

Supplemental data

Methods

Culture of Drosophila S2 cells

Drosophila S2 cells were cultured at 24°C in 1x Schneider's *Drosophila* medium (Gibco/BRL), supplemented with 10% fetal bovine serum (heat-inactivated) and 1% Penicillin/Streptomycin (Invitrogen).

For transfections for luciferase assays, 1.3×10^6 cells per well (in 0.65 ml) were plated in 24-well plates. Cellfectin (Invitrogen) was diluted 1:5 in serum-free medium to a final volume of 21 μ l and incubated for 45' at room temperature, then mixed with 21 μ l of serum-free medium containing the appropriate plasmids and dsRNA, incubated for another 15' at room temperature and finally diluted into 378 μ l serum-free medium and added to the washed cells; 16 h later, the transfection mix was replaced by complete medium and the incubation was continued for the indicated duration of time (typically 48 hours). Each plasmid solution typically contained 650 ng of each of the wt-RLuc and Δ E-FLuc reporters, 130 ng tubulin-RLuc (where needed), and 40 ng dsRNA (where needed); for overexpressions a total of 1.3 μ g DNA (consisting typically of a 1:1 mix of the "driver" plasmid tub-GAL4 on one side, and the different UAS-cDNA plasmids on the other side) was added to each well. ; where indicated, dsRNA was added at 40 ng/ 10^6 cells.

For samples to be analysed by Western blotting or immunoprecipitations, 5×10^6 cells (in 1 ml) were plated per well into 6-well plates; transfections were done in a final volume of 1 ml containing 10 μ l Cellfectin and a total amount of 10 μ g plasmid DNA (3.3 μ g tub-GAL4, and 3.3 μ g of each expression plasmid, or pCaSper4 to bring the total DNA mass to 10 μ g). Cells were typically harvested 48 hours after transfection.

For qRT-PCR analysis of RNAi-treated cells, 5×10^6 cells were plated in each well of a 6-well plate and incubated with 10 μ g dsRNA in 1 ml serum-free medium for 30'. Two ml of complete medium were then added and the cells harvested after the indicated incubation periods.

Analysis of target gene expression.

Luciferase assays: cells were harvested typically 48 h after transfection, washed in 1x PBS and lysed for 15' in 100 μ l 1x Passive Lysis Buffer (Dual-Luciferase Reporter Assay System, Promega). Ten μ l of each lysate was transferred to luminometric 96 well plates (Greiner) and relative reporter gene expression was determined on a Wallac luminometer. The luminometer protocol was adjusted to disperse 50 μ l of each luciferase substrate per measurement. Each transfection was performed in duplicate, and all values are indicated as averages of duplicates with standard deviations.

qRT-PCR: cells were flushed off the plates at the indicated times after transfection, lysed in 1 ml Trizol reagent (Invitrogen) and total RNA was extracted and purified according to the manufacturer's protocol. After precipitation, RNA was redissolved in 20 μ l RNase-free water and 10 μ g of RNA were subjected to a DNase digestion (Ambion TURBO DNA-free-kit). The quality of the purified RNA was confirmed on Bioanalyzer Nano 6000 chips (Agilent). cDNA was synthesised starting with 1 μ g template RNA using the Omniscript Reverse Transcription Kit (Qiagen) and random hexamer primers; as control 1 μ g of template RNA was mock reverse-transcribed. qRT-PCR reactions were performed on an ABI 7900 Real Time PCR Instrument (Applied Biosystems) using the SYBR GREEN PCR Master Mix (Applied Biosystems), and data were analysed with SDS

Supplement “Myc and dHCF”

2.0 software (Applied Biosystems) and Microsoft Excel, using the $\Delta\Delta\text{Ct}$ method. Expression levels of actin5C and Sec24 served as internal references. Primers are listed below.

Protein analysis.

Western blot: cells were harvested at the indicated time points and washed with 1x PBS, lysed in Laemmli sample buffer by boiling for 5' at 95°C and analysed by SDS-PAGE and immunoblotting, using the Enhanced Chemiluminescence kit (Amersham) or fluorescently labeled secondary antibodies. Blots were then either exposed to X-ray films, scanned with a CCD camera (Fuji LAS-3000), or analysed with an Odyssey reader (Li-Cor Biosciences).

***In vitro* interactions:** ^{35}S -methionine labeled proteins were *in vitro* synthesized using the TNT Coupled Reticulocyte Lysate Transcription/Translation kit (Promega) according to the manufacturer's instructions and pRSetB-Myc^{wt}, pRSetB-Myc ^{ΔHBM} , pRSetB-dHCF-N^{wt} or pRSetB-dHCF-N^{PS} as templates. GST-fusion proteins were purified from bacteria according to standard protocols (31; detailed protocol available on request). Equal amounts of bead-coupled GST-fusions were pre-incubated for 2 h in GST Binding Buffer (20 mM Tris-HCl pH 8.0, 200 mM NaCl, 1 mM EDTA, 1 mM DTT, 0.5% NP-40, 10% glycerol, 1% BSA, protease inhibitors), followed by a 2 h incubation at 4°C with ^{35}S -labelled protein, five washes in GST Wash Buffer (20 mM Tris-HCl, 200 mM NaCl, 1 mM EDTA, 1 mM DTT, 0.5% NP-40), analysis by SDS-PAGE (gels were stained with Coomassie Blue to document the amounts of GST-fusion proteins) and autoradiography or exposure to a Phosphorimager screen (Fujifilm FLA-7000).

Immunoprecipitations from S2 cells: 48 hours after transfection, cells were washed once with ice-cold PBS and lysed on ice for 30 minutes in lysis buffer (250 mM NaCl, 50 mM Tris-HCl pH 8.0, 5 mM EDTA pH 8.0, 0.5% Nonidet P-40) containing protease inhibitors (Protease Inhibitor cocktail tablets, Roche). Lysates were centrifuged (10', 13'000 rpm, microfuge) and the supernatants precleared for 1 h at 4°C with protein G Sepharose beads (GE Healthcare), followed by a 3 h incubation with anti-T7 antibodies (0.2 μl) and subsequent 1 hour incubation with protein G Sepharose beads. Beads were washed in Lysis Buffer (3x) and analysed by SDS-PAGE and Western blotting. For the experiment shown in Sup. Fig. 4C, cells were lysed 72 h after transfection and the cleared lysate was incubated for 4 h with 20 μl anti-HA-beads (mouse monoclonal anti-HA-agarose; Sigma), or for 3 h with 200 μl mouse anti-Myc supernatant, followed by a 1 h incubation with protein G sepharose beads.

LacZ assays

Flies were grown under non-crowding conditions; one wandering larva was transferred to an Eppendorf tube and lysed by repeated (3-4x) freezing in liquid nitrogen (for 3-5'), and thawing in a 37° waterbath (for 3-5'), followed by manual homogenization in 100 μl Z-buffer (60 mM Na₂HPO₄, 40 mM NaH₂PO₄, 10 mM KCl, 1 mM MgSO₄). The color reaction was started by mixing the larval lysate with 700 μl Z-buffer (containing 0.3% β -mercaptoethanol) and 160 μl ortho-Nitrophenyl- β -galactoside (0.4% in Z-buffer), incubated for the indicated durations at 30°, and stopped by the addition of 400 μl 1 M Na₂CO₃. Upon 10' centrifugation the supernatant was

Oligonucleotides used for synthesis of dsRNA

Each primer contains a T7 promoter sequence at its 5' end (5'-TAATACGACTCACTATAGGGAGA; not shown below).

Myc: 5'-CCGGCTCTGATAG & 5'-TGCTCATCATGGA

GFP: 5'-TGAGCAAGGGCGAGG & 5'-GCGGCGGTCACGAAC

Supplement "Myc and dHCF"

Luc: 5'-AATCATAGTTTGGGCATCGC-3' & 5'-CAAAGGAGCTCCACCAGAAG-3'
Hcf2: 5'-GACAGTGCCTGGAAGT & 5'-TTTTCTGGCACTCAGC
Hcf3: 5'-GAGAGCCCAAACCTATAG & 5'-GAAAGATCCTTAAACACACC
Atac1: 5'-GTAATGGAAATAGCAGAGATATCTG & 5'-ACTTCTGGACACGACTATACACTTG
Atac2: 5'-CCAAAGATACAAACACAACCTTCAC & 5'-ATCTTGCATTATCTCTTCTAGTGGT
D12: 5'-ACAACCTGTTGGACAGACTACGCTAT & 5'-GCACATAGACCAACCACTTATAGGT
CG10238: 5'-GACAGTGGAAAGTTCCTACTGAAATT & 5'-CTATAACTACACTGGCTTCGCATAC
CG30390: 5'-GTTTTTCATTGCGTAGGTAAACAAAG & 5'-CTCCTCATCAATTCCCTTAGCTAAT
Ash2(2): 5'-CCAGTTCCGATATTACGGCCAATGT & 5'-GTCACCGCCAACCGATCCTCGCTT
(primers "Ash2(1)" are derived from the Eurogentec collection and listed in Sup. Table 1)
Mnn1: 5'-GGCTGTATAAGAAGTTCCAGACGAT & 5'-GATATACGTGATGGTTCCGATAGTG
wds: 5'-CCGCTGATAAACTAATCAAATCTG & 5'-CTTCTCATTCTTGTGACCCGTATAC
CG5585: 5'-CAAAAATGAATTTGGAGCTACTAGG & 5'-AAGGTTTCAACATCCAGTACGAGTA
CG6444: 5'-TTGTTGGACTGCTGCAAAGACGCCA & 5'-TTAGGAGTTGTTGTCCACGGCGGCG

The remaining oligonucleotides were part of a library purchased from Eurogentec, whereby short gene-specific oligonucleotides, containing tags at their 5' ends, are used to generate a primary PCR product that is then re-amplified with tag-specific oligonucleotides. All "R oligonucleotides" contain the same tag (5'- TGGCGCCCCTAGATG), whereas the "S oligonucleotides" contain one of 9 different tags (Table S1).

Oligonucleotides used for generating pWIZ-hcf plasmids

pWIZ-hcf2: MB_XbaHCF_f2: 5'-TACATCTAGAGACAGTGCCTGGAAGT; MB_XbaHCF_r2: 5'-CCGATCTAGATTTTCTGGCACTCAGC
pWIZ-hcf3: MB_XbaHCF_f3: 5'-AGCATCTAGAGCCCAAACCTATA; MB_XbaHCF_r3: 5'-GCAATCTAGAGAAAGATCCTTAAACACACC

Oligonucleotides used for expression analysis quantitative real-time PCR

actin5C: PG_act5C_F1: 5'-GCCCATCTACGAGGGTTATGC; PG_act5C_R1: 5'-AATCGCGACCAGCCAGATC
Sec24: Sec24forw: 5'-CCACTCCCCTGCCATCCT; Sec24rev: 5'-ACCCCAAACCCAGCAACA
myc: dmyc_RTPCR_f: 5'-GAATCGCGCTCGGTTAGTG; dmyc_RTPCR_r: 5'-CTACGCCGCGCTTTAAG
nnp1: PG_nnp1_F1: 5'-CTATACACACGAAAGTTTCCATGCTATA; PG_nnp1_R1: 5'-CCCTTGCTCTTGGAGAATGG
CG5033: PG_CG5033_F1: 5'-TAACCGCTCGGCTTTAATTCA; PG_CG5033_R1: 5'-CCCTTGCTCTTGGAGAATGG
CG12295: CG12295_RTPCR_f: 5'-GGCGGAAGATGGATTTAGCTT; CG12295_RTPCR_r: 5'-CCTCGATTGCCCTTCGTATATAA
fibrillarlin: fib.Left: 5'-ACGACAGTCTCGCATGTGTC; fib.Right: 5'-ATGCGGTA CTTGTGTGGATG
hcf: MF_HCF_qPCR_f: 5'-AATTCTTGGCGACGAGGAGAA; MF_HCF_qPCR_r: 5'-CCCTCCTTGACATCCTTGAA
5sRNA: 5sRNA_fw: 5'-CGTCCGATCACCGAAATTAAG; 5sRNA_rev: 5'-CCAAGCGGTCCCTCATCTAA
snoRNA U3: PG_U3_f: 5'-TTTCACACTAGCTGAAAGCCAAGT; PG_U3_r: 5'-CCTCACGCTGCCGAATAGAA

Supplement "Myc and dHCF"

tRNA(Leu): tRNA^{Leu}.L: 5'-TAAGGCGCCAGACTCAAGAT; tRNA^{Leu}.R: 5'-CCTCAAAGAGGACCAGAAC

transferred into 96-well luminometer plates and the absorption at 420 nm was determined.

Oligonucleotides used for ChIP quantitative real-time PCR

Pka-C1 coding: chr2L_P0_Fw: 5'-CATGACACGGCCAAAGGAGC-3'; chr2L_P0_Rv: 5'-GGACAAGTGGCGACGCAATC-3'
Pka-C1: chr2L_P2_Fw: 5'-TGTGAGTAGGCCAGCGATAG-3'; chr2L_P2_Rv: 5'-GAATAGAACCCGCGCAGTAG-3'
Hoip: chr2L_P3_Fw: 5'-TTTAAGCTAGGGCTGCAGAG-3'; chr2L_P3_Rv: 5'-CGCAGGTGGTTCGGAAATAC-3'
CG4364: chr2L_P7_Fw: 5'-CTTCTTGGGTCTCTCATTG-3'; chr2L_P7_Rv: 5'-ACTTCCTTTCCACGCGAAAC-3'
Nop5: nop5_dHCF_p_Fw: 5'-CAGCCAGCAGCAACTTAACC-3'; nop5_dHCF_p_Rv: 5'-TGTTATGCGCGAACCAAGTG-3'
CG5033: CG5033_dHCF_p_Fw: 5'-ACCGATTACCAGCAGCAGTG-3'; CG5033_dHCF_p_Rv: 5'-CGTGTTCAGTCAGCGATAG-3'

Myc protein mutants used for Fig. S4D

The expression plasmids coding for the indicated Myc mutants have been described in Steiger et al. (2008) and Schwinkendorf et al. (2009), except for HA-Myc^C: this protein contains the HA-tag followed by Myc amino acids 1 to 625, i.e. it lacks the C-terminal BHLHZ domain of Myc.

Drosophila genotypes shown in the figures:

(the symbol ">" represents an FRT-site)

Fig. 2A

- y w; GMR-GAL4/UAS-lacZ[B-4-1-2]
- y w; GMR-GAL4/UAS-T7-dHCF-FLAG
- y w; GMR-GAL4 UAS-Myc[132]/UAS-lacZ[B-4-1-2]
- y w; GMR-GAL4 UAS-Myc[132]/UAS-T7-dHCF-FLAG

Fig. 2B

- y w hs-FLP; UAS-lacZ[B-4-1-2]/+; act>CD2>GAL4 UAS-GFP/+
- y w hs-FLP; UAS-T7-dHCF-FLAG /+; act>CD2>GAL4 UAS-GFP/+
- y w hs-FLP; UAS-lacZ[B-4-1-2]/UAS-Myc[132]; act>CD2>GAL4 UAS-GFP/+
- y w hs-FLP; UAS-T7-dHCF-FLAG/UAS-Myc[132]; act>CD2>GAL4 UAS-GFP/+

Fig. 3A

- y w; sca-GAL4/UAS-lacZ-IR
- y w; sca-GAL4/+; UAS-hcf-IR 3.1/+
- y w; sca-GAL4/UAS-hcf-IR 2.9

Fig. 3B

- y w; ap-GAL4 UAS-Myc[132]/UAS-LacZ-IR^{M3-1}
- y w; ap-GAL4 UAS-Myc[132]/+; UAS-hcf-IR VDRC/+
- y w; ap-GAL4 UAS-Myc[132]/+; UAS-hcf-IR 3.1/+

Fig. 3C

- y w hs-FLP; UAS-lacZ[B-4-1-2]/+; act>CD2>GAL4 UAS-GFP/+

Supplement “Myc and dHCF”

- y w hs-FLP; UAS-hcf-IR 2.42/+; act>CD2>GAL4 UAS-GFP/+
- y w hs-FLP; +; act>CD2>GAL4 UAS-GFP/UAS-hcf-IR 3.1
- y w hs-FLP; UAS-lacZ[B-4-1-2]/UAS-Myc[132]; act>CD2>GAL4 UAS-GFP/+
- y w hs-FLP; UAS-hcf-IR 2.42/UAS-Myc[132]; act>CD2>GAL4 UAS-GFP/+
- y w hs-FLP; UAS-Myc[132]/+; act>CD2>GAL4 UAS-GFP/UAS-hcf-IR 3.1

Fig. 3D

- y w tub>Myc>GAL4 ey-flp/+; UAS-lacZ-IR
- y w tub>Myc>GAL4 ey-flp/+; UAS-hcf-IR 2.9
- y w tub>Myc>GAL4 ey-flp/+;+; UAS-hcf-IR 3.1/+
- y w tub>Myc>GAL4 ey-flp/+;+; UAS-hcf-IR VDRC/+
- y w dm^{P0} tub>Myc>GAL4 ey-flp/+; UAS-lacZ-IR
- y w dm^{P0} tub>Myc>GAL4 ey-flp/+; UAS-hcf-IR 2.9
- y w dm^{P0} tub>Myc>GAL4 ey-flp/+;+; UAS-hcf-IR 3.1/+
- y w dm^{P0} tub>Myc>GAL4 ey-flp/+;+; UAS-hcf-IR VDRC/+

Fig 6B

- (y) w; ap-GAL4 UAS-Myc[132]/UAS-lacZ-IR
- (y) w; ap-GAL4 UAS-Myc[132]/UAS-Ash2-IR
- (y) w; ap-GAL4 UAS-Myc[132]/+ ; UAS-Gcn5-IR(T2)/+

Fig. S2 - LacZ assays:

- blank: buffer alone (no fly)
- control: (y)w; ap-GAL4/CyO,y+ x yw
- LacZ1: (y)w; ap-GAL4/CyO,y+ x yw ; UAS-lacZ[B-4-1-2] ; UAS-GFP
- LacZ1 hcf3: (y)w; ap-GAL4/CyO,y+ x yw; UAS-lacZ[B-4-1-2]/CyO,y+ ; UAS-HCF-IR 3.1/TM6B,Tb
- LacZ1 hcfV: (y)w; ap-GAL4/CyO,y+ x w; UAS-lacZ[B-4-1-2] ; UAS-HCF-IR VDRC/TM6B,Tb

Fig. S3 – knockdown of dHCF in wing imaginal disc clones:

- y w hs-FLP; UAS-LacZ-IR^{M3-1}/+; act>CD2>Gal4 UAS-GFP/+
- y w hs-FLP; UAS-hcf-IR 2.42/+; act>CD2>Gal4 UAS-GFP/+
- y w hs-FLP; +; act>CD2>Gal4 UAS-GFP/UAS-hcf-IR 3.1
- y w hs-FLP; UAS-Myc[132]/UAS-LacZ-IR^{M3-1}; act>CD2>Gal4 UAS-GFP/+
- y w hs-FLP; UAS-Myc[132]/UAS-hcf-IR 2.42; act>CD2>Gal4 UAS-GFP/+
- y w hs-FLP; UAS-Myc[132]/+; act>CD2>Gal4 UAS-GFP/UAS-hcf-IR 3.1

Figure legends

Figure S1. Quantification of dHCF knock-down effects on endogenous Myc targets. S2 cells were incubated with the indicated dsRNAs and RNA isolated 2 d later. Expression levels of the indicated genes were determined by quantitative real-time PCR, using actin 5C as an internal reference. Expression levels in cells treated with *gfp* dsRNA were set to 100 %, and error bars indicate standard deviations.

Figure S2. Knock-down of dHCF *in vivo* does not reduce GAL4 activity. For each time point the average of 3 larvae is shown (\pm standard deviation). Enzymatic activities (calculated from linear regression of the curves shown in the figure) are ($\times 10^{-3}$ Δ OD₄₂₀/min): 0.08 (blank - buffer alone), 0.50 (control - no LacZ-transgene), 6.6 (LacZ1 - no RNAi), 8.1 (LacZ1 + hcf3-RNAi), 8.1 (LacZ1 + hcfV-RNAi).

Supplement "Myc and dHCF"

Figure S3. Knock-down of dHCF *in vivo* impairs (Myc-dependent) growth. Average area of wing imaginal disc clones that have been overexpressing Myc and/or dHCF-dsRNA for 45 h; n=50-80 per genotype; ** indicates $p < 0.01$ as compared to the corresponding control.

Figure S4. Physical interaction between dHCF and Myc *in vitro* and in S2 cells. **A**, *in vitro* translated (IVT) Myc^{WT} preferentially binds to GST-dHCF⁺ (upper panel); GST-dHCF^{PS} was expressed at lower levels in bacteria, so its binding affinity cannot be directly compared to that of GST-dHCF⁺. The lower panel shows a Coomassie Blue staining of the same gel. **B**, *in vitro* translated dHCF⁺ and dHCF^{PS} preferentially bind to GST-Myc^{WT} and GST-Myc^{HBM}. The percentages in panels A and B indicate the relative levels of bound IVT protein, as determined by exposure of the radioactive gels to a PhosphorImager. **C**, anti-HA-epitope antibodies precipitate T7-dHCF when it is co-expressed with HA-Myc, but not when expressed alone. Cells were transfected with T7-dHCF and/or HA-Myc^{WT} (as indicated by a "+" above the lanes) and lysates precipitated with anti-T7 or anti-Myc antibodies. anti-T7-epitope antibodies precipitate HA-Myc^{WT} and HA-Myc^{BHM} when they are co-expressed with T7-dHCF, but not when expressed alone. Labels above the lane indicate the transfected proteins (T7-dHCF and/or HA-Myc^{WT/HBM}). **D**, different Myc mutants still co-immunoprecipitate with dHCF. T7-tagged dHCF was co-expressed in S2 cells with the indicated HA-tagged Myc mutants, followed by cellular lysis and co-immunoprecipitation analysis as described in the main text. The last two lanes contain lysates from untransfected cells (last lane), or from cells expressing HA-Myc^{wt} but no T7-dHCF (penultimate lane).

Figure S5. Efficiency of dHCF and Myc depletion, respectively. S2 cells were treated with the dsRNAs indicated above the lanes, exactly as for the ChIP experiments shown in Figs. 5B, C. Whole cell lysates were probed with the indicated antibodies, revealing efficient depletion of dHCF and Myc, respectively.

Table S2. List of genes that were included in the tissue culture based RNAi screen.

Table S1.

FBgn	Amplicon Length	R oligonucleotide	S oligonucleotide	S tag	Tag Nr
HCF	520	TGGCGCCCCTAGATGCATTAATAGTATATTGCAAAGTTTC	TGAGGTACGCGTGGGATGTGGGTTTGCAATTGATATG	TGAGGTACGCGTGGG	3
Ada2A	520	TGGCGCCCCTAGATGTAGTCCGCGACAACATACA	CGACGCCCGCTGATAGATTGTTGTATGCCCGAACTA	CGACGCCCGCTGATA	4
Ada3	520	TGGCGCCCCTAGATGCACTCTTCGATGACCATTCT	CGCATGTAGCCTGCCAGGGACTCCTCCATTAAGG	CGCATGTAGCCTGCC	7
GCN5	520	TGGCGCCCCTAGATGAACTTTCTGAACCACTACAAC	TAGGTCTAGCCCCGCTCGGTGGGCTCCTTTTTG	TAGGTCTAGCCCCGC	5
CHRAC14	387	TGGCGCCCCTAGATGCGCATCGAGGATCTTAACC	AGCTAGCCCAGGTGAACTCGGGGGCTTCTCT	AGCTAGCCCAGGTGA	1
CG32343	520	TGGCGCCCCTAGATGGTGGTTCTTCTTAAGTACGTTAT	AGCTAGCCCAGGTGAGACTTTTCTTTATATCGGTCCT	AGCTAGCCCAGGTGA	1
NC2b	520	TGGCGCCCCTAGATGGACGACGAGCTGACCCT	TAGGTCTAGCCCCGCCATCGTCATCGTCATCCTC	TAGGTCTAGCCCCGC	5
Sin3A	520	TGGCGCCCCTAGATGGAAATAATCATCATGTACAAAAGTAC	AGCTAGCCCAGGTGAAACCATCTCAGCAGGTGC	AGCTAGCCCAGGTGA	1
ash2	381	TGGCGCCCCTAGATGCCAAAAACAATCGACAGAAAAG	TAGCCTCCCTAGCGCTGTGGCTCGGACCATGC	TAGCCTCCCTAGCGC	8
CG40351	571	TGGCGCCCCTAGATGGCAGGACGTTCCGGAATATC	CGCATGTAGCCTGCCTCCATTACAGACTTTTGATTG	CGCATGTAGCCTGCC	7
ash1	520	TGGCGCCCCTAGATGACCTTTGTGGCCAGGACC	TGACCCGGGTAGCCTGGCAGGCAAGGGATCGT	TGACCCGGGTAGCCT	2
Trx	520	TGGCGCCCCTAGATGTGACGGTTCACCTCAAATGT	AGCTAGCCCAGGTGAATCCAGGGCTGTTAGGGTT	AGCTAGCCCAGGTGA	1
trr	520	TGGCGCCCCTAGATGCAGATGTCCGGACAAATCTC	TAGCCTCCCTAGCGCCTTCTACCTTGAGAACTT	TAGCCTCCCTAGCGC	8

Figure S1

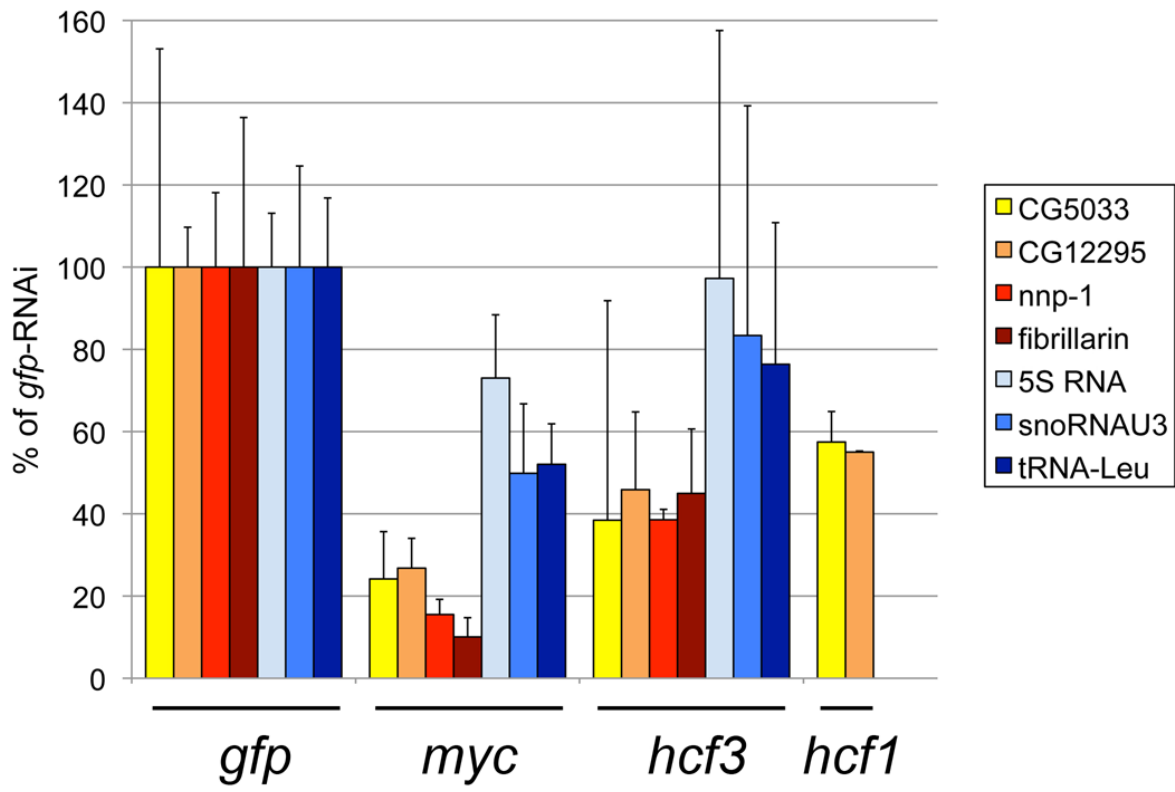


Figure S2

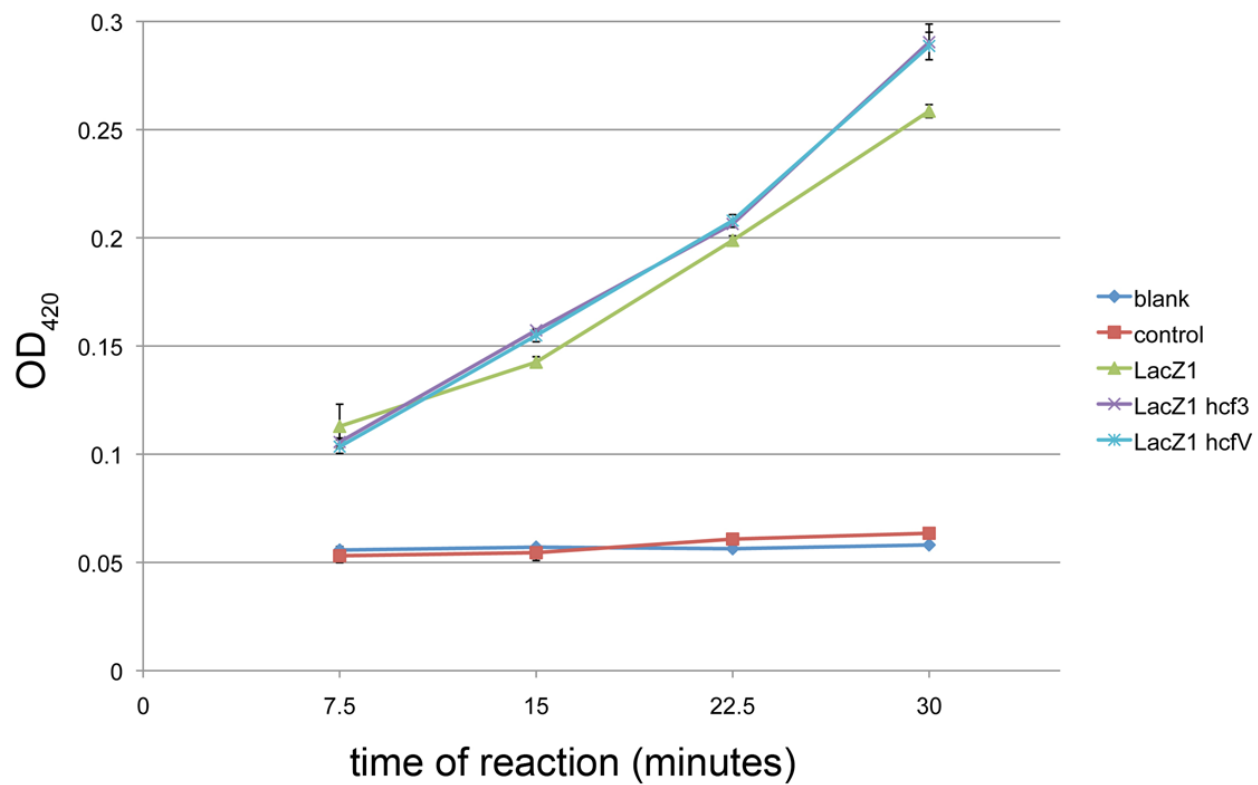


Figure S3

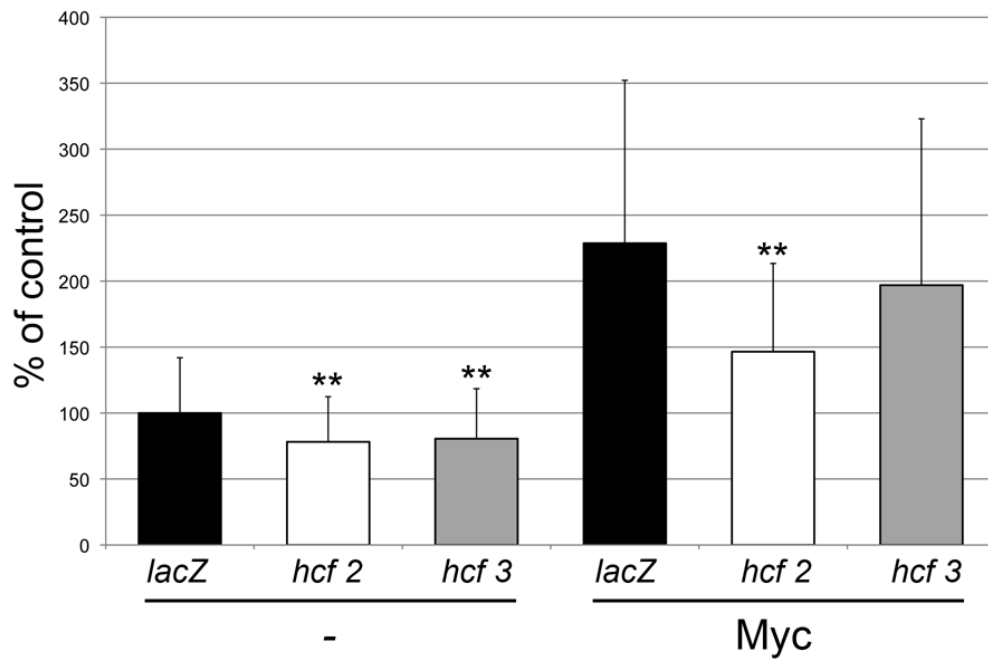


Figure S4

A

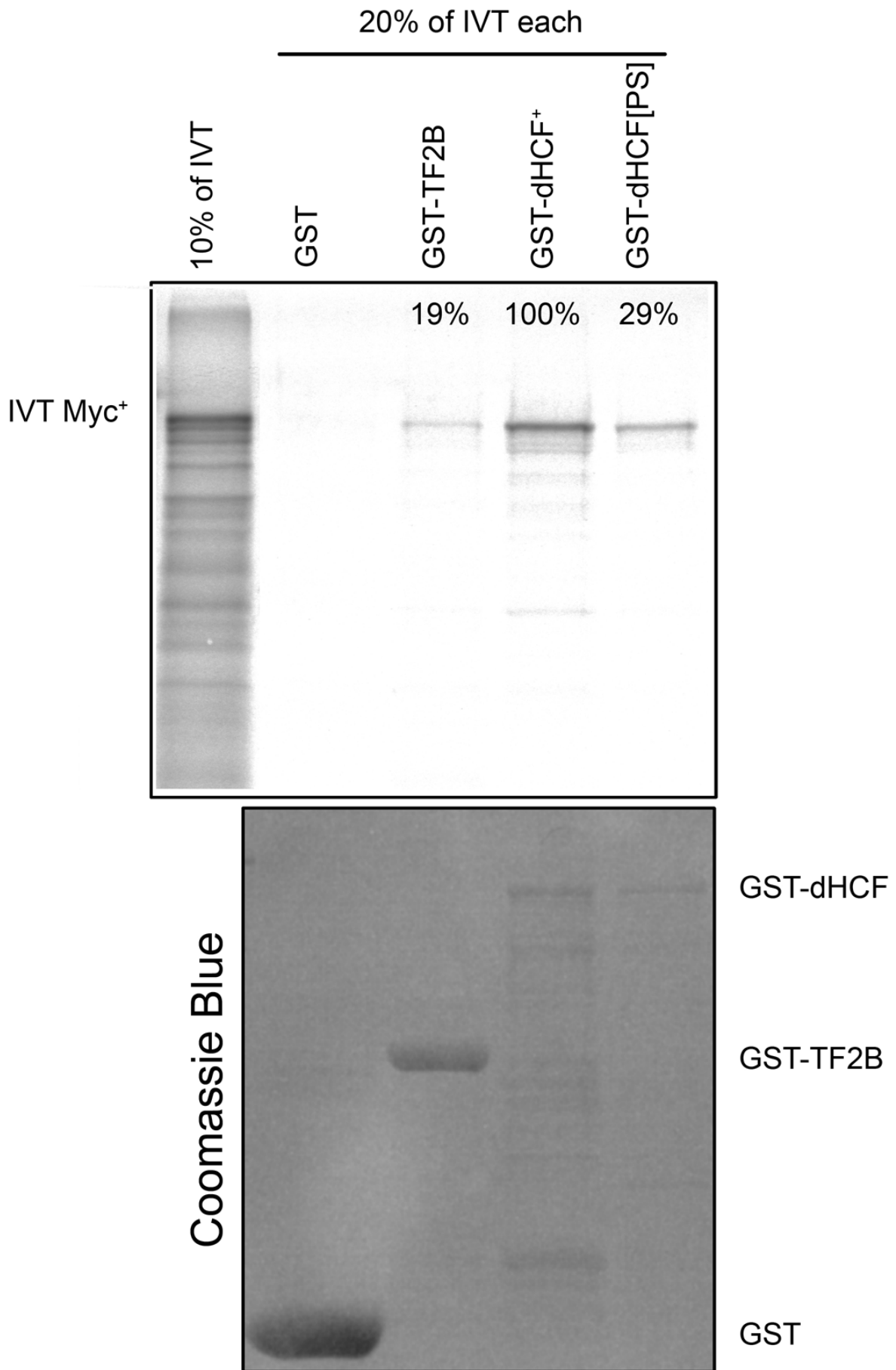


Figure S4

B

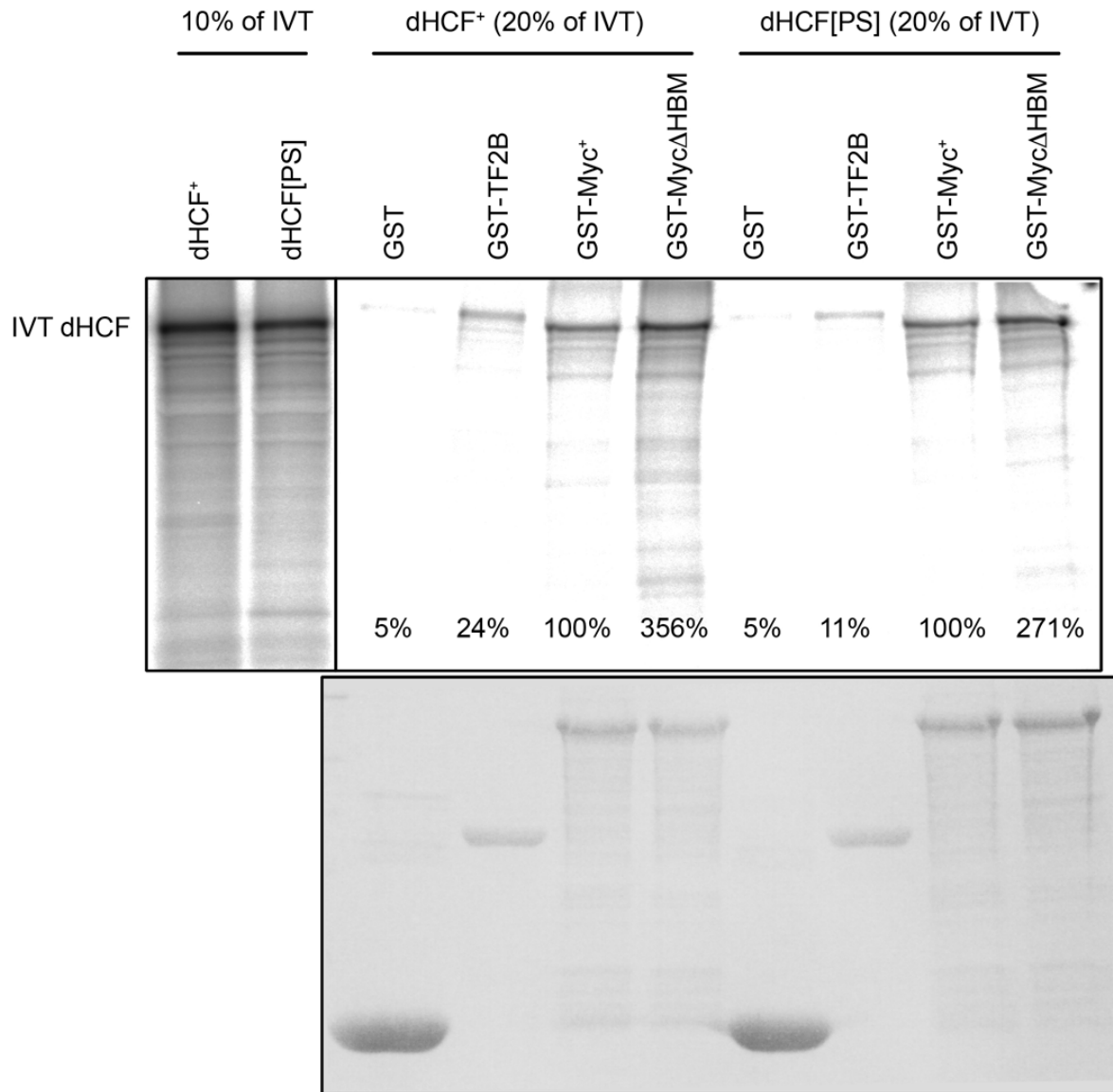
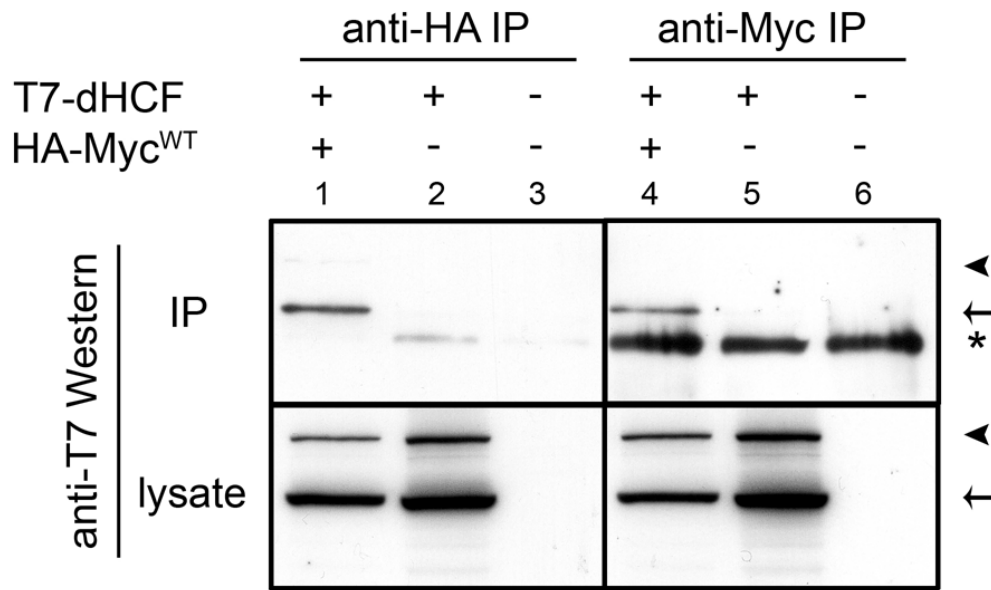


Figure S4

C



D

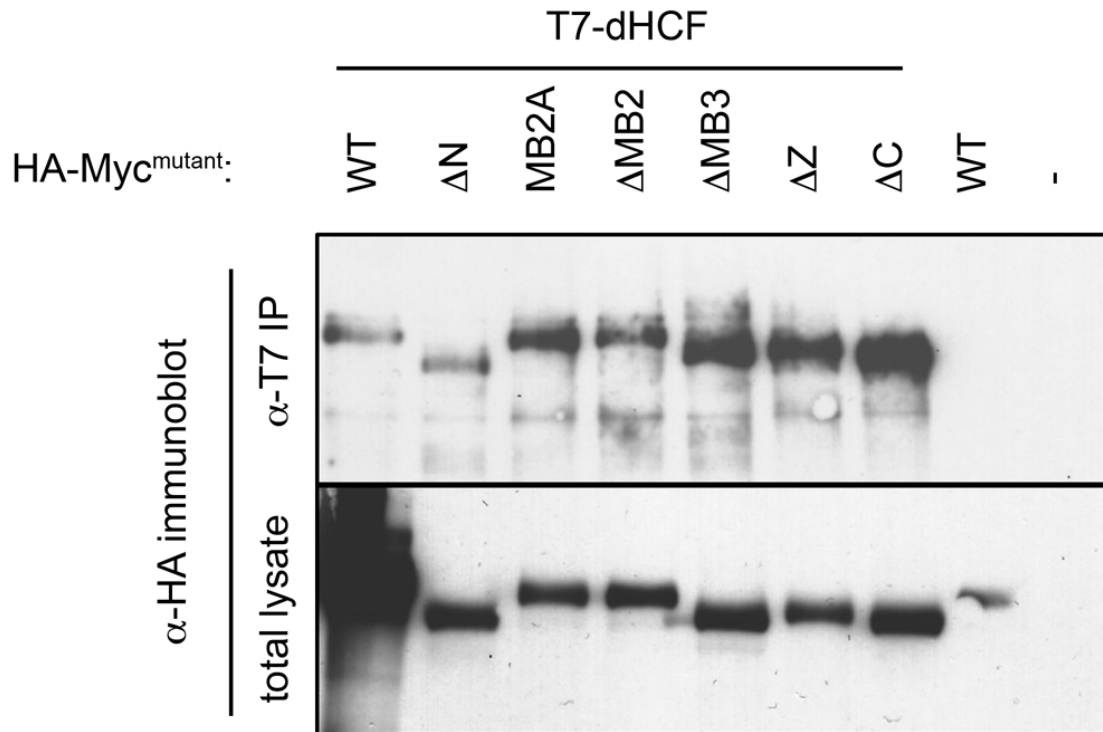
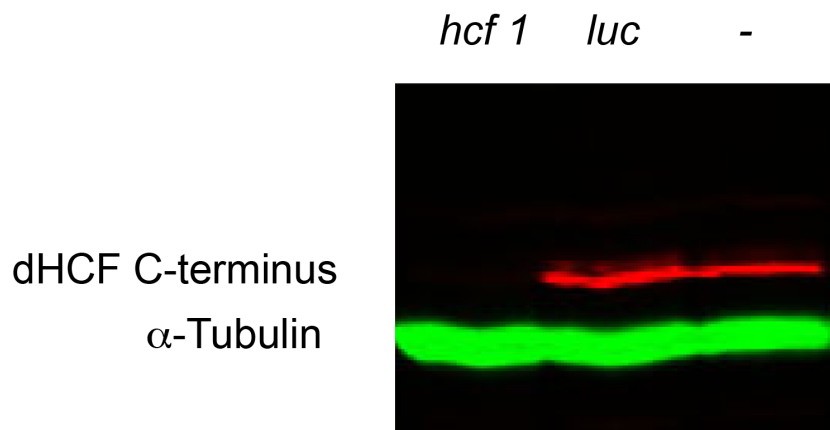


Figure S5

A



B

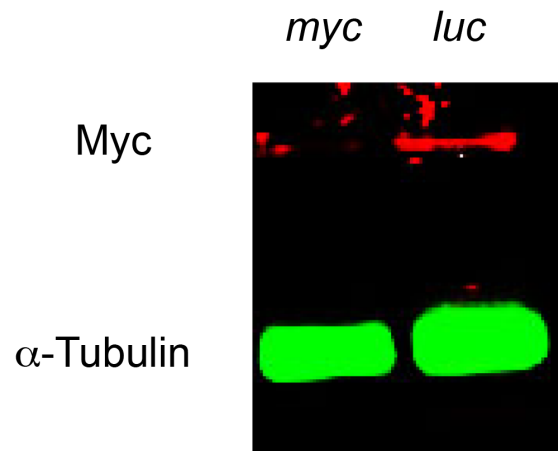


Table S2 / 1

Gene	Synonyms
14-3-3zeta	4-3-3 zeta; leo; 14-3-3zeta; 14-3-3zeta; CG17870; D14-3-3; 2G1; 549; I(2)07103; leonardo; 14-3-3; D14-3-3zeta; Leonardo-13-3-3; par-5
abo	abo; CG6093
ac	ascT5; AS-C T5ac; Hairy wing; 990 E5 F1; CG3796; Ac; ac; ASC; EG:125H10.3; T5; achaete-scute; AS-C T5; sc/T5; Hw
Acf1	Acf-1; CG1966; CHRAC; ACF; Acf; CAF; ACF1; Acf1; acf1; CHRAC-175; dCHRAC; p170/p185; dACF
achi	achintya; CG8819; zaa; achi
acj6	CG9151; I-POU; ACJ6; Acj6; acj6; lpou; tl-POU
Ada2A	ADA2A; Ada2A; CG31318; dAda2A; CG7150
Ada2S	Ada2S; CG9638; BcDNA:LD24527; dAda2S
Adf1	I(2)01349; Adf-1; CG15845; nal; Adf 1; Adf1; adf1; I(2)04065; nalyot
Aef1	CG5683; AEF-1; Aef1
ago	CG15010; ago; DmFbw7
alien	BcDNA:LD10463; Alien; alien; DCH2; Dch2; d-Alien; CG9556; CH2; CSN2
aly	CG2075; ms(3)ry2; aly; ms(3)2
Aly	I(3)02267; Aly; BcDNA:LD24793; cg1101; CG1101; ref1; REF1; dmREF1; DmREF1
aop	Aop; aop; yan/pok; pokkuri; DROYANET; Aop/Yan; aop/yan; yan; Yan; YAN; CG3166; pok; DROYANETSB; SK2-1
AP-2	AP-2; CG7807; DAP-2; dAP-2; stummelbein; dAP-2alpha
apt	TDF/APT; apt; I(2)09049; I(2)k11531; I(2)03041; I(2)06369; 3041; tdf; TDF; CG5393
ara	CG10571; iroquois-complex; Iro; iro; IRO-C; Iro-C; iro-C; iroquois
Arc105	dARC105; BcDNA:GH03922; Med9/ARC105; CG4184; Arc105
Arc32	Med8/ARC32; CG30140; Arc32; CG13867; dARC32
Arc42	CG4703; dARC42; Arc42
Arc92	CG12254; Arc92; dARC92; LD07688
ase	AS-C T8; EG:165H7.2; sc/T8; ascT8; T1; T1a; ASC; AS-C T8ase; ase; T8; CG3258; AS-T8; as-T8
asf1	CG9383; ASF1; Asf1; asf1; dASF1
ash1	dash; I(3)SG29a; CG8887; ash-1; ash; ash1; Ash1; ASH1
ash2	291.8; mad; CG6677; I(3)SG65; 1124/11; 703; I(3)112411; ash-2; I(3)S112411; ash2; ASH2
Asx	CG8787; Asx
atms	CG2503; antimeros; anon-WO0172774.113; anon-WO0172774.114; anon-WO0172774.116; I(3)01456; I(3)02466; I(3)rK509; Paf1; PAF1
Atu	CG1433; I(3)s1938; Another transcription unit
az2	zf43C; az2; CG1605
Bap60	i133; BAP60; Bap60; BAPp60; i127; CG4303
Bbbf1	BBF-1; Bbbf1
bel	DmRH6; I(3)85Ac; BEL; bel; cap; ms(3)Pneo85A; CG9748; cg9748; anon-85Ab; ms(3)neo30; L3; I(3)L3
Bgb	CG7959; rpbeta2; Bgb; bgb; Big-brother; en(lz)D/9
bgcn	ben(2)gcn; fs(2)eo-C; PNBP; CG10330; CG10331; cg10331; CG30170; pep; fs(2)eo6; fs(2)eoQS2; gcn; bgcn; b(2)cgn; b(2)gcn

Table S2 / 2

bi	CG3578; Qd; T3; optomotor-blind; l(1)bi; BI; bi; optomotor blind; Optomotor blind; l(1)omb; dm-omb; Dm-omb; Dm-OMB; omb; Omb; OMB
bic	l(2)49Da; E(Bic); l(2)k10712; 5A; E(2)Bic; BcDNA:GM05329; 107/12; l(2)vr22; CG3644; vr22; Btf; BcDNA.GM05329; bic; Bic
BicD	BicD; CG6605; Bicaudal-D; anon-EST:fe2A11; BIC-D; Bic-D; Bic<up>D</up>
Bin1	dSAP18; dSap18; BcDNA:RE02417; CG6046; bin1/dSAP18; bin1; Bin1; SAP18
bip2	TFIID; dBIP2; i163; CG2009; TAFII155; bip-II; TAF<down>II</down>155; BIP2; bip2; i31; TAF3; dTAF<down>II</down>155
Bj1	CG18640 (Bj1), RCC protein; RCC1; RanGEF; sdt; BJ1; Bj1; CG18640; CG10480
Bka	BcDNA:RE14949; l(2)02695; Bka; mip; CG4539
bl	CG13425; Hrb57A; l(2)k08305; Q18; bl; CG30153; l(2)05056
bon	0487/06; 0249/12; CG15687; 0241/08; bon; Bonus; CG5206
bowl	l(2)k08617; 17-29-5; l(2)c; Bowl; bowl; bowel; org2; Su(tor)2-1; CG10021
brat	l(2)brat; brat; Cf; l(2)37Cf; l(2)E60; anon-37CDa; Brain Tumor; E60; CG10719; fs(2)ltoPM43
Brf	CG4155; BRF; Brf; BRF1; CG31256; CG5419
brk	CG9653; ssg-1; Brinker; Brk; brk
brm	BRM; Brm; brm; CG18438; l(3)72Aa; dBRM; CG5942; E(E2F)3A
Bro	CG7960; Bro; bro; Beta for Runt and OTHERs; rpbeta1
bs	Group IIc; ba; px; Srf; SRF; pruned/DSRF; pruned; DSRF; DSrf; dSRF; dsrf; Serf; l(2)03267; DSrf/bs; CG3411; BS; bs; Serum Response Factor; serum response factor; CG4444; DmSRF; D-SRF
bsh	lambdaE86; Hox11-310; E86; Bsh; bsh; CG10604
btb	btb
BtbVII	BtbVII; BTB protein VII; BTB-VII; CG11494
btd	BTD; btd; CG12653
Bteb2	CG2932; Bteb2
bun	l(2)rl043; bun; l(2)06475; short-sighted; l(2)02687; shortsighted; l(2)k02903; l(2)05479; CG5461; 1550; TSC-22; l(2)00255; EP(2)0488; Tsc22; shs
Bx	fliH; beadex/dLMO; Bd; Ptd; mgt; Lmo; Rho; hdp-a; DLMO; Dlmo; dLMO; dlmo; rhombotin; dttg; CG6500; hld; Bx; mgg; hdp
byn	DTrg; apro; Dm-BYN; Tra; D-TRA; Byn; byn; CG7260; byn/apro; dm-Trg; trg; Trg; D-Trg
C15	C15; Ect5; 93Bal; Hox11-311; CG7937; 311
cact	BG:DS02740.15; cact; CG5848; dip6; cac; fs(2)ltoRN48; n(2)k17003
cad	38E.19; Cad; cad; CG1759; S67; cd
Caf1	NURF-55; Nurf-55; NURF55; dCAF-1 p55; CAF-1; Caf-1; CG4236; 55; p55; CAF1; Caf1; p55/NURF-55; NURF; d-CAF1; dCAF-1; dNURF
Caf1-105	CG12892; Caf1-10; Caf1-105
Caf1-180	Caf1-180; CG12109
can	can; CG6577; dmTAF5b; dTAF<down>II</down>80; TAF5L
Cap	DmSMC3/Cap; Cap; cap; CG9802; SMC3; DmSMC3
cas	l(3)j1C2; l(3)neo33; CG13281; ming; Cas; cas; CG2102
caup	iroquois-complex; iroquois
CCR4	CT33003; CG31137; CT39331; CG5534; CCR4; CG17741

Table S2 / 3

CDC45L	CG3658; anon-1Ec; EG:BACR7A4.11; Cdc45; D; DmCdc45; CDC45L
Cdk7	CDK7; Cdk7; cdk7; CG3319; DmCDK7; DmCdk7; Dmcdk7; DmMO15; p40^{MO15}
Cdk8	CG10572; CDK8; Cdk8; DmCdk8; p58; dTRAP56
Cdk9	CG5179; p43 PITALRE; Cyclin-dependent kinase9 2.7; PTefb; CDK9; Cdk9; cdk9; P-TEF; P-TEFb
Cf2	BcDNA:GM09668; CF2; Cf2; cf2; CG11924; CF2.5
CG10147	CG10147
CG10228	CG10228
CG10267	CG10267
CG10296	CG10296
CG10309	CG10309
CG10366	CG10366
CG10445	CG10445
CG10447	CG10447; BcDNA:RH50436
CG10462	BcDNA:SD07008; CG10462
CG10543	CG10543
CG10563	CG10563
CG10576	BEST:CK00496; CG10576
CG10669	CG10669
CG10685	CG10685
CG10887	CG10887
CG10936	CG10936
CG10959	CG10959
CG11033	CG11033
CG11063	CG11063
CG11107	CG11107; cg11107
CG11183	CG11183
CG11247	CG11247
CG11403	EG:33C11.2; CG11403; cg11403
CG11513	CG11513
CG11552	CG11552
CG11695	CG11695
CG11710	CG11710
CG11762	i36; CG11762
CG11835	CG11835
CG11942	CG11942
CG11990	hyrax
CG12000	CG12000
CG12161	CG12161
CG12175	anon-EST:fe2G7; CG12175
CG12190	CG12190
CG12227	CG12227
CG12236	CG12236
CG12267	CG12267

Table S2 / 4

CG12299	CG12299
CG12460	CG40051; CG12460
CG12605	CG12605
CG12942	CG12942
CG13185	CG13185; CG18329
CG13916	CG13916
CG14216	CG14216
CG14443	CG14443; cg14443
CG14655	CG14655
CG14710	CG14710
CG14711	CG14711
CG14802	dp28b; CG14802; p28; Srb5/Med28b; EG:63B12.13
CG15000	CG15000
CG15073	CG15073
CG15105	CG15105
CG15269	DS04929.3; CG15269; BG:DS04929.3
CG15436	CG15436
CG15800	CG15800
CG15803	CG15803
CG1582	CG1582; cg1582
CG15835	CG15835
CG1602	CG1602
CG16903	CG16903; EG:67A9.2
CG16975	CG16975
CG17023	CG17023
CG17068	CG17068
CG1716	CG1716
CG17181	CG17181
CG17209	CG17209
CG17301	BcDNA:AT30033; CG17301
CG17302	CG17302
CG17328	DS02740.8; BG:DS02740.8; CG17328
CG17331	CG17331
CG17359	CG17359
CG17385	CG17385
CG17568	CG17568
CG17612	CG17612
CG17802	CG17802
CG17806	CG17806
CG1792	CG1792
CG18013	CG18013
CG18262	CG18262
CG1832	CG1832
CG18375	CG18375
CG1845	CG1845

Table S2 / 5

CG18476	CG18476; CG17822
CG18555	CG18555
CG18764	CG18764
CG1884	anon-EST:Liang-1.29; clone 1.29; CG1884
CG1894	CG1894; dmHAG407
CG1957	CG1957; BcDNA:LD14168
CG1965	CG1965
CG1972	CG1972
CG2052	CG10204; CG2052
CG2097	CG2097
CG2120	CG2120
CG2129	CG2129
CG2202	CG2202
CG2469	CG2469
CG2712	EG:95B7.7; anon-3Be; III; CG2712
CG2990	CG2990
CG2995	cab65850 G9a Dm; CG2995; EG:BACR37P7.2
CG3032	CG3032
CG30420	CG3749; CG12850; CG30420
CG30431	CG8341; CG8324; CG30431
CG30443	CG12397; CG30443; BcDNA:RE37461
CG3065	CG3065
CG31156	CG5253; CG31156; CG5257
CG31160	CG13846; CG13851; CG31160
CG31212	CG14279; CG18491; CG31212; CG3602
CG31224	CG17796; CG31224; CG7696
CG31365	CG4639; CG31365
CG31367	CG15187; CG31367
CG31368	CG14729; CG14730; CG31368
CG31441	CG5135; CG31441
CG31453	CG11743; CG31453; CG11744
CG31716	CG5244; CG31716; CG5251; cg5251
CG32067	CG8000; CG32067; CG7983
CG3225	CG3225; cg3225
CG32344	CG32344; DmRH20; CG6994; cg6994
CG32533	CG12211; cg12211; CG14198; CG32533
CG32721	CG32721; BcDNA:GH10333; CG12152
CG32767	i7; CG32767; CG5113; LD34931; CG5086; BcDNA:GM08530
CG32772	CG15469; CG6911; CG32772
CG3281	CG3281
CG33005-O	CG10438; CG33005-ORFA; CG10438a
CG33097	CG15187; CG33097
CG33182	CG4037; CG33182
CG3335	CG3335; cg3335; Dm-RBD-1; Q9VT19
CG3407	CG3407

Table S2 / 6

CG3485	CG3485
CG3561	CG3561; cg3561; DmRH9
CG3654	CG3654
CG3689	CG3689
CG3708	EG:BACR7A4.18; CG3708
CG3726	CG3726
CG3732	CG3732
CG3753	CG3753
CG3756	CG3756
CG3941	CG3941
CG40351	CG17395; CG17396; aaf45425 Dm; CG40351
CG4049	CG4049
CG4078	CG4078
CG4282	CG4282
CG4360	CG4360
CG4413	CG4413
CG4424	CG4424
CG4707	CG4707
CG4730	CG4730
CG4756	CG4756
CG4854	CG4854
CG4901	CG4901; cg4901
CG4935	MET30; BG:DS02740.2; CG4935
CG4936	CG4936
CG5017	CG5017
CG5161	BcDNA:RE62842; CG5161
CG5202	CG5202
CG5205	CG5205; cg5205
CG5222	CG5222
CG5245	CG5245
CG5249	CG5249
CG5319	CG5319
CG5366	BcDNA:GH07774; CG5366
CG5380	CG5380
CG5382	CG5382
CG5591	CG5591
CG5604	CG5604
CG5640	CG5640
CG5641	Interleukin enhancer binding factor; CG5641
CG5684	CG5684
CG5708	CG5708
CG5874	CG5874; BcDNA:SD07139
CG5882	CG5882
CG5899	CG5899
CG6004	CG6004

Table S2 / 7

CG6061	p120; CG6061
CG6118	CG6118
CG6121	EG0007.7; DmEG0007.7; dmHAG405; CG6121; EG:EG0007.7
CG6197	CG6197
CG6204	CG6204
CG6220	CG6220
CG6254	CG6254
CG6418	DmRH27; CG6418; cg6418
CG6654	CG6654
CG6686	CG6686
CG6689	dmCG6689; CG6689
CG6701	CG6701; EP2054; EP(2)2054
CG6751	CG6751
CG6755	CG6755
CG6792	CG6792
CG6808	CG6808; CG31372
CG6843	CG6843
CG6905	CG6905
CG6967	CG6967
CG7099	CG7099
CG7154	CG7154
CG7185	CG7185; cg7185
CG7233	CG7233
CG7246	CG7246
CG7257	DmCG7257; Dm_Rpt4c; CG7257
CG7274	CG7274
CG7312	CG31670; CG7312
CG7339	CG7339
CG7372	CG7372
CG7386	CG7386
CG7504	CG7504
CG7597	AC017581; CG7597
CG7698	CG7698
CG7804	CG7804; cg7804
CG7878	CG7878; cg7878; DmRH26
CG7907	CG7907
CG7922	CG7922; cg7922
CG7928	CG7928
CG7963	CG7963
CG7987	CG7987
CG8117	CG8117
CG8120	CG8120
CG8145	CG8145
CG8159	CG8159
CG8165	CG31123; CG8165

Table S2 / 8

CG8290	BEST:LD29214; LD29214; CG8290
CG8301	CG8301
CG8388	CG8388
CG8484	CG8484
CG8915	CG8915; cg8915
CG8924	CG8924
CG8950	CG8950
CG8974	CG8974
CG9086	CG9086; Ubr1
CG9207	GAS41; CG9207
CG9215	CG9215
CG9323	CG9323; cg9323; 38E.15
CG9418	CG9418; BEST:LD07122; LD07122
CG9425	CG9425
CG9588	CG9588
CG9609	CG9609
CG9650	CG9650
CG9772	CG9772
CG9791	CG9791
CG9793	CG9793
CG9797	CG9797
CG9868	CG9868
CG9899	CG9899
Chd1	Chd1; chd1; DmCHD1; CG3733; dCHD1; CHD-1
Chd3	CHD3; Chd3; chd3; DmCHD3; CG9594
chm	chm; dmHAG404; CG5229; HAT; HAT1
Chrac-14	55A11T; CHRAC; CG13399; CHRAC-14; Chrac-14; CHRAC14; mary; ESTS:55A11T; CG10890
Chrac-16	BcDNA:RE59557; CG15736; CHRAC16; CHRAC; CHRAC-16; Chrac-16; joey
ci	CID; CiD; ciD; CG2125; I(4)13; ci155; Ce; cubitus-interruptus-Dominant; I(4)17; I(4)102ABc; Ci; ci; ci-D; Ci^D; ci^D
cic	CG5067; cic; E(DI)D49; fet; fettucine
Clk	dCLOCK; dClock; dclock; dClck; dCLK/JRK; PAS1; Jrk; jrk; Clk; clk; CLOCK; clock; Jerk; CG7391; dCLK; dClk
Clp	CG3642; c6a; CLP; Clp; clp; Ssb-c6a
cnc	CG4578; cap and collar; CNC; Cnc; cnc; CG17894; CNC_DROME; 5134; Cap 'n' collar; cap 'n' collar; cap'n'collar; I(3)03921
cpsf	CPSF; Cpsf; cpsf; dCPSF-160; CG10110
CrebA	dCREBA; dCrebA; BOX B Binding Factor-2; BBF-2; CREB-a; Creb-A; dCreb-A; dCREB-A; BcDNA:SD05937; BBF2_DROME; I(3)03576; CG7450; creb; Creb; CREB; CrebA; crebA; Bbbf2
CrebB-17A	dCREB; dCREB-2a; dCREB2-a; dCREB2-b; dCbz; S162; CREB2; dCREB-B; Creb2b; CREB2b; dCREB2; dCREB2a; CG6103; dCREB2b; CrebB17-A; CrebB-17A; cAMP-regulated enhancer-binding protein; CREB; Creb; I(1)17Af; dCREB-2
croc	FD1; fd1; Dmfd1; CG5069; fd78E; croc

Table S2 / 9

crol	crol; I(2)04418; I(2)s2346; CG14938; crol gamma; crol beta; crol alpha
crp	CG7664; I(2)35Fd; AP-4; crp; dAP-4; I(2)00232; I(2)k03505; BG:DS02740.3; I(2)k00809
CSN5	CH5; JadBp; CG14884; DCH5; Dch5; dch5; BcDNA:LD14392; I(3)L4032; quo; JAB1/CSN5; jab1/csn5; BcDNA.LD14392; csn5; Csn5; CSN5; Jab1
CstF-50	CstF-50; CG2261
CstF-64	CStF 64; CG7697; CstF-64
CtBP	G9; I(3)03463; I(3)G9; CG7583; I(3)03464; 0256/16; 256/16; BcDNA:GH07572; I(3)87De; CtBP; RE61183; RE01030; EP(3)3528; dCtBP
cul-2	CG1512; cul-2; DMcul-2; I(2)02074; Cul2
cul-4	Cul4; CG8711; cul-4; DMcul-4
cyc	CYCLE; Cycle; dBMAL; dBmal; dBMAL1; dbmal1; CG8727; dBma1; BMAL1; Bmal1; bMAL1; bmal1; Mop3; MOP3; cyc; Cyc
CycC	Cln3; dTRAP33; CycC; cycC; Dmcycc; cyclin C; SRB11; CG7281; Cyc-C
CycH	CG7405; cyclin H; CycH
CycK	CycK; CG15218; cyclin K
CycT	CycT; cyclin T; cyclin T1; Dmcyclin T; p124; dT; cyclin T2; CG6292; P-TEFb
Cyp1	CyP-1; Cyp-1; cyp-1; BcDNA:GM09255; CG9916; Cpy1; Cyp1; cyp1
D	SOX70; CG5893; D; SOX70D; Sox70D; fish-hook; fish; fish hook; I(3)LG9; SOXB2.1; SOXDP; loD
D19A	Zinc finger AT-hook protein; CG10269; D19A
D19B	D19B; CG10270
da	I(2)31Ea; CG5102; daughterless; da
dac	dach; spn; Dm-DAC; dac; Dac; I(2)rK364; dachsund; BG:DS02780.3; I(2)36Ae; CG4952
dalao	dalao; CG7055; BAF57; BAP111; Bap111
Dcr-2	CG6493; cg6493; Dcr-2; dcr-2; Dicer
Ddx1	DDX1; Ddx1; DmDDX1; Dbp79E; CG9054; anon-79E; DmRH12
Deaf1	Deaf1; CG8567; DEAF-1; Deaf-1; deaf-1
Dfd	I(3)84Ae; EbR11; BG:DS00276.5; CG2189; deformed; Dfd; DmDfd
dik	dik; HL-XIV; Ada3; CG7098; DADA3
DIP1	TO67; UbxBP1; klett; clot 10495; CG17686; clot 2020; TO34; klt; dip1; DIP1; dip1a
dl	dL; dl; mat(2)dorsal; CG6667; fs(2)k10816
dlt	CG12021; CG1977; I(3)04276; dlt; Van; Vanaso; CG32315; I(3)62Ba; I(3)dre1; dre1
dom	CG9696; dom; I(2)k08108; 27/4; domino; I(2)81/8; I(2)k02704
Dox-A2	Diphenol oxidase; proPO; I(2)37Bf; DPO; phenol oxidase; phenoloxidase; DXA2_DROME; DmePPO2; I(2)37Bf⁺; CG10484; Dox; Dox-A2; DoxA; p58; DoxA2; PO
Dp	DP; Dp; DmDP; I(2)vr10; dDp; dDP; vr10; dDP1; I(2)49Fk; CG4654; 49Fk
Dp1	BcDNA:LD21677; DDP1; BcDNA:LD21383; Dp1; CG5170
dpa	MCM4; Mcm4; DmMCM4; DmMcm4; Dpa; dpa; CG1616; I(2)43Ca; 43Ca; Drosophila proliferation abnormal
dpld	I(2)k08815-3; dpld; lin-41; CG1624
dpn	anon-EST:fe1B12; dpn; 44C; CG3161; CG8704; deadpan
dre4	DRE4/dSPT16; I(3)62Bg; dSPT16; dspt16; CG1828; spt16; Spt16; I(3)dre4; dre4

Table S2 / 10

dsx	Dmdsx; CG11094; ix-62c; Hr; dsx
E(bx)	NURF-215; Nurf-215; p301; l(3)122; p215; CG17135; CG32346; nurf301; Nurf301; NURF301; CG10894; l(3)ry122; E(bx); CG32478; NURF215; CG7022; En-bx; NURF; NURF-301; dNURF
E(Pc)	l(2)28-28-12; anon-48Ac; E(Pc); e(Pc); GH14582; lll; CG7776; GH05739
e(r)	e(r); CG1871; ER
E(spl)	CG8365; Hes; E(spl)bHLH; En(spl)-C; E(spl); e(spl); m8; l(3)96Fd; Enhancer of split m7; E(spl) m8; Enhancer of split m8; E(spl)m8; E(spl)M8; En(spl); E(spl)-m8; clone 1.71; anon-EST:Liang-1.71
e(y)1	e(y)1; TAF<down>ll</down>; TAF42; Taf42; e(y)4; TAF40/42/e(y)1; TAF<down>ll</down>40; Taf<down>ll</down>40; dTAF42; TAF<down>ll</down>42; d40; dTAF<down>ll</down>40; TAFll40(42); dTAF<down>ll</down>42; e(y)<up>1</u>
E(z)	E(z)1; pco/E(z); pco; enhancer of zeste; l(3)67Fa; Su(z)301; l(3)ds12; E(Z); E(z); l(3)SG17; l(3)B12; CG6502; E[z]; polycombeotic; l(3)1902; Enhancer-of-zeste; Ez; EZ
E103	E103; 90Bre
E2f	CG6376; l(3)j3B1; dE2F; dE2f; l(3)j3C2; drosE2F1; E(Sev-CycE)3A; DmE2F-1; DRTF1/E2F; Evar(3)164; E2f1; E2F1; E(var)93E; E(var)3-93E; l(3)rM729; l(3)07172; dE2F1; de2f1; E(var)3-95E; E2F-1; e2f; E2f; E2F
E2f2	dE2F-2; CG1071; dE2F2; de2f2; E2F; E2F2; E2f2
E81	E81
ear	ear; dENL/AF9; CG4913; ENL/AF-9; ENL/AF9
EcR	Dhr23; snt; EcR-A; NR1H1; EcRB-1; EcR-B1; EcR; ECR; DmEcR; CG1765; DEcR; dECR; EcdR; Ecdysone Receptor; ecdysone receptor
eIB	el; elbow; P10; CG4220; eIB; elb; BG:DS06238.3
Elongin-B	Elongin-B; CG4204; d-elongin B
Elongin-C	d-elongin C; Elongin-C; BcDNA:RH71704; CG9291
emc	CG1007; ms(3)61CD; 0094/26; 0587/01; 0203/10; Emc; emc; l(3)05592; l(3)j4E11; Dm0688; l(3)04322; Ach; gov; 0977/09
en	Es; CG9015; Apa; Eng; en; Engrailed/Invected; V; spt
enok	anon-60Ba; anon-WO0200864.2; S1; rot; CG11290; rotkehlchen; dmHAG406; enok
EP2237	CG4427; EP2237; EP(2)2237
ERR	CG7404; ERR; dERR
esc	extra sex combs; ESC; Esc; esc; CG14941; L41867
esg	CG3758; fleabag; BG:DS07851.7; l(2)br43; 4B7; l(2)esg; shof; l(2)07082; wizard; Fusion-1; dgl; flg; wiz; br43; l(2)4B7; l35Ce; esg; l(2)35Ce; shut off
ESTS:136D	136D12S; ESTS:136D12S
ESTS:42D3	42D3T; ESTS:42D3T; anon-sts30
Fer3	Fer3; Dnato3; ntwist; BcDNA:LD04689; CG6913; nato3; N-twist
fkh	Fkh; fkh; Dmfkh; FORK HEAD; Forkhead; Sebp2; CG10002
fru	CG7690; ms(3)06411; fty; BTB-VI; BtbVI; CG7688; cg7688; sat; cg7689; CG7689; CG14307; fru-satori; CT22773; fru

Table S2 / 11

fs(1)h	fsh; l(1)G0093; fs(1)h; rnc; l(1)G0495; l(1)7Da; fs(1)1456; fs(1)M16; fs(1)R10.4; anon-EST:fe1G2; CG2252; N72; fst(1)h; clone 1.81; fs(1)26/26A; anon-EST:Liang-1.81
ftz-f1	beta-Ftz-F1; alphaFTZF1; betaFTZF1; NR5A1; DmFTZ-F1; DEP1; FTZF1; CG13378; FIP1; alphaFTZ-F1; alphaftz-f1; ftz-f1alpha; FTZ-F1alpha; beta FTZ-F1; betaFTZ-F1; betaftz-F1; betaftz-f1; beta FTZ-F1; l(3)03649; dFtz-
GATAd	GATAd; dGATAd; CG5034
GATAe	GATAe; CG10278; dGATAe
gft	gft; Cul-3; DMcul-3; Cul3; dCul-3; Cullin3; l(2)br34; br34; CG11861; l35Cd; dCul3; l(2)06430; l(2)35Cd; BG:DS07851.2
glu	BcDNA.LD20207; l(2)k08819; Gluon; SMC4; glu; DmSMC4/gluon; BcDNA:LD20207; CG11397
GM130	GM130; CG11061; dGM130; dgm130
gol	g1; anon-G1; CG2679; gol; meso
grh	grh; hsk; NTF-1; EG:191D12.1; Elf1; elf1; Ntf; l(2)s2140; Elf-1/NTF-1; NTF-1/Elf-1; elf1(CAG)<down>7</down>; l(2)IM45; Gh; l(2)06850; Elf-1; NTF1; Ntf1; CG5058; grainyhead; Grainyhead; DREB
grn	dGATA-2; GATAc; GRAIN; l(3)84Fa; CG9656; dGATAc; dGatac; grn; gra; Gata-c; Gata2
gro	m9,m10; CG8384; m9-m10; m9/m10; E(spl)²; m9; E(spl)m9/m10; Gro; gro; BcDNA:LD33829; dGro; E(spl)-WD; E(spl)gro; m10; En-spl; m9/10; Groucho; l(3)gro; BcDNA.LD33829
Gsc	M72; 60Mun1; 60Mun2; CG2851; Muenster 72; l(2)05341; gsc; Gsc; D-gsc; D-Gsc; Pph25; PPH25
gt	CG7952; l(1)giant; Giant; gt; l(1)3Aa; GIAN_DROME; EG:BACH7M4.5
Gug	l(3)01323; l(3)rO116; CG6964; Gug; l(3)j5A3; Atrophin; Atro; atro; l(3)03928
H	H; CG5460; hairless
h	h; CG6494; dDr1; 8247; l(3)08247; brr; l(3)rM384
hay	ERCC3; hwr; hay; nc2; TFIIH; DhR25; DhXPB; ms(3)nc2; DmXPB; Xpb/hay; CG8019; i50
Hcf	Hcf; CG1710; dHCF
HDAC4	dHDAC4; HDAC; CG1770; GC1770; HDAC4; HDAC4a; dmHDA405
HDAC6	CG6170; HDAC; dHDAC6; HDAC2; DmHDAC2; histone deacetylase HDA2; dHDAC2; dmHDA404; HDAC6
Hel89B	89B helicase; 89B; Hel89B; BTAF1; CG4261
Hira	dHira; dhira; Dhh; HIRA; Hira; hira; CG12153
His3	DmeH3; core histone; His; H3 Histone; histone H3; His3; his3; HisC; H3.1; histone-3; histone; Histone; H3; PH3; dH3
His4	DmeH4; core histone; 4; histone H4; H4Ac16; HisC; his4; His4; histone; Histone; Bin2; H4
HLHm3	m3; E(spl)M3; E(spl)m3; split locus enhancer protein m3; HLH-m3; E(Spl)-HLH-m3; HLHm3; HLHM3; CG8346
HLHm5	m5; HLH-m5; E(spl)-m5; HLHm5; CG6096; E(spl) transcription unit m5; E(spl)M5; E(spl)m5

Table S2 / 12

HLHmbeta	E(spl)beta; E(spl); HLHmbeta; HLHmbeta; split locus enhancer protein mA; mbeta; mbeta; Mbeta; HLHmA; Dm-mA; E(spl) mbeta; E(spl)Mbeta; E(spl)mbeta; mA; E(spl)mbeta; CG14548; HLH-mbeta; E(spl)mA; E(Spl) HLH
HLHmdelta	E(spl)delta; E(Spl) HLH-m delta; E(Spl)-HLH-mdelta; HLHmdelta; split locus enhancer protein mC; E(spl)-mdelta; mdelta; HLHmC; HLHMD; E(spl)mbeta; mC; E(spl)mdelta; E(spl)Mdelta; HLHmdelta; HLH-mdelta; E(spl)m
HLHmgamm	E(spl)-mgamma; anon-EST:Liang-1.49; E(spl)gamma; split locus enhancer protein mB; HLHmgamma; HLHmB; Dm-mB; mgamma; Mgamma; mB; mgamma; E(spl)mgamma; E(spl)Mgamma; E(spl)mB; Enhancer of split mgamma; e(spl)mga
HmgD	CG17950; HMG D; HmgD; dHMG-D; clone 1.9; hmg-D; HMG-D; anon-EST:Liang-1.9
HmgZ	anon-EST:Liang-1.58; HMG-Z; hmg-Z; clone 1.58; CG17921; HmgZ; BcDNA:RE28596; dHMG-Z
HP1b	HP1b; Hp1b; CG7041
HP1c	CG6990; HP1c
Hr38	38E.3; DHR38; Dhr38; NR4A4; I(2)02306; 38E.7; CG1864; HR38; Hr38
Hr39	i70; DHR30; betaFTZ-F1; FTZ-F1beta; ftz-F1beta; ftz-f1beta; CG8676; Hr39; EP(2)2490; dFTZ-F1beta; NR5B1; ftz-F1; FTZ-F1; DHR39; FTZ-F1B; DHR39/Ftz-F1beta
Hr4	DHR4; CG16902; EG:133E12.2; Hr4
Hrb87F	Hrb85CD; CG12749; Hrb87F; Hrb87f; Hrb87Fa; P11; P11/Hrb87F; HRB87F/hrp36; HRP36; Hrp36; hrp36; Q14; Q16; p38; Hrb2; hrp40
Hsf	HSF; Hsf; hsf; CG5748; D-HSF; DmHSF; I(2)03091; dHSF; Dm-Hsf
inv	engrailed-related; CG17835; engrailed-invected; Engrailed/Invected; inv; er; in; IV
lswi	dISWI; p140/ISWI; CHRAC; ISW; SWI; anon-EP1279744.124; dCHRAC; p140; ACF; ISWI ATPase; NURF; ISWI; lswi; iswi; Nurf-140; NURF-140; CG8625; dNURF
ix	CG13201; ix
Jra	dJRA; dJra; AP1; I(2R)IA109; dm-Jun; jun; Jun; d-JRA; AP-1; cJun; dJun; dJUN; Djun; DJun; DJUN; I(2)IA109; dAP-1; CG2275; Jun oncogene; c-Jun; Jra; D-Jun; D-jun; d-Jun; d-jun
jumu	Dom; jumu/Dom; Scim31; Dwhn; jumu; Dmjumu; 5295; I(3)06439; Domina; CG4029; E(var)631; Whn; I(3)06142; jumeaux
kay	AP1; kay; fos; Fos; dFos; Dfos; DFos; DFOS; CG15509; AP-1; dAP-1; sro; c-Fos; Fra; d-fos; D-fos; D-Fos; dlhD; DFra; dFRA; dFra
kis	CG3696; EK2-4; I(2)k08827; KIS; kis; 2532; 136/31; CG18326; I(2)07812; GM02209; Su(Pc)21AB; 5841; I(2)s3527; I(2)k14112; I(2)s4771; I(2)k13631; I(2)s4793; CG3660; BEST:GM02209
kn	Collier-Knot; knotted; kn; Kn; collier; CG10197; col; Col
kni	KNI; Kni; kni; NR0A1; Knirps; kn; ri; CG4717
Kr	kruppel; CG3340; Kr; kr; Krpple; lf
kto	CG8491; kohtalo; dTRAP230; DTRAP230; Kto; Kto/Med12; MED12; Med12; siren1; SRB8; Srb8/KTO/TRP230; Trap230; Mediator complex subunit 12
Ku80	Ku80; BG:DS09217.6; CG18801
kz	I(1)N4; CG3228; I67; EG:30B8.2; kz; N8; I(1)2Eb; N1
I(1)10Bb	lethal(1)10Bb; I(1)G14; I(1)10Bb; I(1)GLM14; 10Ba; CG1639; I(1)G0169

Table S2 / 13

I(1)G0007	I(1)G0308; I(1)G0416; I(1)G0176; I(1)G0491; CG1405; cg1405; EP764; I(1)G0476; EP784; CG32604; I(1)G0103; CG1375; I(1)G0007; I(1)G0028
I(2)01424	I(2)01424; CG3845
I(2)05070	CG8392; I(2)05070
I(2)NC136	I(2)NC136; CG8426
I(3)73Ah	lethal(3)73Ah; I(3)02540; I(3)73Ah; CG4195; I(3)133.18
I(3)mbt	CG5954; CG18582; tumor-suppressor; I(3)mbt; MBT; mbt; I(3)malignant braintumor
La	ribonucleoprotein La; DLa/SS-B; 38C.38; CG10922; La; BEST:LD24519; dmLa; D-La
lds	factor 2; lds; DmF2; transcript A; early-B; early; early-3; CG2684; NTef2; lod; early-5
lid	lid; I(2)10424; CG9088
lin19	CG1877; cul-1; I(2)k01207; Cul1; dCul-1; Cullin1; dCul1; I(2)02074; dCullin1; lin19; lin19-like
Lip	I(3)s5196; I(3)j3D2; Lip; 4136; I(3)j3D5; I(3)01086; I(3)rG338
lola	BcDNA:LD17006; CG30012; CG30013; CG30014; BTB-IV; CG12052; lola; I(2)00642; CG18380; CG18381; LD03274; CG18376; CG18378; CG18379; BtbIV; BEST:LD03274; sw59; longitudinals absent; I(2)s3697; misguided
lz	spe; fs(1)A1569; CG1689; amx; Lz; lz; fs(1)M69
Mad	CG12399; MAD; Mad; mad; E(zen)2; 2/23; I(2)K00237; I(2)k00237; apg; En(vvl)
Mat1	MAT1; Mat1; CG7614
Mcm10	CG9241; Mcm10; Scim19; DmMCM10
Mcm2	DmMCM2; DmMcm2; PCR3; CG7538; I(3)rL074; dMCM2; MCM2; Mcm2
Mcm3	MCM3; Mcm3; DmMCM3; DmMcm3; dMCM3; Mcp-PCR2; CG4206; PCR2
Mcm5	MCM5; Mcm5; mcm5; DmMCM5; DmMcm5; DmCDC46; CG4082; PCR4; DmCDC465
Mcm6	CG4039; MCM6; Mcm6; DmMCM6; fs(1)K1214
Mcm7	Mcp-PCR1; MCM7; Mcm7; mcm7; DmMCM7; CG4978; PCR1
Med	I(3)SG70; I(3)XlIm137; anon-EST:Posey121; I(3)SG36; E(zen)3; Med; med; I(3)11m-254; I(3)12m-137; medea; dSmad4; CG1775
MED19	CG5546; Mediator complex subunit 19
Med21	Med21; BcDNA:GH01072; CG6884; dMED21
Med23	BcDNA:GM31575; CG5121; Med23; dMED23
Med24	anon-EST:Liang-1.82; BACR7A4.6; dMED24; Srb6/Surf5; clone 1.82; CG3034; Med24; CG18830; EG:BACR7A4.6
MED26	CG1793; Arc70; ARC 70; CG1823; dARC70; Med26; Mediator complex subunit 26
Med6	dMED6; dMed6; dTRAP32; anon-EST:Posey279; CG9473; Mediator; p35; BcDNA:LD15729; Trap32; Med6; MED6
Med7	CG6529; dMED7; CG31390; dTRAP34; MED7; Med7; Mediator
MED9	CG42517; CG5134; Mediator complex subunit 9; BcDNA:LD07740; BcDNA:RH42446; CG30112; CG30113
Mef2	C; mef2; Mef2; MEF2; DMEF2; DMef2; Dmef2; dMEF2; dMef2; dmef2; SD04091; mef-2; MEF-2; Mef; mef; CG1429; D-MEF2; D-Mef2; D-mef2; Dmef-2; DMef-2; DMEF-2; Dmef; BEST:SD04091
mei-P26	CG12218; mei-P26; BcDNA:GH10646; AF145661
Mes-4	dMES-4; dMes-4; CG4976; Mes-4

Table S2 / 14

Mi-2	0854/01; I(3)j3D4; MI2; Mi 2; I(3)A154.3M3; hip76; I(3)01058; I(3)S000606; Dm-Mi-2; Mi-2; I(3)S085401; CG8103; Pha; pha; dMi-2; dMI-2; dMi; 0006/06
mirr	CG10601; I(3)69Ca; Iroquis complex; I(3)69Da; mir; Sail; crep; Iro; iro; caupalican; mrr; Mrr; I(3)A5-3-42; cre; De1; mirr; iro-C; Iro-C; IRO-C; I(3)6D1; iroquois; De3; Sai; DH1
mle	nap^{ts}; mll; mak; CG11680; no action potential; mls; mle; MLE; nap
Mms19	CG12005; dMMS19; NEST:bs07f08; Mms19
mod(mdg4)	I(3)L3101; CG7836; Mod[mdg4]; CG15500; I(3)j2B7; CG15501; CG7859; CG15802; CG18151; mod(mdg-4); CG32491; mod(gypsy); Doom; doom; E(var)3-93D; E(var)93D; E-var(3)1; modifier of midget4; mod2.2; I(3)03852; E-var(3)3; bpd;
mof	MOF; Mof; mof; dmMOF; CG3025; dMOF; max
mor	I(3)89B1; Moira; E(E2F)3B; dmMOIRA; Swi3D; CG4275; brahma-like; BAP155; mor; CG18740
morgue	CG15437; BcDNA:GH02435; morgue
Mov34	CG3416; Mov34; I(2)k08003; p39B; PRSC_DROME
MRG15	Dmrg15; CG6363; I(3)j6A3; MRG15; DmMRG15
msl-1	i94; male specific lethal; kmB; msl-1; MSL-1; mls-1; CG10385; msl; MSL; km(2)B; msl1; Msl1; MSL1
msl-2	CG3241; male specific lethal; kmA; msl-2; MSL-2; km(2)A; msl; MSL; msl2; Msl2; MSL2
msl-3	mle3; male specific lethal; mle(3)132; CG8631; msl-3; MSL-3; msl; MSL; DmMsl-3; msl3; MSL3; mls3
mTTF	DS01068.4; CG18124; BG:DS01068.4; mTTF; DmTTF
mus304	mus(3)304; mus-304; mus304; CG7347
mus308	mus308; Nuc3; Pol theta; CG6019; 0443/09; mus-308; AAF54858
mus309	DmKu70; mus309; blm; CG6920; RecQ; DmBlm; Dmblm; gesta1
Myb	I(1)XVI; Dm-Myb; Dm-myb; c-Myb; c-myb; myb; Myb; D-myb; Dm Myb; Dm myb; dmMYB; DmMYB; CG9045; dMyb; DMyb; p85
N	dNotch; EG:163A10.2; EG:140G11.1; facet; I(1)3Cb; fa; I(1)Ax; n^{fah}; Abruptex; swb; split; Nintra; CT13012; N; spl; 1.1; Co; co; nd; clone 1.12; 16-178; anon-EST:Liang-1.12; Ax; Chp; notch; I(1)N; 16-55; CG3936; shd
Nap1	NAP1; Nap1; dNAP-1; p56/dCAF-4; dNAP1; dNap1; CG5330; NAP-1; Nap-1
NC2alpha	Drap1; NC2alpha; dDrap; dDrap1/dNC2a; NC2alpha; CG10318; dNC2
NC2beta	CG4185; BG:DS00929.3; dNC2; Dr1; NC2beta; NC2beta
neb	sl(2)ry3; KLP-38B; DmKlp38B; CG10718; tio; sl(2)ry; I(2)03552; Mot; Klp38; I(2)k00802; klp38B; Klp38B; KLP38B; KLP 38B; neb; Neb; Dm0332; 38B.10; I(2)k07614; 38B.12; KIF14
nej	CREB binding protein; dCBP; anon-WO0147981.11; CBP; Cbp; cbp; CG15319; CREB-binding protein; nej; dmCBP; CBP/p300; Crbp; p300/CBP
Nelf-E	anon-66Da; CG5994; cg5994; NELF-E; Nelf-E
nerfin-1	nerfin-1; CG13906
net	Group IId; Shout; shout; CG11450; net
Neu2	Neu2; CG7204
NFAT	MESR1; EP1335; NFAT; NF-AT5; dNFAT; Drosophila TonEBP; CG11172; NFAT5

Table S2 / 15

nht	CG15259; TFIID; dmTAF4b; BG:DS07851.6; dTAF<down>II</down>110; nht; nohitter; no hitter
NK7.1	CG8524; NK7.1
noc	noc; nocA; Sco; I(2)br22; I35Ba; BG:DS04641.1; br22; I(2)35Ba; I(2)35Ba/nocA; Scutoid; CG4491; I(2)br29; br29
nonA	Bj6-1; no-on transient A; Bj6; CG4211; diss; non-A; nonA; NonA; x14; no-on-transient A; Positive spike II group; opm2; nonA/diss
nonA-l	LD09360; no-on transient A-like; nonA-l; CG10328; BEST:LD09360; Z; nonA-1; nonA 1; no-on transient A
nub	Pdm; pdm; dPOU19; Oct-1; nub; dPOU-19; nb; POU33F1; pdm1; Pdm1; twm; dOct1; CG6246; dPOU-19/pdm-1; POU domain protein 1; Pdm-1; pdm-1
Nurf-38	NURF-38; Nurf-38; I(2)k16102; NURF38; 38; CG4634; p38; NURF; p38/NURF-38; dNURF
Nut2	dTRAP15; NUT2; Nut2; CG5057; BcDNA:SD24044
oc	I(1)7Ff; oc; Orthodenticle; orthodenticle; uvi; ort; CG12154; CG7411; Otd; otd; I(1)8Ac
okr	RAD54; Rad54; rad54; DmRAD54; DmRad54; DhR54; okr; CG3736
onecut	CG1922; A1; onecut; D-onecut
Optix	D-Six3; CG18455; Dsix3; opt; Optix; optix; Six3
osa	CG7467; Osa; osa; p300; eld; I(3)04539; E(E2F)3C; I(3)j9C3; I(3)00090; eyelid; eye lid; en(lz)4F/4H
p53	Dm-P53; prac; p53; CG31325; dmp53; Dmp53; dp53; CG33336; CG10873
Parp	PARP-1; CG17718; PARP; Parp; CG40411; CG17685; D.PARP; CG17696; poly(ADP-ribose) polymerase
Pc	CG7618; CG32443; Pc; DmPc; dPC; Pc-G
Pcaf	dGCN5; dGcn5; p/CAF; PCAF; Pcaf; Gcn5; gcn5; CG4107; dGCN5 HAT; dmHAG401; dPCAF; Gcn5/PCAF
Pcl	CG5109; I(2)s1859; PCL; Pcl; pcl
per	Clk; EG:155E2.4; dPER; CG2647; clk-6; dperiod; PER; Per; per
ph-d	CG3895; DROZFP; phm; PH; Ph; ph; ph^D; ph-d; ph-D; PH-d; polyhomeotic; Polyhomeotic; phd; EG:BACN25G24.3
ph-p	PH-p; ph-P; ph-p; ph^P; phm; php; ph; Ph; PH; CG18412; EG:87B1.5; CG18414; polyhomeotic; Polyhomeotic
phol	CG3445; phol
pont	pontin; 0229/05; CG4003; dpon; pont; Tip49/Pontin; Tip49; I(3)S022905; pon
Poxn	pox neuro; Pox-n; pox-n; P4; Poxn; poxn; neuro; pox-neural; pox-neuro; Pox-neuro; CG8246
ppa	I-55; Ppa; ppa; CG9952
Pph13	Mu; PPH13; Pph13; CG2819; Munster; 60Mun1
prod	CG18608; I(2)k08810; PROD; Prod; prod; I(2)88/10
pros	0451/09; 1167/13; I(3)rl160; 0763/13; I(3)rK204; Pros; 0585/13; 0563/18; I(3)j6E2; I(3)rL433; CG17228; pro; 0320/10; I(3)j12C8; DMPROSPER; 0441/16; 1135/07; 0244/09; PROS-1; BcDNA:HL08040; 1135/09; PROS-2; pros; 0664/07; I(3
Pros20S- α p	20S proteasome; 20s proteasome; Pros20S-alpha3
Pros20S- α p	Pros20S-alpha3t; 20S proteasome; 20s proteasome

Table S2 / 16

Pros25	PRC3; PROS-Dm25g; dalpha2; Pros25; 20S proteasome; 20s proteasome; PROS Dm25; alpha2_dm; CG5266; Proteosome
Pros26	DTS5; I(3)DTS5; beta6_dm; 20S proteasome; I(3)73Ai; Pros26-DTS; Pros26; I(3)DTS-5; DTS-5; Proteasome subunit 20S; CG4097
Pros26.4	Dm_Rpt2; DmP26S4; CG5289; proteasome 26S; p56; dRpt2; 26S proteasome subunit 4 ATPase; Pros26.4; P26s4; S4
Pros28.1	20S proteasome; 20s proteasome; a4; CG3422; PROS-28.1; PROSA-28.1; Pros-Dm28.1; PROS-Dm28.1; pros28.1; Pros28.1; Pros28; alpha4_dm
Pros28.1A	CG17268; alpha4t1_dm; 20S proteasome; 20s proteasome; testes-specific proteasome subunit; dalpha7; Pros28.1A; a4-t1
Pros28.1B	CG4569; 20S proteasome; 20s proteasome; testes-specific proteasome subunit; alpha4t2_dm; dalpha7; a4-t2; Pros28.1B
Pros28.2	20S proteasome; Pros28.2
Pros29	20S proteasome; 20s proteasome; PROS-29; alpha3_dm; CG9327; Pros29; pros29
Pros35	PROS-35; PROS-Dm35; Pros-Dm35; alpha_dm; CG4904; 20S proteasome; 20s proteasome; Pros35; pros35
Pros45	CG1489; dRpt6; DUG; Dug; sug1; p42C; Ug; Dm_Rpt6a; Pros45; pros45; sug-1
Pros54	CG7619; p54; S5a; 54 kda mu particle subunit of 26S protease; mu-54; dRpn10; Pros54
Prosalpha3	Prosalpha3T; CG1736; Prosalpha3T
Prosalpha6	Prosalpha1; 20S proteasome; 20s proteasome; 20S proteasome subunit alpha1; CG18495; Prosalpha6
Prosalpha6	CG5648; Prosalpha6T; Prosalpha6T
Prosalpha7	Prosalpha7; CG1519; 20S proteasome; 20s proteasome; alpha7_dm; Prosalpha7; Proteasome alpha3 subunit
Prosbeta2	DTS7; I(3)DTS7; Prosbeta2; Prosbeta2; 20S proteasome; 20s proteasome; anon-EST:fe1E6; anon-EST:fe1G6; CG3329; beta2; beta2_dm; beta2_dm; DTS-7
Prosbeta3	Prosbeta3; Prosbeta3; 20S proteasome; 20s proteasome; 20S proteasome beta3 subunit; CG11981
Prosbeta5	20S proteasome; CG12323; dbeta5; Prosbeta5; Prosbeta5; LD08717
ProsMA5	alpha5_dm; 20S proteasome; 20s proteasome; PSMA5; ProsMA5; prosMA5; PRCZ; CG10938
Psc	I(2)49Ea; 49Ea; CG3886; I(2)Psc; Su(z)2-C; PSC; Psc; psc; D-Bmi; I(2)vr14; vr14
Pur-alpha	PURalpha; pur-alpha; CG1507; Pur-alpha
Rbf	Rb; Rb1; EG:34F3.3; CG7413; rbf; Rbf; RbF; RBF; rbf1; Rbf1; RBF1; dRBF; FBF
Rbf2	CG5083; RBF2; Rbf2; rbf2
rec	CG4828; rec-1; rec; CG14875; rec1; CG31293
RecQ4	DmRECQ4; CG7487; cg7487; RecQ4
RecQ5	RECQ5; RecQ5; RECQE; DmRECQ5; Q1; RECQ5/QE; CG4879; Dm RECQ5/QE; DQ1; Dq1; anon-EST:Posey293
ref(2)P	Ref(2)P; Ref(2)p; ref(2)P; ref(2)p; ref(2)Po2; CG10360; ref; ref(2)Pn; ref2p; Ref2P
REG	CG1591; dREG; REG
Rel	CG11992; ird4; I(3)neo36; Rel; rel; ird; relish
repo	reverse polarity; AbRK2; CG8045(CT24072); CG31240; CT24072; REPO; repo; 3702; I(3)03702; rk2; RK2

Table S2 / 17

rept	I(3)06945; Tip48; reptin; Tip48/Reptin; drep; rept; CG9750; rep
retn	dead ringer; CG5403; retn/dri; retn; BcDNA:LD35748; I(2)02535; EY2-10; 2535; dri; Dri; DRI
RfC40	I(3)SH17; I(3)64Ai; CG14999; rfc; rfc⁴⁰; DRas2; Rfc40; RfC40; rfc4; I(3)rfc40
Rfx	RFX; Rfx; rfx; dRFX; dRfx; Regulatory factor X; CG6312
Rga	I(3)03834; Rga; CG2161
rhi	rhi; CG10683; rno
rno	CG7036; rno
ro	ro; CG6348
Roc1a	Rbx1/Roc; CK01110; dRbx1; EG:115C2.11; CG16982; ROC1; Roc1a; BEST:CK01110; dRoc1a; Rbx1
Roc1b	CG16988; BcDNA:AT21612; dRoc1b; ROC2; ROC1B; Roc1b
Roc2	dRoc2; BcDNA:RE61847; CG8998; Roc2
Rpb10	RPB10; Rpb10; BcDNA:SD08670; CG13628
Rpb11	BcDNA:GM15177; CG6840; RPB11; Rpb11
Rpb4	RPB4; Rpb4; CG31237; CG7150
Rpb5	RPB5; Rpb5; CG11979
Rpb7	CG31155; RPB7; Rpb7; CG6572
Rpb8	CG11246; RPB8; Rpb8
Rpd3	I(3)64Cc; HDAC1; Hdac1; dHDAC1; E(var)3-64BC; HDAC-1; HDAC; dHDAC-1; DmHDAC1; dmHDA401; I(3)04556; Rpd3/HDAC; RPD3; Rpd3; rpd3; CG7471; Su(var)326; dRpd3; dRPD3; Su(var)328
Rpl1	CG10122; RNA polymerase I; RPA1; Rpl1; DmRPA1
Rpl12	CG13418; Rpl12
Rpl135	I(2)k16513; RNA polymerase I; RP135; CG4033; DmRP135; Rpl135; RplII135
RplII140	PolIIc; RNA Pol IIc; RNA polymerase subunit IIc; RNAP II; I(3)RplII140; DmRP140; RplII140; RPII140; RNA polymerase II second largest subunit; II; subunit IIc of RNA Pol II; RNA polymerase II; 150
RplII18	RNAP II; RNA polymerase II; CG1163; Dm6; BcDNA:RH21608; RplII18; RpABC14; polII; Pol II; H5; RNApolII; RNA polII; RNA pol II; RNA Pol II
RplII215	L5; RNAP II LS; RNAP II; Ubl; RNA polymerase II large subunit; POL; RplII215; I(1)L5; I(1)DC912; II; RplII215; I(1)10Ca; I(1)DF912; RplII; RNA polymerase II; 5; RPB1; CG1554; dRPB1; I(1)G0040; 8WG16; H5; polII; PolII;
RplII33	RplII33; I(2)34Dg; CG7885; BG:DS00941.10; I(2)br17; RNA polymerase II; RPB3; RplII33; rplII33; I(2)k05605; br17; polII; Pol II; RNA Pol II; RNA pol II; RNA polII; I34Dg
RplIII128	RplIII128; CG8344; RNA polymerase III; RP128; DmRP128; RNA polymerase IIIb
Rpn1	CG7762; p97; BcDNA:LD21723; Rpn1
Rpn11	Rpn11; p37B; CG18174; yip5
Rpn12	CG4157; p30; Rpn12; dRpn12
Rpn2	p110; Rpn2; CG11888; dRpn2
Rpn5	p55; CG1100; Rpn5
Rpn6	BcDNA:LD18931; p42B; CG10149; BcDNA.LD18931; I(2)k00103; Rpn6; Pros44.5
Rpn7	CG5378; p42A; Rpn7

Table S2 / 18

Rpn9	CG10230; Rpn4; 0718/06; 718/06; rpn9; Rpn9; l(3)S071806; Nobody; l(3)S071806b; Rpn94; p39A
Rpt1	l(2)05643; CG1341; dRpt1; p48B; Dm_Rpt1; Dmp48B; l(2)43Ed; Rpt1
Rpt3	CG16916; Rpt3; Dm_Rpt3a; l(1)G0052; p48A; Dmp48A
Rpt4	l(1)G0227; l(1)G0345; p42D; Rpt4; CG3455; Dm_Rpt4a; Dmp42D; l(1)G0114; Dm_Rpt4b
Rtf1	CG10955; dRtf1
run	CG1849; 1; 2; LB5; l(1)B2/13.1; l(1)LB9; run; l(1)AA33; AA33; leg; Runt; P235; l(1)19Ea; ILB5
SA	DSA; ESTS:92H2T; SA; SCC3; DmSA; CG3423
salm	Sal; sal; salll; SPALT; Spalt; spalt; sal major; l(2)03602; spalt-major; 3602; salm; salM; SalM; CG6464
sc	sisterless-b; scalpha; sis b; sisB; sisb; AS-C T4sc; l(1)1Ba; Sc; sc; scute/sisterlessB; T4; achaete-scute; AS-C T4; T4 AS-C; sc/T4; CG3827; DROACS2; EG:198A6.1; sis-b; ascT4; Hairy-wing; Hw; scute alpha
SC35	CG5442; cg5442; CG5542; dSC35; SC35
Scm	l(3)85Ef; Su(z)302; SCM; Scm; scm; Sex combs on midleg; CG9495
scro	CG17594; scrou; CG18452; scro
SF1	CG5836; cg5836; SF1; dSF1; p70
shn	Shn; shn; l(2)04738; quo; CG7734
sim	CG7771; single-minded; 0716/08; l(3)87Ea; l(3)RD; 0483/09; 0953/08; 1479/04; shm; sim; SIM; l(3)E320; schm; S8; 0899/14; 1002/10; single-minded; 1111/10; 1110/04; 1034/02; 1050/13; l(3)S8; l(3)s8; 1330/08
sima	CG7951; SIMA; Sima; sima; DMU43090; Hif-1A
Sin3A	CG8815; l(2)k09715; dSin3; dSin3A; 97/15; ES2-3; 27/3; ESTS:159A11T; ld; 159A11T; l(2)k02703; EY2-9; l(2)08269; l(2)k05415; SIN3; Sin3; sin3; sni3; Sin 3A; Sin3A
Sir2	SIR2; Sir2; D.mel1; BEST:LD38188; dmSRT406; dSIR2; dSir2; dsir2; CG5216; l(2)05326
Sirt2	dSIRT2; D.mel2; CG5085; Sirt2
Sirt4	dSIRT4; D.mel3; CG3187; dmSRT407; Sirt4
Sirt6	Sirt6; D.mel4; dSIRT6; CG6284; dmSRT408
Sirt7	Sirt7; CG11305; D.mel5; dSIRT7; dmSRT409
Six4	Six4; D-Six4; Dsix4; CG3871; myotonin
skd	SPH203; bls; Pap; pap; pap/dTRAP240; flytrap; skd; CG9936; poils aux pattes; Pap/Trap; l(3)rK760; Scad78; l(3)L7062; TRAP240; blind spot; dTRAP240; Srb9/AMIB/PAP/TRAP240; bli; LD28662
skpA	dSkp-1; l(1)G0058; dSkpA; dskpA; EG:115C2.4; CG16983; l(1)G0389; spkA; skpA; Skp1; l(1)G0109; l(1)G0037
slbo	slbo; fs(2)7; fs(2)8; C/EBP; CG4354; DmC/EBP; DC/EBP; fs(2)ry7; slobo; fs(2)ry8
slmb	l(3)00295; shv; CG3412; Slimb; slimb; pingiel; crd; shiva; BcDNA:GM02031; ica; slmb
slou	S59; s59; slou; NK-1; S59/NK-1; NK1; Nk1; NK1/S59; CG6534; slou/NK1; S-59; PRD

Table S2 / 19

slp1	FD6; slp1; Dmslp1; CG16738; l(2)05965; sloppy-paired; sloppy-paired 1; slp-1; Slp-1; slp-2; slp; Slp
slp2	CG2939; FD7; slp2; Dmslp2; sloppy-paired 2; slp
SMC1	CG6057; SMC1; DmSMC1
SMC2	CG10212; SMC2; DmSMC2
Smox	tmp; l(1)G0348; CG2262; Smad2; smad2; Smox; smox; sad; Sad; DSMAD2; dSMAD2; dSmad2; ted
Smr	CG4013; Smr; E52; SMRTER; Smrter; l(1)G0361
sna	CG3956; sn; sna; l35Db; BG:DS01845.1; l(2)br28; l(2)35Db; l(3)br28; br28
Snr1	snr; BAP45; SNR1; Snr1; snr1; CG1064; l(3)01319
so	CG11121; Drl; mda; So; so; somda; med; ami; old
sob	org1; sob; CG3242
Sox100B	Sox9; CG18674; SoxB; CG15552; Sox100B; SOX100B; CG12098; SOXE
Sox14	DSox-14; Dsox-14; SOX60B; DSox14; CG17263; SOXC; CG3090; DSox60B; SOX14; Sox14
Sox15	Sox F; SOX15; Sox15; SOXF; DSox-15; Dsox-15; SOX50E; Sox50E; CG8404; SoxE
Sox21b	CG32139; sox-like; CG13483; Sox B2-2; CG6419; SOXB2.2; SoxB2.2; Sox21b
SoxN	SoxN; soxN; CG18024; SOX29F; soxneuro; Sox B1; SOXB1
Sp1	Sp1; CG1343; D-Sp1; D.Sp1
spen	E(Sev-CycE)2A; EK2-9; spe; E(Raf)2A; l(2)03350; l(2)k07612; poc; yip1; EY2-7; rhinoceros; l(2)k06805; l(2)k08102; BcDNA:GM01870; E(E2F)2A; spen; 136/24; CG18497; En(yan ^{ACT})2-7; rno
spn-E	Homeless; homeless; fs(1)hls; spn-E; fs(3)hls; Spindle E; spn E; spnE; hls; spn-E/hls; CG3158
Spt3	TFIID; SPT3; Spt3; CG3169
spt4	CG12372; l(2)k05316; SPT4; spt4; Dspt4
Spt5	Dspt5; dSpt5; Spt5; DSIF; CG7626
Spt6	Dspt6; dSpt6; spt 6; SPT6; Spt6; spt6; CG12225; l(1)G0063
sqd	l(3)EP3631; CG17791; Hrb87Fb; RRM3; rrm3; Squid; hnRNP 1; Rbp3; sqd; l(3)j6E3; fs(3)00048; CG16901; Hrb87; hrp40; Hrp40; HRP40
sr	l(3)06948; CG7847; l(3)06948b; Sr; sr; l(3)03999; Stripe
srp	DmGATAb; CG3992; dGATAb; l(3)01549; l(3)89B2; Srp; srp; A7.1; spt; ABF; Abf; abf; l(3)neo45; GATA; GATAb
Sry-delta	EH8; Sry-delta; CG17958; sry-delta; Sry-delta; serendipity delta; srydelta; Srydelta; sry delta; Sry delta; anon-EH8; sry
Ssb-c31a	C31A; p11; CG8396; Ssb-c31a
Ssdp	CG7187; Ssdp; ssdp; l(3)neo48
Ssl1	CG11115; SSL1; Ssl1
Ssrp	SSRP; Ssrp; SSRP1; DssRP; dSSRP; dSSRP1; Cf5; CG4817
Stat92E	DSTAT; Dstat; dSTAT; SD-stat; dSTAT92E/marelle; marelle; D-stat/stat92E; l(3)j6C8; mrl; mrl; DSRC; stat92E; Stat92E; STAT92E; STAT 92E; D-STAT; D-Stat; D-stat; d-STAT; Dstat 92E; Dstat92E; DRODSRC; l(3)06346; mrl stat92E
stc	BcDNA.LD22726; l(2)br33; l35Cb; br33; stc; BG:DS04929.4; l(2)35Cb; BcDNA:LD22726; Cf4; CG3647

Table S2 / 20

stwl	snw; stwl; alpha transcript; fs(3)02024; CG3836
su(f)	R9-18; EC235; l(1)G0393; lethal3Des; 19; 28; CG17170; 29; CstF-77; l(1)su(f); R-9-18; 3DES; l(1)EC235; su⁺-f; l(1)X1; l(1)20Eb; l(1)X3; l3DES; SU-f; su-f; 3-DES; l(1)R-9-18; l(1)3DES; su(f)
Su(H)	CG3497; l(2)35Bh; Su(H); su(H); C; D; RBP-Jkappa; dRBP-JK; dRBP-Jk; br7; BG:DS00929.10; SuH; RBP-J<down>Kappa</down>; oss; dRBP-J<down>Kappa</down>; l(1)br7; FTZ-F2; l(2)br7; l(2)k07904; E(H)
su(Hw)	Su(Hw); Su(hw); su(Hw); su(hw); CG8573; Su[Hw]
su(s)	su-s; EG:115C2.3; su-v; su(s); CG6222
Su(var)2-HP	HP2; Su(var)2-HP2; CG12864
Su(var)205	Su(var); HP1alpha; Suvar2-5; Su(var)²⁰⁵; Su(var)2-05; DmHP-1; HP1; Hp1; Suvar(2)5; E(var)29; HP1a; E(var)29A; dHP1; Su(var)29A; heterochromatin-binding protein; Su-var(2)5; Su(var)2-5; Su(Var)2-5; HP-1; Su(var
Su(var)3-7	l(3)87E1; CG8599; Su(var)(3)3; SU(VAR)3-7; Su(var)3-7; Su-var(3)7; Suvar(3)7; Su(var)(3)7
Su(var)3-9	CG6476; SUV39H1; dIF2; eIF2gamma; SUV39; eIF2G; Suvar(3)9; eIF-2gamma; Su(var)310; eIF-2G; Su(Var)3-9; Su(var)3-9; Su(var)306; Su-var(3)9; Su(var)3-902; Su-var(3)902; caa56376 Suvar39 Dm; Su(var)328
Su(z)2	Su(z)<down>2</down>; Arp; CG3905; l(2)k06344; SUZ2; Su(z)2; su(z)2
sug	CG3850; sugarbabe; sug
SuUR	CG7869; Su(UR); Su(UR)ES; SuUR
sv	spa; l(4)40; pax2/sparkling; Cat; Pax258; CG11049; sv; spa-sv; Pax2; sparkling; Sparkling; pol; D-Pax2; D-pax2; d-Pax2; DPax-2; Dpax-2; dPax258; en(lz)4G/l; dPax2; shaven/sparkling
Taf1	cell; TAF<down>II</down>; TFIID TAF250; TAFII250; CG17603; TAF1; Taf1; TFIID; Taf230; TAF230; Taf250; TAF250; cel; TAF250/230; d230; dTAF<down>II</down>230; SR3-5; dTAF<down>II</down>250; BG:DS00004.13; p230; dmTAF<down>
Taf10	TAF<down>II</down>; TFIID; Taf24; taf24; CG2859; BcDNA:RE73934; TafII24; TAF<down>II</down>24; dTAFII24; dtafII24; dTAF<down>II</down>24; Taf10; TAF10
Taf10b	TAF<down>II</down>; TFIID; Taf16; TAFII16; TafII16; TAF<down>II</down>16; dtafII16; dTAF<down>II</down>16; CG3069; Taf10b; TAF10b
Taf11	TAF<down>II</down>; TAF30b; d30beta; dTAF<down>II</down>30beta; dTAF<down>II</down>30; TFIID; dTAFII30beta; dTAFII30 beta; TFIID-p28beta; dTAFII30; TFIID 28 beta; TAF^{II}30beta; Taf30beta; TAF11; Taf
Taf12	TAF<down>II</down>; Taf32; dTAF<down>II</down>30alpha; dTAF22; dTAF28; TFIID; dTAFII30; p22; TFIID 22; dTAF<down>II</down>30alpha/22; TAF^{II}30alpha; p28; TFIID 28; TAF<down>II</down>30alpha/28 TAF<down>
Taf12L	rye; TAF<down>II</down>; TFIID; dmTAF12b; dTAF<down>II</down>30alpha-2; ryan express; Taf30alpha-2; TAF30alpha-2; dTAF<down>II</down>30a; Taf12L; CG15632; dmTAF12L
Taf13	TAF<down>II</down>; TFIID; 38B.15; TAF18; Taf18; TAF<down>II</down>18; CG10756; dTAF<down>II</down>18; Taf13; TAF13

Table S2 / 21

Taf2	TAF<down>II</down>; TAFII150; TafII150; dTAF II 150; dTAFII150; Taf2; TAF2; TFIID; TAF<up>II</up>150; Taf150; TAF150; dTAF150; Taf<down>II</down>150; TAF<down>II</down>150; CG6711; dTAF<down>II</down>150
Taf4	TAF<down>II</down>; p110; TFIID 110; dTAFII110; I(3)72Dj; SY3-2 TAF110; TAF<up>II</up>110; taf110; Taf110; TAF110; Taf4; TAF4; TFIID; Taf<down>II</down>110; TAF<down>II</down>110; d110; dTAF<down>II</down>110; SR3-3
Taf5	TAF<down>II</down>; TAF80; Taf80; TAF<down>II</down>80/85; TAF<down>II</down>80; Taf<down>II</down>80; Taf85; d80; dTAF<down>II</down>80; TFIID; Taf5; TAF5; TAFII80; dTAFii80; CG7704; TFIID 85; p85; dTAFII85
Taf6	TAF<down>II</down>; TAF60; Taf60; taf60; CG9348; CG32211; Taf62; TAF<down>II</down>60; Taf<down>II</down>60; dTAF62; TAF<down>II</down>62; d60; dTAF<down>II</down>60; dTAF<down>II</down>62; TAFII60(62); TFIID; Taf6; T
Taf6L	TAF<down>II</down>; TAF60-2; Taf60-2; TFIID; CG10390; dTAF<down>II</down>60-2; Taf6L; TAF6L
Taf7	TAF<down>II</down>; TFIID; TAF7; Taf7; E; TAF55; Taf55; CG2670; anon-84Ec; dTAF<down>II</down>55
tai	I(2)k05809; DAIB1; EP(2)2630; CG18494; CG13109; I(2)k05802; I(2)01351; Taiman; 58/2; tai
Tbp	TFIID; TfiID; TBP38; dTFIID; 42kDa polypeptide; CG9874; TBP; Tbp; dTBP; dTbp; TFIIDtau
Tbp-1	BcDNA:GH12068; Tbp-1; CG10370; DmTBP-1; p50; BcDNA.GH12068; I(3)04210; Tbp1; Pros26S-RS6A; Rpt5; Dm_Rpt5a; Dm_Rpt5b; Pros26S; dRpt5
TBPH	dtar; TBPH; CG10327
Tfb1	CG8151; Dmp62; I(2)06949; I(2)06950; TFB1; Tfb1
Tfb2	CG7764; TFB2; Tfb2
Tfb4	TFB4; Tfb4; CG5041
TfIIA-L	dTFIIA; CG5930; TFIIA; TFIIA-L; TfiIA-L
TfIIA-S	dTFIIA; dTFIIA-S; BcDNA:RE44302; CG5163; F121; TfiIA-S; TFIIA-S; TFIIA
TfIIA-S-2	TfIIA-S-2; TFIIA; CG11639; EG:BACR7A4.7
TfIIB	dTFIIB; dTfiIB; CG5193; TFIIB; TfiIB; Tfiib
TfIIEalpha	dTFIIEl; TFIIE; TfiIE; CG10415; TfiIEalpha; TFIIE-L; TfiIEalpha; TfiIEalpha; dTFIIE-L
TfIIEbeta	TFIIE; TfiIE; dTFIIE-S; dTFIIES; CG1276; E<down>S</down>; TfiIEbeta; TfiIEbeta
TfIIFalpha	TFIIF; TfiIF; factor 5a; CG10281; TfiIFalpha; TFIIF-L; F5a; TfiIFalpha; TfiIFalpha; large subunit of transcription factor 5
TfIIFbeta	CG6538; I(3)j3C1; TFIIF; TfiIF; TFIIF small subunit; RAP30; dTFIIF30; F<down>S</down>; TfiIFbeta; TfiIFbeta; TfiIFbeta
TfIIS	I(2)35Cf; I(2)35cF; TFIISA; DmS-II; CG3710; RnpSII; DmSII; I(2)br52; br52; TFS-II; I35Cf; BG:DS00929.12; TfiIS; TfiIS
tgo	Hif1; DARNT; dARNT; darnt; HIF-1beta; Tango; HIF1b; TGO; tgo; CG11987; PRD
TH1	CG9984; TH1; NELF-D
Tif-IA	TIF-IA; Tif-IA; CG16938; CG3278; CG5951

Table S2 / 22

tin	NK-4/msh-2; msh2; NK-4; DmNK-4; DROHOXHK4; NK4/msh-2; Tin; tin; NK4; CG7895; HOX; msh-2; tin/NK4
tj	Dmaf; CG10034; fs(2)eo2; tj; fs(2)eo-B; fs(2)eoPL3; PL3
Top2	CHRAC; type II DNA topoisomerase; CG10223; wind; Topo II; topo II; TOPOII; Topoll; topoll; dCHRAC; TOP2; Top2; top2; TopII; dTopoll; topoisomerase II; Topoisomerase II; type II topoisomerase
tou	tou; Dm Tou; anon-48Ad; CG10897; gene VI; VI
Trap100	Trap100; CG7999; dTRAP100; dTrap100; Mediator
Trap150beta	dSUR2; CG3695; Gal11/SUR2; Trap150beta; SUR2; dTRAP150beta
Trap170	dRGR1; CG12031; dTRAP170; RGR1; p160; Trap170
Trap18	Trap18; p36; SOH1; BcDNA:GM28912; dTRAP18; Mediator; CG1057; dSOH1
Trap19	p18; Trap19; dSRB7; CG17397; dTRAP19; Mediator; SRB7
Trap220	CG7162; Trap220; Med1/SOP3/TRAP220; Mediator; dTRAP220; dTrap220
Trap25	dTRAP25; Med11/TRAP25; CG17183; Trap25
Trap36	Trap36; CG8609; Med4/TRAP36; dp34; dTRAP36; Mediator; p34
Trap37	Trap37; dCRSP34; dTRAP37; CG1245; CRSP34
Trap80	dTRAP80; dTrap80; Mediator; CG7957; p70; I(3)s2956; SRB4; dTRAP80/SRB4; Trap80; TRAP80
Trap95	dTRAP95; Sin4/TRAP95; Trap95; CG5465
Trf	dTRF1; X70838; trf; Trf; TRF; Trf1; TRF1; CG7562
Trf2	dTRF2; CG11195; CG18009; p79/TRF2; TLF; Trf2
Trfp	dTrfp; CG18267; CG18780; I(2)28DE; dTrap26; Tmr; Srb2/TRFP; Mediator; p29; Trfp; TRFP
trh	I(3)10512; 3.1; CG6883; DMU42699; TRH; trh
Trl	TfGAGA/Adf-2; anon-EST:fe2E12; E(var)62; transcription-factor-Adh2; CG13470; Adf-2; Gaf; GAF; Trl-GAGA; I(3)s2325; GAGA factor; Gaga; GAGA; E(var)3-trl; trl; Trl; Adf-2-519; Adf2; CG9343; NC70F; Nc70F; GAGA transcriptio
trr	trr; CG3848; EG:63B12.3; anon-2Bb
trx	I(3)j3A2; Rg-bx; 4733; trx-g; I(3)s5452; I(3)j14A6; NR0A5; R-bx; DMTRXIII; trxl and trxII; 4720; I(3)bx^v; CG8651; trx; Trx; TRX
tst	Ski2; tst; CG10210; cg10210
ttk	1209/05; 1325/15; 0438/31; ttk69; 1049/07; 1372/08; 5311; clone 2.9; ftzf2/ttk; ttkp69; E(yan)100D; ttk; I(3)02667; oversensitive; ovs; FTZ-F2; ftz-f2; 1209/10; 0250/25; 1119/04; 0037/17; Ttk69; TTK88; 1418/06; 1184/16; 1396
Tudor-SN	tudor staphylococcus/micrococcal nuclease; CG7008; Tudor-SN
twi	CG2956; EC9; dip5; twi; DTwist
Uch-L3	BcDNA:LD24440; UCH; p37A; BcDNA.LD24440; Uch-L3; uch-L3; CG3431; dUCH37; I(3)j2B8
unpg	unpg; unpg; upg; anon-45C; CG1650
Upf1	Dm-Upf1; UPF1; Upf1; DmUpf1; CG1559
vas	fs(2)ltoRJ36; BG:DS00929.14; no-relish; DmRH25; EP(2)0812; CG3506; vas; VAS; vasa; Vasa; VASA; cgt
vis	vismay; vis; zaa; CG8821

Table S2 / 23

vnd	l(1)1Bf; l(1)GA100; vnd; Vnd; VND; l(1)RC24; l(1)EA142; l(1)GA122; NK2; l(1)EC6; vnd/NK-2; l(1)VE769; ventral nerve cord defective; EG:118B3.1; NK-2; nk-2; CG6172; dNK-2; EC6; l(1)VA208
vri	vri; l(2)jf23; jf23; argo; CG14029; mat(2)earlyRS32; l(2)25Db; vrille; mat(2)ea-G
vvl	drifter; dfr-vvl; dfr/vvl; CG10037; Cfla; Cf1-a; vvl; VVL; PRD
wdn	CG1454; pqp; Sryc; wdn; sry-h1; sry-c; sry h-l
woc	woc; CG5965
wor	wor; BG:DS03023.1; l35Da; l(2)br35; br35; CG4158; l(2)35Da; schnecke; warniu
XNP	xnp/atrx; XNP; CG4548
Xpd	DhXPD; DhR3; XPD/ERCC2; XPD; Xpd; CG9433; DmXPD
yps	p45; p57; YPS; Yps; yps; Ypsilon Schachtel; CG5654
z	e(bx); en-bx; z; CG7803; EG:BACH59J11.3
zen2	BG:DS00276.10; z2; zpr; zerknüllt 2; CG1048; zen2
zfh1	Zfh1; zfh1; CG1322; zfl-1; l(3)00865; ZFH-1; Zfh-1; zfh-1
zfh2	zfh2; CG1449; ZFH-2; Zfh-2; zfh-2
Zfrp8	l(2)k13705; Zfrp8; zfrp8; CG3260; 137/5
Zyx102EF	Lim102EF; DmLIM-1; lim; Zyxin; zyxin; DLim-1; CG32018; Zyx102EF; BcDNA:LD06023; zyx102; Zyx102; ZYX102