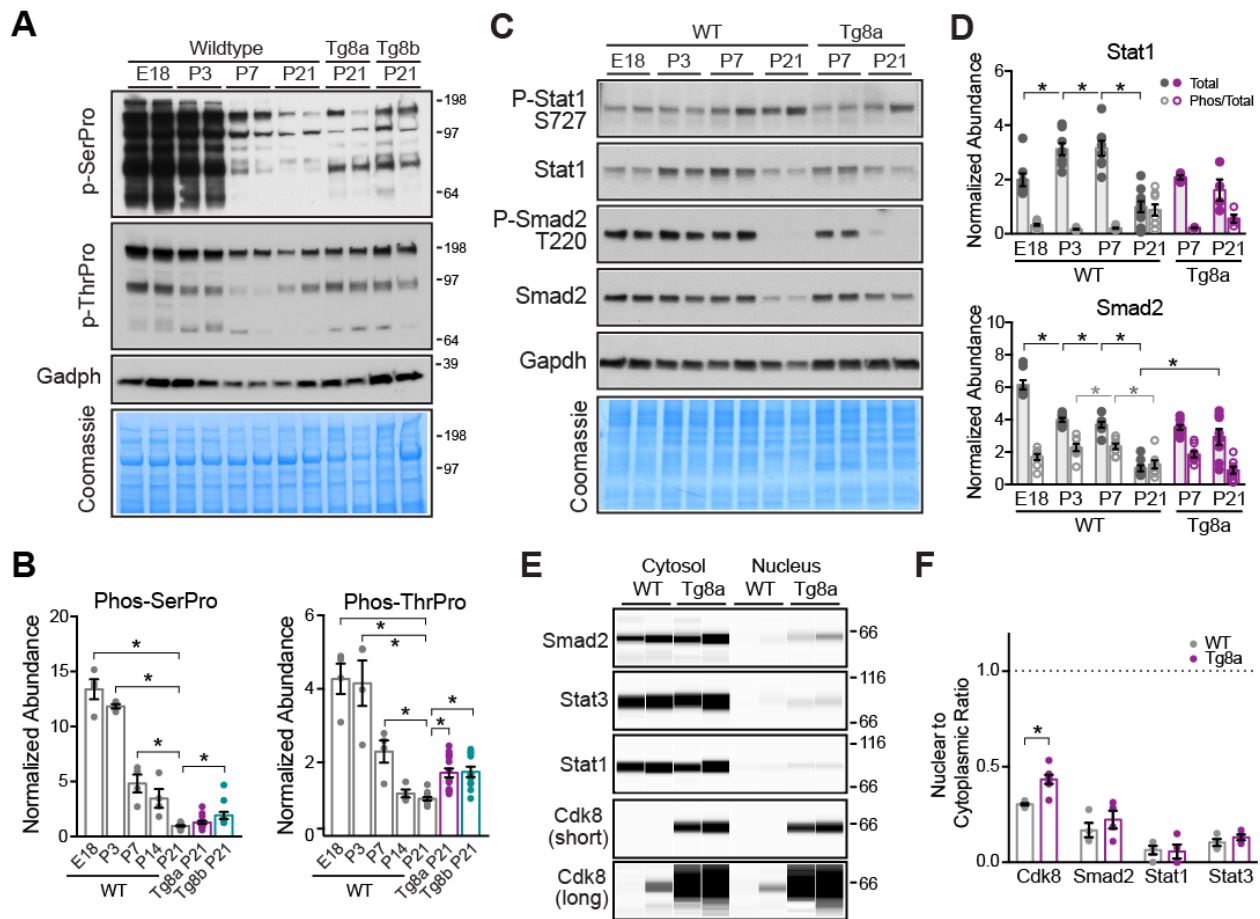
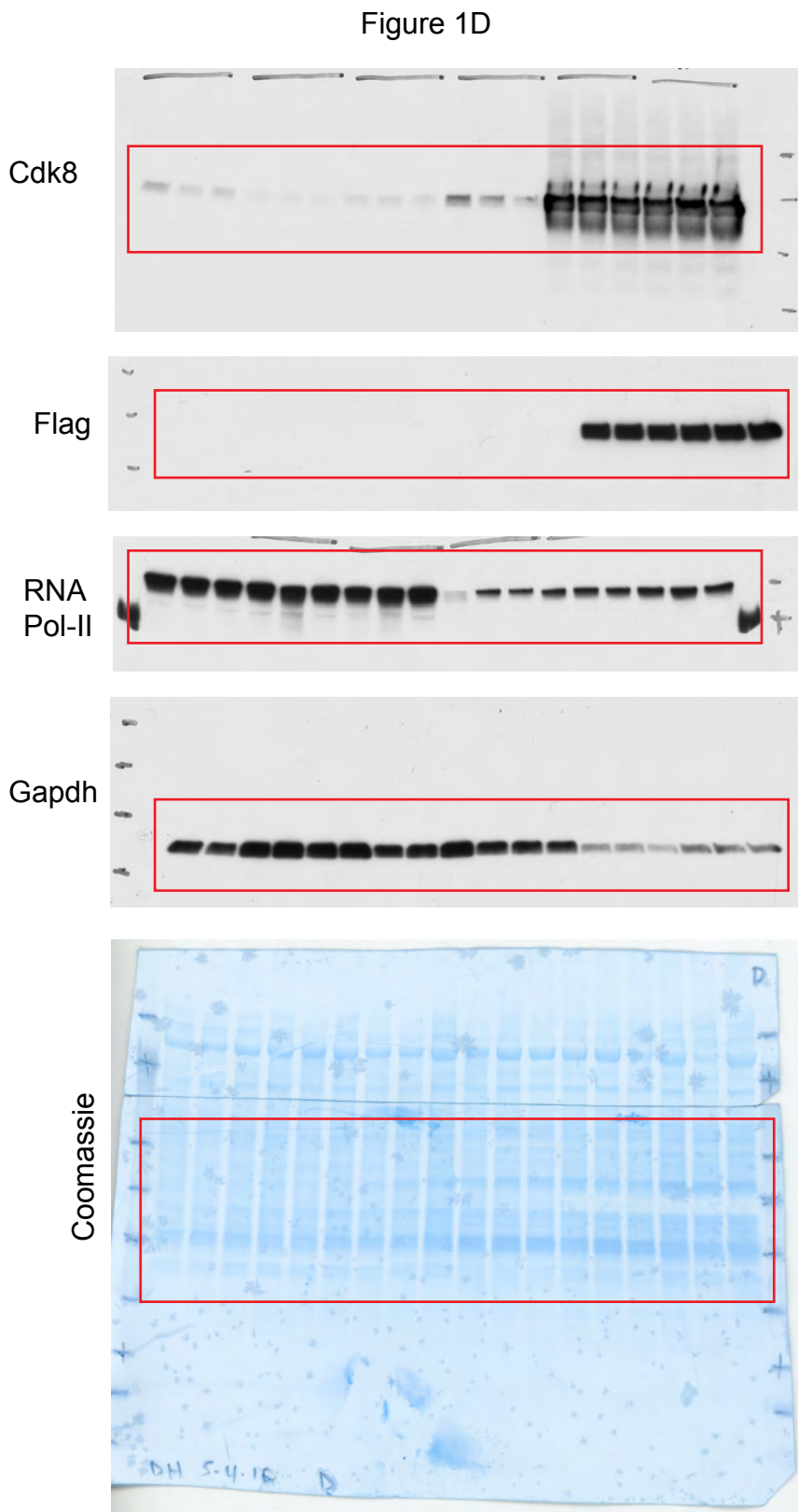
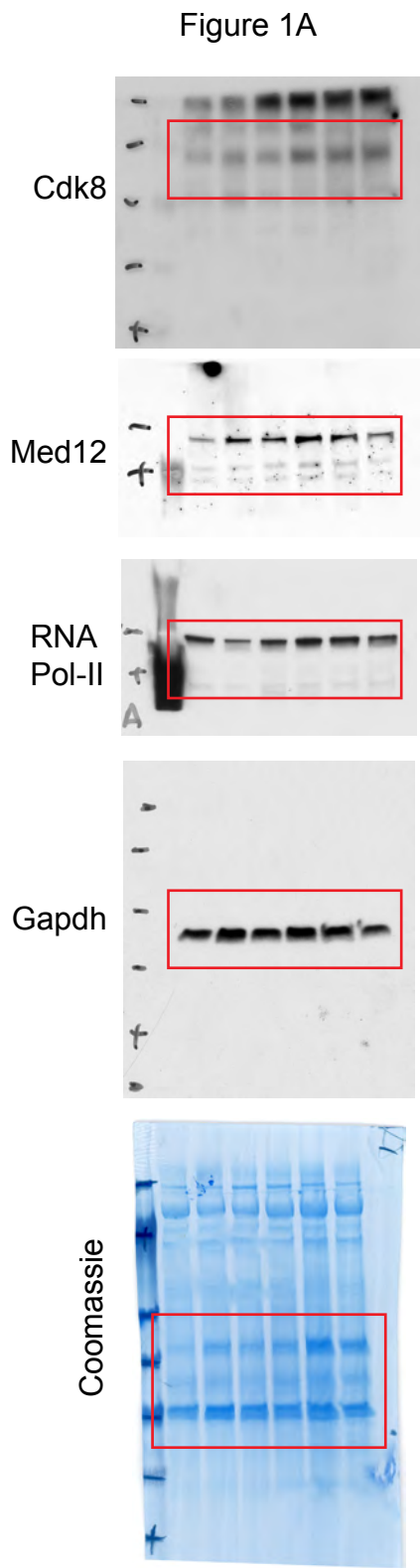


Supplemental Figure 1. Postnatal cardiac expression of mitogen activated protein kinases (Mapks) in WT mice. **A, B.** Changes in cardiac Mapk signaling from embryonic day 18 (E18) through postnatal day 21 (P21) in WT hearts. Example immunoblot (A) and summary analysis (B) of total and active phosphorylated (Phos-) protein levels. *, $p < 0.05$ vs. P21 for total (black) and phosphorylated/total (Phos/total) protein ratio (gray) normalized to Coomassie stain, one-way ANOVA with Tukey's multiple comparisons test, $n=4-10$ from 2-4 experiments.



Supplemental Figure 2. Determination of total and specific phosphorylation levels in developmental and Cdk8 overexpression ventricular lysates. **A.** Example immunoblots assessing Cdk8/Mapk activity in ventricular lysates using two antibodies against proline-directed Ser/Thr kinase substrates (p-SerPro, p-ThrPro) during postnatal WT cardiac development (E18 through P21) compared to P21 Tg8a and Tg8b hearts. **B.** Summary immunoblot data showing decreased levels in total phosphorylated proteins by P21 in WT hearts (gray) that modestly increase upon Cdk8 Tg8a (magenta) and Tg8b (cyan) expression. Phospho-signals were normalized to Coomassie total protein stain. (*), $p < 0.05$; (**), $p < 0.01$; one-way ANOVA with Dunnett's multiple comparisons test (vs. WT P21), $n = 4-15$ from 4-6 experiments. **C, D.** Representative immunoblots (C) and summary data (D) assaying for total (filled symbols) and phosphorylated/total levels (Phos/total, open symbols) of Stat1 and Smad2, known Cdk8 substrates, in ventricular lysates from embryonic day 18 (E18) through postnatal day 21 (P21) WT (gray) and Tg8a (magenta) hearts. Bands were normalized to total protein stain (Coomassie). *, $p < 0.05$, one-way ANOVA with Tukey's multiple comparisons test, $n = 4-8$ from 2-4 experiments. **E, F.** Capillary electrophoresis lane views (E) and summary data (F) of cellular fractionation experiments of P21 WT (gray) and Tg8a (magenta) ventricles examining subcellular localization of Smad2, Stat1, Stat3, and Cdk8. Two exposures are displayed for Cdk8 (short, long) to show transgenic and endogenous levels, respectively. See Figure 5F for the relative segregation of Gapdh and RNA Pol-II of these samples. *, $p < 0.05$, one-way ANOVA, $n = 4$ from two experiments.

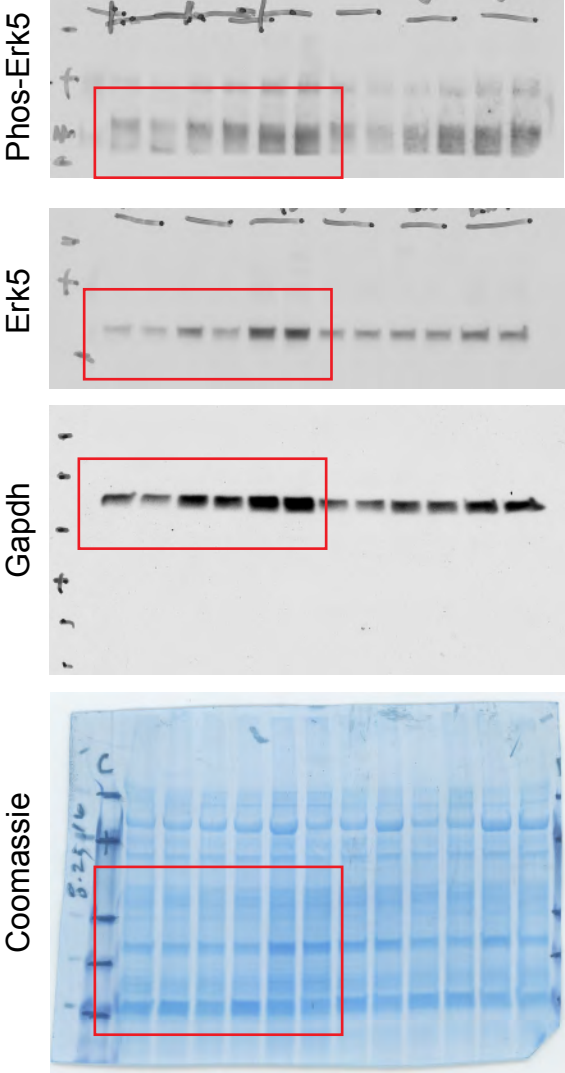
Full unedited gels for Figure 1



Blots were cut prior to probing

Full unedited gels for Figure 5

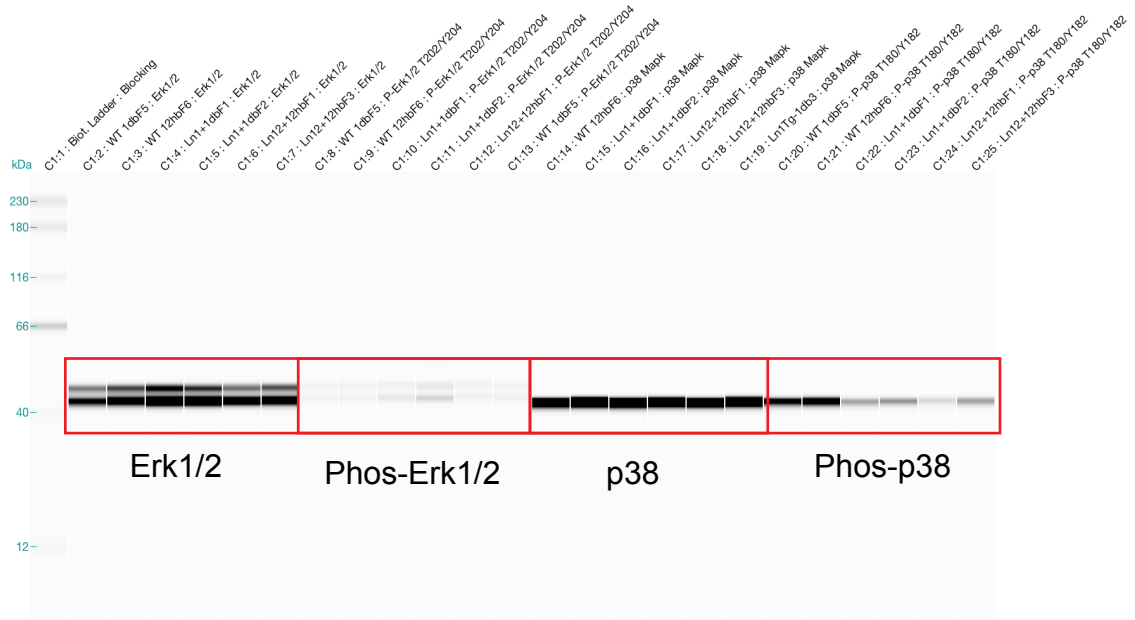
Figure 5A



Blots cut prior to probing

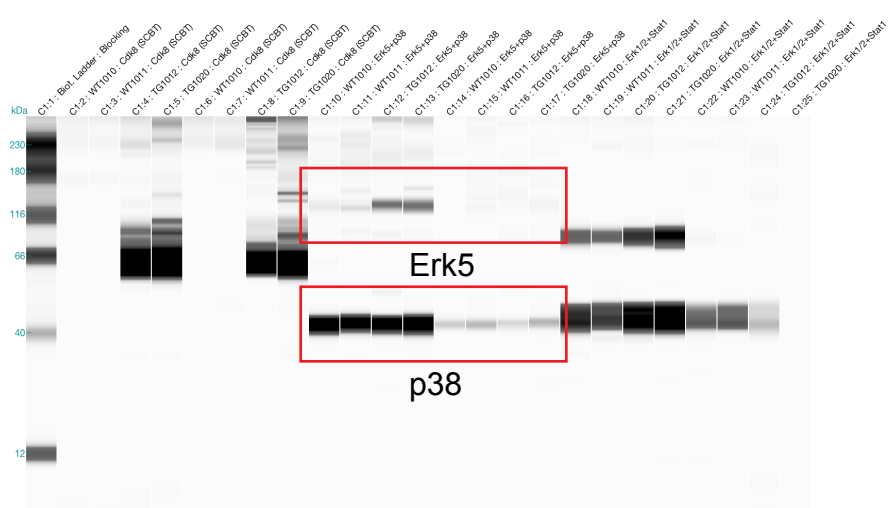
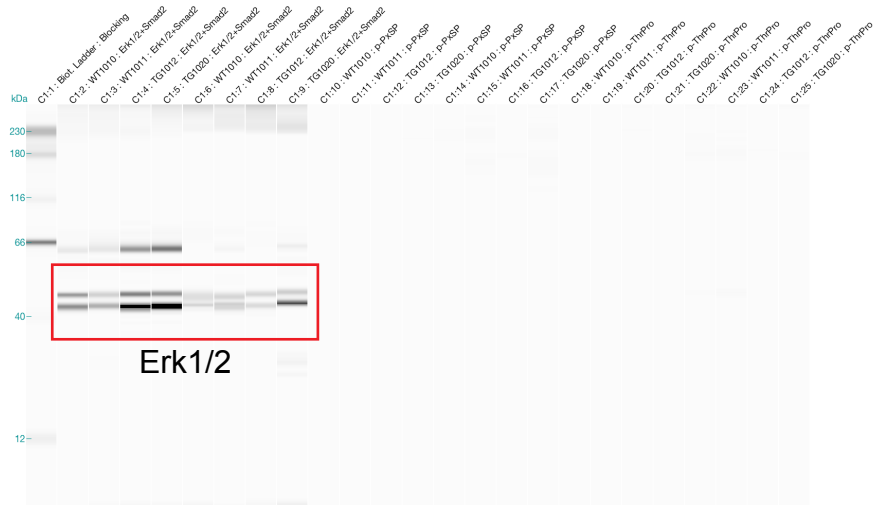
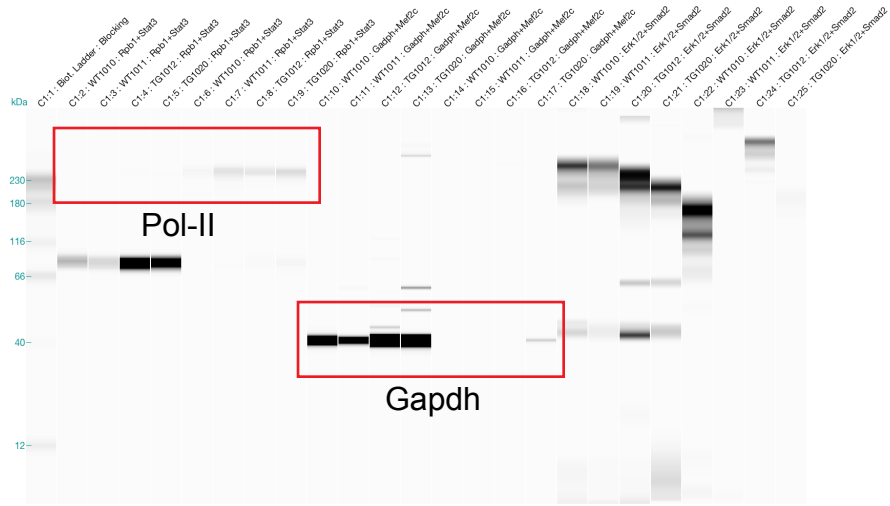
Full unedited gels for Figure 5

Figure 5D



Full unedited gels for Figure 5

Figure 5F



Full unedited gels for Figure 7

Figure 7A

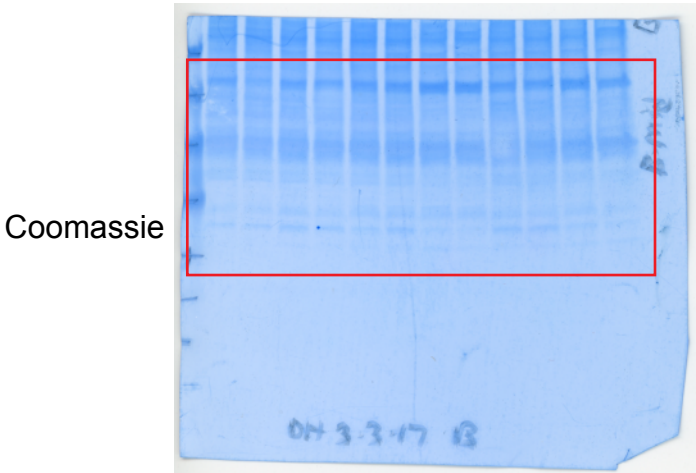
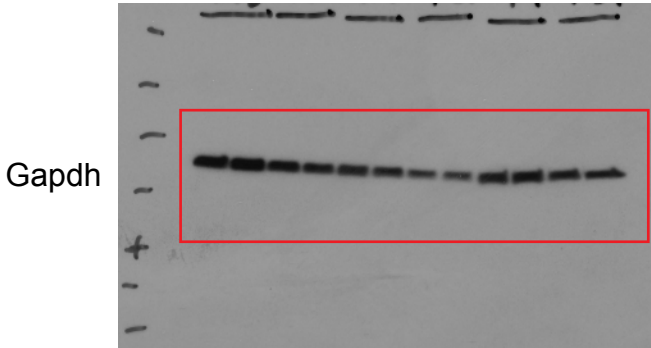
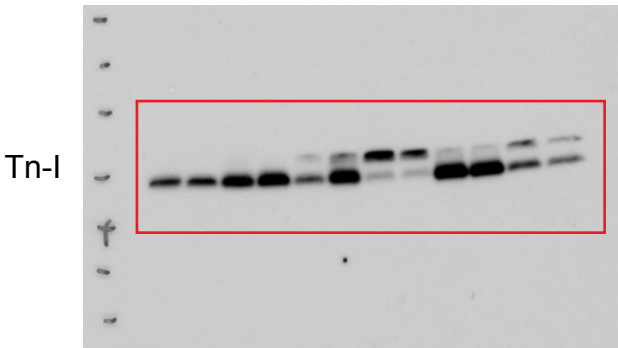
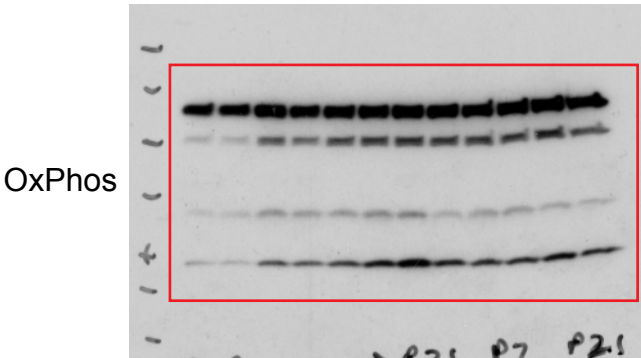


Figure 8D

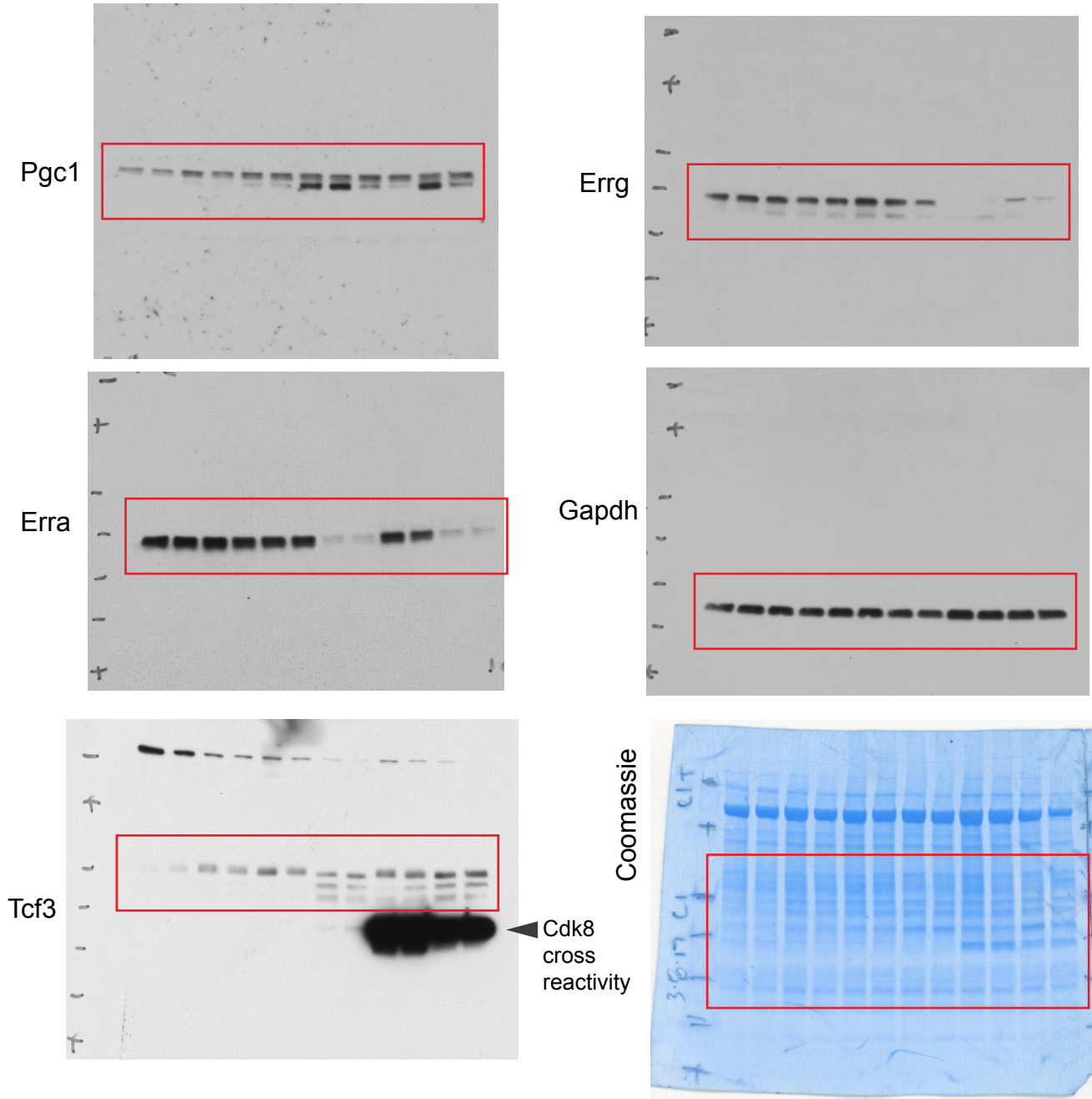
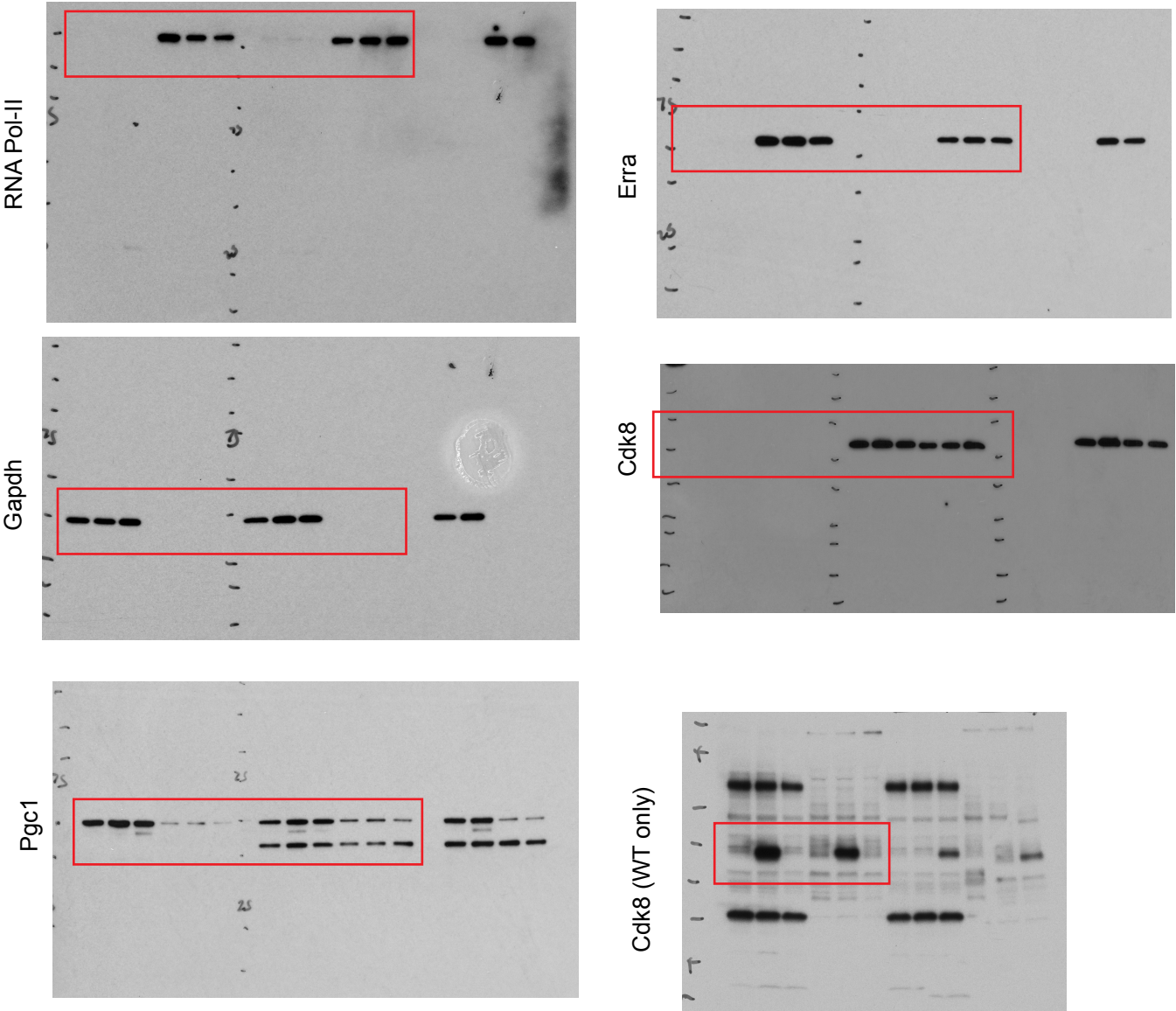
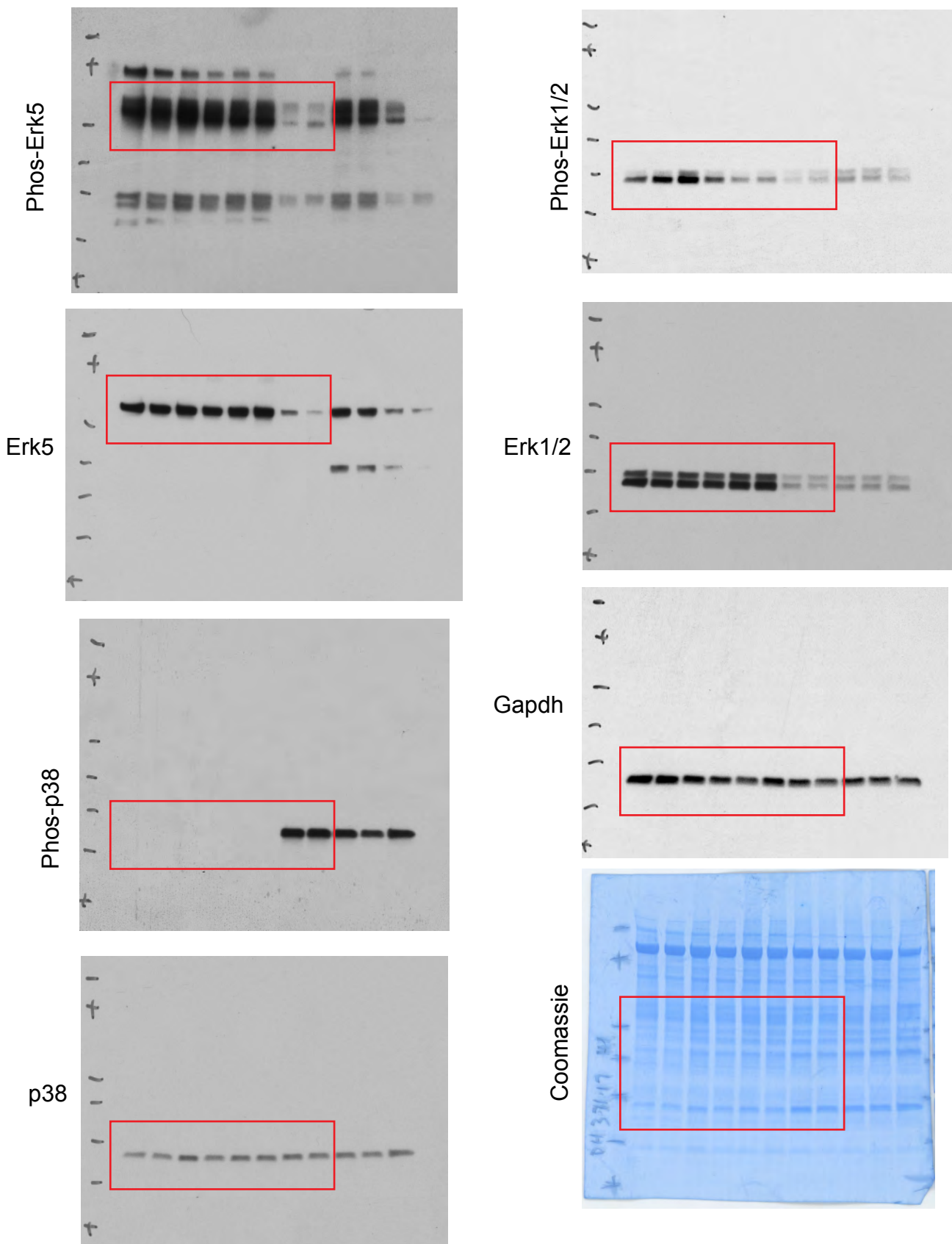


Figure 8F

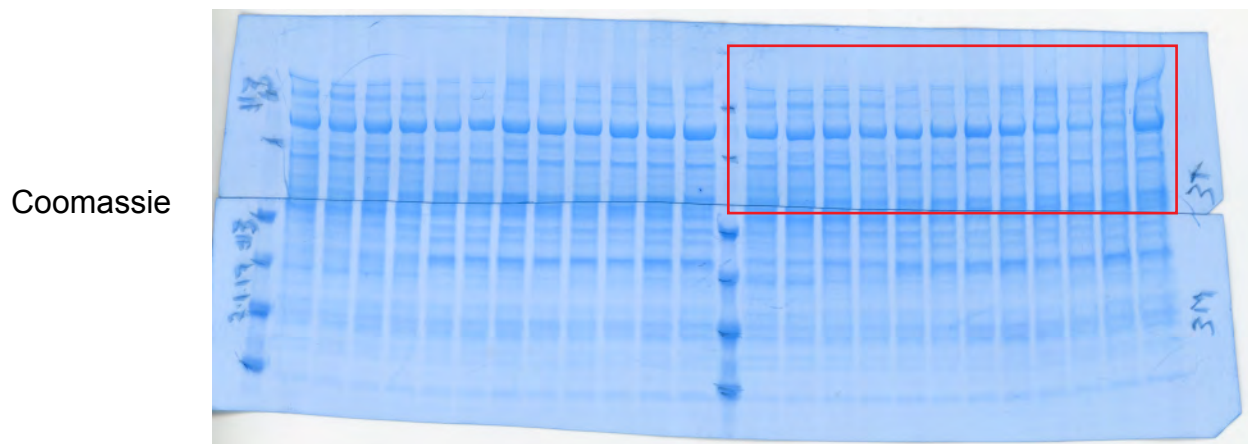
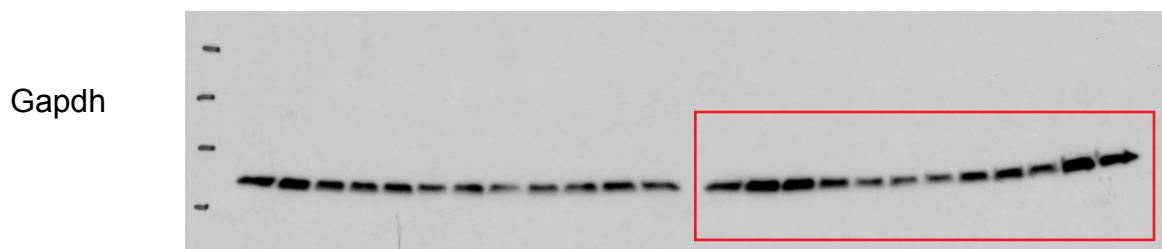
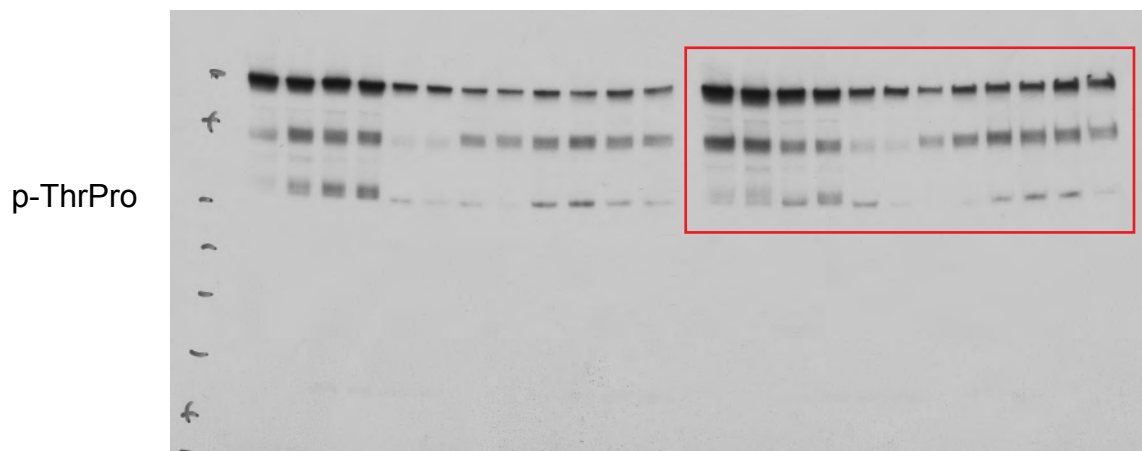
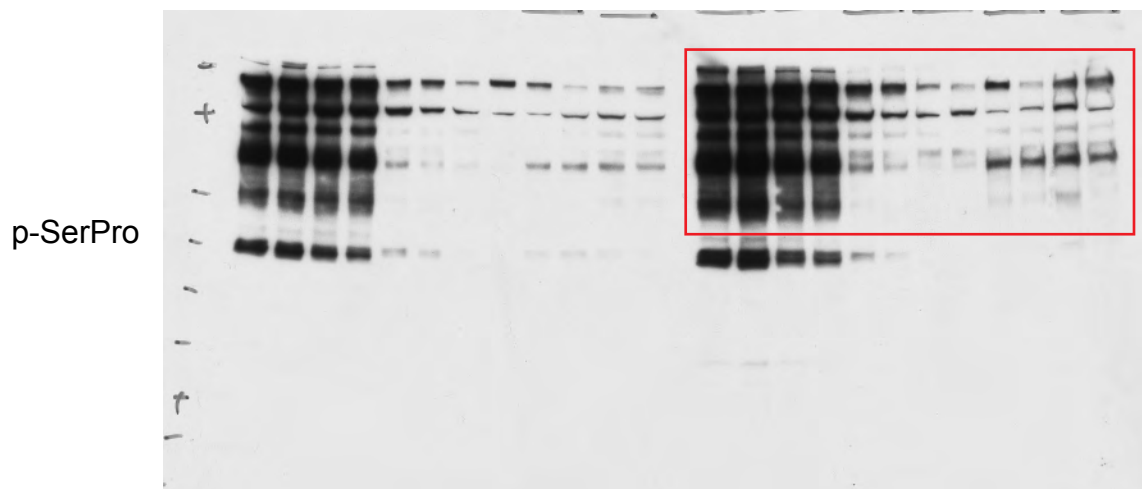


Full unedited gels for Supplemental Figure 1

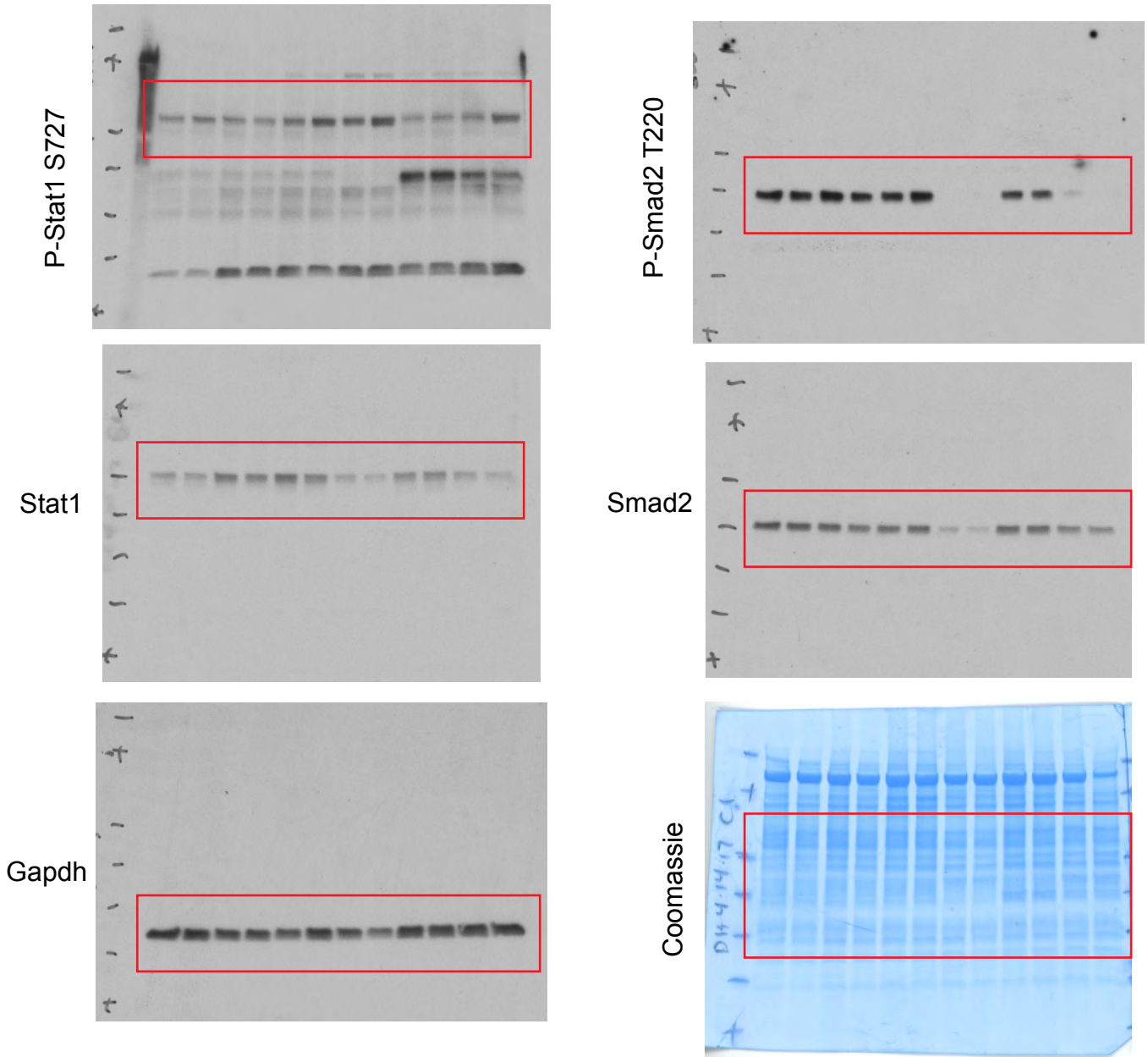


Full unedited gels for Supplemental Figure 2A

Supplemental Figure 2A



Supplemental Figure 2C



Full unedited gels for Supplemental Figure 2

Supplemental Figure 2E

