

Supporting text

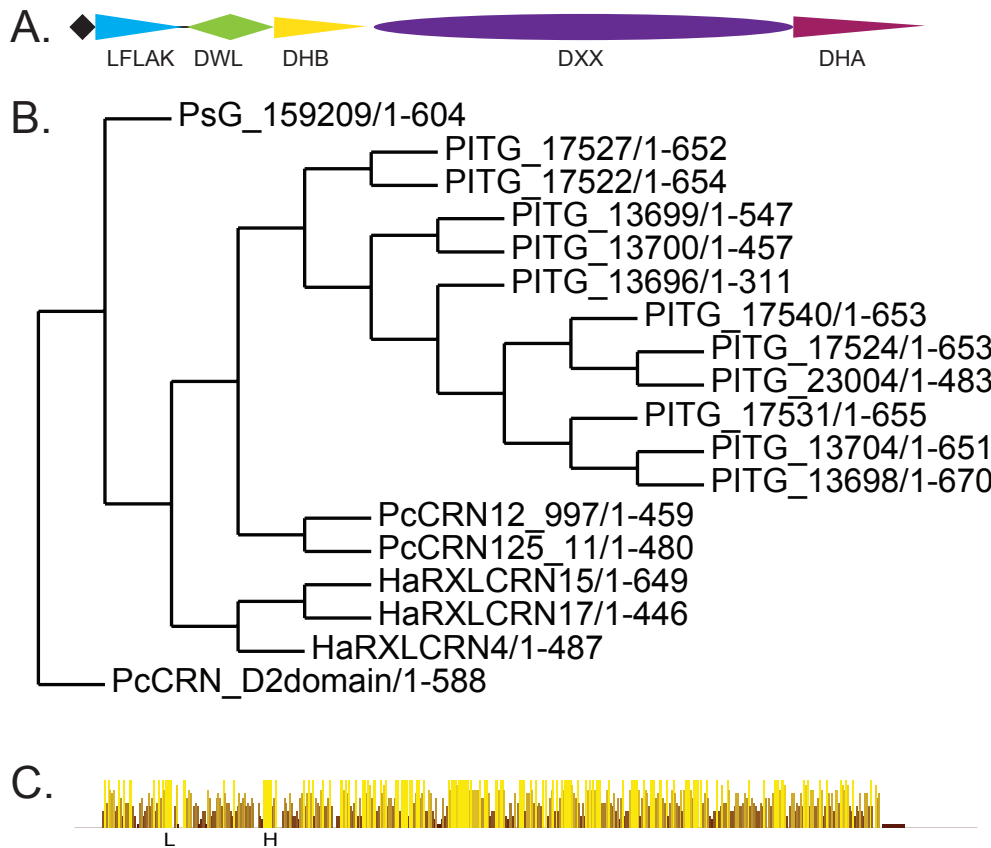


Figure S1

DHB-DXX-DHA domain containing CRN effectors and their conservation.

A) Diagram showing domain structure for the CRN effectors used in this study. CRNs contain a non-canonical putative signal peptide (black diamond), two highly conserved N-terminal domains and three separate C-terminal domains. B) Phylogenetic reconstruction of DHB-DXX-DHA domain containing CRNs, based on maximum likelihood clustering of only the C-terminal domains using 100 bootstraps. C) Conservation motif for DHB-DXX-DHA domain containing Hpa and PcCRNs. Bright yellow bars show highly conserved parts (80% similarity – 100% identical), darker bars are more divergent. LFLAK and HVLVVVP domain are indicated with L and H respectively.

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AtTCP14/1-489      1 MQKPTSSILNVIMDGGDSVGGGGGDDHHRHLHHHR-----PTFPQLLGKHD 49
tTCP14-1/1-416    1 -----MEGGGGDDHLHH-HHHNHQHHQHQQYRPNFPFQLLEKKE- 40
tTCP14-2/1-410    1 -----MDGGGGDDHLQRHQHNHRSI-----ATFPQLLEKKE- 32

AtTCP14/1-489     50 DDNHQQQPSPSSSSSLFSLHQHQLSQSQPQSQSQKSPQTTQKELQQTQEE SAVVAKK 109
tTCP14-1/1-416    41 -----DEPCSSSSAANNINYP SLAISP SDTNTNINPNS-----NDLQITVAST-ETAKK 88
tTCP14-2/1-410    33 -----DEACSSSSNAAAAYTTSLAISNTD-NTHTNPNTPRSTISTLQISASGA-DT SKK 85

AtTCP14/1-489     110 PP LKRA STKDRHTKVDGRGRRIRMP ALCAARVFQLTREL GHKSD GETIEWLLQQAEP SVI 169
tTCP14-1/1-416    89 PA PKRT STKDRHTKVDGRGRRIRMP ALCAARVFQLTREL GHKSD GETIEWLLQQAEP AVI 148
tTCP14-2/1-410    86 PPP KRT STKDRHTKVDGRGRRIRMP ALCAARVFQLTREL GHKSD GETIEWLLQQAEP AVI 145

AtTCP14/1-489     170 AATGTGTIPANFTSLNISLRSSGSSMSLP SHFRSAASTFSPNNIFSPAMLQQQQQQQRGG 229
tTCP14-1/1-416    149 AATGTGTIPANFTSLNISLRSSGSSMSVPSQLRSS-----YFNPNFSLQRRSLF-Q 199
tTCP14-2/1-410    146 AATGTGTIPANFTSLNISLRSSGSSMSVPSQLRSS-----YFNPNFSLQRRGLFP 197

AtTCP14/1-489     230 GVG FHHPHLQGRAPTSSLFP GIDNFTPTTSLNLFHNPTKQEGDQDS EELNSEK-----K 283
tTCP14-1/1-416    200 GIGLS-----SDRSATTTLL-----NFQTGNSNLH-QFQAKQEMRDNSLDLLET S-IEESLS 249
tTCP14-2/1-410    198 GIGLS-----TDT SATTLL-----NFQSANLSSNIQLQTKPELRDNSIDLTESSPAEDNLS 248

AtTCP14/1-489     284 RR IQTTSDLHQQQQHQH-----DQIGGYTLQSSNSGSTATAAAAQQIPGNFWMVAAAAA 339
tTCP14-1/1-416    250 RKRRLDLDLQEQQQNQQQNEQQMGSYLLQSSSSGTMP TSHSS--IPANFWMLTN---- 303
tTCP14-2/1-410    249 RKRRLDLDLEQQQHQQQ-----QQMGSYLLQSS-TGTMP TSHSS--IPANFWMTNP I-- 299

AtTCP14/1-489     340 GGGGGNNNQ TGG LMTASIGTGGGGGEPVWTFP SINTAA---AALYRSGVSGVPSGAVSSG 396
tTCP14-1/1-416    304 -----NNTQV-----LGGDPVWTFP SVNNSGAAAAALYR-----STMSSG 338
tTCP14-2/1-410    300 -----PSNQV-----MGGDP IWP FQSVNSG---ALYR-----GTMP SG 330

AtTCP14/1-489     397 LHF MNFAAPMAFLT GQQQLATT SNHEINEDSNNNEGGRSDGGDHHNTQRHHHQH HHH 456
tTCP14-1/1-416    339 LHF MNFPTPVALLP TQQ-----FGAGSN---GSTLAG-----EGQL 371
tTCP14-2/1-410    331 LQFMNFPTSVALLPSQQ-----LGGSSGGGGGNNGLG-----EGQL 367

AtTCP14/1-489     457 NILSGLNQYGRQVSG--DSQASGSLG---GGDEEDQD----- 489
tTCP14-1/1-416    372 GMVTGLNPY-RPCSGVSESQASGSHSHHGGGGGGDDRHDSTSHHNS 416
tTCP14-2/1-410    368 GMFAGLNPY-RGGGGVSESQASGSHSHH--GGGTDDRHD TSHHS- 409

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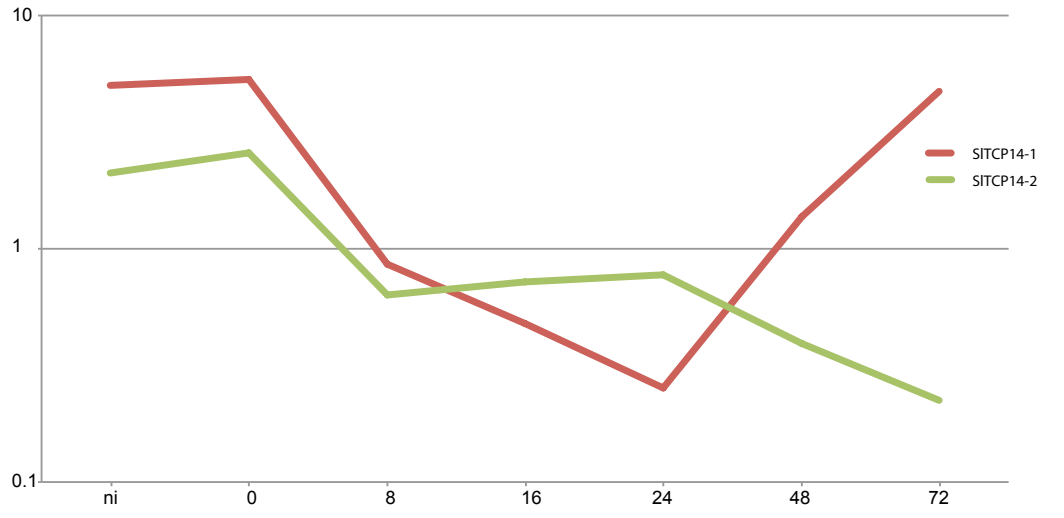


Figure S2

TCP transcription factors conservation and expression patterns.

A) MUSCLE alignment of AtTCP14 and two tomato homologues. Levels of similarity are shown in purple (dark = high similarity). Underlined are conserved basic regions, boxed the helices of the Helix Loop Helix motif. Conserved functional Cysteine is marked with * B) Microarray expression data for tomato TCP14 candidates.

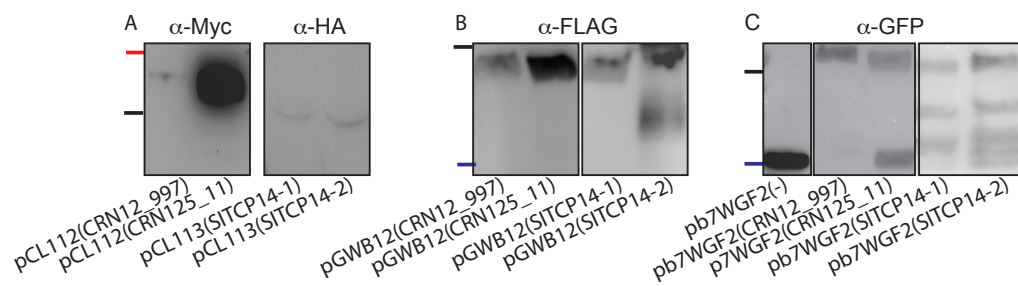


Figure S3

Stable expression of fusion proteins used in this study.

A) Fusion proteins for BiFC microscopy. B) Proteins used for phenotyping assays. C) for Co-IP

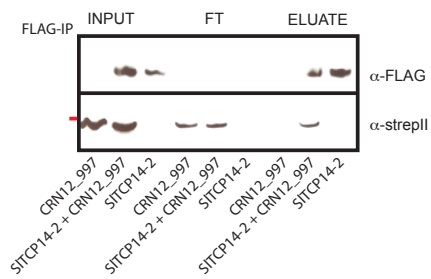


Figure S04

Reversed Co-IP of CRN12_997 and TCP14-2

FLAG-IP of FLAG tagged TCP14-2 co-immunoprecipitates CRN12_997.