Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:35:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524786.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_SRR10524786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:35:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,021,770
Mapped reads	937,583 / 91.76%
Unmapped reads	84,187 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,437 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	27,673 / 2.71%
Duplication rate	2.26%
Clipped reads	938,629 / 91.86%

2.2. ACGT Content

Number/percentage of A's	13,342,683 / 24.88%
Number/percentage of C's	10,355,144 / 19.31%
Number/percentage of T's	16,951,158 / 31.61%
Number/percentage of G's	12,964,994 / 24.18%
Number/percentage of N's	6,302 / 0.01%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1737

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

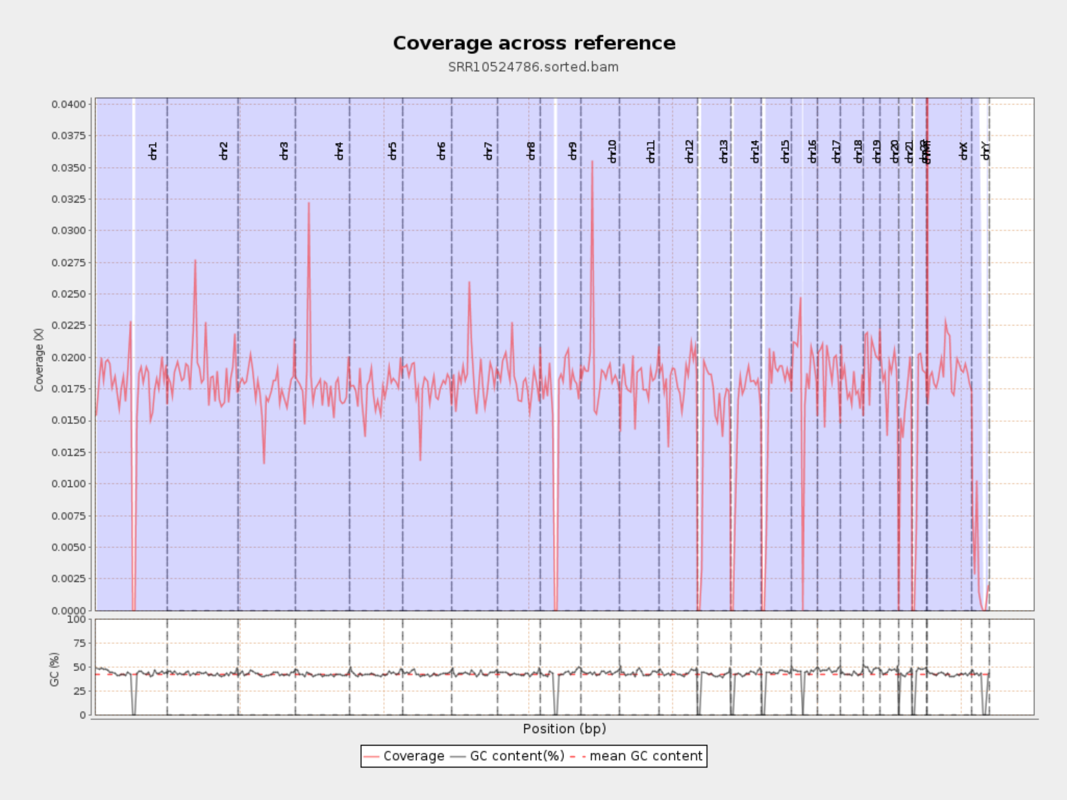
General error rate	0.52%
Mismatches	270,653
Insertions	3,652
Mapped reads with at least one insertion	0.39%
Deletions	10,697
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.39%

2.6. Chromosome stats

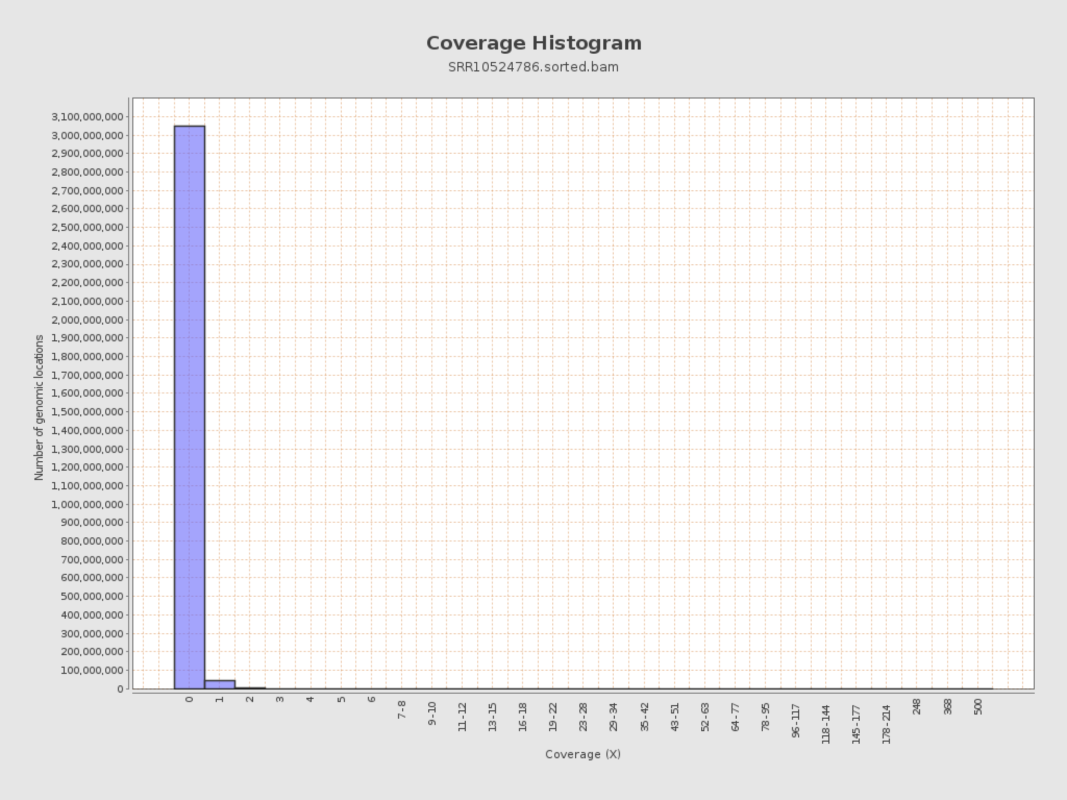
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4245084	0.017	0.2192
chr2	243199373	4574186	0.0188	0.2586
chr3	198022430	3465210	0.0175	0.1433
chr4	191154276	3441258	0.018	0.1565
chr5	180915260	3163555	0.0175	0.1408
chr6	171115067	3042677	0.0178	0.1525
chr7	159138663	2946663	0.0185	0.1984

chr8	146364022	2673629	0.0183	0.1702
chr9	141213431	2284486	0.0162	0.1532
chr10	135534747	2619732	0.0193	0.1979
chr11	135006516	2432618	0.018	0.1599
chr12	133851895	2448830	0.0183	0.1461
chr13	115169878	1653166	0.0144	0.1276
chr14	107349540	1592562	0.0148	0.132
chr15	102531392	1581399	0.0154	0.1341
chr16	90354753	1633916	0.0181	0.155
chr17	81195210	1554541	0.0191	0.1505
chr18	78077248	1381032	0.0177	0.2302
chr19	59128983	1191479	0.0202	0.1988
chr20	63025520	1157440	0.0184	0.1491
chr21	48129895	725427	0.0151	0.1424
chr22	51304566	689658	0.0134	0.1261
chrMT	16571	17768	1.0722	1.1435
chrX	155270560	2950370	0.019	0.1529
chrY	59373566	170877	0.0029	0.0919

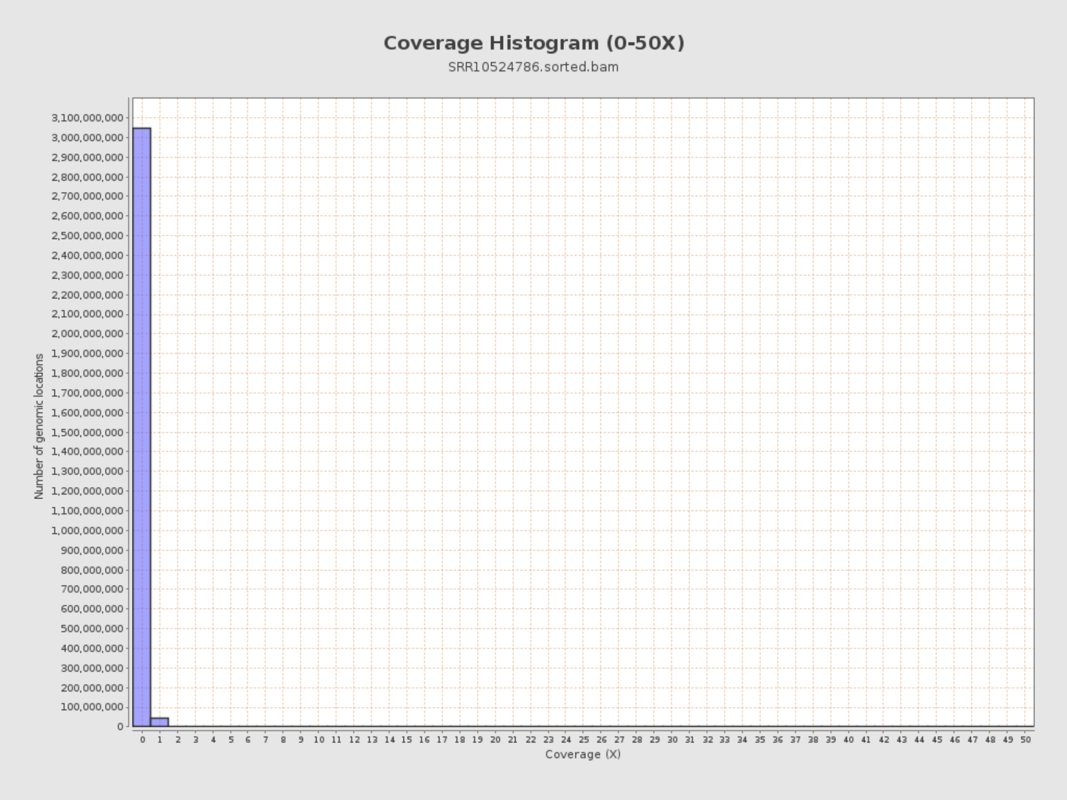
3. Results : Coverage across reference



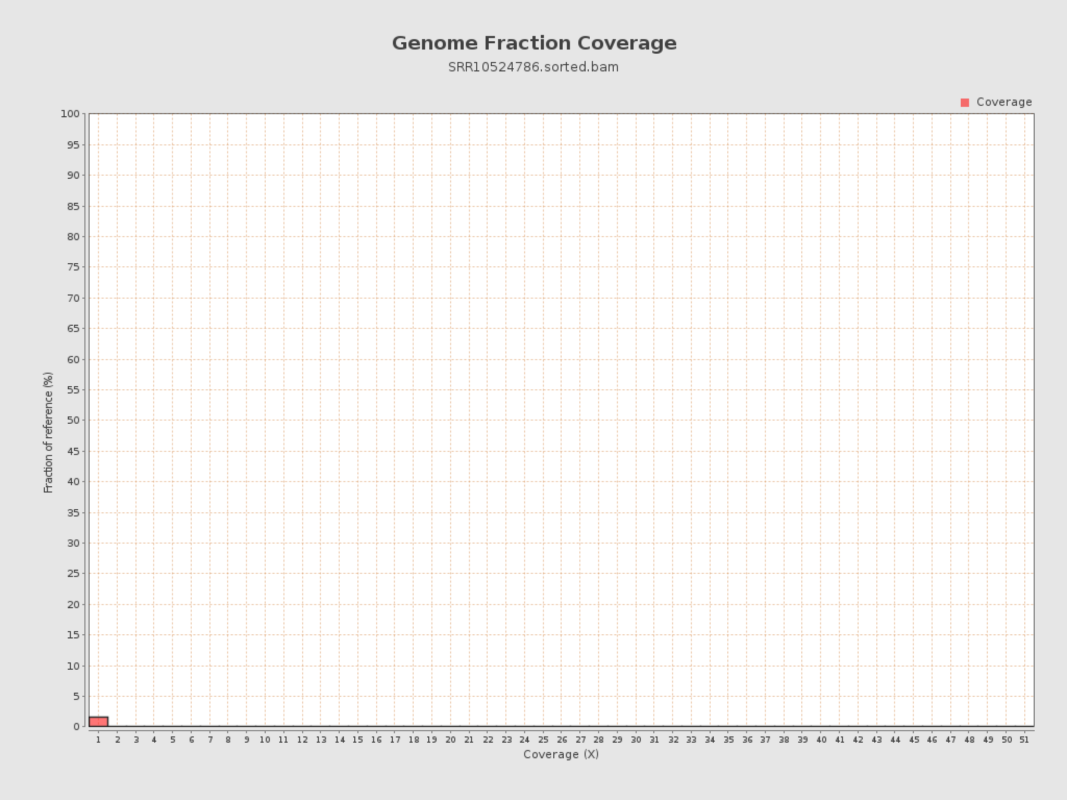
4. Results : Coverage Histogram



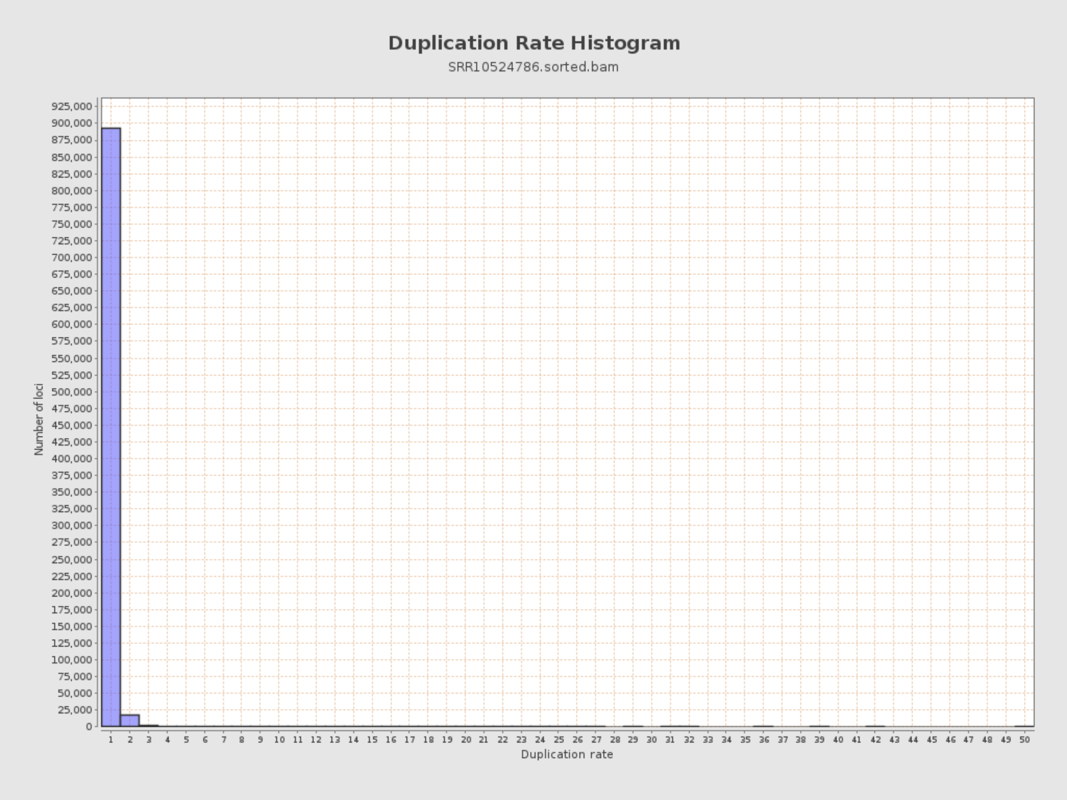
5. Results : Coverage Histogram (0-50X)



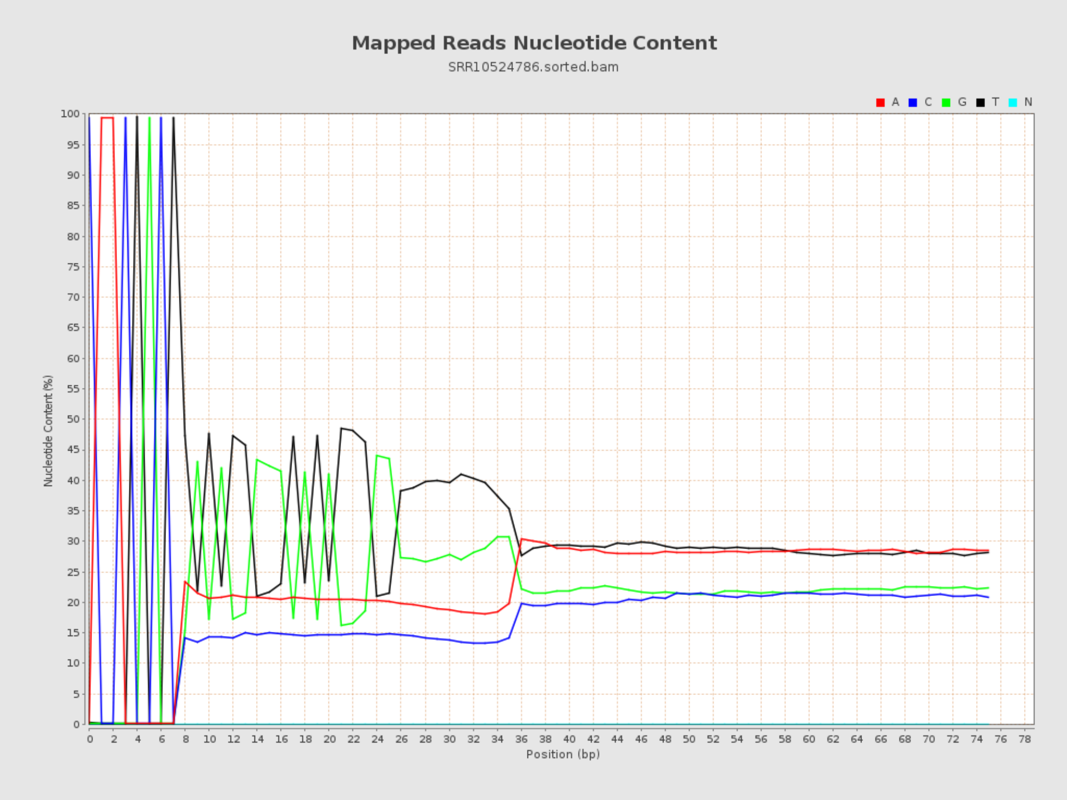
6. Results : Genome Fraction Coverage



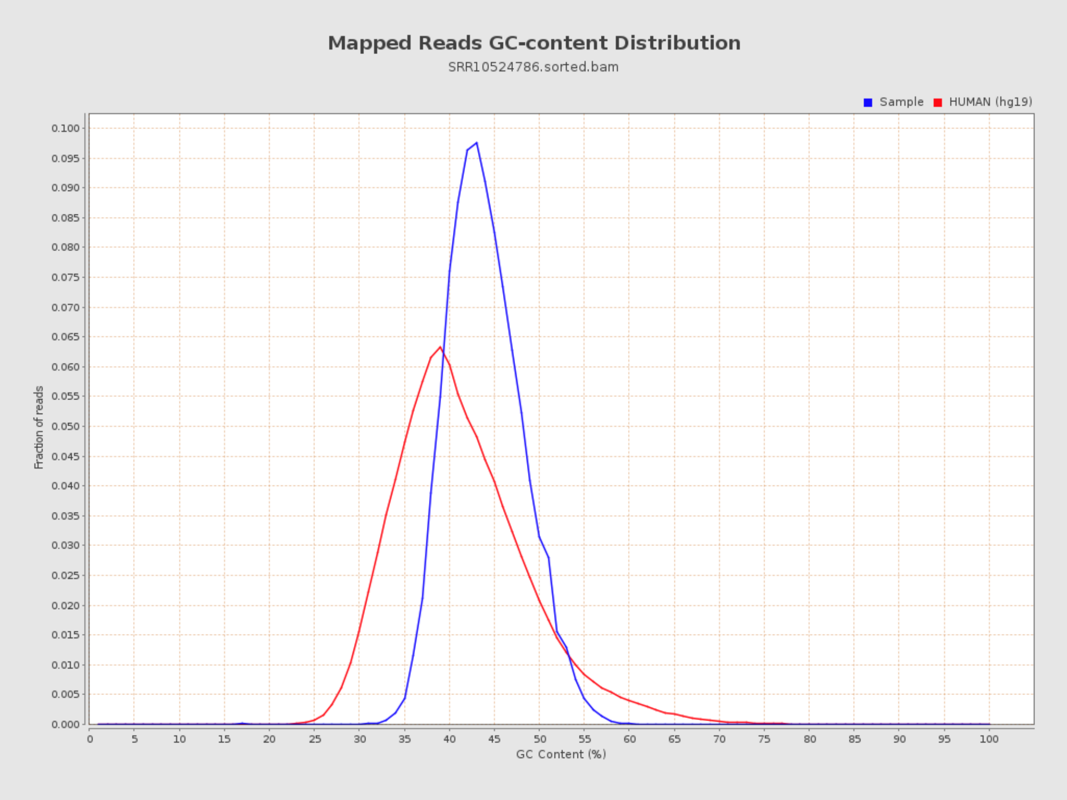
7. Results : Duplication Rate Histogram



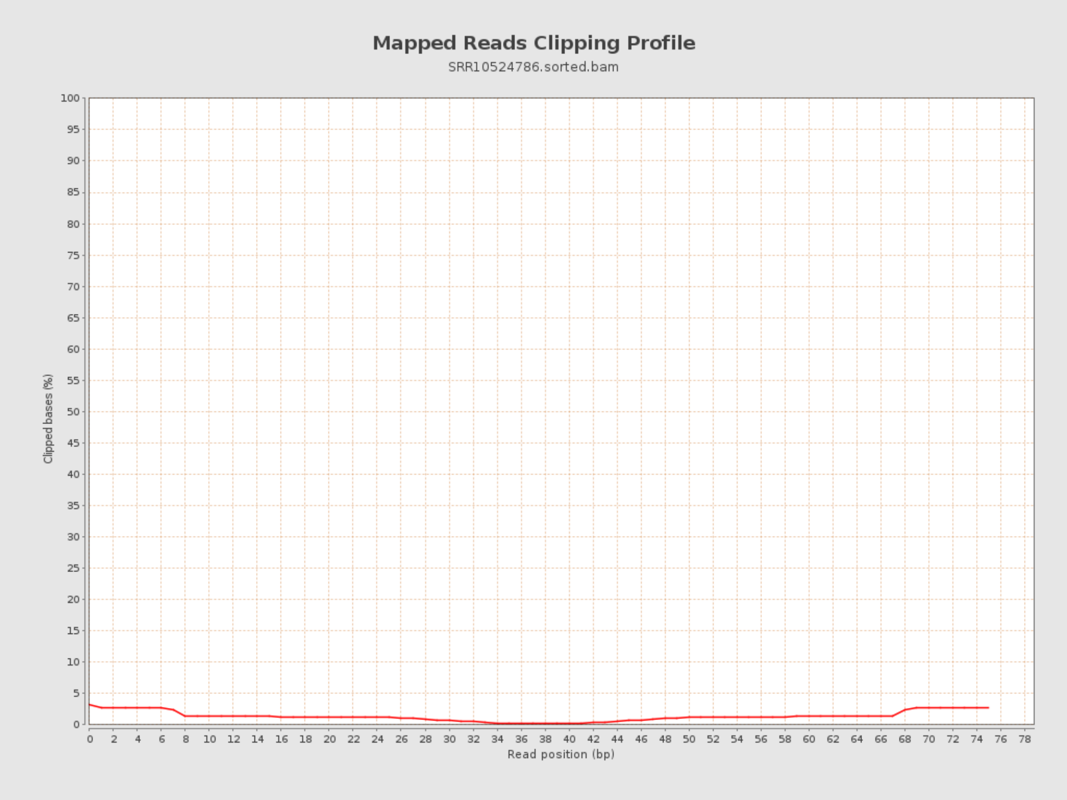
8. Results : Mapped Reads Nucleotide Content



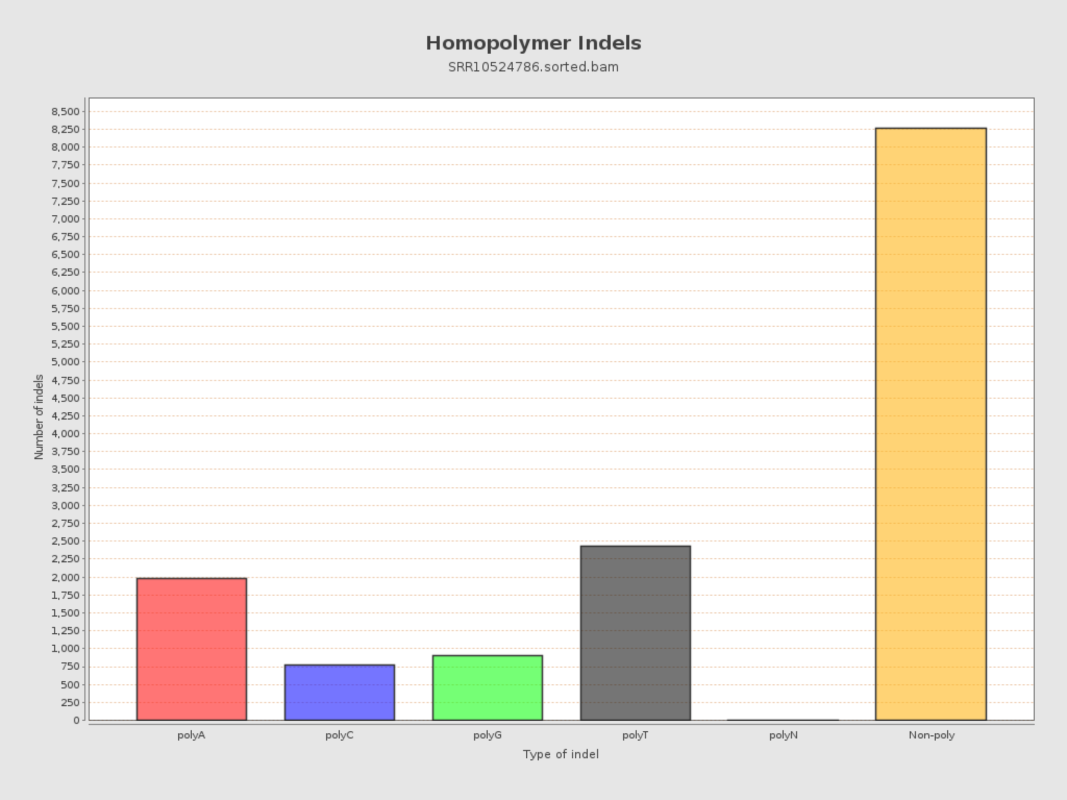
9. Results : Mapped Reads GC-content Distribution



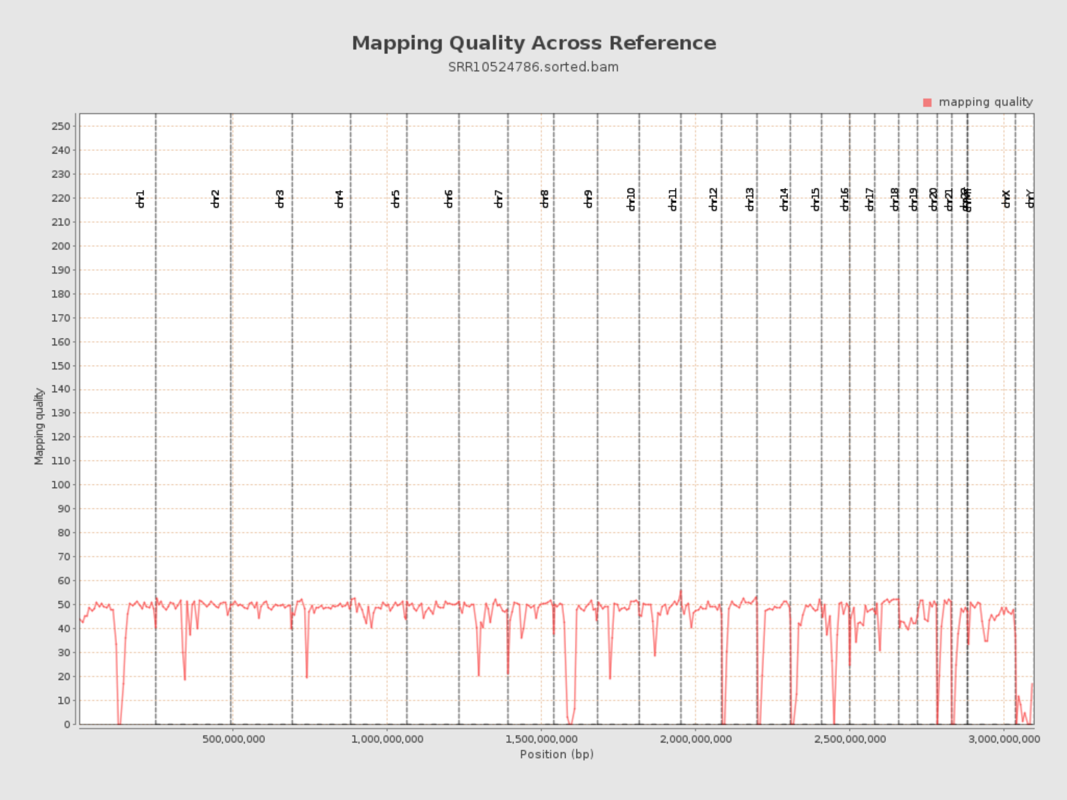
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram