Supporting Information

RNA Signal Amplifier Circuit with Integrated Fluorescence Output

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Supporting Figures

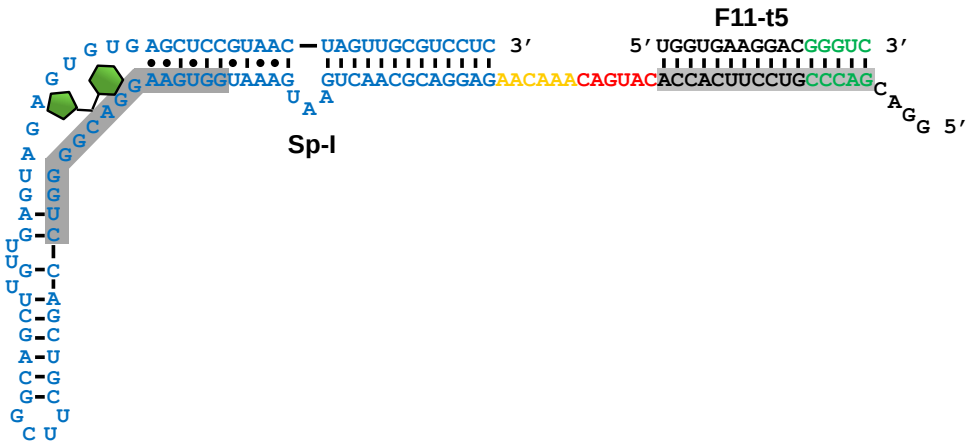

Figure S1. Predicted secondary structure of **Sp-I** complexed with **F11-t5** with the Spinach aptamer shown in the active form. The bases are colored according to Figure 1. The shaded bases engage in the inhibitory helix in the absence of the fuel and catalytic strands as depicted in Figure 1c.

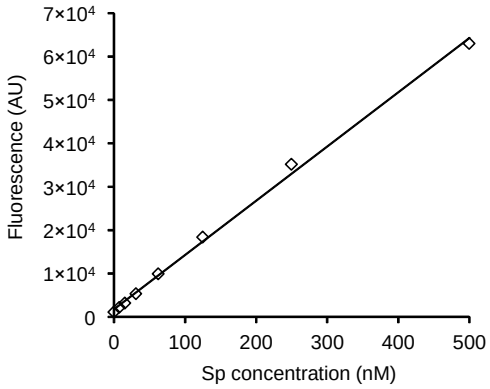

Figure S2. Fluorescence of **Sp** (0-500 nM) in the presence of 3 μM DFHBI measured after 25 min incubation. Plotted values are averages of triplicate measurements. The errors were smaller than the data symbols (< 3.5%) shown.

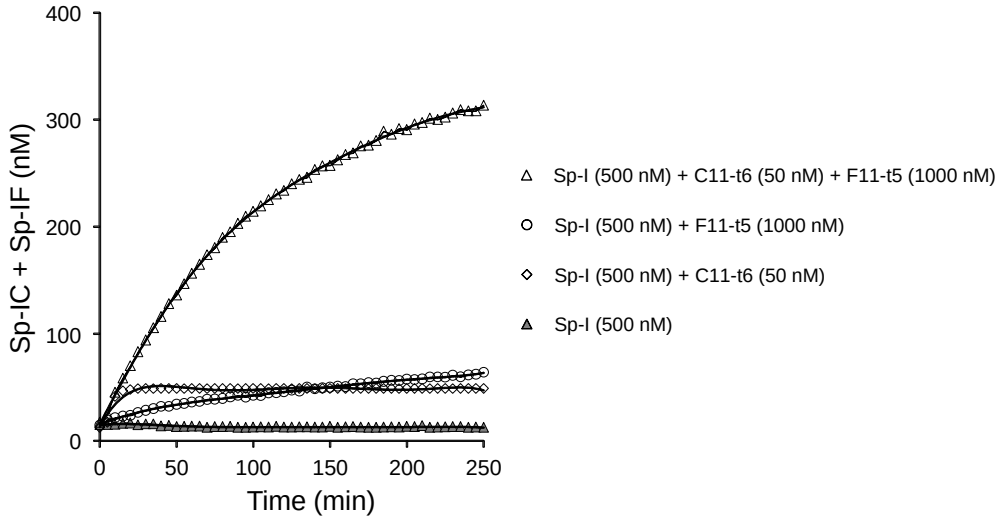

Figure S3. Sp-I (500 nM) is not catalytically activated by **C11-t6** (50 nM) in the absence of the fuel strand **F11-t5** (open diamond). Note that in the absence of the fuel strand, **Sp-IC** rapidly forms almost quantitatively (~50 nM) to reach an equilibrium and no further fluorescence increase is observed. The reactions were performed as described in the Methods and the average fluorescence values from triplicate experiments were plotted. The triplicate measurements were typically within 3% of the plotted average values which were smaller than the data symbols shown.

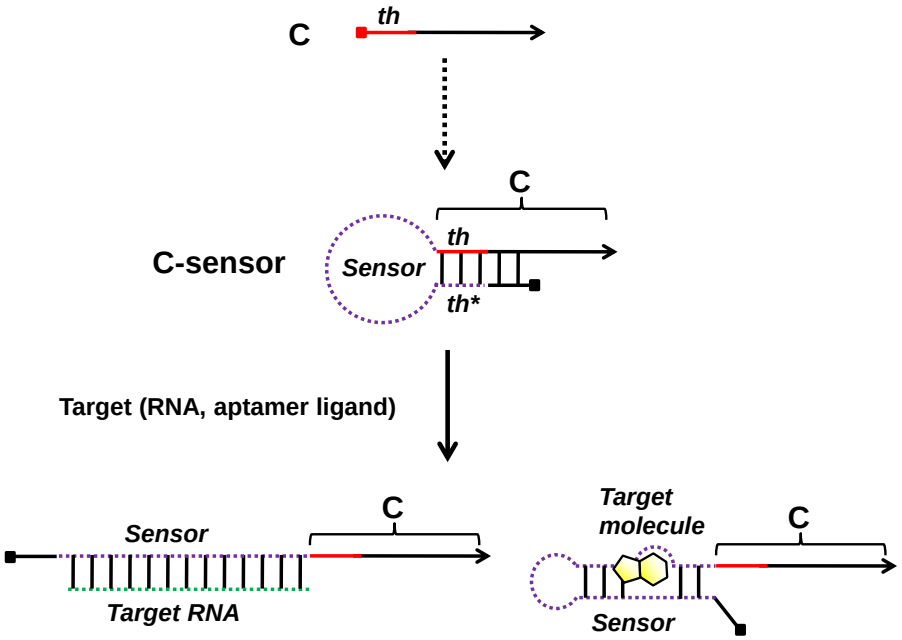

Figure S4. A proposed modification of the catalytic strand (**C**) to accept an arbitrary RNA sequence or a molecule as an input (**C-Sensor**). A "sensor" domain, for example, an antisense sequence for a target RNA or an aptamer sequence for a desired ligand can be attached to the 5' end which is also designed to mask the toe-hold domain (***th***) of **C**. Note that the toe-hold sequence is not constrained by the Spinach sequence, therefore, can be modified to base-pair with various sensor sequences. When the sensor domain engages with the target molecule, it will unmask the toe-hold domain, allowing the catalytic signal amplification to be triggered.