

Table S1: Co-localization of ShcD with EGFR and select compartment markers.
Degree of overlap is expressed as Pearson's r , and compared against signal randomized in the x-axis.

Figure	Signal	$r(\text{obs})$	van Steensel X-translation	
			$r(\text{rand}) \text{ mean} \pm \text{sd}$	$r(\text{obs}) > r(\text{rand})$
Fig. 3B	EGFR T = 5 min	-0.056	-0.055±0.023	65.8%
	EGFR T = 120 min	0.72	0.405±0.098	97.5%
Fig. 3D	EEA1	0.371	0.281 ± 0.079	87.8%
	CD63	0.305	0.319 ± 0.040	29.3%
	Rab11	0.634	0.527 ± 0.057	95.1%
Fig. 7D	EEA1 (T = 10 min)	0.606	0.408 ± 0.084	95.12 %

Table S2: NES motif identified by NetNES 1.1 in ShcA CH1 region.

ANN: Artificial Neural Network. HMM: Hidden Markov Model.

Position	Residue	ANN	HMM	NES	Prediction
345	P	0.074	0.000	0.000	N
346	R	0.070	0.000	0.000	N
347	D	0.085	0.000	0.000	N
348	L	0.082	0.109	0.000	N
349	F	0.076	0.125	0.000	N
350	D	0.135	0.125	0.000	N
351	M	0.086	0.829	0.536	Y
352	K	0.085	0.879	0.589	Y
353	P	0.085	0.879	0.589	Y
354	F	0.082	0.881	0.591	Y
355	E	0.09	0.881	0.594	Y
356	D	0.074	0.881	0.582	Y
357	A	0.079	0.881	0.580	Y
358	L	0.102	0.890	0.592	Y
359	R	0.083	0.882	0.584	Y
360	V	0.103	0.886	0.592	Y
361	P	0.072	0.013	0.000	N
362	P	0.084	0.013	0.000	N
363	P	0.082	0.013	0.000	N
364	P	0.070	0.013	0.000	N
365	Q	0.070	0.013	0.000	N
366	S	0.069	0.013	0.000	N

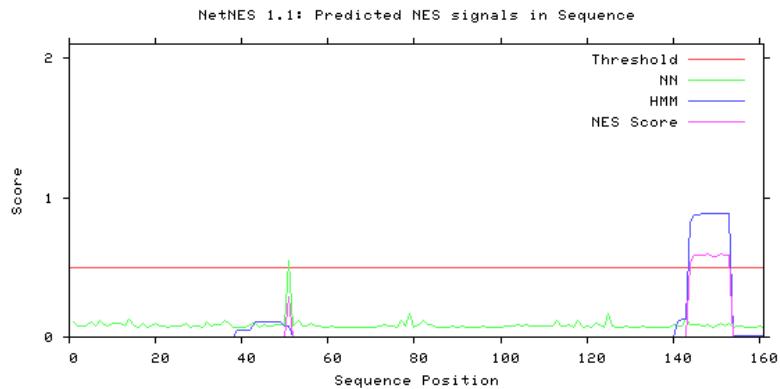


Fig. S1: The ShcA CH1 region contains a nuclear export signal.

NetNES 1.1 was queried with 161 amino acids of p52 ShcA. The pink trace represents a NES score exceeding the (red) threshold. NN: Neural network. HMM: Hidden Markov Model.