

Supplementary

Table S1. Oligonucleotides used in the work.

Oligonucleotide	Nucleotide sequence	Gene or sequence	Received fragment size
1_gRNA_H Up	GATTCGGCCTAAACTAAATCCGAA	Sequence for guide RNA	
1_gRNA_H Lo	AAACTTCGGATTTAGTTTAGGCCG		
npt1	CGACGTTGTCACTGAAGCG	<i>nptII</i> marker gene	487
npt2	AAGCACGAGGAAGCGGTCAG		
Up_H3.3	TAGGCAACGATGGTAAAGCGGATT	Testing the site-specific integration	630/1048
Up_H3.3_1	AATCGCATAATCAAGAAAATCAAAACCC		
Lo_plan3	AGCCGAATAGCCTCTCCACCCAA		
dIFN 1	GATGTAGCGGATAATGGAACCTCTTT	<i>dIFN</i> target gene	478
dIFN 2	TGACTCCTTTTTTCGCTTCCCTG		
VAP27-1_f	AACAAGACAAATAGCGATGTCCCA	12kDa gene of microsomal signal peptidase from <i>A. thaliana</i>	
VAP27-1_r	GCGATTAGATTTCGTCCCGTGA		
VAP27-1_p	[R6G]CACCGTCTCCGGTTCAGAGAGAG[BHQ2]		
HIS3.3_f	CGGTGATCGTGAACTACTGGAAT	Histone H3.3 gene from <i>A. thaliana</i>	
HIS3.3_r	CGGAAGATCATTTCGGCGAAG		
HIS3.3_p	[ROX]CGCTCGATAGGTGGTACGAAATTAGG[BHQ2]		
PARP2_f	GGTGTTTCGTGTAGGTGGAGAGG	PARP2-gene from <i>A. thaliana</i>	
PARP2_r	CCTCTTGCTCTTTGATTCTTCCTTC		
PARP2_p	[Cy5]CTTGAAGAGGCTATCGCAGAAGACA[BHQ2]		
Up_sig.BglII(62)	CCCAGATCTATGGAAGAATTGCTAGAGGC	Primers used to create constructs	
Lo_dIFN(60)	CTGGGATGCTCTTCGACCT		
ifn+Up_GST(60)	AGGTGGAAGAGCATCCCAGATGTCCCCTATACTAGGTTATT		
Lo_GST(GEX)stop A65I(66)	CCCGGTACCTTAACCACCAAACGTGGCTTGCCA		
Up_L_HIII	CCCAAGCTTCGAGCGATTCCAGTAGTTTCACGA		
Lo_L_Acc_Sfr	GGTACCAGAGTAATCTCGAGTTTATTTTCAGCGATCCGCGACG		
Up_R_Sfr_Acc	CTCGAGATTACTCTGGTACCTTCGGATTTAGTTTAGGCCGTCACA		
Lo_R_Sal	CCCGTCGACCATCATCATCCTAAACGACGCCG		
Lo_A-B_pBI(58)	CGAAGGTACCGGATGGATCCCGTGTTCTCTCCAATGAAAT		
Up_Xho-pBI(60)	AATCTCGAGGATCATGAGCGGAGAATTAAG		
Up_L_HIII_gRNA	CCCAAGCTTCGGCCTAAACTAAATCCGAACGGCGAGCGATTCCAGTAGTTTCACGA		
Lo_R_Sal_gRNA	CCCGTCGACGGCCTAAACTAAATCCGAACGGCATCATCATCCTAAACGACGCCG		
Up_Sal_gRNA-pBI(60):	CCCGTCGACCCGTTTCGGATTAGTTTAGGCCGGATCATGAGCGGAGAATTAAG		

Lo_A-B_pBI(58)	CGAAGGTACCGGATGGATCCCGTGTCTCTCCA AATGAAAT		
Lo_Acc_gRNA_G ST(60)	CGAAGGTACCCCGTTCGGATTTAGTTTAGGCCG ACCACCAAACGTGGCTTGCC		

Figure S1. Alignment of nucleotide sequences of PCR fragments obtained with primers UpH3.3_1 and Lo_plan3 from *A. thaliana* cell lines with knock-ins (lines 1, 6, 38 and 4) with DNA sequence of genetic construct pIFN(H3.3).3.

		620		669
1 A.th	(143)	GCTTTCTTGACCAATTCAACGGTCCAGATCTAGCTTTACTGGTTTGACG		
6 A.th	(550)	GCTTTCTTGACCAATTCAACGGTCCAGATCTAGCTTTACTGGTTTGACG		
38 A.th	(617)	GCTTTCTTGACCAATTCAACGGTCCAGATCTAGCTTTACTGGTTTGACG		
4 A.th	(557)	GCTTTCTTGACCAATTCAACGGTCCAGATCTAGCTTTACTGGTTTGACG		
pIFN(H3.3).3	(307)	GCTTTCTTGACCAATTCAACGGTCCAGATCTAGCTTTACTGGTTTGACG		
		670		719
1 A.th	(193)	AGGATCACCCTGCTACATAATTGATTGCTATTGGCTGAATACAAACCGT		
6 A.th	(600)	AGGATCACCCTGCTACATAATTGATTGCTATTGGCTGAATACAAACCGT		
38 A.th	(667)	AGGATCACCCTGCTACATAATTGATTGCTATTGGCTGAATACAAACCGT		
4 A.th	(607)	AGGATCACCCTGCTACATAATTGATTGCTATTGGCTGAATACAAACCGT		
pIFN(H3.3).3	(357)	AGGATCACCCTGCTACATAATTGATTGCTATTGGCTGAATACAAACCGT		
		720		769
1 A.th	(243)	CGCGGATCGCTGAAATAAA	CGTTCGGGATTTAGTTTAGG	CGG--GATCA
6 A.th	(650)	CGCGGATCGCTGAAATAAA	-----	GGCCG--GATCA
38 A.th	(717)	CGCGGATCGCTGAAATAAA	-----	TCGACCG--GATCA
4 A.th	(657)	CGCGGATCGCTGAAATAAAC	-----	TCGACCG--GATCA
pIFN(H3.3).3	(407)	CGCGGATCGCTGAAATAAAC	-----	T---CGAGGATCA
		770		819
1 A.th	(291)	TGAGCGGAGAATTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGG		
6 A.th	(679)	TGAGCGGAGAATTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGG		
38 A.th	(749)	TGAGCGGAGAATTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGG		
4 A.th	(689)	TGAGCGGAGAATTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGG		
pIFN(H3.3).3	(437)	TGAGCGGAGAATTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGG		
		820		869
1 A.th	(341)	ACAAGCCGTTTTACGTTTGGAACTGACAGAACC	GCAACGTTGAAGGAGCC	
6 A.th	(729)	ACAAGCCGTTTTACGTTTGGAACTGACAGAACC	GCAACGTTGAAGGAGCC	
38 A.th	(799)	ACAAGCCGTTTTACGTTTGGAACTGACAGAACC	GCAACGTTGAAGGAGCC	
4 A.th	(739)	ACAAGCCGTTTTACGTTTGGAACTGACAGAACC	GCAACGTTGAAGGAGCC	
pIFN(H3.3).3	(487)	ACAAGCCGTTTTACGTTTGGAACTGACAGAACC	GCAACGTTGAAGGAGCC	
		870		913
1 A.th	(391)	ACTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACATACG		
6 A.th	(779)	ACTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACATACG		
38 A.th	(849)	ACTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACATACG		
4 A.th	(789)	ACTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACATACG		
pIFN(H3.3).3	(537)	ACTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACATACG		