Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:01:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524771.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_SRR10524771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524771.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:01:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524771.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,449,959
Mapped reads	1,330,423 / 91.76%
Unmapped reads	119,536 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,935 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	40,231 / 2.77%
Duplication rate	2.25%
Clipped reads	1,331,973 / 91.86%

2.2. ACGT Content

Number/percentage of A's	18,805,868 / 24.4%
Number/percentage of C's	14,491,122 / 18.8%
Number/percentage of T's	24,634,214 / 31.96%
Number/percentage of G's	19,140,941 / 24.83%
Number/percentage of N's	9,641 / 0.01%
GC Percentage	43.63%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2201

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

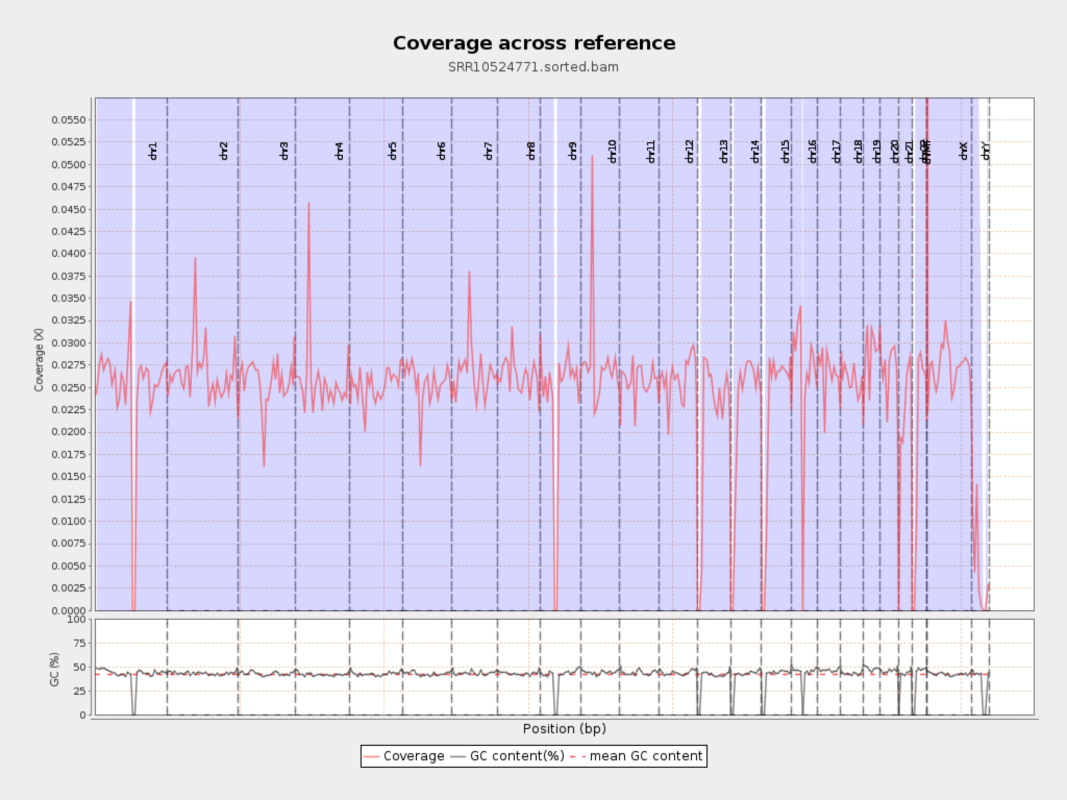
General error rate	0.52%
Mismatches	389,799
Insertions	5,244
Mapped reads with at least one insertion	0.39%
Deletions	15,845
Mapped reads with at least one deletion	1.18%
Homopolymer indels	40.85%

2.6. Chromosome stats

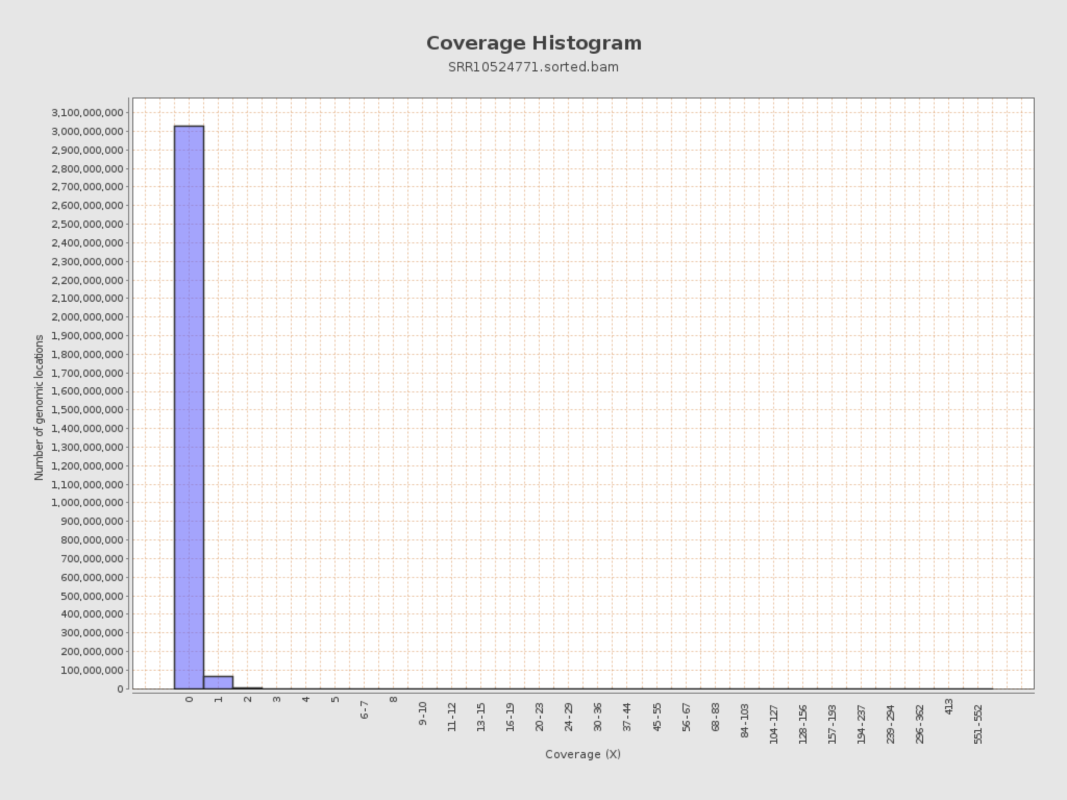
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6146553	0.0247	0.305
chr2	243199373	6485496	0.0267	0.3112
chr3	198022430	5053183	0.0255	0.1745
chr4	191154276	4923500	0.0258	0.1947
chr5	180915260	4581170	0.0253	0.1723
chr6	171115067	4352495	0.0254	0.1816
chr7	159138663	4259428	0.0268	0.2668

chr8	146364022	3857839	0.0264	0.2026
chr9	141213431	3286871	0.0233	0.2003
chr10	135534747	3767901	0.0278	0.2592
chr11	135006516	3488233	0.0258	0.2047
chr12	133851895	3483957	0.026	0.1753
chr13	115169878	2403086	0.0209	0.1557
chr14	107349540	2353348	0.0219	0.1639
chr15	102531392	2228099	0.0217	0.1606
chr16	90354753	2338432	0.0259	0.1901
chr17	81195210	2161817	0.0266	0.1847
chr18	78077248	2021083	0.0259	0.3073
chr19	59128983	1712980	0.029	0.258
chr20	63025520	1692706	0.0269	0.1865
chr21	48129895	1024061	0.0213	0.1757
chr22	51304566	967283	0.0189	0.1499
chrMT	16571	24837	1.4988	1.5037
chrX	155270560	4246664	0.0274	0.1915
chrY	59373566	246525	0.0042	0.1179

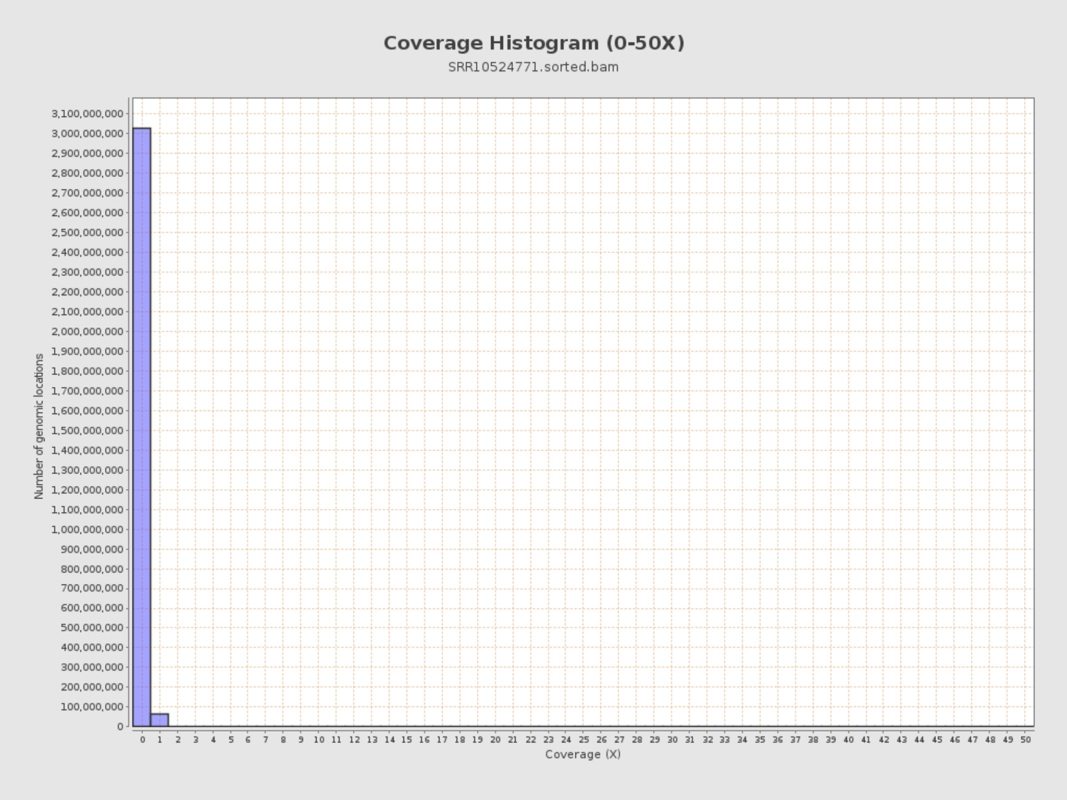
3. Results : Coverage across reference



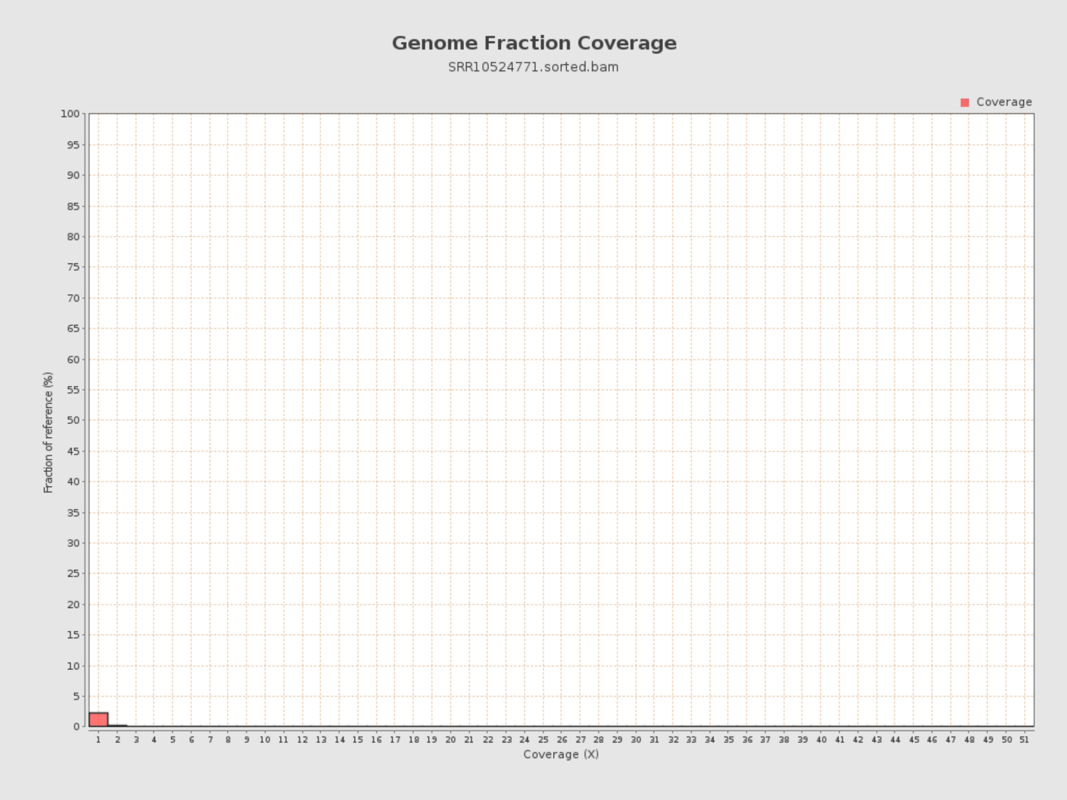
4. Results : Coverage Histogram



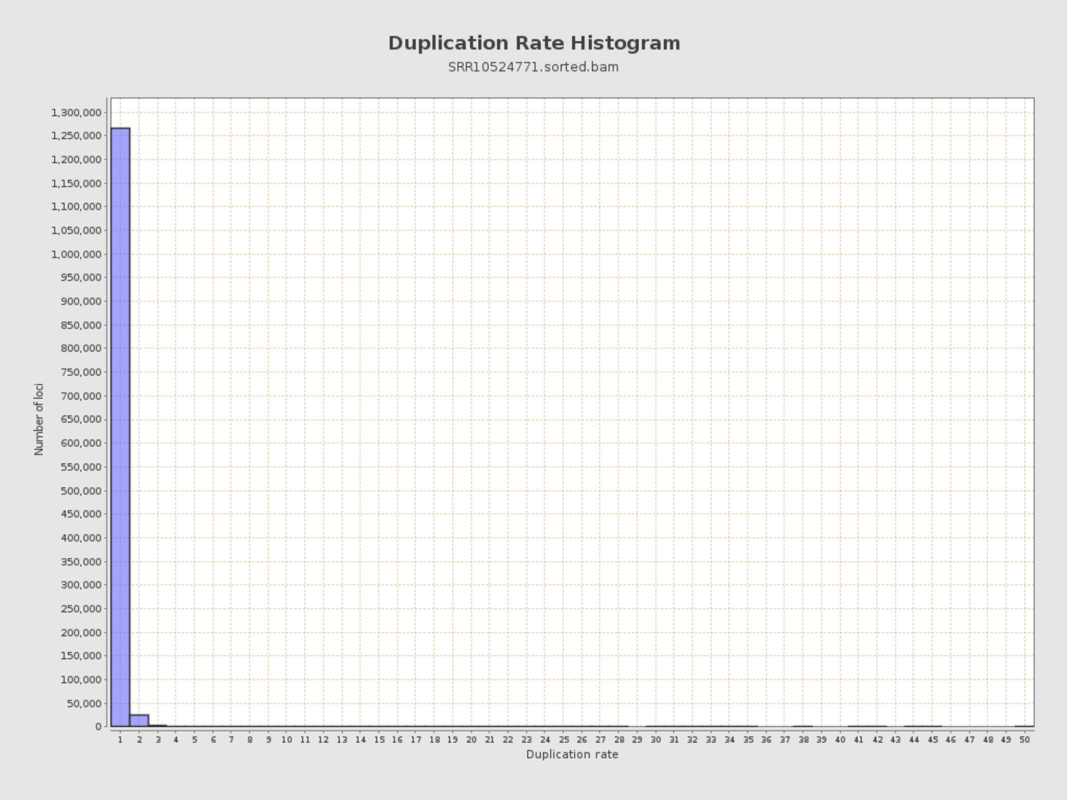
5. Results : Coverage Histogram (0-50X)



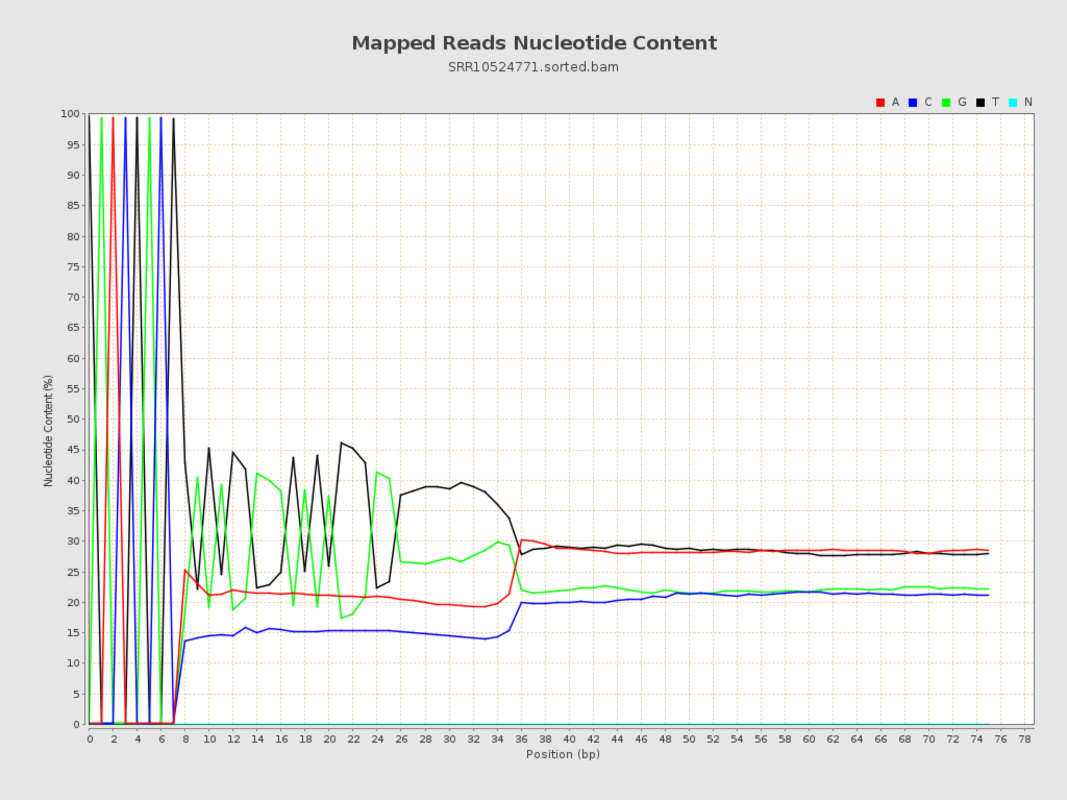
6. Results : Genome Fraction Coverage



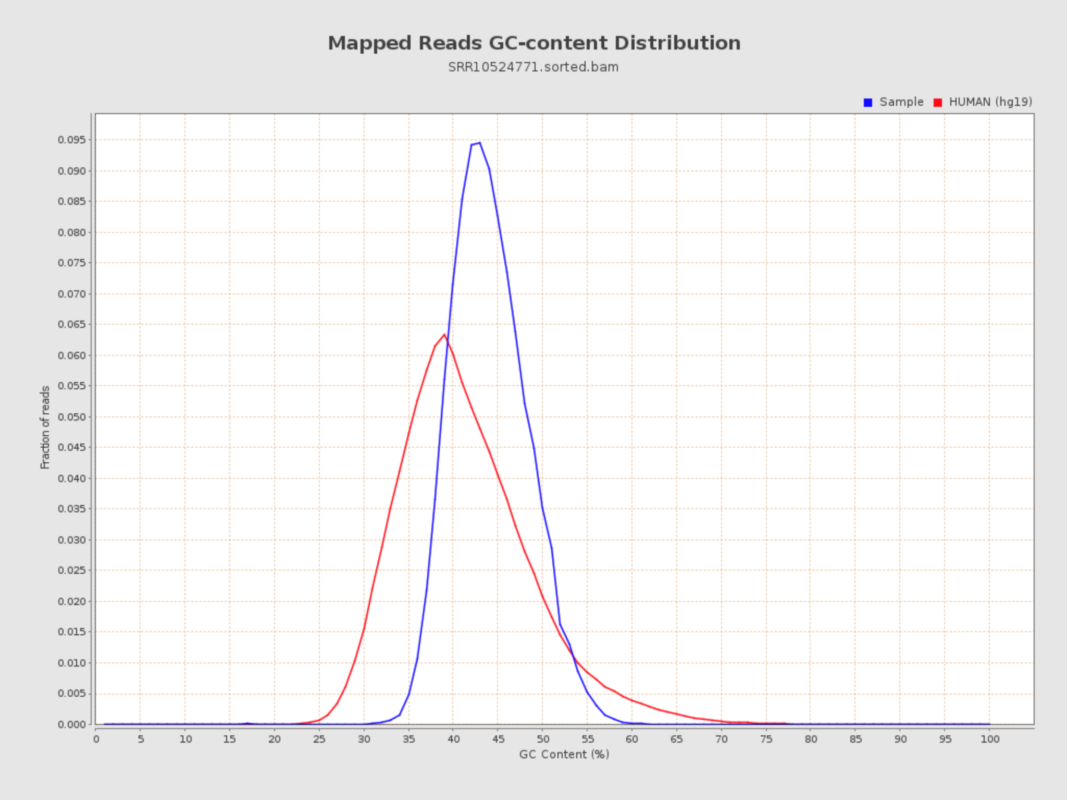
7. Results : Duplication Rate Histogram



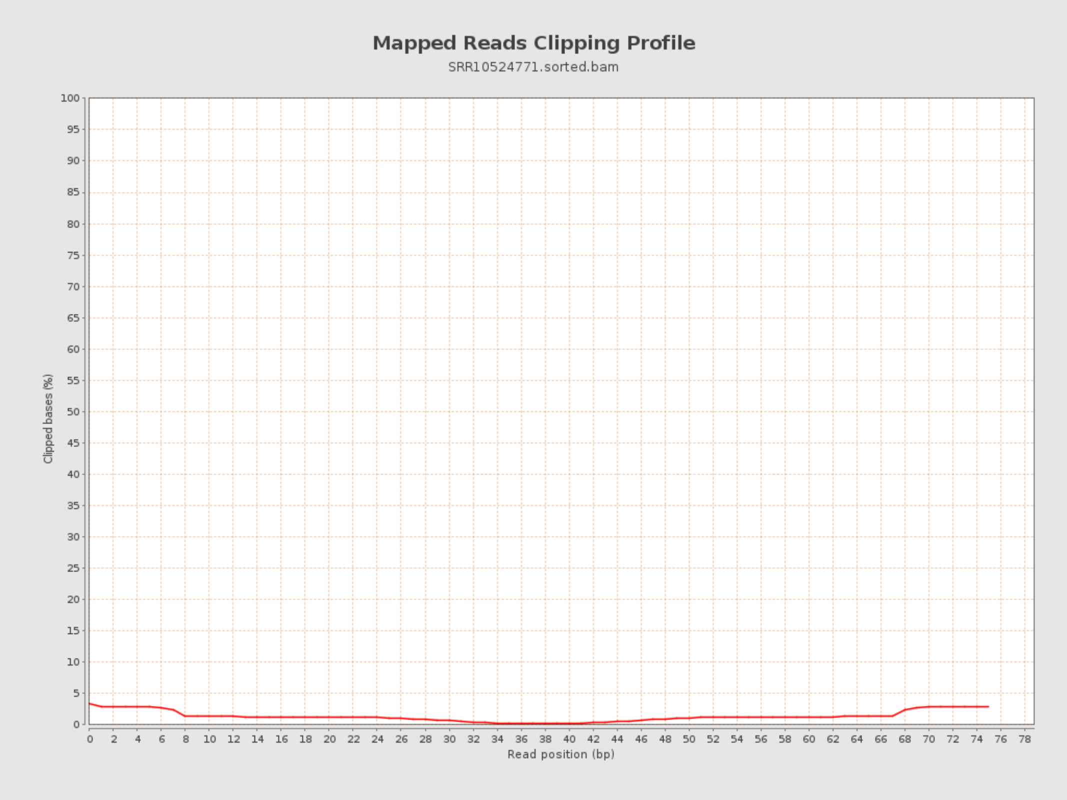
8. Results : Mapped Reads Nucleotide Content



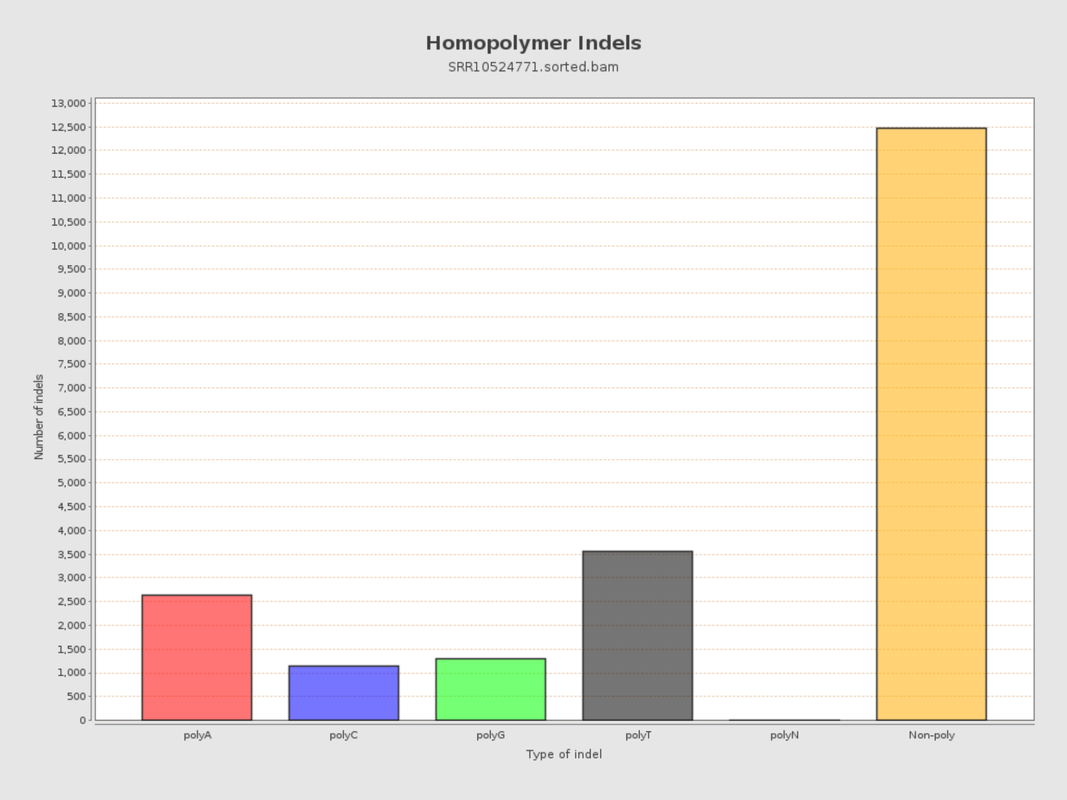
9. Results : Mapped Reads GC-content Distribution



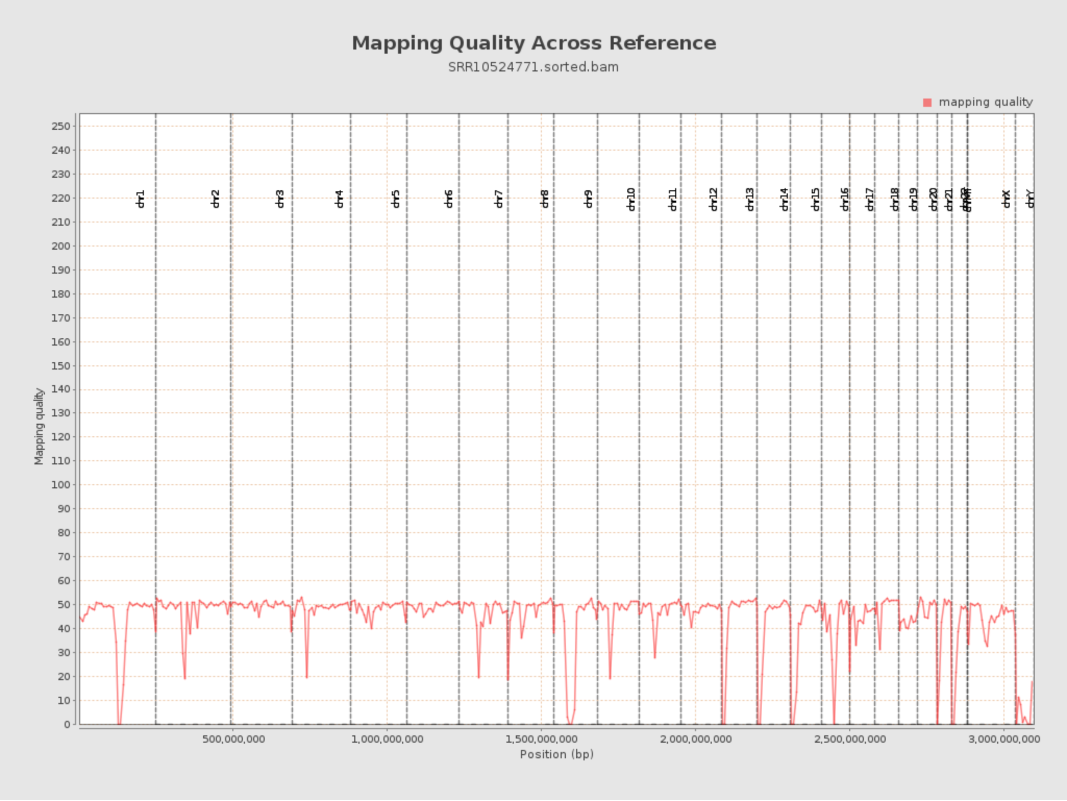
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram