**Figure S1: Proteins used in this study.** a: SDS-PAGE gel with dCas12a (171 kDa) and the fusion protein containing dCas12a and the FKBP domain (dCas12a(FKBP), 180 kDa). b: SDS-PAGE gel with Coomassie stained (left) and maleimide-Alexa488 labeled (right) C-S\textsubscript{10}-B (45 kDa). c: SDS-PAGE gel with Coomassie-stained (left) and maleimide Atto647N labeled (right) fusion protein containing C-S\textsubscript{10} and the FRB domain (C-S\textsubscript{10(FRB)}) (58 kDa). Both C-S\textsubscript{10}-B and C-S\textsubscript{10(FRB)} show aberrant migration in gel because of the high proline content (22%) in the C domain.
Figure S2: C-S\textsubscript{10}-B concentration determines nucleocapsid nucleation and growth.

Kymographs showing binding of C-S\textsubscript{10}-B (magenta) on DNA (dark) at 25 nM and 150 nM polypeptide concentration (left) and percentage of the DNA strand length that is encapsidated by the fluorescent C-S\textsubscript{10}-B (right). Shown are the mean and standard deviation for 10 nucleocapsids per condition.
Figure S3: Decoration of DNA with multiple dCas12a prior to DNA encapsidation by C-S10-B. 

a: YOYO-1 stained DNA molecules (green) decorated with quantum dot-labeled dCas12a (magenta) (top) and distribution of dCas12a along the DNA (bottom) when binding was targeted to 5 (N = 561 dCas12a molecules) or 10 sites (N = 473 dCas12a molecules). Binding sites are shown with stronger magenta in the histograms. 

b: Number of quantum dot-labeled dCas12a proteins per DNA strand after targeting 5 (N = 561) or 10 (N = 473) binding sites. 

c: Distribution of C-S10-B clusters along the DNA with (N = 484) or without (N = 246) decoration with 5 dCas12a. dCas12a binding sites are shown with stronger magenta in the histograms. 

d: Fluorescent quantum dots remaining in the field of view, either bound on the DNA (via dCas12a) or on the lipid surface (N = 100 each) throughout encapsidation with 25 nM C-S10-B.
**Figure S4: Prior decoration with nucleosomes improves DNA encapsidation by C-S10-B**

**a**: Human histone octamers were incubated with the DNA at molar ratios 50:1 and 100:1 prior to tethering in the flowcell. **b**: YOYO-1 stained DNA molecules (green) decorated with quantum dot-labeled nucleosomes (magenta) (top) and distribution of nucleosomes on the DNA (bottom) at the 50:1 ratio (N = 279). **c**: Number of quantum dot-labeled nucleosomes per DNA strand at the 50:1 (N = 279) and 100:1 (N = 832) molar ratios. **d**: Fluorescent quantum dots remaining in the field of view, either bound on the DNA (via nucleosomes) or on the lipid surface (N = 100 each) throughout encapsidation with 25 nM...
C-S\textsubscript{10}-B. e: Double labeling experiment showing co-localization of QD-tagged nucleosomes (magenta, 92\%) with fluorescent C-S\textsubscript{10}-B clusters (green, 57\%). f: Number of C-S\textsubscript{10}-B clusters on naked DNA (N = 246 clusters) versus DNA decorated with nucleosomes at the 50:1 molar ratio (N = 362 clusters). g: Distribution of C-S\textsubscript{10}-B clusters along the DNA with (N = 362) or without (N = 246) decoration with nucleosomes at the 50:1 molar ratio. h: Kymographs showing C-S\textsubscript{10}-B (magenta) binding on naked or nucleosomes-decorated DNA and percentage of the DNA strand length that is encapsidated by the fluorescent C-S\textsubscript{10}-B. Shown are the mean and standard deviation for 10 nucleocapsids per condition. i: Representative kymographs showing faster encapsidation by C-S\textsubscript{10}-B after the DNA (green) is decorated with nucleosomes. j: Condensation profiles at 25 nM C-S\textsubscript{10}-B for naked DNA, and DNA decorated with nucleosomes at the 50:1 and 100:1 molar ratios. Shown are the mean and standard deviation for 25 DNA molecules per condition. k: Violin plots showing the time (t\textsubscript{\text{half}}) required to reach half of maximum condensation for each DNA strand analyzed in (j). Sigmoid curve fitting and extrapolation was used to estimate t\textsubscript{\text{half}} for molecules that did not reach 65.5\% encapsidation during the experiment (30 min).
Figure S5: Decoration of DNA with the previously dimerized complex dCas12a-S\textsubscript{10}. a: YOYO-1 stained DNA molecules (green) decorated with Atto647N-labeled dCas12a-S\textsubscript{10} (magenta) (top) and distribution of dCas12a-S\textsubscript{10} along the DNA (bottom) when binding was targeted to 5 sites (N = 397 dCas12a-S\textsubscript{10} molecules) along the DNA. Binding sites are shown with stronger magenta in the histograms. b: Number of Atto647N-labeled dCas12a-S\textsubscript{10} per DNA strand after targeting 5 sites (N = 397 dCas12a-S\textsubscript{10} molecules) along the DNA.
**Figure S6: Positioning multiple dCas12a-S₁₀ complexes on DNA substrates improves encapsidation by C-S₁₀-B.** C-S₁₀-B binding is assessed via electrophoretic mobility shift assays. 

**a:** A linear 2.5 kbp dsDNA fragment was decorated with ten dCas12a-S₁₀ uniformly distributed along the template. Incubation time with C-S₁₀-B was 3 h. 

**b:** dCas12a-S₁₀ was directed to four sites on a 9.5 kbp pPIC9 plasmid (in supercoiled, linear and nicked open-circular conformations). Incubation time with C-S₁₀-B was 15 h. N/P stands for the stoichiometric ratio between C-S₁₀-B and available DNA binding sites (6 bp).
Figure S7: Encapsidation of cognate and non-cognate DNA templates after selective DNA decoration with dCas12a-S10. Condensation profiles at 10 nM C-S10-B for the non-cognate (20 kbp) and cognate (28.5 kbp) DNA strands after dCas12a-S10 binding at 0, 5, 10 or 25 sites along the cognate DNA. Circles and shaded areas are the mean and standard deviation for 25 DNA molecules per condition.