Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:22:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524384.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_SRR10524384 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524384.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:22:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524384.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,465,463
Mapped reads	1,359,893 / 92.8%
Unmapped reads	105,570 / 7.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,517 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	50,819 / 3.47%
Duplication rate	2.83%
Clipped reads	1,361,798 / 92.93%

2.2. ACGT Content

Number/percentage of A's	20,510,793 / 25.72%
Number/percentage of C's	15,614,457 / 19.58%
Number/percentage of T's	24,796,278 / 31.09%
Number/percentage of G's	18,820,764 / 23.6%
Number/percentage of N's	10,916 / 0.01%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0258

Standard Deviation	0.2599

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

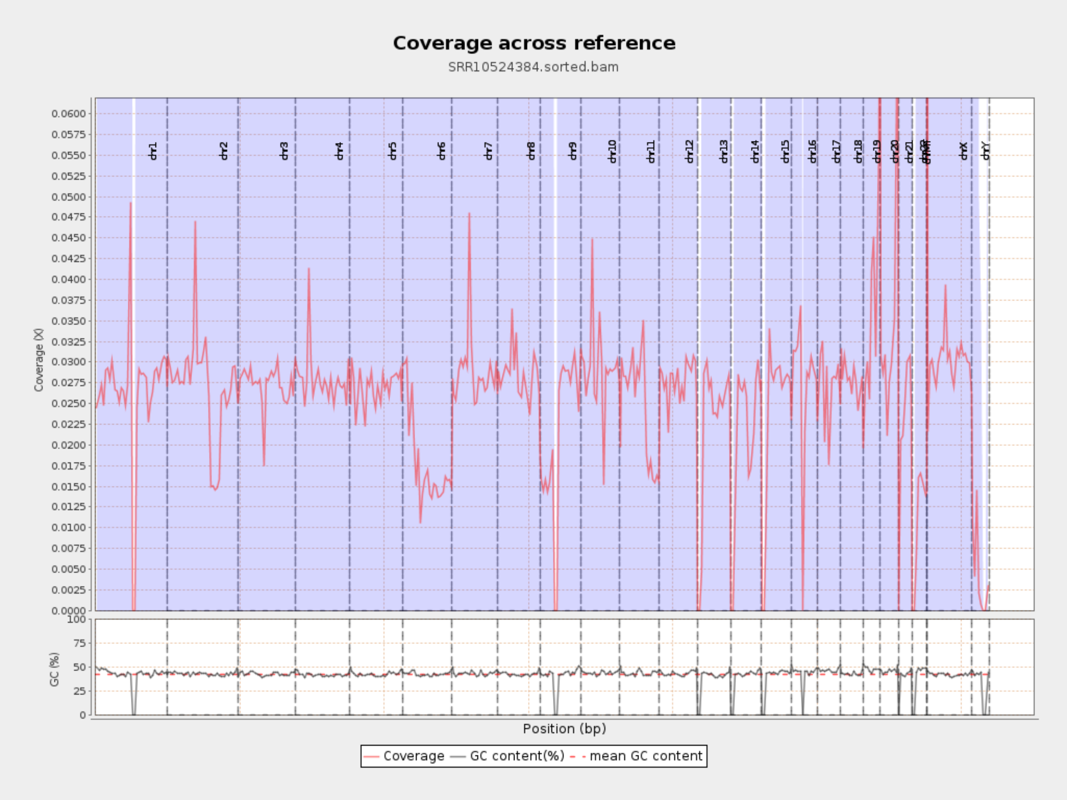
General error rate	0.49%
Mismatches	380,833
Insertions	5,951
Mapped reads with at least one insertion	0.44%
Deletions	14,042
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.83%

2.6. Chromosome stats

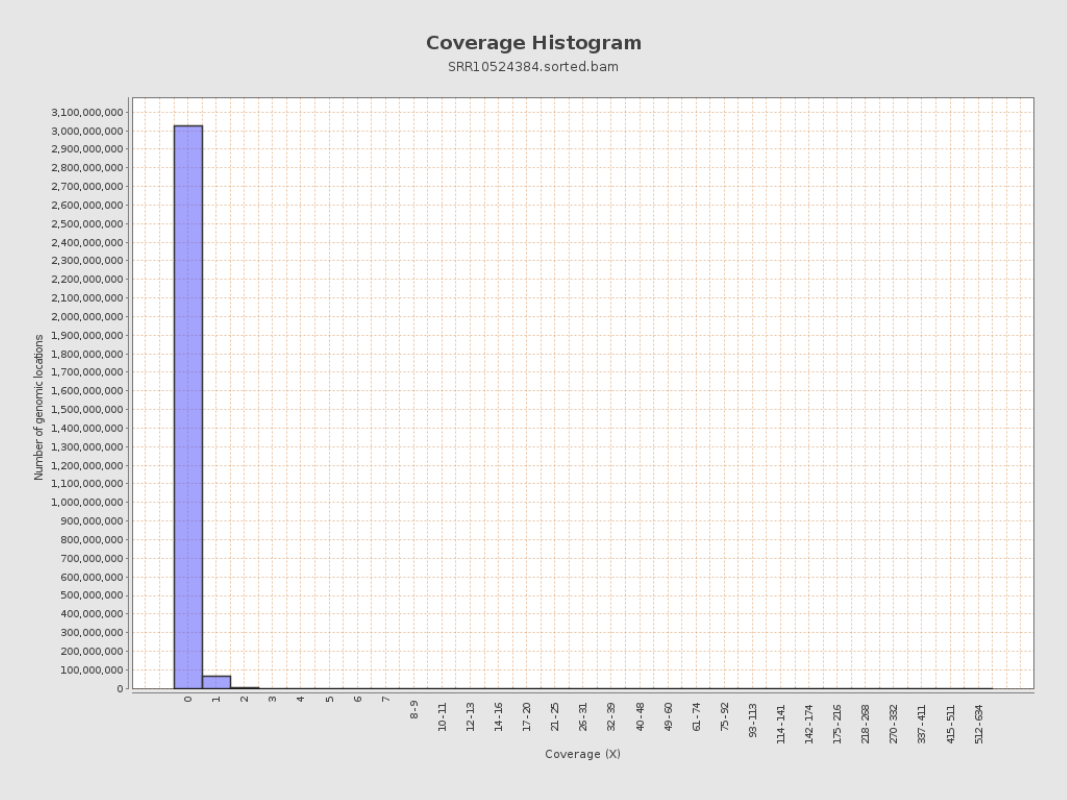
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6563413	0.0263	0.5327
chr2	243199373	6558886	0.027	0.2766
chr3	198022430	5389578	0.0272	0.1781
chr4	191154276	5356192	0.028	0.196
chr5	180915260	4891600	0.027	0.1769
chr6	171115067	3062737	0.0179	0.1544
chr7	159138663	4637197	0.0291	0.3434

chr8	146364022	4179626	0.0286	0.2346
chr9	141213431	2978944	0.0211	0.1993
chr10	135534747	3957371	0.0292	0.2404
chr11	135006516	3364810	0.0249	0.2156
chr12	133851895	3734290	0.0279	0.1876
chr13	115169878	2537945	0.022	0.1602
chr14	107349540	2251950	0.021	0.1611
chr15	102531392	2423818	0.0236	0.1671
chr16	90354753	2429279	0.0269	0.1855
chr17	81195210	2192722	0.027	0.1915
chr18	78077248	2174287	0.0278	0.3483
chr19	59128983	2231492	0.0377	0.3799
chr20	63025520	2232294	0.0354	0.2096
chr21	48129895	1110163	0.0231	0.1804
chr22	51304566	562695	0.011	0.1122
chrMT	16571	22185	1.3388	1.4668
chrX	155270560	4687767	0.0302	0.2038
chrY	59373566	244000	0.0041	0.1188

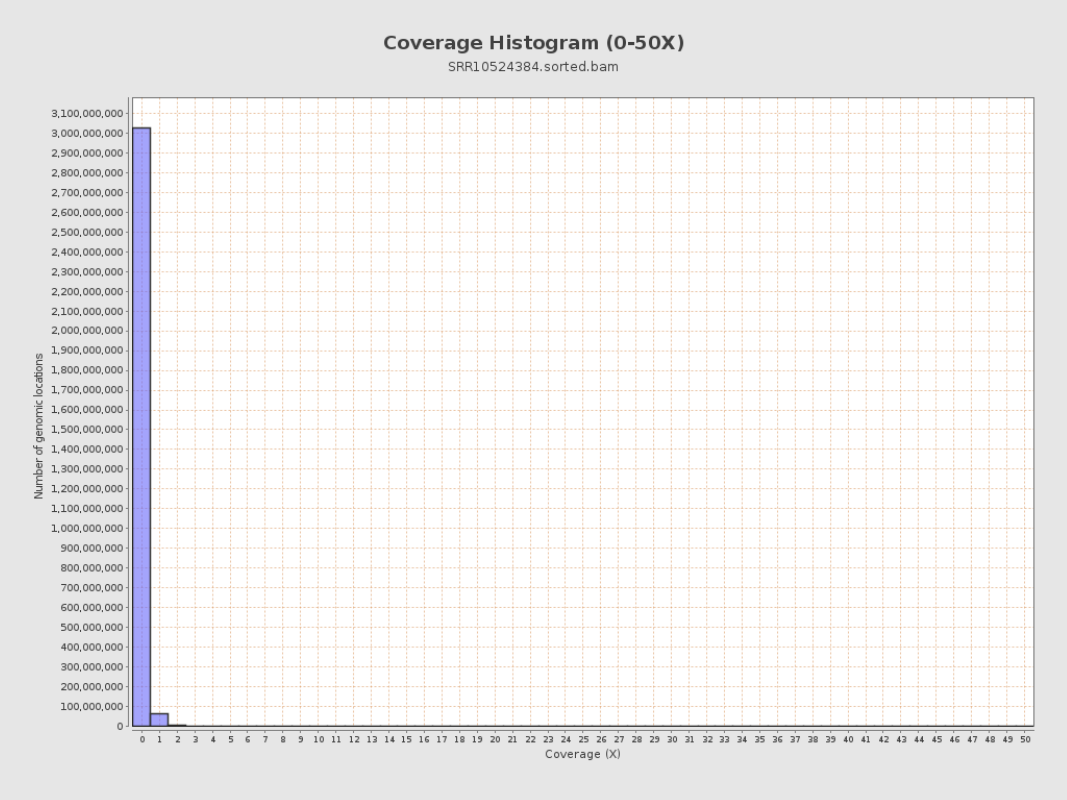
3. Results : Coverage across reference



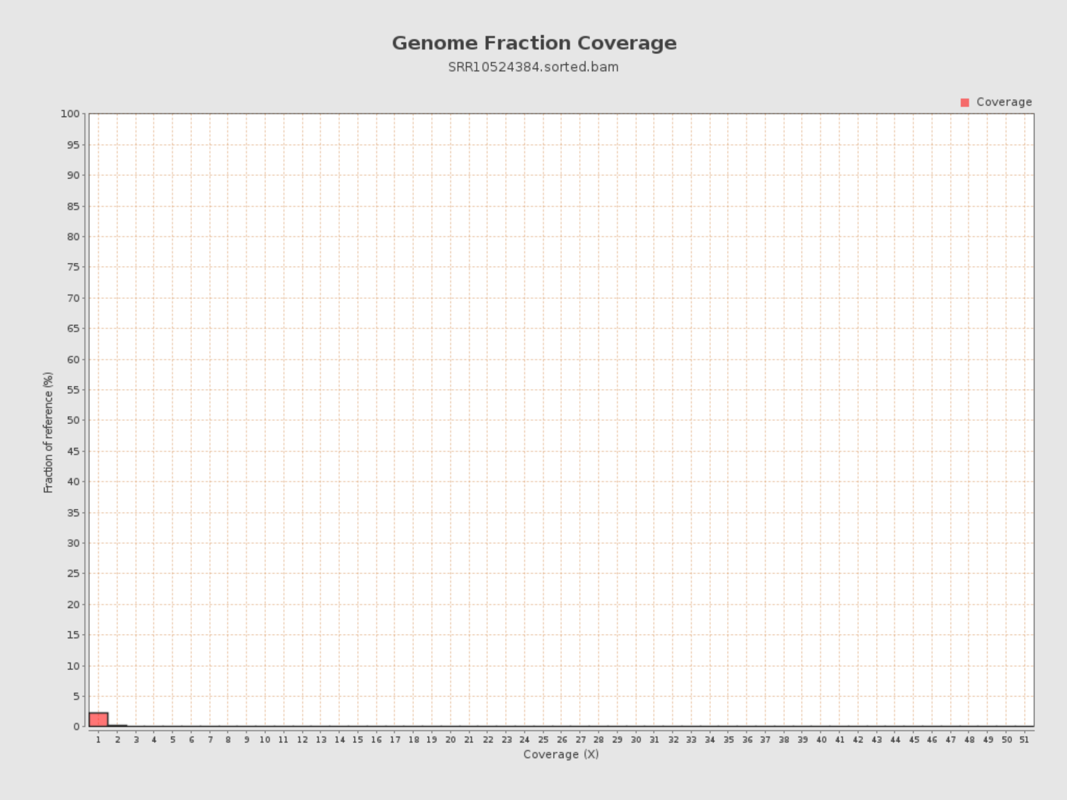
4. Results : Coverage Histogram



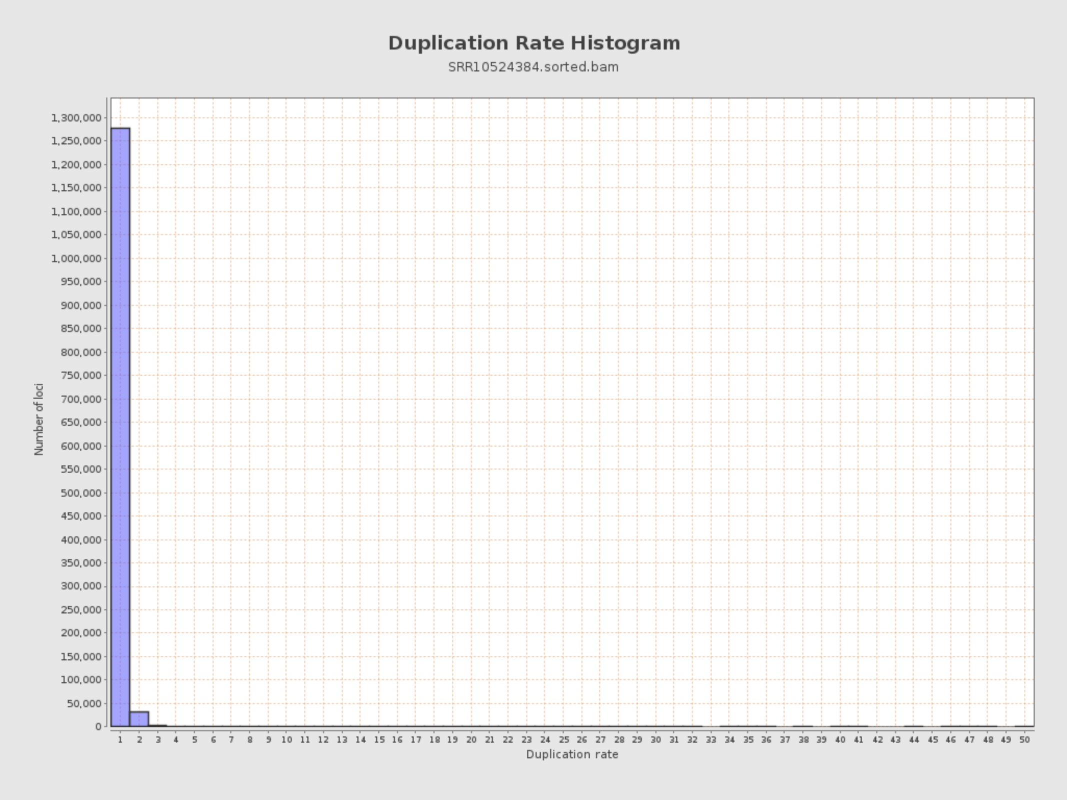
5. Results : Coverage Histogram (0-50X)



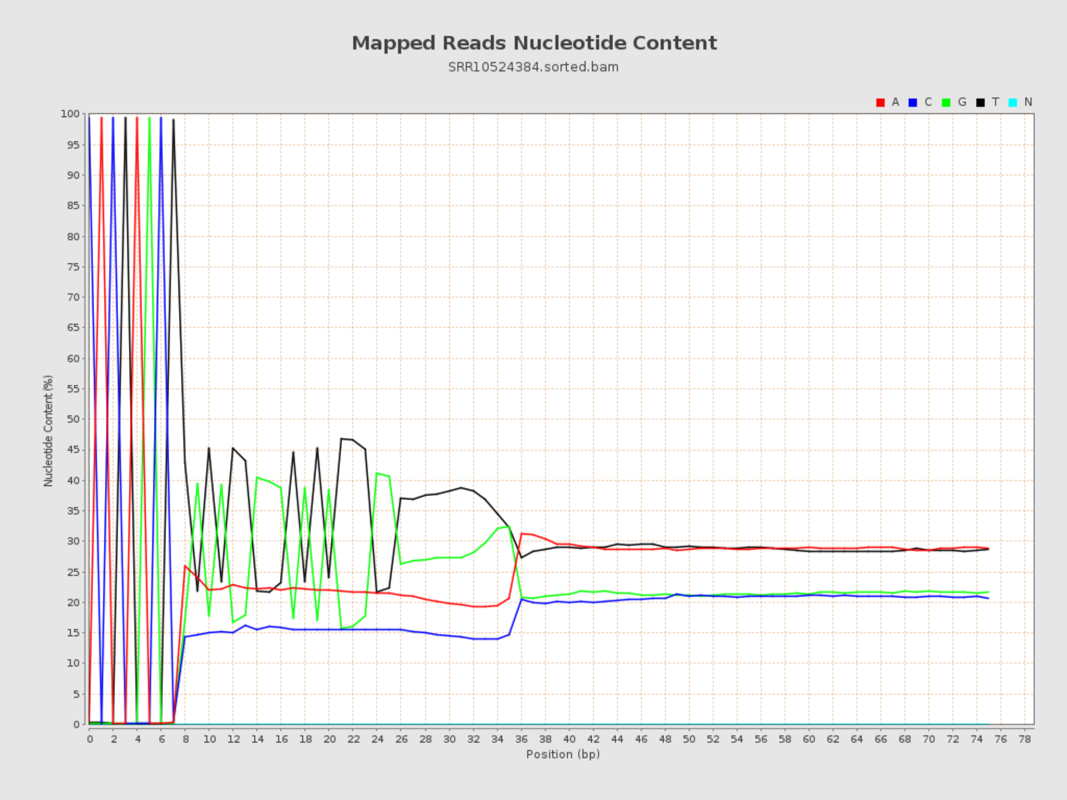
6. Results : Genome Fraction Coverage



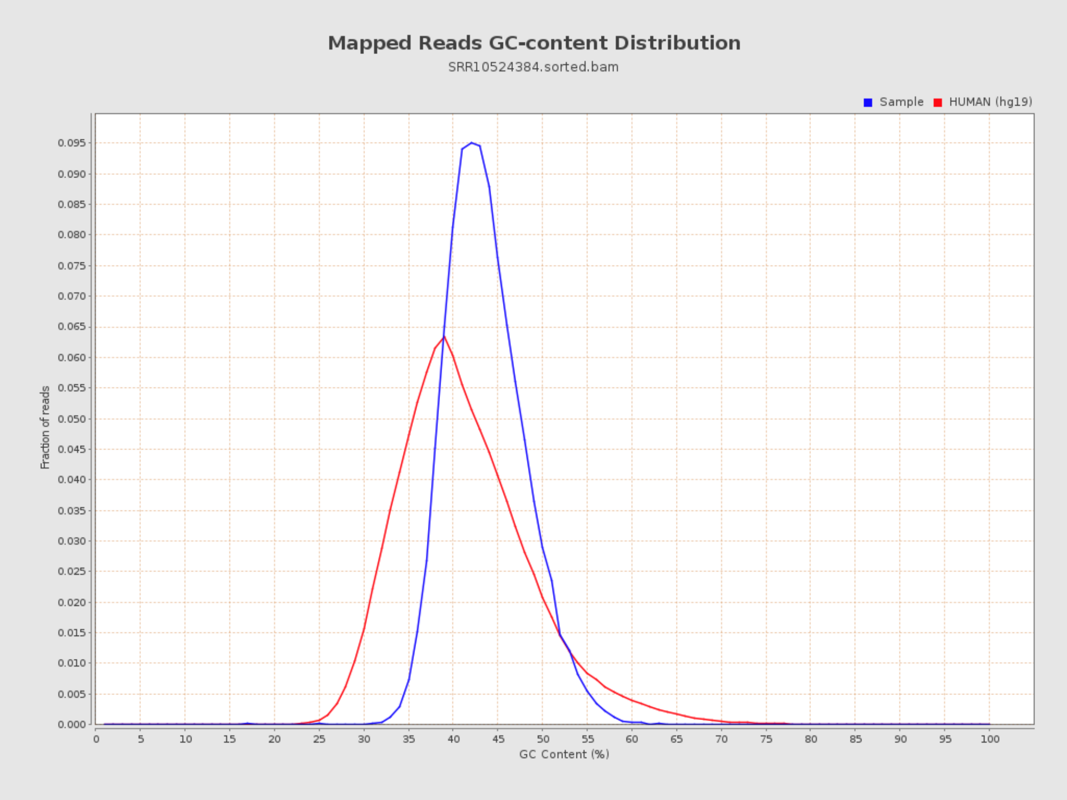
7. Results : Duplication Rate Histogram



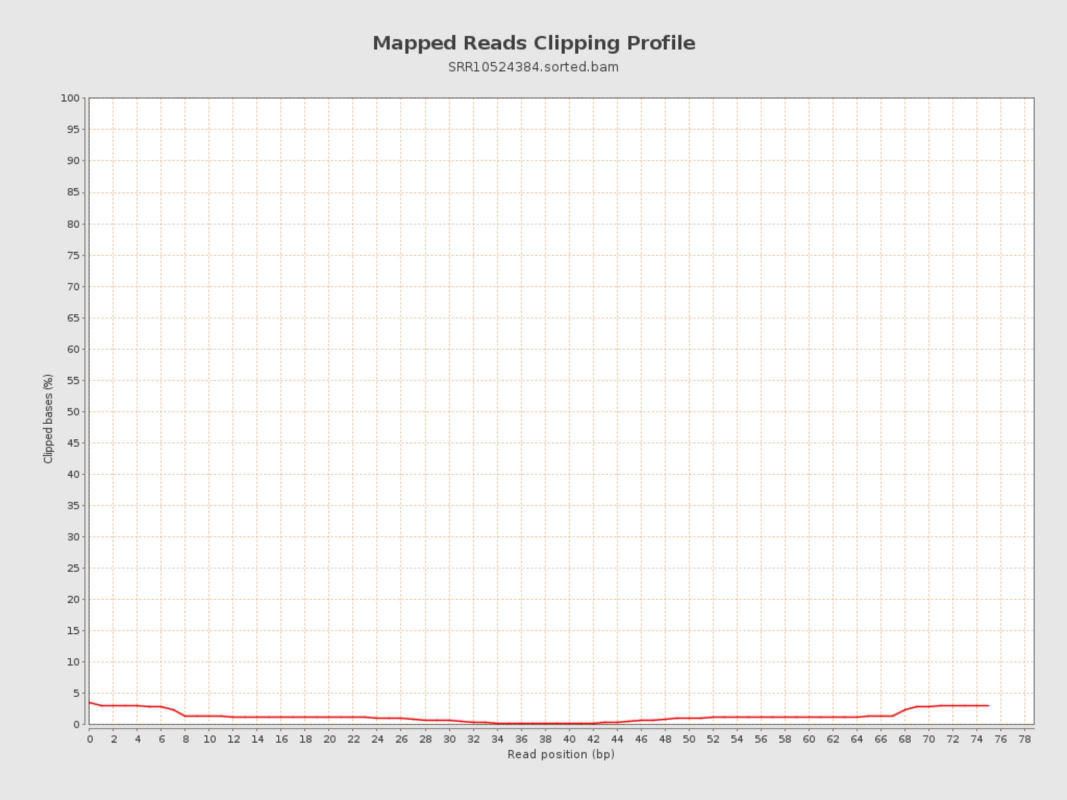
8. Results : Mapped Reads Nucleotide Content



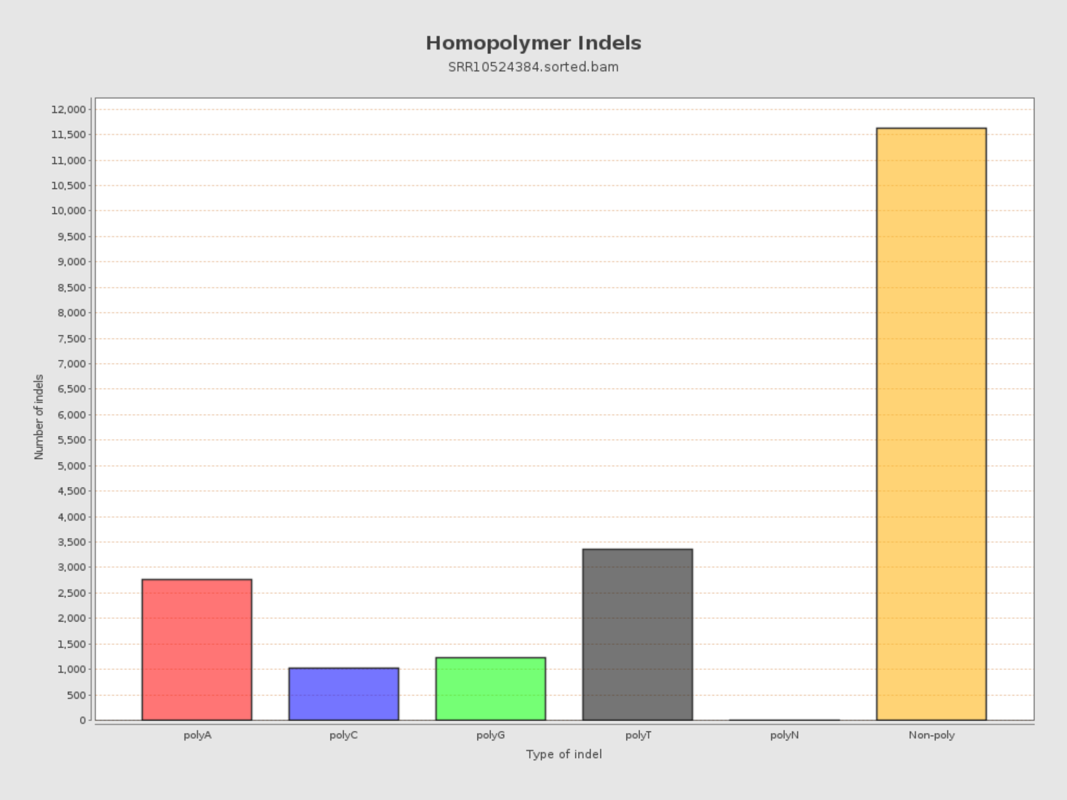
9. Results : Mapped Reads GC-content Distribution



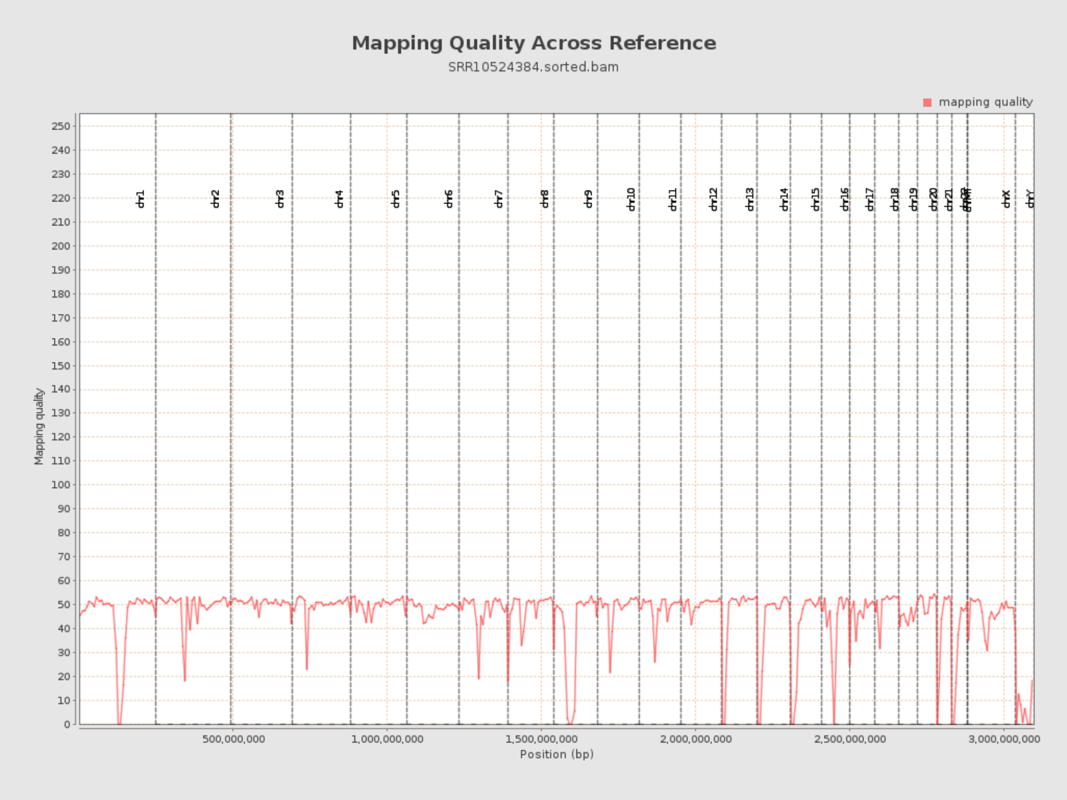
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram