Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:43:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524790.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_SRR10524790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524790.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:43:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,186,248
Mapped reads	1,089,121 / 91.81%
Unmapped reads	97,127 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,119 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	36,006 / 3.04%
Duplication rate	2.56%
Clipped reads	1,089,287 / 91.83%

2.2. ACGT Content

Number/percentage of A's	14,605,276 / 23.36%
Number/percentage of C's	12,068,132 / 19.3%
Number/percentage of T's	20,832,735 / 33.32%
Number/percentage of G's	15,007,260 / 24%
Number/percentage of N's	7,966 / 0.01%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.1921

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

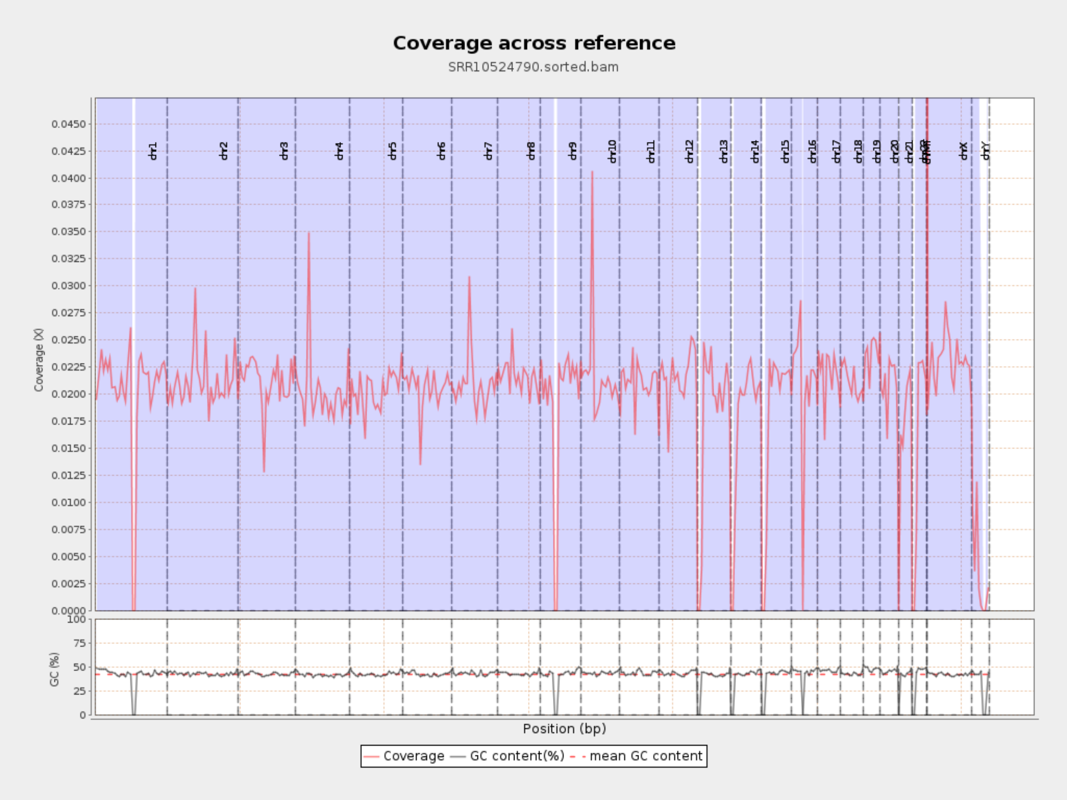
General error rate	0.51%
Mismatches	312,748
Insertions	4,680
Mapped reads with at least one insertion	0.43%
Deletions	12,357
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.14%

2.6. Chromosome stats

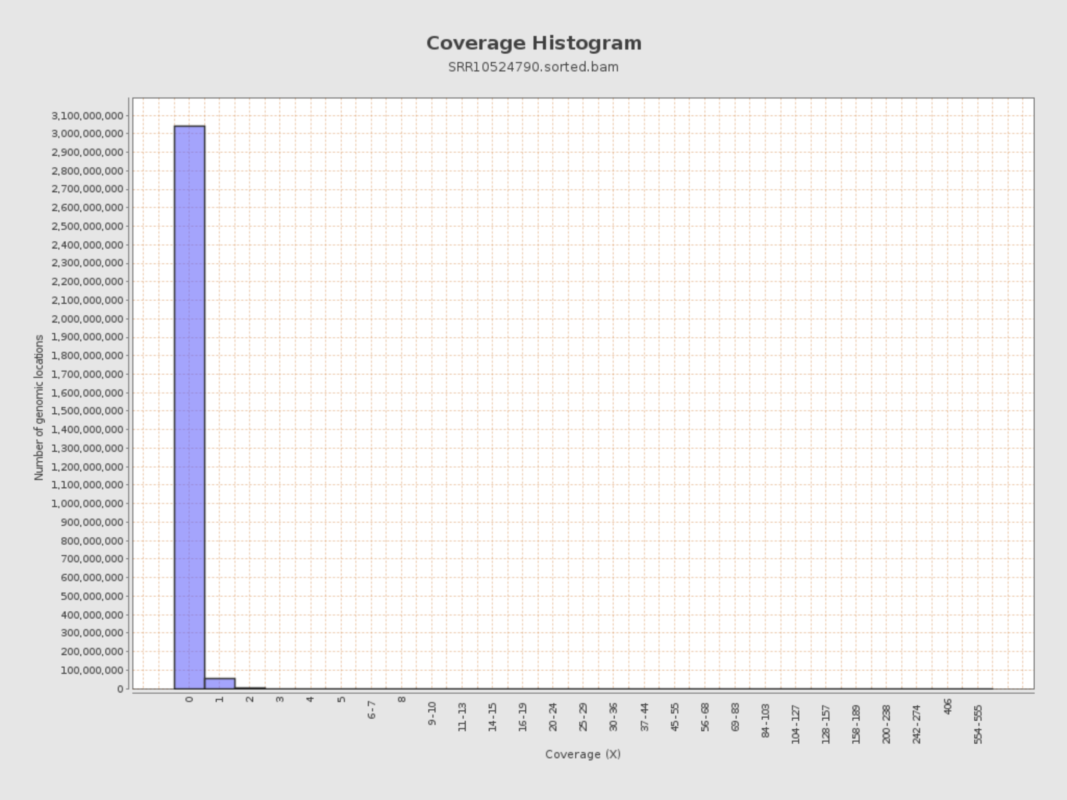
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5048092	0.0203	0.2462
chr2	243199373	5159012	0.0212	0.2844
chr3	198022430	4191775	0.0212	0.1583
chr4	191154276	3901056	0.0204	0.169
chr5	180915260	3693075	0.0204	0.1544
chr6	171115067	3519548	0.0206	0.165
chr7	159138663	3341375	0.021	0.2246

chr8	146364022	3166990	0.0216	0.1853
chr9	141213431	2702373	0.0191	0.1738
chr10	135534747	2948985	0.0218	0.224
chr11	135006516	2868098	0.0212	0.1782
chr12	133851895	2901958	0.0217	0.161
chr13	115169878	2039959	0.0177	0.1435
chr14	107349540	1853982	0.0173	0.146
chr15	102531392	1812262	0.0177	0.1439
chr16	90354753	1857348	0.0206	0.168
chr17	81195210	1775289	0.0219	0.1642
chr18	78077248	1654123	0.0212	0.2526
chr19	59128983	1398087	0.0236	0.2132
chr20	63025520	1304157	0.0207	0.1597
chr21	48129895	811794	0.0169	0.1514
chr22	51304566	787743	0.0154	0.1353
chrMT	16571	12390	0.7477	1.0342
chrX	155270560	3589221	0.0231	0.1747
chrY	59373566	202317	0.0034	0.0991

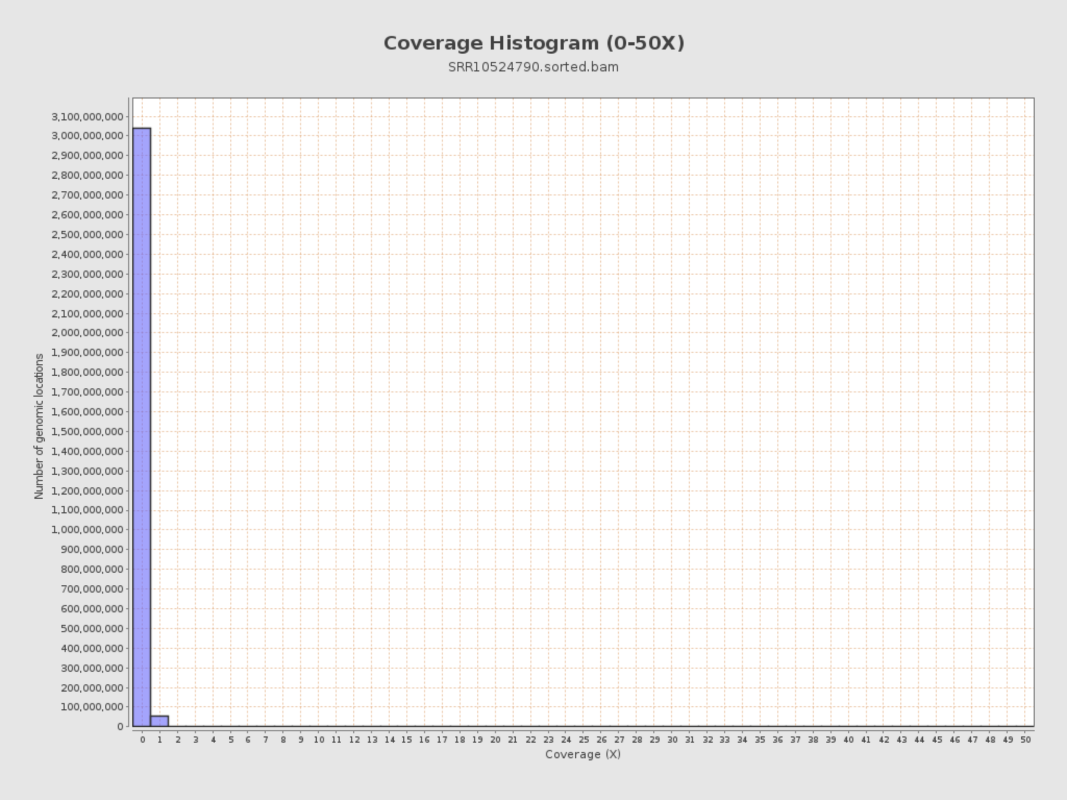
3. Results : Coverage across reference



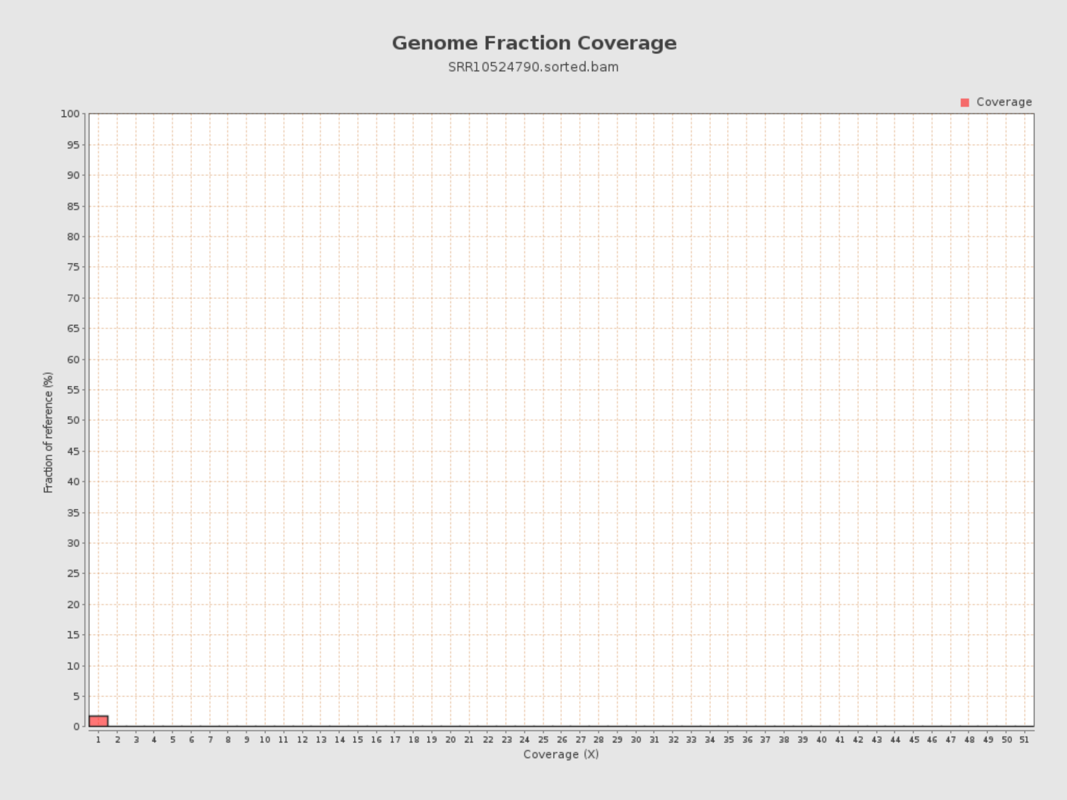
4. Results : Coverage Histogram



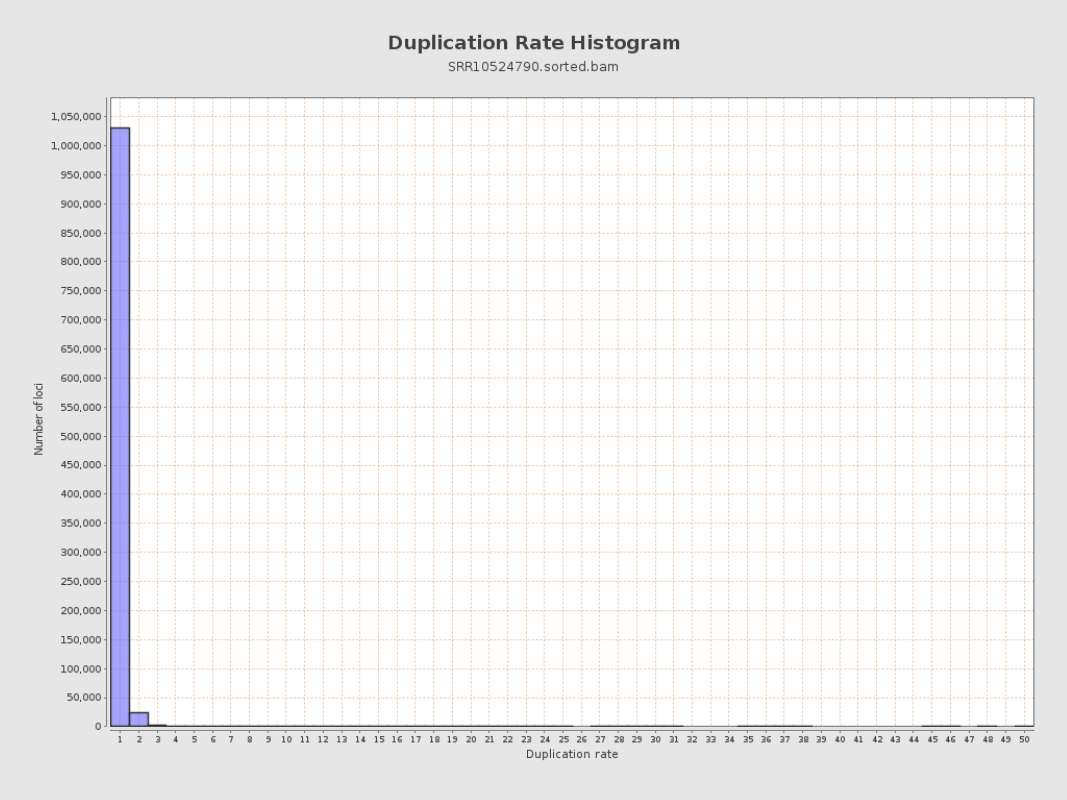
5. Results : Coverage Histogram (0-50X)



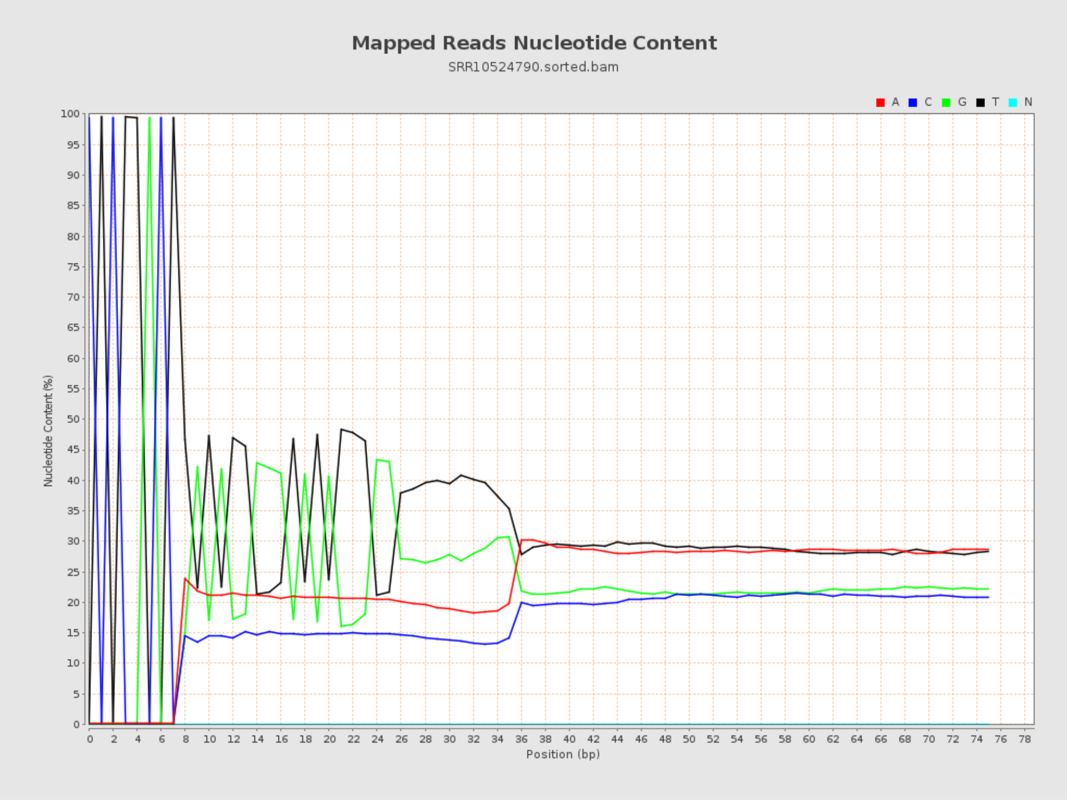
6. Results : Genome Fraction Coverage



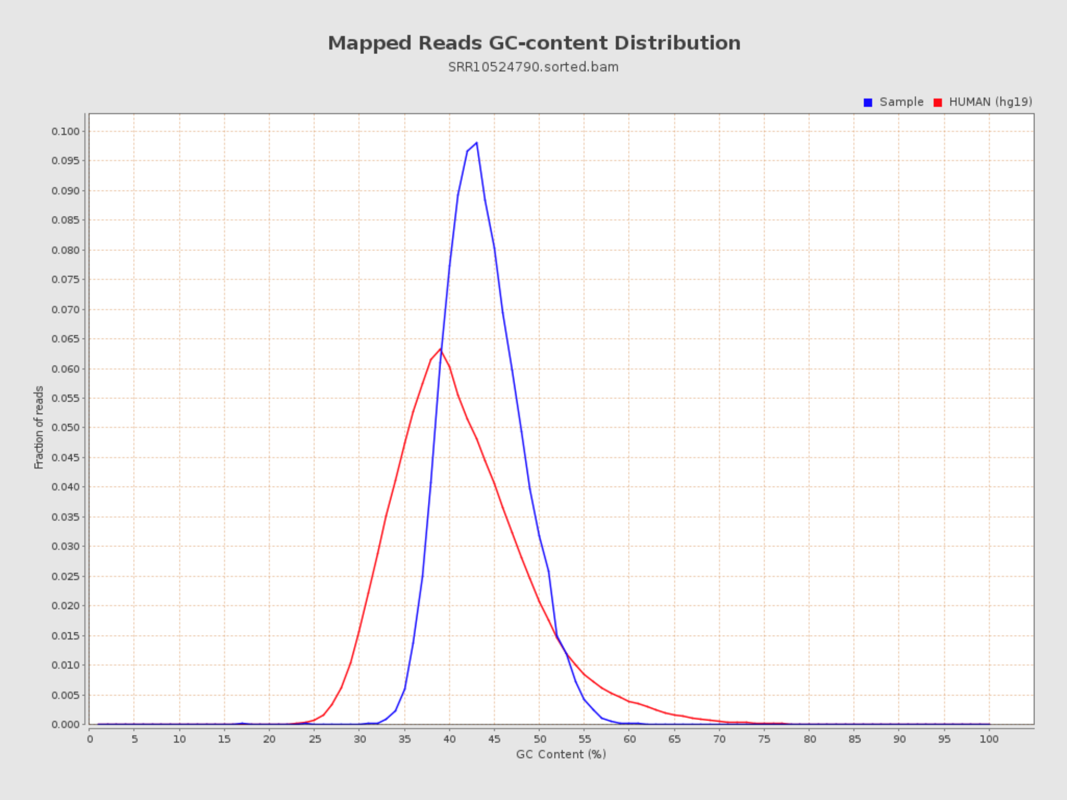
7. Results : Duplication Rate Histogram



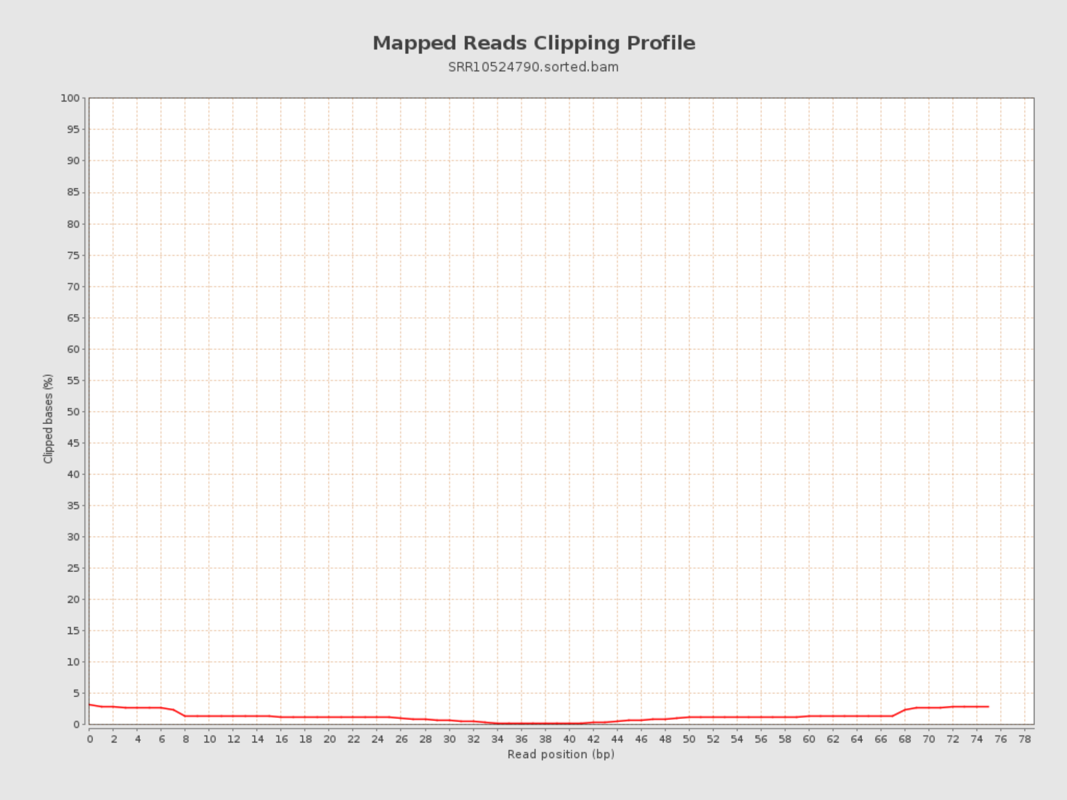
8. Results : Mapped Reads Nucleotide Content



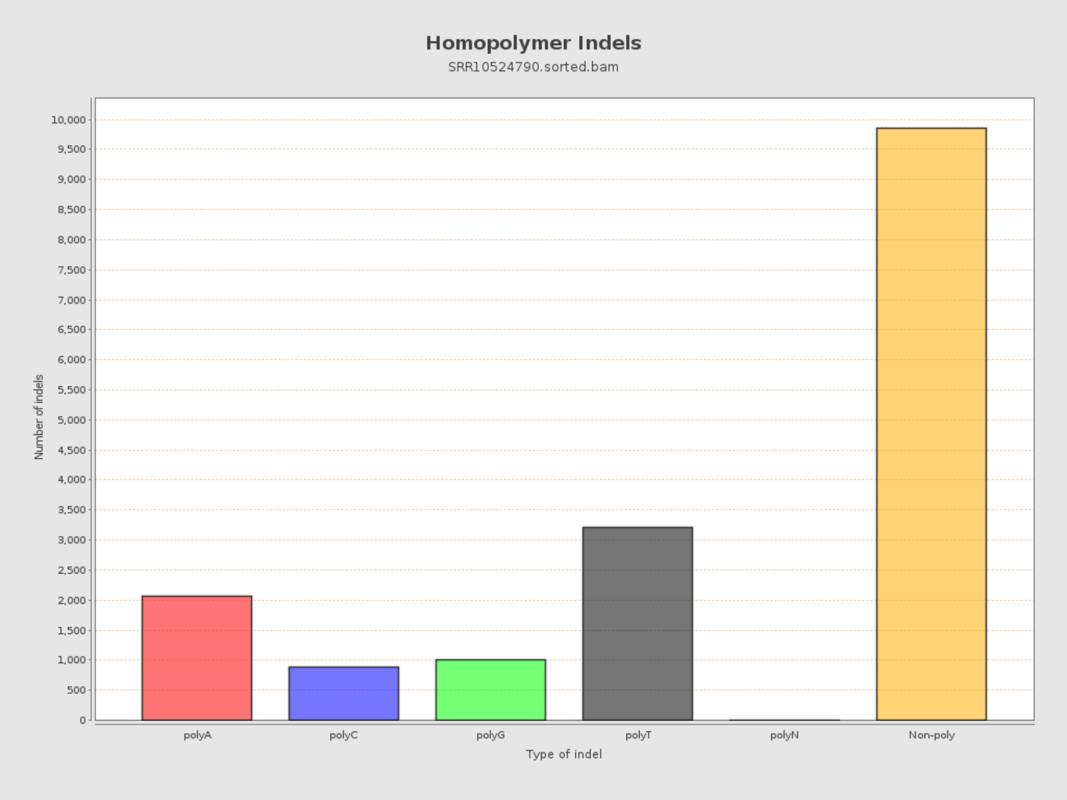
9. Results : Mapped Reads GC-content Distribution



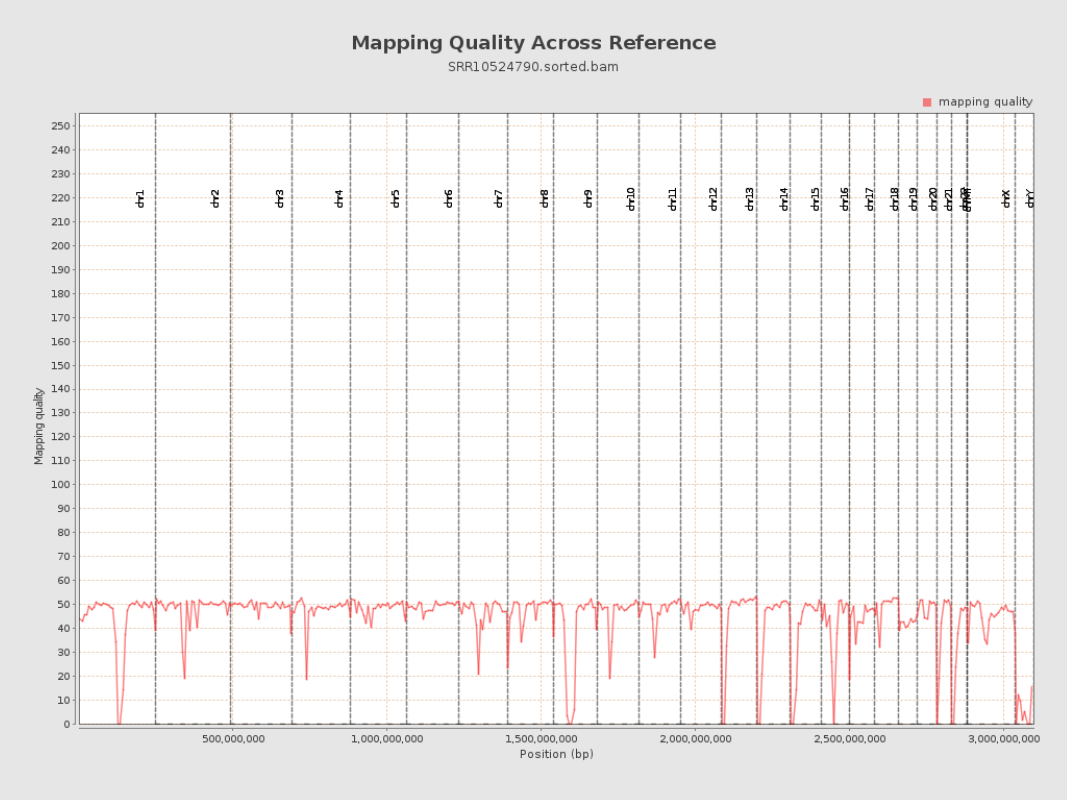
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram