Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:55:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524428.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_SRR10524428 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524428.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:55:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524428.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,036,228
Mapped reads	957,969 / 92.45%
Unmapped reads	78,259 / 7.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,482 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	33,586 / 3.24%
Duplication rate	2.61%
Clipped reads	961,341 / 92.77%

2.2. ACGT Content

Number/percentage of A's	13,270,686 / 23.51%
Number/percentage of C's	10,537,533 / 18.67%
Number/percentage of T's	18,220,293 / 32.28%
Number/percentage of G's	14,408,489 / 25.53%
Number/percentage of N's	5,605 / 0.01%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0182

Standard Deviation	0.2055

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

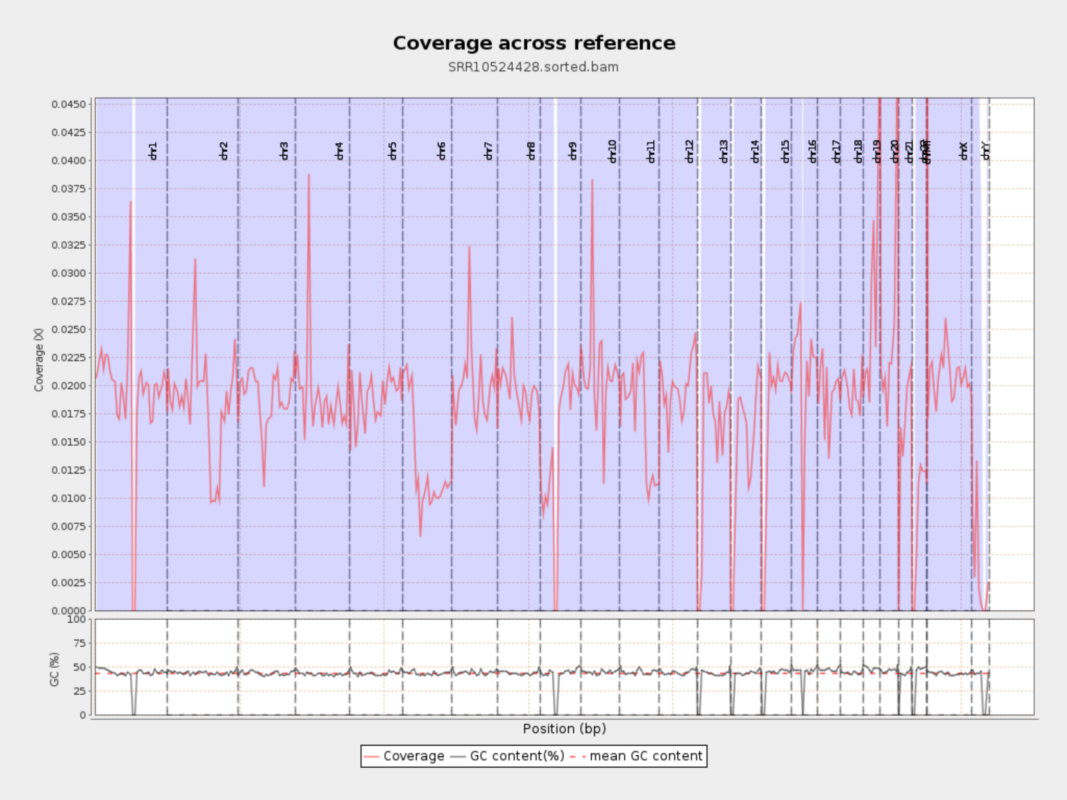
General error rate	0.51%
Mismatches	282,616
Insertions	3,429
Mapped reads with at least one insertion	0.36%
Deletions	9,528
Mapped reads with at least one deletion	0.99%
Homopolymer indels	43.19%

2.6. Chromosome stats

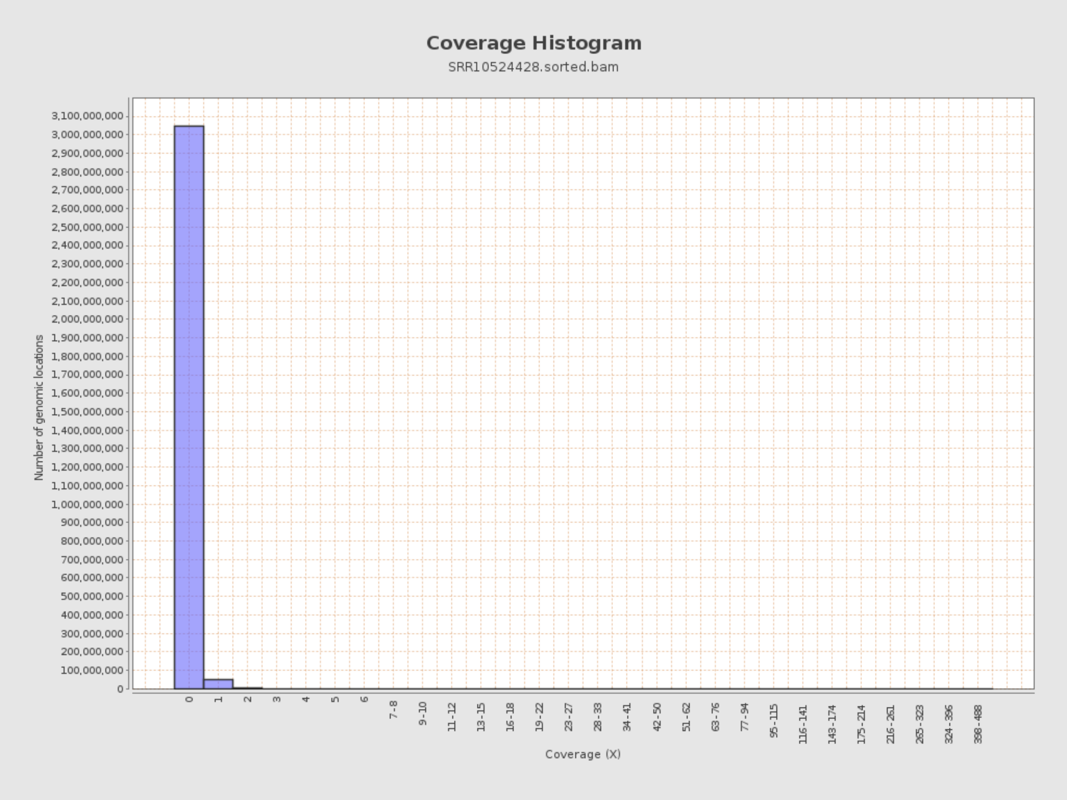
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4807699	0.0193	0.4013
chr2	243199373	4482799	0.0184	0.2367
chr3	198022430	3757379	0.019	0.147
chr4	191154276	3714064	0.0194	0.18
chr5	180915260	3456148	0.0191	0.1477
chr6	171115067	2205691	0.0129	0.1272
chr7	159138663	3226792	0.0203	0.2589

chr8	146364022	2894872	0.0198	0.1714
chr9	141213431	2067560	0.0146	0.1466
chr10	135534747	2879635	0.0212	0.2198
chr11	135006516	2321233	0.0172	0.1639
chr12	133851895	2667739	0.0199	0.1521
chr13	115169878	1732110	0.015	0.1307
chr14	107349540	1549290	0.0144	0.1313
chr15	102531392	1743222	0.017	0.1402
chr16	90354753	1846746	0.0204	0.1607
chr17	81195210	1571334	0.0194	0.1586
chr18	78077248	1527164	0.0196	0.2336
chr19	59128983	1704802	0.0288	0.2961
chr20	63025520	1623218	0.0258	0.178
chr21	48129895	783935	0.0163	0.1574
chr22	51304566	438297	0.0085	0.0991
chrMT	16571	3652	0.2204	0.5086
chrX	155270560	3244487	0.0209	0.1633
chrY	59373566	208416	0.0035	0.1241

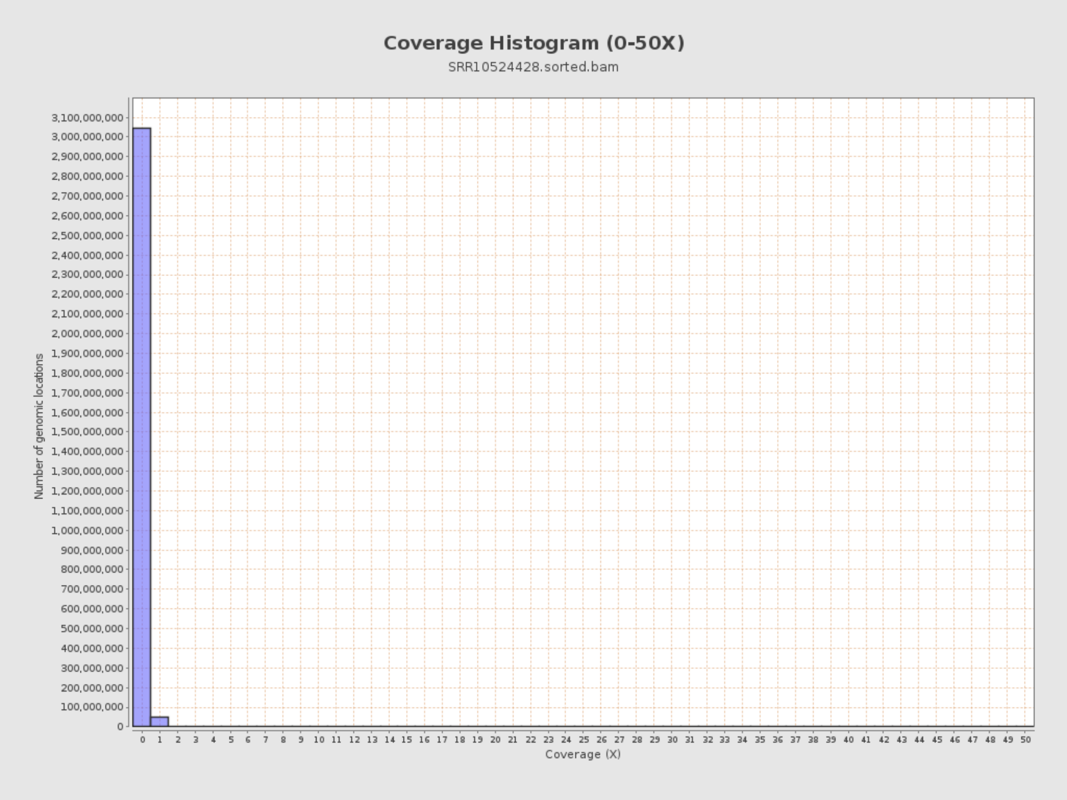
3. Results : Coverage across reference



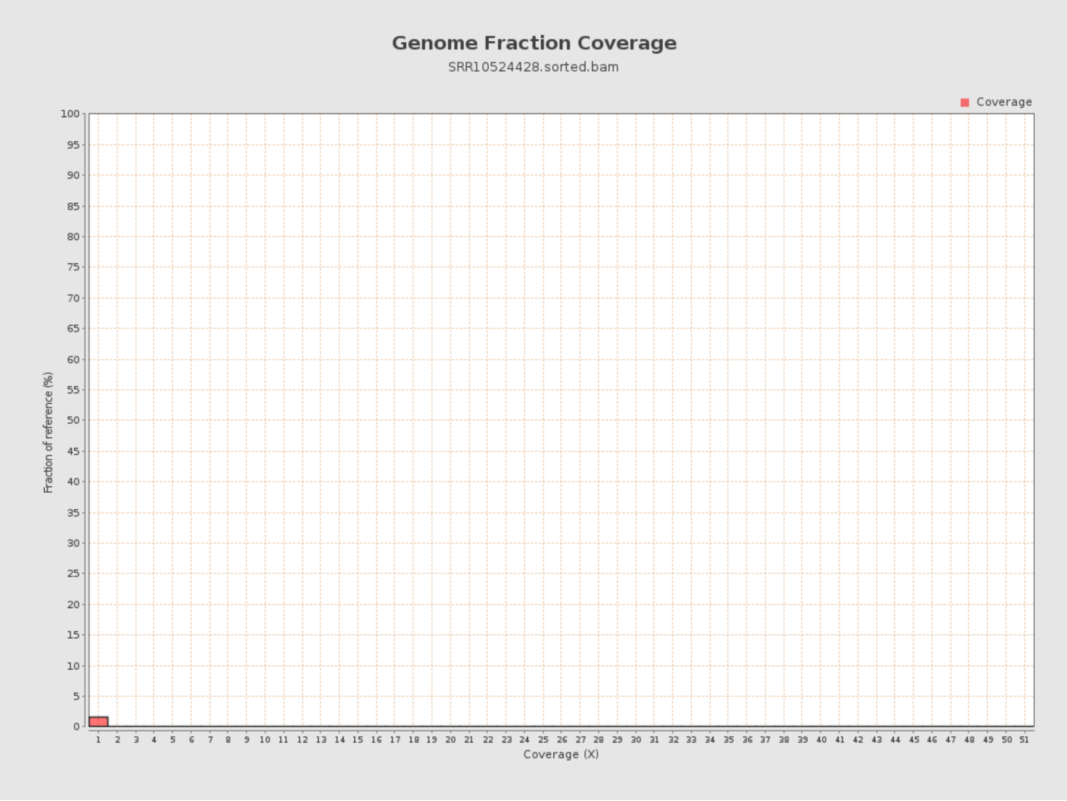
4. Results : Coverage Histogram



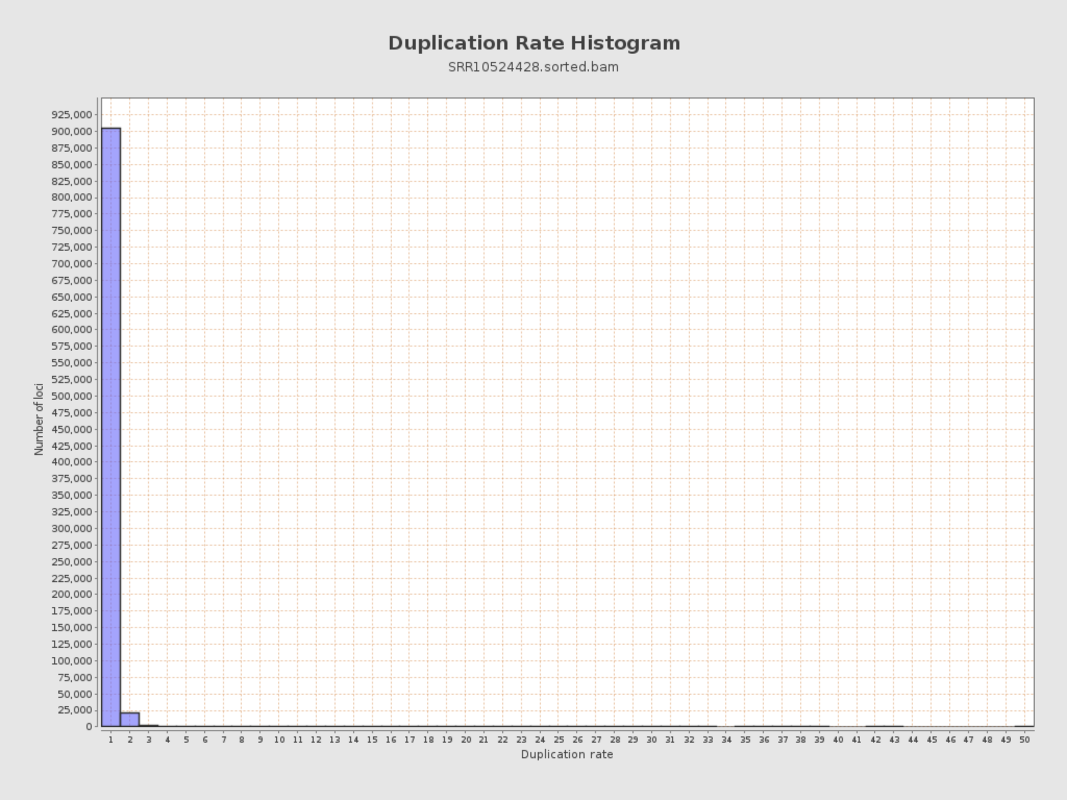
5. Results : Coverage Histogram (0-50X)



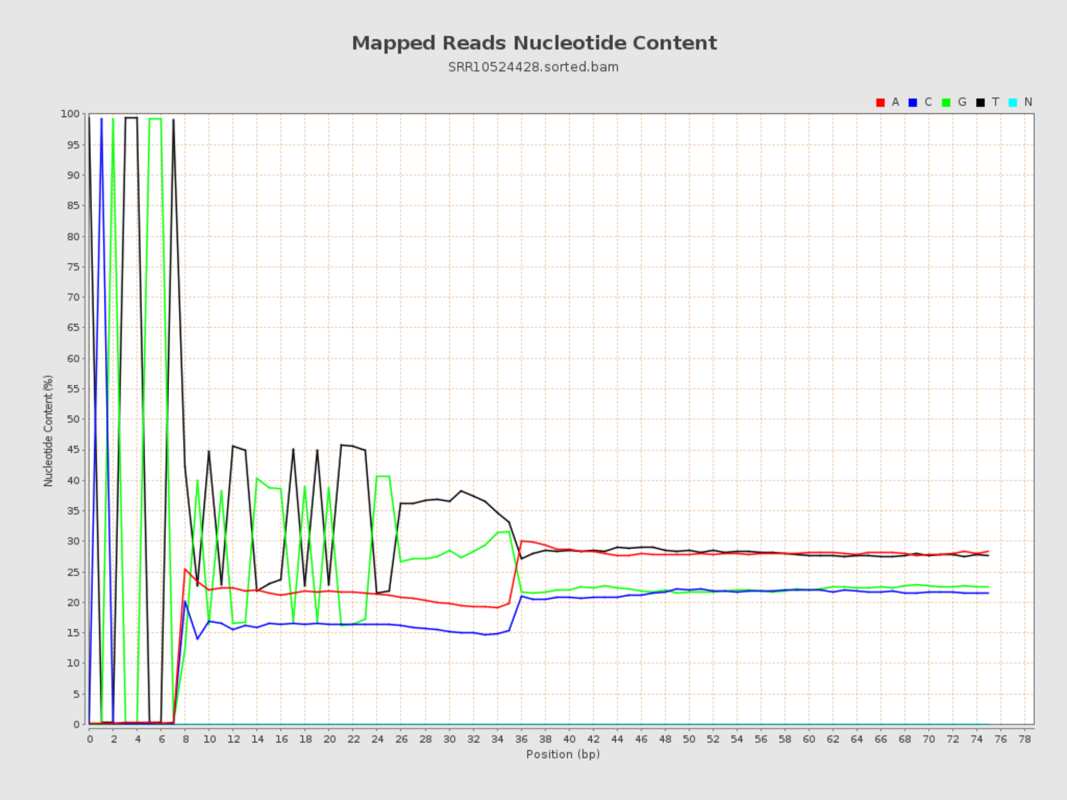
6. Results : Genome Fraction Coverage



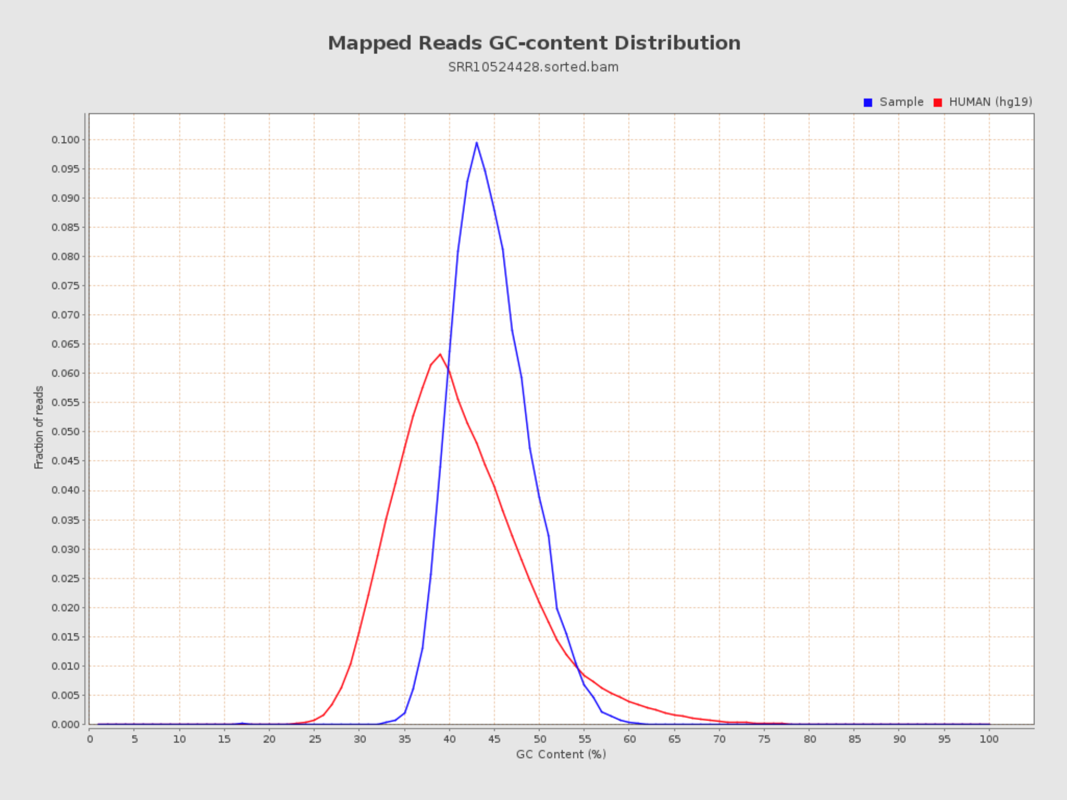
7. Results : Duplication Rate Histogram



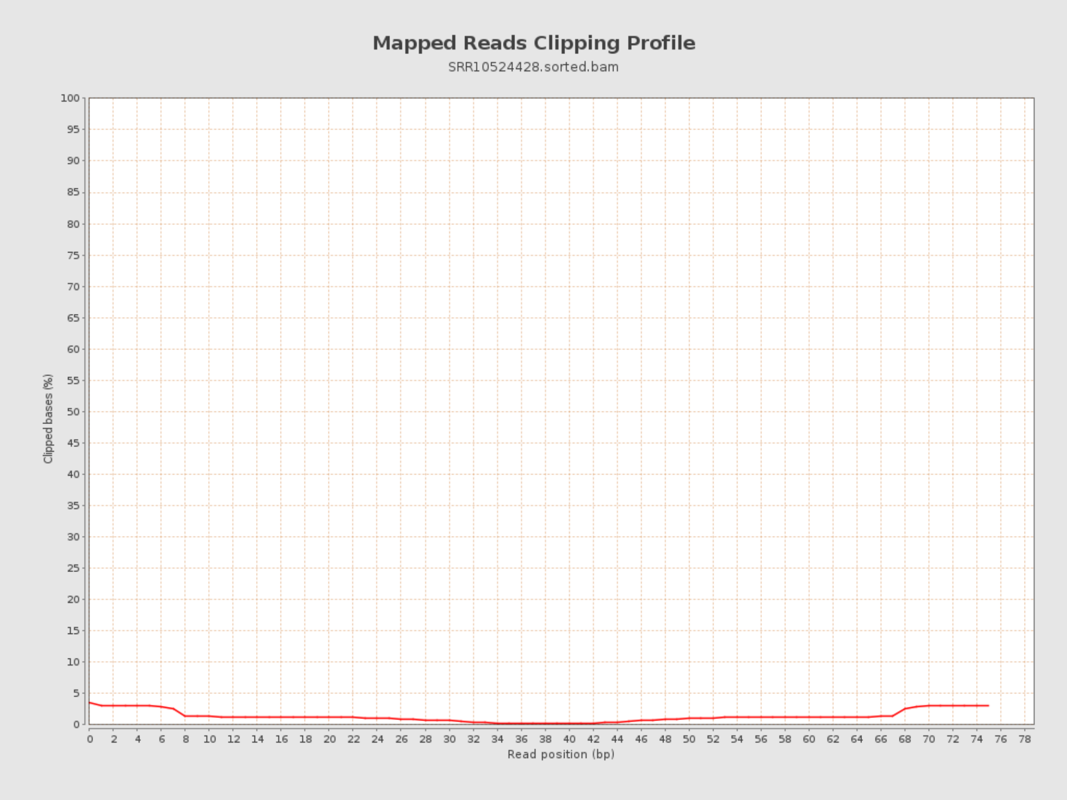
8. Results : Mapped Reads Nucleotide Content



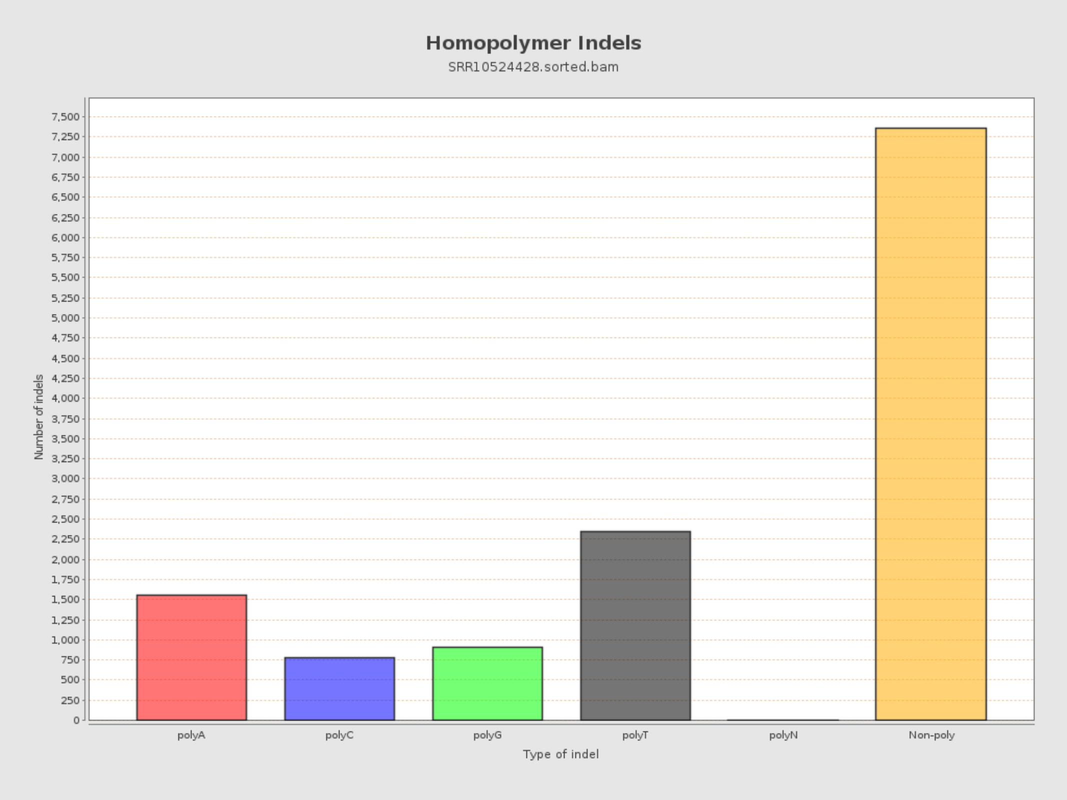
9. Results : Mapped Reads GC-content Distribution



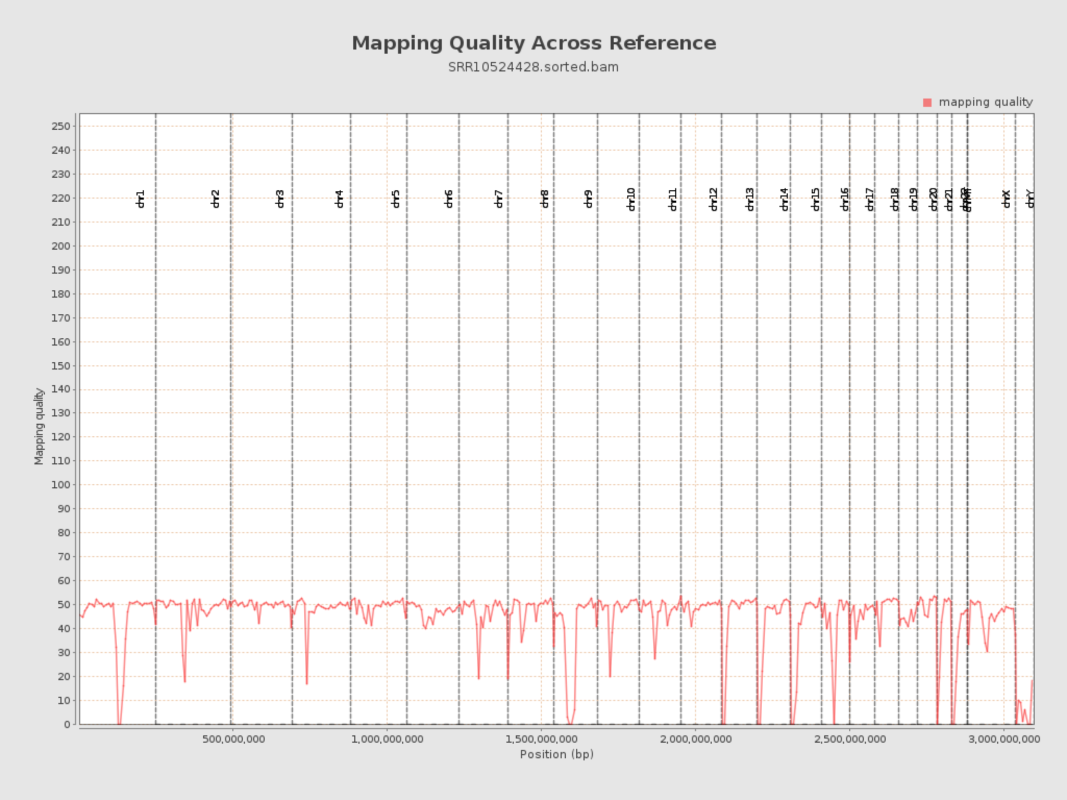
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram