TITLE
CHARACTERISATION OF HRAS LOCAL SIGNAL TRANSDUCTION NETWORKS USING ENGINEERED SITE-SPECIFIC EXCHANGE FACTORS

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ABSTRACT

Ras GTPases convey signals from different types of membranes. At these locations, different Ras isoforms, interactors and regulators generate different biochemical signals and biological outputs. The study of Ras localisation-specific signal transduction networks has been hampered by our inability to specifically activate each of these Ras pools. Here, we describe a new set of site-specific tethered exchange factors, engineered by fusing the RasGRF1 CDC25 domain to sub-localisation-defining tethers, whereby Ras pools at specific locations can be precisely activated. The CDC25 domain has a high specificity for activating HRas but no NRas and KRas. This unexpected finding means that the CDC25 tether constructs mainly activate endogenous H-Ras. Hence, the use of these constructs enabled us to identify distinct pathways regulated by HRas in endomembranes and plasma membrane microdomains. Importantly, these new constructs unveil different patterns of HRas activity specified by their subcellular localisation. Overall, the targeted GEFs described herein constitute ideal tools for dissecting spatially-defined HRas biochemical and biological functions

KEYWORDS

Ras, localisation, Ras-GEF, CDC25 domain, oncogene, signalling network.

Abbreviations:

ER: endoplasmic reticulum
GC: Golgi complex
DM: disordered membrane
LR: Lipid Rafts
GEF: Guanine exchange factor
GAP: GTPase activating protein
PM: Plasma membrane

INTRODUCTION

The proteins of the Ras family of small GTPases, including HRas, KRas4A, KRas4B and NRas, function as molecular switches[1]. Mutations in these proteins occur in over 30% of human tumours and Ras oncogenic mutants are some of the main drivers of cancer[2, 3]. Under physiological conditions, Ras cycles between an active state, bound to GTP, and an inactive state, bound to GDP. The Ras activation/deactivation cycle is tightly regulated by two classes of proteins, Guanine Exchange Factors (GEFs), which facilitate Ras activation, and GTPase Activating Proteins (GAPs), which increase Ras GTPase activity, leading to Ras inactivation[2]. Ras proteins regulate a complex signalling network mediated by several effectors including the Raf family kinases, phosphoinositide-3 Kinase (PI3K) and Ral exchange factors. Ras signalling networks ultimately regulate multiple biological responses, including key events such as proliferation, differentiation, migration or survival[2]. Thus, a refined control of the activity of Ras proteins is crucial for eliciting the correct cell fate decision. Control mechanisms operate at different tiers in order to orchestrate specific Ras-dependent responses, through differential interaction with different effector and regulatory proteins[4]. Another important mechanism for regulating Ras signalling is the localisation-specific control of Ras activation at different membrane domains within the cell, due to the spatially-defined participation of certain exchange factors[5, 6].

Previous studies have unveiled the importance of the site from which Ras signals originate. Initially, it was thought that Ras was functional only at the peripheral plasma membrane, where GEFs would be active[7], but in recent years it has been demonstrated that Ras can also signal from internal localizations such as endoplasmic reticulum (ER)[5], Golgi complex (GC)[8, 9], endosomes[10] or mitochondria[11]. The different Ras isoforms show specific localisation

patterns. HRas and NRas signal from the ER and the GA while KRas signalling is mainly evoked from plasma membrane and mitochondria[12]. Although some Ras interactors are present in all known Ras localisations, a substantial body of data indicates that Ras proteins interact with diverse sets of proteins at distinct sub-localisations, thereby eliciting specific signals from different platforms[12]. Unfortunately, a clear notion of the contribution of the different spatially-defined Ras pools to specific functions is limited by the technical inability to activate the endogenous Ras proteins at, and only at, a specific location. Thus, most of the work done to decipher Ras spatial signalling has been performed by overexpressing tagged constitutively-activated Ras proteins sent to the desired sub-localisations using specific localisation tethers. Such an approach has caveats, since overexpression of these constructs may lead to signal distortions resulting from alterations in Ras regulatory mechanisms such as negative feedback loops. [13]

In this respect, we have previously reported a comprehensive analysis of HRas site specific signalling by using the constitutively activated mutant HRasG12V, which led us to identify several HRas-dependent functions that are mediated by different spatially-defined HRas pools[8, 14, 15]. However, such an approach has pitfalls, since in that scenario negative and positive feedback loops modulating Ras signalling may be lost. In addition, HRas-V12 may exhibit different affinity and kinetics for Ras interacting protein compared to wild type HRas[16]. Thus, signals triggered by mutant Ras at specific locations may differ from those evoked by wt HRas due to their different affinities for GEFs[5, 6, 17] and GAPs[18-20], scaffold proteins[21] and effectors[5, 6, 22, 23]. Therefore, there is an urgent need to develop new methods and strategies in order to characterise local signalling networks activated by Ras under physiological settings.

Here, we present a new set of molecular tools that enable the study of the signalling pathways triggered by endogenous Ras at specific sub-localisations. We demonstrate that these constructs preferentially activate endogenous HRas. Importantly, the signalling networks activated by endogenous HRas reveal similarities but also remarkable differences with those networks evoked by ectopic, site-specific-HRasV12 constructs.

RESULTS

Engineering site-specific Ras activator constructs.

In order to study the signals generated by endogenous Ras populations present at their physiological localisations, we engineered a novel set of molecular utensils based on the RasGRF1 CDC25 catalytic domain. It is known that overexpression of an isolated CDC25 domain targeted to the plasma membrane (PM) is sufficient for activating endogenous Ras[24]. Indeed, we ascertained that the expression of CDC25 caused an increase of RAS-GTP levels similar to those elicited by the whole RasGRF1 protein (Figure 1A). We reasoned that the CDC25 domain specifically targeted to different types of membranes, would be capable of specifically activating the endogenous Ras pools therein, while unaltering physiological regulatory mechanisms acting on RAS signals, such as negative and positive feedbacks or GAPs intervention. To this end, the CDC25 domain was fused to the site-specific tethers previously used to successfully target wt HRas and HRas-V12 to different cellular compartments[14]. These cues comprised: the avian infectious bronchitis virus M protein (referred as M1-CDC25 hereafter) to target CDC25 to the endoplasmic reticulum (ER)[25]. For stable expression at the Golgi complex (GC) we used KDEL receptor D193N mutant[6, 26] (KDEL-CDC25). At the PM we analysed two different domains: disordered membrane (DM), using the transmembrane region of the CD8α receptor [27] (CD8-CDC25), and we

anchored the CDC25 domain to lipid rafts (LR) using LCK myristoylation signal[28, 29] (LCK-CDC25). A FLAG tag was included to enable the detection of the targeted proteins.

To test that the constructs were correctly expressed and localised to the desired locations they were transiently transfected in HEK293T cells and their expression was monitored by western blot (Fig. 1B upper panel). In parallel, we ascertained their localisation by immunofluorescence using anti-FLAG staining in transfected Cos-1 cells by testing their co-localisation with targeted HA-HRas- wt or specific localisation markers. We observed that the targeted CDC25 proteins specifically localised at the desired localisations with similar expression patterns as those previously described for the HRAS V12 constructs [5] (Fig. 1C).

In addition, we generated HeLa cell lines stably expressing the different site–specific GEFs. In these, the expression levels were lower than those obtained by transient expression. In fact, expression was only detectable by previously performing an anti-FLAG immunoprecipitation. (Fig. 1B lower panel).

Altogether, these results indicated that the CDC25 tagged constructs were properly expressed and specifically localized to those compartments where they were aimed at.

Sublocalisation-targeted GEFs specifically activate HRas at different compartments.

Previous studies have shown that RasGRF1 specifically activates HRas, but not NRas and KRas[30, 31]. However, it is unclear why Ras-GRF1 shows such preferences. Structural studies comparing the CDC25 domains of Ras-GRF and SOS1, suggest that such affinity is not dictated by this domain, requiring the participation of other regulatory motifs present in the GEF [32]. For this reason, we expected our constructs to activate the three Ras isoforms. To confirm this, we analysed the ability of untethered, "global" FLAG-CDC25 to activate the three RAS isoforms, by performing Ras-GTP pull down assays in HEK293T cells transiently expressing the GEF plus wild-type versions of H, K and NRas (Figure 2A). As expected,

EGF treatment activated the three Ras isoforms while RasGRF1 only activated H-Ras. Surprisingly, we found that CDC25 prominently activated HRas but not NRAS or KRas (Fig 2A upper panel). Interestingly, only a minimal activation of NRas or KRas could be detected when we doubled the amount of transfected DNA for FLAG-CDC25 (Figure 2A lower panel). This could indicate that the CDC25 can also activate these Ras isoforms, though with diminished efficiency. Though an alternative explanation could be that CDC25-evoked hyperactivation of HRas could promote the activation of the other members of the family, as previously demonstrated[33]. Importantly, this data indicated that the CDC25 domain can contribute to isoform specificity in vivo. These data demonstrated that the CDC25-based constructs are particularly suited for the study of HRas, and therefore we focused on this isoform for the rest of the study.

Next, we investigated the ability of the different site-specific CDC25 constructs to activate the corresponding pools of endogenous HRas. To this end, we utilized the stable HeLa cell lines in which we analysed HRAS activation by Ras-GTP pull-down using GST-Raf-RBD. We found that, compared to parental cells, endogenous HRas activation was augmented in all cases, though to different extents. In this cellular context, the ER and DM exhibited the highest levels of Ras activation (Figure 2B). These results could reflect that, in HeLa cells, HRas is enriched at those sub-localisations where activation is more prominent. Unfortunately, as of today, there is no reliable methodology to quantitate and compare the levels of endogenous Ras proteins existing at different sub-localisations.

It was important to verify that the thethered-CDC25 constructs activated HRas only at the desired localisation and not unspecifically at other localisations. To test this, the location-specific HRAS wild-type versions: M1-HA-HRas (ER-R), LCK-HA-HRas (LR-R), CD8-HA-HRas (DM-R), or KDEL-HA-HRas (GC-R), were co-transfected with the targeted CDC25 proteins. Analysis of their activation in serum deprived HEK293 cells, confirmed

that they were highly GTP-loaded when co-expressed with the CDC25 construct bearing the same tether.

Interestingly, we found that globally expressed CDC25 (TOT-CDC25) activated endogenous Ras to a lesser extent than the site-specific CDC25 constructs (Fig. 2B), except when targeted to LRs (Fig. 2C), suggesting that untargeted CDC25 mainly activates HRas at this sublocalisation.

Noticeably, some unspecific activation was apparent, especially in the case of PM microdomains (Fig. 2C). This could be due to the cross-activation of HRas pools located at the boundaries of DM and LR microdomains. In addition, vesicle trafficking between endomembranes and the peripheral PM may also contribute to some unspecific activation of HRas by reshuffling the localisation of the CDC25 constructs.

In summary, these experiments strongly indicated that the location-specific CDC25 constructs mainly activate the HRas pool located at the specific sublocalisation where these proteins are expressed.

Ras effectors are differentially regulated depending on the subcellular localization where endogenous Ras is activated.

Next, we tested whether the activation of endogenous HRas at different subcellular compartments could differentially activate known Ras effector pathways. Our previous studies of KRas-dependent regulation of RASSF1A/MST2 demonstrated the importance of the differences on the activation kinetics of oncogenic vs wild-type Ras in the regulation of cell death and proliferation[16, 34]. This study also demonstrated that the dynamics and magnitude of Ras signalling network could be cell type specific. Therefore, we compared effector usage in response to endogenous, site-specific HRas activation, as evoked by the tethered CDC25 constructs, to that elicited by the presence of ectopic HRasV12 at the same

sites. We performed these experiments in NIH-3T3 cells, previously used to characterise effector pathway activation by tethered HRasV12 constructs[14]. We found that both sets of constructs elicited a similar pattern of ERK1/2 activation (Fig. 3A). Interestingly, in the case of ER-emanating signals, endogenous HRAS was more efficient than its oncogenic version for triggering ERK activation. Overall, notwithstanding expected differences in intensities, endogenous RAS activation, as evoked by site-specific GEFs, and site-restricted HRasV12 oncoproteins elicit similar patterns of ERK activation.

We extended our analyses to other well-characterised Ras effectors, by monitoring the changes on AKT phosphorylation, one of the key components of the PI3K cascade. The phosphorylation status of AKT exhibited remarkable differences when elicited by endogenous HRas activated by the targeted GEFs at different locations. Interestingly, the two phosphorylatable residues needed for full activation of the kinase[35-37], threonine 308 (T308) and serine 473 (S473), exhibited distinct phosphorylation patterns depending on the sub-localisation where HRas was activated (Fig 3B). While PDK1-dependent T308 phosphorylation[38] was mainly evoked from LR, where PDK1 is located[39], S473 phosphorylation mainly resulted as a consequence of HRas signals coming from disordered membrane and endomembranes but not from LR (Fig. 3B upper panel). Since AKT-S473 is phosphorylated by mTORC2 [36], our results are in line with previous reports indicating that AKT-T308 and S473 residues may be phosphorylated in different cell compartments due to differential localisation of PDK1 and mTORC2 [40, 41]. In the case of mTORC2 which localises to endomembranes, and possibly at some specific PM domains, it suggests that this kinase could be activated by HRas-induced mechanisms at these locations. Thus, these results shed light on the relevance of mTORC2 localization at the PM, hitherto not well characterised. It has been proposed that mTORC2 is recruited to LR by AKT and that this complex may translocate to disordered membrane upon activation to allow its dephosphorylation[40, 41]. Our

results would confirm that mTORC2 is differentially activated at PM microdomains, but contrary to previous reports, they strongly indicate that the activation of mTORC2 induced by HRas [42] occurs at the DM.

The suitability of the site-specific GEFs for deciphering localized HRas signalling, was further confirmed when we studied the activation of the stress activated kinase JNK1. We observed that JNK was differentially regulated, to some extent, from all locations. Although the site-related difference on JNK activation are small, we consistently observed that activation from GC significantly evoked higher levels of phosphorylated JNK (Fig. 3B middle) while JNK activity by HRas activation at ER and DM was less potent. In addition, we analysed STAT3 phosphorylation (Y705) after local HRas activation. This phosphorylation has been reported to be responsible for its dimerization, translocation to the nucleus and DNA binding, which is essential for STAT3-dependent regulation of cell cycle and survival genes[43-45]. We found that site-specific GEFs induced STAT3 phosphorylation, preferentially from the GC (Fig. 3B lower panel).

The above results confirmed that endogenous HRas activates different signalling pathways at distinct cellular localisation. Importantly, these results showed some differences on the pattern of activation of HRas signalling pathways compared to what we observed in our previous studies using constructs expressing site-specific HRasV12[14]. The fact that we did not find the same pattern of effector activation suggest that wild-type and oncogenic HRas are not equivalent in their regulation of effector networks, something that could be related to cellular transformation and other cancer-related processes. Altogether, our data demonstrate that our site-specific GEFs are useful tools for the study of HRas signalling variability as orchestrated by space.

Regulation of proliferation and survival by Ras activity induced by site-specific GEFs.

We next used the CDC25 targeted constructs to investigate the contribution of the different subcellular pools of endogenous HRas to several biological outcomes.

Our previous studies using NIH3T3 stable cell lines expressing targeted HRasV12 proteins, demonstrated that proliferation was differentially regulated depending on localisation[14]. For this reason, we analysed if activation of endogenous HRas by the site-specific GEFs followed the same pattern. We found that Ras signalling from PM microdomains (LR and DM) had the highest impact on proliferation (Fig. 4A). This result was identical to that we had previously observed when using targeted-HRasV12[14]. It confirmed that constant HRas activation from the PM evokes a proliferative advantage, regardless whether the HRas activation is caused by mutation or chronic GEF stimulation.

Next, we examined cell survival using two different assays. First, we measured the bulk survival rates of confluent cells expressing the different targeted CDC25 constructs under conditions of serum depravation (Fig. 4B). In this case, we did not observe significant differences. However, when we measured clonal survival by colony formation assays, where cells are evaluated for their capacity to survive and form colonies originating from single cells. Our data showed that CDC25 chronic activation of HRas provided pro-survival signals from LR, DM and GA but not from the ER (Fig. 4C). Significantly, this result is very different from our previous observations using the oncogenic HRas constructs, where we saw a clear pro-survival advantage emanating from the ER and no regulation from the GA[14]. This difference suggested the existence at the ER of a down-regulatory mechanism of HRas signals that modulates this biological function. Interestingly, the results might indicate that oncogenic HRasV12 is insensitive to such feedback regulation triggering pro-survival signals from the ER that may contribute to HRasV12-dependent transformation. Distinguishing between these possibilities will require the identification of the feedback loop in future studies.

Targeted-CDC25 overexpression does not confer transforming properties.

Constitutively active HRas-V12 is a driver of cell transformation[1], primarily due to aberrant regulation of the activation status of its effector pathways[46]. It has also been reported that expression of full length RasGRF1 and the isolated CDC25 catalytic domain could transform NIH3T3 cells due to hyperactivation of HRas signalling[24, 47]. For this reason, we next examined whether CDC25-induced transformation was differentially regulated by specific HRas pools. To this end, we performed focus formation assays in NIH3T3 fibroblasts using the *bona fide* oncogene HRasV12 as positive control[1]. Surprisingly, contrary to previous studies demonstrating that the expression of an isolated CDC25 domain induces transformation in NIH3T3 cells[7], our results clearly showed that overexpression of the CDC25 GEF motif did not result in cellular transformation (Fig. 5). The discrepancy between both studies is likely due to differences on the sequences spamming by the CDC25 domain on both cases. Similarly, no transformation of NIH3T3 was observed when we expressed the site-specific constructs.

Hence, our findings showed that the targeted CDC25-GEF domains can induce activation of endogenous HRas but, unlike hyperactive HRasV12 this does not result in cellular transformation.

Discussion.

Our understanding of the functional differences among Ras isoforms has increased since the seminal studies by Mark Phillips and John Hancock demonstrated that Ras are active in endomembranes and in different PM microdomains [48, 49], where they have different sets of interactors. Unfortunately, despite the growing importance of space as a regulator of Ras signalling, we still lack the technology to specifically and physiologically activate

compartmentalised pools of Ras. For this reason we must rely on the use of different molecular tools to decipher Ras spatial regulation. Therefore, the CDC25-based site-specific constructs described herein are valuable tools for this purpose. These constructs are an important addition to the series of molecular tools that we and others have developed in the past, to understand the role of the different cellular pools of Ras in the diverse plethora of biological outcomes regulated by these proteins[5, 11, 13, 14]. Unexpectedly, we found that the CDC25 domain cloned here shows strong specificity for HRas and only when the constructs were expressed and high levels in the cells we could see a modest activation of the endogenous NRas and KRas. It is also important to note that the CDC25 construct generated seems to have different properties than the construct previously described by Der's group[7]. This is clearly illustrated by one of the most surprising observation presented here, the lack of transforming properties of the CDC25 constructs that we generated does not induce cell transformation in clear contrast with previous reports. This is likely explained because the RasGRF region cloned by us is shorter than the construct utilized by Der's group which included an 84 extra N-terminal amino acids while our construct is restricted exclusively to the canonical CDC25 domain. Our results indicate that such 84 amino-is essential for conferring transforming properties to the CDC25 domain via Ras activation. This observation is in line with previous findings showing that different regions and domains of RasGRF are necessary for mediating its transformative effect and deletion of RasGRF domains such us the DH and PH domains prevent NIH-3T3 transformation[47].

Using these set of constructs we demonstrate that expression of site-specific CDC25 constructs trigger differential HRas-dependent functions summarised in Figure 6. Remarkably, these findings indicate that site-specific CDC25 constructs are appropriate tools for the study of spatially-defined HRas signalling, by generating a response closer to physiology than that obtained by the use of site-specific HRasV12 constructs, utilized in

previous studies. Thus, our biochemical experiments results indicate that the targeted CDC25 constructs described herein can constantly activate HRas and differentially trigger location specific activation of Ras effector pathways such as the MAPK and AKT without inducing transformation. The difference between the endogenous activated HRas and HRasV12 tethered constructs could be explained by two scenarios. One possibility would be that although the site-specific GEFs can constantly activate HRas and induce proliferative and survival advantages, their effect on local HRas pools is not strong enough to induce cellular transformation. A second, and not mutually exclusive possibility would be that HRas-mediated signals, as induced by site-specific GEFs, remain under the control of negative feedback loops that preclude transforming capacity.

Finally, the current study demonstrates that the combination of these tools in comparative studies can be used to gain insights into the regulatory mechanisms regulating spatially-defined Ras signals, and will help to decipher the spatial cues regulating oncogenic RAS transforming properties. These studies will help in completing our understanding of Ras-dependent signalling networks that have not been fully characterised despite intensive work in the last three decades.

METHODS

Constructs

pGEX-Raf-RBD, HA-RasGRF1, pCEFL-FLAG-RasV12 and the RasV12 plasmids targeted to be expressed at different compartments were previously used and described[5, 14, 31]. CDC25 domain from the RasGRF1 plasmid described before[47](only RasGEF motif containing nucleotides 947-1273) was amplified by PCR and cloned into pCEFL-FLAG vector, sequences of the oligonucleotides utilized are available upon request. The same epitopes and localization signals used for pCEFL-FLAG-HRasV12 [14] were used for the generation of M1-FLAG-CDC25, LCK-FLAG-CDC25, CD8-FLAG-CDC25 and KDEL-FLAG-CDC25 by

cloning the newly generated FLAG-CDC25 in the C-terminal of the different localisation-targeting vectors. All sequences were verified by DNA sequencing.

Cell culture

HEK293T, NIH3T3, HeLa and COS-1 cells were grown in Dulbecco modified Eagle medium (DMEM) supplemented with 10% FBS (foetal bovine serum) and L-glutamine (2 mM) at 37 ºC and 5% CO_2. Cells were transfected with Lipofectamine 2000 (Invitrogen) according with manufacturer's instruction and the amount of DNA indicated in each experiment. For the generation of HeLa stable cell lines, the targeted CDC25 plasmids were transfected in HeLa cells and selection of clones expressing the different CDC25 was performed by G418 (750 μg/ml) treatment during 2 weeks. Hereto, HeLa stable cell lines are named as ER-, LR-, DM- and GC-Flag-CDC25 whereas transiently transfected cells are named as M1-, LCK-, CD8- and KDEL-Flag-CDC25.

Cell lysis and immunoblotting

Total cellular extracts were obtained after cell lysis with HEPES pH 7.5 20 mM, NaCl 150mM, 1% NP-40 and proteases and phosphatases inhibitors. Total lysates were analysed by SDS-polyacrylamide gel electrophoresis and transferred to PVDF membranes. The following antibodies were used for immunoblotting: HA (sc-7392) and total AKT1 (sc-5298) from Santa Cruz; FLAG-M2 (A8592 mouse), FLAG (7425 rabbit), phospho-ERK1/2 (M8159) and total ERK1/2 (M5670) from Sigma; pan-Ras (op40) from Calbiochem; α1 Sodium potassium APTase (AB7671) from Abcam; GM130 (610822) from BD; phospho-AKT T308 (9275), phospho-AKT S473 (9271), phospho-JNK (9251), total JNK1 (9252), phospho-STAT3 (9131), total STAT3 (9132) and GADPH (2118) from Cell Signalling,

secondary mouse (7076) and rabbit (7074) peroxidase-conjugated antibodies from Cell Signalling. EGF was from Upstate Biotechnology Inc.

Immunofluorescence

COS-1 cells were plated and transfected with TransIT-X2 (Mirus) following manufacturer's instruction. Cells were fixed and immunostained as previously described[14]. Briefly, cells were fixed with 3.7% formaldehyde in BS for 10min. Subsequently the fixed cell were permiabilized with 0.5% Triton X-100-PBS (15 min), followed by 0.1 M glycine-PBS (30min). After blocking with 1% BSA-0.01% Tween 20 in PBS (5 min) the cell were incubated with the primary antibodies for an hour. GM130 (mouse) and Na/K ATPase (mouse) specific antibodies were used for the detection of endogenous markers and HA- (mouse) and FLAG- (Rabbit) tagged constructs. Next the cells were wash and incubated with Alexa secondary antibodies conjugated to fluorophores for 45 min. The localisation was determined by confocal microscopy (Leica TCS SP5) at excitation wavelengths of 488 nm (green) and 594 nm (red).

Ras activity assays

Ras activity assays were performed by Raf-RBD pull-down as previously described[14]. Briefly, cell were lysed usig magnesium rich lysis bugger (25 mM HEPES, pH 7.5, 10 mM MgCl2, 150 mM NaCl, 0.5 mM EGTA, 20 mM _-glycerophosphate, 0.5% Nonidet-P40, 10% glycerol, 2 mM sodium orthovanadate, 1, 25 _g/ml leupeptin, and 25 _g/ml aprotinin). Cell lyses were incubated rotating for 1 hour at 4ºC with glutathione agarose beads conjugated with GST-RBD, which contains Raf's Ras binding domain. Ras-GTP bound to the GST-RBD beads was pulled-down by short centrifugations. The beads were washed three times using lysis buffer without glycerol. Laemmli buffer was added to the dry beads and the proteins were denaturalised by boiling the samples which were next analysed by western blot. RasGTP fraction was detected with panRas

antibody for the endogenous Ras or HA antibody for the transfected Ras isoforms. RasGTP levels were normalised against determined total levels of Ras in the corresponding total lysates.

Proliferation assays

Proliferation analysis was performed as previously described[14]. Briefly, NIH3T3 cells were plated at a density of 50,000 cells per well in a six-well plate in duplicates and grown in 5% FBS containing media. Every 24 hours, cells were detached and resuspended using 0.5 ml of trypsin and counted using the Countess Automated Cell Counter (Life Technologies) following manufacturer's instructions.

Survival curves

To estimate survival rates NIH3T3 cells were plated at high density in a six-well plate in duplicates and grown in 1% FBS containing media. Cells were counted every 24 hours for 3 days by standard cell counting techniques as indicated above.

G418-resistant colonies formation

Colony formation assays were performed as described previously in Matallanas et al.[14] NIH3T3 cells were plated at low confluence and transfected with 0.5 μg of the indicated plasmids. Cells were grown in DMEM supplemented with 10% calf serum in the presence of G418 (750 μg/ml) for 10-15 days to allow the formation of discrete colonies. For scoring, cells were fixed, stained with GIEMSA, and colonies with a diameter bigger than 1 mm were counted.

Transformation assays

Focus formation assay was performed as established by Aaronson et al [50]. Briefly, 30% confluent NIH3T3 were plated and transfected using Lipofectaine with the low amounts of the indicated plasmids and grown for 3 weeks in DMEM supplemented with 10% calf serum. The media was changed every 3days and transformation of cells and the formation of foci was monitored using microscopy and visual inspection. When the focus were macroscopically detected by eye the cells were fixed and stained, and foci scored.

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FIGURE LEGENDS

Figure 1. Validation of the constructs for the expression of CDC25 at different compartments within the cell. A. *Expression of RasGRF1 CDC25 domain activates Ras.* HEK293 cells were transfected with 0.5 μg of HA-RasGRF1 or FLAG-CDC25 or stimulated with EGF (100 ng/ml) for 5 minutes. Cell were serum deprived for 16h. Cell lysates were incubated with GST-Raf-RBD and the activation of endogenous Ras was determined by pull-down assays. Activation of Ras and ERK was monitored using the indicated antibodies. The figure is representative of 3 independent experiments. B. *Expression of targeted CDC25 domain at different sub-localisations*. HEK293T cells were transiently transfected with 0.5 μg of DNA with FLAG-CDC25 (TOTAL), M1-FLAG-CDC25 (ER), LCK-FLAG-CDC25 (LR), CD8-FLAG-CDC25 (DM) and KDEL-FLAG-CDC25 (GC). Protein expression was tested by anti-FLAG immunoblotting in total lysates from the transiently transfected HEK293T cells (upper) and from FLAG immunoprecipitates from the stable HeLa cell lines (lower). C. *Cellular sub-localisation of targeted CDC25 domain*. COS-7 cells were co-transfected with 0.5 μg of each CDC25 plasmid and HA-LCK-HRas, HA-M1-Hras or mock plasmid as indicated. Fixed cells were stained with anti-FLAG antibody to detect CDC25 constructs and co-immunostained with anti-HA antibody or the indicated markers of subcellular membranes. Co-localisation was analysed by confocal imaging.

Figure 2. The CDC25 domain is able to activate HRas at different subcellular compartments. A. *Ras activation by CDC25 domain expression is isoform specific*. (*Upper panel)* HEK293 cell were co-transfected with 0.5μg HA-HRas, HA-KRas, HA-NRas, HA-RasGRF1(0.5 μg), FLAG-CDC25 (0.5 μg) or treated with EGF (100 ng/ml) for 5 min as indicated; *(Lower panel*) KEK293 cells were transfected with mock DNA (-) or co-transfected with 0.5 μg of HA-HRas wt, HA-NRas wt or HA-KRas wt and 1μg of FLAG-CDC25 or 1 μg of mock DNA as indicated. 24 hours after transfection the cells were serum

deprived (16 hours), and Ras activation was analysed by pulldown assays using the GST-Raf-RBD recombinant protein. Activation of the different isoforms was measured by Western-blot with anti-HA antibody in the pulled-down fraction and in the total lysates. The data shows HA-Ras-GTP levels normalised to the total HA-Ras, and represented as fold induction relative to the Ras-GTP levels in control cells (in absence of FLAG-CDC25) for each isoform. The data shows the average of two independent experiments and error bars represent standard deviation (SD). Anti-FLAG blot upper panel was spliced from the same gel B. *Activation of endogenous Ras by targeted CDC25 domain at different sub-localisation*. HeLa stable cell lines expressing CDC25 at different subcellular compartments were lysed 16 hours after serum starvation. Total lysates were incubated with GST-Raf-RBD recombinant protein for pulling down active Ras (Ras-GTP). Total Ras levels were determined by immunoblotting. Ras activation was normalised against the total Ras, and is represented as fold induction relative to the Ras-GTP levels in control cells (ST). The data shows the average ± the SD of two independent experiments. C. *Targeted CDC25 domain specifically activates Ras at each subcellular site*. Activated Ras at different compartments was analysed using pulldown assays with GST-Raf-RBD recombinant protein and further anti-Ras immunoblotting. HEK293 cells were transfected with 0.5μg of M1-HA-HRas wt, LCK-HA-HRas wt, CD8-HA-HRas wt, or KDEL-HA-HRas wt, in addition to 0.5μg of empty vector (-), FLAG-CDC25 (TOT), M1-FLAG-CDC25 (ER), LCK-FLAG-CDC25 (LR), CD8-FLAG-CDC25 (DM) and KDEL-FLAG-CDC25 (GA) where indicated. After 24 hours cells were serum deprived for 16 hours and lysed. Active Ras was pulled down using Raf-RBD. The figures are representative of 3 independent experiments.

Figure 3. Biochemical characterisation of Ras effector pathways activation. A. *ERK phosphorylation pattern is similar by comparing HRasV12 expression and HRas activation by CDC25*. NIH3T3 cells were co-transfected in parallel with targeted FLAGRasV12 or targeted FLAGCDC25 (0.5 μg) to different subcellular sites, M1 for ER, LCK for LR, CD8 for DM and KDEL for GC. Cells were serum deprived for 16 hours and the lysates were analysed by western blot by using specific antibodies. The blots were quantified using ImageJ and the graph shows ERK phosphorylation normalized with respect to total ERK and relative to the negative control (empty vector) in this experiment; n=3. B. *Ras activation from different localisation results on distinct level of Ras targets phosphorylation*. NIH3T3 cells were transfected with 0.5μg of empty vector, FLAG-CDC25 (TOT), M1-FLAG-CDC25 (ER), LCK-FLAG-CDC25 (LR), CD8-FLAG-CDC25 (DM) and KDEL-FLAG-CDC25 (GC). 24 hours post-transfection, the cells were starved for 7 hours and then lysed. Phosphorylation of the indicated proteins was determined by blotting with the indicated phospho-specific antibodies Corresponding total protein antibodies (anti-AKT, anti-JNK1 and anti-STAT3) were used for the normalization of the data. The blots where quantify using ImageJ and the numbers show fold of phosphorylation normalised with the control (-); n=3.

Figure 4. Biological characterisation of Ras activation. A. *Compartmentalised CDC25 expression has an effect on cellular proliferation*. NIH3T3 cells were seeded (50,000 cells/well) in six-well plate and transfected with 0.5 μg of the indicated CDC25 constructs. The proliferation rate of transfected cells, growing in media supplemented with 5% FBS, was monitored counting cells every 24 hours during 3 days. Data shows the average of three independent experiments, error bars show SD. B. *CDC25 domains do not confer bulk survival capacity*. Cells were seeded at high confluence (200,000 cells/well) in six-well plates and transfected with 0.5 μg of the indicated CDC25 constructs. Survival curves were monitored by counting cells every 24 hours for 3 days. Data shows the average of three independent experiments, error bars show SD C. *Colonies formation capacity is decrease by*

expression of targeted CDC25 in the endoplasmic reticulum. NIH3T3 were transfected with FLAG-CDC25, M1-FLAG-CDC25, LCK-FLAG-CDC25, CD8-FLAG-CDC25 or KDEL-FLAG-CDC25 (0.5 μg/plate). Transfected cells were selected in the presence of G418 (750 μg/ml). After 12-14 days in culture, colonies were Giemsa stained, and colonies with a diameter bigger than 0.5 mm were scored. Data shows the survival as the average of number of colonies ± SD of two independent experiments.

Figure 5. Physiological activation of Ras by CDC25. *Analysis of the transforming capacities of the CDC25 proteins.* NIH3T3 cells were seeded in low density and transfected with 0.5 μg/plate FLAG-CDC25 (TOT), M1-FLAG-CDC25 (ER), LCK-FLAG-CDC25 (LR), CD8-FLAG-CDC25 DM), KDEL-FLAG-CDC25 (GC) or 0.25 μg of FLAG-HRasV12. Transfected cells with HRas V12 (100 ng/plate) were used as positive control of foci formation. Foci were stained and scored after 3 weeks in culture. Numbers indicate average number of foci per μg of DNA ± SD of three independent experiments.

Figure 6. Summary of Ras effector pathway activation, and changes in phenotype mediated by endogenous HRas from different subcellular localisation. The scheme represents the HRas location specific activation effects observed in the current study. Font letter size indicates stronger effect.

Figure 1

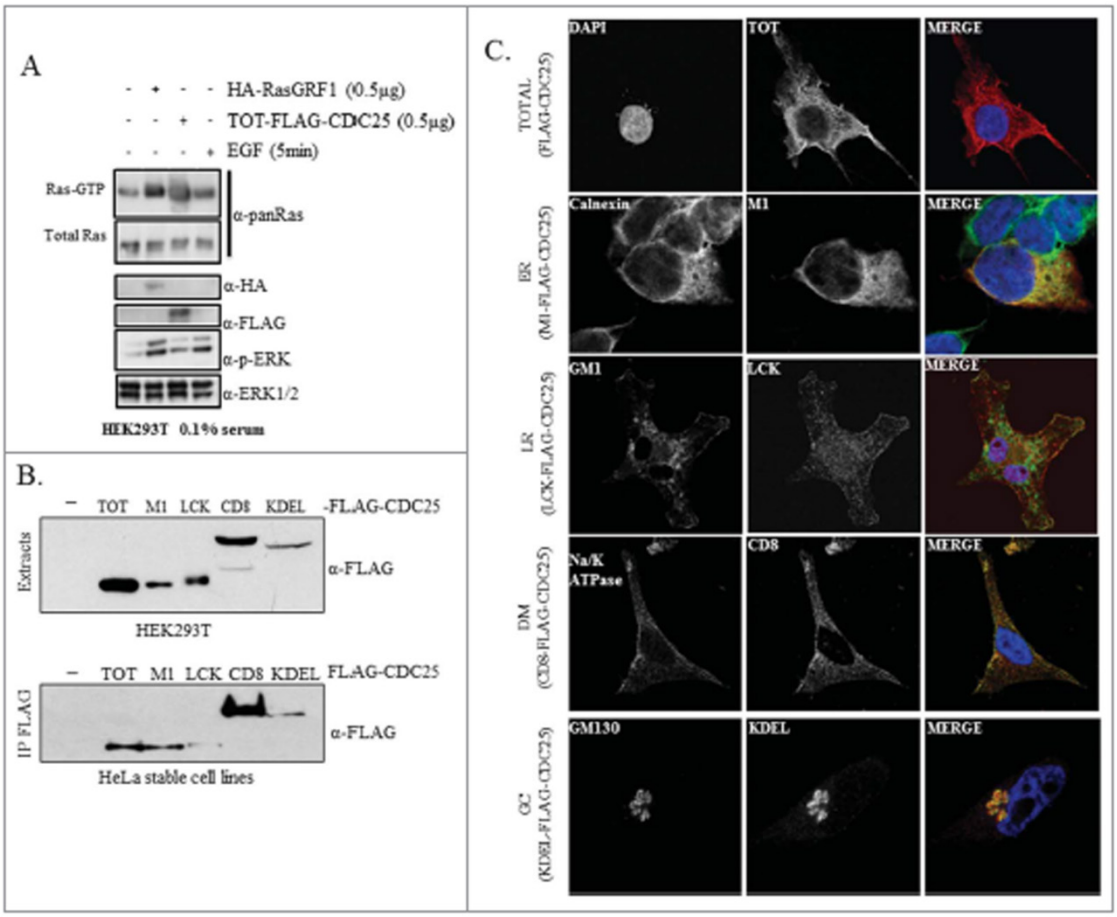

A
- + - - HA-RasGRF1 (0.5μg)
- - + - TOT-FLAG-CDC25 (0.5μg)
- - - + EGF (5min)
Ras-GTP
Total Ras
α-panRas
α-HA
α-FLAG
α-p-ERK
α-ERK1/2
HEK293T 0.1% serum
B.
– TOT M1 LCK CD8 KDEL -FLAG-CDC25
Extracts
α-FLAG
HEK293T
– TOT M1 LCK CD8 KDEL FLAG-CDC25
IP FLAG
α-FLAG
HeLa stable cell lines
C.
TOTAL (FLAG-CDC25)
DAPI
TOT
MERGE
ER (M1-FLAG-CDC25)
Calnexin
M1
MERGE
LR (LCK-FLAG-CDC25)
GM1
LCK
MERGE
DM (CD8-FLAG-CDC25)
Na/K ATPase
CD8
MERGE
GC (KDEL-FLAG-CDC25)
GM130
KDEL
MERGE

Figure 2

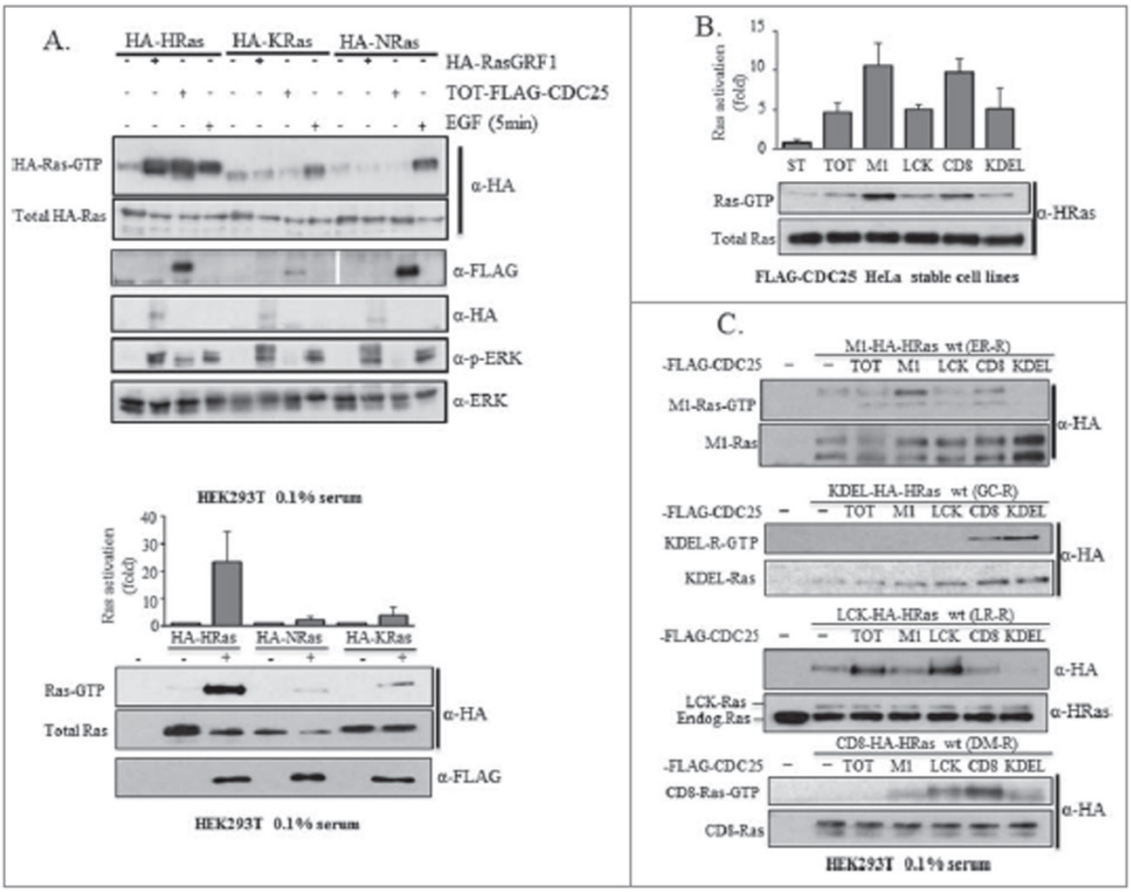

A.
HA-HRas
HA-KRas
HA-NRas
HA-RasGRF1
TOT-FLAG-CDC25
EGF (5min)
HA-Ras-GTP
Total HA-Ras
α-HA
α-FLAG
α-HA
α-p-ERK
α-ERK
HEK293T 0.1% serum
Ras activation (fold)
HA-HRas
HA-NRas
HA-KRas
Ras-GTP
Total Ras
α-HA
α-FLAG
HEK293T 0.1% serum
B.
Ras activation (fold)
ST
TOT
M1
LCK
CD8
KDEL
Ras-GTP
Total Ras
α-HRas
FLAG-CDC25 HeLa stable cell lines
C.
M1-HA-HRas wt (ER-R)
-FLAG-CDC25
TOT
M1
LCK
CD8
KDEL
M1-Ras-GTP
M1-Ras
α-HA
KDEL-HA-HRas wt (GC-R)
KDEL-R-GTP
KDEL-Ras
LCK-HA-HRas wt (LR-R)
LCK-Ras
Endog.Ras
α-HRas
CD8-HA-HRas wt (DM-R)
CD8-Ras-GTP
CD8-Ras
HEK293T 0.1% serum

Figure 3

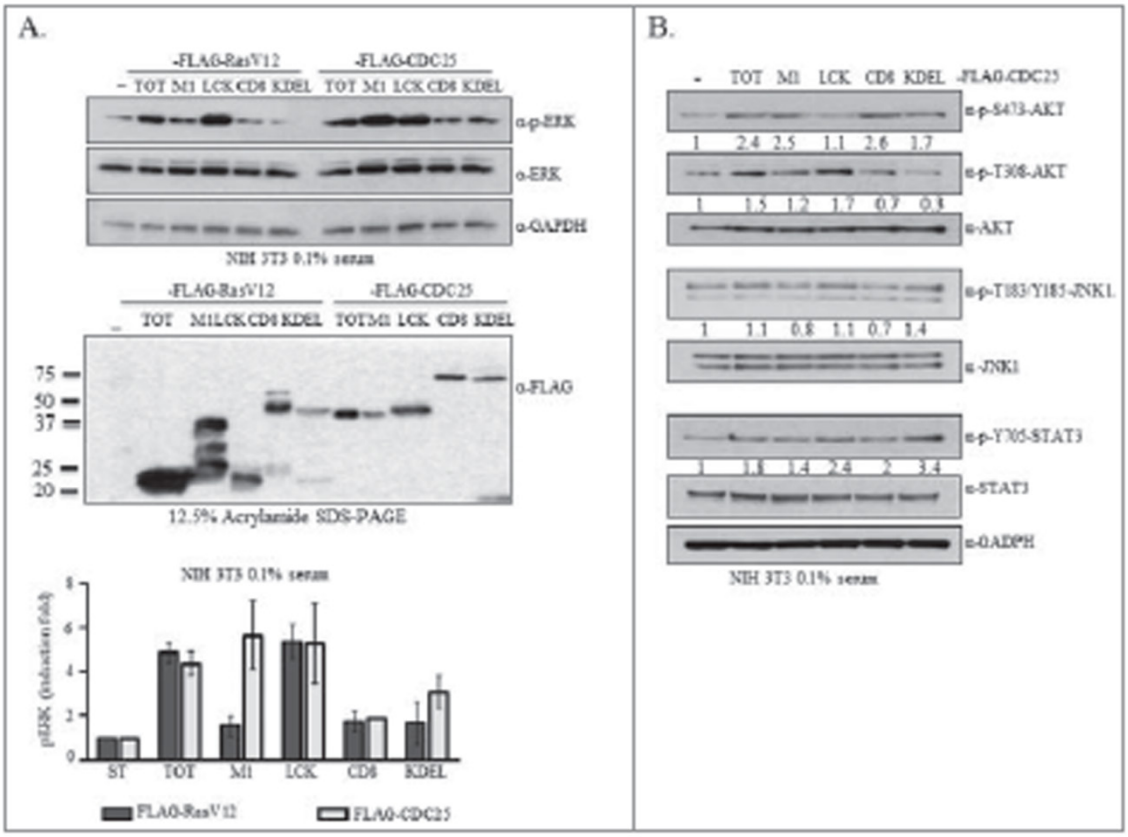

A.
-FLAG-RasV12
-FLAG-CDC25
- TOT M1 LCK CD8 KDEL TOT M1 LCK CD8 KDEL
α-p-ERK
α-ERK
α-GAPDH
NIH 3T3 0.1% serum
-FLAG-RasV12
-FLAG-CDC25
- TOT M1 LCK CD8 KDEL TOT M1 LCK CD8 KDEL
75
50
37
25
20
α-FLAG
12.5% Acrylamide SDS-PAGE
NIH 3T3 0.1% serum
pERK (induction fold)
ST TOT M1 LCK CD8 KDEL
FLAG-RasV12
FLAG-CDC25
B.
- TOT M1 LCK CD8 KDEL -FLAG-CDC25
α-p-S473-AKT
1 2.4 2.5 1.1 2.6 1.7
α-p-T308-AKT
1 1.5 1.2 1.7 0.7 0.8
α-AKT
α-p-T183/Y185-JNK1
1 1.1 0.8 1.1 0.7 1.4
α-JNK1
α-p-Y705-STAT3
1 1.8 1.4 2.4 2 3.4
α-STAT3
α-GADPH
NIH 3T3 0.1% serum

Figure 4

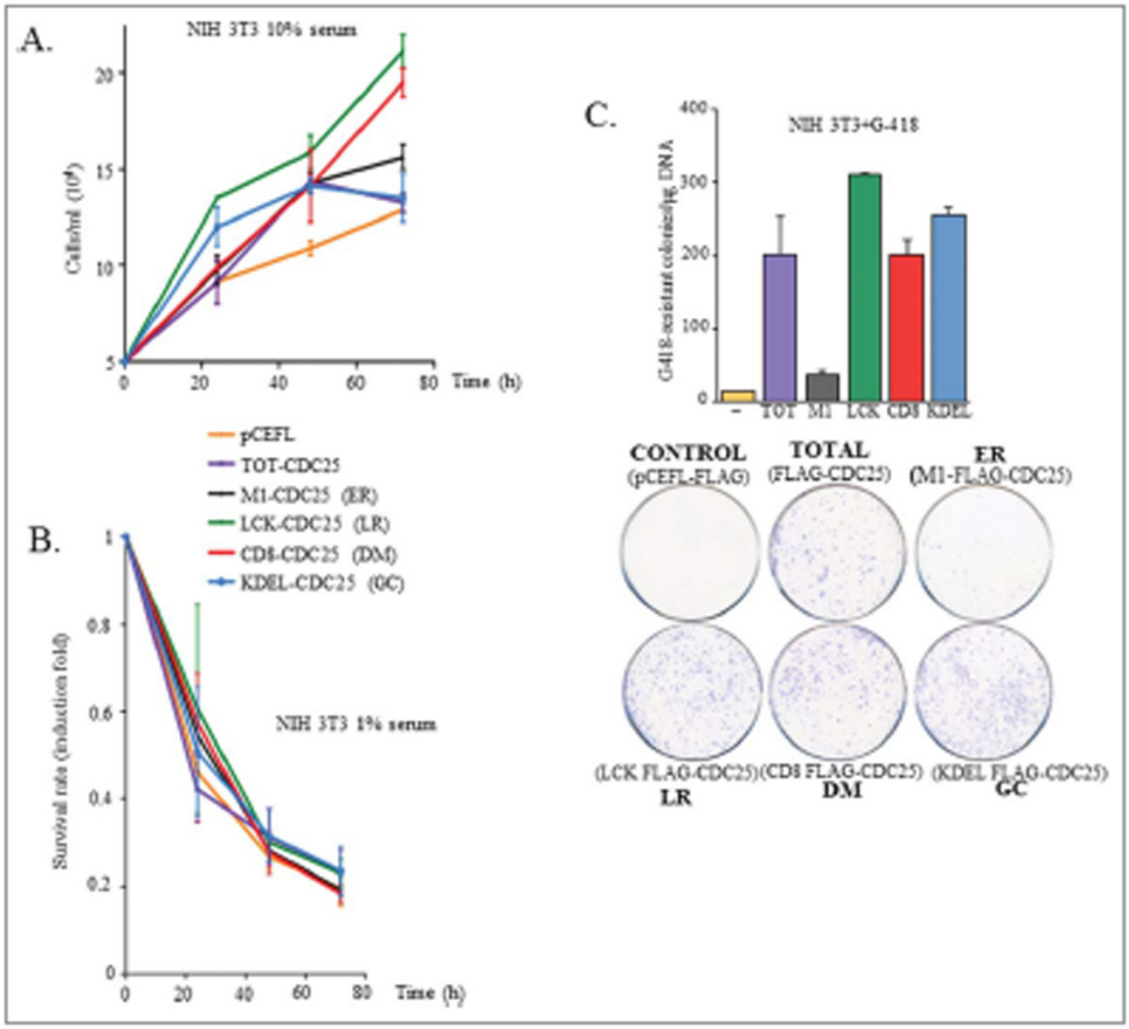

A.
NIH 3T3 10% serum
Cells/ml (10⁴)
Time (h)
pCEFL
TOT-CDC25
M1-CDC25 (ER)
LCK-CDC25 (LR)
CD8-CDC25 (DM)
KDEL-CDC25 (GC)
B.
NIH 3T3 1% serum
Survival rate (induction fold)
Time (h)
C.
NIH 3T3+G-418
G418-resistant colonies/μg DNA
– TOT M1 LCK CD8 KDEL
CONTROL
(pCEFL-FLAG)
TOTAL
(FLAG-CDC25)
ER
(M1-FLAG-CDC25)
(LCK FLAG-CDC25)
LR
(CD8 FLAG-CDC25)
DM
(KDEL FLAG-CDC25)
GC

Figure 5

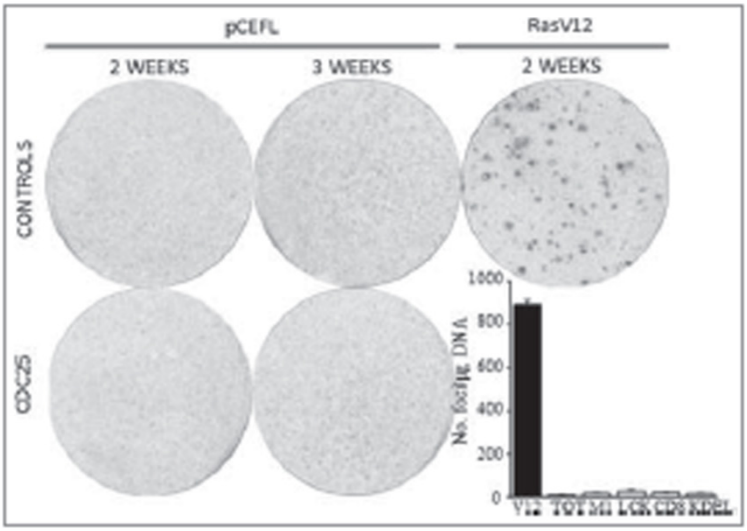
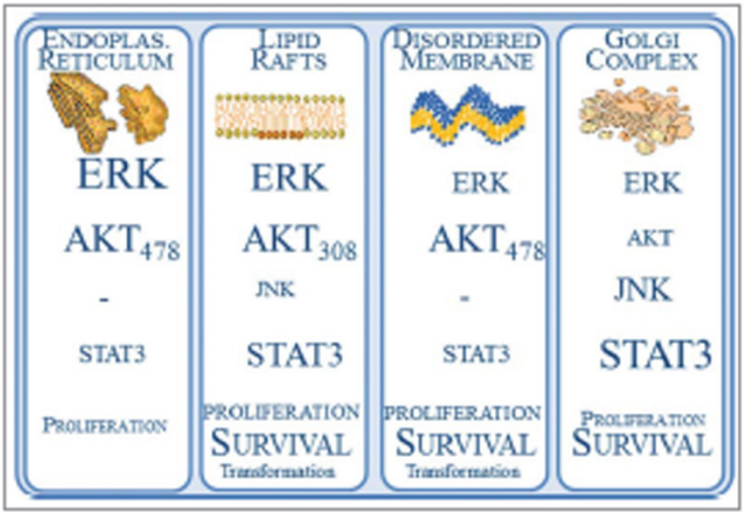

pCEFL
RasV12
2 WEEKS
3 WEEKS
2 WEEKS
CONTROLS
CDC25
1000
800
600
400
200
0

Figure 6


ENDOPLAS. RETICULUM
ERK
AKT478
-
STAT3
PROLIFERATION
LIPID RAFTS
ERK
AKT308
JNK
STAT3
PROLIFERATION
SURVIVAL
Transformation
DISORDERED MEMBRANE
ERK
AKT478
-
STAT3
PROLIFERATION
SURVIVAL
Transformation
GOLGI COMPLEX
ERK
AKT
JNK
STAT3
PROLIFERATION
SURVIVAL