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

hIR8	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGCTGTCGG CATGTGA <mark>CCGACA</mark> ACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCT GTCGGTCATGTGA <mark>CCGACA</mark> TGCAA		
hER13	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>CCGACA</mark> G CACCAAACTTACTGTCGGTGCCCGACAGCACCAAACTTACTGTC GGTGCCCGACAGCACCAAACTTACTGTCGGTGCAA		
hDR5	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>CCGACA</mark> A TTGA <mark>CCGACA</mark> ATTGA <mark>CCGACA</mark> ATTGA <mark>CCGACA</mark> ATTGA <mark>CCGACA</mark> A TTGA <mark>CCGACA</mark> TGCAA		
hDR15	GGGGACAACTTTGTATAGAAAAGT TTGACAAATCTCAGCCGACAATTG ACAAATCTCAGCCGACAATTGACA AATCTCAGCCGACATGCAA	TGCCATGGACC ACAAATCTCAG <mark>C</mark> AATCTCAG <mark>CCG</mark> /	GC <mark>CCGACA</mark> A CCGACAATTG ACAATTGACA
	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
Fr	5	-3	-5
	10	-5	-5
	19	-5	-5
	0	-5	-3
	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	Sco	ore
			-
	hER13		
		(AuxRE pairs	)
	Predicted ARF binding sites		/
	Predicted ARF binding sites Spacing	Score1	, Score2
IR	Predicted ARF binding sites Spacing 20	Score1 -11	Score2 -3
IR DR	Predicted ARF binding sites Spacing 20 16	Score1 -11 -11	Score2 -3 -3
IR DR ER	Predicted ARF binding sites Spacing 20 16 13	Score1 -11 -11 -3	Score2 -3 -3 -3
IR DR ER IR	Predicted ARF binding sites Spacing 20 16 13 3	Score1 -11 -11 -3 -3	Score2 -3 -3 -3 -3 -3
IR DR ER IR FR	Predicted ARF binding sites Spacing 20 16 13 3 13	Score1 -11 -11 -3 -3 -3	Score2 -3 -3 -3 -3 -3
IR DR ER IR ER B	Predicted ARF binding sites Spacing 20 16 13 3 13 3	Score1 -11 -11 -3 -3 -3 -3 -3	Score2 -3 -3 -3 -3 -3 -3 -3
IR DR ER IR ER IR ER	Predicted ARF binding sites Spacing 20 16 13 3 13 3 13	Score1 -11 -3 -3 -3 -3 -3 -3 -3	Score2 -3 -3 -3 -3 -3 -3 -3 -3
R DR ER R ER R ER ER B	Predicted ARF binding sites Spacing 20 16 13 3 13 3 13 13 11	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -3 -3	Score2 -3 -3 -3 -3 -3 -3 -3 -3 -10
R DR R R R R R R R R R R R R R R R R R	Predicted ARF binding sites Spacing 20 16 13 3 13 3 13 13 13 11 7	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -3 -3 -3	Score2 -3 -3 -3 -3 -3 -3 -3 -10 11
R DR R R R R R R R R R R R R R R R R R	Predicted ARF binding sites Spacing 20 16 13 3 13 3 13 13 11 7 20	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 11	Score2 -3 -3 -3 -3 -3 -3 -10 -11 11
IR DR ER IR IR ER IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11
IR DR ER IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20 MEME detection of other TF	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 binding sites	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11
IR DR IR IR IR IR IR IR IR IR IR TF	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Sco	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore
IR DR IR IR IR IR IR IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Scc -10.9526973	Score2 -3 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 -11 -385303955
IR DR IR IR IR IR IR IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT hDR5	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Score1 -10.9526973	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 -11 ore
IR DR IR IR IR IR IR IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT hDR5 Predicted ARF binding sites	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 -11 -3 -3 -3 -3 -3 -3 -3 -3 -3 -3	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 -11 -385303955
IR DR IR IR IR IR IR IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT hDR5 Predicted ARF binding sites Spacing	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 -11 -11 -11 -11	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore 385303955 ) Score2
IR DR IR IR IR IR IR IR IR IR IF IF IF IF	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT hDR5 Predicted ARF binding sites Spacing 20	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -10 -11 -10.9526973 (AuxRE pairs Score1 -11	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore 385303955 ) Score2 -2
IR DR IR IR IR IR IR IR IR LFY IR DR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT ADR5 Predicted ARF binding sites Spacing 20 16	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Score1 -10.952697: (AuxRE pairs Score1 -11 -11	Score2 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore 385303955 ) Score2 -2 -2
IR DR IR IR IR IR IR IR IR IF IF IF IF IF IR IR DR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT DBD5 Predicted ARF binding sites Spacing 20 16 5	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Score1 -10.9526973 (AuxRE pairs Score1 -11 -11 -11	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore 385303955 ) Score2 -2 -2 -2 -2
IR DR IR IR IR IR IR IR IR IF IF IF IF IF IR DR DR DR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT DR5 Predicted ARF binding sites Spacing 20 16 5	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Score1 -10.9526973 (AuxRE pairs Score1 -11 -11 -11 -12 -2	Score2 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore 385303955 Score2 -2 -2 -2 -2 -2 -2 -2 -2 -2
IR DR ER IR IR ER IR IR IR IR IR IF IF IF IF IR IR DR DR DR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT NDR5 Predicted ARF binding sites Spacing 20 16 5 16	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Score1 -10.9526973 (AuxRE pairs Score1 -11 -11 -2 -2	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore 385303955 Score2 -2 -2 -2 -2 -2 -2
IR BR IR IR IR IR IR IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT NDR5 Predicted ARF binding sites Spacing 20 16 5 16 5	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 -10 -11 -10 -10	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 ore 385303955 Score2 -2 -2 -2 -2 -2 -2 -2 -2 -2 -
IR BR IR IR IR IR IR IR IR IR IF IC IR IR IR IR IR IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT NDR5 Predicted ARF binding sites Spacing 20 16 5 16 5 16 5 16	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 binding sites Score1 -11. -11. Score1 -11 -11 -11 -2 -2 -2 -2	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 ore 385303955 Score2 -2 -2 -2 -2 -2 -2 -2 -2 -2 -
IR BR IR IR IR IR IR IR IR IR IR IR IR IR IR	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT NDR5 Predicted ARF binding sites Spacing 20 16 5 16 5 16 5	Score1 -11 -11 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 -11 -11 -11 -11	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 ore 385303955 Score2 -2 -2 -2 -2 -2 -2 -2 -2 -2 -
IR IR IR IR IR IR IR IR IR IR IR IR IR I	Predicted ARF binding sites Spacing 20 16 13 3 3 13 3 13 13 11 7 20 MEME detection of other TF Sequence CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT CATGGACCGCCCGACAATT NDR5 Predicted ARF binding sites Spacing 20 16 5 16 5 16 5 16 5 16 5 16	Score1           -11           -11           -3           -3           -3           -3           -10           -11           binding sites           Score1           -11           -11           -11           -12           -2           -2           -2           -2           -2           -2           -2           -2           -2           -2           -2           -2           -2           -2	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 ore 385303955 ) Score2 -2 -2 -2 -2 -2 -2 -2 -2 -2 -
IR IR IR IR IR IR IR IR IR IR IR IR IR I	Predicted ARF binding sites           Spacing           20           16           13           3           13           3           11           7           20           MEME detection of other TF           Sequence           CATGGACCGCCCGACAATT           hDR5           Predicted ARF binding sites           Spacing           20           16           5           16           5           16           5           16           5           16           5           16           5           16           5           16           5           16           5           16           5           16           5           16           5           16           5           16           5	Score1           -11           -11           -3           -3           -3           -3           -3           -10           -11           binding sites           Score1           -11           -11           -2	Score2 -3 -3 -3 -3 -3 -3 -3 -10 -11 -11 -11 ore 385303955 Score2 -2 -2 -2 -2 -2 -2 -2 -2 -2 -

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	CATGGACCGCCCGACAATT	-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	Sco	re	
LFY	CATGGACCGCCCGACAATT	-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.

hIR8 hER13 Overlapped	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCTAACTTAC <mark>TGTCGG</mark> TGCACCGC <mark>TGT CGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCTAACTTAC <mark>TGTCGG</mark> TCATGTGA <b>TGTCGG</b> TCATGTGA <mark>CCGACA</mark> ACCGCTAACTTAC <mark>TGTCGG</mark> TCAT
hIR8 hER13 Separated	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCTGC <mark>CCGACA</mark> GCACCAAACTTAC <mark>TGT CGG</mark> TGCACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCTGC <mark>CCGACA</mark> GCACCAAACTTAC <mark>TGTCGG</mark> TGCACCGCTGCCGTCATGTGA CCGACAACCGCTGCCCGACAGCAAACTTACTGTCGGTGCA
hIR8 hER13 Juxtaposed	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> GCACCGCGC C <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> TGCAATGC <mark>CCGACA</mark> GCACCAAACTTAC <mark>TGTCGG</mark> TGCCCGACAGCACCAAACTTACTGTCGGTGCC CGACAGCACCAAACTTACTGTCGGTGCAA
hIR8 hDR5 Overlapped	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ATTGA <mark>CCGACA</mark> ATTGCCGC <mark>TGTCGG</mark> TCATG TGA <mark>CCGACA</mark> ATTGA <mark>CCGACA</mark> ATTGCCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ATTGACCGACAATTGCCGC
hIR8 hDR5 Separated	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCCGC <mark>CGACA</mark> ATTGA <mark>CCGACA</mark> ATTG CCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCCGC <mark>CCGACA</mark> ATTGA <mark>CCGACA</mark> ATTGCCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCCGC <mark>CGACA</mark> ATTG CGACAATTGACCGACA
hIR8 hDR5 Juxtaposed	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCG C <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> TGCAAcagg <mark>CCGACA</mark> ATTGA <mark>CCGACA</mark> ATTGACCG
hIR8 hDR15 Overlapped	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CCGACA</mark> ACAATCCGC TGTCGGTCATGTGA <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CCGACA</mark> ACCATCCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CC GACA</mark> ATAGGTCGC
hIR8 hDR15 Separated	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCCGC <mark>CGACA</mark> ATTGACAAATCTCAG <mark>C CGACA</mark> ATTGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGCCGCCCGACAATTGACAAATCTCAG <mark>CCGACA</mark> ATTGACCGCTGTCGGTC ATGTGA <mark>CCGACA</mark> ACCGCCGC <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CCGACA</mark> ATTGA
hIR8 hDR15 Juxtaposed	GGGGACAACTTTGTATAGAAAAGTTGCCATGGACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCGC <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> ACCG C <mark>TGTCGG</mark> TCATGTGA <mark>CCGACA</mark> TGCAAcattgg <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CCGACA</mark> ATTGACAAATCTCAG <mark>CCGACA</mark> ATTGACAAATCTCAG

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