Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:48:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525048.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_SRR10525048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:48:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	531,306
Mapped reads	496,681 / 93.48%
Unmapped reads	34,625 / 6.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,388 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	14,226 / 2.68%
Duplication rate	2.42%
Clipped reads	497,496 / 93.64%

2.2. ACGT Content

Number/percentage of A's	8,208,047 / 27.39%
Number/percentage of C's	5,841,816 / 19.49%
Number/percentage of T's	9,238,260 / 30.82%
Number/percentage of G's	6,679,909 / 22.29%
Number/percentage of N's	3,479 / 0.01%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.1232

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

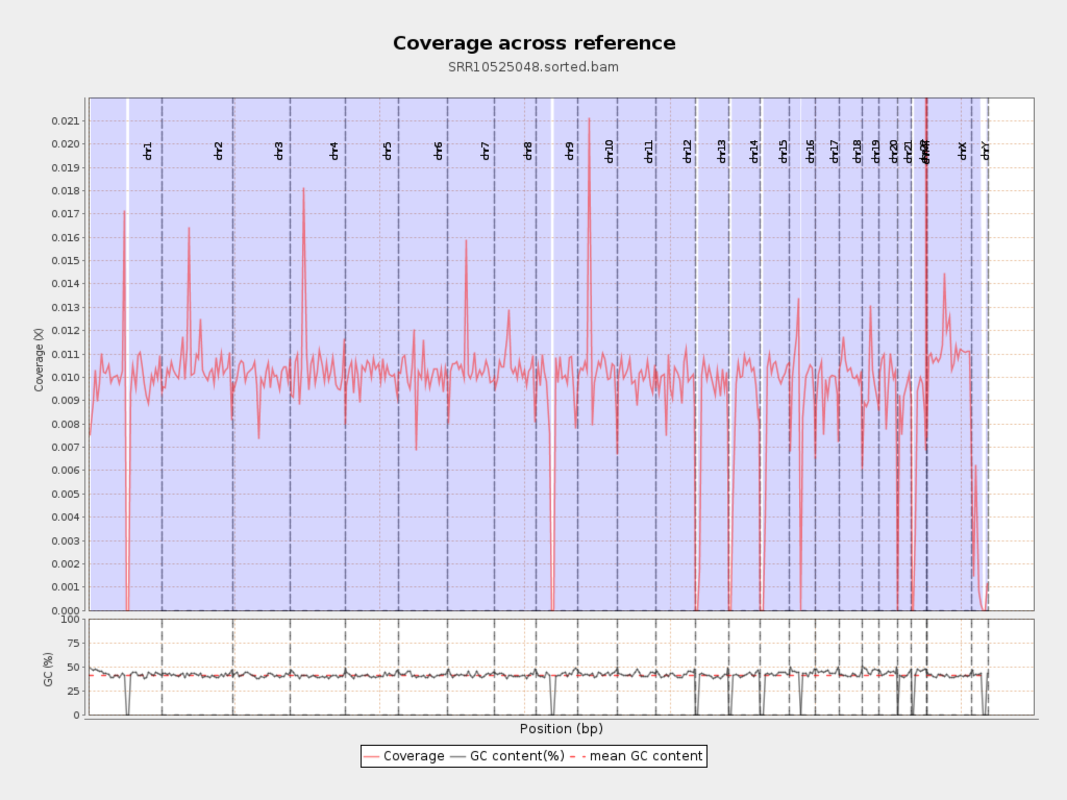
General error rate	0.49%
Mismatches	143,097
Insertions	2,191
Mapped reads with at least one insertion	0.44%
Deletions	6,496
Mapped reads with at least one deletion	1.3%
Homopolymer indels	43.93%

2.6. Chromosome stats

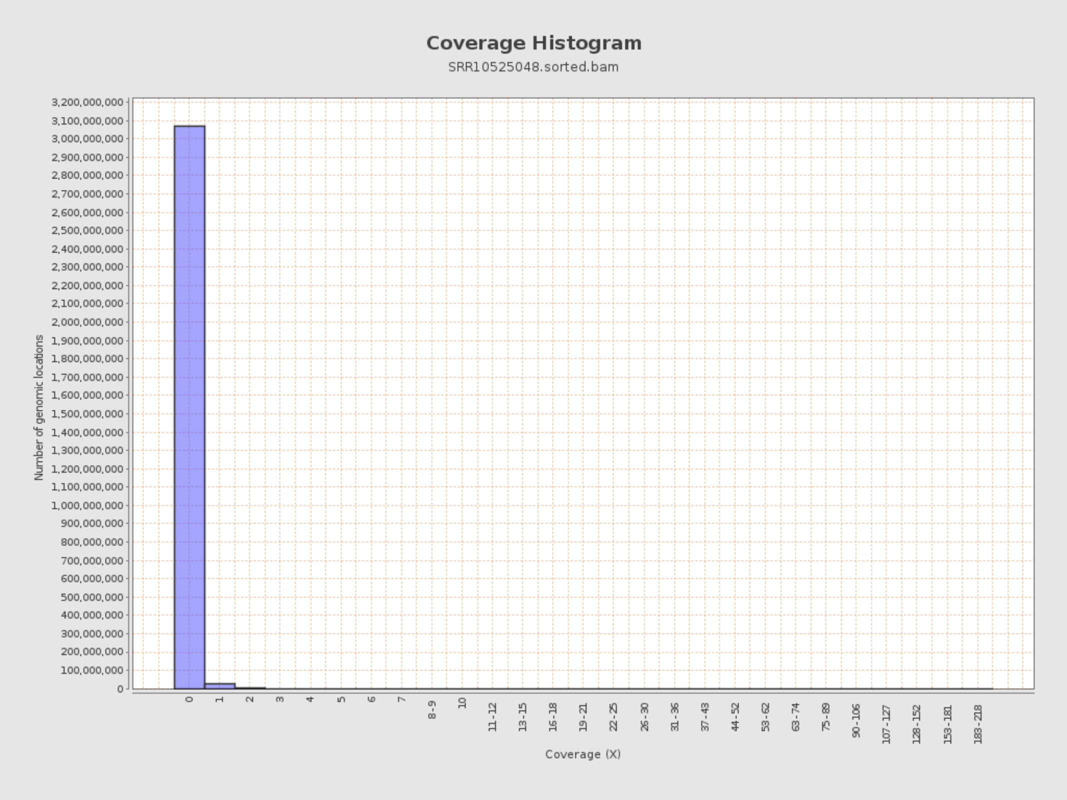
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2377269	0.0095	0.1909
chr2	243199373	2576224	0.0106	0.1364
chr3	198022430	1985697	0.01	0.1044
chr4	191154276	2008595	0.0105	0.1117
chr5	180915260	1839504	0.0102	0.1053
chr6	171115067	1731456	0.0101	0.1084
chr7	159138663	1671297	0.0105	0.1367

chr8	146364022	1518457	0.0104	0.1395
chr9	141213431	1250268	0.0089	0.1079
chr10	135534747	1460962	0.0108	0.1358
chr11	135006516	1348809	0.01	0.1129
chr12	133851895	1319174	0.0099	0.1043
chr13	115169878	955502	0.0083	0.095
chr14	107349540	908443	0.0085	0.0965
chr15	102531392	861224	0.0084	0.0958
chr16	90354753	844533	0.0093	0.1038
chr17	81195210	767419	0.0095	0.1037
chr18	78077248	811795	0.0104	0.1521
chr19	59128983	566529	0.0096	0.1475
chr20	63025520	624667	0.0099	0.105
chr21	48129895	398943	0.0083	0.1011
chr22	51304566	332004	0.0065	0.0835
chrMT	16571	5482	0.3308	0.6443
chrX	155270560	1721246	0.0111	0.1132
chrY	59373566	96647	0.0016	0.0616

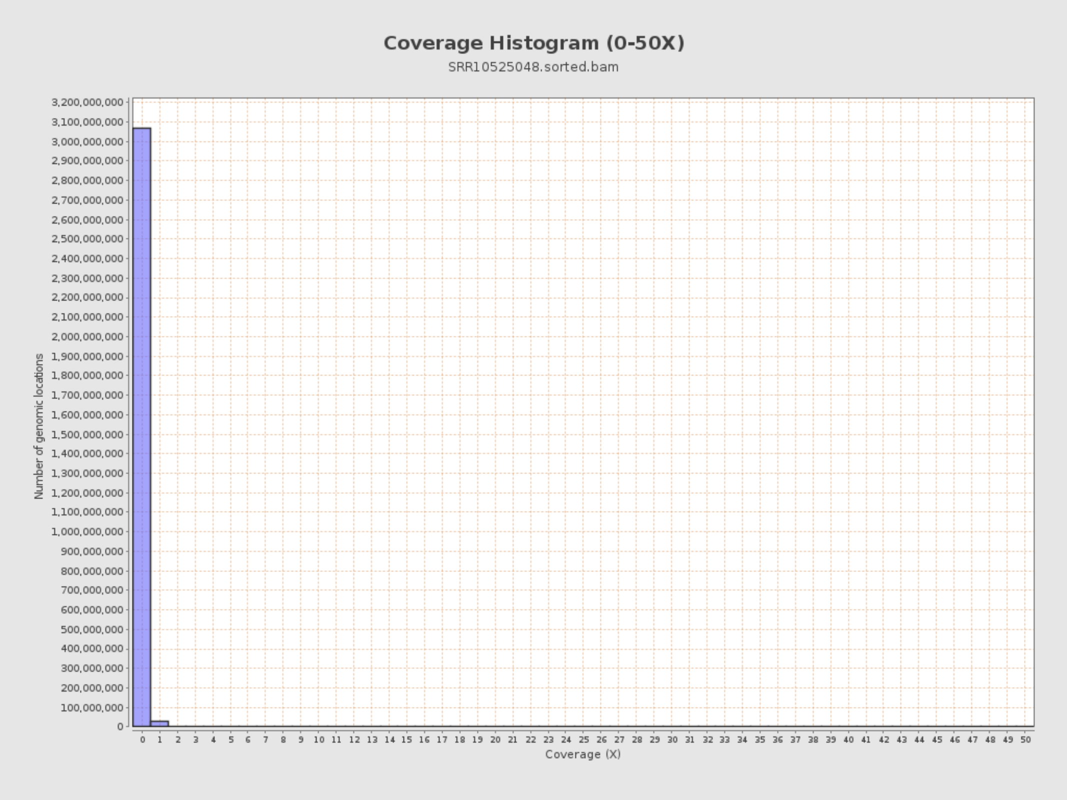
3. Results : Coverage across reference



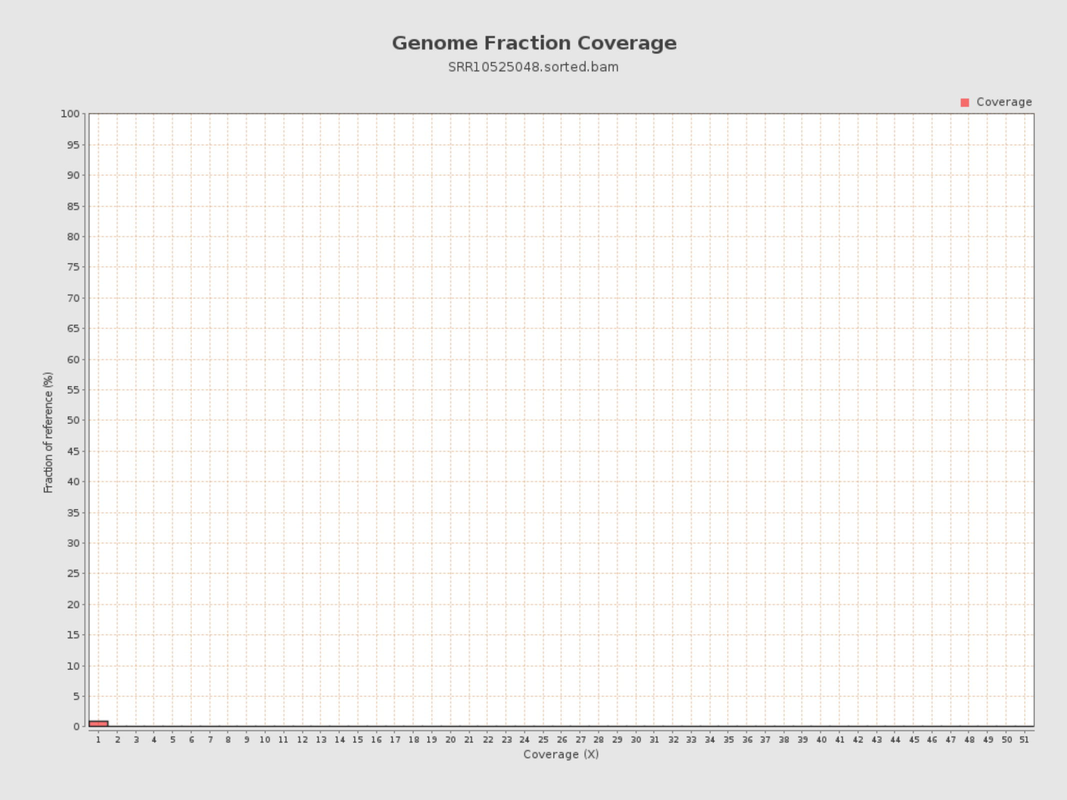
4. Results : Coverage Histogram



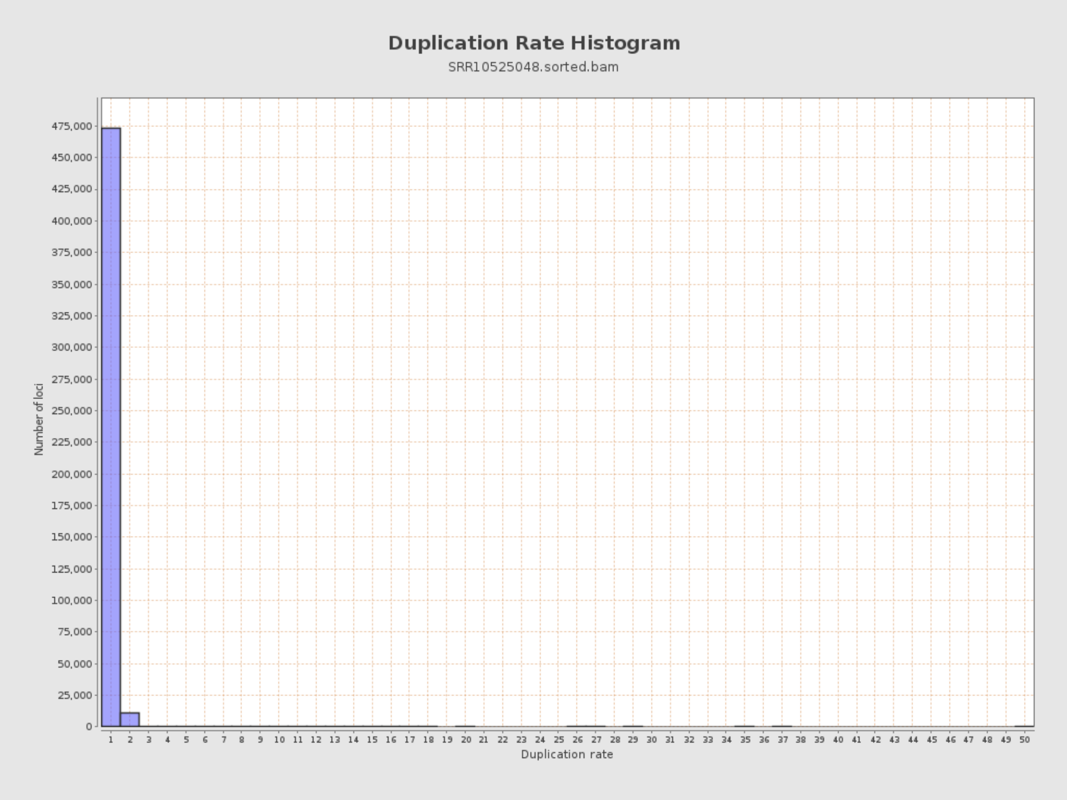
5. Results : Coverage Histogram (0-50X)



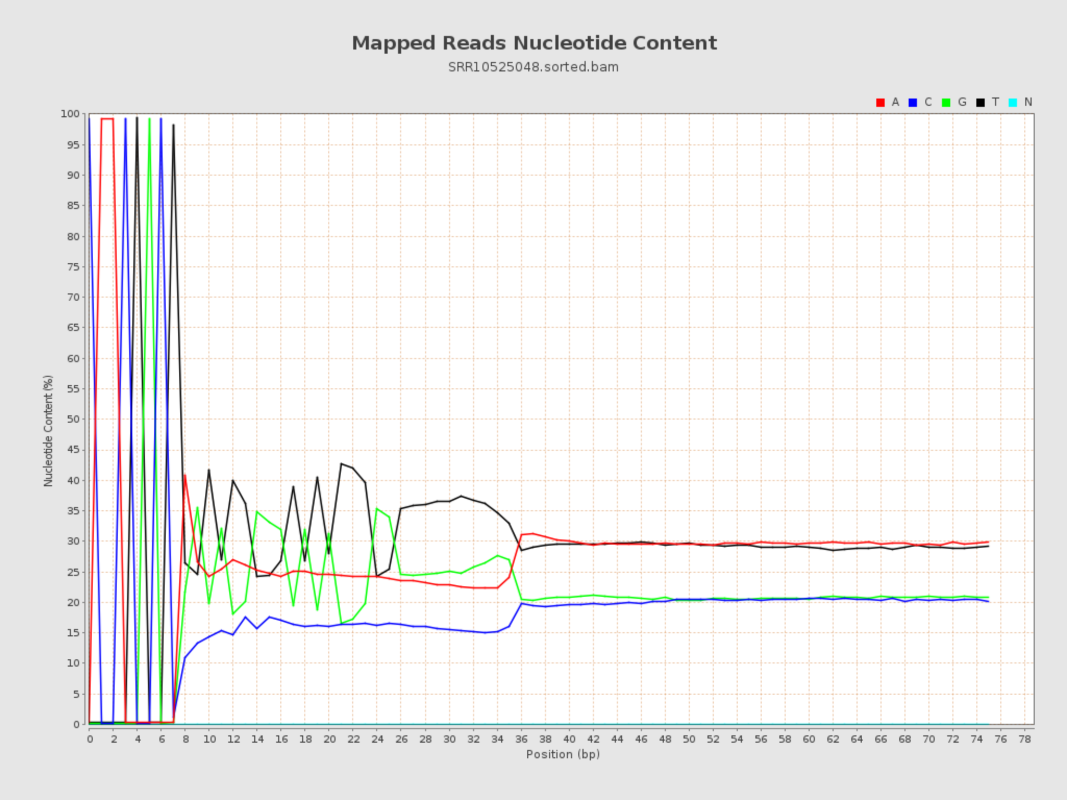
6. Results : Genome Fraction Coverage



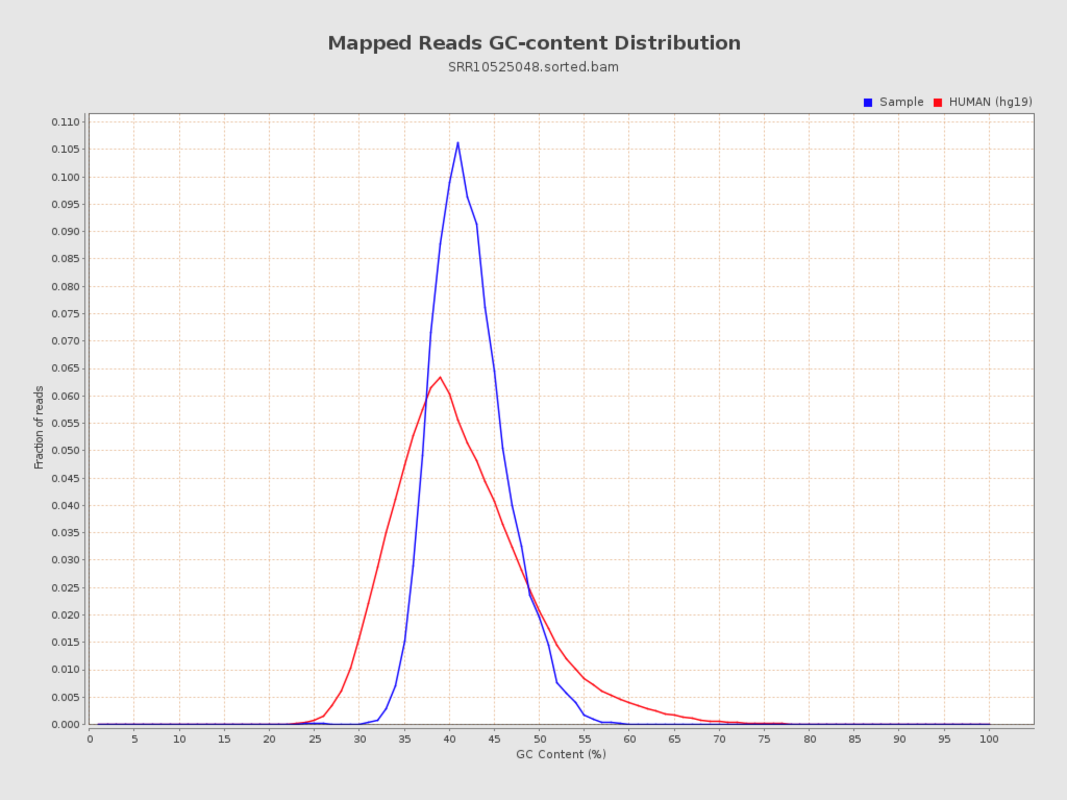
7. Results : Duplication Rate Histogram



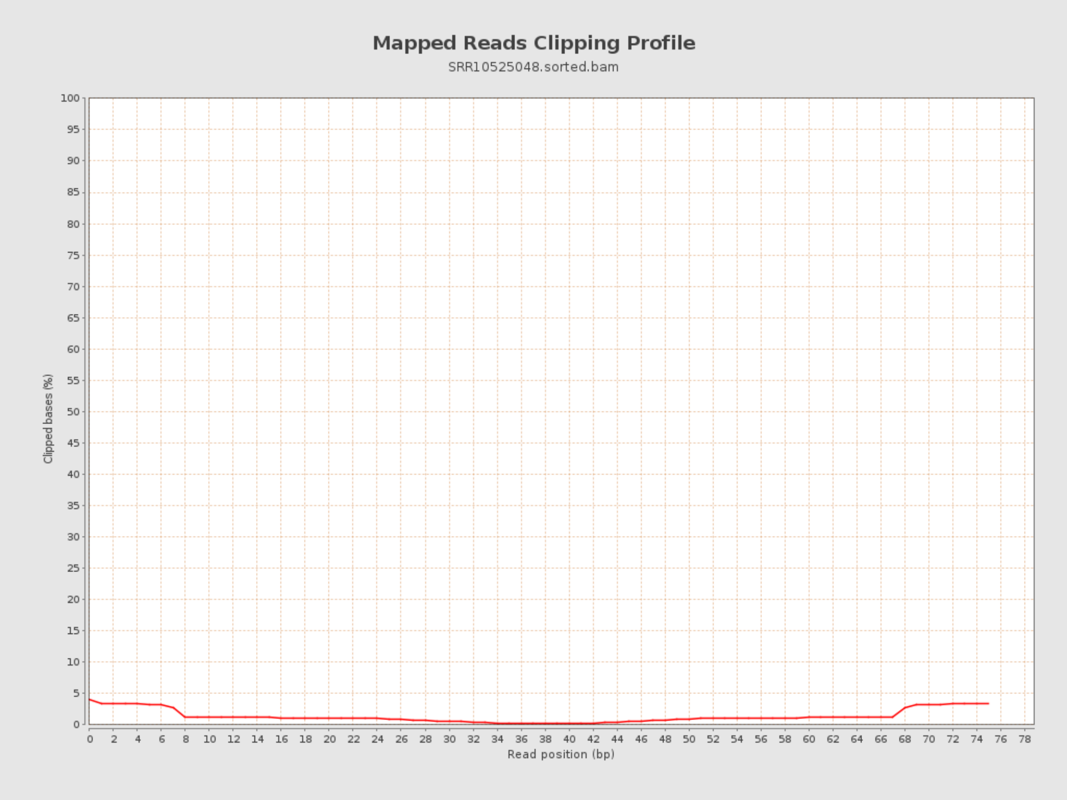
8. Results : Mapped Reads Nucleotide Content



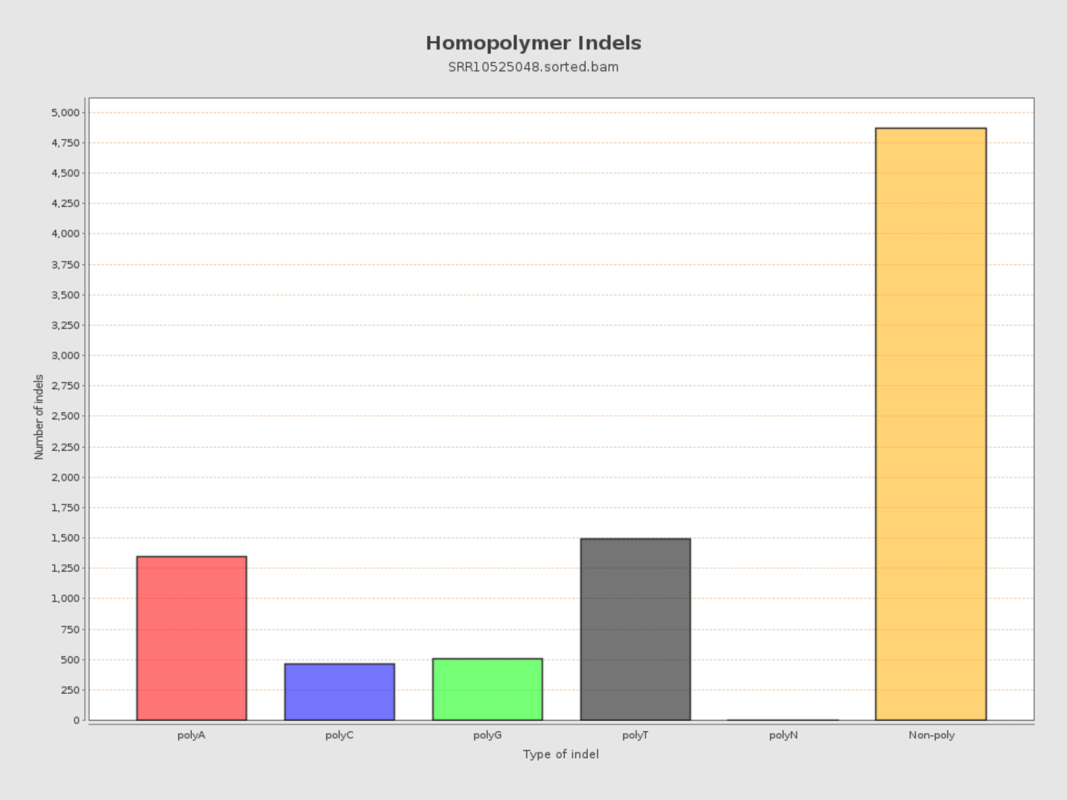
9. Results : Mapped Reads GC-content Distribution



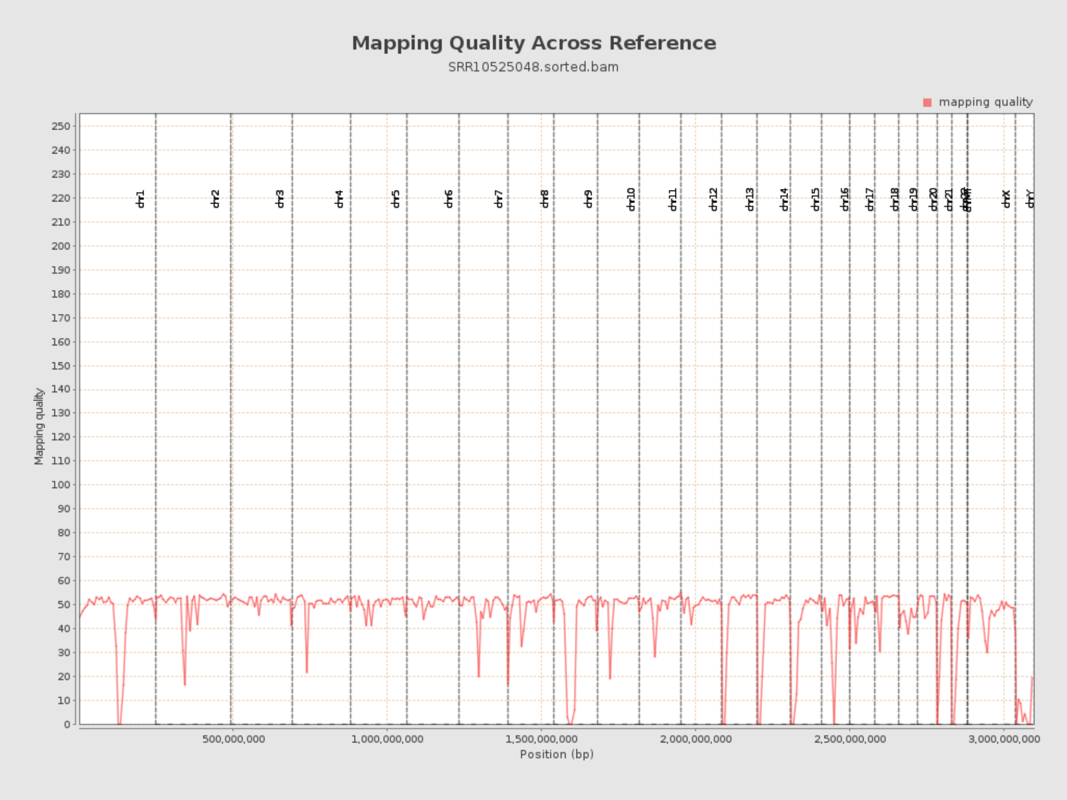
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram