Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:58:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524726.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_SRR10524726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524726.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:58:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	977,314
Mapped reads	894,710 / 91.55%
Unmapped reads	82,604 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,613 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	29,480 / 3.02%
Duplication rate	2.58%
Clipped reads	895,301 / 91.61%

2.2. ACGT Content

Number/percentage of A's	12,768,997 / 24.99%
Number/percentage of C's	8,956,852 / 17.53%
Number/percentage of T's	16,238,097 / 31.78%
Number/percentage of G's	13,127,801 / 25.69%
Number/percentage of N's	6,313 / 0.01%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0165

Standard Deviation	0.1692

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

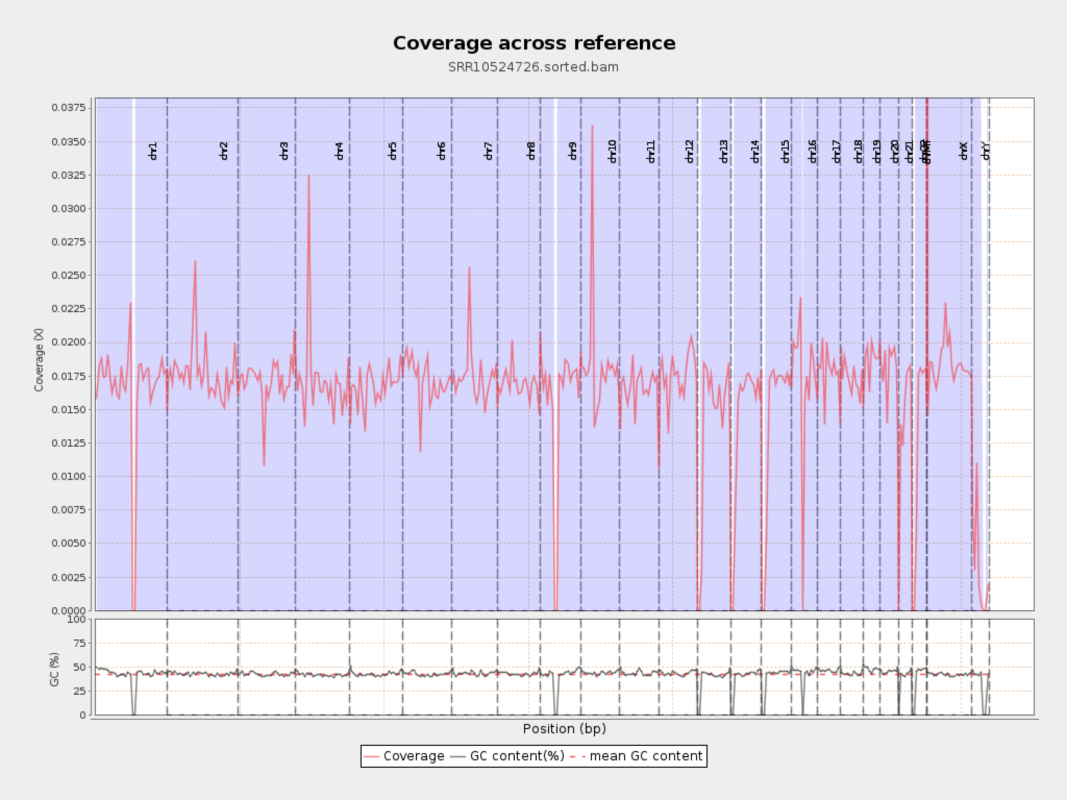
General error rate	0.51%
Mismatches	253,931
Insertions	4,178
Mapped reads with at least one insertion	0.46%
Deletions	10,110
Mapped reads with at least one deletion	1.12%
Homopolymer indels	40.75%

2.6. Chromosome stats

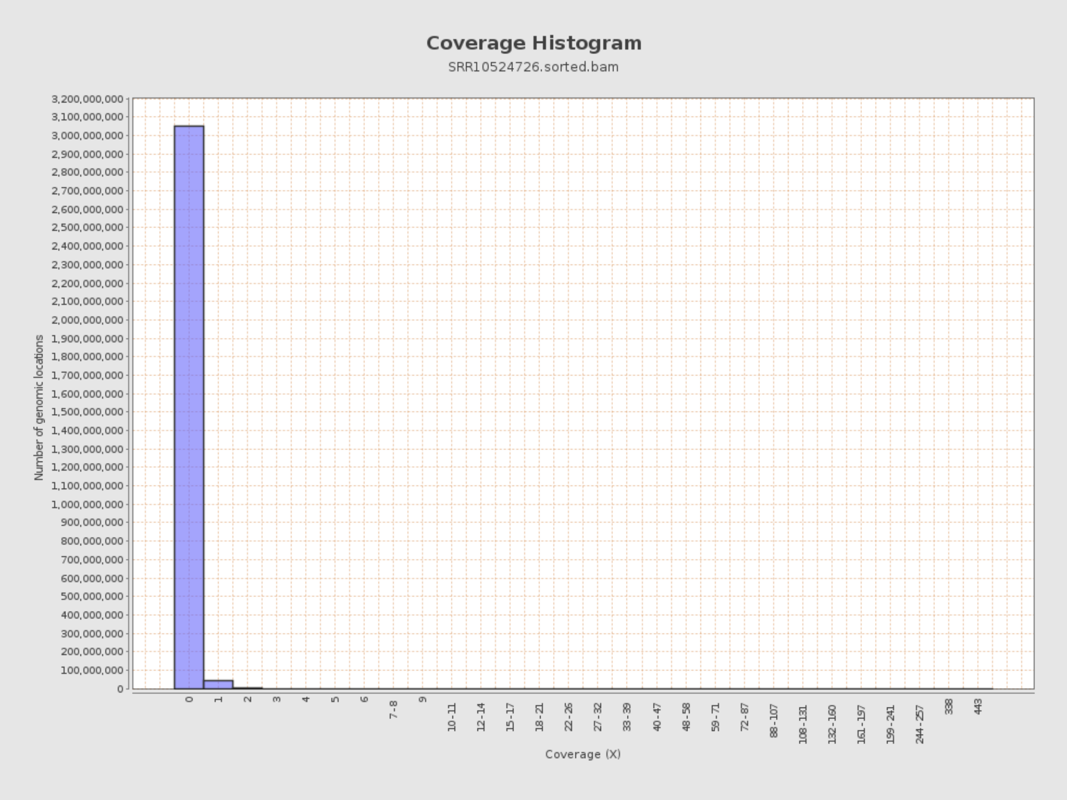
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4092697	0.0164	0.2251
chr2	243199373	4324627	0.0178	0.2402
chr3	198022430	3385264	0.0171	0.1431
chr4	191154276	3301906	0.0173	0.155
chr5	180915260	3051996	0.0169	0.139
chr6	171115067	2936724	0.0172	0.1489
chr7	159138663	2792461	0.0175	0.1917

chr8	146364022	2474361	0.0169	0.1586
chr9	141213431	2176727	0.0154	0.1515
chr10	135534747	2490249	0.0184	0.2
chr11	135006516	2266362	0.0168	0.1565
chr12	133851895	2361186	0.0176	0.1431
chr13	115169878	1586839	0.0138	0.1265
chr14	107349540	1492230	0.0139	0.1284
chr15	102531392	1437737	0.014	0.1271
chr16	90354753	1532824	0.017	0.1486
chr17	81195210	1452260	0.0179	0.1484
chr18	78077248	1349337	0.0173	0.2137
chr19	59128983	1108287	0.0187	0.1867
chr20	63025520	1128248	0.0179	0.1476
chr21	48129895	684531	0.0142	0.1386
chr22	51304566	629332	0.0123	0.1191
chrMT	16571	22386	1.3509	1.4256
chrX	155270560	2854634	0.0184	0.1511
chrY	59373566	181226	0.0031	0.0929

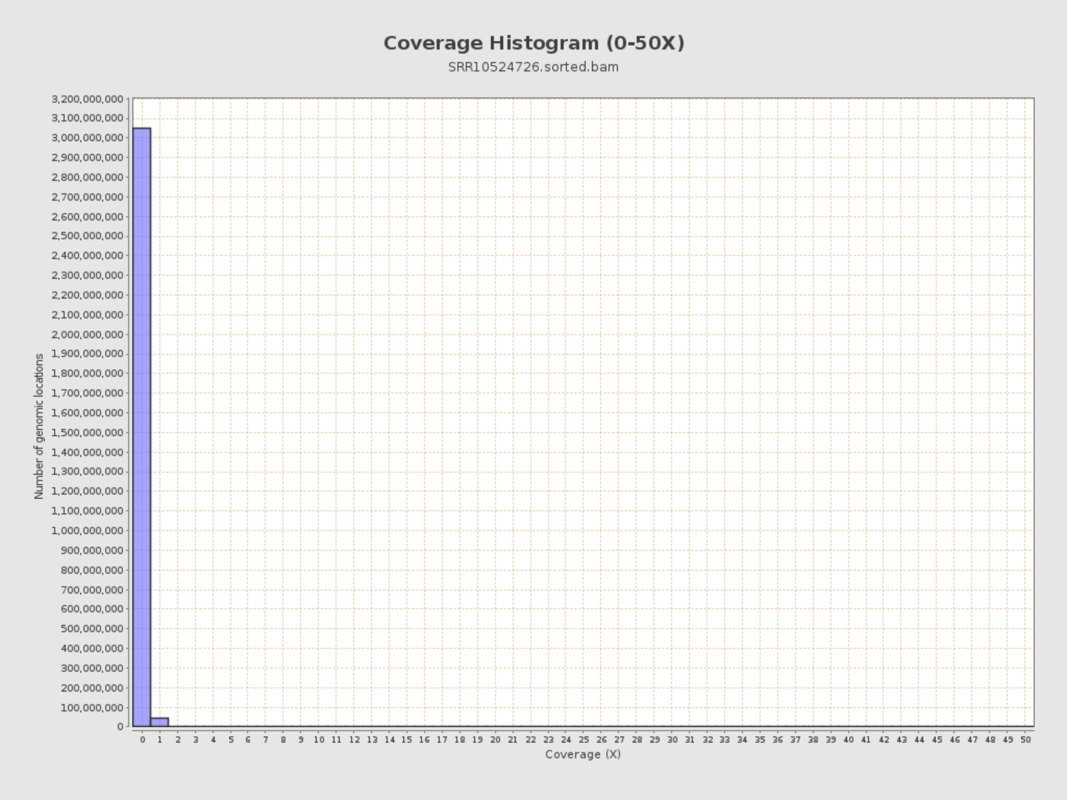
3. Results : Coverage across reference



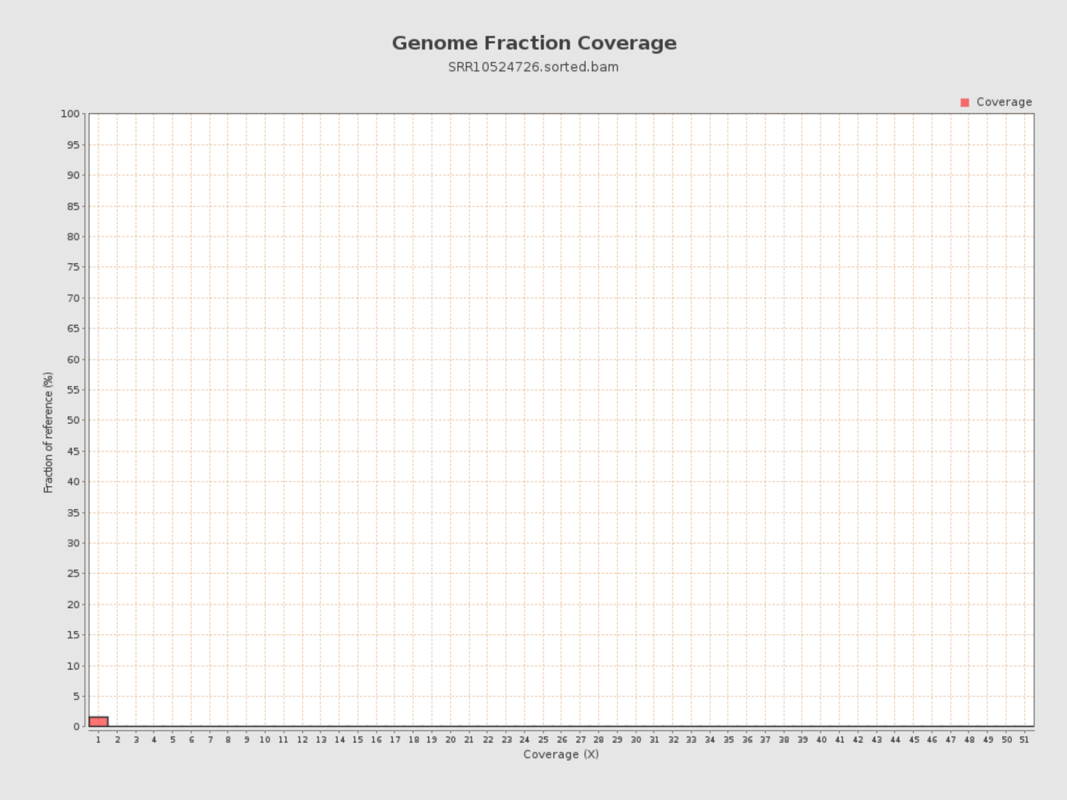
4. Results : Coverage Histogram



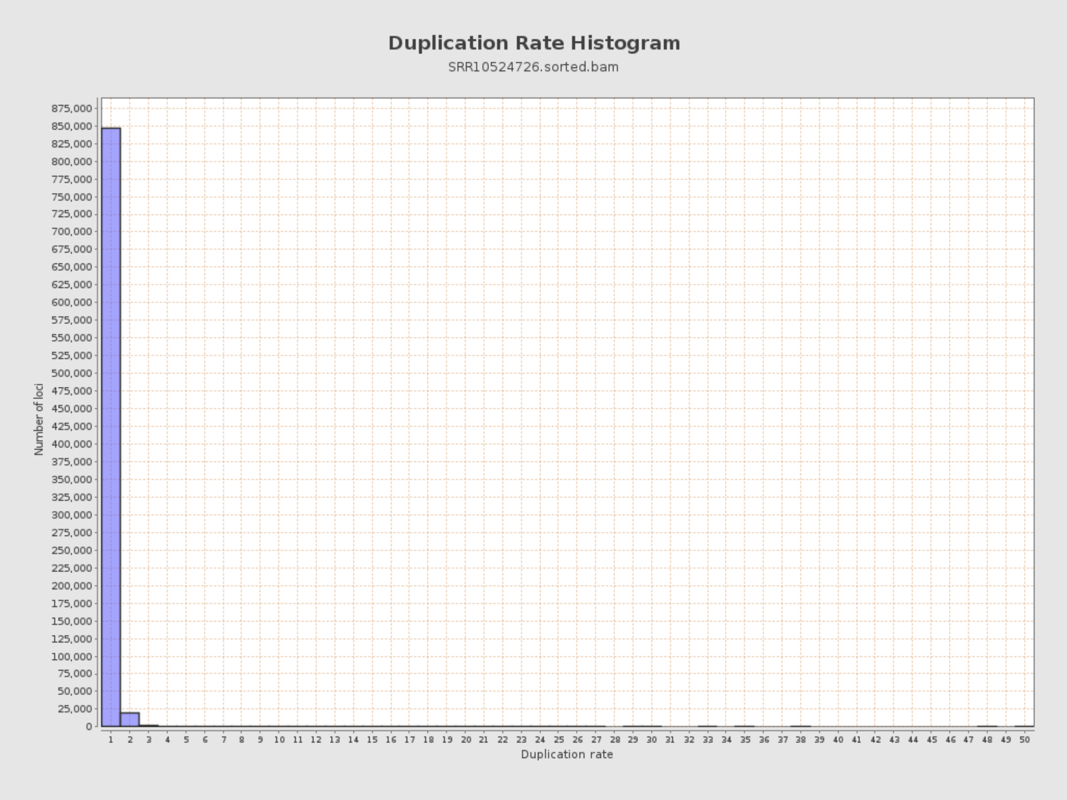
5. Results : Coverage Histogram (0-50X)



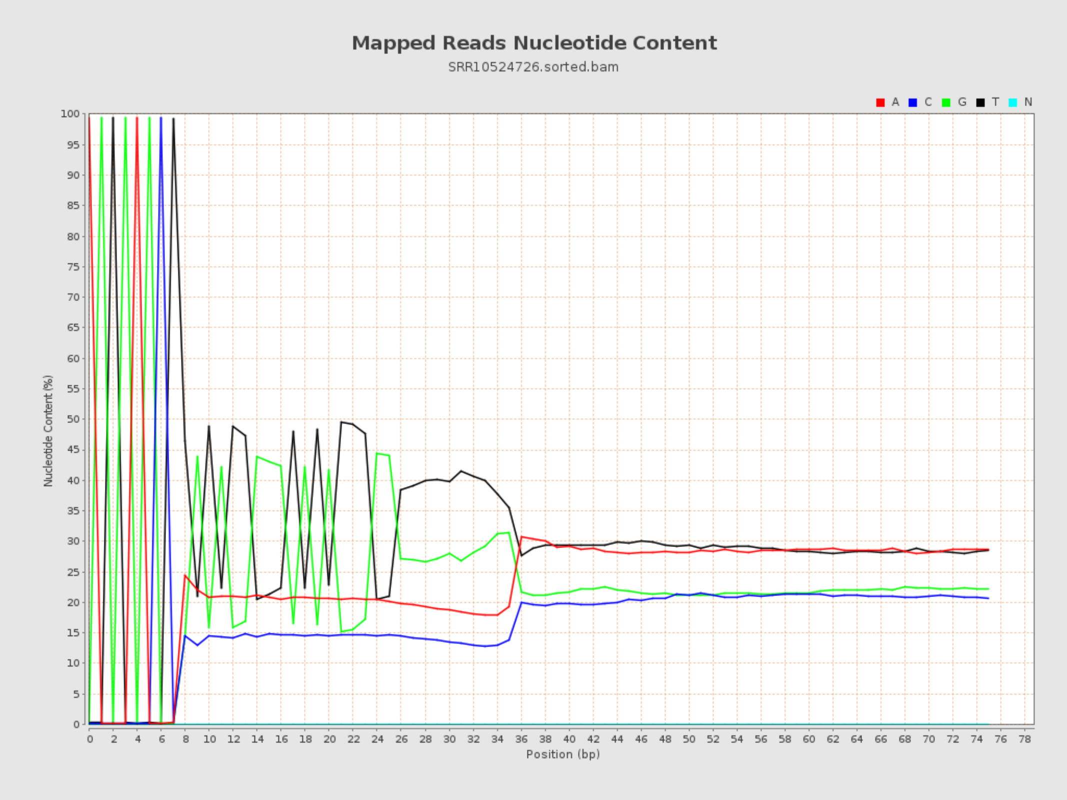
6. Results : Genome Fraction Coverage



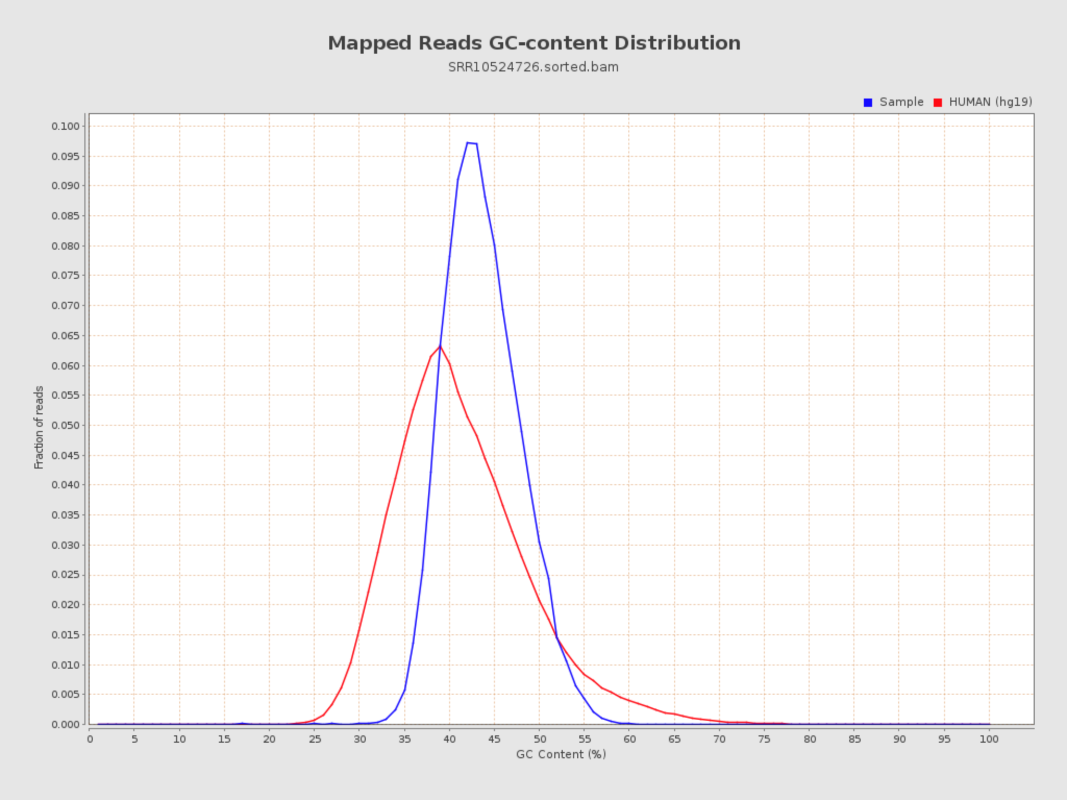
7. Results : Duplication Rate Histogram



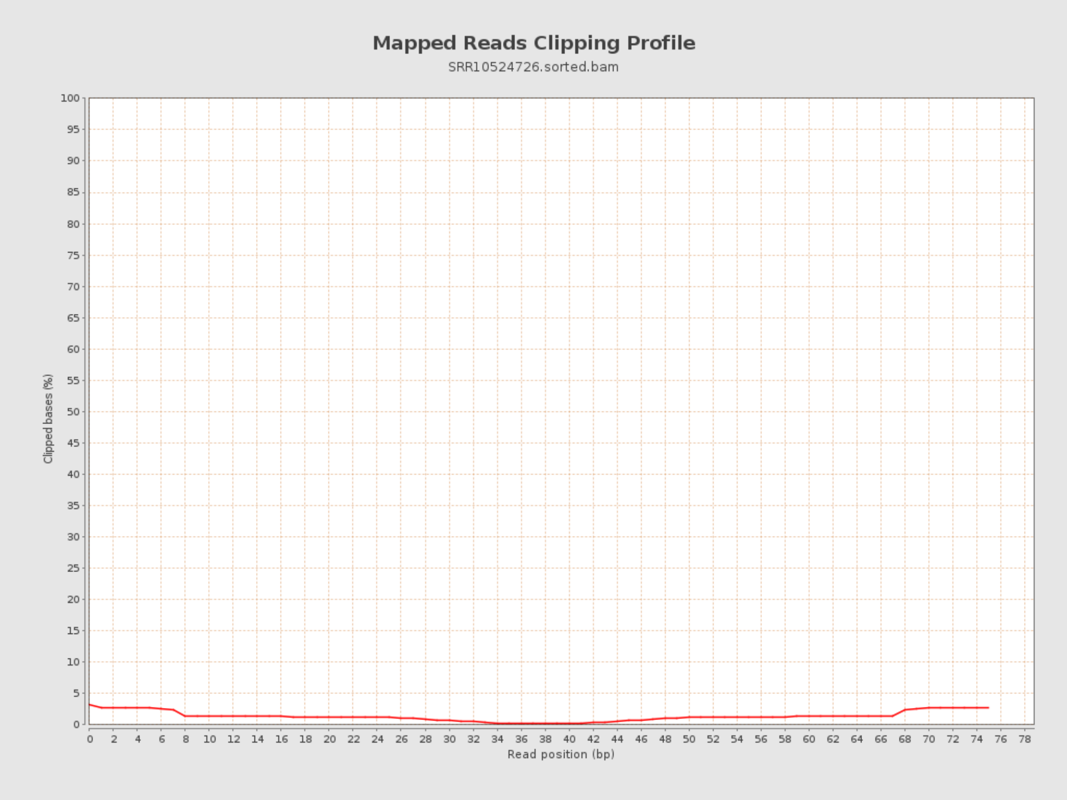
8. Results : Mapped Reads Nucleotide Content



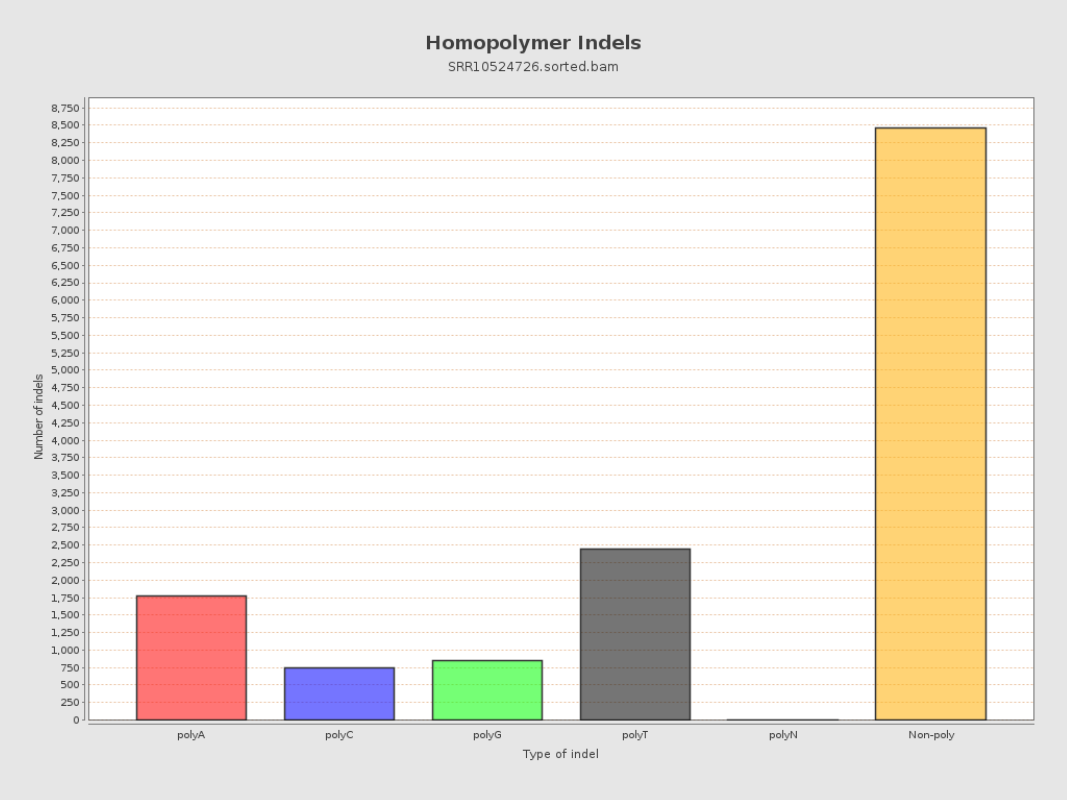
9. Results : Mapped Reads GC-content Distribution



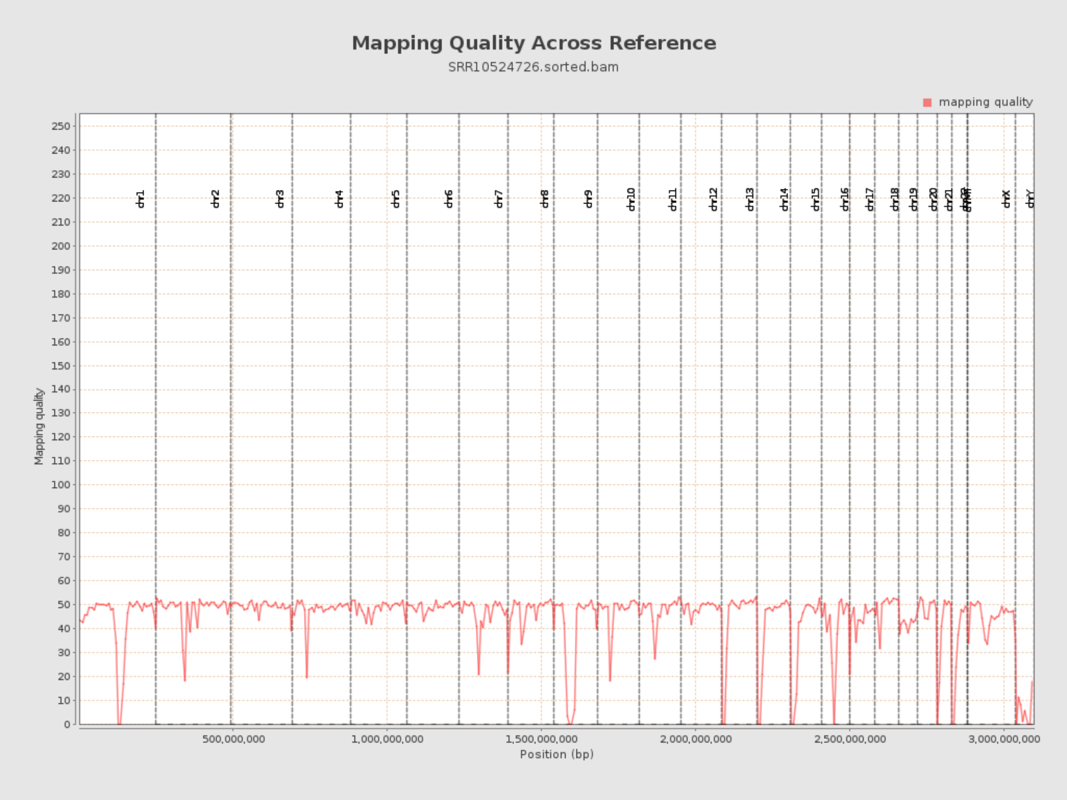
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram