Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:15:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524804.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_SRR10524804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:15:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,409,027
Mapped reads	1,284,289 / 91.15%
Unmapped reads	124,738 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,500 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	54,133 / 3.84%
Duplication rate	3.28%
Clipped reads	1,286,650 / 91.31%

2.2. ACGT Content

Number/percentage of A's	18,306,566 / 24.99%
Number/percentage of C's	13,428,809 / 18.33%
Number/percentage of T's	23,898,014 / 32.62%
Number/percentage of G's	17,614,700 / 24.05%
Number/percentage of N's	8,553 / 0.01%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2225

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

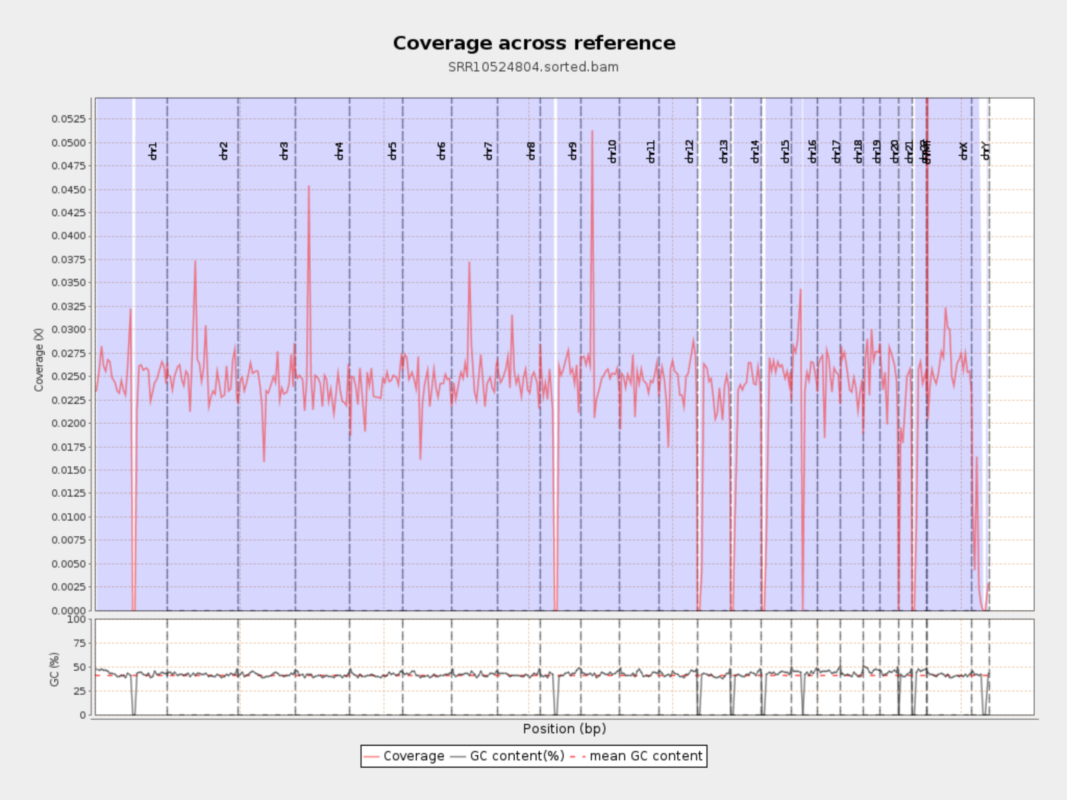
General error rate	0.52%
Mismatches	371,411
Insertions	5,645
Mapped reads with at least one insertion	0.44%
Deletions	14,398
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.96%

2.6. Chromosome stats

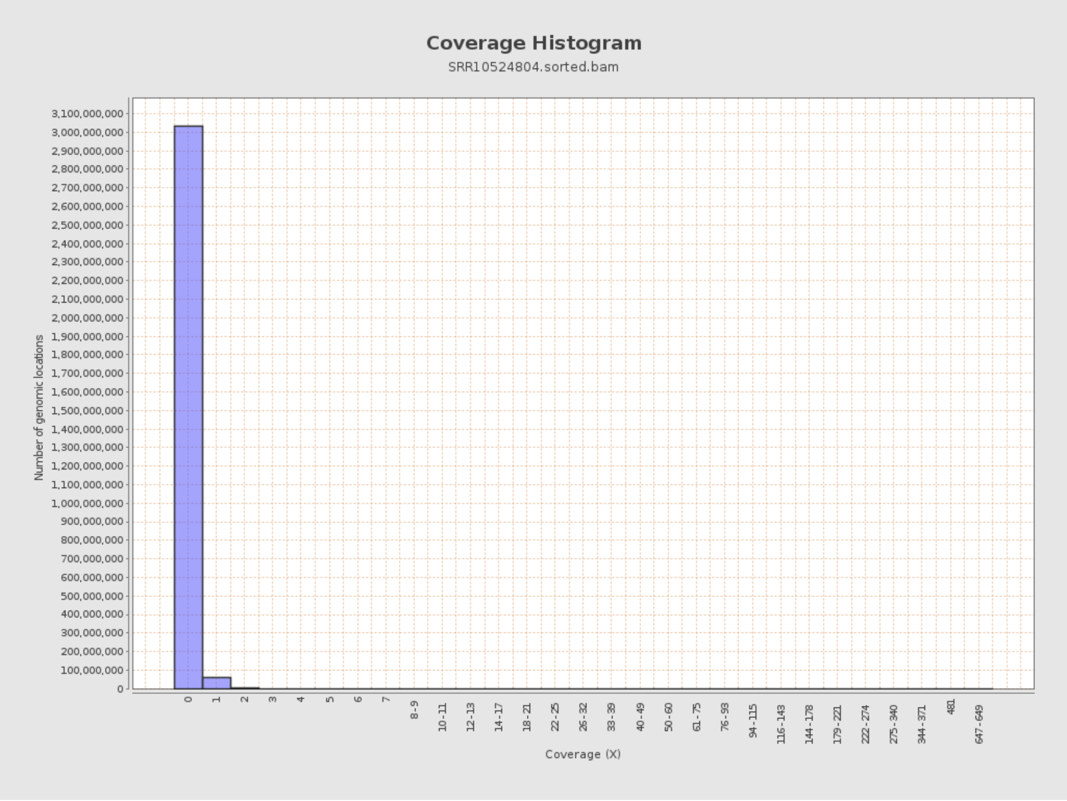
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5892564	0.0236	0.3098
chr2	243199373	6170794	0.0254	0.3356
chr3	198022430	4781475	0.0241	0.1721
chr4	191154276	4708858	0.0246	0.1977
chr5	180915260	4369936	0.0242	0.1708
chr6	171115067	4147749	0.0242	0.1887
chr7	159138663	4012138	0.0252	0.2559

chr8	146364022	3658644	0.025	0.2117
chr9	141213431	3127703	0.0221	0.1888
chr10	135534747	3606468	0.0266	0.273
chr11	135006516	3319334	0.0246	0.2014
chr12	133851895	3302829	0.0247	0.1741
chr13	115169878	2261860	0.0196	0.1546
chr14	107349540	2199820	0.0205	0.1614
chr15	102531392	2129414	0.0208	0.1599
chr16	90354753	2209232	0.0245	0.1887
chr17	81195210	2044497	0.0252	0.1821
chr18	78077248	1924647	0.0247	0.2891
chr19	59128983	1591240	0.0269	0.2468
chr20	63025520	1572978	0.025	0.1832
chr21	48129895	964912	0.02	0.1736
chr22	51304566	906370	0.0177	0.1476
chrMT	16571	29549	1.7832	1.6548
chrX	155270560	4083715	0.0263	0.1885
chrY	59373566	263396	0.0044	0.1346

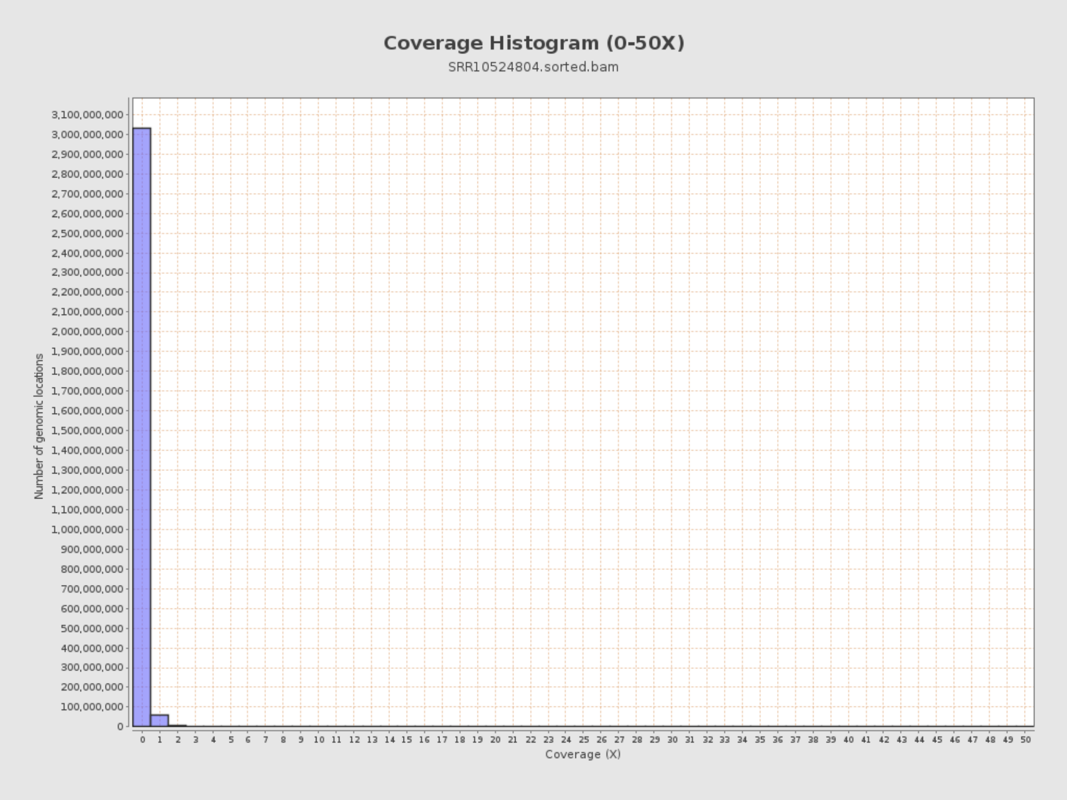
3. Results : Coverage across reference



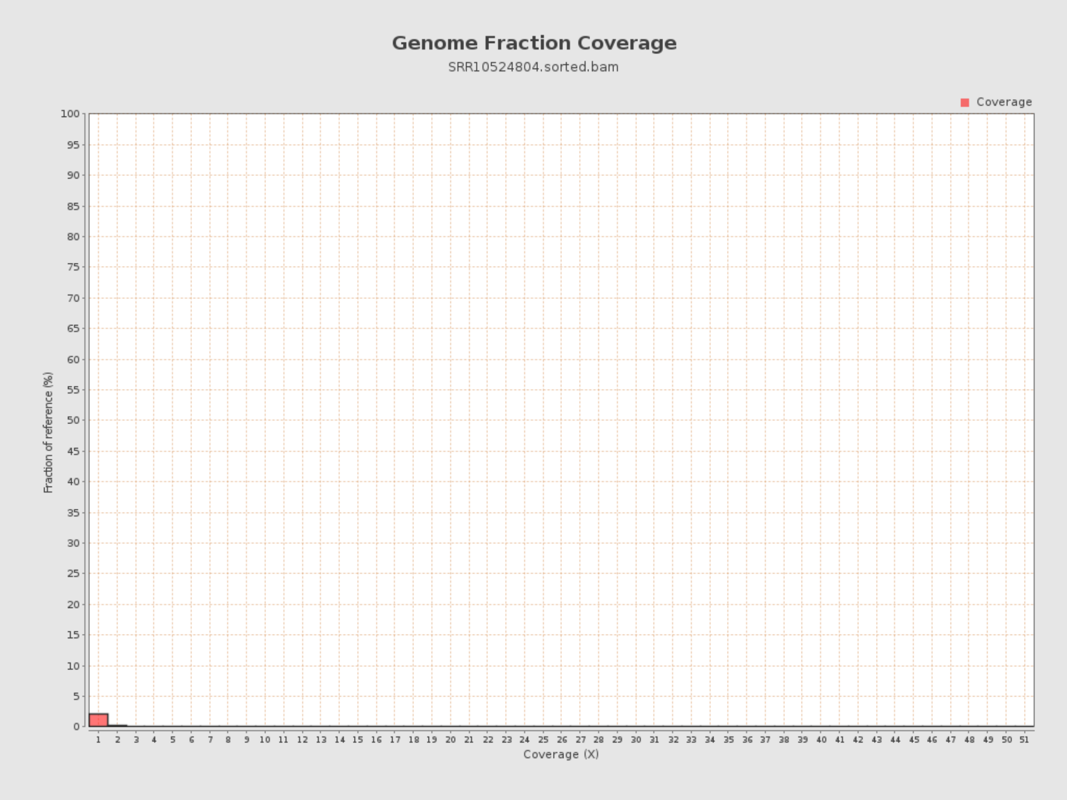
4. Results : Coverage Histogram



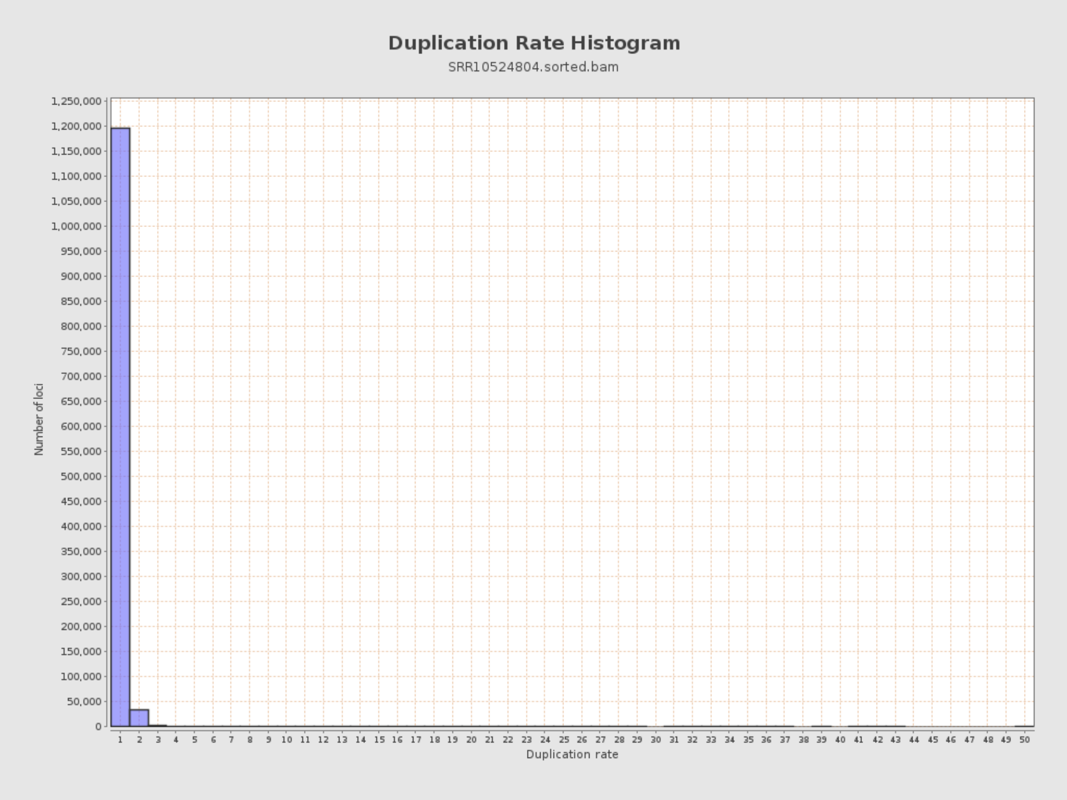
5. Results : Coverage Histogram (0-50X)



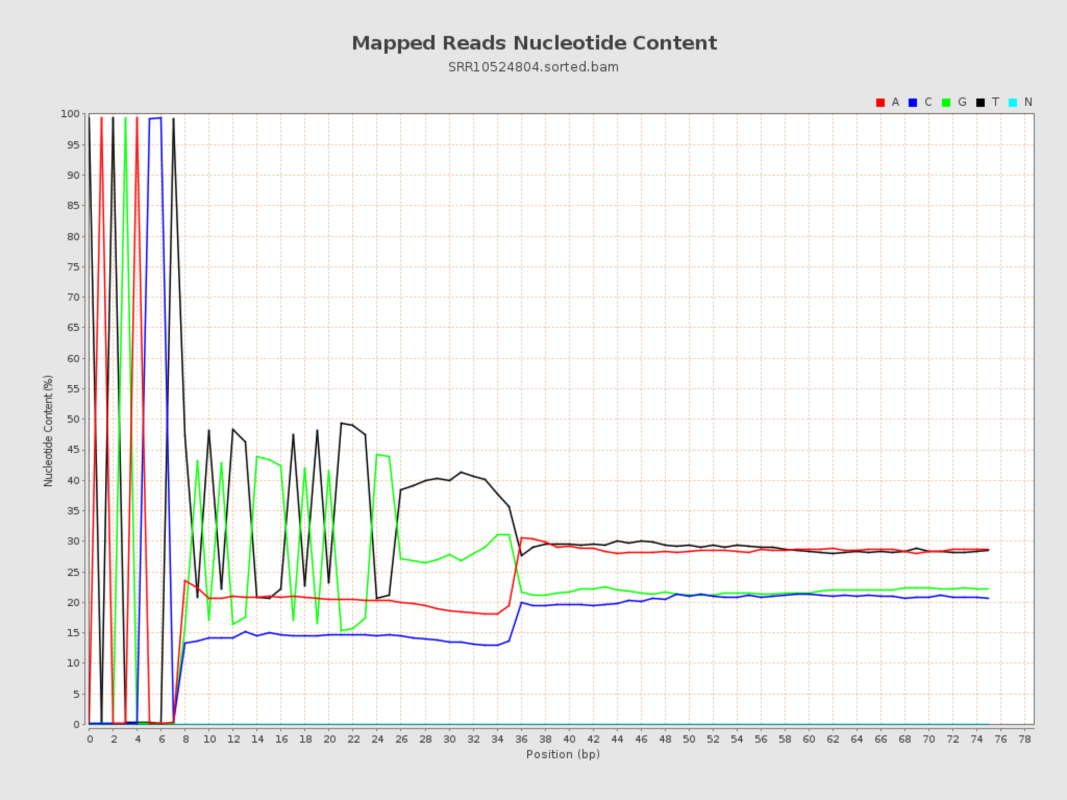
6. Results : Genome Fraction Coverage



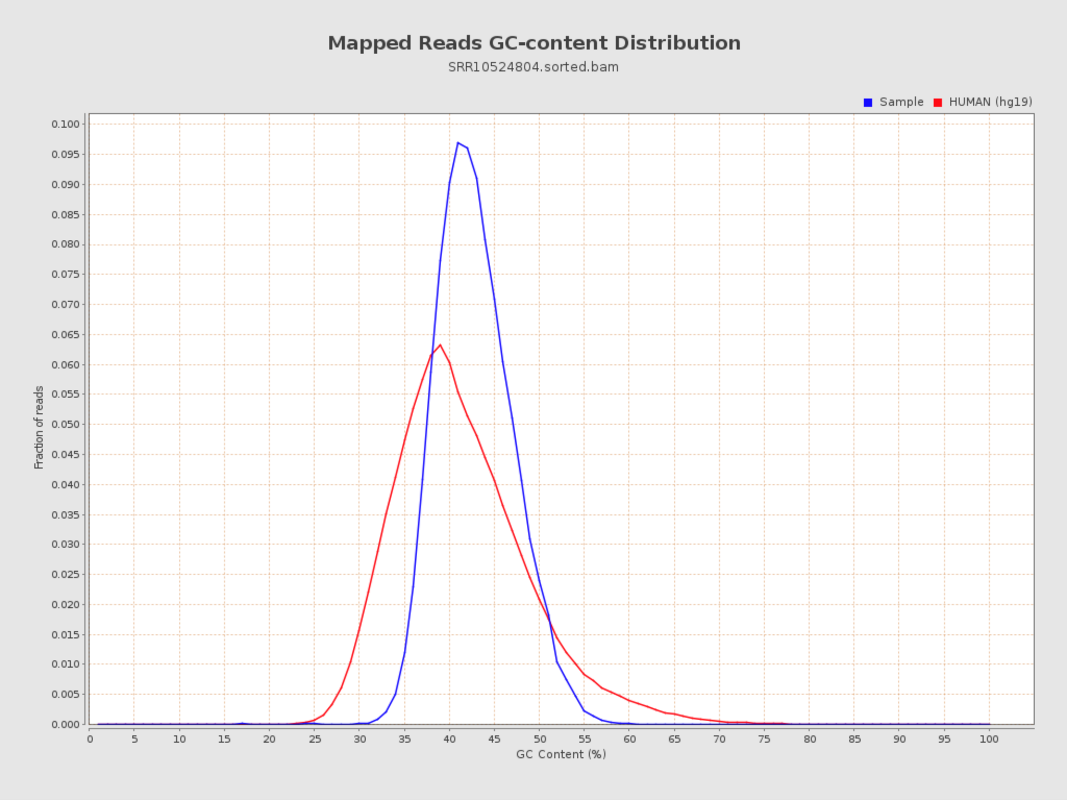
7. Results : Duplication Rate Histogram



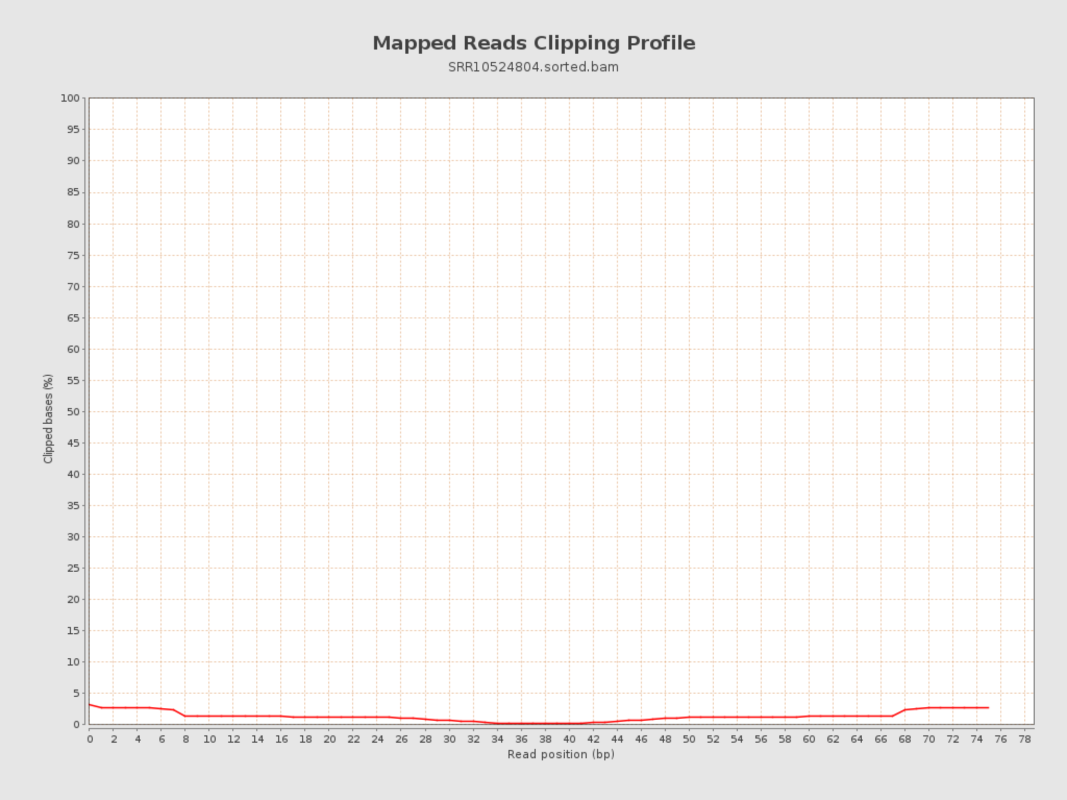
8. Results : Mapped Reads Nucleotide Content



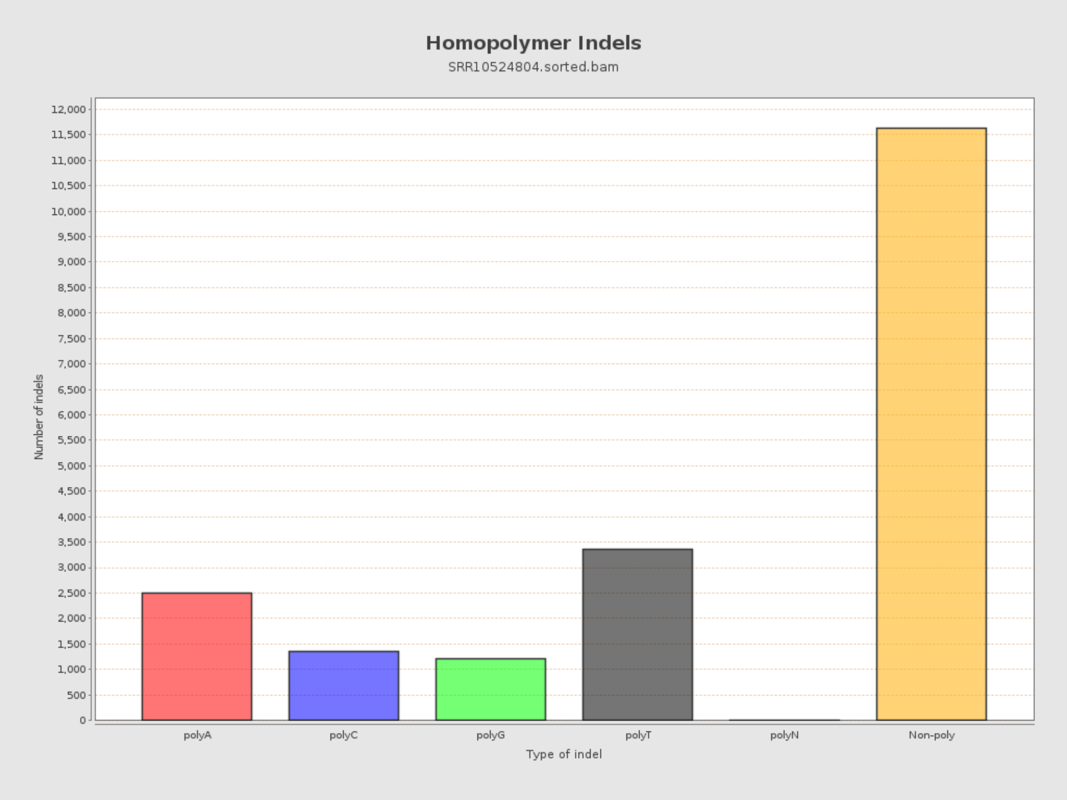
9. Results : Mapped Reads GC-content Distribution



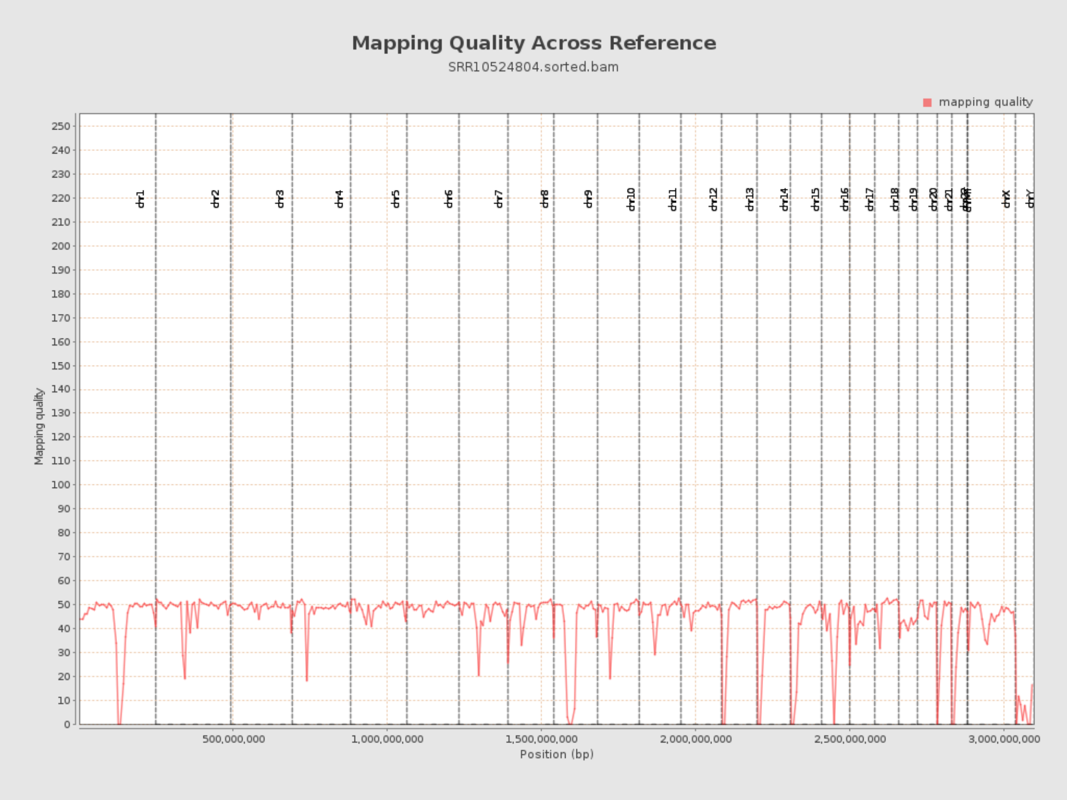
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram