Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:28:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524439.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_SRR10524439 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524439.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:28:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524439.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,092,561
Mapped reads	1,002,213 / 91.73%
Unmapped reads	90,348 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,721 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	40,621 / 3.72%
Duplication rate	3.02%
Clipped reads	1,005,679 / 92.05%

2.2. ACGT Content

Number/percentage of A's	13,781,356 / 23.5%
Number/percentage of C's	11,835,399 / 20.18%
Number/percentage of T's	18,028,284 / 30.74%
Number/percentage of G's	15,000,075 / 25.58%
Number/percentage of N's	5,877 / 0.01%
GC Percentage	45.75%

2.3. Coverage

Mean	0.019

Standard Deviation	0.2174

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

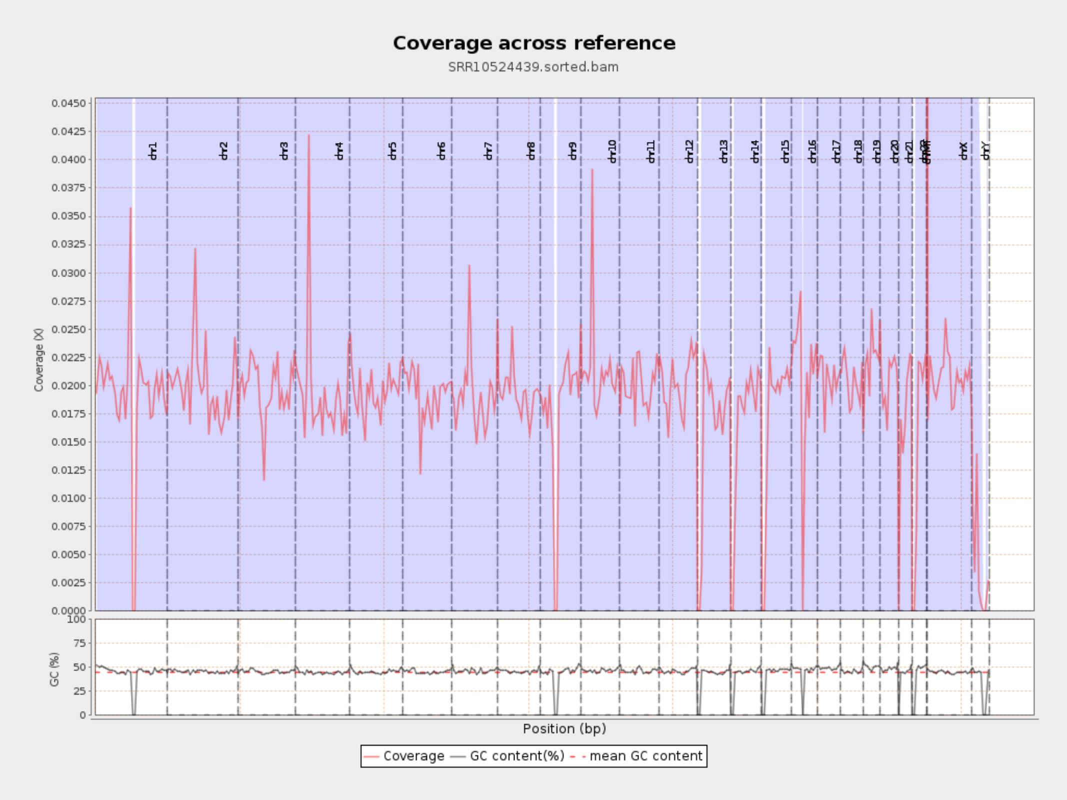
General error rate	0.53%
Mismatches	300,702
Insertions	3,597
Mapped reads with at least one insertion	0.36%
Deletions	10,191
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.11%

2.6. Chromosome stats

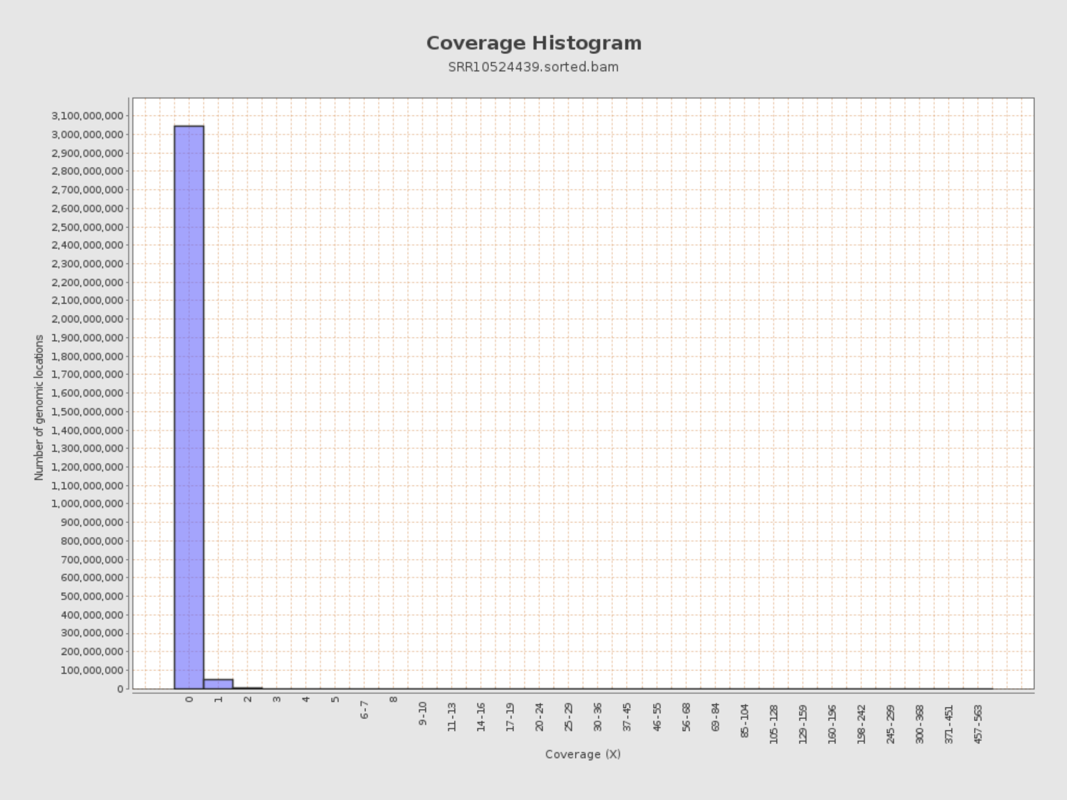
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4730662	0.019	0.4245
chr2	243199373	4880150	0.0201	0.2604
chr3	198022430	3884926	0.0196	0.1511
chr4	191154276	3710222	0.0194	0.1871
chr5	180915260	3520261	0.0195	0.1502
chr6	171115067	3288612	0.0192	0.1616
chr7	159138663	3025077	0.019	0.2434

chr8	146364022	2827449	0.0193	0.1732
chr9	141213431	2452746	0.0174	0.1704
chr10	135534747	2912271	0.0215	0.2336
chr11	135006516	2709474	0.0201	0.1855
chr12	133851895	2701412	0.0202	0.1576
chr13	115169878	1825738	0.0159	0.1367
chr14	107349540	1740571	0.0162	0.1408
chr15	102531392	1725421	0.0168	0.1401
chr16	90354753	1837530	0.0203	0.1633
chr17	81195210	1675507	0.0206	0.1648
chr18	78077248	1585554	0.0203	0.2939
chr19	59128983	1327519	0.0225	0.2915
chr20	63025520	1278571	0.0203	0.1581
chr21	48129895	809807	0.0168	0.1674
chr22	51304566	768751	0.015	0.134
chrMT	16571	8550	0.516	0.8228
chrX	155270560	3219379	0.0207	0.1663
chrY	59373566	221272	0.0037	0.1333

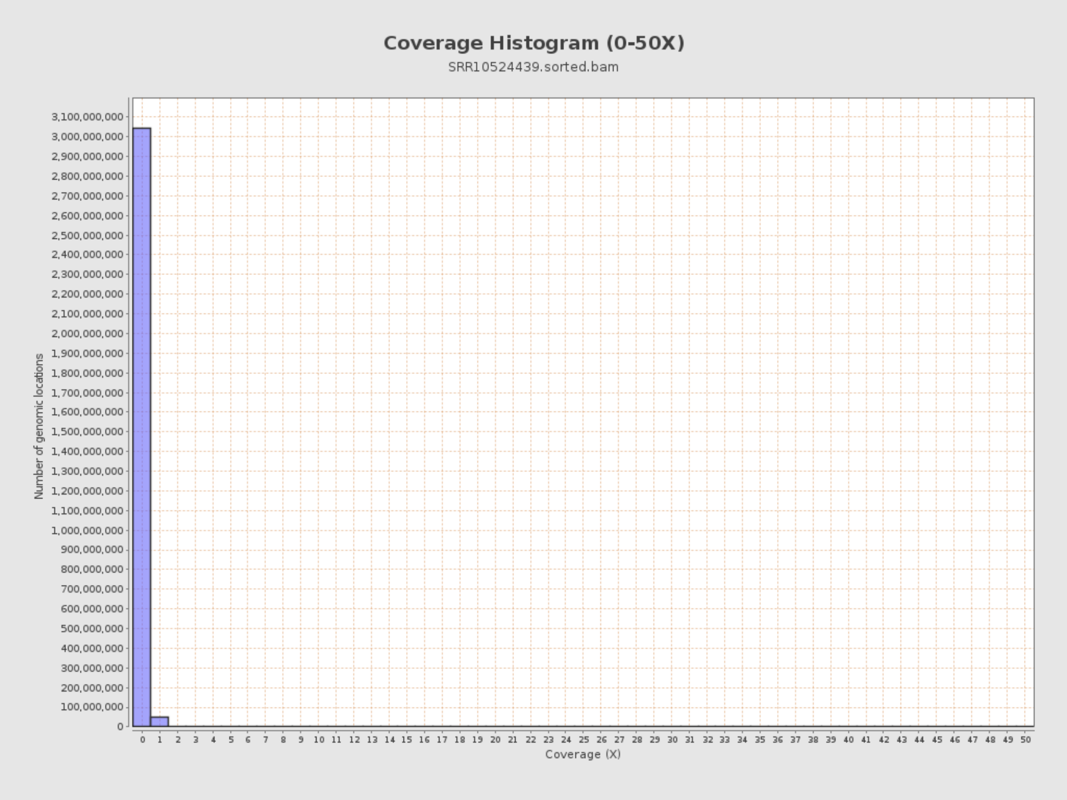
3. Results : Coverage across reference



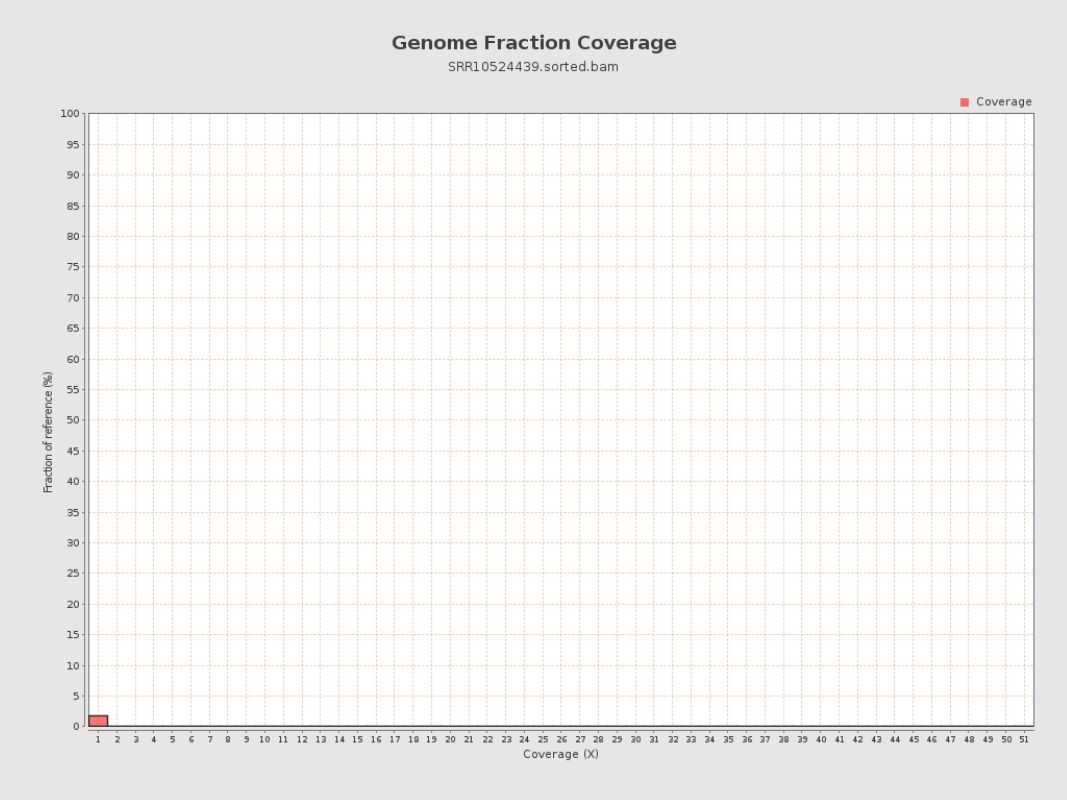
4. Results : Coverage Histogram



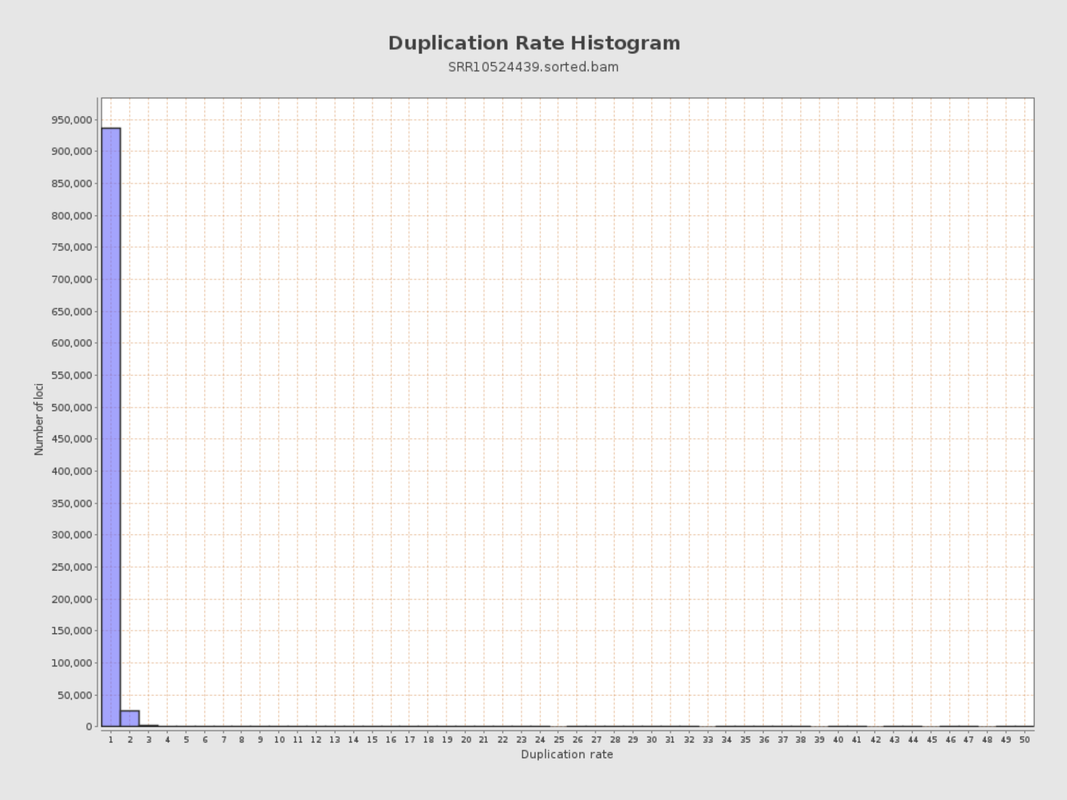
5. Results : Coverage Histogram (0-50X)



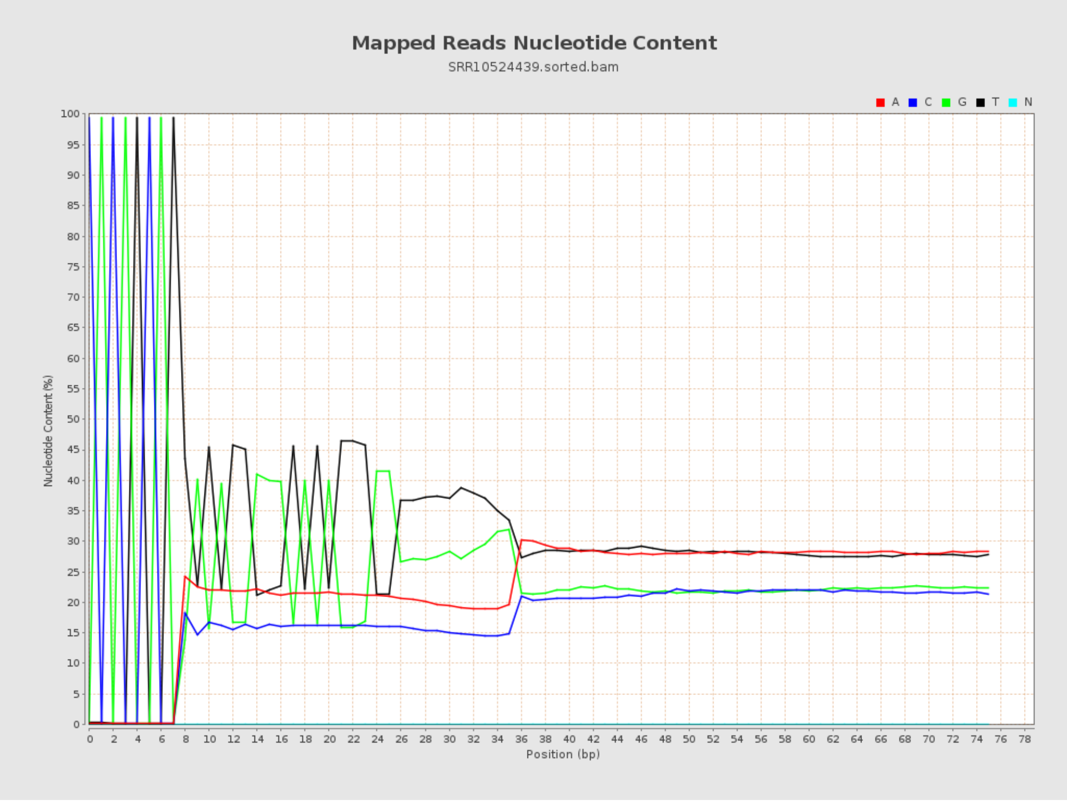
6. Results : Genome Fraction Coverage



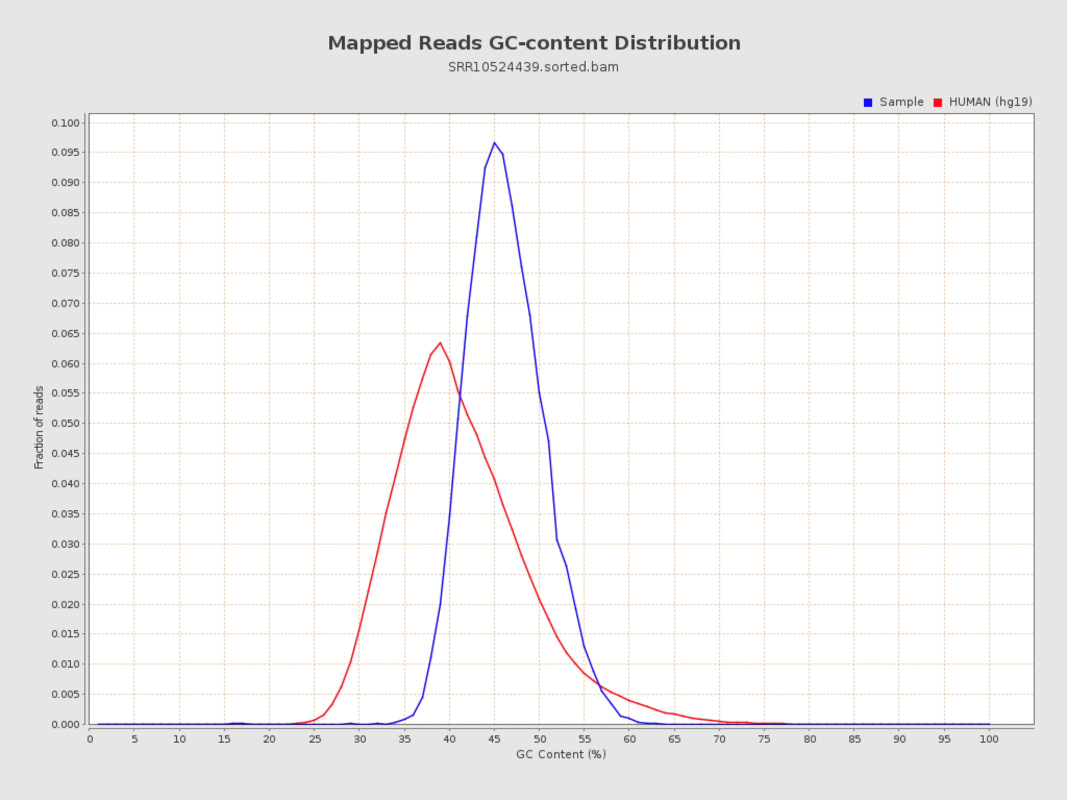
7. Results : Duplication Rate Histogram



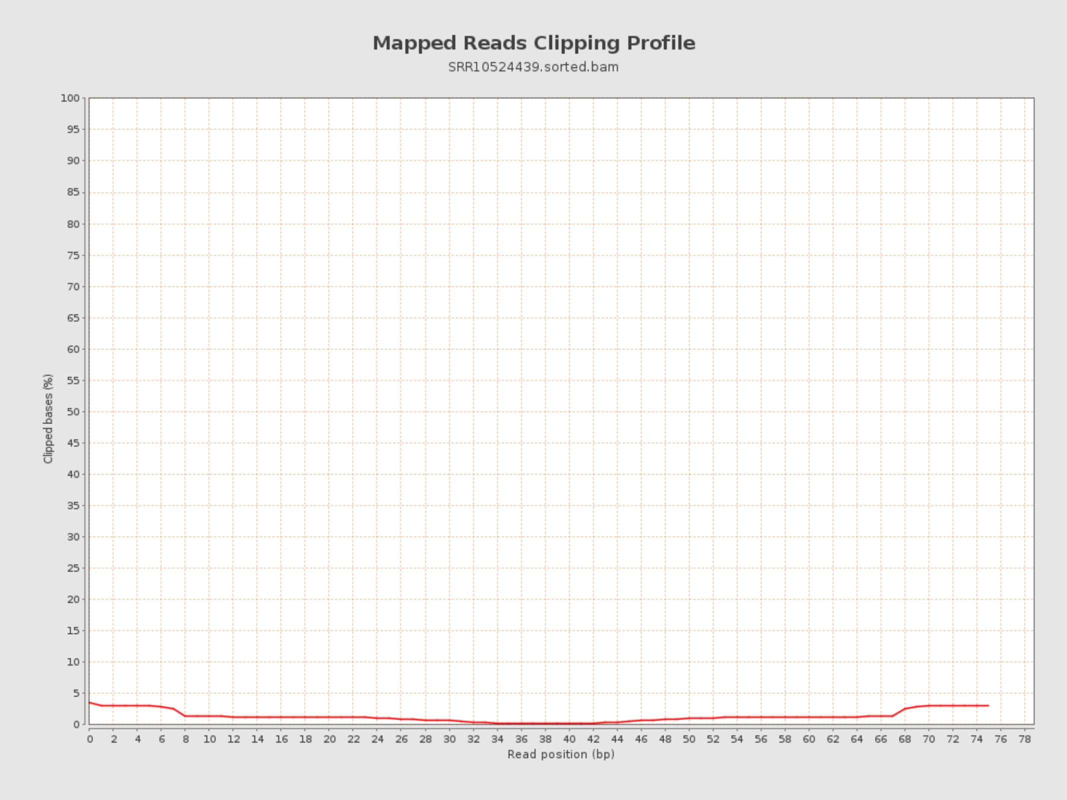
8. Results : Mapped Reads Nucleotide Content



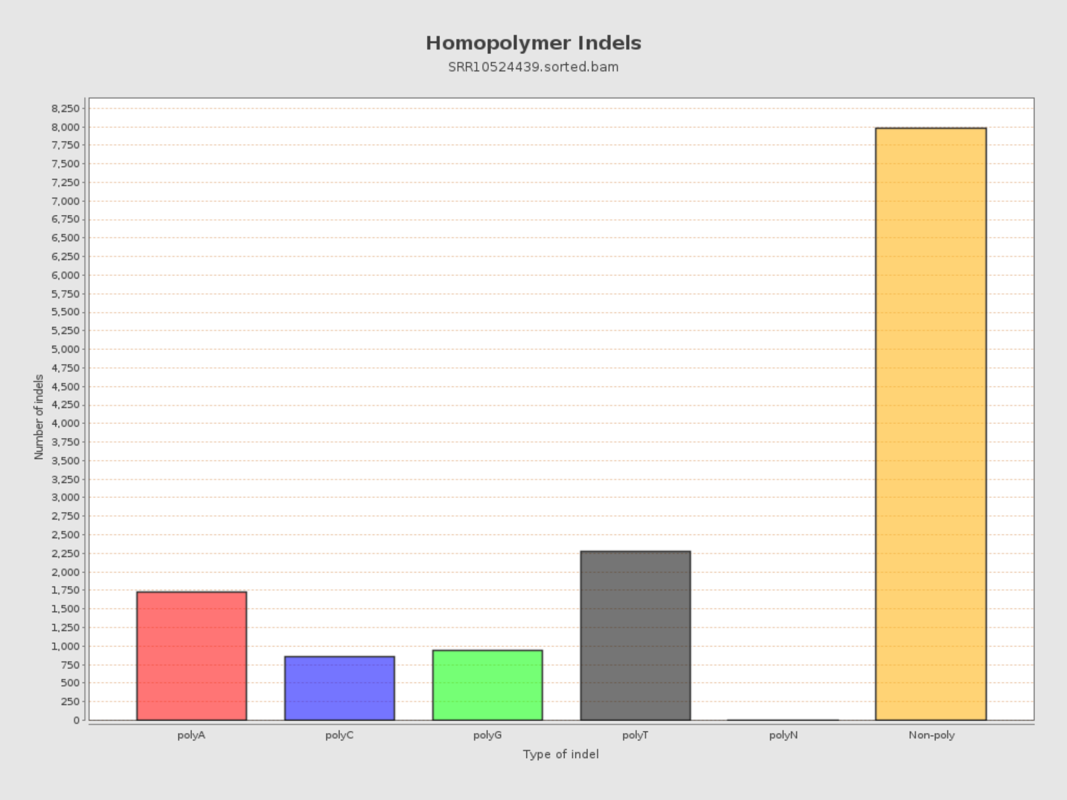
9. Results : Mapped Reads GC-content Distribution



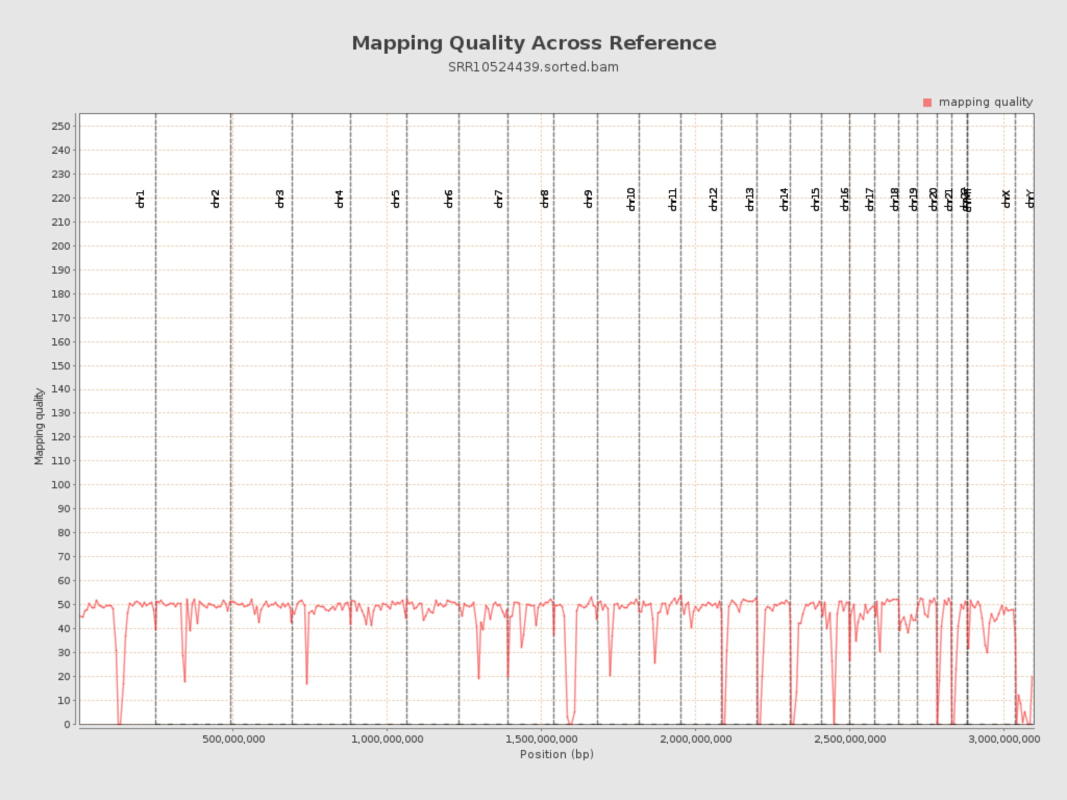
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram