**THIS STOCKLIST IS EDITABLE BY ALL LAB PERSONNEL.**

**PLEASE MARK ANY CHANGES WITH THE DATE AND YOUR INITIALS.**

**ALSO, PLEASE USE THE "TRACK CHANGES" FEATURE WHEN POSSIBLE.**

- **thanks,**
- **the MGMT**

## a stocks = wild type

**a16** ***canton-S*** **(Isogenic 2)**
Source: Constructed 1980, P.M.T.
Ref:
Comments:
wild-type
OK 9/22/83 P.D.L.G.

**a50** ***Oregon-R*** **(Isogenic)**
Source: TRF#a50
Ref:
Comments:

wild-type
there seem to be some lethals in here judged by dead larvae on the walls
OK 9/22/83 P.D.L.G.

**a54 Oregon-R (P2)**
Source: Bloomington #????? 11/20/00
Ref:
Comments:

## b stocks = 1st chromosome stocks

**b96** ***y tsg$^{XB56}$* / FM7b ??? or c, *y w$^{a}$ sn$^{X2}$ v$^{of}$ g$^{4}$ B***
Source: Ken and Jack
Ref: Note nomenclature in diff refs
(1985) Zusman and Wieshaus: *tsg$^{B8}$*
(1991) Ray et al Dev 113: 35: *tsg$^{YB56}$*
(1992) Ferg and Anderson Dev 114: 583: *tsg$^{XB86}$*
Bloomington : ?
Comments:
2nd site lethal tested 7/99 by Vilmos and only 3-5% of expected males live
12/1/97 Homozygote FM7s are not sn thus likely FM7b. The homozygotes are apricot colored in contrast to those in b95. This may be due to different FM7?
jlm

**b129 P[Glass-βGal] on X**
Source: 9/94:Moses
Ref: Moses (1991) G &D
Comments:
on X chromosome
labels all photoreceptor neurons behind furrow and axon projections to brain
Another insert is on ChrII $c272

**b130** ***y* [HS-FLP122] on X**
Source: 10/93:Struhl G
Ref: Moses (1991) G &D
Comments: Flp122 is reportedly 10x as active as Flp1 (Heberlein [Dev121:4085])
on X chromosome

**b159** ***y arm$^{YD35}$/FM7***
Source:JBuratovitch
Ref: Cell 63: 1167 (1990)
Comments: Deletes ~60% of way thro the repeats

**b162 P-sog/FM6.12**
Source: Ethan Bier 4.24/95

Ref:
Comments:

**b175** **y w *arm$^{H8.6}$* FRT18A/FM7**
Source : Heidi Theisen
Ref:
Comments:
*arm$^{H8.6}$* comes from b142

**b180** ***y$^{1}$ nej$^{Q7}$ v$^{1}$ f$^{1}$* / Dp(1;Y) FF1, y$^{+}$ / C(1)DX, *y$^{1}$ w$^{1}$ f$^{1}$***
Source : Received from? (Leslie Thompson knows from whom) Spring 2000
Ref: Bloomington Stock Center stock number B5292,
Comments: Loss of function allele of CBP (Creb Binding Protein)

**b192** ***y w brk$^{M68}$ f* / FM7a**
Source: Uwe Lammel
Ref:
Comments:

**b193** ***y w brk$^{F124}$ f* / FM7a**
Source: Uwe Lammel
Ref:
Comments:
Harbours the P-element enhancer trap 220 on the second chromosome

**b195** ***cv$^{43}$***
Source: 2001 PV
Ref:
Comments:
Stock carries a deletion in the *cv* gene which was obtained by mobilizing the P-element in the EP1349 line. Homozygous viable, crossveins are missing, slight delta-like effect in the LVs. The region surrounding the deletion was sequenced. PV 03/02

**b196** ***cv$^{51}$* / FM7**
Source: 2001 PV
Ref:
Comments:
Stock carries a deletion in the *cv* and the CG3160 (lipase) genes. The deletion was induced by mobilizing the P-element in the EP1349 line. 50% lethality due to second site mutation; crossveins are missing, slight delta-like effect in the LVs. The region surrounding the deletion was sequenced. PV 03/02

**b197** ***cv$^{34}$* / FM7**
Source: 2001 PV
Ref:
Comments:
Stock carries a deletion in the *cv* gene which was obtained by mobilizing the P-element in the EP1349 line. 80% lethality due to second site mutation; crossveins

are missing, slight delta-like effect in the LVs. The region surrounding the deletion was sequenced. PV 03/02

**b203** ***y w* vas-ϕ-zh2A**
Source : K. Basler, University of Zurich
Ref: Bischof et al., PNAS (2007) 104,9:3312-3317
Comments:
yw vas-phi/ vas-phi (2A) – vasa promoter driven germ line specific phiC31 integrase gene on the first chromosome at 2A
integrase is marked with 3xP3-EGFP (eye specific expression in adults)
no AttP (acceptor) site
line number J15 (Basler lab)
"Transgene pjb46 (#17), vas-phi, in ZH-2A (previously: ZH11)" – this comment was on the paperwork that came with the flies

**b204** **y mof[1]/FM6; mei-S332/CyO**
Source: John Lucchesi, lucchesi@biology.emory.edu
Ref:
Comments:
Full genotype: y mof[1]/FM6; (pr) cn mei-S332/CyO, pr cn Cy
Chromosome: 1,2

**b206** **y w mof[2]/FM7**
Source: John Lucchesi, lucchesi@biology.emory.edu
Ref:
Comments:
Chromosome: 1

## c stocks = 2nd chromosome stocks

**c259** **CyS / *Gla Bc***
Source:
Ref:
Comments: CyS = Cy Star

**c260** ***wg$^{CX3}$* / *Gla Bc***
*S*ource:
Ref:
Comments: pupal lethal

**c264** ***Dll$^{B}$* / CyO, [wg-βGal]**
Source:
Ref: Cohen 1989 EMBO J. 8(7):2045-2055
Comments:
LacZ is cytoplasmic
mutant for *wg* by P insert

lethal over $wg^{CX4}$ or $wg^{IG22}$
$Dll^{B}$ = In(2R)48EF; 60E5-6, aka $Dll^{11}$
$Dll^{B}$ available from Bloomington too, stock #1153 (over SM6a)
the CyO chromosome is CyO, P{ry[+t7.2]=en1}wg[en11] as in Bloomington stock #1567

**c289 (w)/w+; $wg^{IL114(ts)}$ /TSTL*, Cy, Tb, Hu, cn-2, e***
Source:2/95: Moses
Ref:
Comments: Clean wg ts
The wg[ts] stock was originally obtained from Amy Bejsovej as w+;wg[ts]/CyO. For convenience of identifying homozygous larva, I replaced the CyO balancer with the TSTL compound balancer by the following cross: w+; wg[ts]/CyO male X w-;M/TSTL/N virgin and obtained the following progeny to set up the new stock: w+/w-; wg[ts]/TSTL X w-; wg[ts]/TSTL. Since I didn't isogenize the X chromosome again, the current stock is a mixture of w+ and w- bearing X chromosomes. This is why you saw red and white eye segregates. The slight difference in the intensity ofthe red color may due to the difference of age

**c321 sdc[10608]/ CyO, [wg-βGal]**
Source: Stefanie PaineSauders
Ref:
Comments:
P element allele enhancer trap in one of introns. Not sure if null

**c330 Df(2R)Δ11,JL/CyoActGFP**
Source Tim Heslip sent the Df, from Lindscomb, I balanced it with CyOActGFP from G57 (CyO, P{w[+mC]=ActGFP}JMR1)BB 20100615
Ref: added to stocks Nov 2000, O. Marcu
Comments:
according to Mike O'Connor, this is a ~6kb deletion in the 2nd intron of SDC that also takes out part of the 2nd exon. In this region he thinks there are regulatory elements for Sara, therefore the deficiency is a double mutant Sdc-Sara-.

**c331 Df48;ubi>Sara183/CyO::TM6B (TSTL)**
Source Mike O'Connor
Ref: added to stocks Nov 2000, O. Marcu
Comments: (Mike's)
This combination has Df48 on 2nd and ubi>sara on 3rd
ubi>Sara183 is a better line than ubi>Sara242? (not sure about this 242 number, it was impossible to decipher-stock c332
Df48 removes Fkbp13, Sara, Syndecan (at least genetically), it probably does not make it past the 3'end of sdc.

**c346 Df(2L)RF / Cy**
Source: Jacques Pradel, Marseille
Ref:
Comments:

Breakpoints: 27E3-F2 ; 28B3-4 (in the *wg* region)

**c357 *w*; *Sco*/CyO**
Source: J. Pallos from an Umea stock noc$^{Sco}$/CyO hs-GFP
Ref:
Comments:

**c358 *w*; *sir2*$^{17}$/CyO**
Source: J. Pallos from a stock from Astrom
Ref: Astrom et al., Genetics 163(3): 931—937 (2003)
Comments:
the original stock they sent was w; Sir2[17]/CyO; Pc[11]/TM3
this is a null allele: comes from an imprecise excision of the P{lacW}k07223 element, removing most of the Sir2 open reading frame (sequences coding for the first 579 amino acids are missing)

**c359 *smt3*$^{AL1}$/CyO Shanti #AL1**
Source: from mutagenesis project with Shanti
Ref:
Comments:
Tamas sequenced: It is a GxA mutation on the DNA that translates into the last four amino acids (GGAP) to become SGAP; therefore it cannot be activated. It is lethal.
Stock AL1 in Shanti's collection

**c360 *dWnt4*$^{AL7}$/CyO Shanti #AL7**
Source: from mutagenesis project with Shanti
Ref:
Comments:
Tamas sequenced. Amino acid sustitution at position 331 S>G
Notably, none of the 7 other mutations identified in this complon had any altered sequence in the coding region or in the first ≥100bp of each intron boundary
See details in Shanti's manuscript

**c361 *dWnt4*$^{RF1}$/CyO Shanti #RF1**
Source: from mutagenesis project with Shanti
Ref:
Comments:
This allele is most promising as it is embryonic lethal BUT no mutation was found on sequencing the coding region or the first ≥100bp of each intron boundary
Defective open head, naked cuticle lost , ventral epidermis fully covered with denticles
See details in Shanti's manuscript

**c362 *dWnt4*$^{RF2}$/CyO Shanti #RF2**
Source: from mutagenesis project with Shanti
Ref:
Comments:

no mutation was found on sequencing the coding region or the first ≥100bp of each intron boundary
Lethal phase = Embryo. Larva 1 &2
Denticle size reduced in each of the 6 rows in all the segments.
See details in Shanti's manuscript

**c363** ***dWnt4$^{RF4}$*/CyO Shanti #RF4**
Source: from mutagenesis project with Shanti
Ref:
Comments:
no mutation was found on sequencing the coding region or the first ≥100bp of each intron boundary!!.
Lethal phase = Embryo. Larva 1 &2
Denticle size reduced in each of the 6 rows in all the segments.
See details in Shanti's manuscript

**c364** ***dWnt4$^{HL11}$*/CyO Shanti #HL11**
Source: from mutagenesis project with Shanti
Ref:
Comments:
no mutation was found on sequencing the coding region or the first ≥100bp of each intron boundary!!.
Lethal phase = Embryo. Larva 1 &2
Denticle size reduced in each of the 6 rows in all the segments.
See details in Shanti's manuscript

**c365** ***dWnt4$^{C1}$*/CyO C1**
Source: from Cohen
Ref: Cohen et al 2002
Comments:
*DWnt4$^{EMS23}$* and *DWnt4$^{C1}$*
The molecular mutation is known for these two alleles that are known described as semi lethal mutations with male and female sterility BUT our mutations complement these! (or not??)
See details in Shanti's manuscript

**c366** ***w[1118];* PBac{RB}CG42389[e02963]/CyO GFP**
Source: Bloomington stock number 18101 rebalanced by J. Purcell with CyO GFP from stock ???
Ref:
Comments:
PiggyBac insertion (49 bp downstream of Exon 3 of CG31738-RB) which results in no detectable B-isoform of CG31738, the A isoform is not affected (qPCR, M. Pomeroy)
CG31738 (the Drosophila homolog of the fibronectin type III domain containing protein family) has been re-annotated by Flybase and is currently listed as CG42389 (Jan.2009)

Lethality in late pupal stage (pharate adult), the occasional (2%) escapers live about a week with progressive degeneration. Possible L3 NMJ defect (M. Pomeroy).

## d stocks = 3rd chromosome stocks

**d76 cn; H1-2 dpp>lacZ/TM2, Ubx**
Source: Heberlein 7/96
Ref:
Comments: B3.0dpp>lacZ of Blackman on Chr III

**d109 *Rpd[m5-5]* w[+] 2AFRT/TM6B *Tb***
Source: Doug Bornemann
Ref:
Comments:
Null allele

**d100 Vucht 1 / TM6B, Tb, P{Ubiquitin>GFP}**
Source : Received from Diane O'Dowd (Originally from T. Kitomoto) Spring 2000
Ref: Bloomington Stock Center stock number B5292,
Comments: Loss of function allele of CBP (Creb Binding Protein)

**d113 *yw* hs-FLP; FRT HDAC3[j]/TM6B *Tb***
Source: Doug Bornemann
Ref:
Comments:
Stronger than the "i" allele

**d114 *yw;* MKRS hs-FLP/TM6 *Tb* Cre**
Source: Istvan Kiss
Ref:
Comments:

**d115 *w;* TM6 Hu/TM3 Ser Act>GFP**
Source: N. Slepko from one of the TM3 GFP lines
Ref:
Comments:

**d116 Taf250$^{EP(3)0421-EX1}$/TM6B**
Source: Dimitri Krainc
Ref: Wassarman DA et al, PNAS 2000 97(3):1154--1159
Comments:
Taf250 = Taf1
imprecise excision of the P element that leaves a 52 bp insertion which contains an in frame stop codon within the first exon
aka EP421-EX1

**d117 Taf250$^{6322}$/TM6B**
Source: Dimitri Krainc
Ref: Wassarman DA et al, PNAS 2000 97(3):1154--1159
Comments:
Taf250 = Taf1
point mutation: W864stop
has a "suppressor" in the background that downregulates expression from UAS (1. eliminates P463 eye degeneration, and 2. reduces UAS-GFP as measured by qRT-PCR) – both the Taf and the TM6 chromosomes do it!

**d118 DMKP-3[P3]**
Source: J Chung, jchung@kaist.ac.kr
Ref: Mol Cell Biol. 2004 Jan;24(2):573-83
Comments:
loss of function mutant of MKP-3 made by remobilizing EP(3)3142
DMKP-3 = Drosophila mitogen-activated protein kinase (MAPK) phosphatase 3
Chromosome: 3

**d119 *w* ; HJS1/TM3 *Ser***
Source: T. Lukacsovics from Daisuke from Wimmer
Ref: Horn et al., Genetics (2003) 163: 647-661
Comments:
HJS = Hermes Jump Starter; line 1
Hermes element for mobilizing PiggyBac constructs
Chromosome: 3

**d120 *w* ; HJS2/TM3 *Ser***
Source: T. Lukacsovics from Daisuke from Wimmer
Ref: Horn et al., Genetics (2003) 163: 647-661
Comments:
HJS = Hermes Jump Starter; line 2
Hermes element for mobilizing PiggyBac constructs
Chromosome: 3

**d121 PBac{WH}huntingtin[f04684]**
Source: Harvard piggy back collection
Ref:
Comments:
Location: in Htt (CG9995) on 3R (98E2)

# E stocks - 4th chromosome

**E1 dTCF$^{1}$/ m(4)579 *??aka m(4)57g?***
Source : Marc Peifer
Ref:
Comments:

dTCF allele
aka l(4) 13B
There is no gene known as m(4)579. However there is a gene known as M(4)57g . The substitution of the "g" by a "9"may be the source of confusion (RSN, 12/00). The mutation corresponds to M(4)57g since flies M/+ have thin bristles and reduced body size. The occasional suppression in the stock may be due to the presence of extra fourth chromosomes( RSN, 5/02).

**E2** **$dTCF^{2}/ Ey^{D}$**
Source : Marc Peifer
Ref:
Comments:
dTCF allele
aka l(4)1B13
Null = frame shift before the HMG box ref VanWettering et al. 1997 -Cell 88:789

**E3** **$dTCF^{3}/ Ey^{D}$**
Source : Marc Peifer
Ref:
Comments:
dTCF allele
aka l(4)BK15
Null = stop codon in HMG box that eliminates the A splicing variant but not the B variant ref VanWettering et al. 1997 -Cell 88:789

**E4** **$l(4)102ABb^{1}/ Ey^{D}$**
Source : Marc Peifer
Ref:
Comments:
dTCF allele

**E5** **w/w; P[UAS>LEF; w+]#8/ P[UAS>LEF; w+]#8 on 3rd; dTcf/ $Ey^{D}$**
Source : Heidi Theisen
Ref:
Comments:
dTCF allele
dTCF allele unkown. Maryam did not keep track. Its either 1, 2, 3,

**E6** **w/w; P[UAS>LEF; w+]#38/ P[UAS>LEF; w+]#38 on 3rd; dTcf/ $Ey^{D}$**
Source : Heidi Theisen
Ref:
Comments:
dTCF allele unkown. Maryam did not keep track. Its either 1, 2, 3,

**E11** ***yw,* T(1,4) sc H $y^{+}$/*Pan*$^{1}$**
Source: HT
Ref:

Comments:
Pan[1] is allele with point mutation E-tail
To get pan[1] larvae bkz yellow

**E12 Df(4) B2-7a**
Source: Rui terminal Df
Ref:
Comments:
How is this maintained? What is on the other 4th chromosome?

**E13 Df(4) B2-2D**
Source: Rui terminal Df
Ref:
Comments:
How is this maintained? What is on the other 4th chromosome?

**E14 Df(4) B6-4a**
Source: Rui terminal Df
Ref:
Comments:
How is this maintained? What is on the other 4th chromosome?

# f stocks = multi chromosome stocks

**f218 *w* ; TM3, *Sb ri p^p bx e* / TM6b, *Tb e ca***
Source:
4/89: Bloomington Stock Center
Engles Stock #4
Ref:
Comments:

**f224 *Sp* / CyO *; Ki hb* / TM3, *Sb* [hb-ßgal]**
Source: 2/92: M O'Connor
Ref:
Comments:
The TM3 has a p insert with *hb* promotor driving ßgal so you can score embryos by ßgal staining in ant *hb* domain.

**f244 y w; T(2;3)apXa/ CyO; TM2**
Source : Kavita
Ref
Comments

**f271 w/Dp(1;Y)y+; Sco/CyO; MKRS/TM6B**
Source:
Ref:
Comments:

y+ bearing Y found by Judy Purcell March/2003- source unknown

**f317 yw; TM6C, Sb Tb e/TM2, Ubx e**
Source:
Ref:
Comments:

**f318 w; TM6B, Hu Tb e/TM3, Ubx>lac e**
Source:
Ref:
Comments:

**f347 (y)w; Xa/CyO, P[w(+mC)=Ubi>GFP]; TM3, P[w(+mC=Act>GFP], Ser**
Source: 1/99 Judy Purcell
Ref:
Comments: Made from #2475 (w, Xa/CyO;TM3) and yw; ln(2R)Gla/CyO, Ubi>GFP and w; Sb+/TM3,Act>GFP, Ser

**f351 *yw* hs-flp ; AttP-zh86Fb ; vas-ϕ-zh102D**
Source : K. Basler, University of Zurich
Ref: Bischof et al., PNAS (2007) 104,9:3312-3317
Comments:
AttP = acceptor line for phiC31 phage attachment site facilitated transformation. vasa promoter driven germ line specific phiC31 integrase gene on the 4th at 102D (homozygous) and attP attachment (acceptor) site (also homozygous) on the third at 86F, hs-flp on X. The flanking genomic sequence of the attP site is given in the supporting material of the paper.
line number J5 (Basler lab)
"Transgene pjb46 (#17), vas-phi, in ZH-attP-102D" – this comment was on the paperwork that came with the flies

**f352 *yw* M{eGFP.vas-int.Dm}ZH-2A ; M{RFP.attP}ZH-51D**
Source : K. Basler, University of Zurich
Ref: Bischof et al., PNAS (2007) 104,9:3312-3317
Comments:
Chromosomes: 1, 2
vasa promoter driven germ line specific phiC31 integrase gene on the first chromosome at 2A; integrase is marked with 3xP3-EGFP (eye specific expression in adults)
AttP attachment site (acceptor for phiC31 phage attachment site facilitated transformation) on the second chromosome at 51D (homozygous); RFP marks the acceptor site on the second chromosome
line number J28 (Basler lab) – short name for it is "ϕX–51D"
"Combined line containing the codon-optimized integrase driven by vasa (vas-int.Dm); access. no. for landing site is EF362407" – this comment was on the paperwork that came with the flies.

**f353** ***yw* M{eGFP.vas-int.Dm}ZH-2A ; M{RFP.attP}ZH-86Fa**

Source : K. Basler, University of Zurich

Ref: Bischof et al., PNAS (2007) 104,9:3312-3317

Comments:

Chromosomes: 1, 3

vasa promoter driven germ line specific phiC31 integrase gene on the first chromosome at 2A; integrase is marked with 3xP3-EGFP (eye specific expression in adults)

AttP attachment (acceptor) site (homozygous) on the third at 86F (this line is supposed to support the strongest expression level as compared to J5 & J28); RFP marks the acceptor site on the second chromosome

line number J35 (Basler lab) short name for it is "ϕX−86Fa"

"Combined line containing the codon-optimized integrase driven by vasa (vas-int.Dm); access. no. for landing site is EF362408" – this comment was on the paperwork that came with the flies.

**f354** ***yw* hs-flp*; act>GAL4, UAS>GFP/CyO***

Source:

Ref:

Comments:

For flipout clones

# G stocks = stocks with GAL4 drivers

**G2** ***y w; Ay GAL4(17bFO3)=actin>GAL4 /TM6B***

Source: Daisuke/Wakae-san 6/98 (Y.Hiromi)

Ref: Rack C-B4

Comments:

## Actin driving GAL4 with y+ already flipped out

**G6** ***Elav> GAL4 on X***

Source: Daisuke/Wakae-san 6/98

Ref: Rack K-A5

Comments:

expresses all neurons all stages per empirical info from USUI

**G14** ***y w; P[w+; UAS> super GFP]T2-1/CyO, y[+])***

Source: Daisuke/Wakae-san 6/98 (Y.Hiromi originally from Barry Dickson)

Ref: Robert M. Dickson* et al. NATURE |VOL 388 | 24 JULY 1997, p355, for the S45T mutation

Comments:

Insertion at 38F-39A

GCGGAATGAAAACAGAA{P}CGGAGCTGAGGAGCGAG

(S65T) means serine 65 changed to Threonine

One of several Enhanced fluoresence GFP reporters

**G18 - P83 wg>Gal4**
Source: Tim? 6/96
Ref:
Comments:
33F1

**G22 - P87 UAS>wg chrII**
Source: Source: Tim? 6/96
Ref:
Comments:

**G23 - P88 y w; UAS>wg[ts]**
Source: Source: Tim? 6/96
Ref:
Comments:

**G25 - P91 Arm>GAL4$^{4}$ ChrIII**
Source: Vincent 11/96
Ref:
Comments: Double insert in ChrIII, homozygous viable, number 4. Construction = Arm>Gal4>K10 = RI/kpn of Arm promoter in Casper4. Gal4 Orf (Not>Kpn) from Gal4(H3) in H3 of BS& K10 terminator Not & blunted Sal into to Not StuI

**G26- P92 Arm>GAL4$^{11}$ ChrII**
Source: Vincent 11/96
Ref:
Comments: Single insert in Chr2, homozygous viable, number 11. Construction = Arm>Gal4>K10 = RI/kpn of Arm promoter in Casper4. Gal4 Orf (Not>Kpn) from Gal4(H3) in H3 of BS& K10 terminator Not & blunted Sal into to Not StuI

**G28 - P179 w/w; P{w+; elav>GAL4}/CyO**
Source: Michelle Musaccio in O'Connor lab 3/97
Ref:
Comments:
Insertion at 42D-E
CTTGCCCGAGCTTTAGG{P}GATCGGGATCGTGGACT
Expression in every CNS neuron starting with segregating neuroblasts and beyond

**G33 - P207 *ptc*-GAL4 on chr II**
Source : Mike O'Connor/ Theo Haerry
Ref:
Comments:
B-#2017 w*; P{w+mW.hs=GawB}559.1 ! GAL4
enhancer trap insert on 2$^{nd}$ but not lethal
Speicher, S. A., U. Thomas, et al. (1994). "The Serrate locus of Drosophila and its role in morphogenesis of the wing imaginal discs: control of cell proliferation." Development **120**(3): 535-44.

**G42 - P268 P[prd>Gal4; w+] on X**

Source:
Ref:
Comments:

**G46 w/w; da>GAL4 chr II**

Source: Kavita lab stock # L36 5/99 orig from O'Connor
Ref:
Comments: daughterless>Gal4

**G49 P[w$^{+}$ UAS>tsg His 51] Chr 3**

Source: O'Connor 6/99
Ref:
Comments:
Is it mutant for w???
6xHIs tag at Cterminal of tsg
gives stonger phenotype w/ sog than His 68

**G62 w, P[w+; UAS>SDCYF28]/CyOActGFP**

Source: Tim Heslip made a construct of syndecan full length with cytoplasmic tyrosines mutated to phenylalanine (YF) into pUAST. Transformed in w/w flies by Oana Marcu, crossed to B2475 females
Ref:
Comment:
Added: June/2000
Location: 2$^{nd}$ chromosome
CyoActGFP (CyO, P{w[+mC]=ActGFP}JMR1) BB 20100615 was crossed in from stock G57

**G68 w, P[w+; UAS>SDC5.6Cyto5]/ CyoActGFP**

Source: Tim Heslip made a construct of syndecan cytoplasmic tail (5.6 indicates the pair of primers) into pUAST. Transformed in w/w flies by Oana Marcu, crossed to B2475 females
Ref:
Comment:
CyoActGFP (CyO, P{w[+mC]=ActGFP}JMR1) BB 20100615 was crossed in from stock G57
Added: Nov/2000
Location: 2nd chromosome

**G73 w, P[w+; UAS>SDC3.4TM-Cyto7]/ SerTM3ActGFP (at 94D10-11, hh 5' untranslated)**

Source: Tim Heslip made a construct of syndecan cytoplasmic tail +transmembrane domain + easter signal sequence (3.4 indicates the pair of primers) into pUAST. Transformed in w/w flies by Oana Marcu, crossed to B2475 females
Comment:
SerTM3ActGFP was crossed in from stock G58
Added: Nov/2000

Location: 3rd chromosome
the homozygous flies have patterned eyes (Namita 6-18-02) that appear as a longitudinal white stripe in the center of the eye. Additionally, homozygous flies do not have claws and the distal part of tarsal segment # 5 (RSN 6-18-02) Since recessive, it is possible that the insertion of Cyto-7 causes the mutant phenotype. According to Tamas, the insertion is in Hh (RSN, 10-2-02)

**G83 UAS>gma = (GFP-moesin fusion) Chr X**
Source: Dan Kiehart (Ruth Montague sent r.montague@duke.edu)8/2001
Ref:
Comments:
A fusion of the actin binding domain of moesin to GFP to label cell outlines.

**G84 UAS>gma = (GFP-moesin fusion) Chr II**
Source: Dan Kiehart (Ruth Montague sent r.montague@duke.edu) 8/2001
Ref:
Comments:
A fusion of the actin binding domain of moesin to GFP to label cell outlines.

**G87 *w ;* elav>GAL4**
Source: George Jackson
Ref:
Comments:
Location = 2nd
This line is different from elav>Gal4/CyO - it's weaker and homozygous viable

**G88 *w ;* dilp2>GAL4.A**
Source: Eric Rulifson
Ref:
Comments:
Location = 2nd
IGF-like gene enhancer

**G90 *y w* (FLP); FRT42D y+ Gal80/SM**
Source: Rui
Ref:
Comments:
to make clones
FLP was not isogenized and thus may be heterozygous for y w this stock is the recombinant #3 from Rui
gal 80 under tubulin promoter (see Liqun Luo somewhere)
SM from f276

**G91 UAS-YFP-FKBP12 RNAi**
Source: from Andrea Brand, Univ. of Cambridge, UK (sent by Melanie Cramton, res. assist) in June 2003
Ref: Van Roessel, Genesis 2002, 34:170-173
Comments:
We got this stock as source of YFP

homozygous on X

**G95 vg>Gal4/CyO; TM6B (floating)**
Source: from Garcia-Bellido lab
Ref:
Comments:
wing margin driver

**G100 WC-316-GAL4**
Source: Scott Weber
Ref:
Comments:
Drives in cells regulating the mushroom body

**G101 w; ap$^{VG035}$/CyO wg-lacZ; ap$^{VNC}$-Gal4-M7/TM6B**
Source: Juan Botas
Ref: *Nature* 2000 Nov 2 **408:6808** 101-6
Comments:
directs expression to a small number of well-defined interneurons (two per hemisegment) in the ventral nerve cord of the adult central nervous system (CNS)
The driver they used in the paper seems to be on the first chromosome… (and doesn't have ap on II)
The ap mutation on the 2nd is sublethal, the Gal4 insert on the third is viable (J.P.)

**G102 Rh1-GAL4**
Source: C. Desplan
Ref:
Comments:
rhodopsin driver
P{ry}
homozygous viable
Location: 1

**G103 Rh1-GAL4**
Source: C. Desplan
Ref:
Comments:
rhodopsin driver
P{ry}
homozygous viable
Location: 2

**G104 Rh1-GAL4**
Source: C. Desplan
Ref:
Comments:
rhodopsin driver
P{ry}
homozygous viable

Location: 3

**G105 w; Sp/CyO ftz-lacZ; elav-GeneSwitch**
Source: received from Haig Keshishian
Ref: Osterwalder et al., 2001 PNAS 98: 12597
Comments:
Conditional RU486-dependent GAL4 line (GSG-301-2)
homozygous viable
Location: 3

**G106 yw;+; elav-GeneSwitch**
Source: received from Haig Keshishian
Ref: Osterwalder et al., 2001 PNAS 98: 12597
Comments:
Conditional RU486-dependent GAL4 line (GSG-301-2)
homozygous viable
Location: 3

**G109 w[1118]; HMLΔ-Gal4 2xe-GFP**
Source: O. Marcu from NASA
Ref: Wernet et al., Cell 115:267279 (2003)
Comments:
labels hemocytes; useful for the inflammation project
inserts (Gal4 and GFP) on the second

**G110 glass-lacZ P(ry+) long gmr**
Source: Jessica Treisman, NYU
Ref:
Comments:
"long" gmr driving lacZ
insert on the third
The vial was marked CyO/Sco/Sp – I assume floating in the background?

**G111 w elav-Gal4; Sco/CyO**
Source: J. Pallos
Ref:
Comments:
elavX from Daisuke (stock G6)
the stock is weak

**G112 w elav-Gal4; Sb/TM6 Ubx**
Source: L. Bodai
Ref:
Comments:
elavX from Daisuke (stock G6)
third chromosome is from Bloomington stock 2960: C(1)M3, y[2]/FM7a; Sb/TM6 – the stock is now in Kyoto, #107496. It is NOT TM2 but TM6 with Hn[P] ss [P88] Ubx[bx-34e] Ubx[P15] e[1]

**G127 elav-Gal4, UAS-GFP, tubP-GAL80[ts], w[*]/FM7c**

Source: Brett Barbaro, by recombining Bloomington stocks B5146 and B7016
Ref:
Comments:
lethality due to Gal80[ts]
UAS-GFP insert is at 4D7 as per Tamas' inverse PCR
Gal80ts is roughly in section 7 or 8, calculated by recombination frequency by Brett Barbaro; Tamas determined it to be in 6F4 (in Sxl)
might have hsFLP present from the BSc5146 stock
Full genotype: P{w[+mW.hs]=GawB}elav[C155], P{w[+mC]=UAS-mCD8::GFP.L}LL4, (P{ry[+t7.2]=hsFLP}1), P{w[+mC]=tubP-GAL80[ts]}9, w[*]/FM7c

**G128 w*; P{w+mC=GAL4-ninaE.GMR}12 ! GAL4**
Source: Bloomington Stock Center, donor: Matthew Freeman
Ref:
Comments:
"gmr-Gal4"
glass enhancer driving GAL4 in the eye disc, provides strong expression in all cells behind the morphogenetic furrow, M.F.
Chromosome affected: 2
Available from Bloomington, stock #1104

**G129 elav-Gal4 UAS-mCD8::GFP**
Source: Bloomington Stock Center, donor: Liqun Luo
Ref:
Comments:
full genotype: P{w[+mW.hs]=GawB}elav[C155], P{w[+mC]=UAS-mCD8::GFP.L}LL4, P{ry[+t7.2]=hsFLP}1 w[*]
GFP labels the cell surface (mouse CD8 is a transmembrane protein), highly concentrated in neuronal processes
May be segregating CyO or FM7c
GFP insert appears to be at 4D7, as determined by Tamas Lukacsovich in early September, 2007
Available from Bloomington, stock #5146

**G130 *w[*];* P{w[+mC]=UAS-GFP.S65T}T10**
Source:Bloomington Stock center, Donor: Corey Goodman
Ref:
Comments:
Insertion site unknown, somewhere on the 3rd chromosome
Might have *y* floating
Available from Bloomington, stock #1522

**G131 P[TG5-286, *ry*$^{+}$,lacZ],*ry*$^{506}$*/TM2. ry***
Source : Chris Merli
Ref:

Comments:
insert on III
line is from remobiliztion of TG5-14
plasmid construct renamed BS3.1 for Development paper
different BS3.1 lines show variable expression, particularly in the wing pouch region
original stock number M16, the only “Merli” stock we kept as of November 2008

**G132 H3N APRD>lacZ 28-2**
Source: AS,HT
Ref:
Comments:
H3N = APRD – 2.8kb fragment that mimics dpp and BS3.0 expression
Line 28-2
Chromosome: II, viable
5/5 lines all mimic dpp expression
used for data collection

**G133 AB1,2 >lacZ 63A**
Source: AS,HT,JP
Ref:
Comments:
APRD reporter derivative: AB1,2 = APRD with both Brk sites mutated
Chromosome: II
Line 63A (used for data collection – published in PLoS)
6/6 lines tested all lost ventral repression

**G134 H3N (1-5) ApRd >lacZ M32**
Source: AS,HT
Ref:
Comments:
APRD reporter derivative: the 5 dTcf sites within APRD are mutated
H3N(1-5) = A*p*R*d* > lacZ
Line M32
Chromosome: II
6/7 lines lose ventral repression
1/7 lines had very weak stain
This line could not be repressed by ectopic Wg
used for data collection

**G135 H3N (M3,4,5) APRd>lacZ F29-2**
Source: AS,HT
Ref:
Comments:
APRD reporter derivative: H3N (M3,4,5) = APR*d*; The distal 3 dTcf sites within APRD are mutated
Chromosome:
4/4 lose ventral repression

used for data collection

**G136 H3B APR>LacZ 30**
Source: AS,HT
Ref:
Comments:
APRD reporter derivative: H3B = APR_ > lacZ (region containing distal Tcf sites is deleted)
Line 30
Chromosome: II
All lines tested lose ventral repression (~5lines)
used for data collection

**G137 SN AP_D>lacZ 21-2**
Source: AS,HT
Ref:
Comments:
APRD reporter derivative: 1.4kb region containing the Co-R (Brinker) binding sites is deleted
SN = AP_D > lacZ
Chromosome: II, viable
used for data collection
7/7 inserts all the same; loss of ventral repression

**G138 M3.1 Ad 10**
Source: AS,HT
Ref:
Comments:
Chromosome: II
M3.1 = BS3.1 with the 2 dTcf sites mutated
This is expressed so Tcf not required for activation
for BS3.1 see Merli's stock M16

**G139 ABTS Aprd>LacZ 15B**
Source: HT,AS,JP
Ref:
Comments:
ABTS = A*prd* = APRD with all 5 dTcf and both Brk binding sites mutated
Line 15B
Chromosome: III
Viable
Kept 2 chromosome II and 2 chromosome III lines because lost track of which lines were used to collect data

## P stocks = stocks with transgenes in new places

**P30** ***w$^{1118}$*; P[*dsh$^{w2}$*, *w$^{+}$*] / TM2**

Source: HT

Ref:

Comments:

EcoR1-BglII genomic fragment into Bam: EcoR1 cut casper transformant 32-2 HT

partially rescues *dsh$^{1}$* and *dsh$^{VA153}$* and does not rescue *dsh$^{V26}$*

**P31** ***w$^{1118}$*; P[*dsh$^{w3}$*, *w$^{+}$*] / CyO**

Source: HT

Ref:

Comments:

EcoR1-BglII genomic fragment into Bam: EcoR1 cut casper transformant 28-4 HT

rescues *dsh$^{1}$*, *dsh$^{V26}$ and dsh$^{VA153}$*

**P41** ***w$^{1118}$*; P[hsp70-*dsh*, *w$^{+}$*]**

Source : transformation of Casper???

Ref:

Comments: #2 chrII

homozygous viable

Able to rescue all *dsh$^{1}$*, but not *dsh$^{VA153}$*, *dsh$^{V26}$* even at 29ºC

**P44** ***cn dpp*-β Gal lacZ chrII**

Source:Mike Buratovitch, Peter Bryant's Lab

Ref:

Comments:

?? dpp enhancer trap on the 2nd chromosome

= BS3.0 from Blackman Development 111:657-666 (1991)

= dpp 3' enhancer driving dpp coding transformed into 55D [i.e. not @ dpp locus]

It does not carry dpp coding. It is marked with ry+ (RSN, 7-15-02)

stock rescued and reestablished by J.P fall 2005 – needs double checking.

Bloomington stock #5527: P{ry[+t7.2]=BS3.0}H1-1, cn[1]; ry[506]

The Chr 3 insert is Bloomington 5528 cn[1]; P{ry[+t7.2]=BS3.0}H1-2, ry[506]/ TM2

**P49** **60X** ***w*/*w*; +/(CyO); [HuCc$^{1}$(60X), *w$^{+}$*] / (TM2)**

Source::

Ref:

Comments:

HuCc$^{1}$ = P[Cc>phb$^{+}$ # 60X, *w$^{+}$*]

insert is on III

**P59** **y w; ciD$^{plac\ ?}$w+? = 4th chromosome**

Source:Buratovitch

Ref: Eton & Kornberg G&D4:1068 (1990).

Comments: Insertion of plarb into ci ($2^{nd}$ exon). Its semi lethal as homozygote (60% homozygotes die as embryos). It's a hypomorph that is lethal over ciD but not over ci alleles. since flies = y but are various shades of red, I assume the plarb = w+ and is homozygous. One will not see the ciD phenotype.

**P93 y w; UAS>Arm[510C]**

Source: Peifer 1/97

Ref:

Comments:

UAS driving activated ARMcDNA- vector =w+ p (Tamas sequenced ~02/2008, it is not "normal" Arm as advertised before)

Insertion: 2L @ 35B, between CG3688 and CG15274, seq.

CGAACTGAGTAATGTGCA in AE003646

**P94 y w; UAS>Arm[52E]**

Source: Peifer 1/97

Ref:

Comments:

UAS driving normal ARMcDNA- vector =w+ p

Insert located at 45B3-4:

GACCGTTGCACTTTTTT{P}GGACAATTTCATGCACTC

**P95 w; P{tsg1.4}/P{tsg1.4} P149-2**

Source: Liz

Ref: Liz's dissertation p.135 tsg mutant rescue stats; p129 how construct was made

Comments:

P149 on chr2 rescues tsg mutants 100%

(P95 -> P178 from LIZ 1/97)

**P106 *w*; P{hsp83-amino 1/2 *tsg*+myc tag}/P{hsp83-amino 1/2 *tsg+myc* tag} NT61-2**

Source: Liz; received hsp83 CaSpeR vector from K. Anderson

Ref: Liz's dissertation p. 132 how construct was made; also see refs in this chapter for hsp83 promoter

Comments: P61 on chr2 does not maternally rescue *tsg* mutants and appears to have no dominant negative effects even at elevated temperatures

**P116 w; P{*twi--tsg*}/P{*twi--tsg*} tt38-2**

Source: Liz

Ref: see Liz's dissertation for *twi* promoter ref; p. 63 for how construct was made; rescue stats p.76

Comments: P38 rescues *tsg* mutants 95%

**P126 y w; P{uas-*tsg*}/P{uas-*tsg*} UT1-2 chr2**

Source:

Ref: See 11/6/96 notebook page 23

Comments: When crossed to blk/blk; blk-Gal4, the F1 progeny that were blk-Gal4, uas-tsg in the heterozygote blk/+ background had many adult defects; the ventral

portion of all eyes are replaced by naked cuticle. See Liz's lab notebook 11/95, page 27-28. This was true for all uas-tsg P126-P133

**P211 UAS dΔN-1/ UAS dΔN-1 dnTcf**
Source : Marc Peifer
Ref:
Comments:
dominant negative dTCF
N terminal 31 amino acids deleted i.e. arm binding site removed
Strong survival, i.e. weak allele
unmapped insertion
Note made by Oana: insert on 2nd as per Adeela - July 16/01
Insertion in 3L @ 64D2-3 between CG10645 and CG10642 (July/2002)

**P212 yw; UAS dΔN-4/ UAS dΔN-4 dnTcf**
Source : Marc Peifer
Ref:
Comments:
dominant negative dTCF
N terminal 31 amino acids deleted i.e. arm binding site removed
moderate
insert on II
Note: this stock is yw (and the insert is w+) - Oana -July 16/01
Insertion site: 3R @ 90D6-E2 in CG 7847 (stripe) (July 2002)

**P213 UAS dΔN-3/ UAS dΔN-3 dnTcf**
Source : Marc Peifer
Ref:
Comments:
dominant negative dTCF
N terminal 31 amino acids deleted i.e. arm binding site removed
Weak [survival, i.e. strong allele]
insert on II
insertion site: 3R @ 90D6-E2 in CG7847 (stripe) (July 2002)

**P214 yw; UAS dTCF10/ UAS dTCF10**
Source : Marc Peifer
Ref:
Comments:
dTCF under UAS control
insert on II
Note: this stock is yw (and the insert is w+) - Oana -July 16/01
insertion: 2R @ 42A2 in CG7865 (July 2002)

**P215 UAS dTCF24/ CyO**
Source : Marc Peifer
Ref:
Comments:
dTCF under UAS control

insert on II (at 35D2)
CCAATTAGAAAGAAACC{P}TATTTAAGCAAAACGCA
homozygous lethal

**P250 *w* ; LEF1(16F1)**
Source : transformation of pUAST-Lef1 from JL Marsh. Sangbin injected on 11/8/96
Ref: a file '-microinjection' in Flylab1
Comments:
line # 16F1
homozygous viable
Injected into *w*
Construct = pUAST-Lef1 from JL Marsh
Location = 2nd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3) males
with A9GAL4, severe wing defect, but mild leg deform; with ptcGAL, all animals died before pupation @25', but died in pupal case @18'

**P280 w; UAS-SDC #20/TM3**
Source:Judy. Maryam injected on 10/10/97
Comments:
line 20
balanced with TM3
injected into w
Construct=UAS-SDC from Judy
location= 3rd
Eye color= orange
Made by crossing to B2475 (w,T(2:3) apXa/SM5; TM3) females

**P296 w; Puast Dsh 94/TM3**
Source Dr. Marsh. Maryam injected on 1/2/98
Comments
line 49
injected into w
Construct=Puast Dsh 94 from Dr.Marsh
location=3rd
Eye Color=orange
Made by crossing to B2475(w;T(2;3)apXa/SM5;TM3) female

**P297 w; Puast Dsh 94/TM3**
Source Dr.Marsh. Maryam injected on 1/2/98
Comments
line 9
injected into w
Construct=Puast Dsh 94 from Dr.Marsh
location=3rd
Eye Color=orange
Made by crossing to B2475(w;T(2;3)apXa/SM5;TM3)female

**P401** ***w ;*** **pUAST Q108+myc/flag #2 / TM3**

Source : Transformation of 108 CAG repeats followed by a myc/flag epitope tag. Construct from the L.Thompson lab. Heli injected Summer 1998.
Ref:
Comments: Q108+myc/flag #2 / Q108+myc/flag #5 flies survive
line # 2
homozygous lethal
Injected into *w*
Location = 3rd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P406** ***w ;*** **pUAST Q108 #12**

Source : Transformation of 108 CAG repeats followed by a myc/flag epitope tag. Stop codon before the tag prevents expression of the tag. Construct from the L.Thompson lab. Heli injected Summer 1998.
Ref:
Comments:
line # 12
homozygous viable
Injected into *w*
Location = 3rd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P409** ***w ;*** **pUAST Q108 #16**

Source : Transformation of 108 CAG repeats followed by a myc/flag epitope tag. Stop codon before the tag prevents expression of the tag. Construct from the L.Thompson lab. Heli injected Summer 1998.
Ref:
Comments:
line # 16
homozygous viable
Injected into *w*
Location = 2$^{nd}$
Insertion at 53A4-5
CAAGCGAAGCGGTTGGGA{P}TCGTCAGTACCGACGAA
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P413** ***w*** **pUAST Q48+myc/flag #30**

Source : Transformation of 48 CAG repeats followed by a myc/flag epitope tag. Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:
line # 30
homozygous viable
Injected into *w*
Location = 1st
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P415 *w ;* pUAST Q48+myc/flag #32**

Source : Transformation of 48 CAG repeats followed by a myc/flag epitope tag.
Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:
line # 32
homozygous viable
Injected into *w*
Location = 2nd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P416 *w ;* pUAST Q48+myc/flag #36**

Source : Transformation of 48 CAG repeats followed by a myc/flag epitope tag.
Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:
line # 36
homozygous viable
Injected into *w*
Location = 2$^{nd}$
Insertion at 70D2-3
GCTCAAAAGTCGGAATG{P}TGGTATTCGGTTTTAGT
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P417 *w* pUAST Q48+myc/flag #42**

Source : Transformation of 48 CAG repeats followed by a myc/flag epitope tag.
Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:
line # 42
homozygous viable
Injected into *w*
Location = 1$^{st}$
Insertion at 9E2
CCGTTATCGCAGCCGGT{P}AGGGATGGCACTTTCGC
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P418 *w ;* pUAST Q56 #1**

Source : Transformation of 56 CAG repeats followed by a myc/flag epitope tag. Stop codon before the tag prevents expression of the tag. Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:
line # 1
homozygous viable
Injected into *w*
Location = 3rd

Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P433 *w ;* pUAST Q22+myc/flag #29**

Source : Transformation of 22 CAG repeats followed by a myc/flag epitope tag. Construct from the L.Thompson lab. Heli injected Summer 1998.

Ref:

Comments:

line # 29
homozygous viable
Injected into *w*
Location = 3rd

Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P435 *w ;* pUAST Q22 #12**

Source : Transformation of 22 CAG repeats followed by a myc/flag epitope tag. Stop codon before the tag prevents expression of the tag.Construct from the L.Thompson lab. Heli injected Summer 1998.

Ref:

Comments:

line # 12
homozygous viable
Injected into *w*
Location = 3rd

Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P441 *w ;* pUAST Q300 #15**

Source : Transformation of 300 CAG repeats followed by a myc/flag epitope tag. Stop codon before the tag prevents expression of the tag. Construct from the L.Thompson lab. Leon injected Spring 1999.

Ref:

Comments:

line # 15
homozygous viable
Injected into *w*
Location = 2nd

Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P451 *w ;* pUAST Q20 Exon1 #111F1L**

Source : transformation of Exon1 from the HD gene, including 20CAG repeats. Construct from the L.Thompson lab. Leon injected Spring 1999.

Ref:

Comments:

line # 111F1L
homozygous viable
Injected into *w*
Location = 3rd

Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P453 *w ;* pUAST Q20 Exon1 #113**

Source : transformation of Exon1 from the HD gene, including 20CAG repeats.
Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:
line # 113
homozygous viable
Injected into *w*
Location = 2nd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P461 *w ;* pUAST Q50 Exon1 #Y4**

Source : transformation of Exon1 from the HD gene, including 50CAG repeats.
Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:
line # Y4
homozygous viable
Injected into *w*
Location = 3rd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P463 *w* ; pUAST Q93 Exon1 #4F1**

Source : transformation of Exon1 from the HD gene, including 93CAG repeats.
Construct from the L.Thompson lab. Heli injected Summer 1999.
Ref:
Comments:
The plasmid sequence has 104 CAGs!!
line # 4F1
homozygous viable
Injected into *w*
Location = 3$^{rd}$
Insertion at 87A-B
CAAATAAACGCGCAGTG{P}AGAAGAGAACATTTTCC
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P465 *w* ; pUAST Q93 Exon1 #8F1**

Source : transformation of Exon1 from the HD gene, including 93CAG repeats.
Construct from the L.Thompson lab. Heli injected Summer 1999.
Ref:
Comments:
The plasmid sequence has 104 CAGs!!
line # 8F1
homozygous viable
Injected into *w*
Location = 2nd
Eye color = position effect

Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P468 *w* ; pUAST Q93 Exon1 #16F1L**

Source : transformation of Exon1 from the HD gene, including 93CAG repeats.
Construct from the L.Thompson lab. Heli injected Summer 1999.
Ref:
Comments:

The plasmid sequence has 104 CAGs!!
line # 16F1L
homozygous viable but weak
Injected into *w*
Location = 2$^{nd}$
Insertion at 25C
TGGGATCTGGGAGCCGG{P}AGAGCTGGTTGAAGGT
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P490 *w ;* pUAST L22 + myc/flag #46A**

Source : transformation of 22 CTG repeats followed by a myc/flag epitope tag.
Construct from the L.Thompson lab. Leon injected Spring 1999.
Ref:
Comments:

line # 46A
homozygous viable
Injected into *w*
Location = 3rd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P491 *w* pUAST L108 + myc/flag #1**

Source : transformation of 108 CTG repeats followed by a myc/flag epitope tag.
Construct from the L.Thompson lab. Heli injected Winter 1999.
Ref:
Comments: PCR of genomic DNA shows deletion of the construct

line # 1
homozygous viable
Injected into *w*
Location = 1st
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P513 *w ;* pUAST H3/H4 Suppressor of aggregation #14**

Source : Construct from the L.Thompson lab; tagged with myc epitope. Leon injected Spring 1999.
Ref:
Comments:

line # 14
homozygous viable
Injected into *w*
Location = 3rd

Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P516** ***w*** **pUAST H3/H4 Suppressor of aggregation #17**
Source : Construct from the L.Thompson lab; tagged with myc epitope. Leon injected Spring 1999.
Ref:
Comments:
line # 17
homozygous viable
Injected into *w*
Location = 1st
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P518** ***w ;*** **pUAST hCBP #4B**
Source : Construct from the L.Thompson lab. Heli injected Summer 2000.
Ref:
Comments:
line # 4B
homozygous viable
Injected into *w*
Location = 3rd
Made by crossing to B2475 (*w*; T(2;3)*ap*$^{Xa}$/ SM5; TM3)

**P563** ***y w ;*** **{p53-pExP-UAS} line # P 1219 B**
Source: Leslie Thompson from Excelexis
Ref:
Comments: Location = 2$^{nd}$
P53 being driven by uas

**P564** ***w ;*** **UAS-tsg$^{His51}$**
Source: M. O'Connor
Ref:
Comments:
Location = 3$^{rd}$.
Source of transgene to make double transgene stock

**P565** ***w ;*** **UAS-sog$^{HA7}$/(TM3 *Sb*)**
Source: M. O'Connor
Ref:
Comments:
Location = 3$^{rd}$.
Source of transgene to make double transgene stock

**P570** ***w ;*** **UAS-sog$^{HA7}$ tsg$^{His51}$ Chr III**
Source:2001 Judit Pallos
Ref:
Comments:

Comes from a single animal and is isogenic (jan. 2001) for chr II and chr III and is supposed to be the same as what Mike sent in stock # P566. Judit isolated a single chr III and the insert location has been tested by PCR
Referred to as pir10 in Judit's notebook.

**P572** ***w*; P{UAS>cv, w+}** ***Chr2***
Source: 2000 PV
Ref:
Comments:
The Tsg-like gene was cloned into pUAST as a PCR product
Stock #7, line #3/1 in Peter's notebook.
aka UAS>tsg-like

**P573** ***w*; P{UAS>cv, w+}** ***Chr3***
Source:2000 PV
Ref:
Comments:
The Tsg-like gene was cloned into pUAST as a PCR product
Stock #17, line #6/5 in Peter's notebook.
aka UAS>tsg-like

**P594** ***w*; 4XPEtsg$^{His39}$** *Chr2*
Source: M. O'Connor, 04/2001
Ref:
Comments:
4 copies of the Twist promoter in front of the tsg gene. Used for the purification of Tsg protein.

**P596 w, UAS>DppGFP.E(X)** *Chr1*
Source: Steve Cohen 05/2001
Ref:
Comments:

**P597 w; UAS>DppGFP.K(2)** *Chr2*
Source: Steve Cohen 05/2001
Ref:
Comments: CyO may be floating

**P598 w; UAS>DppGFP.L(3)** *Chr3*
Source: Steve Cohen 05/2001
Ref:
Comments: TM3 may be floating
replaced one of the copies with the duplicate, since it was contaminated with w-
Oct29/2002

**P601 UAS-brk / TM3**
Source: Uwe Lammel

Ref:
Comments:
Generated using the GM06062 cDNA from the BDGP

**P660 *y w* ; P[w+; UAS> super GFP|T2-1; pUAST Q93 Exon1 #4F1**
Source: Made from G14 and P463 by N. Slepko
Ref:
Comments:
Chromosome: 2,3

**P661 *w* ; P{w[+mC]=UAS-GFP.nls}14; pUAST Q93 Exon1 #4F1**
Source: Made from BSc #4775 and P463 by N. Slepko
Ref:
Comments:
Chromosome: 2,3
N terminal tagged with 15 amino acid SV40 nls (Accession # AF242362)

**P672 *w*; pUAST wnt10**
Source: Construct from T. Lukacsovich, injected by J. Purcell/C. Pace
Ref:
Comments:
homozygous viable
Chromosome: 2

**P673 *w*; pUAST wnt6 – 33m**
Source: Construct from T. Lukacsovich, injected by J. Purcell/C. Pace
Ref:
Comments:
homozygous viable
Chromosome: 2
HA tagged

**P675 *w* ; ptc-Gal4/(CyO); UAS-sog$^{HA7*}$ tsg$^{His51}$/(TM3)**
Source: Stock P566 (from O'Connor) mutagenized with EMS by P. Vilmos/J. Pallos/ A. Lundberg. (ptc-Gal4 introduced later from stock G33.)
Ref:
Comments:
Location = 3rd
Point mutation in UAS-sog (as determined by A.L.) rescues ptc-induced lethality.
Referred to as "Stock B" in Peter's notebook

**P684 *yw* ; UAS-16Qhtt[F24Y]**
Source : Botas
Ref:
Comments:
homozygous viable
Location = 2nd, SM5 may be floating

Theoretically full length htt with 16Qs – that's what Larry requested but the stock came without description

**P685 y*w* ; GMR/SM5; UAS-M64-128Qhtt**
Source : Botas
Ref:
Comments:
homozygous viable (?)
Location = 3rd, TM6 is floating
Theoretically full length htt with 128Qs – that's what Larry requested but the stock came without description
Flies are not Cy, eyes not rough and eye color wild type

**P686 *w* ; UAS-H6-Flag-SUMO/FM6**
Source : Albert Courey at UCLA
Ref:
Comments:
Drosophila SUMO construct
insert on the X
the label on the vial also said "(A'18b)" – line number??

**P687 *w* ; UAS-H6-Flag-SUMO/CyO**
Source : Albert Courey at UCLA
Ref:
Comments:
Drosophila SUMO construct
insert on the second
the label on the vial also said "(A'11c)" – line number??

**P688 *w* ; UAS-H6-Flag-SUMO/TM3 *Sb***
Source : Albert Courey at UCLA
Ref:
Comments:
Drosophila SUMO construct
insert on the third
the label on the vial also said "(A8b)" – line number??

**P689 *w* ; UAS-mRFP-Htt(548)Q15**
Source : Troy Littleton
Ref: Proc Natl Acad Sci U S A (2004) 101, 3224-9
Comments:
insert on the third
548 amino acid long Htt fragment with 15 glutamines and RFP fused on the N terminus
the vial that arrived was labeled Htt(588)

**P690 *w* ; UAS-mRFP-Htt(548)Q138**
Source : Troy Littleton
Ref: Proc Natl Acad Sci U S A (2004) 101, 3224-9

Comments:
insert on the third
548 amino acid long Htt fragment with 138 glutamines and RFP fused on the N terminus
the vial that arrived was labeled Htt(588)

**P691 *w* ; UAS-eGFP-Htt(548)Q15**
Source : Troy Littleton
Ref: Proc Natl Acad Sci U S A (2004) 101, 3224-9
Comments:
insert on the second
548 amino acid long Htt fragment with 15 glutamines and GFP fused on the N terminus
the vial that arrived was labeled Htt(588)

**P692 *w* ; UAS-eGFP-Htt(548)Q138**
Source : Troy Littleton
Ref: Proc Natl Acad Sci U S A (2004) 101, 3224-9
Comments:
insert location unknown
insert on the third per J.P.
548 amino acid long Htt fragment with 138 glutamines and GFP fused on the N terminus
the vial that arrived was labeled Htt(588)
viability with elav on X good, pseudopupil eye phenotype very mild (only a couple of ommatidia with less then 7 rhabdomeres per eye at day 9 and day 17) J.P.

**P693 *w* ; UAS-eGFP-Htt(548)Q138-mRFP**
Source : Troy Littleton
Ref: Proc Natl Acad Sci U S A (2004) 101, 3224-9
Comments:
insert location unknown
insert on third per J.P. Two eye colors found when crossed out to f271.
548 amino acid long Htt fragment with 138 glutamines and GFP fused on the N terminus, RFP on the C terminus
the vial that arrived was labeled Htt(588)
viability with elav on X good, pseudopupil eye phenotype very mild (only a couple of ommatidia with less then 7 rhabdomeres per eye at day 9) J.P.

**P694 *w* ; UAS-exon1Q96-GFP**
Source : Troy Littleton
Ref:
Comments:
insert on the second
first exon of Htt with 96 glutamines and GFP fused on the C terminus

viability with elav on X good, pseudopupil eye phenotype very mild (only a couple of ommatidia with less then 7 rhabdomeres per eye at day 9 and day 17) J.P. Aggregates in discs per NA.

**P696** ***w*** **; UAS-ter-94/CyO**
Source: D. Ruden
Ref: Genes to Cells (2007) 12 , 889; Ruden et al., 2000, Dev. Biol. 218(2): 314--325
Comments:
Ter94 aka Drosophila VCP (valosin-containing protein) = CG2331, is a member of the CDC48p/VCP subfamily of AAA proteins which are involved in homotypic fusion of the endoplasmic reticulum during mitosis
Virginia Kimonis studies this protein (talk title: inclusion body myopathy, Paget disease of Bone and/or Frontotemporal dementia caused by VCP mutations, July 2007)

**P697** ***w;*** **P{UAS-Htt548-Q0}10-2**
Source : Troy Littleton
Ref: Lee et al., PNAS (2004) 101,9:3224-3229
Comments:
548 Htt fragment with 0 glutamines from Hayden
Insert on the 2nd chromosome
line 10-2

**P698** ***w;*** **P{UAS-Htt548-Q128}3-5**
Source : Troy Littleton
Ref: Lee et al., PNAS (2004) 101,9:3224-3229
Comments:
548 Htt fragment with 128 glutamines from Hayden
Insert on the 2nd chromosome
line 3-5

**P700** ***w;*** **P{UAS-Htt588-Q138-RFP}Hi**
Source : Troy Littleton
Ref:
Comments:
588 Htt fragment with 138 glutamines fused to RFP
The fragment length (588) is a guess from Larry's e-mail but the vial sent was labeled "UAS Q138 RFP"
Insert on the 3rd chromosome
This is supposed to express high levels of Htt

**P701** ***w;*** **P{UAS-Htt588-Q138-RFP}Lo**
Source : Troy Littleton
Ref:
Comments:
588 Htt fragment with 138 glutamines fused to RFP
The fragment length (588) is a guess from Larry's e-mail but the vial sent was labeled "UAS Q138 RFP"
Insert on the 3rd chromosome

This is supposed to express low levels of Htt

**P702** ***w;*** **P{UAS-DMKP-3}15; P{UAS-DMKP-3}9/TM6B**
Source: J Chung, jchung@kaist.ac.kr
Ref: Mol Cell Biol. 2004 Jan;24(2):573-83
Comments:
Full length DMKP-3 cloned into a UAS vector
DMKP-3 = Drosophila mitogen-activated protein kinase (MAPK) phosphatase 3
Insert 15 is mild (mild roughness with sev-Gal4), no data on insert 9 in the paper
Chromosome: 2; 3

**P703** ***w;*** **P{UAS-DMKP-3}15/CyO; TM2/TM6B**
Source: J Chung, jchung@kaist.ac.kr
Ref: Mol Cell Biol. 2004 Jan;24(2):573-83
Comments:
Full length DMKP-3 cloned into a UAS vector
DMKP-3 = Drosophila mitogen-activated protein kinase (MAPK) phosphatase 3
Insert 15 is mild (mild roughness with sev-Gal4)
Insert on the 2nd chromosome

**P704** ***w;*** **Bc/Gla; P{UAS-DMKP-3}10**
Source: J Chung, jchung@kaist.ac.kr
Ref: Mol Cell Biol. 2004 Jan;24(2):573-83
Comments:
Full length DMKP-3 cloned into a UAS vector
DMKP-3 = Drosophila mitogen-activated protein kinase (MAPK) phosphatase 3
Insert 10 is strong (very rough eyes with sev-Gal4)
Insert on the 3rd chromosome

**P711 pan-RNAi/TM3**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 25940
Ref:
Comments:
pan (=CG32005) RNAi line
Chromosome: 3, lethal (TM3 balancer is a guess based on Sb)

**P712 CG12717-RNAi**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 17298
Ref:
Comments:
CG17217 RNAi line
CG12717 is a sumo isopeptidase
Chromosome: 2, viable

**P713 CG32110-RNAi**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 34062
Ref:
Comments:
CG32110 RNAi line

CG32110 is a sumo isopeptidase
Chromosome: 3, viable

**P714 CG10107-RNAi/TM3**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 18004
Ref:
Comments:
CG10107 RNAi line
CG10107 is a sumo isopeptidase
Chromosome: 3, lethal (TM3 balancer is a guess based on Sb)

**P715 CG8493-RNAi**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 24110
Ref:
Comments:
CG8493 RNAi line
CG8493 is a sumo isopeptidase
Chromosome: 3, viable

**P716 CG1503-RNAi/TM3**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 32350
Ref:
Comments:
CG1503 RNAi line
CG1503 is a sumo isopeptidase
Chromosome: 3, lethal (TM3 balancer is a guess based on Sb)

**P717 CG12359-RNAi**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 31744
Ref:
Comments:
CG12359 RNAi line
CG12359 is a sumo isopeptidase
Chromosome: 3, viable

**P718 UAS-pan RNAi 32005R-5**
Source: NIG stock center, Japan
Ref: http://www.shigen.nig.ac.jp/fly/nigfly/index.jsp
Comments:
Chromosome 3
CG32005 = CG34403 = pangolin
may have CyO or TM3 Sb Ser floating
Phenotype with Act5c-Gal4 @ 28C: viable (NIG)

**P722 *w;* UAS-PanA**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ S. Woydziak
Ref:
Comments:
Chromosome: 3 (86F)

Homozygous viable
fourth chromosome may still carry the integrase from f351
C-terminal HA tag
severe leg phenotype with Blk-Gal4 at 18°C and lethal at 25°C, severe rough eyes with GMR-Gal4 at 25°C (S. Woydziak)

**P723** ***w;*** **UAS-PanB**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ S. Woydziak
Ref:
Comments:
Chromosome: 3 (86F)
Homozygous viable
fourth chromosome may still carry the integrase from f351
C-terminal HA tag
severe leg phenotype and mild wing phenotype with Blk-Gal4 at 18°C and lethal at 25°C, severe rough eyes with GMR-Gal4 at 25°C (S. Woydziak)

**P724** ***w;*** **UAS-PanC**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ S. Woydziak
Ref:
Comments:
Chromosome: 3 (86F)
Homozygous viable
fourth chromosome may still carry the integrase from f351
C-terminal HA tag
no visible phenotype with Blk-Gal4 at 25°C, no visible phenotype with Ptc-Gal4 at 25°C (S. Woydziak)

**P725** ***w;*** **UAS-PanDA**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ S. Woydziak
Ref:
Comments:
Chromosome: 3 (86F)
Homozygous viable
fourth chromosome may still carry the integrase from f351
C-terminal HA tag
severe leg phenotype with Blk-Gal4 at 25°C, severe leg phenotype with Ptc-Gal4 at 25°C (S. Woydziak)

**P726** ***w;*** **UAS-PanDB**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ S. Woydziak
Ref:
Comments:
Chromosome: 3 (86F)
Homozygous viable
fourth chromosome may still carry the integrase from f351
C-terminal HA tag

no visible phenotype with Blk-Gal4 at 25°C, no visible phenotype with Ptc-Gal4 at 25°C (S. Woydziak)

**P727** ***w;*** **UAS-PanIA**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ S. Woydziak
Ref:
Comments:
Chromosome: 3 (86F)
Homozygous viable
fourth chromosome may still carry the integrase from f351
C-terminal HA tag
no visible phenotype with Blk-Gal4 at 25°C, no visible phenotype with Ptc-Gal4 at 25°C (S. Woydziak)

**P728** ***w;*** **UAS-PanIB**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ S. Woydziak
Ref:
Comments:
Chromosome: 3 (86F)
Homozygous viable
fourth chromosome may still carry the integrase from f351
C-terminal HA tag
severe leg phenotype with Blk-Gal4 at 25°C, severe leg phenotype with Ptc-Gal4 at 25°C (S. Woydziak)

**P729 dPKC-RNAi/TM3**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 27696
Ref:
Comments:
dPKC, PKC 53E (=CG6622) RNAi line
dPKC53E(brain) (Rosenthal, 1987) among Drosophila genes is most similar to the classical genes (PKCalpha, beta and gamma). The third PKC protein, dPKC53E(eye) is a photoreceptor cell-specific PKC, and lies on the second chromosome within 50 kb of dPKC53E(brain) (Schaeffer, 1989) – I don't know if this is brain or eye (C. Aiken)
Chromosome: 3, sterile (TM3 balancer?)
Entered by C. Aiken

**P730 dPKC-RNAi**
Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 27699
Ref:
Comments:
dPKC, PKC 53E (=CG6622) RNAi line
should be most similar to PKC delta
Chromosome: 2, viable
Entered by C. Aiken

**P731 dPKC98F-RNAi/TM3**

Source: VDRC, Vienna Drosophila RNAi Center, Transformant ID: 33434
Ref:
Comments:
dPKC98F, PKC d98F, PKC-brain, Protein C kinase 98E (=CG1954) RNAi line
The 98F sequence contains a 634 amino acid open reading frame with homology to mammalian PKCs. However, the 98F sequence diverges from "classical" mammalian PKC genes in a region near the amino terminus. The more recently identified mammalian PKC-related genes (PKCdelta, epsilon and eta) also diverge in this domain. The 98F gene has greater amino acid identity with, and a domain arrangement characteristic of PKCdelta (also termed nPKC)
Chromosome: 3, sterile (TM3 balancer?)
Entered by: C. Aiken

**P732 w; UAS-DCR/CyO**

Source: Tamas got it from the Benzer lab
Ref:
Comments:
UAS-dicer construct to enhance RNAi effects
line originally from Vienna; might or might not be the same as those available from Bloomington

**P746 w; pUAST-SCA2-Q117[8B]**

Source: cloned by Tamas Lukacsovich; injected by Aditi Iyengar and Yati Bakrania
Ref:
Comments:
full-length human ataxin-2 protein with Q117
background: ‘cs isogenic’
Chromosome: 2

**P747 w; pUAST-SCA2-Q117[9A]**

Source: cloned by Tamas Lukacsovich; injected by Aditi Iyengar and Yati Bakrania
Ref:
Comments:
full-length human ataxin-2 protein with Q117
background: ‘cs isogenic’
Chromosome: 3

**P751 w; pUAST-SCA6-shortQ[3]**

Source: cloned by Tamas Lukacsovich, injected by Aditi Iyengar and Laszlo Bodai
Ref:
Comments:
N-terminal truncated human CACNA1A protein with short polyQ, truncated in the same position as the Q117 versions; translation starts at ~1960 amino acids of CACNA1A with ‘KIYAAM’
The polyQ repeat (of the native gene) is at the C terminal (J.L.M.)

background: ‘cs isogenic’
Chromosome: 2

**P755 w; pUAST-SCA6-Q117[3C]**
Source: cloned by Tamas Lukacsovich, injected by Aditi Iyengar and Yati Bakrania
Ref:
Comments:
N-terminal truncated human CACNA1A protein with Q117; translation starts at ~1960 amino acids of CACNA1A with ‘KIYAAM’
The polyQ repeat (of the native gene) is at the C terminal (J.L.M.)
Patients do not have more than 42Qs and no aggregates have been found in patients (J.L.M.)
background: ‘w’
Chromosome: 3

**P757 w; pUAST-SCA6-Q117[6K]**
Source: cloned by Tamas Lukacsovich, injected by Aditi Iyengar and Yati Bakrania
Ref:
Comments:
N-terminal truncated human CACNA1A protein with Q117; translation starts at ~1960 amino acids of CACNA1A with ‘KIYAAM’
The polyQ repeat (of the native gene) is at the C terminal (J.L.M.)
Patients do not have more than 42Qs and no aggregates have been found in patients (J.L.M.)
background: ‘w’
Chromosome: 2
Has a strong phenotype (J.L.M. based on data from K. Menhaji)

**P758 w; pUAST-SCA6-Q117[14B]**
Source: cloned by Tamas Lukacsovich, injected by Aditi Iyengar and Yati Bakrania
Ref:
Comments:
N-terminal truncated human CACNA1A protein with Q117; translation starts at ~1960 amino acids of CACNA1A with ‘KIYAAM’
The polyQ repeat (of the native gene) is at the C terminal (J.L.M.)
Patients do not have more than 42Qs and no aggregates have been found in patients (J.L.M.)
background: ‘w’
Chromosome: 3
Has a mild phenotype (J.L.M. based on data from K. Menhaji)

**P761 w; pUAST-SCA6-Q117[28B]**
Source: cloned by Tamas Lukacsovich, injected by Aditi Iyengar and Yati Bakrania
Ref:
Comments:

N-terminal truncated human CACNA1A protein with Q117; translation starts at ~1960 amino acids of CACNA1A with 'KIYAAM'
The polyQ repeat (of the native gene) is at the C terminal (J.L.M.)
Patients do not have more than 42Qs and no aggregates have been found in patients (J.L.M.)
background: 'w'
Chromosome: 3

**P763 w; pUAST-SCA17-Q117[18]**
Source: cloned by Tamas Lukacsovich, injected by Yati Bakrania and Laszlo Bodai
Ref:
Comments:
full-length human TBP protein with expanded Q (Q117)
background: 'w'
Chromosome: 2

**P766 w; pUAST-DRPLA-Q117[9]**
Source: cloned by Tamas Lukacsovich, injected by Yati Bakrania and Laszlo Bodai
Ref:
Comments:
full-length human atrophin-1 protein with Q117
background: 'cs'
Chromosome: 2

**P767 w; pUAST-SCA2[3]/CyO**
Source: cloned by Tamas Lukacsovich
Ref:
Comments:
Chromosome: 1; 2
Expresses non-expanded, truncated human ataxin-2
viable

**P768 w; pUAST-SCA6[1]**
Source: cloned by Tamas Lukacsovich
Ref:
Comments:
Chromosome: 1; 2
Expresses human, non-expanded, truncated CACNA1A

**P769 w; pUAST-SCA17[1]**
Source: cloned by Tamas Lukacsovich
Ref:
Comments:
Chromosome: 1; 2
Expresses non-expanded, full-length human TBP

**P770 w; pUAST-TBP-Q8[3]/CyO**
Source: cloned by Tamas Lukacsovich

Ref:
Comments:
Chromosome: 1; 2
Expresses non-expanded, full-length Drosophila TBP

**P771 w; pUAST-TBP-Q116[1]**
Source: cloned by Tamas Lukacsovich
Ref:
Comments:
Chromosome: 1; 3
CyO floating in stock
Expresses expanded, full-length Drosophila TBP

**P772 w; pUAST-TBP-Q116[2]**
Source: cloned by Tamas Lukacsovich
Ref:
Comments:
Chromosome: 1; 2
Expresses expanded, full-length Drosophila TBP

**P773 w pUAST-DRPLA[1]**
Source: cloned by Tamas Lukacsovich
Ref:
Comments:
Chromosome: 1
Expresses human, non-expanded, truncated atrophin-1

**P774 w; pUAST-EGFP[2A] 117Q**
Source: cloned by Tamas Lukacsovich
Ref:
Comments:
Chromosome: 1; 2
EGFP with a long polyQ stretch inserted in the middle
Per Tamas EGFP is codon optimized for human (but works in fly) and has the S65 mutation, The Daisuke lines just have the S65. The DNA sequences are quite different and the proteins are similar but exact aa sequence should be recorded.

**P775 w; pUAST- Pcaf[7]**
Source: cloned and injected by Laszlo Bodai
Ref:
Comments:
Chromosome: 1; 3
Expresses full-length Pcaf cDNA (from DGRC clone GH11602).
Cloning: GH11602-pOT2 was digested with EcoRI (5' site in pOT2 mcs, 3'site in 3'UTR @ 2611 bp) and ligated into EcoRI digested, dephosphorilated pUAST. GH11602-pUAST minipreps were test digested with XhoI and clones having the insert (5'-3') orientation selected.

**P776 w; pUAST- chm[3]**
Source: cloned and injected by Laszlo Bodai
Ref:
Comments:
Chromosome: 1; 3
Expresses full-length chameau cDNA (from DGRC clone LD08307).
Cloning: chm fragment generated by PCR using Bgl II-chm-FW and M13-Rev primers on LD08307-pBS(SK) template. The fragment was digested with Bgl II ($2^{nd}$ site in 3' UTR) and ligated to Bgl II digested pUAST. Orientation tested with Pst I digestion.

**P777 w; pUAST- mof[2]/TM3**
Source: cloned and injected by Laszlo Bodai
Ref:
Comments:
Chromosome: 1; 3
Expresses full-length *males on the first* cDNA (from DGRC clone LD24203)
lethal
Cloning: LD24203-pOT2 was EcoRI-XhoI digested (both sites in the pOT2 mcs) and ligated into EcoRI-XhoI digested pUAST.

**P778 w; pUAST- CG14222[7]/TM3**
Source: cloned and injected by Laszlo Bodai
Ref:
Comments:
Chromosome: 1; 3
Expresses full-length CG14222 cDNA (from DGRC clone LD30731)
Viable, sterile
Cloning: LD30731-pOT2 was digested with EcoRI (5' site in pOT2 mcs, 3'site in 3'UTR @ 675 bp) and ligated into EcoRI digested, dephosphorilated pUAST. LD30731-pUAST clones were tested for insert orientation by PCR using CG14222-Rev and UAS-Fw primers.

**P779 w; pUAST- dTip60[6]**
Source: cloned and injected by Laszlo Bodai
Ref:
Comments:
Chromosome: 1; 3
Expresses full-length dTip60 cDNA (from DGRC clone 31064)
Cloning: LD31064-pOT2 was EcoRI-XhoI digested (both sites in the pOT2 mcs) and ligated into EcoRI-XhoI digested pUAST.

**P780 *(y)w;* UAS-Pan A/CyO [3D 29B]**
Source: HT, TL
Ref:
Comments:
Pan A generated by deleting Pan B (using Flp) from Pan AB transgene line #29B
Chromosome: 2

Transgene is w-
Pan B alone gives strong phenotype – line 29B stronger than 24B, PanA alone very weak. All jumps were identical (4 tested)
From transgenic line 29B; jump #3D

**P781** ***(y)w;*** **UAS-Pan B/CyO [5D 29B]**
Source: HT, TL
Ref:
Comments:
Pan B generated by deleting Pan A (using Cre) from Pan AB transgene line #29B
Chromosome: 2
Transgene is w-
From transgenic line 29B; jump #5D

**P782** ***(y)w;*** **UAS-Pan A/CyO [7A 24B]**
Source: HT, TL
Ref:
Comments:
Pan A generated by deleting Pan B (using Flp) from Pan AB transgene line #24B
Chromosome: 2
Transgene is w-
Pan B alone gives strong phenotype, A alone very weak. All jumps were identical (4 tested)
From transgenic line 24B; jump #7A

**P783** ***(y)w;*** **UAS-Pan B/CyO [8E 24B]**
Source: HT, TL
Ref:
Comments:
Pan B generated by deleting Pan A (using Cre) from Pan AB transgene line #24B
Chromosome: 2
Transgene is w-
Pan B alone gives strong phenotype – line 29 stronger than 24, A alone very weak. All jumps were identical (4 tested)
From transgenic line 24B; jump #8E

**P784** ***+; notum>LacZ/ SM5-TM6***
Source: Tamas got from Jennifer Kennell jkennell@umich.edu in in the Cadigan lab (2 Jan, 2008)
Ref: Originally in 2007 unpublished originating from Basler lab
Comments:
How are the 2 balancers maintained?
This is a fusion of part of the notum promoter fused to LacZ. It supposedly shows all wg expression patterns. Sarah W stained embryos and it shows wg pattern. Information from an e-mail sent to Tamas: "The Tcf reporter plasmid has 12 copies of a consensus TCF binding site with a minimal promoter driving luciferase. It works well in Kc167 cells and it should work in S2 cells as well. We generated transgenic flies that drive lacZ using an enhancer the Basler lab

identified upstream of Notum (a universal responder to Wg signaling). The pattern reflects areas of Wg signaling throughout development (embryo as well as imaginal discs)"

**P785 DEP line driving MEKK1 (10 1799)**
Source: Tamas got from Istvan Kiss
Ref:
Comments:
DEP = double EP
See macVector file 1799 (Mekk1) from Tamas for details of the insert and location.
General activator of the jnk pathway
Strongly suppresses p53 apoptosis

**P786 *w;* UAS-CG31738-AF.4**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ M. Pomeroy
Ref:
Comments:
Isoform A of CG31738 which is the Drosophila homolog of fibronectin type III domain containing protein
CG31738 has been re-annotated by Flybase and is currently listed as CG42389 (Jan.2009), isoform A is now listed as 42389-PG.
Chromosome: 3 (86Fb)
Line number AF.4
Homozygous viable
Fourth chromosome may still carry the integrase from f351
No visible phenotype with actin-Gal4 or elav-Gal4 (M. Pomeroy)

**P787 *w;* UAS-CG31738-BM.1**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ M. Pomeroy
Ref:
Comments:
Isoform B of CG31738 which is the Drosophila homolog of the fibronectin type III domain containing protein family; due to a frameshift mutation, this translates into a truncated protein.
Note that CG31738 has been re-annotated by Flybase and is currently listed as CG42389 (Jan.2009), isoform B is now listed as 42389-PF.
Chromosome: 3 (86Fb)
Line number BM.1
Homozygous viable
Fourth chromosome may still carry the integrase from f351
No visible phenotype with actin-Gal4 or elav-Gal4 (M. Pomeroy)

**P788 *w;* UAS-Httex1p97QT3A(5)**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:
Comments:
Line#: T3A5

Chromosome: 3 (86F)
Homozygous viable
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, and a A to G (ACC to GCC) mutation in the 3rd codon which changes the 3rd amino acid in the protein sequence from T to A.
Driving expression with *elav*>Gal4 at 25 ˚C generates measurable Htt protein and transcript expression in fly heads (determined by Western blot, C. Aiken and qRT-PCR, C. Aiken and J. Pallos)
Phenotype: Driving protein expression with *elav*>Gal4 at 25 ˚C results in reduced viability (eclosion) and photoreceptor neurodegeneration (measured by pseudopupil analysis) at 4, 7, and 11 days, but the degeneration is more mild than that observed with flies expressing site-directed Httex1p97Q (e) (generated by K. Menhaji and J. Purcell). See Aiken et al., 2009

**P789** ***w;*** **UAS-Httex1p97QT3A(9)**

Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:
Comments:
Line#: T3A 9
Chromosome: 3 (86F)
Homozygous viable
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, and a A to G (ACC to GCC) mutation in the 3rd codon which changes the 3rd amino acid in the protein sequence from T to A.
Driving expression with *elav*>Gal4 at 25 ˚C generates measurable Htt protein and transcript expression in fly heads (determined by Western blot, C. Aiken and qRT-PCR, C. Aiken and J. Pallos)
Phenotype: Driving protein expression with *elav*>Gal4 25 ˚C results in reduced viability (eclosion) and photoreceptor neurodegeneration (measured by pseudopupil analysis) at 7days at that is comparable to that observed with T3A line 5. (C. Aiken)

**P790** ***w;*** **UAS-Httex1p97QT3D(1)**

Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:
Comments:
Line#: T3D1
Chromosome: 3 (86F)
Homozygous viable
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, with a the following 3rd codon mutaton: ACC to GAC which changes the 3rd amino acid in the protein sequence from T to D.

Driving expression with *elav*>Gal4 at 25 ˚C generates measurable Htt protein and transcript expression in fly heads (determined by Western blot, C. Aiken and qRT-PCR, J. Pallos)
Phenotype: Driving protein expression with *elav*>Gal4 at 25 ˚C results in reduced viability (eclosion) and photoreceptor neurodegeneration (measured by pseudopupil analysis) at 4, 7, and 11 days, but the degeneration is more mild than that observed with flies expressing site-directed Httex1p97Q (e) (generated by K. Menhaji and J. Purcell). See Aiken et al., 2009

**P791** ***w;*** **UAS-Httex1p97QT3D(12)**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:
Comments:
Line#: T3D12
Chromosome: 3 (86F)
Homozygous viable
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, with a the following 3rd codon mutaton: ACC to GAC which changes the 3rd amino acid in the protein sequence from T to D.
Driving expression with *elav*>Gal4 at 25 ˚C generates measurable Htt protein and transcript expression in fly heads (determined by Western blot, C. Aiken and qRT-PCR, J. Pallos)
Phenotype: Driving protein expression with *elav*>Gal4 results in reduced viability (eclosion) and photoreceptor neurodegeneration (measured by pseudopupil analysis) at 7days at 25 ˚C that is comparable to that observed with T3D line 1. (C. Aiken)

**P792** ***w;*** **UAS-Httex1p97QT3V(1)**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:
Comments:
Line#:T3V1
Chromosome: 3 (86F)
Homozygous viable
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, and a mutation in the 3rd codon which changes the 3rd amino acid in the protein sequence from T to V.
Driving expression with *elav*>Gal4 at 25 ˚C generates measurable Htt transcript expression in fly heads (determined by qRT-PCR, J. Pallos)
Phenotype: Driving protein expression with *elav*>Gal4 results in normal viability (eclosion) and no photoreceptor neurodegeneration (measured by pseudopupil analysis) at 25 ˚C (C. Aiken)

**P793** ***w;*** **UAS-Httex1p97QT3V(42)**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:

Comments:
Line#:T3V42
Chromosome: 3 (86F)
Homozygous viable
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, and a mutation in the 3rd codon which changes the 3rd amino acid in the protein sequence from T to V.
Phenotype: Driving protein expression with *elav*>Gal4 results in normal viability (eclosion) and no photoreceptor neurodegeneration (measured by pseudopupil analysis) at 25 ˚C (C. Aiken)

**P794** ***w;*** **UAS-Httex1p97QT3E(5)/(TM6)**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:
Comments:
Line#:T3E5
Chromosome: 3 (86F)
Homozygous viable (TM6 might be floating)
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, and a mutation in the 3rd codon which changes the 3rd amino acid in the protein sequence from T to E.
Phenotype: Driving protein expression with *elav*>Gal4 results in mild photoreceptor neurodegeneration (measured by pseudopupil analysis) at 25 ˚C (C. Aiken)

**P795** ***w;*** **UAS-Httex1p97QT3E(6)/(TM3)**
Source: construct from T. Lukacsovich, injected into f351 by J. Purcell/ C. Aiken
Ref:
Comments:
Line#:T3E6
Chromosome: 3 (86F)
Homozygous viable (TM3 might be floating)
Fourth chromosome may still carry the integrase from f351
Expresses the Httex1p transgene with 97Q, and a mutation in the 3rd codon which changes the 3rd amino acid in the protein sequence from T to E.
Phenotype: Driving protein expression with *elav*>Gal4 results n mild photoreceptor neurodegeneration (measured by pseudopupil analysis) at 25 ˚C (C. Aiken)

**P796** ***w*****; UAS-C4 sFv; pUAST Q93 Exon1 #4F1 (P463)**
Source: Julie A. McLear (Anne Messer's lab), Utica College, Utica, NY; received - August 2009
Ref: PNAS (2005), vol. 102 no. 32, 11563–11568
Comments:
The anti-HD C4 single chain Fv intrabody binds to an epitope formed by the N-terminal 17 amino acids of htt and has been shown to suppress Huntington's disease pathology in Drosophila

UAS-C4 insert on 2nd chromosome (P463 on 3rd).

**P797 w; Wt Syn/CyO ; UAS-D10 $^{16.2}$/TM2**
Source: Julie A. McLear (Anne Messer's lab), Utica College, Utica, NY; received - August 2009
Ref: PNAS (2005), vol. 102 no. 32, 11563–11568
Comments:
The anti-synuclein D10 single chain Fv intrabody was used as a negative control for the experiments done with anti-HD C4 sFv
UAS insert on 3rd chromosome

## PM stocks = Postranslational modification project

**PM6 *w*; pUAST 97QP Exon1 # 13**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa
showed degeneration
Injected into *w*
Location = III

**PM8 *w;* pUAST 97QP Exon1 # 20**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa
showed degeneration
Injected into *w*
Location = II

**PM12 *w;* pUAST 97QP Exon1 # 30**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa
Showed degeneration
Injected into *w*
Location = III
This is the line Namita always used for experiments

**PM14 *w;* pUAST 97QP Exon1 # 32**
Source : Namita Agrawal
Comments:

transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa
Injected into *w*
Location = III
This line did not survive with elav Gal4 on X at 25°C. PP was done on these flies by raising them at room temperature. Results from this line were published in SUMO Science paper.

**PM19 *w;* pUAST 97QP Exon1 # 43**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa
strong degeneration (an average of 4.28)
Injected into *w*
Location = II

**PM28 *w;* pUAST 97QP Exon1 # 8**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 2 aa (only VL*)
strong degeneration (an average of 4.62)
Injected into *w*
Location = II

**PM33 *w;* pUAST 97QP Exon1 # 17**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 2 aa (only VL*)
showed degeneration
Injected into *w*
Location = II
This is the line Namita always used for experiments.

**PM40 *w;* pUAST Exon1 97QP K6R # 6**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 6 of Exon1 is mutated to R (arginine)
showed degeneration
Injected into *w*
Location = II

**PM41 *w;* pUAST Exon1 97QP K6R # 7**
Source : Namita Agrawal
Comments:

transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 6 of Exon1 is mutated to R (arginine)
showed degeneration
Injected into *w*
Location = III

**PM43 *w;* pUAST Exon1 97QP K6R # 9**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 6 of Exon1 is mutated to R (arginine)
showed degeneration
Injected into *w*
Location = ?

**PM46 *w;* pUAST Exon1 97QP K9R # 17a**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 9 of Exon1 is mutated to R (arginine). Subline of 17
showed degeneration
Injected into *w*
Location = II

**PM48 *w;* pUAST Exon1 97QP K9R # 29**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 9 of Exon1 is mutated to R (arginine)
showed degeneration
Injected into *w*
Location = II

**PM49 *w;* pUAST Exon1 97QP K15R # 1**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 15 of Exon1 is mutated to R (arginine)
Injected into *w*
Location = III

**PM50 *w;* pUAST Exon1 97QP K15R # 2**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 15 of Exon1 is mutated to R (arginine)
Injected into *w*
Location = II

**PM51 *w;* pUAST Exon1 97QP K15R # 4**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 15 of Exon1 is mutated to R (arginine)
showed degeneration
Injected into *w*
Location = II

**PM53 *w;* pUAST Exon1 97QP K15R # 9**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 15 of Exon1 is mutated to R (arginine)
Injected into *w*
Location = ?

**PM56 *w;* pUAST Exon1 97QP K6, 9R # 1**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 6 and 9 of Exon1 are mutated to R (arginine)
showed degeneration
Injected into *w*
Location = III

**PM58 *w;* pUAST Exon1 97QP K6, 9R # 3**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 6 and 9 of Exon1 are mutated to R (arginine)
Injected into *w*
Location = II

**PM59 *w;* pUAST Exon1 97QP K6, 9R # 4**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 6 and 9 of Exon1 are mutated to R (arginine)
showed degeneration
Injected into *w*
Location = III

**PM61 *w;* pUAST Exon1 97QP K6, 9R # 6**
Source : Namita Agrawal
Comments:

transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, lysine 6 and 9 of Exon1 are mutated to R (arginine)
showed degeneration
Injected into *w*
Location = III

**PM63 *w;* pUAST Exon1 97QP 3KR # 14**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, all the three lysines of Exon1 are mutated to R (arginine)
showed degeneration
Injected into *w*
Location = II

**PM64 *w;* pUAST Exon1 97QP 3KR # 18a**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, all the three lysines of Exon1 are mutated to R (arginine)
Injected into *w*
Location = II

**PM69 *w;* pUAST Exon1 97QP 3KQ # 3**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, all the three K (lysines) are mutated to Q (glutamine) to mimic acetylation
showed degeneration
Injected into cs-*w*
Location = III

**PM73 *w;* pUAST Exon1 97QP 3KQ # 9**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, all the three K (lysines) are mutated to Q (glutamine) to mimic acetylation
died as pupae
Injected into cs-*w*
Location = II

**PM76 *w;* pUAST Exon1 97QP 3KQ # 12**
Source : Namita Agrawal
Comments:

transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, all the three K (lysines) are mutated to Q (glutamine) to mimic acetylation
showed degeneration
Injected into cs-*w*
Location = II

**PM79 *w;* pUAST Exon1 97QP 3KQ # 15**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, all the three K (lysines) are mutated to Q (glutamine) to mimic acetylation
died as pupae
Injected into cs-*w*
Location = II

**PM83 *w;* pUAST Exon1 97QP 3KQ # 20**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, all the three K (lysines) are mutated to Q (glutamine) to mimic acetylation
died as pupae
Injected into cs-*w*
Location = III

**PM86 *w;* pUAST Exon1 97QP S13A # 1**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, Serine13 of Exon1 is mutated to A (alanine)
showed degeneration
Injected into *w*
Location = II

**PM87 *w;* pUAST Exon1 97QP S13A # 2**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, Serine13 of Exon1 is mutated to A (alanine)
showed degeneration
Injected into *w*
Location = III

**PM103 *w;* pUAST Exon1 97QP S16A # 25**
Source : Namita Agrawal
Comments:

transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, Serine16 of Exon1 is mutated to A (alanine)
showed degeneration
Injected into *w*
Location = II

**PM106** ***w;* pUAST Exon1 97QP S16A # 41**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa, Serine16 of Exon1 is mutated to A (alanine)
showed degeneration
Injected into *w*
Location = III

**PM110** ***w;* pUAST Exon1 97QP S13, 16A # 2**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa. Both Serines 13 and 16 of Exon1 are mutated to A (alanine)
showed degeneration
Injected into *w*
Location = III

**PM111** ***w;* pUAST Exon1 97QP S13, 16A # 4**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa. Both Serines 13 and 16 of Exon1 are mutated to A (alanine)
showed degeneration
Injected into *w*
Location = II

**PM121** ***w;* pUAST Exon1 97QP 3KR S16A # 1**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa. All 3 lysines are mutated to R (arginine) and Serine16 of Exon1 are mutated to A (alanine)
all 7, no phenotype
Injected into cs-*w*
Location = II

**PM124** ***w;* pUAST Exon1 97QP 3KR S16A # 4**
Source : Namita Agrawal
Comments:

transformation of Exon1 from the HD gene, including 97CAG repeats and has extra 14 aa. All 3 lysines are mutated to R (arginine) and Serine16 of Exon1 is mutated to A (alanine)
all 7, no phenotype
Injected into cs-*w*
Location = III

**PM137 *w;* pUAST Exon1 97QP S13D # 1**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). Serine13 of Exon1 is mutated to D (aspartic acid)
showed degeneration
Injected into *w*
Location = III

**PM139 *w;* pUAST Exon1 97QP S13D # 3**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). Serine13 of Exon1 is mutated to D (aspartic acid)
died as larvae/pupae
Injected into *w*
Location = II

**PM145 *w;* pUAST Exon1 97QP S16D # 3 S16A!!!**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). Serine16 of Exon1 is mutated to D (aspartic acid)
died as larvae/pupae
Injected into *w*
Location = II
Tamas checked by PCR and this turns out to be S16A (October 2009)

**PM146 *w;* pUAST Exon1 97QP S16D # 4**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). Serine16 of Exon1 is mutated to D (aspartic acid)
died as larvae/pupae
Injected into *w*
Location = III
This line is still S16D (PCR by Tamas October 2009), unlike PM145 (line 3)

**PM151 *w;* pUAST Exon1 97QP S13, 16D # 3**
Source : Namita Agrawal

Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). Both Serine 13 and 16 of Exon1 is mutated to D (aspartic acid)
showed degeneration
Injected into *w*
Location = II

**PM156** ***w;* pUAST Exon1 97QP S13, 16D # 10**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). Both Serine 13 and 16 of Exon1 is mutated to D (aspartic acid)
died as larvae/pupae
Injected into *w*
Location = II

**PM159** ***w;* pUAST Exon1 25QP S13, 16D # 2**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 25CAG repeats and has 2 extra aa (VL*). Both Serine 13 and 16 of Exon1 is mutated to D (aspartic acid)
all 7, no degeneration
Injected into cs-*w*
Location = III

**PM160** ***w;* pUAST Exon1 25QP S13, 16D # 5**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 25CAG repeats and has 2 extra aa (VL*). Both Serine 13 and 16 of Exon1 is mutated to D (aspartic acid)
all 7, no degeneration
Injected into cs-*w*
Location = II

**PM169** ***w;* pUAST Exon1 97QP 3KR S16D # 1**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). All 3 lysines are mutated to R (arginine) and Serine 16 of Exon1 is mutated to D (aspartic acid)
showed degeneration
Injected into *w*
Location = III

**PM172** ***w;* pUAST Exon1 97QP 3KR S16D # 4**
Source : Namita Agrawal
Comments:

transformation of Exon1 from the HD gene, including 97CAG repeats and has 2 extra aa (VL*). All 3 lysines are mutated to R (arginine) and Serine 16 of Exon1 is mutated to D (aspartic acid)
showed degeneration
Injected into *w*
Location = II

**PM175** ***w;* pUAST His-Exon1 97QP # 2**
Source : Namita Agrawal
Comments:
transformation of Exon1 from the HD gene, including 97CAG repeats and has His tag on N terminus.
all 7, no degeneration
Injected into *w*
Location = II

**PM180** ***w;* pUAST CG12717 # 1**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM181** ***w;* pUAST CG12717 # 2**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM182** ***w;* pUAST CG12717 # 3**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM183** ***w;* pUAST CG12717 # 4**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM184** ***w;* pUAST CG12717 # 5**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*

Location = III

**PM185** ***w;*** **pUAST CG12717 # 6**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM186** ***w;*** **pUAST CG12717 # 7**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM187** ***w;*** **pUAST CG12717 # 8**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM188** ***w;*** **pUAST CG12717 # 9**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = ?

**PM189** ***w;*** **pUAST CG12717 # 10**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM190** ***w;*** **pUAST CG1503 # 2**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM191** ***w;*** **pUAST CG1503 # 12**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463, mild rescue, statistically not significant
injected into *w*

Location = III

**PM192** ***w;* pUAST CG1503 # 17**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM193** ***w;* pUAST CG1503 # 39**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463, mild rescue, statistically not significant
injected into *w*
Location = III

**PM194** ***w;* pUAST CG1503 # 49**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463, mild rescue, statistically not significant
injected into *w*
Location = II

**PM195** ***w;* pUAST CG1503 # 55**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463, mild rescue, statistically not significant
injected into *w*
Location = III

**PM196** ***w;* pUAST CG1503 # 60**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM197** ***w;* pUAST CG1503 # 66**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM198** ***w;* pUAST CG11023 # 2**
Source : Namita Agrawal
Comments:

Isopeptidase overexpression construct.
injected into *w*
Location = I

**PM199** ***w;* pUAST CG11023 # 3**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM200** ***w;* pUAST CG11023 # 4**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav;P463 makes phenotype worse

injected into *w*
Location = II

**PM201** ***w;* pUAST CG11023 # 7**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM202** ***w;* pUAST CG11023 # 10**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM203** ***w;* pUAST CG11023 # 37**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM204** ***w;* pUAST CG11023 # 44**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM205** ***w;* pUAST CG11023 # 50**
Source : Namita Agrawal

Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM206** ***w;* pUAST CG32110 # 18**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM207** ***w;* pUAST CG32110 # 25**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463
injected into *w*
Location = II ?

**PM208** ***w;* pUAST CG32110 # 40**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463, rescued
injected into *w*
Location = III

**PM209** ***w;* pUAST CG8493 # 1**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM210** ***w;* pUAST CG8493 # 2**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM211** ***w;* pUAST CG8493 # 4**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = ?

**PM212** ***w;*** **pUAST CG8493 # 18**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM213** ***w;*** **pUAST CG8493 # 25**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM215** ***w;*** **pUAST CG8493 # 47**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = II

**PM216** ***w;*** **pUAST CG8493 # 54**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463, significant rescue
injected into *w*
Location = II

**PM217** ***w;*** **pUAST CG8493 # 61**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
injected into *w*
Location = III

**PM218** ***w;*** **pUAST CG8493 # 62**
Source : Namita Agrawal
Comments:
Isopeptidase overexpression construct.
tested with elav>P463
injected into *w*
Location = III

**PM235** ***w;*** **pUAST SUMO-1 ΔG # 1**
Source : Namita Agrawal
Comments:
The plasmid was made by Joan. Last 4 amino acids at the C terminus are missing and construct works as activated SUMO (according to Tamas)

Normal Sumo sequence ends with GGHSTV, this one is GAMA (sequenced by Tamas), therefore cannot be activated (04/2008, JP).
injected into *w*
Location = ?

## Stock center stocks

**B-#5879 Df(2R)BSC3, w[+mC] unch[k15501] cn[1] bw[1] sp[1]/SM6a, bw[k1]**
Source : Bloomington Drosophila Stock Center
Comments:
Deleted segment: 48E12--49B6
deletes CG8493 (in 48F10), a SUMO peptidase

**B-#6130 Df(2L)PM4/SM6a**
Source : Bloomington Drosophila Stock Center
Comments:
Deleted segment: 21A1--21B1
deletes CG11023 (in 21A5), a SUMO peptidase

**B-#6232 In(1)w[m4h]; Su(var)2-1[1]/In(2L)t, In(2R)Cy, Cy[1] amos[Roi-1] pr [1] cn[1]**
Source: Bloomington, donor: Umea Stock Center
Ref:
Comments:

**B-#6456 Df(3L)BSC10, rho[ve-1] e[1]/TM3, Ser[1]**
Source : Bloomington Drosophila Stock Center
Comments:
Deleted segment: 69D4--69F7
deletes CG32110 (in 69E4), a SUMO peptidase

**B-#6659 y[*] w[*]; P{w[+mC]=UAS-2xEYFP}AH2**
Source: Bloomington, donor: Alan Michelson
Ref:
Comments:
Chromosome: 2 (58D8)

**B-#6660 y[*] w[*]; P{w[+mC]=UAS-2xEYFP}AH3**
Source: Bloomington, donor: Alan Michelson
Ref:
Comments:
Chromosome: 3 (68C)

**B-#6661 y[*] w[*] P{w[+mC]=UAS-2xEYFP}AX**
Source: Bloomington, donor: Alan Michelson
Ref:
Comments:

Chromosome: 1 (10B)

**B-#7064 w[*]; P{w[+mC]=UAS-ECFP-beta-actin}2**
Source: Bloomington, donor: Andrea Brand
Ref:
Comments:
Expresses CFP-tagged human cytoplasmic beta-actin
Chromosome: 2

**B-#7118 w[1118]; P{w[+mC]=UAS-myr-mRFP}1**
Source: Bloomington, donor: Henry Chang
Ref:
Comments:
P{UAS-myr-mRFP} expresses membrane-targeted monomeric RFP
Chromosome: 2

**B-#8505 w[*]; P{w[+mC]=UAS-Rab4-mRFP}2**
Source: Bloomington, donor: Henry Chang
Ref:
Comments:
Expresses a Rab4-RFP fusion protein under UAS control to label early endosomes
Chromosome: 2

**B-#11633 P{ry[+t7.2]=PZ}Rpd3[04556] ry[506]/TM3, ry[RK] Sb[1] Ser[1]**
Source: Bloomington, donor: Berkeley Drosophila Genome Proj. donor's source: Allan Spradling
Ref:
Comments:
Breakpts/Insertion: 64B12 (R4 flank)
hypomorph – P element inserted in the 5' UTR 47 bp from the start

**B-#5938 y[1] w[1118]; P{w[+mC]=UAS-Gal4.H}3A] chr 3**
Source: Bloomington 5938
Ref:

**Comments: UAS>GAL4 on 3**

**B-#5939 y[1] w[1118]; P{w[+mC]=UAS-Gal4.H}12B chr 2**
Source: Bloomington
Ref:
Comments: UAS>GAL4 on 2

**B-#5940 P{w[+mC]=UAS-Gal4.H}24, y[1] w[1118]; P{UAS-Gal4.H}12B; P {UAS-Gal4.H}3A chr 1;2;3**
Source: Bloomington
Ref:

Comments: UAS>GAL4 on all 3 chromosomes

**B-#8141 w[*]; P{w[+mC]=UAS-Hsap\MJD.tr-Q78}c37.3 SCA3 Chr 3**
Source: Bloomington
Ref:
Comments: Machado Joseph SCA3 Bonini

**B-#8149 w[*]; P{w[+mC]=UAS-Hsap\MJD.tr-Q27}N18.3d SCA3 Chr3**
Source: Bloomington
Ref:
Comments: Machado Joseph SCA3 Bonini

**B-#8150 w[*]; P{w[+mC]=UAS-Hsap\MJD.tr-Q78}c211.2 SCA3 Chr2**
Source: Bloomington
Ref:

**Comments: Machado Joseph SCA3 Bonini**

**B-#23650 w[*]; P{w[+mC]=His2Av-mRFP1}III.1 Chr 3**
Source: Bloomington
Ref:
Comments: 3L (71A4-71B1)
P{His2Av-mRFP1} is composed of three distinct fragments. First, a 2240 bp His2Av PCR fragment encompassing 751 bp upstream of the His2Av translational initiation codon and the complete His2Av coding region up to the ultimate codon. This is fused to a second PCR fragment encompassing the T:Disc\RFP$^{mRFP}$ coding region. A third PCR fragment encompassing 1690 bp of genomic His2Av 3' flanking DNA is cloned downstream of the His2Av-T:Disc\RFP$^{mRFP}$ fusion protein.
The gene Histone H2A variant is referred to in FlyBase by the symbol Dmel\His2Av (CG5499, FBgn0001197). It is a protein_coding_gene from Drosophila melanogaster. Its sequence location is 3R: 22692653..22694630. It has the cytological map location 97D3. There is experimental evidence that it has the molecular function: SUMO binding. There is experimental evidence that it is involved in the biological process: cellular response to DNA damage stimulus. 33 alleles are reported.

**B-#5428 P{w[+mC]=UAS-EGFP}8, w[1118]**
Source: Bloomington 5428
Ref:
Comments: GFP on X
Hugh has it

**B-#5431 w[1118]; P{w[+mC]=UAS-EGFP}5a.2**
Source: Bloomington 5431
Ref:

**Comments: GFP on 2L 29C**