TABLE S1. Molecular analysis of some GOF modifiers of the Vpu-induced wing and eye phenotypes

Uyi[1]	Gene[2]	Insertion site[3]	Molecular information / Function	wing[4]	eye[4]	Human homolog[5]
Class 1: Transcriptional factors						
146	*cropped (crop)*	2nd intron	Unknown domain / Function	S	0	*TFAP4*
181	***tramtrack (ttk)***	-11700 pb	Transcription factor / Peripheral nervous system	S	0	BTB/POZ family proteins
195	*lola*	According to transcripts	Transcription factor / Axonal guidance	S	0	BTB/POZ family proteins
1238*	*su(H)*	+32pb (AS)	Transcription activator / Notch transduction	E	E	*CBF1/RBPJ*
1526	*mes*$^{-4}$	+40pb (AS)	Histone methyl transferase / Gene silencing	S	0	*NSD1*
1877	*emc*	+208pb	Transcription repressor / Cell-cell signaling; cell proliferation	L	0	*Inhibitor of DNA binding4*
1170	*shnurri (shn)*	-3490pb (AS)	Transcription factor / Wing morphogenesis; Cell proliferation	E	0	*HIV-EP3*
Class 2: Translation, splicing						
1028	*Rpl7*	-1983pb	Structural constituent of ribosome / Mitosis	0	S	*RPL7*
1276**	*eIF3-S10*	-85pb	Translation initiation factor / Mitosis	S	E	*EiF3A*
1652*	*heph*	4th intron	Translation repressor / Notch signaling pathway	E	E	*hnRNP1/PTB1*
3006	***fusilli***	(AS)	mRNA binding / EGFR signaling	S	0	*ESRP1*
1051**	*waharan*	-38bp (AS)	Aminoacyl-tRNA ligase activity; ATP binding / Multiple processes	E	S	-
Class 3: Apoptosis						
1206	*mir-278 stem loop*	NK	miRNA-gene / Negative regulation of apoptosis	S	0	-
15	*anterior open (aop)*	-107bp	Transcription repressor / Positive regulation of apoptosis	S	L	*ETV6*
1835	***thread (th)/diap1***	+2088bp	Apoptosis inhibitor / Apoptosis	S	0	*IAP*
1027*	*malic enzyme (men)*	2nd exon	Malate dehydrogenase / Regulation of apoptosis	S	S	*malic enzyme I cytosolic*
1238*	*l(2)35Bg*	-713bp	Unknown / Apoptosis inhibitor related	E	E	*Ciapin1*

Class 4: Ubiquitin, Proteasome						
1339*	*partner of paired (ppa)*	-45bp	Unknown domain / Ubiquitin-dependent protein catabolic process	E	E	*FBXL14*
1323	*CG2218*	-186bp	Ubiquitin-protein ligase activity / Ubiquitylation	S	0	*UBOX5*
Class 5: Signaling pathways						
1261	*CG14945*	-45bp	Phospholipase C activity / intracellular signal transduction	0	L	*Phosopholipase C family*
1726	*target of wingless(tow)*	+126bp (AS)	Unknown domain / Regulation of Smoothened signaling pathway	S	0	-
1755	*pxb*	-43bp (AS)	Unknown domain / Smoothened signaling pathway	S	0	-
1033	*eathbound 1 (ebd1)*	1st exon	DNAbinding / Positive regulation of WG signaling	0	S	-
Class 6: Metabolism						
1283	*CG2098*	-364bp	Ferrochelatase / Protoporphyrinogen IX biosynthetic process	0	E	*FECH*
1030	*CG7910*	+162bp (AS)	Fatty acid amide hydrolase / Unknown function	S	0	*fatty acid amide hydrolase*
1730	*O-GlcNAcase (oga)*	+54bp (AS)	Hyaluronoglucosaminidase / Unknown function	0	L	*MGEA5*
1751	*Ssadh*	+2281bp (AS)	Succinate-semialdehyde dehydrogenase / Gamma-aminobutyric acid catabolic process	S	0	*ALDH5A1*
Class 7: Cell adhesion, extracellular matrix, cytoskeleton						
1228**	*CG14394*	-2682bp	Unknown domain / Tissue regeneration; Cell adhesion	S	E	*Ninjurin 2*
1526	*CG5514*	-800bp	Structural constituent of cell wall / Unknown function	S	0	-
1702	*Kuzbanian (Kuz)*	1st intron	Metallo-endopeptidase / Peripheral nervous system	S	0	*ADAM10*
1332	***scr64***	+1500bp	Tyrosine kinase / Actin filament-based process	0	E	*FYN*
1116	*viking (vkg)*	+8bp	Extracellular matrix structural constituent / Skeletal muscle development	0	L	*Type IV collagen*
1290	*Laminine B1 (LanB1)*	-39bp	Unknown / Organ development; Cell migration; Basement membrane assembly	0	S	*Laminin B*
Class 8: Traffic						
3113*	***liprin alpha***	-48bp	Protein binding / Axon guidance	L	E	*PPFIA1/Liprin*

1051**	*c(3)G*	-410bp	Reciprocal meiotic recombination	E	S	*Restin/CLIP-170*
1228	*Past1*	+562bp	Calcium ion binding / Endocytosis	S	0	*HPAST1/EHD1*
1824	*CG8451*	-374bp	Multivitamin transmembrane transporter / Membrane transport	S	0	*SSSF*
Class 9: Others						
1199	***grapes (grp)***	-99bp	Ser/thr kinase / Cell cycle; DNA damage checkpoint.	0	E	*CHEK1*
1213		-183bp		0	E	*CHEK1*
1776		-200bp		0	E	*CHEK1*
1324	*CG4552*	+634bp (AS)	Rab GTPase activator activity / Phagocytosis, engulfment	S	0	*TBC1D23*
1751	*CG4673*	-900bp (AS)	Structural constituent of nuclear pore / Neurogenesis	S	0	*NPLOC4*
5377	*amnesiac (amn)*	+1010bp	Neuropeptide hormone / Learning, memory;Antimicrobial humoral response	E	0	-
1702	*B4*	-1843bp (AS)	Unknown domain / Imaginal disc development; Circadian rythm.	S	0	-
3110	*cht11*	+1269bp	ChitinaseII / Chitin catabolic process	E	0	-
1348	*CG8003*	-448bp	Zinc ion binding / Unknown function	E	0	*ANKMY2*
1730	*CG3353*	-100bp	Zinc ion binding / Unknown function	0	L	*SMYD5*
1001	*CG32369*	1st intron (AS)	Zinc ion binding / Proteolysis	S	0	*LONRF2*
1657	*Esyt2*	-8553bp	C2 membrane targeting protein / Unknown function	0	L	*ESYT2*

[1] P[yellow+ -UAS] insertion line number

[2] In **bold** are the genes verified to be deregulated by the insertion of the P[yellow$^+$ -UAS] element

[3] Insertion site corresponds to the location of the P element relative to the known/putative transcriptional start site of the candidate gene. All P element insertions are in the sense transcriptional orientation relative to the candidate gene unless specified by (AS). NK: transcription start site not known

[4] Modification of the Vpu-induced phenotype in the wing or in the eye. S: suppressor, E: enhancer, L: léthal, 0: no modification.

[5] - No human homolog identified

* Insertion lines that modified both wing and eye Vpu-induced phenotypes in the same direction

** Insertion lines that modified wing and eye Vpu-induced phenotypes in the opposite direction