Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:03:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524728.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_SRR10524728 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524728.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:03:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524728.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,349,659
Mapped reads	1,232,420 / 91.31%
Unmapped reads	117,239 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,381 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	49,339 / 3.66%
Duplication rate	3.09%
Clipped reads	1,233,579 / 91.4%

2.2. ACGT Content

Number/percentage of A's	16,307,253 / 23.21%
Number/percentage of C's	12,842,367 / 18.28%
Number/percentage of T's	22,903,342 / 32.6%
Number/percentage of G's	18,188,643 / 25.89%
Number/percentage of N's	8,038 / 0.01%
GC Percentage	44.17%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.2159

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

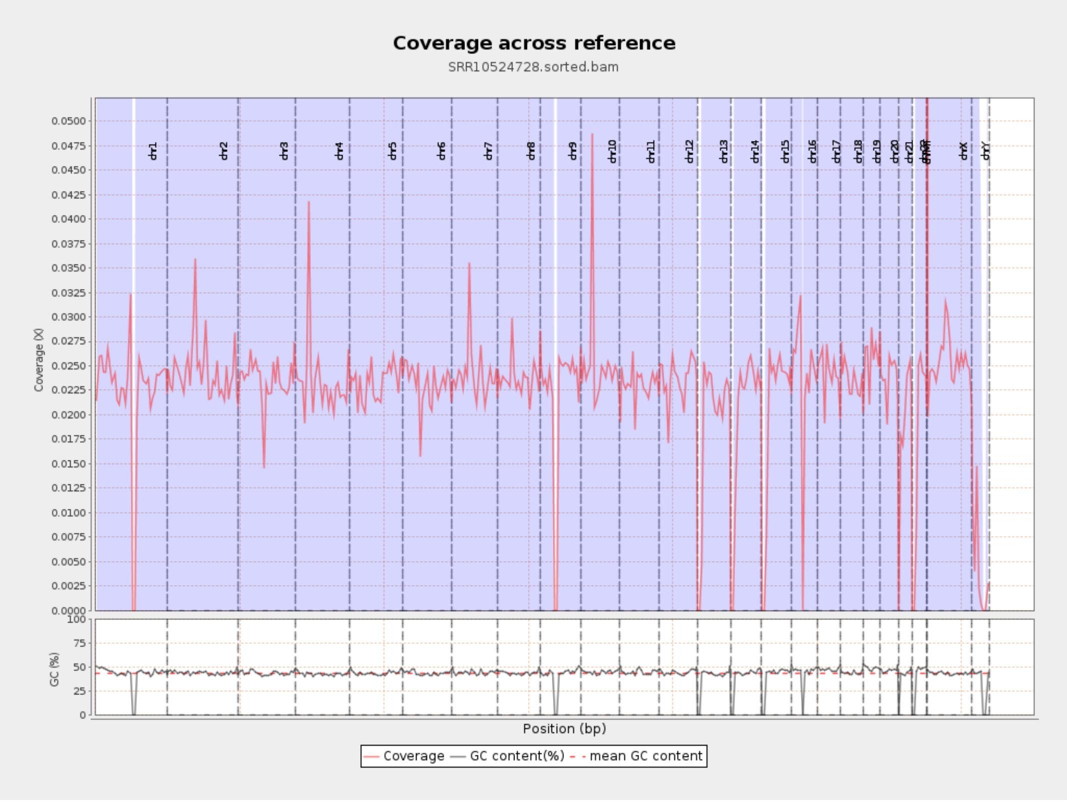
General error rate	0.52%
Mismatches	357,075
Insertions	4,800
Mapped reads with at least one insertion	0.39%
Deletions	14,118
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.04%

2.6. Chromosome stats

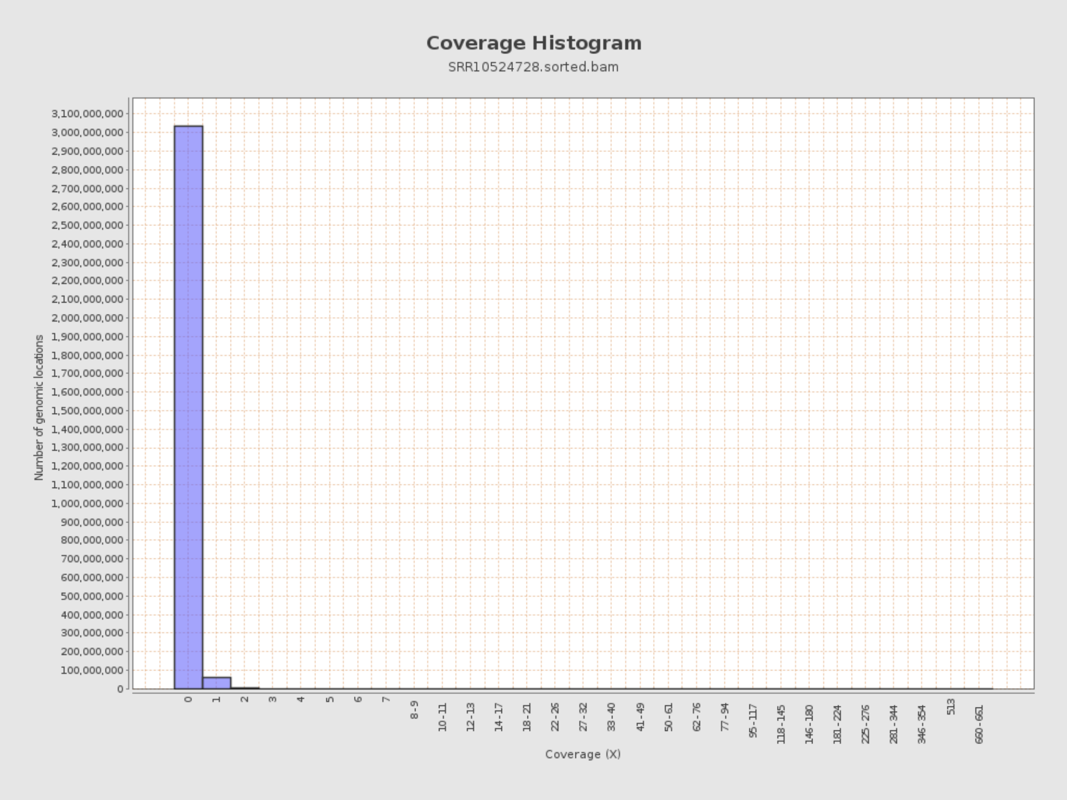
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5563575	0.0223	0.2896
chr2	243199373	5957505	0.0245	0.3316
chr3	198022430	4641371	0.0234	0.1698
chr4	191154276	4500017	0.0235	0.1882
chr5	180915260	4233382	0.0234	0.1674
chr6	171115067	3951938	0.0231	0.1825
chr7	159138663	3859997	0.0243	0.2555

chr8	146364022	3472759	0.0237	0.2001
chr9	141213431	3047724	0.0216	0.1917
chr10	135534747	3428050	0.0253	0.2572
chr11	135006516	3130096	0.0232	0.1906
chr12	133851895	3165977	0.0237	0.1709
chr13	115169878	2164736	0.0188	0.1526
chr14	107349540	2123464	0.0198	0.157
chr15	102531392	2041810	0.0199	0.1554
chr16	90354753	2114916	0.0234	0.1824
chr17	81195210	1974179	0.0243	0.1775
chr18	78077248	1846386	0.0236	0.2887
chr19	59128983	1523642	0.0258	0.2489
chr20	63025520	1503226	0.0239	0.1763
chr21	48129895	919626	0.0191	0.1648
chr22	51304566	876362	0.0171	0.1441
chrMT	16571	27474	1.658	1.6284
chrX	155270560	3959561	0.0255	0.186
chrY	59373566	244759	0.0041	0.1225

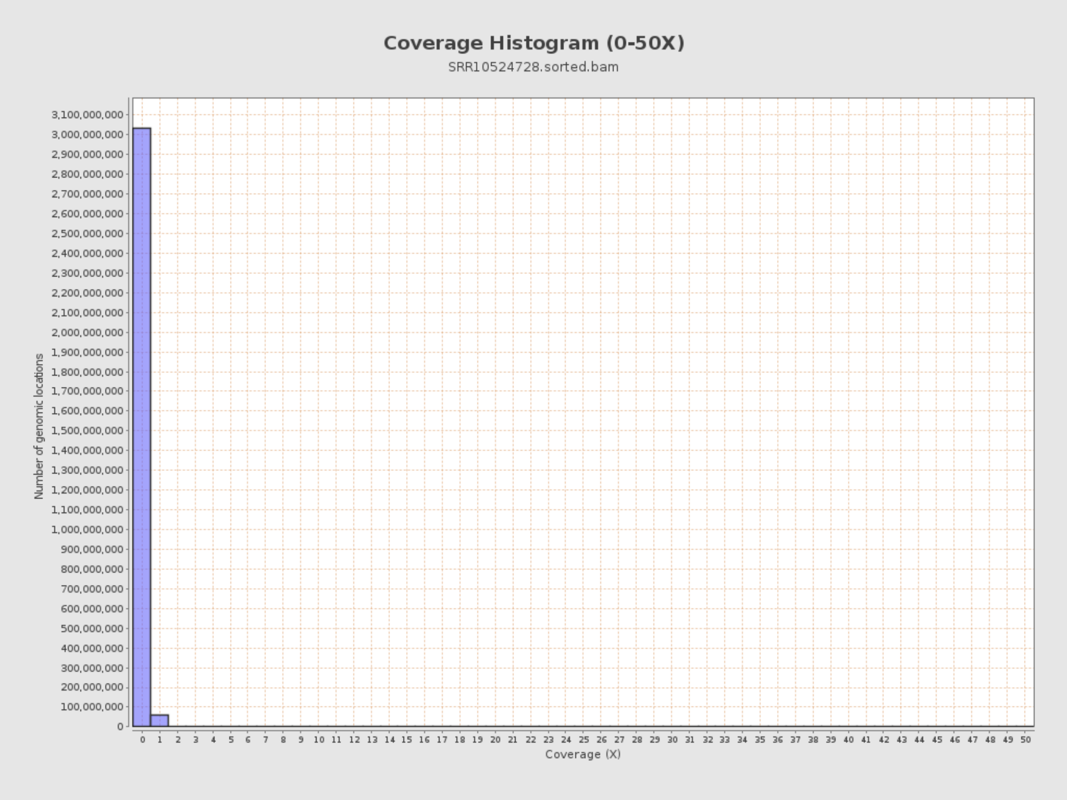
3. Results : Coverage across reference



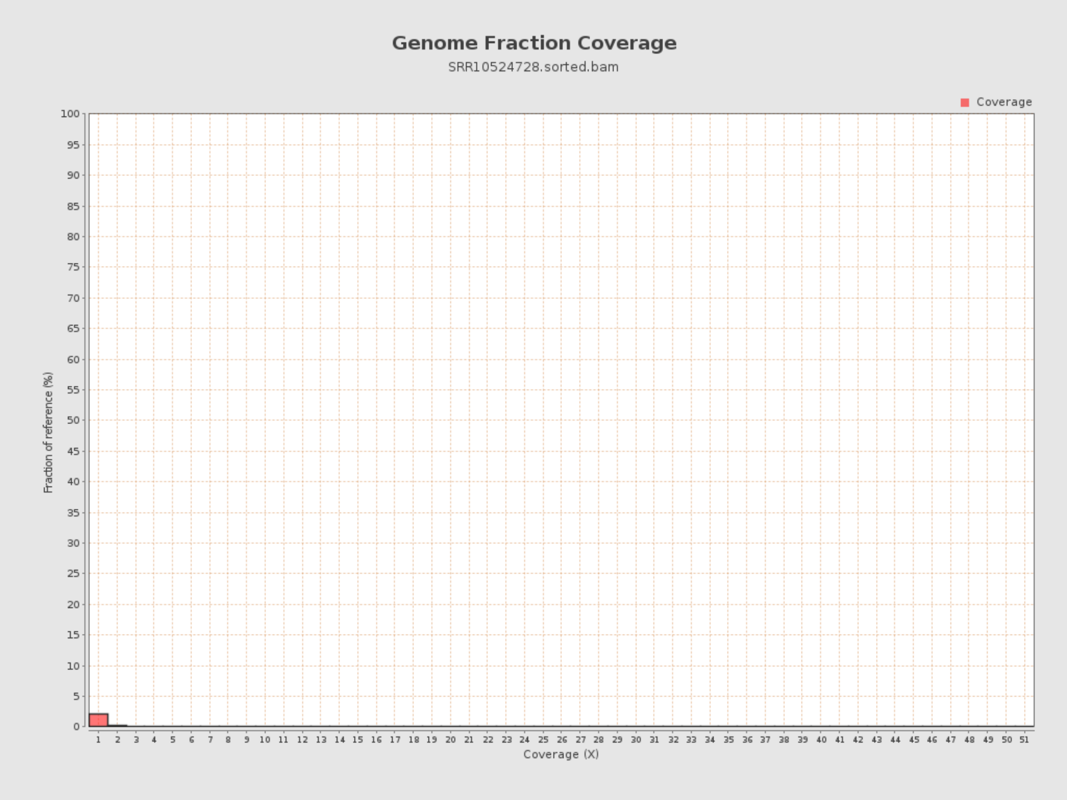
4. Results : Coverage Histogram



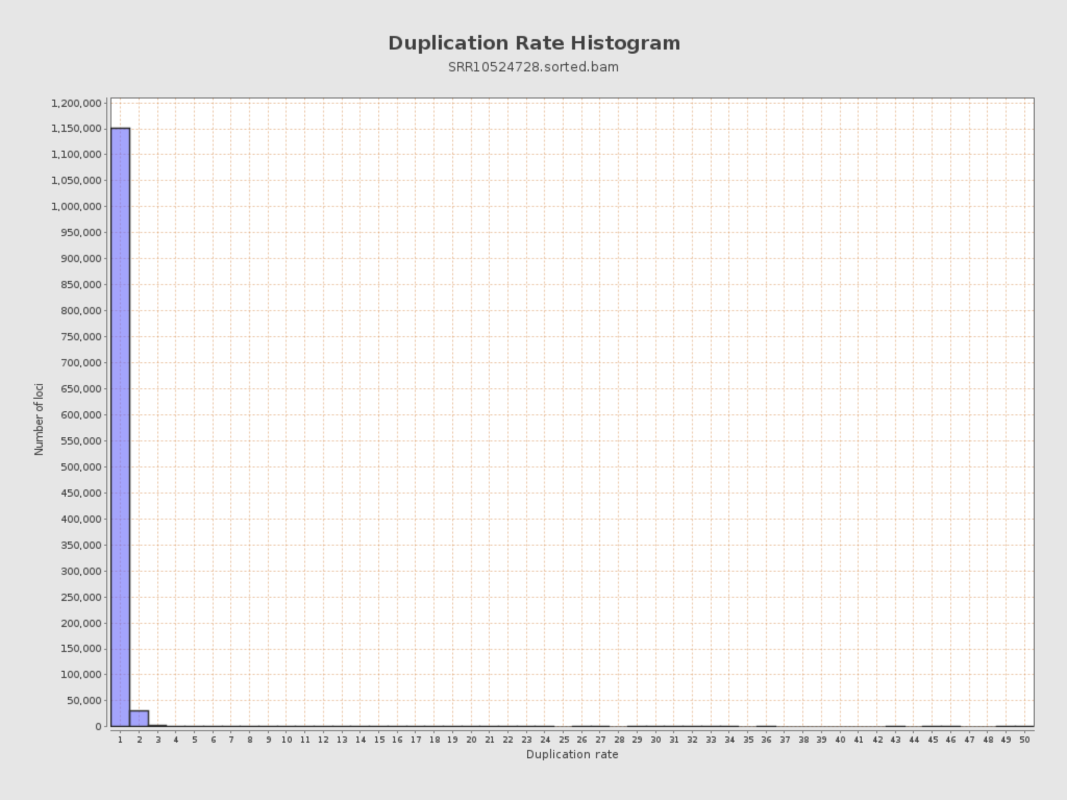
5. Results : Coverage Histogram (0-50X)



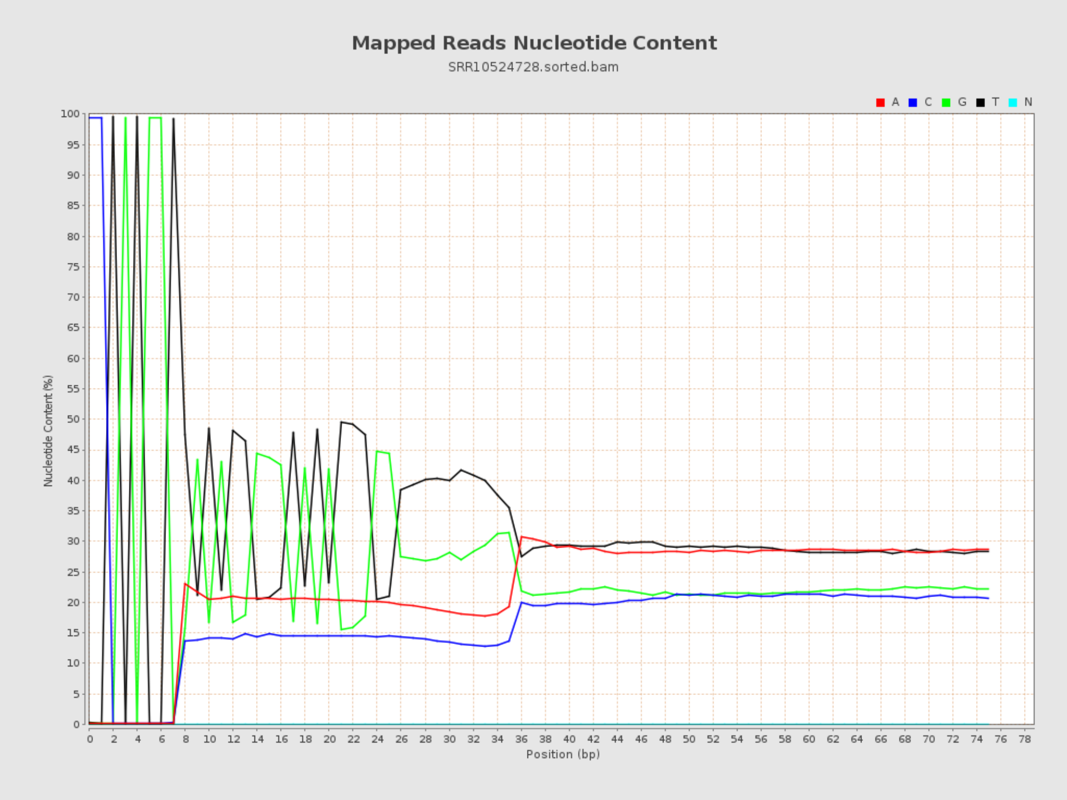
6. Results : Genome Fraction Coverage



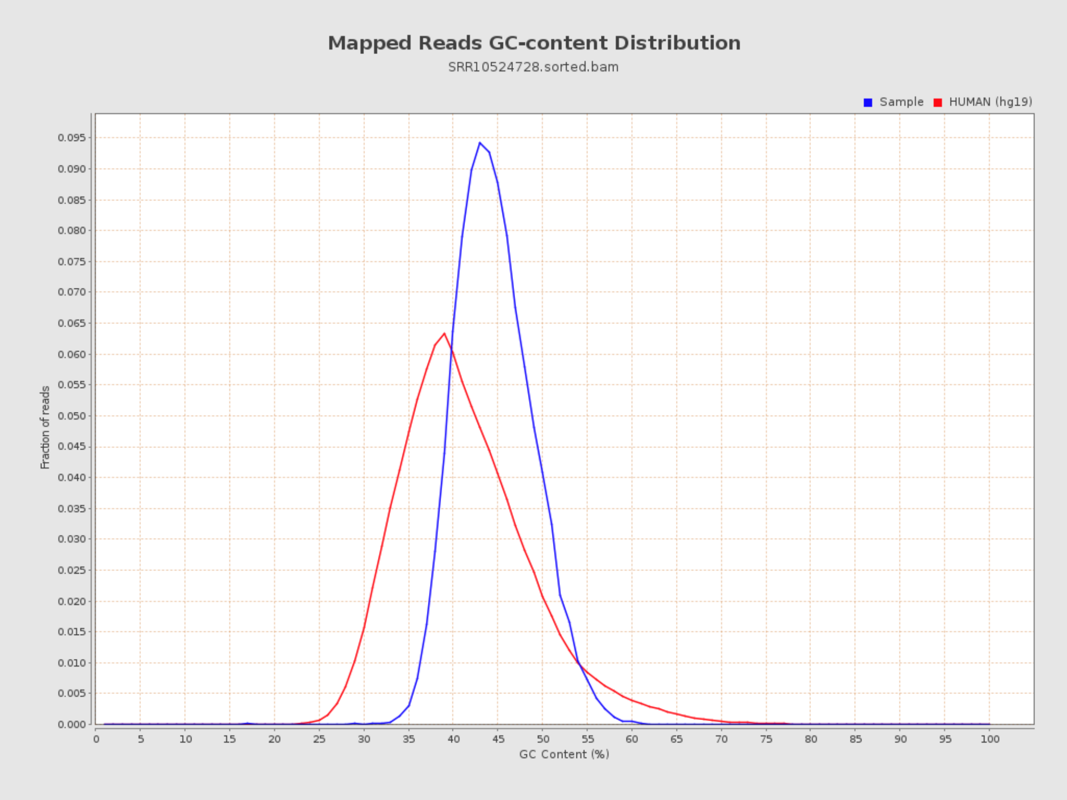
7. Results : Duplication Rate Histogram



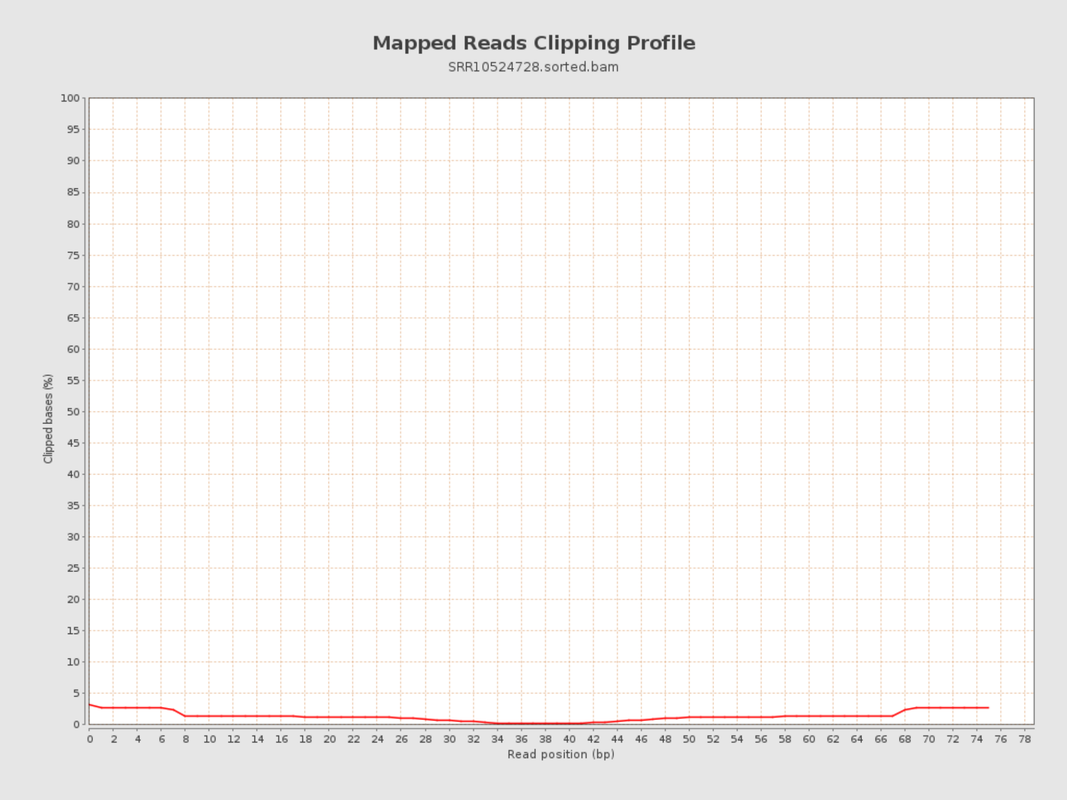
8. Results : Mapped Reads Nucleotide Content



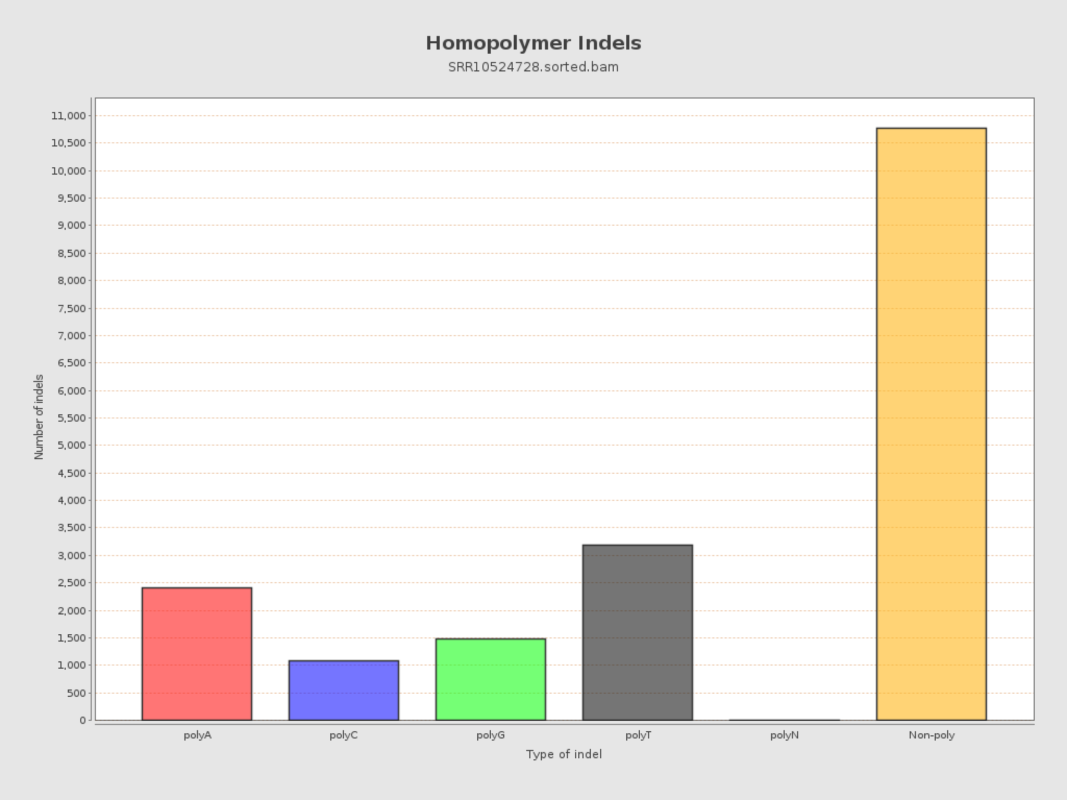
9. Results : Mapped Reads GC-content Distribution



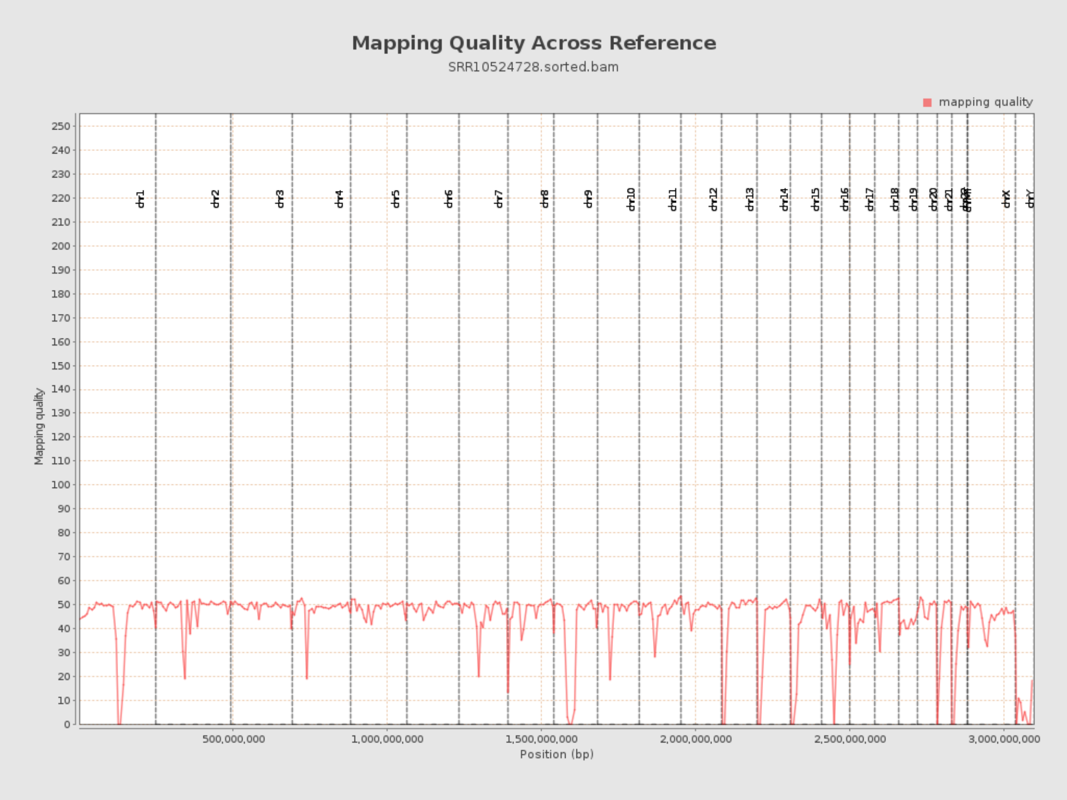
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram