Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:06:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524800.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_SRR10524800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:06:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,580,332
Mapped reads	1,437,059 / 90.93%
Unmapped reads	143,273 / 9.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,534 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	49,138 / 3.11%
Duplication rate	2.43%
Clipped reads	1,436,729 / 90.91%

2.2. ACGT Content

Number/percentage of A's	19,606,535 / 23.91%
Number/percentage of C's	15,173,185 / 18.5%
Number/percentage of T's	27,921,885 / 34.05%
Number/percentage of G's	19,298,424 / 23.53%
Number/percentage of N's	1,763 / 0%
GC Percentage	42.04%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.271

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

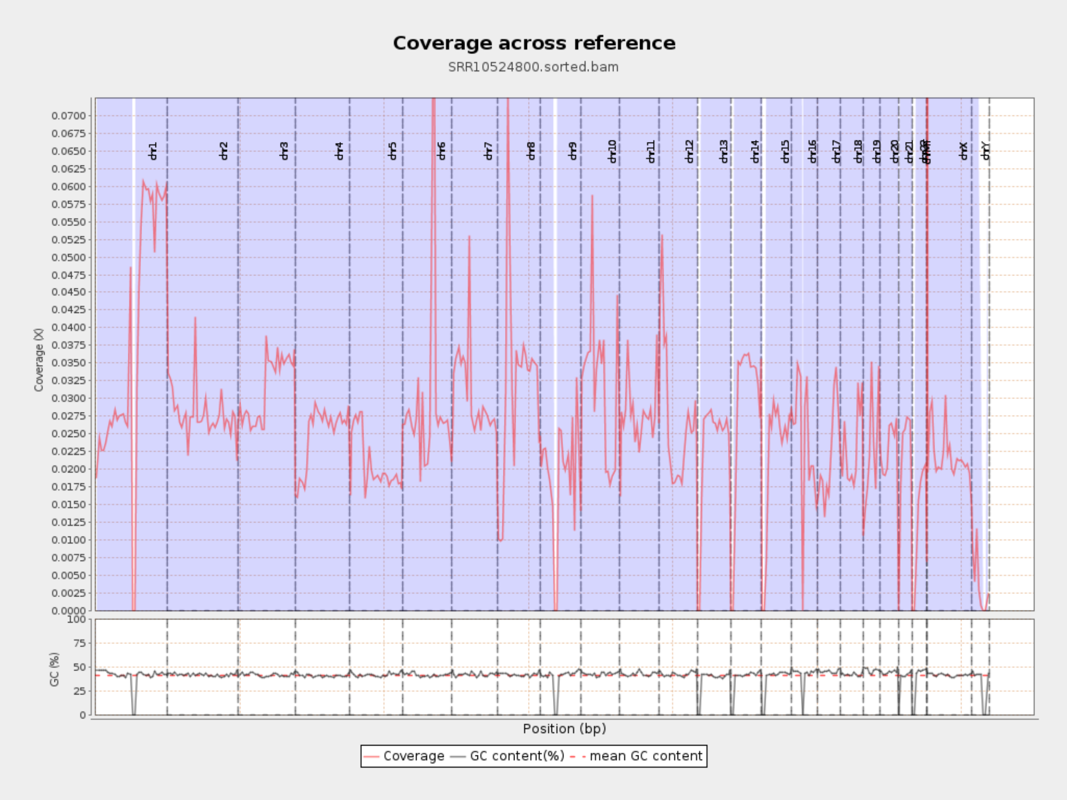
General error rate	0.52%
Mismatches	420,106
Insertions	6,006
Mapped reads with at least one insertion	0.42%
Deletions	16,854
Mapped reads with at least one deletion	1.17%
Homopolymer indels	43.67%

2.6. Chromosome stats

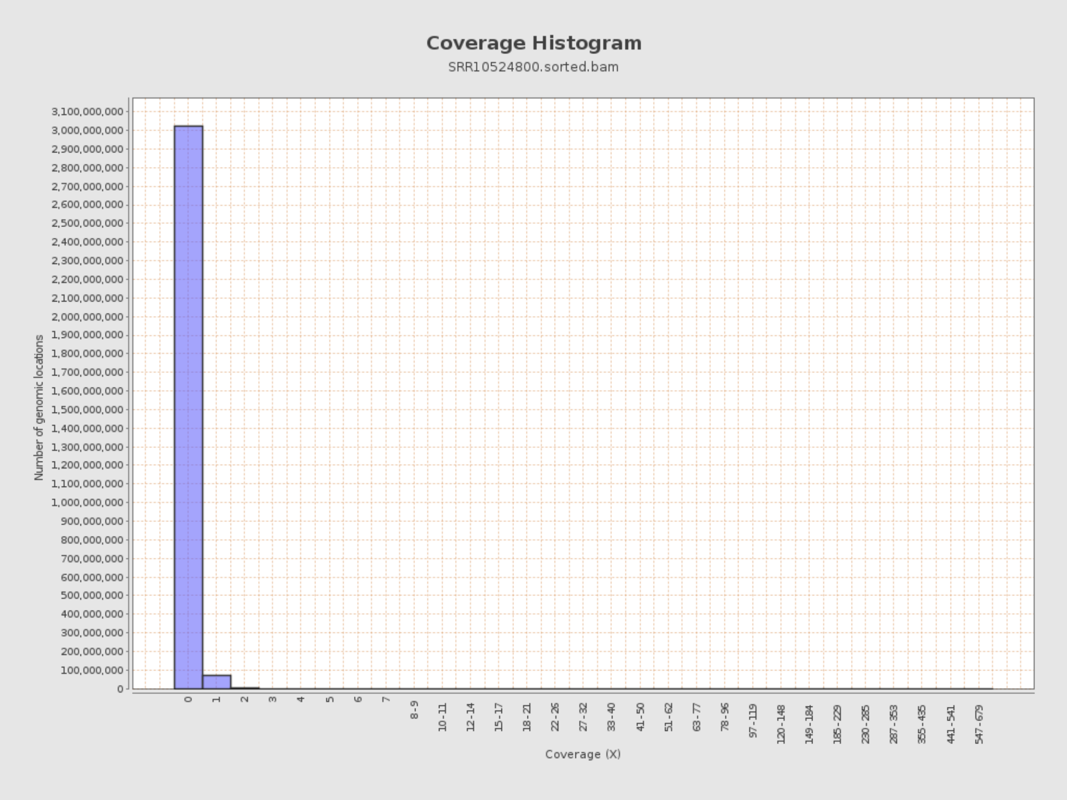
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9408024	0.0377	0.4999
chr2	243199373	6769655	0.0278	0.3365
chr3	198022430	6207314	0.0313	0.193
chr4	191154276	4781414	0.025	0.1761
chr5	180915260	3784252	0.0209	0.1562
chr6	171115067	5185408	0.0303	0.2127
chr7	159138663	4896707	0.0308	0.4265

chr8	146364022	4733824	0.0323	0.2766
chr9	141213431	2712234	0.0192	0.2023
chr10	135534747	4356704	0.0321	0.3106
chr11	135006516	3754600	0.0278	0.219
chr12	133851895	3650372	0.0273	0.1812
chr13	115169878	2639826	0.0229	0.1657
chr14	107349540	3053816	0.0284	0.1854
chr15	102531392	2201484	0.0215	0.1623
chr16	90354753	2133268	0.0236	0.1858
chr17	81195210	1796299	0.0221	0.1643
chr18	78077248	1771738	0.0227	0.3605
chr19	59128983	1350073	0.0228	0.3501
chr20	63025520	1431582	0.0227	0.1645
chr21	48129895	1047331	0.0218	0.1645
chr22	51304566	644884	0.0126	0.12
chrMT	16571	78961	4.765	3.2688
chrX	155270560	3423917	0.0221	0.1799
chrY	59373566	214406	0.0036	0.0972

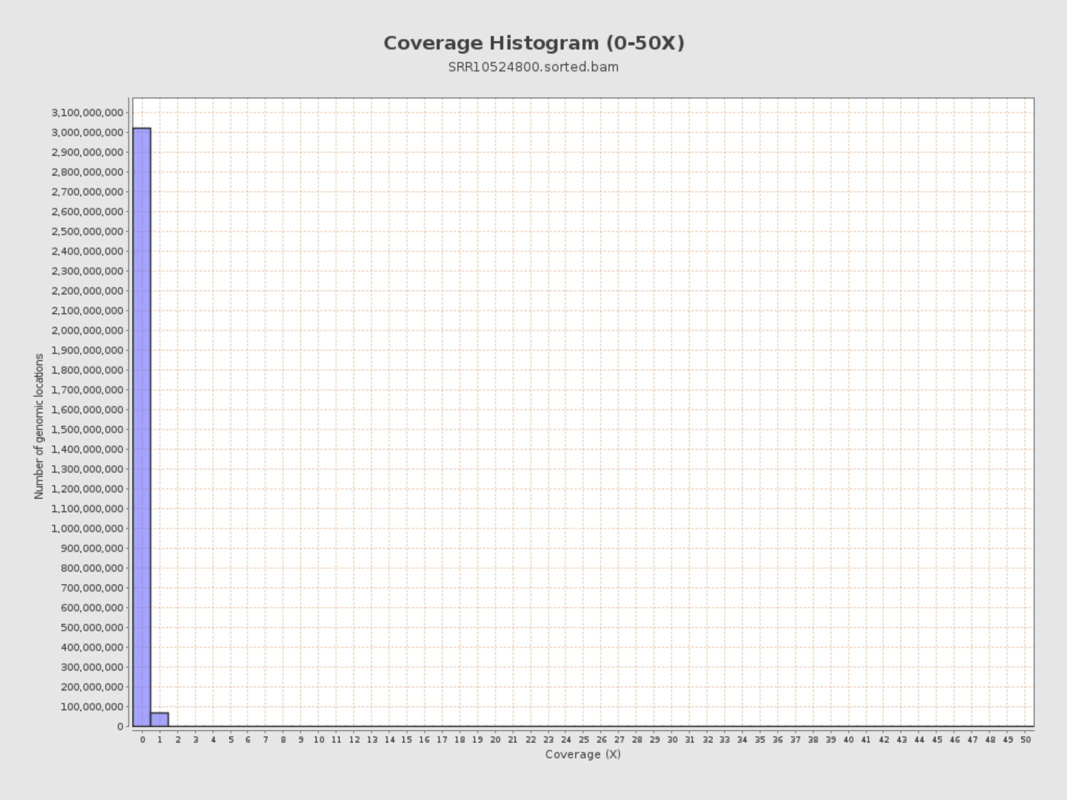
3. Results : Coverage across reference



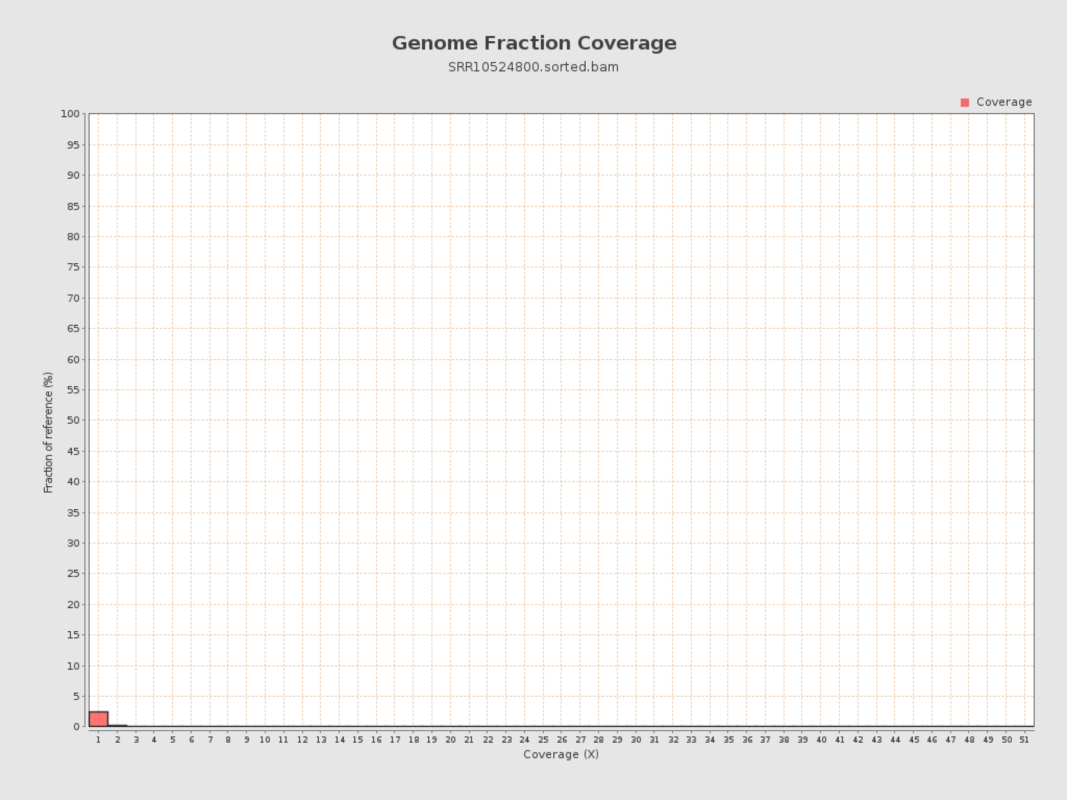
4. Results : Coverage Histogram



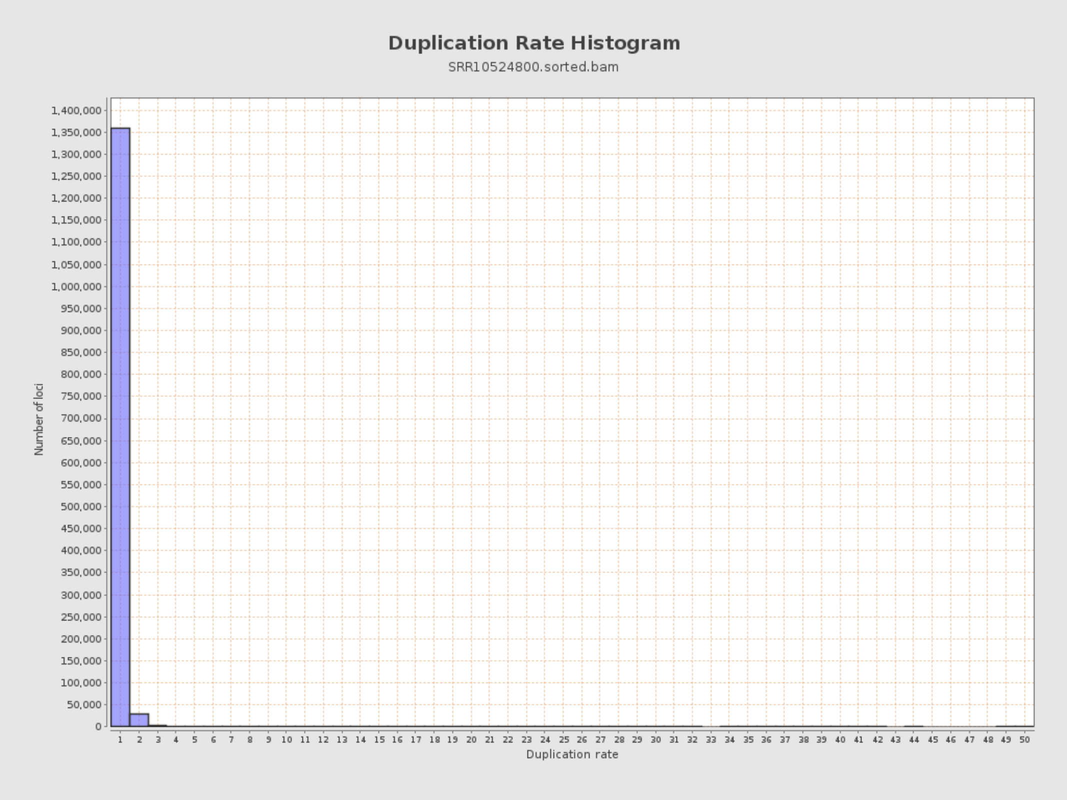
5. Results : Coverage Histogram (0-50X)



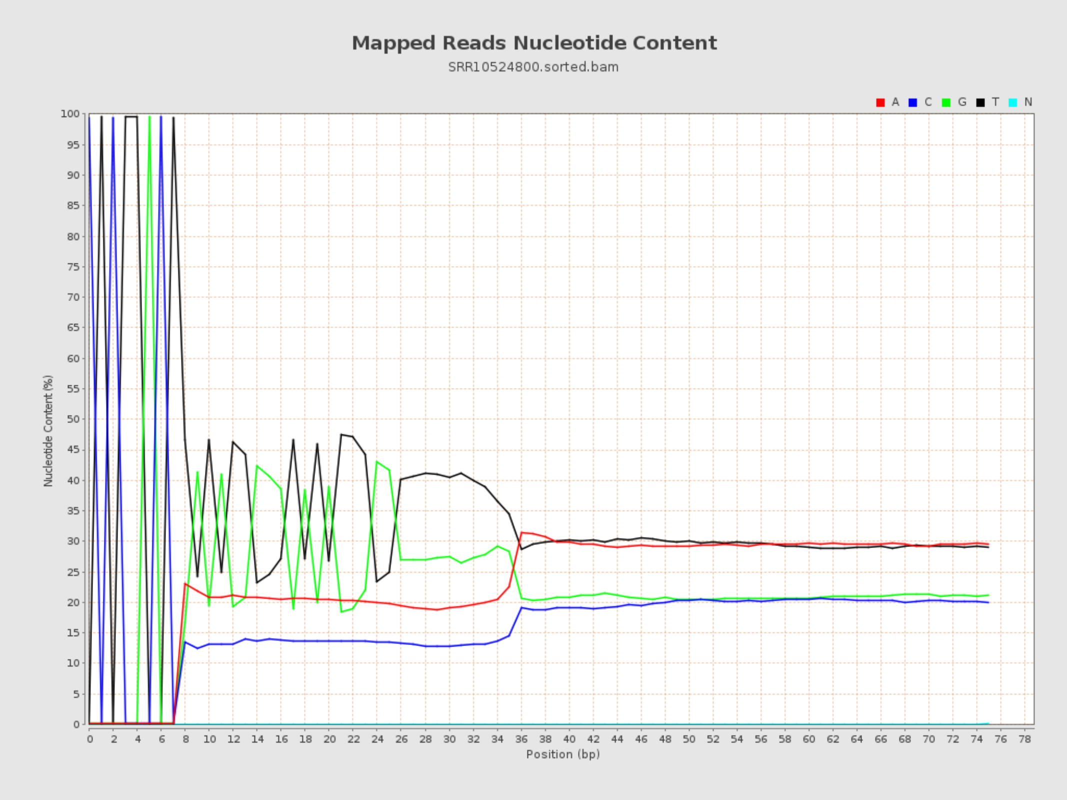
6. Results : Genome Fraction Coverage



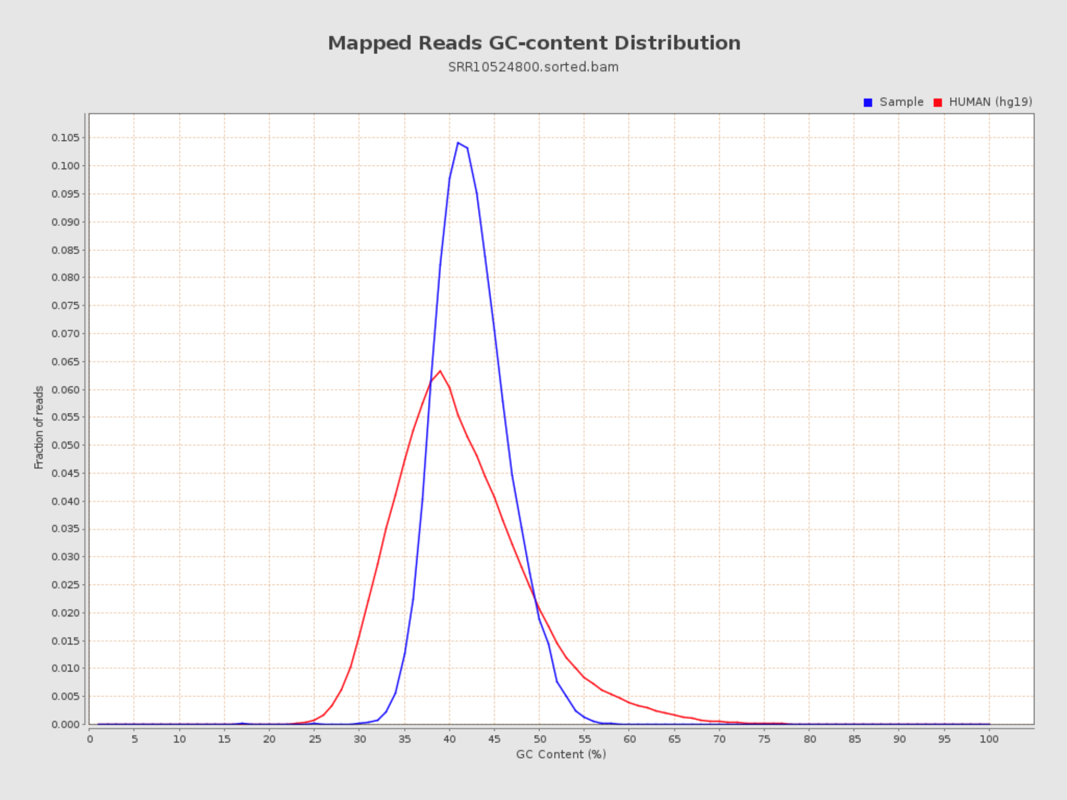
7. Results : Duplication Rate Histogram



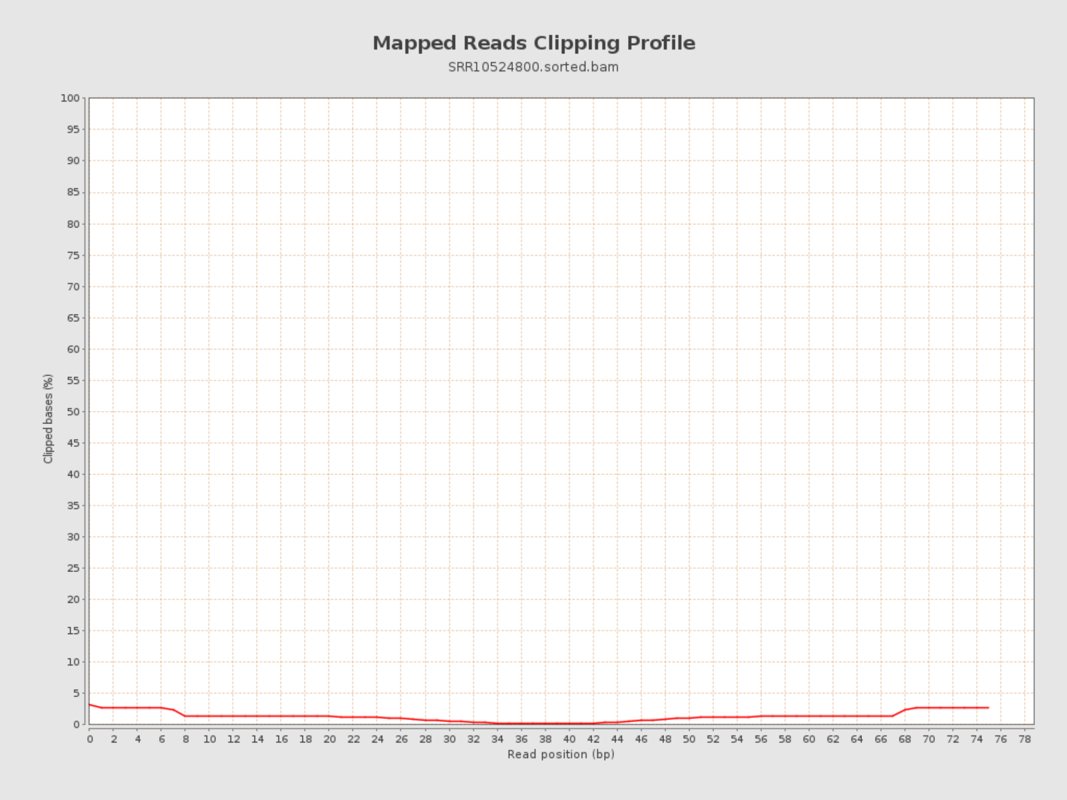
8. Results : Mapped Reads Nucleotide Content



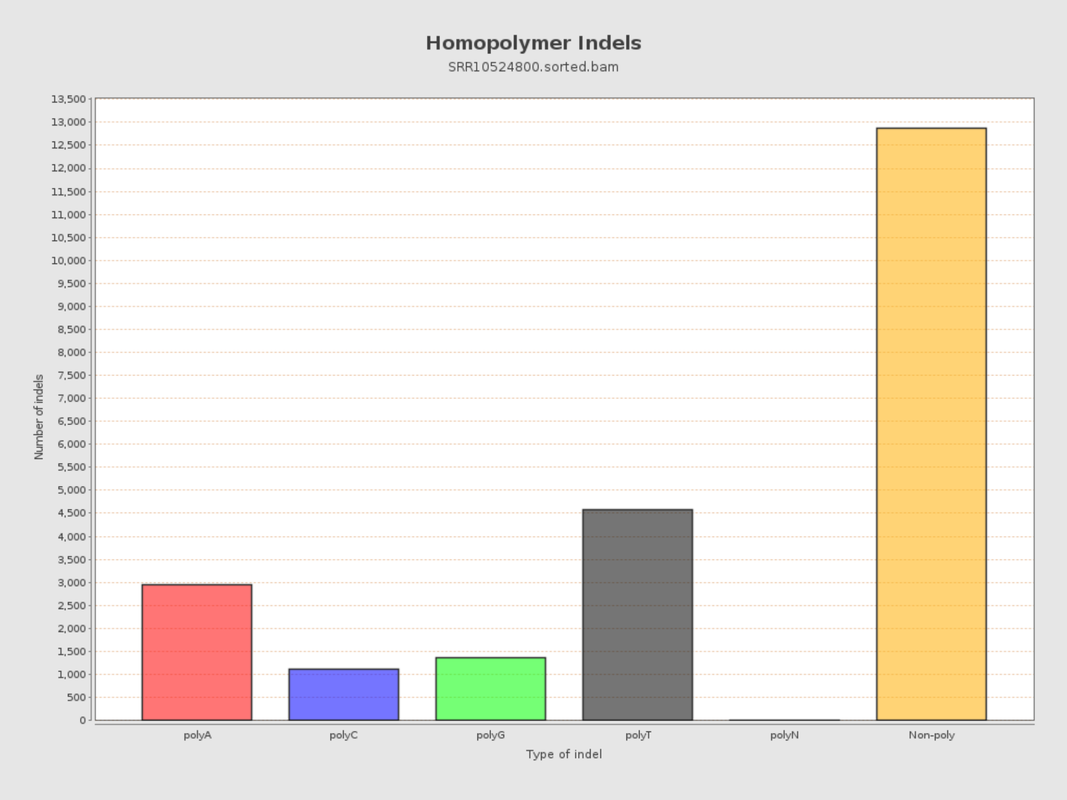
9. Results : Mapped Reads GC-content Distribution



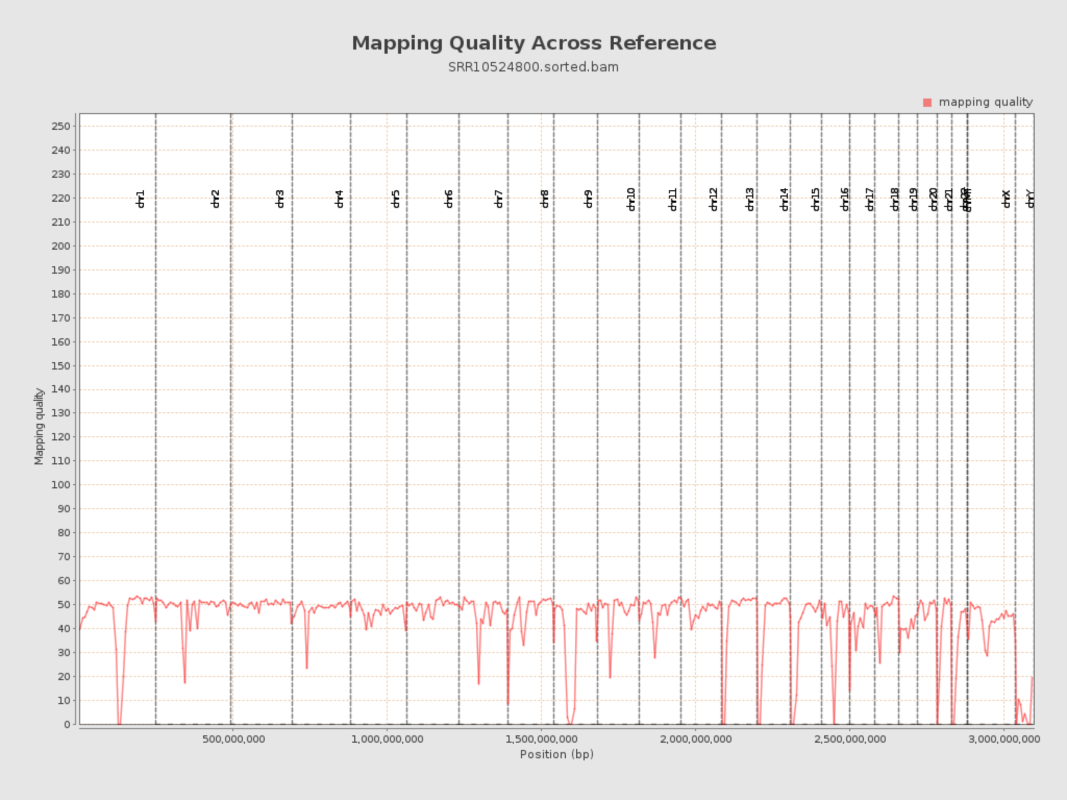
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram