Supplementary Material

Oligonucleotides and plasmid constructs

The oligonucleotides used in this study are listed in table 1. The two-hybrid constructs were generated in vectors pEG202, pJG4-5 or pJG4-5Y (pJG4-5 in which a polylinker has been introduced between the *Eco*RI and *Xho*I restriction sites), a kind gift from Drs. C. Antoniewski and J-Y. Roignant. The cDNAs were amplified using DyNAzyme™ EXT DNA polymerase (Finnzymes), subcloned as indicated below and sequenced.

Primers corto1-s and corto550-as were used to generate the full-length *corto* cDNA. The amplification product was subcloned as a *Bam*HI/*Eco*RI fragment in pBluescript and in pGEX4T-1 in frame with the GST domain. It was also subcloned as an *Eco*RI/blunt fragment in pJG4-5 in frame with the activation domain B42 of *E.coli* and in pEG202 in frame with the LexA DNA binding domain. These constructs were designated pBS-Corto, pGEX-Corto, pEG-Corto and pJG-Corto, respectively. Plasmid pEG-Corto was digested by *Pvu*II and *Sal*I, then treated with Klenow polymerase and religated to give plasmid pEG-C1/324 which encodes amino-acids 1 to 324 of Corto. The region corresponding to amino-acids 107 to 203 was amplified using primers corto127-s and corto203-as and subcloned as a *Bam*HI/*Eco*RI fragment in pGEX4T-1 and as an *Eco*RI/blunt fragment in pEG202 to give plasmids pGEX-C127/203 and pEG-C127/203. The region corresponding to amino-acids 440 to 550 was amplified with primers corto440-s and corto550-as. The resulting fragment was subcloned as an *Eco*RI/blunt fragment in pEG202 to give plasmid pEG-C440/550.

EST SD03549, which contains the *esc* cDNA, was digested by *Asu*II, blunt-ended with Klenow polymerase, and digested with *Xho*I. The resulting 1.6 kb fragment, which corresponds to the full-length ESC cDNA, was sub-cloned in pJG4-5 previously digested with *Sma*I and *Xho*I to give plasmid pJG-ESC. The full-length *esc* cDNA was also amplified using primers esc2-s and esc425-as. It was subcloned as a blunt/*Xho*I fragment in pJG4-5Y

previously digested with *Sma*I and *Xho*I. Sequencing of this subclone revealed two mutations in the *esc* cDNA. The first mutation leads to the substitution of the glutamic acid at position 125 by a glycine and the second one to the substitution of the leucine at position 142 by a phenylalanine (E125G, L142F). This clone was named pJG-ESC*. The full-length *E(z)* cDNA was amplified using primers E(z)1-s and E(z)760-as and subcloned as an *Eco*RI/blunt fragment in pJG4-5 to give plasmid pJG-E(Z). This construct was digested by *Sgr*AI and *Sma*I, then treated with S1 nuclease and religated to obtain pJG-E(Z)1/315 which encodes amino-acids 1 to 315 of E(Z). pJG-E(Z) was also digested by *Eco*RI and *Xma*I, then treated with Klenow polymerase and religated to obtain pJG-E(Z)315/760 which encodes amino-acids 315 to 760 of E(Z). The E(Z) SET domain was amplified using primers E(z)601-s and E(z)760-as. This fragment was subcloned as an *Eco*RI/blunt fragment in pJG4-5 to give plasmid pJG-E(Z)SET. The full-length *Pc* cDNA was amplified using primers Pc1-s and Pc390-as and subcloned as an *Eco*RI/blunt fragment in pJG4-5 to give plasmid pJG-PC. The full-length *Scm* cDNA was amplified using primers Scm1-s and Scm877-as and subcloned in pJG4-5 as an *Eco*RI/blunt fragment to give plasmid pJG-SCM. The full-length *Trl* cDNA was amplified using primers Trl1-s and Trl519-as and subcloned as a *Bgl*II/blunt fragment in pJG4-5Y to give plasmid pJG-GAGA. The region coding the GAGA BTB/POZ domain was amplified using primers Trl1-s and Trl99-as. This fragment was subcloned as a *Bgl*II/blunt fragment in pJG4-5Y to give plasmid pJG-GAGABTB.

Yeast strains

The yeast strains were transformed using the displayGREEN™ transformation kit (Display systems Biotech). The bait strain RFY231 (*MATα trp1Δ::hisG his3 ura3-1 leu2::*3Lexop-*LEU2*) was co-transformed with the URA3 pSH18-34 plasmid, which contains the *LacZ* reporter gene under the control of eight LexA binding sequences and the minimal TATA region from the *GAL1* promoter, and with the HIS3 pEG202 bait constructs expressing LexA-tagged Corto or Corto sub-domains (pEG-Corto, pEG-C127/203 and pEG-C440/550). As

pEG-C1/324 activates the *LacZ* reporter gene of pSH18-34 by itself, it was introduced into strain EGY48SHΔSpe (*MATα his3 trp1 ura3* 6LexAop-*LEU2*) which contains a single copy of the *LacZ* gene integrated in the yeast genome. In that strain, no trans-activation of *LacZ* by pEG-C1/324 could be detected. The prey strain RFY206 (*MATa ura3-52 his3Æ200 leu2-3 lys2Æ201 trp1::hisG*) was transformed with the different TRP1 prey plasmids derived from pJG4-5 and pJG4-5Y and expressing the B42 activation domain-tagged Corto, PcG and GAGA constructs (pJG-Corto, pJG-ESC, pJG-ESC*, pJG-E(Z), pJG-E(Z)SET, pJG-E(Z)1/315, pJG-E(Z)315/760, pJG-PC, pJG-PH, pJG-PHΔN, pJG-PHΔS, pJG-SCM, pJG-GAGA and pJG-GAGABTB).

TABLE 1. Oligonucleotides used for subcloning

corto1-s	5’-ACGATGACGATGGCCGCCTGTTATGCCACCTACG-3’
corto127-s	5’-ACTGCCAGCAGCAACAGCAACACAGCCCCC-3’
corto203-as	5’-CACCGCCCGCGCGGTCGCATGC-3’
corto325-s	5’-GCTGCGGCCCAGGCCTCGATAGCC-3’
corto440-s	5’-GGCCCTGACACCAATCCC-3’
corto550-as	5’-CACGTTGTAGCAGGAGATCTGCGG-3’
esc2-s	5’-CAGCAGTGATAAAGTGAAAAACGGCAACGAGCCC-3’
esc425-as	5’-TCAGATGGAAGTTGTTTGTCTGCG-3’
E(z)1-s	5’-AATAGCACTAAAGTGCCGCCCGAGTGG-3’
E(z)760-as	5’-TCAAACAATTTCCATTTCACGCTCTATGCCC-3’
E(z)601-s	5’-CAGGCCTGCGGAGCGGATCAGTTTAAGC-3’
Pc1-s	5’-ACTGGTCGAGGCAAGGGGAGTAAGG-3’
Pc390-as	5’-TCAAGCTACTGGCGACGAATCGCC-3’
Scm1-s	5’-TCGGGCGGACGTGATAGCAGTACC-3’
Scm877-as	5’-GAGTGCCAGATTATTTCGACGACCATTGACC-3’
Trl1-s	5’-TCGCTGCCAATGAATTCGCTGTATTCG-3’
Trl519-as	5’-CTGCGGCTGCGGCTGTTGCTGCTGCGG-3’
Trl99-as	5’-GGCGTGATCCACGCTCACCTCTCCGCG-3’

Adapters (*Bam*HI: *cgc**ggatcc**gcg*, *Eco*RI: *cgc**gaattc**cgg*, *Nco*I: *catg**ccatgg**catg*, *Bgl*II *gga**agatct**tcc*, *Xho*I: *ccg**ctcgag**cgg*) were added at their 5’ ends as indicated in Materials and Methods