

Supplemental Figure 1. Alignment of ZIX C-terminus with the Ataxin-10 related domain pfam09759 of other eukaryotes

Red residues: highly conserved, blue residues: moderately conserved.

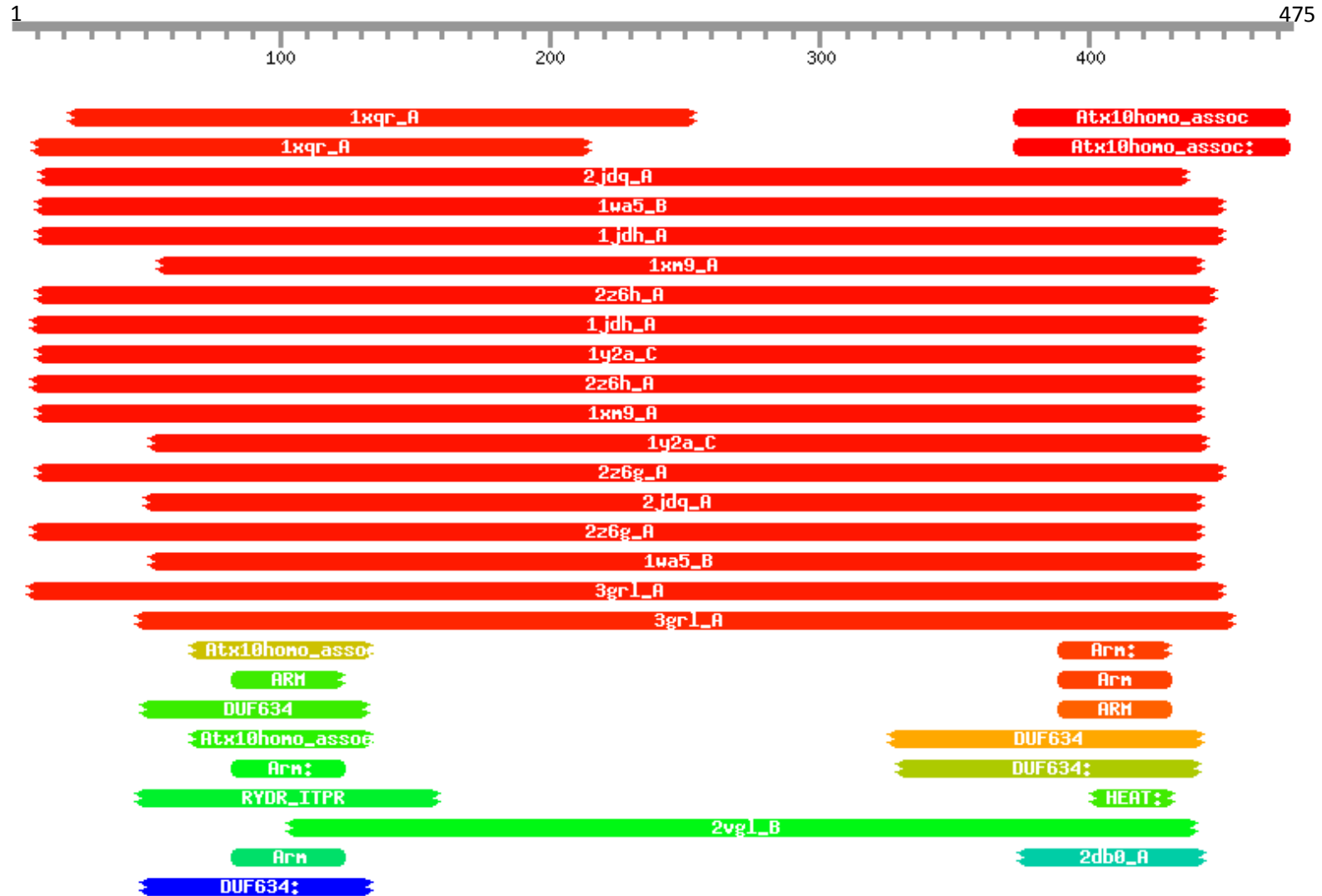
		10	20	30	40	50	60	70	80	
	*.....*.....*.....*.....*.....*.....*.....*.....								
ZIX	372	GFRRDIVSVIGNCAYRRKEVQDEIRERDG-LFLMLQQCVTDDENPFLREWGLWCIRNLLLEGNPENQEVVAELEIKGS--V	448							
gi 122016228	197	GYRTEHMRLMANLTLDNVEACSFIVSNSALLAAVLTSTRFDEENPGMVEWAEFCIRNLCCTKEAHEKIRRLMPVGIsdE	276							
gi 1351646	324	GVKRECVRFIAFICSKFSTAPDLVRHFNG-VALIISQANYDDWNPYIREISVLCRLLQNNIENQKIIGGLTPITT--T	400							
gi 74670950	807	NLKKLVVLVLSLWKCPEVQDQIRRHGG-VETILSCTNFDAHNPYIKEHAVMCLKFLLEGNRENQKLVEALEAREVvrD	885							
gi 74606966	420	GIKCFLVELLGFMSYEQKDVQDSVRELHG-LELVLSNCIIIDNPNPFIKERICICIRYLLANNSTNQEFISQLEAKKA--V	496							
gi 74695766	419	ECKSLIIIEILGFLT YKNREVQDKCRELHG-LELVLSNCVIDDNDPFIKERSIMCIRFLLKDNKENQNFVANLESKRV--A	503							
gi 74608914	427	ECKLLIIIEIIAMLT HENREIQNQVRELGG-LGVILSNCVIDDNDPFIKERSIMCIRFLLKDNKENQNFVANLESKRV--A	503							
gi 140514	445	HCKLVIIEILASLVYAHPEIQDQIRELGG-LALILSNCVIDDNDPFIKERSIVCLKFLKKNNAKNQEVVKMEAQDV--V	521							
gi 74627407	363	SVKTNIIITILSYLSYDSFQFQEKIRELGG-LSLVLSNCIIIDNPNPFIKERQAIIVCLKYLLQKNPKNQQFVADLEAKKV--V	439							
gi 74601194	381	QVKSLIIIEVIAFLVHGSFEIQEKMRELHG-LELVLSNCMIIDNNDPFIKERAIIVCVKFLLANNEKNQQFVADLEAKQT--V	457							
gi 75151733	361	GYRRDVVAVIANCLHRSKVKQDEVRLHDG-IILLLQQCVVDEENPYLREWGLFAVKNLLEGNNEENQKEVSGLKMQEA--V	437							
gi 74858970	499	GFKIELIRILGNLSYKNRGNQDEIRELGG-IEIILNHCRFDVNNPYIKESVFAIRNLCEDNVENQNLIESLKVKGV--A	575							
gi 82178990	379	GFKAHLIRLIGNLICYQNKENQEKVYQLDG-IALILDNCSIDNPNPFLNQWAVFAIRNLTENNNDKNQELIASMERQGL--A	455							
gi 122144951	369	GFKSHLIRLIGNLICYKNKDNQDKVNELDG-IPLILDNCSIDNPNPFLNQWAVFAIRNLTENNNDKNQELIASMERQGL--A	445							
gi 122093877	348	SLKSSLVKALVNLSYKNKKNQNLARDMQI-MAAILECTNLDARNPLIKESVILAIRNLCDDNLENQKVASLTKVGD--A	424							
gi 74685004	431	NLKRDLVRLLGVLTFNDTRVGDQVREYEG-VQLVLSLSTEIDEGNPFLREHALFCIRNLMMLNPNANQAIKEMDPVGV---	506							
gi 74830132	196	GFRRHVRLVANLTYENKEVCSAVLGDTRLTLTAI LGATRIDLENPGMGEWATFVIRNLCYCSNEAREILRGLTPISIV-E	274							
gi 75036035	198	GFKTECMRLIANLTHNNVDVNAALVERDTfLNFNLSATQIDEENPGMVEWAEFALRNICESAAAREKIRKLAPQGV--T	275							
gi 122160642	468	GYRVDLIAIIGNASFNRAQVCDLVVSLGG-VPMVLNHTRGEDGEAYLREWALWAVRNMTEVSDAARQKIEIQPQAV--E	544							
gi 24654554	255	ELKTLVRCANLLYDNKANKGYCLDTQL-LPTLLECTTMDARNPLMREWSILAIRNACINCPEAQQVIAGLTMQGS--A	331							
		90	100							
	*.....*.....*.....								
ZIX	449	DVPQLREIGLRVEIDPKtARPKLVNd	474	(Arabidopsis thaliana)						
gi 122016228	277	SKELLSSGRVDCHLNSE-GKLVLSNP	301	(Trypanosoma cruzi)						
gi 1351646	401	HSDALEEAGFTSYINDK-GKVVLQPK	425	(Saccharomyces pombe)						
gi 74670950	886	ENGLLERSGFEAVIDKT-GKLAIRPK	910	(Aspergillus fumigates)						
gi 74606966	497	DGDVLKKAGYKVDIDGK-GNIKLTAD	521	(Kluyveromyces lactis)						
gi 74695766	496	NDDVLAEEAGYEVKVGAD-GKIGLTKN	520	(Eremothecium gossypii) (Ashbya gossypii)						
gi 74608914	504	NDETLEAGYEVDISKD-GKLSLKST	528	(Candida glabrata)						
gi 140514	522	QDDALSKAGFEISVEKG-GKVRVLSK	546	(Saccharomyces cerevisiae)						
gi 74627407	440	DDQVLSEVGQVEV-ID-GKVAVKRK	463	(Candida albicans)						
gi 74601194	458	DDDALKEVGYEVI-ED-GNVKLRKT	481	(Debaryomyces hansenii)						
gi 75151733	438	ITPEIADIGLRVEIDKEtGHPKLVNN	463	(Oryza sativa)						
gi 74858970	576	NNDELKDLGLEVGVTEN-GTIKFKNV	600	(Dictyostelium discoideum)						
gi 82178990	456	DSSLLKSMGLQAEERD-GKLLLKSV	479	(Xenopus (Silurana) tropicalis)						
gi 122144951	446	DASLLKMGFEVEK-RG-DKLILKST	469	(Bos Taurus)						
gi 122093877	425	ENSLLTEYNSAG-----GTIRIKDS	444	(Aedes aegypti) (Stegomyia aegypti)						
gi 74685004	507	----LSETGELLPV--P-DKMKKKSI	525	(Filobasidiella neoformans) (Cryptococcus neoformans)						
gi 74830132	275	EAEDELFGKAVDPHATPE-GRSAMEPL	299	(Trypanosoma brucei)						
gi 75036035	276	DQSREILAGRCSYSFSStGKVQLHTQ	301	(Leishmania major)						
gi 122160642	545	ESEELLAKGLDVELNREtGRPRVVKR	570	(Ostreococcus tauri)						
gi 24654554	332	PNDILTELNLDM-----GALRISDR	351	(Drosophila melanogaster)						

Supplemental Figure 2. Predicted secondary structure of ZIX by HHpred based on sequence alignment with proteins of known structures.

Six representative hits (1, 3, 5, 21, 22, 23) were selected to show secondary structure alignment below the graphic presentation.

Query ZIX (seq=MEASLP EEVL...TARPKLVNDT Len=475 Neff=4.0 Nseqs=45)

Parameters score SS:yes search:local realign with MAP:no



Supplemental Data. Ngo et al. (2012). Plant Cell 10.1105/tpc.112.102384

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
<input type="checkbox"/> 1	pfam09759	Atx10homo_assoc Spin	100.0	7.7E-42	0	294.8	11.0	102	372-474	1-102 (102)
<input type="checkbox"/> 2	PF09759	Atx10homo_assoc: Spin	100.0	9.8E-40	2.2E-44	283.0	8.9	103	372-474	1-105 (105)
<input type="checkbox"/> 3	2jdg A	Importin alpha-1 subuni	98.9	2E-06	4.6E-11	85.7	27.7	324	11-436	23-353 (450)
<input type="checkbox"/> 4	lwa5 B	Importin alpha subunit;	98.8	1.1E-06	2.6E-11	90.1	25.0	341	10-449	89-431 (530)
<input type="checkbox"/> 5	ljdh A	Beta-catenin; beta-cate	98.8	8.3E-07	1.9E-11	90.0	21.7	337	10-449	22-358 (529)
<input type="checkbox"/> 6	lxm9 A	Plakophilin 1; armadill	98.7	4.3E-07	1E-11	86.9	16.3	355	55-441	7-370 (457)
<input type="checkbox"/> 7	2z6h A	Catenin beta-1, beta-ca	98.7	1.6E-06	3.6E-11	92.2	21.2	334	10-446	19-352 (644)
<input type="checkbox"/> 8	ljdh A	Beta-catenin; beta-cate	98.7	1.1E-05	2.6E-10	81.8	25.3	407	8-442	62-500 (529)
<input type="checkbox"/> 9	ly2a C	SRP1-alpha, importin al	98.6	5.4E-05	1.3E-09	73.4	26.7	330	10-441	9-349 (428)
<input type="checkbox"/> 10	2z6h A	Catenin beta-1, beta-ca	98.6	1.4E-05	3.2E-10	85.0	23.5	408	8-441	59-496 (644)
<input type="checkbox"/> 11	lxm9 A	Plakophilin 1; armadill	98.5	4.3E-05	1E-09	73.2	21.6	387	10-441	7-417 (457)
<input type="checkbox"/> 12	ly2a C	SRP1-alpha, importin al	98.4	0.00018	4.1E-09	69.8	25.4	299	52-443	9-308 (428)
<input type="checkbox"/> 13	2z6g A	B-catenin; FULL-length,	98.4	1.7E-05	3.9E-10	87.2	20.3	337	10-449	155-491 (780)
<input type="checkbox"/> 14	2jdg A	Importin alpha-1 subuni	98.2	0.00068	1.6E-08	67.7	23.4	295	50-441	20-316 (450)
<input type="checkbox"/> 15	2z6g A	B-catenin; FULL-length,	98.1	0.00062	1.4E-08	75.0	23.2	406	8-441	192-632 (780)
<input type="checkbox"/> 16	lwa5 B	Importin alpha subunit;	97.8	0.0028	6.6E-08	65.3	21.3	293	52-441	89-381 (530)
<input type="checkbox"/> 17	3grl A	General vesicular trans	97.6	0.018	4.1E-07	63.7	25.1	359	7-449	24-413 (651)
<input type="checkbox"/> 18	lxqr A	HSPBP1 protein; armadil	97.6	0.0017	4E-08	63.1	15.0	225	22-253	56-291 (296)
<input type="checkbox"/> 19	lxqr A	HSPBP1 protein; armadil	97.5	0.0026	6.1E-08	61.8	14.9	200	9-214	86-289 (296)
<input type="checkbox"/> 20	3grl A	General vesicular trans	96.8	0.023	5.4E-07	62.7	14.8	325	47-453	21-365 (651)
<input type="checkbox"/> 21	PF00514	Arm: Armadillo/beta-c	94.7	0.065	1.5E-06	37.3	4.6	40	388-429	1-40 (41)
<input type="checkbox"/> 22	pfam00514	Arm Armadillo/beta-c	94.6	0.062	1.5E-06	37.7	4.4	41	388-430	1-41 (41)
<input type="checkbox"/> 23	smart00185	ARM Armadillo/beta-	91.9	0.28	6.6E-06	34.4	4.1	41	388-430	1-41 (41)

Supplemental Data. Ngo et al. (2012). Plant Cell 10.1105/tpc.112.102384

```

Q ss_pred          ccCCCCHHHHHHHHHHHHHHhCCHHHHHHHHHhCccccCcC
Q ZIX              410 TDDENPFLREWGLWCIRNLLLEGNPENQEVVAELEIKGSVD 449 (475)
Q Consensus        410 ~D~Np~lreW~i~aiRnL~e~n~nQ~Ia~le~qg~ 449 (475)
                   .+..++-+++..+++++|++..++..+....-.....|.++
T Consensus        319 ~~~~~v~~~a~~aL~~L~~~~~i~~~~~ 358 (529)
T ljdh_A           319 RAGDREDITEPAICALRHILTSRHQEAEMAQNAVRLHYGLP 358 (529)
T ss_dssp          HHTTCHHHHHHHHHHHHHHTSSSTTHHHHHHHHHHTCCHH
T ss_pred          hhhhhhhhHHHHHHHHhhhhccccchhhhhhhHHhccCch

```

No 21

>[PF00514](#) Arm: Armadillo/beta-catenin-like repeat; InterPro: The armadillo (Arm) repeat is an approximately 40 amino acid long tandemly repeated sequence motif first identified in the Drosophila melanogaster segment polarity gene armadillo involved in signal transduction through wingless. Animal Arm-repeat proteins function in various processes, including intracellular signalling and cytoskeletal regulation, and include such proteins as beta-catenin, the junctional plaque protein plakoglobin, the adenomatous polyposis coli (APC) tumour suppressor protein, and the nuclear transport factor importin-alpha, amongst others . A subset of these proteins is conserved across eukaryotic kingdoms. In higher plants, some Arm-repeat proteins function in intracellular signalling like their mammalian counterparts, while others have novel functions . The 3-dimensional fold of an armadillo repeat is known from the crystal structure of beta-catenin, where the 12 repeats form a superhelix of alpha helices with three helices per unit . The cylindrical structure features a positively charged groove, which presumably interacts with the acidic surfaces of the known interaction partners of beta-catenin. ; PDB: [2bct](#) [1jpp](#) [A](#) [li7x](#) [C](#) [lmle](#) [A](#) [li7w](#) [A](#) [3bct](#) [1v18](#) [A](#) [1jpw](#) [B](#) [1th1](#) [B](#) [1qz7](#) [A](#)
Probab=94.70 E-value=0.065 Score=37.34 Aligned_cols=40 Identities=20% Similarity=0.281 Sum_probs=0.0

```

Q ss_pred          ChhhHHHHHhCCcHHHHhCccCCCHHHHHHHHHHHHHh
Q ZIX              388 RKEVQDEIRERDGLFLMLQQCVTDDENPFLREWGLWCIRNLL 429 (475)
Q Consensus        388 ~~~~qd~vr~l~Gi~liL~c~D~Np~lreW~i~aiRnL~ 429 (475)
                   +++++..+..+..+|||.+++.=. .+|-+++|=..|++|++
T Consensus        1 ~~~~~i~~~g~i~~l~~L~~~~~v~~~a~~~L~nl~ 40 (41)
T PF00514_consens 1 SPENRQAITI EAGALPALVQLLK--SSDEEVQENAAWALS NLA 40 (41)
T ss_dssp          SHHHHHHHHTTTHHHHHHHHTT--SSSHHHHHHHHHHHHH
T ss_pred          CcHHHHHHHhCCcHHHHHHhC--CCCHHHHHHHHHHHhC

```

No 22

>[pfam00514](#) Arm Armadillo/beta-catenin-like repeat. Approx. 40 amino acid repeat. Tandem repeats form super-helix of helices that is proposed to mediate interaction of beta-catenin with its ligands. CAUTION: This family does not contain all known armadillo repeats.
Probab=94.62 E-value=0.062 Score=37.72 Aligned_cols=41 Identities=20% Similarity=0.262 Sum_probs=0.0

```

Q ss_pred          ChhhHHHHHhCCcHHHHhCccCCCHHHHHHHHHHHHHh
Q ZIX              388 RKEVQDEIRERDGLFLMLQQCVTDDENPFLREWGLWCIRNLL 430 (475)
Q Consensus        388 ~~~~qd~vr~l~Gi~liL~c~D~Np~lreW~i~aiRnL~e 430 (475)
                   +++++..+..+..+|||.+.+.+. .+~+~+~+~+~+..|++|+|.
T Consensus        1 ~~~~~v~~~g~v~~Lv~lL~~~~~v~~~a~~aL~nL~ 41 (41)
T pfam00514       1 SPENKQAVIEAGALPPLVQLLS--SPDEEVQEEAAWALS NLA 41 (41)
T ss_pred          CcHHHHHHHhCCcHHHHHHhC--CCcHhHHHHHHHHHHhC

```

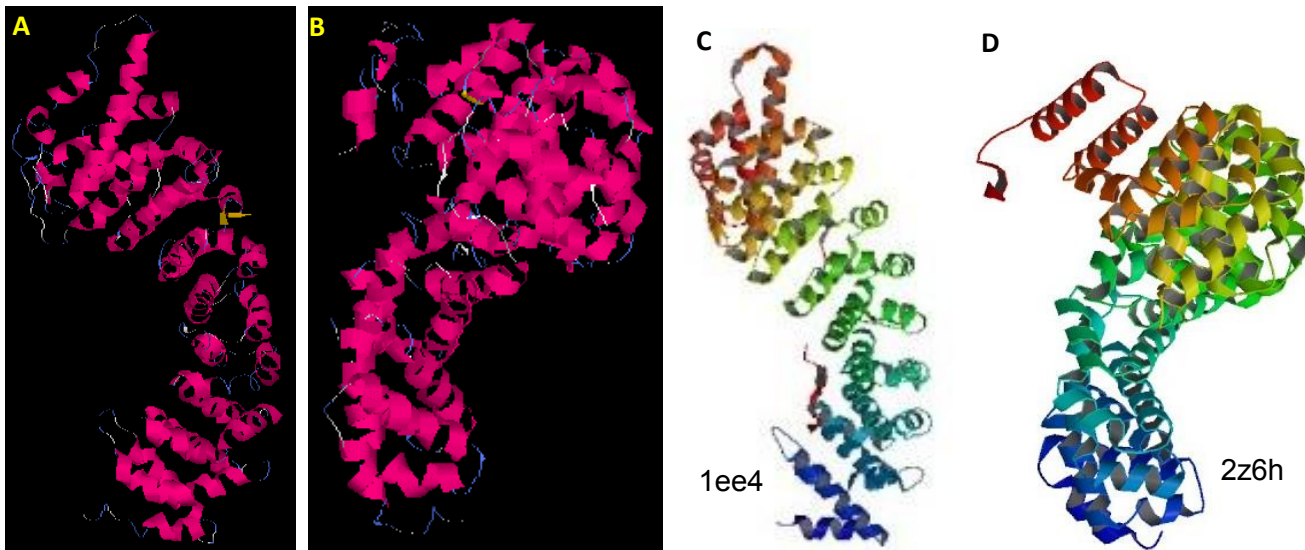

Supplemental Figure 3. Identification of Arm repeats in ZIX

Putative ZIX Arm repeat motifs were aligned with known Arm repeats of two proteins with crystal 3-D structure (yeast importin- α and mouse β -catenin) and with the consensus pfam00514 and smart00185 protein domains.

H1	H2	H3	
Yeast importin-α (SRP1)			
HRPPIDVVI	QAGV VPRLVEFMR-ENQP	EMLQLEAAWALTNIA	
TSAQTKVVV	DADA-VPLFIQLLY--TGS	VEVKEQAIWALGNVA	
DSTDYRDYV	LQCNAM EPIILGLFN--SNK	PSLIR TATWTL SNLC	
PQEAIQAVI	DVR-IPKRLVELLS--HES	TLVQTPALRAVGNIV	
NDLQTQVVI	NAG-VLPALRLLLS--SPK	ENIKKEACWTISNIT	
NTEQIQAVI	DANL-IPPLVKLLEV--AE	YKTKKEACWALSNAS	
RPDIIRYLV	SQG-CIKPLCDLLEIA--D	NRIIEVTLDALENIL	
Mouse β-catenin			
NYQDDAELA	TR--AIP ELTKLLN--DED	QVVVNKAAVMVHQLS	
KEASRHAIM	RSPQM VSAIVR TMQ-NTND	VE TARCTAGT LHNLS	
CSSNKPAIV	EAG-GMQALGLHLT--DPS	QRLVQNC LWT LRNLS	
NQESKLIIL	ASG-GPQALVNIMR-TYTY	EKLLWTT SRVLKVL S	
DKEAAEAIE	AEG-ATAPL TELLH--SRN	EGVATYAAAVLFRMS	
QEGAKMAVR	LAG-GLQKMVALLN--KTN	VKFLAITTDCLQILA	
AEMAQNAV R	LHY-GLPVVKLLH-PPSH	WPLIKATVGLIRNLA	
HREGLLAIF	KSG-GIPALVKMLG--SPV	DSVLFYAITTLHNLL	
NYKNKMMVC	QVG-GIEALVRTVLRAGDR	EDITEPAICALRHLLT	
CPANHAPLR	EQG-AIPRLVQLLV RGVRM	EEIVEGCTGALHILA	
pfam00514			
SPENRQAI I	EAG-AIPALVQLLK--SSD	EEVQENAAWALS NL	
smart00185			
DEKQQAVVD	AG--GLPALV ELLK--SED	EEVVKEAAWALS NLS	
ZIX			
SDLASKSIL	P---SILRLIQLLP-YPSS	RHYLNLSLKVLRNLC	(33-79)
VSNQNSFVD	HD--GSAIVSDLLDSA IAD	FETVRFGLQVLANVV	(83-122)
RKEVQDEIR	ERD-GLFLMLQQCVTD DEN	PFLEWGLWCIRNLL	(388-429)

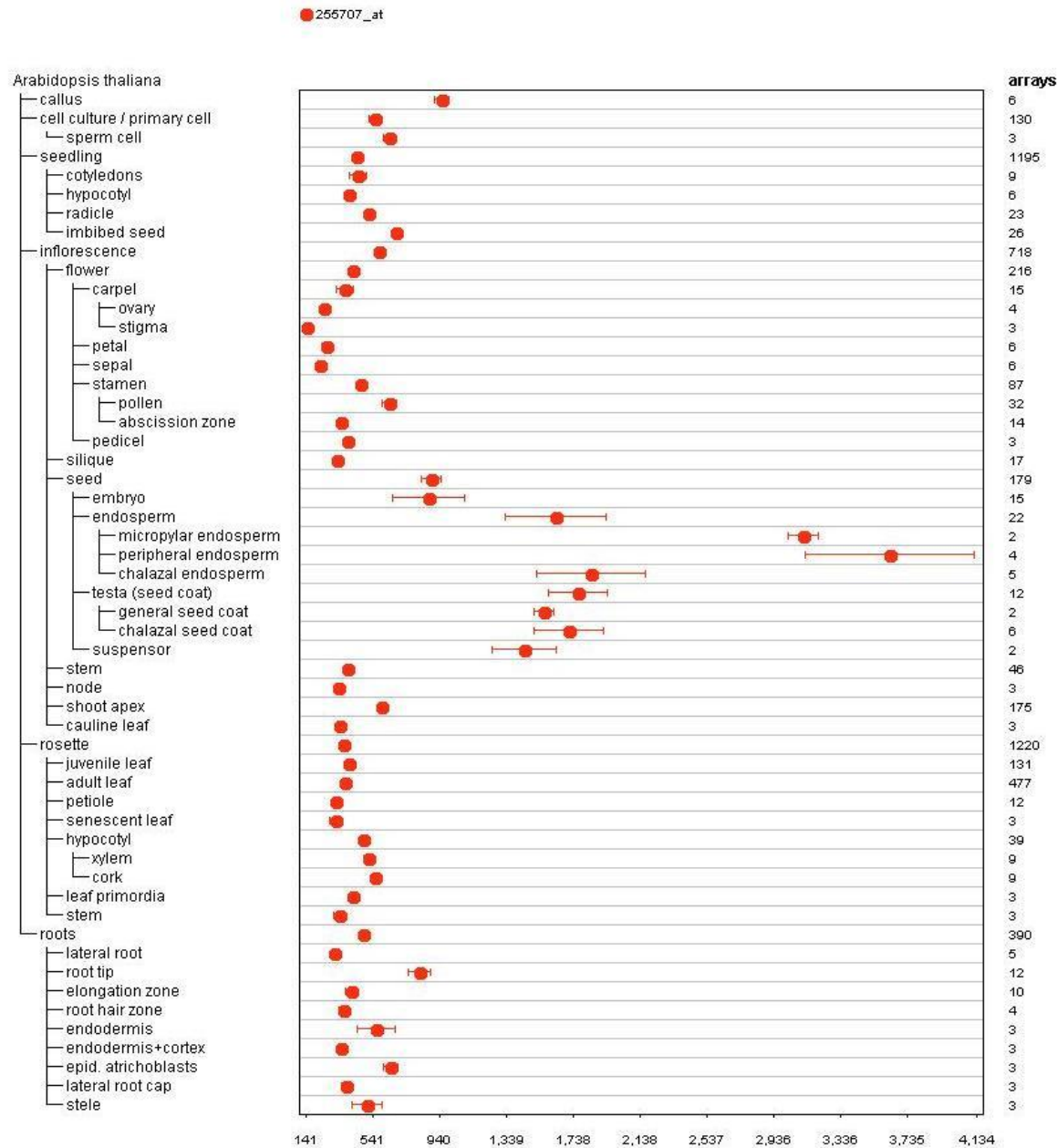
The three helices of Arm repeats were designated as H1, H2, and H3. The amino acid positions of three putative ZIX Arm repeat motifs were given in parentheses. Color codes for amino acid residues: blue: aliphatic; green: basic; red: acidic; gray shade: conserved amino acid.

Supplemental Figure 4. Two top 3-D thread models of ZIX predicted by I-TASSER using proteins of known crystallized structures. **A** and **B**: predicted 3-D models of ZIX. **C**: crystal structure of yeast importin- α (SRP1) complexed with c-myc NLS peptide (1ee4). **D**: crystal structure of human β -catenin Arm repeat region and C-terminus (2z6h).

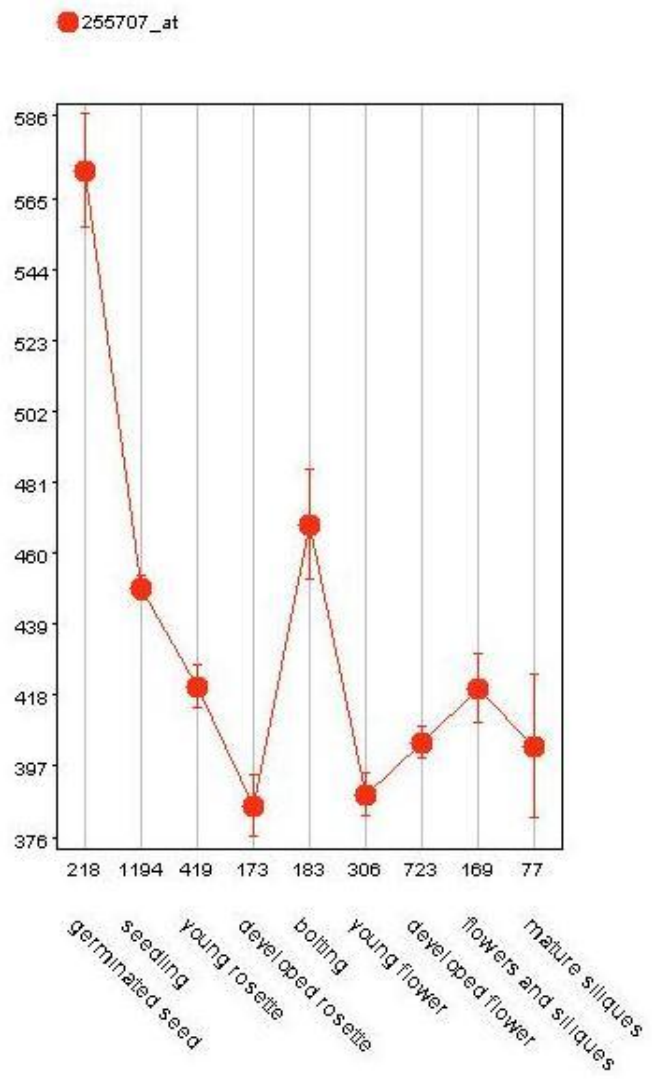


Supplemental Figure 5. Expression data of ZIX transcripts and proteins from public databases

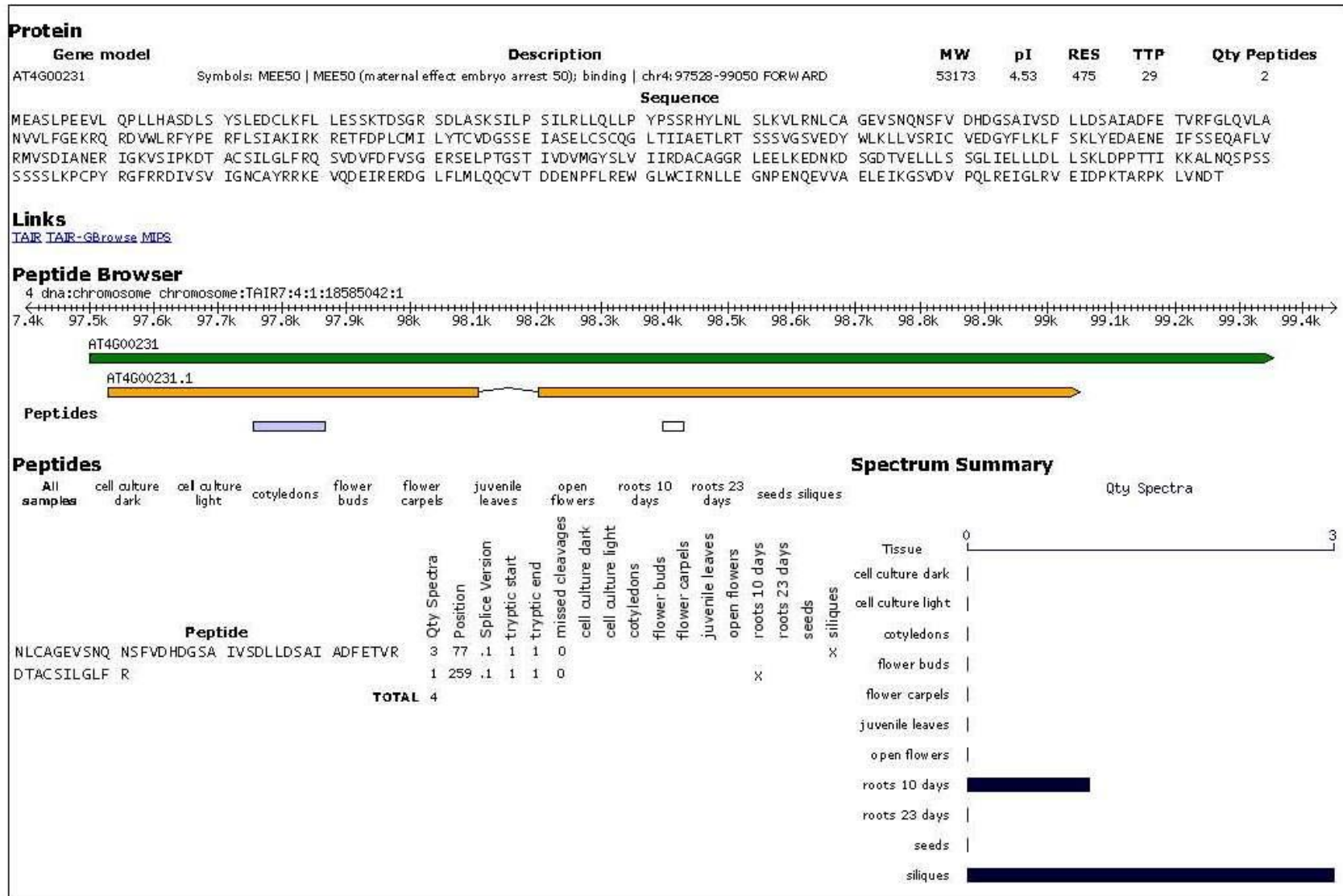
A. ZIX spatial expression data were extracted from Genevestigator v3. The x-axis indicates expression levels.



B. ZIX developmental expression data were extracted from Genevestigator v3. The y-axis indicates expression levels.

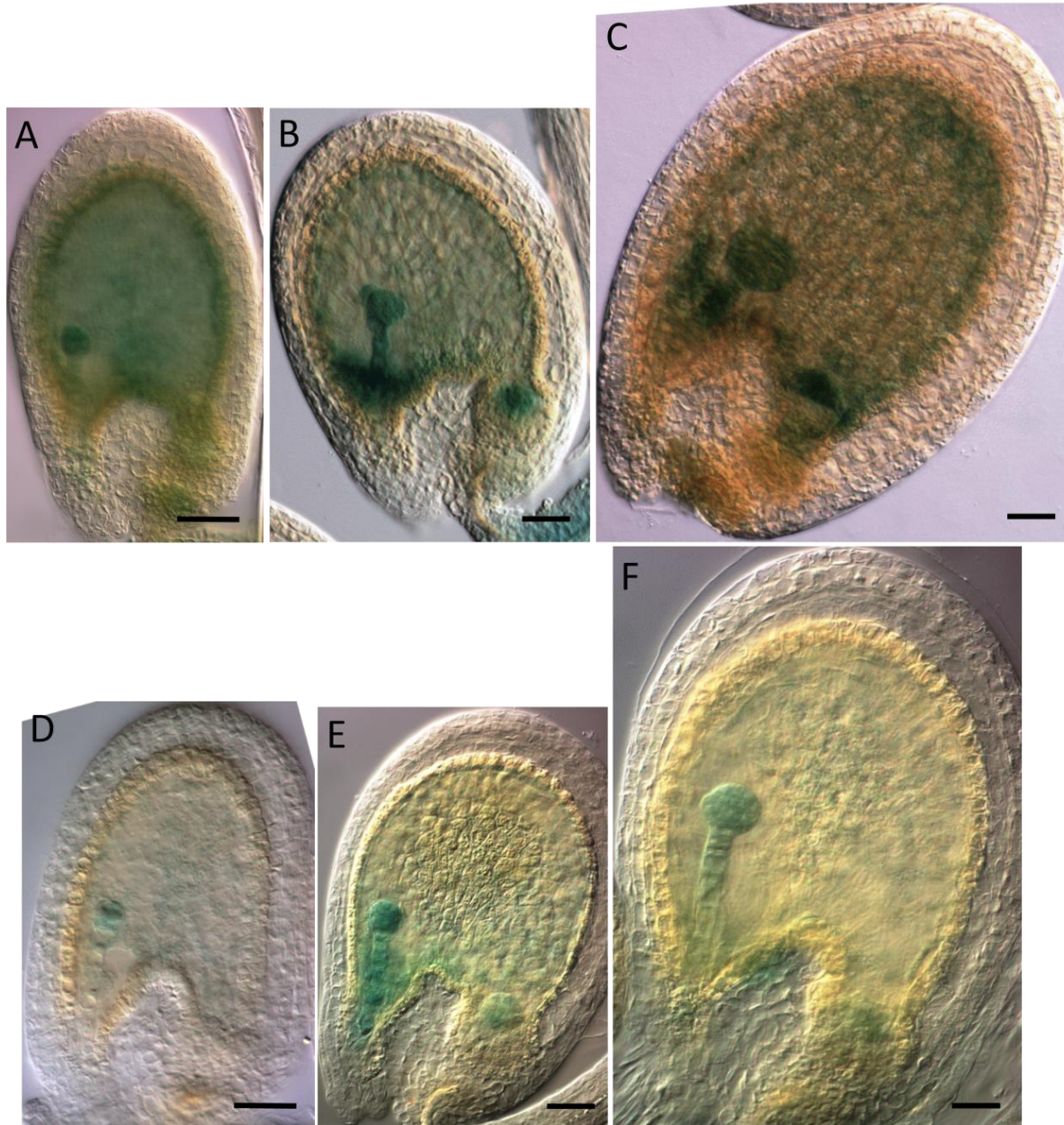


C. ZIX protein expression data were extracted from AtProteom. Two peptides were detected from roots and siliques.



Supplemental Figure 6. *ZIX* promoter activities in early seeds

A-C: maternal *ZIX*:GUS. D-F: paternal *ZIX*:GUS. A,D: 4-cell embryo. B,E: 8-cell embryo. C,F: globular embryo. Scale bar: 20 μ m.



Supplemental Figure 7. Chromatin mark and small RNA distributions at *ZIX* locus from public databases.
A. DNA cytosine methylation, small RNAs, and mRNAs in wild-type and mutant immature floral tissues.



mC: methylated cytosine, **smRNA;** small RNAs, **ddc:** *drm1,drm2,cmt3*, **rdd:** *ros1,dml2,dml3*
 yellow bars: CG, blue bars: CHG, red bars : CHH (absent from this locus)
 green squares: RNA-sequencing reads.

Data were extracted from <http://neomorph.salk.edu/epigenome/epigenome.html>.

Supplemental Figure 7 (cont.). Chromatin mark and small RNA distributions at *ZIX* locus obtained from public databases.

B. DNA cytosine methylation and histone methylation, acetylation and ubiquitylation marks compiled from multiple data sources at <http://epigara.biologie.ens.fr/cgi-bin/gbrowse/a2e/>.

Showing 4 kbp from Chr4, positions 96,426 to 100,425

Instructions

Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.

Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.

Examples: AT1G01040, AT3G52910.1, Chr1:1504365..1514364, Chr4:1-25000, ChrC:63781..68780, At4g25530.

[Bookmark this] [Upload your own data] [Hide banner] [Share these tracks] [Link to Image] [High-res Image] [Help] [Reset]

Search

Landmark or Region:

Chr4:96426..100425

Data Source

EPIGARA [TAIR8]

Overview

Reports & Analysis:

Scroll/Zoom: Show 4 kbp

Details

DNA/GC Content



Locus (gene, pseudogene, transposable_element_gene)



Protein Coding Gene Models (mRNA)



CDS (protein)



Pseudogenes (pseudogenic_transcript)

Noncoding RNAs (ncRNA, miRNA, tRNA, snoRNA, snRNA, rRNA)

Transposable Elements

Chromatin states (Chr4)



H3K9me2 Col0 native - Bernatavichute et al. (2008)



H3K9me2 Col0 crosslinked - Bernatavichute et al. (2008)

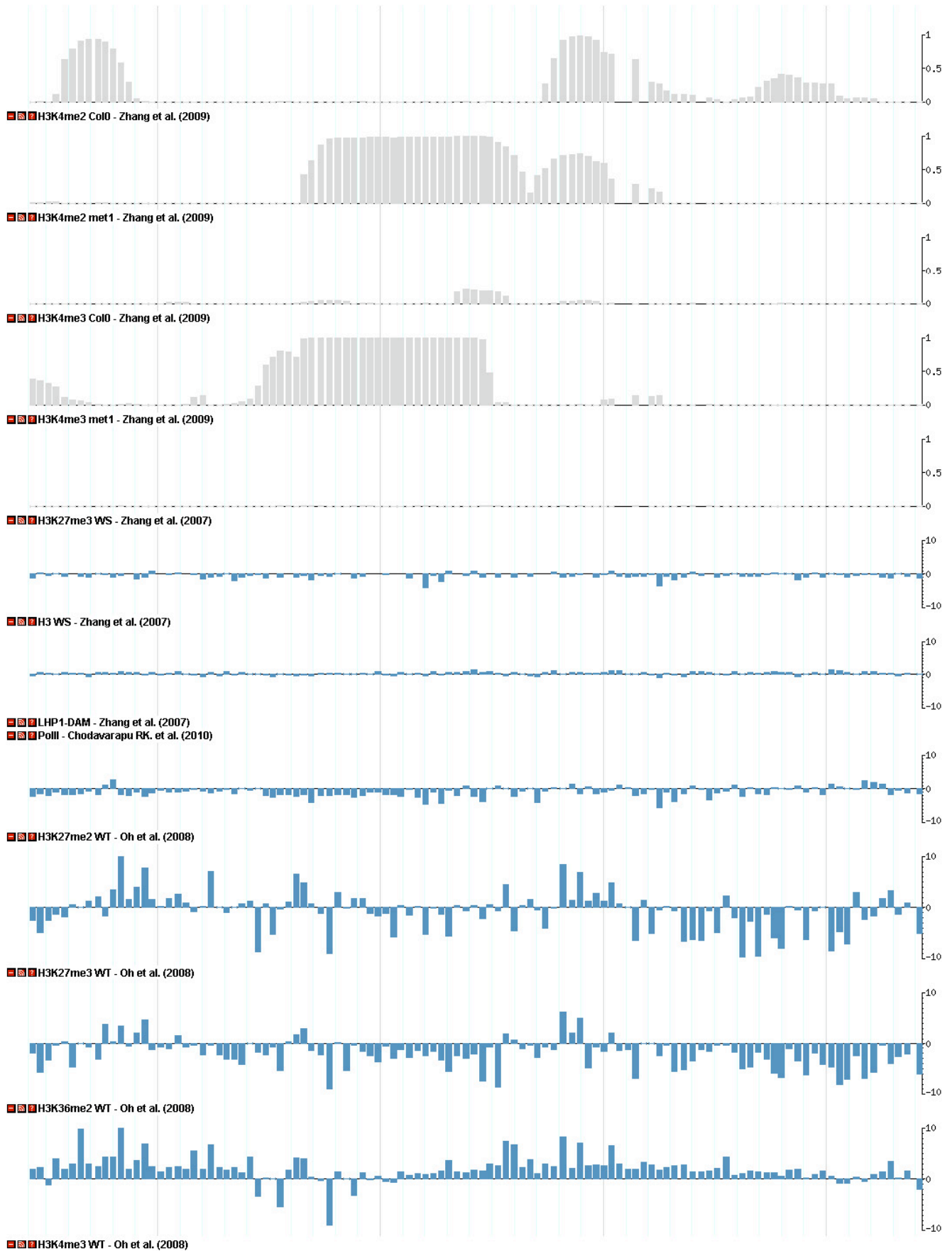


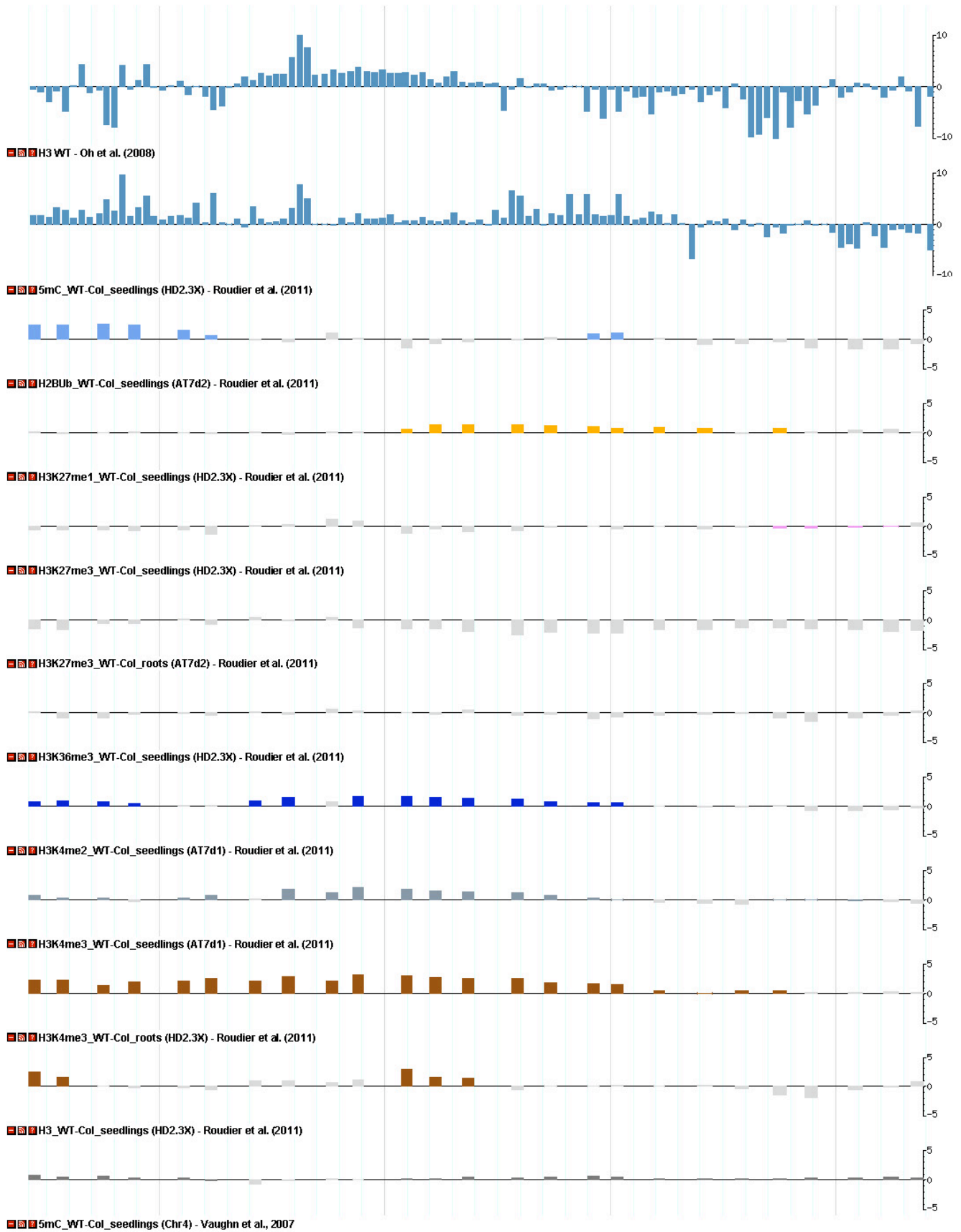
H3K4me1 Col0 - Zhang et al. (2009)

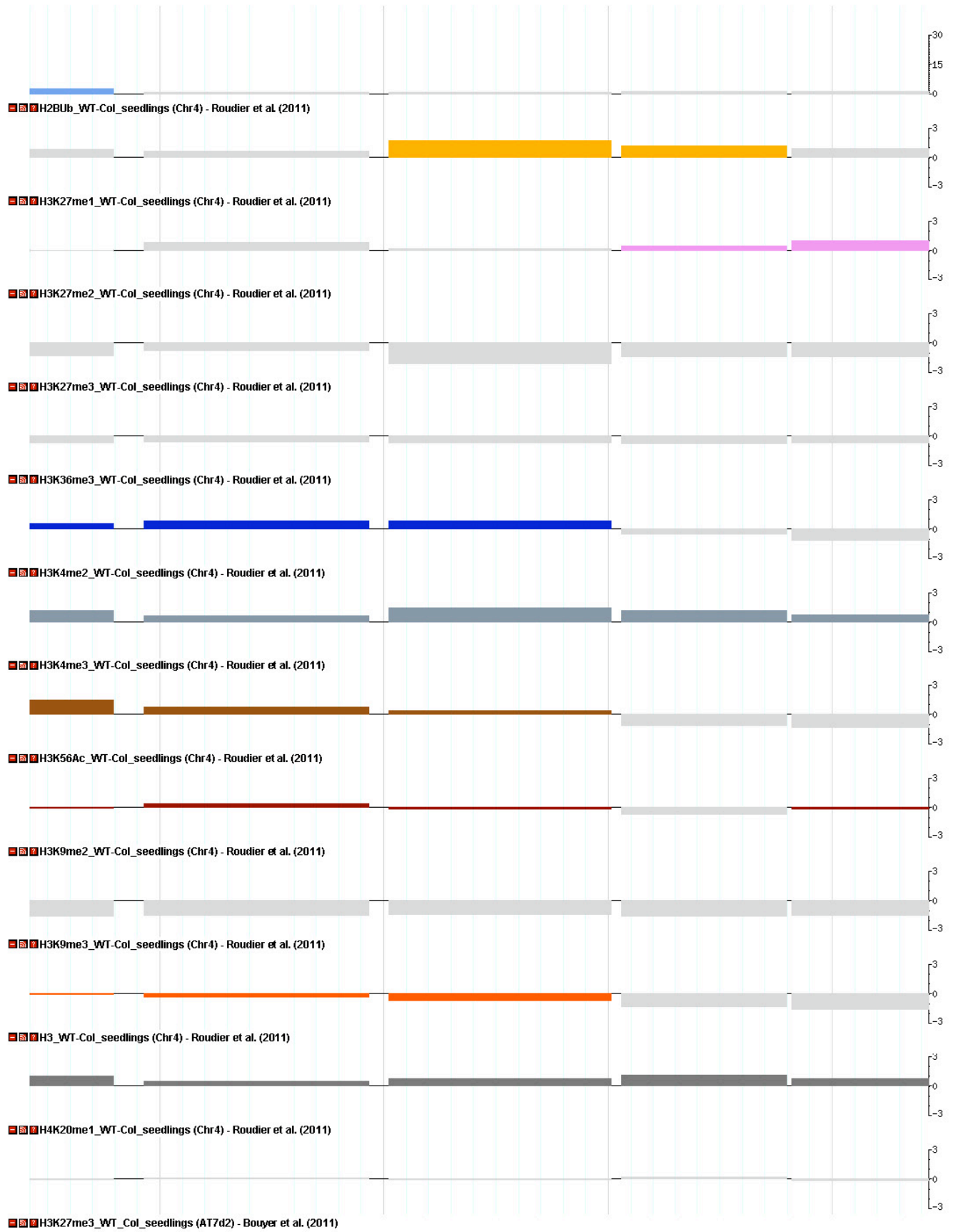


H3K4me1 met1 - Zhang et al. (2009)



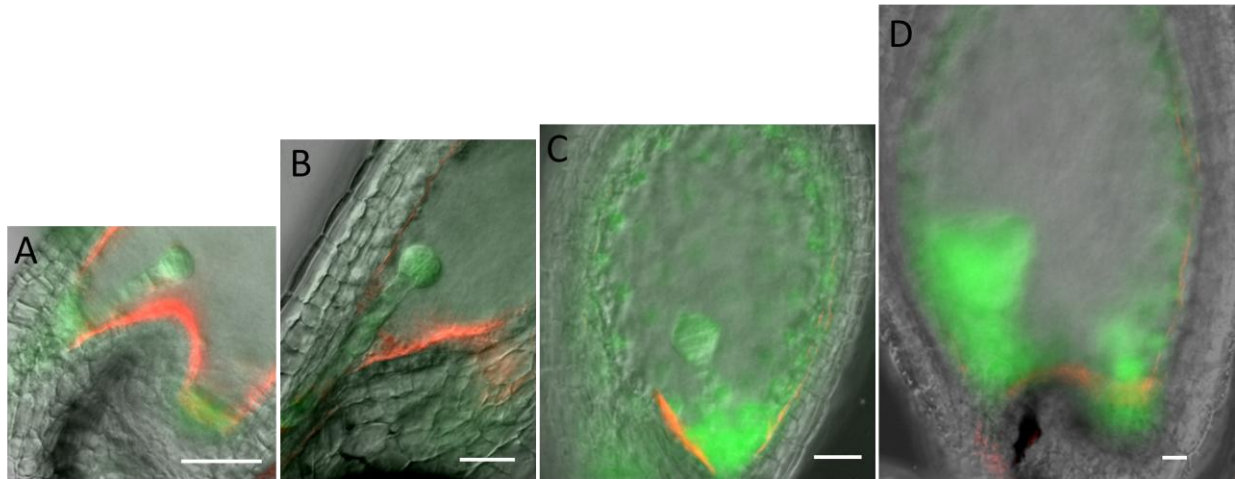






Supplemental Figure 8. ZIX-GFP protein localization in early seeds

DIC and GFP overlay images. A: 4-cell embryo. B: 8-cell embryo. C: early globular embryo. D: early heart stage embryo. Scale bar: 20 μ m.



Supplemental Figure 9. Maternal *MINI3:GUS* expression in *zix* seeds

A: 1DAP wild-type (wt) seed. B-D: 2DAP *zix* seeds. Scale bar: 20 μ m.



Supplemental Table 1. Primers and PCR parameters

allele	primer	sequence (5' to 3')
<i>Ds</i> borders of	Ds5-2	CGTCCGTTTTTCGTTTTTTACC
all 3 <i>zix</i>	Ds3-2	CCGGTATATCCCGTTTTTCG
<i>zix-1</i>	SET2325 5'	ATTGCTTGAAATTTCTTCTAGAGTCTTC
	SET2325 3'	GCCCTTGACAGCTACAAAGC
<i>zix-2</i>	SET3862 5'	ACTGTCTCGAAATCCGCAAT
	SET6076 3'	GTGGTGAAGGCCAAACAAT
<i>zix-3</i>	SGT8064 5'	CATCCTCACAAGAAAGGCTTG
	SET5779 3'	GGCCATTACACGAAACACT
<i>At4g00231</i>	LP <i>At4g00231</i> exon2 Dral	GTAGCTGTCAAGGGCTCACC
SNP	RP <i>At4g00231</i> exon2 Dral	TCAGGGTTCCCTTCCAGTAA
<i>Ler met1</i> &	met1 For	CTCTTTAGTAGAAGTTGGCATG
<i>Col met1</i>	met1 Rev	ATATGTATGTATAGATATTTTCTCC
<i>Ler ddm1-2</i>	DDM1f	CAGATCTCTACCCTCCTGT
	ddm1-2dRsa	TGAGCTACGAGCCATGGGTTTGTGAAACGTA
<i>Col ddm1-1</i>	ddm1-1 for	TTTGAGGTTTGCAGAATCGATGGCA
	ddm1-1 rev	CCTATAAACATGAACAGGTTTCGTCTGCCCGAT
<i>Ler cmt3-7</i>	cmt3-7 for	TTGACTACCCCGGGAATGAACCCATTTGT
	cmt3-7 rev	GATCTGCAACAAATCTCAGC
<i>Lg At4g00231</i> transgene	ad1 gMEE	AAAAAGCAGGCTGCGGTCCAATCGCCGATTA
	ad2 gMEE	AGAAAGCTGGGTAGCATCATCATCCAGTTAGATGCT
	attB1 for	GGGGACAAGTTTGTACAAAAAAGCAGGCT
	attB1 rev	GGGGACCACTTTGTACAAGAAAGCTGGGT
<i>ZIX:ZIX-GFP</i>	ad1 gMEE	AAAAAGCAGGCTGCGGTCCAATCGCCGATTA
	ad2 gMEEfuse	AGAAAGCTGGGTGGTGTTCATTGACAAGCTTTGG

All PCRs were carried out for 30 cycles, except for At4g00231 SNP, which was done for 35 cycles, at 94⁰C / 30 sec, 55⁰C / 30 sec, 72⁰C / 60 sec, with 94⁰C / 2 min at the beginning and 72⁰C / 3 min at the end. The annealing temperatures for *met1*, *ddm1-2*, and *ddm1-1* alleles were 45⁰C, 48⁰C, and 67⁰C, respectively. PCR parameters for amplifying the Lg *At4g00231* transgene were performed as recommended by the Gateway cloning protocol per manufacturer (Invitrogen, CA, USA).