Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:51:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524982.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_SRR10524982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:51:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,534,498
Mapped reads	1,405,520 / 91.59%
Unmapped reads	128,978 / 8.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,315 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	54,235 / 3.53%
Duplication rate	3%
Clipped reads	1,404,207 / 91.51%

2.2. ACGT Content

Number/percentage of A's	20,033,826 / 24.73%
Number/percentage of C's	15,423,008 / 19.04%
Number/percentage of T's	26,991,161 / 33.32%
Number/percentage of G's	18,556,133 / 22.91%
Number/percentage of N's	968 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.2338

2.4. Mapping Quality

Mean Mapping Quality	45.57

2.5. Mismatches and indels

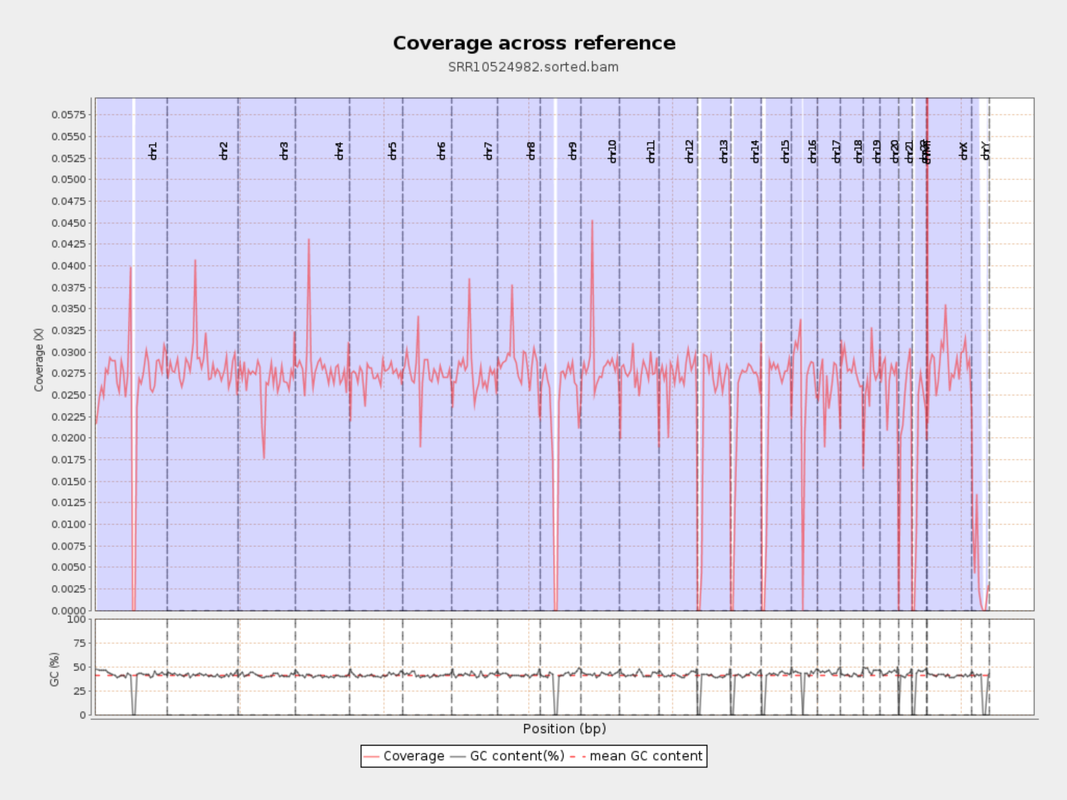
General error rate	0.51%
Mismatches	406,050
Insertions	5,160
Mapped reads with at least one insertion	0.37%
Deletions	15,783
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.11%

2.6. Chromosome stats

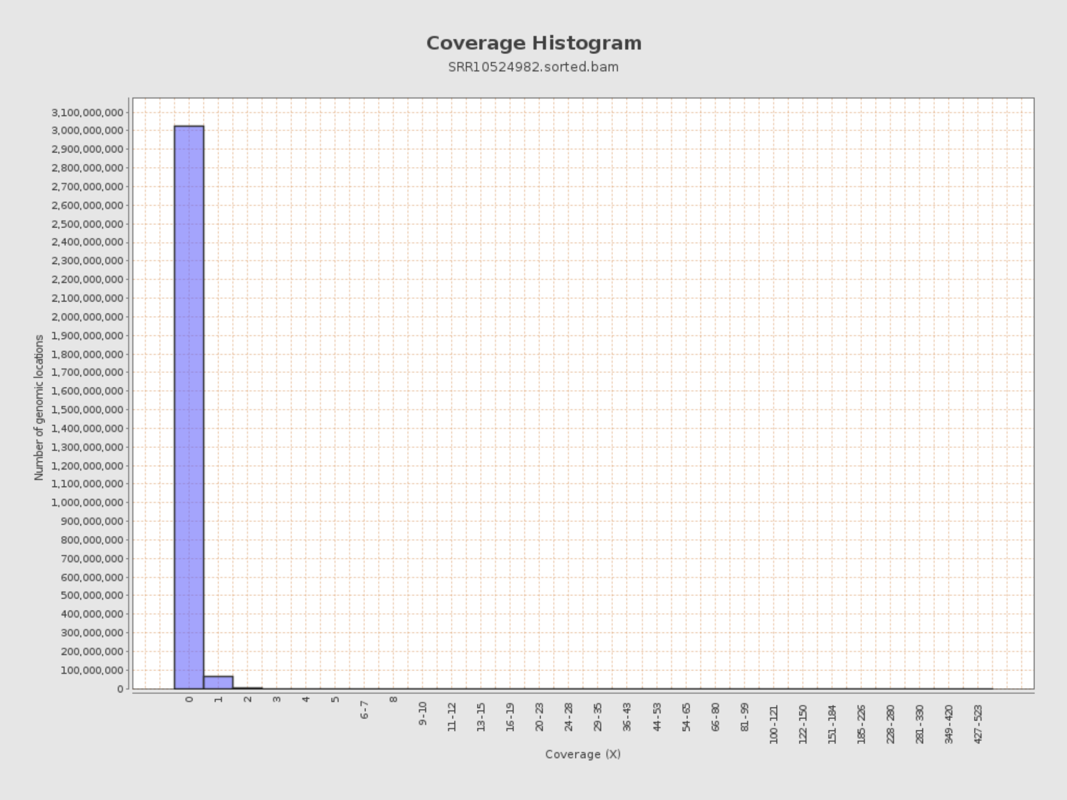
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6449413	0.0259	0.3889
chr2	243199373	6945094	0.0286	0.2728
chr3	198022430	5287389	0.0267	0.1791
chr4	191154276	5437689	0.0284	0.2045
chr5	180915260	4976534	0.0275	0.1823
chr6	171115067	4722040	0.0276	0.2025
chr7	159138663	4394420	0.0276	0.2659

chr8	146364022	4226188	0.0289	0.2652
chr9	141213431	3275348	0.0232	0.1998
chr10	135534747	3909974	0.0288	0.2446
chr11	135006516	3738322	0.0277	0.2284
chr12	133851895	3678363	0.0275	0.183
chr13	115169878	2651053	0.023	0.1676
chr14	107349540	2463827	0.023	0.1691
chr15	102531392	2318398	0.0226	0.1731
chr16	90354753	2315068	0.0256	0.1819
chr17	81195210	2094993	0.0258	0.1907
chr18	78077248	2194500	0.0281	0.3105
chr19	59128983	1588050	0.0269	0.2871
chr20	63025520	1683686	0.0267	0.1822
chr21	48129895	1088455	0.0226	0.1786
chr22	51304566	898552	0.0175	0.1438
chrMT	16571	6045	0.3648	0.6677
chrX	155270560	4449295	0.0287	0.1993
chrY	59373566	239249	0.004	0.1061

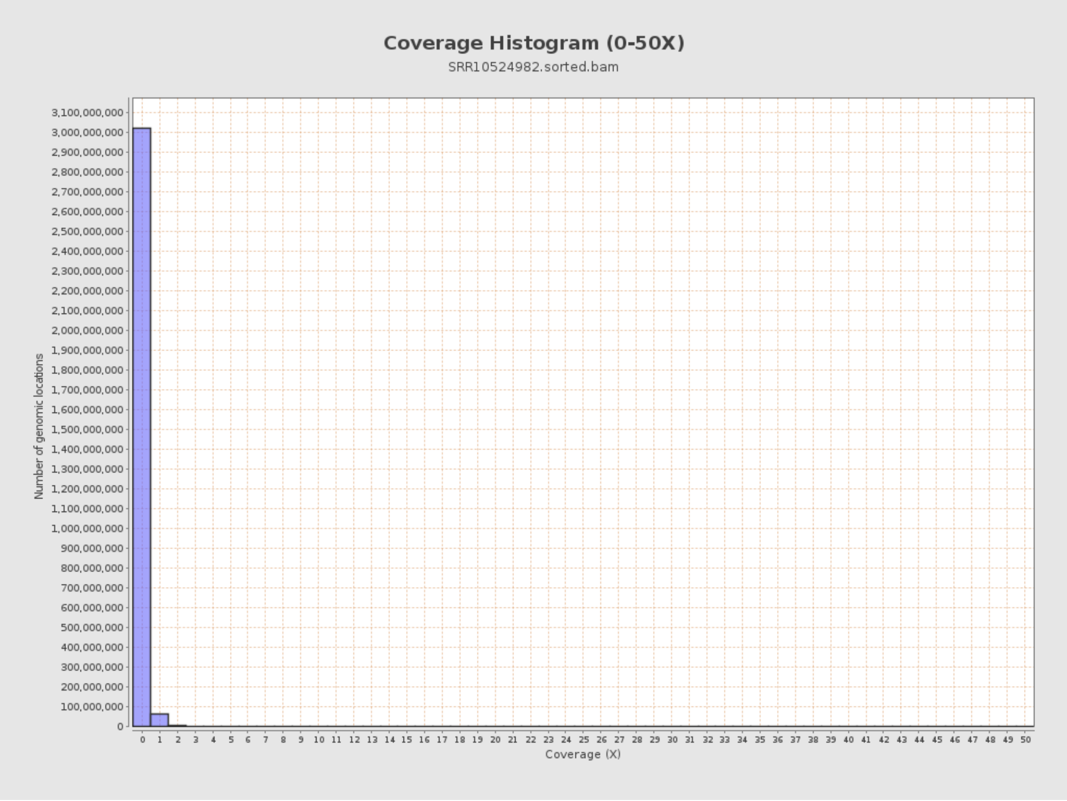
3. Results : Coverage across reference



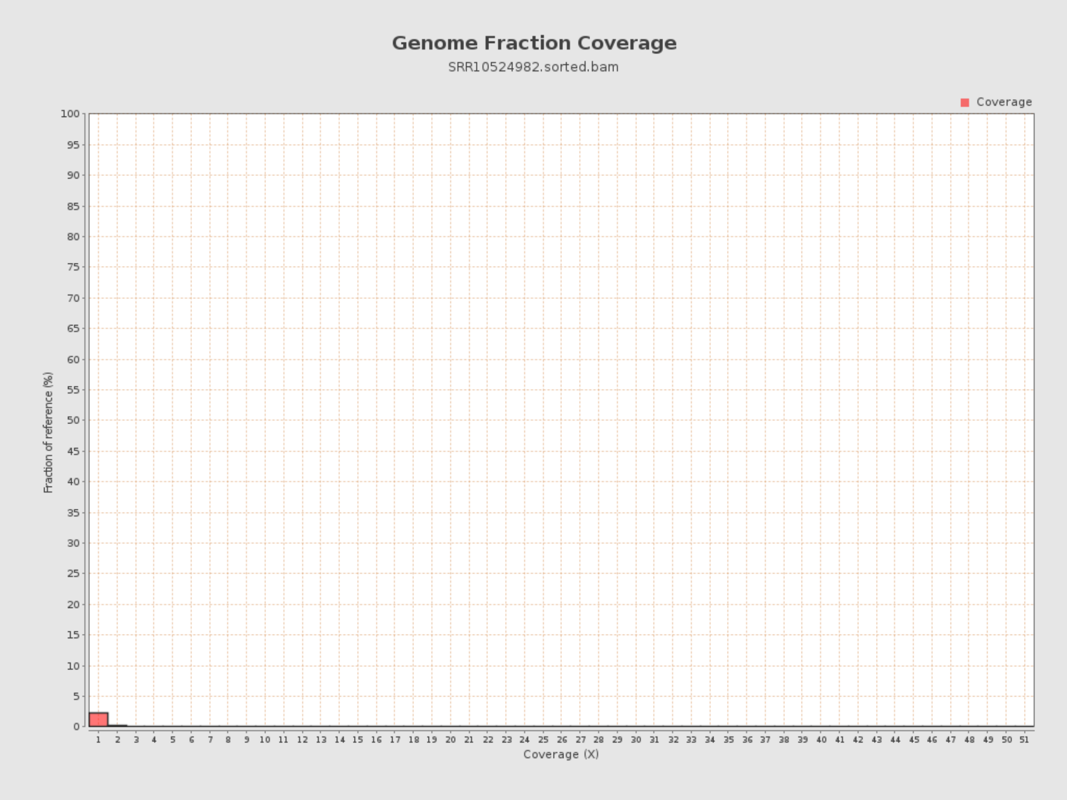
4. Results : Coverage Histogram



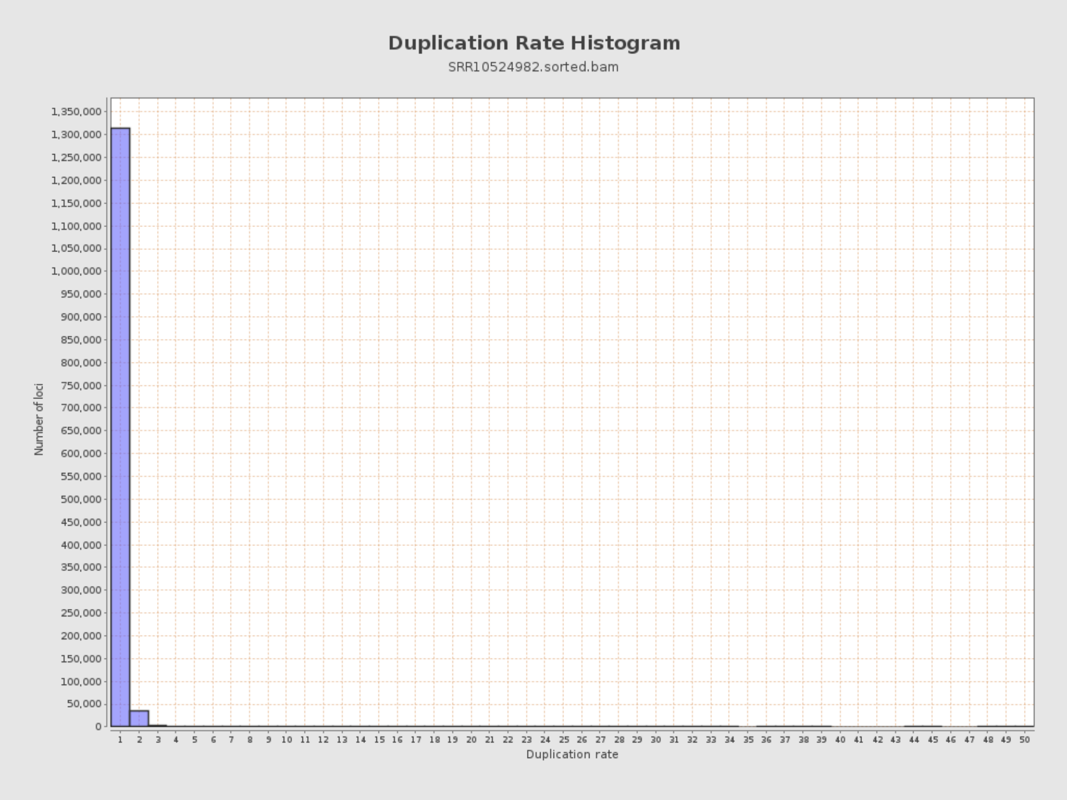
5. Results : Coverage Histogram (0-50X)



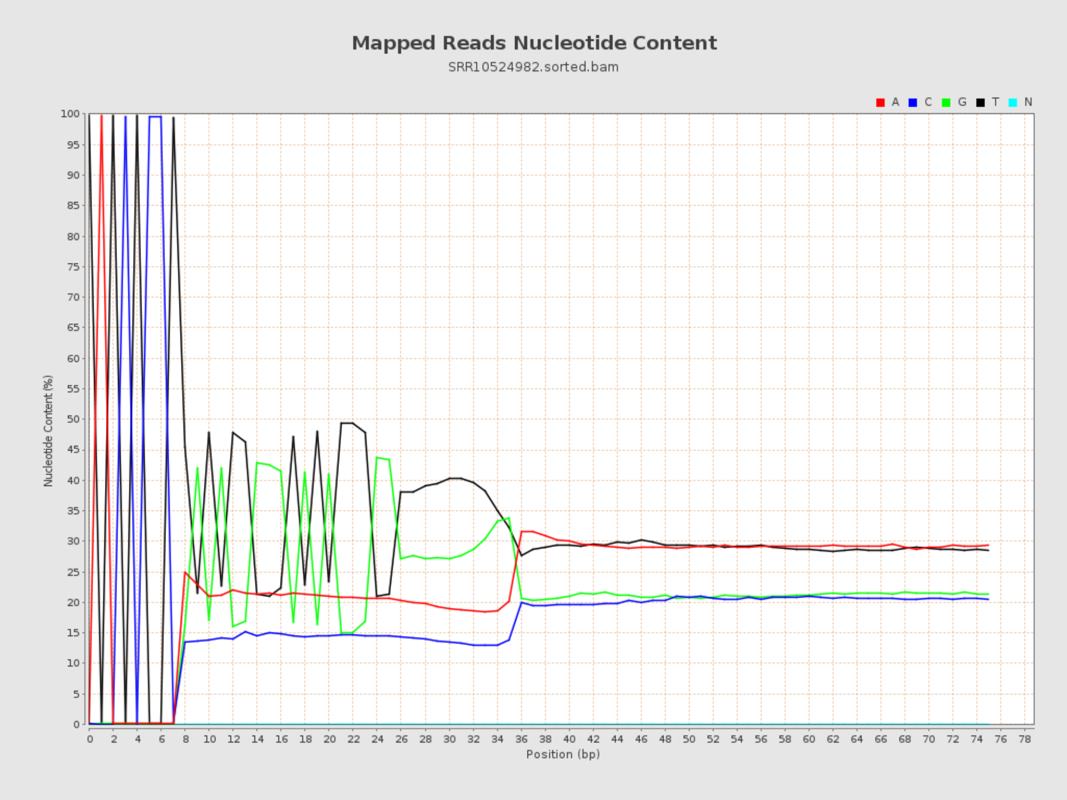
6. Results : Genome Fraction Coverage



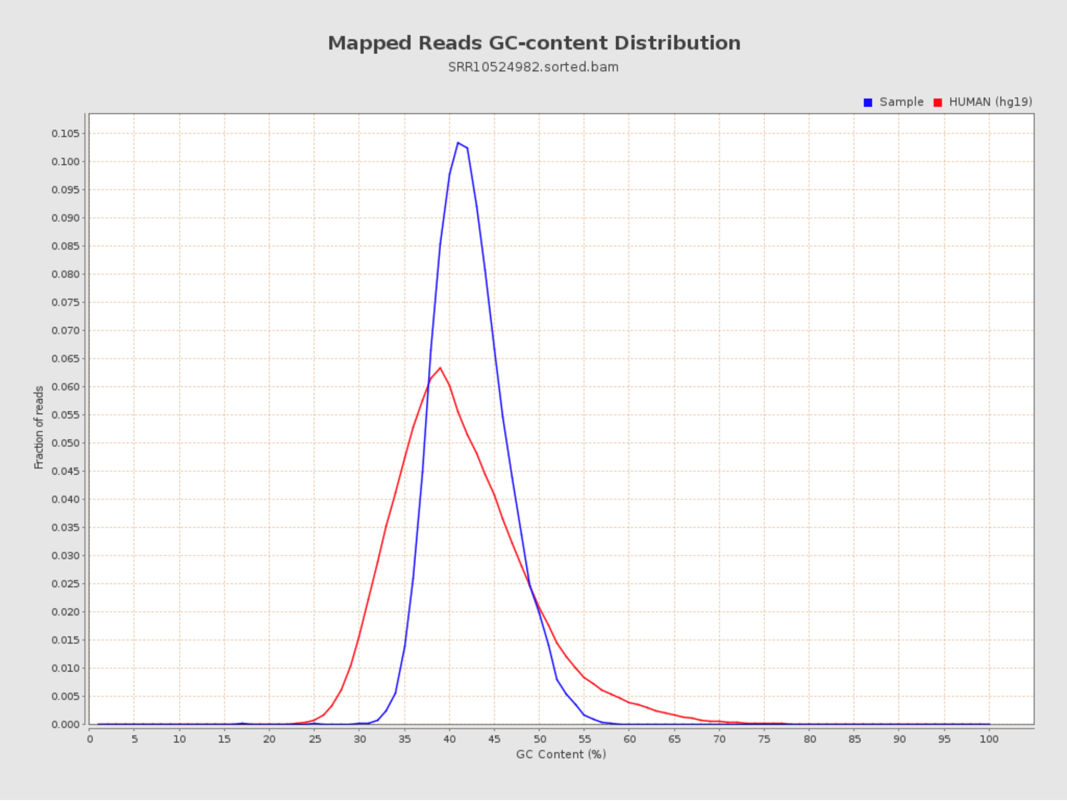
7. Results : Duplication Rate Histogram



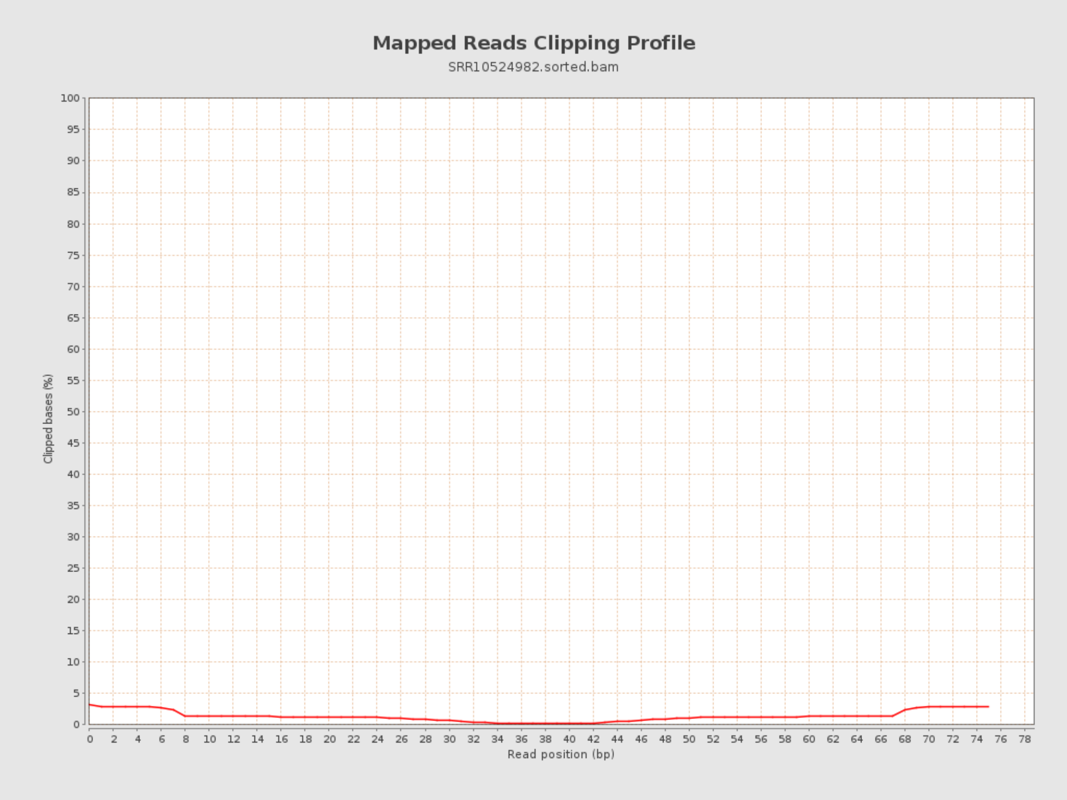
8. Results : Mapped Reads Nucleotide Content



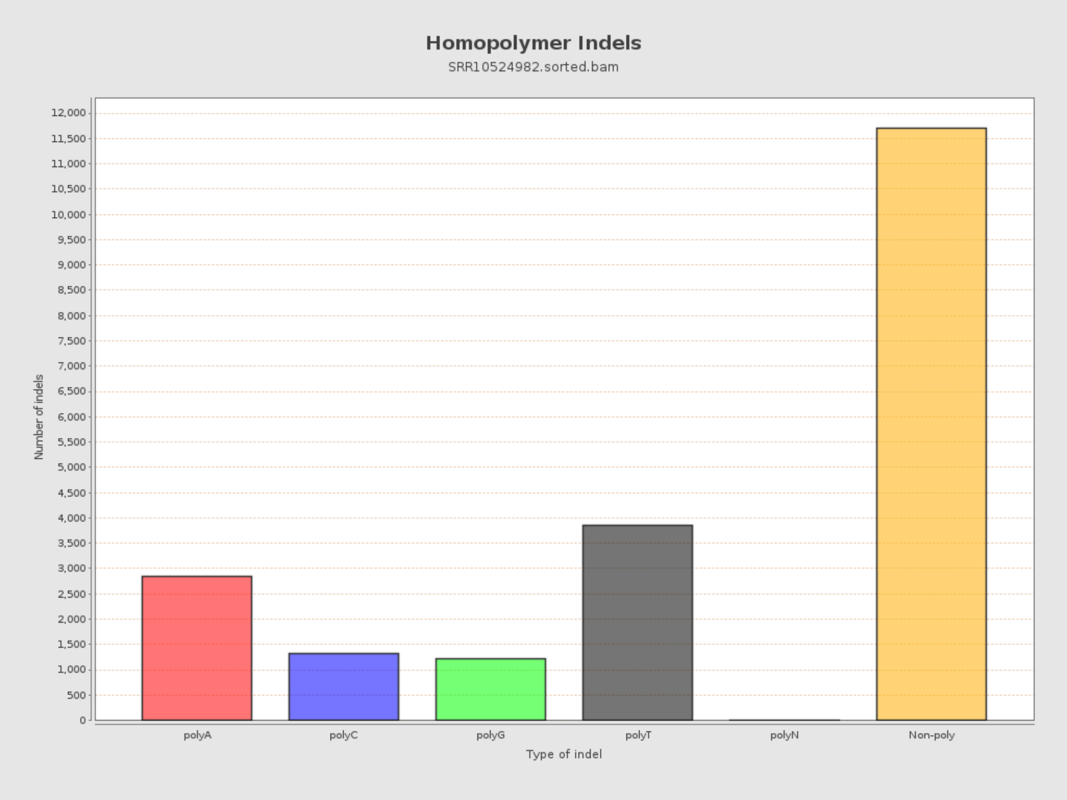
9. Results : Mapped Reads GC-content Distribution



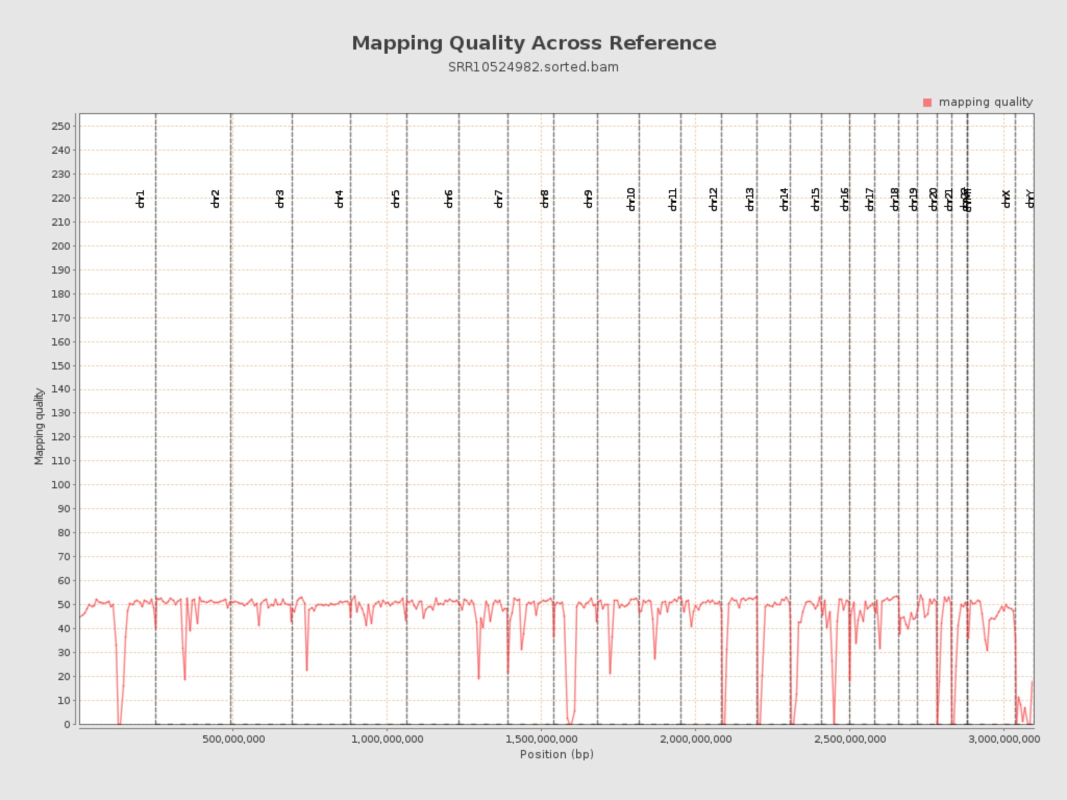
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram