Supplemental Figure 1



Figure S1. A) A significant increase in β -gal activity is observed in cells co-transfected with both plasmids (4), compared to cells transfected with individual plasmids and mixed together (3), demonstrating the specificity of the assay. **B**) Box-and-whisker plots showing Z-scores of negative control RNAi (*C.elegans* gene *ZK686.3* or *GFP*) show little variation from the median, whereas technical positive RNAi controls, targeting the transfected plasmids (*Dome, LacZ, RLuc*) show significant Z-scores. Further positive control (Rab5), targeting the endocytic machinery and causing an increase in Dome stability, shows a significant increase in enzyme activity. **C-D**) Example western blot (C) and quantification (D) from secondary RNAi screen analysis, measuring Dome protein levels. **E**) Dome-FLAG protein levels increase in Kc₁₆₇ cells upon knockdown of *Act42A*, resulting in a 2.5-fold increase compared to a *LacZ* control. **F**) qPCR of the Dome-FLAG construct also shows an approximately 2.5-fold increase in expression upon knockdown of *Act42A*. Efficiency of RNAi is confirmed by qPCR of *Act42A*.

Supplemental Figure 2



Figure S2. A) mRNA expression levels of *MASK* in Kc₁₆₇ cells assayed by qPCR after indicated RNAi treatment (MASK1= BKN20625; MASK2 = HFA16018) relative to housekeeping gene RpL32. Knockdown of *MASK* levels are confirmed. *** p < 0.01. **B**) *6x2xdRafluc* STAT92E reporter assay is reduced after indicated RNAi treatment. **C**) Three different STAT92E-dependent luciferase reporters were used to measure JAK/STAT activity after stimulation with Upd. Significant changes were observed after indicated RNAi treatment for all STAT92E-dependent reporters. **D**) Z-scores derived from the Dome dimerisation genome-scale RNAi screen comparing the effect of MASK knockdown (column 1) to the Ras/Raf pathway components *csw, Ras85D, Ras64B, raf* and for the Hippo pathway genes *hpo, wts* and *yki*. None of the interactions were significant (ns). **E**) Z-scores derived from a previous genome-scale RNAi screen for modulators of the *6x2xDrafLuc* STAT92E activity reporter (Fisher et al., 2012). The effect of MASK (column 1) is compared to the Ras/Raf pathway genes *csw, Ras85D, Ras64B, raf* and to the Hippo pathway genes *hpo, wts, yki*. None of the interactions were significant (ns). **F-H**) Dorsal view of eye overgrowth phenotypes caused by ectopic Upd ligand expression driven by *GMR-Upd*Δ3'. Panels show an alternative control (OreR), which was scored as normal, and two further MASK alleles (*MASK*^{5.8} and *MASK*^{7.29}), which were scored as having moderate suppression.

Supplemental Figure 3



Figure S3

A) mRNA expression of *ANKHD1* indicated from HeLa cells, after siRNA treatment against *ANKHD1* or non-targeting control. Measurements were taken relative to β -actin.

B) phospho-STAT1 (pSTAT1) and phospho-STAT3 (pSTAT3) protein are increased by ligand stimulation (OSM) in HeLa cells treated with control siRNA. Induction of phosphorylated STATs was suppressed when treating cells with non-overlapping siRNA reagents targeting ANKHD1. β -actin was used as a loading control.

Table S1.

Click here to Download Table S1

Table S2.

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Table S3: Primers used in this study

Gene	Purpose	Primers
MASK-A1A2	Gateway	F: caccCGGCTGCTTTGCAAGG
	cloning	R: CTTAAGAGGAGCAGCCTGTTGTGTGGCAG
RpL32	qPCR	F: GACGCTTCAAGGGACAGTATCTG
		R: AAACGCGGTTCTGCATGAG
MASK	qPCR	F: CCGTTTCAGAGGACGATATTC
		R: CTTCCGACTCTTCCTCCGTTT
Socs36E	qPCR	F: AGTGCTTTACTGCTGCGACT
		R: TCGTCGAGTATTGCGAAGT
SOCS3	qPCR	F: AGCTGGTCTCCTTTTCCTACTCATACTA
		R: GGTGAAAGATGTCCCGTCTCC
		probe: TGGGTGGATGGAGCGGGAGGA
ANKHD1	qPCR	F: AGCGGTACGGGCGGAG
		R: AAATAAATGATTCAACCTCGGACAC
		probe: CGCTGGATTTCAAGTTGGCGGC
β -actin	qPCR	F: ATCATTGCTCCTCCTGAGCG
		R: GACAGCGAGGCCAGGATG
		probe: TACTCCGTGTGGATCGGCGGCT