Supplemental Figures and Tables.

Figure S1. Scatter plots of differential genome-wide correlations between codon usage and mRNA levels between constitutive and facultative genes from indicated organisms and tissues. Pearson correlation coefficients are shown in Figure 1.

Figure S2. (A) Northern blot analysis of De-*Luc* and Opt-*Luc* mRNAs expressed under the control of the *Myc* core promoter and the *Myc* or DSCP IDR. (B) Northern blot analysis of De-*Luc* and Opt-*Luc* mRNA under control of the *Hsp70* core promoter with mutations in the left (MutL), middle (MutM), and right (MutR) 10 nt of the 20-nt CDE sequence. (C) Northern blot analysis of De-*Luc* and Opt-*Luc* mRNA expressed under control of the *Act5C* core promoter with indicated CDE sequences.

Figure S3. (A) Northern blot analysis of *gapdh* and U6 RNA levels in nuclear and total fractions. (B) Northern blot analysis of mRNA levels of *hph* and *Gal4* in indicated stable cell lines. (C) Quantification of the relative *hph* mRNA levels for experiment shown in panel A. (D) Quantification of the relative *Gal4* mRNA levels for experiment shown in panel A. (E) Positive and negative controls for Pol II CTD ChIP assay.

Figure S4. (A) Positive and negative controls for H3K27ac ChIP assay. (B) H3K9me3 ChIP assay for H3K9me3 over the 5' *Myc*-tag region of different constructs. qPCR primers amplify the 5' *Myc*-tag sequence, and data were normalized to F22. (C) H3K27me3 ChIP assay for H3K27me3 over the 5' *Myc*-tag region of indicated constructs. qPCR primers amplify the 5' *Myc*-tag sequence, and data were normalized to a region in 3L. (D) Positive and negative controls for H3K9me3 ChIP assay. (E) Positive and negative controls for H3K27me3 ChIP assay. (F) Positive and negative controls for H3 ChIP assay. Data are means ± SD. ns: not significant.

Figure S5. Northern blot analyses showing the downregulation of the indicated mRNA after introducing gene specific dsRNA.

Table S1: Nucleotide sequences of the reporter genes and promoters used in this study.

Table S2: RNA-seq samples of human (different tissues), *Drosophila Melanogaster* (different tissues and different time points) and *Neurospora crassa* (different carbo sources) analyzed in Figure 1B-D.

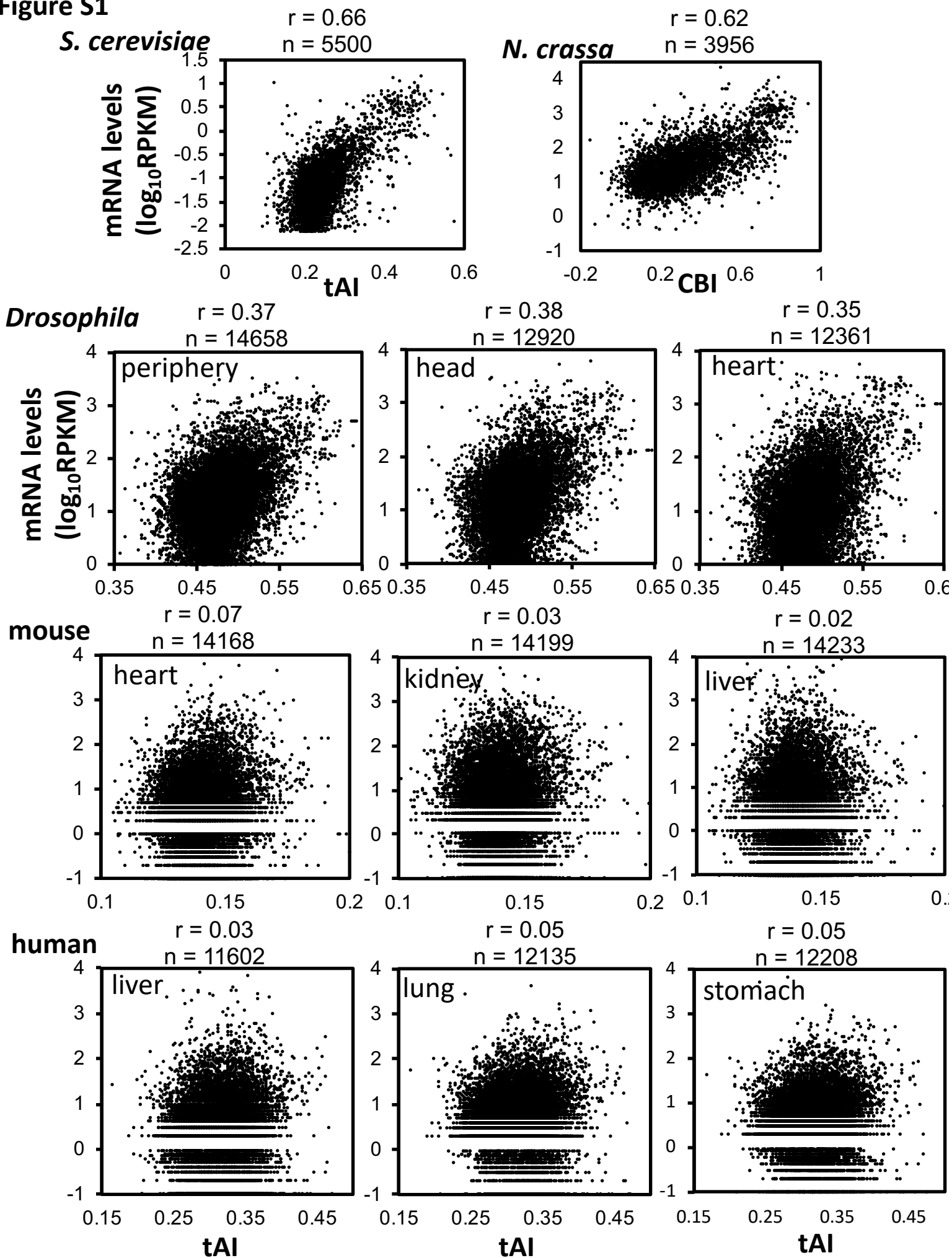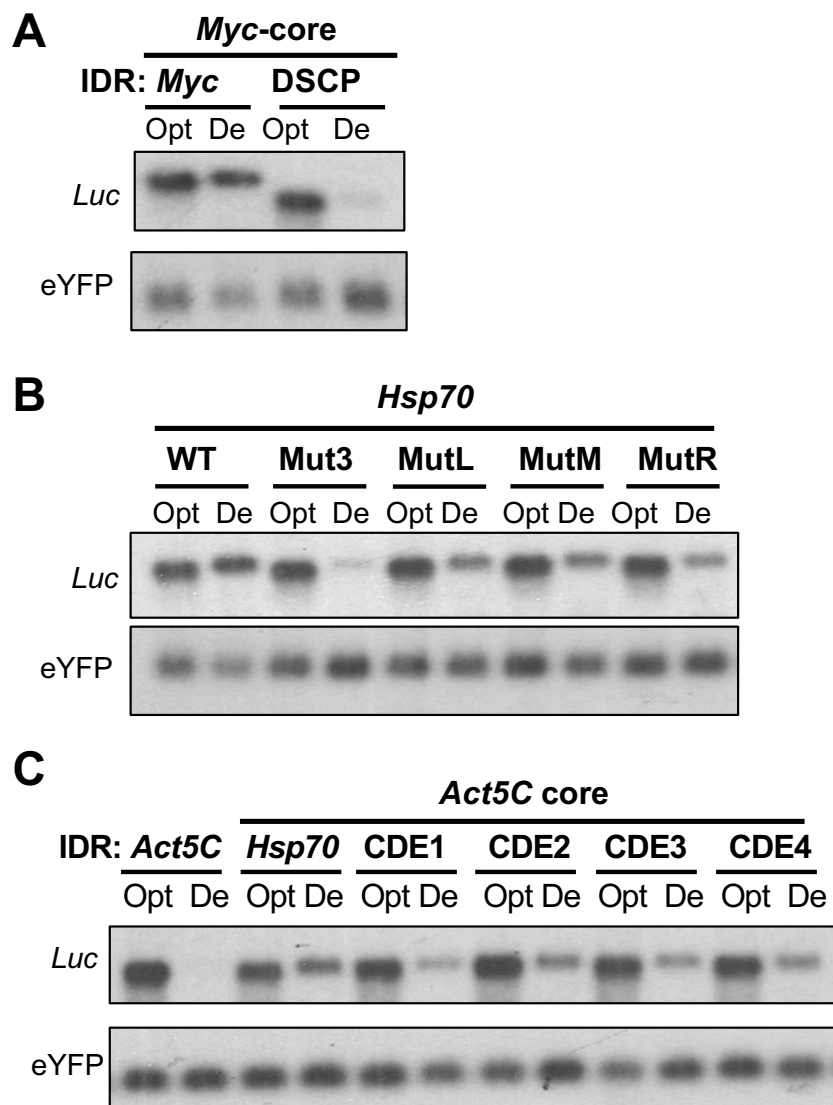**Table S3: Primer sequences used for probe amplification in Northern blot analyses.**

Figure S1

Figure S2

A

Myc-core

IDR: *Myc*   DSCP

Opt De   Opt De

Luc

eYFP

B

Hsp70

WT   Mut3   MutL   MutM   MutR

Opt De   Opt De   Opt De   Opt De   Opt De

Luc

eYFP

C

Act5C core

IDR: *Act5C*   *Hsp70*   CDE1   CDE2   CDE3   CDE4

Opt De   Opt De   Opt De   Opt De   Opt De   Opt De

Luc

eYFP

Figure S3

A

Nuclear Total

Gapdh

U6

rRNA

B

	Hsp70		*Act5C*		DSCP	
	Opt	De	Opt	De	Opt	De

Hph

Gal4

rRNA

C

Hph

Relative mRNA level

1.5

1.0

0.5

0.0

Opt De | Opt De | Opt De
Hsp70 | *Act5C* | DSCP

D

Gal4

Relative mRNA level

1.5

1.0

0.5

0.0

Opt De | Opt De | Opt De
Hsp70 | *Act5C* | DSCP

E Pol II CTD ChIP Control

Input%

2.5

2.0

1.5

1.0

0.5

0.0

Act-intron   3L1

Figure S4

Figure S5

A   Ctl   *Ars2*-KD

Ars2

rRNA

B   Ctl   *Mtr4*-KD

Mtr4

rRNA

C   Ctl   *ZCCHC8*-KD

Zcchc8

rRNA

D   Ctl   *Rrp40*-KD

Rrp40

rRNA

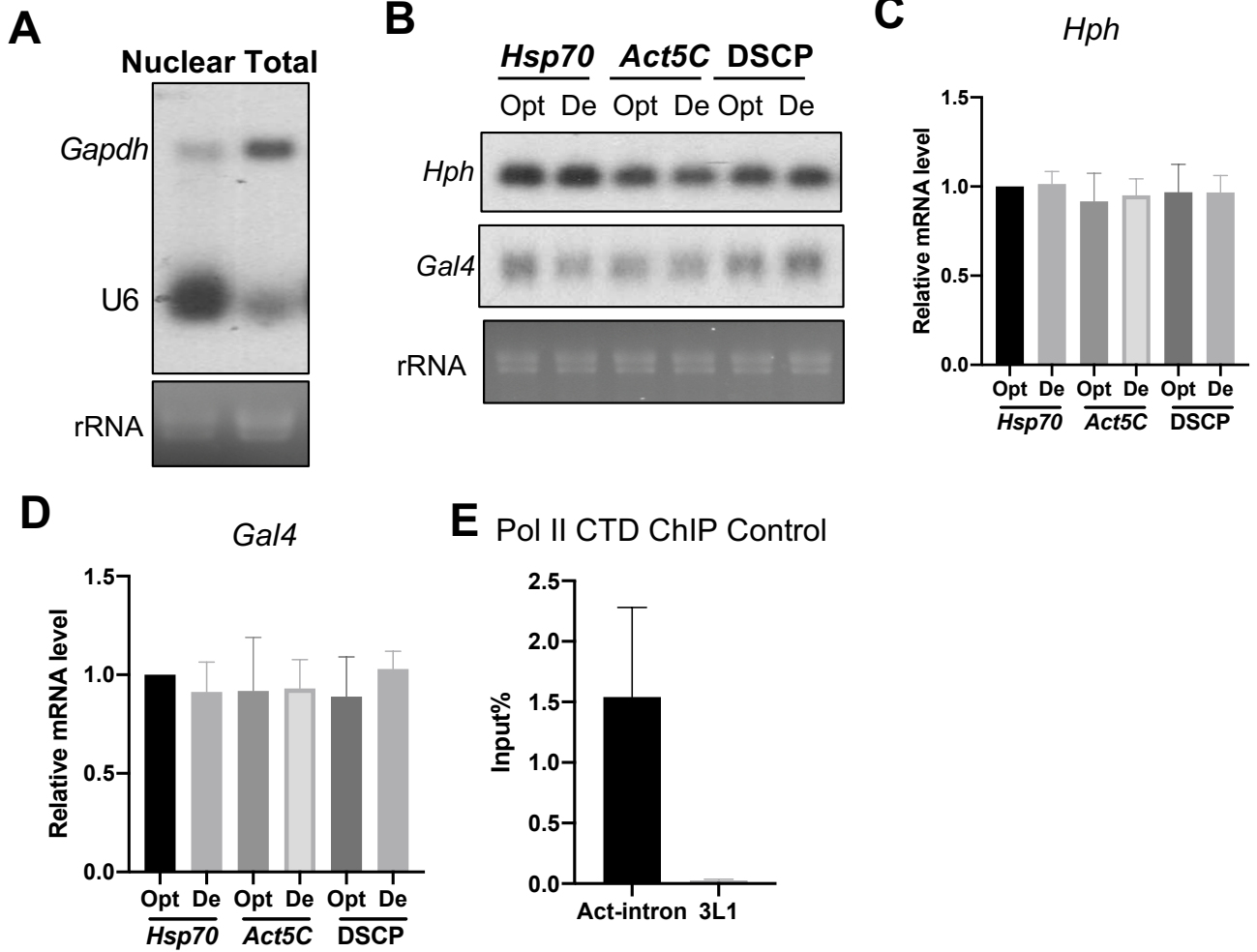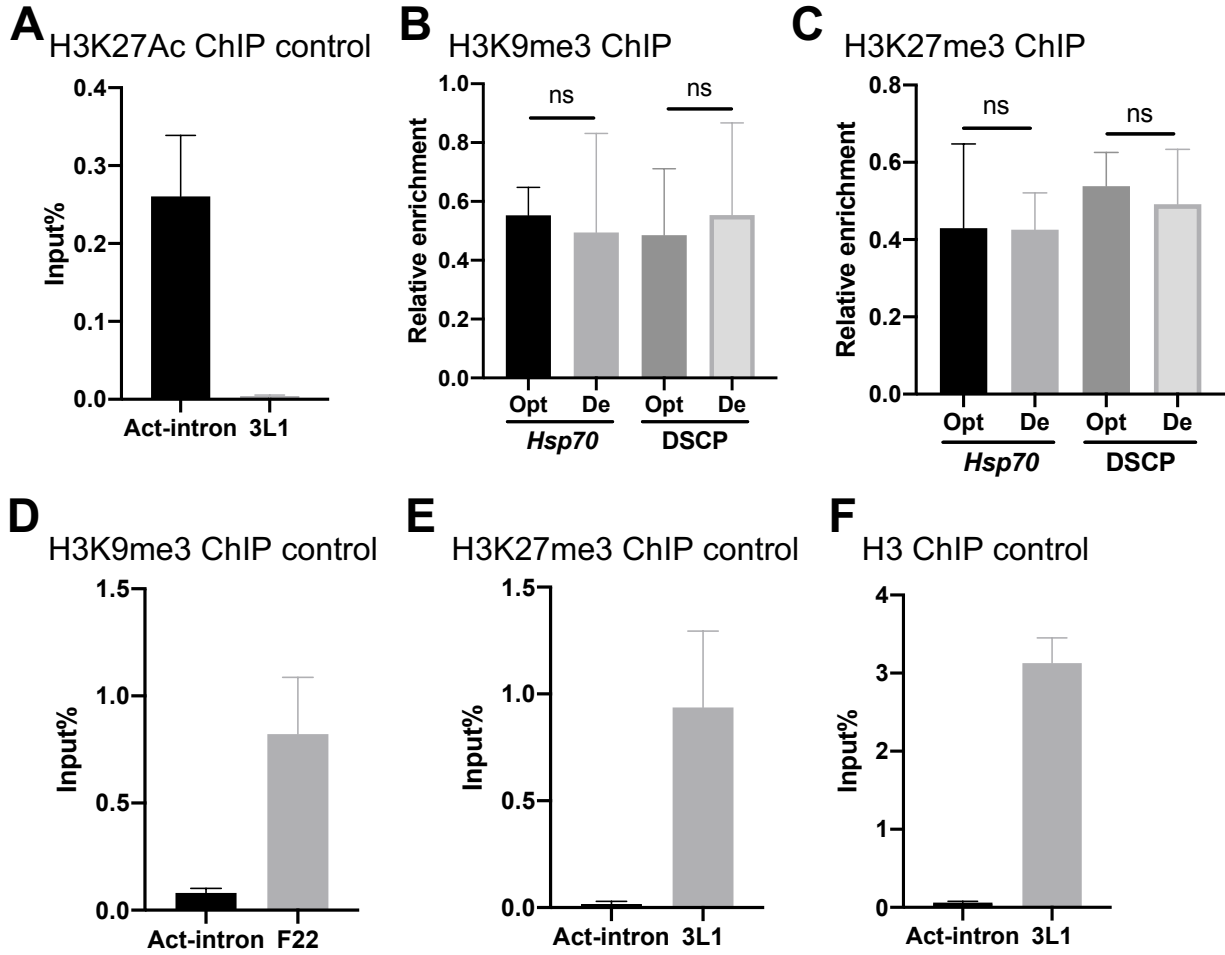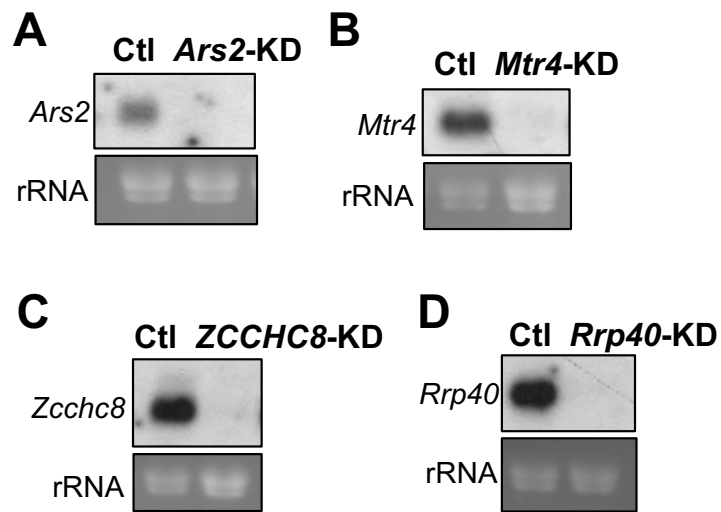**Table S1. Nucleotide sequences of the reporter genes and promoters used in this study**

> Opt luciferase
ATGGAAGACGCCAAAAACATAAAGAAAGGCCCCGCCCCCTTCTACCCCCTGGAGGATGGCACCGCCGG
CGAGCAGCTGCACAAGGCCATGAAGCGCTACGCCCTGGTGCCCGGCACCATCGCCTTCACCGATGCCCA
CATCGAGGTGGATATCACCTACGCCGAGTACTTCGAGATGAGCGTGCGCCTGGCCGAGGCCATGAAGC
GCTACGGCCTGAACACCAACCACCGCATCGTGGTGTGCAGCGAGAACAGCCTGCAGTTCTTCATGCCCG
TGCTGGGCGCCCTGTTCATCGGCGTGGCCGTGGCCCCCGCCAACGATATCTACAACGAGCGCGAGCTGC
TGAACAGCATGGGCATCAGCCAGCCCACCGTGGTGTTCGTGAGCAAGAAGGGCCTGCAGAAGATCCTG
AACGTGCAGAAGAAGCTGCCCATCATCCAGAAGATCATCATCATGGATAGCAAGACCGATTACCAGGGC
TTCCAGAGCATGTACACCTTCGTGACCAGCCACCTGCCCCCCGGCTTCAACGAGTACGATTTCGTGCCCG
AGAGCTTCGATCGCGATAAGACCATCGCCCTGATCATGAACAGCAGCGGCAGCACCGGCCTGCCCAAG
GGCGTGGCCCTGCCCCACCGCACCGCCTGCGTGCGCTTCAGCCACGCCCGCGATCCCATCTTCGGCAACC
AGATCATCCCCGATACCGCCATCCTGAGCGTGGTGCCCTTCCACCACGGCTTCGGCATGTTCACCACCCT
GGGCTACCTGATCTGCGGCTTCCGCGTGGTGCTGATGTACCGCTTCGAGGAGGAGCTGTTCCTGCGCAG
CCTGCAGGATTACAAGATCCAGAGCGCCCTGCTGGTGCCCACCCTGTTCAGCTTCTTCGCCAAGAGCACC
CTGATCGATAAGTACGATCTGAGCAACCTGCACGAGATCGCCAGCGGCGGCGCCCCCCTGAGCAAGGA
GGTGGGCGAGGCCGTGGCCAAGCGCTTCCACCTGCCCGGCATCCGCCAGGGCTACGGCCTGACCGAGA
CCACCAGCGCCATCCTGATCACCCCCGAGGGCGATGATAAGCCCGGCGCCGTGGGCAAGGTGGTGCCC
TTCTTCGAGGCCAAGGTGGTGGATCTGGATACCGGCAAGACCCTGGGCGTGAACCAGCGCGGCGAGCT
GTGCGTGCGCGGCCCCATGATCATGAGCGGCTACGTGAACAACCCCGAGGCCACCAACGCCCTGATCG
ATAAGGATGGCTGGCTGCACAGCGGCGATATCGCCTACTGGGATGAGGATGAGCACTTCTTCATCGTGG
ATCGCCTGAAGAGCCTGATCAAGTACAAGGGCTACCAGGTGGCCCCCGCCGAGCTGGAGAGCATCCTG
CTGCAGCACCCCAACATCTTCGATGCCGGCGTGGCCGGCCTGCCCGATGATGATGCCGGCGAGCTGCCC
GCCGCCGTGGTGGTGCTGGAGCACGGCAAGACCATGACCGAGAAGGAGATCGTGGATTACGTGGCCA
GCCAGGTGACCACCGCCAAGAAGCTGCGCGGCGGCGTGGTGTTCGTGGATGAGGTGCCCAAGGGCCT
GACCGGCAAGCTGGATGCCCGCAAGATCCGCGAGATCCTGATCAAGGCCAAGAAGGGCGGCAAGATC
GCCGTGTAA

> De luciferase
ATGGAAGACGCCAAAAACATAAAGAAAGGCCCTGCACCTTTTTATCCTTTAGAAGACGGGACTGCAGGG
GAACAATTACATAAAGCAATGAAAAGATATGCATTAGTACCTGGGACTATAGCATTTACTGACGCACAT
ATAGAAGTAGACATAACTTATGCAGAATATTTTGAAATGTCTGTAAGATTAGCAGAAGCAATGAAAAGA
TATGGGTTAAATACTAATCATAGAATAGTAGTATGTTCTGAAAATTCTTTACAATTTTTTATGCCTGTATT
AGGGGCATTATTTATAGGGGTAGCAGTAGCACCTGCAAATGACATATATAATGAAAGAGAATTATTAAA
TTCTATGGGGATATCTCAACCTACTGTAGTATTTGTATCTAAAAAAGGGTTACAAAAAATATTAAATGTA
CAAAAAAAATTACCTATAATACAAAAAATAATAATAATGGACTCTAAAACTGACTATCAAGGGTTTCAAT
CTATGTATACTTTTGTAACTTCTCATTTACCTCCTGGGTTTAATGAATATGACTTTGTACCTGAATCTTTTG
ACAGAGACAAAACTATAGCATTAATAATGAATTCTTCTGGGTCTACTGGGTTACCTAAAGGGGTAGCATT
ACCTCATAGAACTGCATGTGTAAGATTTTCTCATGCAAGAGACCCTATATTTGGGAATCAAATAATACCT
GACACTGCAATATTATCTGTAGTACCTTTTCATCATGGGTTTGGGATGTTTACTACTTTAGGGTATTTAAT
ATGTGGGTTTAGAGTAGTATTAATGTATAGATTTGAAGAAGAATTATTTTTAAGATCTTTACAAGACTAT
AAAATACAATCTGCATTATTAGTACCTACTTTATTTTCTTTTTTTGCAAAATCTACTTTAATAGACAAATAT
GACTTATCTAATTTACATGAAATAGCATCTGGGGGGGCACCTTTATCTAAAGAAGTAGGGGAAGCAGTA

GCAAAAAGATTTCATTTACCTGGGATAAGACAAGGGTATGGGGTTAACTGAAACTACTTCTGCAATATTAA
TAACTCCTGAAGGGGACGACAAACCTGGGGCAGTAGGGAAAGTAGTACCTTTTTTTGAAGCAAAAGTA
GTAGACTTAGACACTGGGAAAACTTTAGGGGTAAATCAAAGAGGGGAATTATGTGTAAGAGGGCCTAT
GATAATGTCTGGGTATGTAAATAATCCTGAAGCAACTAATGCATTAATAGACAAAGACGGGTGGTTACA
TTCTGGGGACATAGCATATTGGGACGAAGACGAACATTTTTTTATAGTAGACAGATTAAAATCTTTAATA
AAATATAAAGGGTATCAAGTAGCACCTGCAGAATTAGAATCTATATTATTACAACATCCTAATATATTTG
ACGCAGGGGTAGCAGGGTTACCTGACGACGACGCAGGGGAATTACCTGCAGCAGTAGTAGTATTAGAA
CATGGGAAAACTATGACTGAAAAGAAATAGTAGACTATGTAGCATCTCAAGTAACTACTGCAAAAAAA
TTAAGAGGGGGGGTAGTATTTGTAGACGAAGTACCTAAAGGGTTAACTGGGAAATTAGACGCAAGAAA
AATAAGAGAAATATTAATAAAAGCAAAAAAGGGGGGAAAATAGCAGTATAA

> Opt YFP
ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACG
TAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTG
AAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCTTCGGCTACGGCC
TGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAG
GCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAG
TTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACAT
CCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGA
ACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACT
ACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGT
CCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCC
GGGATCACTCTCGGCATGGACGAGCTGTACAAGTAA

> De YFP
ATGGTATCTAAAGGGGAAGAATTATTTACTGGGGTAGTACCTATATTAGTAGAATTAGACGGGGACGTA
AATGGGCATAAATTTTCTGTATCTGGGGAAGGGGAAGGGGACGCAACTTATGGGAAATTAACTTTAAA
ATTTATATGTACTACTGGGAAATTACCTGTACCTTGGCCTACTTTAGTAACTACTTTTGGGTATGGGTTAC
AATGTTTTGCAAGATATCCTGACCATATGAAACAACATGACTTTTTTAAATCTGCAATGCCTGAAGGGTA
TGTACAAGAAGAACTATATTTTTTAAAGACGACGGGAATTATAAAACTAGAGCAGAAGTAAAATTTGA
AGGGGACACTTTAGTAAATAGAATAGAATTAAAAGGGATAGACTTTAAAGAAGACGGGAATATATTAG
GGCATAAATTAGAATATAATTATAATTCTCATAATGTATATATAATGGCAGACAAACAAAAAAATGGGAT
AAAAGTAAATTTTAAAATAAGACATAATATAGAAGACGGGTCTGTACAATTAGCAGACCATTATCAACA
AAATACTCCTATAGGGGACGGGCCTGTATTATTACCTGACAATCATTATTTATCTTATCAATCTGCATTAT
CTAAAGACCCTAATGAAAAAGAGACCATATGGTATTATTAGAATTTGTAACTGCAGCAGGGATAACTTT
AGGGATGGACGAATTATATAAATAA

Core promoter is unlined region
> Act5C promoter
<u>GCTAAGCGGGCTTTATAAAACGGGCTGCGGGACCAGTTTTCATATCACTACCGTTTGAGTTCTTGTGCTG
TGTGGATACTCCTCCCGACAC</u>AAAGCCGCTCCATCAGCCAGCAGTCGTCTAATCCAGAGACACCAAACCG
AAAGACTTAATTTATATTTATTTAATTAATTTTAATAAAACACACCAAAT

> DSCP promoter

CGCCCGGGGATCGAGCGCAGCGGTATAAAAGGGCGCGGGGTGGCTGAGAGCATCAGTTGTGAATGAA
TGTTCGAGCCGAGCAGACGTGCCGCTGCCTTCGTTAATATCCTTTGAATAAGCCAACTTTGAATCACAAG
ACGCATACCAAACGGCATTCCGGTACTGTTGGTAAAGCCACC

> Tub promoter
TGGCCACACTGCGGCCATCGTATAAAAGCCCGCGCTCTCCAAAGCGAATGCACTAATTTTTCCAAGTGTG
TGAAGCGGACAGTTTGTGTTGTGTTCGACTGCTATAAGCGAAAGATAATTTTAAGTTAAAAGTTCAAAA
GCCTAAAACAAATACAAAATGAGGGAAATCGTTCACATCCAAGCTGGTCAGTGCGGCAACCAAATCGGC
GCCAAG

> Hsp70 promoter
CGCCGGAGTATAAATAGAGGCGCTTCGTCTACGGAGCGACAATTCAATTCAAACAAGCAAAGTGAACAC
GTCGCTAAGCGAAAGCTAAGCAAATAAACAAGCGCAGCTGAACAAGCTAAACAATCTGCAGTAAAGTG
CAAGTTAAAGTGAATCAATTAAAAGTAACCAGCAAC

> cMyc promoter
TACGATAGAAATTTTATTTAAGCCACAGACAACATGAAACGGGCACTATTTCTGTGGCGTCGCGTGTTCA
GTTCACCGCGGGTAATTCAGAGAATCGCTTTGTGGATTGGATTTTTGCCTGTTTTCCGCCCGATACAAAA
AAAAAAAACCAAACGCTATATAAATAGTTCTGTAGTAAAACCTGAAGCAACACGTTTTAAAATATACAAC
TACTACTAACAACTGTCACAGCCAAGTTACAAAAGTGCTAAATC

> Per promoter
TGCGAGTGCACGGGGGCTTATACACCGGAGCTTGCGATGCGAGCACTAGTGTTCGTGCGAATTTAGAG
CCAGAAGGTCGACAACGCGTTCGTCGCACAGTAGAAAGTATTGCCATATACCAAATAAATCGCAACAAC
GACCTGTCGAATCACGCAAACAAACAGCTTCGTTTTTTTTTTTTTAATTTCGACCAGAAACAAACCGTTAT
TCTTT

Table S1: RNA-seq samples used for the analyses in Figure 1B-D.

	Human		N. crassa		D. Melanogaster
1	Brodmann.1909.area.24	1	X2..sucrose	1	Periphery_Wk3_ALF_ZT00
2	Brodmann.1909.area.9	2	X1..miscanthus	2	Periphery_Wk3_ALF_ZT06
3	C1.segment.of.cervical.spinal.cor	3	X1..Amylopectin	3	Periphery_Wk3_ALF_ZT12
4	EBV.transformed.lymphocyte	4	X1..amylose	4	Periphery_Wk3_ALF_ZT18
5	adrenal.gland	5	X1..Arabinan	5	Periphery_Wk3_TRF_ZT00
6	amygdala	6	X1..avicel	6	Periphery_Wk3_TRF_ZT06
7	aorta	7	X1..corn.stover	7	Periphery_Wk3_TRF_ZT12
8	atrium.auricular.region	8	X1..eastern.cottonwood	8	Periphery_Wk3_TRF_ZT18
9	blood	9	X1..Energy.cane	9	Periphery_Wk5_ALF_ZT00
10	breast	10	X1..galactan	10	Periphery_Wk5_ALF_ZT03
11	caudate.nucleus	11	X1..Galactomannan	11	Periphery_Wk5_ALF_ZT06
12	cerebellar.hemisphere	12	X1..Lobloly.Pine	12	Periphery_Wk5_ALF_ZT09
13	cerebellum	13	X1..MLG	13	Periphery_Wk5_ALF_ZT12
14	cerebral.cortex	14	X1..Pectin.Esterified	14	Periphery_Wk5_ALF_ZT15
15	coronary.artery	15	X1..Pectin	15	Periphery_Wk5_ALF_ZT18
16	cortex.of.kidney	16	X1..Rhamnogalacturonan	16	Periphery_Wk5_ALF_ZT21
17	ectocervix	17	X1..sherbourne.willow	17	Periphery_Wk5_TRF_ZT00
18	endocervix	18	X1..Switchgrass	18	Periphery_Wk5_TRF_ZT03
19	esophagogastric.junction	19	X1..Wing.nut	19	Periphery_Wk5_TRF_ZT06
20	esophagus.mucosa	20	X1..Xylan	20	Periphery_Wk5_TRF_ZT09
21	esophagus.muscularis.mucosa	21	X1..Xyloglucan	21	Periphery_Wk5_TRF_ZT12
22	fallopian.tube	22	X2mM.arabinose	22	Periphery_Wk5_TRF_ZT15
23	greater.omentum	23	X2mM.cellobiose	23	Periphery_Wk5_TRF_ZT18
24	heart.left.ventricle	24	X2mM.fructose	24	Periphery_Wk5_TRF_ZT21
25	hippocampus.proper	25	X2mM.fucose	25	Periphery_Wk7_ALF_ZT00
26	hypothalamus	26	X2mM.galactose	26	Periphery_Wk7_ALF_ZT06
27	liver	27	X2mM.galacturonic.acid	27	Periphery_Wk7_ALF_ZT12
28	lower.leg.skin	28	X2mM.glucuronic.acid	28	Periphery_Wk7_ALF_ZT18
29	lung	29	X2mM.glycerol	29	Periphery_Wk7_TRF_ZT00
30	minor.salivary.gland	30	X2mM.maltose	30	Periphery_Wk7_TRF_ZT06
31	nucleus.accumbens	31	X2mM.mannitol	31	Periphery_Wk7_TRF_ZT12
32	ovary	32	X2mM.mannose	32	Periphery_Wk7_TRF_ZT18
33	pancreas	33	X2mM.rhamnose	33	Head_Wk3_ALF_ZT00
34	pituitary.gland	34	X2mM.ribose	34	Head_Wk3_ALF_ZT06
35	prostate.gland	35	X2mM.sorbose	35	Head_Wk3_ALF_ZT12
36	putamen	36	X2mM.trehalose	36	Head_Wk3_ALF_ZT18
37	sigmoid.colon	37	X2mM.xylose	37	Head_Wk3_TRF_ZT00
38	skeletal.muscle.tissue	38	citrus.peel	38	Head_Wk3_TRF_ZT06
39	small.intestine.Peyer.s.patch	39	Starvation	39	Head_Wk3_TRF_ZT12
40	spleen	40	X0.4..NaNO3	40	Head_Wk3_TRF_ZT18
41	stomach	41	X0.25mM.Methionine..low.sulfur.	41	Head_Wk5_ALF_ZT00
42	subcutaneous.adipose.tissue	42	X1..Abies.alba.sapwood	42	Head_Wk5_ALF_ZT03
43	substantia.nigra	43	X1..BSA	43	Head_Wk5_ALF_ZT06
44	suprapubic.skin	44	X1..cedrus.libani.kearn.or.heartwo	44	Head_Wk5_ALF_ZT09
45	testis	45	X1..Cedrus.libani.splint.wood	45	Head_Wk5_ALF_ZT12
46	thyroid.gland	46	X1..Glucomannan	46	Head_Wk5_ALF_ZT15
47	tibial.artery	47	X1..inulin	47	Head_Wk5_ALF_ZT18
48	tibial.nerve	48	X1..lignin	48	Head_Wk5_ALF_ZT21
49	transformed.skin.fibroblast	49	X1..picea.abies.heartwood	49	Head_Wk5_TRF_ZT00
50	transverse.colon	50	X1..Picea.abies.sapwood	50	Head_Wk5_TRF_ZT03
51	urinary.bladder	51	X1..Polygalacturonic.acid	51	Head_Wk5_TRF_ZT06
52	uterus	52	X1..Quercas.robur.sapwood	52	Head_Wk5_TRF_ZT09
53	vagina	53	X1..robina.pseudoararia.heartwoo	53	Head_Wk5_TRF_ZT12
		54	X1..robina.pseudoararia.sapwood	54	Head_Wk5_TRF_ZT15
		55	X2mM.mannobiose	55	Head_Wk5_TRF_ZT18
		56	X3.4mM.arginine	56	Head_Wk5_TRF_ZT21
		57	X4.3mM.proline	57	Head_Wk7_ALF_ZT00
		58	X5mM.glutamate	58	Head_Wk7_ALF_ZT06
		59	X5mM.glutamine	59	Head_Wk7_ALF_ZT12
		60	X5mM.Methionine..high.sulfur.	60	Head_Wk7_ALF_ZT18
		61	X10.1mM.alanine	61	Head_Wk7_TRF_ZT00
		62	X20mM.glycine	62	Head_Wk7_TRF_ZT06

Table S3: The primer sequences used for the template amplification used for making probes for Northern blot analysis.

5xMyc-luciferase 5' end (5'- TGATATCATCGATTTAAAGCA -3', 5'-TGCTAATACGACTCACTATAGGGAGCATGTCGCCCAAGCTCTCCAT -3')

 eYFP 5' end (5'- ATGGTGAGCAAGGGCGAGGAGCTG -3', 5'-TGCTAATACGACTCACTATAGGGAGCCTCGCCGGACACGCTGAAC -3')

YFP 3'UTR (5'- TCTTTGTGAAGGAACCTTAC -3', 5'-TGCTAATACGACTCACTATAGGGAGTTCATCAGTTCCATAGGTTG -3')

Ars2 3'UTR (5'- TATCGGTTACCATGATTTGG -3', 5'-TGCTAATACGACTCACTATAGGGAGTCGCACTTTATTTCCTTGTG -3')

Mtr4 3'UTR (5'- CGACTGGAGGAGCTTCTGCG -3', 5'-TGCTAATACGACTCACTATAGGGAGATTTACAAAGGTTGTTAGGG -3')

ZCCHC8 3'UTR (5'- GCTCGTCGCCTTGGAAGGCG -3', 5'-TGCTAATACGACTCACTATAGGGAGTCCAGCCAAGCAGGCGGATA -3')

Rrp40 3'UTR (5'- GAGCTGGTCTGCGTCAACTC -3', 5'-TGCTAATACGACTCACTATAGGGAGTAAGGGTAGTACTATCTTTC -3')

Hsp70 5'end (5'- ATGCCTGCTATTGGAATCGATCTG -3', 5'-TGCTAATACGACTCACTATAGGGAGCCGATCAGTCGCTTGGCGTCAAAC -3')

U6 (5'- CGGCAGAACATATACTAAAATTGG -3', 5'-TAATACGACTCACTATAGGGAGTGTGGAACGCTTCACGATTTTGCG -3')

gapdh (5'- AGTCCACCGGAGTGTTCACC -3', 5'-TGCTAATACGACTCACTATAGGGAGAGAAGTCGGTGGAGACCACC -3')

Gal4 (5'- ATGAAGCTACTGTCTTCTATCG -3', 5'-TGCTAATACGACTCACTATAGGGAGTGTGCCCTAGTCAGCGGAGACC -3')

hph (5'- ATGAAAAAGCCTGAACTCACCG -3', 5'-TGCTAATACGACTCACTATAGGGAGTTTGTAGAAACCATCGGCGCAGC -3').