

Figure S1. Cell viability of PEI-LBL-NCs and Se@CS NPs in RAW 264.7 cells. Cell viability, measured by the metabolic CellTiter Glo assay, after 4h incubation with PEI-LBL-NCs and Se@CS NPs as a function of Se concentration (ppm).

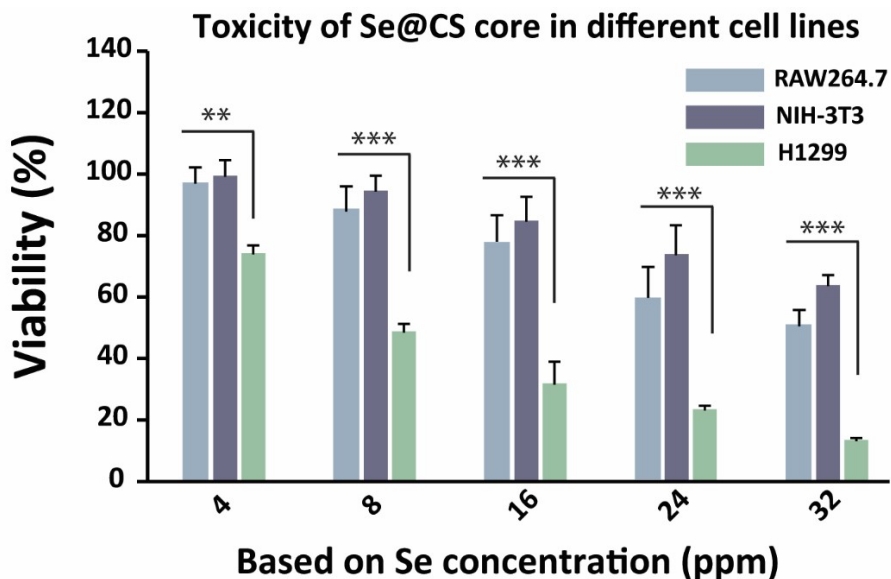
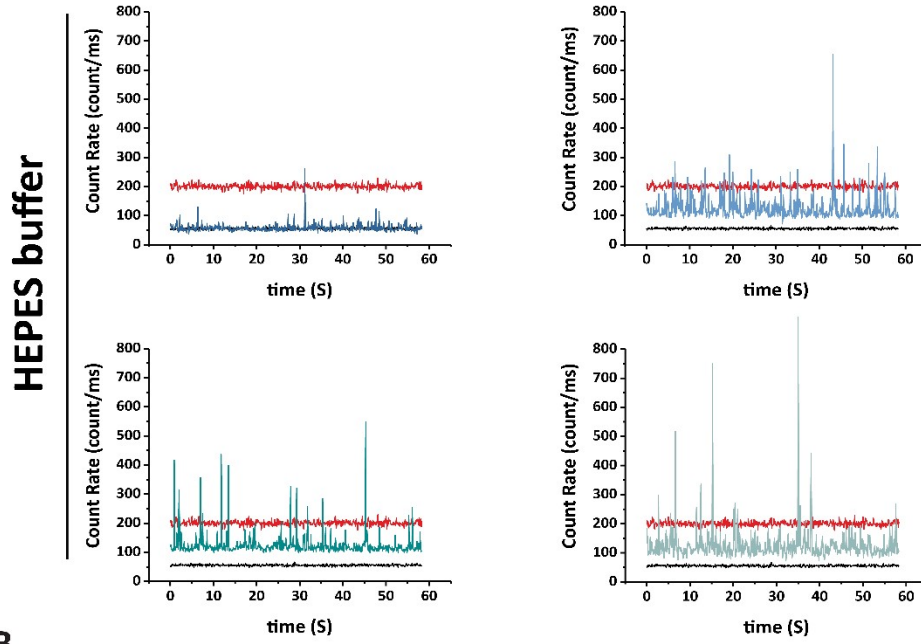


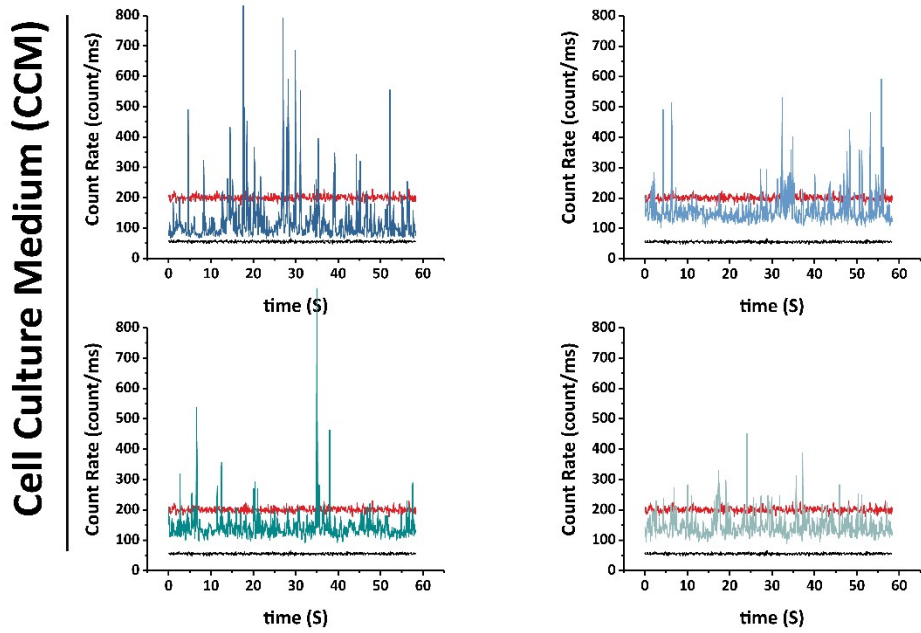
Figure S2. Cell viability of Se@CS core in RAW 264.7, NIH-3T3, and H1299 cells. Cell viability, measured by the metabolic CellTiter Glo assay, after 4h incubation with Se@CS as a function of Se concentration (ppm). Bars represent mean \pm standard deviation, (ns = not significant, n = 3, *: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$).

A

— BG — Naked siRNA — PEI-LBL-NCs — CS-LBL-NCs — jetPRIME-NCs — RNAiMAX-NCs

**B**

— BG — Naked siRNA — PEI-LBL-NCs — CS-LBL-NCs — jetPRIME-NCs — RNAiMAX-NCs



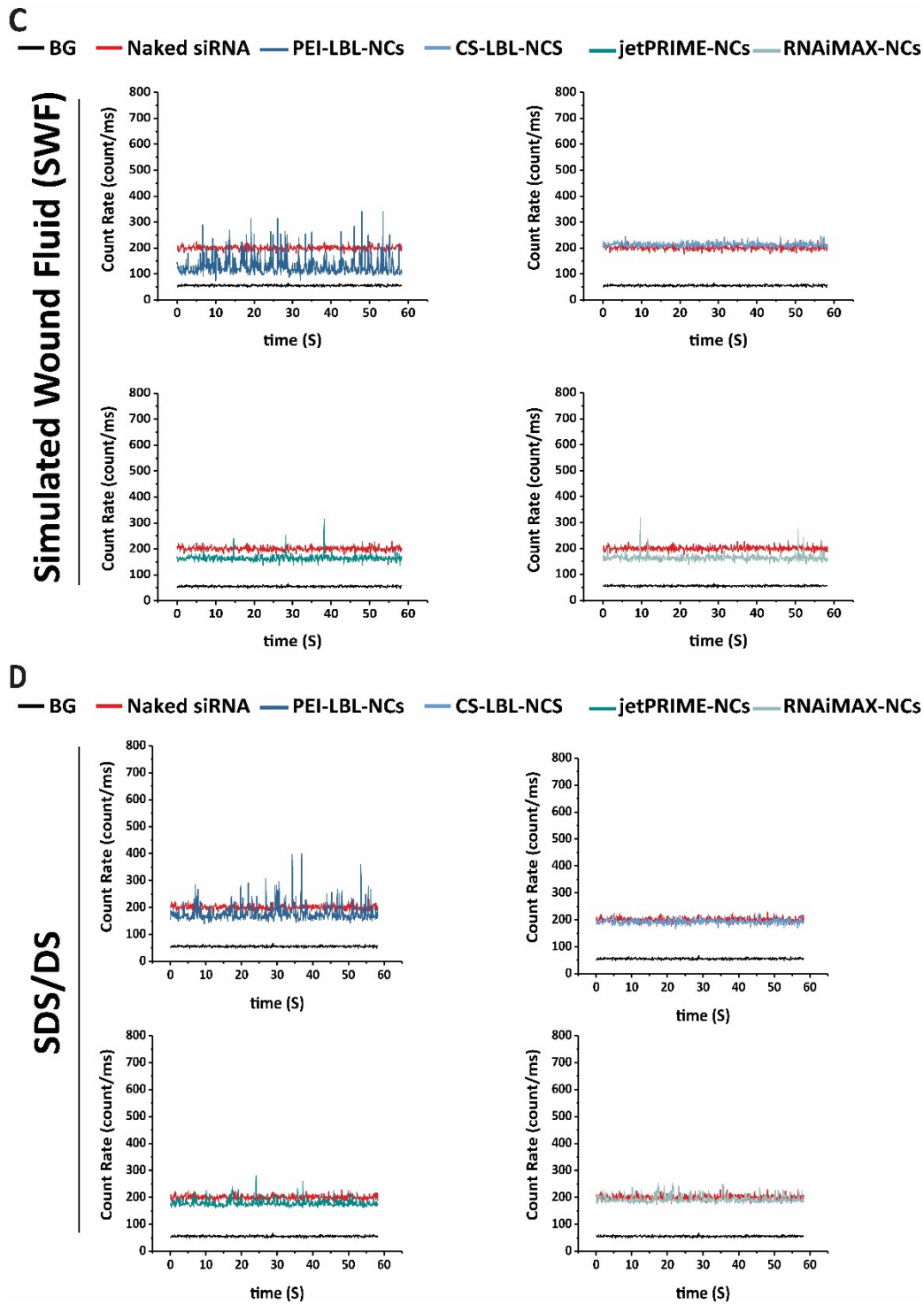


Figure S3. FFS decomplexation assay. Representative fluorescence fluctuations as measured with FFS for naked siRNA (red) Water Background (BG, Black), NCs (PEI-LBL-NCs, CS-LBL-NCs, jetPRIME-NCs, and RNAiMAX-NCs) 4h incubated in **(A)** HEPES, **(B)** CCM, **(C)** SWF, and **(D)** NCs 15 min incubated in SDS/DS (PEI-LBL-NCs, CS-LBL-NCs, and jetPRIME-NCs were incubated in sodium dodecyl sulfate (SDS) 2%, and RNAiMAX-NCs incubated with dextran sulfate (DS) 0.1%).