Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:26:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524359.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_SRR10524359 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524359.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:26:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524359.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,598,534
Mapped reads	2,363,437 / 90.95%
Unmapped reads	235,097 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,059 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	129,082 / 4.97%
Duplication rate	3.97%
Clipped reads	2,371,369 / 91.26%

2.2. ACGT Content

Number/percentage of A's	34,105,477 / 24.98%
Number/percentage of C's	27,067,128 / 19.83%
Number/percentage of T's	42,466,836 / 31.11%
Number/percentage of G's	32,851,889 / 24.07%
Number/percentage of N's	18,251 / 0.01%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.4131

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Mismatches and indels

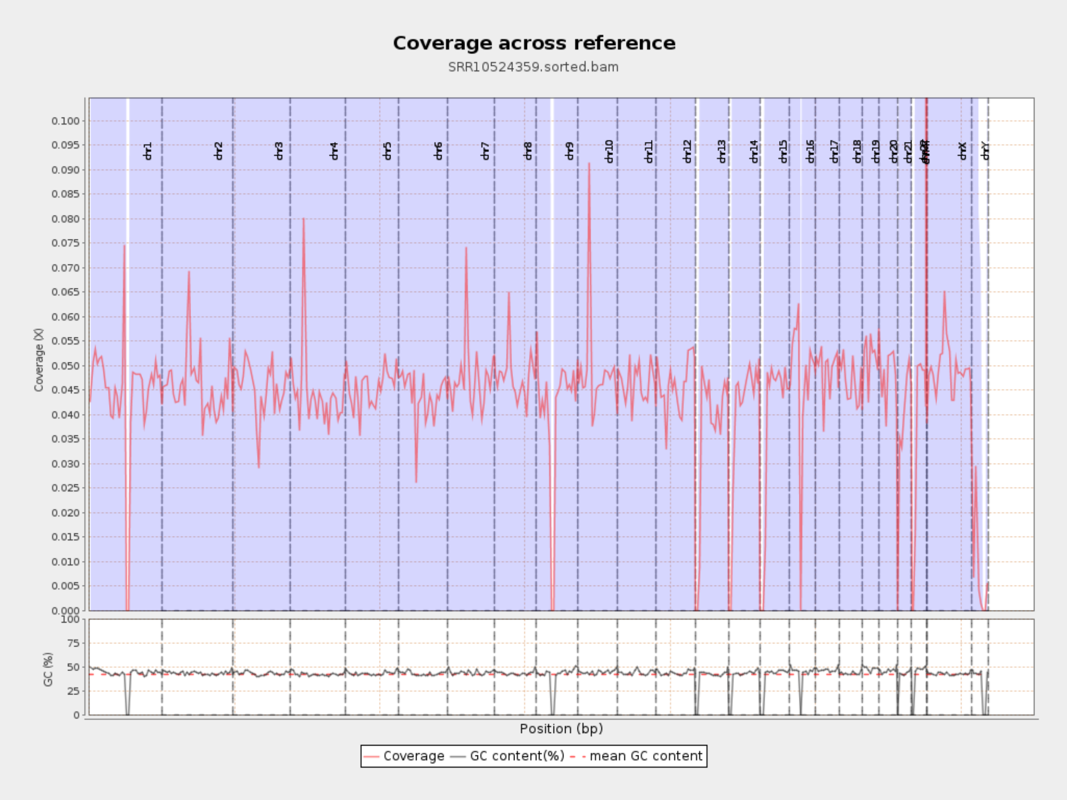
General error rate	0.54%
Mismatches	717,159
Insertions	8,319
Mapped reads with at least one insertion	0.35%
Deletions	23,033
Mapped reads with at least one deletion	0.97%
Homopolymer indels	42.5%

2.6. Chromosome stats

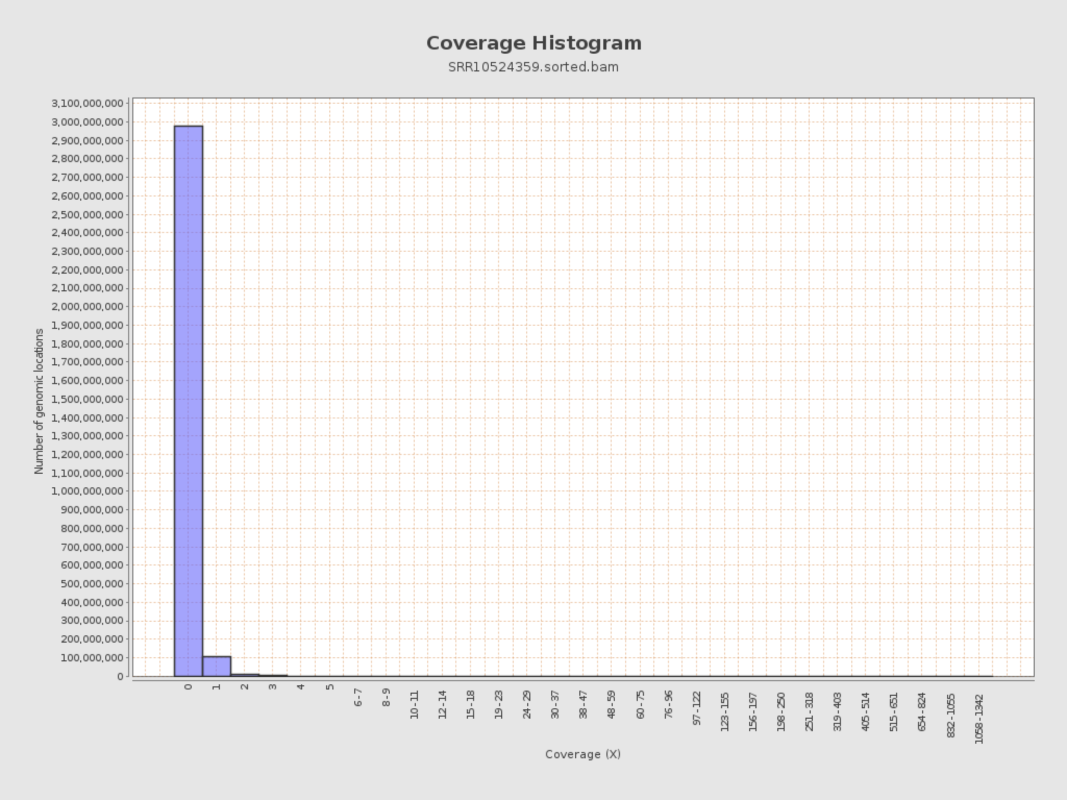
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11006413	0.0442	0.8063
chr2	243199373	11221941	0.0461	0.6038
chr3	198022430	9012472	0.0455	0.2479
chr4	191154276	8454392	0.0442	0.2957
chr5	180915260	8240821	0.0456	0.2448
chr6	171115067	7520359	0.0439	0.2672
chr7	159138663	7544134	0.0474	0.5107

chr8	146364022	6997888	0.0478	0.3319
chr9	141213431	5603944	0.0397	0.3179
chr10	135534747	6614590	0.0488	0.4151
chr11	135006516	6253997	0.0463	0.3564
chr12	133851895	6168431	0.0461	0.2511
chr13	115169878	4140957	0.036	0.2174
chr14	107349540	4151901	0.0387	0.2453
chr15	102531392	3892770	0.038	0.2252
chr16	90354753	4263448	0.0472	0.2807
chr17	81195210	3975464	0.049	0.2694
chr18	78077248	3659179	0.0469	0.6425
chr19	59128983	3049280	0.0516	0.5161
chr20	63025520	3022975	0.048	0.2587
chr21	48129895	1833705	0.0381	0.2676
chr22	51304566	1746796	0.034	0.2141
chrMT	16571	29646	1.789	1.7082
chrX	155270560	7663528	0.0494	0.2946
chrY	59373566	477275	0.008	0.2226

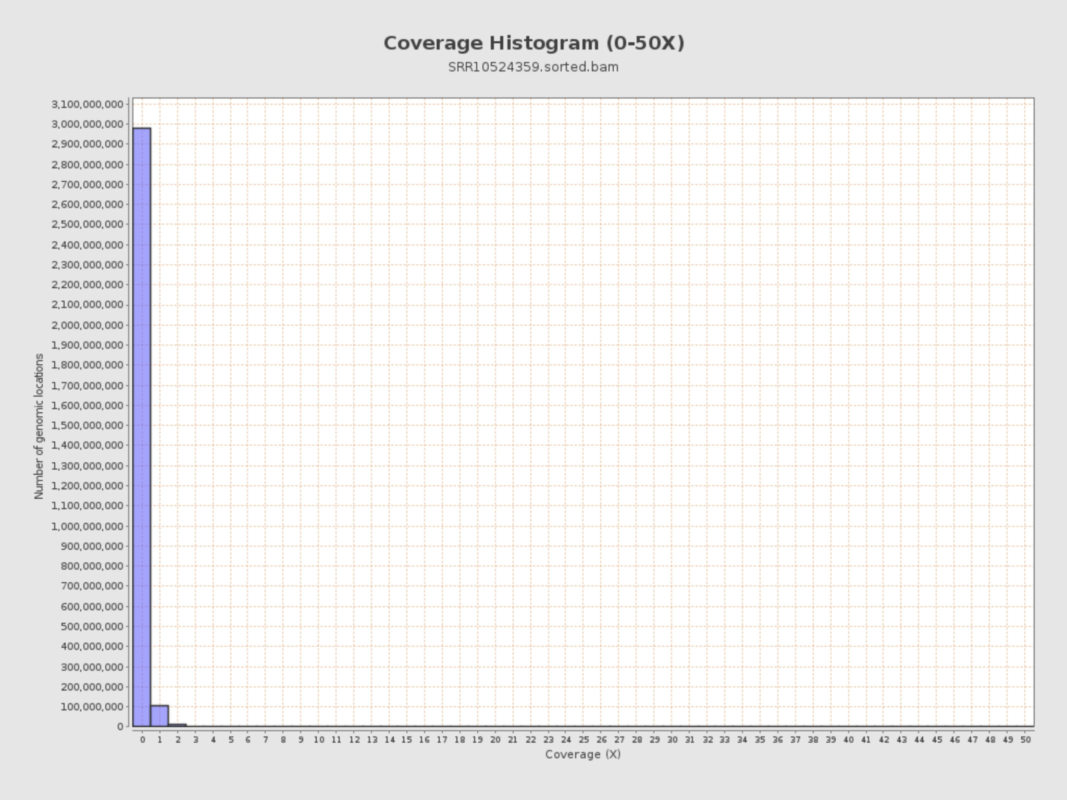
3. Results : Coverage across reference



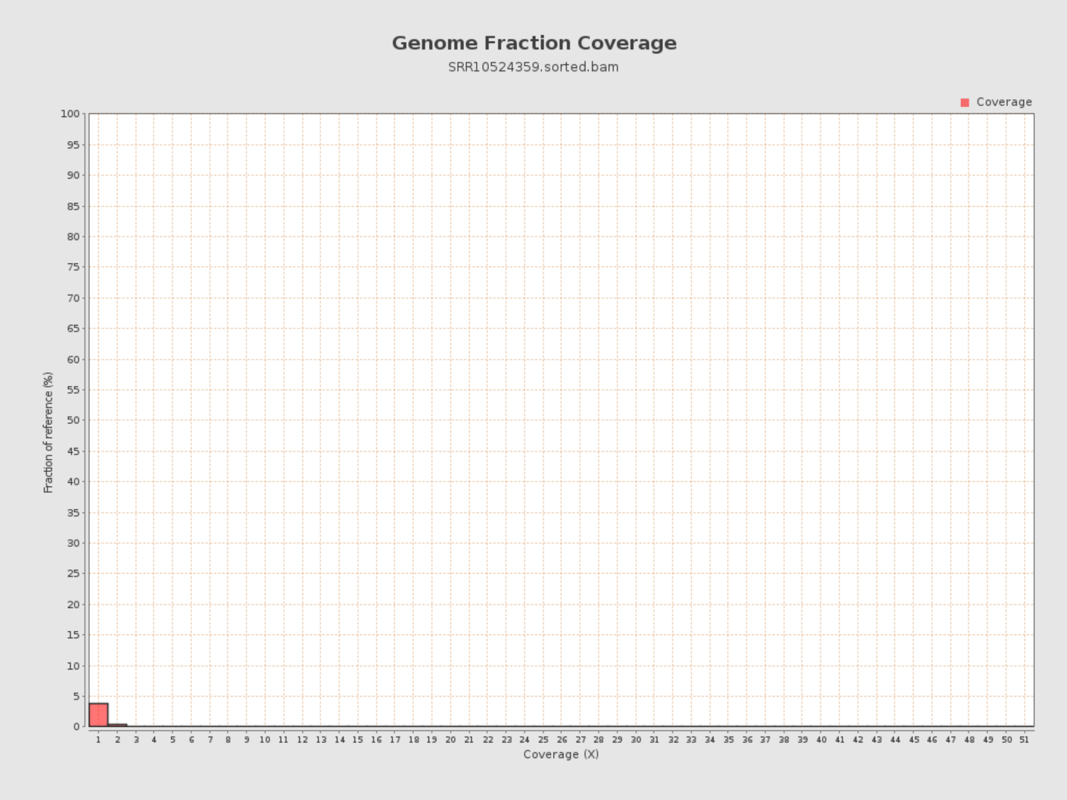
4. Results : Coverage Histogram



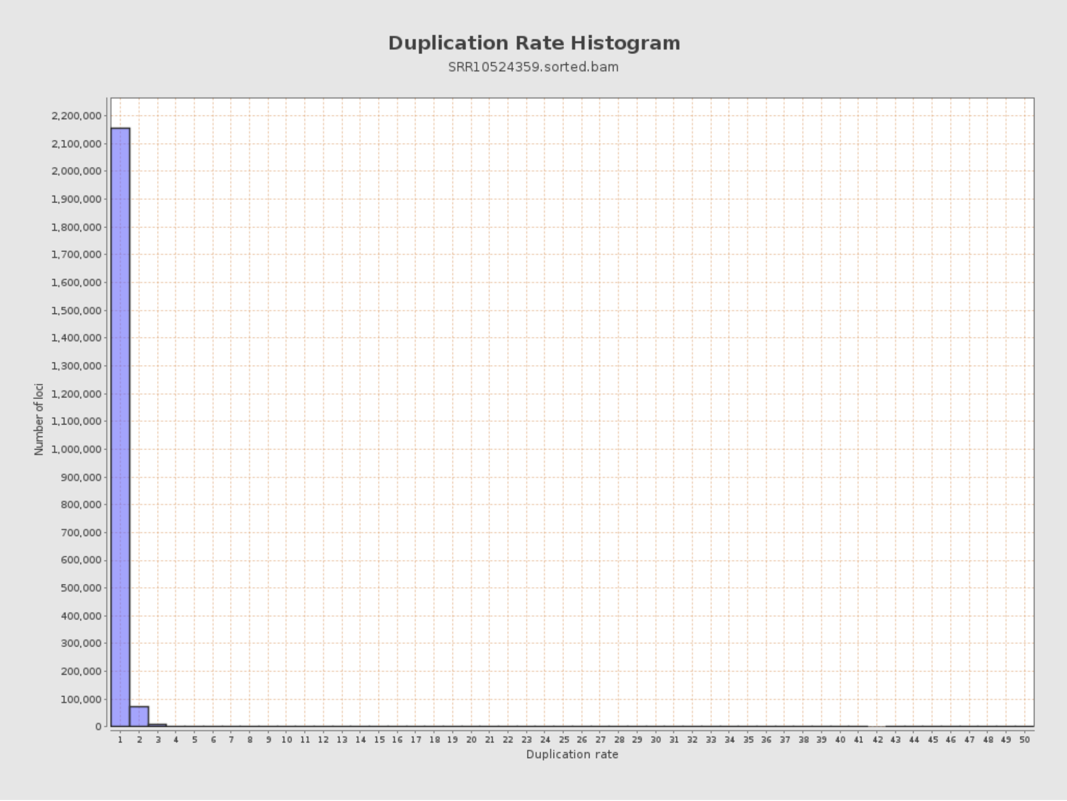
5. Results : Coverage Histogram (0-50X)



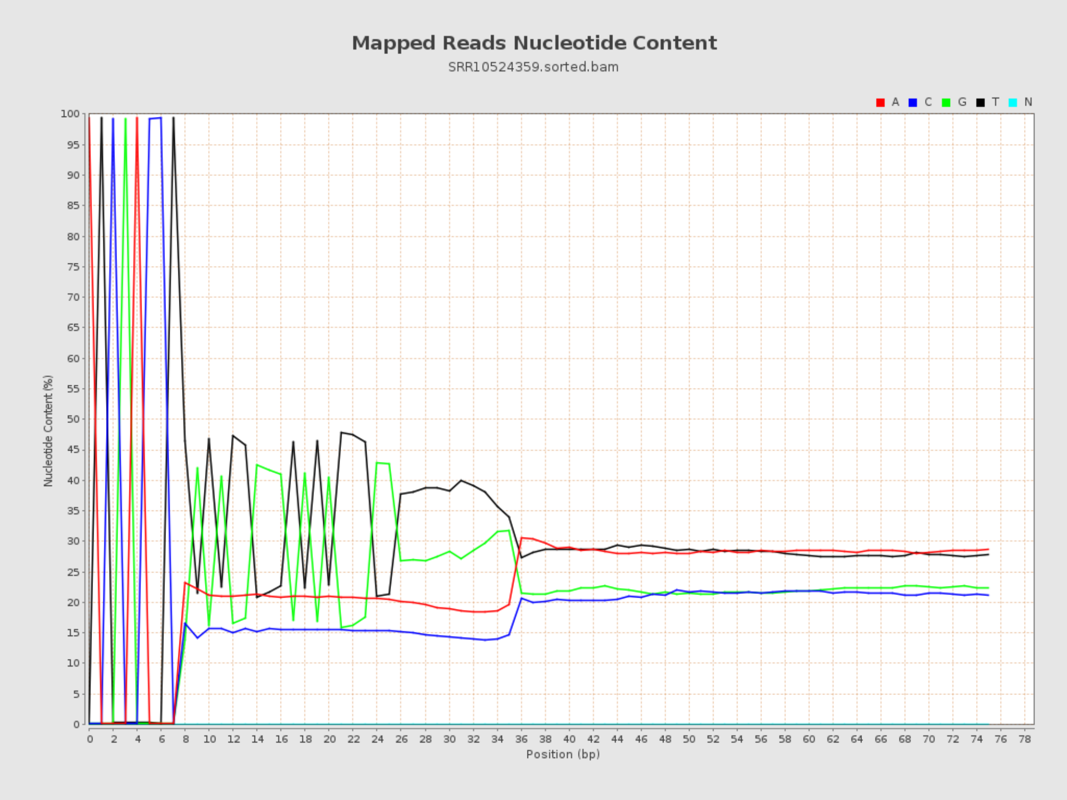
6. Results : Genome Fraction Coverage



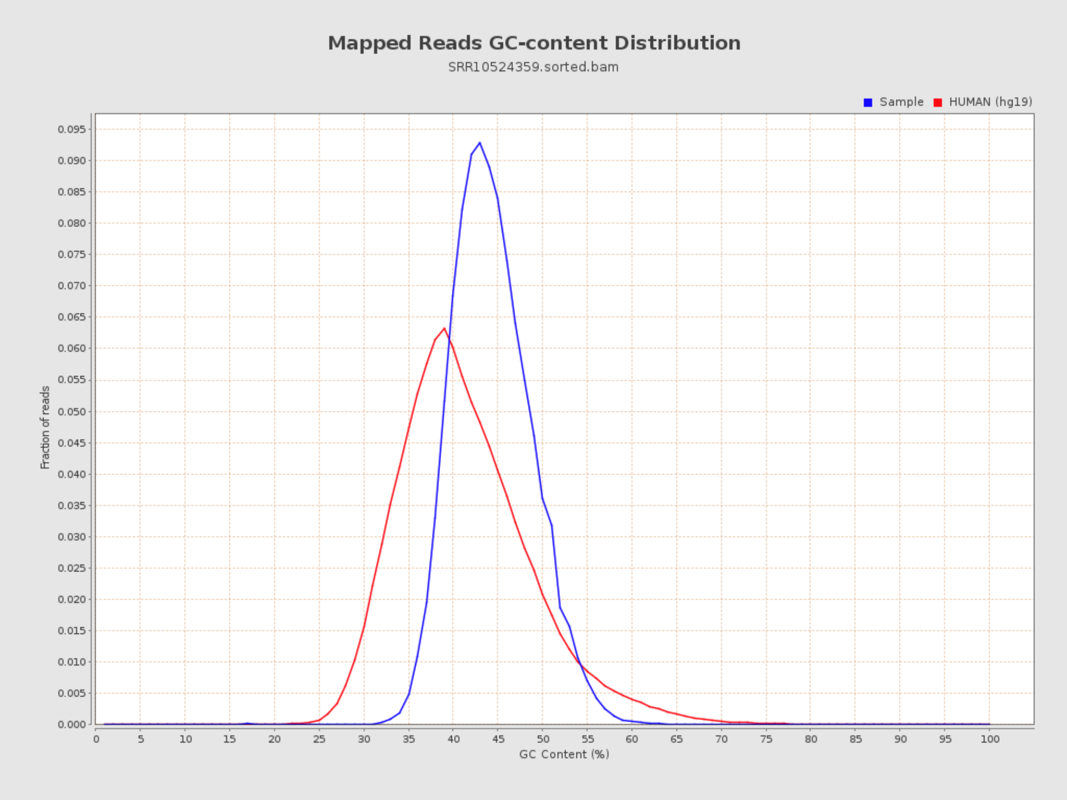
7. Results : Duplication Rate Histogram



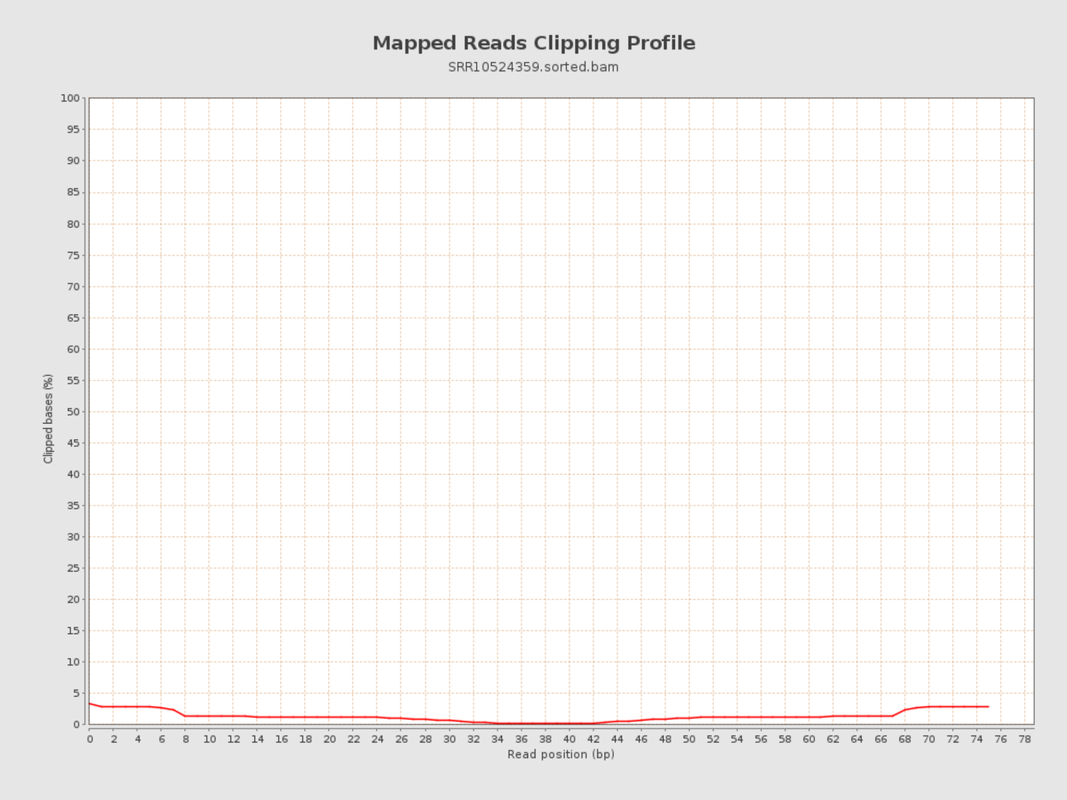
8. Results : Mapped Reads Nucleotide Content



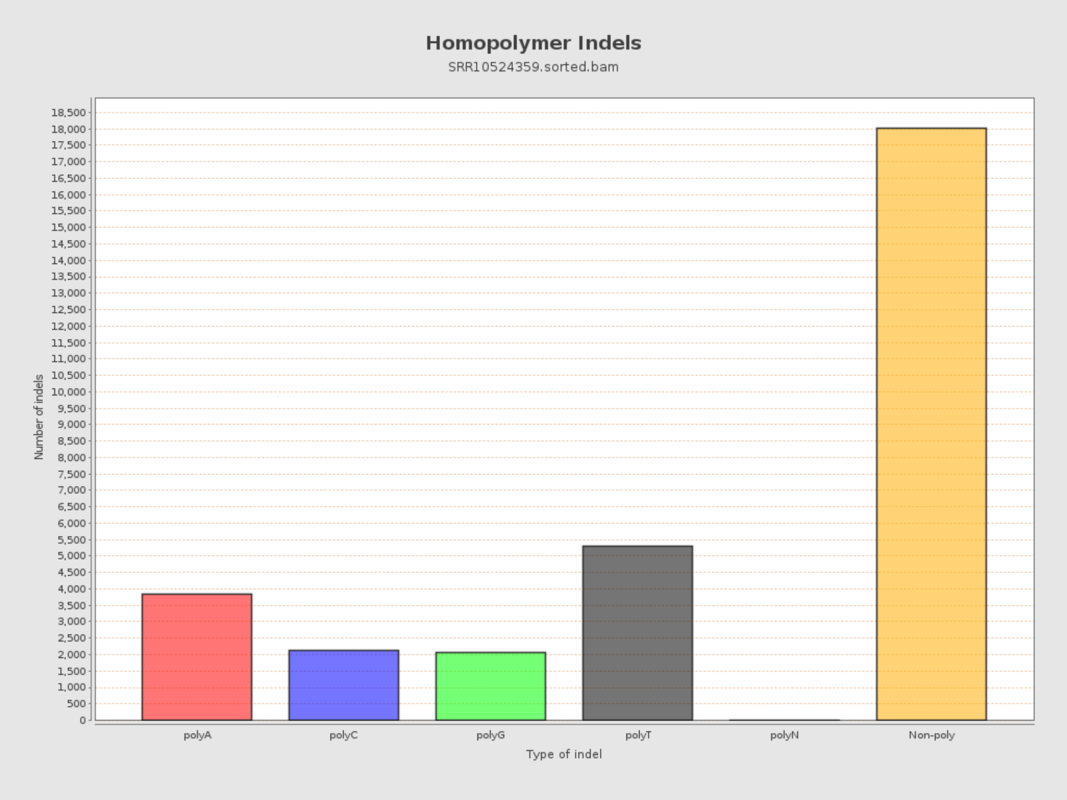
9. Results : Mapped Reads GC-content Distribution



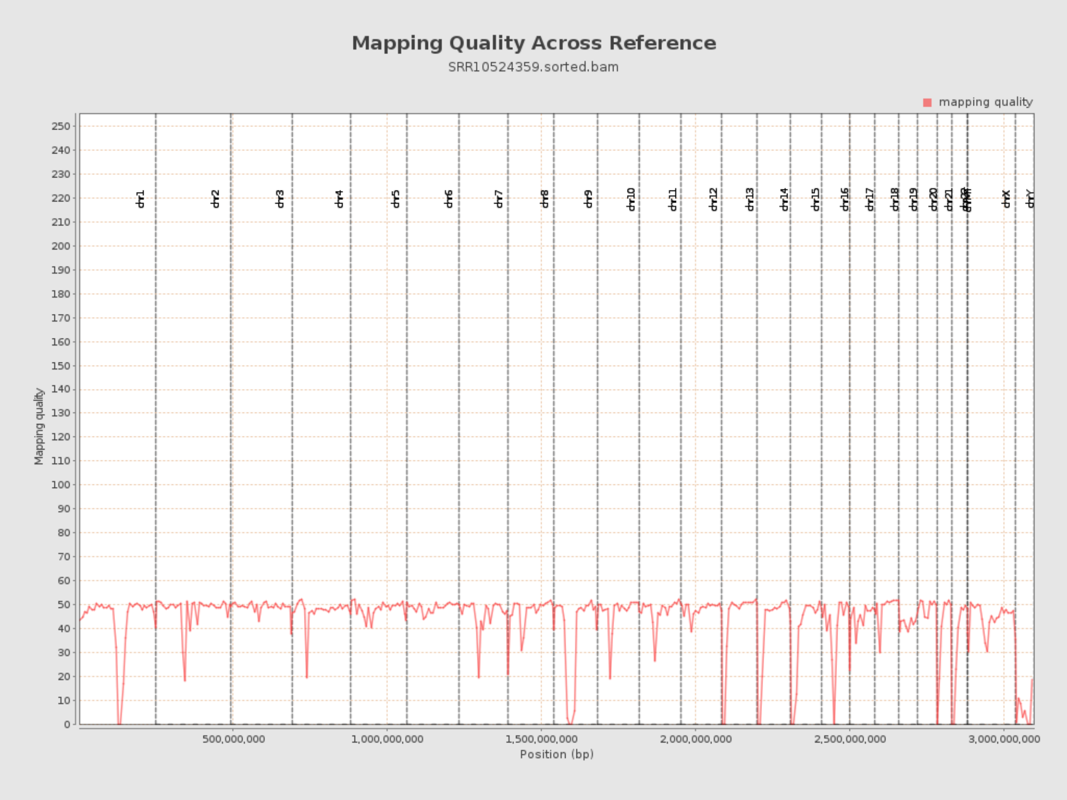
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram