Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 20:49:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524279.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_SRR10524279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524279.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 20:49:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,350,917
Mapped reads	1,249,401 / 92.49%
Unmapped reads	101,516 / 7.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,010 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	38,618 / 2.86%
Duplication rate	2.19%
Clipped reads	1,250,540 / 92.57%

2.2. ACGT Content

Number/percentage of A's	18,556,801 / 25.3%
Number/percentage of C's	13,587,251 / 18.53%
Number/percentage of T's	23,596,986 / 32.18%
Number/percentage of G's	17,586,934 / 23.98%
Number/percentage of N's	9,886 / 0.01%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2464

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

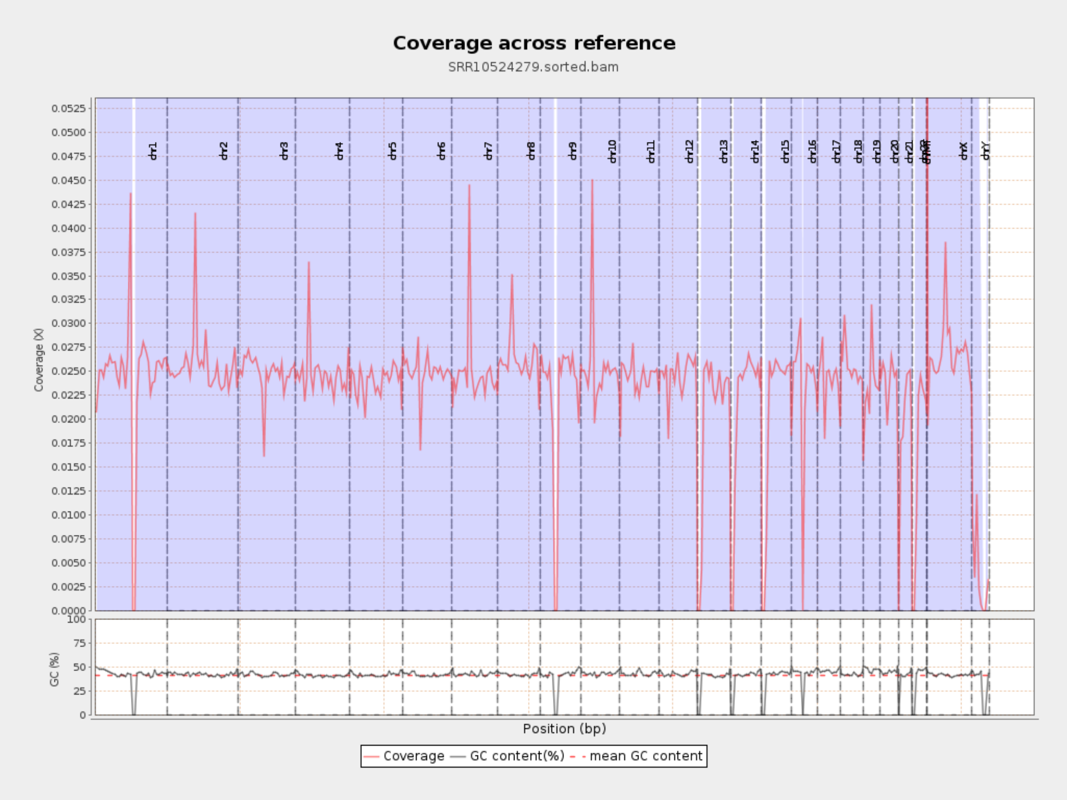
General error rate	0.5%
Mismatches	357,798
Insertions	5,173
Mapped reads with at least one insertion	0.41%
Deletions	14,523
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.73%

2.6. Chromosome stats

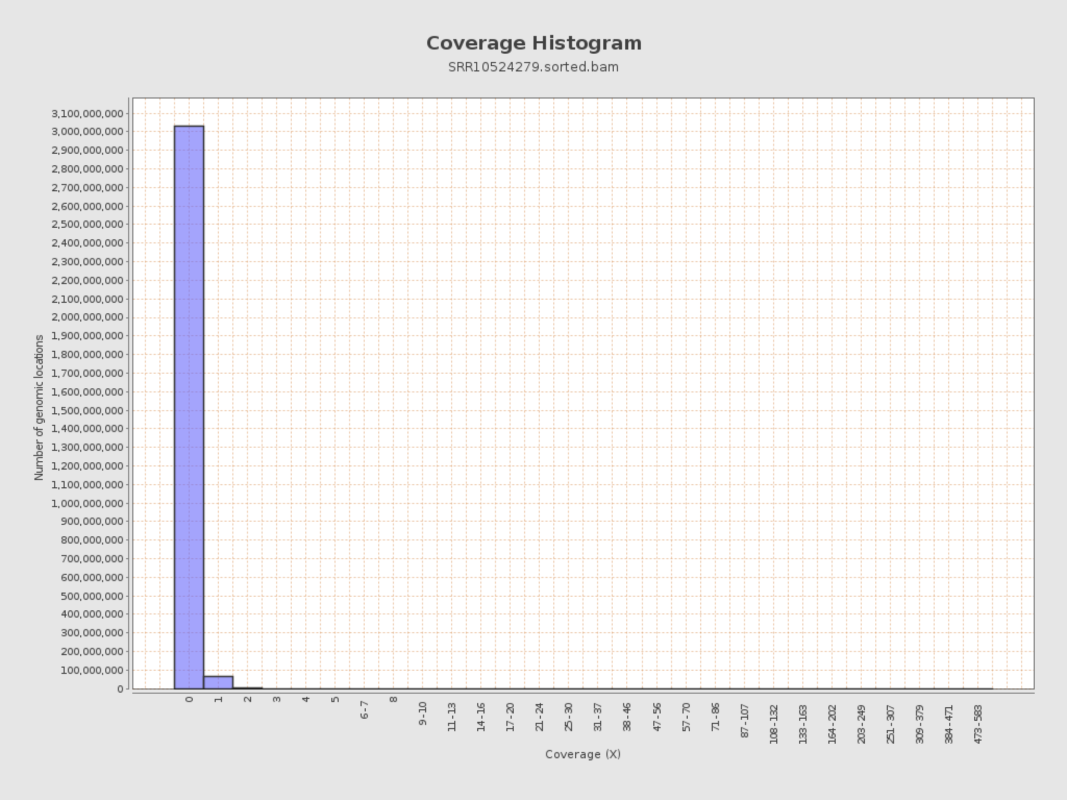
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6040909	0.0242	0.4668
chr2	243199373	6241938	0.0257	0.2638
chr3	198022430	4923314	0.0249	0.1677
chr4	191154276	4737902	0.0248	0.1793
chr5	180915260	4356027	0.0241	0.1658
chr6	171115067	4263427	0.0249	0.1803
chr7	159138663	3982191	0.025	0.3399

chr8	146364022	3846108	0.0263	0.2428
chr9	141213431	3117061	0.0221	0.2217
chr10	135534747	3453908	0.0255	0.2316
chr11	135006516	3306977	0.0245	0.2164
chr12	133851895	3299595	0.0247	0.1711
chr13	115169878	2307220	0.02	0.1504
chr14	107349540	2262399	0.0211	0.1615
chr15	102531392	2095196	0.0204	0.1516
chr16	90354753	2075360	0.023	0.175
chr17	81195210	1959126	0.0241	0.1769
chr18	78077248	1999850	0.0256	0.4146
chr19	59128983	1407576	0.0238	0.3153
chr20	63025520	1508377	0.0239	0.1677
chr21	48129895	937862	0.0195	0.1618
chr22	51304566	827062	0.0161	0.1343
chrMT	16571	4000	0.2414	0.511
chrX	155270560	4190621	0.027	0.1983
chrY	59373566	216614	0.0036	0.0977

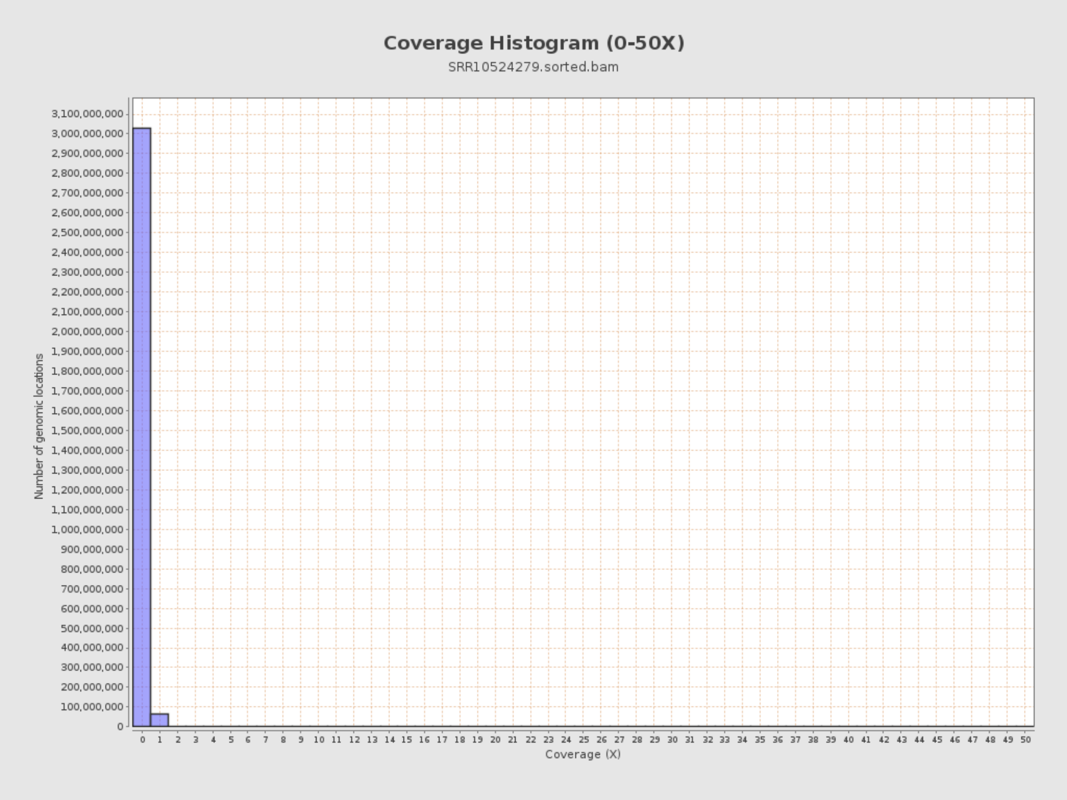
3. Results : Coverage across reference



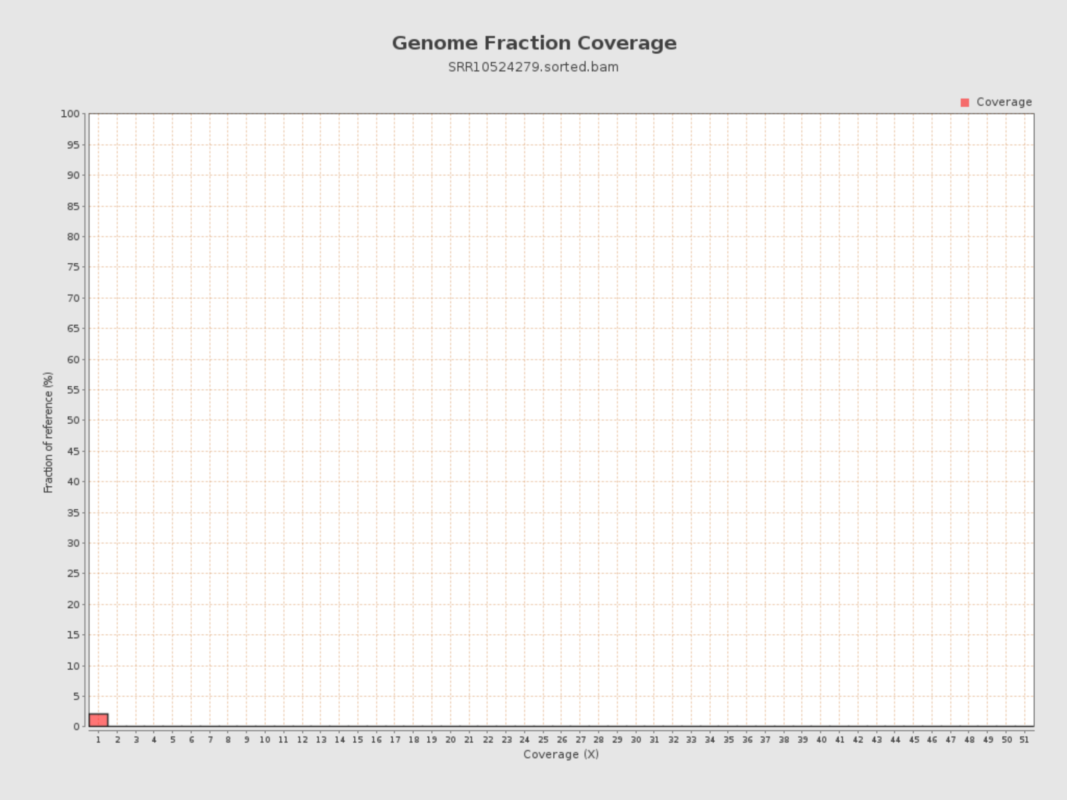
4. Results : Coverage Histogram



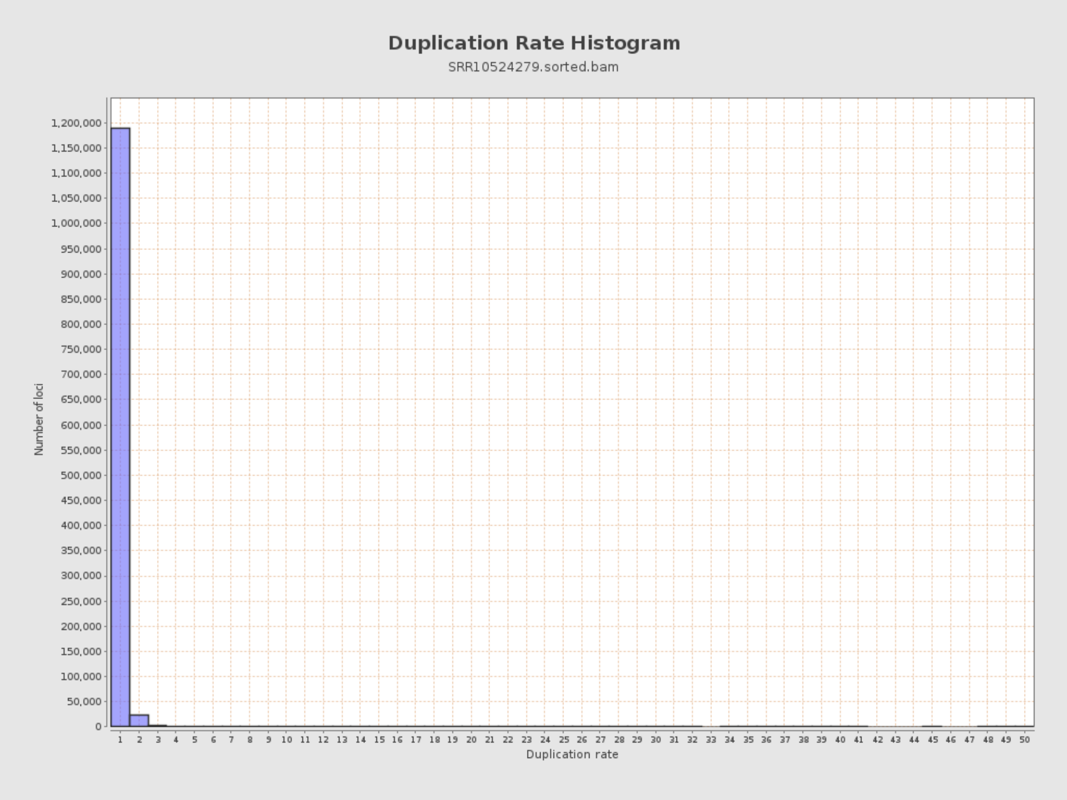
5. Results : Coverage Histogram (0-50X)



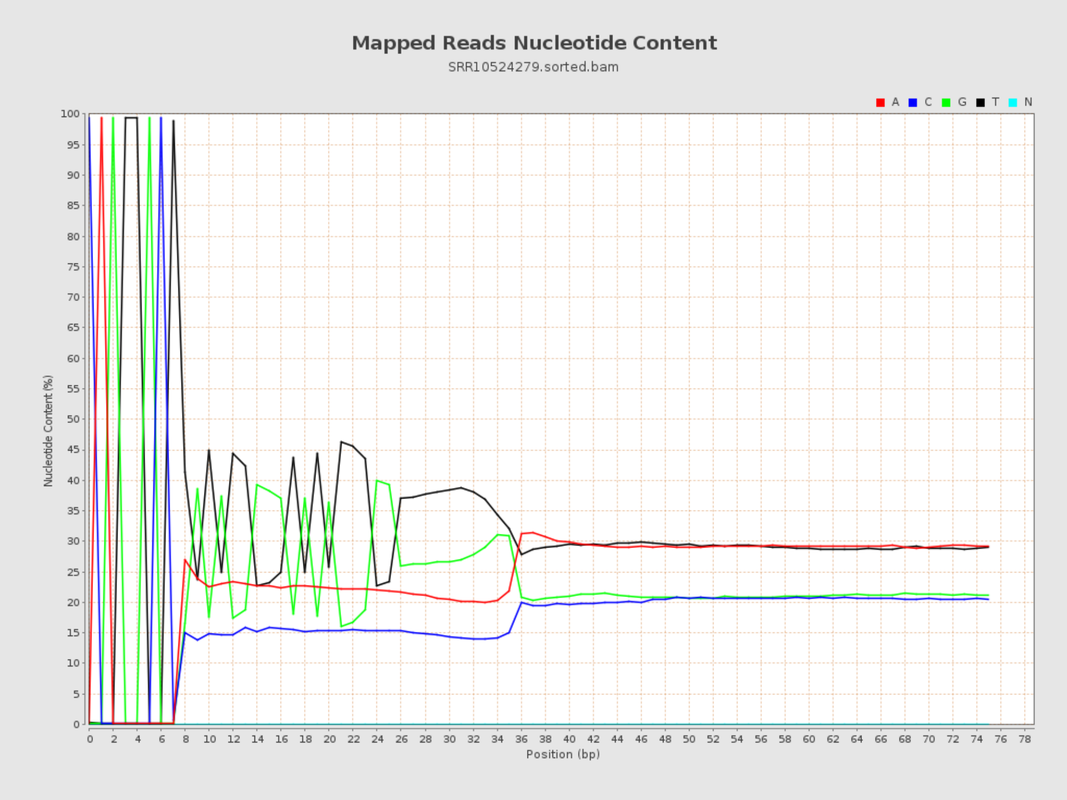
6. Results : Genome Fraction Coverage



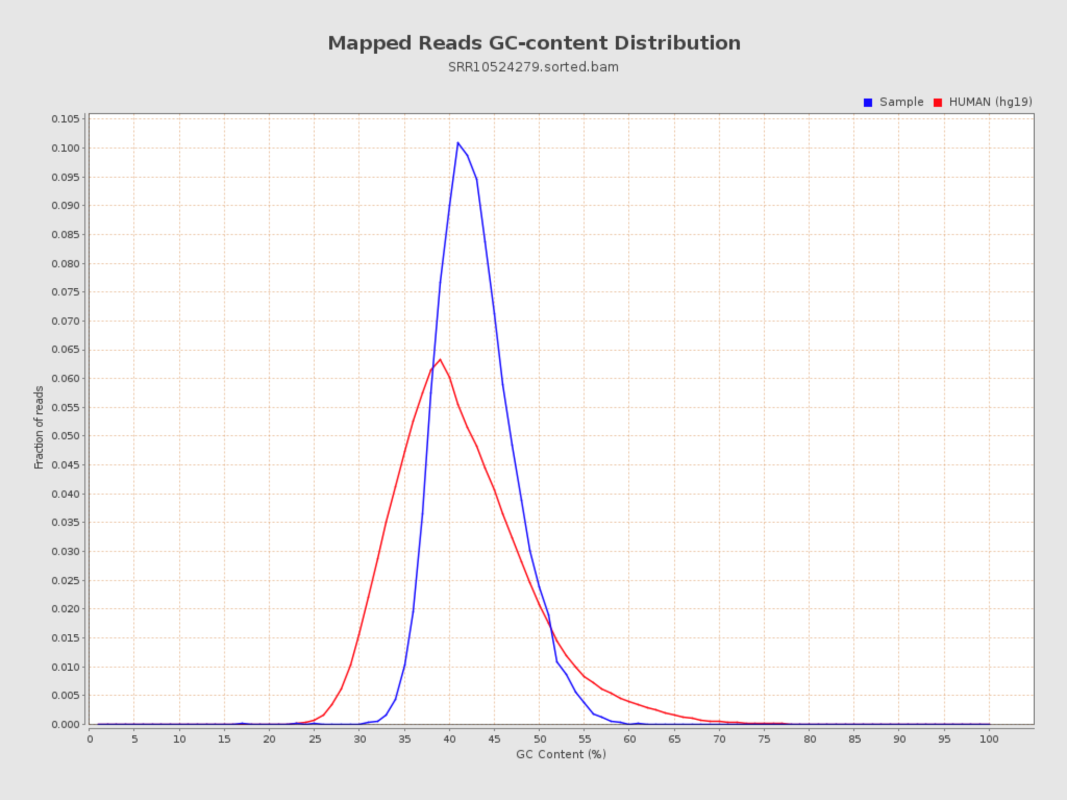
7. Results : Duplication Rate Histogram



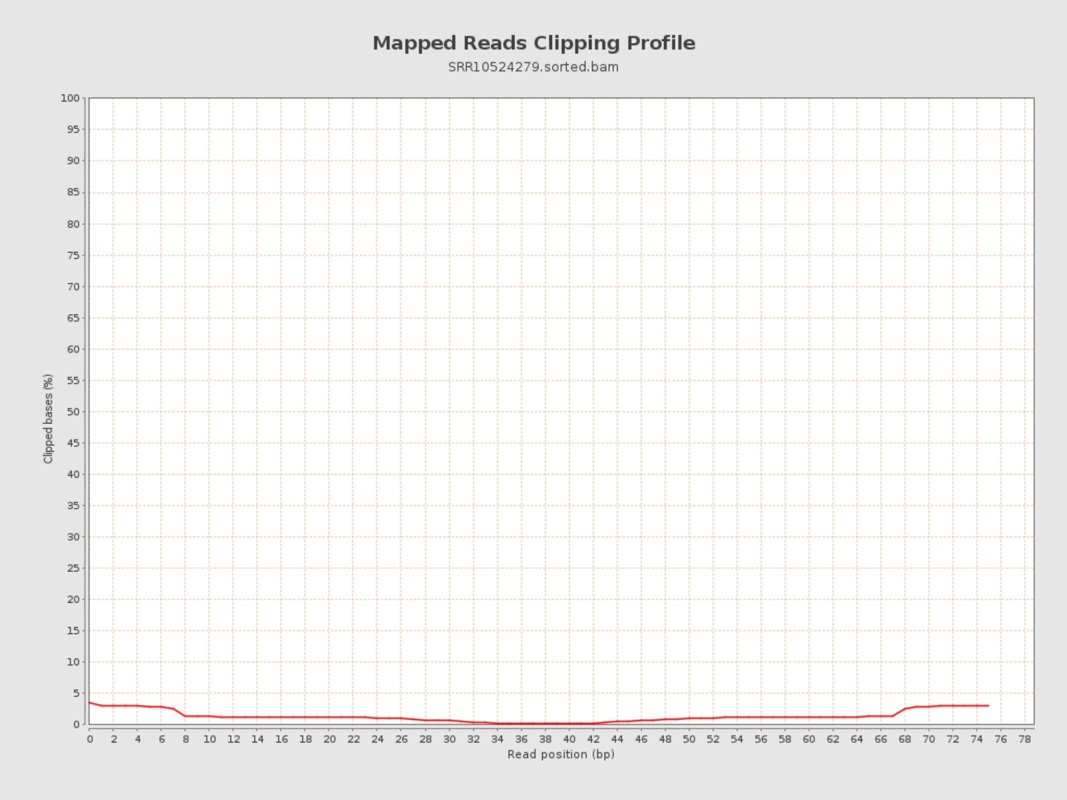
8. Results : Mapped Reads Nucleotide Content



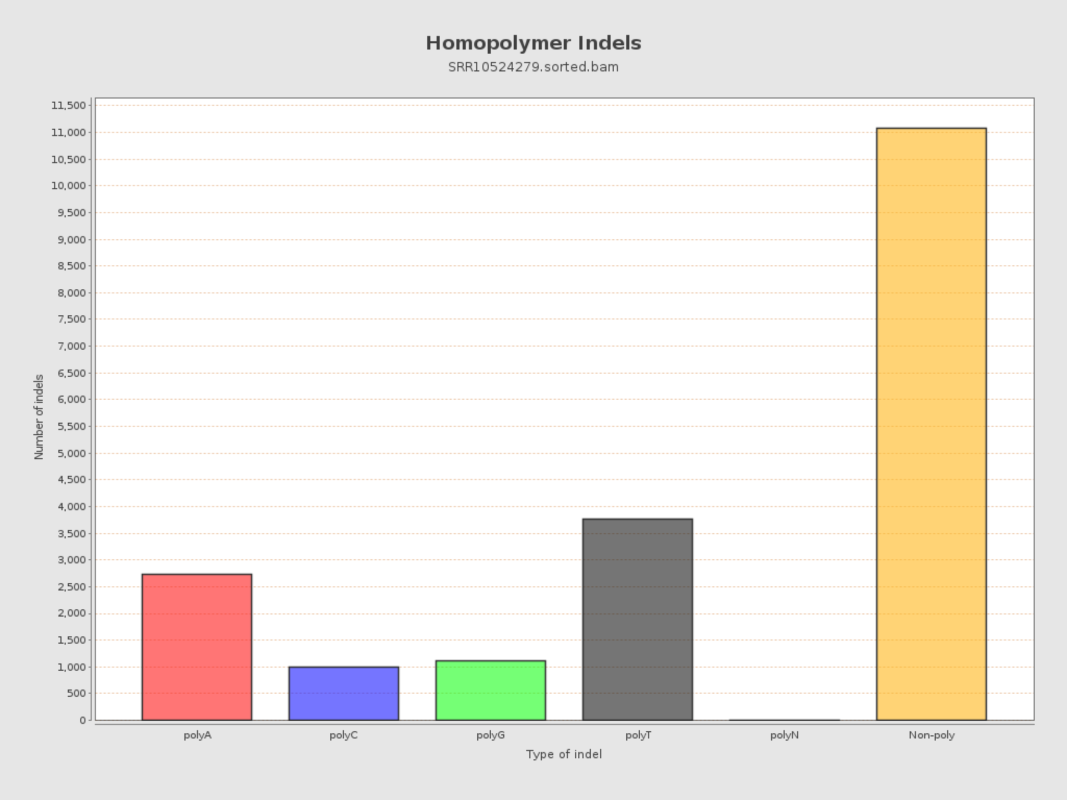
9. Results : Mapped Reads GC-content Distribution



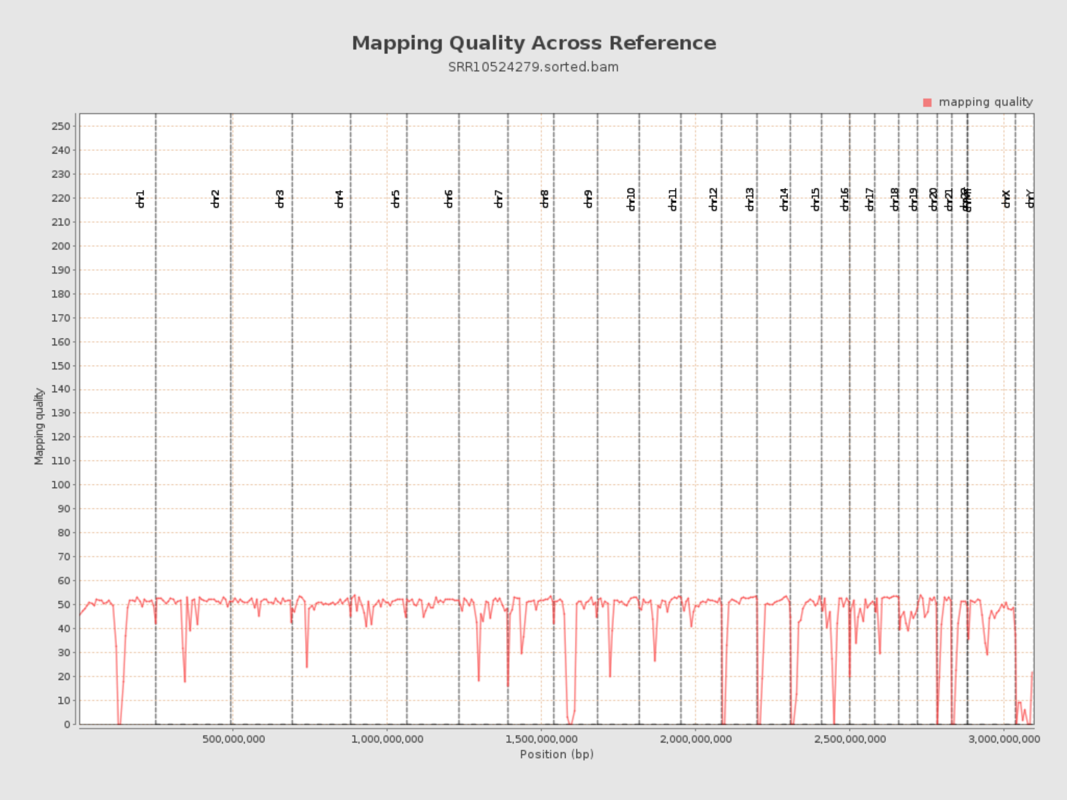
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram