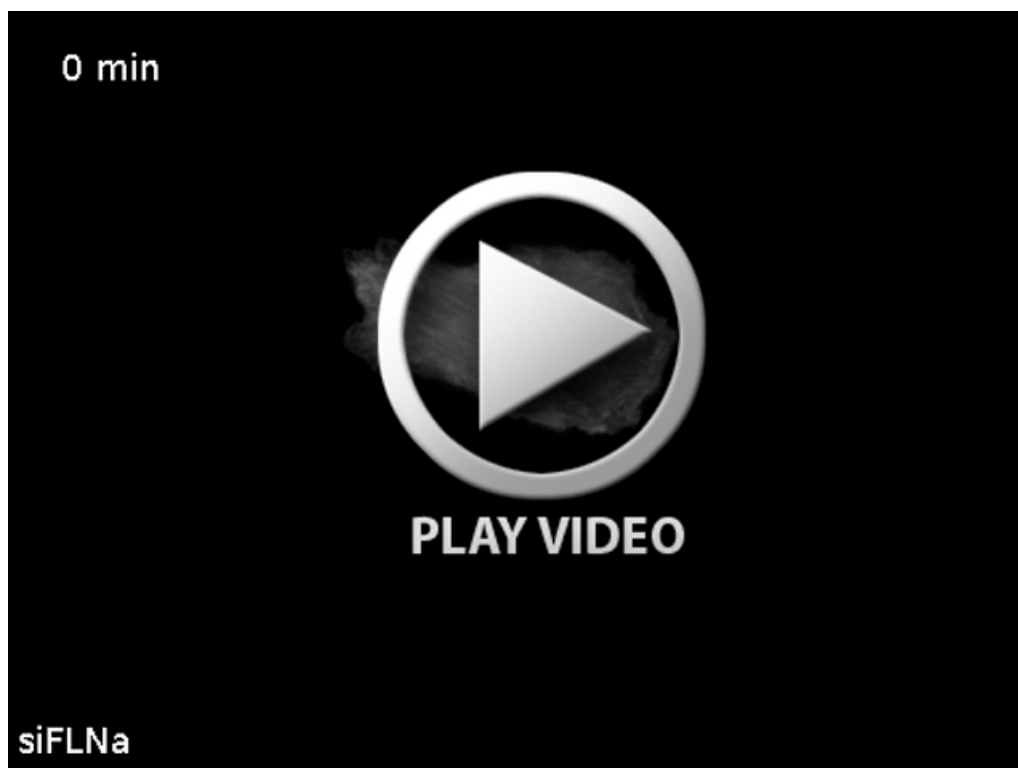**Movie 1. Protrusion dynamics in siCTRL U2OS cell, related to figure 6.** siCTRL U2OS cells transiently expressing Lifeact-mEGFP were plated on FN for 4 h and imaged at 37°C on an Axiovert 200M live cell imaging system (Carl Zeiss) for 420 min at 1 frame every 180 s.

Movie 2. Protrusion dynamics in siFLNa U2OS cell, related to figure 6. siFLNa U2OS cells transiently expressing Lifeact-mEGFP were plated on FN for 4 h and imaged at 37°C on an Axiovert 200M live cell imaging system (Carl Zeiss) for 420 min at 1 frame every 180 s.

Movie 3. Protrusion dynamics in siIQGAP1 U2OS cell, related to figure 6. siIQGAP1 U2OS cells transiently expressing Lifeact-mEGFP were plated on FN for 4 h and imaged at 37°C on an Axiovert 200M live cell imaging system (Carl Zeiss) for 420 min at 1 frame every 180 s.

Movie 4. Protrusion dynamics in siRacGAP1 U2OS cell, related to figure 6. siRacGAP1 U2OS cells transiently expressing Lifeact-mEGFP were plated on FN for 4 h and imaged at 37°C on an Axiovert 200M live cell imaging system (Carl Zeiss) for 420 min at 1 frame every 180 s.

Table S1. Proteins identified in the FLNa-GFP, IQGAP1-GFP, Rac1-GFP, RCC2-GFP and GFP pull-downs, related to figure 4. Proteins recruited to FLNa-GFP, IQGAP1-GFP, Rac1-GFP, RCC2-GFP and GFP were analysed by liquid chromatography–tandem mass spectrometry. Three biological replicates were performed for each GFP pull-down. Relative protein abundance was calculated using the unweighted spectral count of a given protein normalised to the total number of spectra observed in the entire sample and to the molecular weight of that protein (normalised spectral count).

Download Table S1

Table S2. Proteins enriched in the FLNa-GFP pull-downs, related to figure 4. List of the proteins enriched to FLNa-GFP. Relative protein abundance was calculated using the unweighted spectral count of a given protein normalised to the total number of spectra observed in the entire sample and to the molecular weight of that protein (normalised spectral count). Proteins in the FLNa-GFP dataset enriched more than two-fold over controls (GFP and RCC2) were considered to be specifically recruited.

Download Table S2

Table S3. Proteins enriched in the IQGAP1-GFP pull-downs, related to figure 4. List of the proteins enriched to IQGAP1-GFP. Relative protein abundance was calculated using the unweighted spectral count of a given protein normalised to the total number of spectra observed in the entire sample and to the molecular weight of that protein (normalised spectral count). Proteins in the IQGAP1-GFP dataset enriched more than two-fold over controls (GFP and RCC2) were considered to be specifically recruited.

Download Table S3

Table S4. Proteins enriched in the Rac1-GFP pull-downs, related to figure 4. List of the proteins enriched to Rac1-GFP. Relative protein abundance was calculated using the unweighted spectral count of a given protein normalised to the total number of spectra observed in the entire sample and to the molecular weight of that protein (normalised spectral count). Proteins in the Rac1-GFP dataset enriched more than two-fold over the GFP control were considered to be specifically recruited.

Download Table S4

Table S5. Proteins enriched in the RCC2-GFP pull-downs, related to figure 4. List of the proteins enriched to RCC2-GFP. Relative protein abundance was calculated using the unweighted spectral count of a given protein normalised to the total number of spectra observed in the entire sample and to the molecular weight of that protein (normalised spectral count). Proteins in the RCC2-GFP dataset enriched more than two-fold over the GFP control were considered to be specifically recruited.

Download Table S5