

Figure S1. Number of missing values per fraction, mixture and channel (replicate). Extreme amounts of missing values in one sample of 786-O WT (channel 127N) and 786-O^{PARK2} (channel 128C). EV, empty vector; NA, not available; WT, wild-type.

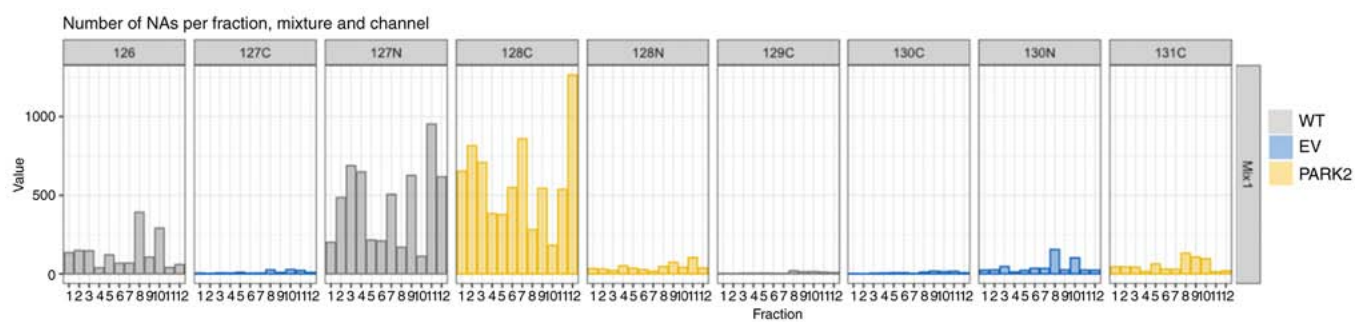


Figure S2. PARK2 overexpression has no effect on cell cycle progression or apoptosis. (A) Cell cycle was analyzed by flow cytometry, and the PARK2 overexpression group showed no difference in the number of cells in G₁, S or G₂/M phase. (B) Apoptosis was analyzed by Annexin V-FITC staining. No effect on apoptosis was observed between the control or the wild-type cells compared with the PARK2-overexpressing cells. EV, empty vector; PARK2, parkin.

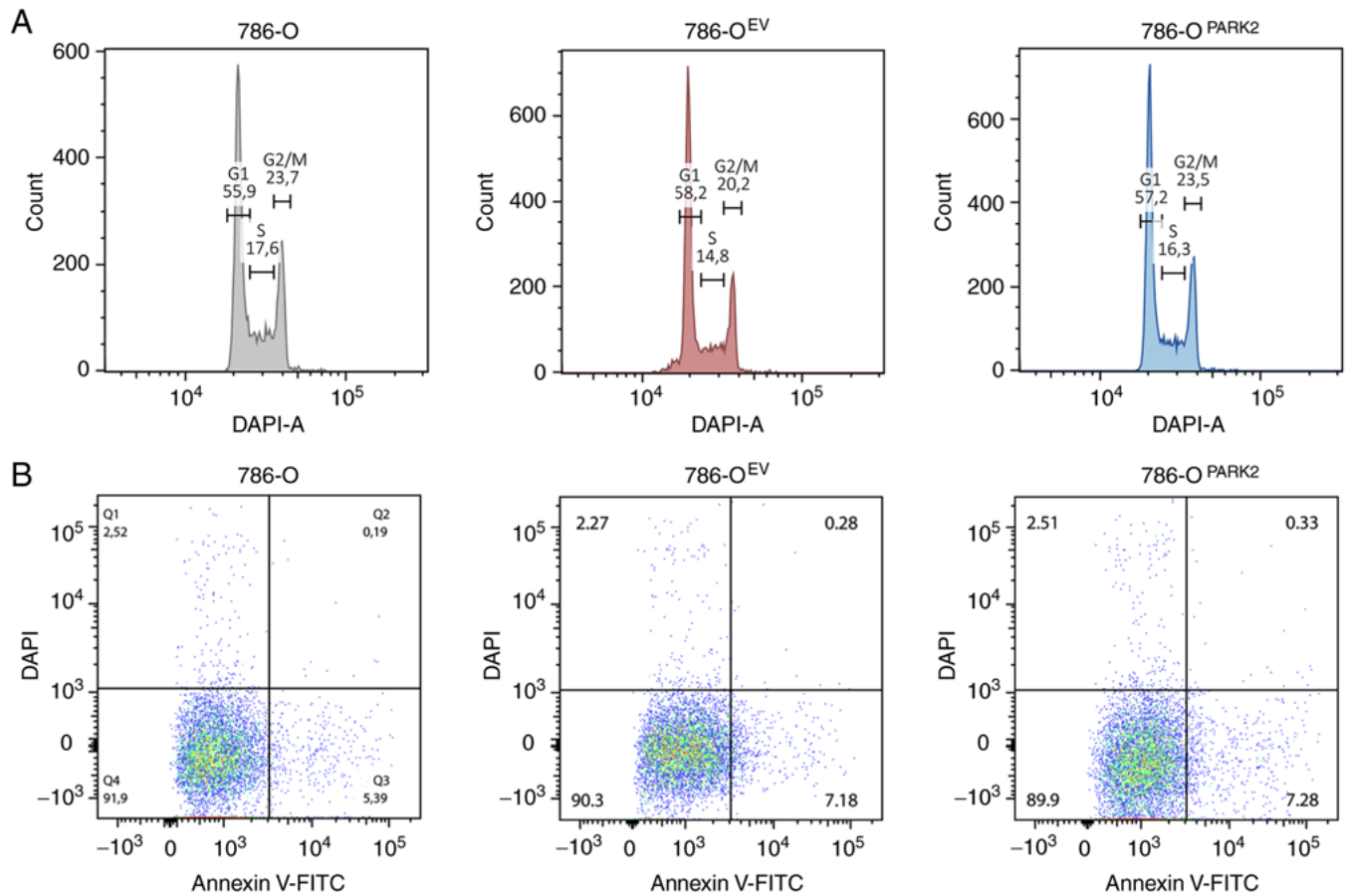


Figure S3. RNA sequencing of 786-O cells revealed no difference in the gene expression profile. The gene expression profiles of the samples were projected onto the first two principal components in a principal component analysis plot.

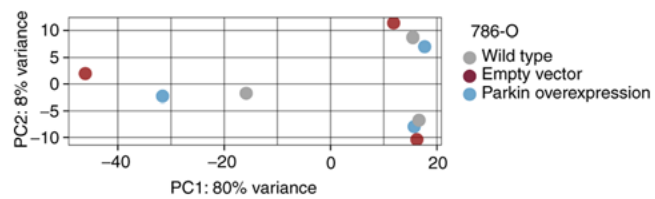


Table SI. Primer sequences used in quantitative PCR.

Gene	Primer sequence (5'-3')
PARK2	F: TAGCTTTGCACCTGATCGC R: CCACACAAGGCAGGGAGTAG
CKS2	F: GCTCTTCGCGCTCTCGTTTCATTT R: CTCTGGGTAAACATAACATGCCGGT
TBP	F: GCCGAATATAATCCCAAGCG R: TGGACTGTTCTTCACTCTTGGC
β -actin	F: AGAGCTACGAGCTGCCTGAC R: AGCACTGTGTTGGCGTACAG

CKS2, CDC28 protein kinase regulatory subunit 2; F, forward; PARK2, parkin; R, reverse.

Table SII. RNA sequencing analysis of transduced 786-O cells revealed no difference in the molecular gene profile except for PARK2.

A, Wild-type 786-O vs. 786-O^{PARK2}

Gene	baseMean	log ₂ (FC)	lfcSE	P-value	p.adjust
PARK2	33.9896130	-4.88402	0.716252534	1.11x10 ⁻¹²	3.25x10 ⁻⁰⁸
DDX11L1	2.2721059	-1.32x10 ⁻⁷	0.001442695	0.77050596	0.9999447
WASH7P	69.9607934	3.55x10 ⁻⁷	0.001442691	0.83914998	0.9999447
MIR1302-2HG	0.3675501	-1.57x10 ⁻⁷	0.001442695	0.71903402	0.9999447
FAM138A	0.6905265	-2.05x10 ⁻⁷	0.001442695	0.39418555	0.9999447
OR4G4P	1.7573551	-2.08x10 ⁻⁷	0.001442695	0.59224827	0.9999447
OR4F5	0.3601597	-9.74x10 ⁻⁸	0.001442695	0.60158002	0.9999447
AL627309.1	4.5598300	3.75x10 ⁻⁷	0.001442694	0.57489685	0.9999447
CICP27	8.7093328	3.01x10 ⁻⁶	0.001442695	0.36275494	0.9999447
AL627309.6	2.7953695	-5.42x10 ⁻⁷	0.001442695	0.40018298	0.9999447

B, 786-O^{EV} vs. 786-O^{PARK2}

Gene	baseMean	log ₂ (FC)	lfcSE	P-value	p.adjust
PARK2	33.9896130	-5.00106	0.763408501	6.98x10 ⁻¹²	2.04x10 ⁻⁷
DDX11L1	2.2721059	-5.82x10 ⁻⁷	0.001442695	0.07978226	0.9994839
WASH7P	69.9607934	4.80x10 ⁻⁷	0.001442691	0.78385611	0.9994839
MIR1302-2HG	0.3675501	2.78x10 ⁻⁸	0.001442695	0.90240207	0.9994839
FAM138A	0.6905265	-1.42x10 ⁻⁷	0.001442695	0.59401627	0.9994839
OR4G4P	1.7573551	1.33x10 ⁻⁷	0.001442695	0.79312307	0.9994839
OR4F5	0.3601597	-7.07x10 ⁻⁸	0.001442695	0.82930561	0.9994839
AL627309.1	4.5598300	-9.65x10 ⁻⁷	0.001442695	0.06565381	0.9994839
CICP27	8.7093328	-4.39x10 ⁻⁷	0.001442693	0.69893500	0.9994839
AL627309.6	2.7953695	-5.23x10 ⁻⁷	0.001442695	0.42197480	0.9994839

C, 786-O^{EV} vs. wild-type 786-O

Gene	baseMean	log ₂ (FC)	lfcSE	P-value	p.adjust
DDX11L1	2.2721059	-5.36x10 ⁻⁷	0.001442695	0.14078113	0.99478187
WASH7P	69.9607934	1.31x10 ⁻⁷	0.001442691	0.942794721	0.99478187
MIR1302-2HG	0.3675501	1.60x10 ⁻⁷	0.001442695	0.630041961	0.99478187
FAM138A	0.6905265	1.29x10 ⁻⁷	0.001442695	0.758135271	0.99478187
OR4G4P	1.7573551	3.27x10 ⁻⁷	0.001442695	0.433992336	0.99478187
OR4F5	0.3601597	1.25x10 ⁻⁷	0.001442695	0.764081727	0.99478187
AL627309.1	4.5598301	-1.13x10 ⁻⁶	0.001442695	0.021561027	0.99478187
CICP27	8.7093328	-1.42x10 ⁻⁶	0.001442694	0.207238438	0.99478187
AL627309.5	14.7681642	8.05x10 ⁻⁶	0.001442704	0.360169959	0.99478187
RNU6-1100P	0.4969637	2.06x10 ⁻⁷	0.001442695	0.442763178	0.99478187

Top 10 genes are sorted according to p.adjust. FC, fold change; lfcSE, log2 fold change standard error; p.adjust, adjusted P-value; PARK2, parkin.

Table SIII. Comparison of proteins in wild-type 786-O, 786-O^{EV} and 786-O^{Parkin} cells following liquid chromatography-mass spectrometry.

A, Wild-type 786-O vs. 786-O^{PARK2}

Gene	Protein	log ₂ (FC)	P-value	p.adjust
CASC4	Q6P4E1	1.906497758	0.00076719	0.16313711
COX4I1	P13073	1.636215670	0.01328973	0.29729017
LUC7L;LUC7L2	Q9NQ29;Q9Y383	1.619143278	0.00449151	0.25575769
CAVIN3	Q969G5	1.601144344	0.00038075	0.16287758
CEP131	Q9UPN4	1.574897872	0.00120607	0.19261649
S100A6	P06703	1.572996165	7.48x10 ⁻⁵	0.09221914
SNRPD1	P62314	1.421997148	0.00250319	0.24434690
HMGB2	P26583	1.403681058	0.00579499	0.25942692
TRAM1	Q15629	1.379748741	0.00014372	0.09221914
UBE2Z	Q9H832	1.329082117	6.27x10 ⁻⁶	0.01468176
P/SMD4/I/SL	P55036;A2A3N6	1.314499787	0.00018621	0.10241587
FAM98B	Q52LJ0	1.308267653	0.00084584	0.16313711
RPL36L/A	Q969Q0;P83881	1.305046083	0.01491832	0.30358648
IFI35	P80217	1.295985181	0.02286751	0.33861512
COMMD6	Q7Z4G1	1.273804336	0.00742947	0.28144293
OSBPL10	Q9BXB5	1.248222170	7.63x10 ⁻⁶	0.01468176
USE1	Q9NZ43	1.192647425	0.01787605	0.31715569
GPT2	Q8TD30	1.182492216	0.00165222	0.21203508
EXOSC7	Q15024	1.167749418	0.00012121	0.09221914
PEA15	Q15121	1.107112256	0.00061561	0.16313711
HDAC2	Q92769	1.105577758	0.00173882	0.21595078
GSPT1	P15170	1.098692029	0.00320009	0.25031880
KHDRBS3	O75525	1.091078211	0.00079661	0.16313711
TPM/4/3	P67936;P06753	1.085333035	0.02150016	0.33612192
SMARCC1	Q92922	1.074104998	0.02420964	0.34502522
APIP	Q96GX9	1.046699047	0.00349304	0.25031880
GPRIN1	Q7Z2K8	1.043104857	0.00407110	0.25031880
SLIRP	Q9GZT3	1.028073826	0.06117870	0.43785561
SPECC1	Q5M775	1.023900487	0.00130079	0.19261649
ACT/G2/B	P63267;P60709	-1.00024334	0.14059155	0.55041941
SNX27	Q96L92	-1.00447612	0.00087441	0.16313711
KLF16	Q9BXX1	-1.01538213	0.02163654	0.33612192
AATF	Q9NY61	-1.02012130	0.19869568	0.63169148
PIGG	Q5H8A4	-1.03872103	0.00255860	0.24434690
FAM45BP	Q6NSW5	-1.04838469	0.08568078	0.47420854
YBX3	P16989	-1.08539596	0.07048920	0.45610657
HINT1	P49773	-1.12897571	0.01332675	0.29729017
H/3F3A/IST3/3	P84243;Q16695	-1.16304277	0.25613898	0.67915638
HMGN4	O00479	-1.20380566	0.09870832	0.50302587
AHSG	P02765	-1.21075999	0.17981348	0.60823001
FBLN1	P23142	-1.35383655	0.04673596	0.40503852
PARK2	O60260	-1.86848344	0.00147746	0.21067426
SLC6A8	P48029	-2.02788007	0.00010871	0.09221914

B, 786-O^{EV} vs. 786-O^{PARK2}

Gene	Protein	log ₂ (FC)	P-value	p.adjust
COX4I1	P13073	2.022996844	0.00262662	0.22982908
CASC4	Q6P4E1	1.662323774	0.00102823	0.17211613
CEP131	Q9UPN4	1.553085223	0.00073838	0.14961837
CAVIN3	Q969G5	1.534277426	0.00027429	0.10237014
IFI35	P80217	1.429118441	0.0093935	0.27632266

Table SIII. Continued.

B, 786-O^{EV} vs. 786-O^{PARK2}

Gene	Protein	log ₂ (FC)	P-value	p.adjust
LUC7L;LUC7L2	Q9NQ29;Q9Y383	1.396022682	0.00613253	0.27404238
SNRPD1	P62314	1.387958265	0.00167629	0.22094489
UBE2Z	Q9H832	1.362294557	2.57x10 ⁻⁶	0.00494211
TRAM1	Q15629	1.359457847	8.37x10 ⁻⁵	0.05954009
OSBPL10	Q9BXB5	1.346968509	2.10x10 ⁻⁶	0.00494211
GPT2	Q8TD30	1.343660246	0.00040666	0.12043425
HMGB2	P26583	1.338260519	0.00457035	0.25983629
HDAC2	Q92769	1.336829804	0.00028295	0.10237014
P/SMD4/I/SL	P55036;A2A3N6	1.296489578	0.00010825	0.05954009
EXOSC7	Q15024	1.237454402	4.13x10 ⁻⁵	0.05302231
GSPT1	P15170	1.153238644	0.00139031	0.21410758
IMUP	Q9GZP8	1.127156944	0.16903833	0.61862886
SMARCC1	Q92922	1.108169042	0.01389880	0.30753099
CKS2	P33552	1.093649818	0.00054893	0.13625458
S100A6	P06703	1.078688821	0.00053796	0.13625458
COMMD6	Q7Z4G1	1.070808966	0.01128923	0.28879367
YTHDC1	Q96MU7	1.061134659	0.00164653	0.22094489
SDF2	Q99470	1.050471248	0.09357897	0.51093537
RPL36A/L/	Q969Q0;P83881	1.048393780	0.02640772	0.34347885
STXBP1	P61764	1.041731852	0.01015926	0.28381847
APIP	Q96GX9	1.026993416	0.00229553	0.22094489
PKMYT1	Q99640	1.025024326	0.04391947	0.39259199
RBM22	Q9NW64	1.009516940	0.01368827	0.30610696
GNE	Q9Y223	1.003774644	9.48x10 ⁻⁵	0.05954009
HMGNA4	O00479	-1.00293440	0.12670711	0.57121137
HINT1	P49773	-1.09733279	0.00979125	0.28300057
AFP	P02771	-1.14276615	0.37628294	0.77908499
C3	P01024	-1.15619182	0.20681796	0.64572084
KCNAB2	Q13303	-1.18400825	0.06324699	0.44597237
FBLN1	P23142	-1.58411238	0.01668296	0.31793728
AHSG	P02765	-1.78489300	0.04473948	0.39325798
PARK2	O60260	-1.98312346	0.00056625	0.13625458
SLC6A8	P48029	-2.02968081	5.62x10 ⁻⁵	0.05411216

C, 786-O vs. 786-O^{EV}

HRG	P04196	1.62717409	0.08854260	0.99980451
KRT16	P08779	1.14727457	0.00485898	0.99980451
H/IST2/2AC/IST3/ 2A/IST2/2AB/2AFX	Q16777;Q7L7L0; Q8IUE6;P16104	0.83645710	0.05473729	0.99980451
HIST2H2AC	Q16777	-0.69116610	0.20795500	0.99980451

Proteins with |log₂FC|>1 are displayed in the table. FC, fold change; p.adjust, adjusted P-value; PARK2, parkin.