Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:46:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524866.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_SRR10524866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524866.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:46:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	917,376
Mapped reads	824,363 / 89.86%
Unmapped reads	93,013 / 10.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,036 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	22,026 / 2.4%
Duplication rate	1.87%
Clipped reads	826,064 / 90.05%

2.2. ACGT Content

Number/percentage of A's	12,080,931 / 25.74%
Number/percentage of C's	8,314,520 / 17.71%
Number/percentage of T's	15,581,534 / 33.19%
Number/percentage of G's	10,964,357 / 23.36%
Number/percentage of N's	1,015 / 0%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0152

Standard Deviation	0.1849

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

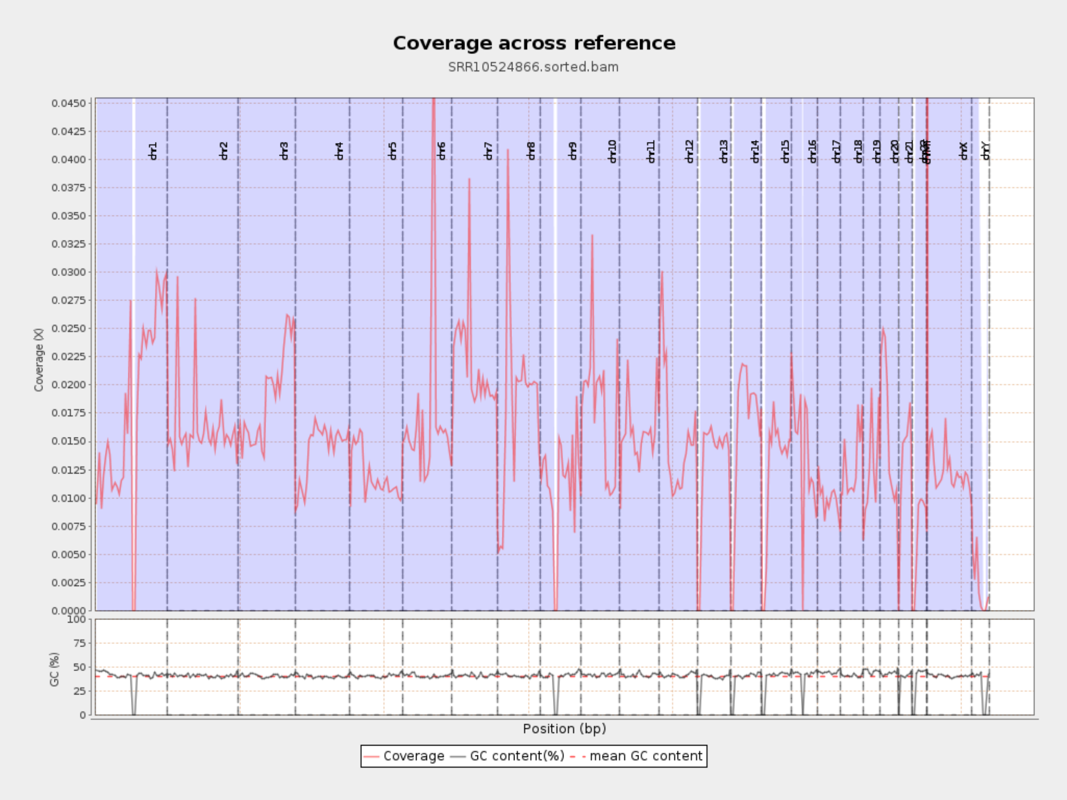
General error rate	0.54%
Mismatches	250,116
Insertions	3,258
Mapped reads with at least one insertion	0.39%
Deletions	10,155
Mapped reads with at least one deletion	1.22%
Homopolymer indels	41.64%

2.6. Chromosome stats

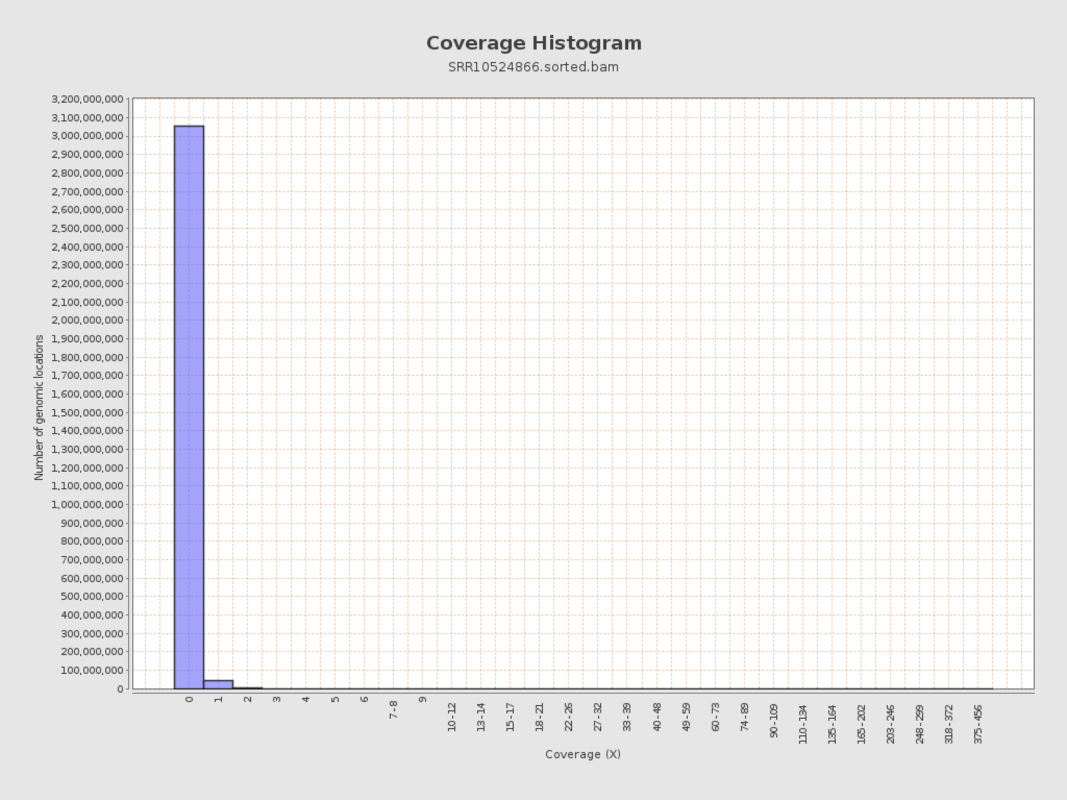
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4443835	0.0178	0.3101
chr2	243199373	3921350	0.0161	0.2401
chr3	198022430	3730326	0.0188	0.1443
chr4	191154276	2734797	0.0143	0.1278
chr5	180915260	2174313	0.012	0.1157
chr6	171115067	3033345	0.0177	0.1503
chr7	159138663	3492487	0.0219	0.325

chr8	146364022	2715555	0.0186	0.1793
chr9	141213431	1569120	0.0111	0.1395
chr10	135534747	2459798	0.0181	0.1967
chr11	135006516	2129881	0.0158	0.1531
chr12	133851895	2109439	0.0158	0.1338
chr13	115169878	1503230	0.0131	0.1198
chr14	107349540	1731296	0.0161	0.1343
chr15	102531392	1254103	0.0122	0.1179
chr16	90354753	1264433	0.014	0.1326
chr17	81195210	804339	0.0099	0.1067
chr18	78077248	1002089	0.0128	0.2191
chr19	59128983	758337	0.0128	0.2099
chr20	63025520	1022818	0.0162	0.1341
chr21	48129895	645576	0.0134	0.1223
chr22	51304566	341562	0.0067	0.0849
chrMT	16571	65167	3.9326	3.0134
chrX	155270560	1927601	0.0124	0.1261
chrY	59373566	123488	0.0021	0.0684

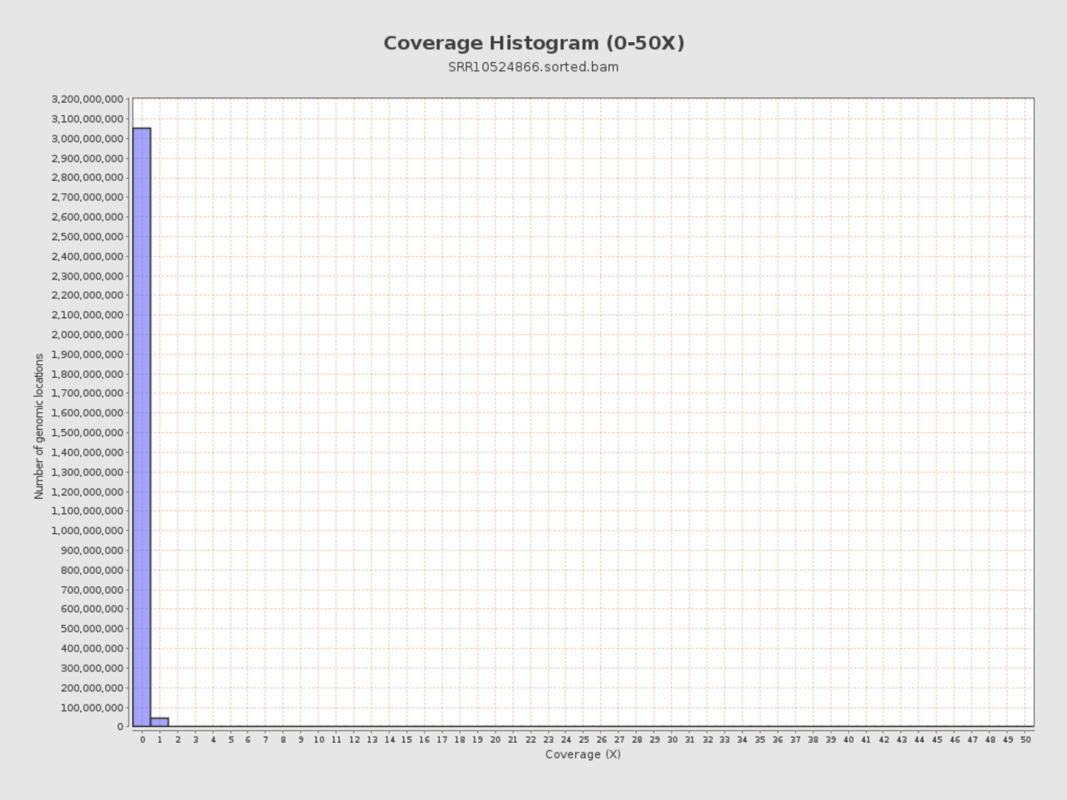
3. Results : Coverage across reference



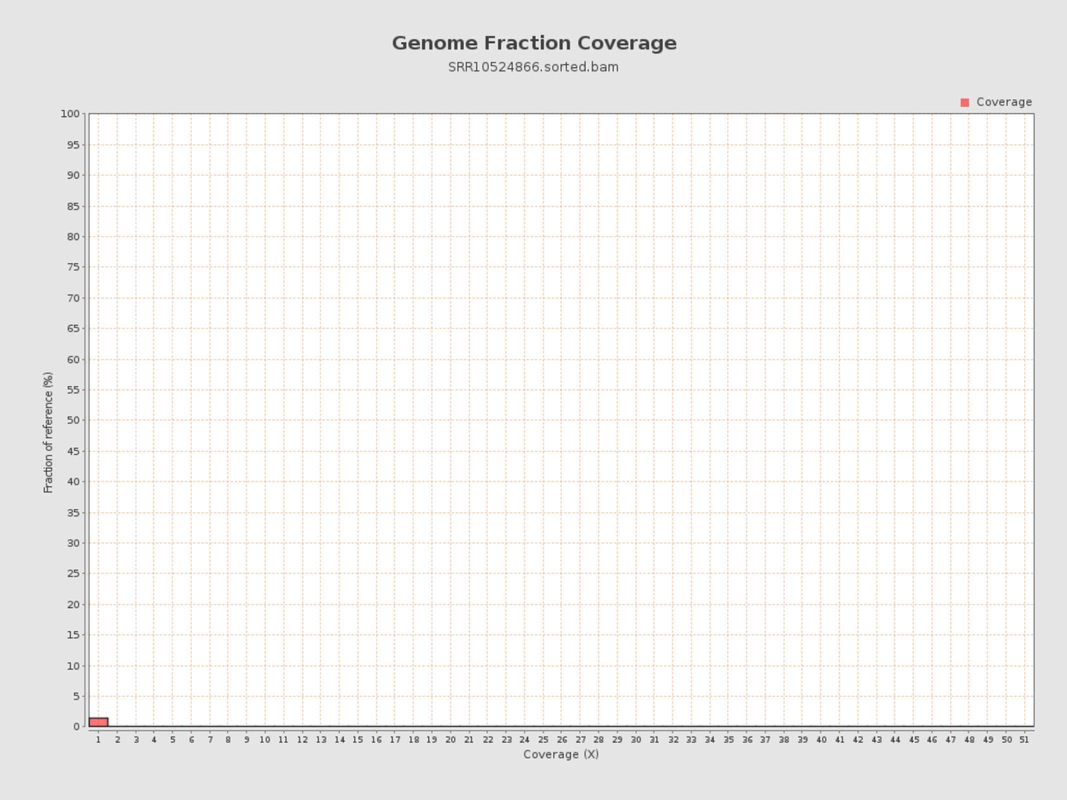
4. Results : Coverage Histogram



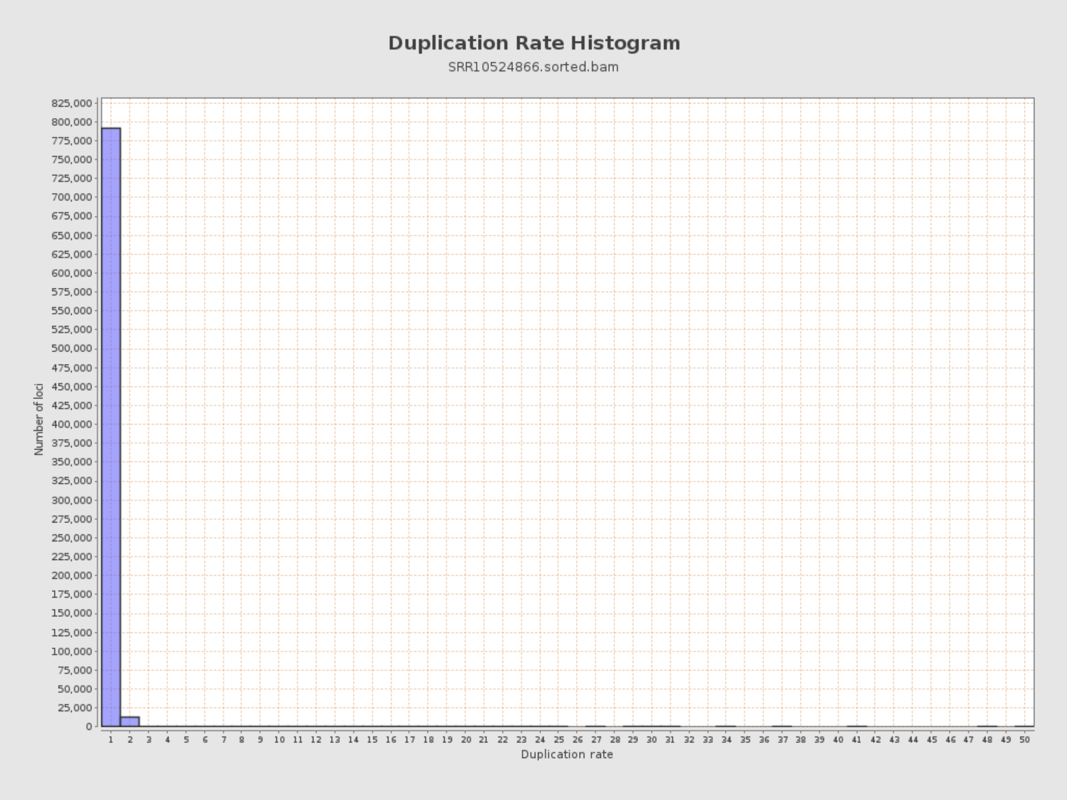
5. Results : Coverage Histogram (0-50X)



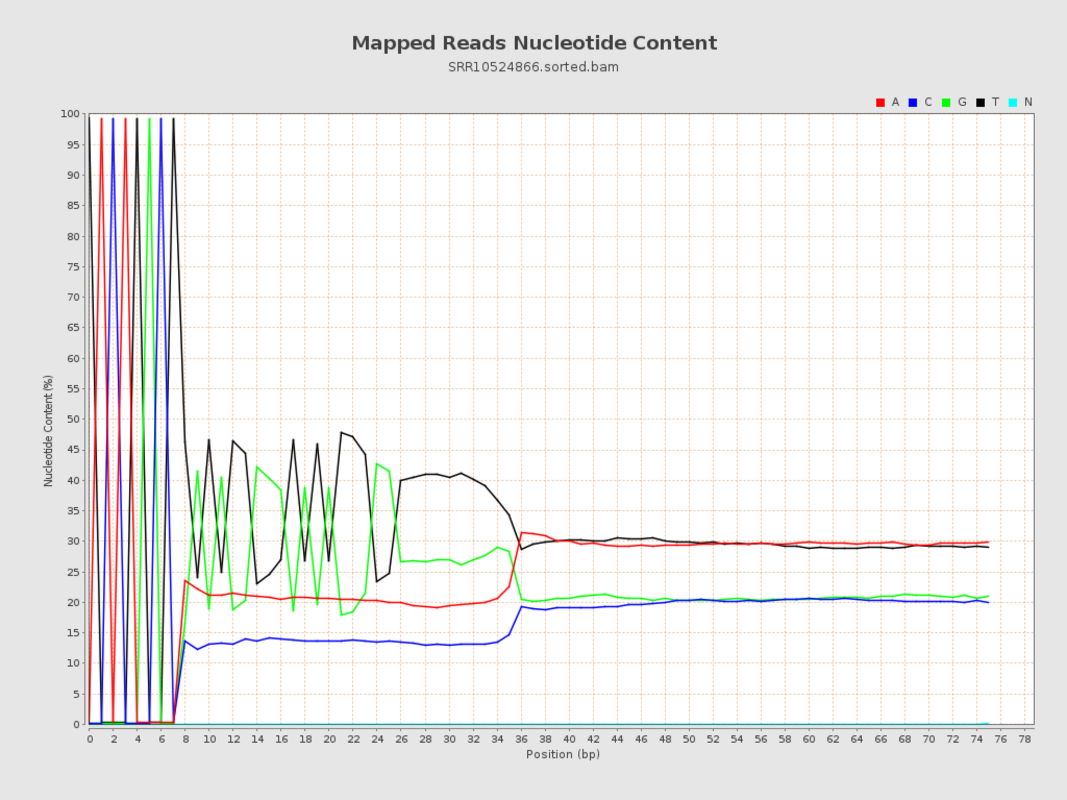
6. Results : Genome Fraction Coverage



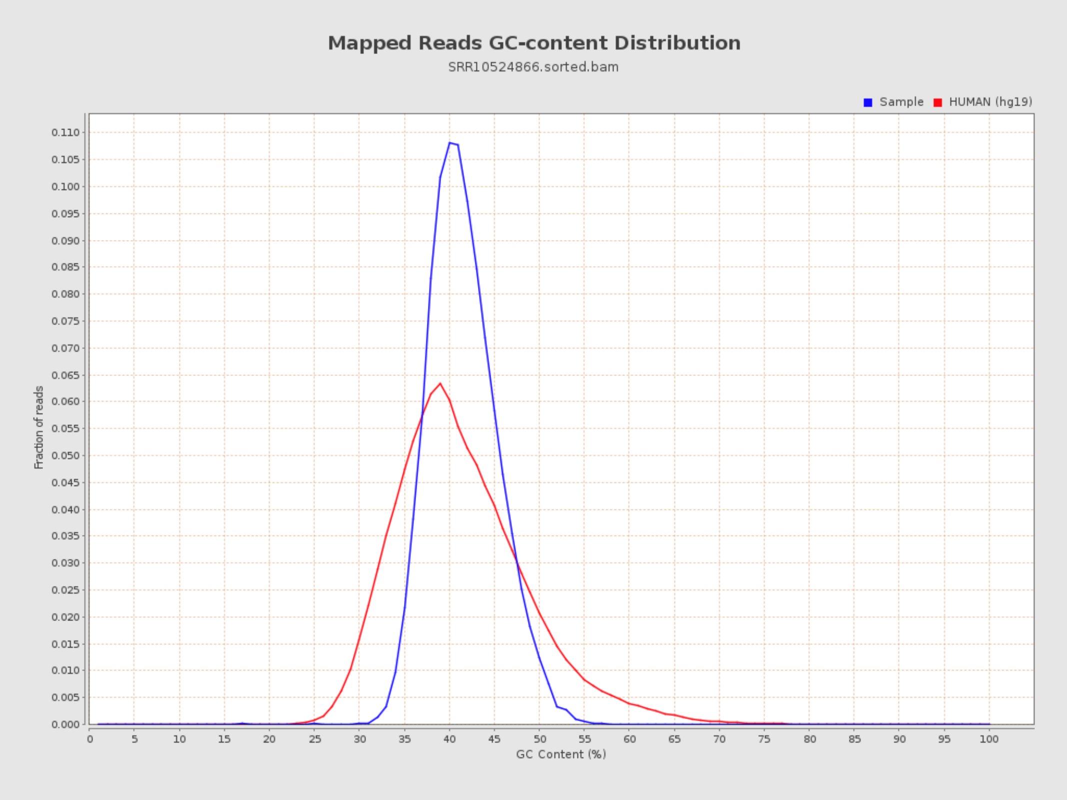
7. Results : Duplication Rate Histogram



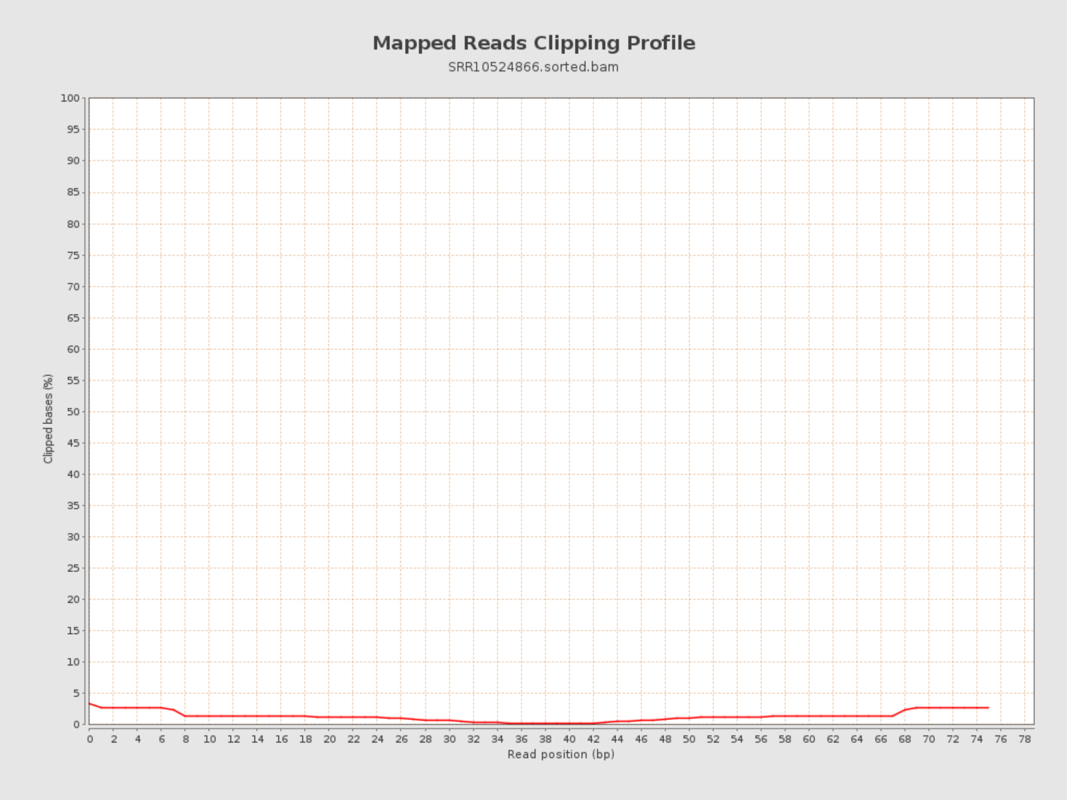
8. Results : Mapped Reads Nucleotide Content



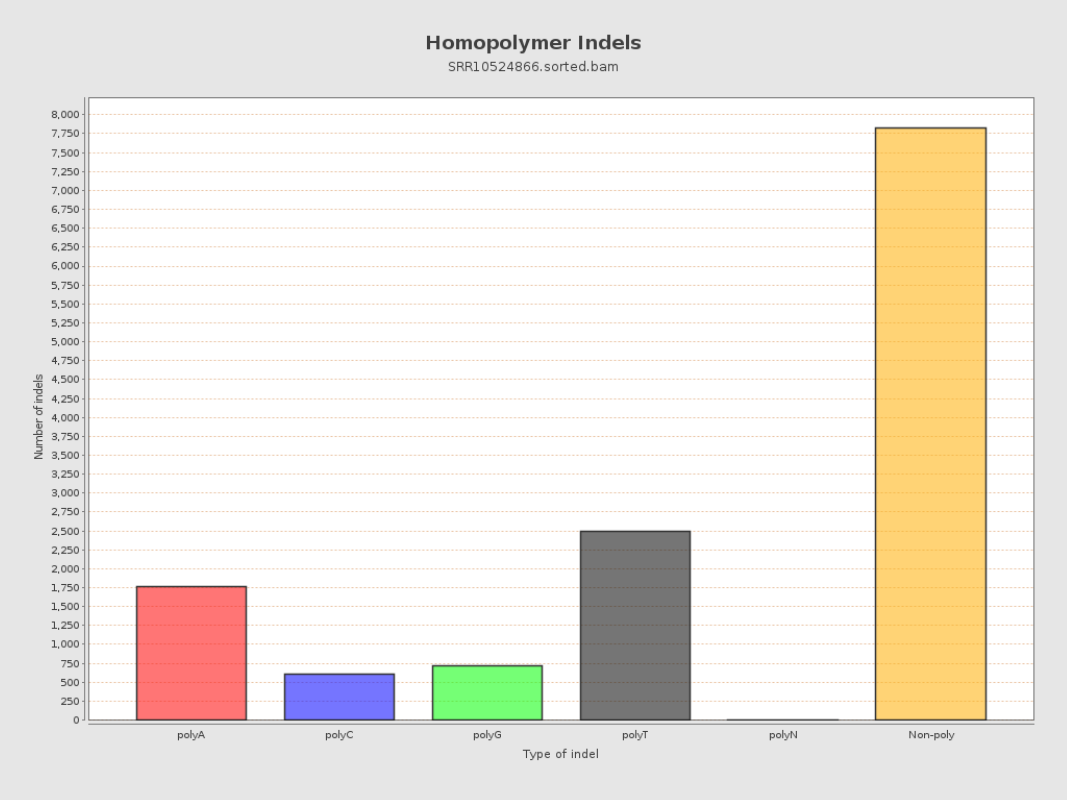
9. Results : Mapped Reads GC-content Distribution



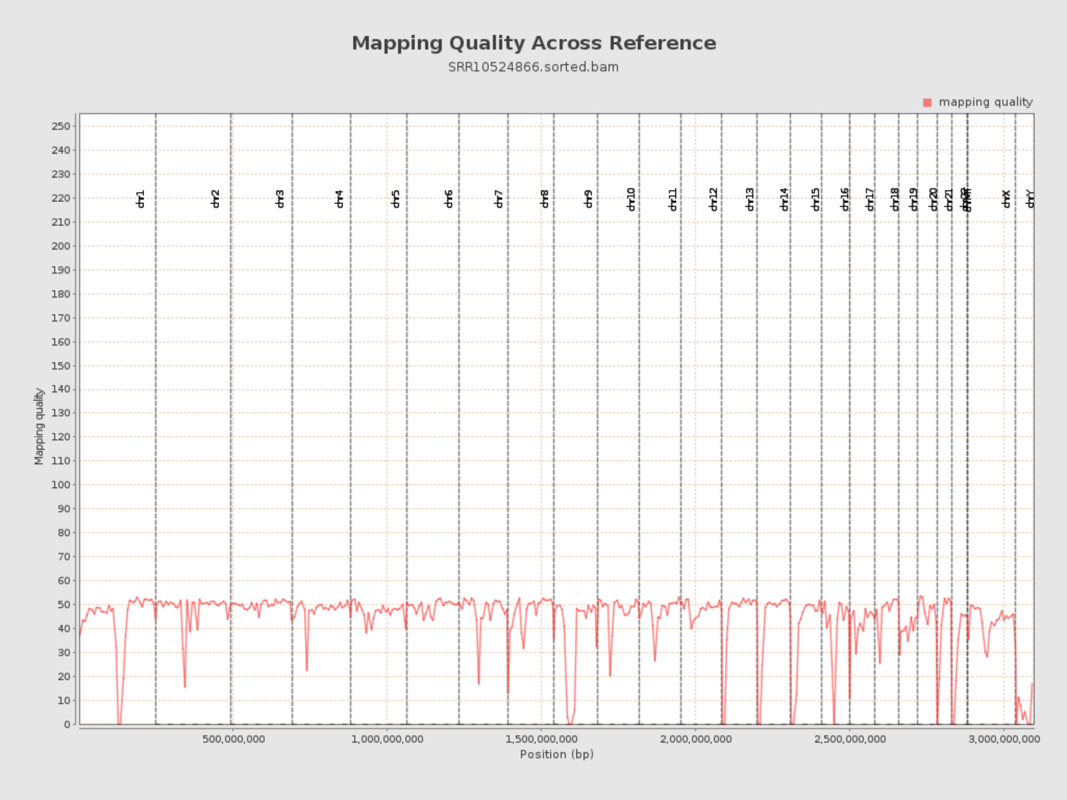
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram