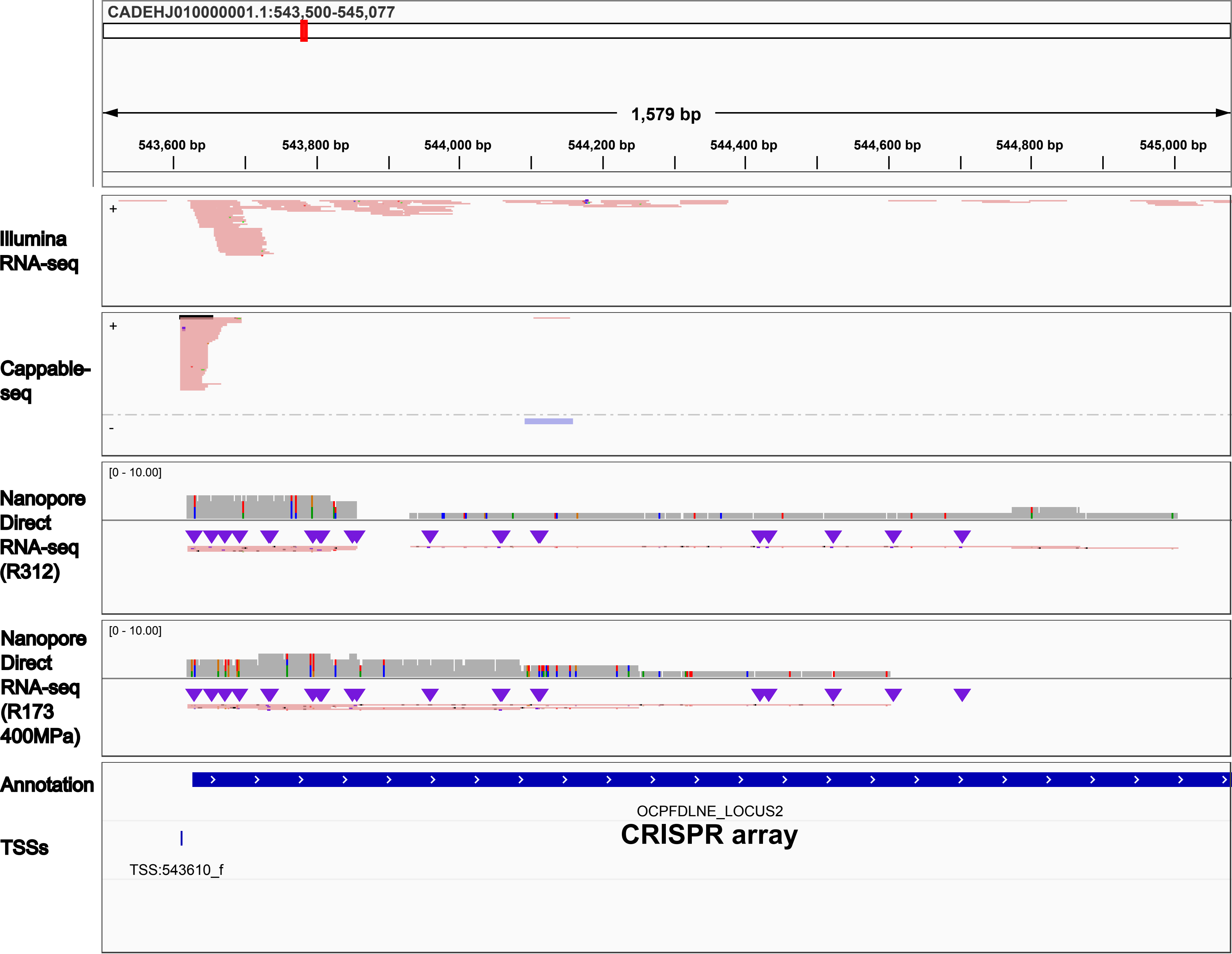
Figure S8. Visualization of CRISPR array location on *L. monocytogenes* RO15 region 543550 bp - 545050 Mbp. Six data rows, in descending order: combined Illumina RNA-seq reads, combine cap-seq reads, Nanopore direct RNA-seq for control sample (R312) reads, Nanopore direct RNA-seq for sample 400 MPa treated (R173) reads, Genbank annotation, and TSS prediction annotation. Red lines are forward reads, and blue lines are reverse reads. Grey bars are coverage bar plots. Purple triangle indicates insertion regions on the sequencing read. The region includes the CRISPR array with 54 spacer sequences. One forward TSS was predicted at the beginning of the CRISPR array.


CADEHJ010000001.1:543,500-545,077
1,579 bp
543,600 bp
543,800 bp
544,000 bp
544,200 bp
544,400 bp
544,600 bp
544,800 bp
545,000 bp
Illumina RNA-seq
+
Cappable-seq
+
-
Nanopore Direct RNA-seq (R312)
[0 - 10.00]
Nanopore Direct RNA-seq (R173 400MPa)
[0 - 10.00]
Annotation
OCPFDLNE_LOCUS2
CRISPR array
TSSs
TSS:543610_f