A

	ADF expression	Other expression	% expression per line				
tph-1 prom17 (99bp)	+	NO	95	93	90		
Mutation SCAN#1	-	NO	0	0	0		
Mutation SCAN#2	-	NO		3	2		
Mutation SCAN#3	+	NO		83	88		
Mutation SCAN#4	+/-	NO	52	43	37		
Mutation SCAN#5	+	NO	93	92	83		
3X [GGCTCATTTATTCTCCCACGGAAACCATGACAGCAAAAAT]	+	NO		88	93		
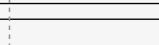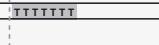
B

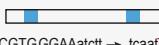|	ADF expression	Other expression	% expression per line		
1X [GGCTCATTTATTCTCCCACGGAAACCATGACAGCAAAAAT] gcy-5 minimal promoter	-	ASER	0	0	0
gcy-5 minimal promoter	-	ASER	0	0	0
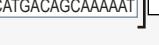
C

■ CSL

	ADF expression	Other expression	% expression per line				
tph-1							
tph-1prom17::gfp (-283/-184)	+	NO	95	93	90		
ttattCTCCCACGgaaac → ttattCTCTTACGgaaac							
tph-1prom42::gfp CSL MUT	-	NO	0	0	0		
cat-4							
cat-4prom6::gfp (-629/-3)	+	NSM, HSN, AIM, CEPs, ADE, PDE	88	87	85	82	
agattTACCCACGgctca → agattTACTTACGgctca							
cat-4prom69::gfp CSL MUT	-	NSM, HSN, AIM, CEPs, ADE, PDE	27	3	2		
cataaGTGGGAAaagat → cataaTTTGGAAaagat							
cat-4prom73::gfp CSL MUT	-	NSM, HSN, AIM, CEPs, ADE, PDE	5	12			
bas-1							
bas-1prom7::gfp (-166/-4)	+	NO	97	97	88		
tcaatCGTGGGAAatctt → tcaatTTTGGGAAatctt							
bas-1prom74::gfp CSL MUT	+/-	NO	78	67	58		
ctcggTTCCCATAgcgaa → ctcggGGGCCATAgcgaa							
bas-1prom90::gfp CSL MUT	-	NO	20	0			
cat-1							
cat-1prom14::gfp (-1088/-566)	+	NSM, HSN, CEPs, ADE, PDE	90	80	80	77	72
tatagTTCCCATAtataa → tatagTTCCTTTAtataa							
cat-1prom80::gfp CSL MUT	+/-	NSM, HSN, CEPs, ADE, PDE	48	20	0		
cat-1prom37::gfp (-180/+5)	+	Yes, Unidentified	98	95	92		
ttagaTTCCCACGgtctg → ttagaTTCCCTTTgtctg							
cat-1prom77::gfp CSL MUT	-	Yes, Unidentified	37	12	10		
mod-5							
mod-5prom8::gfp (+1490/+2133)	+	Yes, Unidentified	87	82	82		
gaataTTCCCACGcatgt → gaataTTCTTACGcatgt							
mod-5prom10::gfp CSL MUT	+/-	Yes, Unidentified	43	37	35		
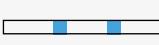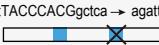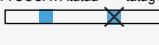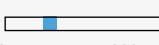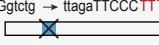
Supplementary Figure 1

Supplementary Figure 1. Primary data for CSL/LAG-1 binding site mutational analysis of the ADF serotonin pathway gene CRMs

A) Primary data for the scanning mutation analysis of *tph-1* minimal CRM from figure 1D. Each number represents the % of GFP cells in a particular transgenic line. +: > 80% of mean wild type construct expression, +/−: values indicate a penetrance of 80- 20% the mean wild type expression value; −: values are less than 20% of mean wild type values. "Other expression" refers to expression in other neurons.

B) A single copy of the CSL motif is not sufficient to drive ADF expression. Results of the *tph-1prom45* construct that consists of one copy of the first 40bp of the *tph-1p17* minimal CRM cloned in front of the *gcy-5* minimal promoter which is expressed only in the ASER neuron.

C) Primary data for the mutational analysis of predicted CSL binding sites from figure 1G. Above each construct, the wild type consensus sequence is included in capital letters in the context of a longer region and after the arrow introduced point mutations are highlighted in red. Each number represents the % of GFP cells in a particular transgenic line. +, +/- and - are the same as in A. "Other expression" refers to expression in other neurons.