

Supplementary figure legends



Figure S1. Mfold schematics of shRNAs with traditional Brummelkamp (BK) loop and miR30 adapted structures. The PB1 siRNA sequence was embedded in the miR30 structure (miR30-PB1) with both the sense and antisense sequence connected by a loop. The natural miRNA sequence is shown alongside of miR30-PB1.

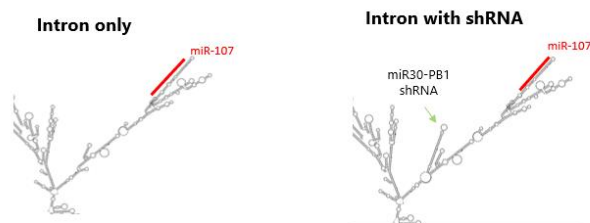


Figure S2. The predicted RNA secondary structures of a section of the natural intron 5 of PANK1 without (left) and with shRNA (right). The miR107 sequence is highlighted in red colour and the green arrow indicates the inserted miR30-PB1 shRNA within the intron. .

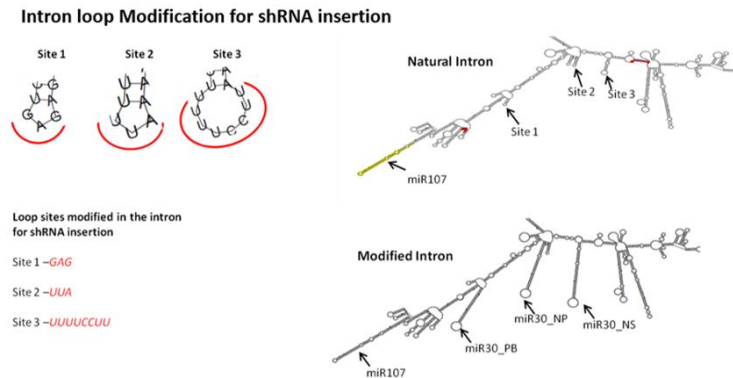


Figure S3. The selected loop sequences downstream of miR107 to be replaced with the miR30-PB1, miR30-NP and miR30-NS are highlighted in red colour. The comparison of the predicted secondary structure of the natural intron (top) and intron with three shRNAs (bottom) is also shown.

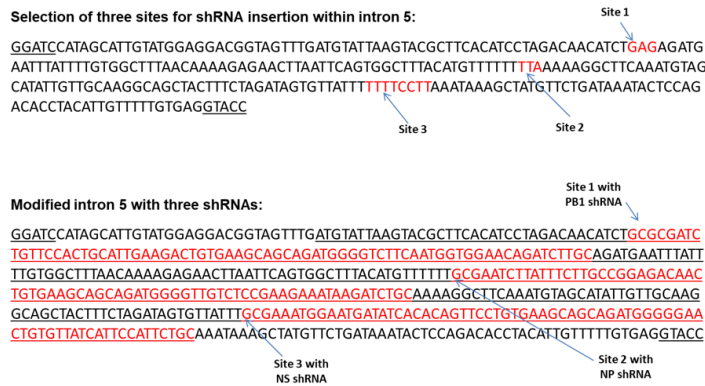


Figure S4. The selected intron 5 region of the PANK1 gene to insert three shRNAs. The three selected sites downstream to miR-107 are highlighted in red (top) and the intron sequence with PB1, NP and NS shRNA was provided (bottom). The intron containing three shRNAs (466 bp) was oligo-synthesised and used to clone into pGI vector.

Table S1. Synthesised oligonucleotides used in this study.

Name	sequence
GFP_fwd	ACTGTCGACATGGTGAGCAAGGGGCGAGG
GFP_rwd	ACTGCGGCCGCTTACTTGTACAGCTCGTCC
SmaI_fwd	GACCCGGGCCGAGGTGAAG
SmaI_rev	CTTCACCTCGGCCCGGGTC
Intron_107_fwd	GTAAGATGGTGTATTTACTATGAGC
Intron_107_rev	CTGTAAAATTGAAAAGCAG
BamHI_int_fwd	ACTAGATGGGATCCATAGC
BamHI_int_rev	GCTATGGATCCCATCTAGT
KpnI_int_fwd	TGTGAGGTACCGCTCTAAC
KpnI_int_rev	GTTAGAGCGGTACCTCACA

BK_PB1_fwd	GATCGATCTGTTCCACCATTGAATTCAAGAGATTC AATGGTGGAACAGATCGTAC
BK_PB1_rev	GATCTGTTCCACCATTGAATCTCTTGAATTCAATGG TGGAACAGATC
miR30_ PB1_fwd	GATCGCGACAGATCTGTTCCACCATTGAAGACTGT GAAGCAGCAGATGGGGTCTTCAATGGGAACAGAT CTGCTGCGTAC
miR30_PB1_rev	GCAGCAGATCTGTTCCCATTTGAAGACCCCATCTGC TGCTTCACAGTCTTCAATGGTGGAACAGATCTGTCC C
PB1_luc_fwd	CTCGAGGGAGATCATTCGAGCTGAAG
PB1_luc_rev	GCGGCCGCCCCGTCTGAGTTCTTCAATGG
NP_luc_fwd	GCGCTCGAGACCAAATGAGAATCCAGCAC
NP_luc_rev	AGCGCGGCCGCAATTGTCGTAATCCTCTGCA
NS_luc_fwd	ATGCTCGAGGTACTCTCGGTCTGGACATC
NS_luc_rev	ATCGCGGCCGCTTCCCGCCATTTCTCGTTTC
miR-PTA	GAGGCGAGCACAGAATTAATACGACTCCATATAG GTTTTTTTTTTTTVN
PAM-URP	GAGGCGAGCACAGAATTAATACGAC
miR107	GCAGCAGCATTGTACAGGGCT
miR26a	GCCTTCAAGTAATCCAGGATAGG
PB1	CGCTTCAATGGTGGAACAGATC
5S	TGGGAATACCGGGTGCTGT
Poly-A_fwd	ACTGCGGCCGCGACTCTAGATCA
Poly-A_rev	ACTGAATTCACGCTTACAATTTACGC

Table S2. siRNA sequences used in this study.

Name	Sequence (5' – 3')
PB1-2257	GATCTGTTCCACCATTGAA
NP	GATCTGTTCCACCATTGAA
NS1/NEP	AATGGAATGATAACACAGT