Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:52:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524794.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_SRR10524794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524794.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:52:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,002,199
Mapped reads	906,887 / 90.49%
Unmapped reads	95,312 / 9.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,537 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	29,455 / 2.94%
Duplication rate	2.5%
Clipped reads	908,118 / 90.61%

2.2. ACGT Content

Number/percentage of A's	12,986,219 / 25.03%
Number/percentage of C's	9,998,699 / 19.27%
Number/percentage of T's	16,410,497 / 31.63%
Number/percentage of G's	12,474,503 / 24.05%
Number/percentage of N's	5,725 / 0.01%
GC Percentage	43.32%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.1755

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

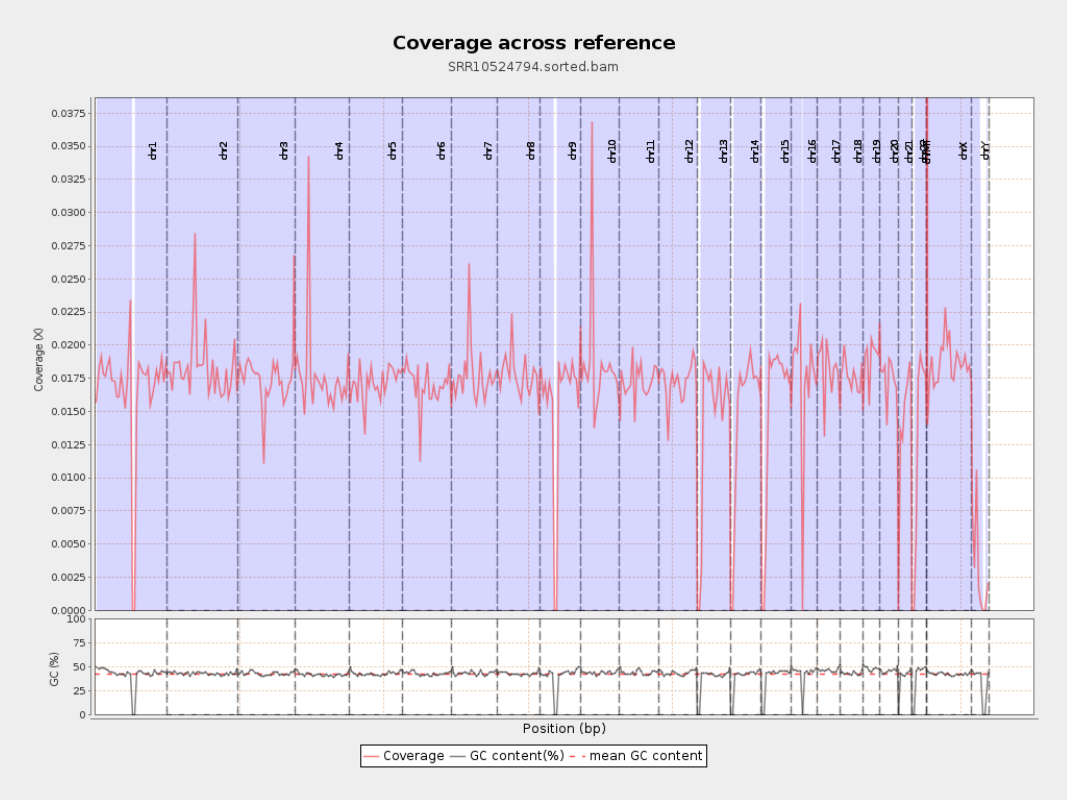
General error rate	0.53%
Mismatches	266,714
Insertions	4,018
Mapped reads with at least one insertion	0.44%
Deletions	10,112
Mapped reads with at least one deletion	1.11%
Homopolymer indels	40.94%

2.6. Chromosome stats

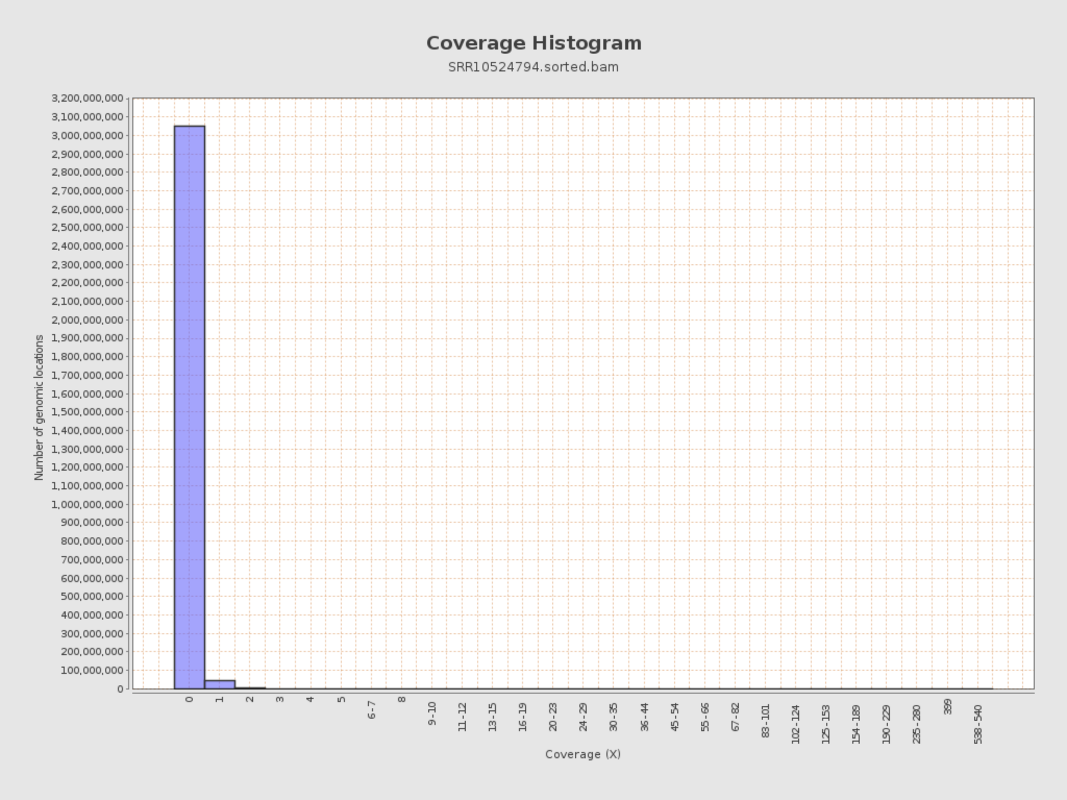
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4118821	0.0165	0.2282
chr2	243199373	4455584	0.0183	0.2718
chr3	198022430	3439165	0.0174	0.1425
chr4	191154276	3382716	0.0177	0.1598
chr5	180915260	3112285	0.0172	0.1402
chr6	171115067	2899542	0.0169	0.1483
chr7	159138663	2823563	0.0177	0.2004

chr8	146364022	2596171	0.0177	0.1623
chr9	141213431	2178330	0.0154	0.1553
chr10	135534747	2511548	0.0185	0.2079
chr11	135006516	2332674	0.0173	0.156
chr12	133851895	2305012	0.0172	0.1425
chr13	115169878	1618354	0.0141	0.1271
chr14	107349540	1567732	0.0146	0.1322
chr15	102531392	1524096	0.0149	0.1311
chr16	90354753	1540498	0.017	0.1517
chr17	81195210	1473912	0.0182	0.1487
chr18	78077248	1378958	0.0177	0.2182
chr19	59128983	1124074	0.019	0.1988
chr20	63025520	1093249	0.0173	0.1459
chr21	48129895	685066	0.0142	0.1391
chr22	51304566	637932	0.0124	0.1198
chrMT	16571	23193	1.3996	1.4102
chrX	155270560	2891163	0.0186	0.1519
chrY	59373566	178301	0.003	0.0924

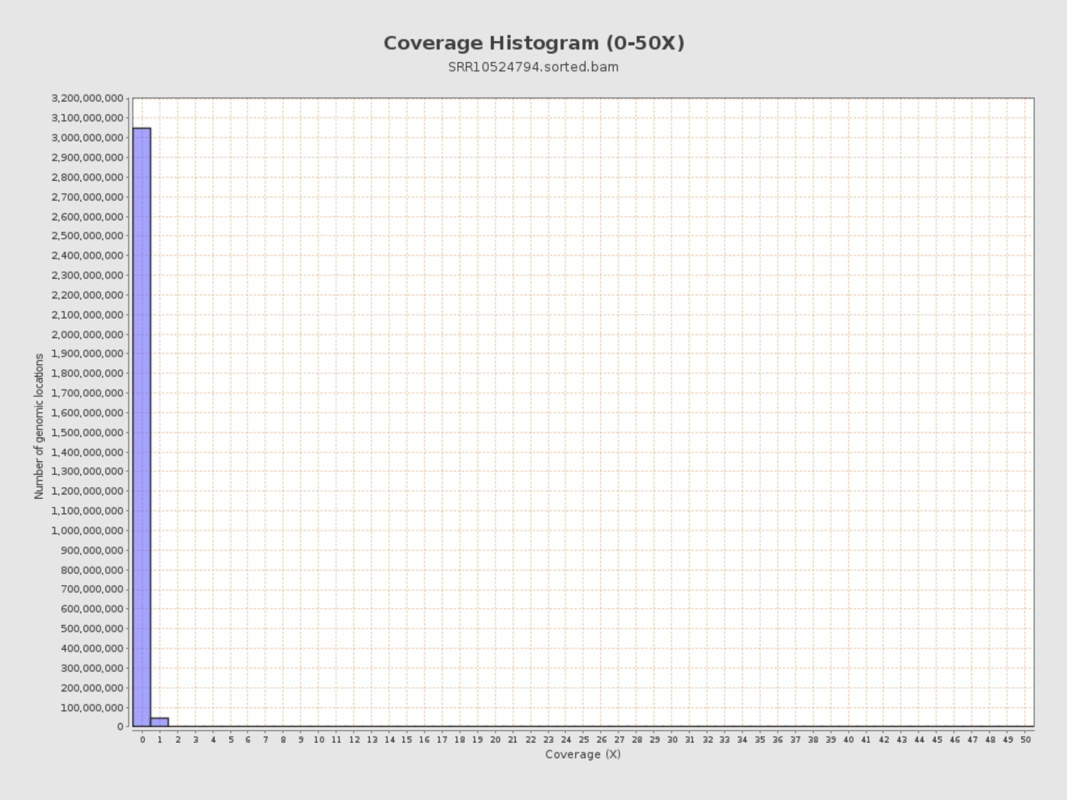
3. Results : Coverage across reference



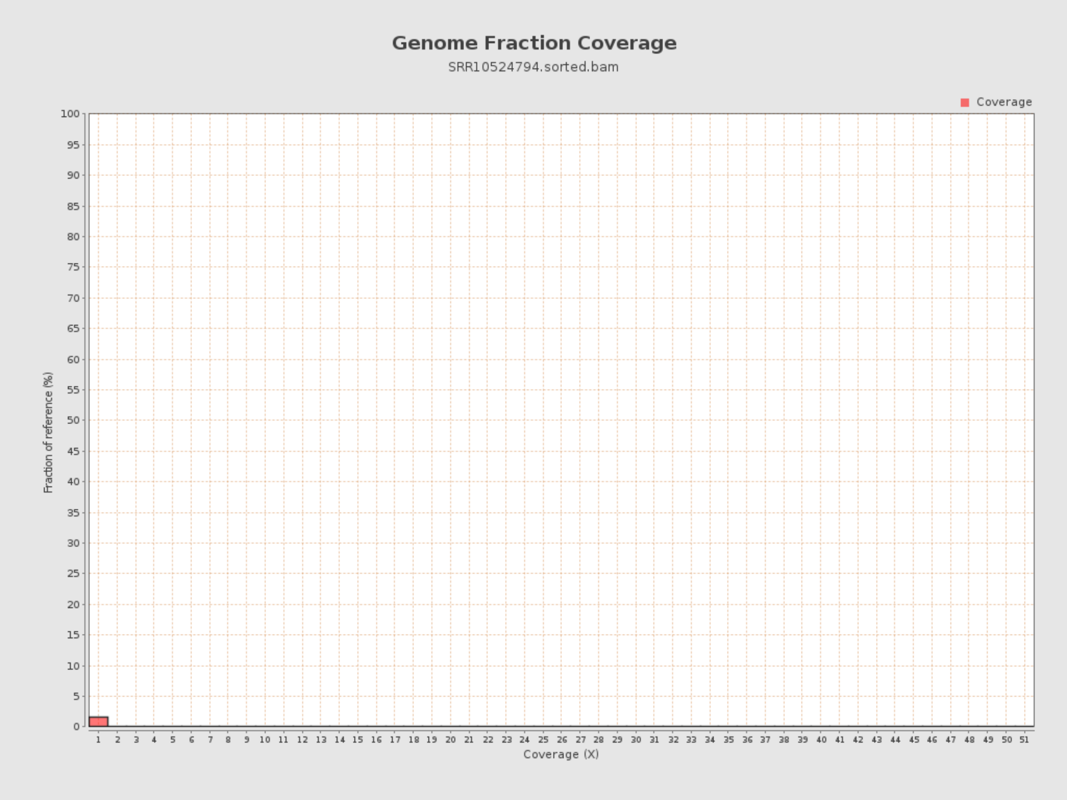
4. Results : Coverage Histogram



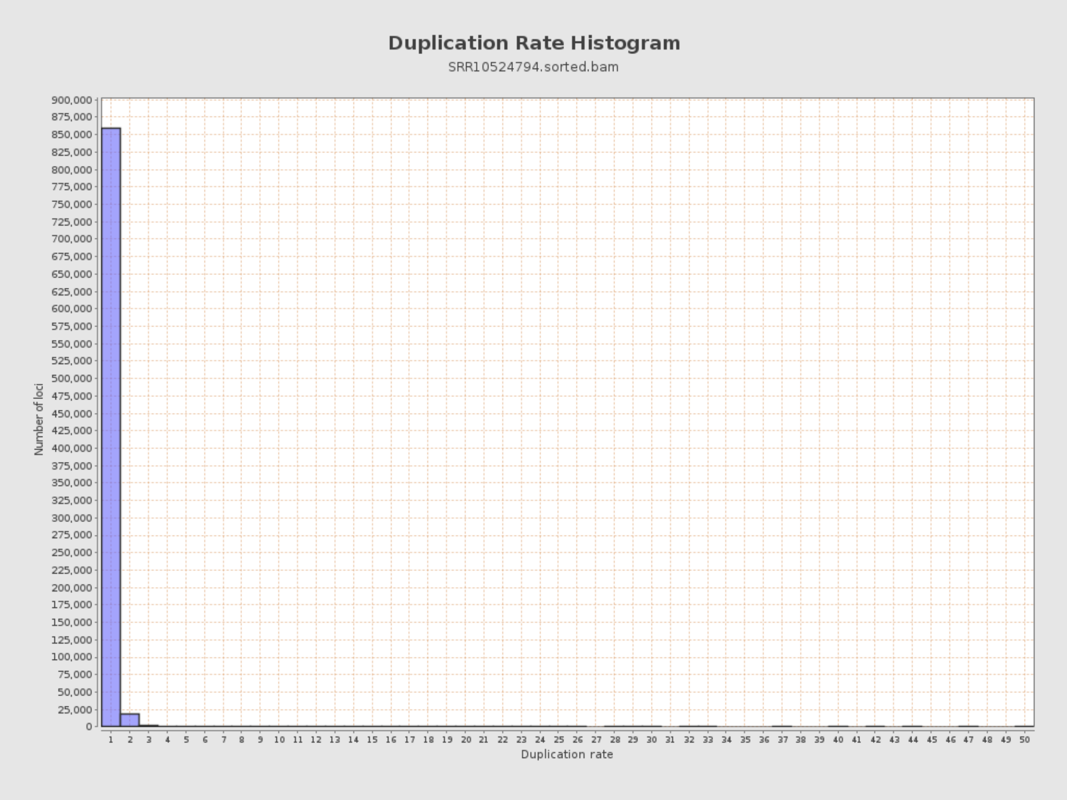
5. Results : Coverage Histogram (0-50X)



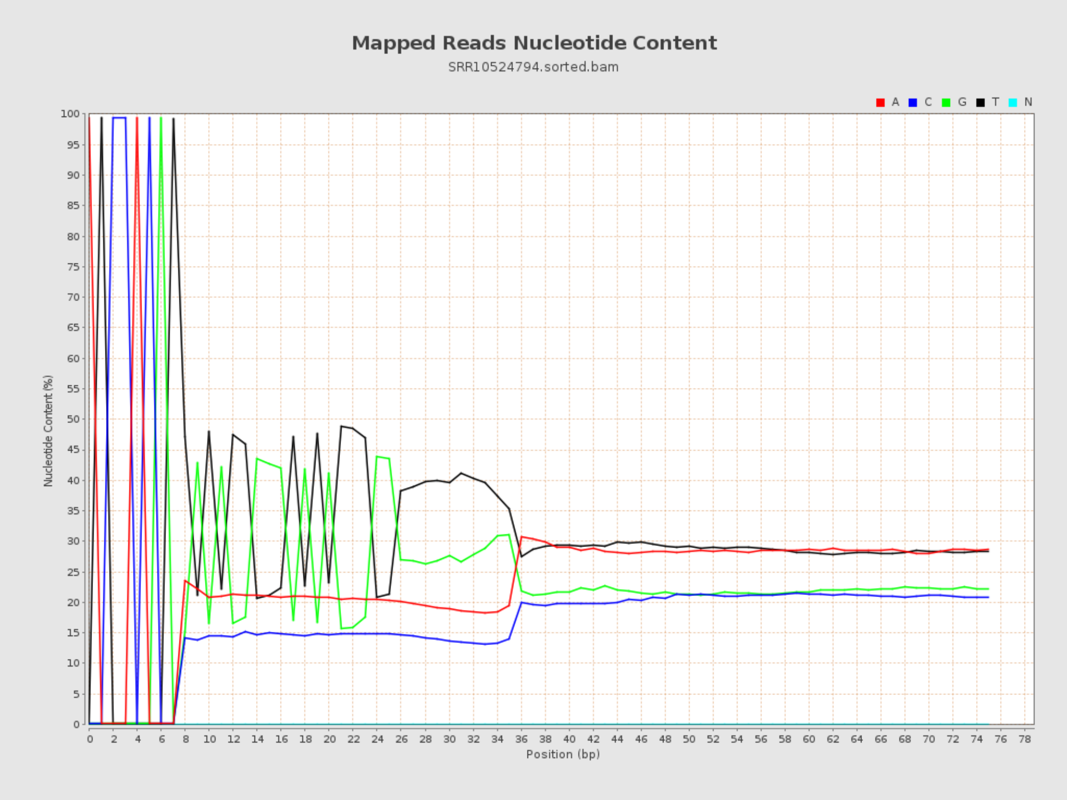
6. Results : Genome Fraction Coverage



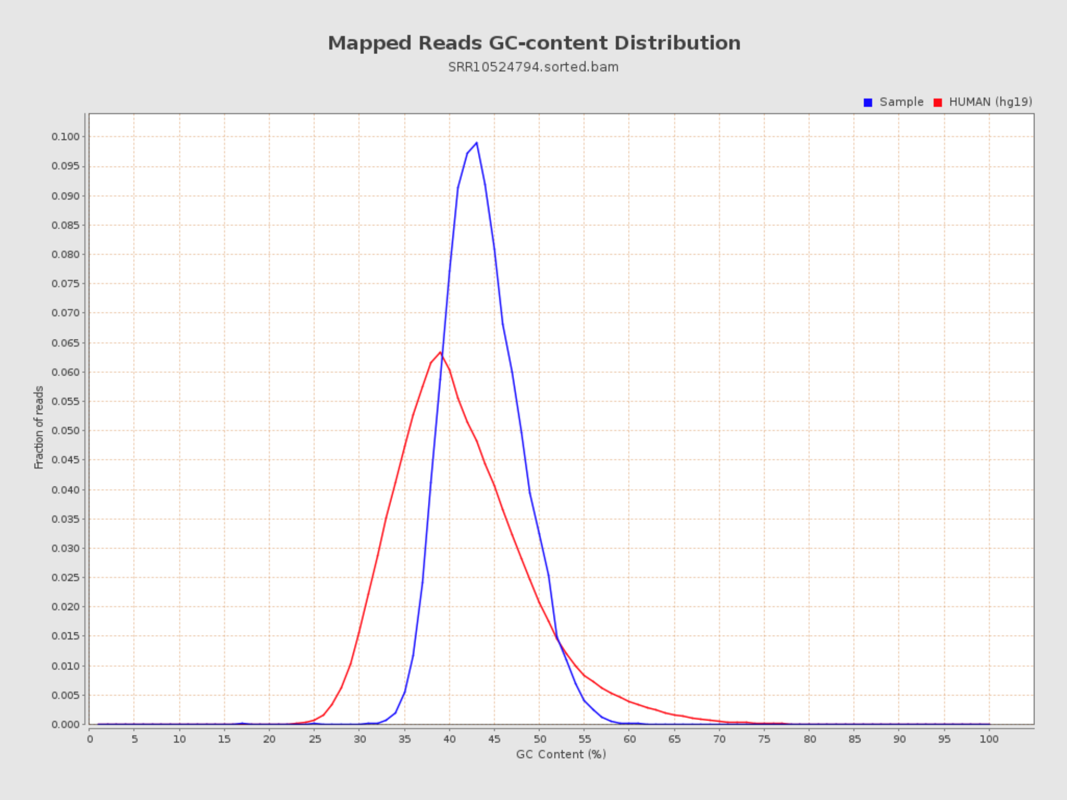
7. Results : Duplication Rate Histogram



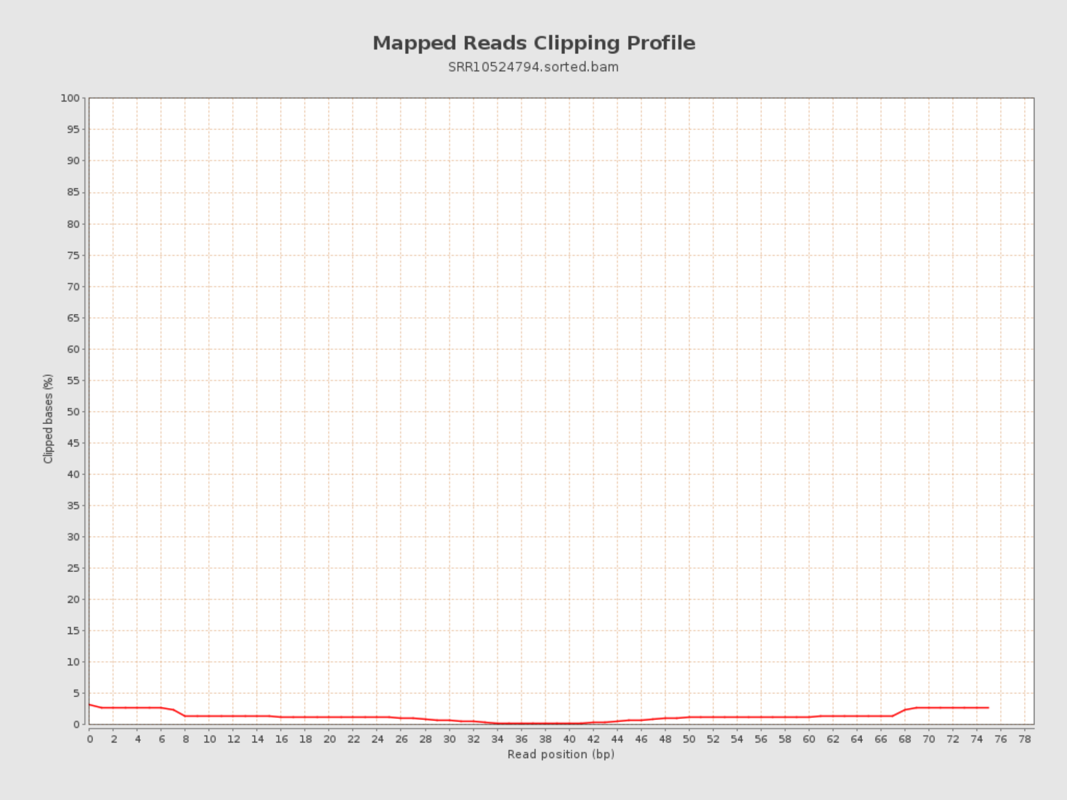
8. Results : Mapped Reads Nucleotide Content



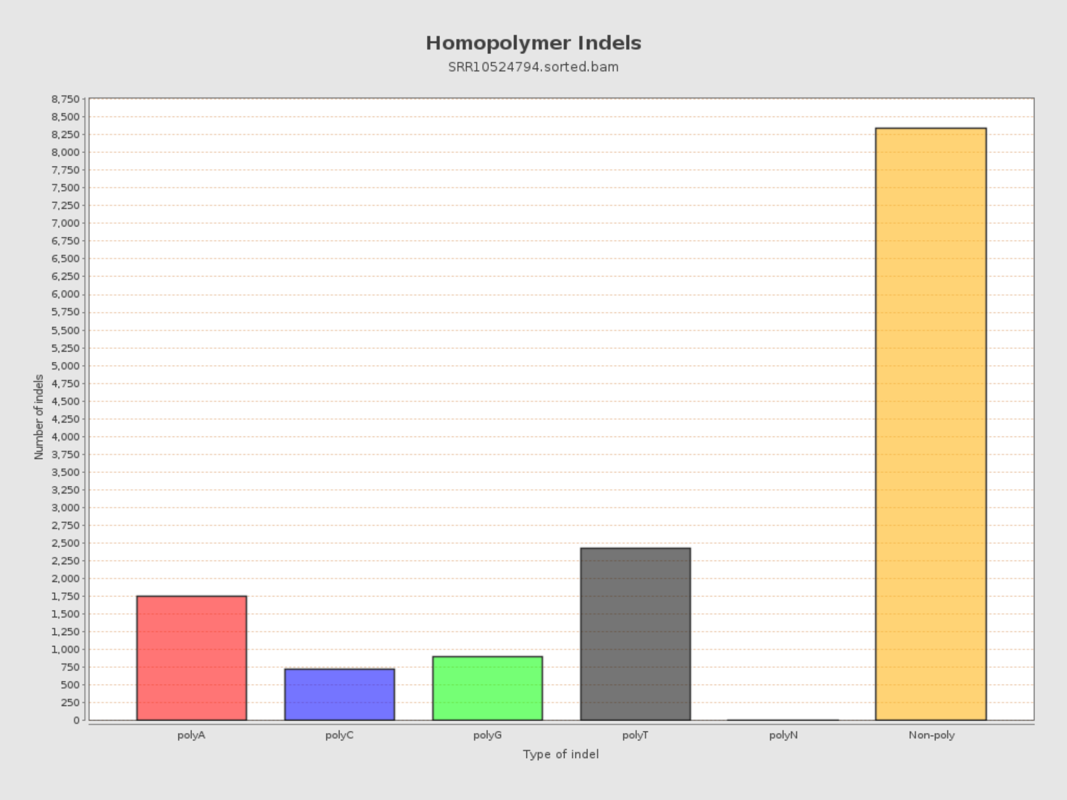
9. Results : Mapped Reads GC-content Distribution



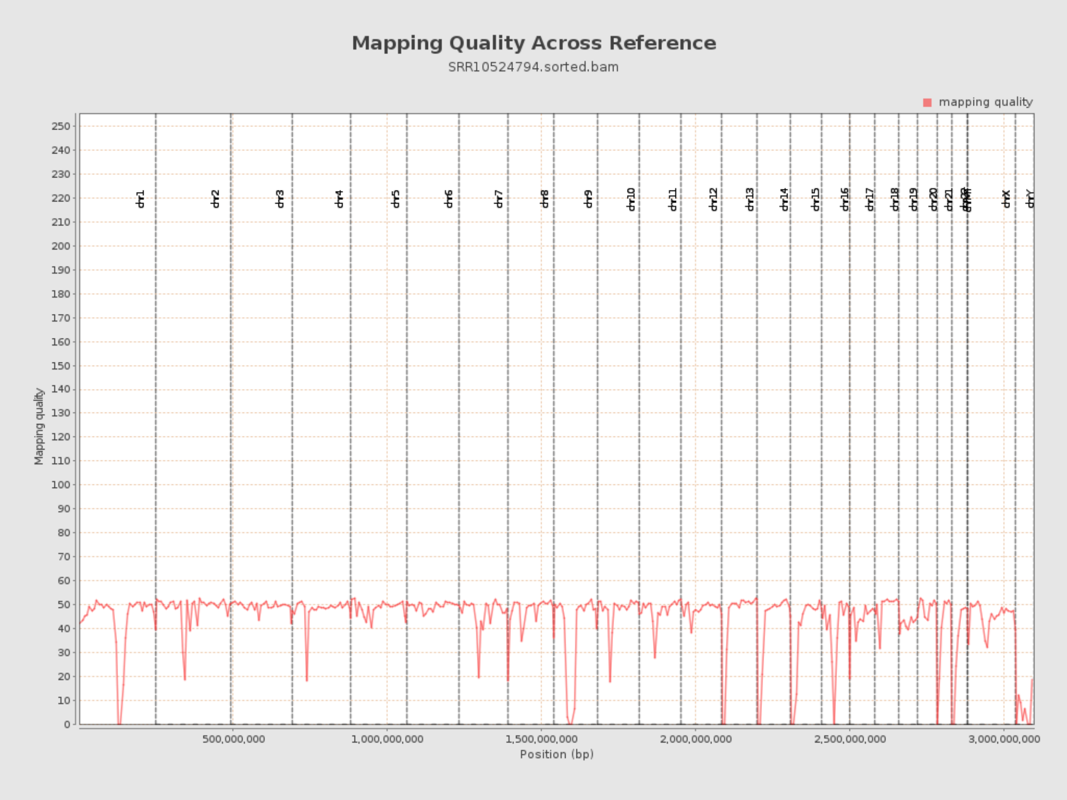
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram