Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:42:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524414.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_SRR10524414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524414.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:42:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,597,732
Mapped reads	5,157,407 / 92.13%
Unmapped reads	440,325 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,116 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	407,379 / 7.28%
Duplication rate	5.64%
Clipped reads	5,159,825 / 92.18%

2.2. ACGT Content

Number/percentage of A's	75,769,259 / 25.1%
Number/percentage of C's	58,627,914 / 19.42%
Number/percentage of T's	94,221,861 / 31.22%
Number/percentage of G's	73,185,254 / 24.25%
Number/percentage of N's	37,405 / 0.01%
GC Percentage	43.67%

2.3. Coverage

Mean	0.0975

Standard Deviation	0.8754

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

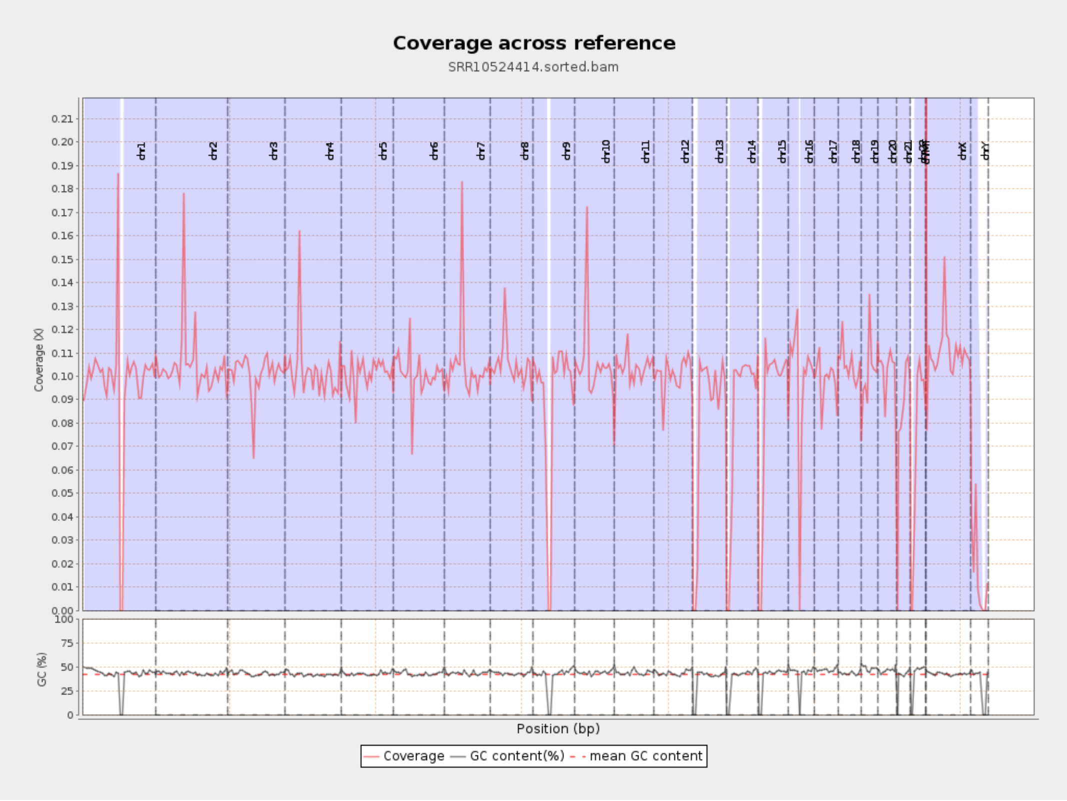
General error rate	0.51%
Mismatches	1,476,067
Insertions	24,661
Mapped reads with at least one insertion	0.48%
Deletions	54,235
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.84%

2.6. Chromosome stats

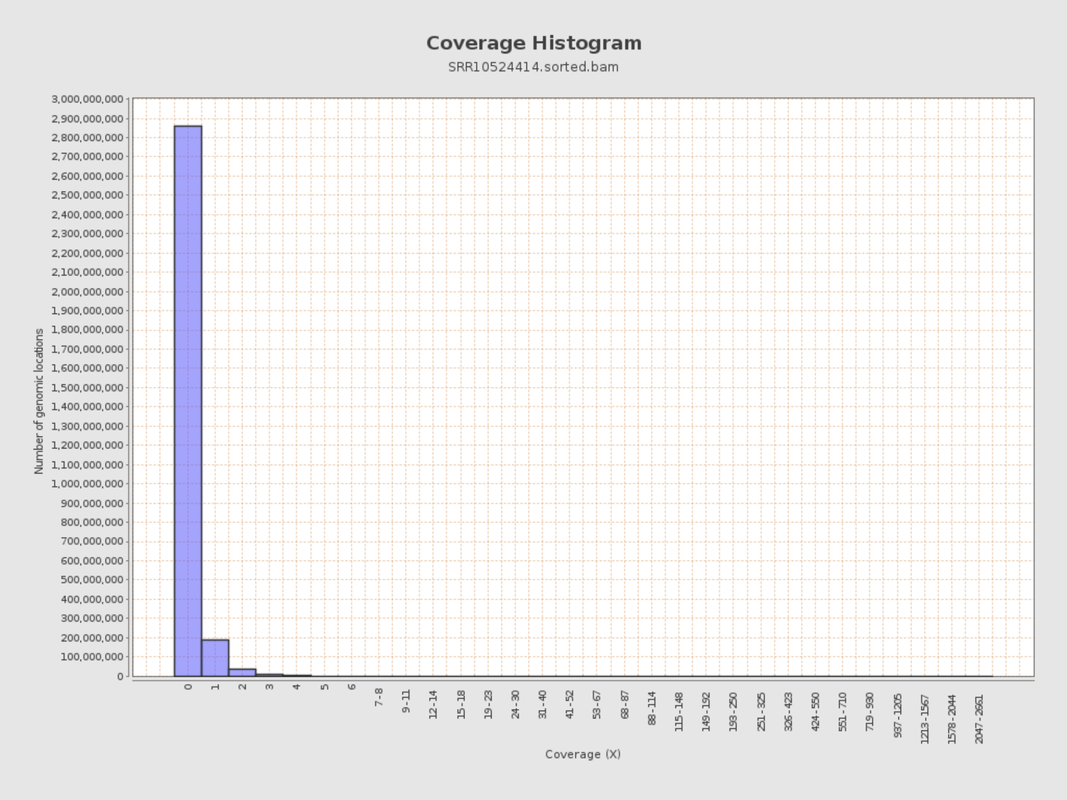
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24148512	0.0969	2.0135
chr2	243199373	25515651	0.1049	0.9561
chr3	198022430	20029585	0.1011	0.3943
chr4	191154276	19656917	0.1028	0.5121
chr5	180915260	18318420	0.1013	0.3992
chr6	171115067	17263688	0.1009	0.5133
chr7	159138663	16728358	0.1051	1.2646

chr8	146364022	15325203	0.1047	0.7347
chr9	141213431	12644289	0.0895	0.6734
chr10	135534747	14317256	0.1056	0.7434
chr11	135006516	13933634	0.1032	0.7342
chr12	133851895	13539379	0.1012	0.4254
chr13	115169878	9499116	0.0825	0.3562
chr14	107349540	9141268	0.0852	0.4029
chr15	102531392	8824431	0.0861	0.3681
chr16	90354753	8692067	0.0962	0.4514
chr17	81195210	8051104	0.0992	0.4709
chr18	78077248	8204637	0.1051	1.3918
chr19	59128983	6058003	0.1025	1.2949
chr20	63025520	6436724	0.1021	0.4194
chr21	48129895	4016214	0.0834	0.4701
chr22	51304566	3574331	0.0697	0.3276
chrMT	16571	13128	0.7922	1.1068
chrX	155270560	17072609	0.11	0.5422
chrY	59373566	923374	0.0156	0.3934

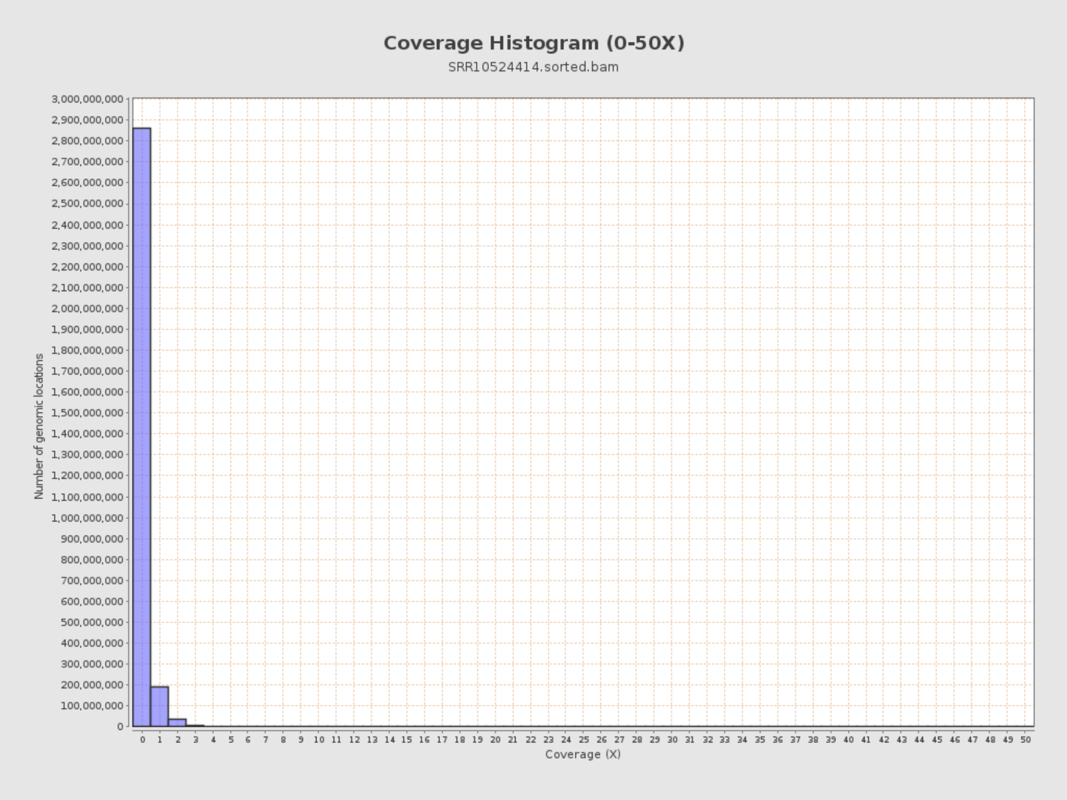
3. Results : Coverage across reference



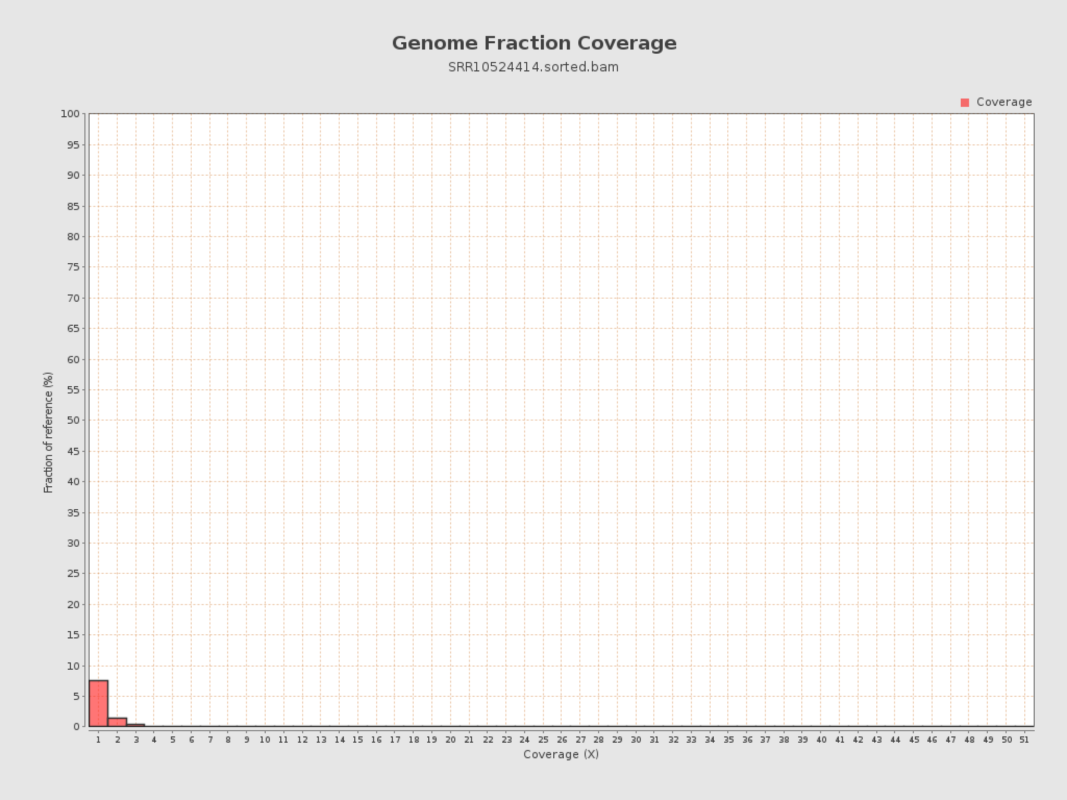
4. Results : Coverage Histogram



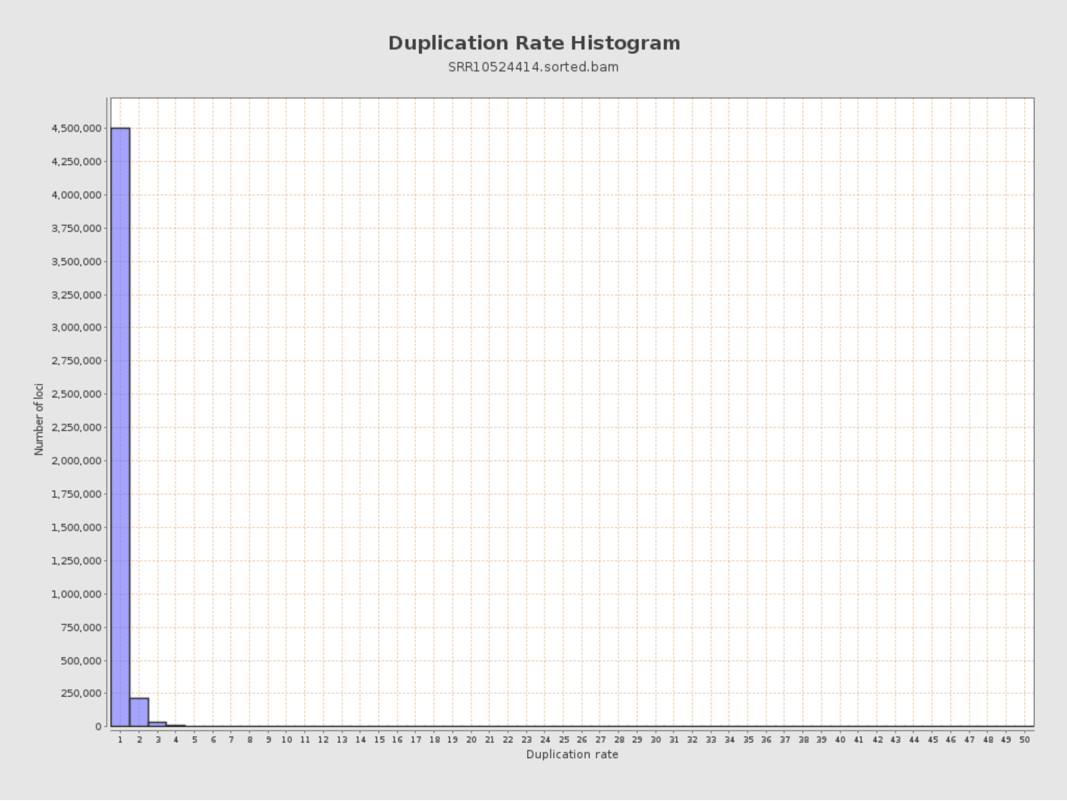
5. Results : Coverage Histogram (0-50X)



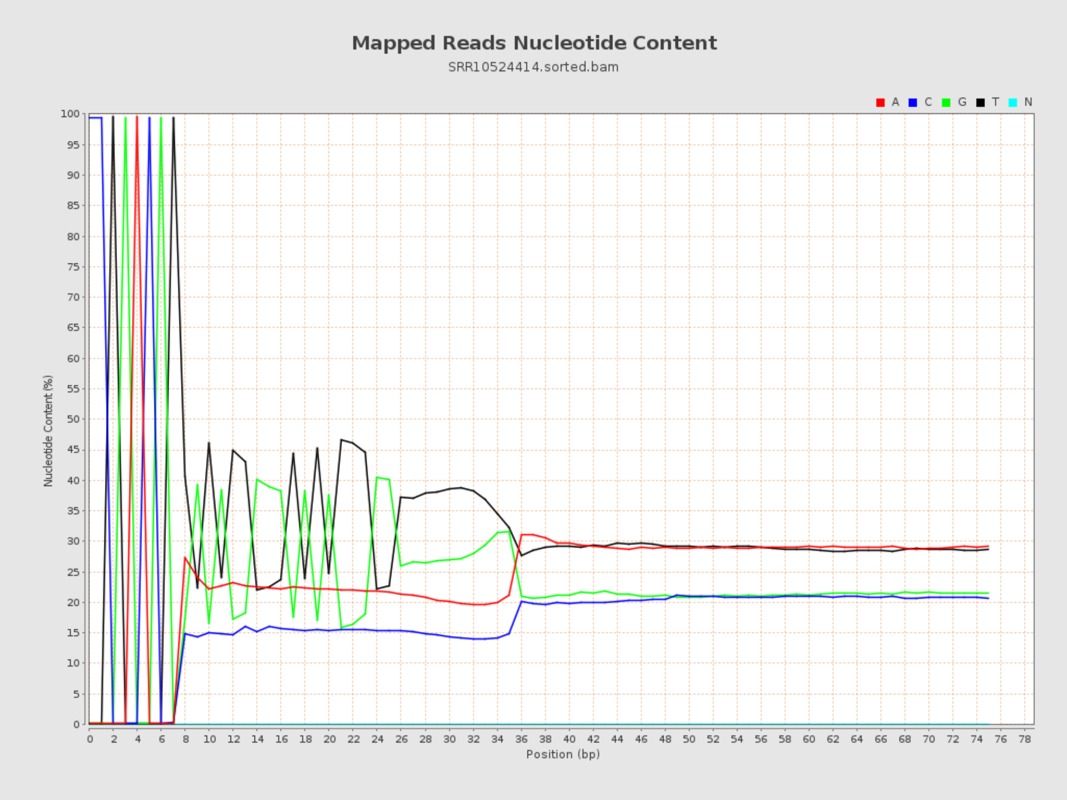
6. Results : Genome Fraction Coverage



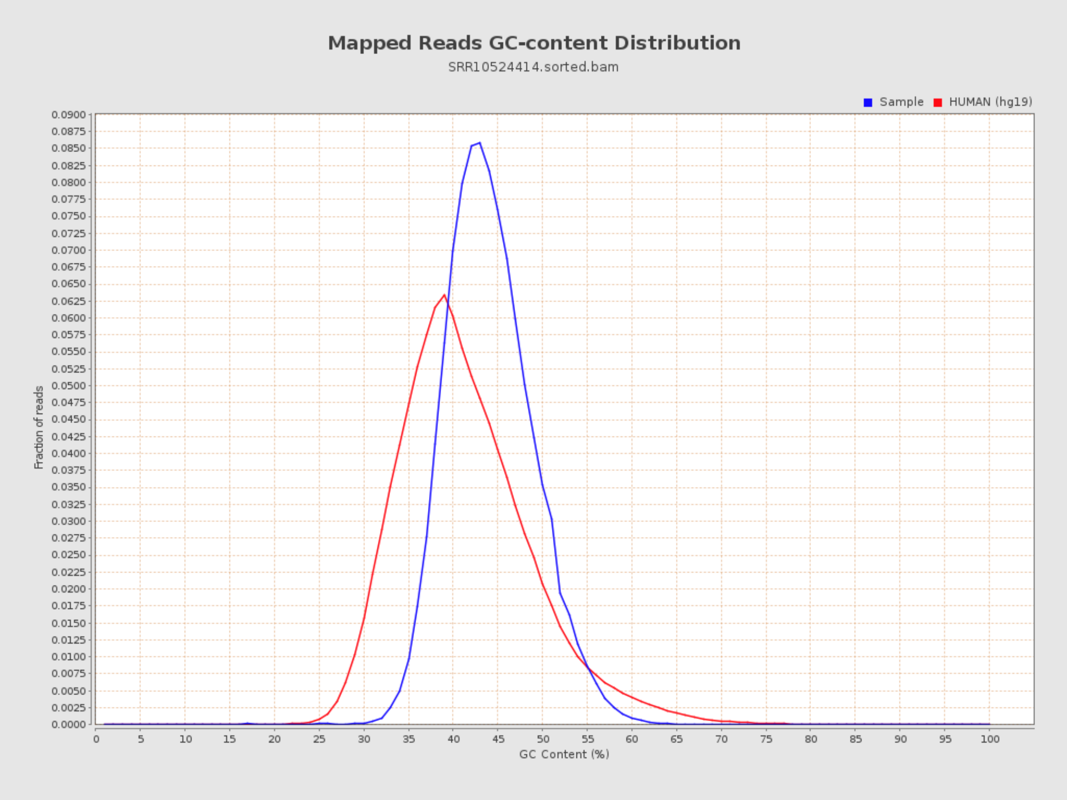
7. Results : Duplication Rate Histogram



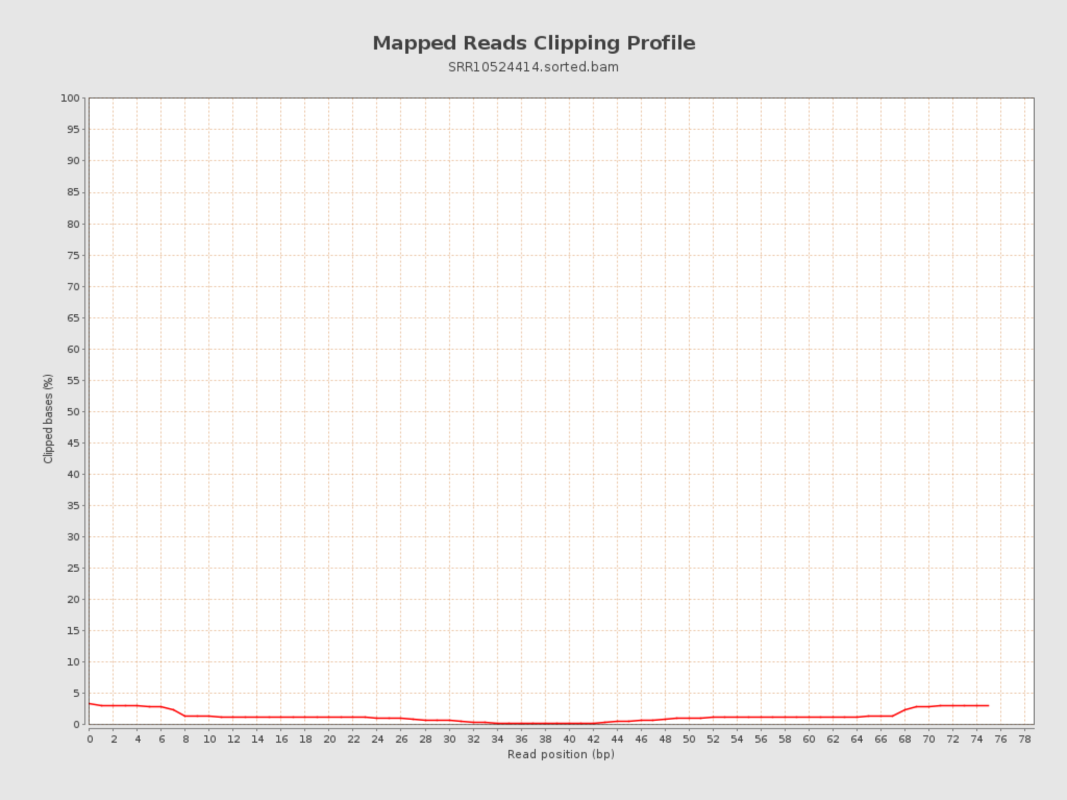
8. Results : Mapped Reads Nucleotide Content



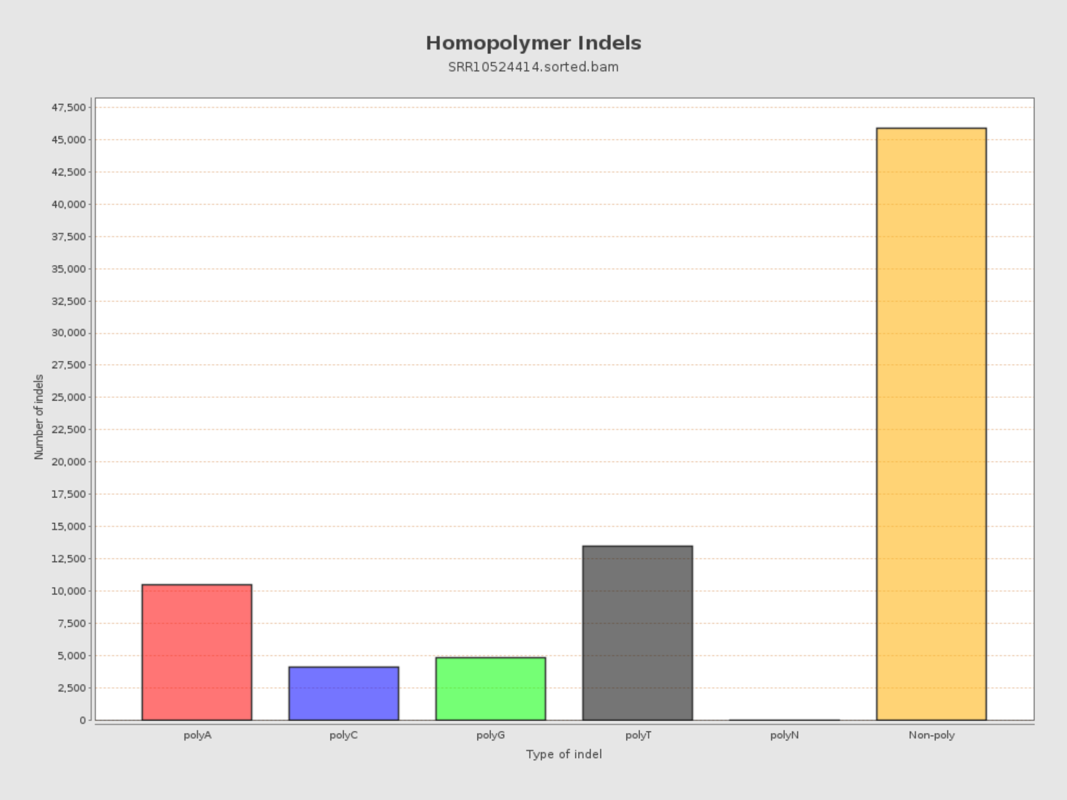
9. Results : Mapped Reads GC-content Distribution



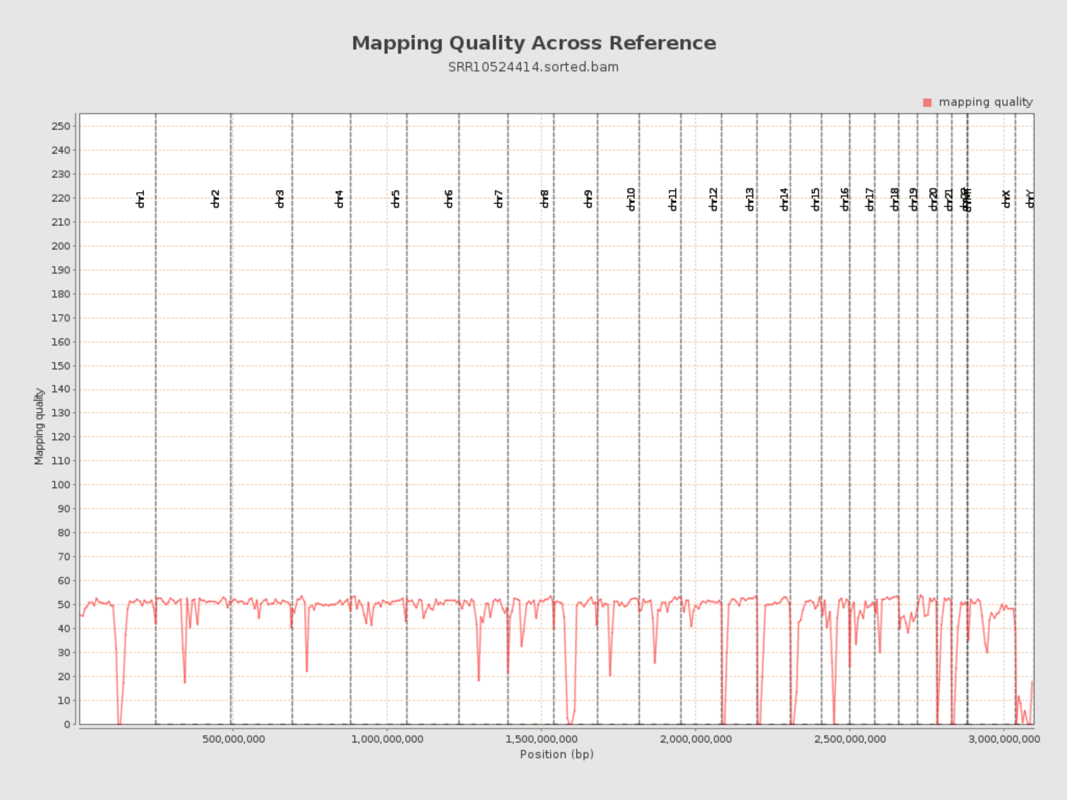
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram