

Table S1. hIR8, hER13, hDR5 and hDR15 synthetic promoter sequences and binding sites predicted in each sequence, related to Figure 2

hIR8	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGCTGTCGGT CATGTGACCCGACAACCGCTGTCTGGTTCATGTGACCCGACAACCGCT GTCTGGTTCATGTGACCGACATGCAA		
hER13	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGCCCGACAG CACCAAACCTTACTGTCTGGTGCCTCGGACGACCAAACTTACTGTCT GGTGCCCGGACAGCACCAAACTTACTGTCTGGTGCACAA		
hDR5	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGCCCGACAA TTGACCCGACAATTGACCGACAATTGACCGACAATTGACCCGACAA TTGACCGACATGCAA		
hDR15	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGCCCGACAA TTGACAAATCTCAGCCGACAATTGACAAATCTCAGCCGACAATTG ACAAATCTCAGCCGACAATTGACAAATCTCAGCCGACAATTGACA AATCTCAGCCGACATGCAA		
hIR8			
Predicted ARF binding sites (AuxRE pairs)			
	Spacing	Score1	Score2
DR	20	-11	-5
ER	16	-11	-5
DR	19	-5	-5
IR	8	-5	-3
DR	19	-3	-3
Er	5	-3	-5
DR	19	-5	-5
IR	8	-5	-3
DR	19	-3	-3
Er	5	-3	-5
IR	8	-5	-3
DR	11	-3	-10
ER	7	-10	-11
IR	20	-11	-11
MEME detection of other TF binding sites			
TF	Sequence	Score	
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hER13			
Predicted ARF binding sites (AuxRE pairs)			
	Spacing	Score1	Score2
IR	20	-11	-3
DR	16	-11	-3
ER	13	-3	-3
IR	3	-3	-3
ER	13	-3	-3
IR	3	-3	-3
ER	13	-3	-3
IR	11	-3	-10
ER	7	-10	-11
IR	20	-11	-11
MEME detection of other TF binding sites			
TF	Sequence	Score	
LFY	CATGGACCGCCCCGACAATT	-10.952697385303955	
hDR5			
Predicted ARF binding sites (AuxRE pairs)			
	Spacing	Score1	Score2
IR	20	-11	-2
DR	16	-11	-2
DR	5	-2	-2
DR	16	-2	-2
DR	5	-2	-2
DR	16	-2	-2
DR	5	-2	-2
DR	16	-2	-2
DR	5	-2	-2
DR	16	-2	-3

DR	5	-2	-3
DR	11	-3	-10
ER	7	-10	-11
IR	20	-11	-11
MEME detection of other TF binding sites			
TF	Sequence	Score	
LFY	CATGGACCGCCCCACAATT	-10.952697385303955	
hDR15			
Predicted ARF binding sites (AuxRE pairs)			
	Spacing	Score1	Score2
IR	20	-11	-2
DR	16	-11	-2
DR	1	-2	-8
DR	15	-2	-2
DR	8	-8	-2
DR	15	-8	-8
DR	1	-2	-8
DR	15	-2	-2
DR	8	-8	-2
DR	15	-8	-8
DR	1	-2	-8
DR	15	-2	-2
DR	8	-8	-2
DR	15	-8	-8
DR	1	-2	-8
DR	15	-2	-2
DR	8	-8	-2
DR	15	-8	-8
DR	1	-2	-8
DR	15	-2	-3
DR	8	-8	-3
DR	11	-3	-10
ER	7	-10	-11
IR	20	-11	-11
MEME detection of other TF binding sites			
TF	Sequence	Score	
LFY	CATGGACCGCCCCACAATT	-10.952697385303955	

All sequences were ordered as synthetic DNA (Thermofisher). TGTCGG sequences in forward or reverse are indicated in blue. The synthetic promoters included these sequences followed by CMV or 35S minimal promoters for CHO-K1, or protoplast and *in planta* experiments, respectively. For each sequence we verified the presence of IR8, ER13, DR5 or DR15 repeats and of other potential transcription factor binding sites (see methods). ARF binding sites predictions provide the orientation of the two AuxREs (ER, IR or DR), the number of nucleotides in between (spacing) and the score of each AuxRE (Score 1 and score 2). IR8, ER13, DR5 and DR15 repeats are shown in blue. Sequences were optimized to avoid the presence of other AuxREs pairs with high scores (the closest to zero the higher the score is) and/or preferentially bound by ARFs according to DAP-seq data. Although other AuxRE pairs and binding sites for LEAFY transcription factor were predicted to be present in the synthetic promoter sequences, the scores for these other sites are much lower than for IR8, ER13, DR5 and DR15 sites.

Table S5. Combined synthetic promoter sequences, related to Figure 7

hIR8 hER13 Overlapped	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ACCGCTAACTTAC TGTCGG TGCACCGC TGT CGG TCATGTGA CCGACA ACCGCTAACTTAC TGTCGG TCATGTGA TGTCGG TCATGTGA CCGACA ACCGCTAACTTAC TGTCGG TCAT
hIR8 hER13 Separated	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ACCGCTGC CCGACA GCACCAAACTTAC TGT CGG TGCACCGC TGTCGG TCATGTGA CCGACA ACCGCTGC CCGACA GCACCAAACTTAC TGTCGG TGCACCGC TGTCGG TCATGTGA CCGACA ACCGCTGC CCGACA GCACCAAACTTAC TGTCGG TGCA
hIR8 hER13 Juxtaposed	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ACCGC TGTCGG TCATGTGA CCGACA ACCG C TGTCGG TCATGTGA CCGACA TGCAATGC CCGACA GCACCAAACTTAC TGTCGG TGC CCGACA GCACCAAACTTAC TGTCGG TGC C CGACA GCACCAAACTTAC TGTCGG TGCAA
hIR8 hDR5 Overlapped	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ATTGA CCGACA ATTGCCGC TGTCGG TCATG TGA CCGACA ATTGA CCGACA ATTGCCGC TGTCGG TCATGTGA CCGACA ATTGA CCGACA ATTGCCGC
hIR8 hDR5 Separated	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ACCGCCGC CCGACA ATTGA CCGACA ATTG CCGC TGTCGG TCATGTGA CCGACA ACCGCCGC CCGACA ATTGA CCGACA ATTGCCGC TGTCGG TCATGTGA CCGACA ACCGCCGC C CGACA ATTGA CCGACA ATTG
hIR8 hDR5 Juxtaposed	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ACCGC TGTCGG TCATGTGA CCGACA ACCG C TGTCGG TCATGTGA CCGACA TGCAAcagg CCGACA ATTGA CCGACA ATTGA CCGACA ATTGA CCGACA ATTGA CCGACA ATTGA CCG ACA TGCAA
hIR8 hDR15 Overlapped	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ATTGACAAATCTCAG CCGACA ACAATCCGC TGTCGG TCATGTGA CCGACA ATTGACAAATCTCAG CCGACA ACCATCCGC TGTCGG TCATGTGA CCGACA ATTGACAAATCTCAG CC GACA ATAGGTCGC
hIR8 hDR15 Separated	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ACCGCCGC CCGACA ATTGACAAATCTCAG C CGACA ATTGACCGC TGTCGG TCATGTGA CCGACA ACCGCCGC CCGACA ATTGACAAATCTCAG CCGACA ATTGACCGC TGTCGG TC ATGTGA CCGACA ACCGCCGC CCGACA ATTGACAAATCTCAG CCGACA ATTGA
hIR8 hDR15 Juxtaposed	GGGGACAACCTTTGTATAGAAAAGTTGCCATGGACCGC TGTCGG TCATGTGA CCGACA ACCGC TGTCGG TCATGTGA CCGACA ACCG C TGTCGG TCATGTGA CCGACA TGCAAcattgg CCGACA ATTGACAAATCTCAG CCGACA ATTGACAAATCTCAG CCGACA ATTGACAAAT CTCAG CCGACA ATTGACAAATCTCAG CCGACA ATTGACAAATCTCAG CCGACA TGCAA