Table S1. GEO accession numbers for data analyzed in this study

TEAD1 – muscle : GSM1331246 (RD HUMAN TEAD-CHIPSEQ _48240-treat)

TEAD1 – astrocyte : GSM1515741 (TEAD1-SF268_REP1_54611_treat)

TEAD1 – lung : GSM1664955 (MSTO TEAD1_56535_treat)

TEAD1 – carcinoma : GSM11667161 (HUCCT1 TEAD1_56542_Treat)

H3K4me1 (HUVEC) – GSM733690 (BERNSTEIN_HUVEC_H3K4ME1_45367_treat)

H3K4me3 (HUVEC) – GSM733673 (BERNSTEIN_HUVEC_H3K4ME3_45376_treat)

H3K27ac (HUVEC) – GSM733691 (BERNSTEIN_HUVEC_H3K27AC_45360_treat)

Supplemental Figure 1

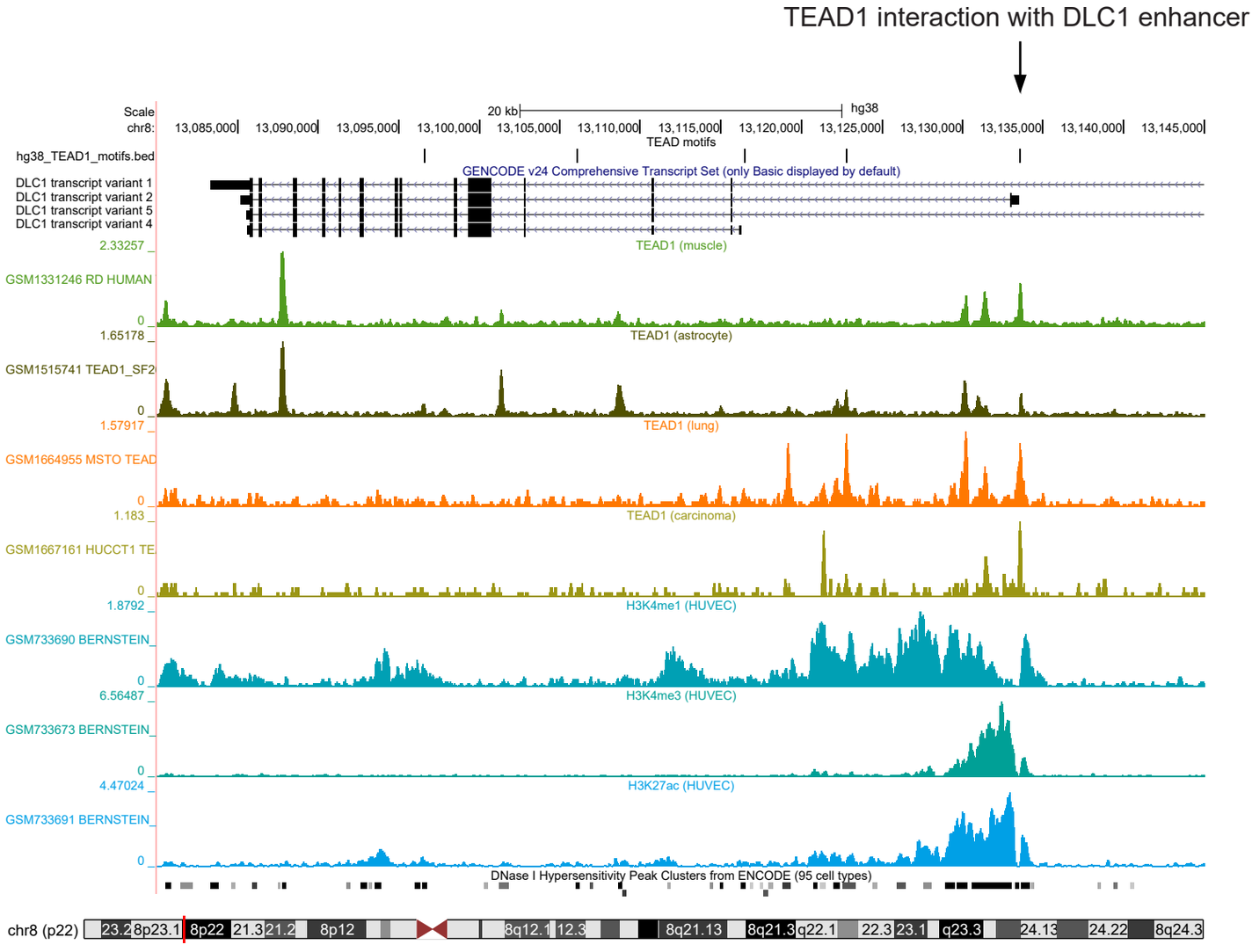


Figure S1. Full detailed schematics of UCSC genome browser results at position chr8:13,074,715-13,142,890 of the human genome (GRCh38/hg38) showing the genomic location of DLC1 transcript variants 1 (NP_872584.2), 2 (NP_006085.2), 5 (NP_001303597.1) and 4 (NP_001157743.1) and the presence of a TEAD motif at the transcriptional start site (TSS) of DLC1 transcript variant 2. Plotted are the results from publicly available GEO data TEAD1 ChIP-Seq data from various cell types and corresponding histone modification profiles in HUVECs in ENCODE. The data show a binding peak of TEAD1 at the TSS of DLC1 transcript variant 2. Histone modification profiles indicate that there is an open conformation of chromatin and an active promoter region around the TEAD binding motif, defined as the bimodal presence of both histone H3 trimethylation at lysine 4 (H3K4me3) and histone H3 acetylation at lysine 27 (H3K27ac), combined with increased DNase hypersensitivity.

Figure S2. Full scans of Western experiments in Figure 1. Molecular weights of the marker, exposure times, sensitive scanning mode and following order of antibody probing are indicated.

Supplemental Figure 2

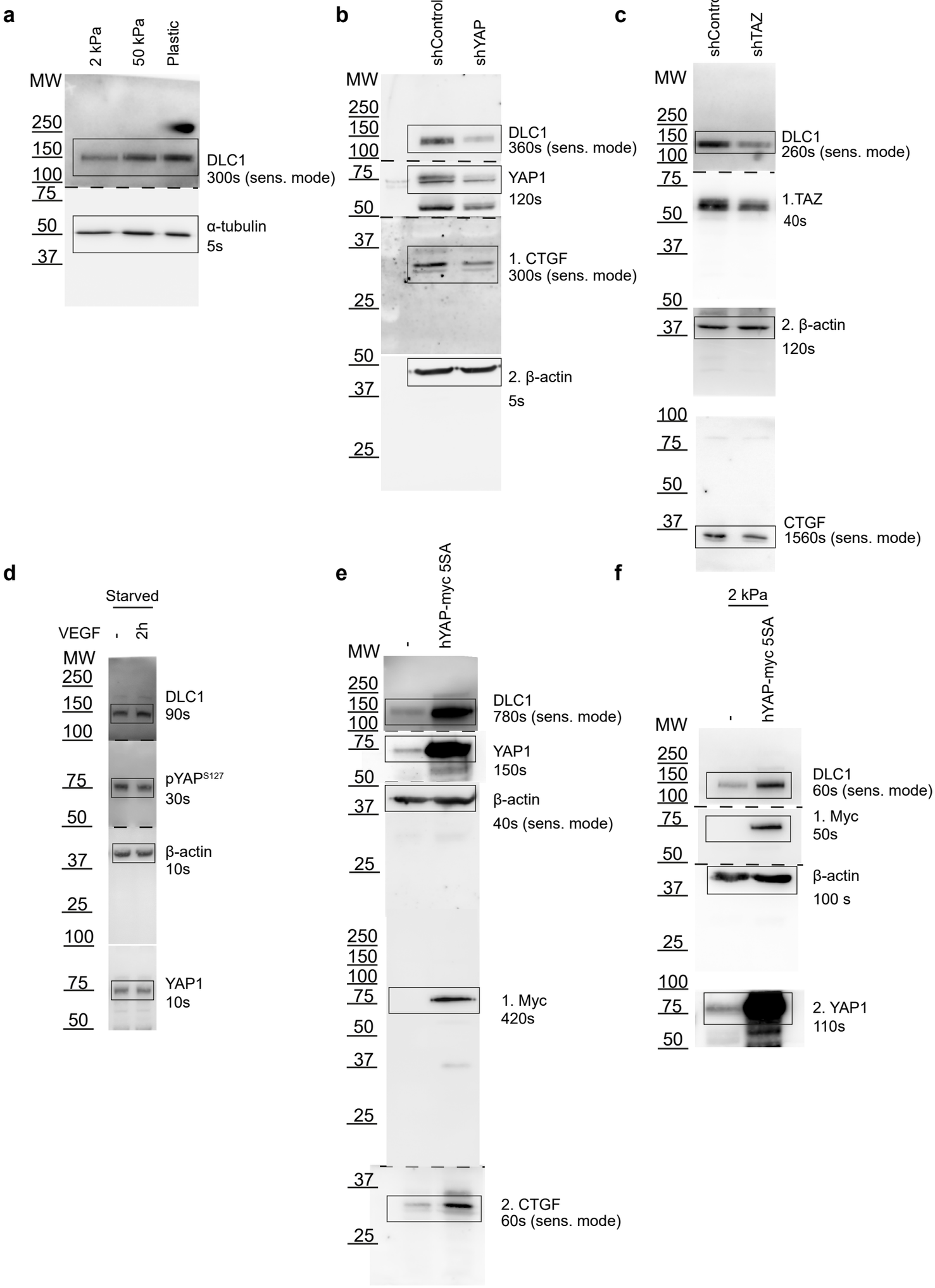


Figure S2. Full scans of Western experiments in Figure 1. Molecular weights of the marker, exposure times, sensitive scanning mode and following order of antibody probing are indicated.

Supplemental Figure 3

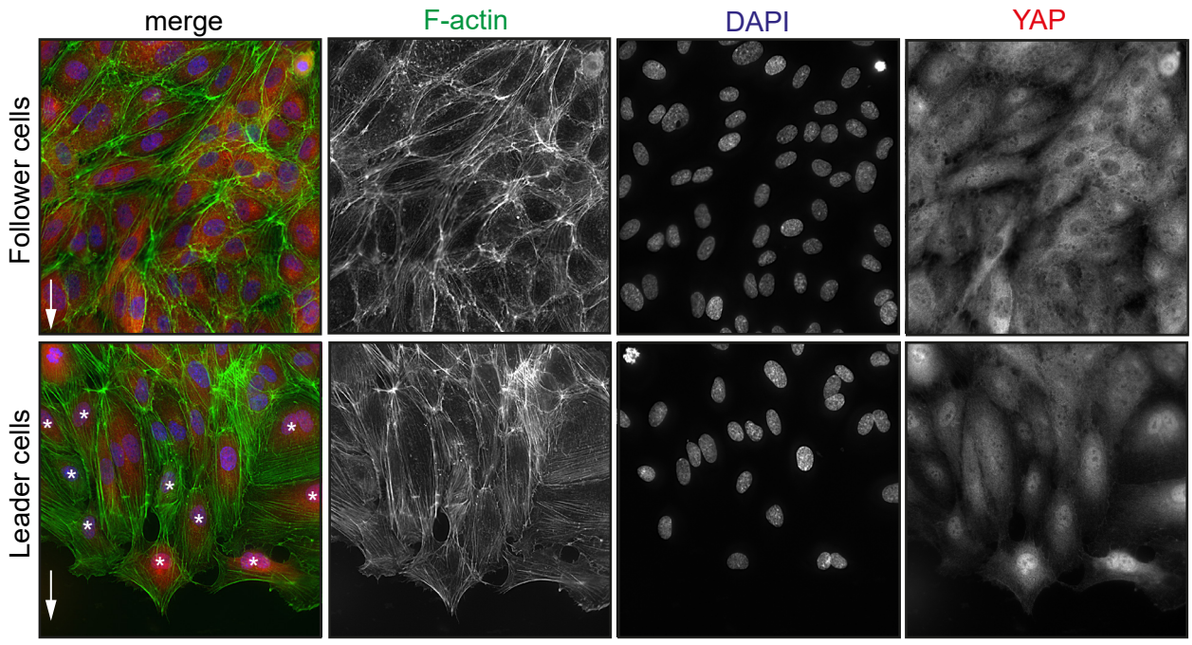


Figure S3. Widefield IF images of HUVECs fixed 6 hours after initiation of scratch wound assays stained for DAPI (blue), F-actin (green) and YAP (red). Pictures taken of the follower cells in the center of the monolayer and of the leader cells at the scratch wound edge. Asterisks highlight cells with nuclear enrichment of YAP compared to the cytoplasm.

Supplemental Figure 4

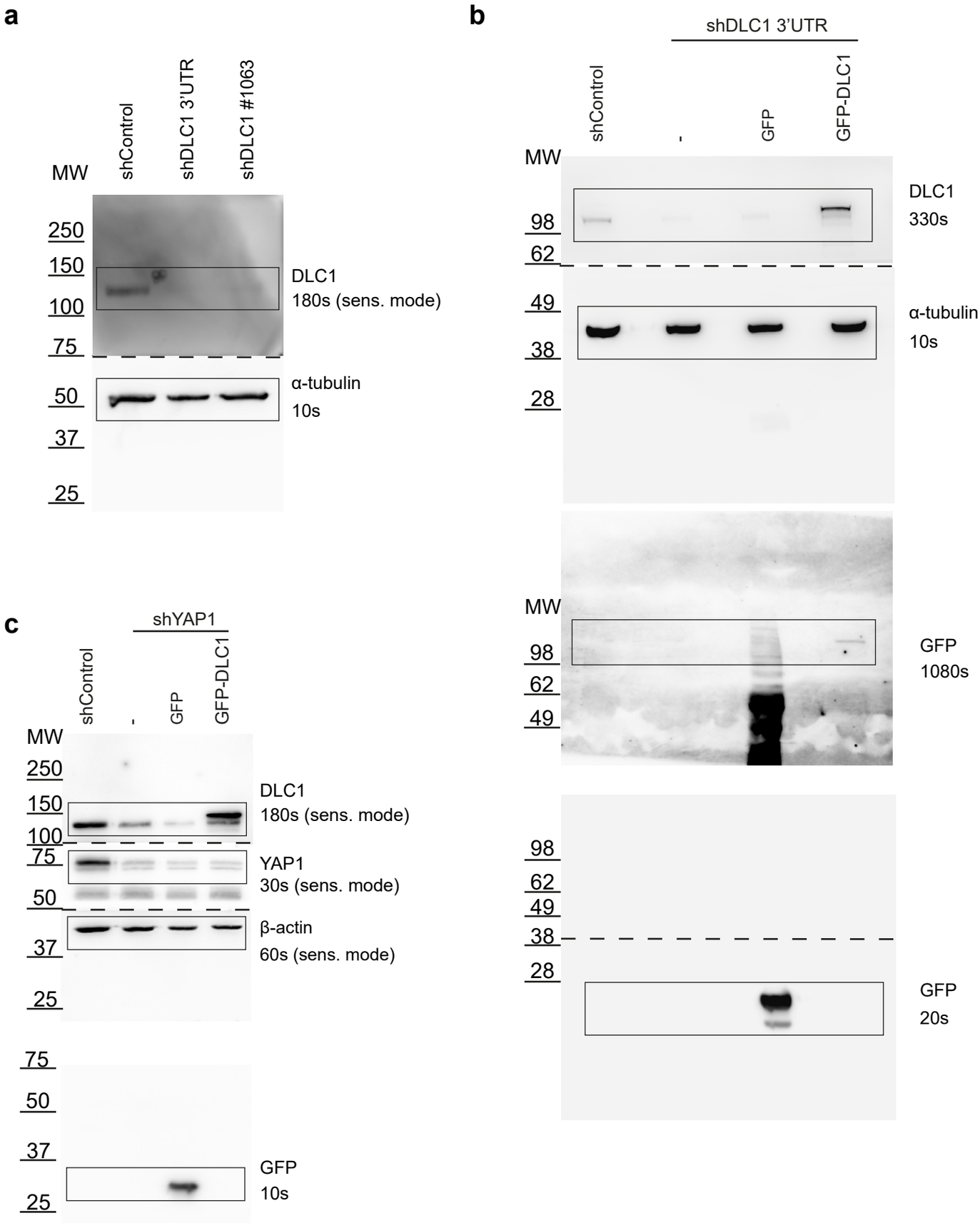
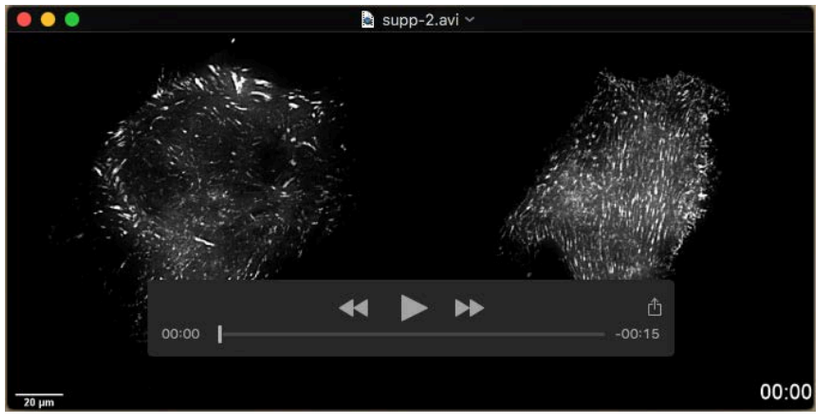
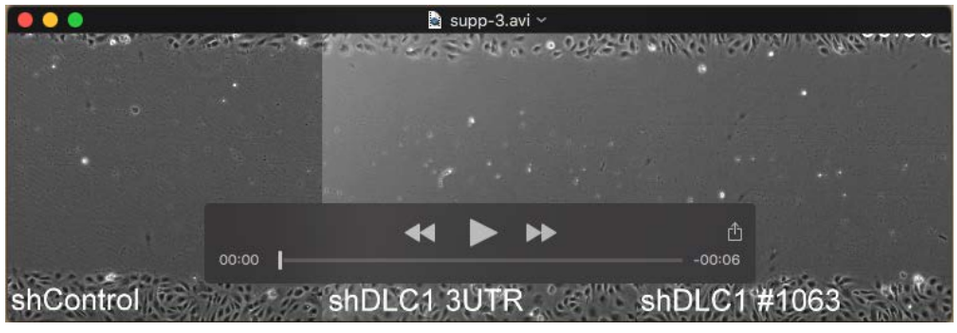


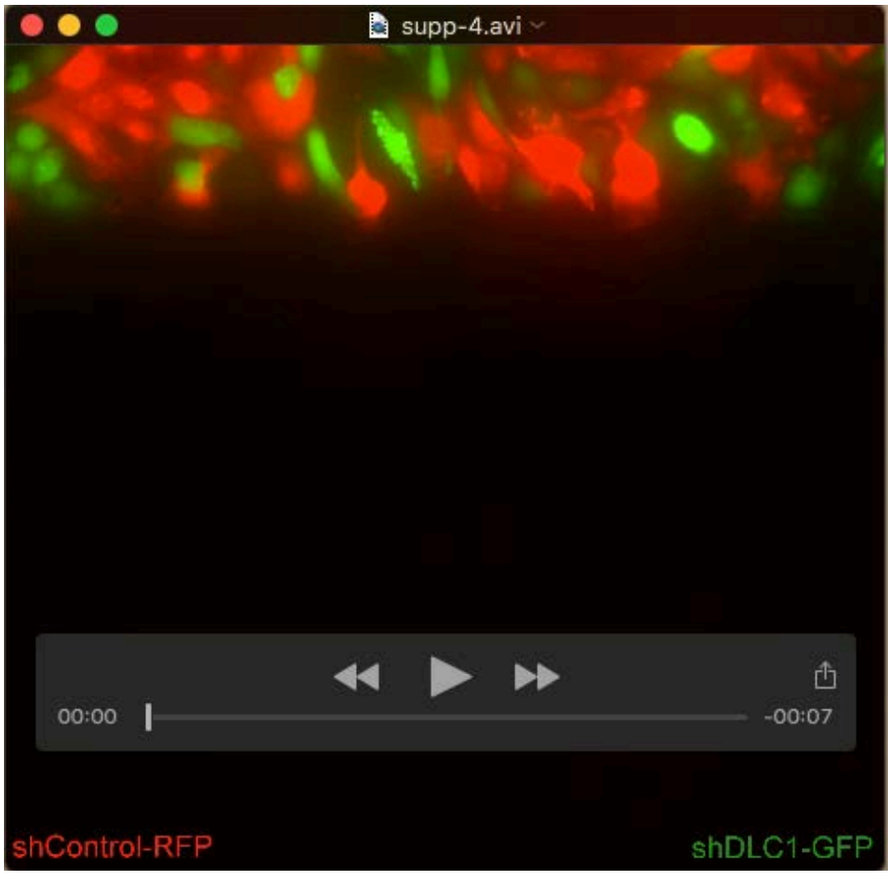
Figure S4. Full scans of Western experiments in Figure 3-5. Molecular weights of the marker, exposure times, sensitive scanning mode and following order of antibody probing are indicated.



Movie 1. DLC1 controls endothelial focal adhesion dynamics. Time lapse recording of HUVECs transduced with shControl or shDLC1 and expressing paxillin-mCherry. Images were acquired by time-lapse TIRF microscopy (NIKON Eclipse Ti) using a 60x/1.49 NA oil objective. Frames were taken every 30 sec for ~ 2,5 hours.



Movie 2. DLC1 is needed for endothelial directional migration. Time lapse recording of HUVECs transduced with shControl, shDLC1 3'UTR or shDLC1 #1063 during scratch wound migration. Images were acquired by time-lapse phase-contrast microscopy (NIKON Eclipse Ti) using a 10x dry objective. Frames were taken every 10 min for ~ 16 hours.



Movie 3. DLC1 is needed to establish leader cells during directional migration. Time lapse recording of mosaic cultures of HUVECs transduced with shControl (RFP) or shDLC1 (GFP) during scratch wound migration. Images were acquired by time-lapse fluorescence microscopy (NIKON Eclipse Ti) using a 20x/0.75 NA dry objective. Frames were taken every 10 min for ~ 17 hours.