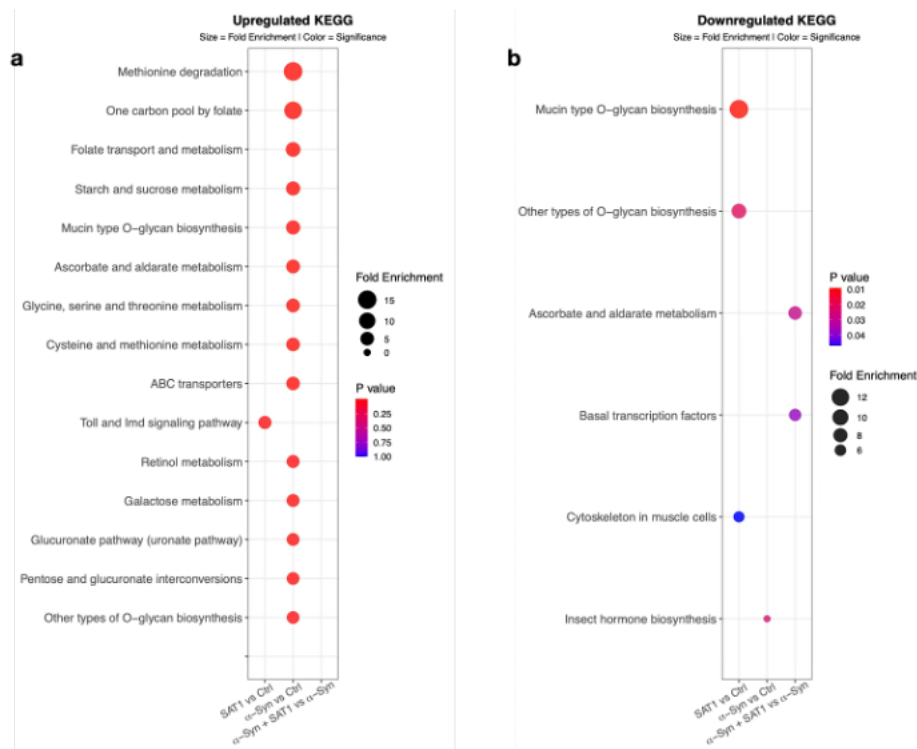


# Polyamine metabolic enzyme SAT1 remodels the neuronal transcriptome and rescues $\alpha$ -synuclein toxicity in *Drosophila*

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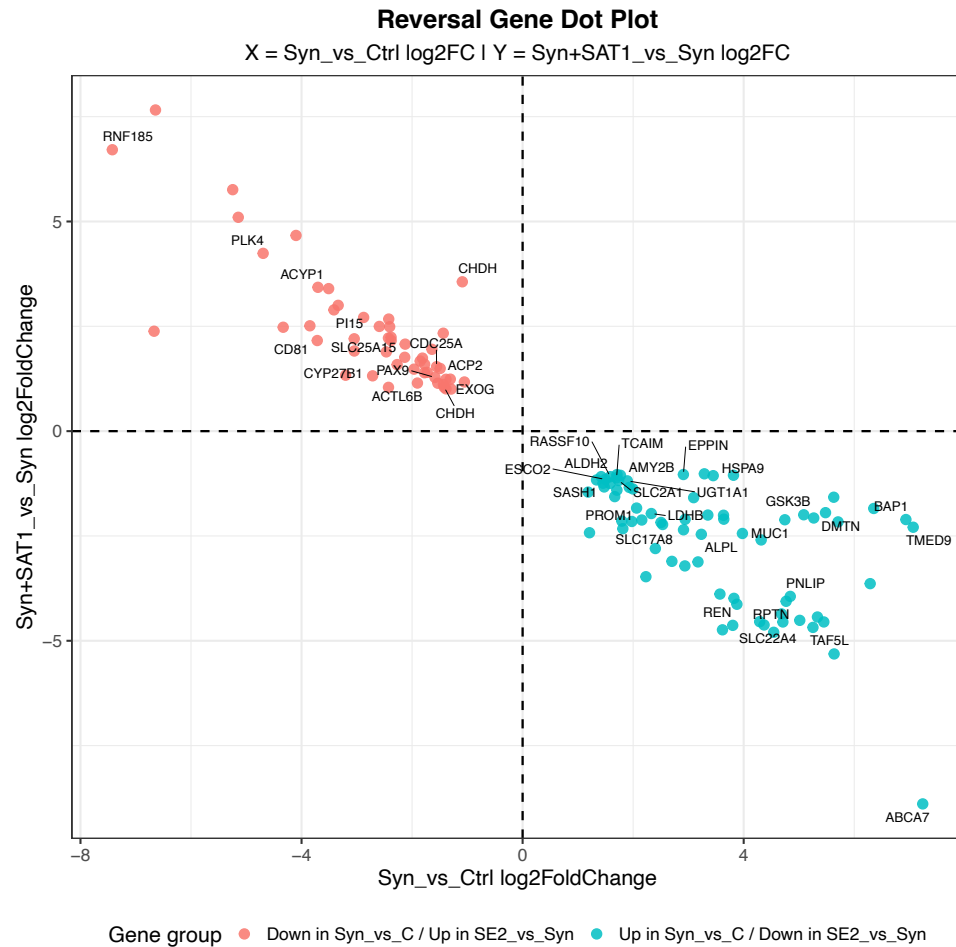
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**Supplementary fig. 1.**

## SAT1 and $\alpha$ -Syn differentially regulate neuronal biological pathways.

Dot plots showing functional enrichment of significantly differentially expressed genes from three comparisons, SAT1 vs control,  $\alpha$ -Syn vs control, and  $\alpha$ -Syn+SAT1 vs  $\alpha$ -Syn. KEGG pathway enrichment for upregulated (a) and downregulated (b) gene sets. Dot size indicates fold enrichment, and dot color denotes enrichment significance (p value). Only significantly enriched terms are shown.



## Supplementary figure 2.

### Reversal of $\alpha$ -Syn-associated gene expression by SAT1 co-expression.

To identify genes whose  $\alpha$ -Syn-associated expression changes were reversed by SAT1 co-expression, DESeq2 results from the  $\alpha$ -Syn versus control and  $\alpha$ -Syn+SAT1 versus  $\alpha$ -Syn comparisons were integrated. Each gene is plotted by its  $\log_2$  fold change in  $\alpha$ -Syn versus control (x-axis) and  $\alpha$ -Syn+SAT1 versus  $\alpha$ -Syn (y-axis). Genes were required to be significantly differentially expressed in both contrasts (adjusted p value < 0.05;  $|\log_2$  fold change| > 1).

Genes downregulated by  $\alpha$ -Syn but upregulated upon SAT1 co-expression are shown as salmon-colored dots and cluster in the upper-left quadrant. Genes upregulated by  $\alpha$ -Syn but suppressed by SAT1 are shown as teal-colored dots and cluster in the lower-right quadrant. Dashed lines indicate zero  $\log_2$  fold change in each comparison. Gene-level results were merged by FlyBase gene identifier and annotated with corresponding human ortholog symbols for visualization.

Supplementary figure 3.

Uncropped Blots

Figure 1b

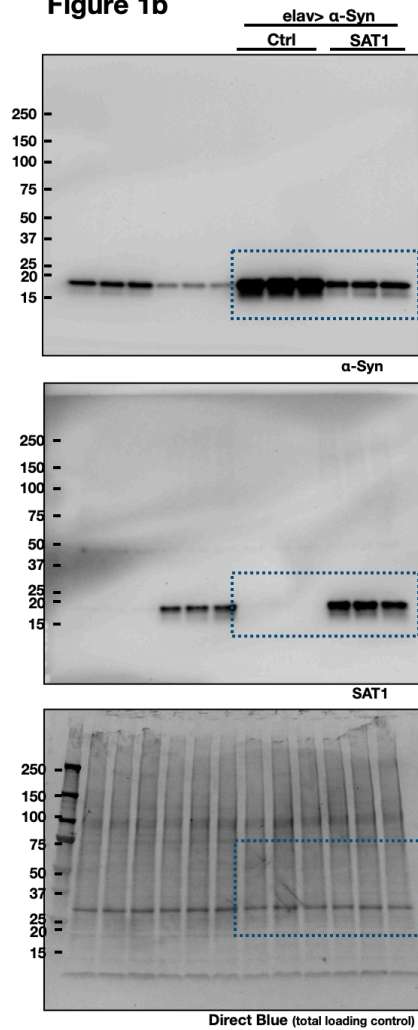


Figure 5b

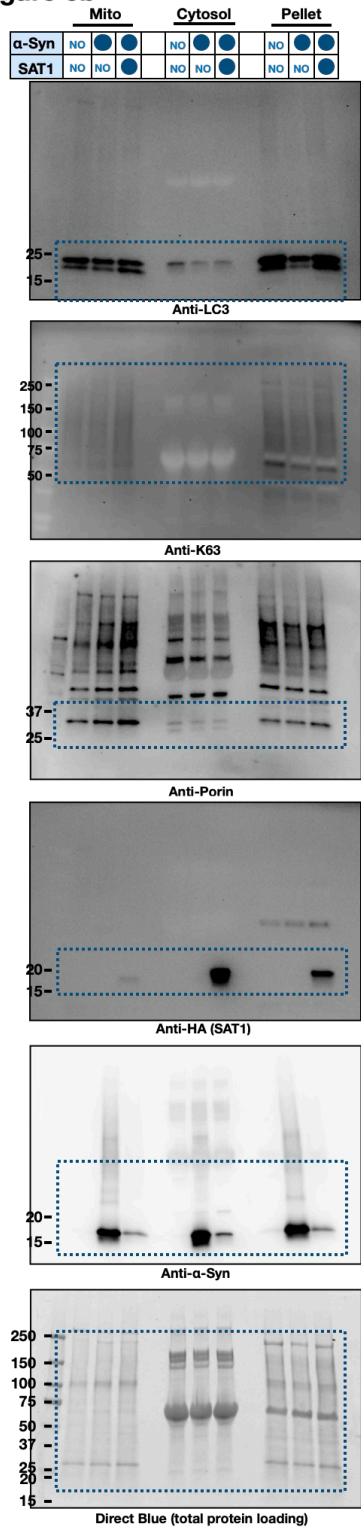


Figure 5c

