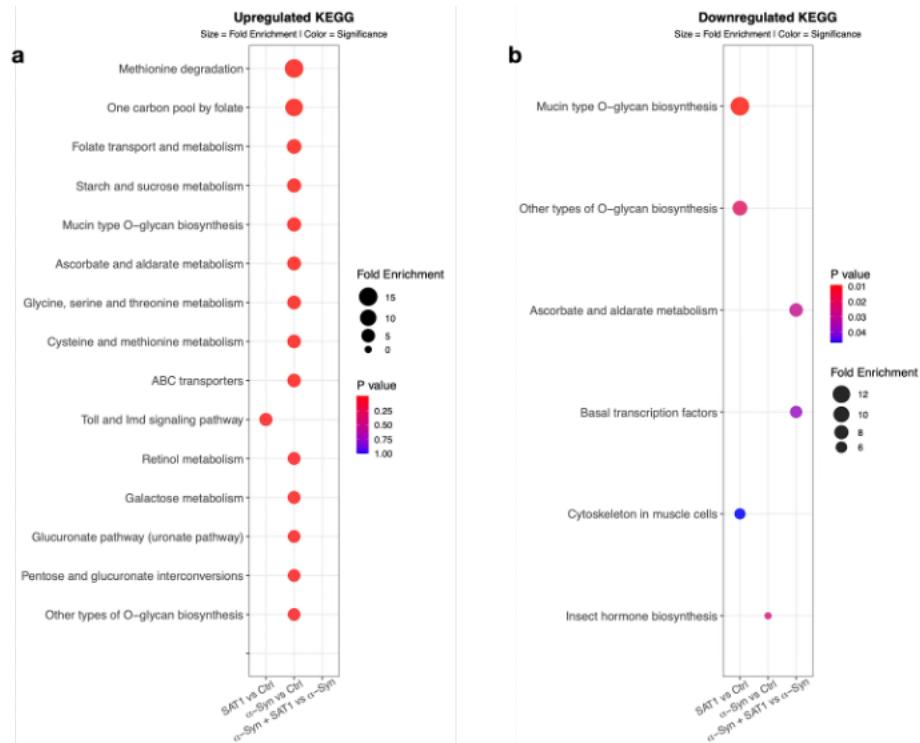


Polyamine metabolic enzyme SAT1 remodels the neuronal transcriptome and rescues α -synuclein toxicity in *Drosophila*

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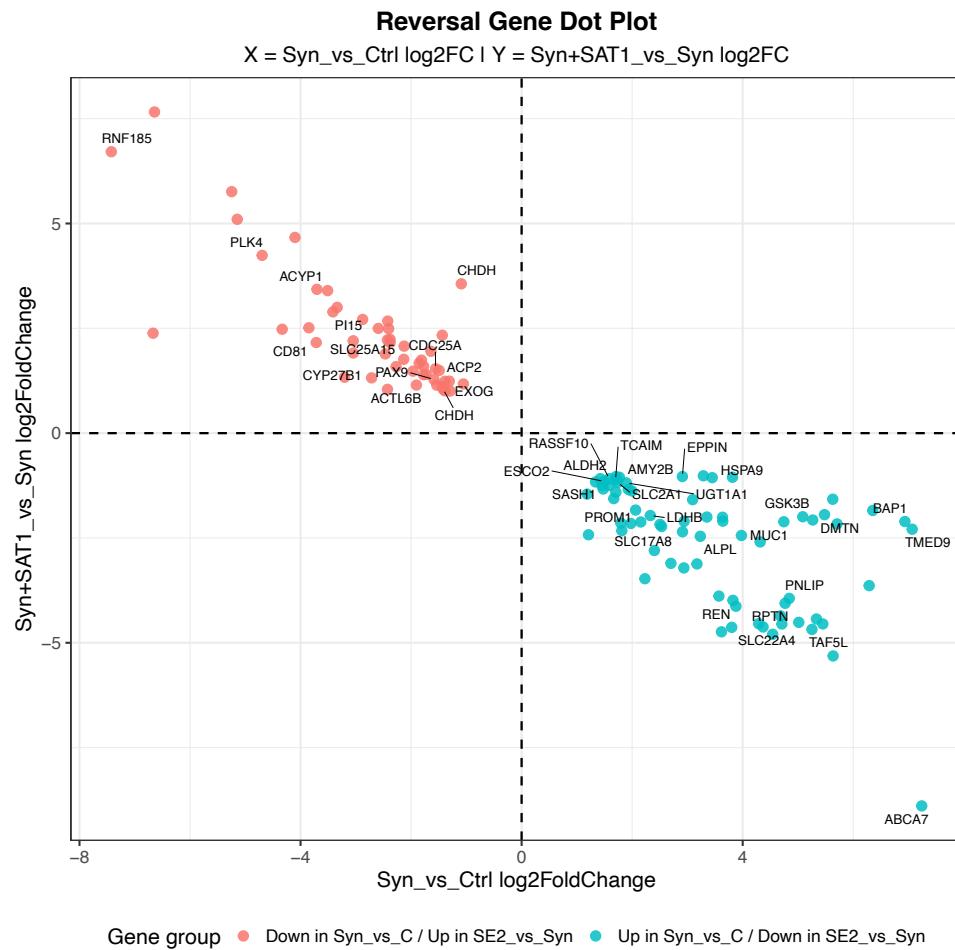
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Supplementary fig. 1.

SAT1 and α -Syn differentially regulate neuronal biological pathways.

Dot plots showing functional enrichment of significantly differentially expressed genes from three comparisons, SAT1 vs control, α -Syn vs control, and α -Syn+SAT1 vs α -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 α -Syn-associated gene expression by SAT1 co-expression.

To identify genes whose α -Syn-associated expression changes were reversed by SAT1 co-expression, DESeq2 results from the α -Syn versus control and α -Syn+SAT1 versus α -Syn comparisons were integrated. Each gene is plotted by its log₂ fold change in α -Syn versus control (x-axis) and α -Syn+SAT1 versus α -Syn (y-axis). Genes were required to be significantly differentially expressed in both contrasts (adjusted p value < 0.05; |log₂ fold change| > 1).

Genes downregulated by α -Syn but upregulated upon SAT1 co-expression are shown as salmon-colored dots and cluster in the upper-left quadrant. Genes upregulated by α -Syn but suppressed by SAT1 are shown as teal-colored dots and cluster in the lower-right quadrant. Dashed lines indicate zero log₂ 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

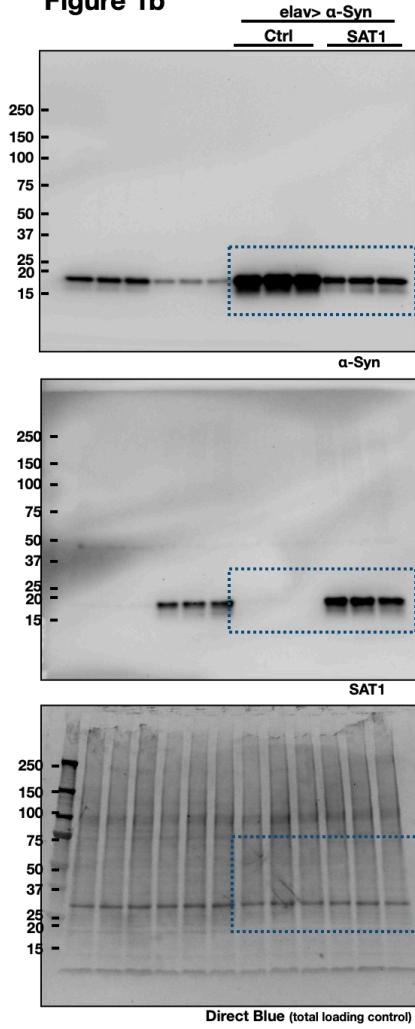


Figure 5b

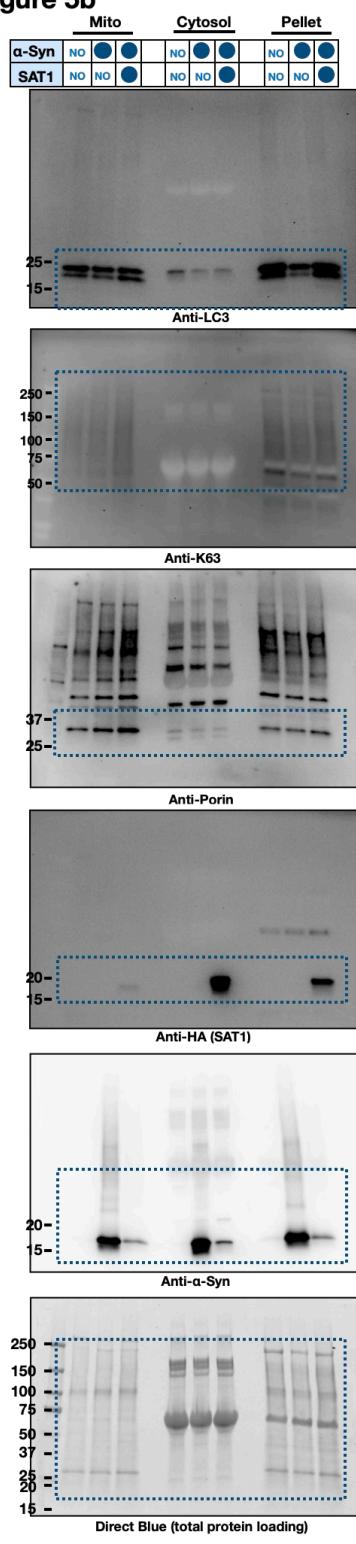


Figure 5c

