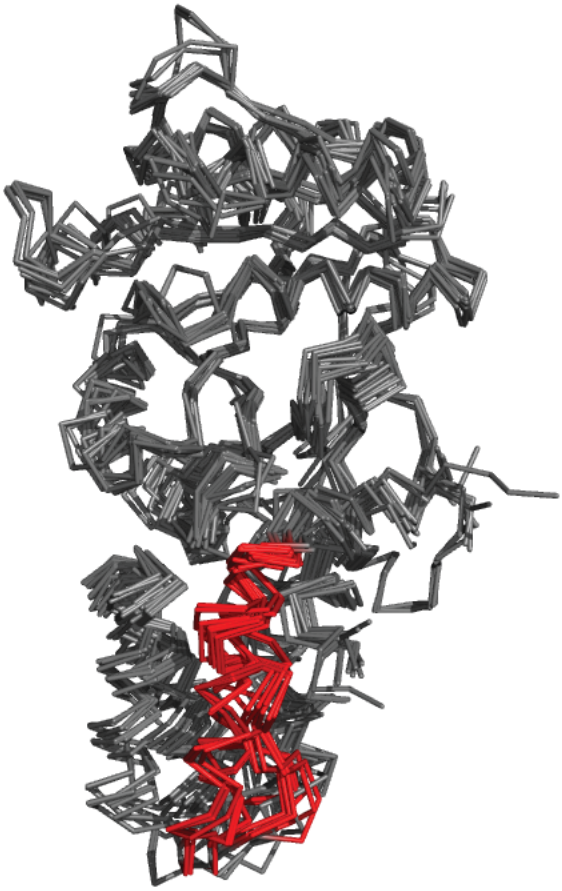
Supplementary figures for:

SRP RNA controls a conformational switch regulating the SRP-SRP receptor interaction

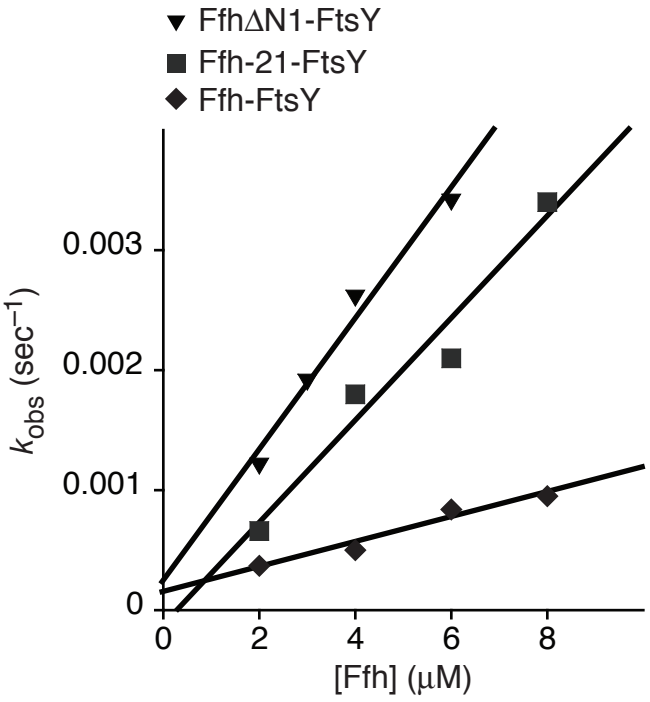
Saskia B. Neher*[1,2], Niels Bradshaw*[1,2], Stephen N. Floor[3,4], John D. Gross[3], and Peter Walter[1,2]

Howard Hughes Medical Institute[1],
Department of Biochemistry and Biophysics[2],
Department of Pharmaceutical Chemistry[3],
and Graduate Group in Biophysics[4]
University of California at San Francisco
600 16th Street,
San Francisco, CA 94158

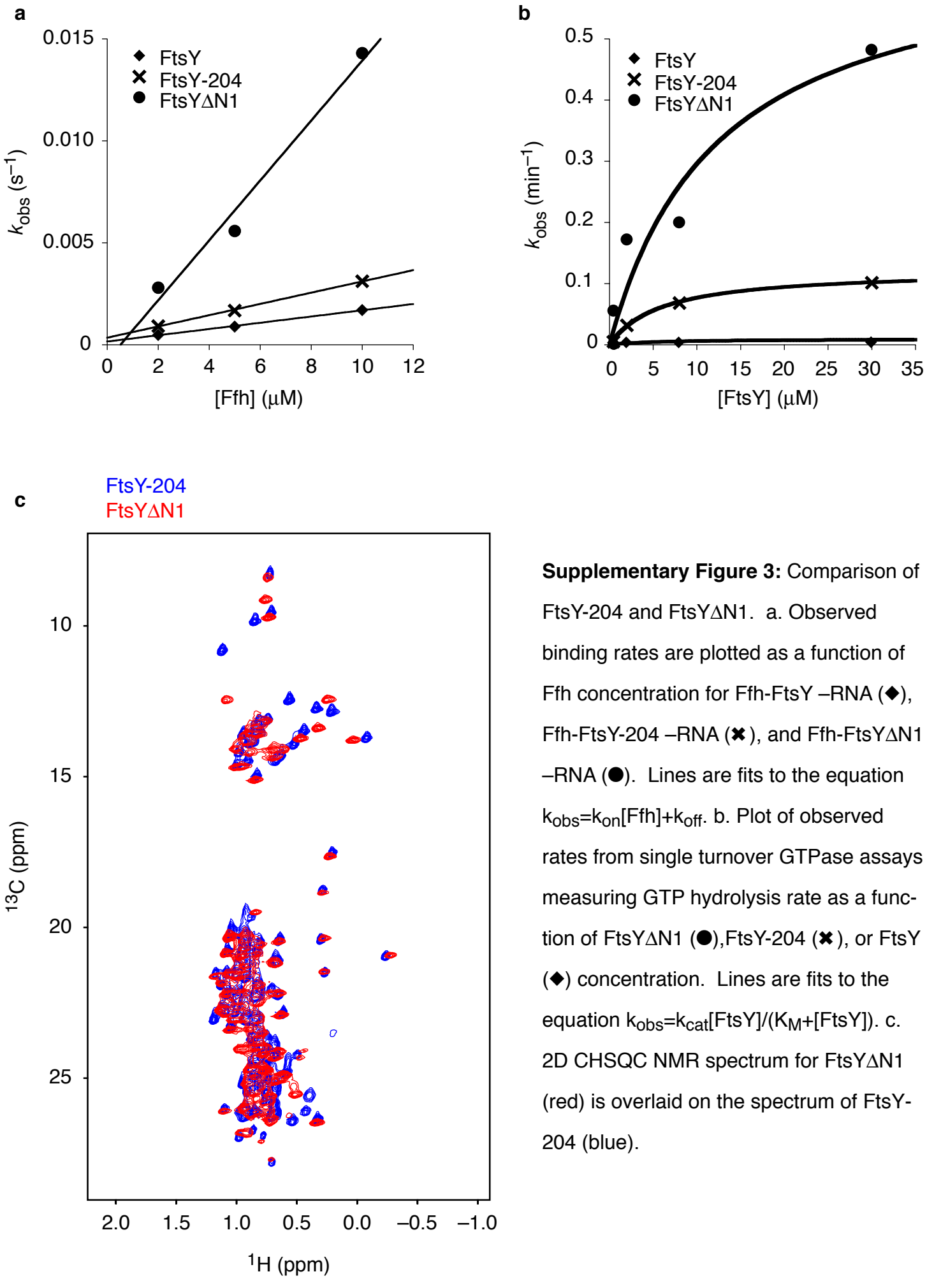
Corresponding author: Peter Walter (pwalter@biochem.ucsf.edu) *These authors made equal contributions



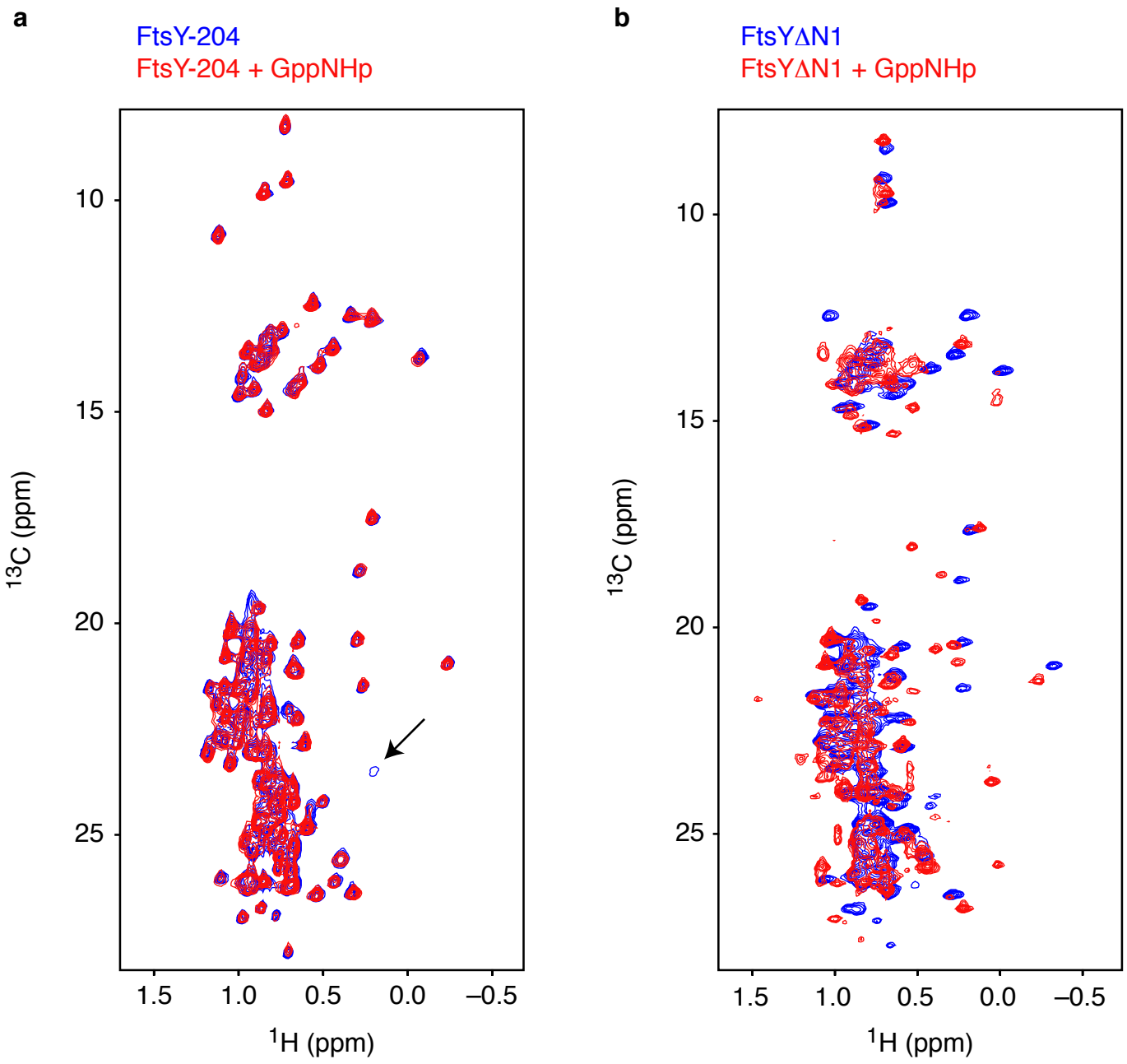
Supplementary Figure 1: Helix N1 is present in structures of uncomplexed FtsY. Allignment of FtsY structures from PDB files 1FTS, 2QY9, 1ZU4, 1ZU5, 2Q9C, 2Q9B, 2Q9A, 1VMA, 3B9Q, and 2OG2. Residues homologous to *E. coli* residues 204-221 of helix N1 are shown in red.



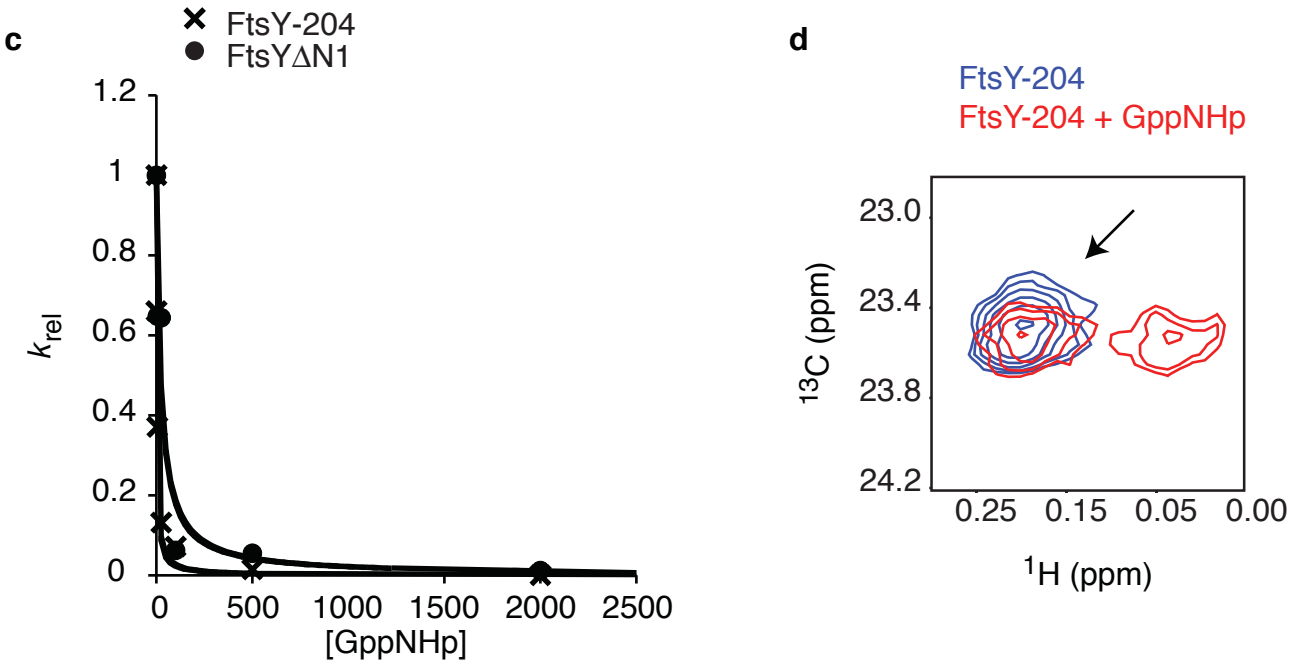
Supplementary Figure 2: Effect of length of Ffh N-terminal truncation. Truncation of the entire Ffh helix N1 (amino acids 1-20, called Ffh-21 here) is functionally equivalent to truncation of the first 8 amino acids (FfhΔN1). Observed binding rates are plotted as a function of Ffh concentration for FfhΔN1-FtsY –RNA (▼), Ffh-21-FtsY –RNA (■), and Ffh-FtsY –RNA (◆). Lines are fits to the equation $k_{obs}=k_{on}[Ffh]+k_{off}$.



Supplementary Figure 3: Comparison of FtsY-204 and FtsYΔN1. a. Observed binding rates are plotted as a function of Ffh concentration for Ffh-FtsY –RNA (◆), Ffh-FtsY-204 –RNA (✖), and Ffh-FtsYΔN1 –RNA (●). Lines are fits to the equation $k_{obs}=k_{on}[Ffh]+k_{off}$. b. Plot of observed rates from single turnover GTPase assays measuring GTP hydrolysis rate as a function of FtsYΔN1 (●),FtsY-204 (✖), or FtsY (◆) concentration. Lines are fits to the equation $k_{obs}=k_{cat}[FtsY]/(K_M+[FtsY])$. c. 2D CHSQC NMR spectrum for FtsYΔN1 (red) is overlaid on the spectrum of FtsY-204 (blue).



Supplementary Figure 4: FtsYΔN1 but not FtsY-204 undergoes a GppNHp dependent conformational change. a. 2D CHSQC spectrum for FtsY-204+GppNHp (red) is overlaid on the spectrum of FtsY-204 (blue). A peak that broadens in the FtsY-204 spectrum +GppNHp is marked with an arrow. b. 2D CHSQC spectrum for FtsYΔN1+GppNHp (red) is overlaid on the spectrum of FtsY-ΔN1 (blue).



Supplementary Figure 4. FtsYΔN1 but not FtsY-204 undergoes a GppNHp dependent conformational change. c. The affinity of GppNHp for FtsYΔN1 and FtsY-204 was measured by GTPase inhibition assays. Relative rates of GTP hydrolysis are plotted as a function of concentration of GppNHp. Lines are fits to the equation $k_{rel}=K_I/(K_I+[GppNHp])$ d. A region of the 2D CHSQC spectrum containing the peak marked in a is magnified with decreased contour cutoff.