

Fig. S1 pre-miR-LRRK2-5 and pre-miR-LRRK2-5NB direct silencing of a complementary dual-luciferase target sequence A) Dual-luciferase reporter assay showing knockdown of LRRK2 target sequence following co-transfection with indicated pre-miRNA variants. Values represent mean ratios of *Renilla*:Firefly luciferase +/- S.D. from n=6. Pre-miRNA variants are normalised to cells transfected with a non-specific U6 pre-miRNA hairpin. *= P<0.05 relative to normalising control.

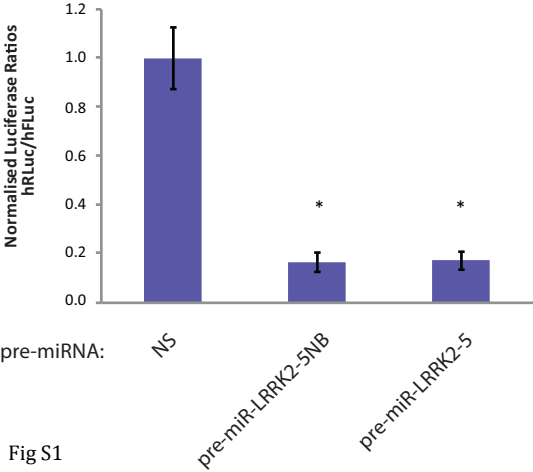
Fig. S2 mirt-LRRK2-5NB directs silencing in a sequence-specific manner A) Codon-modified scrambled target sequence to mirt-LRRK2-5NB. B) Dual-luciferase reporter assays showing knockdown of a codon-modified scrambled LRRK2 target following co-transfection with indicated mirtron (left panel) and pre-miRNA control (right panel) variants. Values represent mean ratios of *Renilla*:Firefly luciferase +/- S.D. from n=6. Mirtron variants are normalized to cells transfected with the NAD variant. Pre-miRNA variants are normalised to cells transfected with a non-specific U6 pre-miRNA hairpin. *= P<0.05 relative to respective normalising control.

Fig. S3 Direct comparison of synthetic mirtrons to U6-transcribed pre-miRNAs (shRNAs) A) Dual-luciferase reporter assays showing knockdown of a LRRK2 target following co-transfection with indicated mirtron (left panel) and pre-miRNA control (right panel) variants at equivalent hairpin concentrations of 2.5 fm. Values represent mean ratios of *Renilla*:Firefly luciferase +/- S.D. from n=3. Mirtron variants are normalized to cells transfected with the NAD variant. Pre-miRNA variants are normalised to cells transfected with a non-specific U6 pre-miRNA hairpin. *= P<0.05 relative to respective normalising control.

Fig. S4 Algorithm design of a synthetic mirtron targeting α -synuclein. A) Predicted hairpin alignments of α -synuclein targeting synthetic mirtron, α -syn-mirt-1, designed using an in-house algorithm. B) Representative fluorescent microscopy images of different intron variants 48hrs after transfection in HEK-293 cells. C) Quantification of eGFP fluorescence following expression indicated intron variants in HEK-293 cells. Values represent mean fluorescence +/- S.D. from n=3. *= P<0.05 relative to non-transfected cells. D) Dual-luciferase reporter assays showing

knockdown of an α -synuclein target following co-transfection with indicated mirtron (left panel) and pre-miRNA control (right panel) variants. Values represent mean ratios of *Renilla*:Firefly luciferase \pm S.D. from n=3. Mirtron variants are normalized to cells transfected with the NAD variant. Pre-miRNA variants are normalised to cells transfected with a non-specific U6 pre-miRNA hairpin. *= P<0.05 relative to respective normalising control. E) Quantification of mCherry tagged α -synuclein fluorescence following co-expression with the NAD intron or mirt- α -Syn-1 in HEK-293 cells. Values represent mean fluorescence \pm S.D. from n=3. Mirt- α -Syn-1 fluorescence is normalized to cells transfected with the NAD intron. *= P<0.05 relative to respective normalising control.

Fig. S5 A) Quantification of eGFP fluorescence following expression of indicated intron variants in SH-SY5Y cells and Hela cells. Values represent mean fluorescence \pm S.D. from n=3. *= P<0.05 relative to non-transfected cells.



A.

LRRK2 sequence: acc t t t att cct gac tct tct atg

Amino-acid seq: Thr Phe Ile Pro Asp Ser Ser Met

Codon replaced: acG ttC atC ccG gaT tcG tcG atg

B.

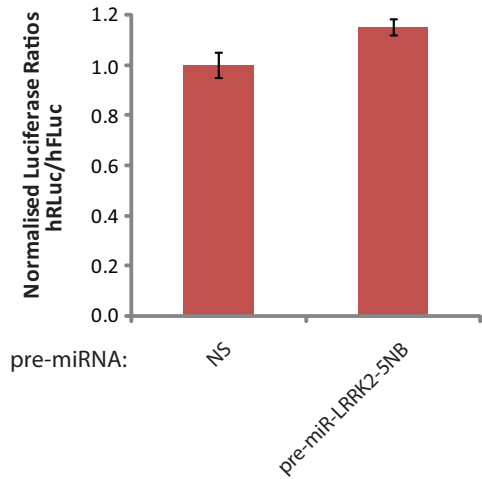
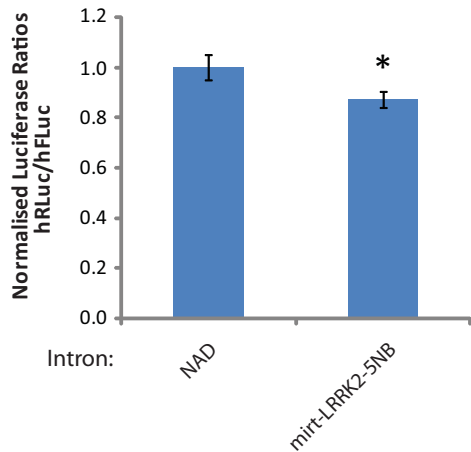


Fig S2

A.

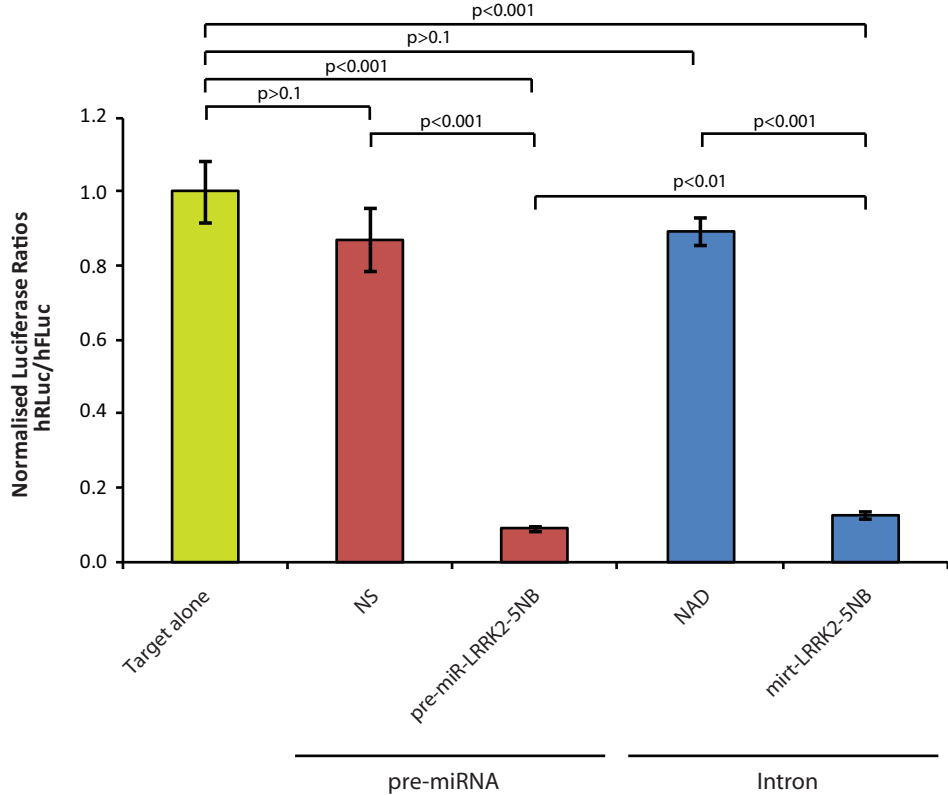
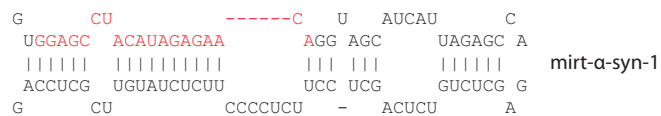
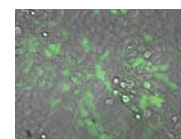
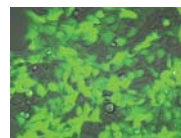


Fig S3

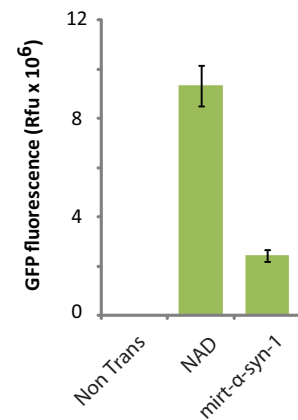
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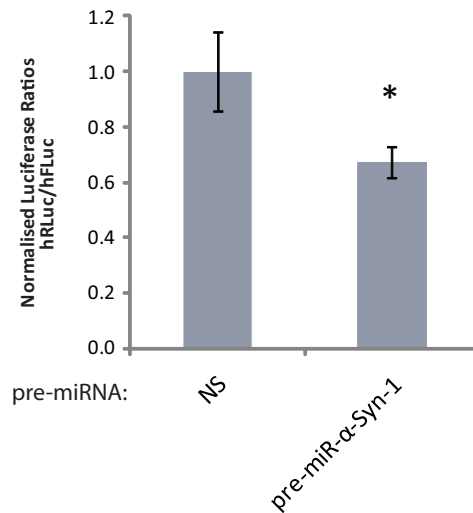
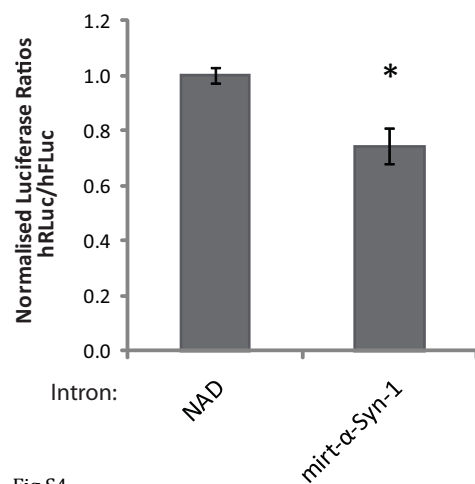
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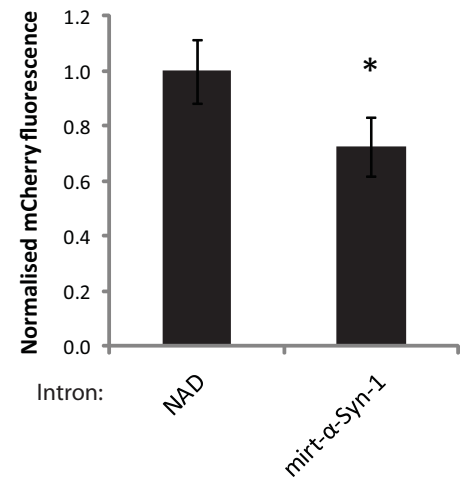
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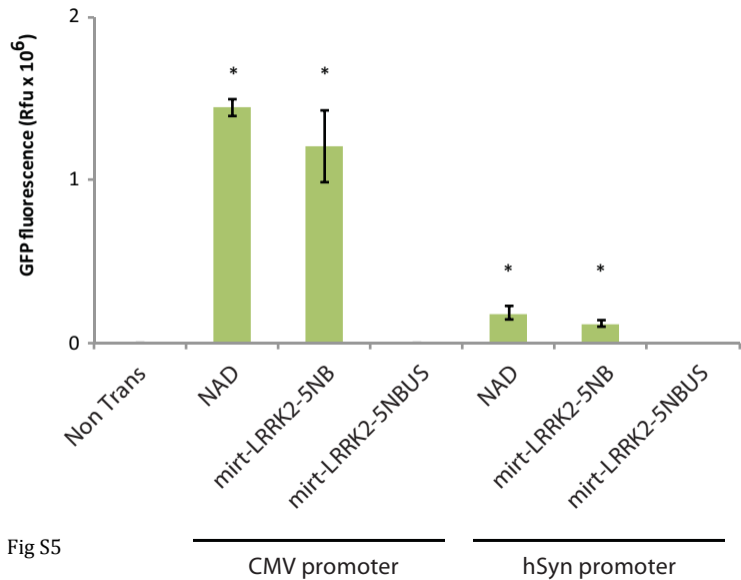
D.



E.



SH-SY5Y cells



Hela cells

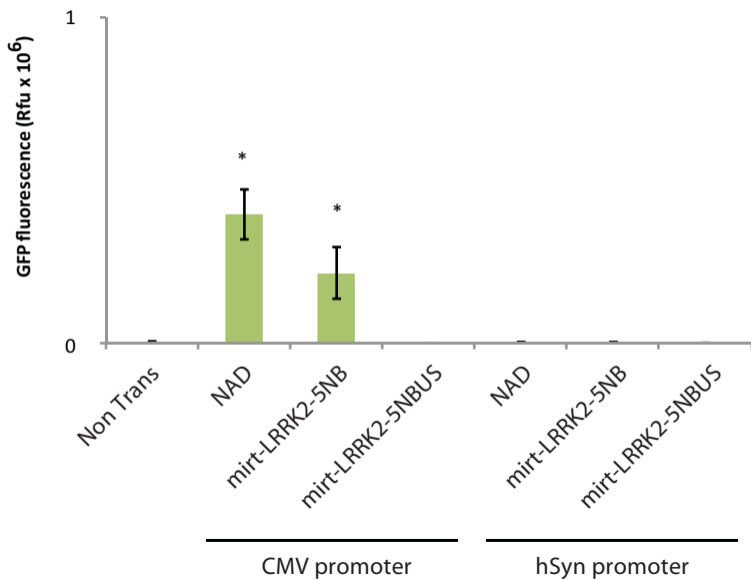


Fig S5