Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:51:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524722.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_SRR10524722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524722.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:51:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	799,302
Mapped reads	733,020 / 91.71%
Unmapped reads	66,282 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,490 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	16,932 / 2.12%
Duplication rate	1.68%
Clipped reads	735,319 / 92%

2.2. ACGT Content

Number/percentage of A's	10,527,772 / 24.92%
Number/percentage of C's	7,578,698 / 17.94%
Number/percentage of T's	13,945,793 / 33.01%
Number/percentage of G's	10,199,591 / 24.14%
Number/percentage of N's	895 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0137

Standard Deviation	0.1582

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

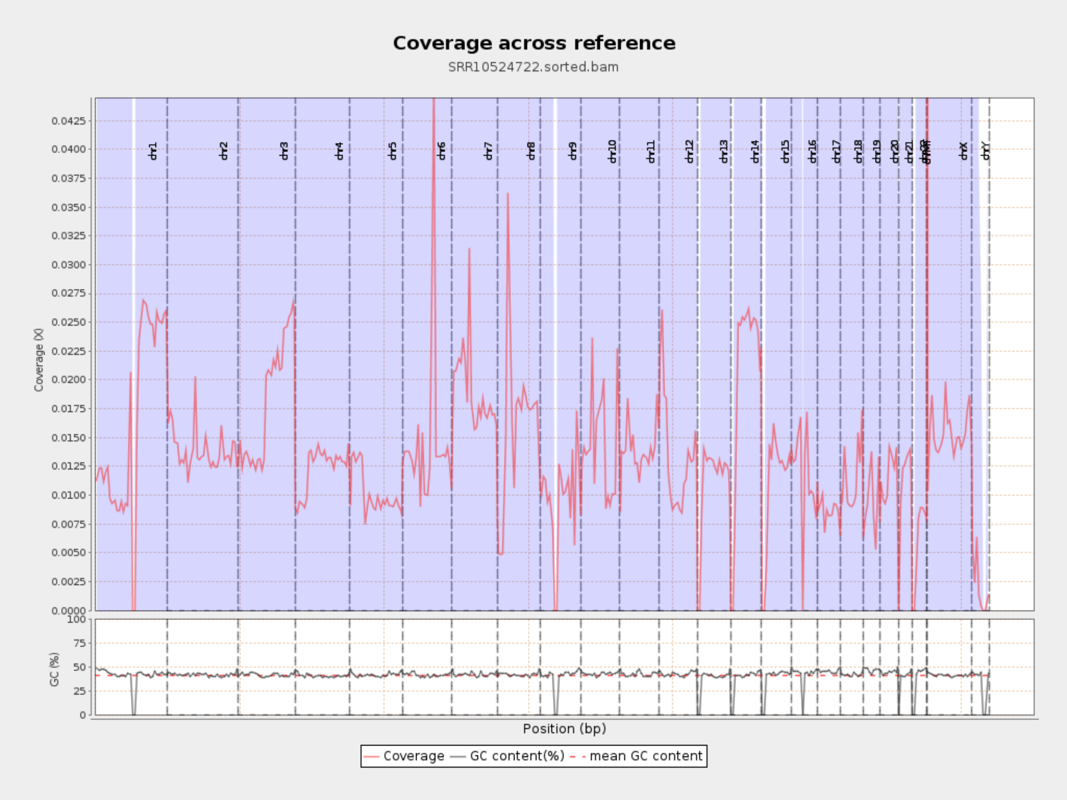
General error rate	0.51%
Mismatches	211,904
Insertions	2,591
Mapped reads with at least one insertion	0.35%
Deletions	8,839
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.37%

2.6. Chromosome stats

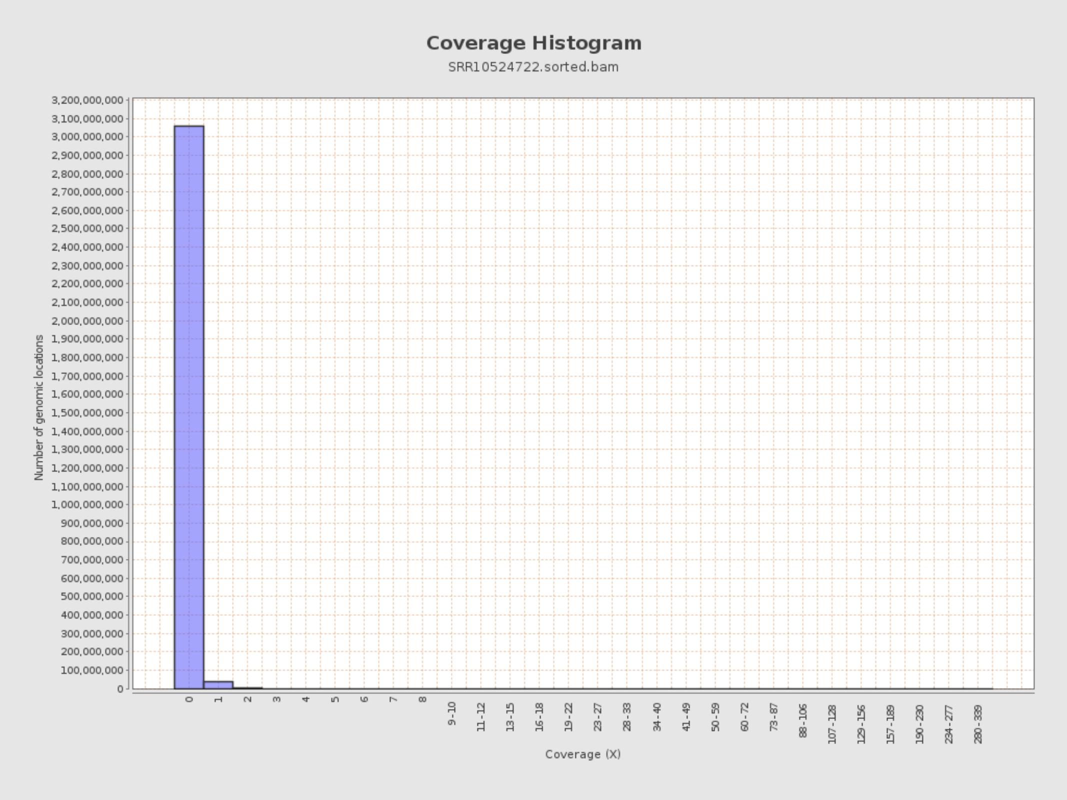
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4045648	0.0162	0.2399
chr2	243199373	3387545	0.0139	0.1876
chr3	198022430	3586133	0.0181	0.1406
chr4	191154276	2362125	0.0124	0.1183
chr5	180915260	1851873	0.0102	0.105
chr6	171115067	2590918	0.0151	0.137
chr7	159138663	3044002	0.0191	0.2595

chr8	146364022	2410838	0.0165	0.1677
chr9	141213431	1367850	0.0097	0.1221
chr10	135534747	1964438	0.0145	0.1563
chr11	135006516	1878568	0.0139	0.1487
chr12	133851895	1806774	0.0135	0.1219
chr13	115169878	1270463	0.011	0.1106
chr14	107349540	2200951	0.0205	0.1504
chr15	102531392	1115940	0.0109	0.1102
chr16	90354753	1055235	0.0117	0.1201
chr17	81195210	698373	0.0086	0.0978
chr18	78077248	886604	0.0114	0.2118
chr19	59128983	572398	0.0097	0.1639
chr20	63025520	734338	0.0117	0.1135
chr21	48129895	536494	0.0111	0.1135
chr22	51304566	308759	0.006	0.0803
chrMT	16571	69243	4.1786	2.8983
chrX	155270560	2401074	0.0155	0.1347
chrY	59373566	119992	0.002	0.0688

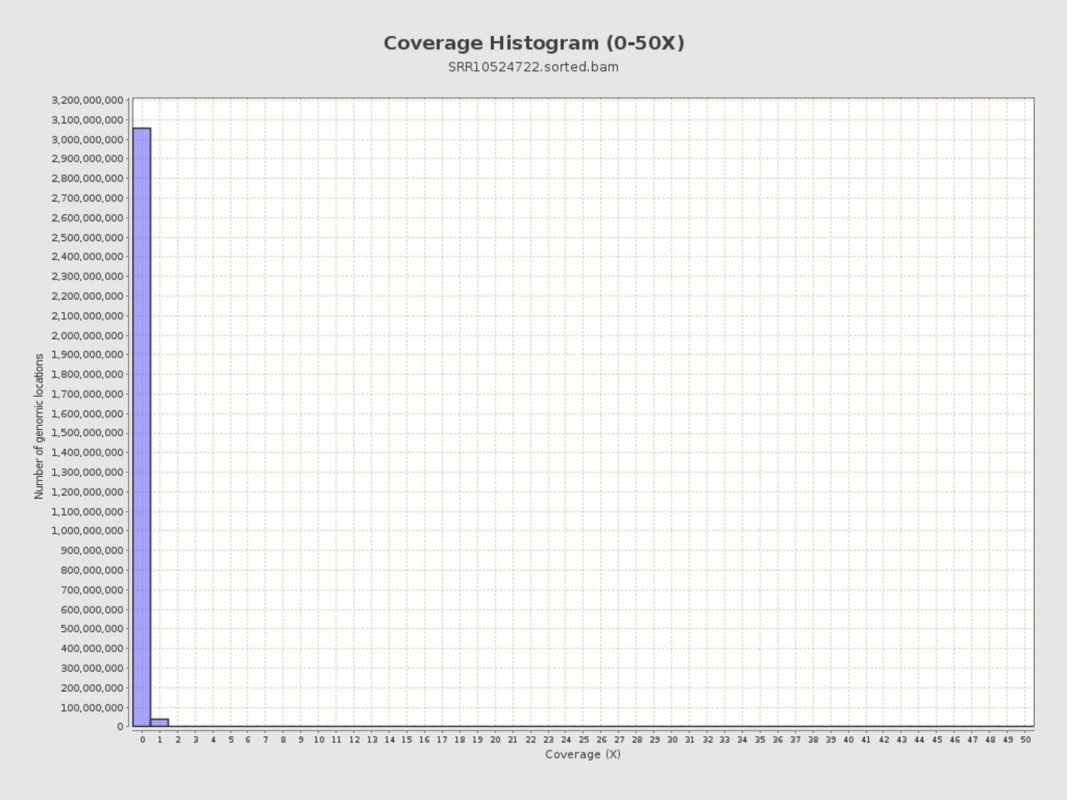
3. Results : Coverage across reference



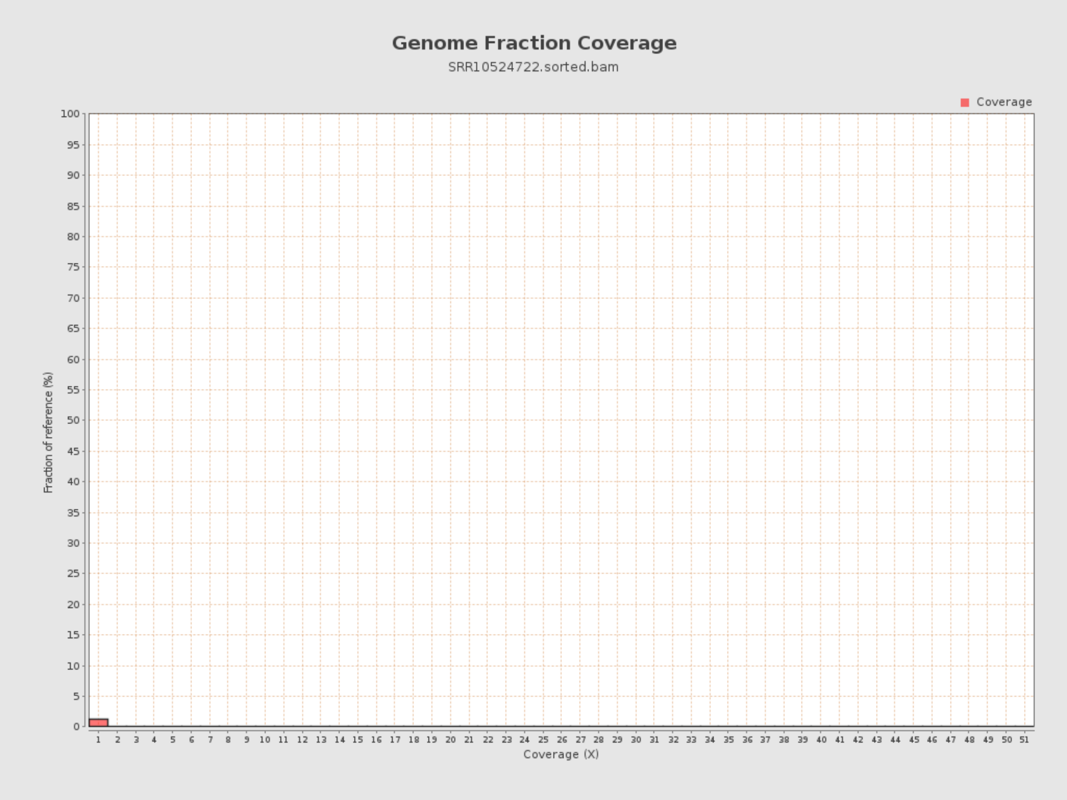
4. Results : Coverage Histogram



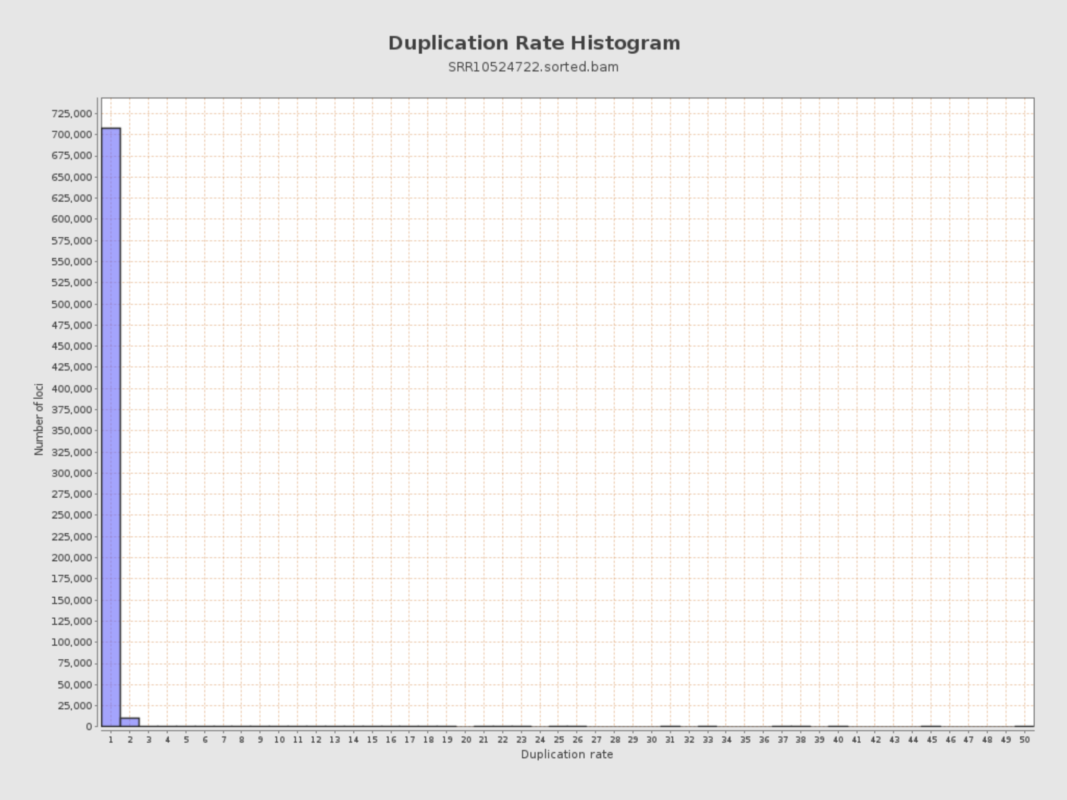
5. Results : Coverage Histogram (0-50X)



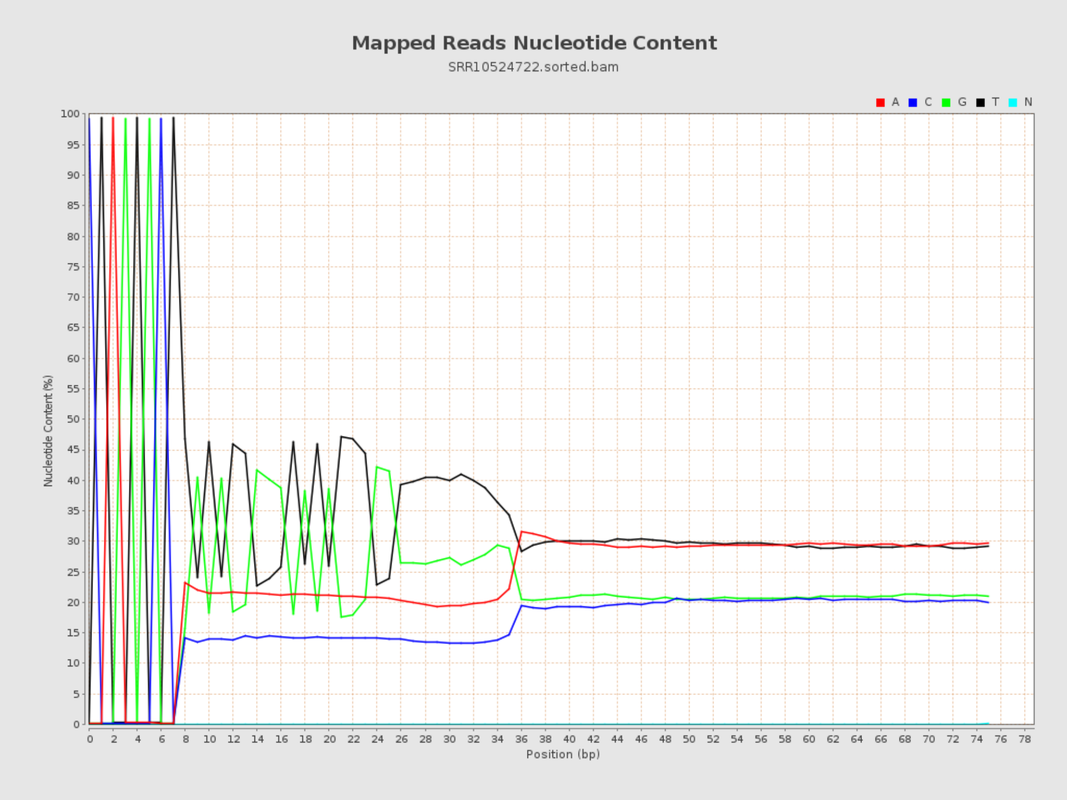
6. Results : Genome Fraction Coverage



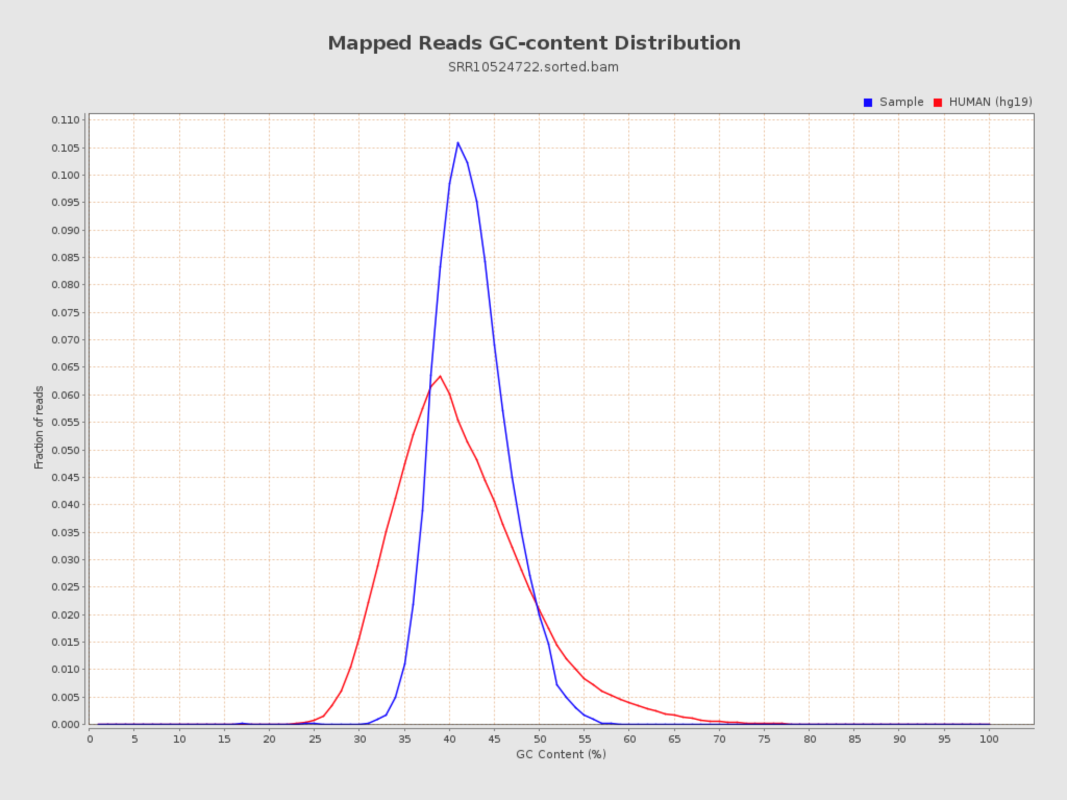
7. Results : Duplication Rate Histogram



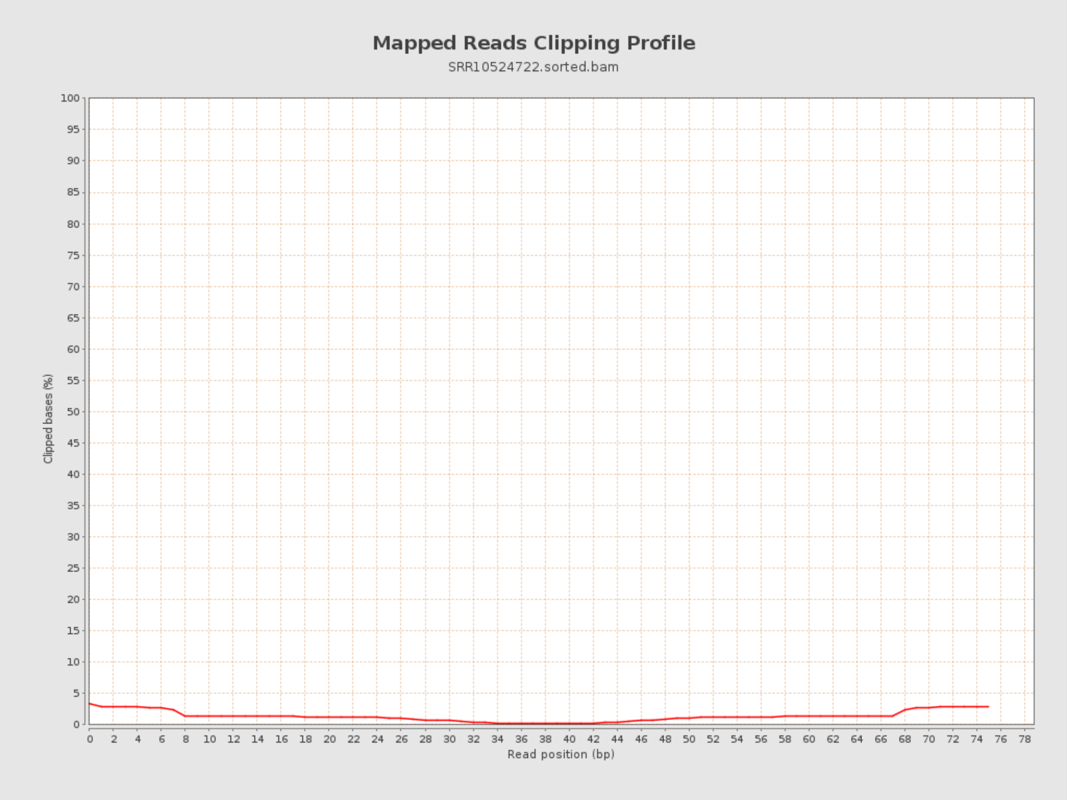
8. Results : Mapped Reads Nucleotide Content



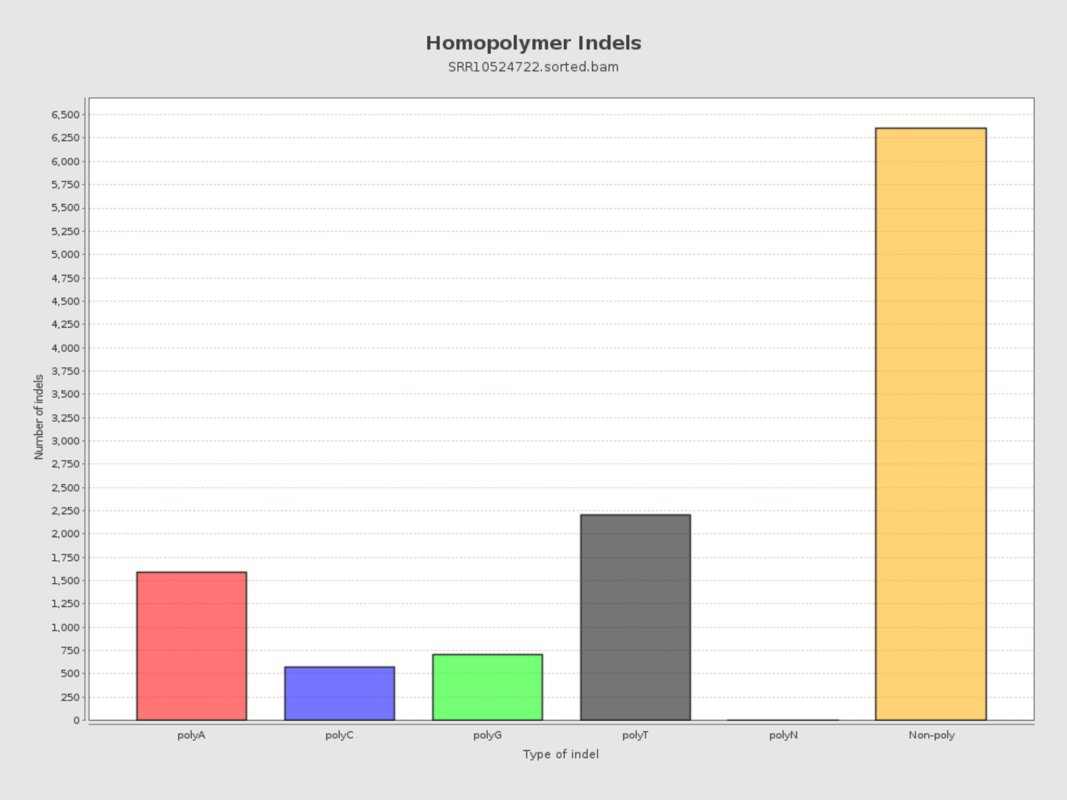
9. Results : Mapped Reads GC-content Distribution



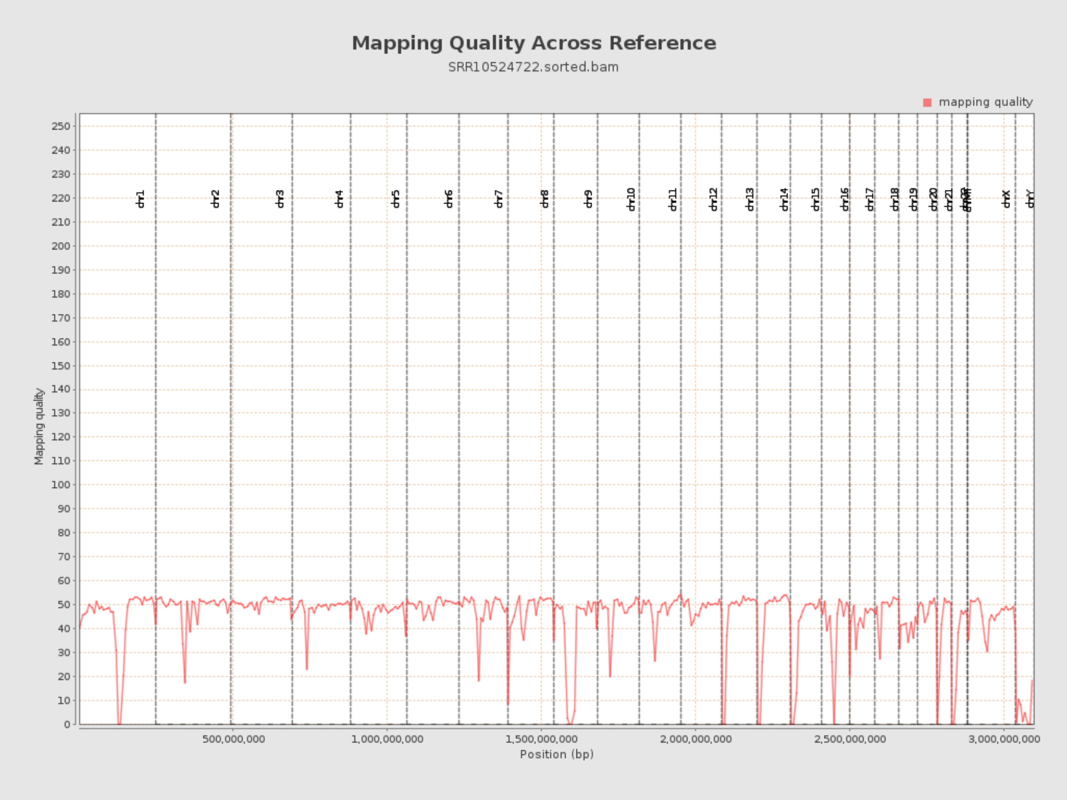
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram