

# Figure S1

A.

Sites 1 through 100

```
ORTH1 MAIEKPCDDGDGVMRCVYPPSEELCGTCVTPWHVSCIPESASSGEWECPCDSGVVVPAAFGTGNARPESSGSVAAIRAIADETEA
ORTH2 MARDIIPCDGDGVMCRCKSNPPPEESCGTCVTPWHVSCSSPPKIASIWHCPDCSGEIDPPVSGGALGFESAGSDVAIRAIEADESIEE
ORTH3 MIPACYPCEPDEGVMCRCKSNPPPEESCGTCVTPWHVSCSSPPKIASIWHCPDCSGEIDPPVSGVAAGYGSVSDVAAIHIEADESAE
ORTH4 MAIQGICDDGDGVMRCVYPPSEELCGTCVTPWHVSCIPESASSGDWECPCDSGVVVPAAFGTGISGPESSGSVAAIRAIAADVTEA
ORTH5 MAIQGICDDGDGVMRCVYPPSEELCGTCVTPWHVSCIPESASSGDWECPCDSGVVVPAAFGTGISGPESSGSVAAIRAIAADVTEA
ORTHlikeMIRVNGPCD-----CYSAAESISGCIITHTVTSIS-----SPIDRSQDVPVPSD-----ESGGS-----KAESMIDA
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Sites 101 through 200

```
ORTH1 EKAKKRKMSGGDDGVDEEEKK-----EIFSCICQPERPII-----PCGHFCKCFEKWAVGGKRLC
ORTH2 EKAKMRKRSKGVVEEDDEEERKKGKGNPNLDVSAIGDMCSFCMQPERPVTK-----PCGHACKCFEKW-MGGKRLC
ORTH3 EKAKKRKMSKGVVEEDDEEKKKISKGKR-IDYIS-----HFECFCMSKQVSVRVIFAALMVWFESPCGHACKCFEKW-MGGHRSC
ORTH4 EKAKKRKMSGGDDGVDEEEKK-----EIFSCICQPERPII-----PCGHFCKCFEKWAVGGKRLC
ORTH5 EKAKKRKMSGGDDGVDEEEKK-----EIFSCICQPERPVII-----PCGHFCKCFEKWAVGGKRLC
ORTHlikeDEIKRKRKISGDCADENKSDGEIASNDG--VDAFAICEDINCSKQCDRPII-----PCGHFCKCFDKW-IDGKRLC
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Sites 201 through 300

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ORTH1 MLCRSKIPRHVAKNPRISIAVSARAVVTKCSVEAAAKVHHIIRNDRPEKAFTERAVKTKGANAASGKFFVTPRDHFGPIAENDVTRKGGYV
ORTH2 GRCRSIPEKMAKNPRISIVAAARAKVSKS-AAATISVVFHISNDRDPKAFTERAKKTGANAASGKIYVTPPDHFGPIAENDPVRKGVV
ORTH3 GLCRSVIPESMVKNPRISIVSARARVSEK-ADARISVVHYDNDRDPKAFTERAKKTGANAASGKIFVTPRDHFGPIAENDPVRKGVV
ORTH4 MLCRSKIPRHVAKNPRISIAVSARAVVTKCSGEAAAKVHHIIRNDRPEKAFTERAVKTKGANAASGKFFVTPRDHFGPIAANDVTRKGGYV
ORTH5 MLCRSKIPRHVAKNPRISIAVSARAVVTKCSGEAAAKVHHIIRNDRPEKAFTERAVKTKGANAASGKFFVTPRDHFGPIAANDVTRKGGYV
ORTHlikeALCRSIPDKMAANPRVSSVSVRYVVKVAKI-AGVGTIAFFPFSKQDQPEAFRIRKRA-KIGEEAAR--IYVVFDFHGPAAHDEVRKGVV
```

Sites 301 through 400

```
ORTH1 GESWEDRECRVWGAHFPHTAGIAGSVAAGASVAISGGYDDDEDHGEWFTYSGGRD-SGNKRINKKSSDAFKNMESR-SCKMGYPVVRVRSWK
ORTH2 GESWEDRECRVWGAHFPHTAGIAGSVAAGASVAISGGYDDDEDHGEWFTYSGGRD-SGNKRINKKESDFKFEKSAALR-SCKLGYPVVRVRSWK
ORTH3 GESWGRACRQWGAHFPHTAGIAGSVAAGASVYISGGYDDDEDHGEWFTYSG-----RKNVYAFDVFNFNEAR-SCKLGYPVVRVRSWK
ORTH4 GESWEDRECRVWGVHFPHTAGIAGAAVGAASVAISGGYDDDEDHGEWFTYSGGRD-SGNKRINKKSSDAFKNMESR-SCKMGYPVVRVRSWK
ORTH5 GESWEDRECRVWGVHFPHTAGIAGAAVGAASVAISGGYDDDEDHGEWFTYSGGRD-SGNKRINKKSSDAFKNMESR-SCKMGYPVVRVRSWK
ORTHlikeGESWEDRECRVWGVHFPHTAGIAGSVAAGASVVIISGGYKDDDEDHGEWFTYSG-----KSRGRHFANEDQEFEDNEARVSCMGYPVVRVRSWK
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Sites 401 through 500

```
ORTH1 EKRSAYAPEEG-VRYDGVYRIKCVSNGVYGSFKVCRYFVRCNENAPWTSDEHGDRPRFPVPEEIAADFVRKESPSWDFDEAGRWKWKPPP
ORTH2 EKRSAYAPEEG-VRYDGVYRIKCVKRVGVYGSFKVCRYFVRCNENAPWTSDEHGDRPRFPVPEEIAADFERKESPSWDFDEAGRWKWKPPP
ORTH3 DKRSYAPVGG-VRYDGVYRIKCVRIVGI-----MCRFVRCNENAPWTSDEHGDRPRFPVPEEIAADFERKESPSWDFDEAGRWKWKPPP
ORTH4 EKRSAYAPEEG-VRYDGVYRIKCVSNGVYGLHKMCRYFVRCNENAPWTSDEHGDRPRFPVPEEIAADFVRKESPSWDFDEAGRWKWKPPP
ORTH5 EKRSAYAPEEG-VRYDGVYRIKCVSNGVYGLHKMCRYFVRCNENAPWTSDEHGDRPRFPVPEEIAADFVRKESPSWDFDEAGRWKWKPPP
ORTHlikeDRYSAYAPEEG-VRYDGVYRIKCVKRAFDSFKVCRYFVRCNENAPWTSDESGDRPRFPVPEEIASDFERKESPSWDFDEAGRWKWKPPP
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Sites 501 through 600

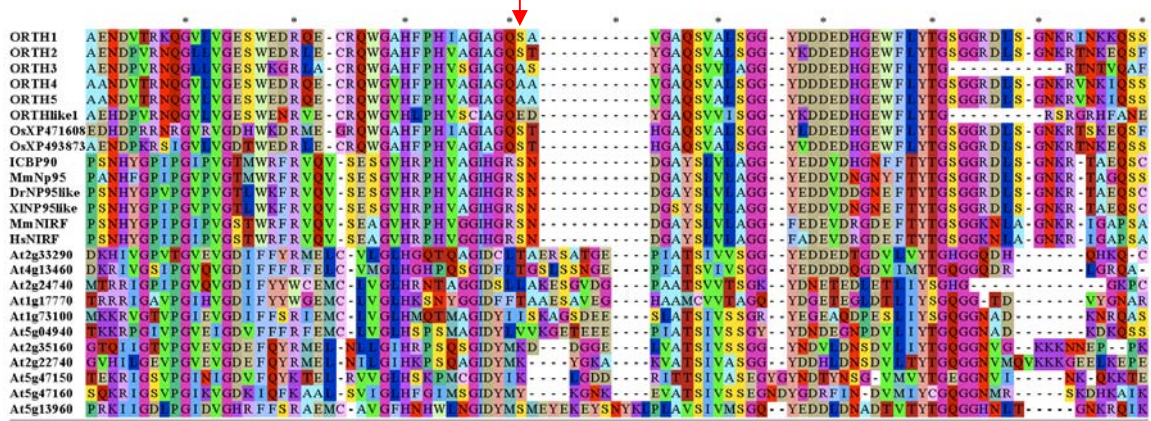
```
ORTH1 VSR---MADPEERKKNRAK-----AMKARREFSCICREVSPIVTPCAHNFCKAC-EAKFAGITQRRERSNGGRKRAKKNLMI-CPCCTDI
ORTH2 ASKKSVA-VAPEERKNRAIAAHSNIMRARREFKCIICREVSPIVTPCAHNFCKAC-EAKFAGITQRRERSNGGRKRAKKNVMI-CPCCTDI
ORTH3 ASKKSVA-VAPEERKNRAIAKSNIMRARREFKCIICREVSPIVTPCAHNFCKAC-EAKFAGITQRRERSNGGRKRAKKNVMI-CPCCTDI
ORTH4 VSR---MADPEERKKNRAKKN-----AMKARREFSCICREVSPIVTPCAHNFCKAC-EAKFAGITQRRERSNGGRKRAKKNLMI-CPCCTDI
ORTH5 VSR---MADPEERKKNRAKKN-----AMKARREFSCICREVSPIVTPCAHNFCKAC-EAKFAGITQRRERSNGGRKRAKKNLMI-CPCCTDI
ORTHlikeAVH-----EIRE-----RMKMAMC-----FVLIIVGSSIVYQ
```

Sites 601 through 673

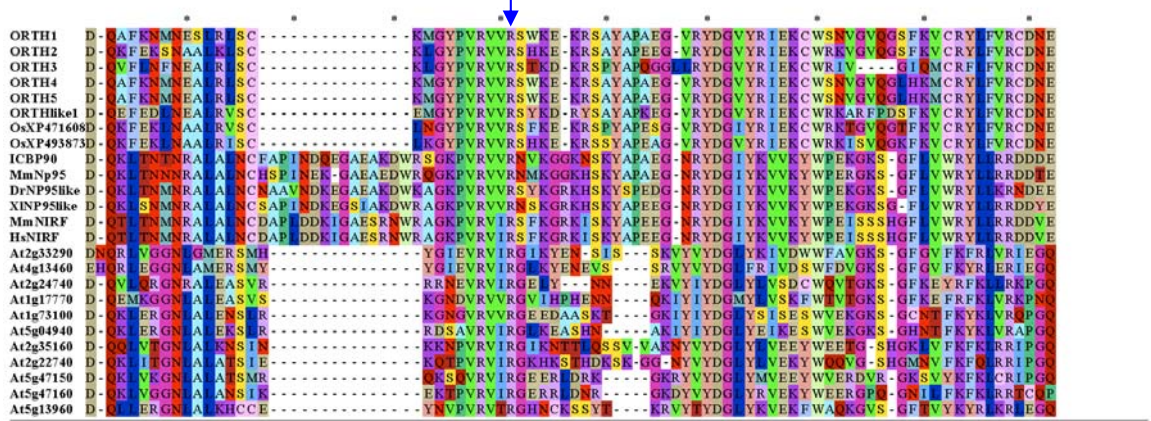
```
ORTH1 SEF--NPVREMMEIENFKKSEEE---ADAS---ISEEE-EESEPPPKKIKMDNSVGGSCISISA--
ORTH2 SDF--NPVREVAEVIKKTQEDAEDEDEGECSGTPPEE-DSEPKKRKIDTDAIVSALIR---
ORTH3 AEFV--NPVREVAEVIKKTQEDAE-ENASDEGCSGHEEEDDEPKKRKIDTDAEVSAAVVESDMK
ORTH4 SEF--NPVREMMEIENFKKSEEE---AEVAESSNISEEE-EESEPPPKKIKMDNSVGG--DMSISA--
ORTH5 SEF--NPVREMMEIENFKKSEEE---AEVAESSNISEEE-EESEPPPKKIKMDKNSVG--GTSISA--
ORTHlike-----
```

B.

Sites 1 through 100

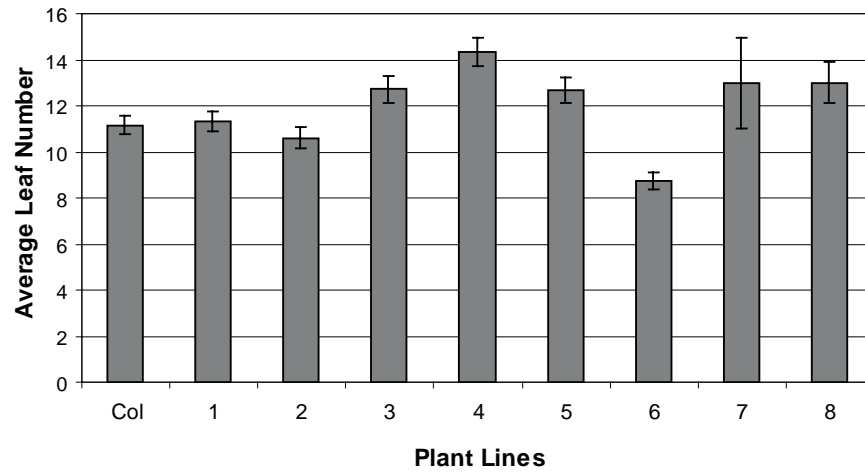


Sites 101 through 192



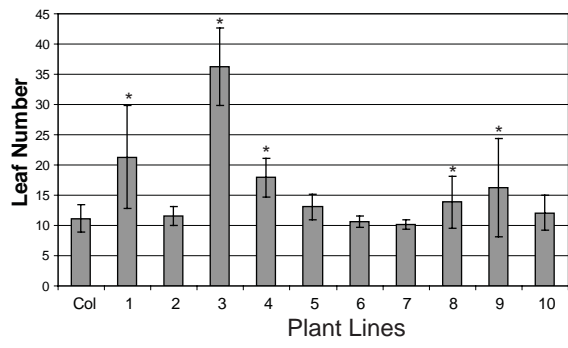
**Figure S1.** CLUSTAL X generated protein alignment of ORTH proteins and SRA domain. (a) Alignment of the entire protein coding region of the Arabidopsis ORTH proteins. Domains are indicated as follows: blue bar shows position of PHD domain, red bar indicates position of N-terminal RING domain, green bar indicates position of the SRA domain, purple bar indicates position of the C-terminal RING domain. All domain limits are based on SMART predictions. (b) The core SRA domain alignment of all Arabidopsis SRA domain-containing proteins as well as representative orthologues of the ORTH proteins in rice (OsXP471608; OsXP493873), human (ICBP90; NIRF), mouse (NIRF; NP95), Danio (DrNP95like), and Xenopus (XINP95like) (See Figure 1 for NCBI locus codes for each protein.). SRA domain-only and SRA-SET domain-containing proteins are listed by their AGI code. Arrows indicate positions in ORTH1 and other SRA domain-containing proteins known to disrupt methylated DNA association (Johnson et al., 2007).

## GFP-ORL

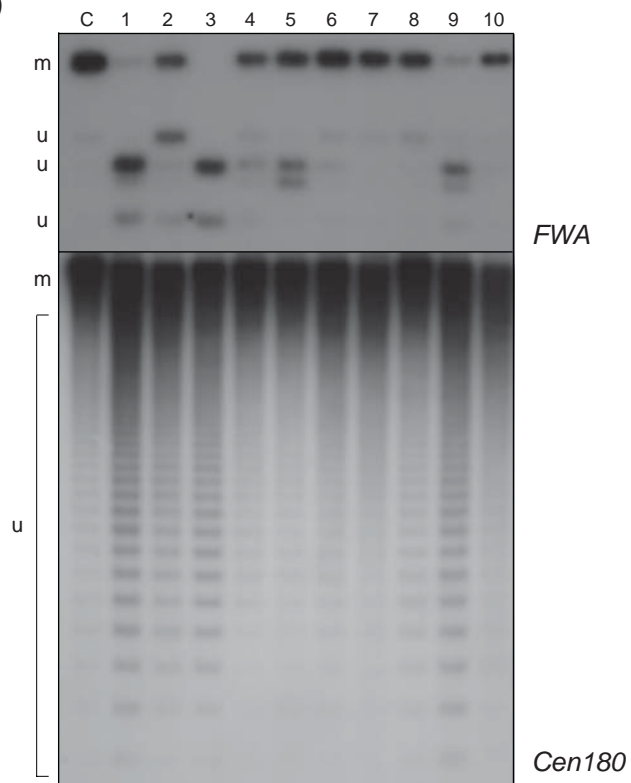


Supplemental Figure 2.

(a)



(b)



Supplemental Figure 3.

**Figure S2.** Overexpression of GFP-ORL does not cause a late-flowering phenotype. Eight independent insertional lines expressing GFP-ORL under the 35S promoter were analyzed for a flowering time phenotype. The number of leaves produced before the transition to reproductive tissue was counted from at six to twenty segregating T2 individuals. Each bar represents mean  $\pm$  SEM.

**Figure S3.** Overexpression of ORTH1 causes a late flowering phenotype. (a) The flowering time of seven to nineteen T2 plants from ten independent 35S::ORTH1 lines and wild type (Col) was measured by counting leaves produced before the transition to reproductive tissue. Each bar represents mean  $\pm$  SD. Asterisk is above lines that are statistically different from Col based on a student's t test ( $P < 0.005$ ). (b) Southern blots for FWA (upper) and Cen180 bp repeats (lower) with DNA pooled from all T2 plants from ten ORTH1 independent plants. The upper band from Col (C) DNA is fully methylated (m), while lower bands are products from unmethylated (u) DNA.