Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:01:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524675.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_SRR10524675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524675.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:01:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524675.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	718,558
Mapped reads	664,454 / 92.47%
Unmapped reads	54,104 / 7.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,945 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	16,056 / 2.23%
Duplication rate	1.8%
Clipped reads	665,038 / 92.55%

2.2. ACGT Content

Number/percentage of A's	9,871,764 / 25.18%
Number/percentage of C's	7,998,044 / 20.4%
Number/percentage of T's	12,529,862 / 31.96%
Number/percentage of G's	8,795,728 / 22.44%
Number/percentage of N's	5,801 / 0.01%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.148

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

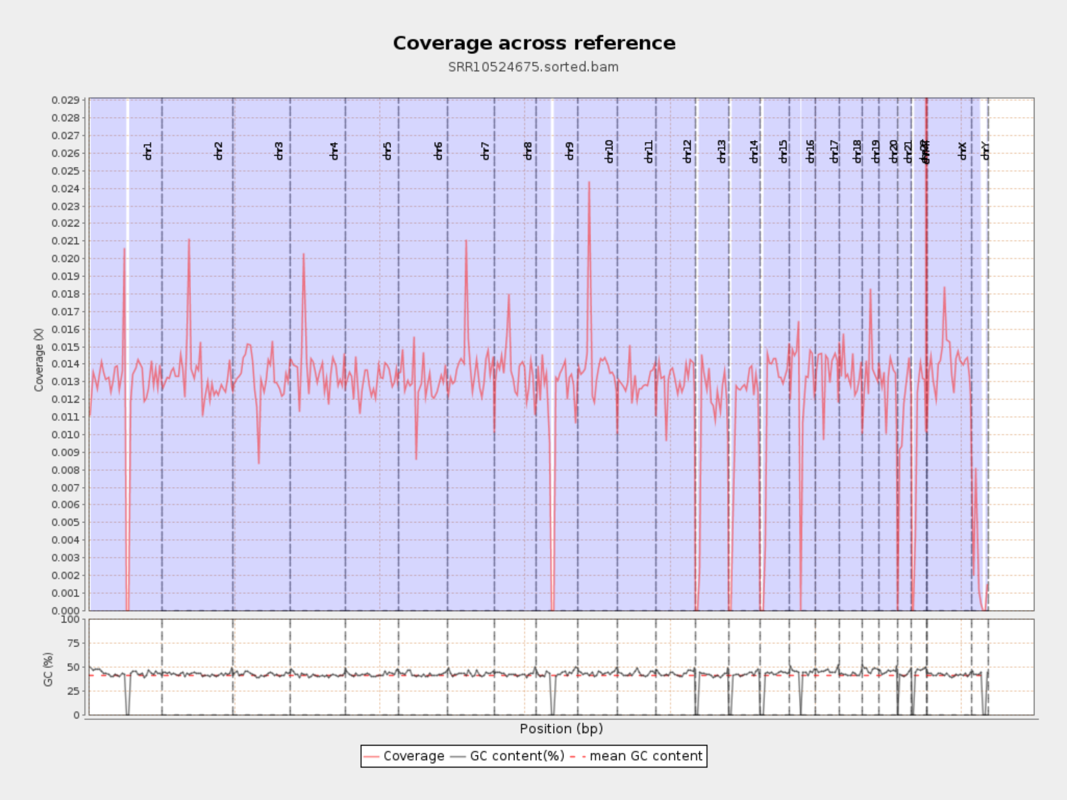
General error rate	0.52%
Mismatches	196,643
Insertions	3,117
Mapped reads with at least one insertion	0.47%
Deletions	7,605
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.45%

2.6. Chromosome stats

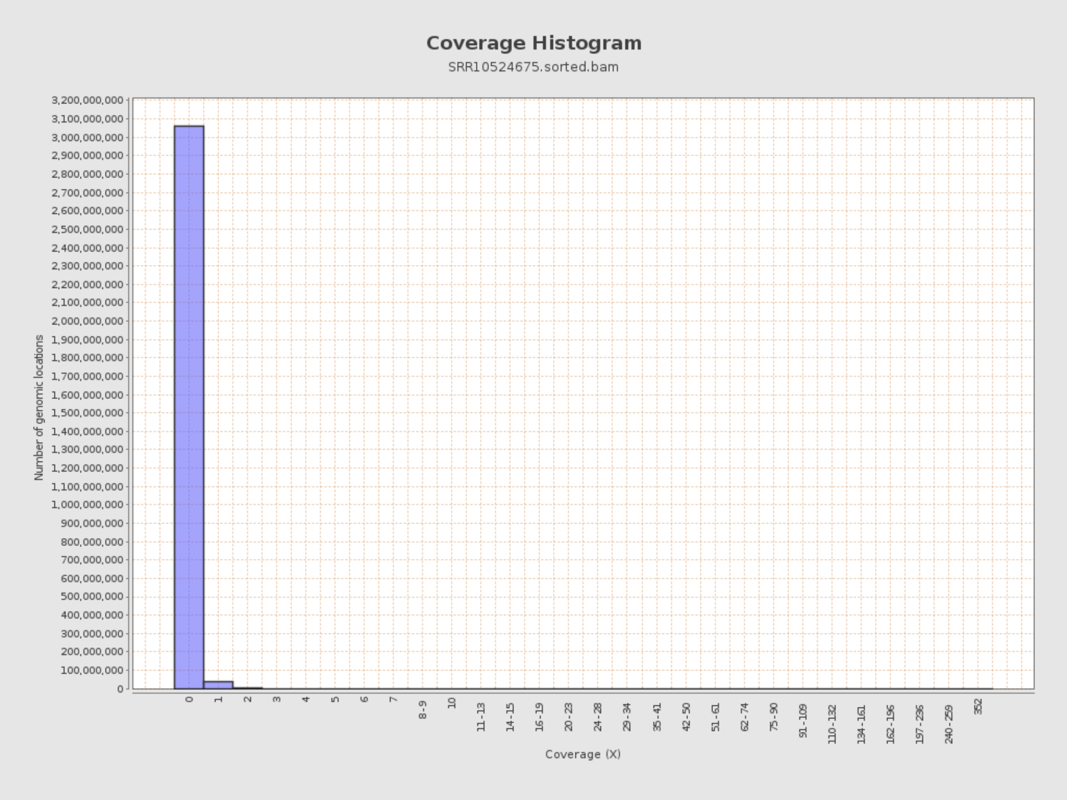
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3140058	0.0126	0.2229
chr2	243199373	3263876	0.0134	0.1925
chr3	198022430	2617519	0.0132	0.1202
chr4	191154276	2625062	0.0137	0.1297
chr5	180915260	2367947	0.0131	0.1195
chr6	171115067	2218181	0.013	0.1272
chr7	159138663	2222213	0.014	0.1709

chr8	146364022	1995658	0.0136	0.1534
chr9	141213431	1621076	0.0115	0.1266
chr10	135534747	1919594	0.0142	0.1507
chr11	135006516	1748915	0.013	0.1381
chr12	133851895	1753166	0.0131	0.1202
chr13	115169878	1205759	0.0105	0.1071
chr14	107349540	1149128	0.0107	0.1108
chr15	102531392	1139032	0.0111	0.1102
chr16	90354753	1142409	0.0126	0.1227
chr17	81195210	1106143	0.0136	0.1252
chr18	78077248	1059480	0.0136	0.2099
chr19	59128983	812101	0.0137	0.1863
chr20	63025520	814678	0.0129	0.1196
chr21	48129895	509740	0.0106	0.1139
chr22	51304566	461969	0.009	0.0989
chrMT	16571	12759	0.77	1.0598
chrX	155270560	2180617	0.014	0.1283
chrY	59373566	126109	0.0021	0.0873

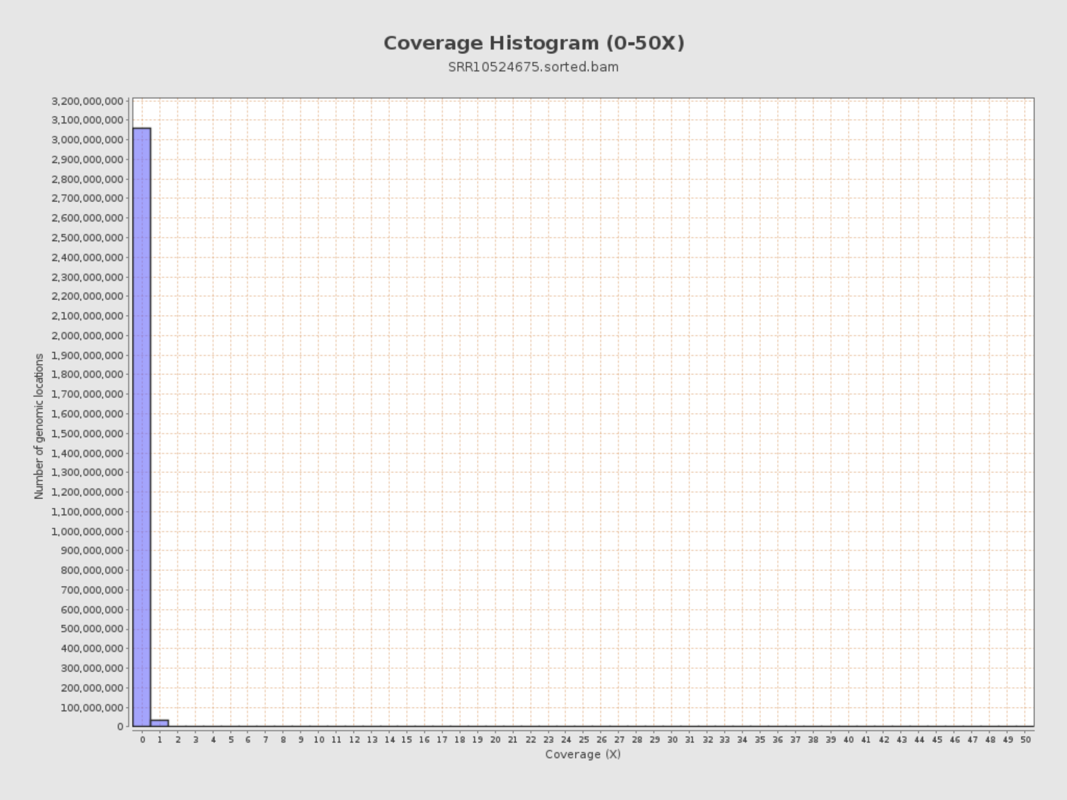
3. Results : Coverage across reference



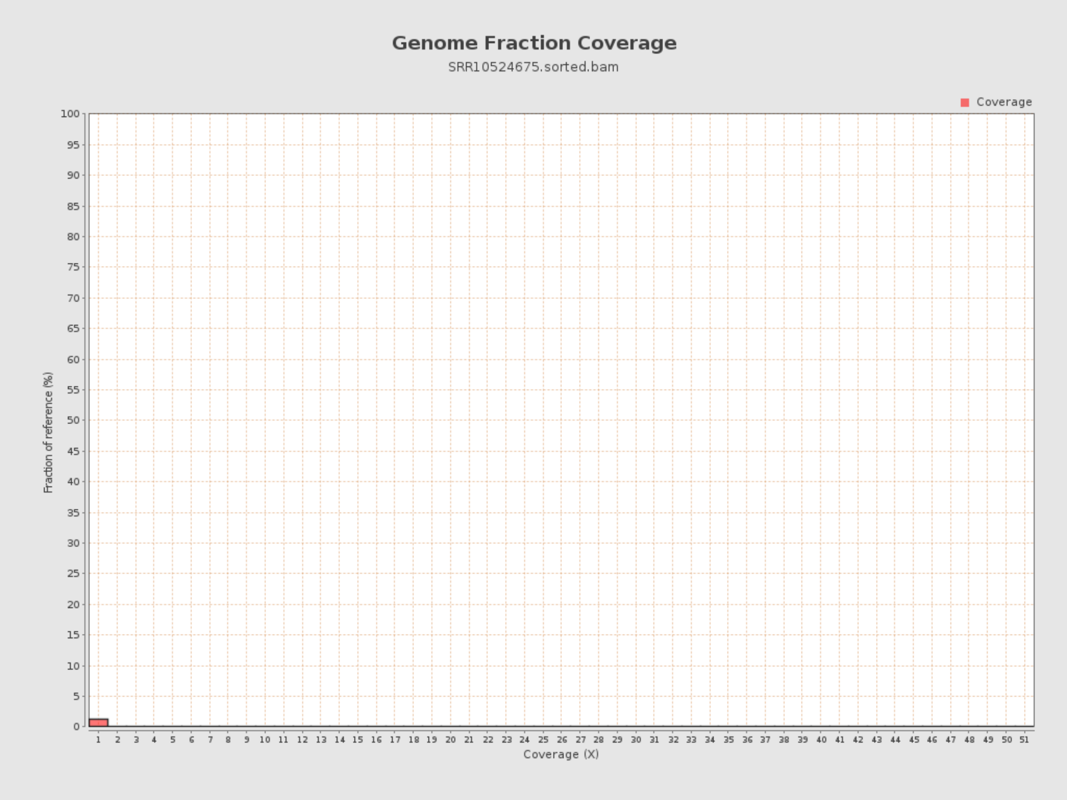
4. Results : Coverage Histogram



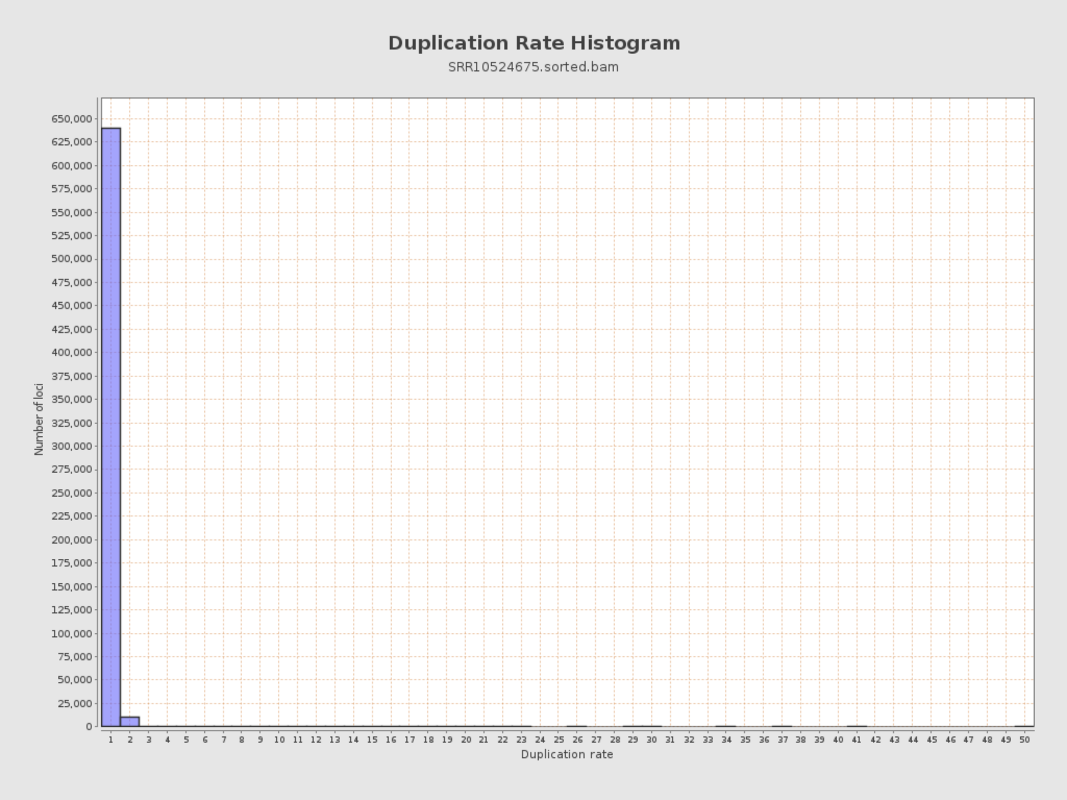
5. Results : Coverage Histogram (0-50X)



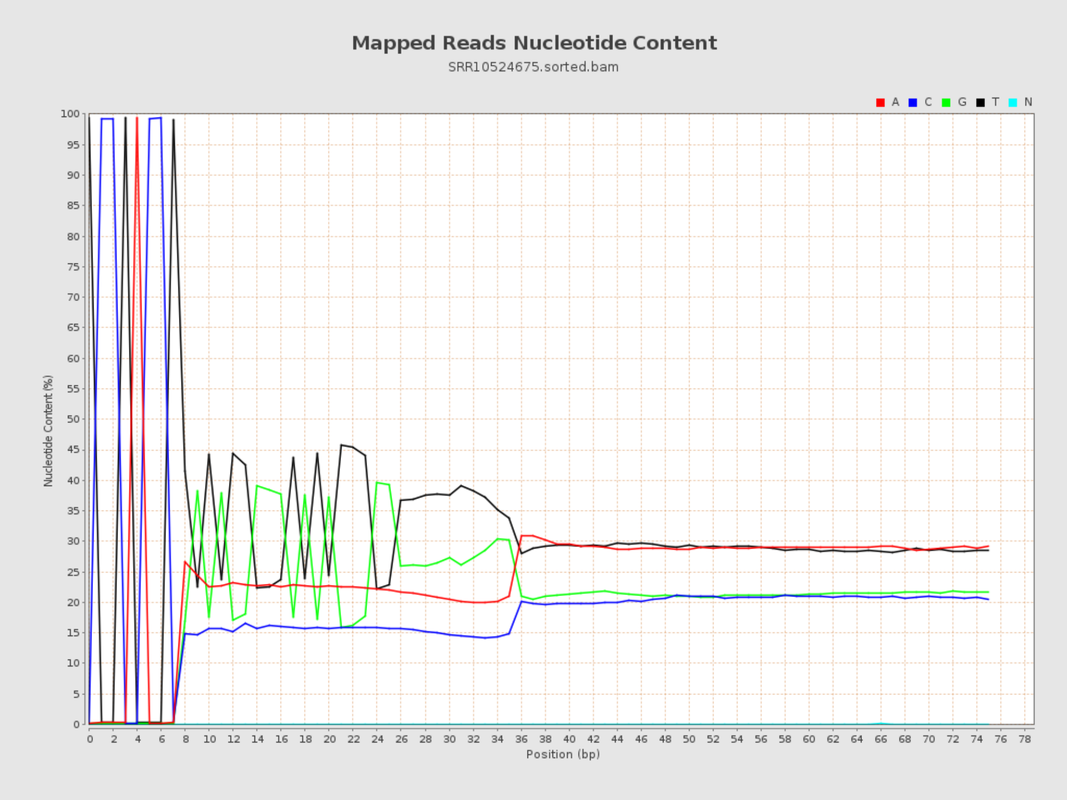
6. Results : Genome Fraction Coverage



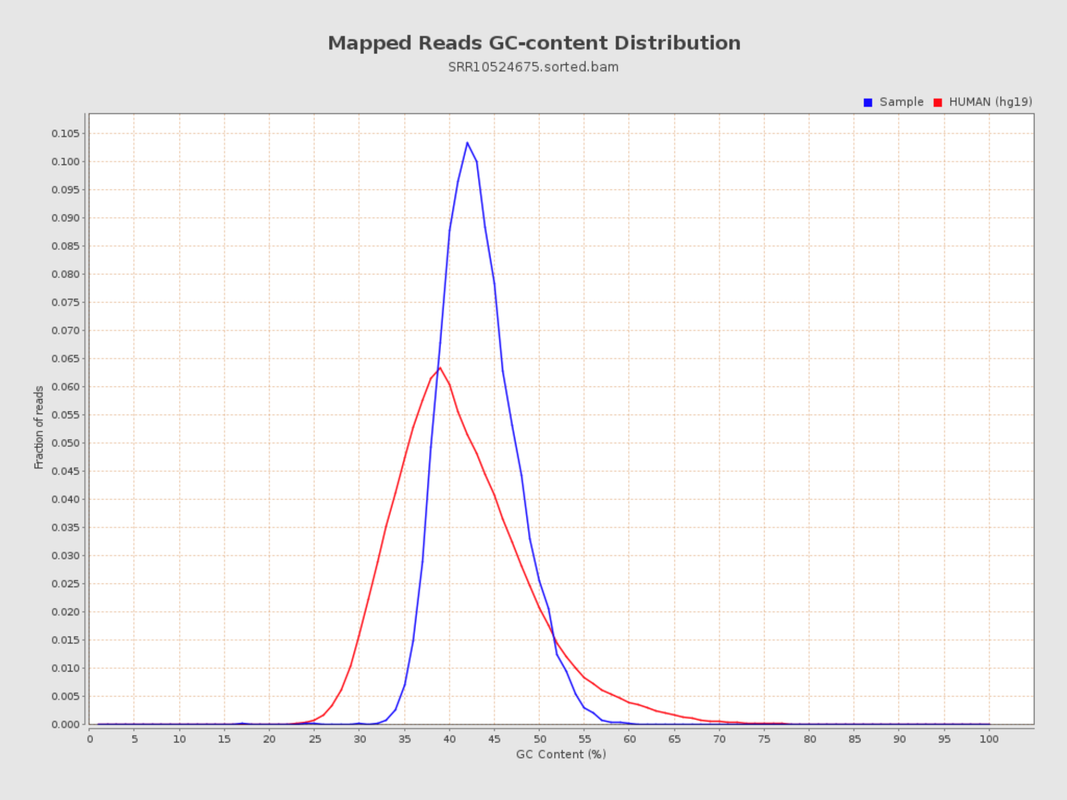
7. Results : Duplication Rate Histogram



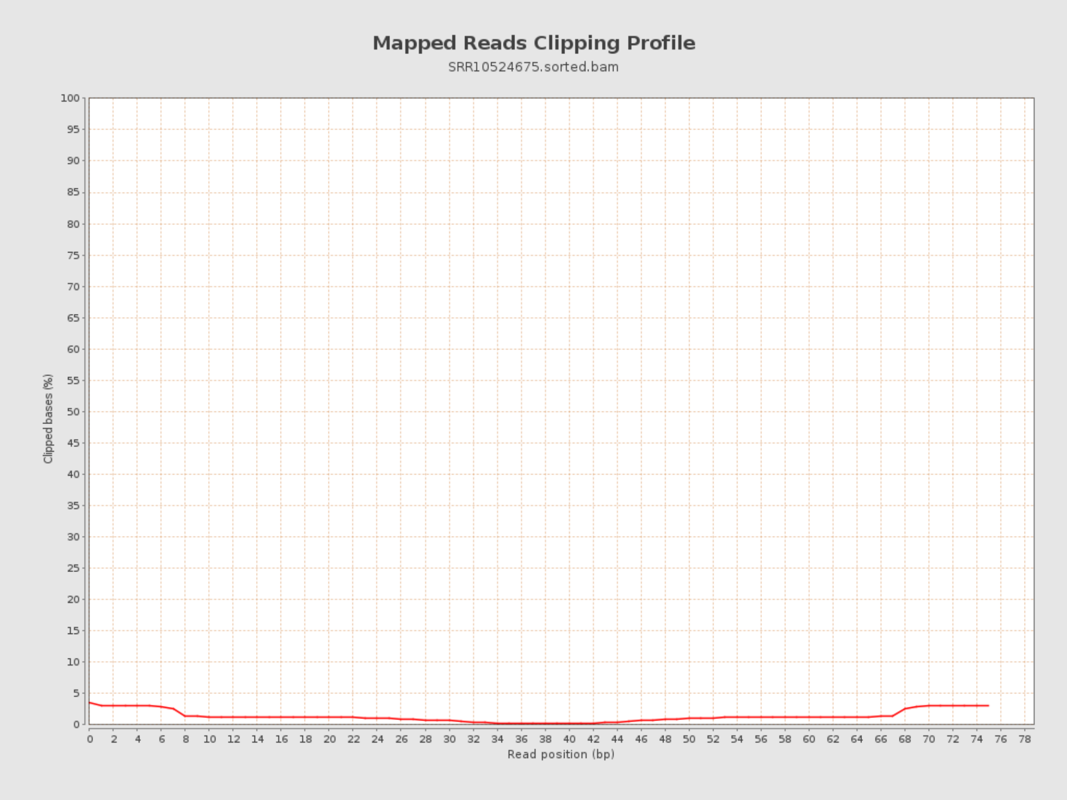
8. Results : Mapped Reads Nucleotide Content



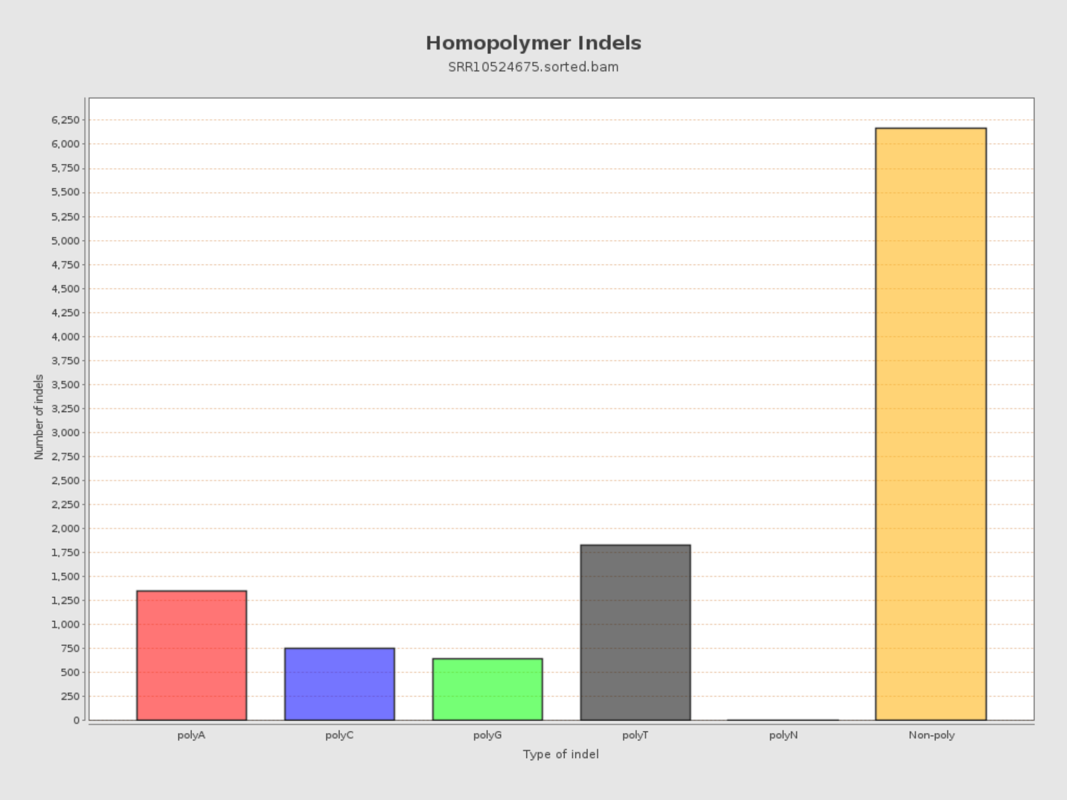
9. Results : Mapped Reads GC-content Distribution



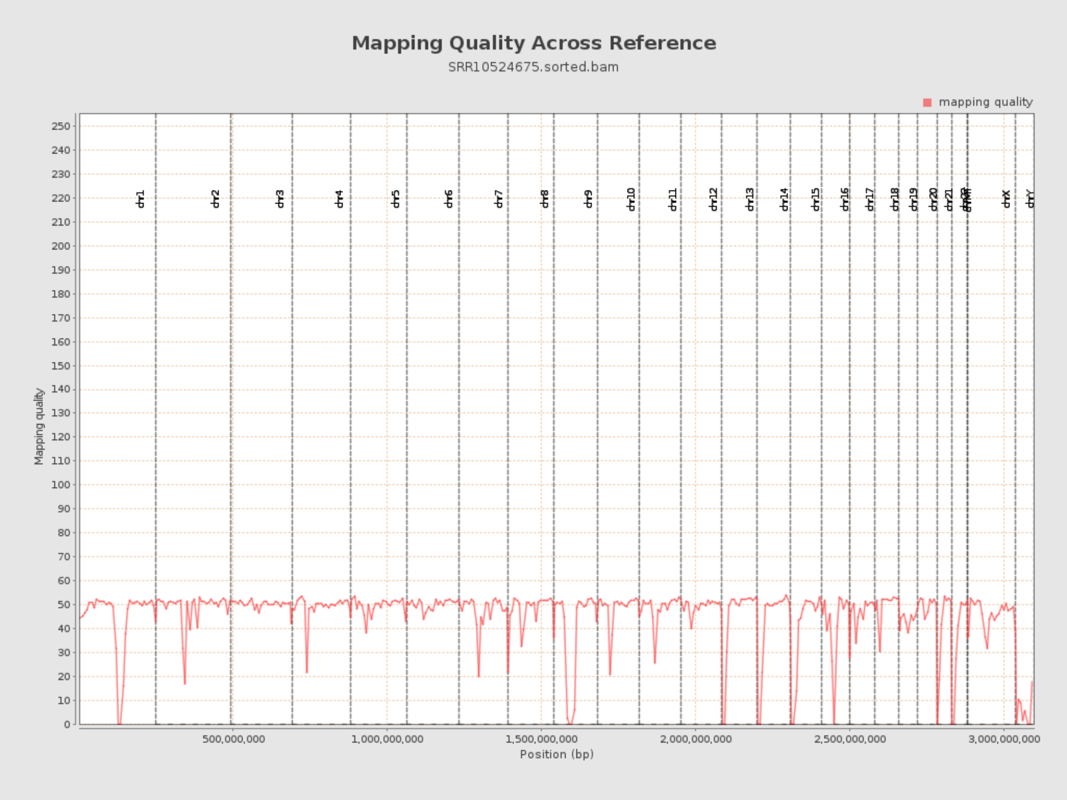
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram