Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:50:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524986.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_SRR10524986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524986.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:50:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	919,346
Mapped reads	848,920 / 92.34%
Unmapped reads	70,426 / 7.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,251 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	20,845 / 2.27%
Duplication rate	1.83%
Clipped reads	848,785 / 92.32%

2.2. ACGT Content

Number/percentage of A's	12,844,029 / 25.62%
Number/percentage of C's	8,909,281 / 17.77%
Number/percentage of T's	16,326,958 / 32.56%
Number/percentage of G's	12,056,107 / 24.05%
Number/percentage of N's	678 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.1678

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

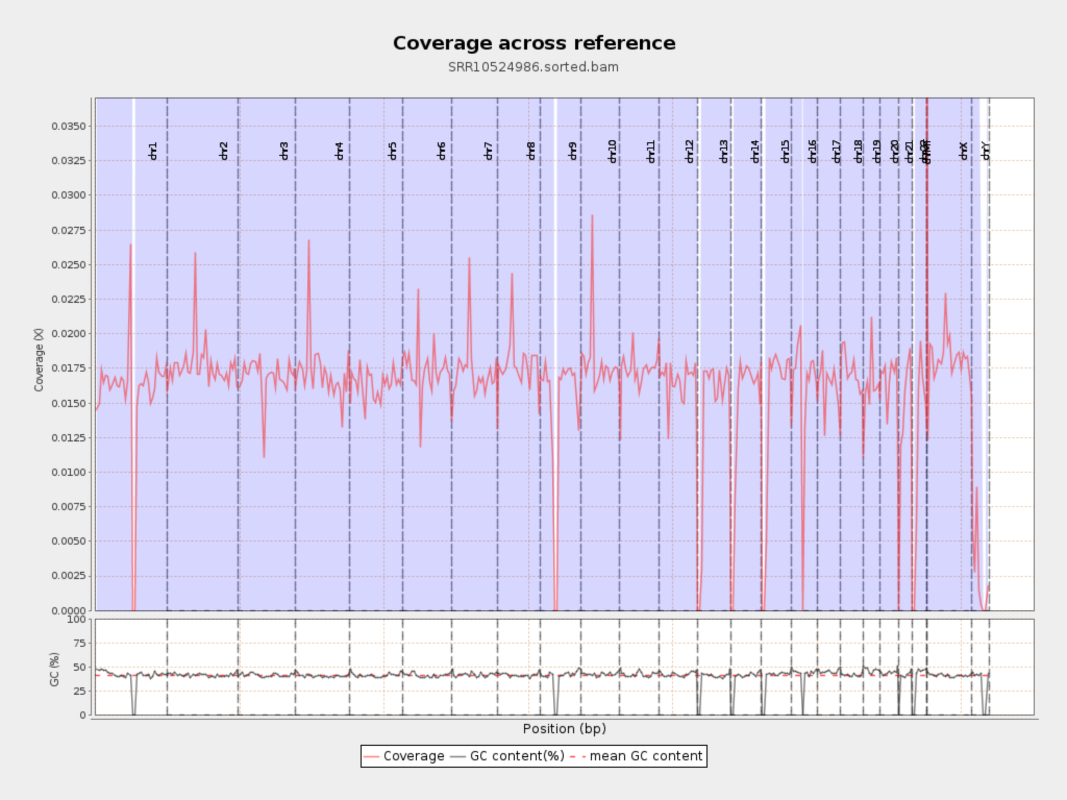
General error rate	0.49%
Mismatches	238,915
Insertions	3,173
Mapped reads with at least one insertion	0.37%
Deletions	9,201
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.07%

2.6. Chromosome stats

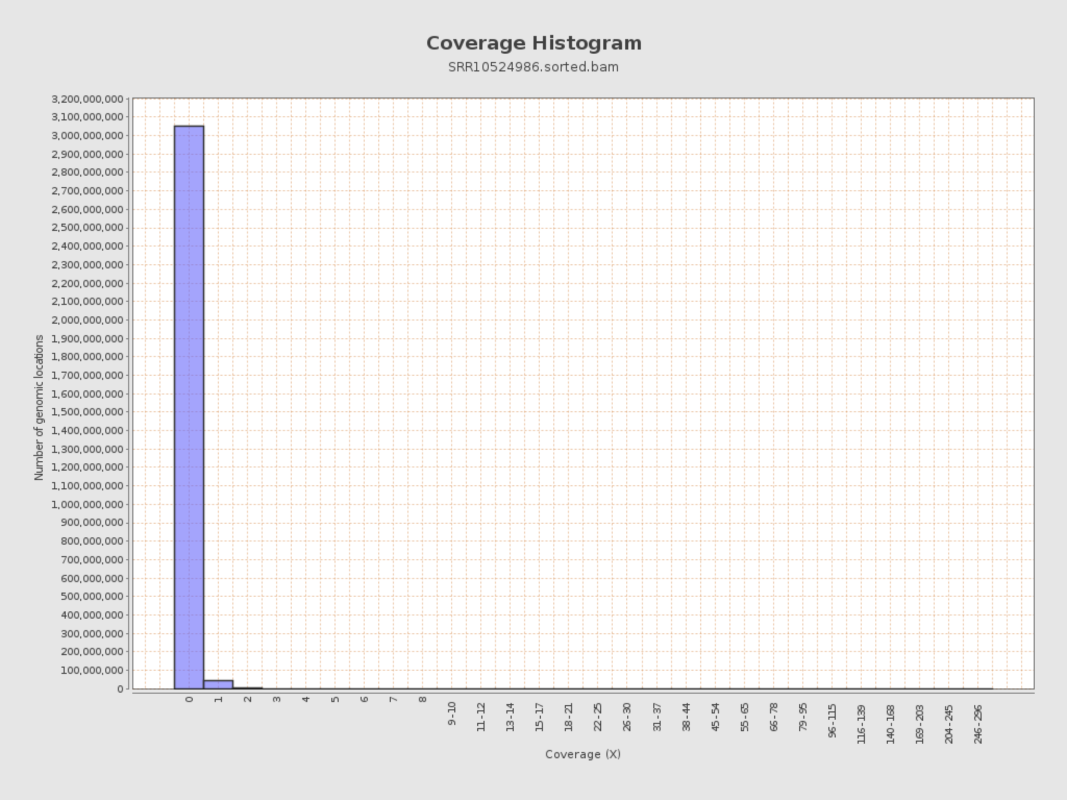
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3907075	0.0157	0.2645
chr2	243199373	4316685	0.0177	0.1806
chr3	198022430	3340693	0.0169	0.1369
chr4	191154276	3291957	0.0172	0.1493
chr5	180915260	2969506	0.0164	0.1354
chr6	171115067	2968491	0.0173	0.161
chr7	159138663	2749660	0.0173	0.1928

chr8	146364022	2623573	0.0179	0.1883
chr9	141213431	2051389	0.0145	0.1466
chr10	135534747	2437370	0.018	0.1725
chr11	135006516	2345748	0.0174	0.1684
chr12	133851895	2217194	0.0166	0.1366
chr13	115169878	1598361	0.0139	0.1246
chr14	107349540	1515902	0.0141	0.1279
chr15	102531392	1463182	0.0143	0.1277
chr16	90354753	1419520	0.0157	0.1353
chr17	81195210	1317491	0.0162	0.1421
chr18	78077248	1357866	0.0174	0.2256
chr19	59128983	966943	0.0164	0.2043
chr20	63025520	1054231	0.0167	0.1391
chr21	48129895	672985	0.014	0.1309
chr22	51304566	592654	0.0116	0.1128
chrMT	16571	1133	0.0684	0.2734
chrX	155270560	2823851	0.0182	0.1508
chrY	59373566	149373	0.0025	0.0791

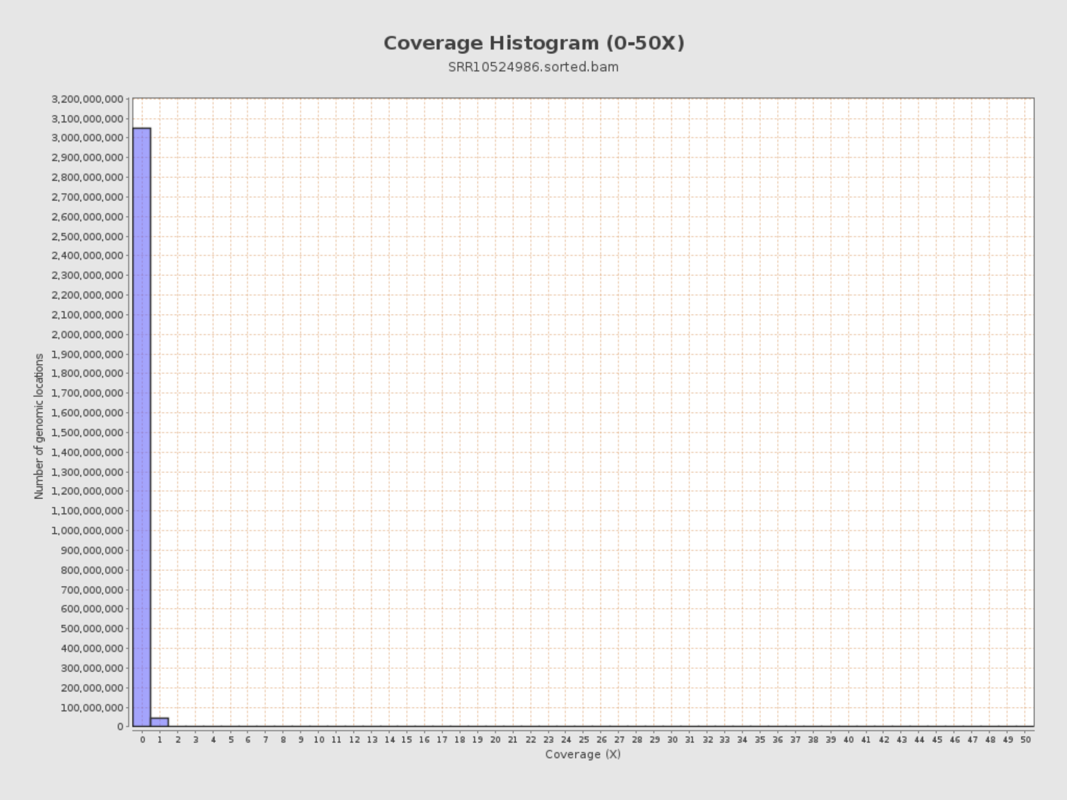
3. Results : Coverage across reference



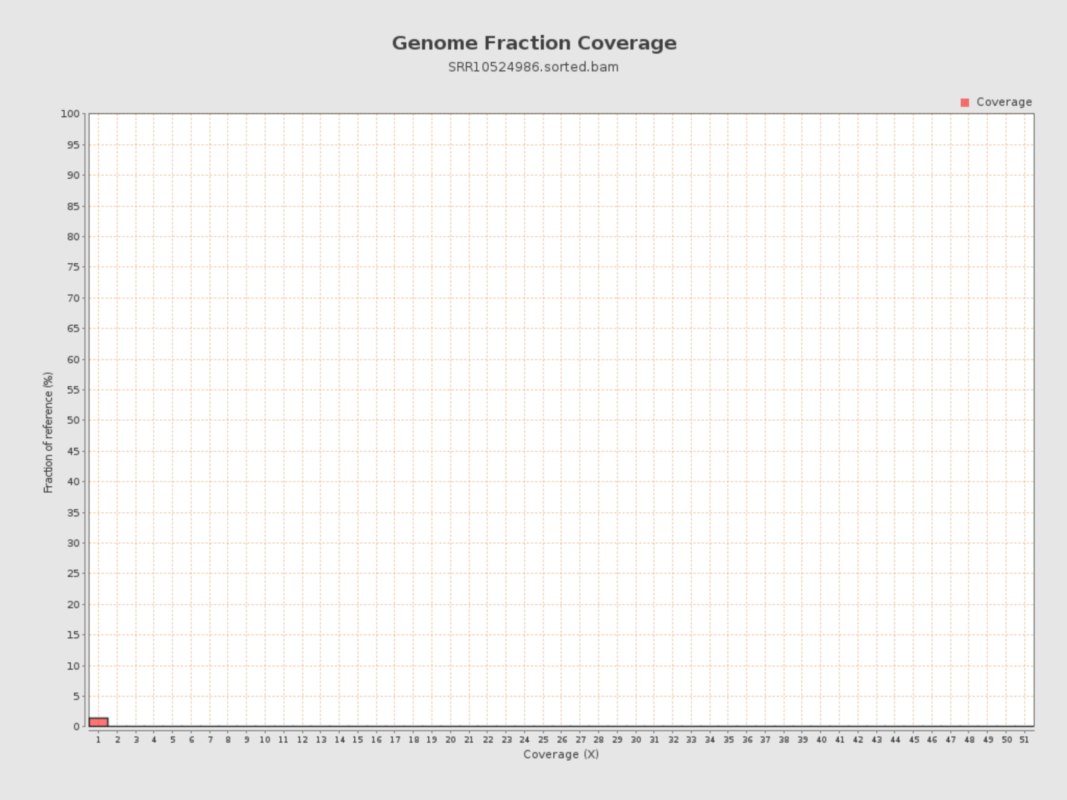
4. Results : Coverage Histogram



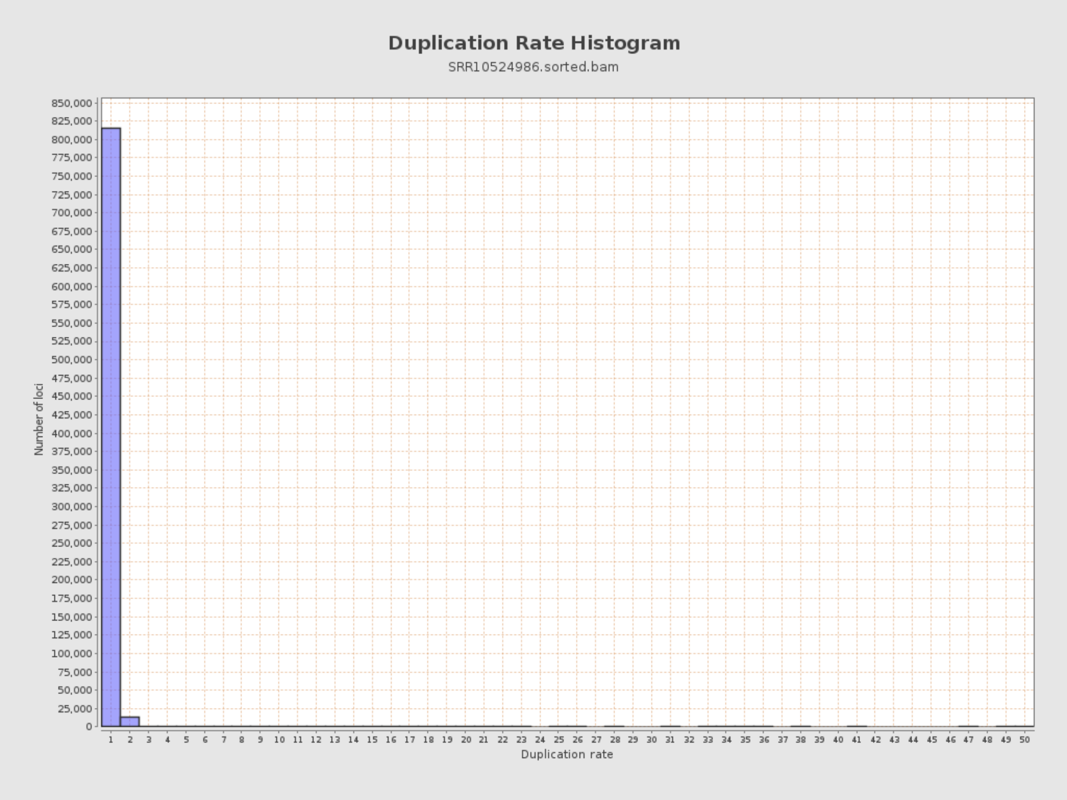
5. Results : Coverage Histogram (0-50X)



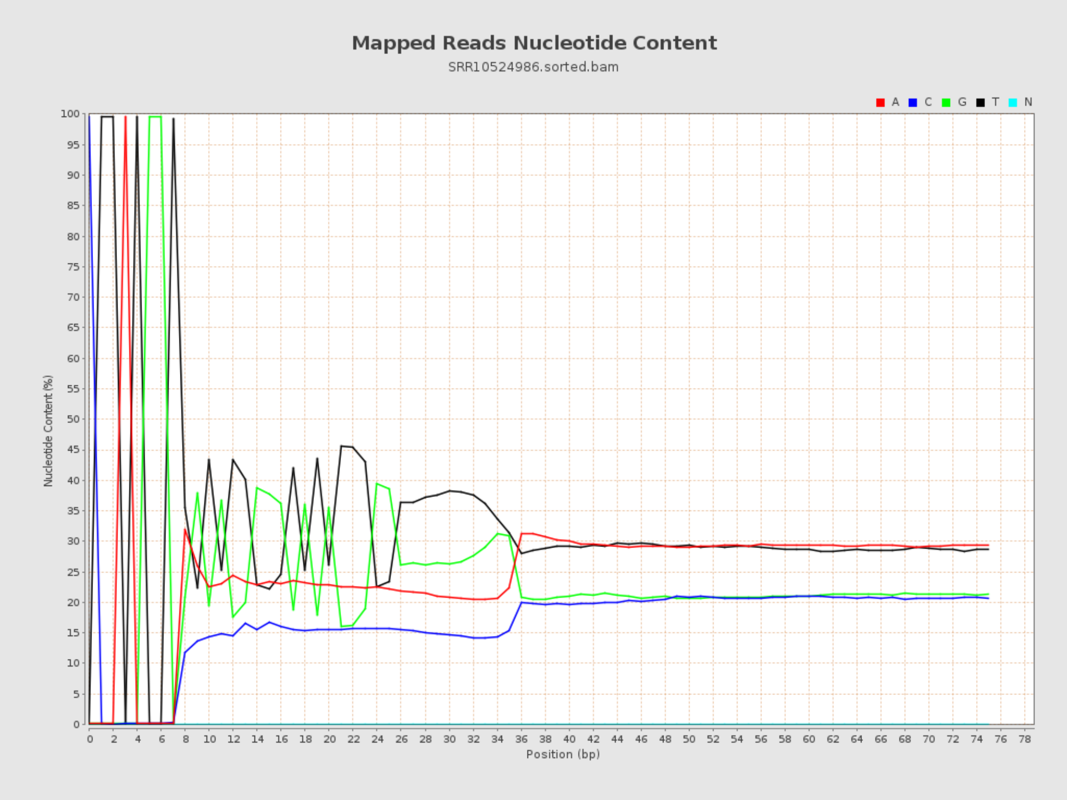
6. Results : Genome Fraction Coverage



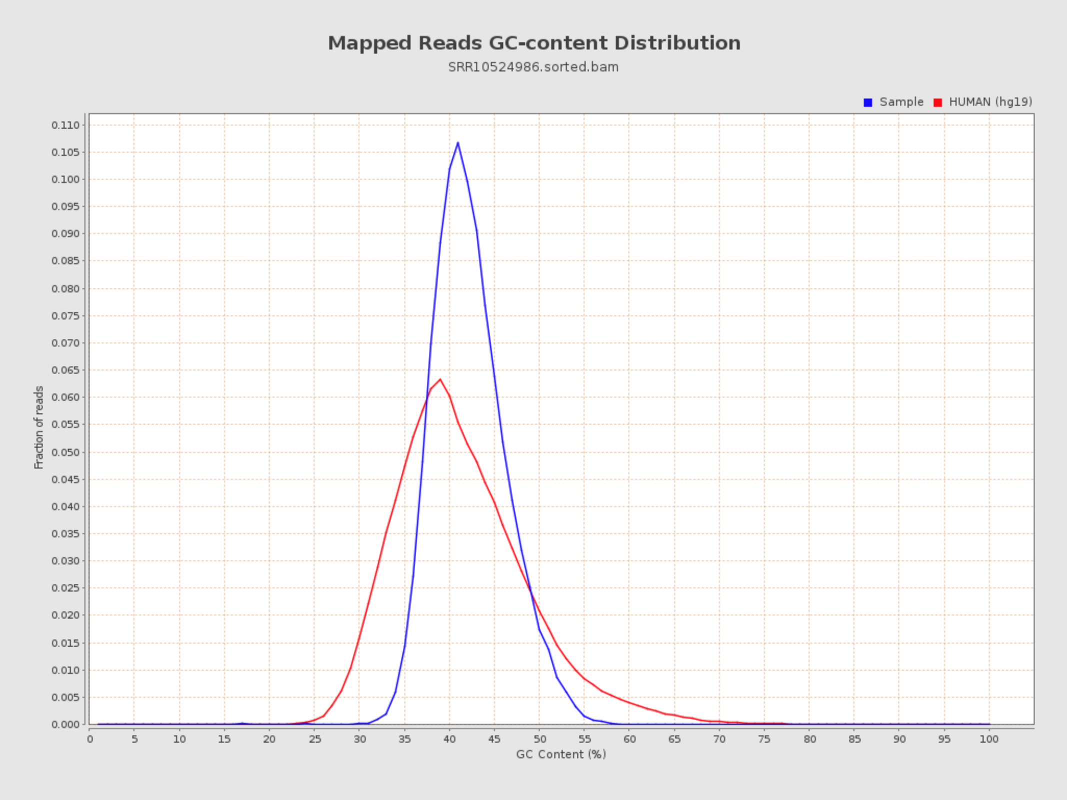
7. Results : Duplication Rate Histogram



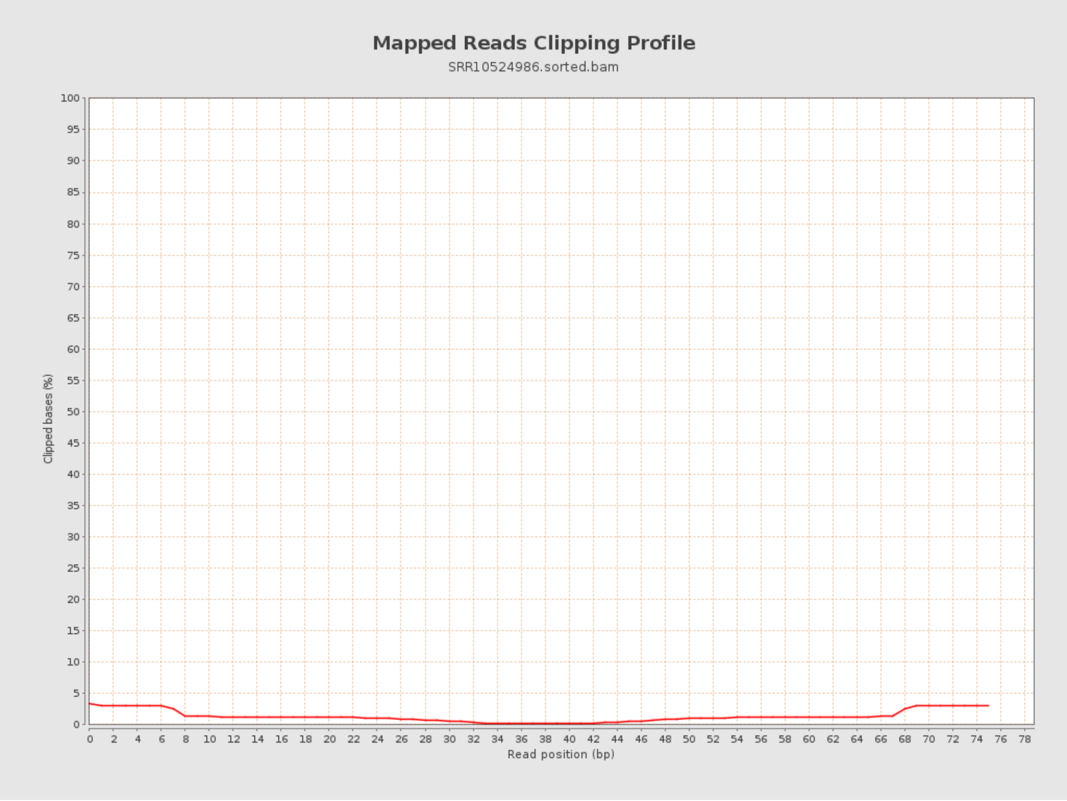
8. Results : Mapped Reads Nucleotide Content



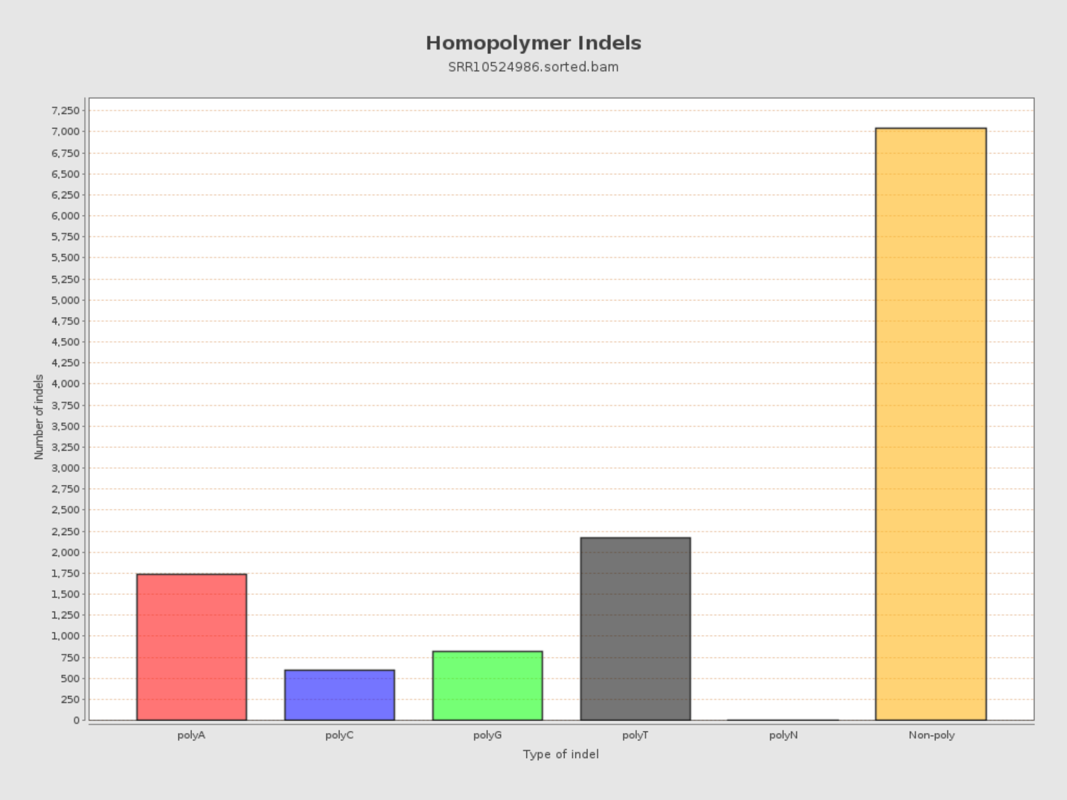
9. Results : Mapped Reads GC-content Distribution



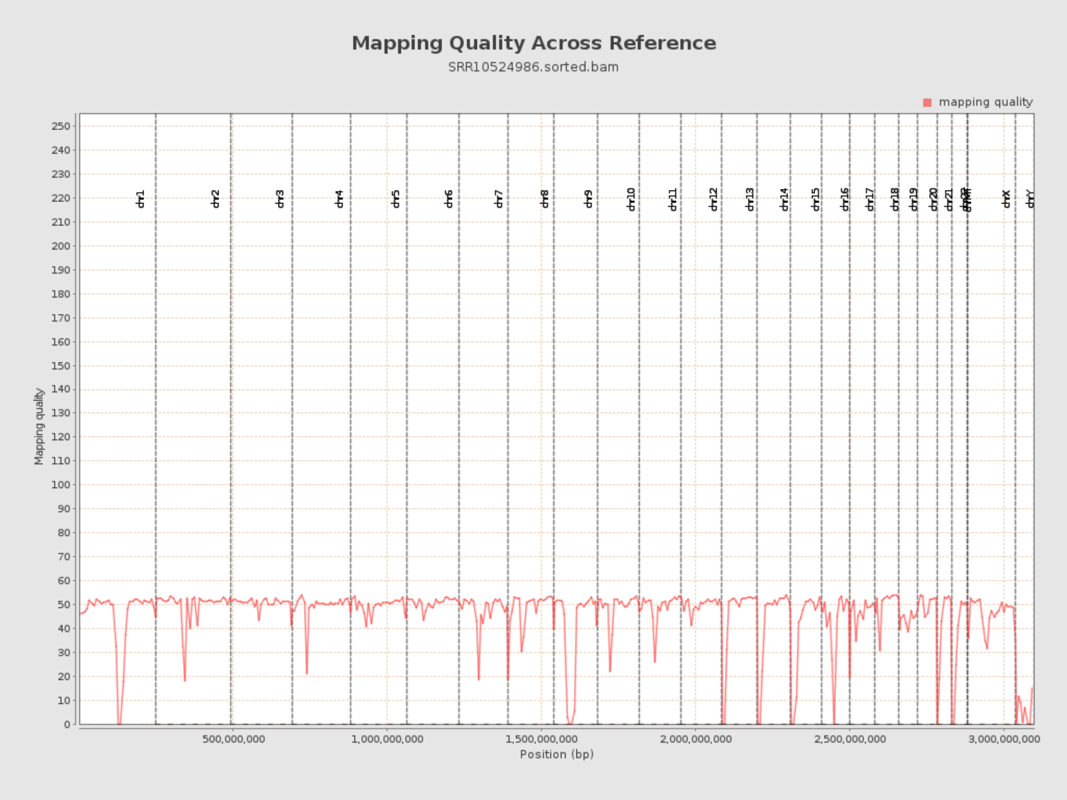
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram