Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:36:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524760.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_SRR10524760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:36:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,344,973
Mapped reads	1,239,625 / 92.17%
Unmapped reads	105,348 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,160 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	37,728 / 2.81%
Duplication rate	2.33%
Clipped reads	1,240,863 / 92.26%

2.2. ACGT Content

Number/percentage of A's	17,299,820 / 24.12%
Number/percentage of C's	14,733,969 / 20.54%
Number/percentage of T's	21,722,143 / 30.29%
Number/percentage of G's	17,956,352 / 25.04%
Number/percentage of N's	8,703 / 0.01%
GC Percentage	45.58%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2051

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

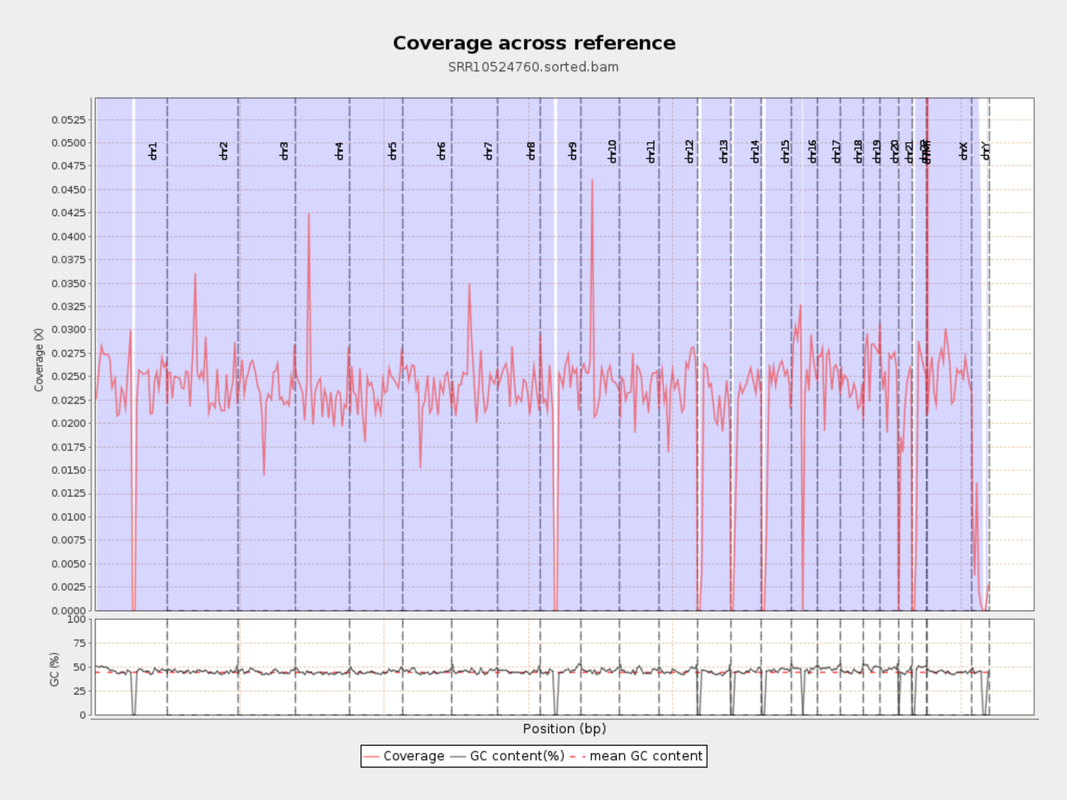
General error rate	0.51%
Mismatches	355,151
Insertions	5,206
Mapped reads with at least one insertion	0.42%
Deletions	13,802
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.52%

2.6. Chromosome stats

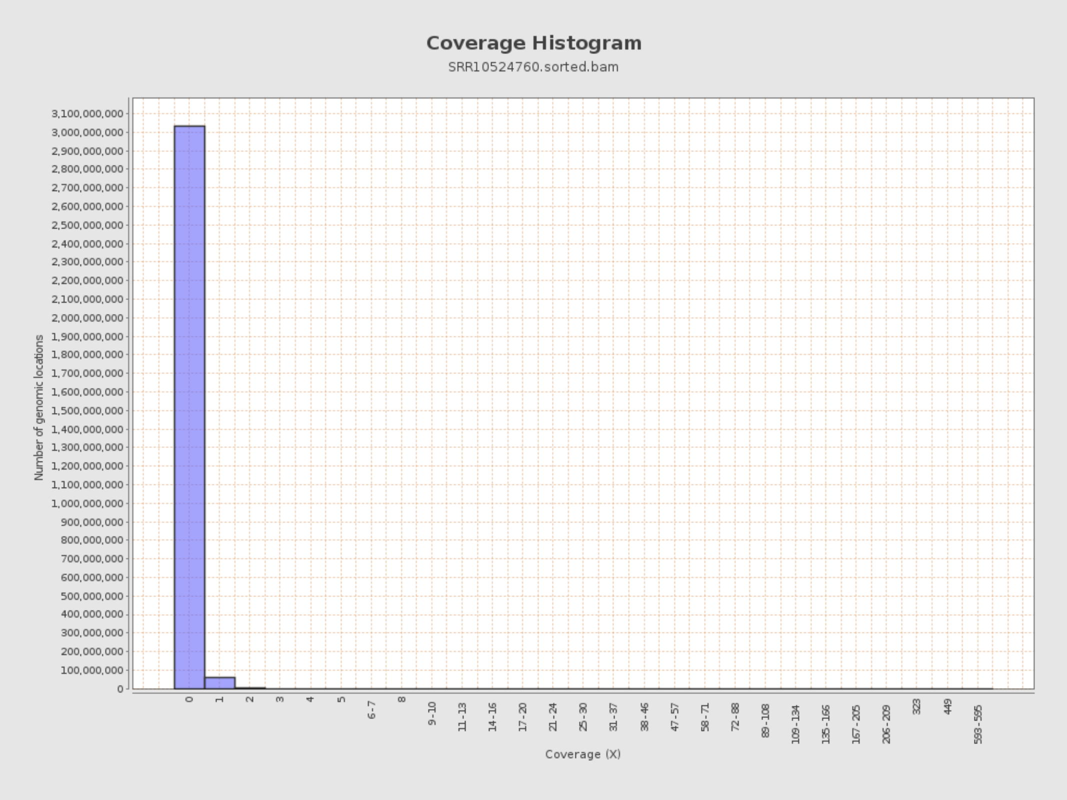
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5812193	0.0233	0.2423
chr2	243199373	5985427	0.0246	0.31
chr3	198022430	4695663	0.0237	0.1681
chr4	191154276	4535792	0.0237	0.1875
chr5	180915260	4272434	0.0236	0.1659
chr6	171115067	4040273	0.0236	0.1765
chr7	159138663	3926489	0.0247	0.2475

chr8	146364022	3515625	0.024	0.1883
chr9	141213431	3075667	0.0218	0.1867
chr10	135534747	3493935	0.0258	0.2443
chr11	135006516	3241536	0.024	0.1922
chr12	133851895	3246793	0.0243	0.1708
chr13	115169878	2187916	0.019	0.1496
chr14	107349540	2157333	0.0201	0.1567
chr15	102531392	2089841	0.0204	0.1568
chr16	90354753	2244486	0.0248	0.1864
chr17	81195210	2083358	0.0257	0.1817
chr18	78077248	1847432	0.0237	0.271
chr19	59128983	1612106	0.0273	0.2273
chr20	63025520	1576932	0.025	0.1785
chr21	48129895	956401	0.0199	0.1679
chr22	51304566	938727	0.0183	0.1478
chrMT	16571	24099	1.4543	1.5252
chrX	155270560	3951206	0.0254	0.1827
chrY	59373566	231550	0.0039	0.1083

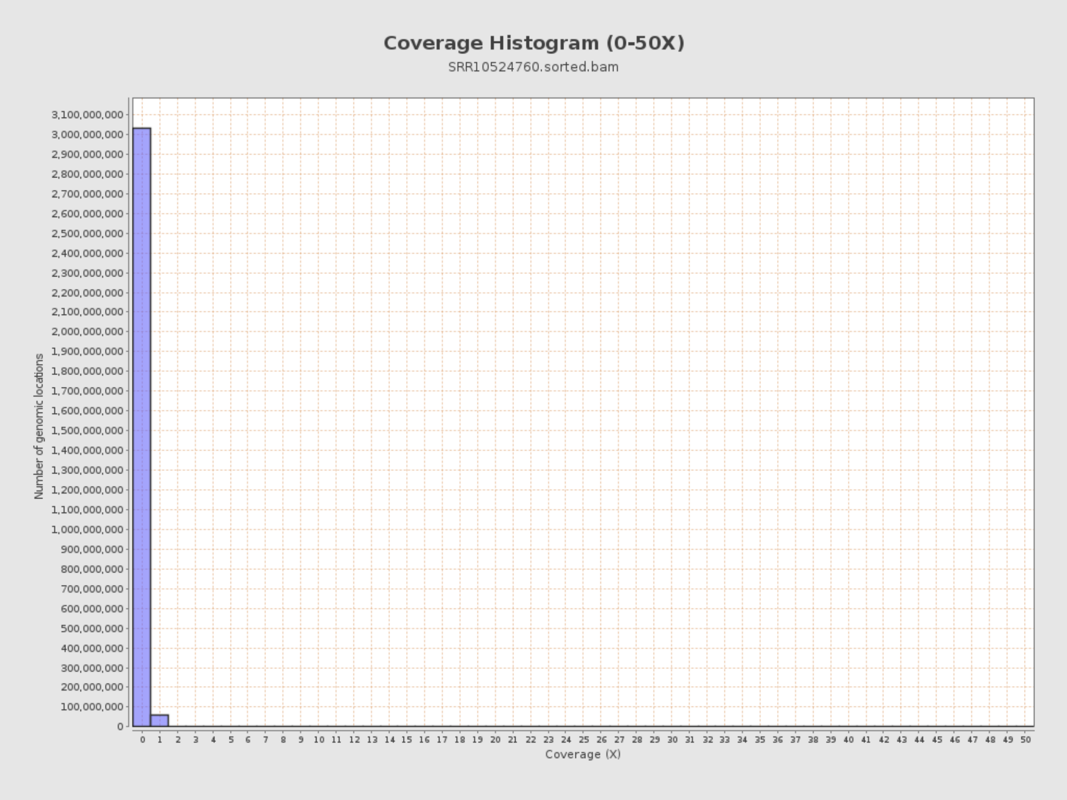
3. Results : Coverage across reference



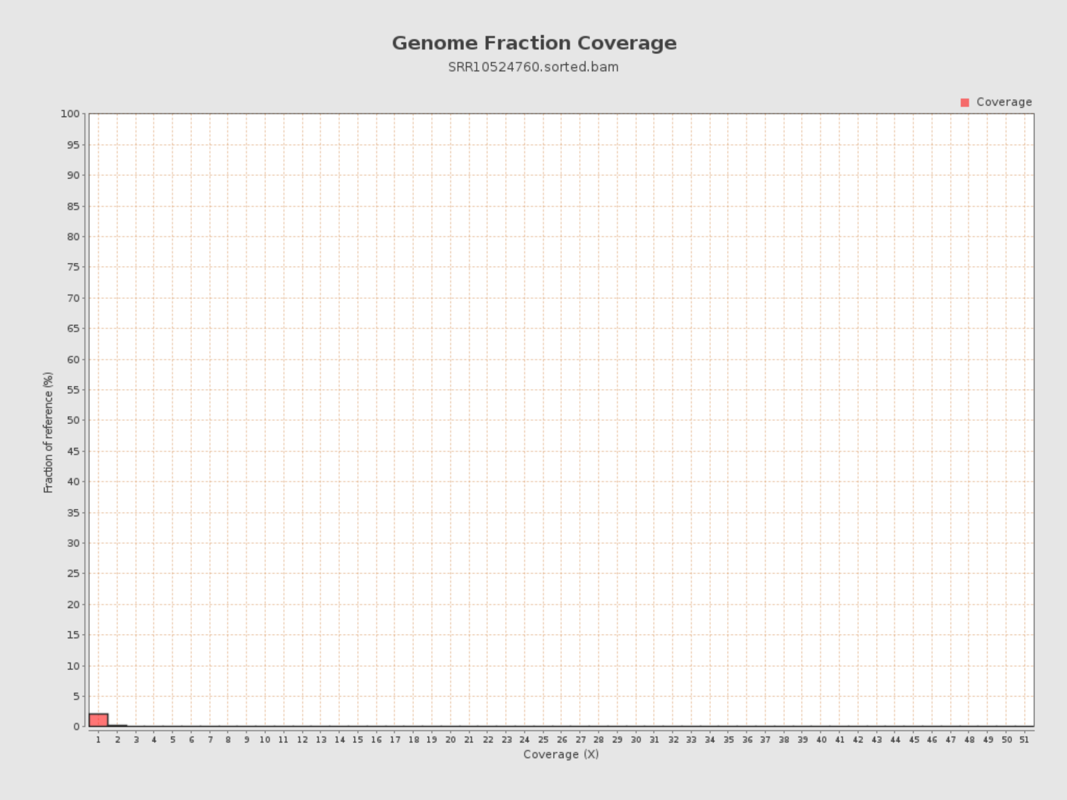
4. Results : Coverage Histogram



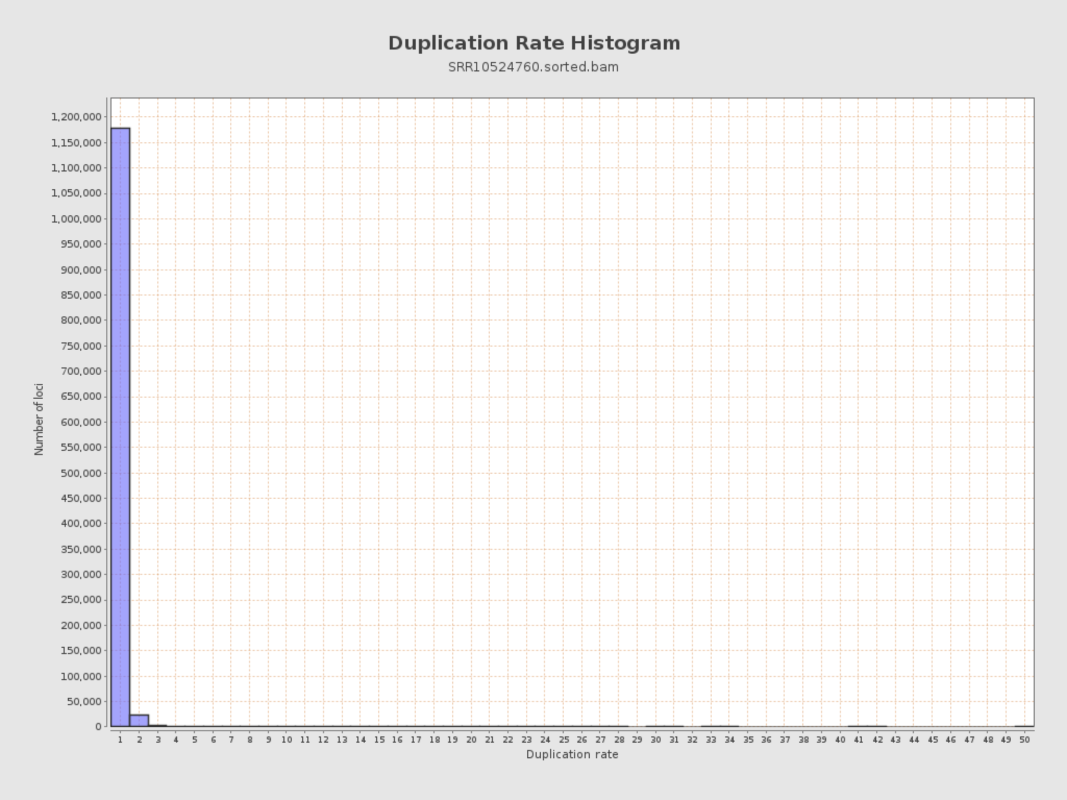
5. Results : Coverage Histogram (0-50X)



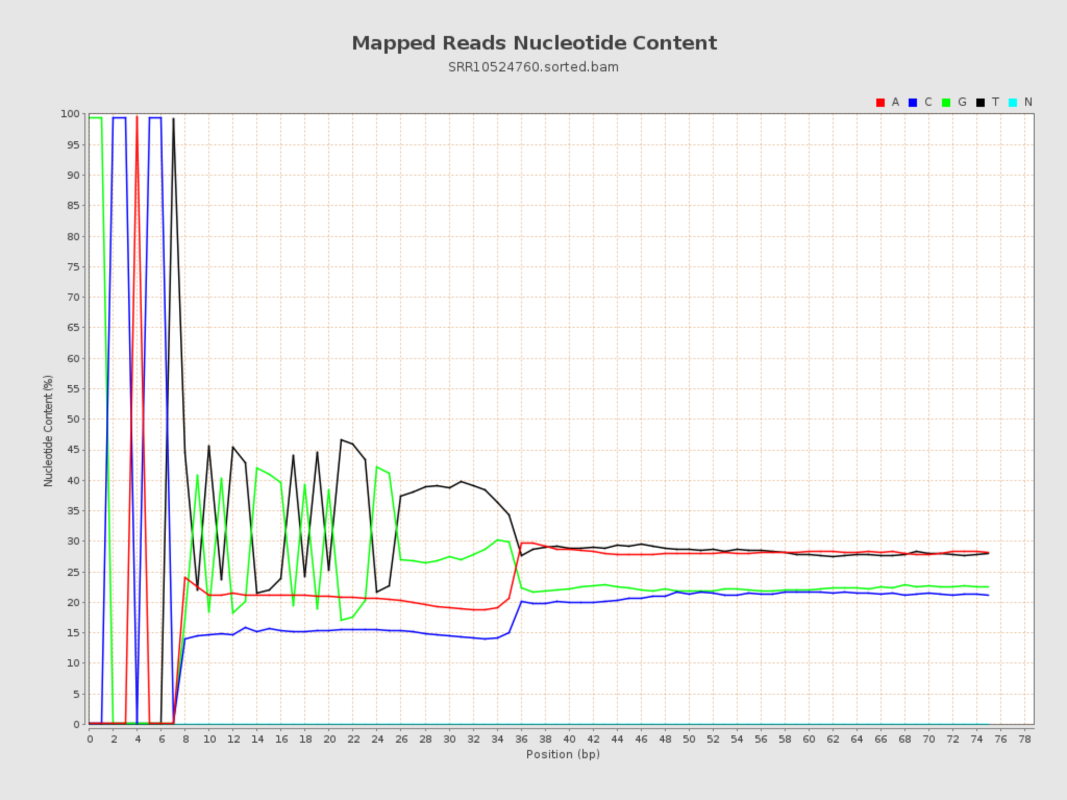
6. Results : Genome Fraction Coverage



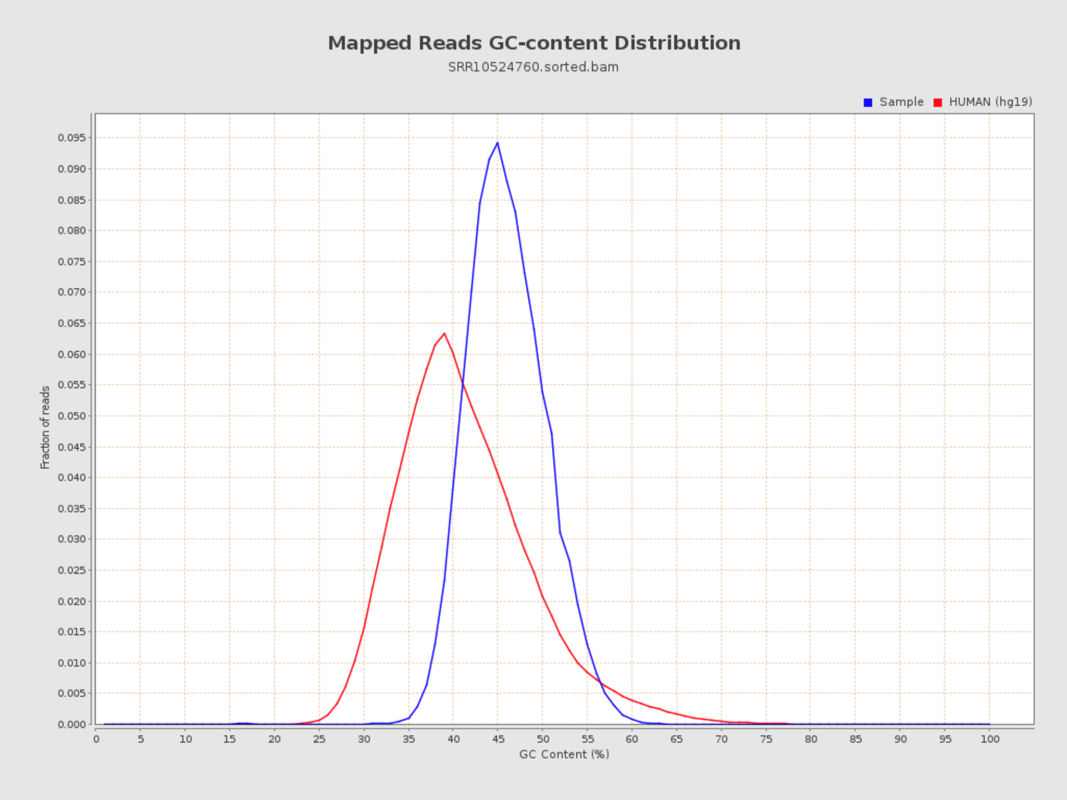
7. Results : Duplication Rate Histogram



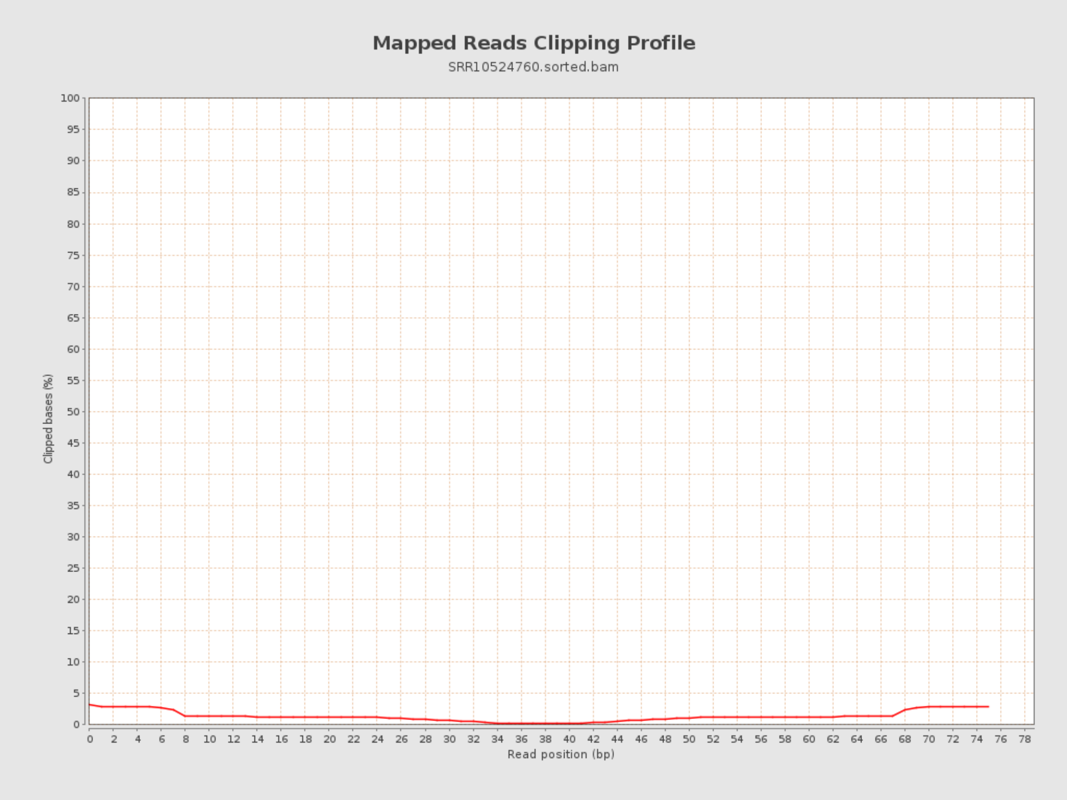
8. Results : Mapped Reads Nucleotide Content



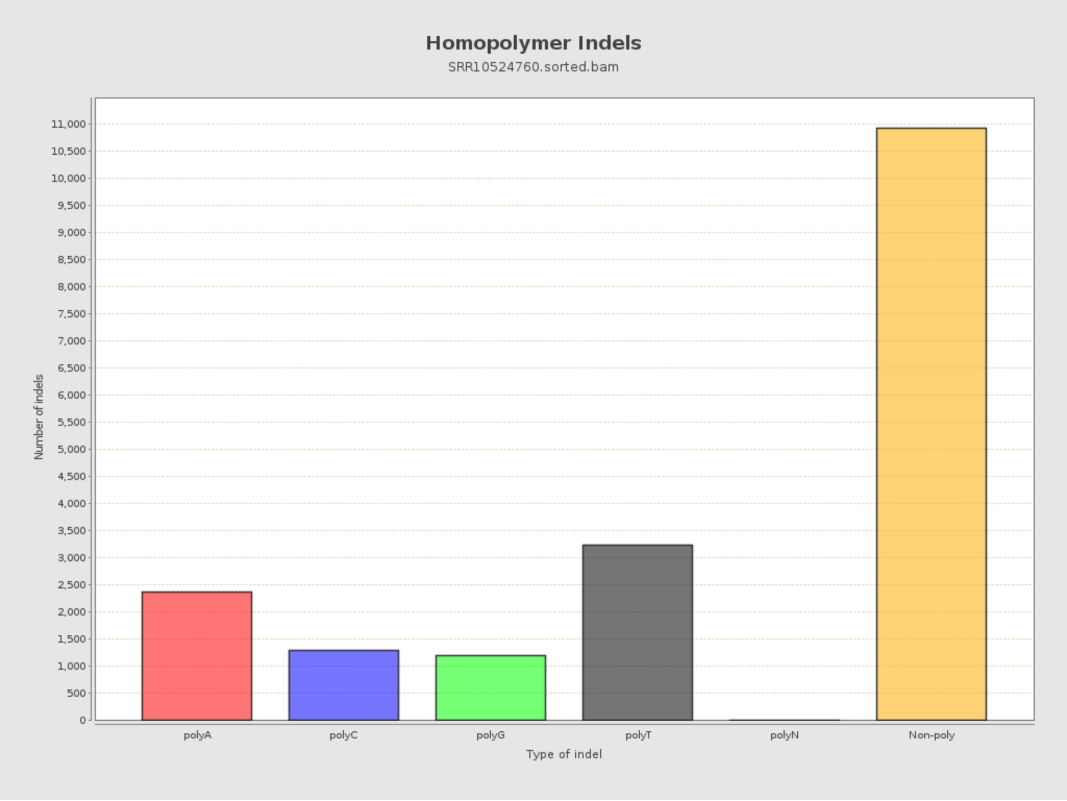
9. Results : Mapped Reads GC-content Distribution



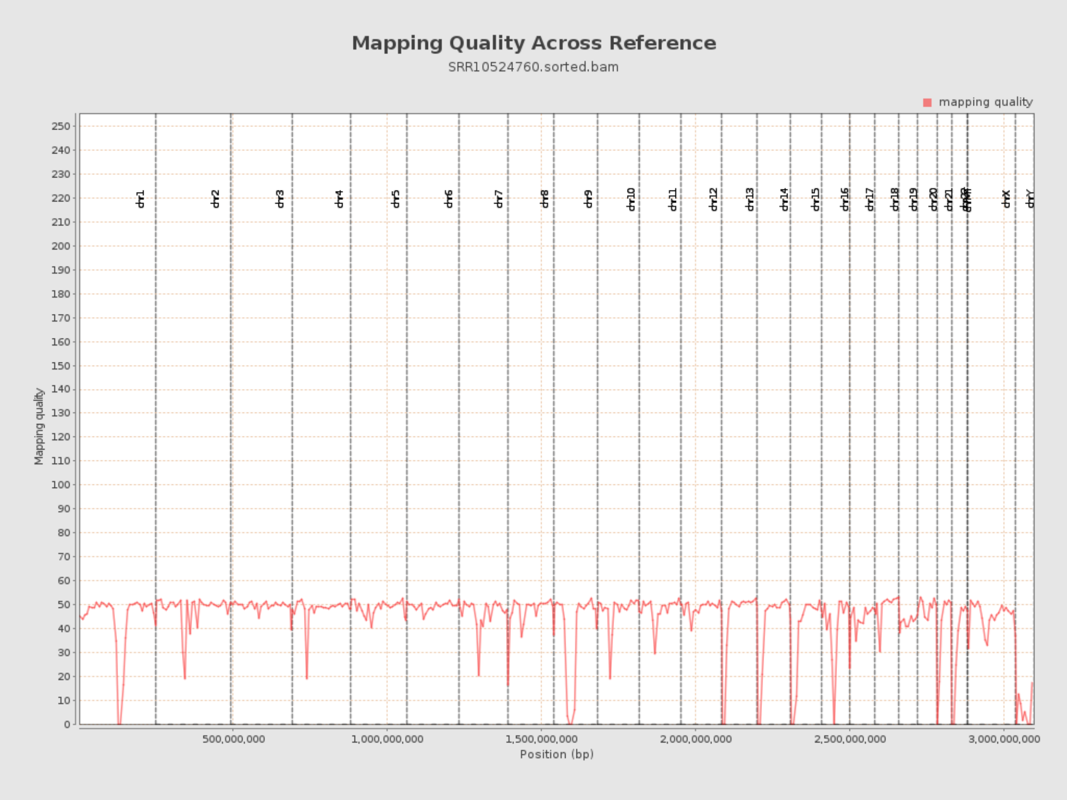
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram