

**“A conserved, non-canonical insert in FIS1 mediates TBC1D15 and DRP1 recruitment for mitochondrial fission”**

**Figure S1. Rational design and validation of  $\Delta$ SKY FIS1 variants**

**S1**,  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectral overlays of FIS1 wildtype (black) with  $\Delta$ SKYD49G(left panel) and  $\Delta$ N $\Delta$ SKYD49G (right panel) with colors as indicated. Data were collected on 100  $\mu\text{M}$  samples at 25 °C, pH 7.4 at 14.1 T. FIS1 arm crosspeaks are indicated in magenta. **S1A**, The midpoint of the thermal unfolding transition was determined by fitting light scattering data collected from 25-95°C with the mean  $\pm$  standard deviation from 3-5 technical replicates shown as a box-and-whisker plot. **S1B-F**, Full  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectral overlays of FIS1 wildtype (black) with  $\Delta$ N $\Delta$ SKYD49G, AAA,  $\Delta$ SKY,  $\Delta$ SKYD49G, and D49G, respectively. Arm residue crosspeaks are labeled in magenta.

**Figures S2-S3. Confocal image gating methods and correlational analyses.**

**S2A**, Western blot showing FIS1 expression in HCT116 cells co-transfected with pcDNA-mitoYFP and pcDNA-FIS1. FIS1 expression in each sample is first normalized to total protein expression and then quantified (n=1) as relative ratios to wildtype FIS1. **S2B**, Prior to analyzing confocal microscopy images shown in **Figure 3**, cells were gated to exclude cells that overexpressed FIS1 (mean A.U. >1600). Each point in the scatter plot represents a cell cropped for image analysis. Only cells with A.U. < 1600 were included in quantitative analyses presented in Figure 3. **S2C**, Correlational plots to determine the relationship between FIS1 expression and mitochondrial network area, and DRP1 recruitment (**S2D**). Each point is colored based on the gated population average FIS1 expression of gated cells.

**S3A**, Scatter plots of all cropped cells from confocal microscopy images shown in **Figure 5**, showing the relationship between FIS1 expression and mitochondrial network area and DRP1 recruitment. (**S3B**) without and without ectopic YFP-TBC1D15. The red shaded area in **S3A** and **S3B** shows which cells were included for analyses after gating. **S3C**, Correlational plots to determine the relationship between FIS1 expression and mitochondrial network area and DRP1 recruitment (**S3D**). Each point is colored based on the gated population's average FIS1 expression of gated cells. **S3E**, Western blot showing FIS1 and YFP-TBC1D15 expression levels (top), and the quantification (n =1) of relative expression to wildtype FIS1 (bottom).

Fig. S1.

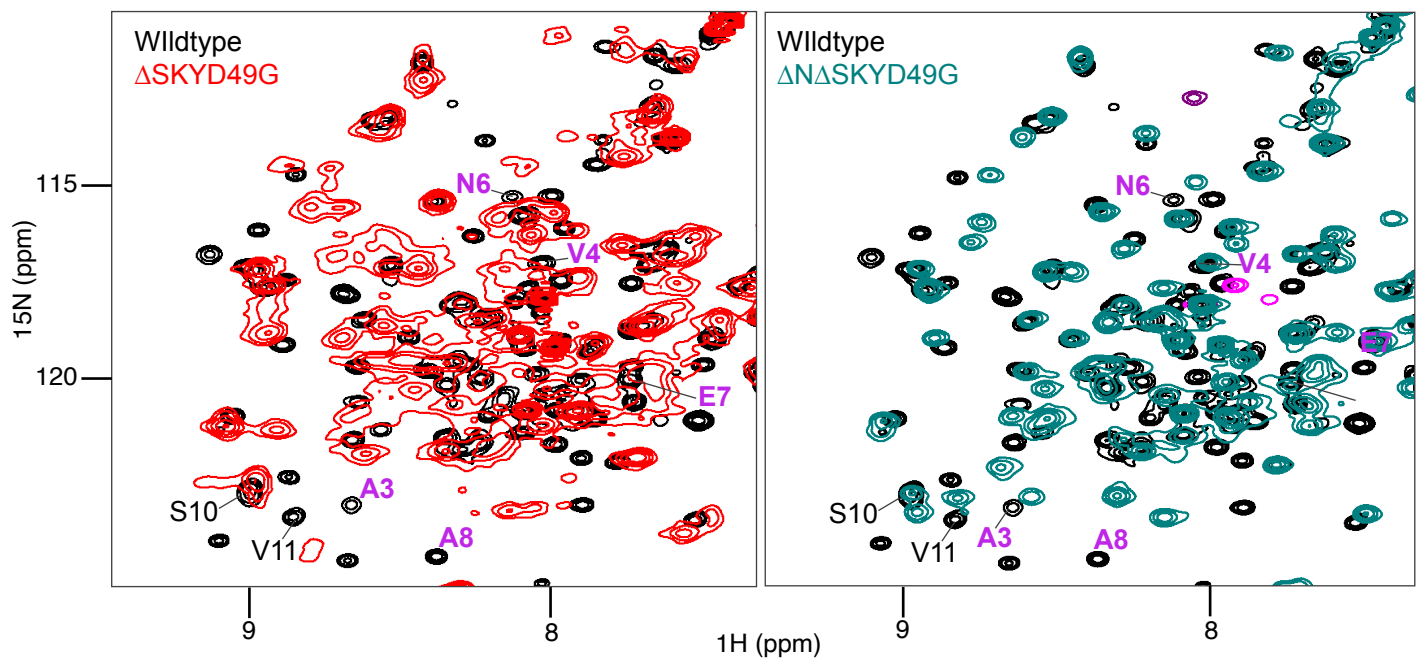
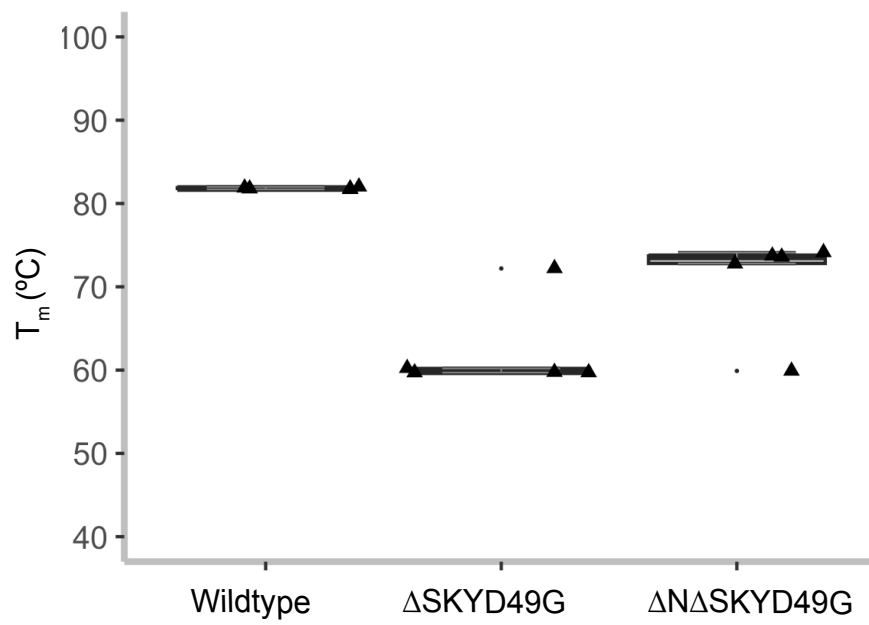
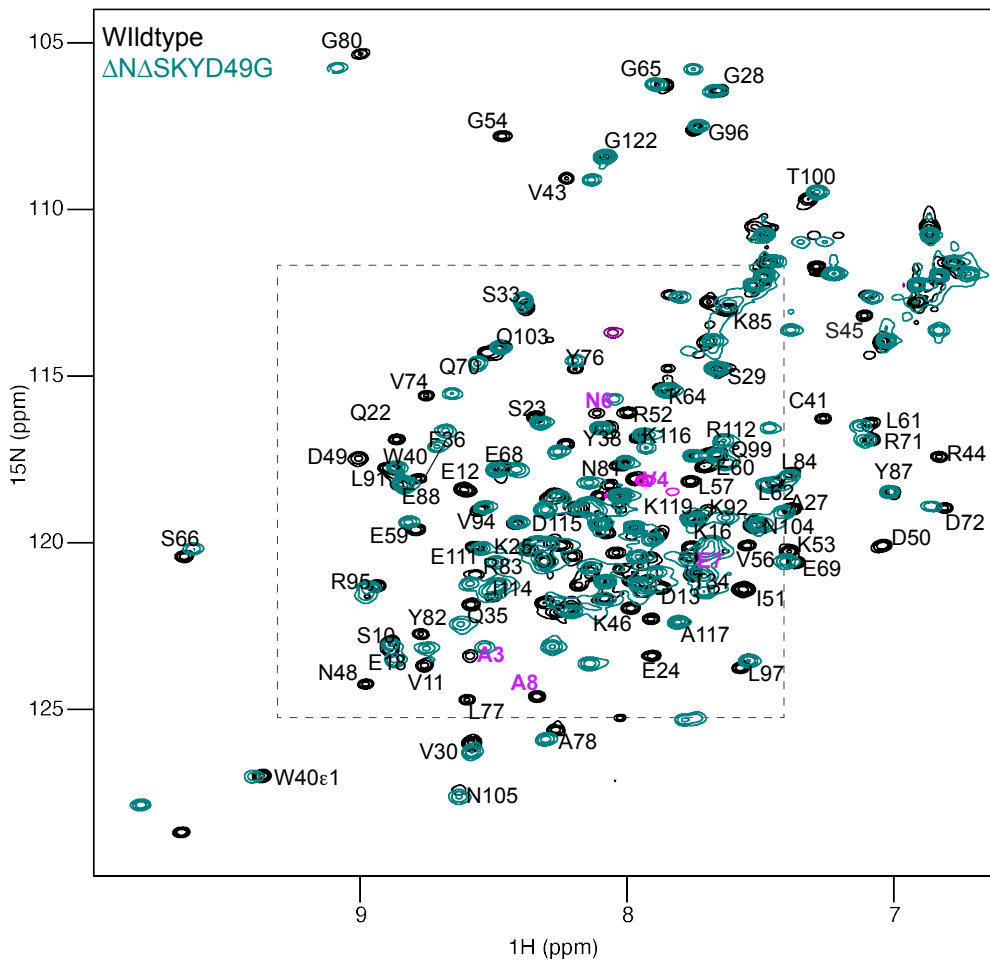


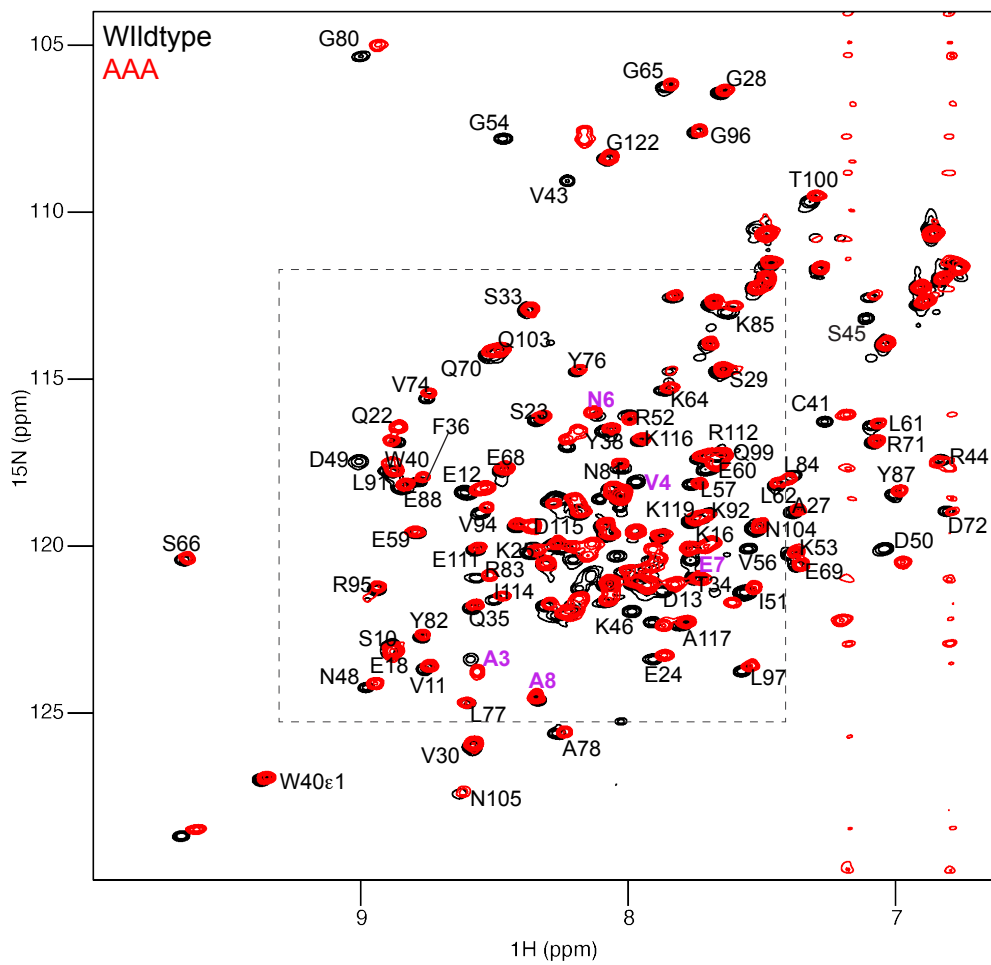
Fig. S1a.



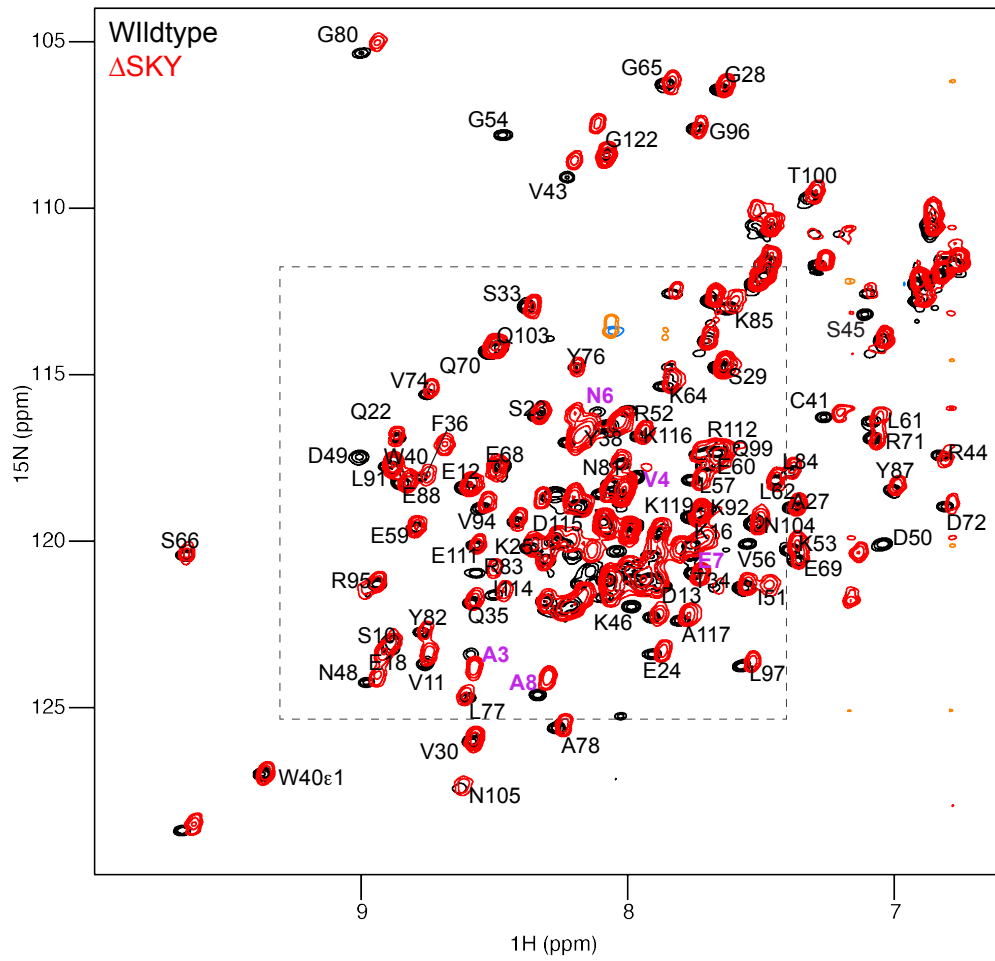
S1b.



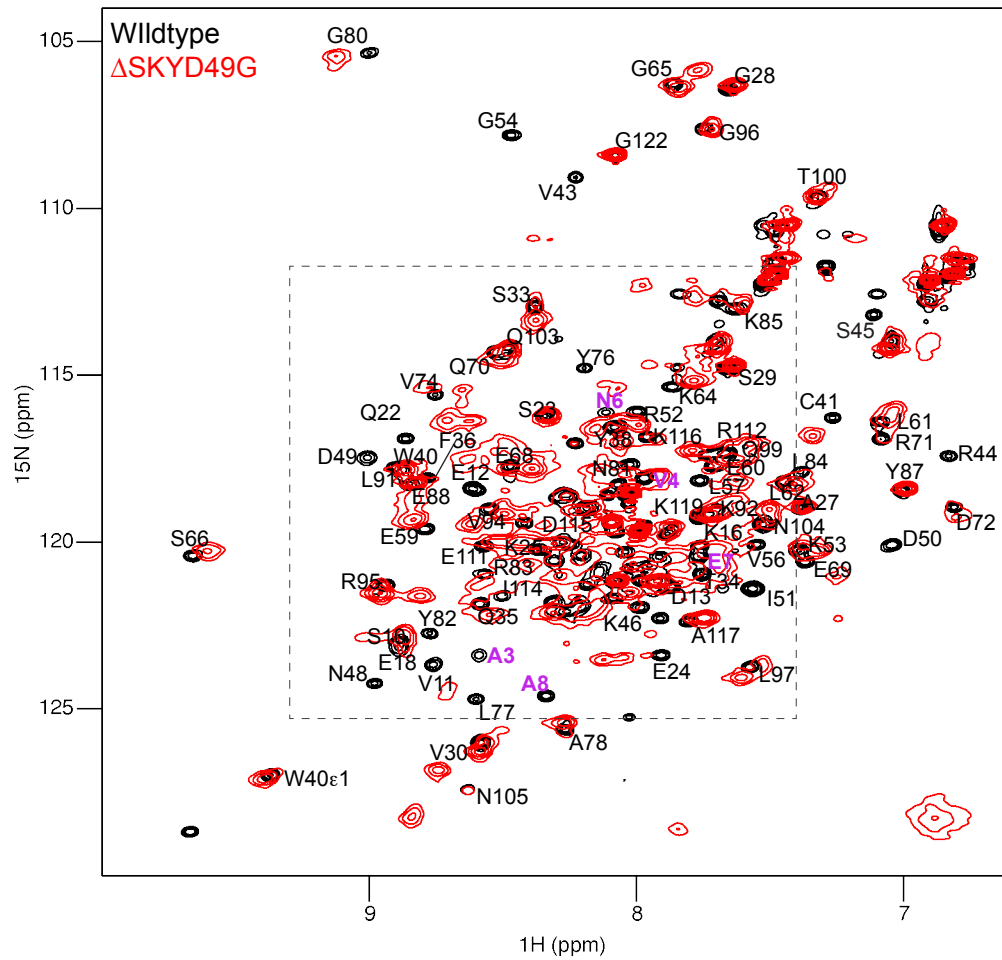
S1c.



S1d.



S1e.



S1f.

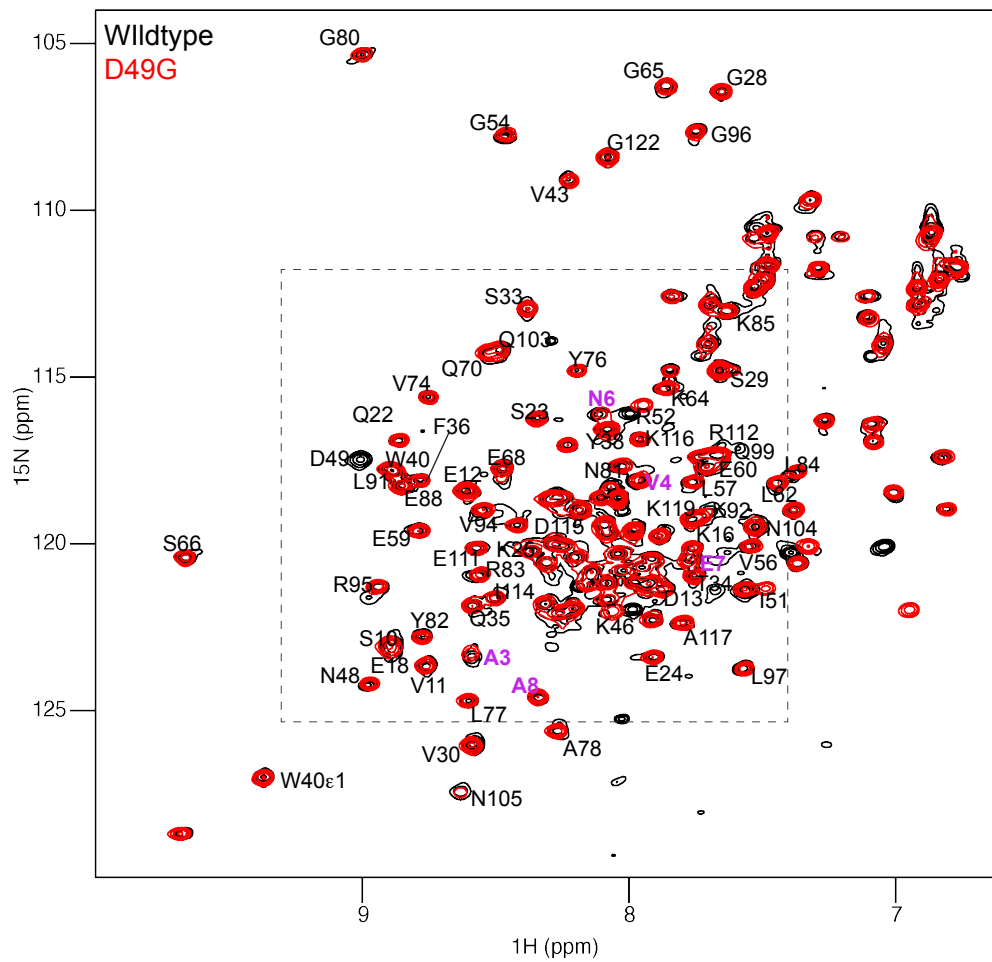


Fig. S2A.

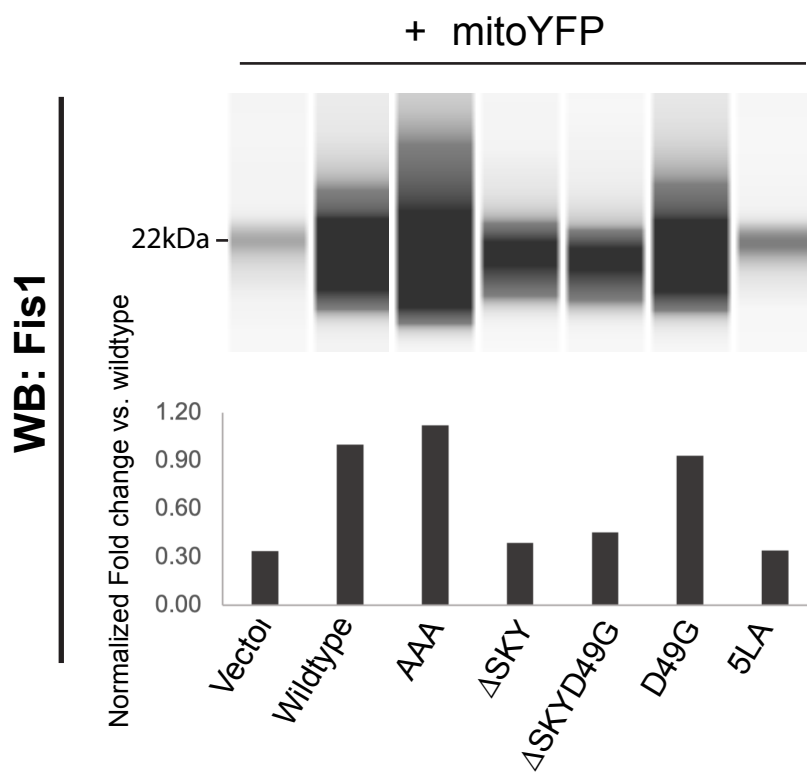


Fig. S2A. continued

Total protein assay

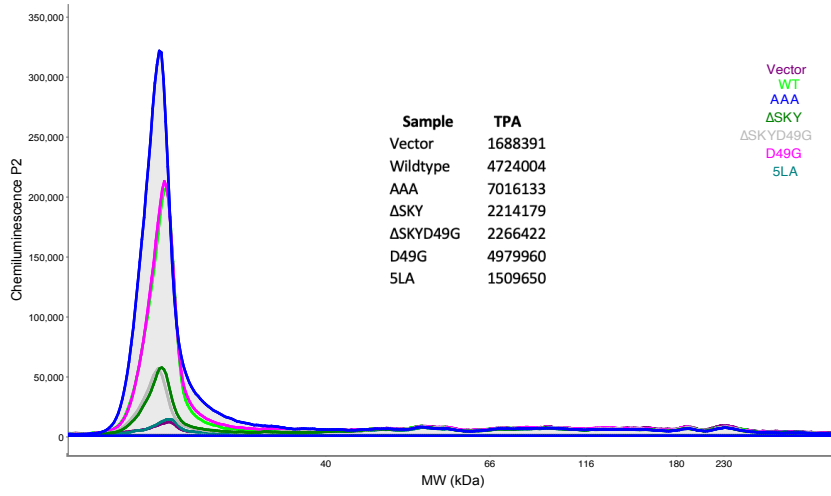
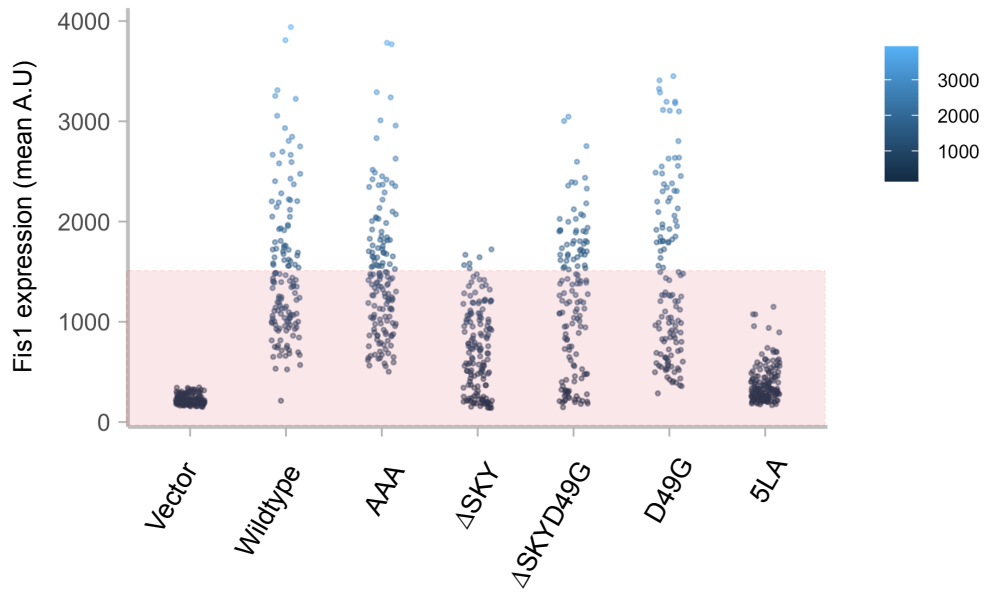
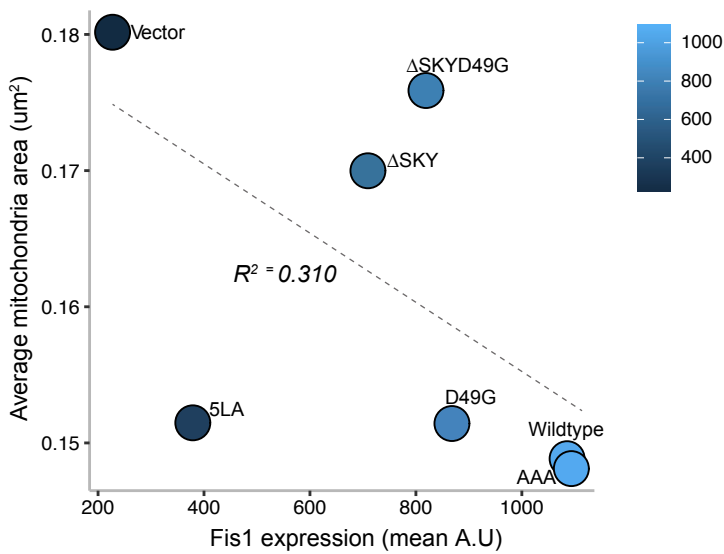


Fig. S2B.

Gating



S2C.



S2D.

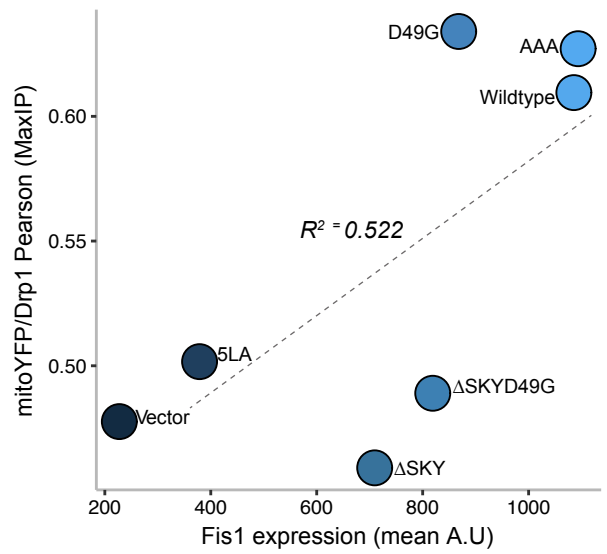


Fig. S3A.

### Gating

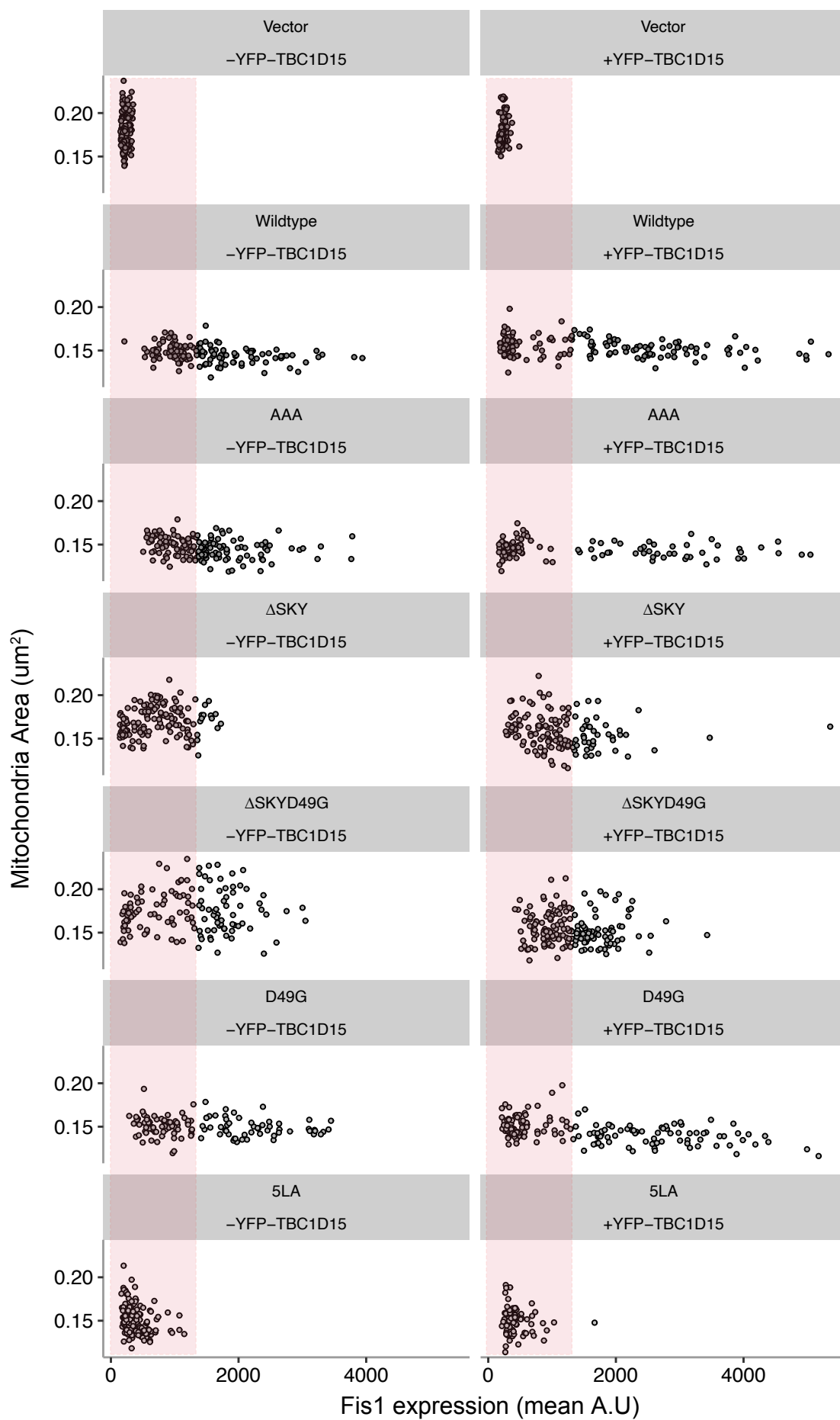


Fig. S3B.

### Gating

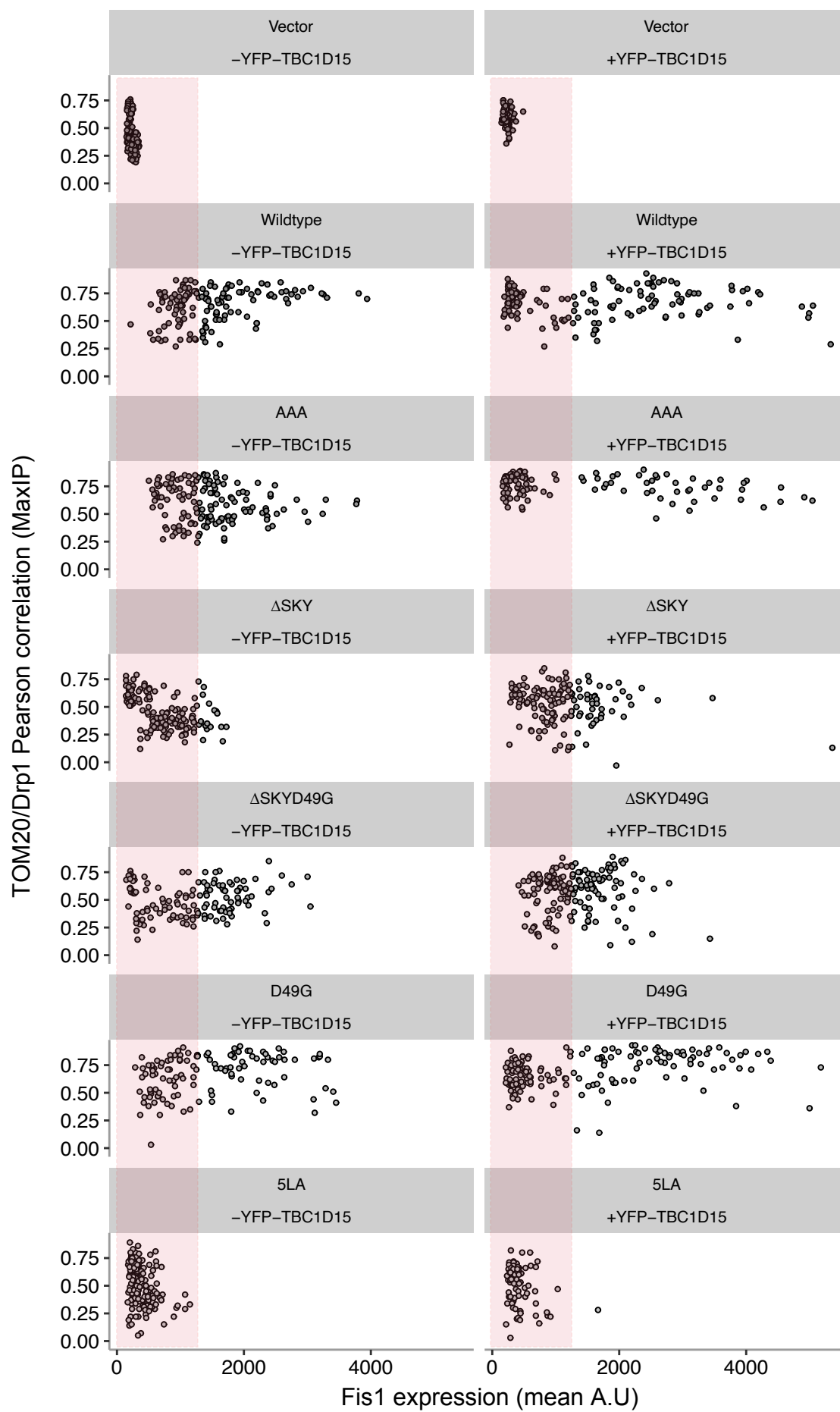
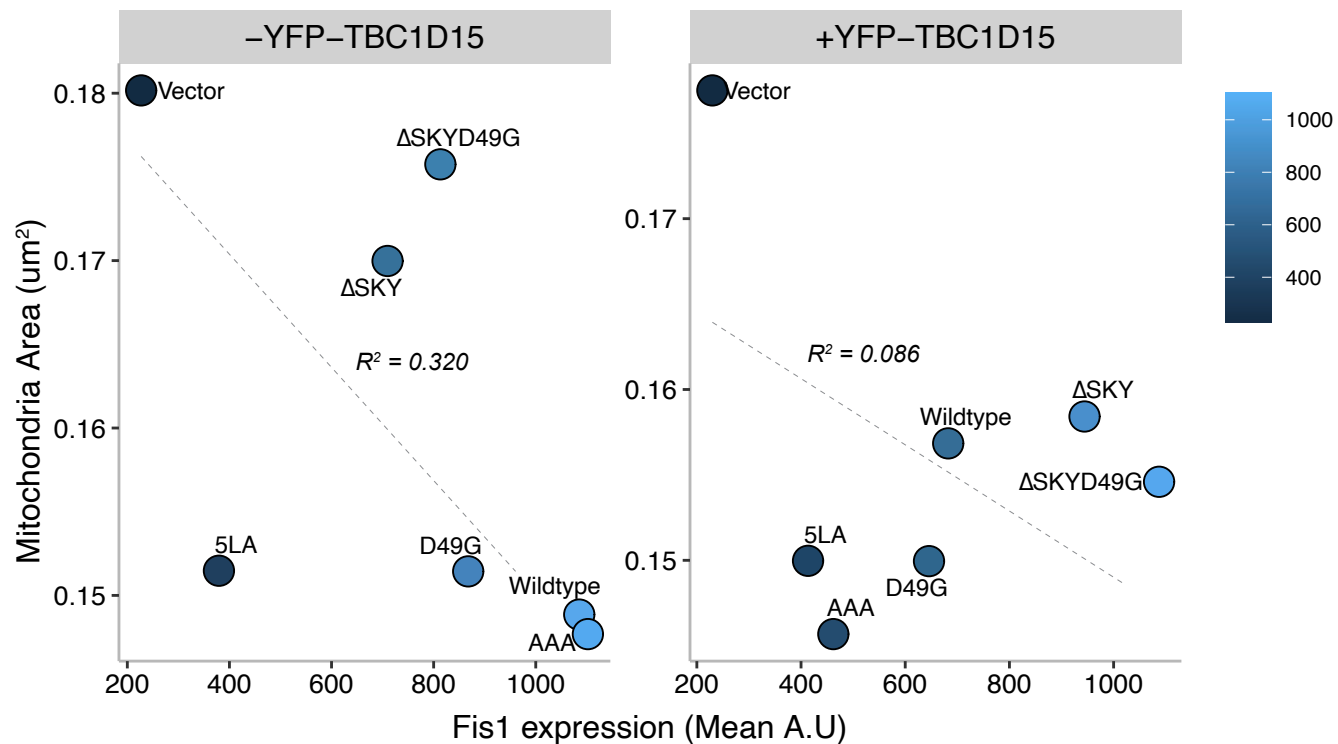
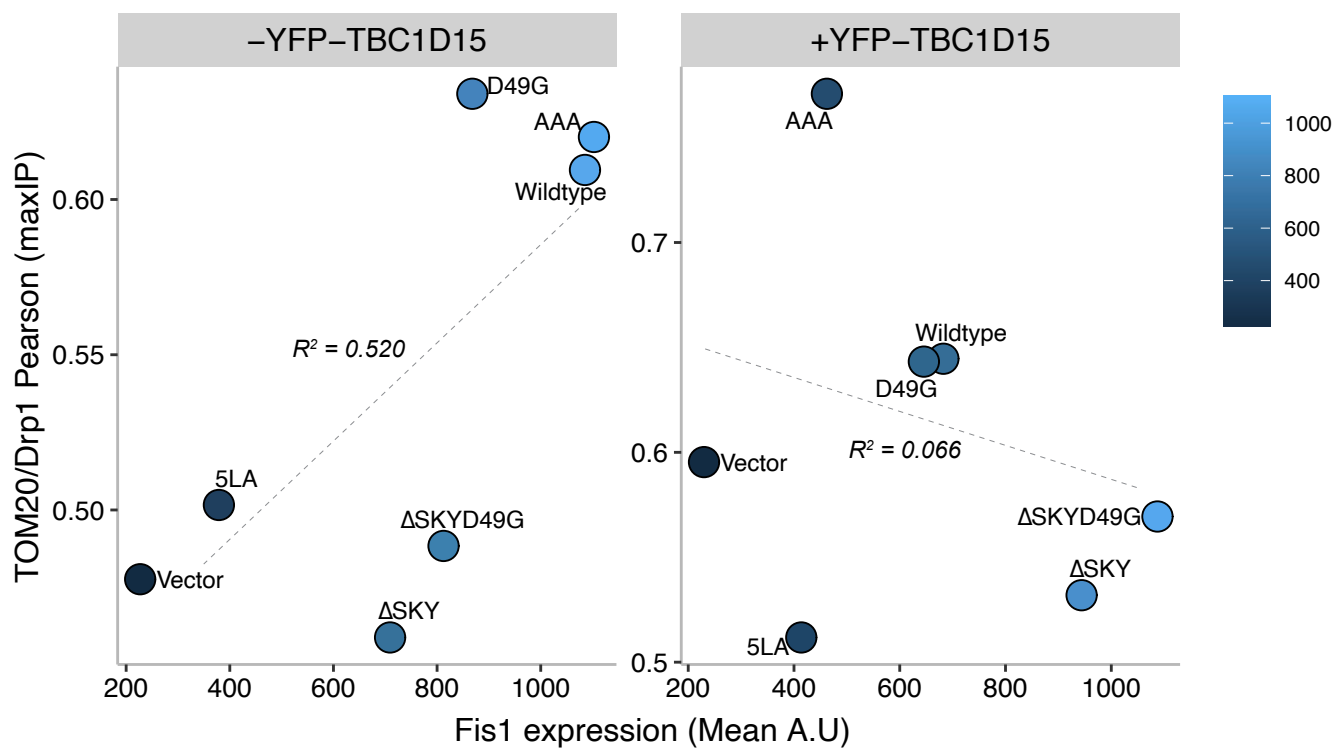




Fig. S3C.



S3D.



S3E.

