Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:21:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524659.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_SRR10524659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:21:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,634,225
Mapped reads	1,517,280 / 92.84%
Unmapped reads	116,945 / 7.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,711 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	54,169 / 3.31%
Duplication rate	2.6%
Clipped reads	1,519,234 / 92.96%

2.2. ACGT Content

Number/percentage of A's	23,500,893 / 26.07%
Number/percentage of C's	16,267,341 / 18.04%
Number/percentage of T's	28,025,534 / 31.09%
Number/percentage of G's	22,343,652 / 24.78%
Number/percentage of N's	12,550 / 0.01%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0291

Standard Deviation	0.2724

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

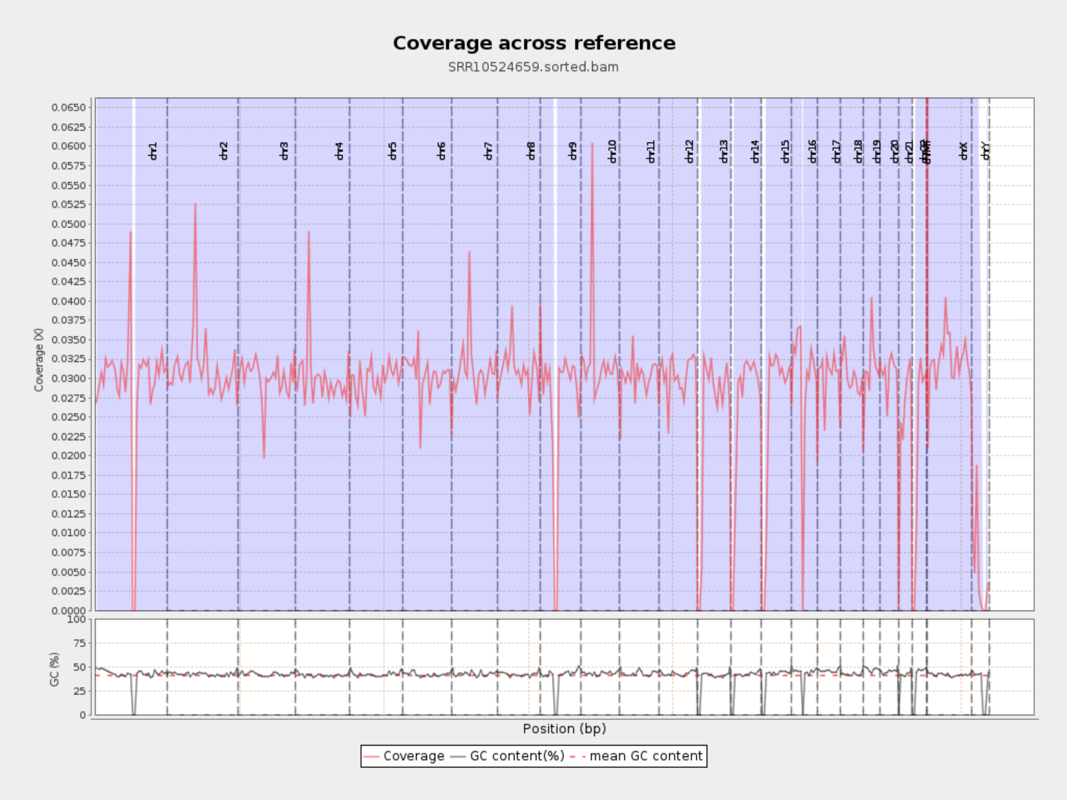
General error rate	0.51%
Mismatches	446,784
Insertions	6,340
Mapped reads with at least one insertion	0.42%
Deletions	16,882
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.49%

2.6. Chromosome stats

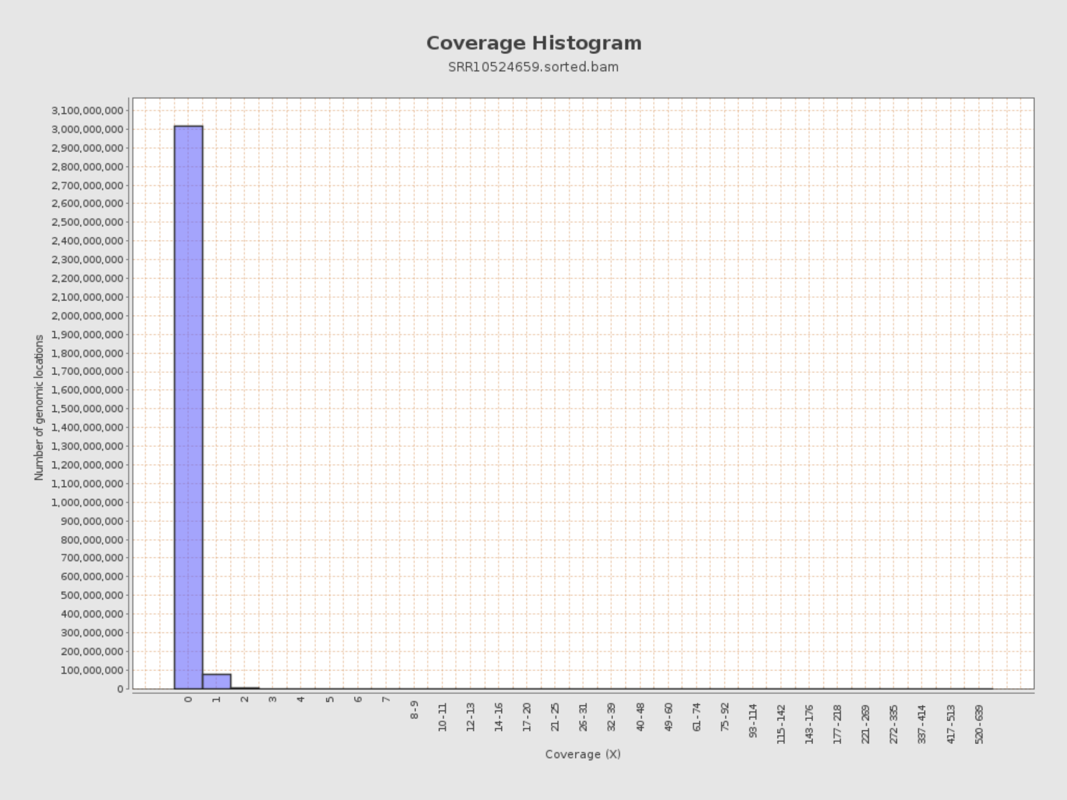
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7271229	0.0292	0.4719
chr2	243199373	7621707	0.0313	0.3603
chr3	198022430	5937944	0.03	0.1877
chr4	191154276	5775734	0.0302	0.2159
chr5	180915260	5421109	0.03	0.1875
chr6	171115067	5199737	0.0304	0.2112
chr7	159138663	4986401	0.0313	0.3188

chr8	146364022	4552874	0.0311	0.2983
chr9	141213431	3769067	0.0267	0.2313
chr10	135534747	4403231	0.0325	0.2912
chr11	135006516	4109264	0.0304	0.2335
chr12	133851895	4070715	0.0304	0.1912
chr13	115169878	2857108	0.0248	0.1709
chr14	107349540	2710914	0.0253	0.177
chr15	102531392	2598224	0.0253	0.1738
chr16	90354753	2638299	0.0292	0.198
chr17	81195210	2473137	0.0305	0.1982
chr18	78077248	2377912	0.0305	0.4131
chr19	59128983	1878114	0.0318	0.3696
chr20	63025520	1923359	0.0305	0.195
chr21	48129895	1190379	0.0247	0.1949
chr22	51304566	1072674	0.0209	0.1559
chrMT	16571	22067	1.3317	1.2772
chrX	155270560	5022644	0.0323	0.2116
chrY	59373566	293064	0.0049	0.1743

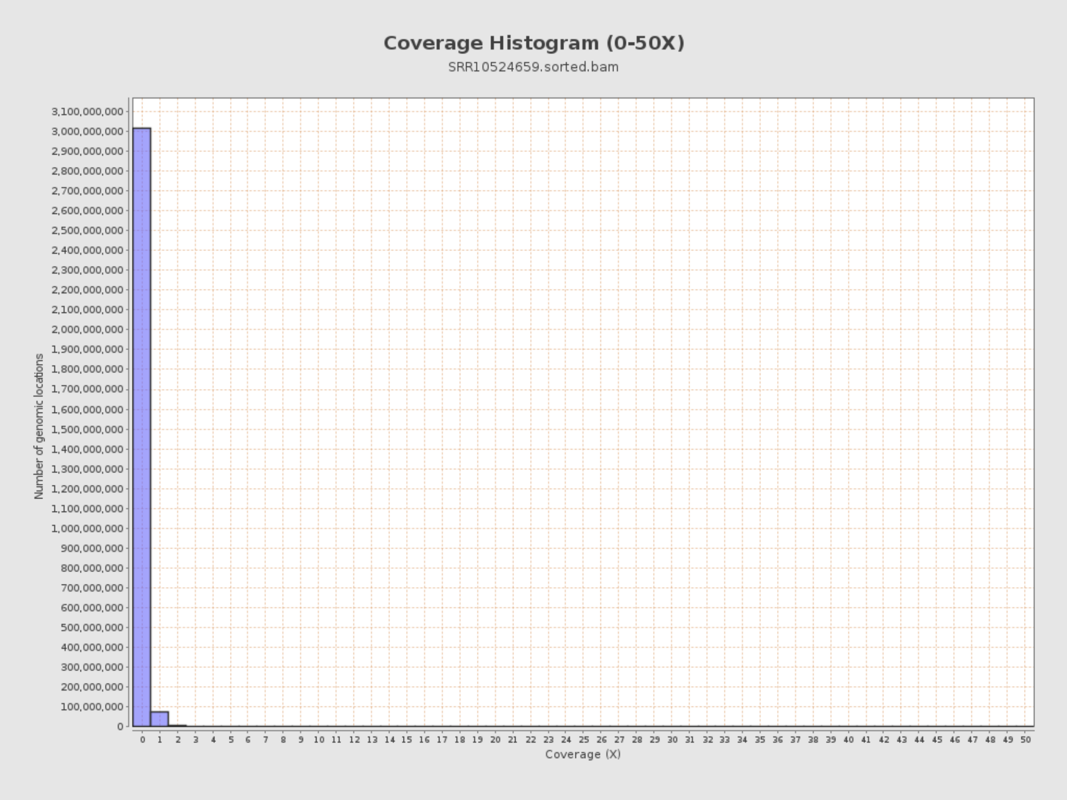
3. Results : Coverage across reference



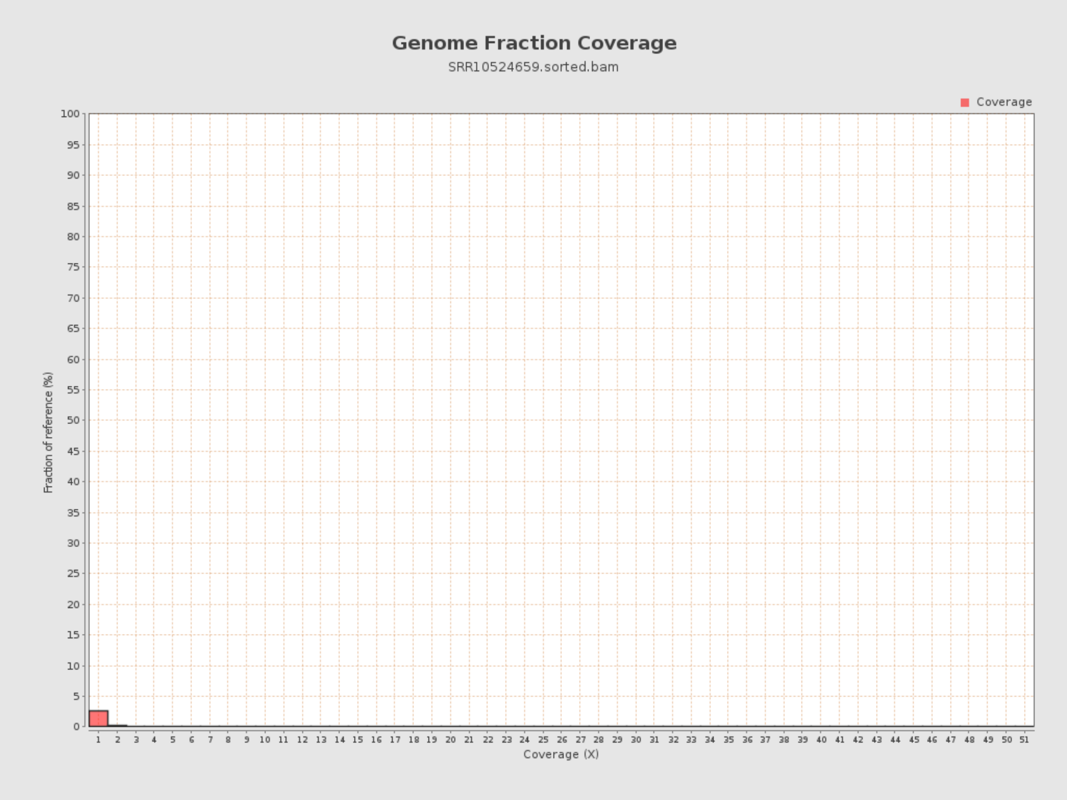
4. Results : Coverage Histogram



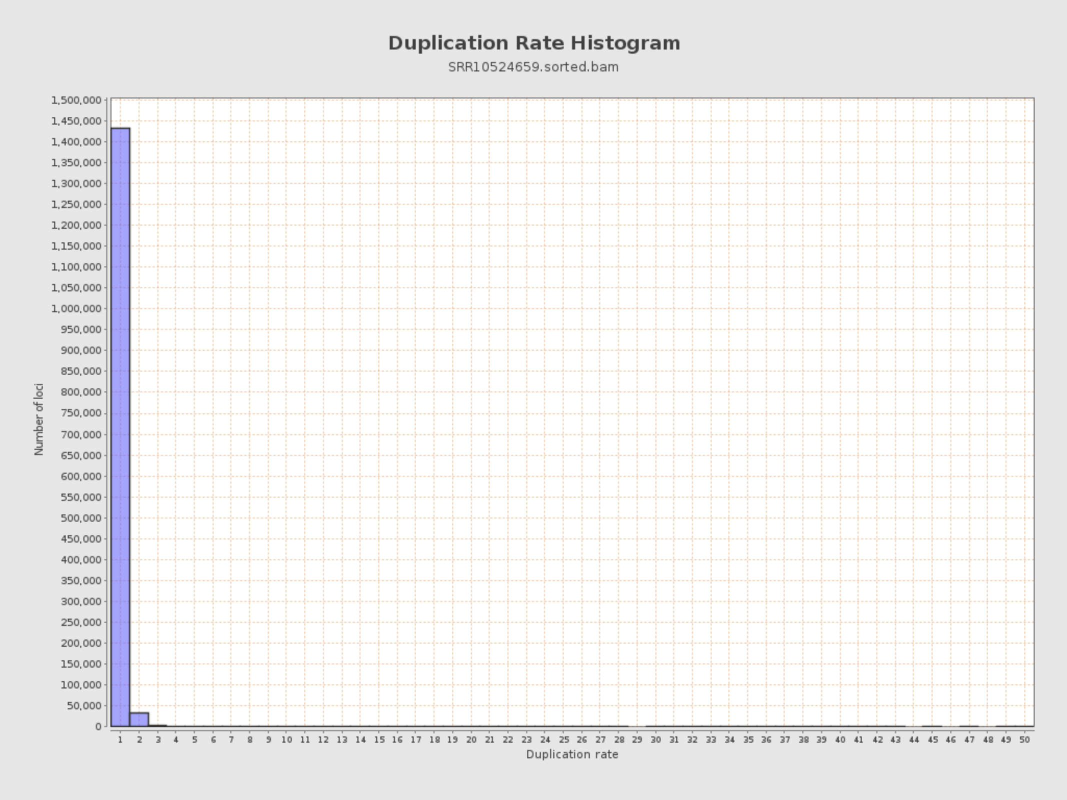
5. Results : Coverage Histogram (0-50X)



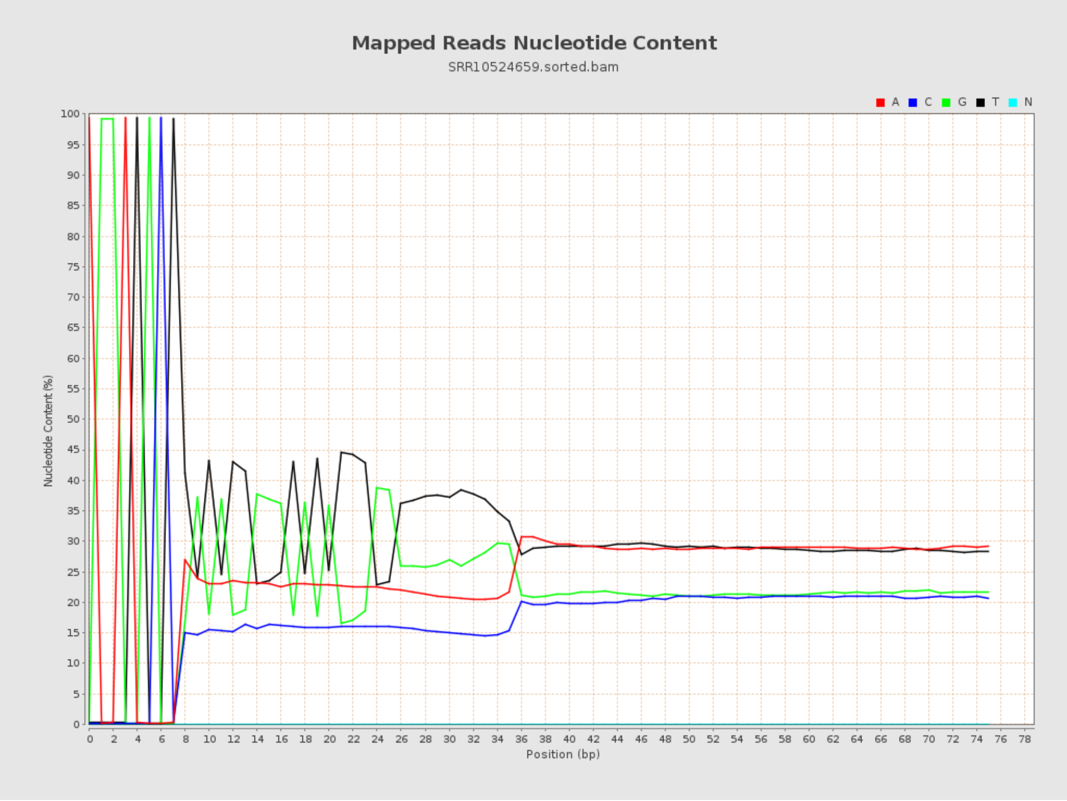
6. Results : Genome Fraction Coverage



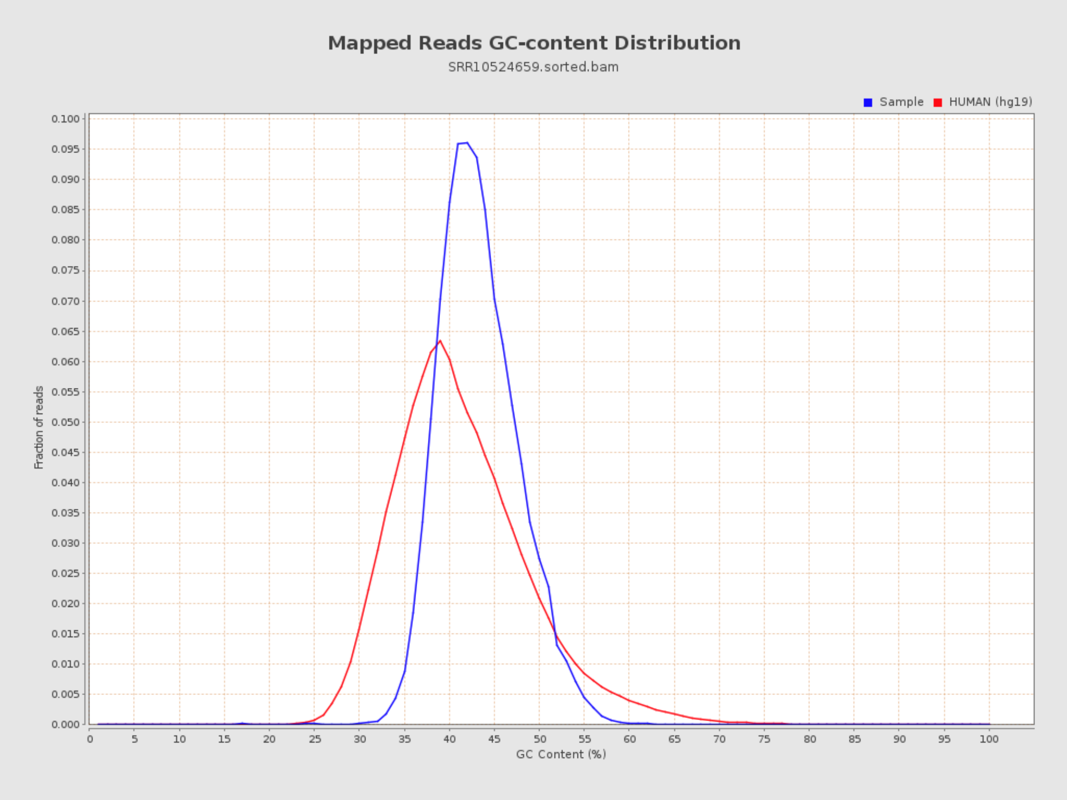
7. Results : Duplication Rate Histogram



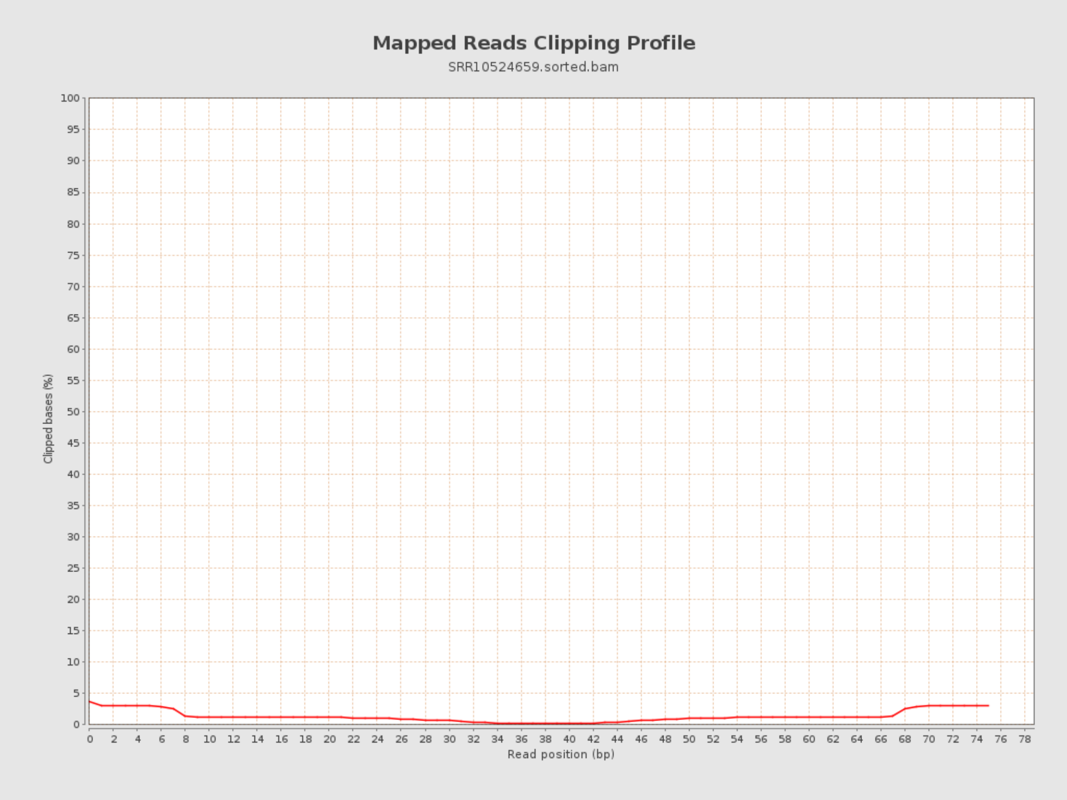
8. Results : Mapped Reads Nucleotide Content



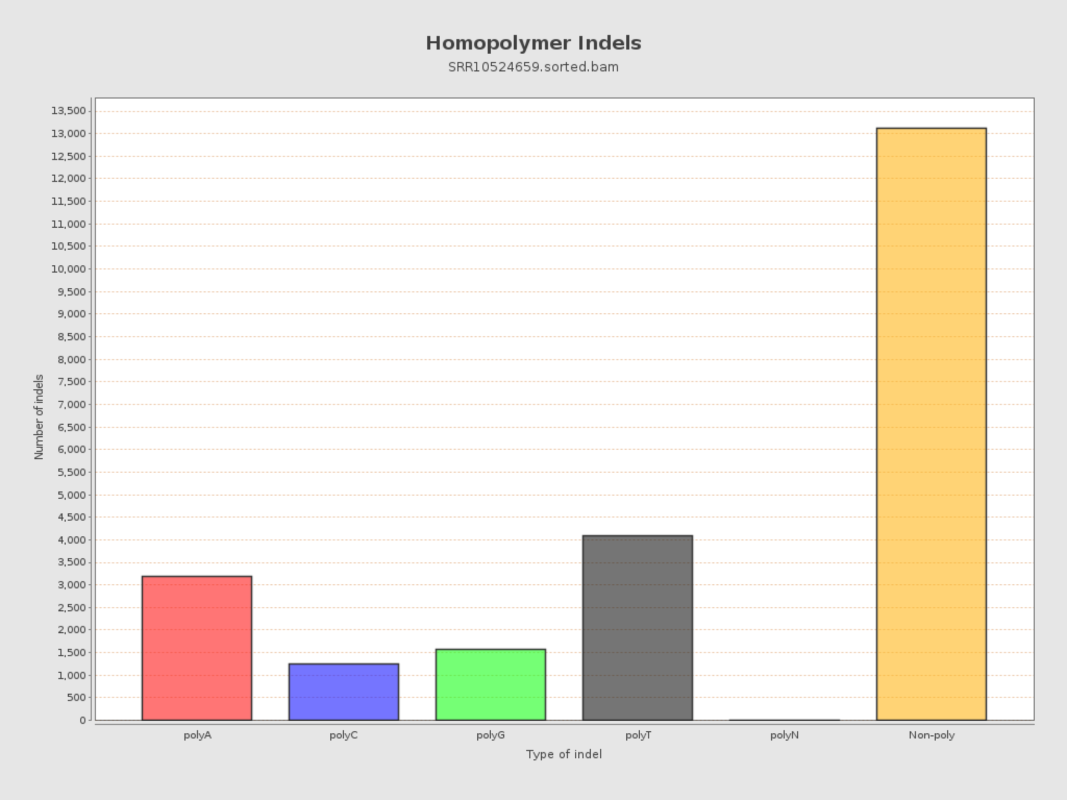
9. Results : Mapped Reads GC-content Distribution



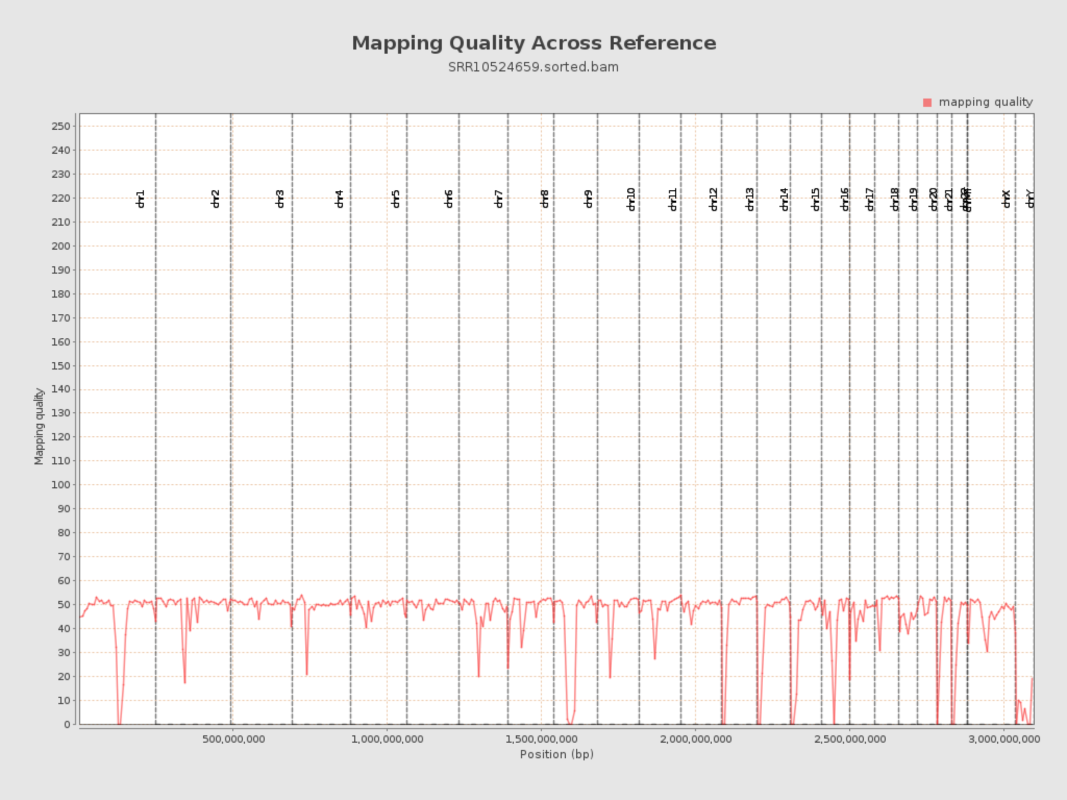
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram