Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:28:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525038.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_SRR10525038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:28:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,218,587
Mapped reads	1,119,696 / 91.88%
Unmapped reads	98,891 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,622 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	34,104 / 2.8%
Duplication rate	2.28%
Clipped reads	1,120,703 / 91.97%

2.2. ACGT Content

Number/percentage of A's	16,074,954 / 24.74%
Number/percentage of C's	11,471,151 / 17.66%
Number/percentage of T's	21,512,796 / 33.11%
Number/percentage of G's	15,911,438 / 24.49%
Number/percentage of N's	701 / 0%
GC Percentage	42.15%

2.3. Coverage

Mean	0.021

Standard Deviation	0.2008

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

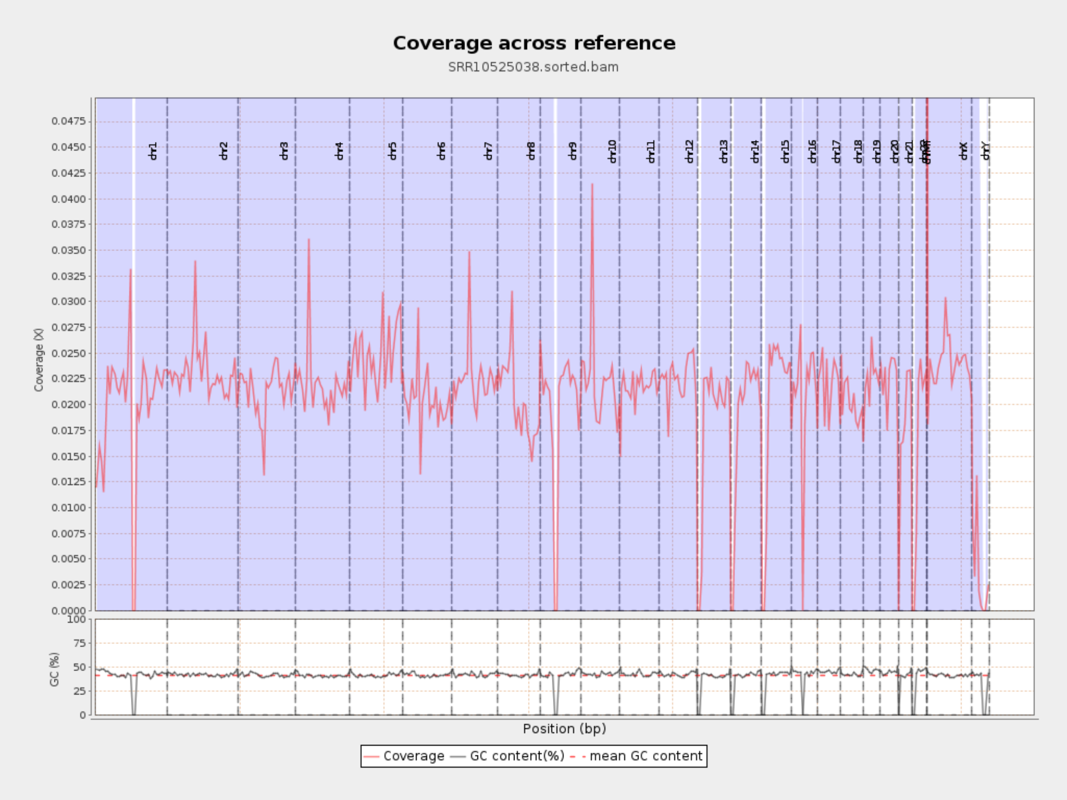
General error rate	0.5%
Mismatches	319,349
Insertions	4,137
Mapped reads with at least one insertion	0.37%
Deletions	12,227
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.26%

2.6. Chromosome stats

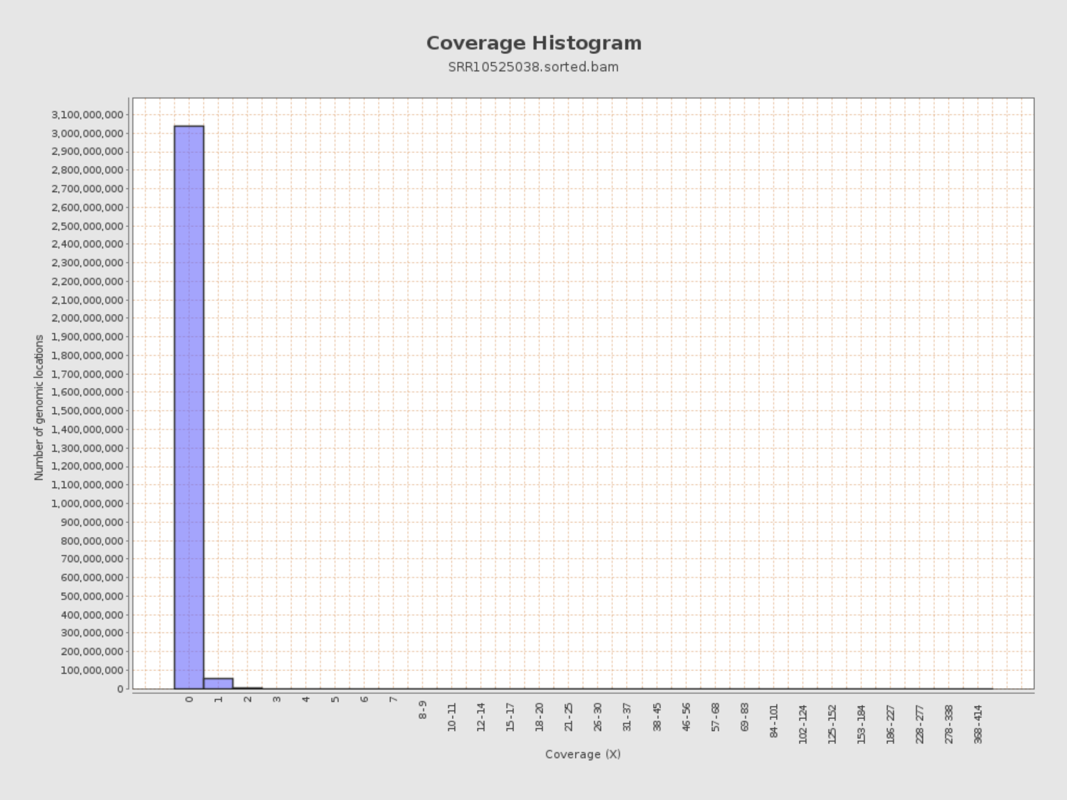
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4908227	0.0197	0.3148
chr2	243199373	5633027	0.0232	0.2326
chr3	198022430	4226955	0.0213	0.1568
chr4	191154276	4218517	0.0221	0.1761
chr5	180915260	4516905	0.025	0.1694
chr6	171115067	3498571	0.0204	0.1772
chr7	159138663	3600654	0.0226	0.238

chr8	146364022	2980272	0.0204	0.2153
chr9	141213431	2741988	0.0194	0.1787
chr10	135534747	3063717	0.0226	0.22
chr11	135006516	2939621	0.0218	0.1891
chr12	133851895	3016950	0.0225	0.1615
chr13	115169878	2063063	0.0179	0.145
chr14	107349540	1970789	0.0184	0.1488
chr15	102531392	2025200	0.0198	0.1558
chr16	90354753	1855330	0.0205	0.1599
chr17	81195210	1804553	0.0222	0.1763
chr18	78077248	1567616	0.0201	0.2692
chr19	59128983	1330672	0.0225	0.2324
chr20	63025520	1411346	0.0224	0.1613
chr21	48129895	857253	0.0178	0.1571
chr22	51304566	804717	0.0157	0.133
chrMT	16571	7368	0.4446	0.7597
chrX	155270560	3739944	0.0241	0.177
chrY	59373566	208252	0.0035	0.1137

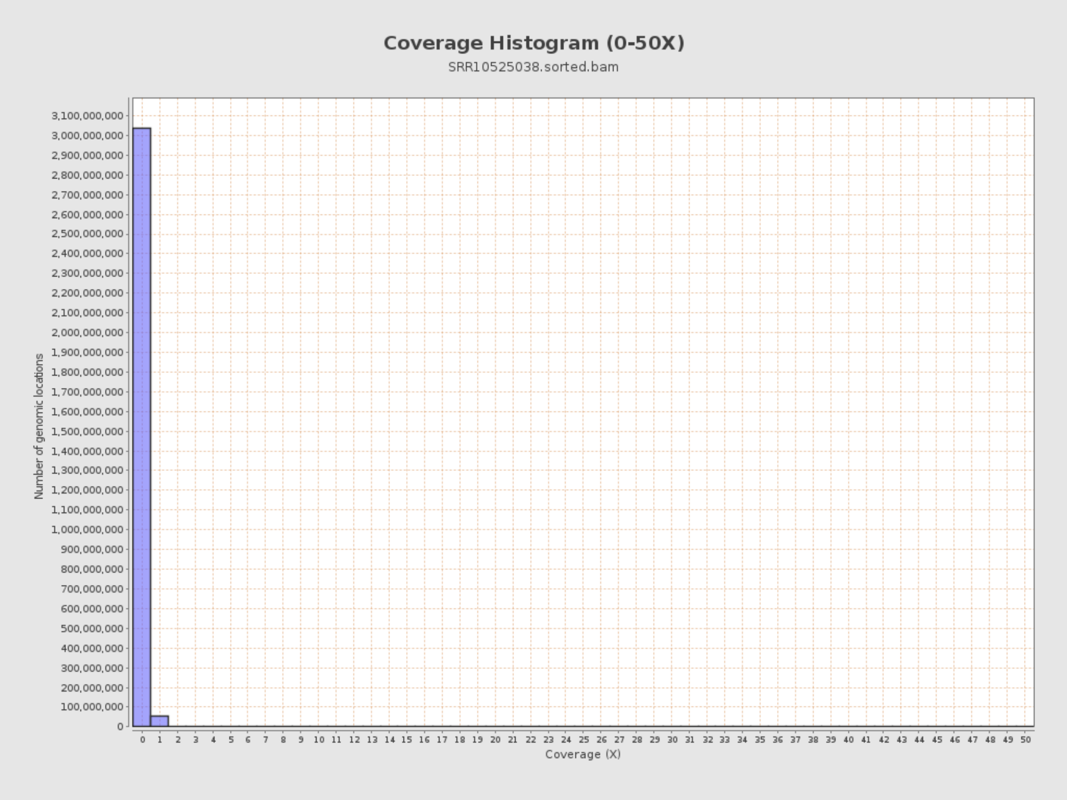
3. Results : Coverage across reference



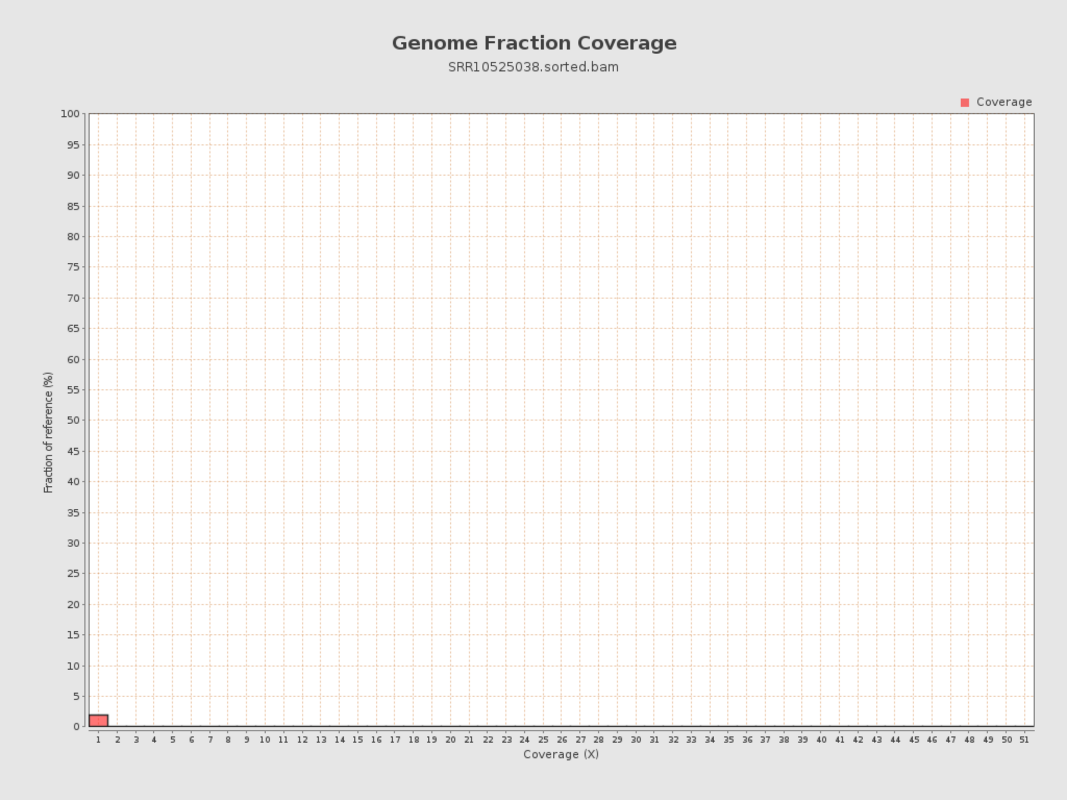
4. Results : Coverage Histogram



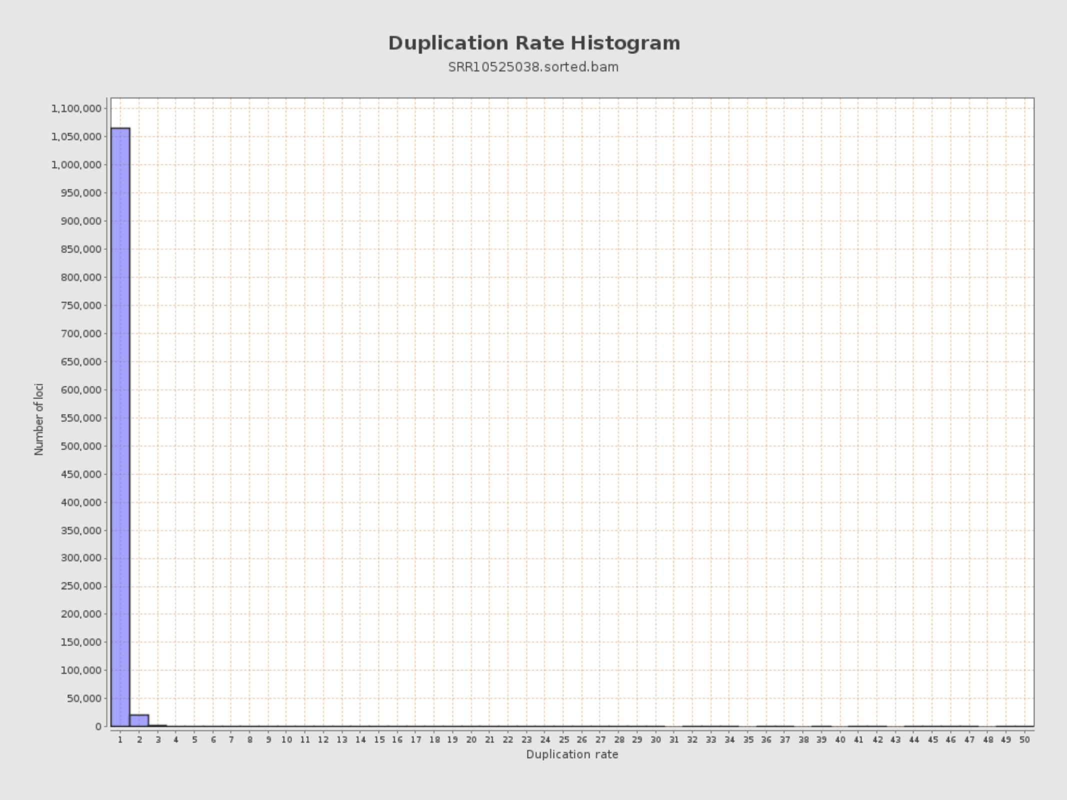
5. Results : Coverage Histogram (0-50X)



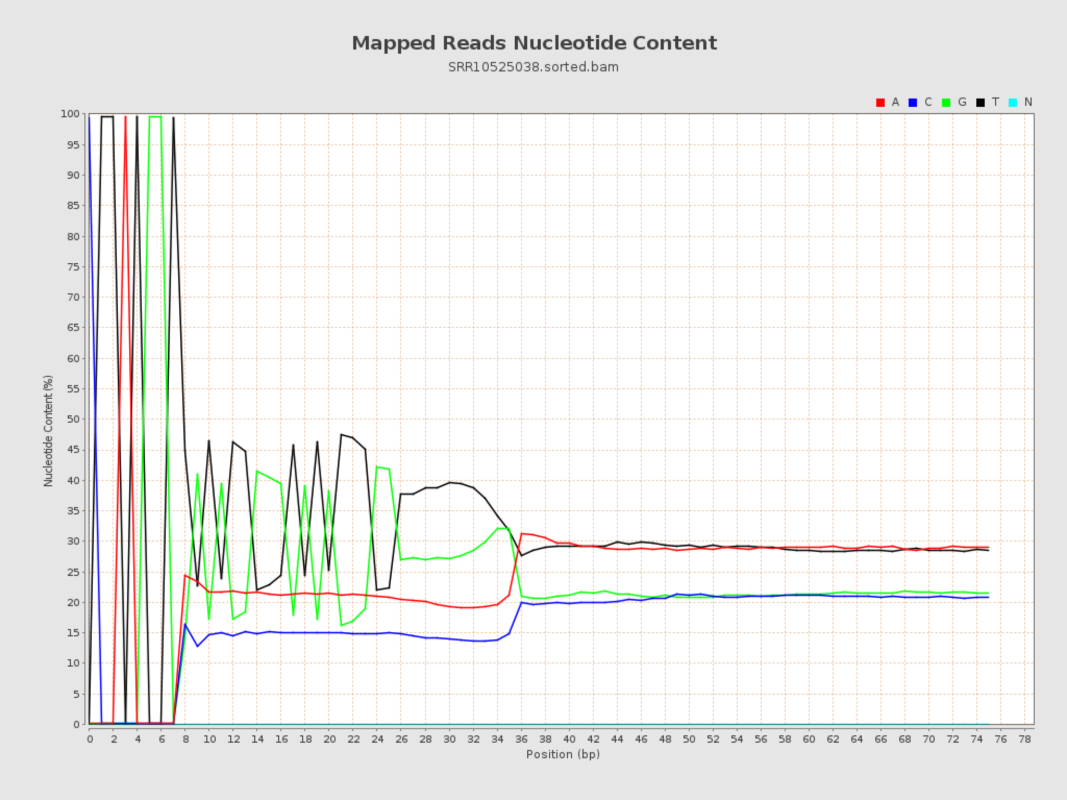
6. Results : Genome Fraction Coverage



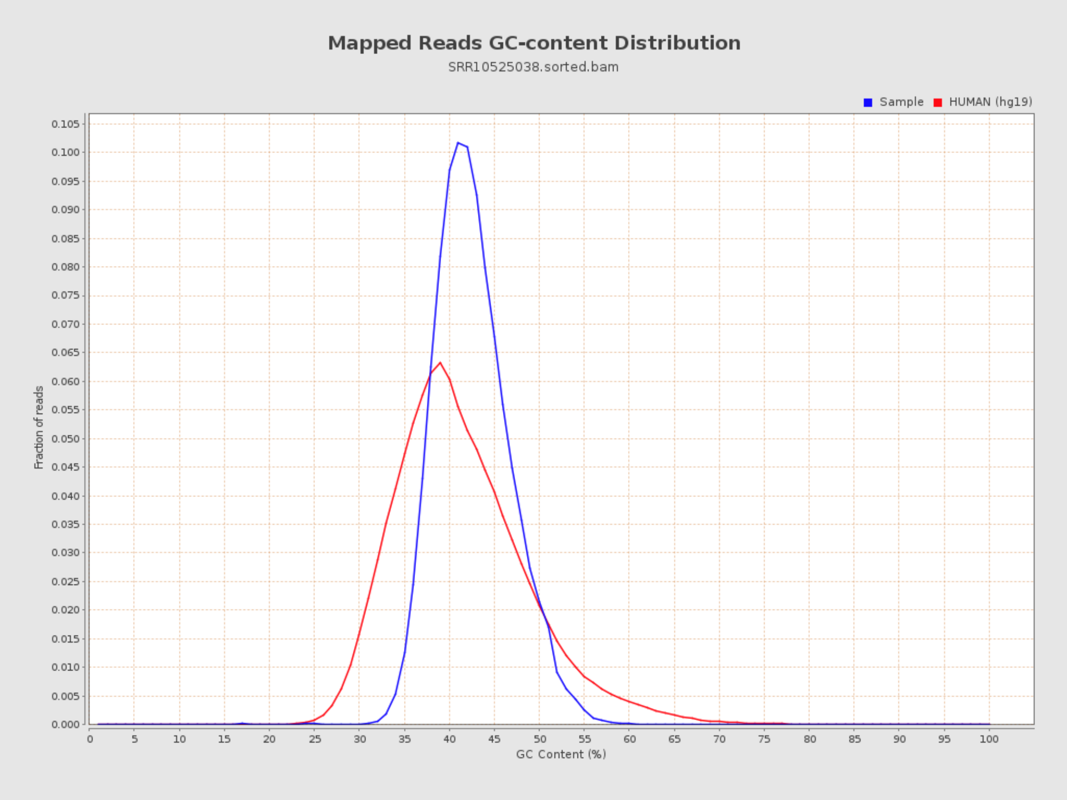
7. Results : Duplication Rate Histogram



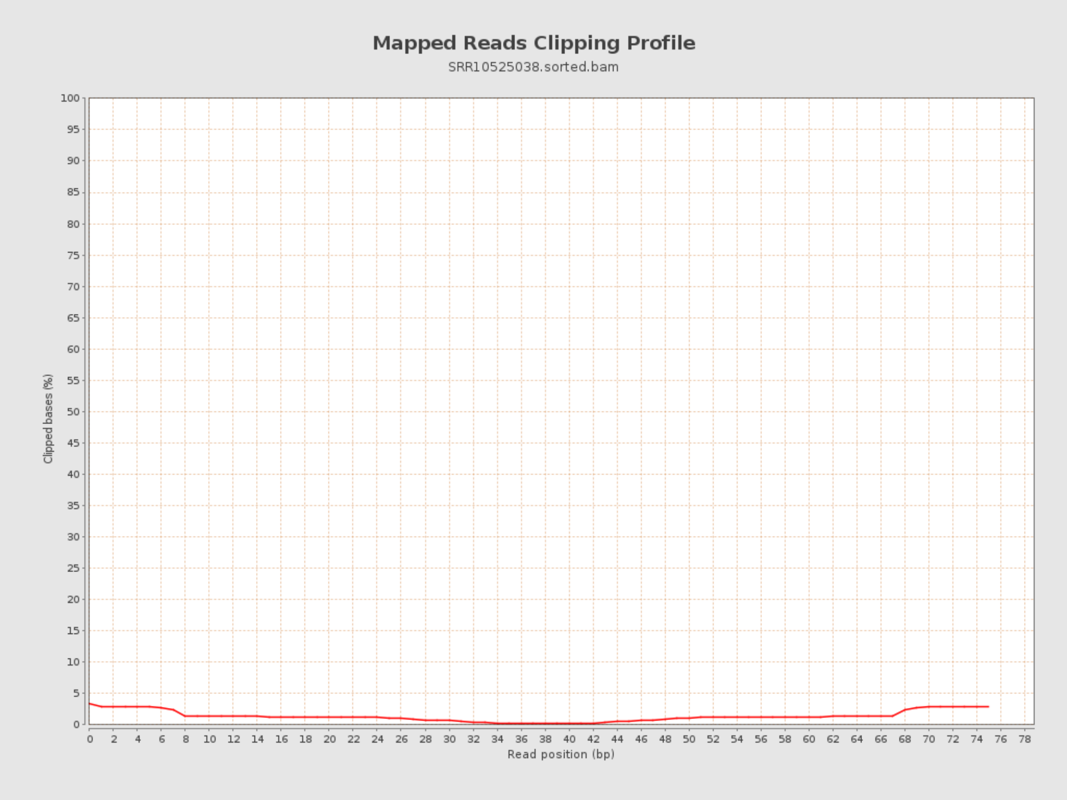
8. Results : Mapped Reads Nucleotide Content



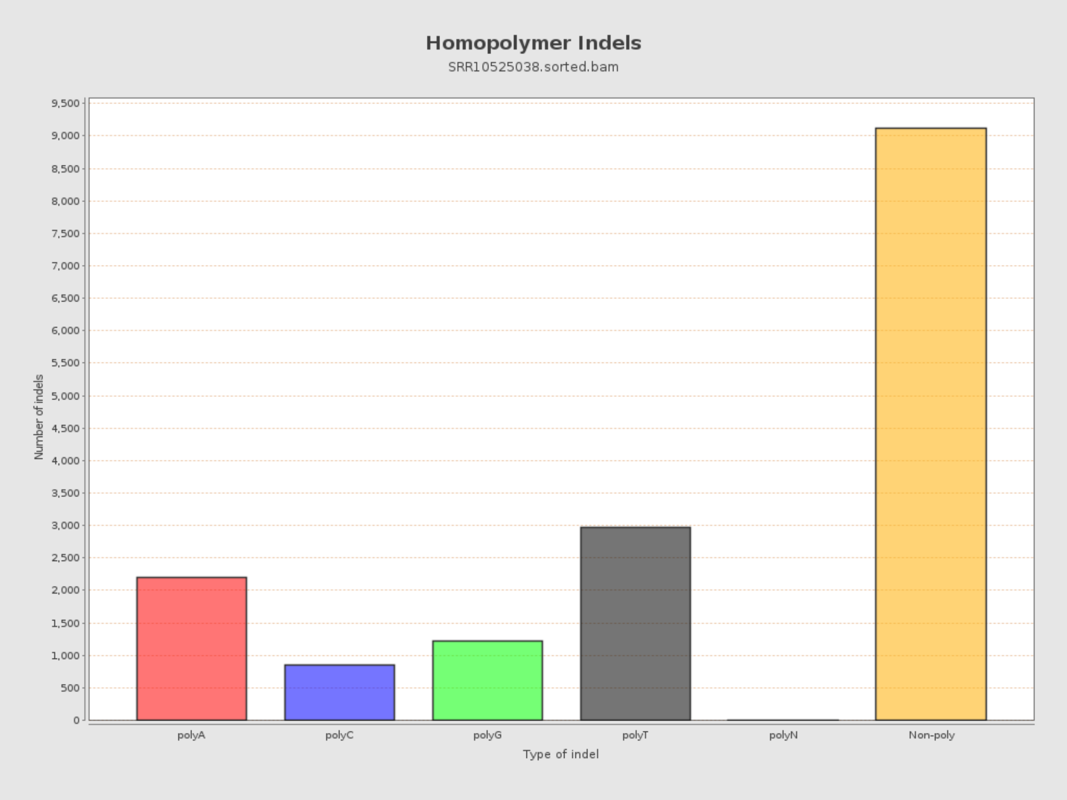
9. Results : Mapped Reads GC-content Distribution



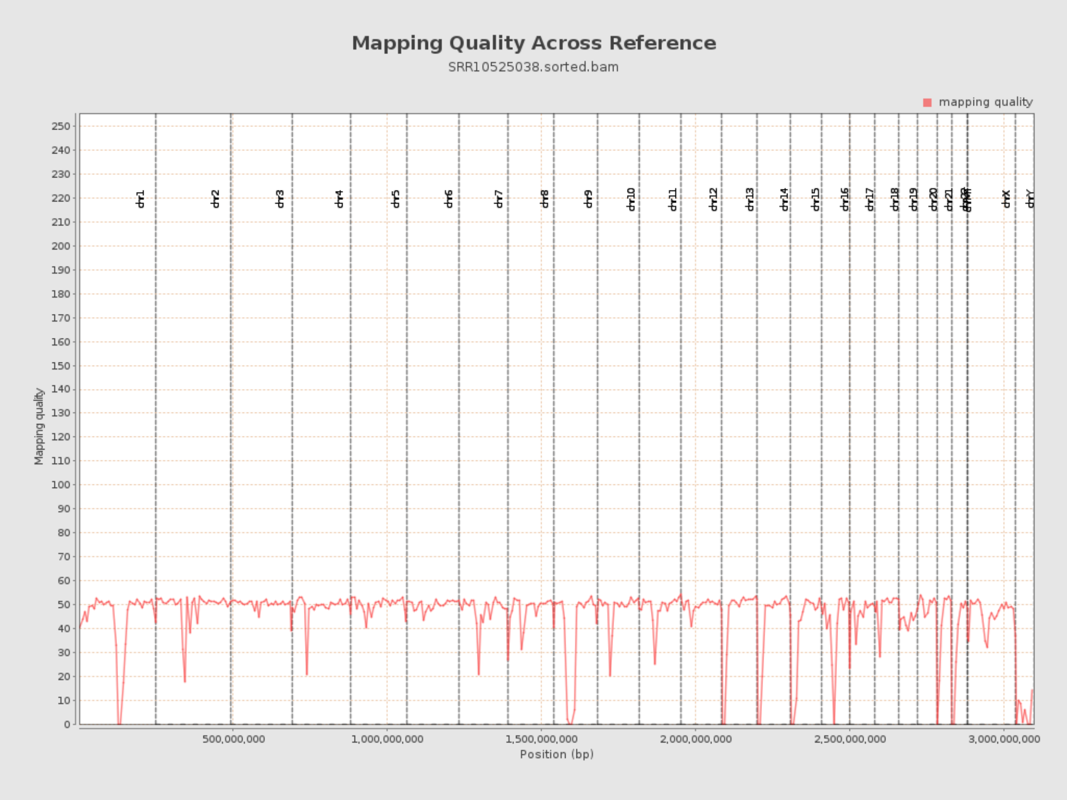
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram