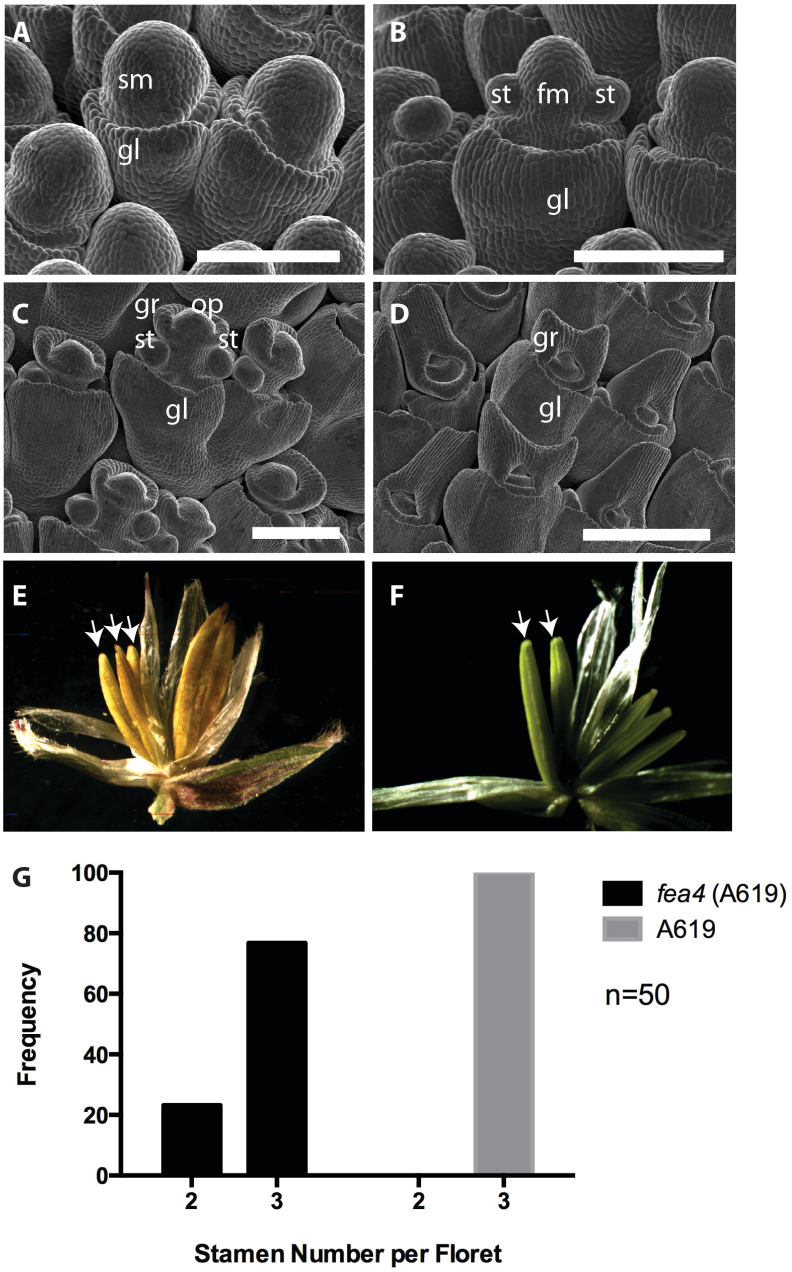

Supplemental Figure 1: *fea4* floral phenotypes. There is a normal progression of floral development in *fea4* mutants (A-D; wild type not shown). Wild type A619 male florets each contain 3 stamens (arrows, E), whereas florets of *fea4* plants introgressed into A619 frequently contain only 2 stamens (arrows, F), quantified in (G). sm= spikelet meristem; gl= glume; fm= floral meristem; st= stamen primordium; op= ovule primordium; gr= gynoecial ridge. Scale bars = 200 μm in (A,B), 250 μm in (C), and 500 μm in (D) .

A.

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PAN      1 MQSSFKTVPFTPDPYSQSSYFFRGDSCLEEFHQPVNGFHHESAIDLSPNVTIASANLHYT
FEA4     1 ----MHRQPSPHAPSSSGSWAEQGAGGYRHGRDGAT-FLLPELLQRSPNPSSKSS--SAA

PAN     61 TPDTVMDCGGGGGGGLRERLEGGEEECLDTGQLVYQKGTRLVGGGVGEVNSSWCDSVSAM
FEA4    54 TPVPPLAAAHGGGVAAPFGMAPLGVAAADEARFCMTPWS------AAAHFENWGDSG-IV

PAN    121 ADNSQHTDTSTDIDTDDKTQLNGGHQGMLLATNCSDQSNVKSSDQRTLRRLAQNREAARK
FEA4   107 VTSPLAETASTDVDMGGGGAMAQSVDG---HDNSLPACKVEPRDHKAQRRLAQNREAARK

PAN    181 SRLRKKAYVQQLENSRIRLAQLEEELKRARQQGSLVERGVSADHTHLAAGNGVFSFELEY
FEA4   164 SRMRKKAYIVELENSRSKLSHLEQELQRARQQGMFIASGRSGDHGCSTG--GALAFDLEY

PAN    241 TRWKEEHQRMINDLRSGVNSQLGDNDLRVLVDAVMSHYDEIFRLKGIGTKVDVFFMLSGM
FEA4   222 ARWLDEHQHMMNDLRVALSAQIGDDDLGVLVDGAMLHYDQMFRLKGVATRTDVFHVLSGM

PAN    301 WKTPAERFFMWLGGFRSSELLKILGNHVDPLTDQQLIGICNLQQSSQQAEDALSQGMEAL
FEA4   282 WMSPAERFFMWLGGFRSSELLKVLARHVEPLTEQQLVGICGLQQSLQQAEDALSQGMEAL

PAN    361 QQSLLETLSSASMGPNSSANVADVMGHMAMAMGKLGTLENFLRQADLLRQQTLQQLHRIL
FEA4   342 QQALGDTLAAAAT-PCAADSVTNYMGQMAVAMSKLATVENFLRQADLLRQQTLKQVRRIL

PAN    421 TTRQAARAFLVIHDYISRLRALSSLWLARPRD
FEA4   401 TTRQAARALLVISDYFSRLRALSSLWLTRPTD
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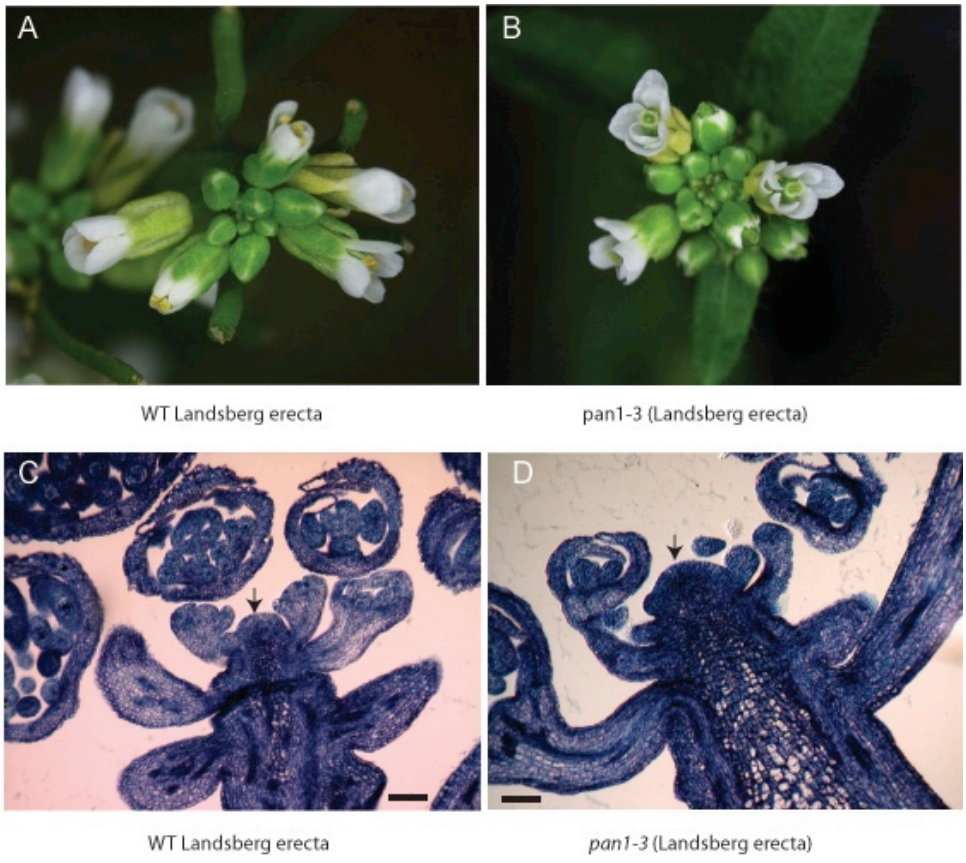
B.

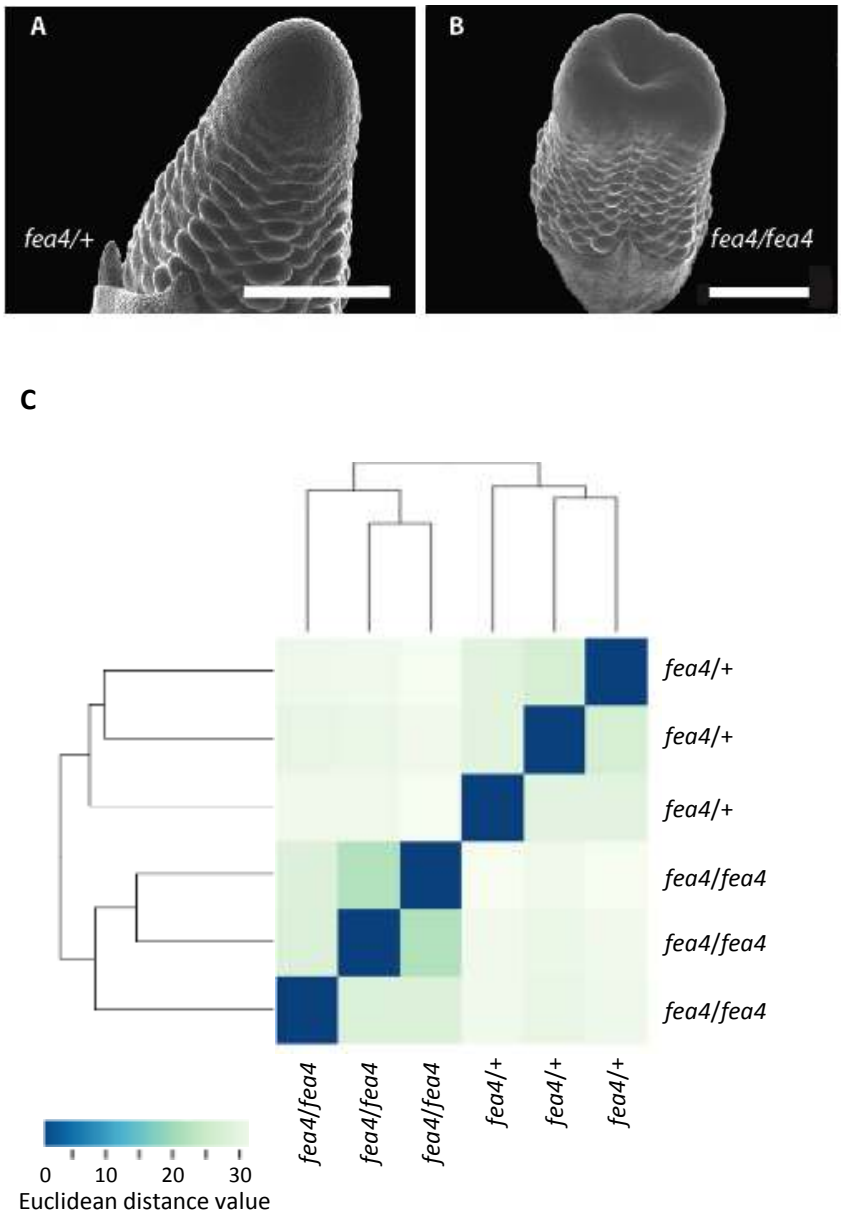
Supplemental Figure 2:

(A) A CLUSTAL alignment of FEA4 and PERIANTHIA visualized with the Boxshade program. Black boxes represent identical residues, grey boxes conservative substitutions, and white boxes non-conservative substitutions. FEA4 and PAN share approximately 59% identity.

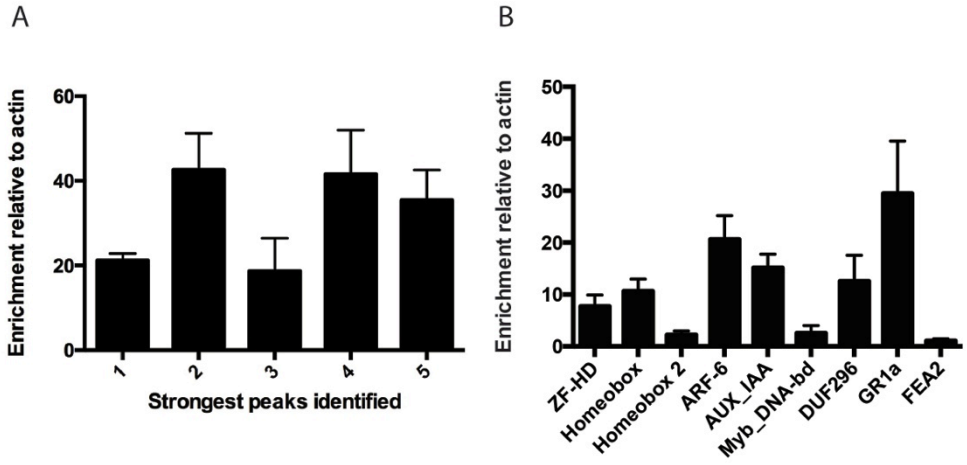
(B) Phylogenetic tree of top 100 FEA4 BLAST hits; the clade shown in Fig. 3C is indicated. Red font used to indicate location of FEA4 and PERIANTHIA sequences. Blue font used to indicate location of other maize bZIP sequences.



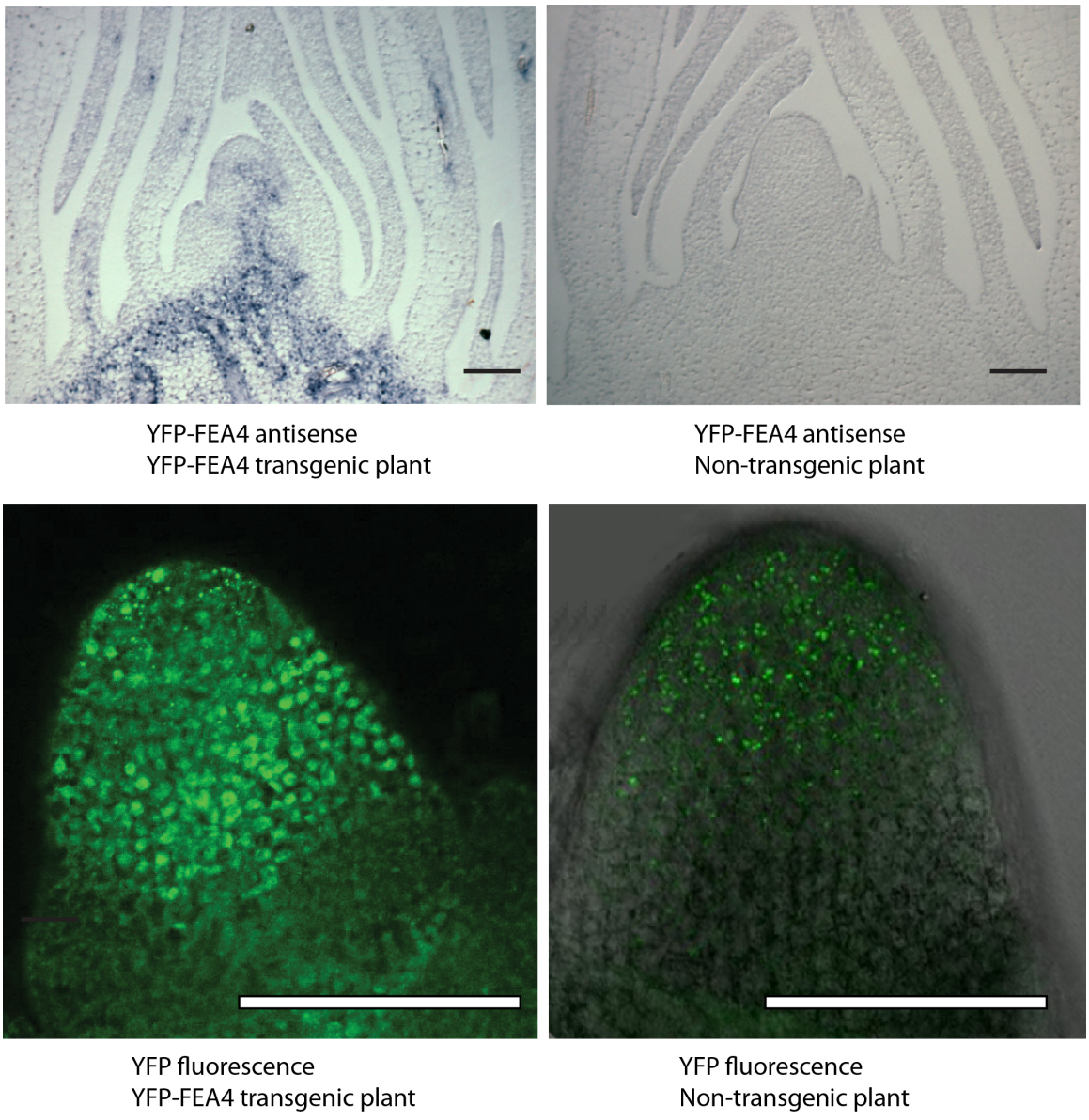
Supplemental Figure 3: Reproductive phenotypes of the *perianthia (pan)* mutant of *Arabidopsis*. Mutant flowers (B) have extra petals and sepals in the outer whorls compared to wild-type flowers (A) (Running et al., 1996). Mutant inflorescences also contain an increased number of flowers compared to the wild type, likely due to larger inflorescence meristems (C, D). *pan* meristems averaged 327 µm +/- 29 µm compared to 256 µm +/- 35 µm in wild type. Histological sections were stained with Toluidine Blue O. Scale bars = 100 µm in C and D.



Supplemental Figure 4. Three biological replicates for *fea4*/*fea4* mutant and for *fea4*/+ heterozygous "wild-type" siblings consisted of pools of >10 ~1-mm ear primordia. *fea4*/*fea4* ears have enlarged inflorescence meristems at this stage, but otherwise appear normal. Scale bars=500 □m (A-B). Biological replicates for both *fea4*/+ and *fea4*/*fea4* were closely correlated with each other. Heat map shows Euclidean distances between samples based on normalized gene expression data from DESeq analysis (C).



Supplemental Figure 5: qPCR validation of ChIP-seq peaks. Five strong peaks of FEA4 occupancy with high enrichment and low False Discovery Rate (FDR) were selected and validated (A). We also validated the enrichment of binding associated with bound and modulated targets (B). For validation, we performed three biologically replicated ChIP experiments, and each CT value used was the average of at least two technical replicates. Enrichment of bound regions relative to an actin control region was calculated by the delta CT method. The graphs represent the average enrichment +/- standard deviation. The *fea2* locus served as a negative control as no binding peaks were observed in the ChIP-seq experiments.



Supplemental Figure 6: YFP anti-sense *in situ* hybridization demonstrates concordance between mRNA and fusion protein accumulation. Apices from transgenic YFP-FEA4 plants and non-transgenic sibling plants were hybridized with a YFP anti-sense probe, which showed peripheral zone-specific expression in the transgenic plants, and no signal in the control. Scale bars = 100 μm. YFP-FEA4 protein was visualized using a Zeiss 710 confocal microscope. Note that background, punctate fluorescence is observed in the apical region of the SAM.

Supplemental Table 1: Summary of *fea4* mutant alleles.

Seven independent alleles were obtained from various sources, including Ethyl Methane Sulfonate (EMS)-induced mutagenesis, and the Trait Utility System in Corn (TUSC) population.

Name	Source	DNA	Protein	Complementation(F1)	Allelism(F2)
fea4-ref	EMS	C-T	W282➔STOP	N/A	N/A
*fea4-rel*09-5171*	EMS	G-A	Q242➔STOP	All fasciated, n=20	All fasciated, n=40
*fea4-rel*07-167*	EMS	G-A	R307➔R*	All fasciated	All fasciated n=20
fea4-369	EMS	G-A	G213➔S	All fasciated	
fea4-33	EMS	C-T	Q229➔STOP		
fea4-TUSC1	TUSC	Mu		Fasciated	
fea4-TUSC2	TUSC	Mu		Fasciated	

*** This allele has a silent mutation. No other mutations were found in the coding region of this allele.**

Supplemental Table 2. Summary statistics for RNA-sequencing and mapping.

Sample type	Biological Replicate	Mapped reads (101 bp)[a]	% mapped	% properly paired	Genes expressed (FPKM)[b]	
					≥ 0.001	≥ 1
fea4/+ (wild-type)	Rep. 1	39,148,856	61.3	82.4	25,576	21,170
	Rep. 2	36,243,349	64.2	82.2		
	Rep. 3	46,909,941	64.1	81.4		
fea4/*fea4*	Rep. 1	18,245,968	67	81.6	26,232	21,124
	Rep. 2	44,380,258	71.2	80.1		
	Rep. 3	63,213,521	71.7	79.6		

[a] 101-bp PE reads were mapped to the maize reference genome Refgen_AGPv2 using *Tophat2* and an *a priori* set of 110,028 gene models (maize Working Gene Set).
[b] Based on a Filtered Gene Set (FGS) of 39,656 high-confidence models, *Cufflinks* was used to call expressed genes. Listed are numbers of FGS genes detected with FPKMs of at least 0.001 and 1, respectively.

Supplemental Table 3: Gene expression analysis of meristem marker genes in *fea4* and wild type inflorescences.

Normalized read count averages among all samples (baseMean.Avg), wild-type biological replicates (baseMean.wt) and *fea4* mutant biological replicates (baseMean.fea4) based on DESeq analysis. These values were used in determine fold changes. Genes are deemed significantly differentially expressed at an adjusted p-value of <0.05.

Gene name	Maize Gene ID	Significant	Adjusted p-value	baseMean Average	baseMean WT	baseMean *fea4*	Fold Change
FEA4	GRMZM2G133331	no	1	108.03	106.32	109.73	1.03
CT2	GRMZM2G064732	no	0.5802	1475.85	1372.26	1579.44	1.15
KN1	GRMZM2G017087	no	1	14962.85	14966.66	14959.05	1.00
FEA2	GRMZM2G104925	no	0.6814	724.38	785.54	663.22	0.84
TD1	GRMZM2G300133	no	0.3992	452.61	542.97	362.25	0.67
WUS1	GRMZM2G047448	no	1	22.22	22.56	21.88	0.97
WUS2	GRMZM2G028622	no	1	7.42	4.95	9.90	2.00
WUS-like	GRMZM2G069028	no	1	18.26	17.37	19.14	1.10
WUS-like	GRMZM2G108933	no	0.3546	11.39	20.80	1.98	0.10
WUS-like	GRMZM2G069274	no	1	262.82	270.02	255.63	0.95
WOX3A	GRMZM2G122537	no	0.7541	593.33	678.20	508.46	0.75
WUS-like	GRMZM2G409881	no	0.9635	202.42	219.96	184.88	0.84
WUS-like	GRMZM2G133972	no	1	6.55	7.48	5.63	0.75
WUS11	GRMZM2G170958	no	0.9913	2.08	0.35	3.81	10.88
CLV1like	GRMZM2G123178	no	1	139.09	142.86	135.32	0.95
CLV1like	GRMZM2G066248	no	1	139.09	142.86	135.32	0.95
ZmCLV3	GRMZM2G315601	no	N.A.	0.00	0.00	0.00	N.A.
ZmFCP1	GRMZM2G165836	no	1	14.10	15.67	12.53	0.80

Supplemental Table 4. ChIP-seq library sequencing and alignment summary statistics.

		Reads sequenced	Reads aligned	Suppressed alignments[a]	Reads post filter	Redundant rate[b]	Called peaks[c]
rep1	ChIP	3,208,913	1,187,974 (37.02%)	1,326,255 (41.33%)	979,775	0.18	5,020
	Input	3,045,051	1,155,697 (37.95%)	1,525,800 (50.11%)	1,153,854	0	
rep2	ChIP	4,890,975	1,657,898 (39.63%)	1,693,350 (40.48%)	1,570,715	0.05	9,644
	Input	4,346,850	1,408,355 (37.44%)	1,887,325 (50.17%)	1,405,914	0	

[a] Suppressed alignments due to multiple mapping reads; only unique alignments were kept. [b] Rate of tag redundancy in ChIP-seq libraries; only unique tags were used for peak-calling with MACS v1.0.4. [c] Significance threshold for calling enriched peaks was $p < 1.0e-05$.

Supplemental Table 5: Primers used in this study.

Primer Name	Primer Sequence	Purpose
MP 510	ACTGGATTCCTTGGGAAGGT	CAPS marker for mapping
MP 511	TGGAGTGCACAATCCACAAT	CAPS marker for mapping
MP 516	GCATCCACTTTAGCTTCTGGA	CAPS marker for mapping
MP 517	CGACAACTGGTTCTGTTACCAA	CAPS marker for mapping
MP 900	TGATCCTGTGCAATGTAAAGC	*fea4-ref* genotyping (Cac8I)
MP 901	CAGCTGCTGCTCCGTCAG	*fea4-ref* genotyping (Cac8I)
FEA2-D	AACCTGCAGTCCCTGCCTCCA	*fea2-o* genotyping
FEA2-ASA	AATAGGTCAGGTTCCCTATC	*fea2-o* genotyping
Mu58	CCAWSGCCTCYATTTCGT	*fea2-o* genotyping
MP 815	ATGCATCGTCAGCCATCTC	*fea4* full length probe
MP 816	TCAATCCGTCGGCCGCGTC	*fea4* full length probe
MP 833	TCCCATTCGAAAACAAAAGC	*fea4* short probe
MP 834	GAAGCTCCTGCTCAAGATGG	*fea4* short probe
MP 220	GGGGACAAGTTTGTACAAAAAAGCAGG-CTTCATAAATTTGATTTAGGGGGTGTT	YFP-FEA4 construction
MP 201	GGGGACAACTTTTGTATACAAAGTTGT-CATCGGGCACGGATCAGAGCG	YFP-FEA4 construction
MP 202	GGGGACAACTTTTCTATACAAAGTTGTC-ATGCATCGTCAGCCATCTC	YFP-FEA4 construction
MP 203	GGGGACAACTTTATTATACAAAGTTGT-GCACCGAAATCGCTCTACTC	YFP-FEA4 construction
MP 204	GGGGACAACTTTGTATAATAAAGTTGTC-TCTGTATCCGTTGTGAGATGG	YFP-FEA4 construction
MP 205	GGGGACCACTTTGTACAAGAAAGCTGGGT A- GCGAAAGCAAACATTAAATCA	YFP-FEA4 construction