Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:16:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524882.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_SRR10524882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524882.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:16:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,156,029
Mapped reads	1,065,184 / 92.14%
Unmapped reads	90,845 / 7.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,728 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	33,176 / 2.87%
Duplication rate	2.28%
Clipped reads	1,065,966 / 92.21%

2.2. ACGT Content

Number/percentage of A's	16,234,368 / 26.02%
Number/percentage of C's	12,033,450 / 19.28%
Number/percentage of T's	19,642,607 / 31.48%
Number/percentage of G's	14,485,108 / 23.21%
Number/percentage of N's	7,720 / 0.01%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.216

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

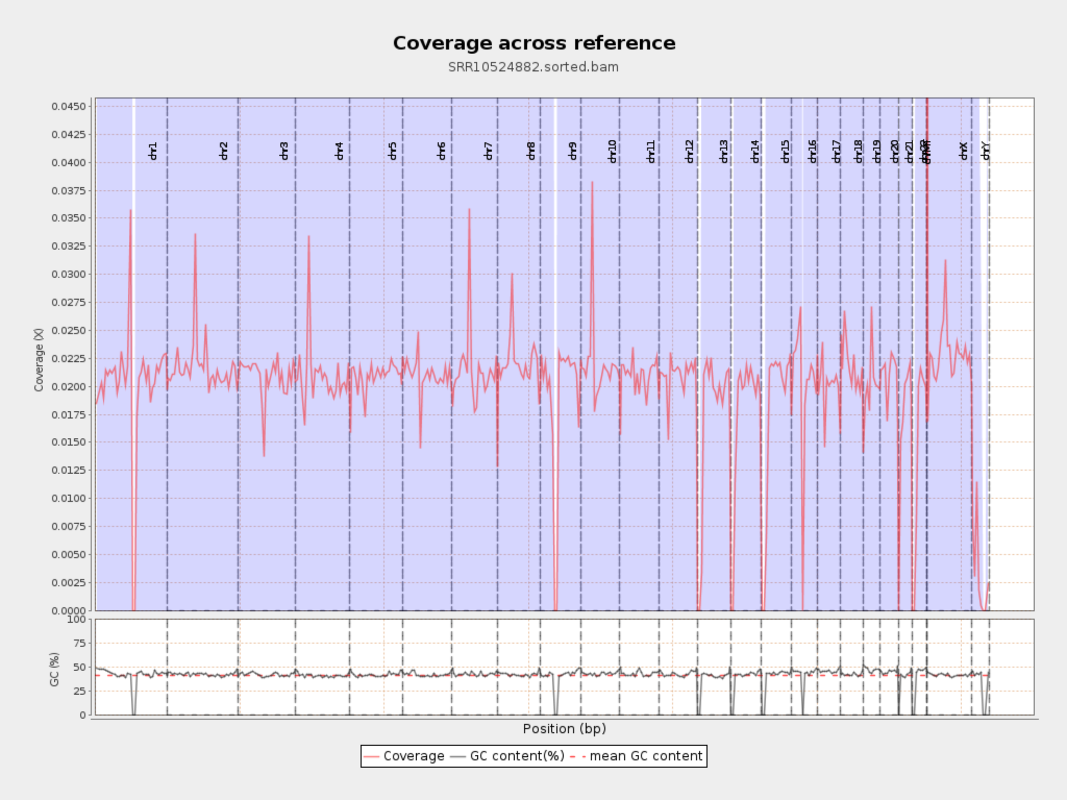
General error rate	0.51%
Mismatches	306,677
Insertions	4,733
Mapped reads with at least one insertion	0.44%
Deletions	11,665
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.33%

2.6. Chromosome stats

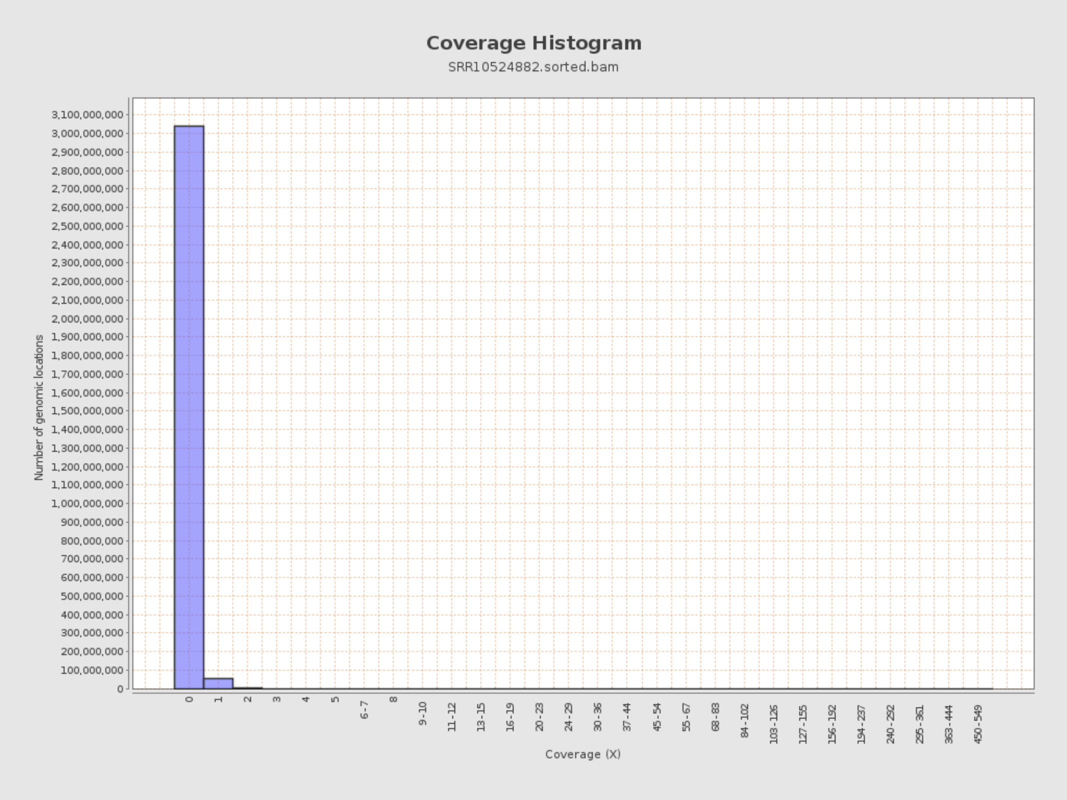
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4990873	0.02	0.408
chr2	243199373	5291999	0.0218	0.2282
chr3	198022430	4144927	0.0209	0.1531
chr4	191154276	4009479	0.021	0.1668
chr5	180915260	3800836	0.021	0.1541
chr6	171115067	3596767	0.021	0.1644
chr7	159138663	3430229	0.0216	0.2723

chr8	146364022	3253649	0.0222	0.207
chr9	141213431	2655407	0.0188	0.1957
chr10	135534747	2993340	0.0221	0.2046
chr11	135006516	2845977	0.0211	0.1974
chr12	133851895	2808348	0.021	0.1564
chr13	115169878	1967043	0.0171	0.1385
chr14	107349540	1841924	0.0172	0.1458
chr15	102531392	1789428	0.0175	0.1404
chr16	90354753	1795397	0.0199	0.158
chr17	81195210	1618394	0.0199	0.1581
chr18	78077248	1704788	0.0218	0.3476
chr19	59128983	1203273	0.0203	0.2705
chr20	63025520	1326046	0.021	0.1562
chr21	48129895	829857	0.0172	0.1505
chr22	51304566	734470	0.0143	0.1265
chrMT	16571	41361	2.496	2.0681
chrX	155270560	3558342	0.0229	0.1791
chrY	59373566	189750	0.0032	0.0921

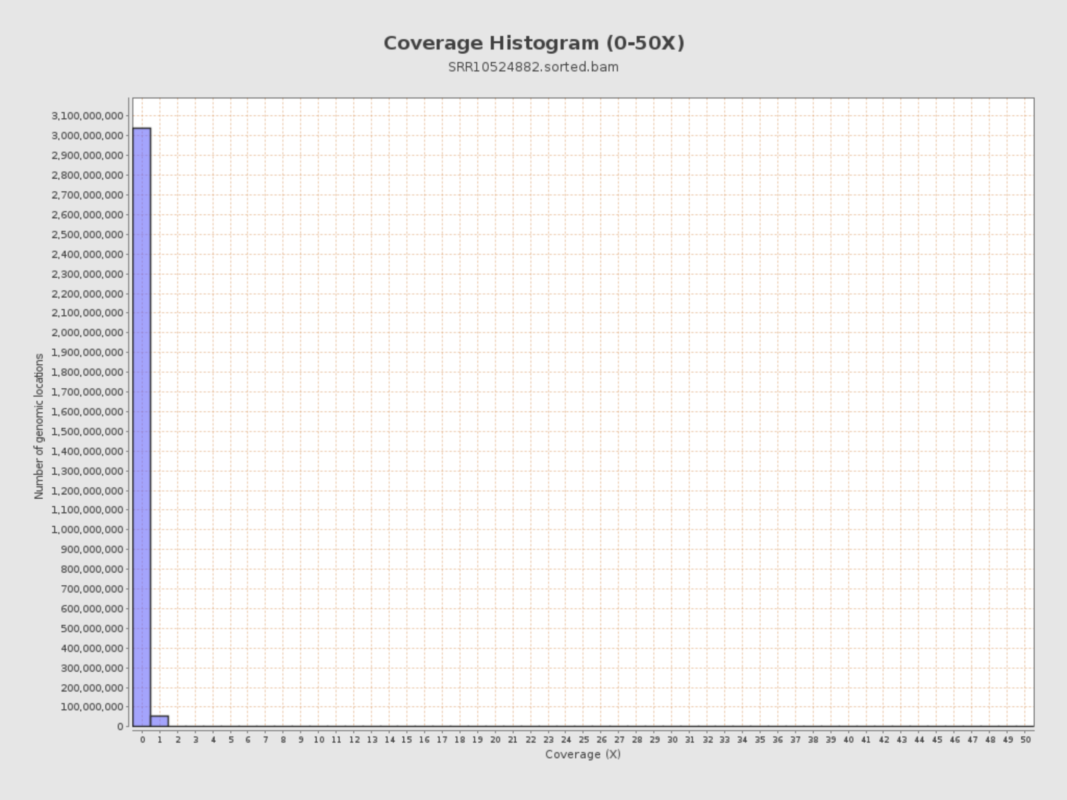
3. Results : Coverage across reference



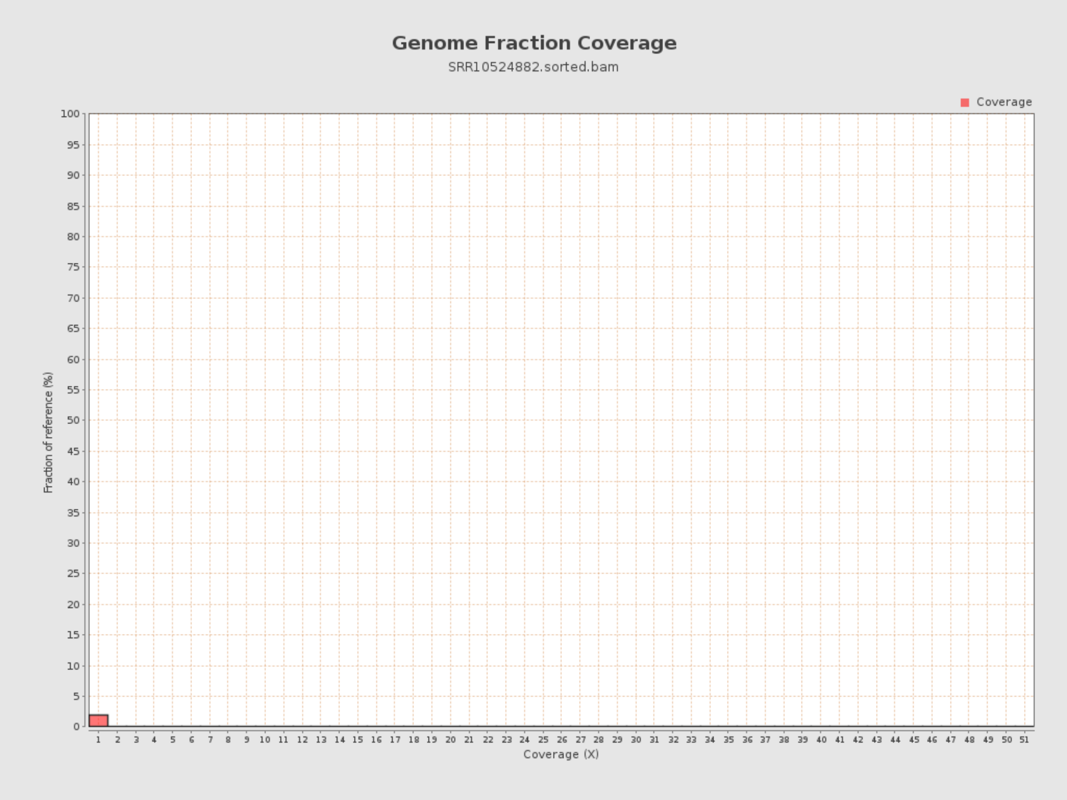
4. Results : Coverage Histogram



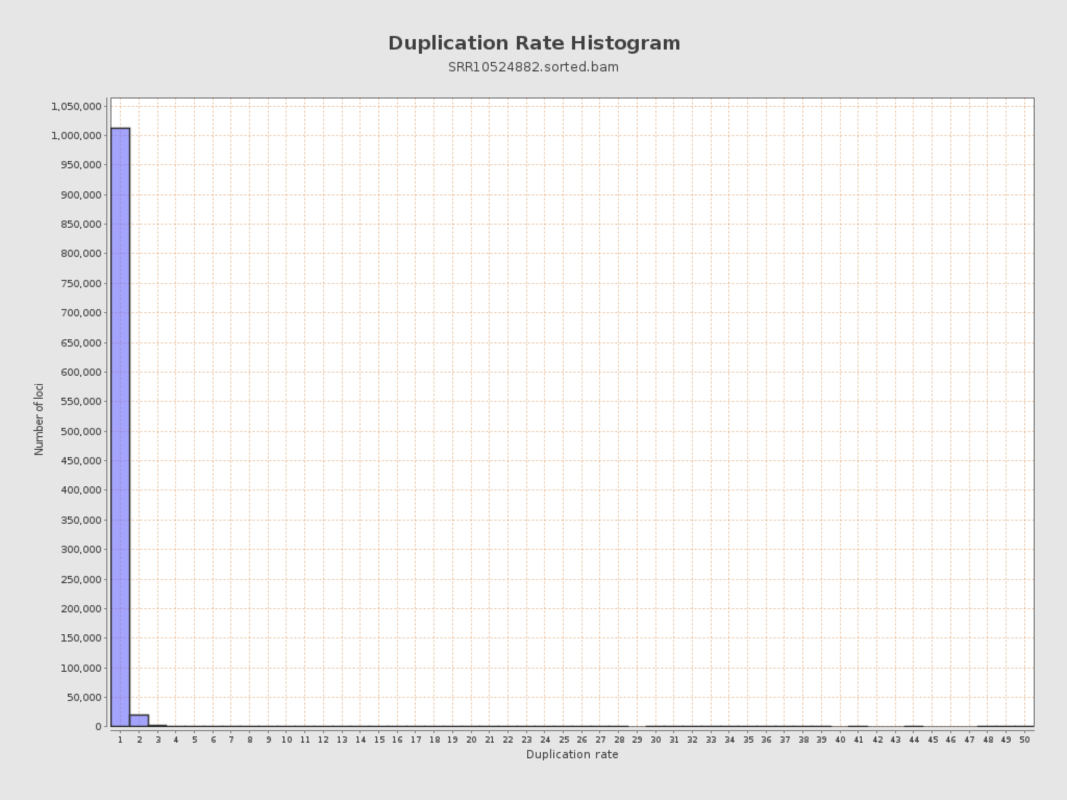
5. Results : Coverage Histogram (0-50X)



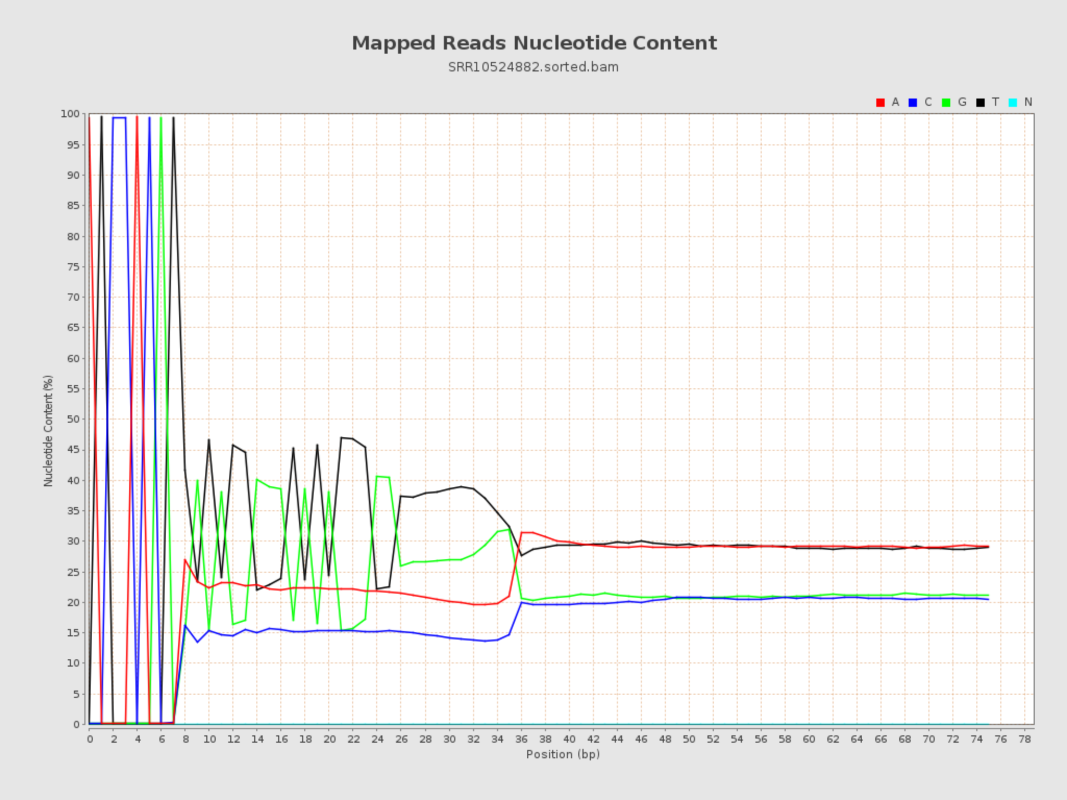
6. Results : Genome Fraction Coverage



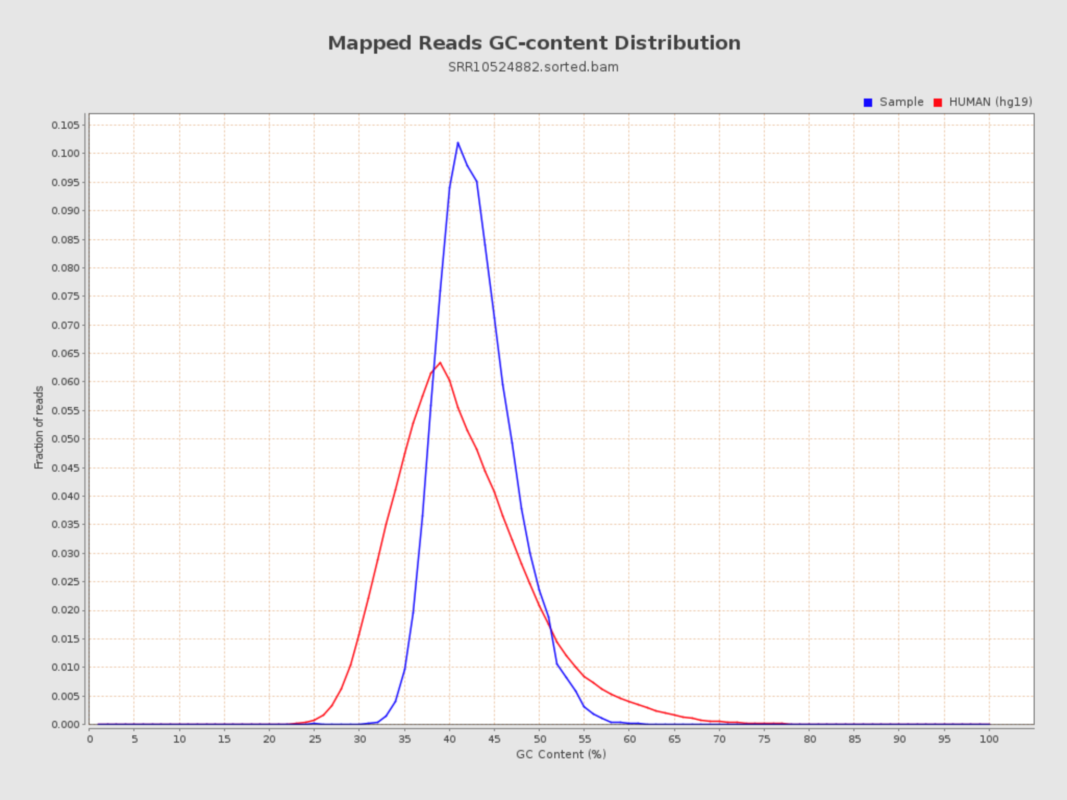
7. Results : Duplication Rate Histogram



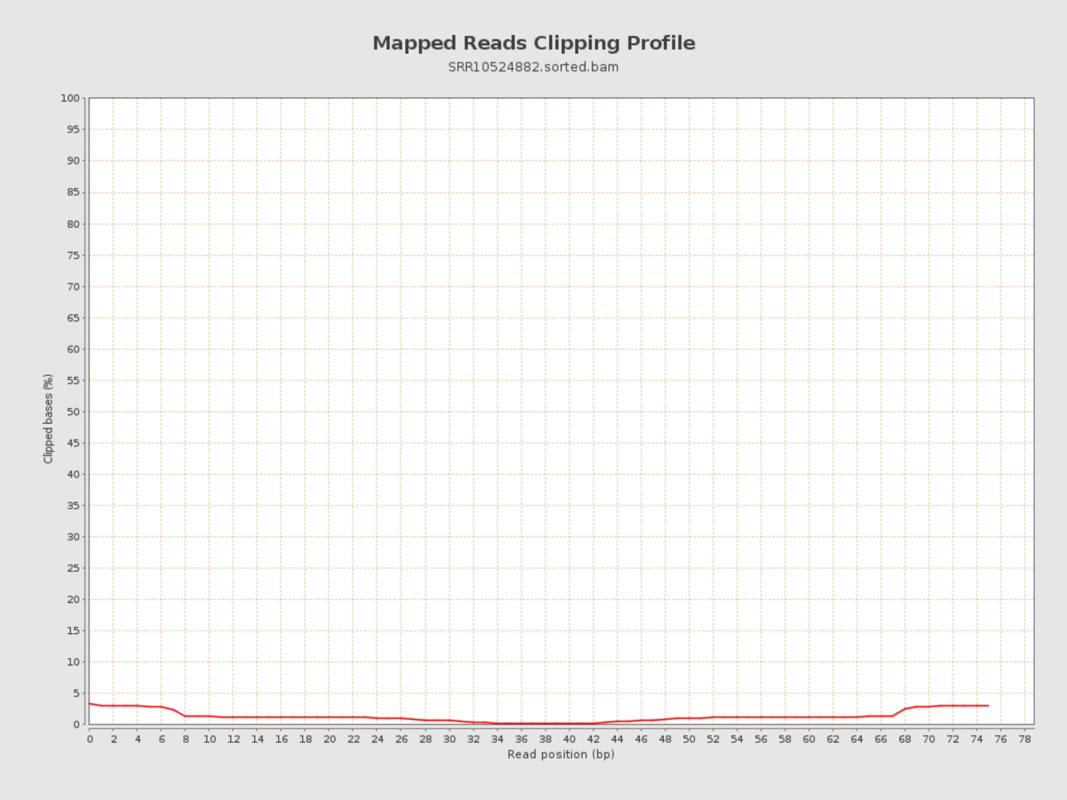
8. Results : Mapped Reads Nucleotide Content



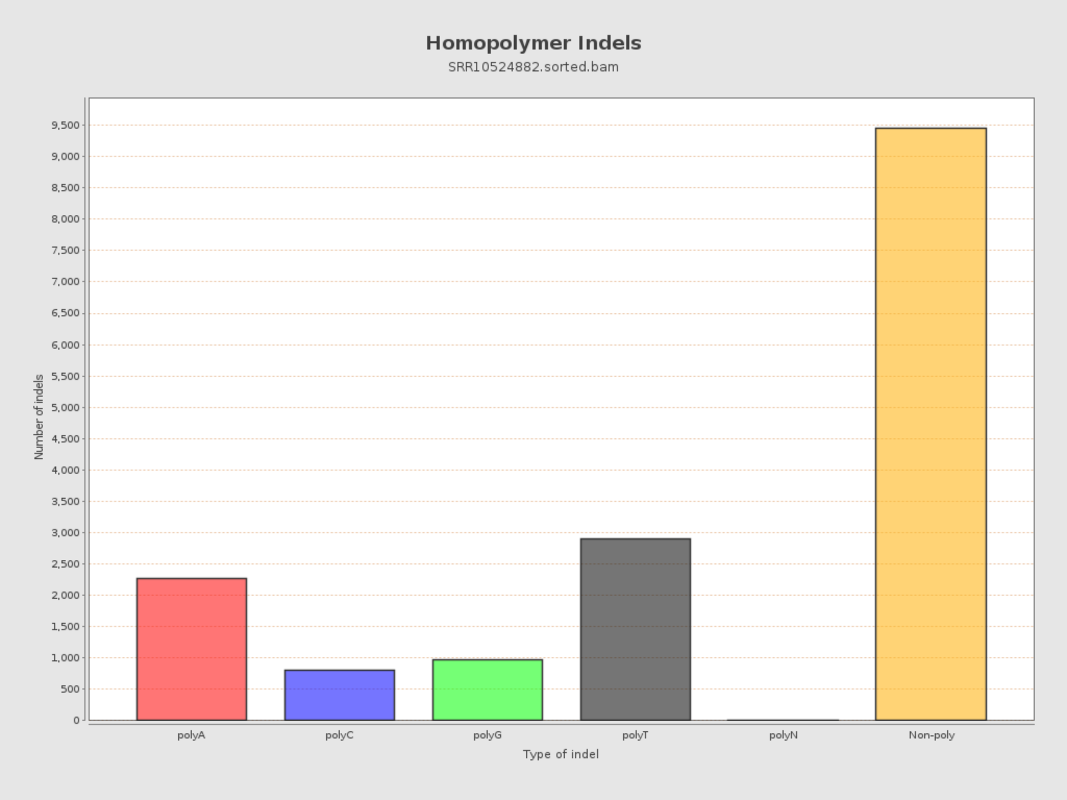
9. Results : Mapped Reads GC-content Distribution



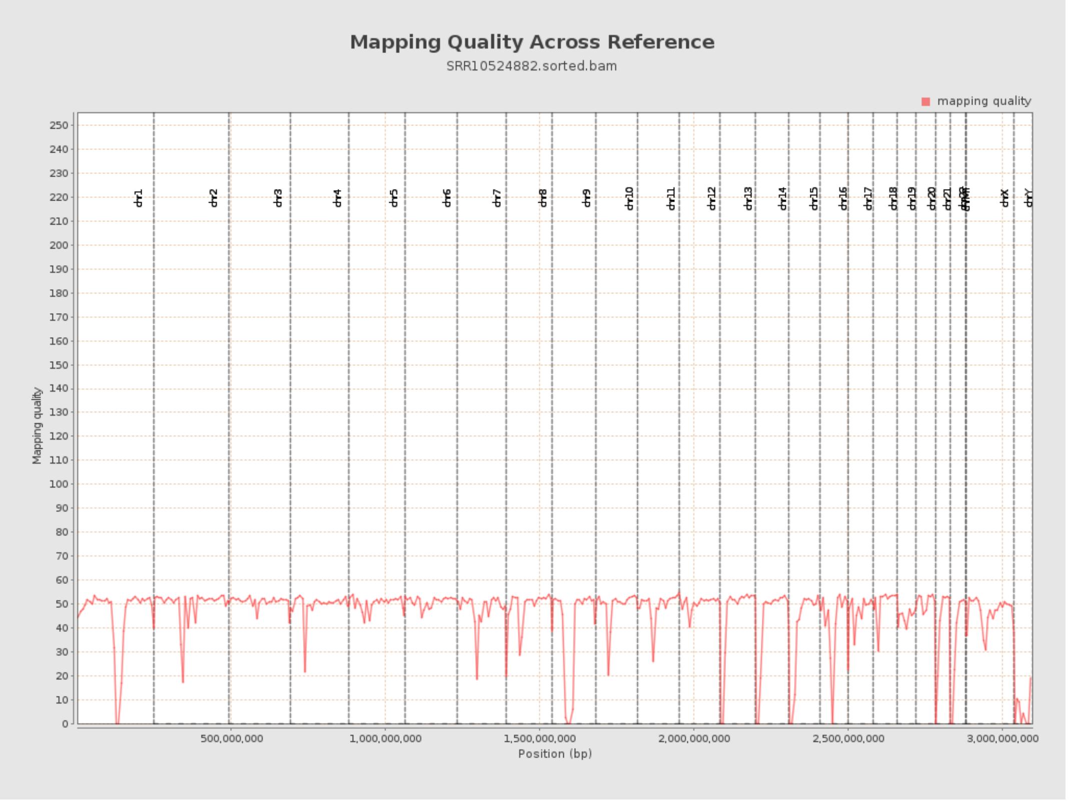
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram