A

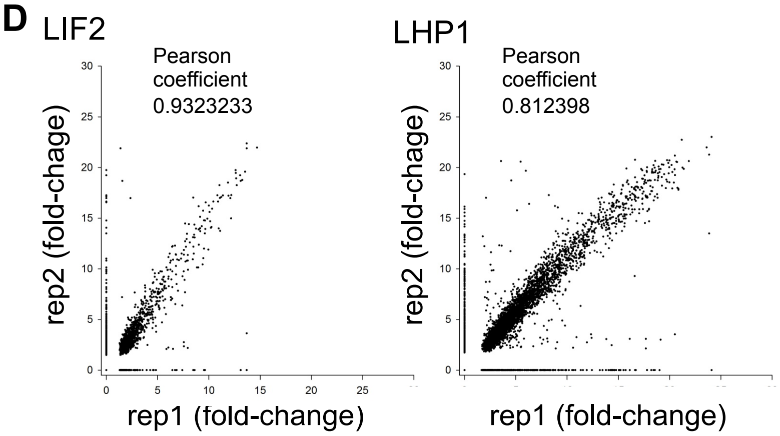
Reads	Total Number	Uniquely mapped
LHP1 IP rep1	49 337 103	22 535 892
LHP1 INPUT rep1	44 858 478	26 075 751
LHP1 IP rep2	51 830 947	17 161 379
LHP1 INPUT rep2	47 477 630	17 480 420
LIF2 IP rep1	46 292 522	17 954 623
LIF2 INPUT rep1	50 345 677	21 072 356
LIF2 IP rep2	47 453 337	12 953 623
LIF2 INPUT rep2	47 070 104	18 201 752

B

	Covered nucleotides	Nbre regions covered
LIF2 rep1	5034884	1750
LIF2 rep2	6913458	2442
Intersect beween LIF2 rep1 & rep2	3937459	1457
LHP1 rep1	23794547	4901
LHP1 rep2	23881395	5095
Intersect beween LHP1 rep1 & rep2	21988263	4844

C

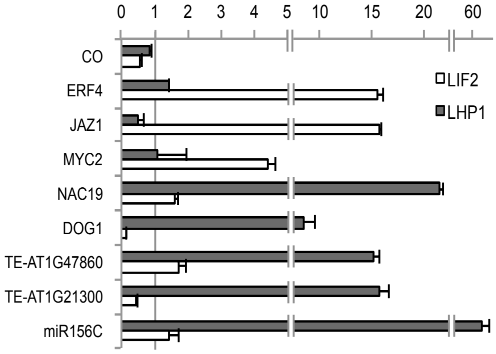
Overlap between replicates	%
In nucleotides	
related to LIF2 rep1	78.20
related to LIF2 rep2	56.95
related to LHP1 rep1	92.41
related to LHP1 rep2	92.07
In numbrer of regions	
related to LIF2 rep1	83.26
related to LIF2 rep2	59.66
related to LHP1 rep1	98.84
related to LHP1 rep2	95.07



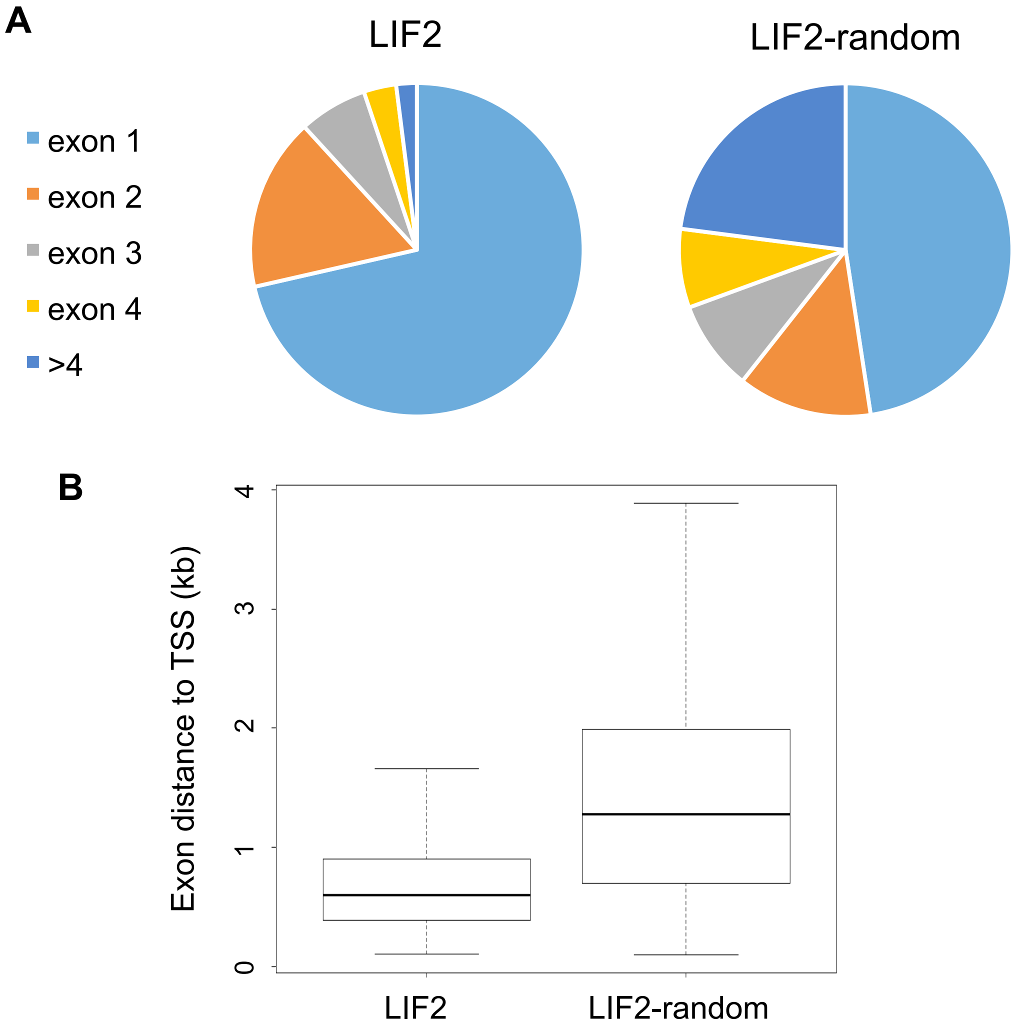
E

AGI		Annotation	LHP1 rep1	LHP1 rep2	LIF2 rep1	LIF2 rep2
AT5G60390	EF1	CDS	0	0	0	0
AT5G15840	CO	CDS	0	0	0	0
AT3G15210	ERF4	CDS	0	0	12.09	16.97
AT1G19180	JAZ1	5'UTR	0	0	7.97	9.9
AT1G32640	MYC2	CDS	0	0	4.05	5.7
AT1G52890	NAC19	CDS	7.68	9.08	2.86	2.21
AT5G45830	DOG1	CDS	11.59	11.2	0	0
AT1G47860		TE	4.41	5.18	3.65	4.03
AT1G21300		TE	8.33	11.47	0	0
AT4G31877	miR156C	ncRNA	15.71	15.98	0	0

F



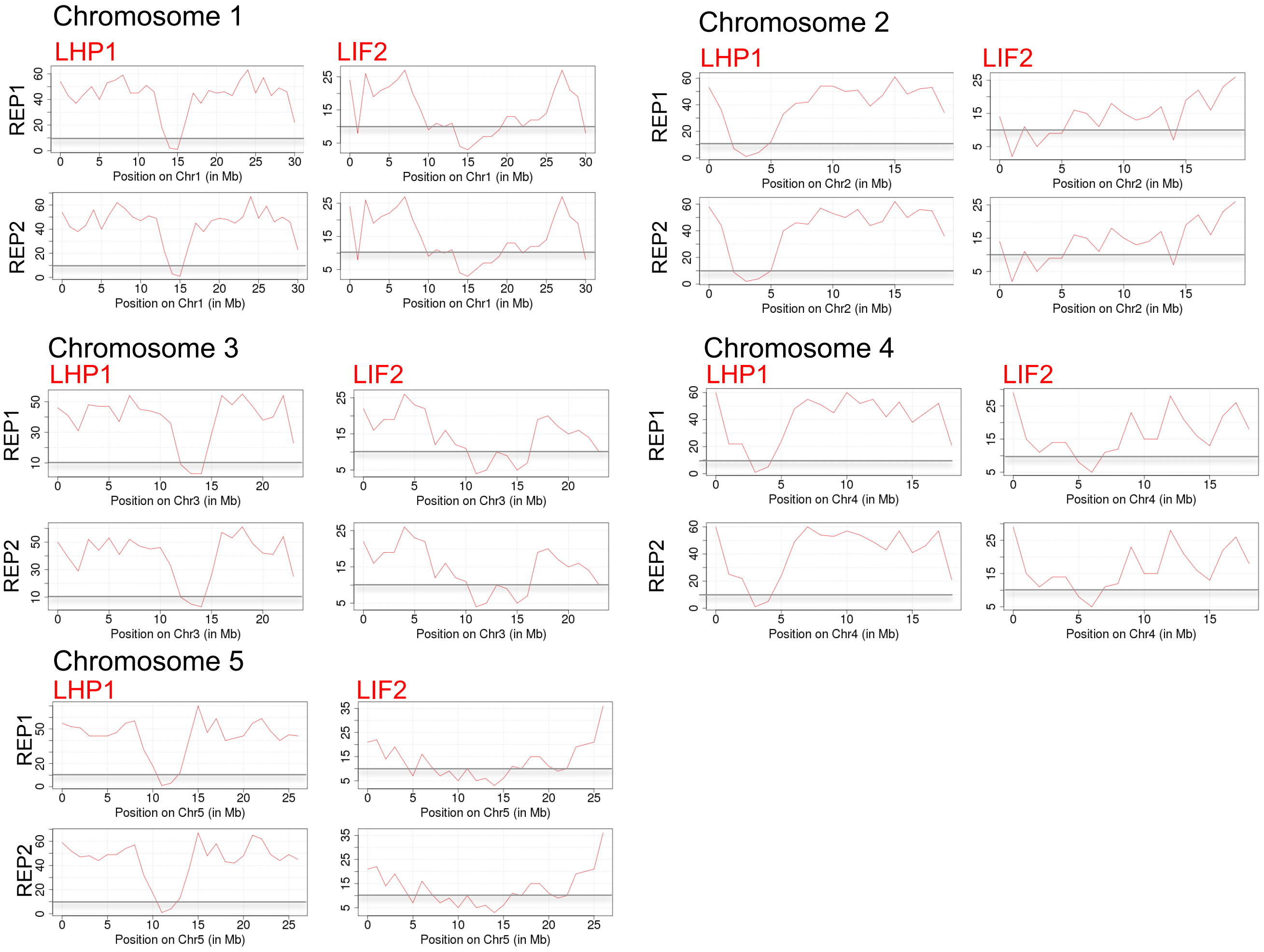
Supplemental Figure 1: ChIP-seq experiments.
(**A**) Read counts and mapping in the two ChIP-seq biological replicates.
(**B**) Comparisons between replicates.
(**C**) Overlaps between replicates.
(**D**) MACS peak fold-change correlations between ChIP-seq replicates.
(**E**) Fold-changes in the two ChIP-seq biological replicates of selected target regions.
(**F**) Confirmation by ChIP-QPCR at targets identified by ChIP-seq. Protein enrichments were relative to input and the internal reference gene, *EF1α*. The values correspond to the mean of two biological replicates and three technical replicates for each ±SE.



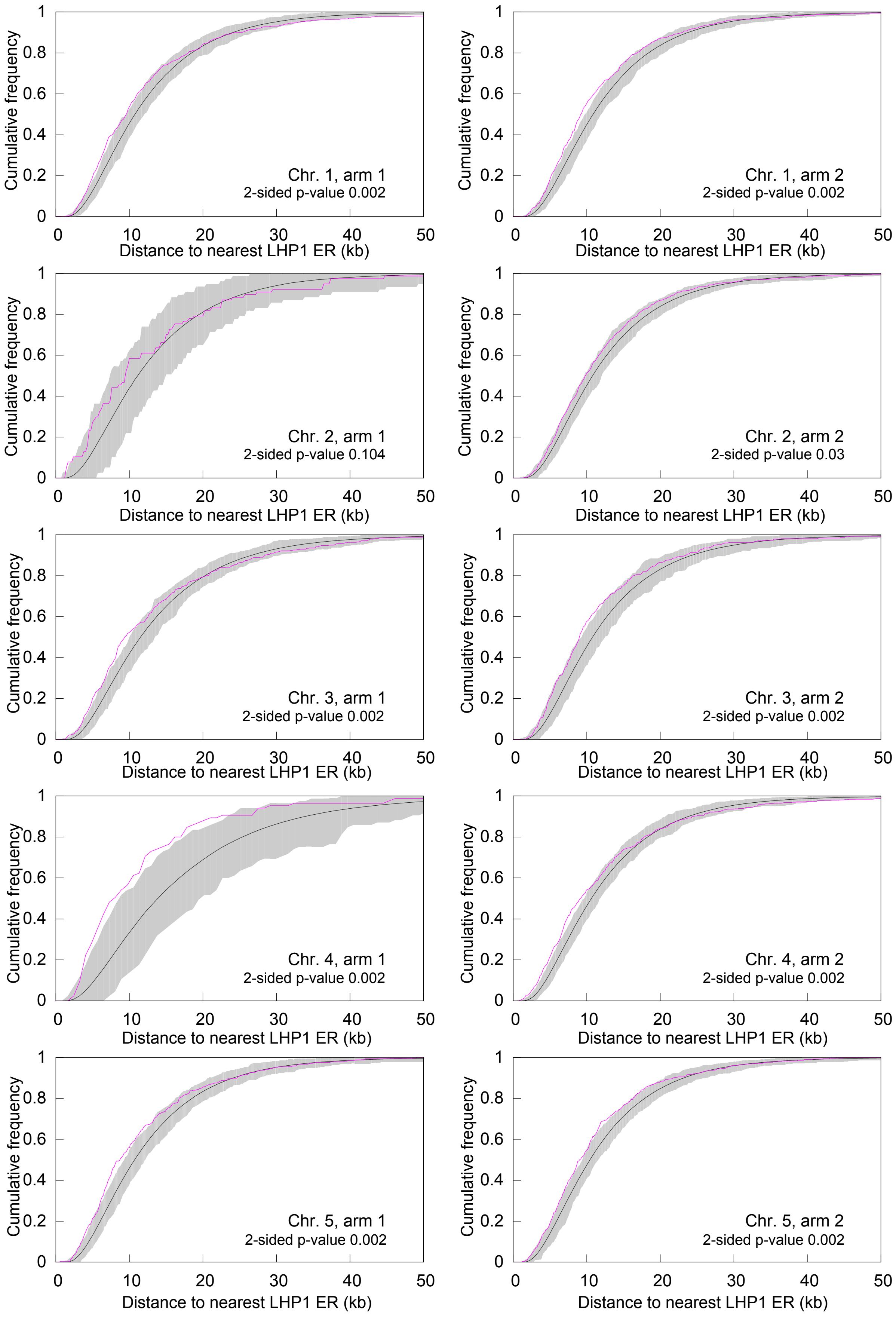
Supplemental Figure 2: Exon distributions of LIF2 ERs.

(**A**) Exon number distribution of LIF2 ERs and comparisons with the randomly shuffled control regions.

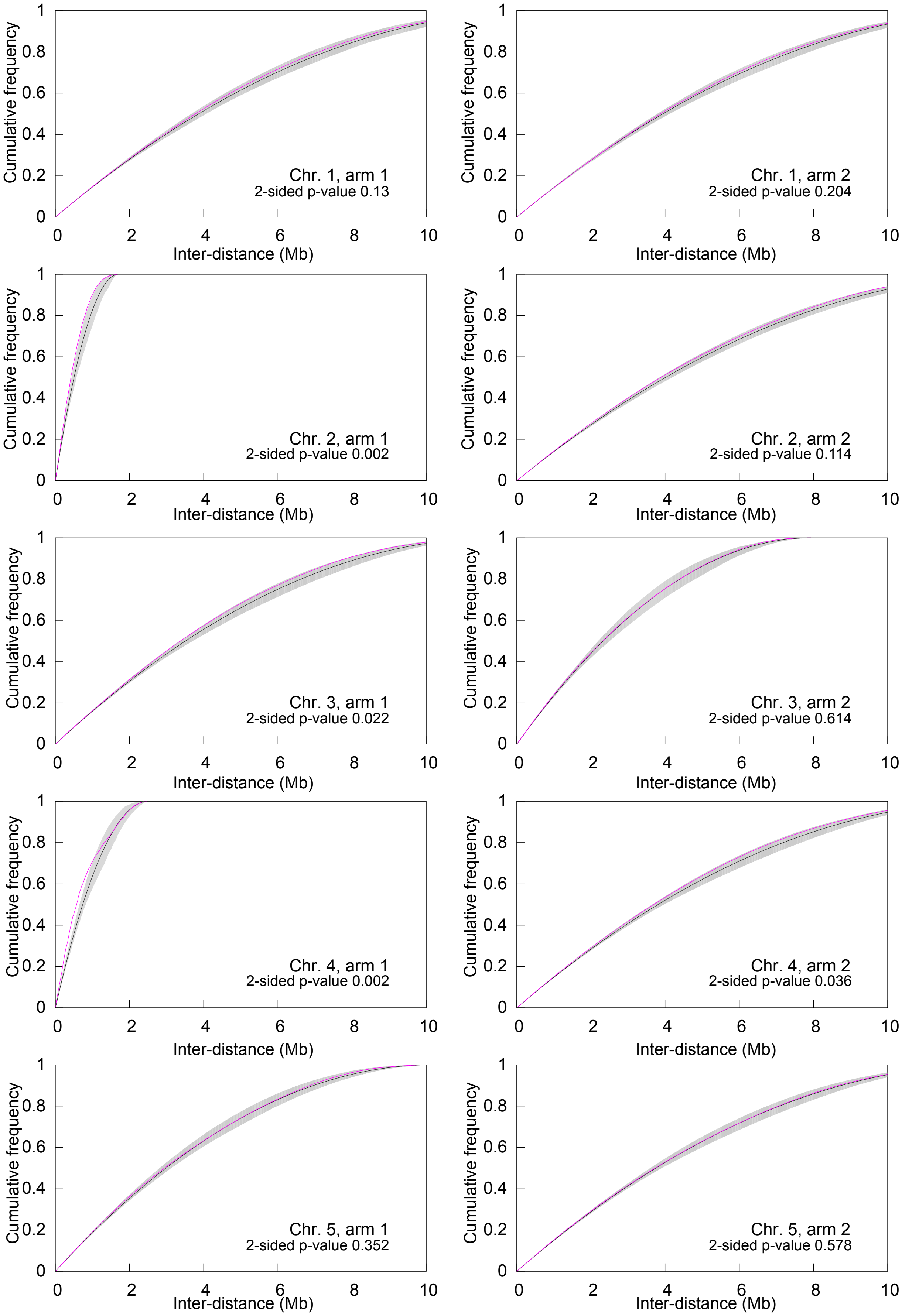
(**B**) Distance to TSS of the LIF2-bound exons and comparisons with the randomly shuffled control regions.



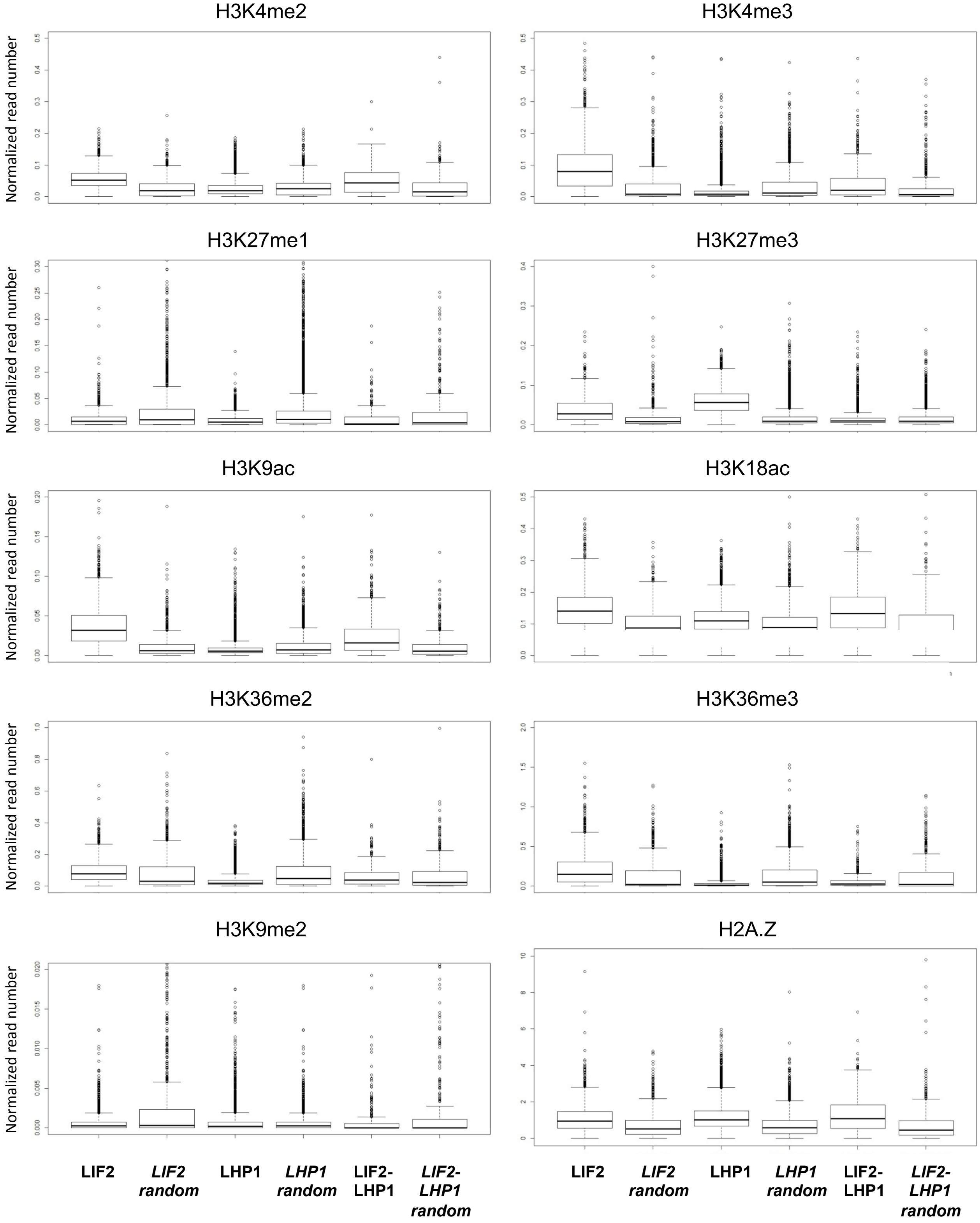
Supplemental Figure 3: Distributions of the sums of the summits in 1-Mb windows. For the two biological replicates, LHP1 and LIF2 distributions on the five chromosomes were compared by plotting the sums of their summits in 1-Mb windows.



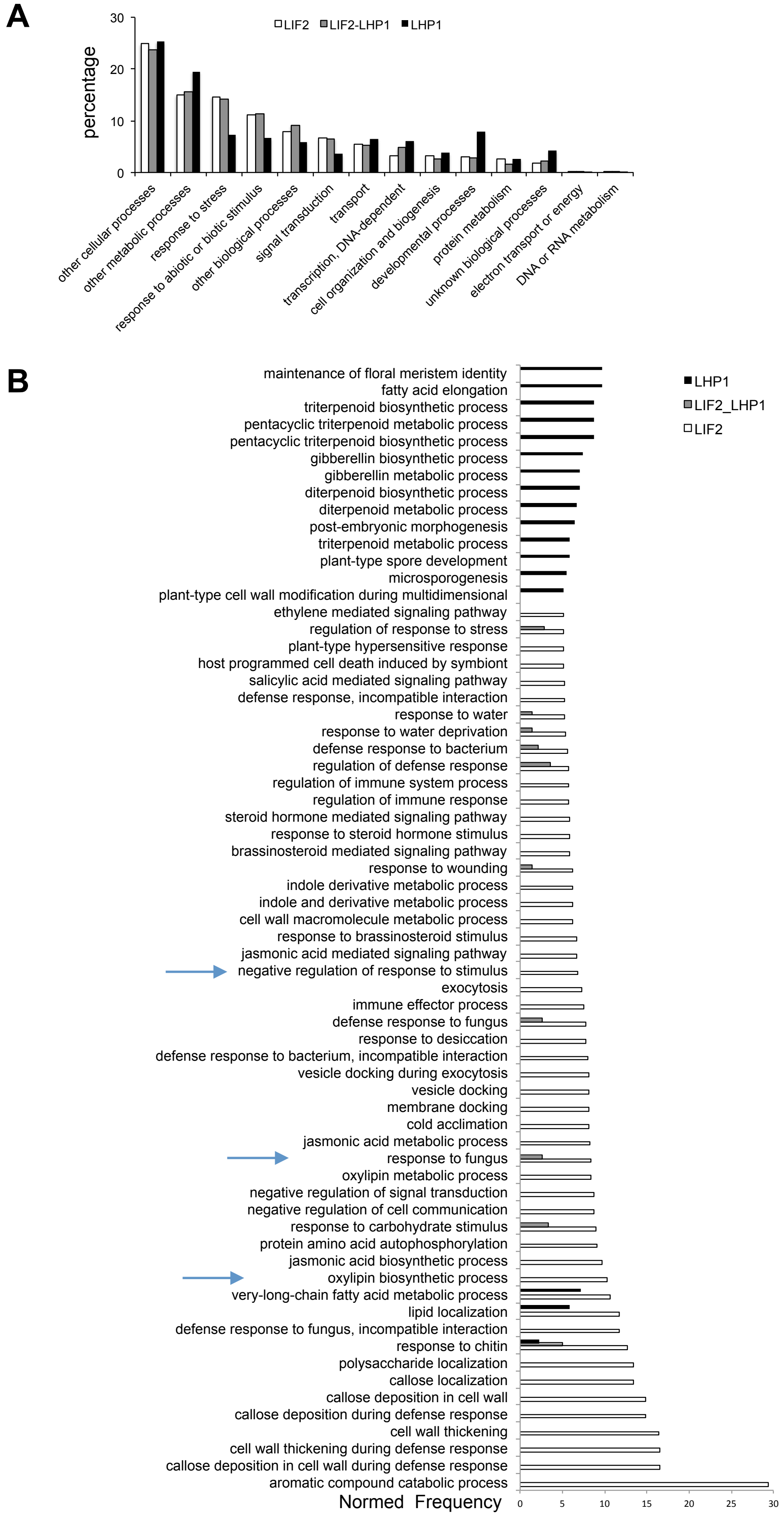
Supplemental Figure 4: Cumulative distribution of the distance to the nearest LHP1 summit. Pink: observed distribution; black: average distribution under the random model; grey: 95% envelope under the random model. Arm 1 of chromosome 2 and arm 1 of chromosome 4 bear the NOR and the knob, respectively, which introduce spatial constraints.



Supplemental Figure 5: Cumulative distribution of LHP1 summit inter-distances.
Pink: observed distribution; black: average distribution under the random model; grey: 95% envelope under the random model. Arm 1 of chromosome 2 and arm 1 of chromosome 4 bear the NOR and the knob, respectively, which introduce spatial constraints.



Supplemental Figure 6: Post-translational histone modifications and their distributions in LIF2 ERs, LHP1 ERs and LIF2-LHP1 IRs.



Supplemental Figure 7: GO term analysis of the target loci of LIF2 and LHP1.

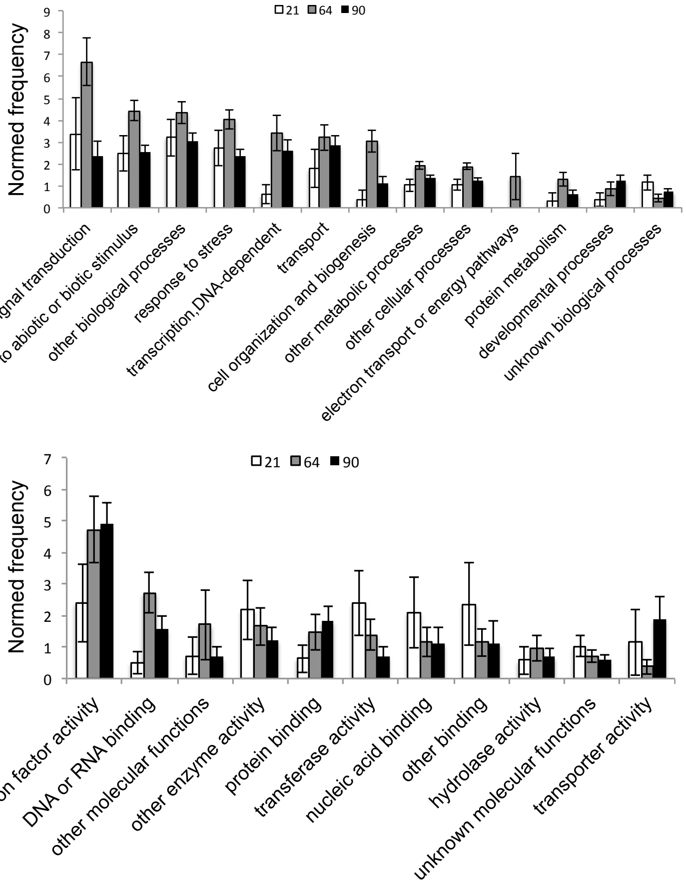
(**A**) Functional categorization of the LIF2 ERs, LHP1 ERs and LIF2-LHP1 IRs (TAIR GO toolkit).

(**B**) Normed frequencies (NF) of the GO terms in the biological process categories with an over 4-fold enriched NF in at least one of the input lists (*i.e.,* LIF2 target genes, LHP1 target genes, genes of LIF2-LHP1 IRs) were compiled using AgriGO toolkit. Arrows: GO terms related to JA.

A

LIF2-LHP1 targets		
Set-90	Set-64	Set-21
AT1G03850	AT1G02390	AT1G21010
AT1G03870	AT1G02400	AT1G21550
AT1G09950	AT1G02920	AT1G58420
AT1G12110	AT1G12090	AT1G61890
AT1G22570	AT1G13260	AT1G65390
AT1G22710	AT1G17420	AT1G69900
AT1G24530	AT1G18570	AT1G72520
AT1G25440	AT1G21910	AT1G78850
AT1G25550	AT1G24140	AT2G04495
AT1G26250	AT1G25400	AT2G43060
AT1G29280	AT1G28370	AT4G18950
AT1G34245	AT1G30720	AT4G23170
AT1G35560	AT1G33610	AT4G30280
AT1G37130	AT1G33760	AT4G39640
AT1G44350	AT1G35140	AT5G11550
AT1G52890	AT1G35210	AT5G19230
AT1G54740	AT1G36060	AT5G20230
AT1G58270	AT1G53170	AT5G59820
AT1G68520	AT1G61260	AT5G61600
AT1G70170	AT1G66090	AT5G64260
AT1G71880	AT1G66180	AT5G66650
AT1G72430	AT1G77640	
AT1G75500	AT1G80840	
AT1G75710	AT2G05520	
AT1G80450	AT2G18690	
AT2G02680	AT2G22500	
AT2G05380	AT2G24600	
AT2G19810	AT2G25450	
AT2G22470	AT2G26560	
AT2G32030	AT2G30362	
AT2G32140	AT2G35930	
AT2G36950	AT2G44840	
AT2G40750	AT3G01290	
AT2G41100	AT3G10300	
AT2G42350	AT3G10720	
AT2G45400	AT3G22160	
AT2G46160	AT3G48520	
AT2G47485	AT3G49120	
AT2G48030	AT3G50260	
AT3G07350	AT3G50480	
AT3G15500	AT3G52400	
AT3G18950	AT3G52450	
AT3G22910	AT3G56400	
AT3G23030	AT3G56710	
AT3G23250	AT4G00360	
AT3G28910	AT4G01950	
AT3G44720	AT4G02330	
AT3G46090	AT4G08950	
AT3G48650	AT4G20000	
AT3G49780	AT4G22690	
AT3G50740	AT4G25470	
AT3G52470	AT4G30270	
AT3G60520	AT4G32800	
AT3G62690	AT5G04340	
AT4G00730	AT5G17350	
AT4G16780	AT5G21960	
AT4G16820	AT5G25250	
AT4G17460	AT5G26920	
AT4G23880	AT5G35735	
AT4G25480	AT5G42380	
AT4G32290	AT5G43760	
AT4G32480	AT5G47220	
AT4G34380	AT5G54720	
AT4G36010	AT5G64120	
AT4G36670		
AT4G36900		
AT4G37540		
AT4G38620		
AT4G39950		
AT5G06300		
AT5G07080		
AT5G09440		
AT5G12340		
AT5G14730		
AT5G14920		
AT5G24930		
AT5G26340		
AT5G37540		
AT5G40720		
AT5G41810		
AT5G46295		
AT5G49280		
AT5G49520		
AT5G49700		
AT5G54710		
AT5G62020		
AT5G62470		
AT5G64750		
AT5G67430		
AT5G67450		

B



C

Biological process	Description	NO. Genes in Overlap	Tot. NO. Genes in GO	p-value	FDR
Set-21					
Response to wounding	GO:0009611	6	340	1.34e-07	7.93e-05
Oxylipin metabolic process	GO:0031407	5	167	1.35e-07	7.93e-05
JA metabolic process	GO:0009694	5	159	1.07e-07	7.93e-05
Set-64					
Response to chitin	GO:0010200	22	421	3.33e-24	1.43e-20
Reg. of innate immune response	GO:0045088	20	415	2.57e-21	3.3e-18
Reg. of immune system process	GO:0002682	20	419	3.08e-21	3.3e-18
Set-90					
Response to chemical stimulus	GO:0042221	37	953	1.78e-10	7.95e-07
Response to stimulus	GO:0050896	45	6222	3.09e-09	4.6e-06
Response to organic substance	GO:0010033	29	2739	2.46e-09	4.6e-06

D

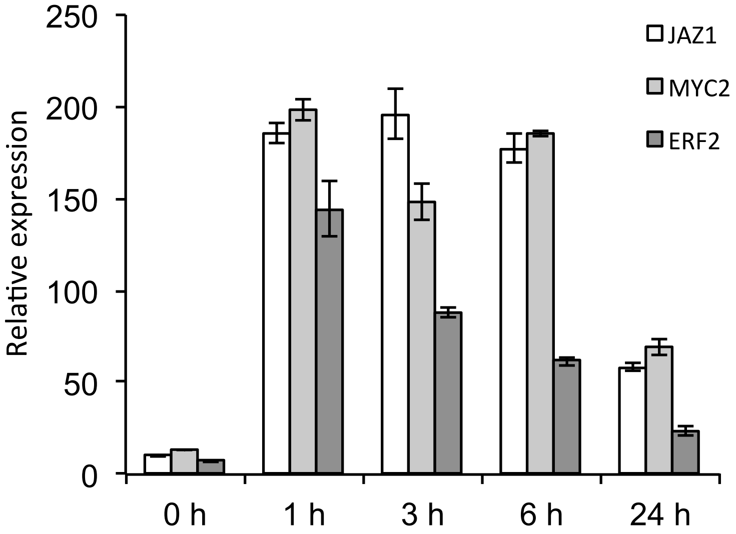
Expression profiles	Set-90	Set-64	Set-21
No change in transcriptomes	54 (60.0%)	26 (40.6%)	7 (33.3%)
Deregulation in *lif2*	19	31	9
Deregulation in *lhp1*	28 (31.1%)	22	11
Deregulation in *lif2 & lhp1*	11	15	6
Down in *lif2*	14	29 (45.3%)	8
Up in *lif2*	5	0	1
Down in *lhp1*	7	9	4
Up in *lhp1*	18	10	4
Down in *lif2 & lhp1*	2	7	3
Up in *lif2 & lhp1*	3	0	1

Supplemental Figure 8: Analyses of the LIF2-LHP1 IRs with binding alterations in the mutant backgrounds.

(**A**) Lists of the three sets of genes.

(**B-C**) GO analyses using BAR and Plant GSEA toolkits, respectively.

(**D**) Expression profiles of the gene sets. Percentages related to the number of genes in the Set were calculated for the largest classes.



Supplemental Figure 9: Expression kinetics of JA-induced marker genes in response to MeJA treatment in wild-type plants.

Two-week-old seedlings were treated with JA for 1 to 24 hours and *JAZ1*, *MYC2* and *ERF2* expression was recorded. *EF1* was used as reference gene.

Tandem duplications (T-Clusters)	**Chromosome 4**	**Whole genome**
T-Clusters	248	1564
T-Cluster genes	681	4176
Average T-Cluster size (gene number)	2.75	2.67
T-Clusters & LHP1 targets genes	132	861
% of T-Cluster genes targeted by LHP1	19.4	20.6
% of LHP1 target genes in T-Clusters	23.8	23.1
LHP1 target genes in T-Clusters (with no unannotated genes in the cluster)	n.d.	848
Clusters with 1 LHP1 target gene per cluster	n.d.	484
Clusters with 2 LHP1 target gene per cluster	n.d.	138
Clusters with 3 LHP1 target gene per cluster	n.d.	20
Clusters with 4 LHP1 target gene per cluster	n.d.	7
% of LHP1 targeted genes in T-clusters that have multiple LHP1 targets	n.d.	9.6%

Supplemental Table 1 : Tandem duplications and LHP1 target genes.
n.d. non determinded.

	LIF2		**LIF2-LHP1**	
	Normed Frequency	p-value	Normed Frequency	p-value
Biological process				
signal transduction	3.34	1.753e-50	2.82	2.213e-11
other biological processes	3.22	1.652e-87	3.27	8.384e-29
response to abiotic or biotic stimulus	3	1.399e-78	2.7	2.662e-19
response to stress	2.98	2.398e-87	2.67	5.353e-21
transport	2.32	2.349e-36	2.22	5.928e-11
transcription,DNA-dependent	1.71	8.047e-10	2.15	1.356e-07
other cellular processes	1.35	1.633e-24	1.24	4.149e-05
other metabolic processes	1.34	3.208e-20	1.32	6.090e-07
cell organization and biogenesis	1.2	5.091e-03	0.97	0.079
electron transport or energy pathways	1.19	0.060	0.33	0.043
developmental processes	1.13	0.013	1.04	0.071
protein metabolism	1.05	0.026	0.63	1.059e-03
unknown biological processes	0.58	1.403e-18	0.68	1.004e-04
DNA or RNA metabolism	0.27	6.744e-06	0.12	2.346e-03
Molecular function				
transcription factor activity	2.39	3.730e-18	3.7	2.739e-17
DNA or RNA binding	1.16	0.011	1.39	6.066e-03
receptor binding or activity	1.43	0.100	1.31	0.255
protein binding	1.9	1.958e-13	1.29	0.031
other enzyme activity	1.2	0.033	1.25	0.082
other molecular functions	1.2	3.401e-03	1.25	0.022
transporter activity	1.12	0.050	1.16	0.097
other binding	1.17	6.249e-04	1.12	0.032
transferase activity	1.52	4.876e-07	1.05	0.078
nucleic acid binding	0.53	1.859e-04	0.72	0.068
unknown molecular functions	0.66	3.823e-12	0.71	3.973e-04
hydrolase activity	1.01	0.045	0.7	0.022
kinase activity	1.83	5.319e-07	0.68	0.070
nucleotide binding	1.15	0.011	0.64	9.169e-03
structural molecule activity	0.52	0.016	0.63	0.154

Supplemental Table 2: GO term analysis of the genes present in LIF2 ERs and LIF2-LHP1 IRs using the Plant Functional Genomics (BAR) classification Superviewer program.

TF family	**Nbr Genes**	**Total in family**	**p-value**	**FDR**
LIF2				
AP2-EREBP	24	138	1.57e-11	1.79e-08
WRKY	12	72	2.82e-06	1.07e-03
LIF2_LHP1				
AP2-EREBP	17	138	2.72e-14	1.11e-11
C2C2-CO-Like	4	30	1.97e-04	0.0202
C2H2	8	211	6.24e-04	0.0488
WRKY	6	72	5.63e-05	7.68e-03
LHP1				
C2H2	34	211	1,00E-04	0.0146
BASIC HELIX-LOOP-HELIX (bHLH)	33	162	1.94e-06	5.27e-04
BHLH	33	161	1.73e-06	5.27e-04
MADS	31	109	7.36e-09	4.66e-06
MADS-BOX	31	108	6.13e-09	4.66e-06
HOMEOBOX	29	91	2.66e-09	4.66e-06
MYB	27	131	1.34e-05	2.82e-03
MYB3R- and R2R3- TYPE MYB-encoding genes	27	132	1.5e-05	2.86e-03
NAC	19	96	3.76e-04	0.0434
WRKY	18	72	4.29e-05	6.79e-03
ZINC FINGER-HOMEOBOX - ZHD subfamily	7	14	3.88e-04	0.0434

Supplemental Table 3: Enrichments of LIF2 and LHP1 targets in specific transcription factor families using the PlantGSEA resource.

TF	Genes targeted	Total genomic targets	p-value	FDR	Genes targeted by TF in ERs
LIF2					
AGL15 (MADS box)	7	22	9.89e-06	1.69e-04	AT1G02400 AT1G14920 AT4G25470 AT2G45830 AT4G38680 AT1G68840 AT1G13260
AP2 (AP2/EREBP)	18	165	2.87e-06	5.73e-05	AT1G11050 AT1G13260 AT1G22530 AT1G23390 AT1G71030 AT3G55980 AT4G00730 AT4G01250 AT4G02540 AT4G08950 AT4G16490 AT4G20260 AT4G25480 AT4G26690 AT4G29190 AT5G19140 AT5G20250 AT5G49360
PIF1 (AtbHLH15)	22	189	8.38e-08	2.51e-06	AT1G25550 AT1G28330 AT1G52890 AT1G56220 AT1G60190 AT1G68670 AT2G01570 AT2G16660 AT2G27500 AT2G45820 AT2G46710 AT3G02550 AT3G04730 AT3G12920 AT3G24050 AT3G24503 AT3G25870 AT4G17460 AT5G24930 AT5G54380 AT5G64260 AT5G65430
HY5 (bZIP)	61	221	6.37e-37	7.64e-35	AT1G07135 AT1G09070 AT1G17420 AT1G18300 AT1G18570 AT1G20510 AT1G21910 AT1G24140 AT1G24530 AT1G53170 AT1G56660 AT1G60190 AT1G61340 AT1G61890 AT1G66160 AT1G68840 AT1G69760 AT1G73500 AT1G77640 AT1G78850 AT2G22500 AT2G25460 AT2G27660 AT2G30040 AT2G33580 AT2G35290 AT2G35930 AT2G39650 AT2G41100 AT2G41640 AT3G06080 AT3G14440 AT3G25250 AT3G46080 AT3G48520 AT3G52400 AT3G54810 AT3G55980 AT3G56880 AT3G62260 AT3G62720 AT4G08950 AT4G17500 AT4G25490 AT4G27310 AT4G29780 AT4G32800 AT4G33920 AT4G34150 AT4G36670 AT5G01100 AT5G43890 AT5G45110 AT5G45340 AT5G49280 AT5G49520 AT5G52020 AT5G59550 AT5G62020 AT5G62520 AT5G66650
LIF2_LHP1					
AGL15 (MADS box)	4	22	6.71e-05	7.64e-04	AT1G02400 AT1G13260 AT2G45830 AT4G25470
AP2 (AP2/EREBP)	6	165	3.61e-03	0.0274	AT4G00730 AT4G37540 AT4G25480 AT4G08950 AT5G54470 AT1G13260
PIF1 (AtbHLH15)	6	189	6.79e-03	0.0441	AT1G03850 AT1G25550 AT1G52890 AT4G17460 AT5G24930 AT5G64260
HY5 (bZIP)	30	221	1.75e-25	7.97e-24	AT1G17420 AT1G18570 AT1G21910 AT1G24140 AT1G24530 AT1G25400 AT1G53170 AT1G61890 AT1G77640 AT1G78850 AT2G22500 AT2G27660 AT2G35290 AT2G35930 AT2G37430 AT2G41100 AT3G25250 AT3G46080 AT3G48520 AT3G52400 AT4G08950 AT4G32800 AT4G36670 AT5G43890 AT5G49280 AT5G49520 AT5G52020 AT5G59820 AT5G62020 AT5G66650
LHP1					
AP2 (AP2/EREBP)	30	165	3.73e-05	1.68e-03	AT2G16760 AT2G14210 AT5G54470 AT1G71050 AT4G00730 AT4G04630 AT5G67180 AT5G07030 AT3G58780 AT4G36870 AT2G40435 AT5G15310 AT4G13210 AT2G18550 AT2G43620 AT2G45660 AT1G35910 AT1G70560 AT4G18960 AT5G64870 AT4G37540 AT5G13790 AT1G73590 AT5G67060 AT1G13260 AT1G35730 AT3G55710 AT2G42830 AT4G08950 AT4G24050
HY5 (bZIP)	42	221	4.27e-07	5.86e-05	AT1G24530 AT5G52020 AT5G25810 AT1G78990 AT1G17420 AT3G52400 AT2G47460 AT1G61890 AT5G23010 AT4G27250 AT1G02810 AT2G22500 AT5G49520 AT5G57510 AT1G16850 AT4G36670 AT3G55120 AT2G37430 AT1G53170 AT5G59820 AT5G66650 AT1G32450 AT5G44120 AT5G42800 AT2G28630 AT3G48520 AT5G62490 AT5G24140 AT5G59780 AT2G15020 AT3G21720 AT5G49280 AT1G17380 AT5G10100 AT4G08950 AT4G05100 AT2G41100 AT3G22830 AT5G62020 AT1G78850 AT1G12950 AT5G13930
SEP3 (MADS box)	11	15	5.4e-07	5.86e-05	AT3G54340 AT2G22540 AT3G58780 AT3G02310 AT2G45660 AT4G18960 AT5G13790 AT2G03710 AT4G24540 AT2G42830 AT5G15800

Supplemental Table 4: LIF2 and LHP1 targets are also bound by specific transcription factors.
The PlantGSEA and AGRIS toolkits were used.

Segment Name	Unique sequence occurrences	Total occurrence	Expected unique sequence	Expected occurrences	Rank	Score
ACGTGGCA word						
Distal Promoter	598	621	497.582	503.982	1175	109.93
Proximal Promoter	414	431	353.216	358.329	1251	65.7371
Core Promoter	172	174	141.099	152.113	539	34.061
5'UTR	26	26	15.5612	16.4062	3156	13.3462
Intron	48	48	38.8425	40.5848	21162	10.161
3'UTR	26	27	21.3065	22	14830	5.1762
Genome-wide	5	1265	5	1020.69	2410	0
AAACCCTA word						
Intron	764	802	652.752	686.061	672	120.231
5'UTR	911	952	825.505	908.536	26	89.7771
Distal Promoter	3116	3674	3041.64	3238.08	2631	75.2602
Core Promoter	639	658	568.781	618.048	51	74.3858
Proximal Promoter	1606	1779	1540.73	1598.78	1209	66.6328
3'UTR	91	92	75.7094	78.332	2976	16.7401
Genome-wide	5	11340	5	9887.71	55	0

Supplemental Table 5: Occurrences of the two identified DNA words.
The word frequency calculation was performed in non-coding segments of the *A. thaliana* genome, using the Arabidopsis *cis*-regulatory element database (http://arabidopsis.med.ohio-state.edu/AtcisDB/).

GO term	Description	Normed frequency	p-value	FDR
lhp1 LIF2 depleted				
Biological process				
GO:0052542	callose deposition during defense response	31,5	1.4e-06	2.4e-05
GO:0033037	polysaccharide localization	28,5	2.2e-06	3.3e-05
GO:0052545	callose localization	28,5	2.2e-06	3.3e-05
GO:0010200	response to chitin	24,5	2.1e-31	5.0e-29
GO:0009631	cold acclimation	20,6	8.7e-06	0.00013
GO:0002252	immune effector process	19,3	1.2e-05	0.00016
GO:0031408	oxylipin biosynthetic process	18,7	1.3e-05	0.00018
GO:0009867	jasmonic acid mediated signaling pathway	17,1	4.1e-07	7.6e-06
GO:0009743	response to carbohydrate stimulus	16,9	1.5e-29	2.4e-27
GO:0031407	oxylipin metabolic process	15,3	3.2e-05	0.00041
GO:0002682	regulation of immune system process	14,6	4.0e-05	0.00049
GO:0050776	regulation of immune response	14,6	4.0e-05	0.00049
GO:0042434	indole derivative metabolic process	13,5	9.7e-06	0.00014
GO:0042430	indole and derivative metabolic process	13,5	9.7e-06	0.00014
GO:0050832	defense response to fungus	13,3	4.1e-10	1.4e-08
GO:0009873	ethylene mediated signaling pathway	12,9	4.3e-07	7.7e-06
GO:0031347	regulation of defense response	12,7	2.6e-06	3.9e-05
GO:0080134	regulation of response to stress	11,5	9.6e-07	1.7e-05
GO:0009620	response to fungus	11,3	2.0e-11	1.1e-09
GO:0000160	two-component signal transduction system (phosphorelay)	10,4	2.0e-06	3.2e-05
GO:0009611	response to wounding	10,3	3.8e-12	2.3e-10
GO:0042742	defense response to bacterium	10,1	9.0e-11	4.3e-09
GO:0009415	response to water	10,0	8.4e-14	7.3e-12
GO:0009414	response to water deprivation	9,9	3.8e-13	3.0e-11
GO:0019760	glucosinolate metabolic process	9,6	0.00024	0.0026
GO:0016143	S-glycoside metabolic process	9,6	0.00024	0.0026
GO:0019757	glycosinolate metabolic process	9,6	0.00024	0.0026
GO:0048585	negative regulation of response to stimulus	8,7	9.5e-05	0.0011
GO:0006955	immune response	8,5	5.5e-16	6.2e-14
GO:0002376	immune system process	8,4	5.9e-16	6.2e-14
GO:0045087	innate immune response	8,3	1.2e-14	1.2e-12
GO:0009642	response to light intensity	8,0	0.00015	0.0018
GO:0009617	response to bacterium	7,7	8.6e-10	2.7e-08
GO:0009723	response to ethylene stimulus	7,2	2.4e-07	4.9e-06
GO:0006952	defense response	7,2	9.6e-25	1.3e-22
Molecular function				
GO:0016564	transcription repressor activity	17,1	9.0e-09	8.9e-07
lif2 LHP1 depleted				
Biological process				
GO:0010876	lipid localization	16,7	5.6e-13	3.6e-11
GO:0010076	maintenance of floral meristem identity	16,7	1.2e-05	0.00037
GO:0046087	cytidine metabolic process	16,7	1.2e-05	0.00037
GO:0006216	cytidine catabolic process	16,7	1.2e-05	0.00037
GO:0009972	cytidine deamination	16,7	1.2e-05	0.00037
GO:0046135	pyrimidine nucleoside catabolic process	15,0	1.8e-05	0.00053
GO:0046133	pyrimidine ribonucleoside catabolic process	15,0	1.8e-05	0.00053
GO:0010022	meristem determinacy	13,9	0.00013	0.0027
GO:0009164	nucleoside catabolic process	13,6	2.8e-05	0.00075
GO:0042454	ribonucleoside catabolic process	13,6	2.8e-05	0.00075
GO:0034656	nucleobase, nucleoside and nucleotide catabolic process	12,5	4.0e-05	0.001
GO:0034655	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	12,5	4.0e-05	0.001
GO:0045962	positive regulation of development, heterochronic	12,5	0.00018	0.0038
GO:0046131	pyrimidine ribonucleoside metabolic process	10,7	7.8e-05	0.0019
GO:0006213	pyrimidine nucleoside metabolic process	10,0	0.00011	0.0023
GO:0009886	post-embryonic morphogenesis	9,3	2.1e-08	9.7e-07
GO:0045596	negative regulation of cell differentiation	8,1	8.1e-07	3.2e-05
GO:0065001	specification of axis polarity	7,9	9.1e-05	0.0021
GO:0016145	S-glycoside catabolic process	7,9	0.0003	0.006
GO:0019759	glycosinolate catabolic process	7,9	0.0003	0.006
GO:0019762	glucosinolate catabolic process	7,9	0.0003	0.006
GO:0010089	xylem development	7,8	0.001	0.017
GO:0016139	glycoside catabolic process	7,5	0.00038	0.0073
GO:0010074	maintenance of meristem identity	7,4	4.4e-05	0.0011
GO:0048440	carpel development	7,4	3.6e-11	2.0e-09
GO:0009943	adaxial/abaxial axis specification	7,3	0.00014	0.0031
GO:0019827	stem cell maintenance	7,3	1.7e-05	0.0005
GO:0048864	stem cell development	7,3	1.7e-05	0.0005
GO:0009944	polarity specification of adaxial/abaxial axis	7,1	0.00048	0.0088
GO:0006722	triterpenoid metabolic process	7,1	0.00048	0.0088
GO:0048467	gynoecium development	7,0	2.7e-11	1.5e-09
GO:0048863	stem cell differentiation	7,0	2.1e-05	0.00059

Supplemental Table 6: GO term analysis of LIF2 or LHP1 depleted regions in the mutant backgrounds (AgriGO).
Lists of GO terms with NF ≥7.

Primer	Sequence (5' to 3')	Application
3HA-1	ACACACACTGCAGGGGTTAATTAACATCTTTTACCC	Cloning
3HA-2	CGGAATCTAGAGTCGACGCTGCACTGAGCAGCGTAA	Cloning
3HA-2	CCGGATATCGTCGACGGGTTAATTAACATCTTTTACCC	Cloning
3HA-2	CGGGATATCTTACTCGAGGCACTGAGCAGCGTAATCTGG	Cloning
Nost-1	CCTAAGGTACCGAATTTCCCCGATCGTTCA	Cloning
Nost-2	CGGGAATTCCCGATCTAGTAACATA	Cloning
AD379-28	TACGCAGCTGTTGTAATCCAA	Cloning
AD379-29	CATTATCCTGCAGGTCTGACATCTGGTCATC	Cloning
AD379-30	TTCCCCTCGAGATGTCAGACGCAAGAGATAA	Cloning
AD379-32	TTGAAAGTTGAAACAAAATCAATCA	Cloning
JAZ1_F	AGCTTCACTTCACCGGTTCTTGGA	qRT-PCR
JAZ1_R	TCTTGTCTTGAAGCAACGTCGTCA	qRT-PCR
JAZ9_F	TGCTGTCGAAGAACGAGGGT	qRT-PCR
JAZ9_R	CTTCCCCCATTCTCTAGCTGC	qRT-PCR
LOX3_F	CGGATAGAGAAAGAGATTGAGAAAAGGAAC	qRT-PCR
LOX3_R	GGTACACCTCTACACGTAACACCAGGC	qRT-PCR
MYC2_F	GCCGAAGGAATACACGCAAT	qRT-PCR
MYC2_R	CGGGTTGTGAACGGGCTA	qRT-PCR
VSP2_F	TAGGCTTCAATATGAGATGCTTCCAGT	qRT-PCR
VSP2_R	ACCGTTGGAAATTGTGGAAGAATG	qRT-PCR
JAZ6_A_F	GTCTGCTCAGCCGGTACTTG	qChIP/qRT-PCR
JAZ6_A_R	TTCGAGCCAACCCCATATTA	qChIP/qRT-PCR
CO_F	AAC AAT GAC CGA TCC AGA GAA	qChIP/qRT-PCR
CO_R	CCT CCT TGG CAT CCT TAT CA	qChIP/qRT-PCR
EF1_F	CCA AGG GTG AAA GCA AGA AGA	qChIP/qRT-PCR
EF1_R	CTG GAG GTT TTG AGG CTG GTA T	qChIP/qRT-PCR
MYC2_A_F	CTCTTCCGATATCTCAACTTTATGG	qChIP
MYC2_A_R	GGCGTCGGAGTTGTTTCA	qChIP
miR156C_F	TTGCGTGCTCACTGCTCTAT	qChIP
miR156C_R	AGAGAAAGTGAGAGATGGGAACA	qChIP
AT1G21300-F	TGTACCAACAACGCTCCACT	qChIP
AT1G21300_R	TTTCCAGATAGCGAAGTTGTCTT	qChIP
AT1G47860_F	CCGCGTTTGCACCATTAT	qChIP
AT1G47860_R	CCATTGCCTACACGTACCG	qChIP
DOG1_F	TCTCGAGTGGATGAGTTTGC	qChIP
DOG1_R	TCTTCATCACCGTGAGAT CG	qChIP
ERF4_F	GTTTTCTTGCCCGGATCTC	qChIP
ERF4_R	CGTTAGGAAGCGTCCTTGG	qChIP
NAC19_F	TCTTCATCGGTCGGGTAAAATCGG	qChIP
NAC19_R	TCCAAGAAACTGACCCGTTAACGC	qChIP
JAZ1_B_F	GCAGAGAAGCAACAGCAACA	qCHIP
JAZ1_B_R	TCTCGAATAGCTAAATCGATACAAAG	qCHIP
JAZ9_A_F	GTCGAGAATAATGGAACATATTAAACC	qCHIP
JAZ9_A_R	GCAATAGGACGAACACAGTTATCA	qCHIP
JAZ9_B_F	TCTTCCTCTTCTTTAAATTGGATGTT	qCHIP
JAZ9_B_R	CAAACTCTCAAATTAACGTGTTTCTC	qCHIP
LOX3_A_F	CATCACAGAAAGGTCATCACTTG	qCHIP
LOX3_A_R	TTGATCGAGAACTGTGTTGACTG	qCHIP
LOX3_C_F	TTGGTACTCAGAATCAATCAACG	qCHIP
LOX3_C_R	GGTCGTCGACGGTTGATAA	qCHIP

Supplemental Table 7: List of primers.