Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:14:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524827.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_SRR10524827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524827.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:14:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	930,611
Mapped reads	846,558 / 90.97%
Unmapped reads	84,053 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,585 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	19,412 / 2.09%
Duplication rate	1.71%
Clipped reads	847,711 / 91.09%

2.2. ACGT Content

Number/percentage of A's	12,216,086 / 25.14%
Number/percentage of C's	9,080,363 / 18.69%
Number/percentage of T's	14,773,222 / 30.4%
Number/percentage of G's	12,514,937 / 25.76%
Number/percentage of N's	5,947 / 0.01%
GC Percentage	44.44%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.1583

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

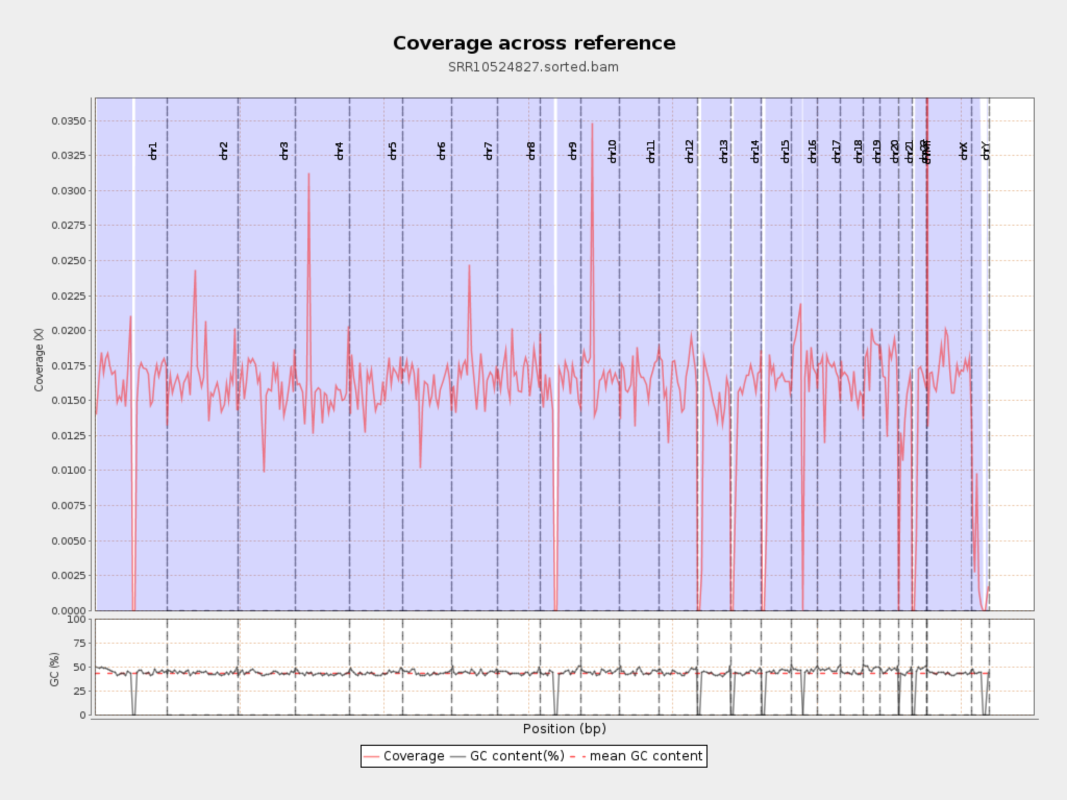
General error rate	0.52%
Mismatches	244,559
Insertions	3,697
Mapped reads with at least one insertion	0.43%
Deletions	9,493
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.27%

2.6. Chromosome stats

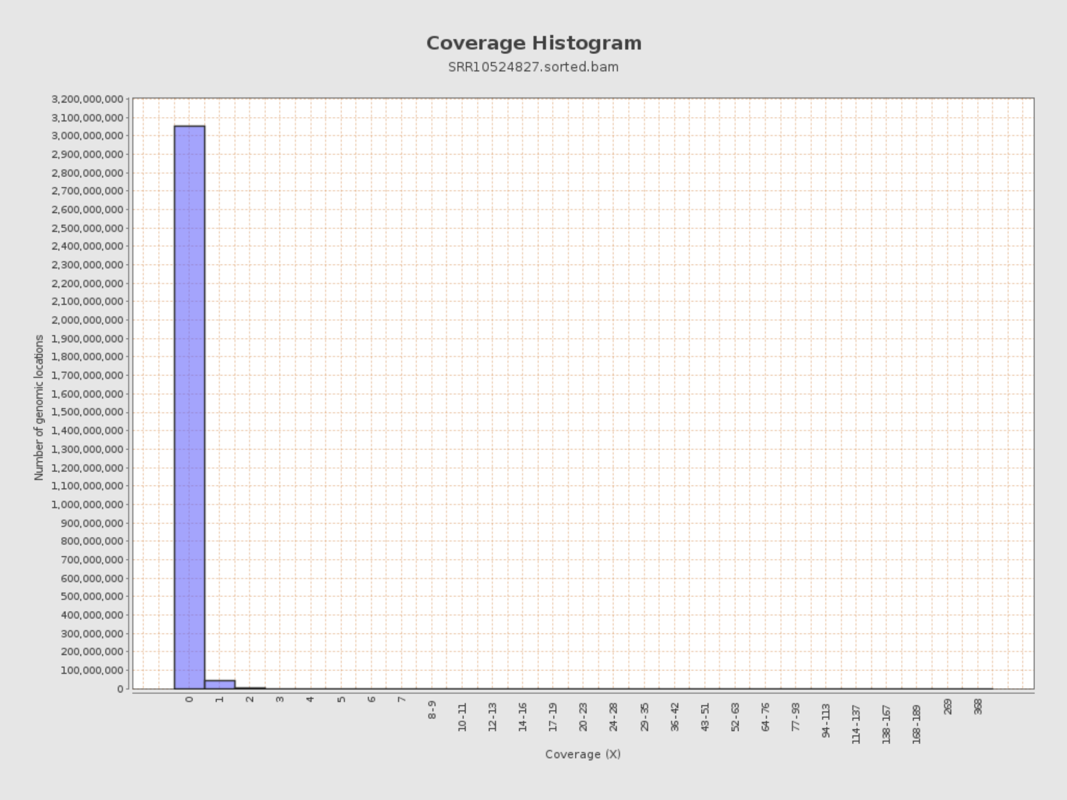
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3918623	0.0157	0.1879
chr2	243199373	4034838	0.0166	0.2171
chr3	198022430	3170297	0.016	0.1357
chr4	191154276	3081152	0.0161	0.1501
chr5	180915260	2925509	0.0162	0.1344
chr6	171115067	2734865	0.016	0.138
chr7	159138663	2697102	0.0169	0.1877

chr8	146364022	2477661	0.0169	0.1508
chr9	141213431	2040381	0.0144	0.1412
chr10	135534747	2403358	0.0177	0.1971
chr11	135006516	2243586	0.0166	0.1529
chr12	133851895	2201717	0.0164	0.136
chr13	115169878	1487237	0.0129	0.1203
chr14	107349540	1467596	0.0137	0.1254
chr15	102531392	1385645	0.0135	0.1236
chr16	90354753	1512032	0.0167	0.1475
chr17	81195210	1372246	0.0169	0.1416
chr18	78077248	1255265	0.0161	0.2055
chr19	59128983	1080945	0.0183	0.1762
chr20	63025520	1080462	0.0171	0.1427
chr21	48129895	613408	0.0127	0.132
chr22	51304566	597545	0.0116	0.1151
chrMT	16571	10182	0.6144	0.8634
chrX	155270560	2654435	0.0171	0.1448
chrY	59373566	159756	0.0027	0.0854

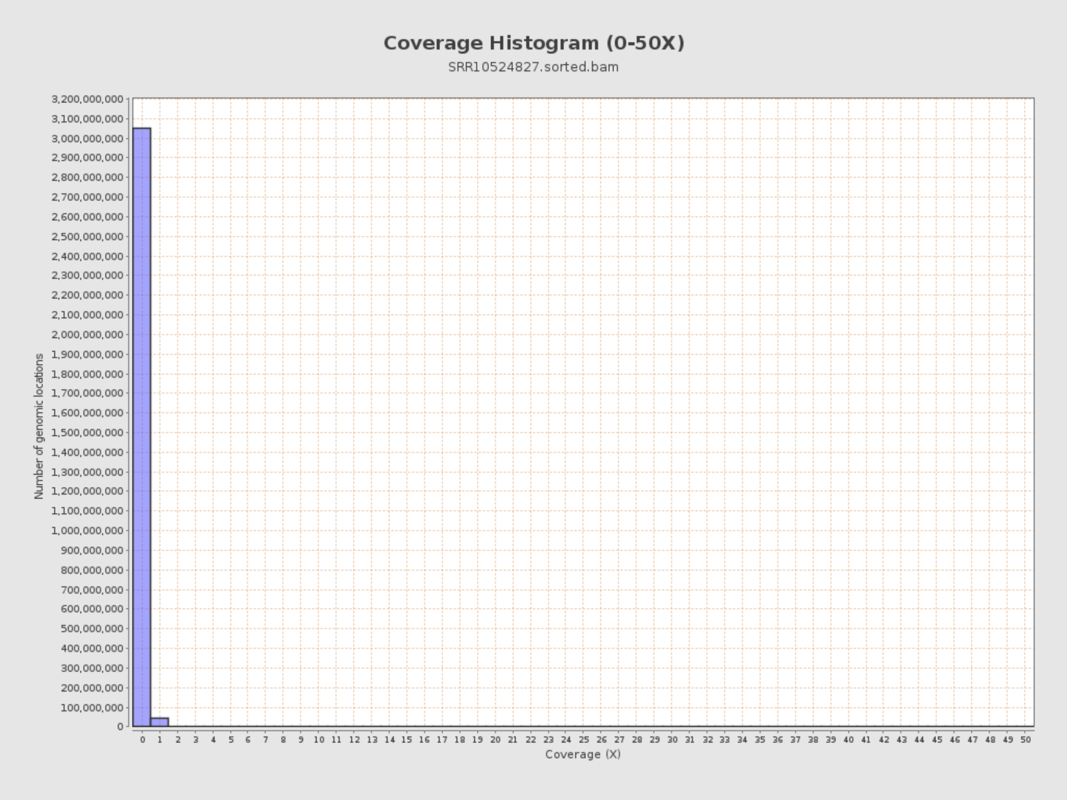
3. Results : Coverage across reference



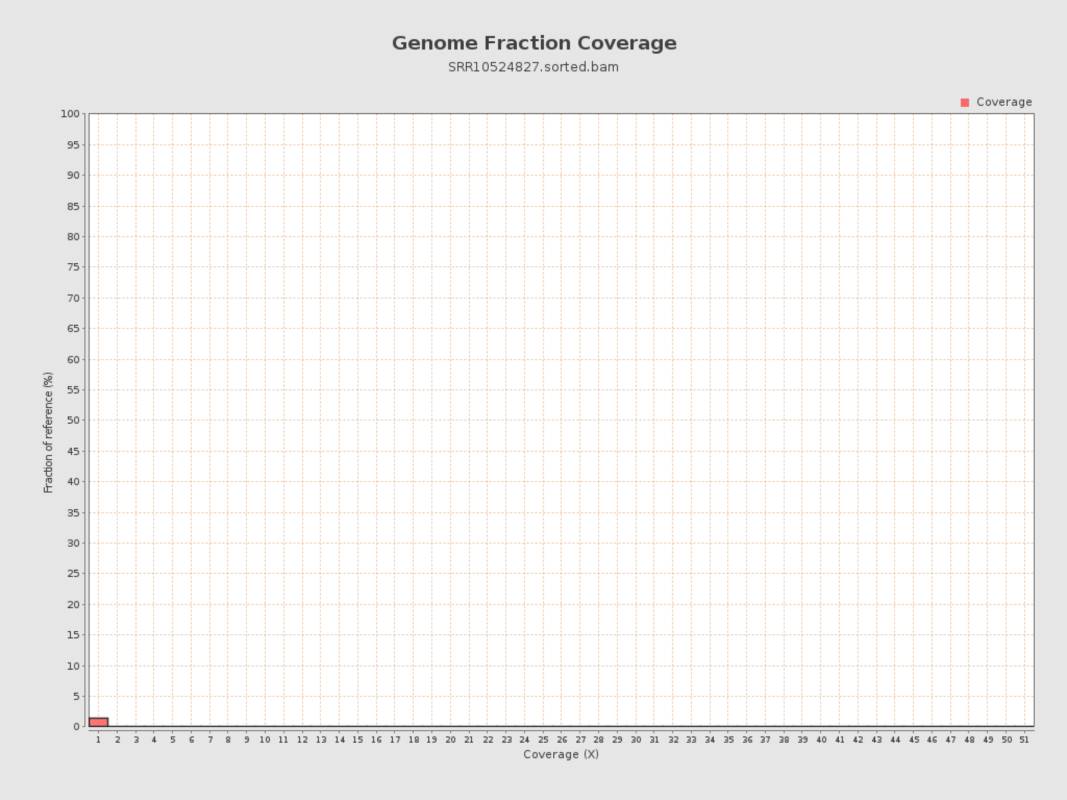
4. Results : Coverage Histogram



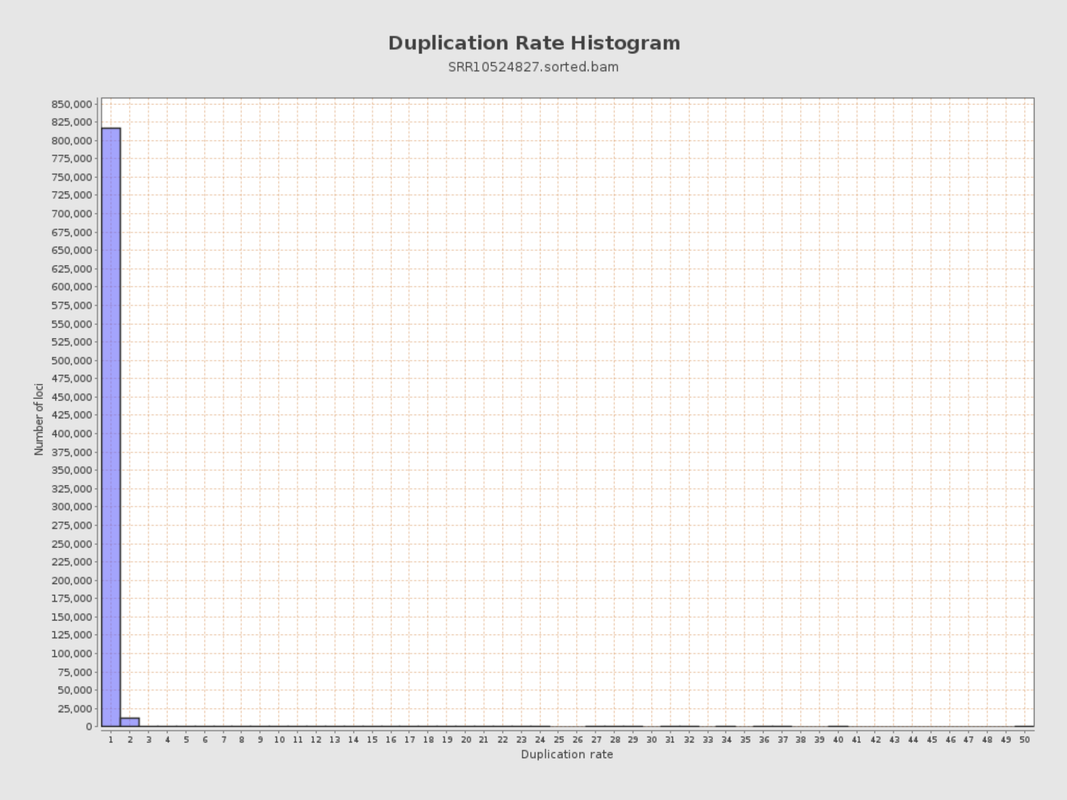
5. Results : Coverage Histogram (0-50X)



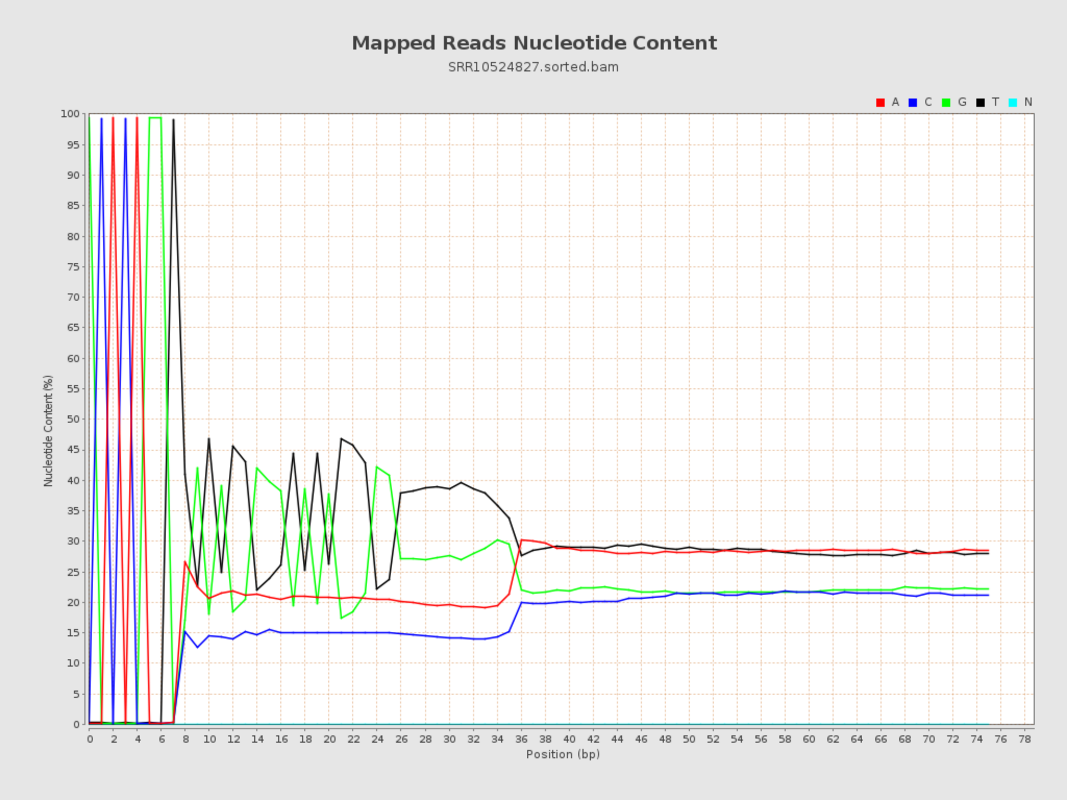
6. Results : Genome Fraction Coverage



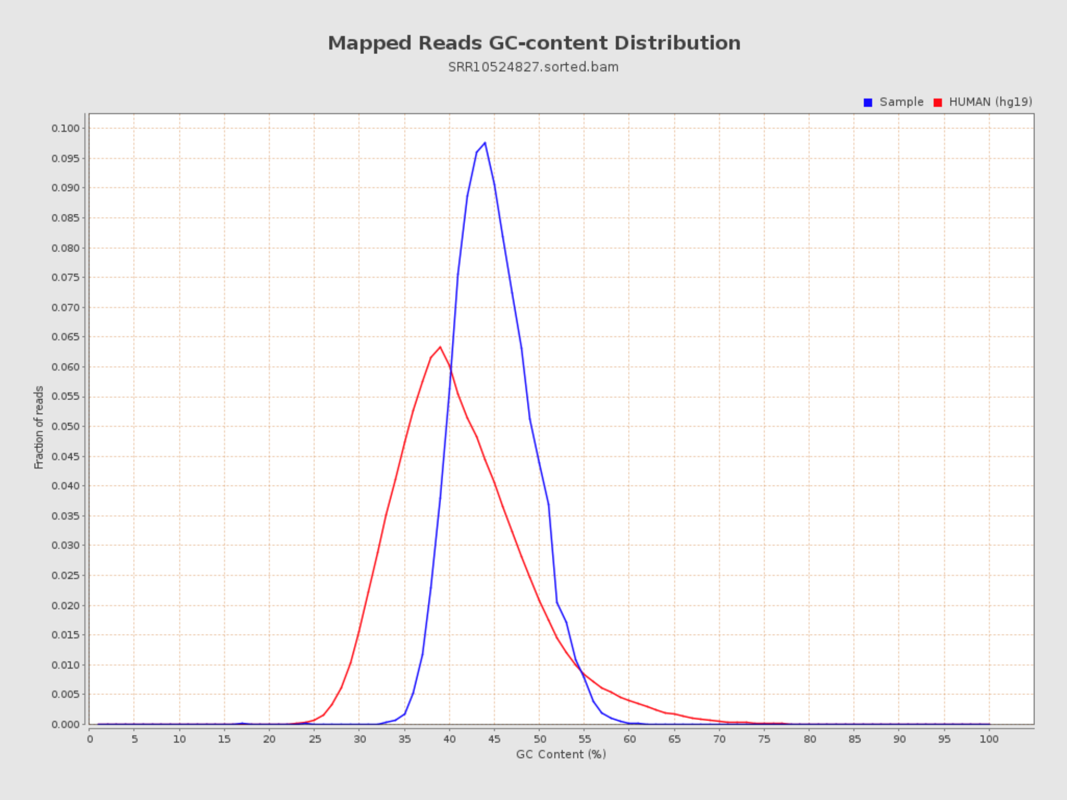
7. Results : Duplication Rate Histogram



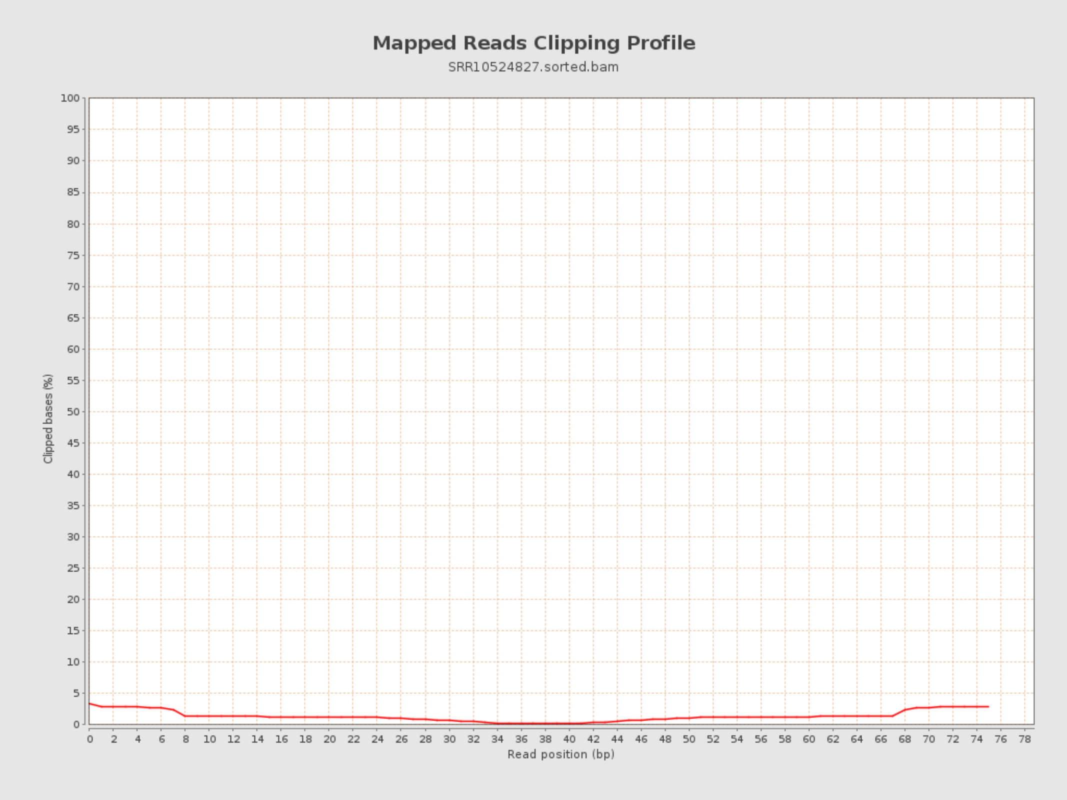
8. Results : Mapped Reads Nucleotide Content



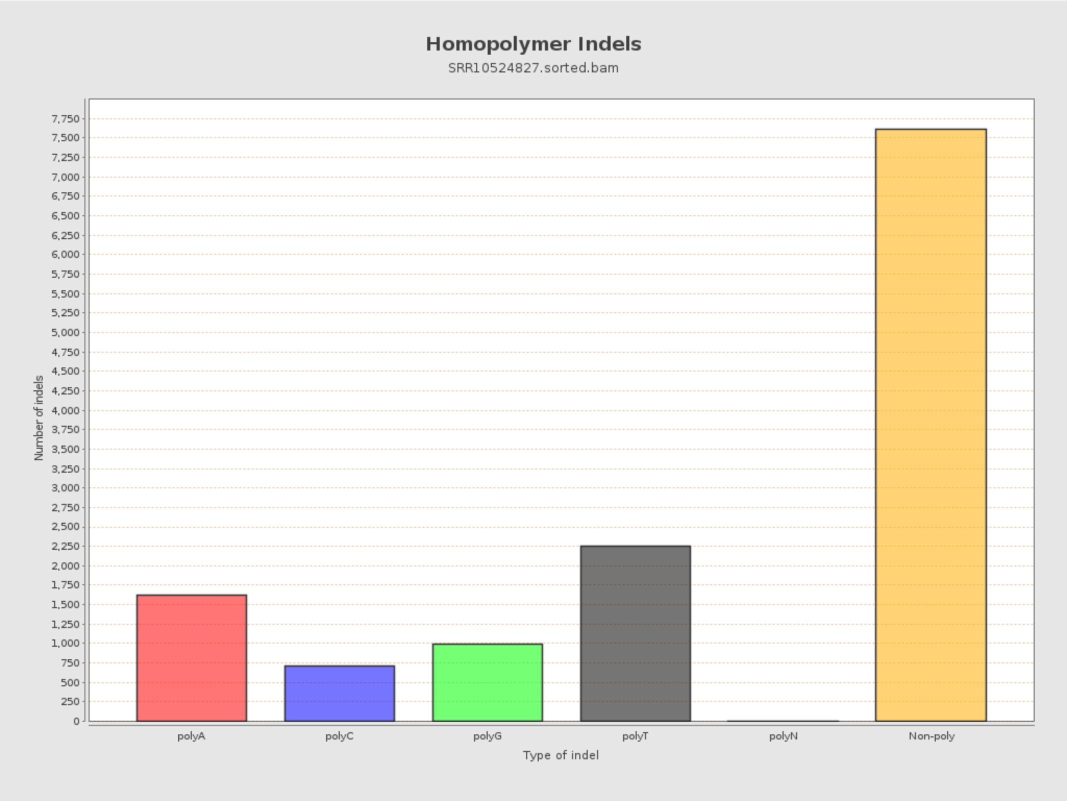
9. Results : Mapped Reads GC-content Distribution



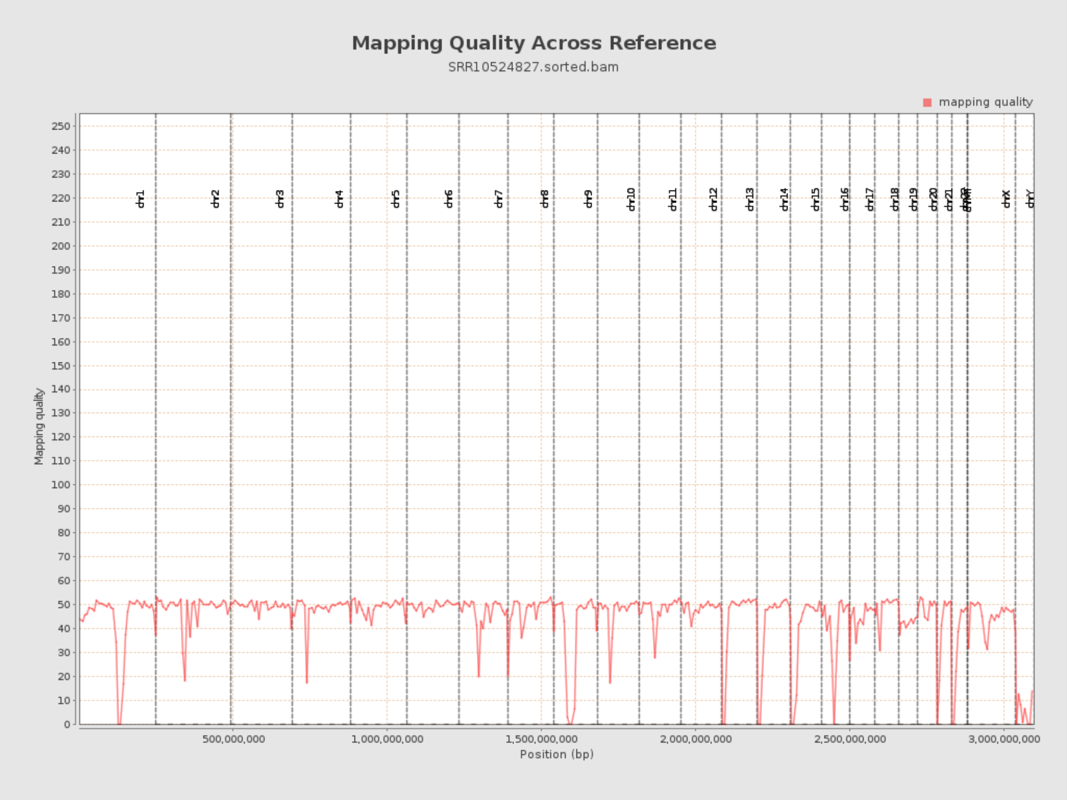
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram