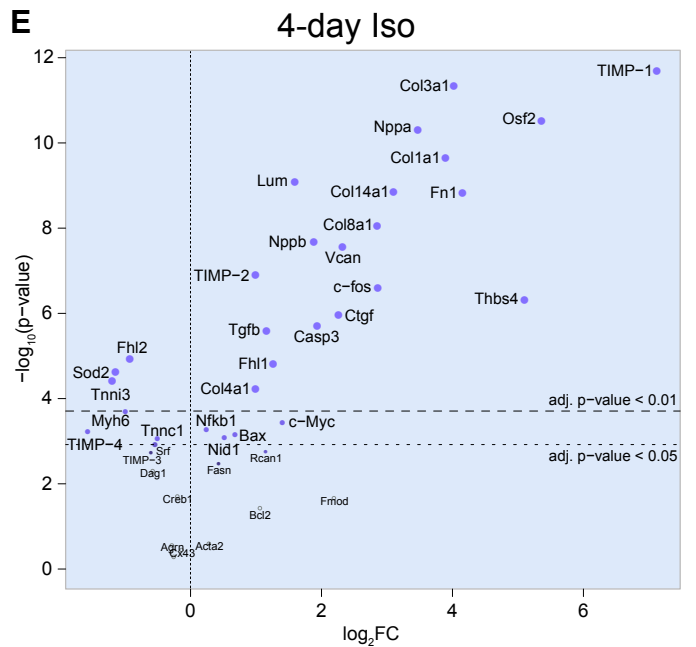
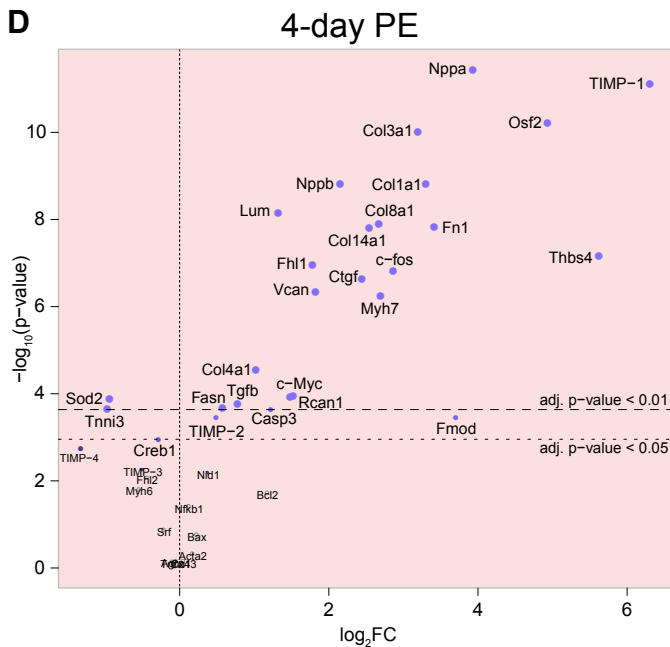
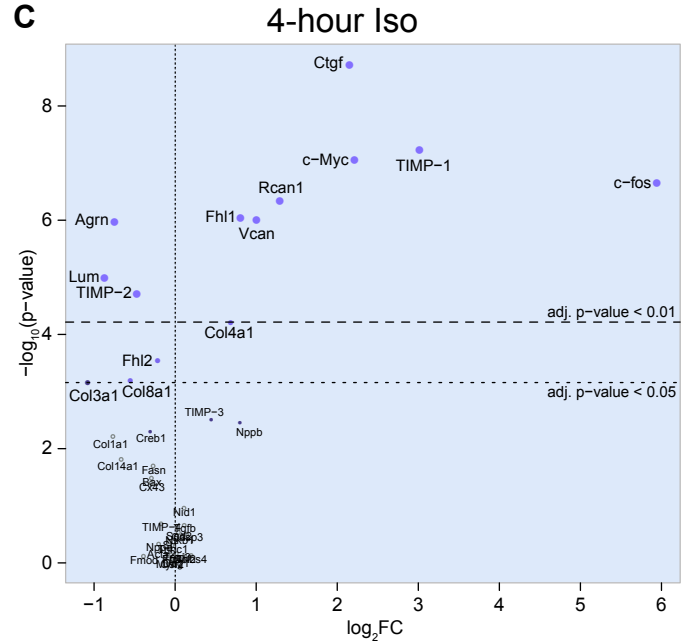
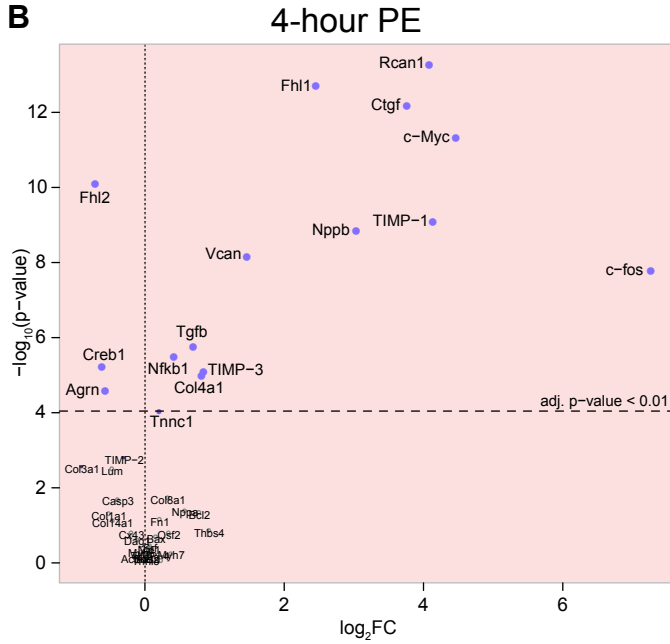
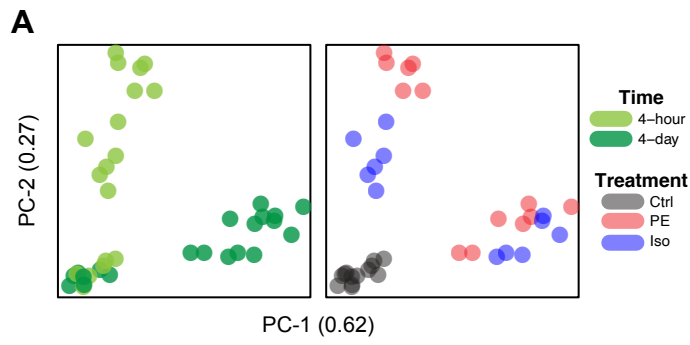
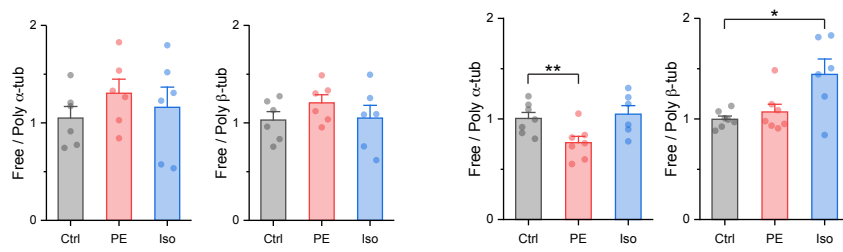
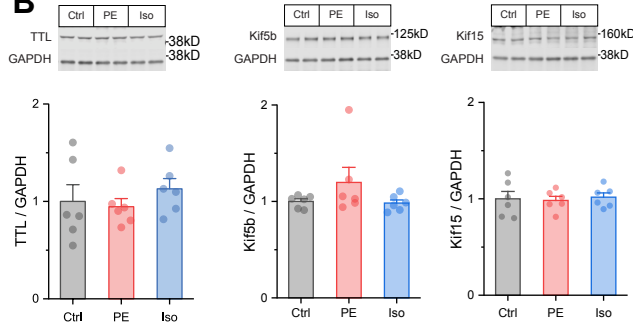
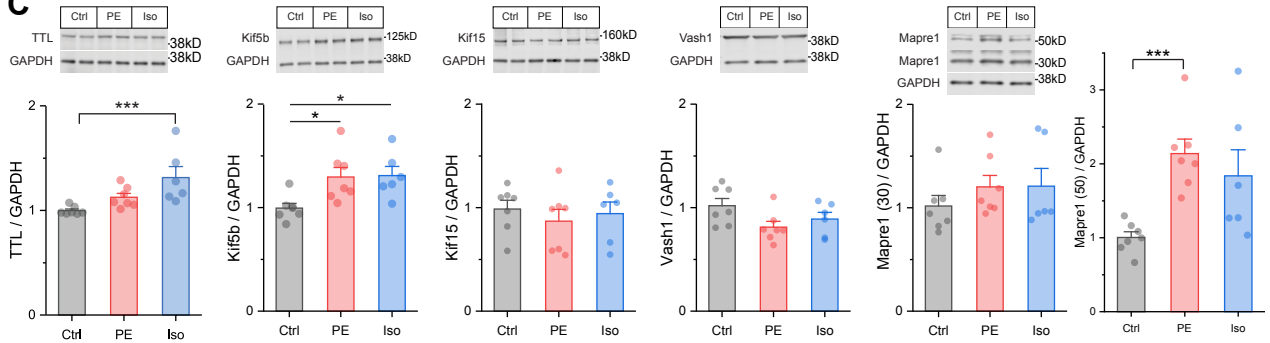


**Supplemental Figure 1.** Summary of the tubulin code. **(A)** Free & polymerized tubulins are in dynamic equilibrium. **(B)** The tubulin code is the permutation of the tubulin post-translational modifications & isoforms.

# Hypertrophy & Fibrosis



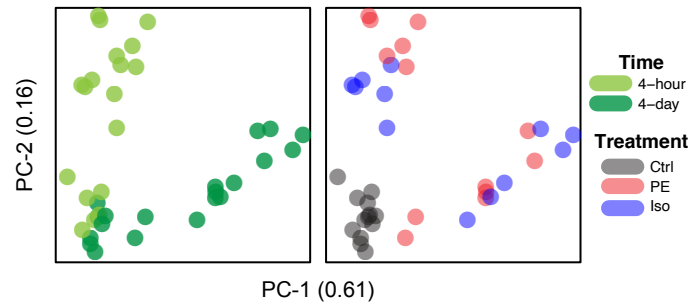
**Supplemental Figure 2. (A)** Principal component analysis (PCA) of nCounter mRNA counts from 4-hour and 4-day mice heart tissues using the hypertrophy & fibrosis panel. Volcano plots of all mRNA counts from the hypertrophy & fibrosis panel for **(B)** 4-hour PE, **(C)** 4-hour Iso, **(D)** 4-day PE, & **(E)** 4-day Iso. (n = 4h:6, 4d: Ctrl:7, PE:7, Iso:6)

**A****B****C**

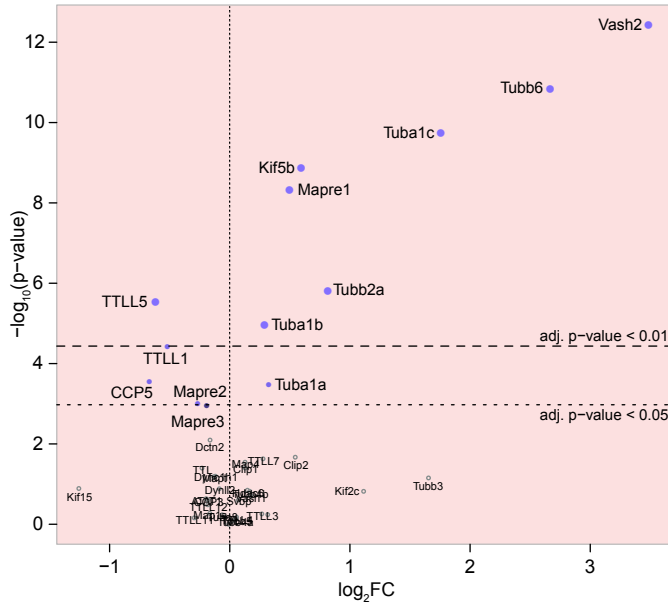
**Supplemental Figure 3. (A)** Free/Poly quantifications for  $\alpha$  and  $\beta$ -tubulins at 4-hour (**left**) and 4-day (**right**). **(B)** Western blot analyses of TTL, Kif5b, and Kif15 at 4-hour. (n: Ctrl, PE, Iso = 6) **(C)** Western blot analyses of TTL, Kif5b, Kif15, Vash1, and Mapre1 at 4-day. (n: Ctrl=7, PE=7, Iso=6). For Mapre1, we provided quantifications of two prominent bands at different molecular weights that were changed in the experimental groups: 30kDa band, which is the predicted molecular weight according to the amino acid sequence, and 50kDa band, which is also observed using the Anti-EB1 antibody produced in rabbit (Sigma: E3406) in certain cell types. For all graphs, \* represents p-value from Welch-corrected two-tailed two-sample t-test  $< 0.025$ , \*\* represents  $p < 0.01$ , and \*\*\* represents  $p < 0.001$ .

# Tubulin isoforms, tubulin modifying enzymes, & motors

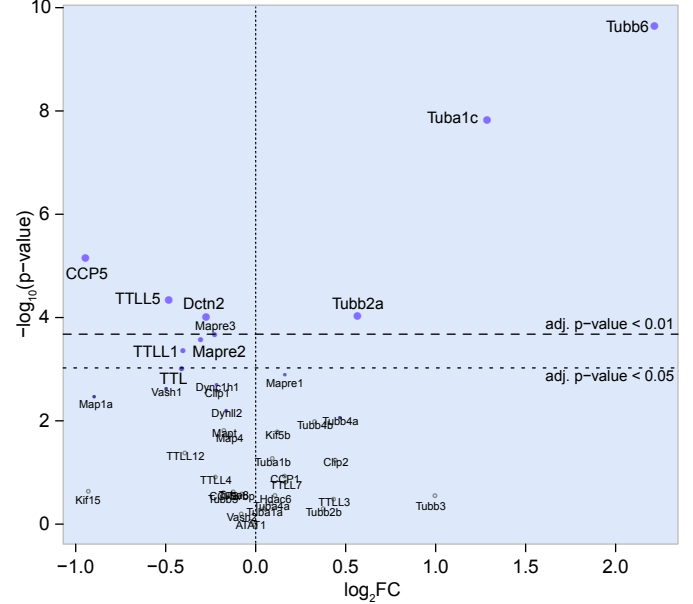
**A**



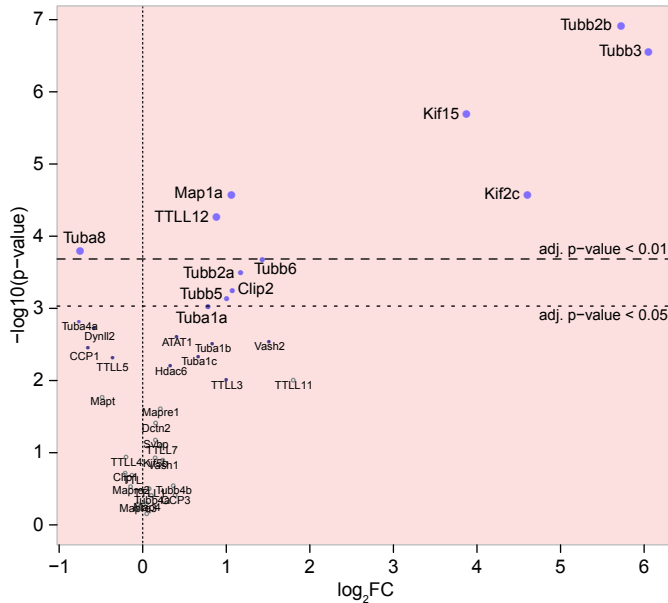
**B** 4-hour PE



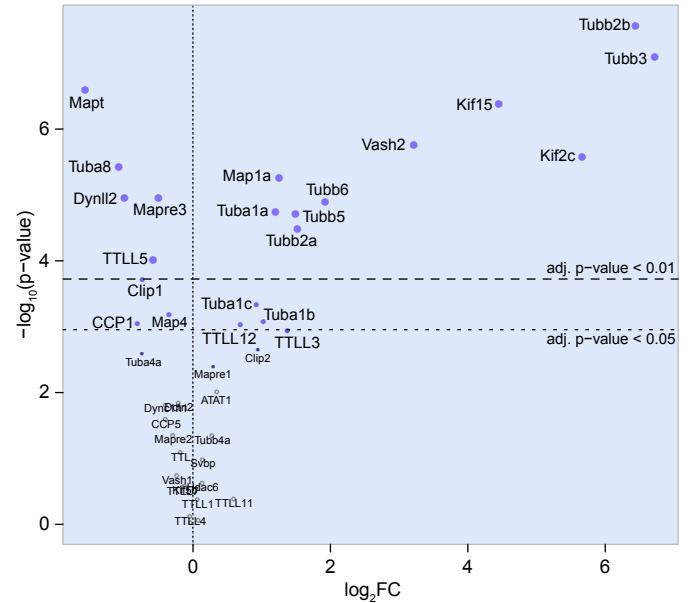
**C** 4-hour Iso



**D** 4-day PE

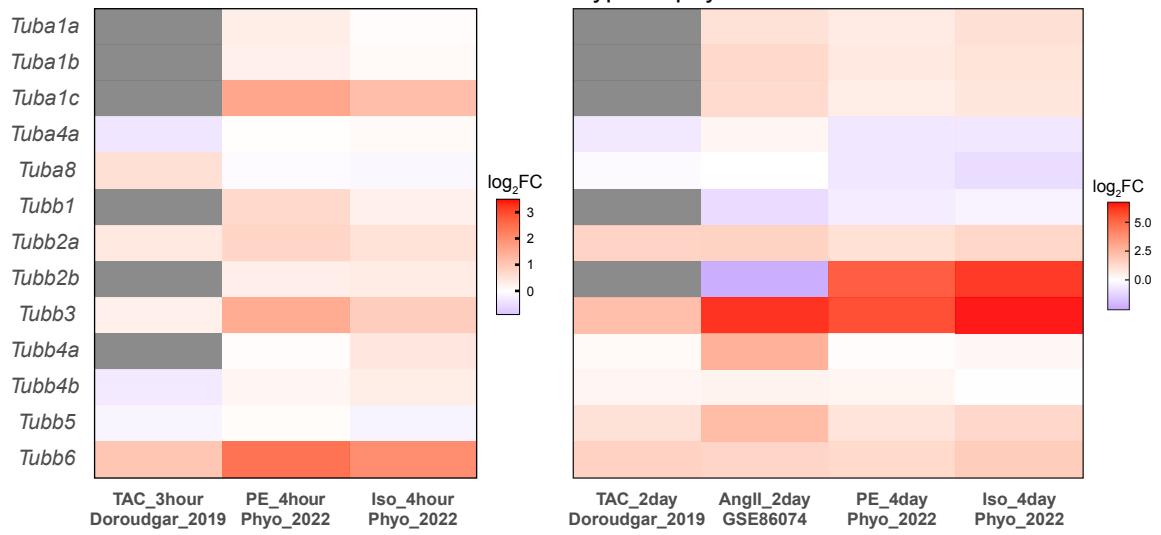


**E** 4-day Iso

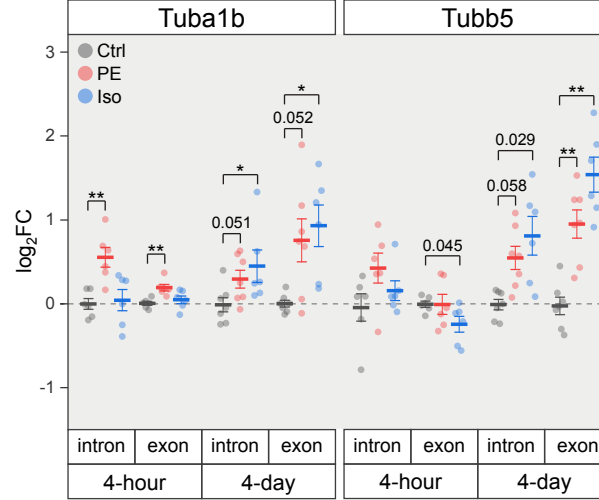


**Supplemental Figure 4. (A)** Principal component analysis (PCA) of nCounter mRNA counts from 4-hour and 4-day mice heart tissues using the tubulin panel. Volcano plots of all mRNA counts from the tubulin panel for **(B)** 4-hour PE, **(C)** 4-hour Iso, **(D)** 4-day PE, & **(E)** 4-day Iso. (n = 4h:6, 4d: Ctrl:7, PE:7, Iso:6)

mRNA from cardiac hypertrophy mouse models



**Supplemental Figure 5.** Previously published & current studies' mRNA data of mouse  $\alpha\beta$ -tubulin isoforms following different pathological stimulations (Bottermann et al., 2018, Doroudgar et al., 2019).

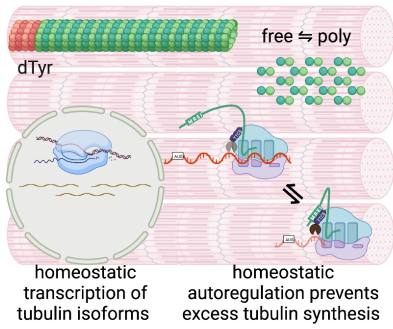


**Supplemental Figure 6.** Unspliced and spliced mRNA counts of Tuba1b and Tubb5 (n = 4h:6, 4d: Ctrl:7, PE:7, Iso:6); \* represents p-value from Welch-corrected two-tailed two-sample t-test on non-log data < 0.025 (Bonferroni-corrected for two comparisons), \*\* represents p < 0.01, and \*\*\* represents p < 0.001.

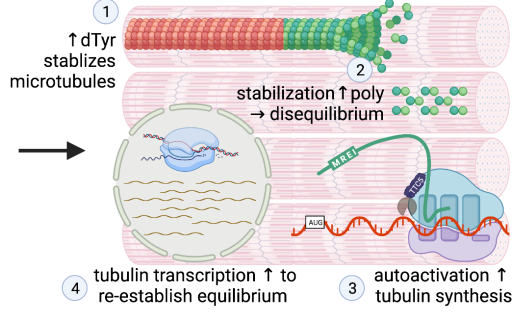
### Hypertrophic stimuli



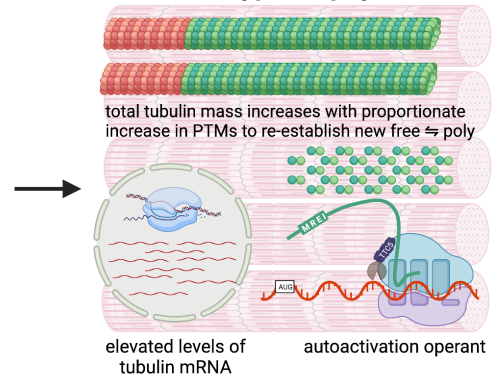
### Normal



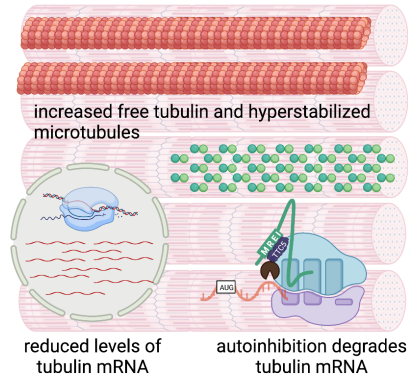
### Pre-hypertrophy



### Hypertrophy



### Heart Failure



Supplemental Figure 7. Schematic model of the summary