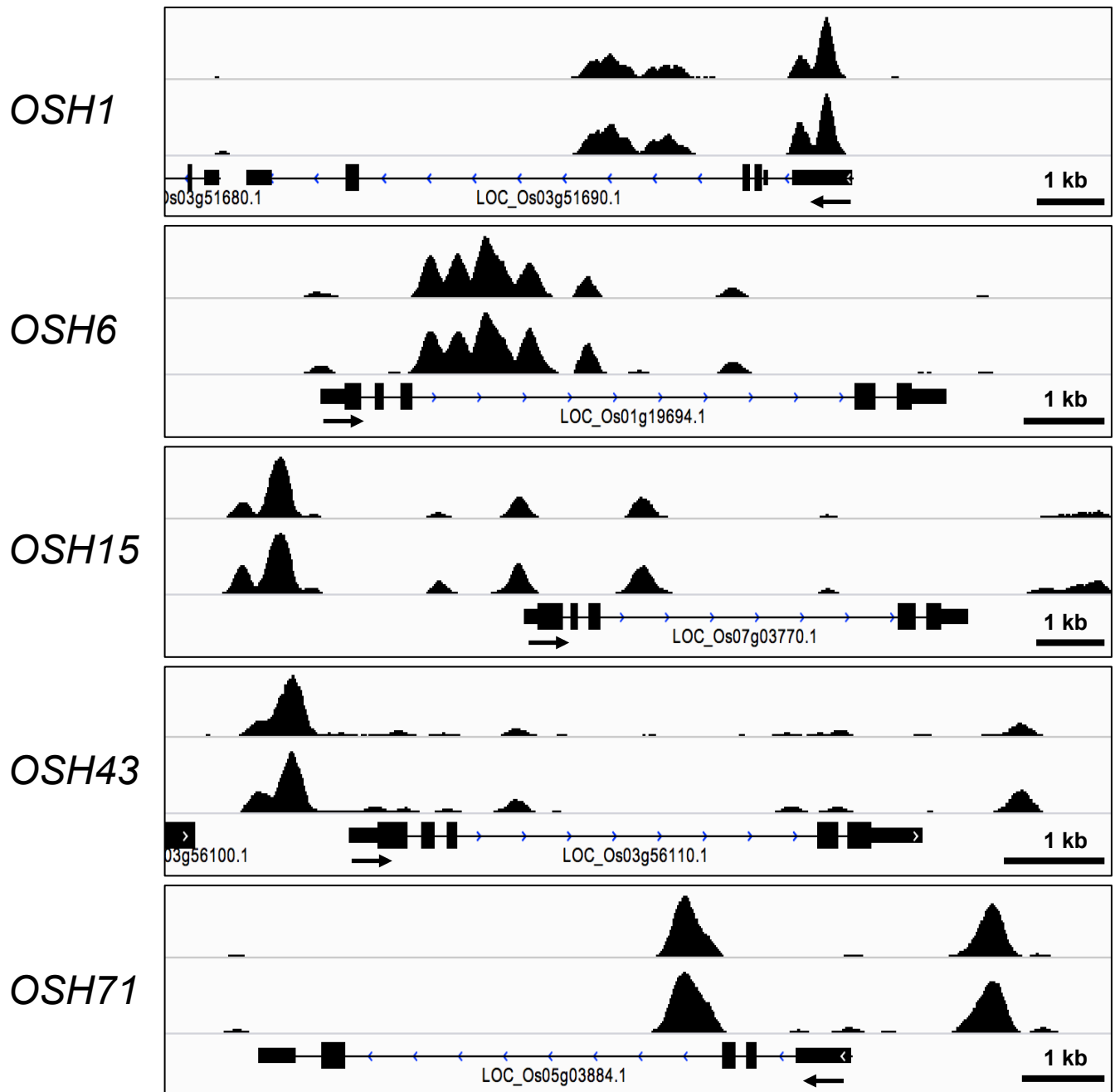
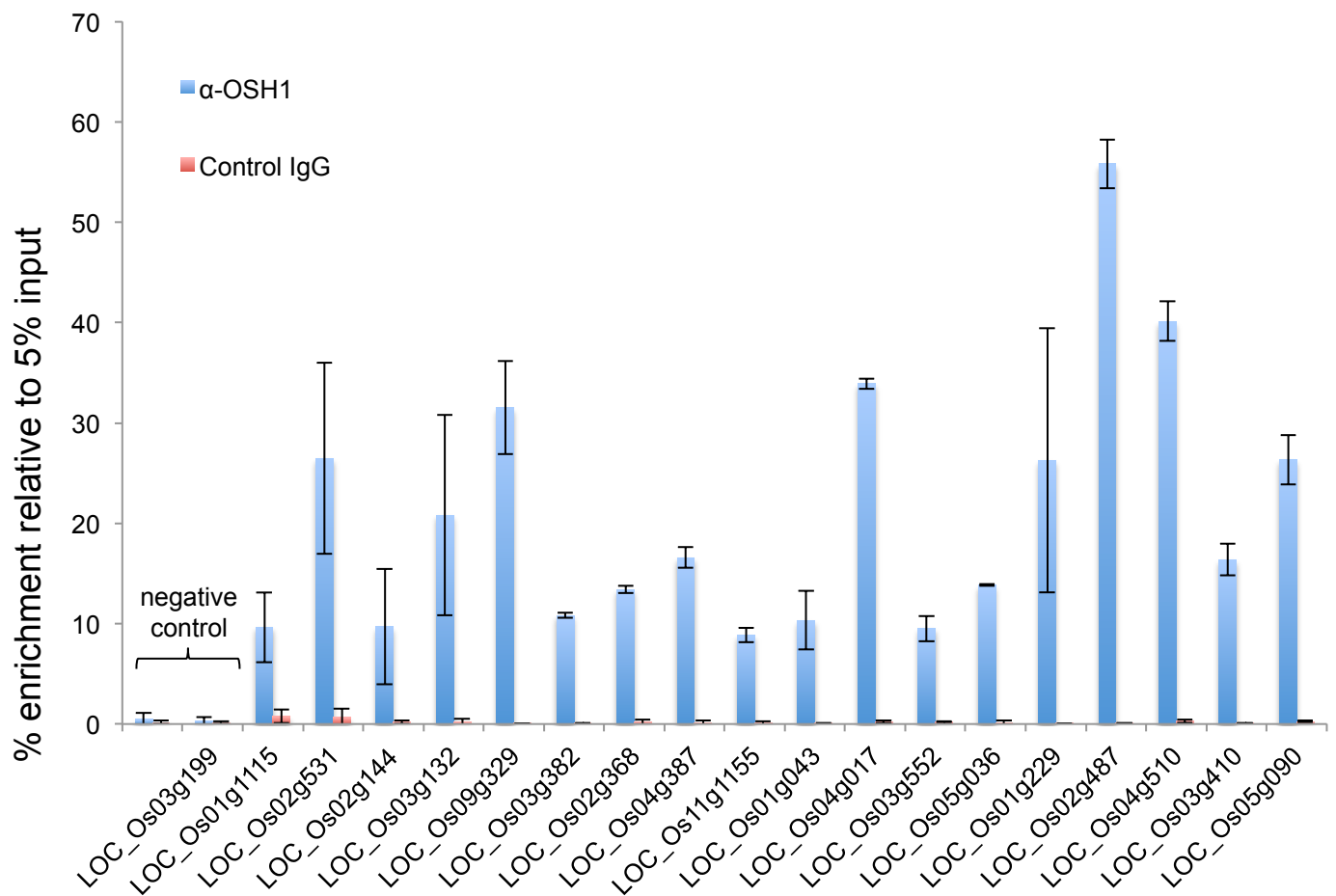


Supplemental Figure 1

**Supplemental Figure 1. OSH1 ChIP-seq data on class I *KNOX* loci.**

OSH1 ChIP-seq data from two biological replicates are shown with gene structures indicated below.

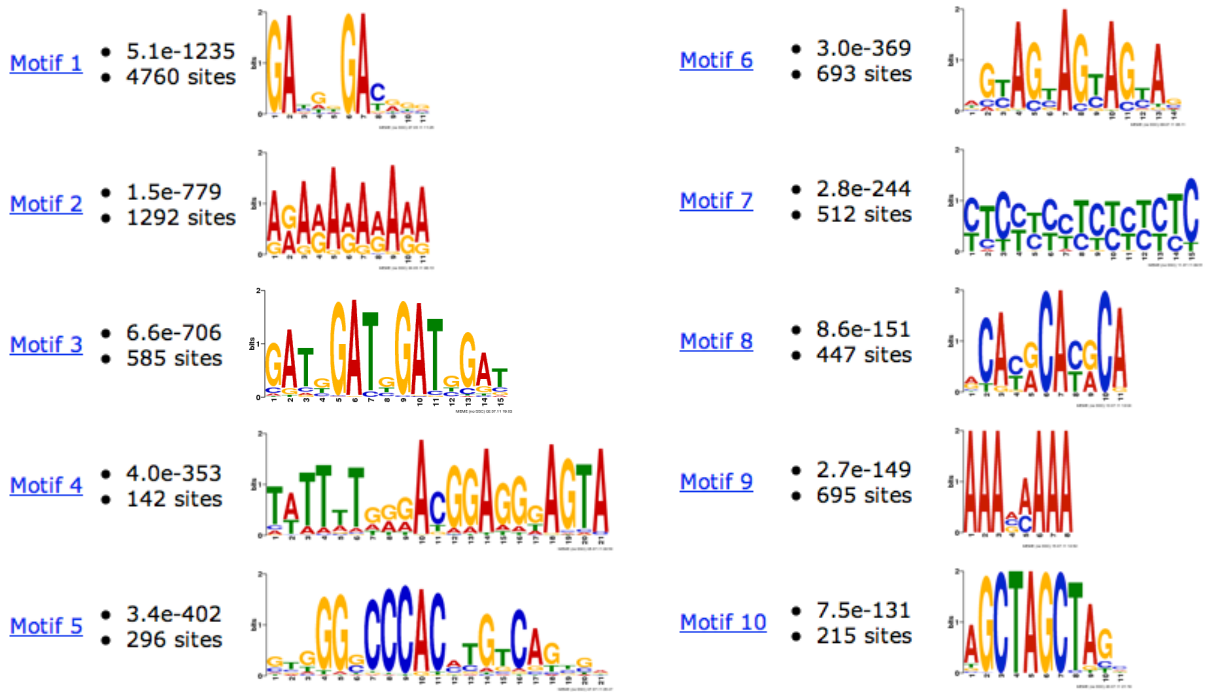
Supplemental Figure 2

**Supplemental Figure 2. Verification of OSH1-bound loci found in ChIP-seq.**

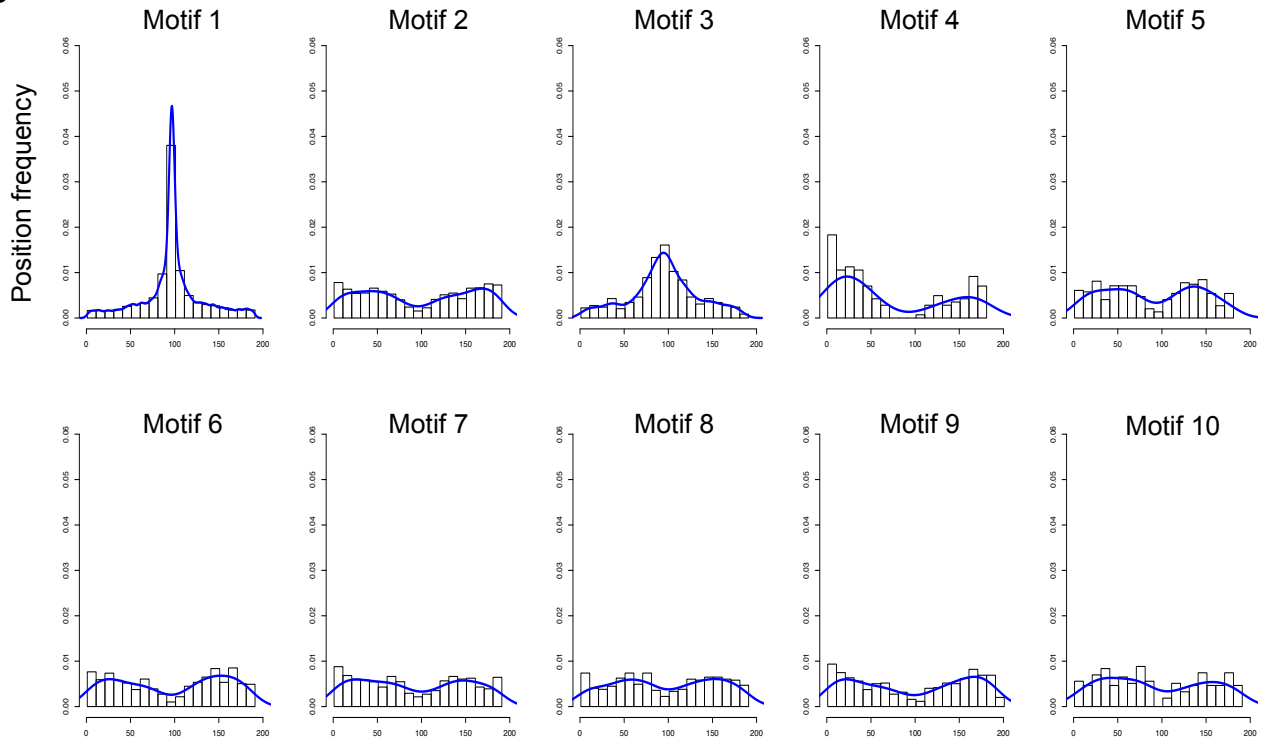
Enrichment of 18 OSH1 bound and 2 unbound loci was examined by ChIP using α -OSH1 antibody and control IgG followed by qPCR. The percentage of enrichment represents the amount of immunoprecipitated DNA relative to 5% of input DNA. Each data is the average of three biological replicates. Error bars represent the SD. Primers used in this experiment are listed in Supplemental Table 1.

Supplemental Figure 3

A



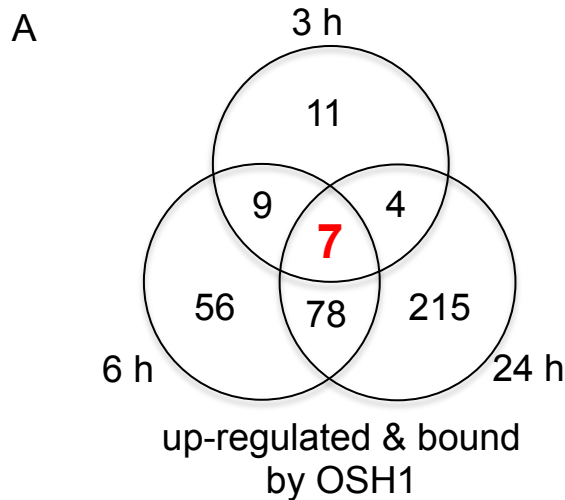
B

**Supplemental Figure 3. Motif enrichment analysis among OSH1 bound regions.**

(A) Ten highly enriched DNA motifs. *p*-values and number of the motifs found in 5,547 OSH1 binding regions are shown left to the DNA motif logos.

(B) Distribution of the motifs in 200 bp region of peaks. The peak summits were positioned in the center. Vertical axis shows the position frequency of OSH1 bound peak summits.

Supplemental Figure 4



B

Gene ID	annotation
LOC_Os01g65920	'F-BOX protein'
LOC_Os01g66120	'NAC domain transcription factor'
LOC_Os05g11210	'not assigned.unknown'
LOC_Os05g29810	'AP2/EREBP transcription factor'
LOC_Os06g39880	'misc.cytochrome P450' (CYP734A4)
LOC_Os06g46030	'not assigned.unknown'
LOC_Os08g30520	'not assigned.unknown'

Supplemental Figure 4. Seven OSH1 bound genes up-regulated in all time points after DEX induction in 35S:OSH1-GR.

(A) Venn diagram of OSH1 bound genes up-regulated in 35S:OSH1-GR. The number of OSH1 direct target genes that were up-regulated at all time points after OSH1 induction is shown in red.

(B) List of seven genes up-regulated in all time points after DEX induction.

Supplemental Figure 5

OSH1 binding peak in *CYP734A2* 3'UTR

tggcgccccacccaggttgccaagaataccctccttaaca **gaccg** **gatcaga**
 ccagcctttttaa **gattg** **atgac**acacagcaacgtggggcccactc

OSH1 binding peak in *CYP734A4* 3'UTR

cagactagtggtagc **gatcaga**gcacaacttttagg **gattg** **atggtcagaaa**
 ctctcaga **gagaga** **gaagaga**gacagtagggtagtagcagtagc

OSH1 binding peak in *CYP734A6* promoter

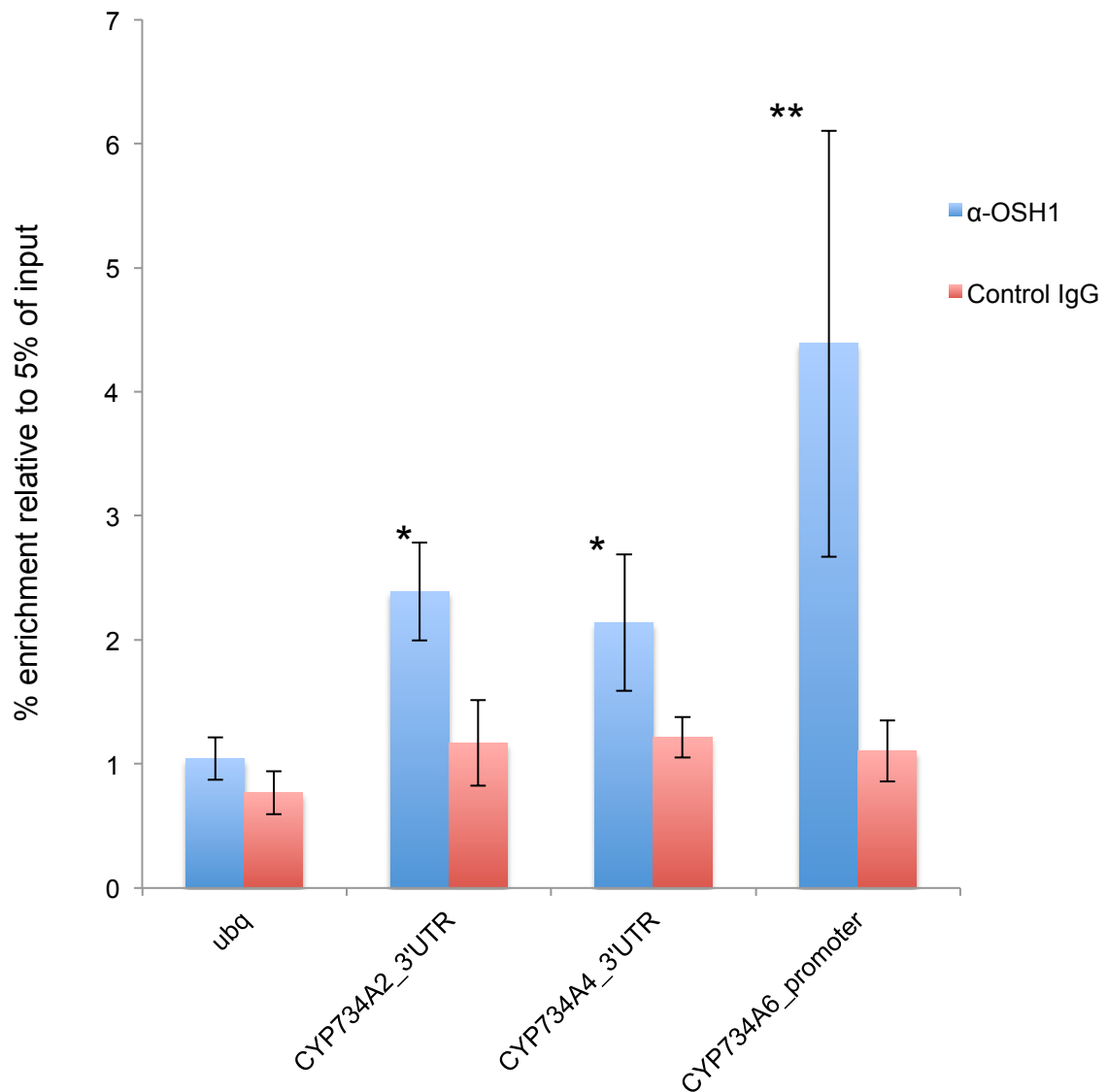
tcagccggcgccatgggcgcat **gacacga**cacgg **tcgactcga**tggtcgat
gacatgagcccat **gacac**gctcgat **gagctgatctgatctgatc**gtgaga

Supplemental Figure 5. OSH1 binding motifs found in ChIP-seq peaks at three *CYP734A* loci.

Sequences 50 bp upstream and downstream from the center of OSH1 binding peaks are represented for three *CYP734A* loci. Motif 1 (GANNNGA) shown in Figure 4C is indicated in red color with brackets.

TGAC/GTCA motif previously identified as KNOX binding site by in vitro binding assays (Smith et al. 2002) is shown in blue.

Supplemental Figure 6



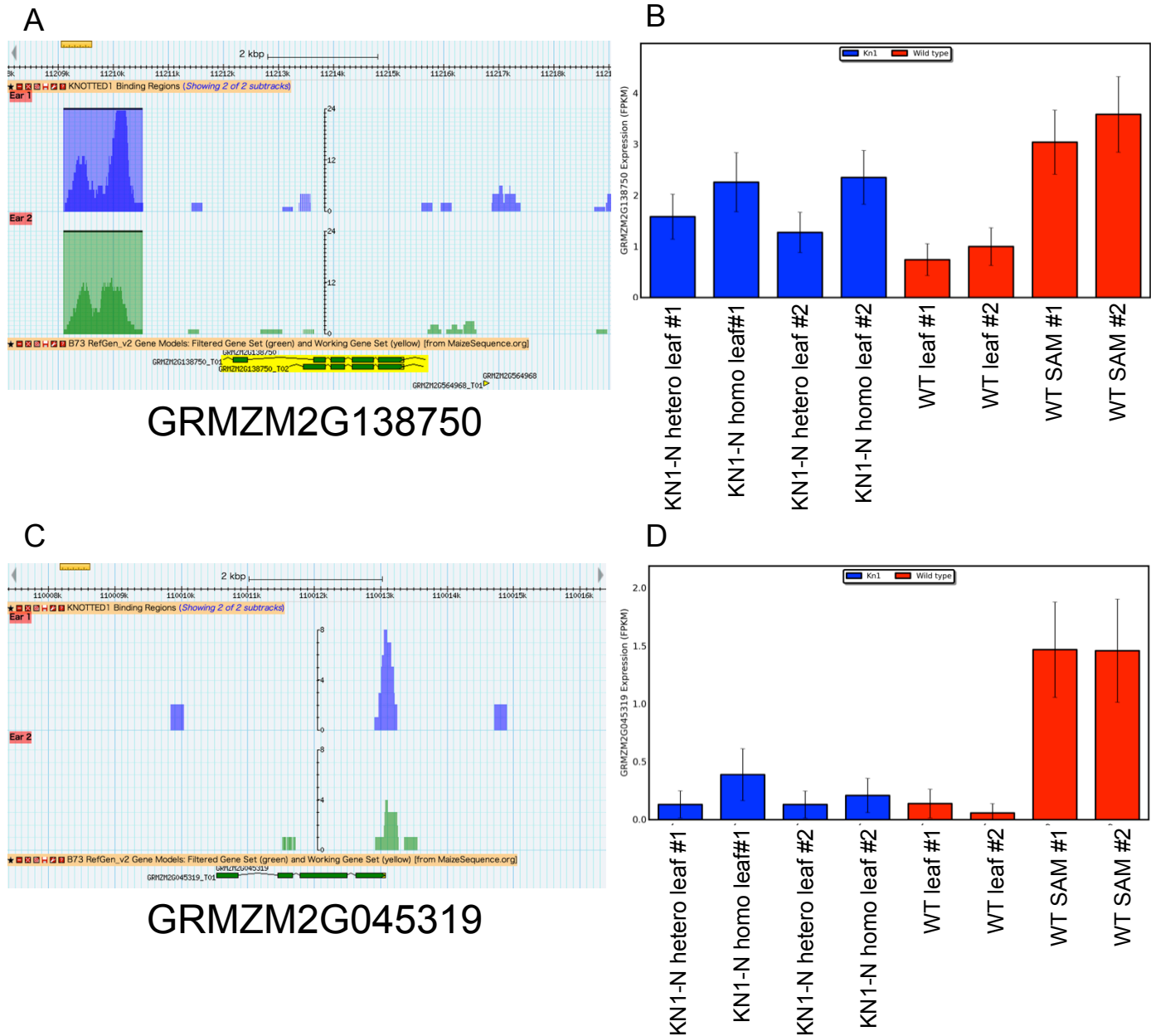
Supplemental Figure 6. ChIP assay using α -OSH1 antibody followed by qPCR on three *CYP734A* loci in 2-week-old shoot apices.

The percentage of enrichment represents the amount of immunoprecipitated DNA relative to 5% of input DNA. Each data point is the average of three biological replicates. Error bars represent the SD. Primers used in this experiment are listed in Supplemental Table 1. Asterisks indicate significant enrichment at $p < 0.05$ (*) and at $p < 0.01$ (**) compared to the control ubiquitin locus in Student's *t*-test.

Supplemental Figure 7. Expression of BR pathway genes bound by OSH1.

ChIP-seq data and RNA-seq data are shown in left and middle column. Validation of RNA-seq data by qRT-PCR is shown in right column. For expression data, vertical axis represent the relative expression level. Expression level at each time point is relative to that of before DEX treatment (0 h). For qRT-PCR, the data represent the average of three biological replicates. Error bars represent SD. Primers used in this experiment are listed in Supplemental Table 1.

Supplemental Figure 8

**Supplemental Figure 8. KN1 targets *CYP734A* genes in maize.**

(A and C) Snapshots of KN1 ChIP-seq data tracks of MaizeGDB genome browser (<http://www.maizegdb.org/>) on GRMZM2G138750 and GRMZM2G045319 are shown in (A) and in (C), respectively. Two sets of KN1 ChIP-seq data from B73 ears are indicated in the top and middle rows, and the gene structures are shown in the bottom.

(B and D) Relative expression levels of GRMZM2G138750 and GRMZM2G045319 are shown in (B) and in (D), respectively. The data were collected from maize gene expression database qTeller (<http://qteller.com/>). The data represent the average of two or three biological replicates. Error bars represent SD.

Supplemental Data. Tsuda et al. (2014). Plant Cell 10.1105/tpc.114.129122

Supplemental Table 1. Oligo nucleotide sequences used in this study

Experiment	Forward Primer	Sequence	Reverse Primer	Sequence	Target
ChIP-seq validation	KT9	AACCAGCTGAGGCCCAAGA	KT10	ACGATTGATTTAACCAGTCCATGA	ubq
	KT7	CGTACAACTTTGCAGAGCCA	KT8	TCGGAATCTCCACAAGAACC	LOC_Os03g19900
	KT1	TGGTCACTTCTGCTGTTTCG	KT2	CAAGTAACCGTGCCTTGATG	LOC_Os01g11150
	KT13	GCCCCACATGATGGAGAAA	KT14	TTTTTGTCTGTTGCTGGACTG	LOC_Os03g19900
	KT17	ATGCCAGAAACATATCGGA	KT18	GAAGGCGAGAGAGACGTTTG	LOC_Os02g14430
	KT21	CAATGCGACGTCAACTTCAT	KT22	ATGTCTGCTCCAGTCCAGT	LOC_Os03g13200
	KT33	TTGGTCTCCTCAGCTCTCGT	KT34	TTTGTGGCATAAAAATACTCCAC	LOC_Os09g32948
	KT37	CTGATGTACAGAGGCTTCAGAGG	KT38	TCATGGAACAAGATCAAAGGC	LOC_Os03g38210
	KT41	GGTAGCCAAAGGAAAGGGAC	KT42	TAGCACGTACCGCCTCTTCT	LOC_Os02g36880
	KT45	GCAGGCTCCAGAGATTTTCA	KT46	ATGGATCCTACACGGGATGA	LOC_Os04g38720
	KT49	TCCTAGATGTCTTGTCGGG	KT50	CTGTGTGGGCCACCATACTA	LOC_Os11g11550
	KT53	AATTGTCAATCGCAAATGGCT	KT54	CCTCATTGCACGAAAATGTG	LOC_Os01g04350
	KT57	TGCATTTTCACTGTCTCACTCC	KT58	GGAGTTGAATTGGCAGAAA	LOC_Os04g01740
	KT61	TGATCCATCCGATGCAGATA	KT62	AGTGCTACAGTGTTCGCTGC	LOC_Os03g55250
	KT65	GCAAATGCAATTCAGAGCAA	KT66	CTCCATGAAGGAAGAGCAGC	LOC_Os05g03640
	KT69	TTCGGACTTTCAAGCAGAA	KT70	TTCTGTGTGGTATGGTGACA	LOC_Os01g22900
	KT73	TAGGACGATATGCCAGGAGG	KT74	TGAGCACACGAGTCACTCA	LOC_Os02g48770
	KT77	AGGACACTTGAGACGTGCG	KT78	GCCGGTACATAAAAAGTAGGCA	LOC_Os04g51000
	KT85	GGTACCACGAGCTGAAGAGC	KT86	GTCCGTCCCGGTGGTAG	LOC_Os03g41060
KT89	ATCAAGTGCAGCTCAGGGAT	KT90	GAGATGCCTCACCTGTCAA	LOC_Os05g09020	
ChIP qPCR in shoot apex	KT583	ccaccaggttgccaagaat	KT584	ggcaacaaaagaagggcgag	LOC_Os02g11020 (CYP734A2) 3'UTR
	KT461	gtacgatcagagcacaacttttagg	KT462	ggggctactgctactacctactac	LOC_Os06g39880 (CYP734A4) 3'UTR
	KT671	actcgcaaggatctctctca	KT672	atcgacgtgcatgggctc	LOC_Os01g29150 (CYP734A6) promoter
qRT-PCR	KT408	ATGTGCGTAGGCCAGAACCT	KT409	GGTATAGGAGCATCAGCACTGTC	LOC_Os02g11020 (CYP734A2)
	KT410	GACAGCGGCTTCAACGACTT	KT411	AGGTTGGTGGTCTGCTGCTT	LOC_Os06g39880 (CYP734A4)
	KT412	GTTTACACCGTTCCGGCTTG	KT413	GACGTATCTGGCCGACAACC	LOC_Os01g29150 (CYP734A6)
	KT394	GGAGGAAGAAGGTAACAACAATA	KT395	tcctatctaactcgcaaaatgttc	LOC_Os03g40540 (OsBR6ox)
	KT392	CACATCGTCAACTTCCCAC	KT393	tctactagttagatggtgacg	LOC_Os01g10040 (D2/CYP90D2)
	KT396	AGAATGAGGAGAGGCTGTTTCAGT	KT397	AGTGCTAGAGCAAGGTTCTGAG	LOC_Os04g39430 (D11)
	KT388	CAAGGGTATGTTTATAGCTATGGT	KT389	GTTATTGTCTCGCCAAAGTCT	LOC_Os01g52050 (BRI1)
35S:OSH1-GR	KT694	ccctctagaATGGAGGAGATCTCCACCAC	KT695	GAA'TcccgggGCCGAGCCTGTAGAGGCCGCCGT	OSH1 coding region
	KT696	CGGCcccgggATTGAGCAAGCCACTGCAGGAG	KT697	aaaggtacctcaTTTTGATGAAACAGAAGC	GR domain
CYP734A6 reporter	KT604	ccctctagagtagtgagcaaatgctaggatg	KT607	CTTGCTCACCATcacctccaggaagccgagaac	CYP734A6 promoter
	KT608	ccgtggaggtagGGTGTAGCAAGGGCGAGGAGCTGTT	KT609	cactgacacggCTACTTGTACAGCTCGTCCATGCCG	GFP
	KT610	AGCTGTACAAGTAGccgtgtcagtgatgaggtgctg	KT611	cccggtaaccttggcgtgaactaaacacaacctatc	CYP734A6 3' region
CYP734A2 RNAi	KT469	caccATCTACGGGCATAGGTTCTTGAT	KT470	GTCGGCCTTCTCGCCTTGCTCGGC	CYP734A2

Supplemental Table 2. Summary statistics for ChIP-seq library alignment

Antibody	DRA Accession #	Read Length	Total # of Paired End Reads	Mapped Paired End Reads	% Mapping
α -OSH1	DRR000602	106	22132344	8954827	40.46
control IgG	DRR000603	106	23042540	5386883	23.38
α -OSH1	DRR000743	106	31055647	16376288	52.73
control IgG	DRR000744	106	31299193	5178433	16.54

Supplemental Table 3. Summary statistics for RNA-seq library alignment

Sample Genotype	DEX treatment (hr)	DRA Accession #	Sample name	Total Reads	Reads aligned	Reads not aligned	Alignment %
35S:OSH1-GR	0	DRA002287	KTSH001A	35884679	28545859	7338820	79.55
35S:OSH1-GR	3	DRA002287	KTSH001B	30777093	25204304	5572789	81.89
35S:OSH1-GR	6	DRA002287	KTSH001C	30557139	25093360	5463779	82.12
35S:OSH1-GR	24	DRA002287	KTSH001D	26420016	21712958	4707058	82.18
WT	0	DRA002287	KTSH001E	22139758	18335746	3804012	82.82
WT	3	DRA002287	KTSH001F	26531266	21468643	5062623	80.92
WT	6	DRA002287	KTSH001G	22912448	18853872	4058576	82.29
WT	24	DRA002287	KTSH001H	23647083	19755083	3892000	83.54
35S:OSH1-GR	0	DRA002287	KTSH002A	21058015	17457838	3600177	82.9
35S:OSH1-GR	3	DRA002287	KTSH002B	19362290	16050943	3311347	82.9
35S:OSH1-GR	6	DRA002287	KTSH002C	30120078	24726402	5393676	82.09
35S:OSH1-GR	24	DRA002287	KTSH002D	21922524	17940091	3982433	81.83
WT	0	DRA002287	KTSH002E	21522988	17873397	3649591	83.04
WT	3	DRA002287	KTSH002F	20713953	17236425	3477528	83.21
WT	6	DRA002287	KTSH002G	21114305	17662248	3452057	83.65
WT	24	DRA002287	KTSH002H	20859761	17424922	3434839	83.53