## Supplementary figure legends

**Fig. S1.** Co-expression network analysis using RNA-seq data. **A**, We analyzed publicly available RNA-seq data from the prefrontal cortex of individuals with 29 of PD and 44 of control. **B**, We conducted an unsupervised co-expression modules associated with PD. Of the 17 co-expression modules that were generated with this combined data. Correlation coefficients (R) and P-values between co-expression modules and disease status \*R: Correlation coefficients

**Fig. S2.** PC12 cells were differentiated for 5 days upon stimulation with NGF (100 ng/ml) after introduction of parkin shRNA. To study neurite outgrowth, the medium was changed to RPMI containing 100 ng/ml NGF. The cells were further cultured for 5 days. Cells with at least one neurite longer than two-body length were counted as neurite positive. At least 500 cells were counted for each group performed in triplicate.

Fig. S3. Docking model of parkin with p21 as described in methods.

**Fig. S4.** Schematic model of regulation of p21 by parkin in neurogenesis. The E3 ligase parkin regulates p21 levels through the ubiquitin proteasome pathway. p21 normally opposes the development of neurogenesis. Genetic mutations or knockout of parkin result in impaired parkin function that leads to the accumulation of p21 and a disruption of neurogenesis.



Module	R	P-value
PD_M1	0.18931	0.1087
PD_M2	-0.02	0.86647
PD_M3	0.49808	7.33E-06
PD_M4	0.18533	0.11647
PD_M5	0.0036	0.97588
PD_M6	0.43161	0.00014
PD_M7	0.30238	0.00932
PD_M8	0.45093	6.24E-05
PD_M9	0.35155	0.00229
PD_M10	-0.4249	0.00018
PD_M11	-0.3241	0.00516
PD_M12	-0.2076	0.07808
PD_M13	-0.3417	0.00309
PD_M14	-0.1318	0.26623
PD_M15	-0.1193	0.31455
PD_M16	-0.2529	0.03087
PD_M17	-0.4856	1.33E-05

В









p21 amino acid residues interacting with parkin:

Ser42 - Val45 Glu124 - Pro129 Arg210 Asp232 - Pro234 Tyr250 - Ile255 Parkin amino acid residues interacting with p21:

Leu187 – Asn190 **His279 – Tyr285** Asn295 – His302 Tyr312 – Cys323

