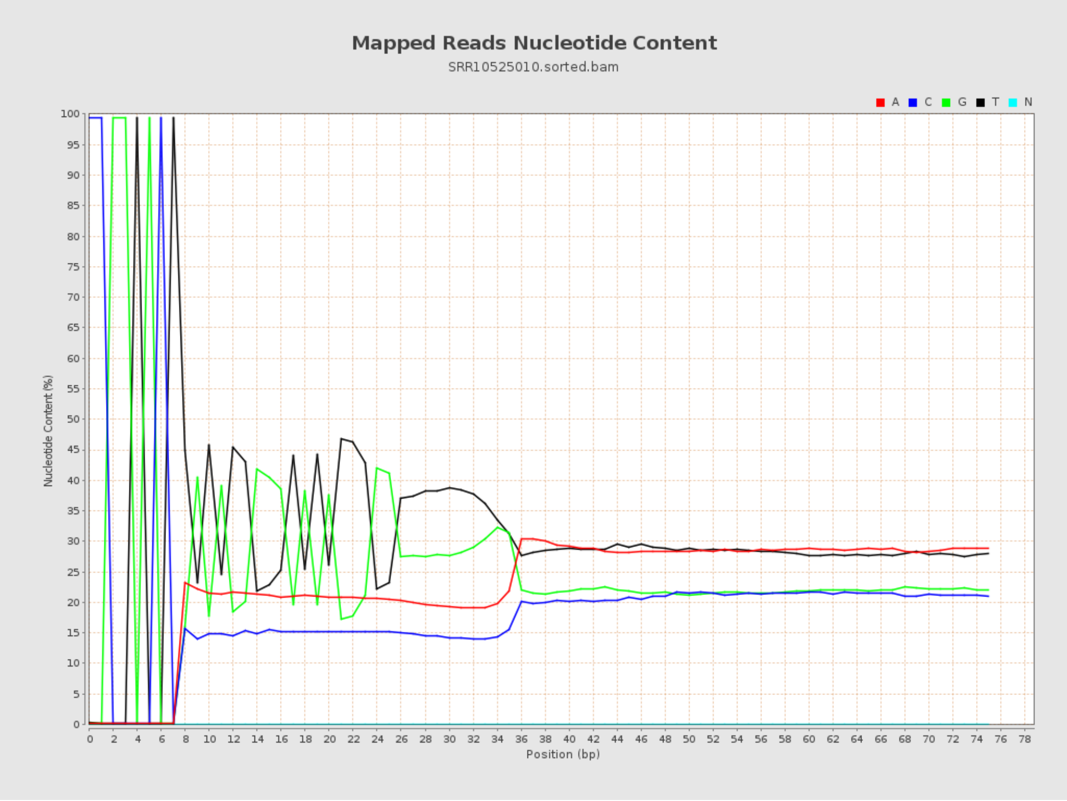
6. Results : Genome Fraction Coverage



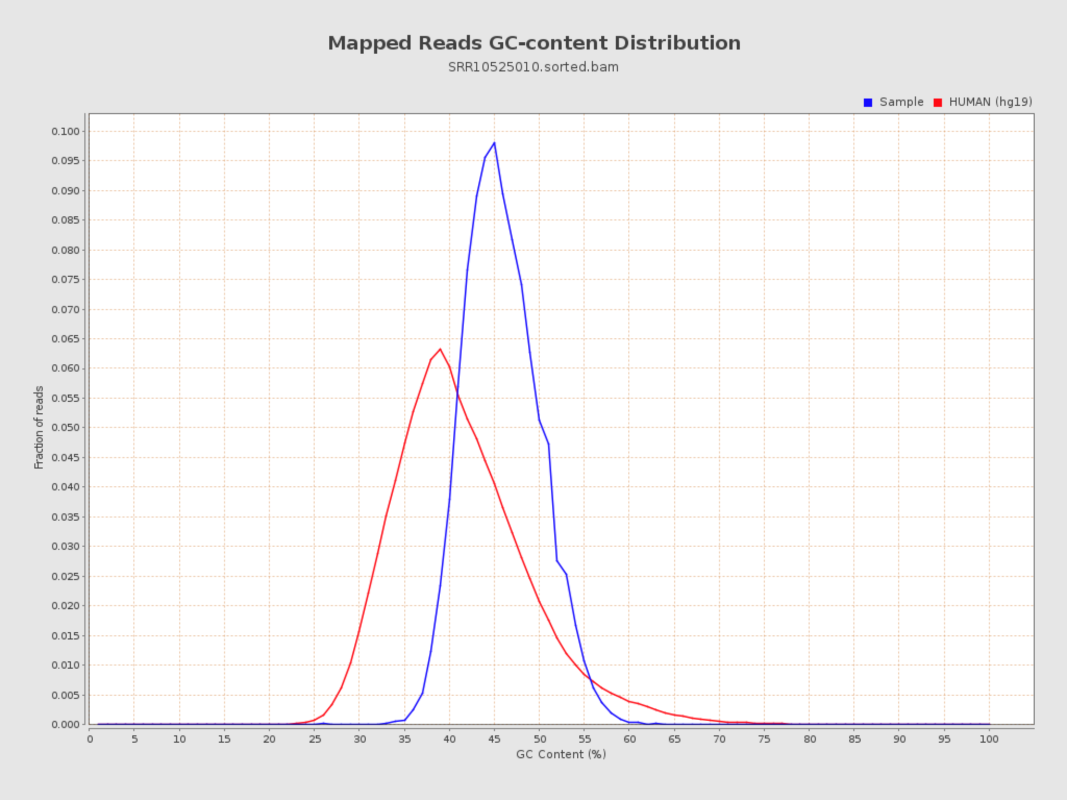
7. Results : Duplication Rate Histogram



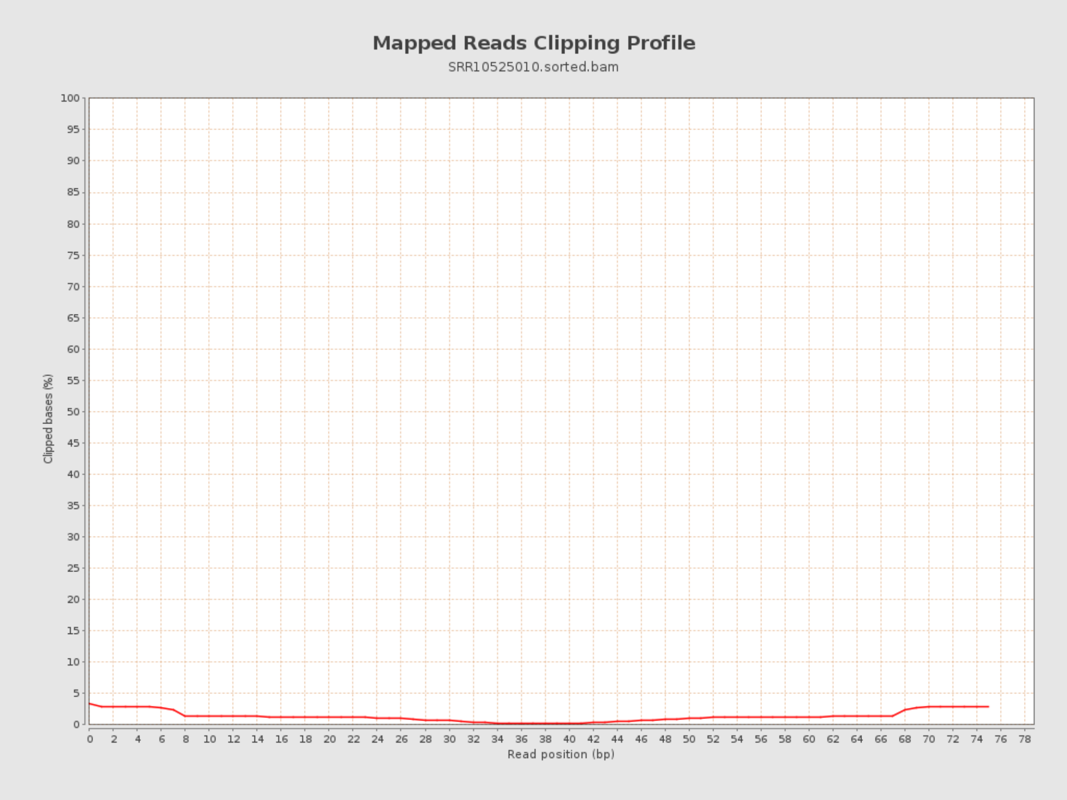
8. Results : Mapped Reads Nucleotide Content



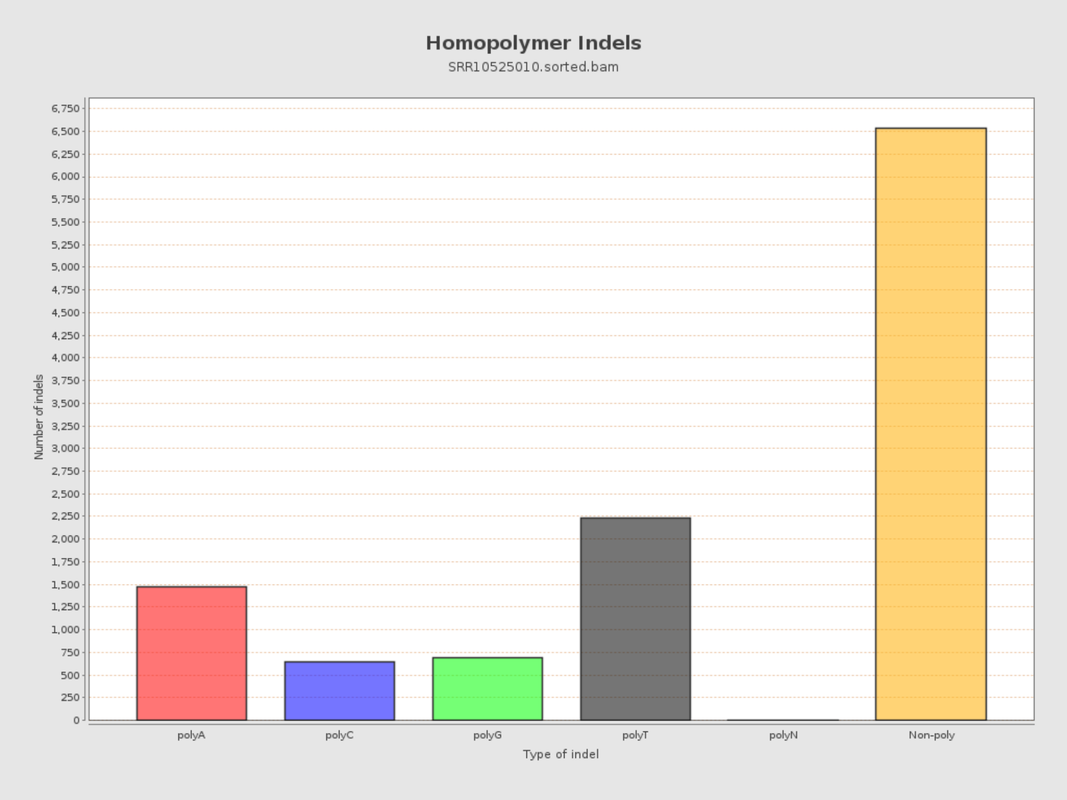
9. Results : Mapped Reads GC-content Distribution



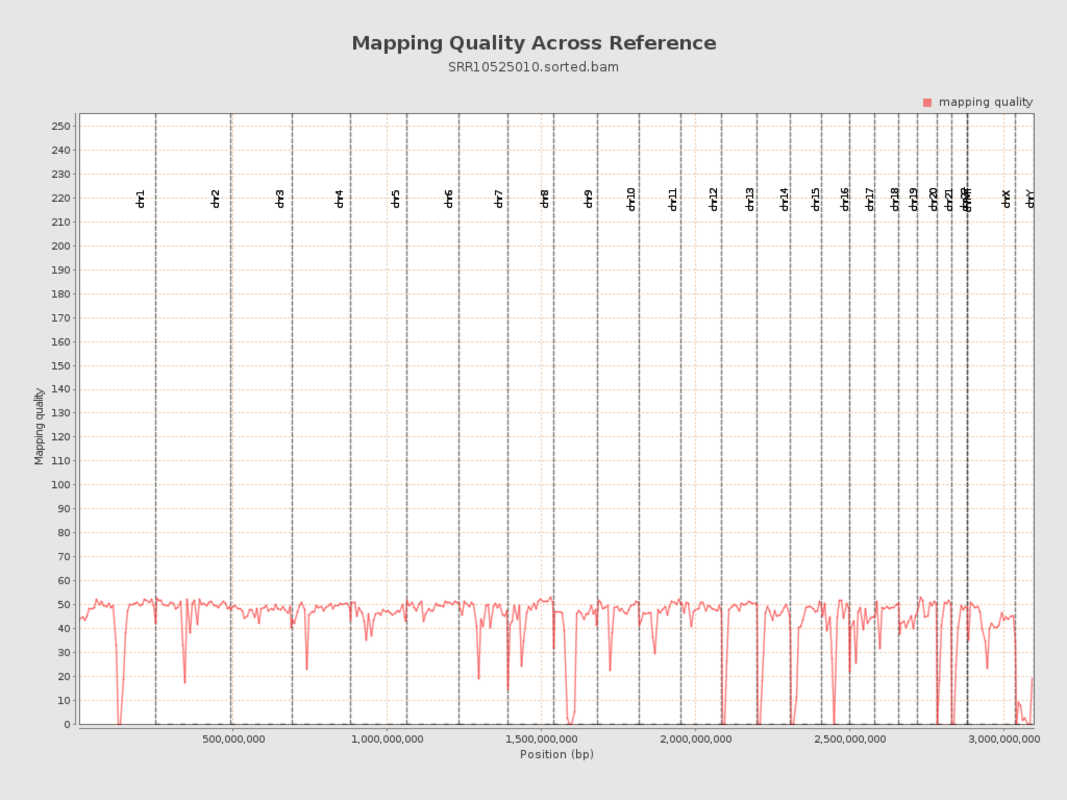
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram