Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:52:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524650.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_SRR10524650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524650.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:52:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	770,082
Mapped reads	712,594 / 92.53%
Unmapped reads	57,488 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,028 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	21,010 / 2.73%
Duplication rate	2.29%
Clipped reads	713,285 / 92.62%

2.2. ACGT Content

Number/percentage of A's	10,615,890 / 25.51%
Number/percentage of C's	7,780,923 / 18.7%
Number/percentage of T's	13,426,964 / 32.27%
Number/percentage of G's	9,785,218 / 23.52%
Number/percentage of N's	324 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0134

Standard Deviation	0.1534

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

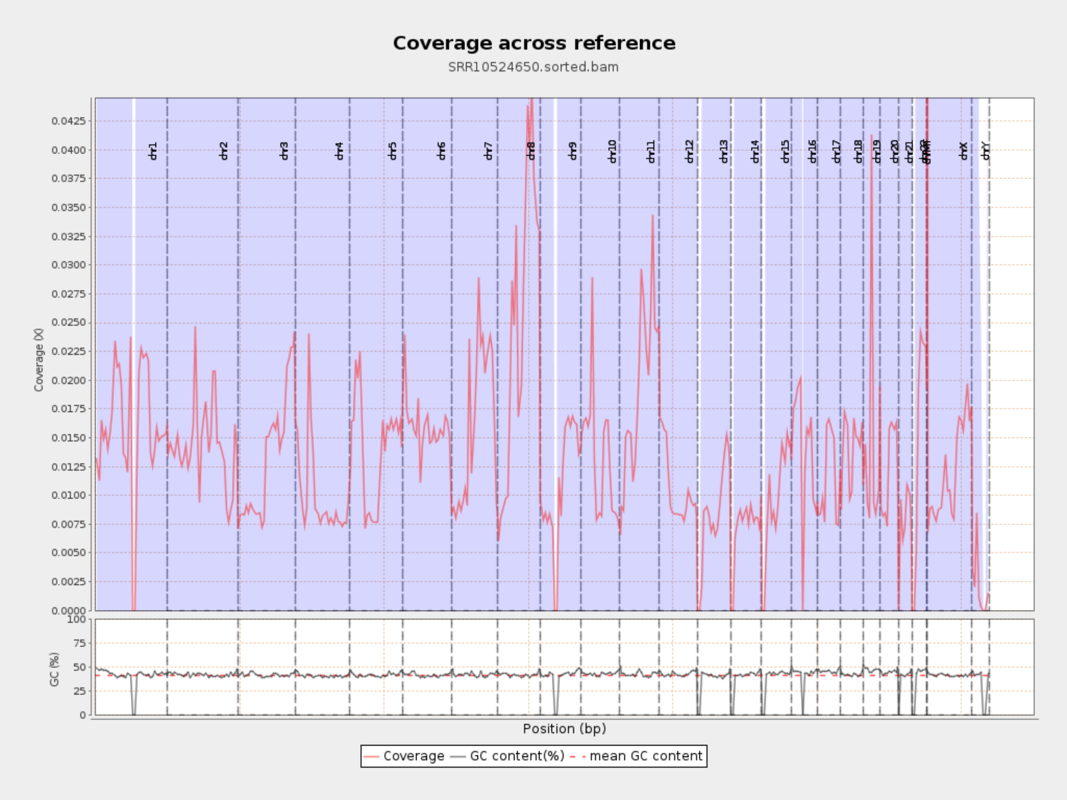
General error rate	0.51%
Mismatches	208,455
Insertions	2,965
Mapped reads with at least one insertion	0.41%
Deletions	7,863
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.45%

2.6. Chromosome stats

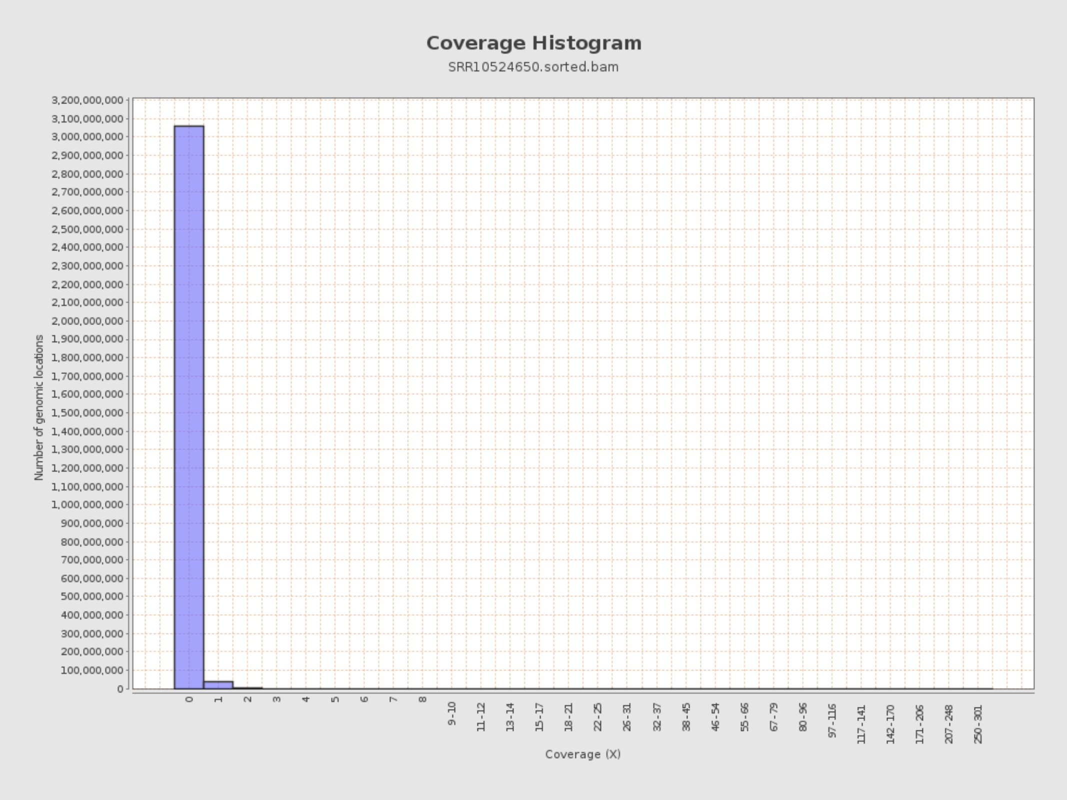
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3934798	0.0158	0.2453
chr2	243199373	3477954	0.0143	0.1778
chr3	198022430	2607130	0.0132	0.1211
chr4	191154276	1924438	0.0101	0.1201
chr5	180915260	2551490	0.0141	0.1252
chr6	171115067	2727017	0.0159	0.1376
chr7	159138663	2582683	0.0162	0.1867

chr8	146364022	3706536	0.0253	0.2053
chr9	141213431	1518295	0.0108	0.1276
chr10	135534747	1833069	0.0135	0.1676
chr11	135006516	2619441	0.0194	0.1572
chr12	133851895	1422594	0.0106	0.1108
chr13	115169878	952156	0.0083	0.0957
chr14	107349540	751801	0.007	0.0904
chr15	102531392	963097	0.0094	0.1026
chr16	90354753	1252838	0.0139	0.1281
chr17	81195210	918040	0.0113	0.1147
chr18	78077248	1097542	0.0141	0.1961
chr19	59128983	856407	0.0145	0.1796
chr20	63025520	771874	0.0122	0.1191
chr21	48129895	375252	0.0078	0.1078
chr22	51304566	776375	0.0151	0.1305
chrMT	16571	5378	0.3245	0.6009
chrX	155270560	1873793	0.0121	0.122
chrY	59373566	122648	0.0021	0.0848

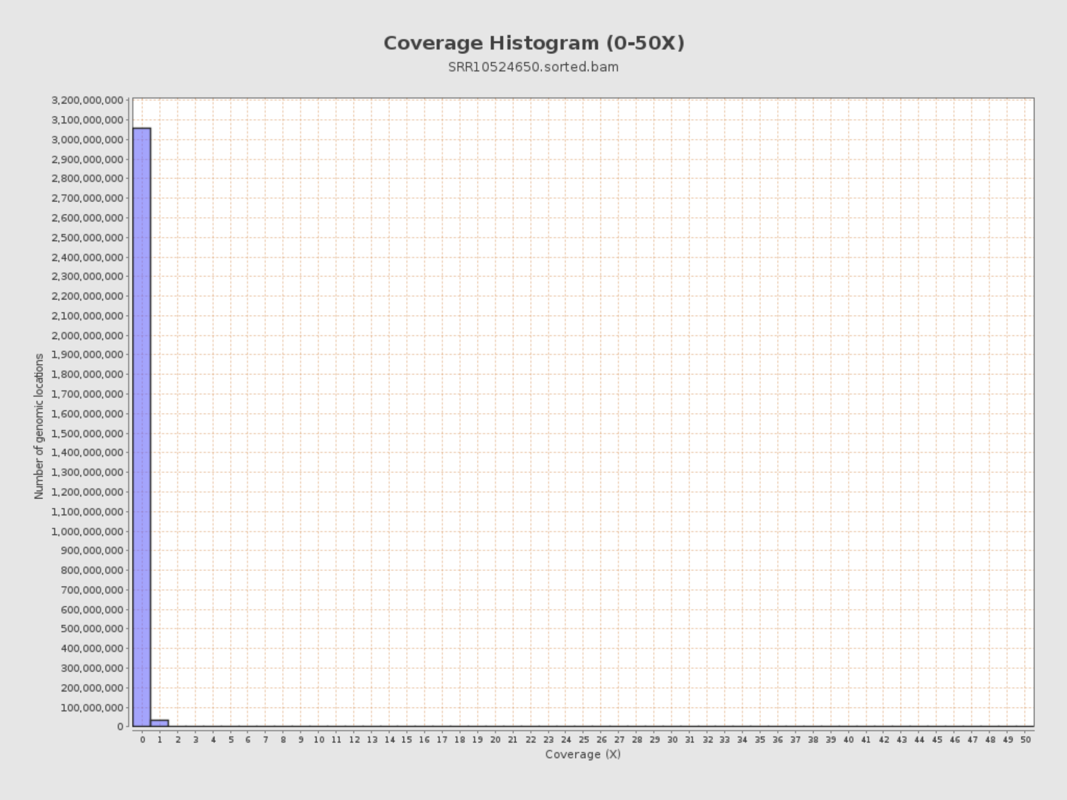
3. Results : Coverage across reference



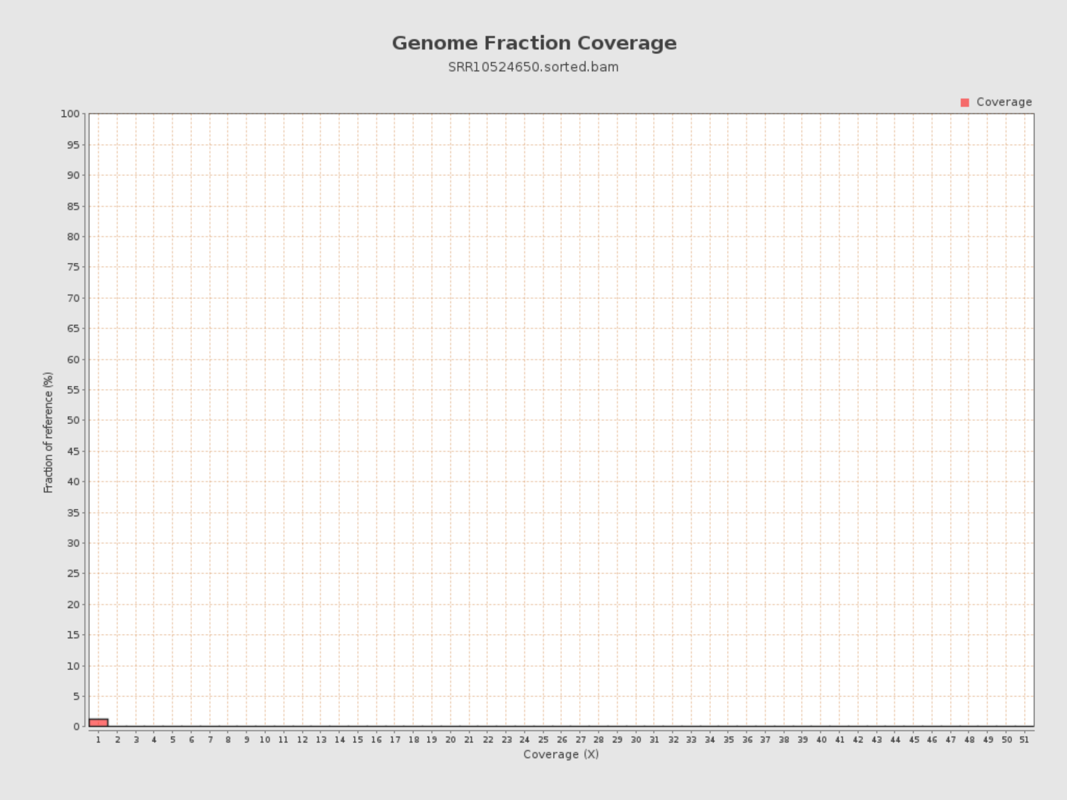
4. Results : Coverage Histogram



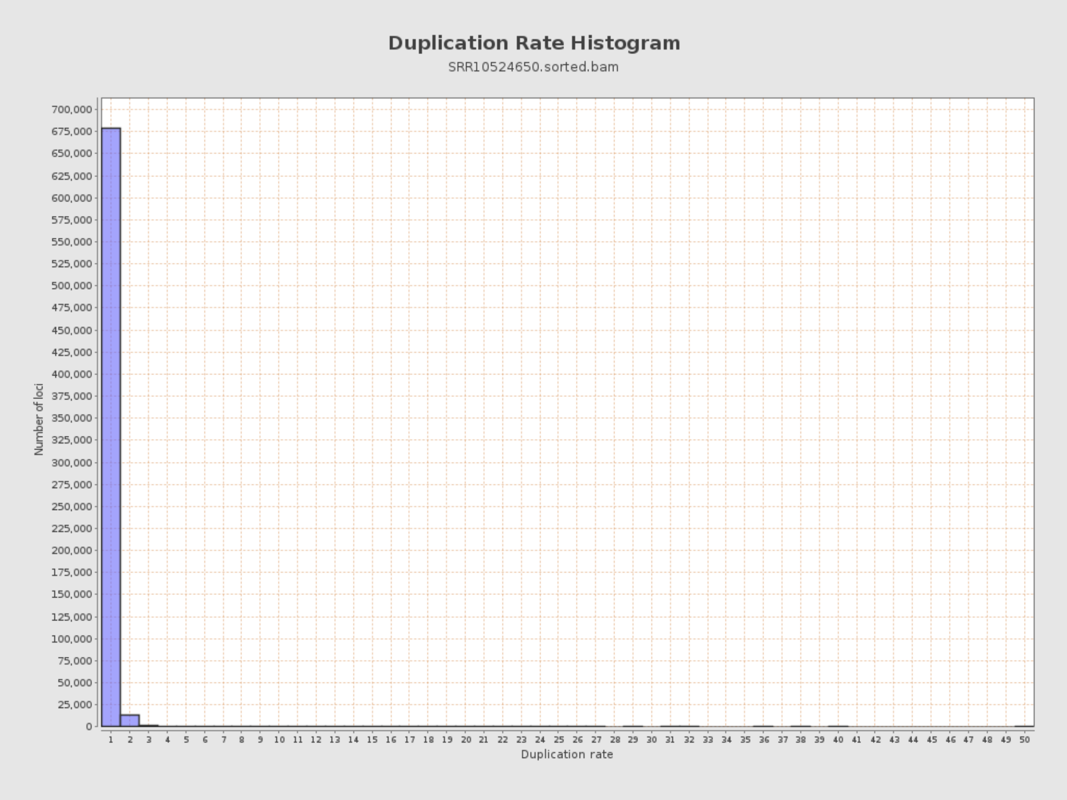
5. Results : Coverage Histogram (0-50X)



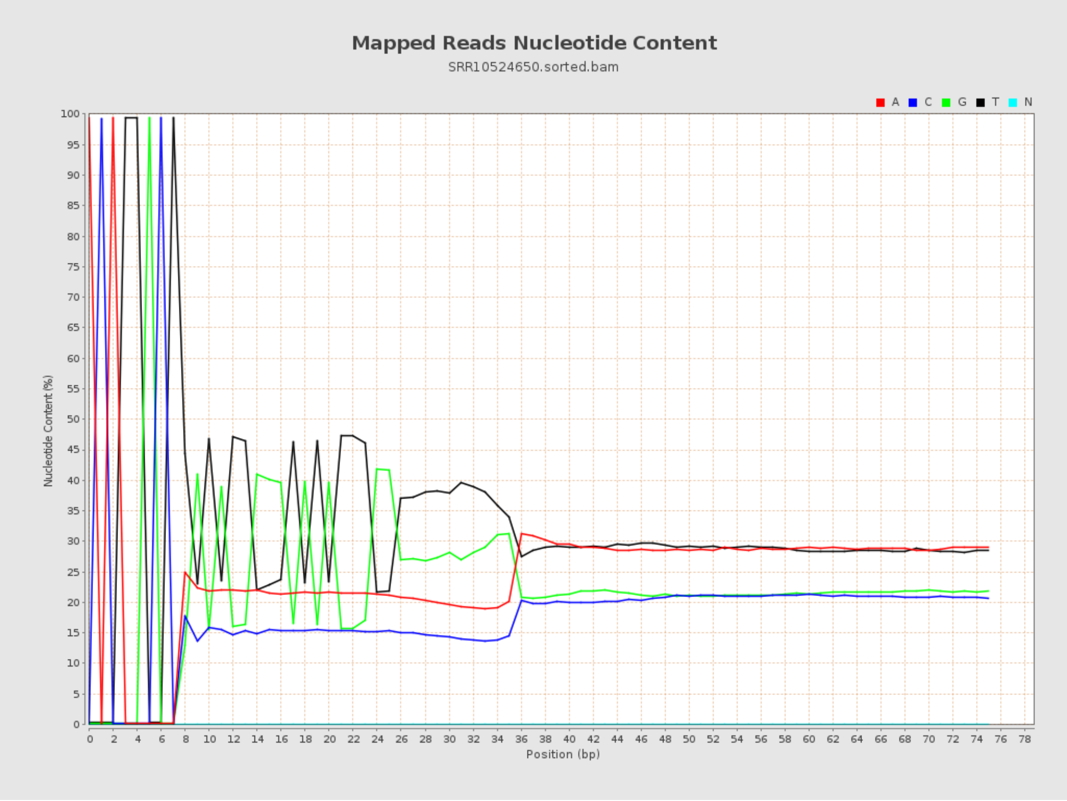
6. Results : Genome Fraction Coverage



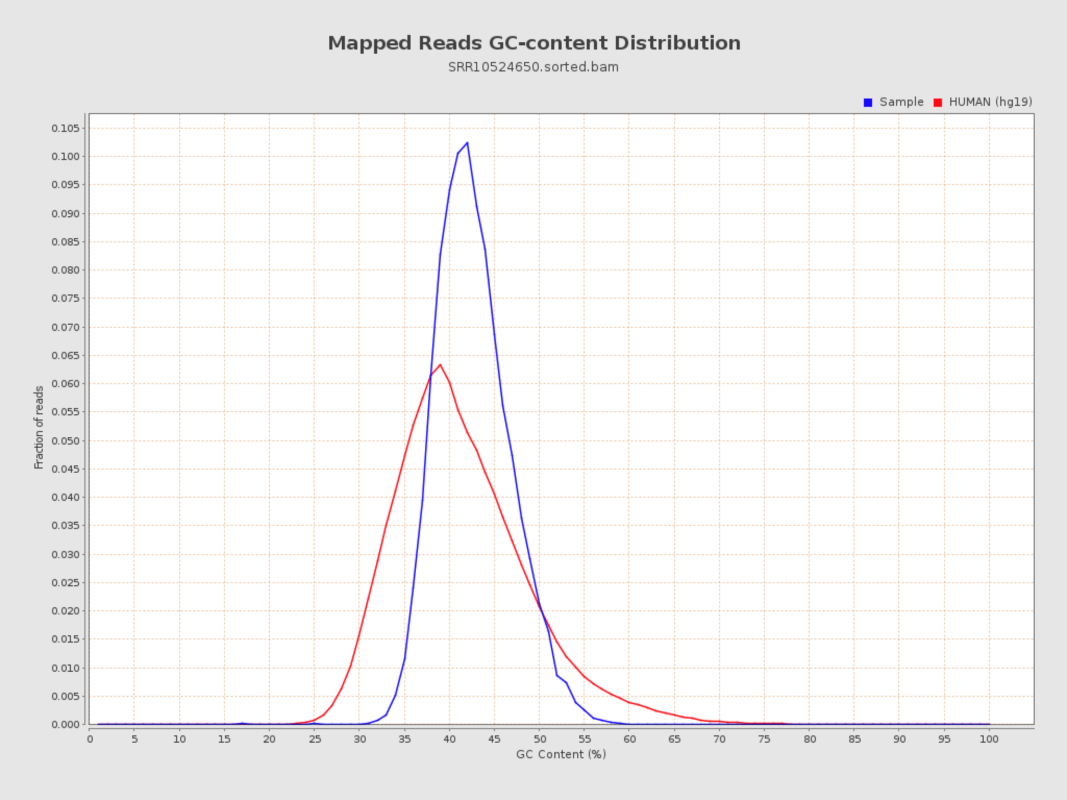
7. Results : Duplication Rate Histogram



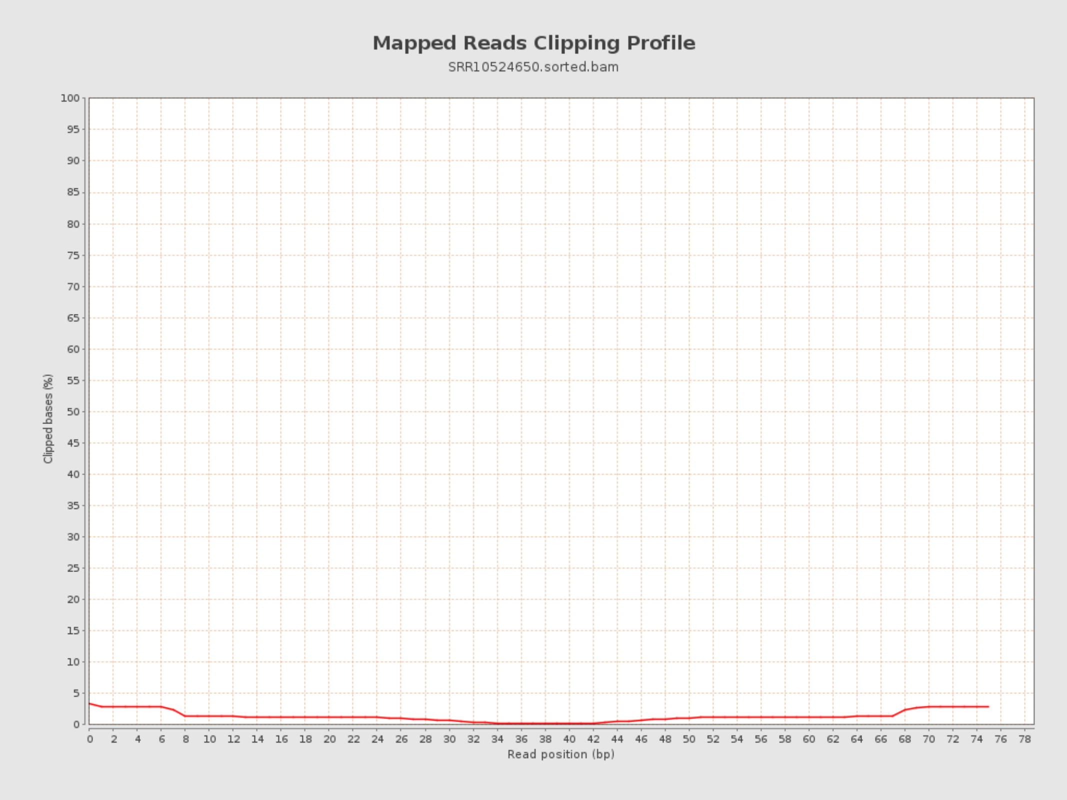
8. Results : Mapped Reads Nucleotide Content



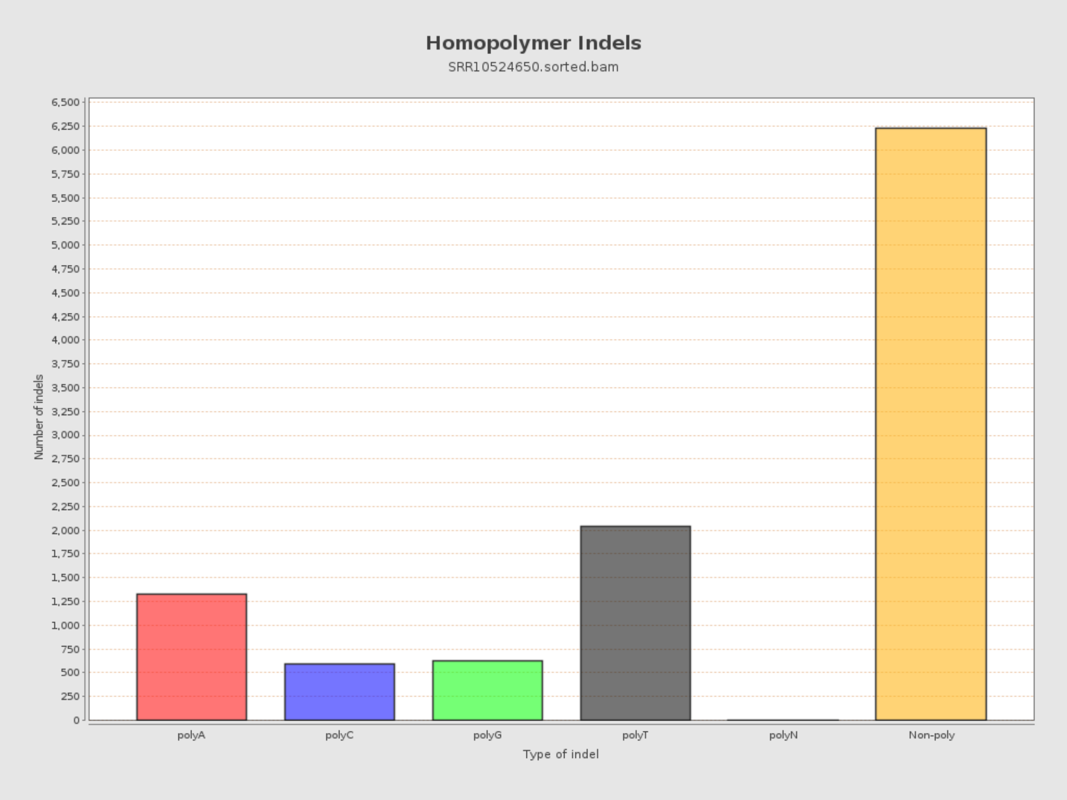
9. Results : Mapped Reads GC-content Distribution



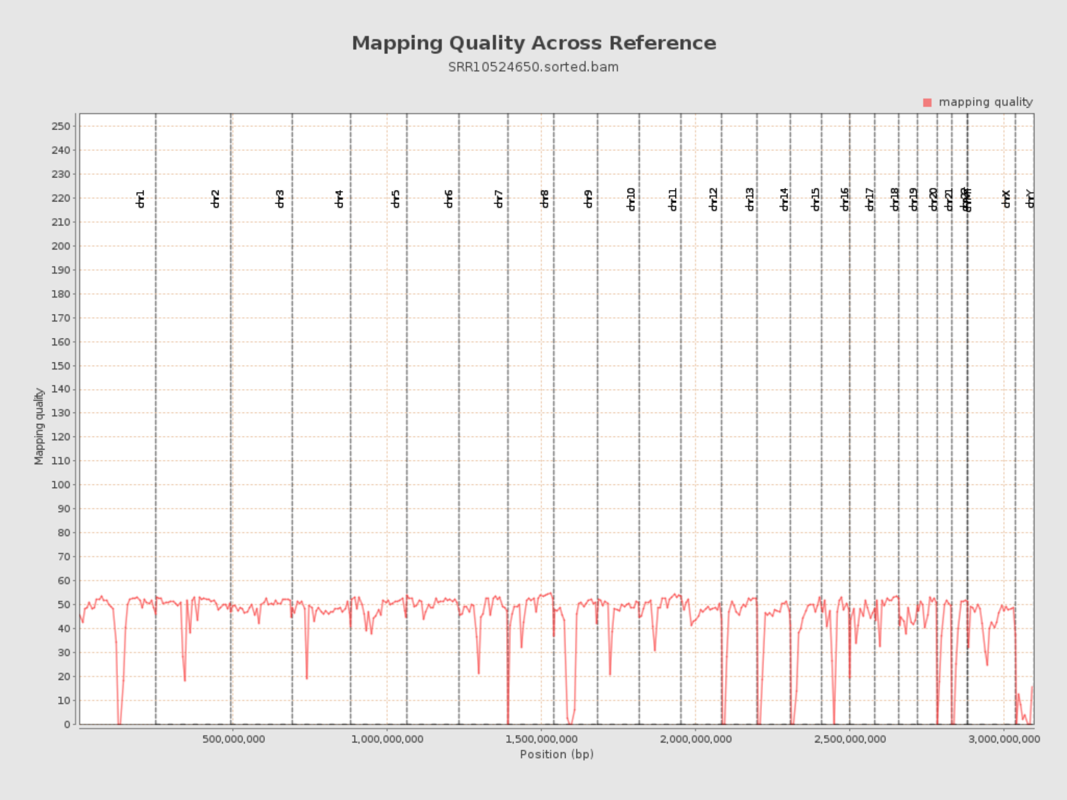
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram