Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:15:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524752.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_SRR10524752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:15:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,352,829
Mapped reads	1,237,260 / 91.46%
Unmapped reads	115,569 / 8.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,055 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	38,353 / 2.84%
Duplication rate	2.34%
Clipped reads	1,236,866 / 91.43%

2.2. ACGT Content

Number/percentage of A's	17,845,646 / 25.04%
Number/percentage of C's	13,906,400 / 19.51%
Number/percentage of T's	22,261,413 / 31.23%
Number/percentage of G's	17,249,913 / 24.2%
Number/percentage of N's	8,676 / 0.01%
GC Percentage	43.71%

2.3. Coverage

Mean	0.023

Standard Deviation	0.2098

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

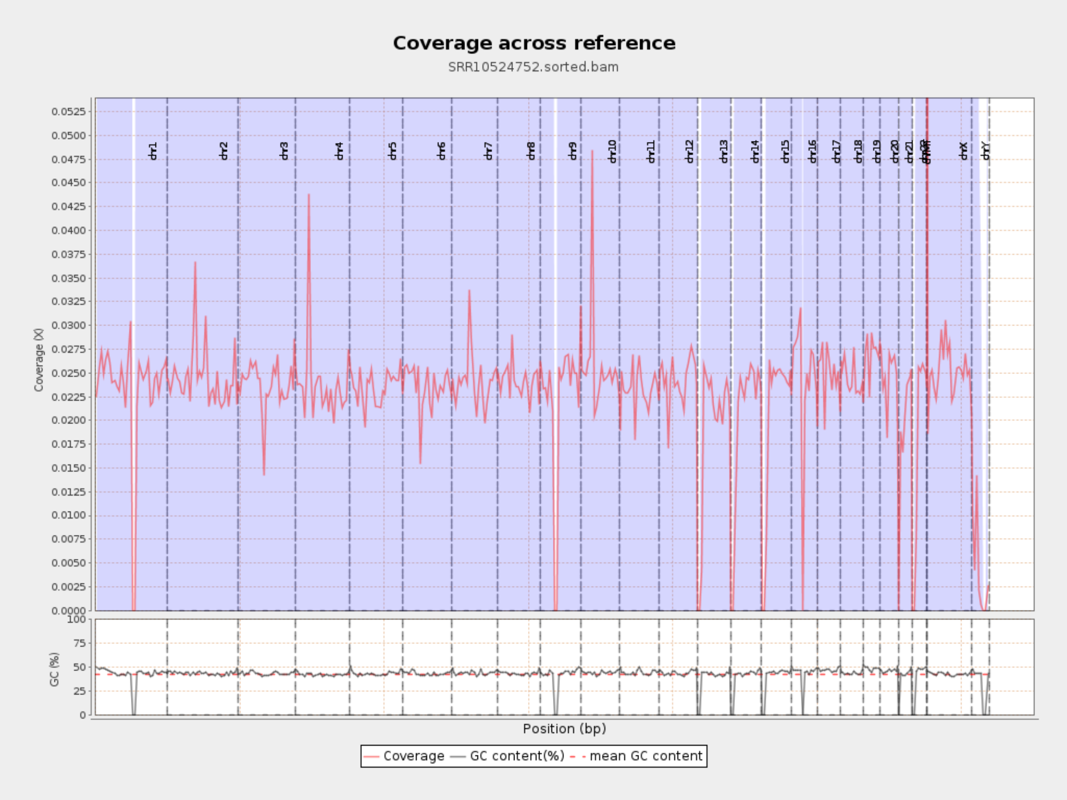
General error rate	0.52%
Mismatches	357,695
Insertions	5,713
Mapped reads with at least one insertion	0.46%
Deletions	14,005
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.96%

2.6. Chromosome stats

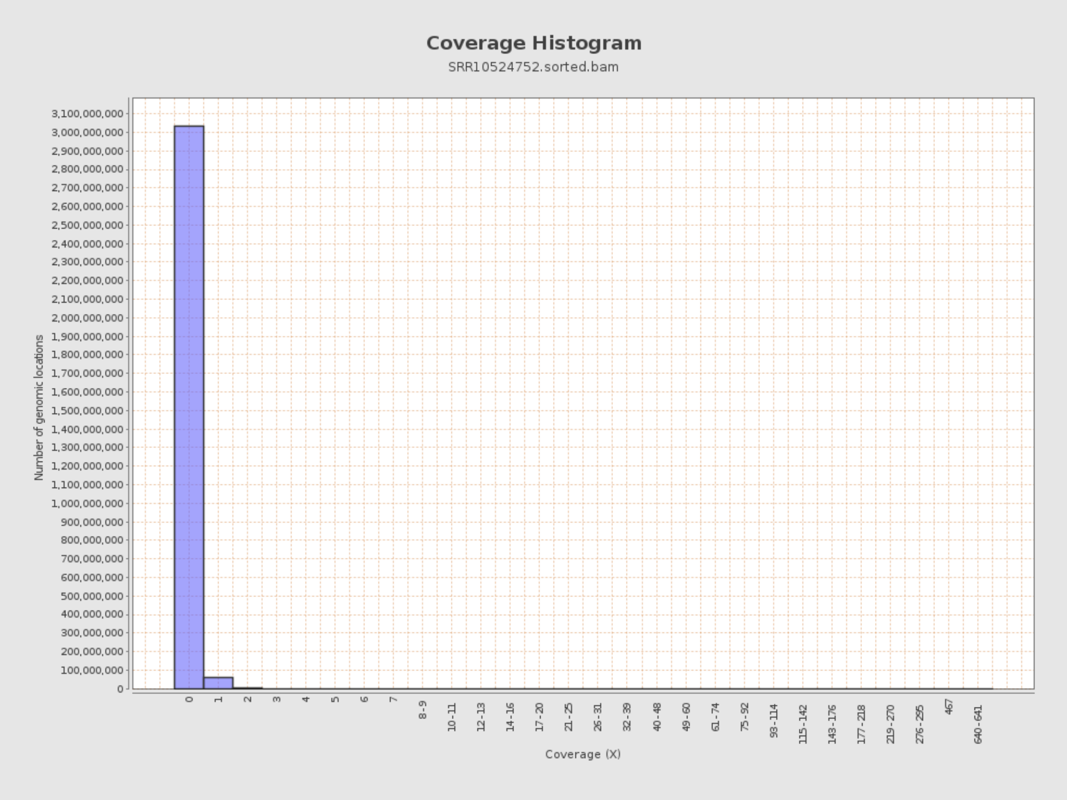
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5794478	0.0232	0.2644
chr2	243199373	5960991	0.0245	0.3241
chr3	198022430	4693187	0.0237	0.1681
chr4	191154276	4575127	0.0239	0.1892
chr5	180915260	4268558	0.0236	0.167
chr6	171115067	4023650	0.0235	0.178
chr7	159138663	3853859	0.0242	0.2386

chr8	146364022	3529900	0.0241	0.1911
chr9	141213431	3079192	0.0218	0.1874
chr10	135534747	3495245	0.0258	0.2541
chr11	135006516	3161752	0.0234	0.1925
chr12	133851895	3253632	0.0243	0.1705
chr13	115169878	2176443	0.0189	0.1491
chr14	107349540	2135919	0.0199	0.1564
chr15	102531392	2051039	0.02	0.1551
chr16	90354753	2163736	0.0239	0.1817
chr17	81195210	2034069	0.0251	0.1773
chr18	78077248	1907811	0.0244	0.2874
chr19	59128983	1592518	0.0269	0.2319
chr20	63025520	1539843	0.0244	0.1764
chr21	48129895	933503	0.0194	0.1646
chr22	51304566	898712	0.0175	0.1444
chrMT	16571	25510	1.5394	1.4873
chrX	155270560	3907887	0.0252	0.1839
chrY	59373566	237891	0.004	0.1219

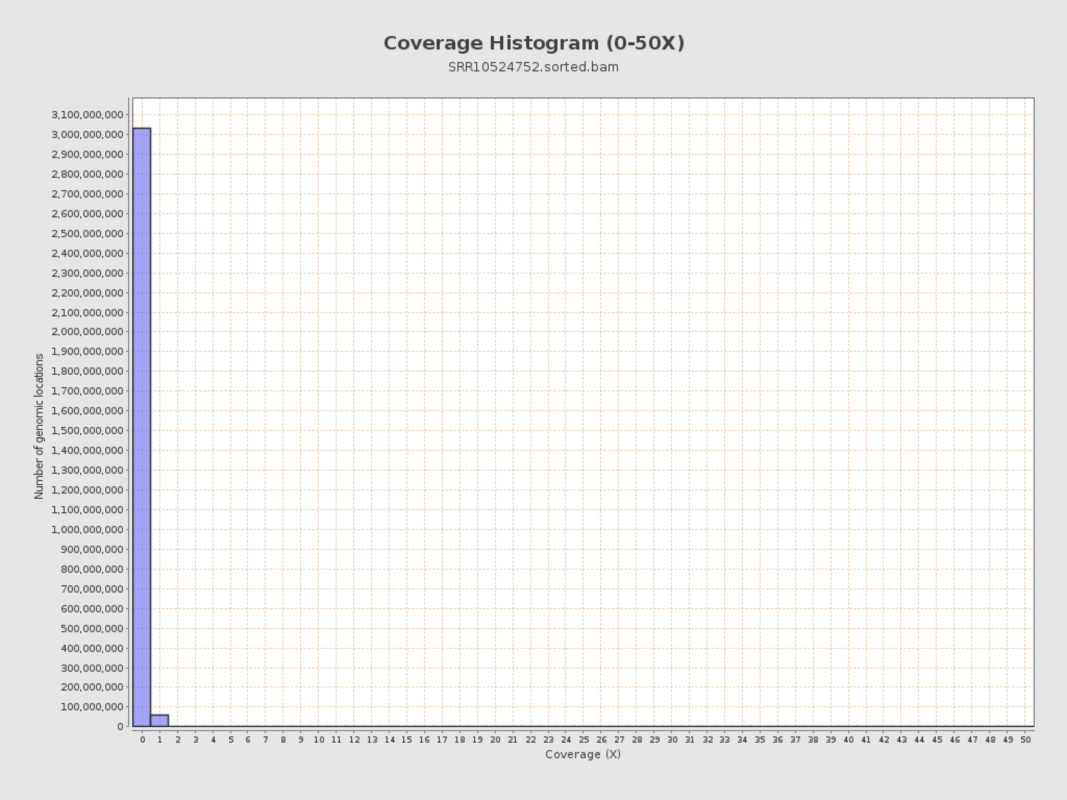
3. Results : Coverage across reference



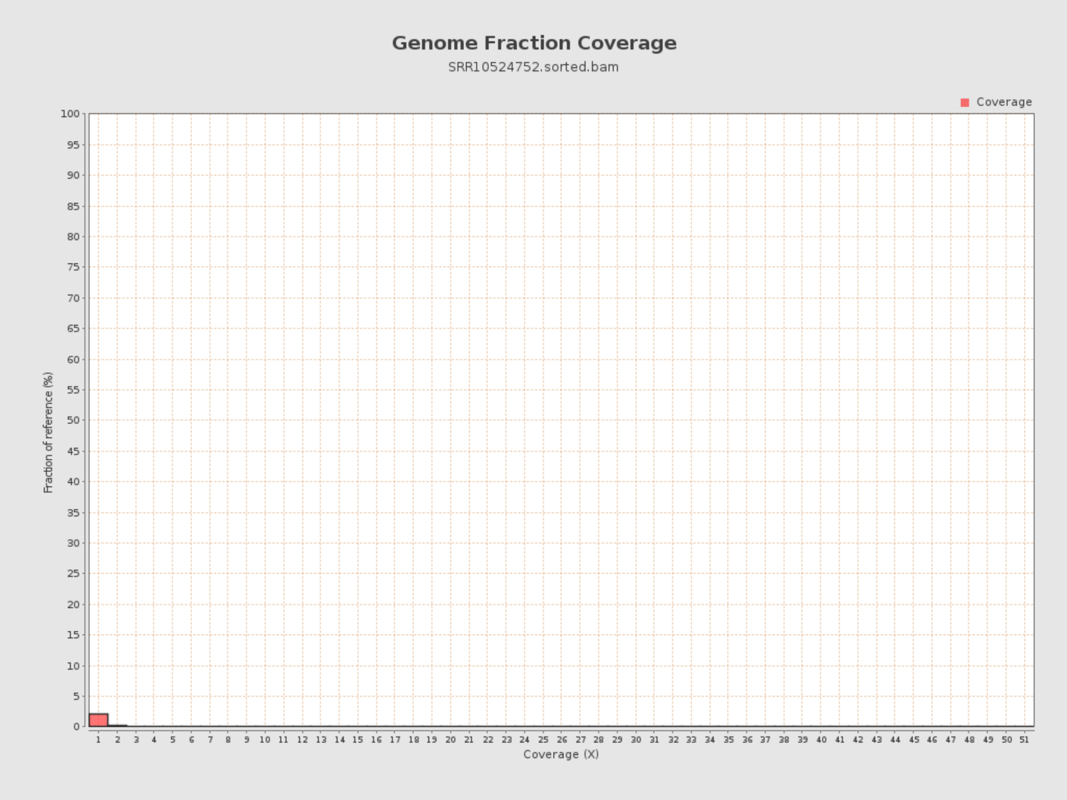
4. Results : Coverage Histogram



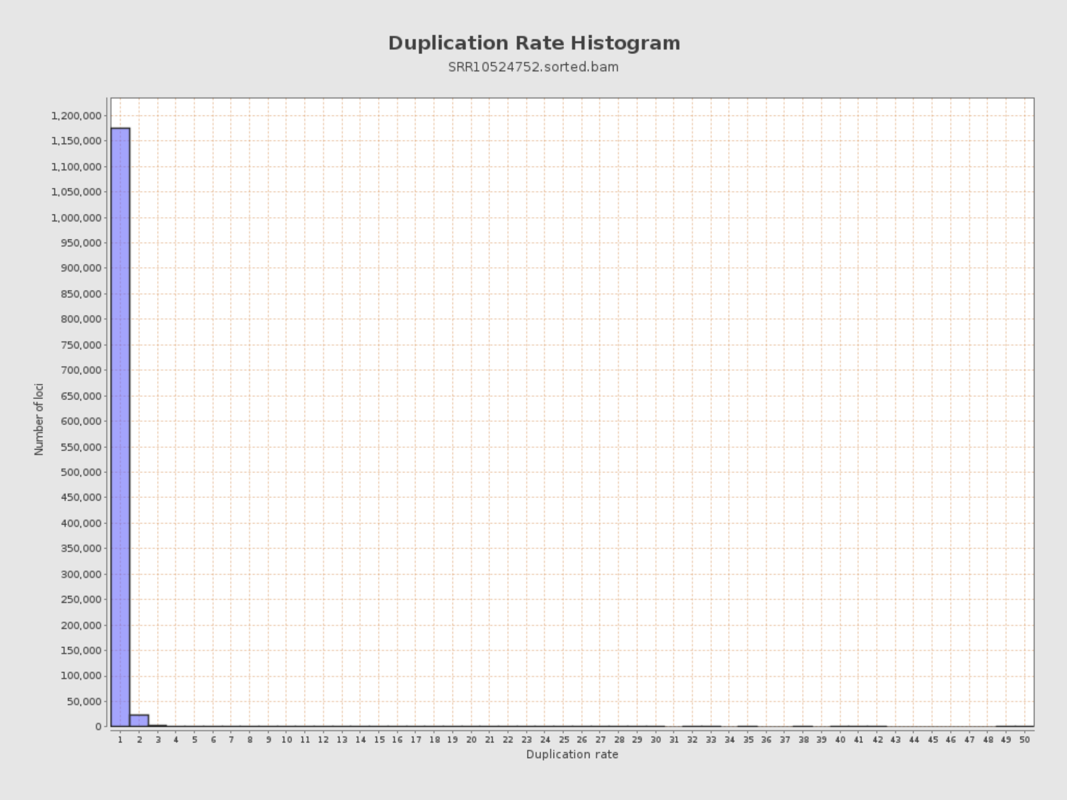
5. Results : Coverage Histogram (0-50X)



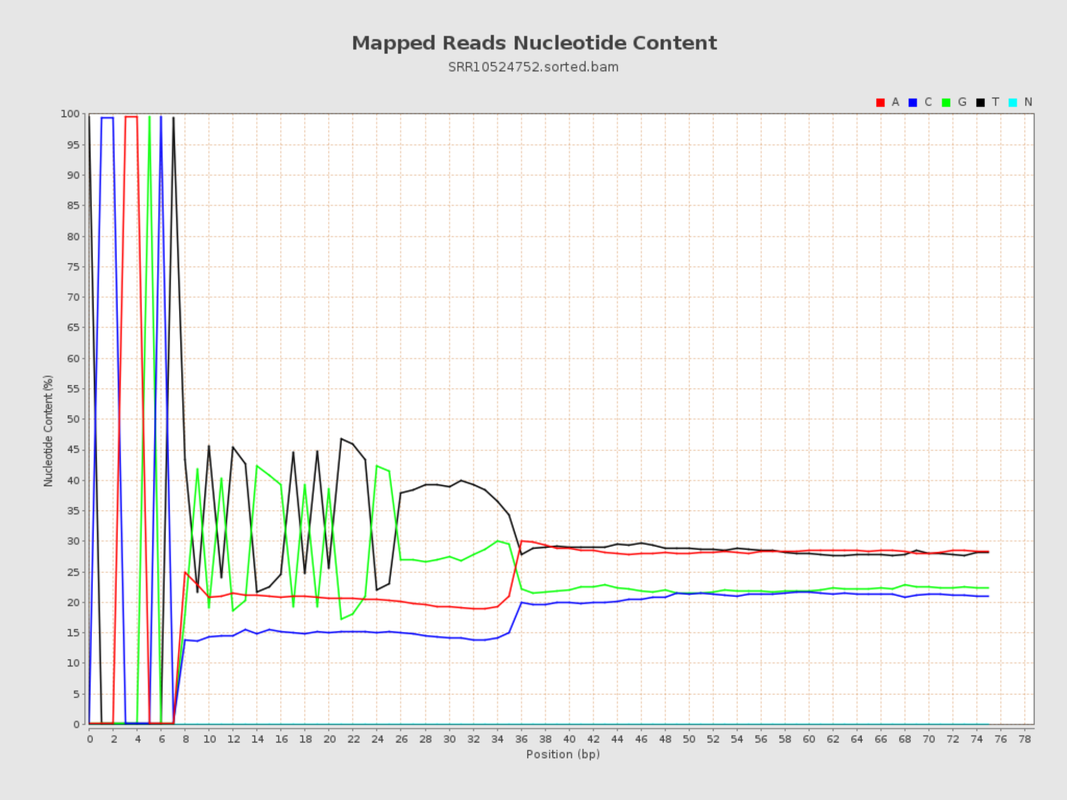
6. Results : Genome Fraction Coverage



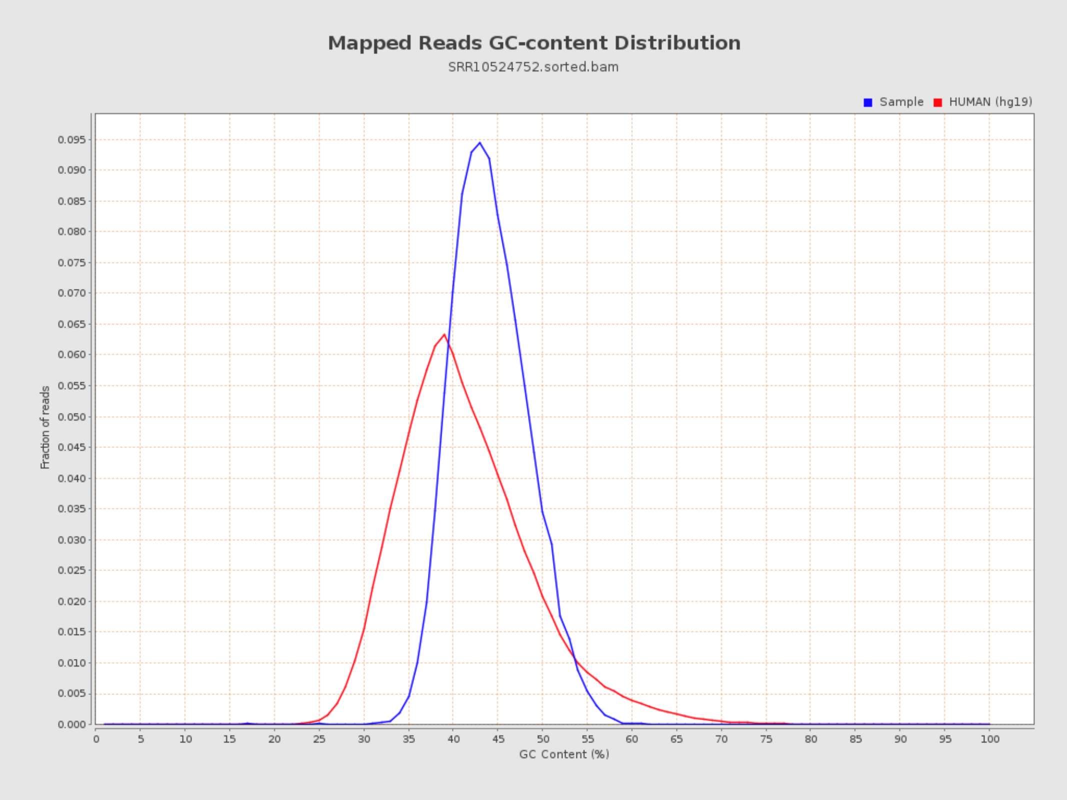
7. Results : Duplication Rate Histogram



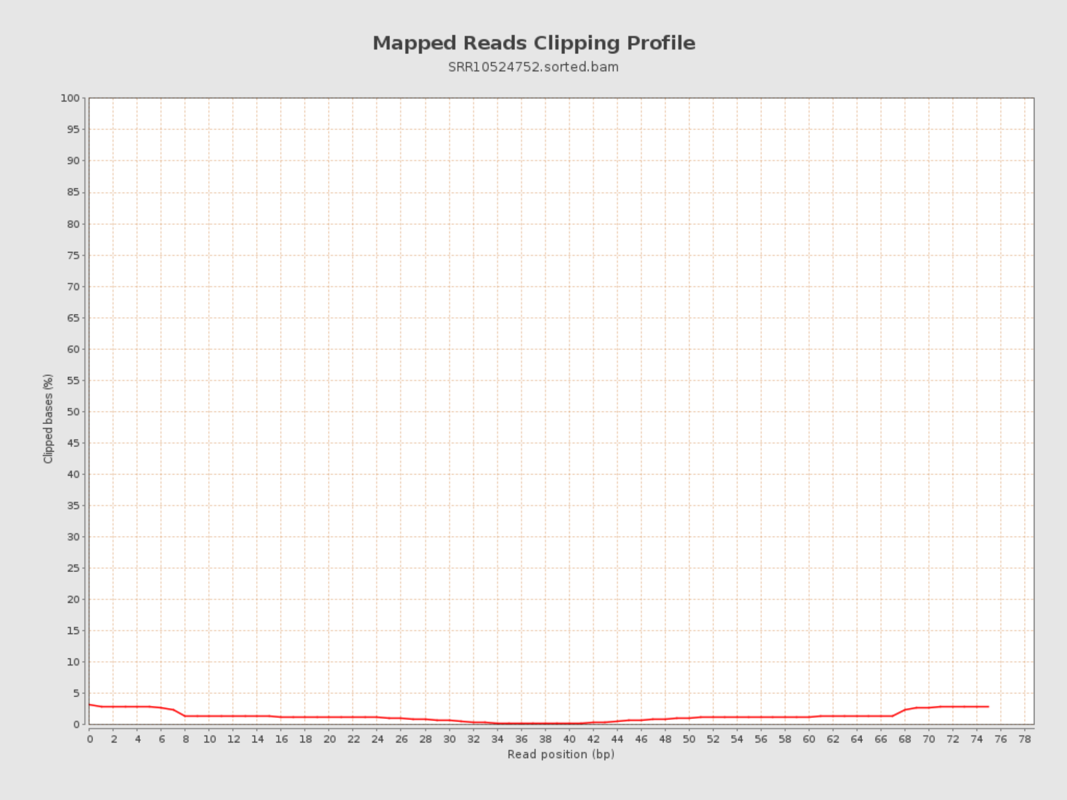
8. Results : Mapped Reads Nucleotide Content



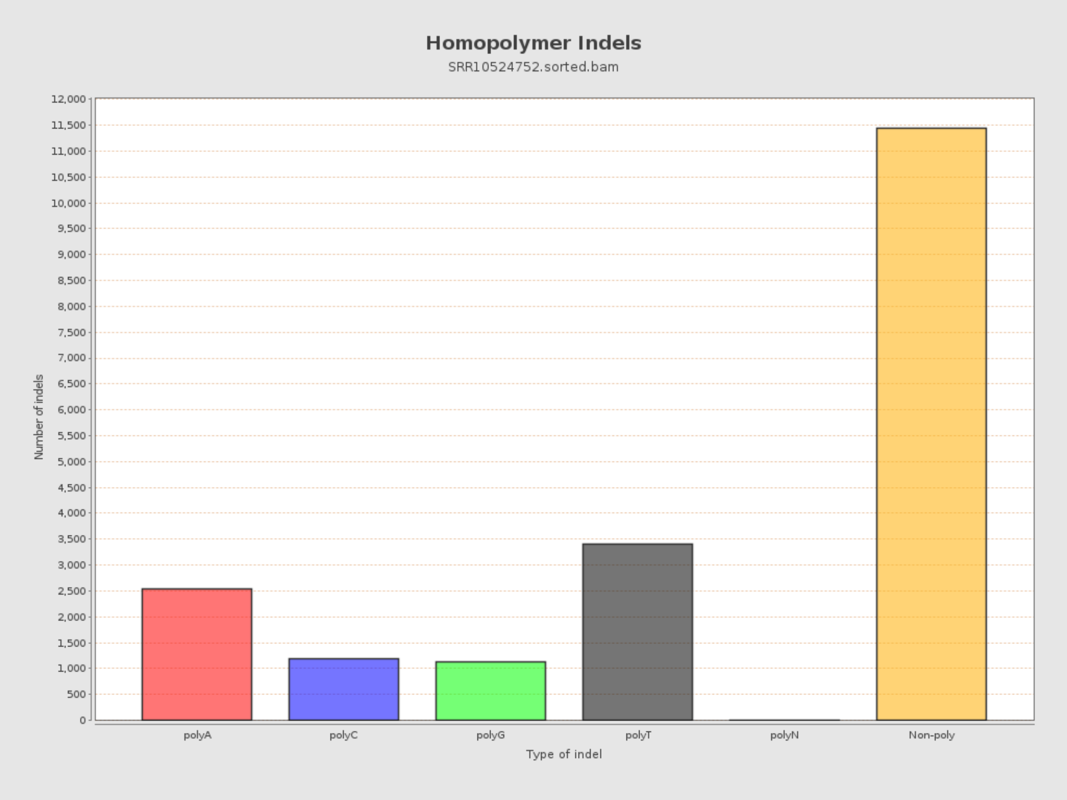
9. Results : Mapped Reads GC-content Distribution



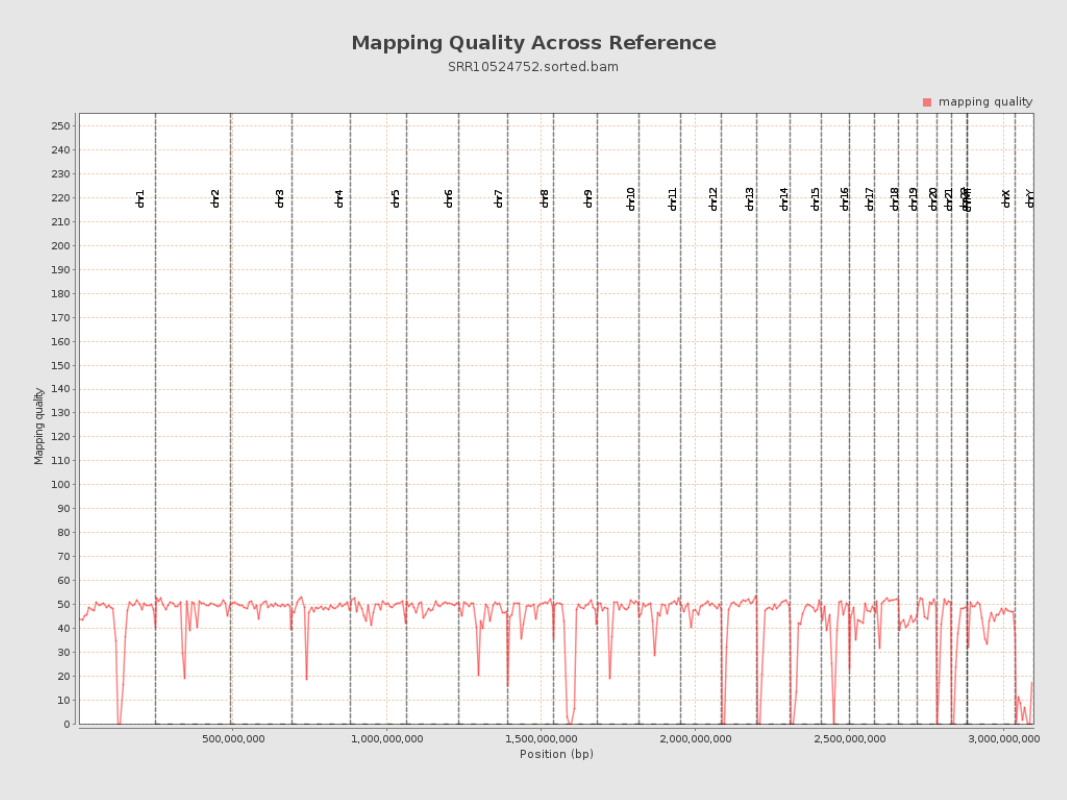
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram