

Supplemental legends and Data for:

Identification of evening complex associated proteins in *Arabidopsis* by affinity purification and mass spectrometry.

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Figure S1. Characterization of ELF4::ELF4-HFC complementation lines. A) Multiple lines independent ELF4::ELF4-HFC transgenic lines complement the *elf4-3* loss of function allele and restore *CAB::LUC* rhythms. Seedlings were entrained in 12 hours light and 12 hours dark conditions for 6 days before transferring to constant light. n= 16, error bars= 95% confidence interval. B) Scatter plots of average period length of ELF4::ELF4-HFC complementation lines. Measurements were repeated twice in independent biological experiments with similar results. C) Relative amplitude error (RAE) plots of complementation lines. The line at RAE =0.6 represents the upper bounds of values that are considered reliably rhythmic. D) ELF4::ELF4-HFC complementation lines rescue hypocotyl elongation defects of *elf4-3* mutants. Scatter plots show of hypocotyl length of the independent insertion lines. N≥20, line is the mean, and error is 95% confidence interval. Measurements were repeated twice in independent biological experiments with similar results.

Figure S2. Characterization of circadian expression patterns of identified co-interacting proteins. Data was derived from a circadian time course analysis in the *Col* background (110). The genes identified by AP-MS were determined to have a circadian expression pattern if their expression matched a cosine wave with an adjusted p value of  $\leq 0.05$ , and were graphed. Black indicates genes common to both ELF4 and ELF3 pull downs (any genetic background), blue indicates genes specific to ELF4 pulldowns (any genetic background), and red are specific to ELF3 pulldowns (any genetic background).

Figure S3. Characterization of the ELF4::ELF4-HFC *elf3-1 elf4-3* lines. A) ELF4::ELF4-HFC *elf3-1 elf4-3* is arrhythmic. Comparison of wild type, *elf4-3 elf3-1*, ELF4::ELF4-HFC-51 *elf4-3*, and ELF4::ELF4-HFC *elf3-1 elf4-3* in constant light conditions. Seedlings were entrained in 12 hours light and 12 hours dark conditions for 6 days before transferring to constant light. n= 16, error bars= s.e.m. B) RAE plots of wild type, *elf4-3 elf3-1*, ELF4::ELF4-HFC-51 *elf4-3*, and ELF4::ELF4-HFC *elf3-1 elf4-3* lines. The line at RAE =0.6 represents the upper bounds of values that are considered reliably rhythmic. C) Comparison of hypocotyl elongation phenotypes of wild type, *elf4-3 elf3-1*, ELF4::ELF4-HFC-51 *elf4-3*, and ELF4::ELF4-HFC *elf3-1 elf4-3* lines. N=20. Measurements were repeated twice with similar results. Note that *wild type*, ELF4::ELF4-HFC-51 *elf4-3*, and *elf4-3* mutant data for all subpanels are shared with Figure 1 and S1, and were re-graphed for comparison.

Figure S4. Characterization of ELF3::ELF3-HFC complementation lines. A) Multiple lines independent ELF3::ELF3-HFC transgenic lines complement the *elf3-2* loss of function allele and restore *CCA1::LUC* rhythms. Seedlings were entrained in 12 hours light and 12 hours dark conditions for 6 days before transferring to constant light. n= 8, error = 95% confidence interval. Measurements were repeated twice in independent biological experiments with similar results. B) RAE plots of ELF3::ELF3-HFC complementation lines. The line at RAE =0.6 represents the upper bounds of values that are considered reliably rhythmic. C) Scatter plots of the period length of wild type, ELF3::ELF3-HFC #1 *elf3-2*,

ELF3::ELF3-HFC #3 *elf3-2*, and ELF3::ELF3-HFC #15 *elf3-2*. Line is at mean, n= 8, error = 95% confidence interval. Measurements were repeated twice in independent biological experiments with similar results. D) ELF3::ELF3-HFC complementation lines also rescue hypocotyl elongation defects of *elf3-2* mutants. Scatter plots show the average and range of hypocotyl length of the independent insertion lines. N= 20. Measurements were repeated twice in independent biological experiments with similar results.

Figure S5. Characterization of the ELF3::ELF3-HFC #3 *elf3-2 elf4-2* lines. A) ELF3::ELF3-HFC #3 *elf3-2 elf4-2* has dampened rhythms. Comparison of wild type, *elf4-2*, ELF3::ELF3-HFC #3 *elf3-2*, and ELF3::ELF3-HFC #3 *elf3-2 elf4-2* in constant light conditions. Seedlings were entrained in 12 hours light and 12 hours dark conditions for 6 days before transferring to constant light. error = 95% confidence interval. Measurements were repeated twice in independent biological experiments with similar results. B) RAE plots of wild type, *elf4-2*, ELF3::ELF3-HFC #3 *elf3-2*, and ELF3::ELF3-HFC #3 *elf3-2 elf4-2*. The line at RAE =0.6 represents the upper bounds of values that are considered reliably rhythmic. Measurements were repeated twice in independent biological experiments with similar results. C) Scatter plots of the period length of wild type, *elf4-2*, ELF3::ELF3-HFC #3 *elf3-2*, and ELF3::ELF3-HFC #3 *elf3-2 elf4-2* lines. Line is at mean, n= 8, error = 95% confidence interval. Measurements were repeated twice in independent biological experiments with similar results. D) Characterization ELF3::ELF3-HFC #3 *elf4-2* lines hypocotyl elongation phenotypes. Scatter plots show the average and range of hypocotyl length of the independent insertion lines. N= 20. Measurements were repeated twice in independent biological experiments with similar results. Note that *wild type*, ELF3::ELF3-HFC #3 *elf3-2* and *elf3-2* mutant data in all subpanels are shared with Figure S4, and re-graphed for comparison.

Figure S6. Characterization of the circadian rhythmicity of the *mlk* lines. A) Wild type compared to the *mlk* single mutants. Seedlings were entrained in 12 hours light and 12 hours dark conditions for 6 days before transferring to constant red light. N=15-16, error = 95% confidence interval. Measurements were

repeated twice with similar results. B) RAE plots of wild type and *mlk* single mutants. The line at RAE =0.5 represents the upper bounds of values that are considered reliably rhythmic. Measurements were repeated twice with similar results. C) Wild type compared to the *mlk* double mutants. Seedlings were entrained in 12 hours light and 12 hours dark conditions for 6 days before transferring to constant red light. N=15-16, error = 95% confidence interval. Measurements were repeated twice in independent biological experiments with similar results. D) RAE plots of wild type and *mlk* double mutants. The line at RAE =0.6 represents the upper bounds of values that are considered reliably rhythmic. Measurements were repeated twice in independent biological experiments with similar results. E) Wild type compared to the *mlk* triple mutants. Seedlings were entrained in 12 hours light and 12 hours dark conditions for 6 days before transferring to constant red light. N=15-16, error = 95% confidence interval. Measurements were repeated twice with similar results. F) RAE plots of wild type and *mlk* triple mutants. The line at RAE =0.6 represents the upper bounds of values that are considered reliably rhythmic. Measurements were repeated twice in independent biological experiments with similar results. Note that the data for *wild type* are shared among all panels for comparison.

**Table S1. Gene ontology enrichment of proteins that co-precipitate with ELF4-HFC in the elf4-3 background. AGRIGO website (<http://bioinfo.cau.edu.cn/agriGO/>) output for queried Arabidopsis locus IDs that co-precipitate with ELF4::ELF4-HFC #51.**

GO term	Ontology	Description	Number in input list	Number in Background	p-value	FDR
GO:0048511	Process	rhythmic process	6	75	9.80E-13	1.10E-10
GO:0007623	Process	circadian rhythm	6	75	9.80E-13	1.10E-10
GO:0010017	Process	red or far-red light signaling pathway	5	41	1.30E-11	9.80E-10
GO:0050789	Process	regulation of biological process	13	3697	1.30E-10	7.10E-09
GO:0009639	Process	response to red or far red light	6	210	3.80E-10	1.70E-08
GO:0065007	Process	biological regulation	13	4188	6.00E-10	2.30E-08
GO:0009416	Process	response to light stimulus	7	596	4.30E-09	1.40E-07
GO:0009314	Process	response to radiation	7	613	5.20E-09	1.50E-07
GO:0050794	Process	regulation of cellular process	11	3375	2.20E-08	5.50E-07
GO:0051716	Process	cellular response to stimulus	7	840	4.40E-08	1.00E-06
GO:0007242	Process	intracellular signaling cascade	6	659	3.00E-07	6.20E-06
GO:0009605	Process	response to external stimulus	5	429	1.10E-06	2.00E-05
GO:0009628	Process	response to abiotic stimulus	7	1471	1.90E-06	3.30E-05
GO:0019219	Process	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7	1847	8.50E-06	0.00012
GO:0031326	Process	regulation of cellular biosynthetic process	7	1881	9.60E-06	0.00012
GO:0009889	Process	regulation of biosynthetic process	7	1881	9.60E-06	0.00012
GO:0051171	Process	regulation of nitrogen compound metabolic process	7	1888	9.80E-06	0.00012
GO:0010556	Process	regulation of macromolecule biosynthetic process	7	1843	8.40E-06	0.00012
GO:0045449	Process	regulation of transcription	7	1802	7.30E-06	0.00012
GO:0007165	Process	signal transduction	6	1228	1.10E-05	0.00012
GO:0006350	Process	transcription	7	1923	1.10E-05	0.00012
GO:0009791	Process	post-embryonic development	5	705	1.20E-05	0.00012
GO:0080090	Process	regulation of primary metabolic process	7	1952	1.20E-05	0.00012
GO:0010468	Process	regulation of gene expression	7	2001	1.40E-05	0.00013
GO:0031323	Process	regulation of cellular metabolic process	7	2036	1.60E-05	0.00014
GO:0060255	Process	regulation of macromolecule metabolic process	7	2060	1.70E-05	0.00015
GO:0032501	Process	multicellular organismal process	7	2094	1.90E-05	0.00016
GO:0019222	Process	regulation of metabolic process	7	2210	2.70E-05	0.00022
GO:0006139	Process	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	8	3198	3.20E-05	0.00025
GO:0006355	Process	regulation of transcription, DNA-dependent	5	987	5.90E-05	0.00044
GO:0051252	Process	regulation of RNA metabolic process	5	996	6.10E-05	0.00044
GO:0032774	Process	RNA biosynthetic process	5	1040	7.50E-05	0.00051
GO:0006351	Process	transcription, DNA-dependent	5	1039	7.50E-05	0.00051
GO:0006807	Process	nitrogen compound metabolic process	8	3826	0.00012	0.00077
GO:0009987	Process	cellular process	13	11684	0.00015	0.00095
GO:0050896	Process	response to stimulus	8	4057	0.00018	0.0011
GO:0043170	Process	macromolecule metabolic process	10	7127	0.0003	0.0018
GO:0044238	Process	primary metabolic process	11	8995	0.0004	0.0024
GO:0044249	Process	cellular biosynthetic process	8	4925	0.00068	0.0036
GO:0034645	Process	cellular macromolecule biosynthetic process	7	3661	0.00065	0.0036
GO:0009059	Process	macromolecule biosynthetic process	7	3685	0.00068	0.0036
GO:0016070	Process	RNA metabolic process	5	1657	0.00065	0.0036
GO:0048856	Process	anatomical structure development	5	1726	0.00078	0.0041
GO:0044260	Process	cellular macromolecule metabolic process	9	6447	0.0008	0.0041
GO:0009058	Process	biosynthetic process	8	5118	0.00088	0.0044
GO:0010467	Process	gene expression	7	3962	0.0011	0.0051
GO:0007275	Process	multicellular organismal development	5	2020	0.0016	0.0076
GO:0044237	Process	cellular metabolic process	10	8722	0.0016	0.0077
GO:0008152	Process	metabolic process	11	10614	0.0018	0.0084
GO:0032502	Process	developmental process	5	2304	0.0028	0.013

AGRIGO query using these gene IDs

AT2G25930  
 AT3G46640  
 AT1G12910  
 AT3G22380  
 AT5G61380  
 AT2G18790  
 AT5G35840  
 AT4G18130  
 AT4G16250  
 AT1G09570  
 AT2G32950  
 AT2G46340  
 AT5G43630  
 AT2G16365  
 AT3G13670  
 AT3G19390  
 AT5G10450

Background list contained annotated 37767 genes from TAIR9

**Table S2. Gene ontology enrichment of proteins that co-precipitate with ELF3::ELF3-HFC in the elf3-2 background. AGRIGO website (<http://bioinfo.cau.edu.cn/agriGO/>) output for queried Arabidopsis locus IDs that co-precipitate with ELF3::ELF3-HFC #3.**

GO term	Ontology	Description	Number in input list	Number in Backgro	p-value	FDR
GO:0048511	Process	rhythmic process	7	75	2.60E-13	2.90E-11
GO:0007623	Process	circadian rhythm	7	75	2.60E-13	2.90E-11
GO:0009639	Process	response to red or far red light	7	210	2.60E-10	1.40E-08
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GO:0009416	Process	response to light stimulus	8	596	1.30E-08	5.70E-07
GO:0009314	Process	response to radiation	8	613	1.60E-08	5.90E-07
GO:0009628	Process	response to abiotic stimulus	10	1471	8.40E-08	2.60E-06
GO:0050789	Process	regulation of biological process	14	3697	1.40E-07	3.80E-06
GO:0065007	Process	biological regulation	14	4188	6.60E-07	1.60E-05
GO:0009791	Process	post-embryonic development	7	705	8.90E-07	2.00E-05
GO:0050794	Process	regulation of cellular process	12	3375	3.20E-06	6.40E-05
GO:0045449	Process	regulation of transcription	9	1802	5.50E-06	0.0001
GO:0019219	Process	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	9	1847	6.70E-06	0.0001
GO:0031326	Process	regulation of cellular biosynthetic process	9	1881	7.70E-06	0.0001
GO:0009889	Process	regulation of biosynthetic process	9	1881	7.70E-06	0.0001
GO:0051171	Process	regulation of nitrogen compound metabolic process	9	1888	8.00E-06	0.0001
GO:0010556	Process	regulation of macromolecule biosynthetic process	9	1843	6.50E-06	0.0001
GO:0006350	Process	transcription	9	1923	9.20E-06	0.00011
GO:0080090	Process	regulation of primary metabolic process	9	1952	1.00E-05	0.00012
GO:0006139	Process	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	11	3198	1.30E-05	0.00014
GO:0010468	Process	regulation of gene expression	9	2001	1.30E-05	0.00014
GO:0031323	Process	regulation of cellular metabolic process	9	2036	1.50E-05	0.00015
GO:0060255	Process	regulation of macromolecule metabolic process	9	2060	1.60E-05	0.00015
GO:0032501	Process	multicellular organismal process	9	2094	1.80E-05	0.00017
GO:0044260	Process	cellular macromolecule metabolic process	15	6447	2.10E-05	0.00018
GO:0019222	Process	regulation of metabolic process	9	2210	2.80E-05	0.00024
GO:0051716	Process	cellular response to stimulus	6	840	3.80E-05	0.00031
GO:0006807	Process	nitrogen compound metabolic process	11	3826	7.10E-05	0.00054
GO:0043170	Process	macromolecule metabolic process	15	7127	7.20E-05	0.00054
GO:0007242	Process	intracellular signaling cascade	5	659	0.00014	0.001
GO:0044237	Process	cellular metabolic process	16	8722	0.00019	0.0013
GO:0044238	Process	primary metabolic process	16	8995	0.00028	0.0019
GO:0010467	Process	gene expression	10	3962	0.00049	0.0033
GO:0009987	Process	cellular process	18	11684	0.00053	0.0034
GO:0050896	Process	response to stimulus	10	4057	0.0006	0.0037
GO:0007275	Process	multicellular organismal development	7	2020	0.00069	0.0042
GO:0006355	Process	regulation of transcription, DNA-dependent	5	987	0.00087	0.0051
GO:0051252	Process	regulation of RNA metabolic process	5	996	0.0009	0.0052
GO:0032774	Process	RNA biosynthetic process	5	1040	0.0011	0.006
GO:0006351	Process	transcription, DNA-dependent	5	1039	0.0011	0.006
GO:0034645	Process	cellular macromolecule biosynthetic process	9	3661	0.0013	0.0067
GO:0009059	Process	macromolecule biosynthetic process	9	3685	0.0013	0.0069
GO:0016070	Process	RNA metabolic process	6	1657	0.0014	0.0073
GO:0032502	Process	developmental process	7	2304	0.0015	0.0075
GO:0008152	Process	metabolic process	16	10614	0.002	0.0097
GO:0007165	Process	signal transduction	5	1228	0.0023	0.011
GO:0044249	Process	cellular biosynthetic process	10	4925	0.0027	0.013
GO:0009058	Process	biosynthetic process	10	5118	0.0036	0.016
GO:0048856	Process	anatomical structure development	5	1726	0.0095	0.043

AGRIGO query using these gene IDs

AT2G40080  
AT3G46640  
AT5G59570  
AT3G22380  
AT5G61380  
AT1G12910  
AT1G72630  
AT2G06255  
AT1G17455  
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AT2G18790  
AT5G35840  
AT4G18130  
AT4G16250  
AT1G09570  
AT2G32950  
AT2G46340  
AT4G11110  
AT3G15354  
AT5G61270  
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AT2G16365  
AT5G06850  
AT3G42170  
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AT5G18190  
AT2G25760  
AT5G20630

Background list contained annotated 37767 genes from TAIR9



















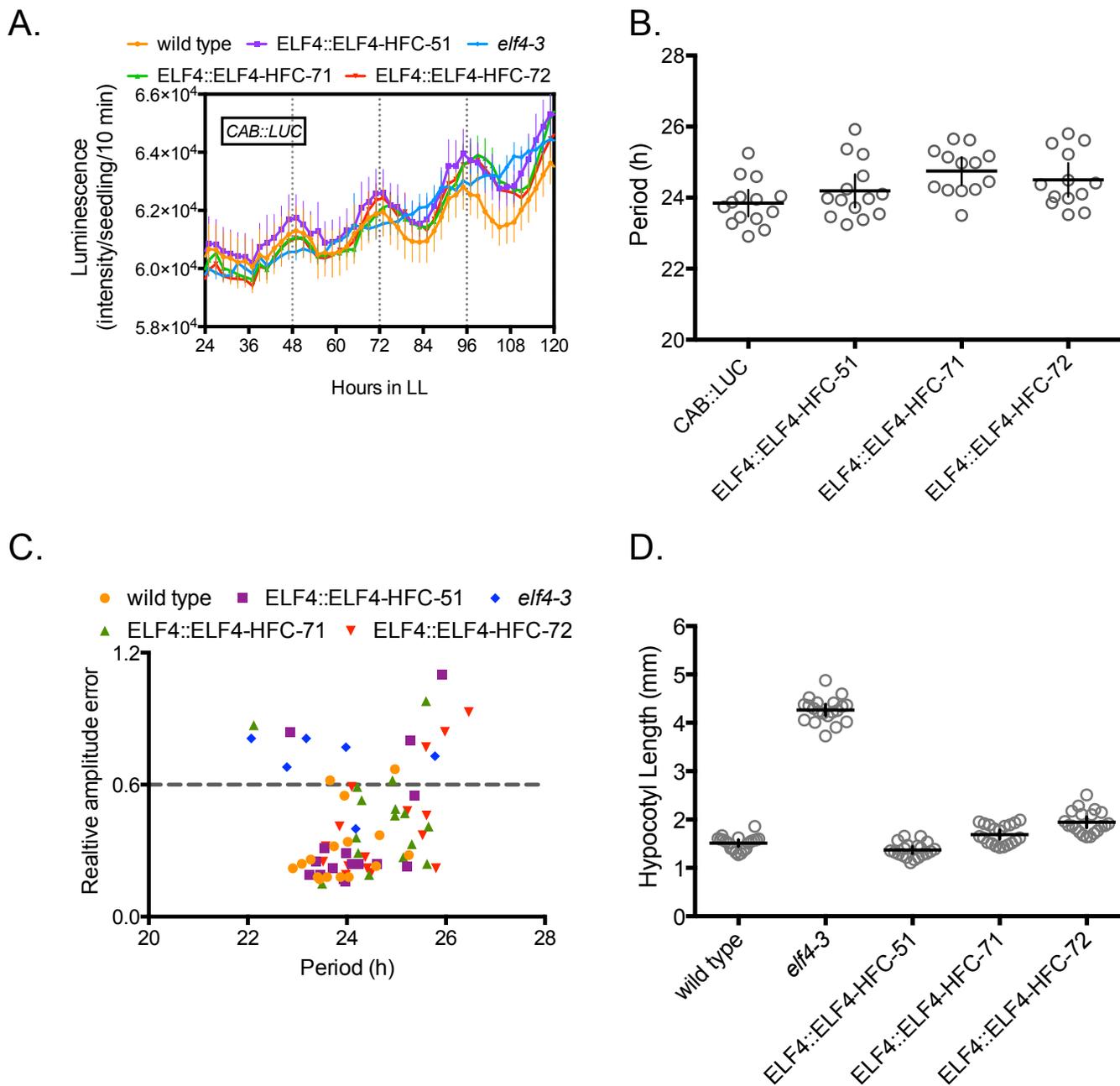




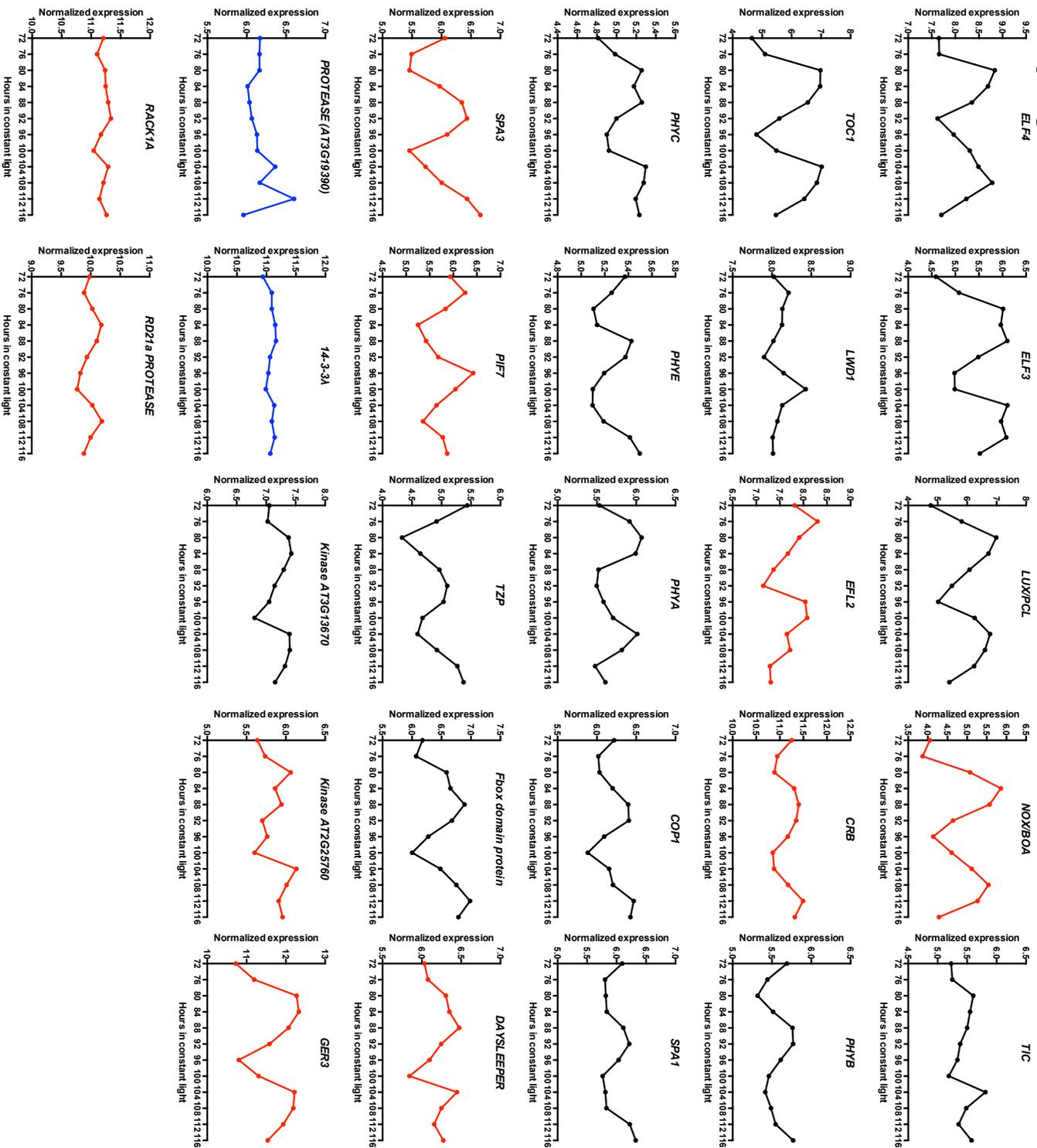


ELF3- <i>hnc</i> <i>phd8</i> nap 2	1	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% EEDPAFPYVNRG	99.70%	63.5	30.2	5.1	1,667.79
ELF3- <i>hnc</i> <i>phd8</i> nap 2	2	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% FQDVPNDGK	99.70%	67.5	29.4	4.4	1,137.05
ELF3- <i>hnc</i> <i>phd8</i> nap 2	3	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% FQSDGER	99.70%	57.2	30.1	20.9	1,144.59
ELF3- <i>hnc</i> <i>phd8</i> nap 2	4	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% LKQKAAK	99.00%	57.8	29.1	13	812.416
ELF3- <i>hnc</i> <i>phd8</i> nap 2	5	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% LPHNDGAK	99.00%	57.7	27	26	911.482
ELF3- <i>hnc</i> <i>phd8</i> nap 2	6	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% LKQKAAK	99.70%	43.6	26.7	23.1	2,734.86
ELF3- <i>hnc</i> <i>phd8</i> nap 2	7	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% LKASQKLLLEKPKLQK	99.70%	85.9	25	83.6	1,312.08
ELF3- <i>hnc</i> <i>phd8</i> nap 2	8	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% LKQKAAK	99.70%	51	27.8	24.6	2,408.52
ELF3- <i>hnc</i> <i>phd8</i> nap 2	9	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% LKQKAAK	99.70%	86.1	28.5	78.6	1,978.75
ELF3- <i>hnc</i> <i>phd8</i> nap 2	10	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% LKQKAAK	99.70%	32.9	30.7	23.9	1,551.76
ELF3- <i>hnc</i> <i>phd8</i> nap 2	11	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% NLYVQKGGKAAKATGK	99.70%	117	30.9	13.1	1,612.04
ELF3- <i>hnc</i> <i>phd8</i> nap 2	12	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% GQSDSPSPDQSDGK	99.70%	64.6	29.1	5.6	1,614.77
ELF3- <i>hnc</i> <i>phd8</i> nap 2	13	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% QVNSLQKQVPRV	99.70%	68.9	30.2	5.1	1,661.81
ELF3- <i>hnc</i> <i>phd8</i> nap 2	14	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% SDNFAKQDQDQFKTK	99.70%	58.7	28.8	48.7	1,699.79
ELF3- <i>hnc</i> <i>phd8</i> nap 2	15	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% QPFFKAAQGGDNNAAKTTTITTTTTT	99.70%	64.6	31.1	5.3	1,315.23
ELF3- <i>hnc</i> <i>phd8</i> nap 2	16	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% DVNLTFLVPPSGQSDQVDR	99.70%	65.1	30.5	6.1	2,224.04
ELF3- <i>hnc</i> <i>phd8</i> nap 2	17	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% TTVVETTR	99.00%	50	28	40.8	907.464
ELF3- <i>hnc</i> <i>phd8</i> nap 2	18	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% VFKQLTVLR	99.70%	39.4	28.7	23.6	1,392.76
ELF3- <i>hnc</i> <i>phd8</i> nap 2	19	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT202990.1	FAM10_20101214.fam	77,204.80	100.00%	19	28	35	0.21%	38.00% NQVQNKALR	99.70%	73.1	36.2	16.2	1,915.52
ELF3- <i>hnc</i> <i>phd8</i> nap 2	20	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	8	12	0.07%	60.40% NNVALEAGQSDPAAWVNLDR	99.70%	70.6	25.7	64.0	2,314.98
ELF3- <i>hnc</i> <i>phd8</i> nap 2	21	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	8	12	0.07%	60.40% NNVALEAGQSDPAAWVNLDR	99.70%	306	28.6	8.2	1,514.82
ELF3- <i>hnc</i> <i>phd8</i> nap 2	22	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	8	12	0.07%	60.40% LKQKAAKNGKAR	99.70%	55.3	30.4	47.4	1,538.77
ELF3- <i>hnc</i> <i>phd8</i> nap 2	23	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	8	12	0.07%	60.40% VNNVQKGLVDFVPSGSGK	99.70%	56.3	29.4	48.1	2,162.98
ELF3- <i>hnc</i> <i>phd8</i> nap 2	24	Symbolic: ELF3, PKZ02   Hydroxyproline-rich glycoprotein family protein   chr2:11059459-11061378 FORWARD LENGTH=695	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	1	2	6	0.04%	18.00% LKQKAAK	99.70%	17.2	24.4	2.4	1,025.54
ELF3- <i>hnc</i> <i>phd8</i> nap 2	25	Symbolic: PCL1, LUX   Homodomain-like superfamily protein   chr3:17381248-1738219 FORWARD LENGTH=923	AT204664.1	LAT304664.0	18,648.50	100.00%	2	2	6	0.04%	18.00% PVDVHARLQK	99.70%	32.8	25	51.6	1,197.70
ELF3- <i>hnc</i> <i>phd8</i> nap 2	26	Symbolic: PCL1, LUX   Homodomain-like superfamily protein   chr3:17381248-1738219 FORWARD LENGTH=923	AT204664.1	LAT304664.0	18,648.50	100.00%	1	2	6	0.04%	18.00% GGGGPPNNSNNWVEEIVDRSSSSSSGSK	99.70%	80	27	0	3,028.27
ELF3- <i>hnc</i> <i>phd8</i> nap 2	27	Symbolic: PCL1, LUX   Homodomain-like superfamily protein   chr3:17381248-1738219 FORWARD LENGTH=923	AT204664.1	LAT304664.0	18,648.50	100.00%	1	2	6	0.04%	18.00% LKQKAAK	99.70%	65.8	25.4	27.4	2,271.95
ELF3- <i>hnc</i> <i>phd8</i> nap 2	28	Symbolic: TIC   Time for caffeine   chr3:7913181-7913879 FORWARD LENGTH=150	AT202280.1	LAT302280.2	16,449.80	100.00%	4	4	5	0.03%	4.13% ENAKDHFVQKSDPSTDR	99.70%	54.3	26.4	43.6	1,317.63
ELF3- <i>hnc</i> <i>phd8</i> nap 2	29	Symbolic: TIC   Time for caffeine   chr3:7913181-7913879 FORWARD LENGTH=150	AT202280.1	LAT302280.2	16,449.80	100.00%	4	4	5	0.03%	4.13% NQSDQFKT	99.70%	30.9	29	19.1	1,330.22
ELF3- <i>hnc</i> <i>phd8</i> nap 2	30	Symbolic: TIC   Time for caffeine   chr3:7913181-7913879 FORWARD LENGTH=150	AT202280.1	LAT302280.2	16,449.80	100.00%	4	4	5	0.03%	4.13% SGGSGGKGLDQSPVTR	99.70%	65.1	31.3	56.3	1,979.99
ELF3- <i>hnc</i> <i>phd8</i> nap 2	31	Symbolic: TIC   Time for caffeine   chr3:7913181-7913879 FORWARD LENGTH=150	AT202280.1	LAT302280.2	16,449.80	100.00%	4	4	5	0.03%	4.13% GEAADKDFEAK	99.70%	53.7	28.3	44.9	1,917.63
ELF3- <i>hnc</i> <i>phd8</i> nap 2	32	Symbolic: TIC   Time for caffeine   chr3:7913181-7913879 FORWARD LENGTH=150	AT202280.1	LAT302280.2	16,449.80	100.00%	4	4	5	0.03%	4.13% SGGSGGKGLDQSPVTR	99.70%	60.9	30.9	19.1	1,979.99
ELF3- <i>hnc</i> <i>phd8</i> nap 2	33	Symbolic: TOCA, APR1, PRL1, AT2OC1   C/EBP motif-containing response regulator protein   chr5:2467540-2467876 FORWARD LENGTH=638	AT206180.1	FAM10_20101214.fam	69,269.40	100.00%	3	3	4	0.02%	7.28% FQVNSAGSKPK	99.70%	42.4	29.5	31.5	2,449.60
ELF3- <i>hnc</i> <i>phd8</i> nap 2	34	Symbolic: TOCA, APR1, PRL1, AT2OC1   C/EBP motif-containing response regulator protein   chr5:2467540-2467876 FORWARD LENGTH=638	AT206180.1	FAM10_20101214.fam	69,269.40	100.00%	3	3	4	0.02%	7.28% GNSHQKNEVSWATPAPHAR	99.70%	41.7	31.2	34	2,209.26
ELF3- <i>hnc</i> <i>phd8</i> nap 2	35	Symbolic: TOCA, APR1, PRL1, AT2OC1   C/EBP motif-containing response regulator protein   chr5:2467540-2467876 FORWARD LENGTH=638	AT206180.1	FAM10_20101214.fam	69,269.40	100.00%	3	3	4	0.02%	7.28% NQVQNKALR	99.70%	42.4	29.5	31.5	2,449.60
GRF- <i>hnc</i> <i>Col</i> nap 1	1	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	6	7	20	0.04%	30.00% NNVALEAGQSDPAAWVNLDR	99.70%	84.2	27.2	70.7	1,515.84
GRF- <i>hnc</i> <i>Col</i> nap 1	2	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	2	6	7	0.02%	30.00% VNNVQKGLVDFVPSGSGK	99.70%	87.1	30.1	81.1	2,146.99
GRF- <i>hnc</i> <i>Col</i> nap 1	3	Symbolic: PVE1   Phytochrome E 1   chr8:10042112-10042848 REVERSE LENGTH=112	AT648130.1	FAM10_20101214.fam	12,213.10	100.00%	4	6	0.03%	3.87% NNVALEAGQSDPAAWVNLDR	99.70%	101	31.5	101	2,566.23	
GRF- <i>hnc</i> <i>Col</i> nap 1	4	Symbolic: PVE1   Phytochrome E 1   chr8:10042112-10042848 REVERSE LENGTH=112	AT648130.1	FAM10_20101214.fam	12,213.10	100.00%	2	4	6	0.03%	3.87% NNVALEAGQSDPAAWVNLDR	99.70%	173	30.5	143	2,280.08
GRF- <i>hnc</i> <i>Col</i> nap 1	5	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	3	8	21	0.11%	48.00% NNVALEAGQSDPAAWVNLDR	99.70%	77.1	25.1	77.1	2,319.98
GRF- <i>hnc</i> <i>Col</i> nap 2	1	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	3	8	21	0.11%	48.00% NNVALEAGQSDPAAWVNLDR	99.70%	132	27.2	127	1,512.84
GRF- <i>hnc</i> <i>Col</i> nap 2	2	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	8	21	0.11%	48.00% VNNVQKGLVDFVPSGSGK	99.70%	99.4	29.4	97.4	2,162.08
GRF- <i>hnc</i> <i>Col</i> nap 2	3	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	10	28	0.15%	49.50% NNVALEAGQSDPAAWVNLDR	99.70%	89.1	26.6	89.1	2,302.99
GRF- <i>hnc</i> <i>Col</i> nap 2	4	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	10	28	0.15%	49.50% NNVALEAGQSDPAAWVNLDR	99.70%	107	27.2	96.6	1,512.84
GRF- <i>hnc</i> <i>Col</i> nap 2	5	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	10	28	0.15%	49.50% NNVALEAGQSDPAAWVNLDR	99.10%	109	28.6	10.9	2,460.07
GRF- <i>hnc</i> <i>Col</i> nap 2	6	Symbolic: ELF4   Protein of unknown function [DFP13131]   chr2:16784548-16784880 REVERSE LENGTH=111	AT204000.1	FAM10_20101214.fam	12,375.40	100.00%	4	10	28	0.15%	49.50% VNNVQKGLVDFVPSGSGK	99.70%	100	29.7	109.2	2,146.99

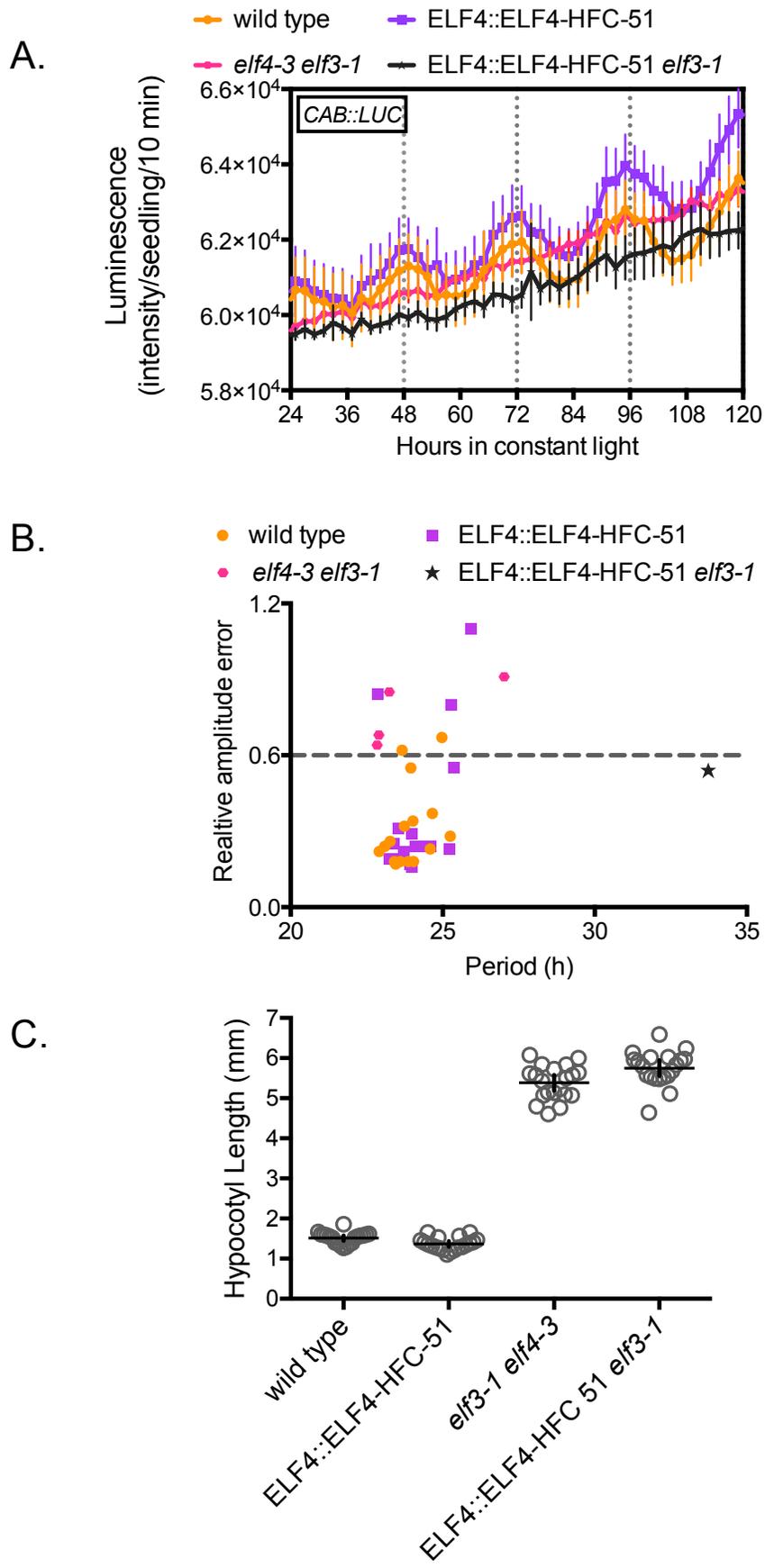
# Supplementary Figure S1



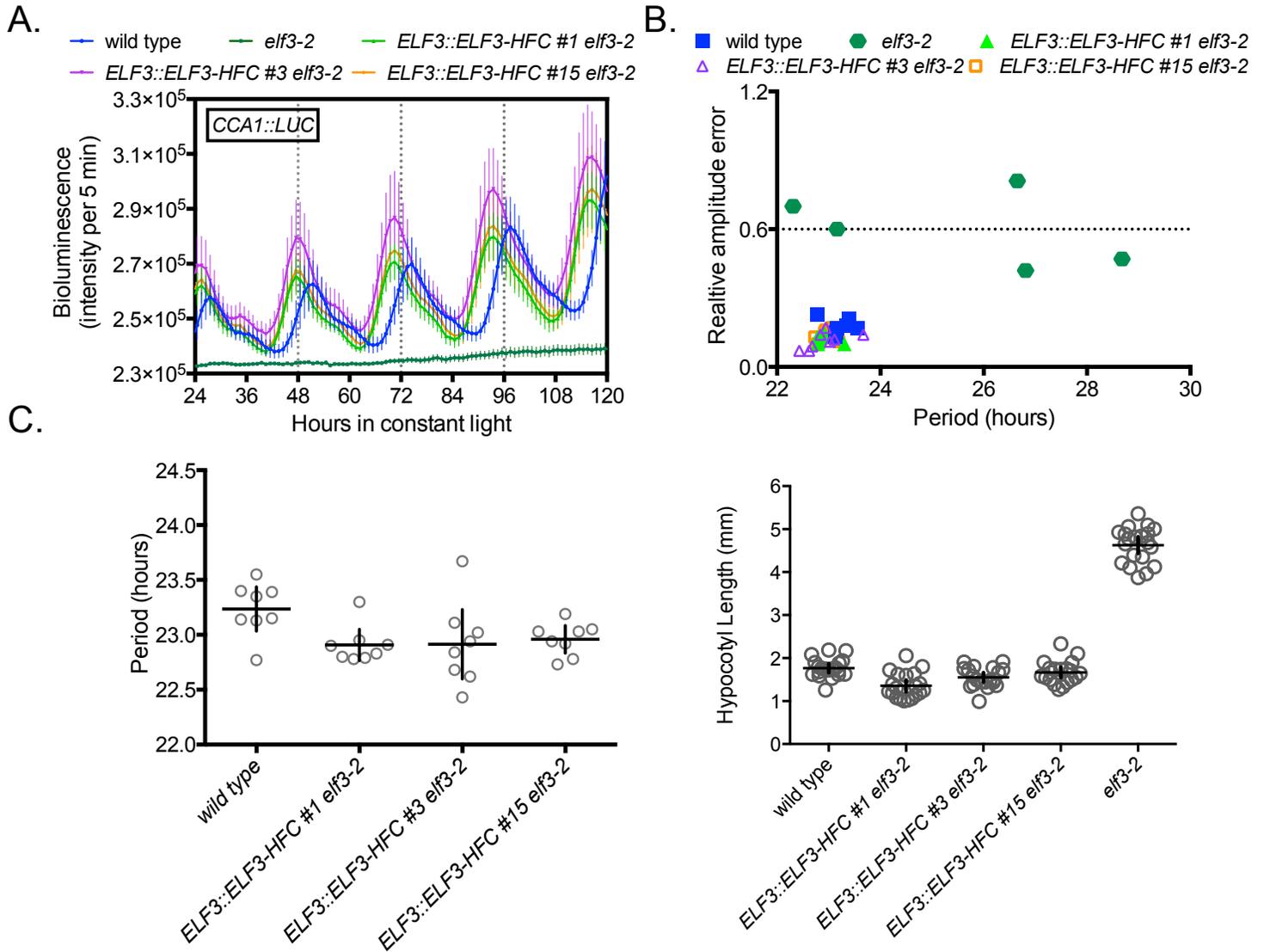
# Supplementary Figure S2



## Supplementary Figure S3

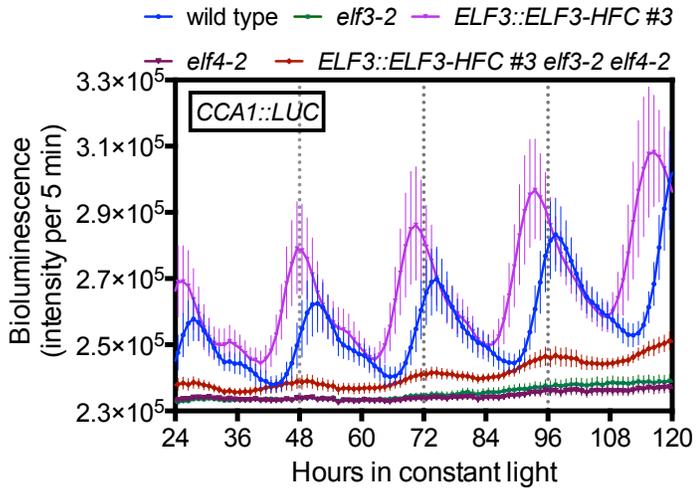


# Supplementary Figure S4

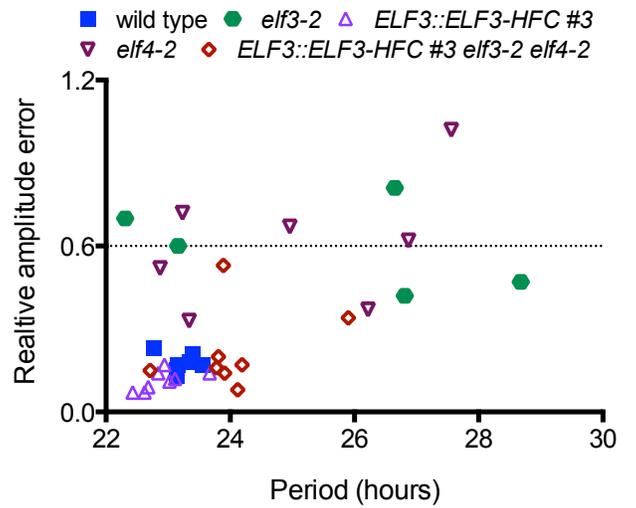


# Supplementary Figure S5

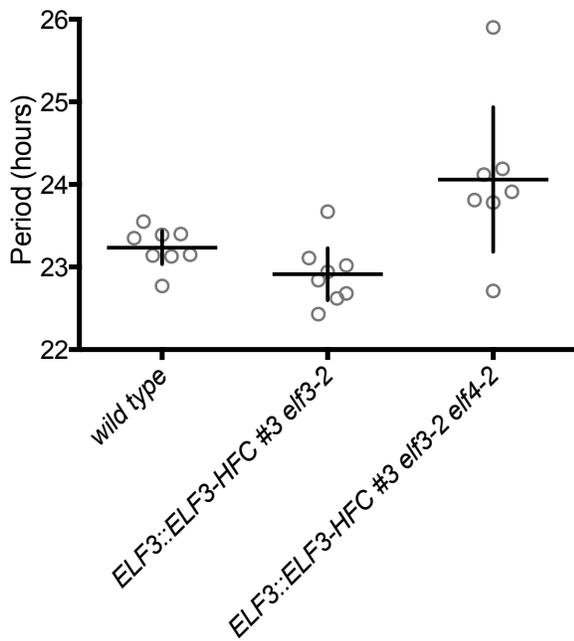
A.



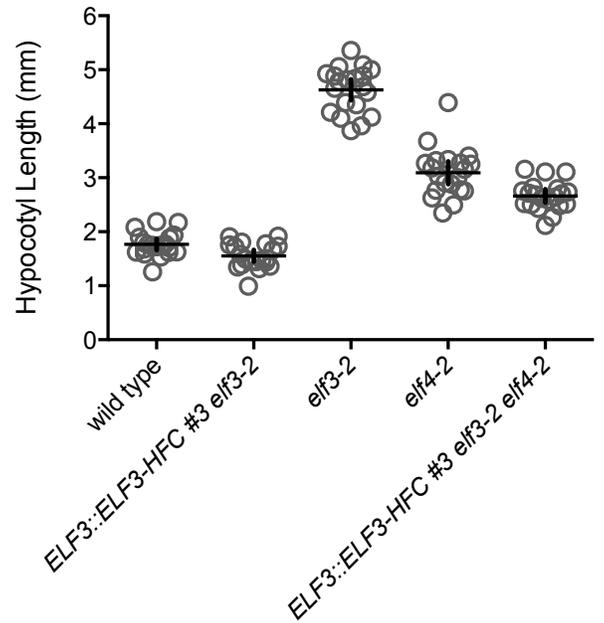
B.



C.



D.



# Supplementary Figure S6

