Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:27:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524782.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_SRR10524782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:27:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	847,318
Mapped reads	775,771 / 91.56%
Unmapped reads	71,547 / 8.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,215 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,456 / 2.77%
Duplication rate	2.37%
Clipped reads	777,785 / 91.79%

2.2. ACGT Content

Number/percentage of A's	10,716,768 / 24.2%
Number/percentage of C's	8,091,060 / 18.27%
Number/percentage of T's	14,458,777 / 32.66%
Number/percentage of G's	11,003,431 / 24.85%
Number/percentage of N's	5,005 / 0.01%
GC Percentage	43.13%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.1555

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

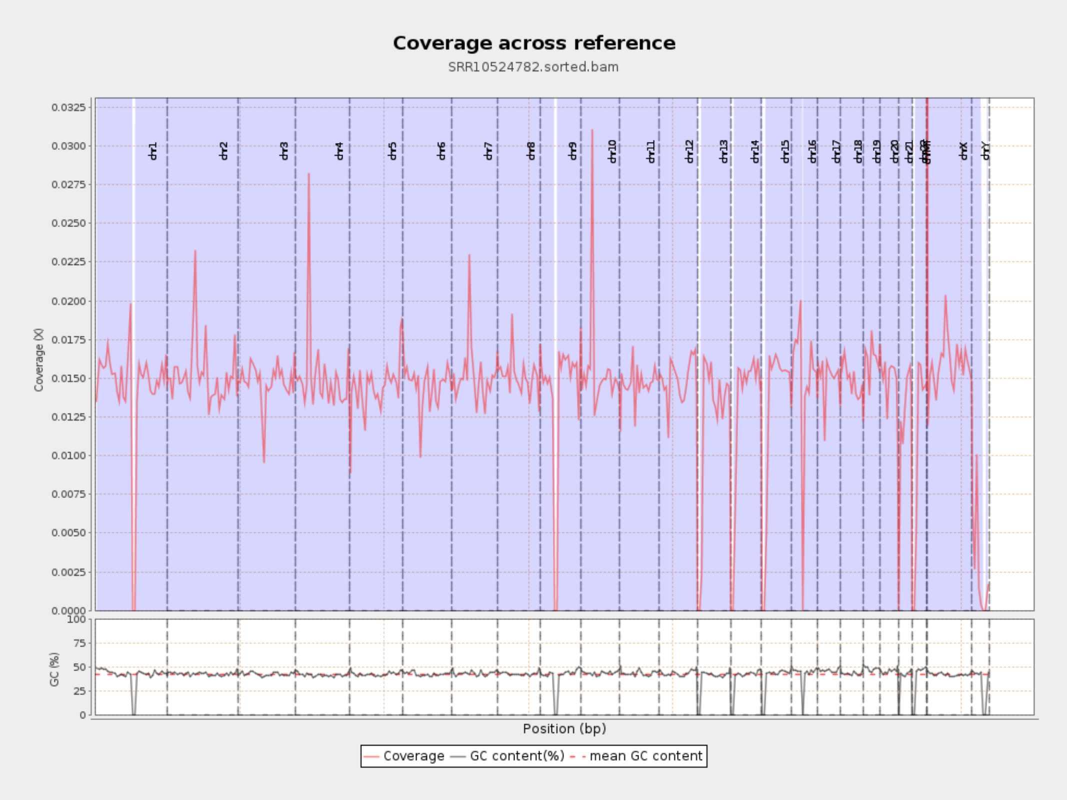
General error rate	0.52%
Mismatches	223,495
Insertions	2,870
Mapped reads with at least one insertion	0.37%
Deletions	9,017
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.79%

2.6. Chromosome stats

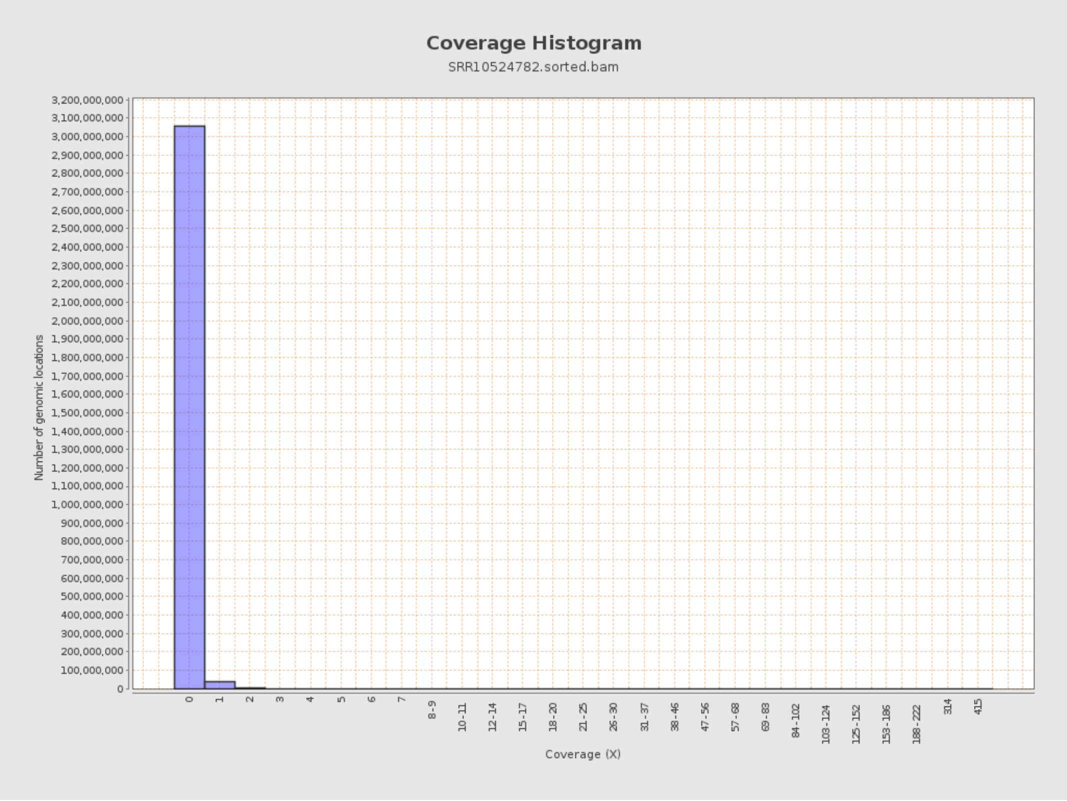
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3558291	0.0143	0.203
chr2	243199373	3695320	0.0152	0.2235
chr3	198022430	2911760	0.0147	0.1299
chr4	191154276	2891776	0.0151	0.1425
chr5	180915260	2633958	0.0146	0.1288
chr6	171115067	2498336	0.0146	0.1361
chr7	159138663	2416615	0.0152	0.1789

chr8	146364022	2215567	0.0151	0.1465
chr9	141213431	1936372	0.0137	0.1431
chr10	135534747	2118356	0.0156	0.1781
chr11	135006516	1983178	0.0147	0.1394
chr12	133851895	1994721	0.0149	0.1313
chr13	115169878	1379559	0.012	0.117
chr14	107349540	1365399	0.0127	0.1222
chr15	102531392	1304681	0.0127	0.1204
chr16	90354753	1324105	0.0147	0.1371
chr17	81195210	1217164	0.015	0.1344
chr18	78077248	1163402	0.0149	0.1998
chr19	59128983	952771	0.0161	0.1654
chr20	63025520	941002	0.0149	0.1338
chr21	48129895	588316	0.0122	0.1252
chr22	51304566	540561	0.0105	0.1101
chrMT	16571	28584	1.7249	1.6687
chrX	155270560	2470639	0.0159	0.1395
chrY	59373566	159320	0.0027	0.088

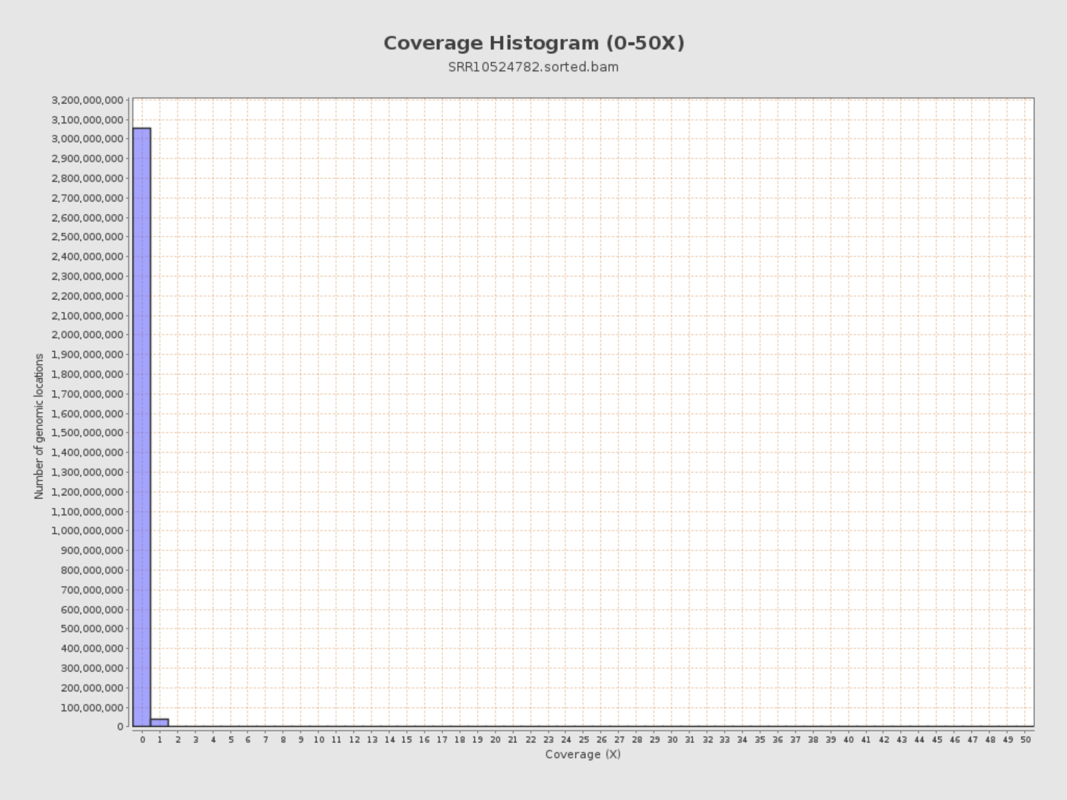
3. Results : Coverage across reference



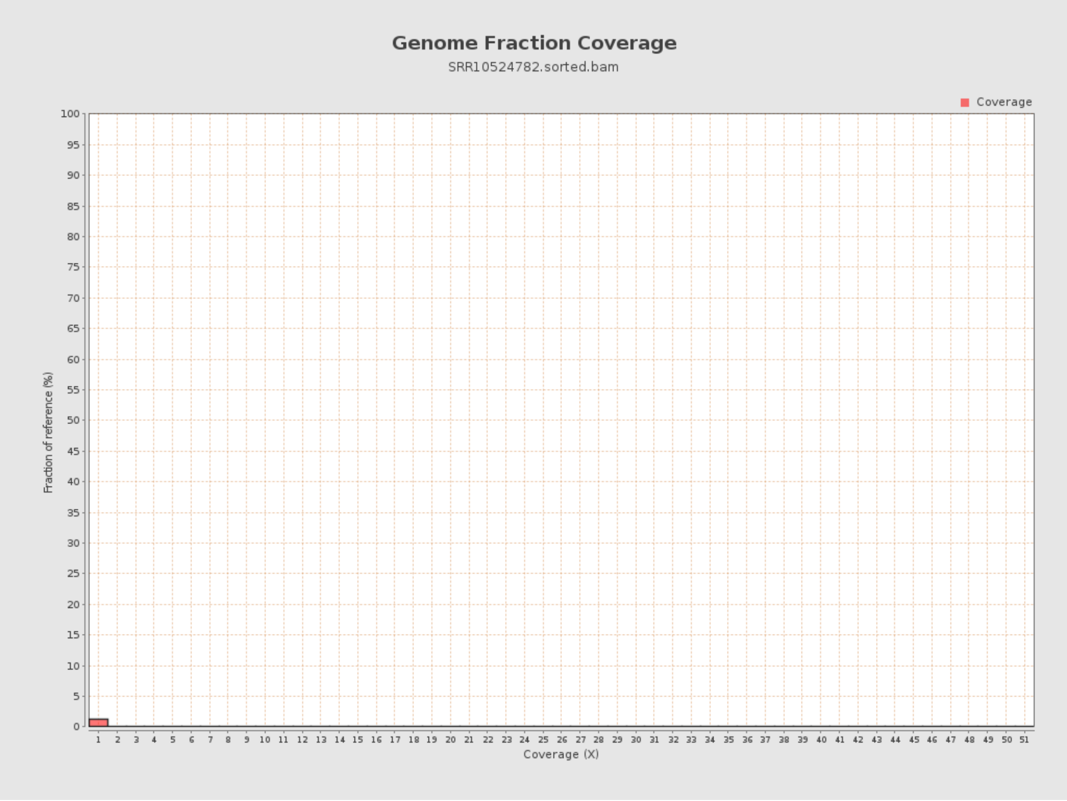
4. Results : Coverage Histogram



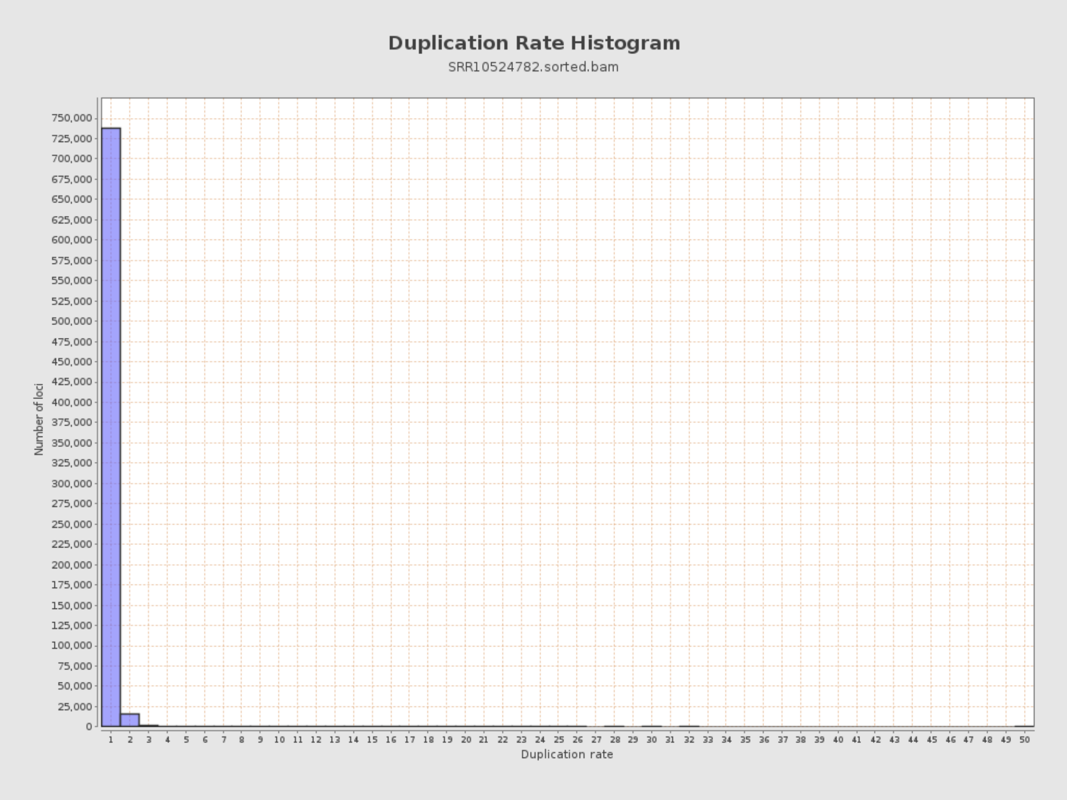
5. Results : Coverage Histogram (0-50X)



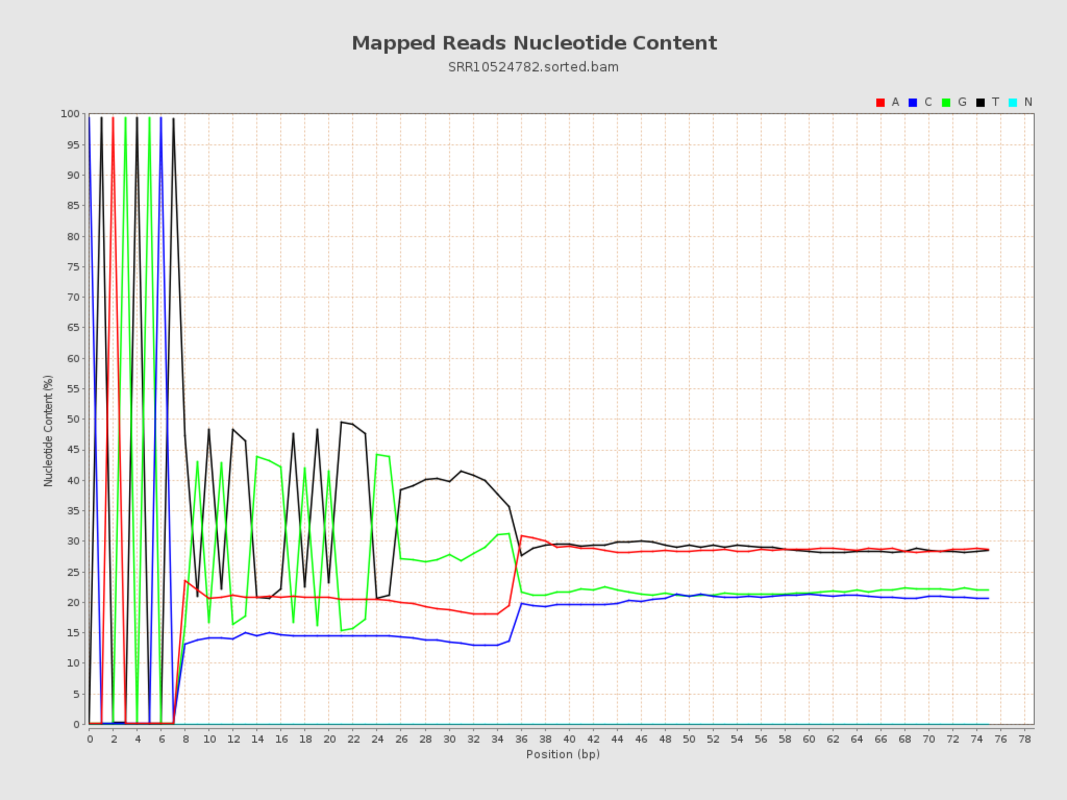
6. Results : Genome Fraction Coverage



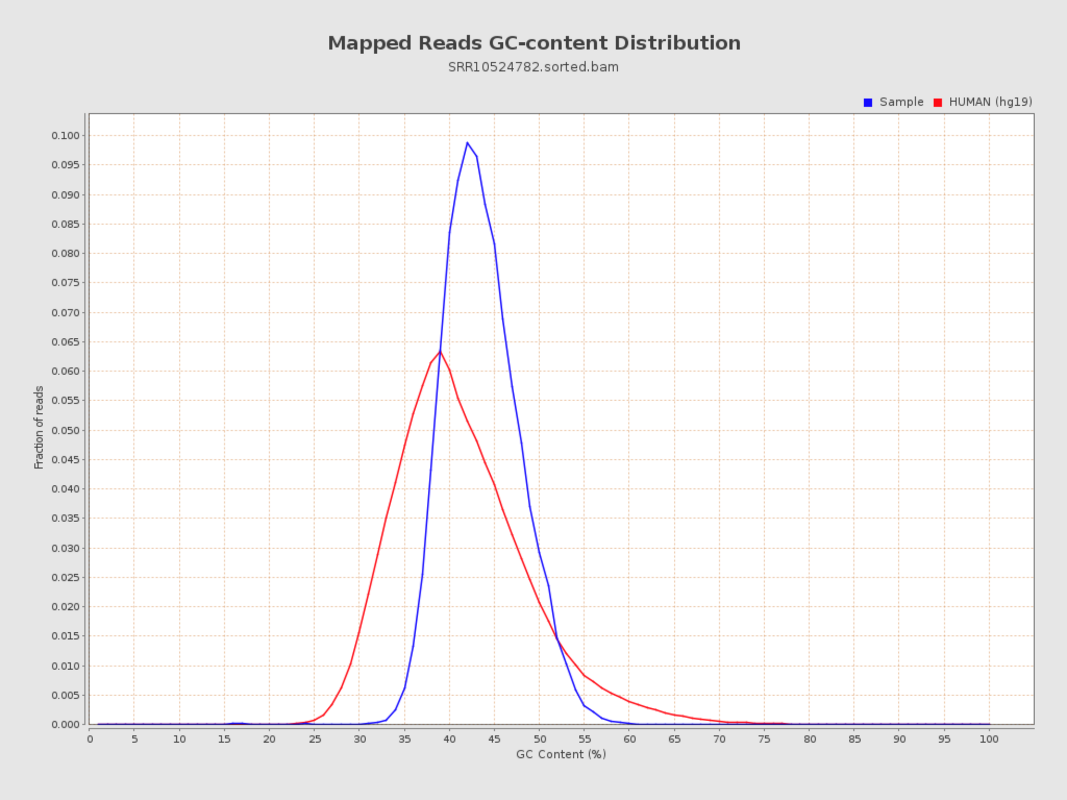
7. Results : Duplication Rate Histogram



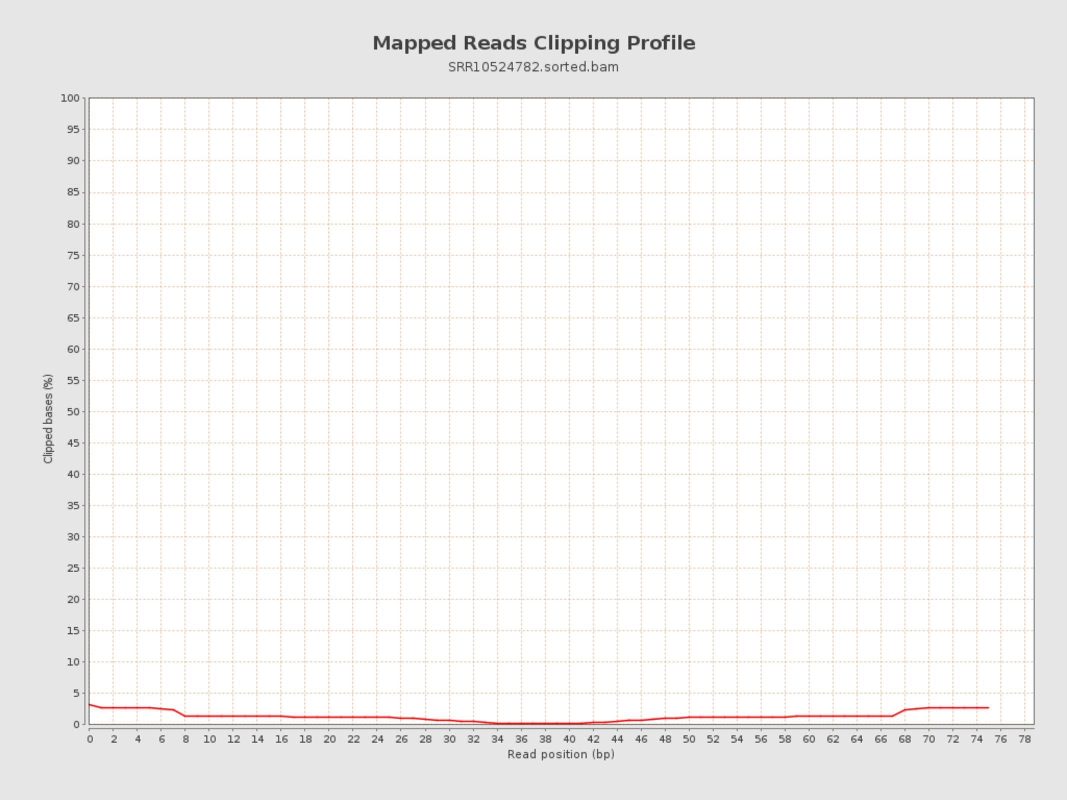
8. Results : Mapped Reads Nucleotide Content



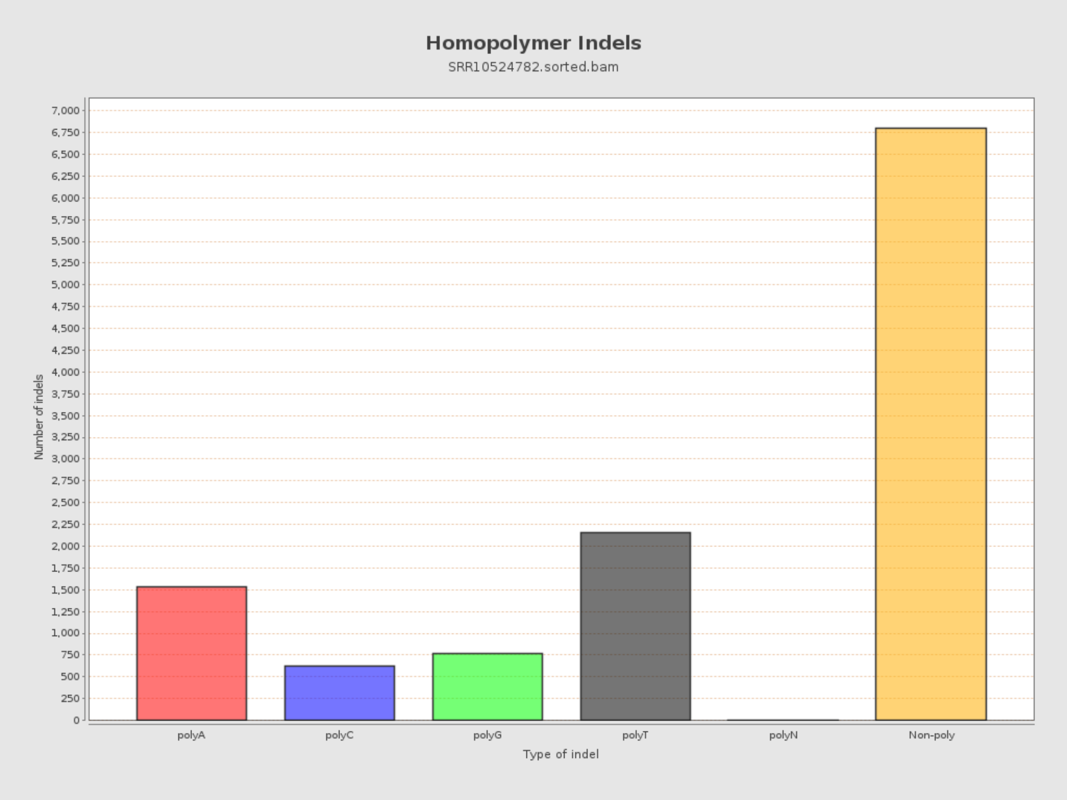
9. Results : Mapped Reads GC-content Distribution



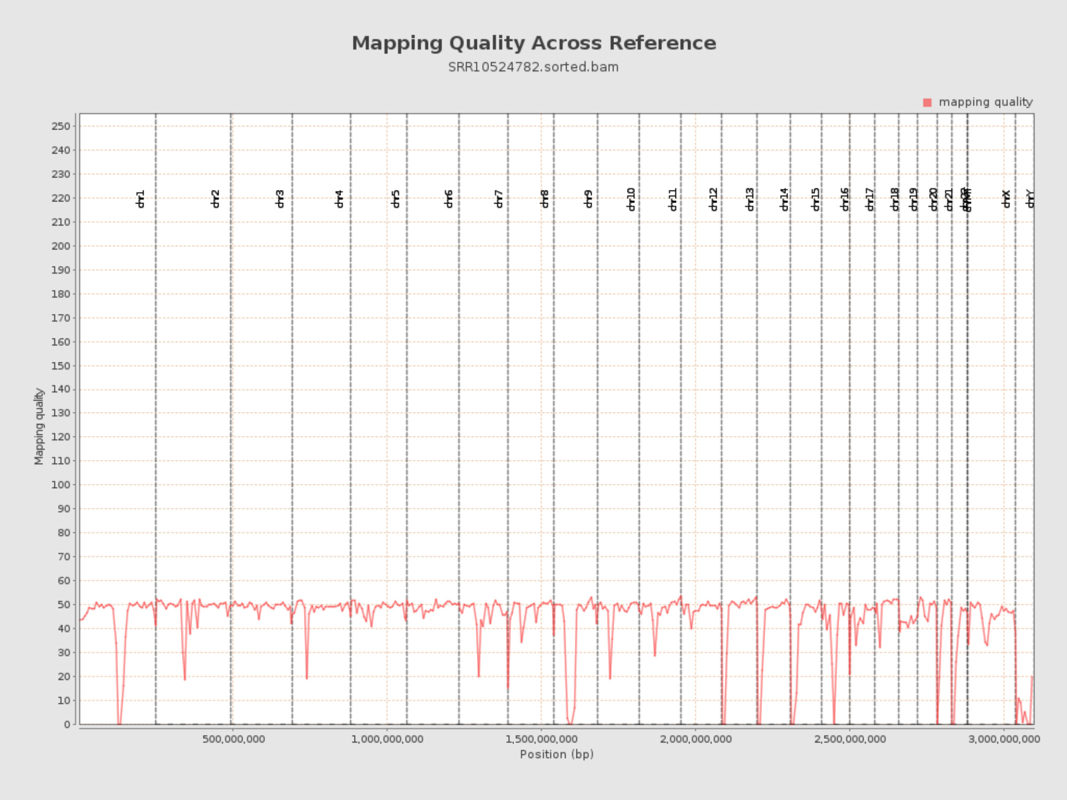
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram