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Local and global Cdc42 GEFs for fission yeast cell polarity are coordinated by microtubules and the Tea1/Tea4/Pom1 axis

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ABSTRACT

The conserved Rho-family GTPase Cdc42 plays a central role in eukaryotic cell polarity. The rod-shaped fission yeast *Schizosaccharomyces pombe* has two Cdc42 guanine-nucleotide exchange factors (GEFs), Scd1 and Gef1, but little is known about how they are coordinated in polarized growth. Although the microtubule cytoskeleton is normally not required for polarity maintenance in fission yeast, we show here that when *scd1* function is compromised, disruption of microtubules or the polarity landmark proteins Tea1, Tea4, or Pom1 leads to disruption of polarized growth. Instead, cells adopt an isotropic-like pattern of growth, which we term PORTLI growth. Surprisingly, PORTLI growth is due to spatially inappropriate activity of Gef1. Although most Cdc42 GEFs are membrane-associated, we find that Gef1 is a broadly-distributed cytosolic protein rather than a membrane-associated protein at cell tips like Scd1. Microtubules and the Tea1/Tea4/Pom1 axis counteract inappropriate Gef1 activity by regulating the localization of the Cdc42 GTPase-activating protein Rga4. Our results suggest a new model of fission yeast cell polarity regulation, involving coordination of “local” (Scd1) and “global” (Gef1) Cdc42 GEFs via microtubules and microtubule-dependent polarity landmarks.

INTRODUCTION

Cell polarity is essential for many eukaryotic cell functions, including migration and/or directional growth, intracellular transport, cell signaling, asymmetric cell division, and tissue organization (Campanale et al., 2017; Mayor and Etienne-Manneville, 2016; Rodriguez-Boulan and Macara, 2014; Schelski and Bradke, 2017; St Johnston and Ahringer, 2010). Cell polarization involves generation of spatial cues (intrinsic or extrinsic) for polarity site selection, recruitment of specific proteins to regions of plasma membrane, and reorganization of the actin and microtubule cytoskeleton and of intracellular trafficking. The Rho-family GTPase Cdc42 has important roles in many of these processes (Chiou et al., 2017; Etienne-Manneville, 2004; Etienne-Manneville, 2013; Hall, 2012; Harris and Tepass, 2010; Martin and Arkowitz, 2014; Perez and Rincon, 2010). Like other small GTPases, Cdc42 binds effector proteins in its active, GTP-bound, state. Control of Cdc42 activity by GTPase activating proteins (GAPs) and guanine-nucleotide exchange factors (GEFs) is thus a critical feature of polarity regulation (Bos et al., 2007; Cook et al., 2014; Hodge and Ridley, 2016; Moon and Zheng, 2003; Rossman et al., 2005).

Unicellular eukaryotes such as budding yeast *Saccharomyces cerevisiae* and fission yeast *Schizosaccharomyces pombe* are excellent models for studying Cdc42-dependent cell polarity, due to their simple geometries and reduced complexity relative to metazoans (Chiou et al., 2017; Martin and Arkowitz, 2014). Budding yeast are ovoid and form a single bud once per cell cycle, while fission yeast are rod-shaped and grow at their tips. In recent years, work in budding yeast has led to key insights into the mechanism(s) by which a stable, self-organized polarity cluster based on Cdc42-GTP can emerge on the plasma membrane to establish a presumptive bud site (Chiou et al., 2017; Goryachev and Leda, 2017; Woods and Lew, 2017). Cdc42 cluster formation depends on spontaneous symmetry-breaking via likely multiple converging positive feedback loops involving active Cdc42, Cdc42 effectors, and the Cdc42 GEF, Cdc24. Local enrichment of these factors via positive feedback can be sufficient for the establishment of cell polarity at a site designated by internal and/or external cues (Chiou et al., 2017; Goryachev and Leda, 2017; Woods and Lew, 2017).

While many of the components and mechanisms involved in budding yeast polarity are conserved in fission yeast, there are also distinct differences. Scd1, the fission yeast ortholog of budding yeast Cdc24, is thought to have a similar role to Cdc24, functioning in a positive feedback loop to organize polarity clusters of Cdc42-GTP on the plasma membrane at cell tips (Chang et al., 1999; Chang et al., 1994; Chiou et al., 2017; Endo et al., 2003). However, while Cdc24 is essential for viability, Scd1 is non-essential, as fission yeast has a second Cdc42 GEF, Gef1. Scd1 and Gef1 are thought to share an overlapping essential

function, because single-deletion mutants of either gene (*scd1* Δ or *gef1* Δ) are viable, while the double-deletion mutant (*scd1* Δ *gef1* Δ) is lethal (Coll et al., 2003; Hirota et al., 2003).

Both Scd1 and Gef1 have been described to localize to the cell midzone during cytokinesis and to the cell tips during interphase (Coll et al., 2003; Das et al., 2009; Hirota et al., 2003) (Das et al., 2015; Kokkoris et al., 2014; Vjestica et al., 2013). However, phenotypes associated with Scd1 and Gef1 differ significantly. Unlike rod-shaped wild-type cells, *scd1* Δ cells have a mostly round morphology (Chang et al., 1994) and lack detectable enrichment of Cdc42-GTP at cell tips (Kelly and Nurse, 2011; Tatebe et al., 2008). By contrast, *gef1* Δ cells have a largely wild-type morphology, albeit with mild defects in bipolar tip growth and septum formation (Coll et al., 2003). Similarly, Scd1 overexpression leads to no significant change in cell morphology, whereas Gef1 overexpression causes cells to become wider or rounder (Coll et al., 2003; Das et al., 2012). It is currently unclear how Scd1 and Gef1 activities are coordinated in the activation of Cdc42 at cell tips.

Another significant difference between fission yeast and budding yeast is that in fission yeast, interphase MTs make important contributions to cell polarity regulation (Huffaker et al., 1988; Jacobs et al., 1988; Martin and Arkowitz, 2014) (Chiou et al., 2017). In this regard, fission yeast may be more similar to mammalian cells, in which MTs can interact directly or indirectly with multiple polarity regulators and also provide tracks for directed transport of vesicles and signaling molecules (Etienne-Manneville, 2013; Neukirchen and Bradke, 2011; Siegrist and Doe, 2007; Sugioka and Sawa, 2012). Interphase MTs in fission yeast are nucleated from multiple intracellular sites and form ~3-5 bundles, each containing ~2-5 MTs, that extend along the long axis of the cell (Chang and Martin, 2009; Sawin and Tran, 2006). Landmark proteins such as Tea1 and Tea4 are continuously delivered to the cell tip via the plus ends of dynamic MTs (Martin et al., 2005; Mata and Nurse, 1997; Tatebe et al., 2005). Landmark proteins further recruit polarity factors such as the protein kinase Pom1, PP1 protein phosphatase Dis2, formin For3 and actin-associated protein Bud6, (Alvarez-Tabares et al., 2007; Bahler and Pringle, 1998; Glynn et al., 2001; Martin et al., 2005).

The importance of MTs in fission yeast cell polarity has been demonstrated by pharmacological inhibition (Sawin and Nurse, 1998; Sawin and Snaith, 2004) and by mutation of genes involved in microtubule biogenesis and function (Hirata et al., 1998; Radcliffe et al., 1998; Umesono et al., 1983; Vardy and Toda, 2000) (Anders et al., 2006; Samejima et al., 2005; Sawin et al., 2004). Mutations affecting MT nucleation and organization often lead to curved cells, while mutations affecting landmark proteins tend to lead to bent or branched cells, particularly after stress. By contrast, mutations in the Cdc42 polarity module lead to round- or wide-cell phenotypes (Chang et al., 1994; Kelly and Nurse, 2011; Miller and Johnson, 1994). Collectively, these findings have led to the view that MTs

and MT-dependent landmark proteins are important for selecting sites of polarity establishment but not for polarity establishment *per se* or maintenance of polarized growth (Chang and Martin, 2009; Sawin and Snaith, 2004). The differences in phenotypes mentioned above (i.e. mispositioned polarity vs. lost/impaired polarity) further highlight our limited understanding of how MTs and MT-dependent landmarks contribute to regulation of Cdc42-dependent cell polarity.

Here we address both the question of how the two fission yeast Cdc42 GEFs are coordinated in cell polarity regulation and how MTs and their effectors contribute to regulation of the core cell polarity machinery. Previous work showed that although *scd1* Δ cells are wide/round, they are nevertheless polarized during interphase (Kelly and Nurse, 2011). Here we find that polarized growth of *scd1* Δ cells, unlike wild-type cells, absolutely requires interphase MTs: after MT disruption, *scd1* Δ cells grow in an isotropic-like manner. We show that MTs promote polarized growth in *scd1* mutants via a pathway involving polarity proteins Tea1, Tea4, and Pom1 (the Tea1/Tea4/Pom1 “axis”), as well as Cdc42 GAP Rga4 (Das et al., 2007; Kokkoris et al., 2014; Tatebe et al., 2008). Remarkably, this pathway serves to counteract the activity of Gef1, which, contrary to some previous reports (Das et al., 2015; Das et al., 2009; Kokkoris et al., 2014; Vjestica et al., 2013), we find to be a cytosolic “global” Cdc42 GEF rather than a membrane-associated “local” GEF like Scd1. Our results reveal a previously unrecognized role for MTs and the Tea1/Tea4/Pom1 axis in the maintenance of fission yeast cell polarity and suggest a model in which local and global Cdc42 GEFs are active in parallel but regulated by different mechanisms. If not coordinated, these can impair rather than promote polarized growth.

RESULTS

***Polarized growth of scd1* Δ cells**

Previously it was shown that hydroxyurea (G1/S phase)-arrested *scd1* Δ cells have a polarized shape (Kelly and Nurse, 2011). This suggested that *scd1* Δ cells are normally polarized, but because of their round shape, polarization can be observed unambiguously only during extended interphase. To investigate polarization of *scd1* Δ without using hydroxyurea, we overexpressed the CDK-inhibitory kinase Wee1 (*adh13:wee1*) in *scd1* Δ cells that also expressed CRIB-3mCitrine, a reporter for active (GTP-bound) Cdc42 (Jaquenoud and Peter, 2000; Mutavchiev et al., 2016; Tatebe et al., 2008). Compared to *scd1* Δ cells, *adh13:wee1 scd1* Δ cells were clearly polarized, although also wider than wild-type cells (Fig. S1). Interestingly, in spite of this polarization, we did not detect CRIB-3mCitrine at cell tips in *adh13:wee1 scd1* Δ cells (Fig. S1A), similar to observations of hydroxyurea-arrested *scd1* Δ cells (Kelly and Nurse, 2011).

To characterize *scd1Δ* polarized growth in further detail, we used *cdc2-asM17* cells, which have a mutation in the ATP-binding pocket of Cdc2 and can be arrested in interphase by treatment with nucleotide-competitive analogs (Aoi et al., 2014; Bishop et al., 2000; Cipak et al., 2011). We imaged several different fluorescent-tagged cell polarity reporters in *scd1Δ cdc2-asM17* cells (Fig. 1). After treatment with the nucleotide-competitive analog 3-BrB-PP1, *scd1Δ cdc2-asM17* cells were clearly polarized, and beta-glucan synthase Bgs4 (Cortes et al., 2005; Cortes et al., 2015), exocyst component Sec8 (Snaith et al., 2011; Wang et al., 2002), F-actin reporter Lifeact (Huang et al., 2012; Riedl et al., 2008), and polarity landmark Tea1 (Mata and Nurse, 1997) were all localized to cell tips, as in wild-type cells (Fig. 1A-E). By contrast, CRIB, polarity kinase Shk1 (Qyang et al., 2002), and Cdc42 itself (Bendezu et al., 2015) were either not detected (CRIB, Shk1) or not visibly enriched (Cdc42) at cell tips after the same treatment (Fig. 1F-H).

We conclude that *scd1Δ* cells can grow in a polarized manner, with nearly all of the hallmarks of normal polarized growth. Due to the increased width of *scd1Δ* cells, their polarized growth is most easily apparent during extended interphase. In addition, polarized growth in *scd1Δ* is not associated with detectable levels of the CRIB reporter or Shk1 at cell tips ((Kelly and Nurse, 2011); see Discussion).

Polarized growth in scd1 mutants depends on microtubules and on polarity landmark proteins Tea1 and Tea4

Inability to detect CRIB-3mCitrine at cell tips in *scd1Δ* cells led us to ask what other factors might be important for *scd1Δ* polarized growth. Although MTs are not required for polarized growth in wild-type (*scd1+*) cells (Sawin and Snaith, 2004), we hypothesized that MTs might contribute specifically to polarized growth in *scd1Δ* cells. We imaged mCherry-Bgs4 in *scd1Δ cdc2-asM17* cells during extended interphase after 3-BrB-PP1 treatment, both in the presence and absence of the MT-depolymerizing drug MBC (Fig. 2; Movie 1). Inhibition of Cdc2-asM17 allowed imaging of cell growth for several hours without intervening cell division. In the absence of MBC, *scd1Δ cdc2-asM17* grew in a polarized manner, as did control (*scd1+*) *cdc2-asM17* cells in the presence of MBC. Strikingly, after addition of MBC to *scd1Δ cdc2-asM17* cells, Bgs4 no longer localized mainly to cell tips and instead formed transient, mobile patches on the plasma membrane (Fig. 2A). Accordingly, instead of growing in a polarized manner, MBC-treated cells became increasingly round over time (Fig. 2B,C). While average growth in these cells appeared to be isotropic, because of the dynamic, non-uniform distribution of Bgs4 on the plasma membrane we will refer to this growth pattern as “PORTLI” (POLaRity Transience Leading to Isotropic-like) growth. We conclude that MTs are critical for polarized growth in *scd1Δ* cells, but not in wild-type (*scd1+*) cells.

We hypothesized that MTs may contribute to polarized growth in *scd1* Δ cells via landmark proteins Tea1 and Tea4. Interestingly, and consistent with this hypothesis, *tea1* Δ *scd1* Δ double mutants are inviable (Papadaki et al., 2002). Therefore, to construct double mutants of *scd1* with *tea1* Δ and *tea4* Δ , we generated a strain in which expression of 3HA-tagged Scd1 is controlled by the weak, thiamine-repressible *nmt81* promoter (Basi et al., 1993) (Fig. 3A). For simplicity, we will refer to the repressed *nmt81:3HA-scd1* allele as *scd1*^{low}. Under repressing conditions, *scd1*^{low} cells had a round morphology and lacked detectable CRIB-3mCitrine at cell tips. We note, however, that other mutant phenotypes (see below) indicate that some biologically relevant, functional Scd1 is produced in these cells, albeit at very low levels.

We introduced *tea1* Δ and *tea4* Δ mutations into *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* backgrounds. Under repressing conditions, *tea1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* and *tea4* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* were viable but showed slightly increased frequency of cell death (see Methods). We repressed Scd1 expression for 24 h and then imaged cells after 3-BrB-PP1 addition (Fig. 3B; Movie 2). In control 3-BrB-PP1-treated cells, mCherry-Bgs4 remained highly polarized at cell tips, and cells grew in a polarized manner. By contrast, in *tea1* Δ and *tea4* Δ mutants even before 3-BrB-PP1 addition, cells were round, and mCherry-Bgs4 was present on the plasma membrane as small, randomly-positioned patches (sometimes barely detectable) and on internal membranes. After 3-BrB-PP1 addition, *tea1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* and *tea4* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* showed PORTLI growth, with transient, mobile mCherry-Bgs4 patches (Fig. 3B; Movie 2; Fig. 4B). This indicates that when Scd1 is expressed at very low levels, the absence of either Tea1 or Tea4 leads to loss of normal polarity. We further confirmed these results by imaging exponentially growing *scd1*^{low} and *scd1*^{low} *tea1* Δ cells in *cdc2+* backgrounds (Fig. S2; Movie 3).

***gef1* loss-of-function relieves the requirement for Tea1 and Tea4 in *scd1*^{low} polarized growth**

We next tested whether Gef1 contributes to polarized growth when *scd1* function is compromised (Fig. 4). Because *gef1* Δ *scd1* Δ double mutants are inviable, we introduced *gef1* Δ into *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* cells. Under repressing conditions, *gef1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* cells remained viable. Moreover, mCherry-Bgs4 was strongly enriched at cell tips both before and after 3-BrB-PP1 addition, and cells grew in a highly polarized manner (Fig. 4A,B; Movie 4). These results indicate that Gef1 is not required for polarized growth in *scd1*^{low} cells and thus that the very low level of Scd1 expressed in *scd1*^{low} cells is sufficient for viability and polarized growth. This in turn raised the question of why Tea1 and Tea4 are required for polarized growth in *scd1*^{low} cells.

We hypothesized two possible roles for the Tea1/Tea4 system. The first possibility was that Tea1 and Tea4 might enhance the intrinsic ability of Scd1 to serve as a GEF when expressed at very low levels. The second possibility, which was motivated by the observation that Gef1 overexpression causes cell rounding (Coll et al., 2003; Das et al., 2012), was that rather than supporting Scd1 function directly, Tea1 and Tea4 may prevent or counteract any inappropriate function of Gef1, which would otherwise somehow interfere with the ability of low levels of Scd1 to promote polarized growth.

To distinguish between these possibilities, we introduced *gef1* Δ into *tea1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* cells and imaged cells after *scd1* repression and 3-BrB-PP1 addition. Remarkably, *gef1* Δ completely reversed the PORTLI growth of *tea1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* cells, which now grew in a highly polarized manner (Fig. 4A,B; Movie 4). We obtained qualitatively similar results without Cdc2 inhibition (i.e. in the absence of 3-BrB-PP1; Fig. S3A). These results provide strong support for the second of the two possible roles proposed above.

In addition to a central catalytic Dbl homology (DH) domain required for GEF activity, Gef1 contains an N-terminal region of unknown function and a C-terminal region that is proposed to contain a Bin/amphiphysin/Rvs (BAR) domain (Das et al., 2015). Because *gef1* Δ abolishes expression of the entire Gef1 protein, it remained unclear whether the polarized growth seen in *gef1* Δ *tea1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* cells was specifically due to a loss of Gef1's GEF activity. We therefore mutated conserved residues E318 and N505 in the Gef1 DH domain to generate a mutant (*E318A, N505A*; termed *gef1-EANA*) that, based on previous structural and *in vitro* biochemical analyses, should be folded properly but unable to bind Cdc42 (Aghazadeh et al., 1998; Rossman et al., 2005; Rossman et al., 2002a; Rossman et al., 2002b). Consistent with this, we found that *gef1-EANA* is a loss-of-function allele, even though Gef1-EANA protein localized *in vivo* identically to wild-type Gef1 (Fig. S3B-E). In further imaging experiments, we found that after *scd1* repression, *gef1-EANA tea1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* cells were polarized both before and after 3-BrB-PP1 addition (Fig. 4A,B; Movie 4). This indicates that the reversal of PORTLI growth seen in our experiments can be attributed specifically to the loss of Gef1 GEF activity, rather than to the absence of Gef1 protein more generally.

Collectively, these results suggest not only that Gef1 is not required for polarized growth in *scd1*^{low} cells but also that preventing or counteracting Gef1 activity is a prerequisite for polarized growth in *scd1*^{low} cells. According to this view, the main role of Tea1 (and Tea4) in promoting polarized growth in *scd1*^{low} cells is to prevent PORTLI growth caused by inappropriate Gef1 activity, because if Gef1 is not present, then Tea1 is no longer required for polarized growth.

During unperturbed interphase, Gef1 is cytosolic rather than membrane-associated

How is Gef1 localized *in vivo* such that it can promote PORTLI growth in *scd1^{low}* cells? Initial characterization of Gef1 showed that it localized to the septum during cell division but did not have any specific localization during interphase (Coll et al., 2003; Hirota et al., 2003). However, it was later reported that Gef1 is also localized to cell tips during interphase (Das et al., 2015; Das et al., 2009; Kokkoris et al., 2014; Vjestica et al., 2013). Because it was not obvious to us how cell tip-localized Gef1 would lead to PORTLI growth, we reinvestigated Gef1 interphase localization.

Using several different fluorescent Gef1 fusion proteins, including previously published ones, we observed Gef1 at the septum during cell division, but we did not observe any specific localization of Gef1 during interphase, even with sensitive detection (Fig. 5A; Fig. S4A). We also did not observe specific localization of Gef1 in interphase *scd1Δ* cells (Fig. 5A,B), and we confirmed that our method of preparing cells for imaging does not introduce artifacts (Fig. S4B; see Methods). These results indicate that Gef1 is normally cytosolic and not enriched on the plasma membrane during interphase.

Interestingly, however, we did find conditions under which Gef1 becomes localized to cell tips. We treated cells expressing Gef1-3YFP with thiabendazole (TBZ), a drug that not only depolymerizes MTs but also leads to a stress that depolarizes the actin cytoskeleton for 60-90 min, via a non-MT-related mechanism (Sawin and Nurse, 1998; Sawin and Snaith, 2004). Upon TBZ treatment, Gef1-3YFP transiently localized to cell tips before becoming associated with mobile patches on the plasma membrane on cell sides (Fig. S4C,D; Movie 5). As we have recently found that stress signaling regulates the Cdc42 cell-polarity module (Mutavchiev et al., 2016), we speculate that during some imaging protocols, it is possible that some form of mild unintended stress may cause cytosolic Gef1 to associate with the plasma membrane at cell tips (see Discussion).

Targeting to cell tips converts Gef1 from a global to a local Cdc42 GEF

Together with our finding that *gef1Δ* and *gef1-EANA* mutations restore polarized growth to *tea1Δ scd1^{low}* cells, our observation that Gef1 is normally cytosolic suggested that the PORTLI growth seen in *scd1* mutants in the presence of MBC or in *tea1Δ* or *tea4Δ* backgrounds is due to Gef1 acting on membrane-associated Cdc42 from a cytosolic pool, as a “global” Cdc42 GEF. To support this view, we asked whether artificial targeting of Gef1 to cell tips—that is, changing a “global” Cdc42 GEF into a “local” GEF--would convert it from a promoter of PORTLI growth into a promoter of polarized growth.

In one set of experiments, we used GFP and GFP-binding protein (GBP; (Rothbauer et al., 2008)) to heterodimerize Gef1 with Tea1 (Fig. 5B). Fusion of Gef1-mCherry to GBP rescued the synthetic lethality of *gef1Δ scd1Δ* cells, indicating that Gef1-mCherry-GBP is

functional. In *gef1Δ scd1Δ* cells expressing untagged Tea1, Gef1-mCherry-GBP was cytosolic during interphase, and cells displayed the wide/round morphology expected for *scd1Δ* mutants. By contrast, in *gef1Δ scd1Δ* cells expressing Tea1-GFP, which is normally localized to cell tips (Behrens and Nurse, 2002), Gef1-mCherry-GBP relocated from the cytosol to cell tips, and cells displayed a normal, wild-type morphology. This demonstrates that targeting Gef1 to cell tips is sufficient to promote highly robust polarized growth in *scd1Δ* cells.

In a second set of experiments, we used rapamycin-induced dimerization (Chen et al., 1995; Haruki et al., 2008) to target Gef1 to cell tips (Fig. 5C). We tagged Gef1 with an Frb (FKBP-rapamycin binding) domain, and Tea1 with 2FKBP12 (2x12kD-FK506- and rapamycin-binding protein) (Ding et al., 2014). Because this does not require GFP-tagging of Gef1 or its dimerization partner, it allowed us to image CRIB-3mCitrine as a reporter of the Cdc42 cell-polarity module. We first validated dimerization by replacing endogenous Gef1 and Tea1 with Gef1-Frb-GFP and Tea1-2FKBP12 fusion proteins, in a *scd1Δ* background. Upon rapamycin addition, Gef1-Frb-GFP was rapidly recruited from the cytosol to cell tips, and cells became more polarized (Fig. S5A; Movie 6). We then replaced Gef1 and Tea1 with Gef1-Frb (i.e. without GFP) and Tea1-2FKBP12 in a *scd1Δ CRIB-3mCitrine* background. Before rapamycin addition, interphase cells showed nearly undetectable levels of CRIB-3mCitrine at cell tips. However, upon addition of rapamycin, CRIB-3mCitrine quickly appeared at cell tips, and morphology and polarized growth became similar to wild-type cells (Fig. 5D; Fig. S5B,C). By contrast, in control cells expressing Gef1-Frb, rapamycin did not induce CRIB-3mCitrine localization to cell tips. Taken together, these results indicate that relocating Gef1 from the cytosol to cell tips converts it from a global to a local Cdc42 GEF.

Pom1 kinase activity is required for polarized growth of scd1Δ cells

To understand how MTs, Tea1, and Tea4 may counteract Gef1 to allow polarized growth in *scd1* mutants, we investigated the polarity protein kinase Pom1 (Bahler and Pringle, 1998). Pom1 is localized to the plasma membrane and enriched at cell tips, and this depends both on Tea1 and Tea4 and on Pom1 kinase activity (Hachet et al., 2011). We introduced the analog-sensitive allele *pom1-as1-tdTomato* (Hachet et al., 2011), or control *pom1-tdTomato*, into *scd1Δ GFP-Bgs4 cdc2-asM17* cells and used 3-BrB-PP1 to simultaneously inhibit analog-sensitive Pom1 and Cdc2 (Fig. 6A,B; Fig. S6A; Movie 7). In control *pom1-tdTomato* cells, GFP-Bgs4 and Pom1-tdTomato localized to cell tips both before and after 3-BrB-PP1 addition, and cells grew in a polarized manner. In *pom1-as1-tdTomato* cells, GFP-Bgs4 and Pom1-as1-tdTomato localized to cell tips before 3-BrB-PP1 addition, but after 3-BrB-PP1 addition, both proteins became delocalized, and cells showed

PORTLI growth. This demonstrates that Pom1 kinase activity is required for polarized growth of *scd1* Δ cells.

To determine whether PORTLI growth after Pom1 inhibition depends on Gef1, we introduced either a *pom1* Δ single mutation or *pom1* Δ *gef1* Δ double mutation into *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* cells. After 3-BrB-PP1 addition, *pom1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* showed PORTLI growth, while *pom1* Δ *gef1* Δ *scd1*^{low} *mCherry-Bgs4 cdc2-asM17* grew in a polarized manner (Fig. S6B; Movie 8). These results suggest that Pom1, like Tea1 and Tea4, contributes to polarized growth of *scd1* mutant cells by counteracting Gef1.

One role of Pom1 is to regulate localization of the Cdc42 GTPase activating protein (GAP) Rga4 (Das et al., 2007; Tatebe et al., 2008). In wild-type cells, Rga4 is localized to the plasma membrane and enriched on cell sides but excluded from cell tips. By contrast, in *pom1* Δ and *pom1* kinase-inactive mutants, Rga4 is no longer excluded from non-growing cell tips (Tatebe et al., 2008). We therefore examined Rga4-3GFP localization in *pom1-as1-tdTomato* and *pom1-tdTomato* cells in *scd1* Δ *cdc2-asM17* backgrounds after 3-BrB-PP1 addition (Fig. 6C; Fig. S7). In control *pom1-tdTomato scd1* Δ *cdc2-asM17* cells, Rga4-3GFP remained largely excluded from cell tips. By contrast, in *pom1-as1-tdTomato scd1* Δ *GFP-Bgs4 cdc2-asM17* cells, Rga4-3GFP quickly became much more uniformly distributed on the plasma membrane, coincident with redistribution of Pom1-as1-tdTomato and the onset of PORTLI growth.

Cdc42 GAP Rga4 counteracts Gef1-dependent PORTLI growth

In principle, the more uniform distribution of Rga4-3GFP after Pom1 inhibition could be either a consequence or a cause of PORTLI growth. To distinguish between these possibilities, we investigated how Rga4 contributes to polarized growth when *scd1* function is compromised, and how this is affected by Gef1.

We first analyzed *rga4* Δ *scd1* Δ double mutants. Previous single-time-point images indicated that *rga4* Δ *scd1* Δ double mutants are especially wide (Kelly and Nurse, 2011) and, after hydroxyurea arrest, nearly round (Revilla-Guarinos et al., 2016). We introduced *rga4* Δ into *scd1* Δ *cdc2-asM17 mCherry-Bgs4* cells and imaged cell growth over several hours after 3BrB-PP1 addition. In contrast to the polarized growth of *scd1* Δ *cdc2-asM17* cells, *rga4* Δ *scd1* Δ *cdc2-asM17* cells showed PORTLI growth, with transient, mobile patches of mCherry-Bgs4 on the plasma membrane (Fig. 7A; Movie 9).

To investigate the role of Gef1 in Rga4-dependent polarized growth, we generated *rga4* Δ and *rga4* Δ *gef1* Δ mutants in a *scd1*^{low} *cdc2-asM17* background and analyzed them both with and without 3-BrB-PP1 (these cells also expressed CRIB-3mCitrine and Bgs4-mCherry; see Fig. S8). During extended interphase after 3-BrB-PP1 addition, *rga4* Δ *scd1*^{low}

cdc2-asM17 cells were compromised in polarity, becoming wider and rounder than control *scd1^{low} cdc2-asM17* cells. While these polarity defects were not as extreme as in *rga4Δ scd1Δ cdc2-asM17* or *tea1Δ scd1^{low} cdc2-asM17* cells under similar conditions, they were almost completely rescued by additional deletion of *gef1* (Fig. S8; see Discussion). During exponential growth (i.e. without 3-BrB-PP1), *rga4Δ scd1^{low} cdc2-asM17* cells were also significantly wider than isogenic control (*rga4+*) cells, and this was also rescued by the additional deletion of *gef1* (Fig. 7B,C). Collectively, these results indicate that polarity defects associated with *rga4Δ* in *scd1* mutants are mediated through Gef1.

Rescue of *rga4Δ* polarity defects by *gef1Δ* in a *scd1^{low}* background appeared to conflict with a previous report that *rga4Δ gef1Δ* double mutants were wider than either *rga4Δ* or *gef1Δ* single mutants (Kelly and Nurse, 2011). We therefore reinvestigated cell dimensions of *rga4Δ* and *gef1Δ* single and double mutants in a fully wild-type background (Fig. 7D,E). Consistent with an earlier characterization (Das et al., 2007), *rga4Δ* cells were wider than wild-type cells. However, we also found that additional deletion of *gef1* restored *rga4Δ* cells to normal width. Our results in a wild-type (*scd1+*) background thus contradict previous work (Kelly and Nurse, 2011) and suggest that increased width of *rga4Δ (scd1+)* cells is a consequence of global Gef1 activity competing, albeit with limited success, against relatively strong local Scd1 activity.

DISCUSSION

Cell polarity regulation by local and global Cdc42 GEFs

Our results suggest a conceptual model for Cdc42- and MT-mediated cell polarity regulation in fission yeast (Fig. 8) that is significantly different from previous models (Chang and Martin, 2009; Hachet et al., 2012; Rincon et al., 2014; Sawin and Snaith, 2004)(Chiou et al., 2017; Kokkoris et al., 2014; Martin and Arkowitz, 2014). While details of the model are presented in Fig. 8, we mention a few key points here.

We have shown that Gef1 is a cytosolic, “global” Cdc42 GEF, unlike Scd1, which is a cell tip-localized, “local” Cdc42 GEF (Hirota et al., 2003) (Kelly and Nurse, 2011). Moreover, the functional outputs of these two GEFs are controlled by distinct mechanisms, working in parallel. Promotion of polarized growth by Scd1 is thought to be a direct consequence of its localization at cell tips, dependent on a positive feedback mechanism similar to that in budding yeast (Chiou et al., 2017; Endo et al., 2003; Kelly and Nurse, 2011; Woods and Lew, 2017). By contrast, the spatially uniform cytosolic distribution of Gef1 during interphase would allow it, in principle, to activate Cdc42 anywhere on the plasma membrane. However, global Gef1 activity is normally spatially antagonized by Cdc42 GAP Rga4, whose localization is restricted to the cell sides by MTs and the Tea1/Tea4/Pom1 axis (Tatebe et al., 2008), leading to a “channeling” of net Gef1 activity towards cell tips. The importance of

restricting net Gef1 activity to cell tips is underscored by our finding that artificial targeting of Gef1 to cell tips in *scd1* Δ cells restores wild-type morphology and CRIB localization at tips.

We have shown that when *scd1* function is compromised, MTs and the Tea1/Tea4/Pom1 axis become essential for polarity maintenance. Previous work by us and others strongly supported the view that MTs and the Tea1/Tea4/Pom1 axis are important for specifying sites of cell polarity establishment but not for polarity establishment *per se*, or polarity maintenance (Bahler and Pringle, 1998; Mata and Nurse, 1997) (Chang and Martin, 2009; Martin et al., 2005; Sawin and Snaith, 2004; Tatebe et al., 2005). Our new results indicate that such a view is incomplete, and that a key role of the Tea1/Tea4/Pom1 axis is to counteract, via Rga4, any spatially inappropriate Gef1 activity at cell sides. In mammalian cells, there are similar examples of MTs regulating RhoGEF or RhoGAP distribution or activity, either directly or indirectly, in cell migration, cytokinesis, and tissue organization (Birkenfeld et al., 2008; Etienne-Manneville, 2013; Meiri et al., 2012; Ratheesh et al., 2012; Siegrist and Doe, 2007; Yuce et al., 2005). Although not addressed in the current work, we note that MTs and Tea1/Tea4/Pom1 axis are also important for New-End Take-Off (NETO), the transition from monopolar to bipolar growth (Bahler and Pringle, 1998; Martin et al., 2005; Mata and Nurse, 1997; Mitchison and Nurse, 1985; Nunez et al., 2016).

Our work further suggests that MTs provide the means for coordinating Gef1 function with Scd1 function. Normally, alignment of MTs along the long axis of the cell leads to positioning of MT-dependent landmarks at cell tips (Minc et al., 2009; Terenna et al., 2008) and therefore, ultimately, to enrichment of Rga4 at cell sides. Thus when MTs and landmarks are present, the Scd1 and Gef1 systems cooperate to promote polarized growth at the same sites, i.e. the cell tips. By contrast, when MTs and/or landmarks are absent, the Scd1 (local) and Gef1 (global) systems can end up competing with each other, with Gef1 promoting PORTLI rather than polarized growth (e.g. in *scd1^{low} tea1* Δ).

Our model also provides new mechanistic interpretations of previously-reported results. For example, *scd1* Δ and *rga4* Δ mutations were previously described as having additive effects on cell width, because the *scd1* Δ *rga4* Δ double mutant was found to be wider than either single mutant (Kelly and Nurse, 2011). However, our work demonstrates that the difference between the single mutants and the double mutant is in fact qualitative rather than quantitative, because while each single mutant is polarized, the *scd1* Δ *rga4* Δ double mutant shows PORTLI growth. Moreover, within the context of our model, the difference in cell shape between *scd1* Δ single mutants and *scd1* Δ *rga4* Δ double mutants, together with the rescue of *rga4* Δ phenotypes by *gef1* Δ , strongly suggests that the major physiological role of Rga4 in cell polarity regulation is to counteract the effects of Gef1.

Polarized and PORTLI growth in cells with impaired Scd1 function

To analyze polarized growth in *scd1* Δ and *scd1*^{low} cells, we imaged fluorescently-tagged beta-glucan synthase Bgs4, whose localization normally correlates precisely with polarized growth (Cortes et al., 2005), and we extended interphase by inhibiting analog-sensitive Cdc2 (Aoi et al., 2014). Interestingly, during PORTLI growth, Bgs4 appears as transient and mobile patches on the plasma membrane instead of being distributed homogeneously. The transient nature of these patches will be interesting to investigate in the future.

Imaging during extended interphase allowed us to unambiguously identify growth patterns in *scd1* mutants, which normally do not elongate very much during a single cell cycle because of their short/wide shape. Extended interphase can also circumvent problems that arise if strains have abnormal phenotypes associated with cytokinesis (e.g. *pom1* Δ ; (Bahler and Pringle, 1998) see Methods). While there may be caveats to the use of analog-sensitive Cdc2, we observed similar differences in polarized vs. PORTLI growth in several strains without Cdc2 inhibition; we therefore do not anticipate that Cdc2 inhibition significantly affects the overall interpretation of our results. In fission yeast, polarized growth continues when Cdc2 kinase is inactivated by either temperature- or analog-sensitive mutations (Dischinger et al., 2008; Nurse et al., 1976). In this context, fission yeast may be different from budding yeast, which has both polarized and isotropic growth periods during interphase, depending on the stage of bud formation (Chiou et al., 2017; Martin and Arkowitz, 2014). In the absence of inhibition, *cdc2-asM17* retains essentially all functionality of wild-type *cdc2+* (Aoi et al., 2014), unlike an earlier *cdc2-as* allele (Dischinger et al., 2008), and to inhibit Cdc2-asM17, we used the minimum concentration of analog required to prevent mitotic entry (see Methods). Under these conditions (i.e. in the absence of any other perturbations), both wild-type and *scd1* Δ cells show robust polarized growth.

While our initial experiments involved *scd1* Δ cells, many subsequent experiments involved *scd1*^{low} cells. This was critical for deciphering the relationship between Scd1, Gef1 and the Tea1/Tea4/Pom1 axis, because *scd1* Δ is synthetically lethal with *tea1* Δ and *gef1* Δ , while *scd1*^{low} is not. At the same time, these differences in synthetic lethality highlight the fact that because *scd1*^{low} cells retain some Scd1 function, they are not equivalent to *scd1* Δ cells. In particular, after 3-BrB-PP1 treatment (in *cdc2-asM17* backgrounds), *scd1* Δ *rga4* Δ cells show PORTLI growth, while *scd1*^{low} *rga4* Δ cells have less severe polarity defects (which are nevertheless rescued by *gef1* Δ). The simplest explanation for this is that in *scd1*^{low} *rga4* Δ cells, the polarity system set up by low levels of Scd1 can partially compete against the Gef1-dependent drive towards PORTLI growth. How low levels of Scd1 achieve this at a mechanistic level remains to be explored.

In this context, it is also interesting to compare polarity phenotypes of *scd1^{low} rga4Δ* with *scd1^{low} tea1Δ*, because *scd1^{low} tea1Δ* cells show more severe PORTLI growth (as do *scd1^{low} tea4Δ*, and *scd1^{low} pom1Δ*). We can imagine two non-exclusive explanations for this difference. First, in addition to regulating Rga4, the Tea1/Tea4/Pom1 axis could have a separate role in either bolstering *scd1^{low}* function or countering *gef1* function. Tea1 was recently shown to have a role in limiting the distribution of sterol-rich membrane domains to cell poles (Makushok et al., 2016), via an unknown mechanism; however, it is unclear whether this could be important for polarized vs. PORTLI growth, as *rga4Δ scd1Δ* cells are *tea1+* but still show PORTLI growth. Tea1 is also important for polarized growth of *for3Δ* cells (Feierbach et al., 2004) and in a *cdc42* allele with an added (engineered) transmembrane domain (Bendezu et al., 2015). Second, the different phenotypes could be due to the presence vs. the absence of Rga4. That is, in *scd1^{low} tea1Δ* cells, the GAP activity of Rga4 will be distributed essentially evenly over the entire plasma membrane, including at “prospective tip” regions, thereby counteracting the weak polarizing activity of Scd1^{low}; by contrast, in *scd1^{low} rga4Δ* cells, there is no Rga4 GAP activity anywhere, and therefore low levels of Scd1 may have a greater net effect on cell polarity.

Currently it is unclear why CRIB-3mCitrine is not detectable at cell tips in polarized *scd1Δ* and *scd1^{low}* cells. While it is formally possible that polarized growth in these cells does not involve GTP-bound Cdc42 at cell tips, it is equally plausible that the levels of GTP-bound Cdc42 and/or other factors required for CRIB reporter localization (Takahashi and Pryciak, 2007) are simply below the threshold necessary for detection. In this context, it is important to note that even though CRIB-3mCitrine is not detected at cell tips in *scd1^{low}* cells, cell-polarity phenotypes indicate that these cells nevertheless produce biologically-important levels of Scd1.

Gef1 localization during interphase

As we find that in unperturbed interphase cells, Gef1 is cytosolic, both in wild-type and in *scd1Δ* backgrounds, it is unclear why some (but not all) reports observed Gef1 at interphase cell tips (Das et al., 2015; Das et al., 2009; Kokkoris et al., 2014; Vjestica et al., 2013). Our own results lead us to speculate that these reports could be due to unintended mild cell stress, possibly because of how cells are prepared for imaging, or because of phototoxicity during imaging (Laissue et al., 2017). In our experiments, cells are imaged under conditions that are essentially identical to those of cells growing in flasks, apart from shaking. This minimizes stress ((Mutavchiev et al., 2016); see Methods) and allows imaging of polarized growth under the microscope for several hours.

Previous work has suggested that Gef1 is negatively regulated by phosphorylation via the NDR kinase Orb6 (Das et al., 2015; Das et al., 2009); specifically, Orb6 is thought to prevent Gef1 from localizing to the plasma membrane on cell sides. Our results are not inconsistent with this view. However, because we find that Gef1 can be active as a cell-polarity GEF from the cytosol, we would argue that regulation of Gef1 membrane localization (specifically, to cell sides) is separable from regulation of Gef1's GEF activity *per se*. It is possible that localization of Gef1 to the plasma membrane on cell sides might further potentiate its net biological activity relative to any countering GAP activity from Rga4. These will be interesting questions to address in the future.

Regulated localization of Cdc42 GEFs to the plasma membrane may also be relevant to mammalian cells. Gef1 is unusual among RhoGEFs in that while it contains a catalytic DH domain, it lacks a pleckstrin homology (PH) domain, which is present in nearly all DH-family RhoGEFs and is important for association with membrane lipids (Cook et al., 2014; Rossman et al., 2005). The mammalian Cdc42 GEF Tuba also lacks a PH domain and instead contains a BAR domain (Salazar et al., 2003); Gef1 has also been proposed to contain a BAR domain, although this has not been confirmed experimentally (Das et al., 2015). Interestingly, in MCDK epithelial cells, Tuba is localized to the cytoplasm when cells are grown in a monolayer but is concentrated subapically when cells are grown to form cysts (Qin et al., 2010). Thus, like Gef1, the localization of Tuba may be subject to regulation, during development and/or differentiation.

Links from polarity landmarks to Gef1 and Rga4

We showed previously that MT-based targeting of Tea1 to cell sides can promote new polarity axis formation, leading to branched cells (Sawin and Snaith, 2004). More recently, Kokkoris *et al.* reported that ectopically-localized Tea4 can specify growth sites through a mechanism involving Gef1 and Rga4 (Kokkoris et al., 2014). These experiments were based on fusing an N-terminal Tea4 fragment (Tea4N) to the cortical node protein Cdr2 (Morrell et al., 2004; Wu et al., 2006), leading to localization of the Cdr2-Tea4N fusion protein to nodes at cell sides. The Cdr2-Tea4N fusion induced an ectopic “bulge” at cell sides, and further experiments suggested this was due to local activation of Cdc42 via localized plasma-membrane recruitment of Gef1 and exclusion of Rga4. While both our current work and that of Kokkoris *et al.* suggest functional links from Tea4 to Gef1 and Rga4, there are several distinctions between the two studies. First, and most generally, the work of Kokkoris *et al.* suggests that the Tea4 landmark is *sufficient* for growth at ectopic sites, while one aspect of our work has been to show that the Tea4 landmark (together with Tea1 and Pom1) is *necessary* for polarized growth at normal cell tips, specifically when Scd1 function is compromised. Second, Kokkoris *et al.* reported that Gef1 is recruited to ectopic sites

containing the Cdr2-Tea4N fusion. In contrast, we have shown that Gef1 is not detected on the plasma membrane of unperturbed wild-type or *scd1* Δ cells, although it can be enriched on the plasma-membrane under certain conditions (e.g. TBZ treatment, independent of Tea4; Fig. 5; Fig. S4; Movie 5). Third, the bulge induced by Cdr2-Tea4N did not require Pom1, whereas we find that Pom1 is essential for polarized growth in *scd1* Δ cells (Fig. 6; Fig. S6; Fig. S7; Movie 7; Movie 8). Fourth, bulging induced by Cdr2-Tea4N was dependent not only on Gef1 but also, surprisingly, on Rga4. In contrast, our data suggest that Rga4 on the plasma membrane at cell sides locally counteracts the effect of global Gef1 activity, thereby preventing growth in the cell middle. Finally, the ectopic bulge induced by Cdr2-Tea4N is qualitatively different from the conventional polarized growth seen at normal cell tips and in cells that establish a new polarity axis in the cell middle by other means (so-called “T” shape; (Sawin and Snaith, 2004; Snell and Nurse, 1994)). These differences suggest that the detailed mechanisms that lead to the Cdr2-Tea4N-induced ectopic bulge may be distinct from those that polarize growth at a normal cell tip.

Concluding remarks

What might be the purpose of regulating cell polarity by both local and global Cdc42 GEFs? While here we can only speculate, we note that *gef1* Δ cells have a mild defect/delay in NETO (Coll et al., 2003; Das et al., 2012). Computational modeling suggests that Gef1’s contribution to total Cdc42 GEF activity may be an important feature in the timing of NETO and in the symmetry of Cdc42 activation at the two cell tips (Das et al., 2012). In light of our results, it may be of interest to investigate, in a more detailed spatial model, how the particular properties of a local vs. a global GEF may influence the NETO transition. A second possible purpose relates to our observation that although Gef1 is cytosolic in unperturbed cells, it associates with the plasma membrane upon TBZ treatment (this work), as well as upon inhibition/inactivation of Orb6 (Das et al., 2009). Thus, Gef1 may have a specific role in regulating cell polarity in response to stress or cell signaling.

METHODS

Yeast culture

Standard fission yeast methods were used throughout (Forsburg and Rhind, 2006; Petersen and Russell, 2016). Growth medium was either YE5S rich medium (using Bacto yeast extract; Becton Dickinson) or PMG minimal medium, with glucose added after autoclaving (PMG is equivalent to EMM2 minimal medium but uses 4 g/L sodium glutamate instead of ammonium chloride as nitrogen source). PMG was used only for experiments involving *scd1*^{low} cells (i.e. *nmt81:3HA-scd1* cells), in which case cells were grown first in

PMG (i.e. without thiamine) and then in PMG plus 20 μ M thiamine for 24 hr prior to use in imaging experiments. In all other experiments (i.e. all experiments not involving *scd1^{low}* cells) YE5S was used. Supplements such as adenine, leucine, and uracil were used at 175 mg/L. Solid media used 2% Bacto agar (Becton Dickinson).

Plasmid and yeast strain construction

Mating for genetic crosses (Ekwall and Thon, 2017) was performed on SPA5S plates with supplements at 45 mg/L. Crosses were performed using tetrad dissection or random spore analysis. Tagging and deletion of genes were performed using PCR-based methods (Bahler et al., 1998), with the exception of the strains described below, which involved integration of newly-constructed plasmids. All plasmid constructions (below) were confirmed by sequencing. For rapamycin-induced dimerization, endogenous Gef1 and Tea1 were tagged with Frb/Frb-GFP (Gef1) and 2FKBP12 (Tea1), using PCR-based methods (Ding et al., 2014). To prevent rapamycin-based inhibition of normal cellular pathways via the endogenous TOR system, these alleles were crossed into a *tor2-S1837E fkh1 Δ* background (note that *tor2-S1837E* is different from the *tor1-S1834E* allele described in Ding et al.) (Ding et al., 2014; Laor et al., 2014; Takahara and Maeda, 2012). All strains used in this study are listed in Table S1.

***adh13:wee1* plasmid/strain construction.** The *wee1* open reading frame (ORF) was amplified by PCR from genomic DNA and cloned into the NdeI site of pNATZA13 (kind gift from Y. Watanabe) to form pNATZA13-Wee1 (pKS1448). Apal-linearized pKS1448 was then integrated at the Z locus (Sakuno et al., 2009) of KS515, and positive clones were screened by microscopy and confirmed by colony PCR.

gef1-EANA-3mCherry. TOPO-Gef1-3mCherry:kan plasmid (pKS1632) was constructed using 3-piece Gibson assembly approach (NEB). Briefly, PCR fragments of TOPO vector (pCR2.1), Gef1 ORF (flanked by 180bp upstream of Gef1 ORF), and 3mCherry-Kan fragment (flanked by 180bp downstream of Gef1 ORF) were assembled to generate pKS1632. A PCR fragment of Gef1 (internal fragment corresponding to amino-acid residues 314-508 but containing two point mutations, E318A and N505A) was subsequently introduced into pKS1632 via a 2-piece Gibson assembly approach to generate pKS1699. A Gef1-containing SpeI-XbaI fragment from pKS1699 was then purified and transformed into strain KS7656 to generate strain KS9183.

gef1-mCherry-GBP. The *gef1+* ORF was amplified from genomic DNA and introduced into pINTH41.3HA-mCherry-GBP-3PK:natMX6 plasmid (kind gift from I. Hagan) via 2-piece Gibson assembly to generate pKS1488. NotI-linearized pKS1488 was then transformed into strain KS7742 to generate strain KS8152.

Microscopy sample preparation and imaging

All imaging experiments were performed with exponentially growing cells cultured at 25°C. Imaging was performed either in coverslip dishes (MatTek; P35G-0.170-14-C.s) or 4-chamber glass bottom micro-slides (Ibidi; 80427). Imaging dishes/slides were placed on a 25°C heat block, coated with 1 mg/mL soybean lectin (Sigma; L1395), left for 10 min, and washed with appropriate medium to remove excess lectin. Log-phase culture was added to dishes/slides and left to settle for 15 minutes. The dishes/slides were washed extensively with media using aspiration with at least 3 full exchanges of media (approximately 1 mL each). Finally, 500 μ L of medium was added to the dish/slide before imaging. For lectin-free imaging, a 4-chamber micro-slide was used. 300 μ L of *gef1-3mCitrine* culture ($OD_{595}=0.25$) was added directly to one chamber and imaged within 10 mins. Cells immobilized on a lectin-coated glass bottom in an adjacent chamber were used to first find the correct focal plane for imaging.

Live-cell fluorescence imaging was performed using a custom spinning-disk confocal microscope unit [Nikon TE2000 microscope base, attached to a modified Yokogawa CSU-10 unit (Visitech) and an iXon+ Du888 EMCCD camera (Andor), 100x/1.45 NA Plan Apo objective (Nikon), Optospin IV filter wheel (Cairn Research), MS-2000 automated stage with CRISP autofocus (ASI), and thermo-regulated chamber maintained at 25°C (OKOlab)]. Metamorph software (Molecular Devices) was used to control the spinning-disc confocal microscope.

3-BrB-PP1 (4-Amino-1-tert-butyl-3-(3-bromobenzyl)pyrazolo[3,4-d]pyrimidine; A602985) was obtained from Toronto Research Chemicals and dissolved in methanol to make a 50 mM stock solution. 3-BrB-PP1 was used at a final concentration of 8 μ M; 4 μ M was insufficient to completely prevent mitotic entry. Thiamine, methyl-2-benzimidazole carbamate (MBC), and thiabendazole (TBZ) were obtained from Sigma. Thiamine was dissolved in water as 200 mM stock and used at a final concentration of 20 μ M. MBC stock solution was 2.5 mg/mL in DMSO and was used at a final concentration of 25 μ g/mL (therefore 1% DMSO final concentration). In MBC experiments, DMSO-only control used 1% DMSO final. TBZ stock solution was 30 mg/mL in DMSO and was used at a final concentration of 150 μ g/mL (therefore 0.5% DMSO final concentration). Rapamycin was obtained from Fisher Scientific Ltd (Cat No. 10798668). Rapamycin was dissolved in DMSO as a 1 mg/mL stock and used at a final concentration of 2.5 μ g/mL. All drug additions during imaging were performed by medium exchange using a 1 mL polyethylene transfer pipette (Fisher Scientific, 1346-9118).

We note that when grown on solid PMG medium without thiamine, *scd1^{low} tea1Δ*, *scd1^{low} tea4Δ*, and *scd1^{low} pom1Δ* double mutants formed colonies that were noticeably smaller than wild-type cells and *scd1^{low}* single mutants. Under these conditions, the double mutants also showed some defects in septum positioning and in completion of cytokinesis. Accordingly, we found that during normal growth in liquid PMG medium without thiamine, 22% (9/41) of non-dividing *scd1^{low} tea1Δ* cells were binucleate, compared to 0% (0/87) of *scd1^{low} (tea1+)* cells. After nine hours repression in thiamine, 58% (32/55) of non-dividing *scd1^{low} tea1Δ* cells were binucleate, compared to 0% (0/151) of *scd1^{low} (tea1+)* cells. In all *scd1^{low}* mutants, analysis of growth patterns after inhibition of Cdc2-asM17 by 3-BrB-PP1 was limited to mononucleate cells.

Numbers of independent biological replicate experiments are provided for each yeast strain, in each figure, in the yeast strain list in Table S1. We define an independent biological replicate as growing/culturing a given yeast strain and then using it for a given biochemistry experiment or imaging session. Up to a few hundred cells of the same genotype may be imaged in any given replicate imaging session.

Analysis of microscopy images

Processing of the acquired raw images was executed using ImageJ (Fiji, NIH). Unless otherwise stated, all images and videos shown are maximum projections of eleven Z-sections with 0.7 μm step-size. For rigid body registrations, ImageJ StackReg and Linear Stack Alignment with SIFT plugins were used. Image formatting and assembly were performed using Photoshop (Adobe) and Illustrator CS3 (Adobe). Cell outlines were drawn by hand in Illustrator, using images from individual video time-points as templates. In some cases, cell outlines were aligned slightly due to limited cell movement during imaging. In a few cases where cell borders were more difficult to discern (e.g. in late-stage depolarized cells), images from successive time-points were superimposed and then used as a template for drawing. Videos were edited using ImageJ and QuickTime (Apple).

Quantification of the percentage of cells with polarized mCherry-Bgs4 or GFP-Bgs4 signals on cell tips (Figs. 2, 3, 4 and 6) was performed manually, based on analysis of videos. Cells with persistent mCherry-Bgs4 or GFP-Bgs4 signals on the cell tips (over a period of four hr) were scored as polarized cells. To avoid confusing depolarized cells with cells that simply had a diminished Bgs4 signal (because of photo-bleaching), quantification was performed using only on the first four hr of videos. Occasional cells that transiently lost the tip signal but then regained it shortly afterwards (i.e. in the same place) were also scored as polarized cells. Graphs were created using Graphpad Prism software. Statistical analysis was carried out using online tools (<http://www.graphpad.com/quickcalcs/>; <http://www.socscistatistics.com>]

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Figures

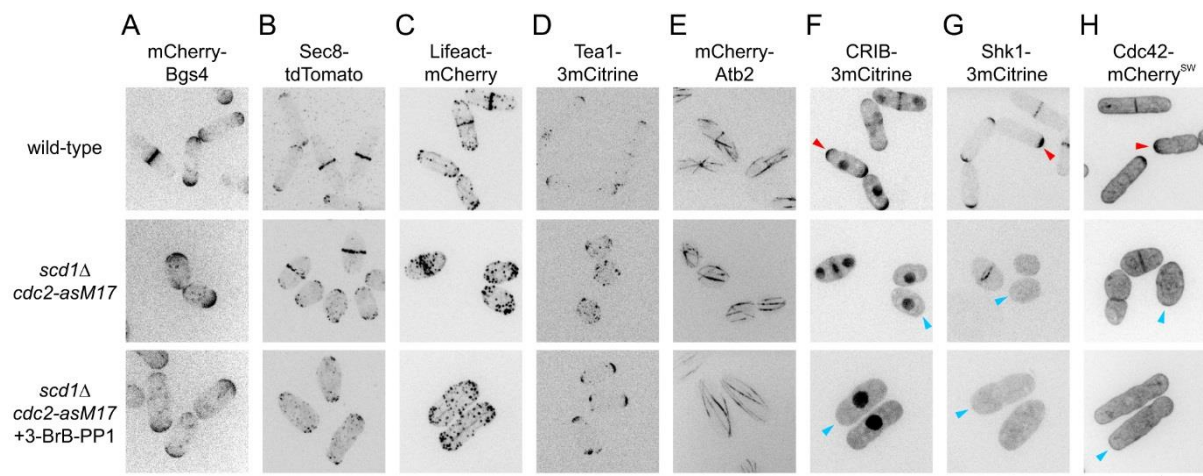


Figure 1. Polarized growth of *scd1* Δ cells during extended interphase.

(A-H) Cell morphology and localization of polarity-associated proteins in cells of the indicated genotypes. In bottom panels, 3-BrB-PP1 was added 5 hr before imaging to inhibit analog-sensitive Cdc2. Arrowheads in F, G indicate detection (red) or no significant detection (blue) at cell tips. Arrowheads in H indicate enrichment (red) or no enrichment (blue) at tips. Bar, 10 μ m. See also Figure S1.

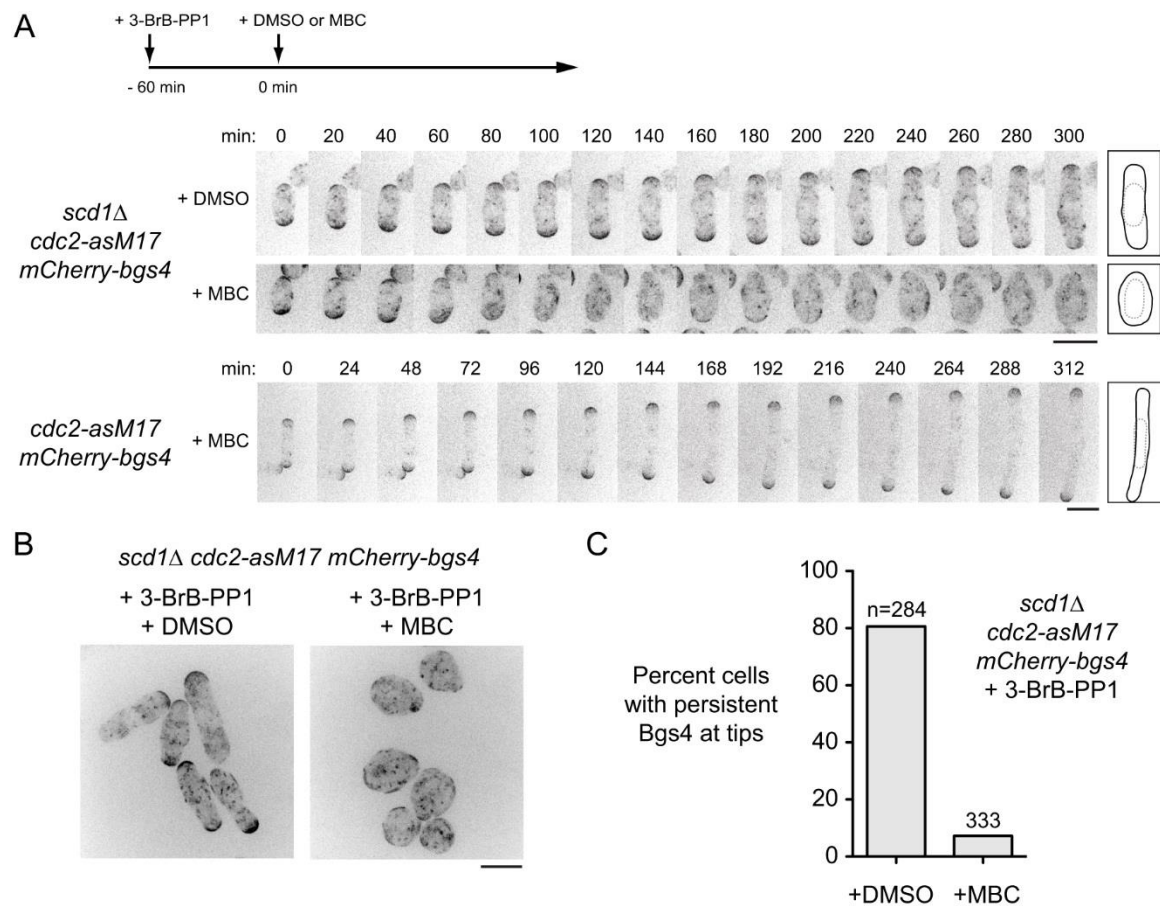


Figure 2. Microtubule depolymerization in *scd1* Δ cells leads to PORTLI growth.

(A) Movie time-points showing cell morphology and mCherry-Bgs4 distribution in indicated genotypes, treated with 3-BrB-PP1 at -60 min and then with DMSO or MBC (plus 3-BrB-PP1). Diagrams show outlines at beginning and end of movies. (B) Fields of cells as in A, after 3-BrB-PP1 and DMSO or MBC treatment for 300 min. (C) Quantification of mCherry-Bgs4 at cell tips during DMSO or MBC treatment (see Methods); n indicates number of cells scored. Difference between DMSO and MBC treatment was highly significant ($p < 0.0001$; Fisher's exact test). Bars, 10 μ m. See also Movie 1.

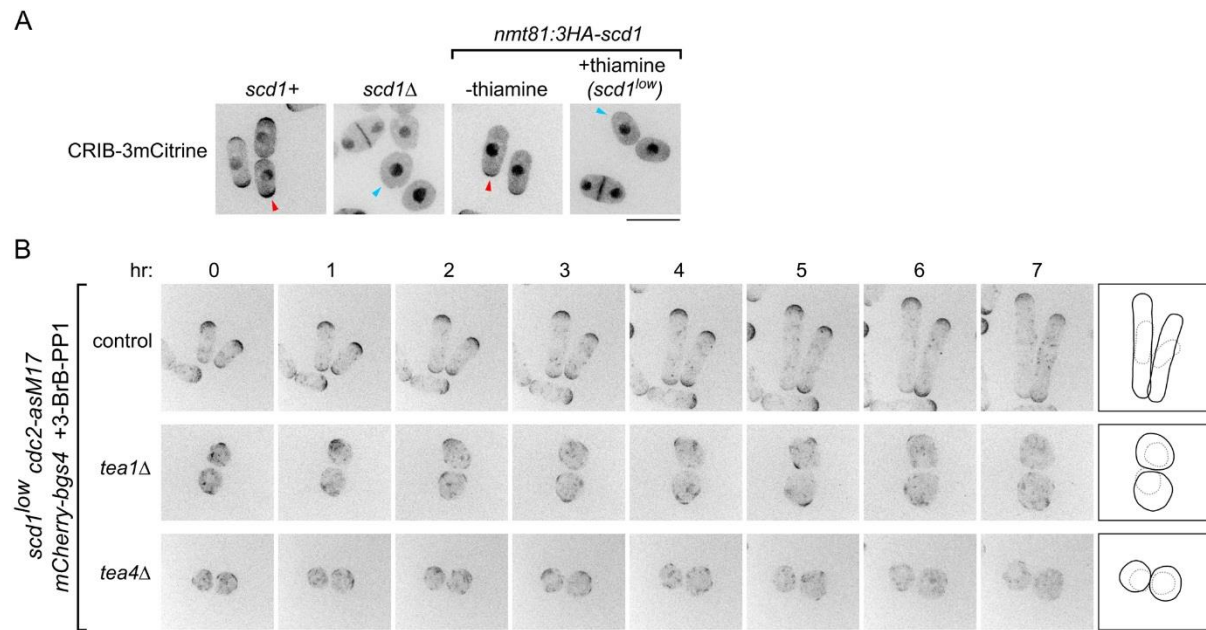


Figure 3. When *scd1* is expressed at very low levels, *tea1Δ* and *tea4Δ* cells show PORTLI growth.

(A) Cell morphology and CRIB-3mCitrine localization in indicated genotypes. Thiamine represses *nmt81:3HA-scd1* expression ("*scd1^{low}*"). Arrowheads indicate detection (red) or no significant detection (blue) of CRIB-3mCitrine at tips. (B) Movie time-points showing cell morphology and mCherry-Bgs4 distribution in indicated genotypes. *scd1* expression was repressed 24 hr before imaging. 3-BrB-PP1 was added 30 min before imaging. Diagrams show outlines at beginning and end of movies. Bars, 10 μ m. See also Movie 2.

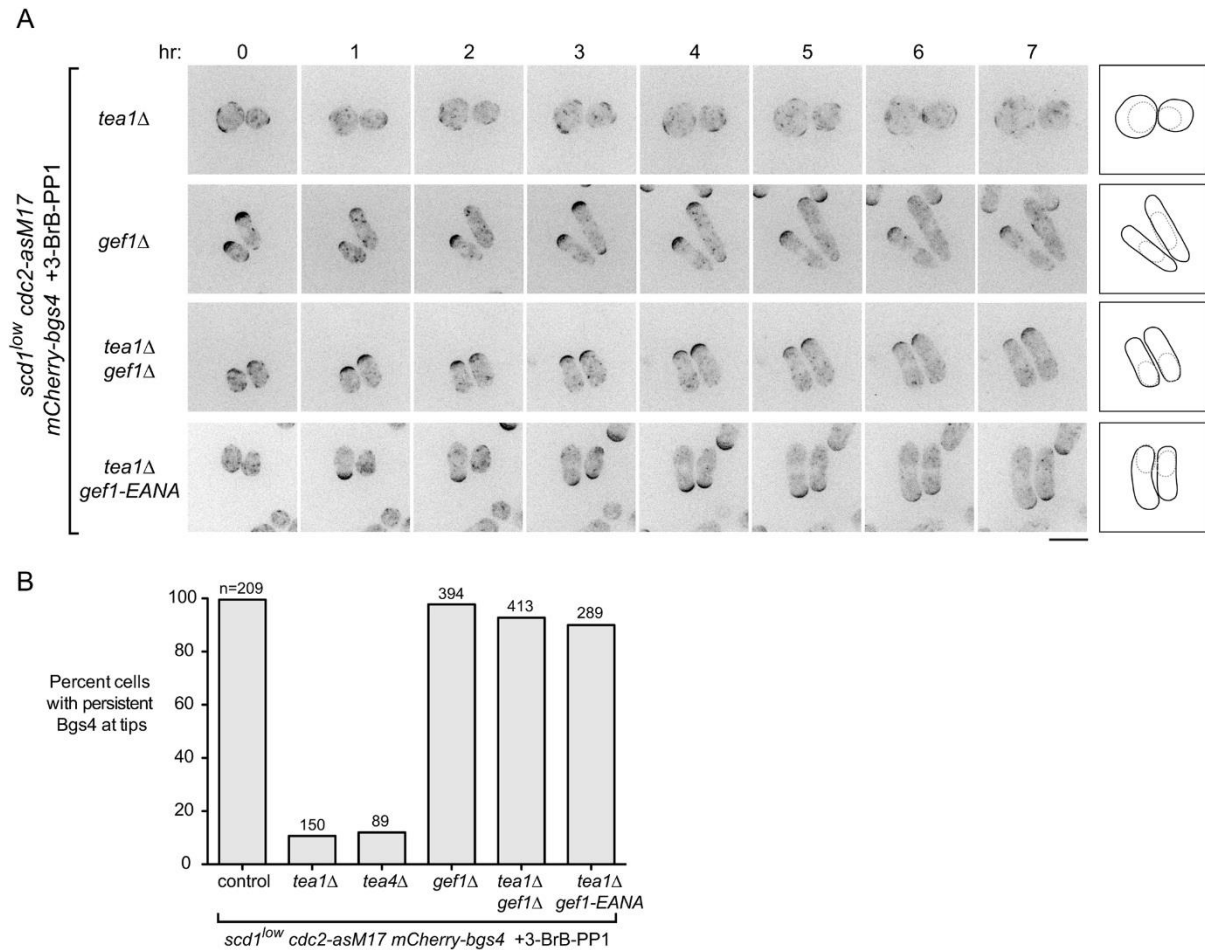


Figure 4. Loss of *gef1* function restores polarized growth to *scd1^{low} tea1*Δ cells.

(A) Movie time-points showing cell morphology and mCherry-Bgs4 distribution in indicated genotypes. *scd1* expression was repressed 24 hr before imaging. 3-BrB-PP1 was added 30 min before imaging. Diagrams show outlines at beginning and end of movies. Note newborn daughter cells often have less mCherry-Bgs4 at cell tips. (B) Quantification of mCherry-Bgs4 at cell tips, from movies of the type in Fig. 3 and Fig. 4A; n indicates number of cells scored. Pairwise differences relative to control (first column) were highly significant for all strains except *gef1*Δ, ($p < 0.0001$; Fisher's exact test, with correction for multiple comparisons). Bar, 10 μ m. See also Figure S3 and Movie 4.

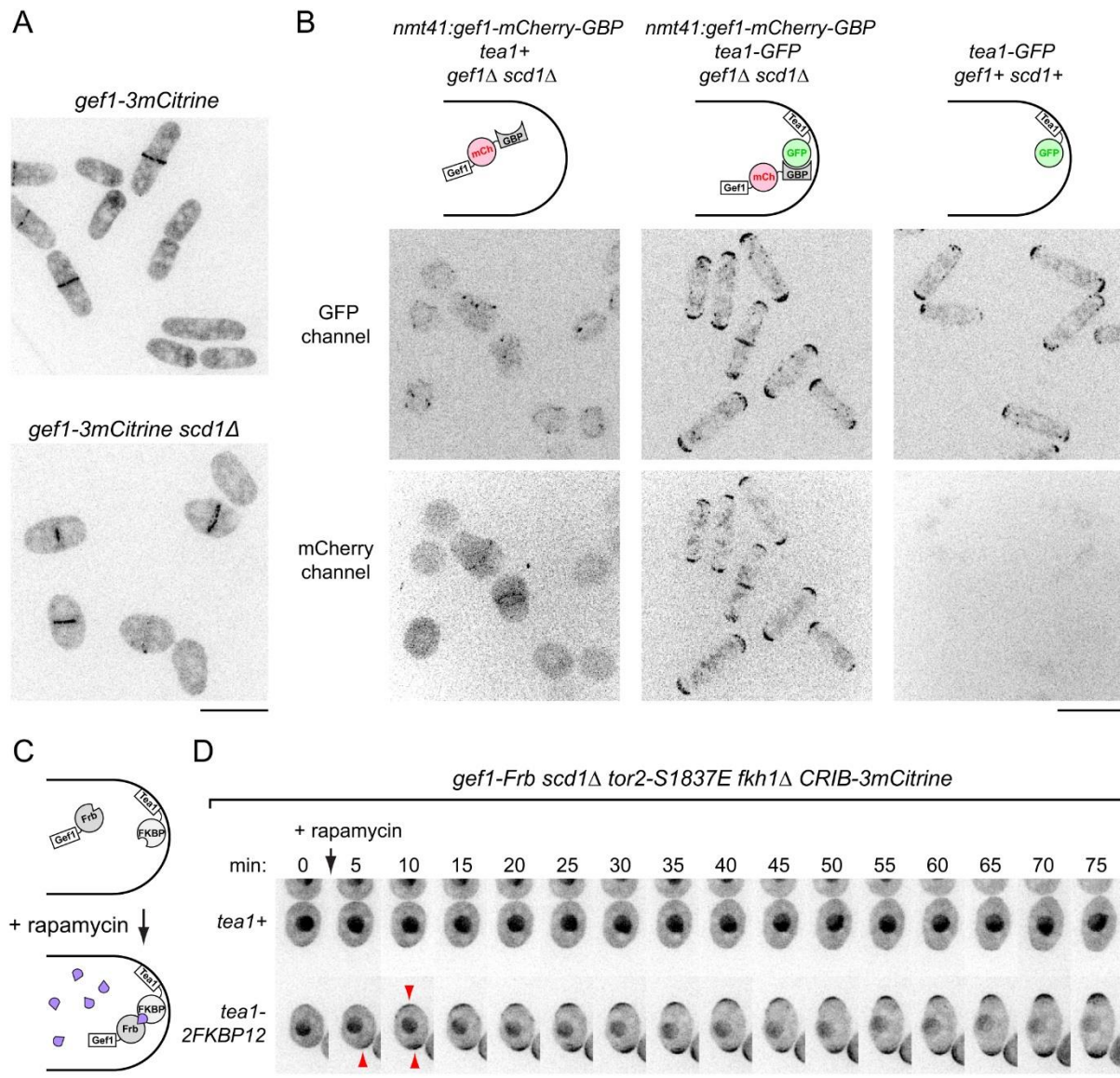


Figure 5. Gef1 is normally cytosolic and is active during interphase, as targeting Gef1 to cell tips in *scd1Δ* cells restores wild-type morphology and Cdc42-GTP enrichment at tips.

(A) Localization of Gef1-3mCitrine in wild-type and *scd1Δ* cells. In both cases, Gef1 is present at septum but not at cell tips. (B) Ectopic targeting of Gef1-mCherry-GBP to cell tips by coexpression of Tea1-GFP, in *scd1Δ* background. In untagged *tea1+* cells (left), Gef1-mCherry-GBP remains cytosolic, and cells are round. In *tea1-GFP* cells (middle), Gef1-mCherry-GBP is at cell tips, and cells are polarized. Right panels show absence of bleed-through from GFP channel to mCherry channel. (C) Schematic of targeting Gef1 to cell tips by rapamycin-induced dimerization. (D) CRIB-3mCitrine localization after time-resolved targeting of Gef1 to cell tips by rapamycin-induced dimerization with Tea1-2FKBP12. Negative control cells express untagged Tea1 (*tea1+*). Rapamycin was added just after the 0 min time-point. Arrowheads indicate appearance of CRIB-3mCitrine at tips after rapamycin addition. Bars, 10 μ m. See also Figures S4, S5 and Movies 5, 6.

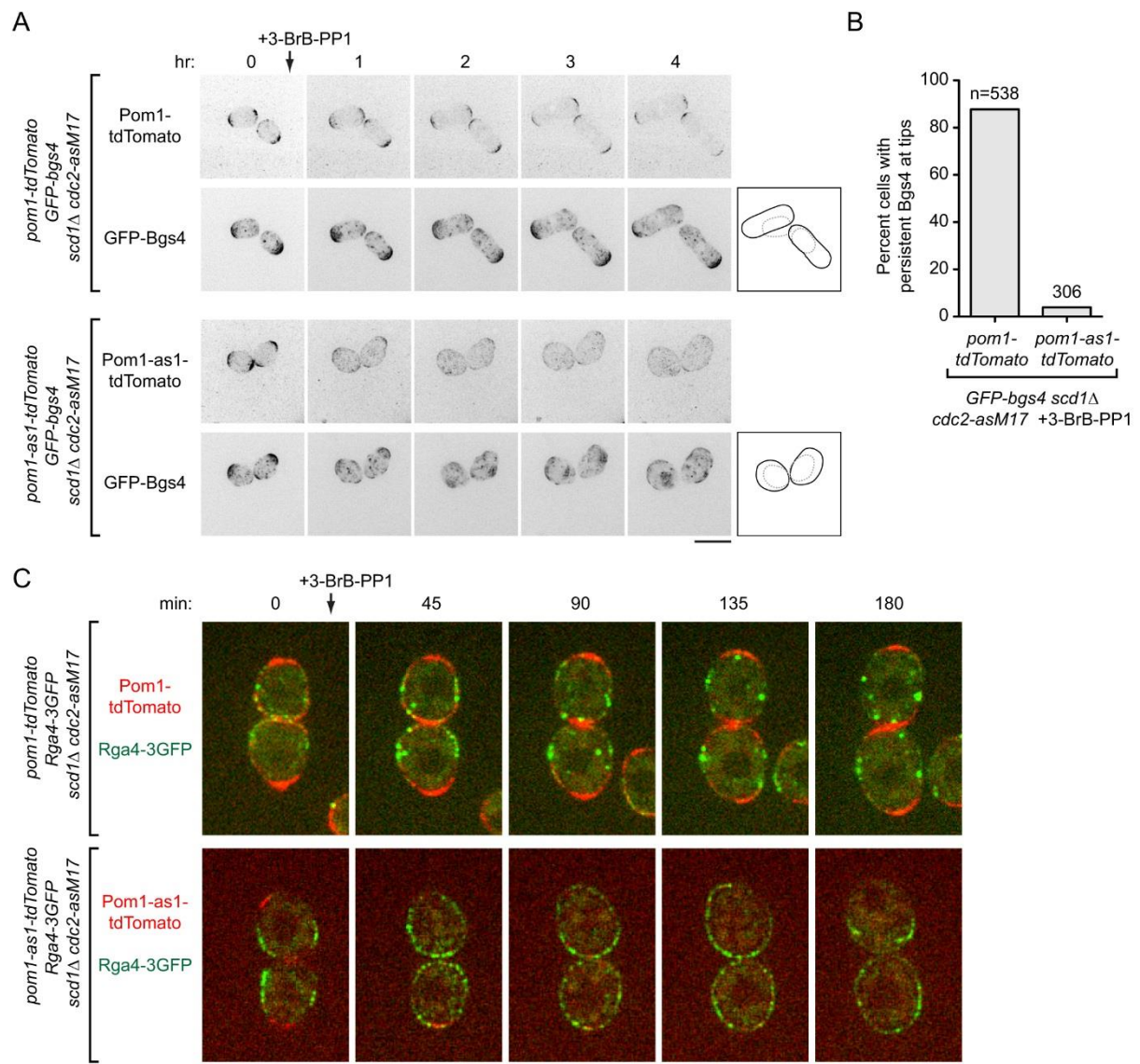


Figure 6. Inhibition of Pom1 kinase activity in *scd1*Δ cells leads to PORTLI growth and randomized localization of Cdc42 GAP Rga4.

(A) Movie time-points showing cell morphology and distribution of Pom1-tdTomato or Pom1-as1-tdTomato and GFP-Bgs4 in indicated genotypes after 3-BrB-PP1 treatment (added just after 0 hr time-point). 3-BrB-PP1 inhibits both Cdc2-asM17 and Pom1-as1-tdTomato. Diagrams show outlines at beginning and end of movies. (B) Quantification of GFP-Bgs4 at cell tips, from movies of the type in A. Differences were highly significant ($p < 0.0001$; Fisher's exact test). (C) Single focal-plane movie time-points showing cell morphology and distribution of Pom1-tdTomato or Pom1-as1-tdTomato and Rga4-3GFP in indicated genotypes after 3-BrB-PP1 treatment. Bars, 10 μ m. See also Figures S6, S7 and Movies 7, 8.

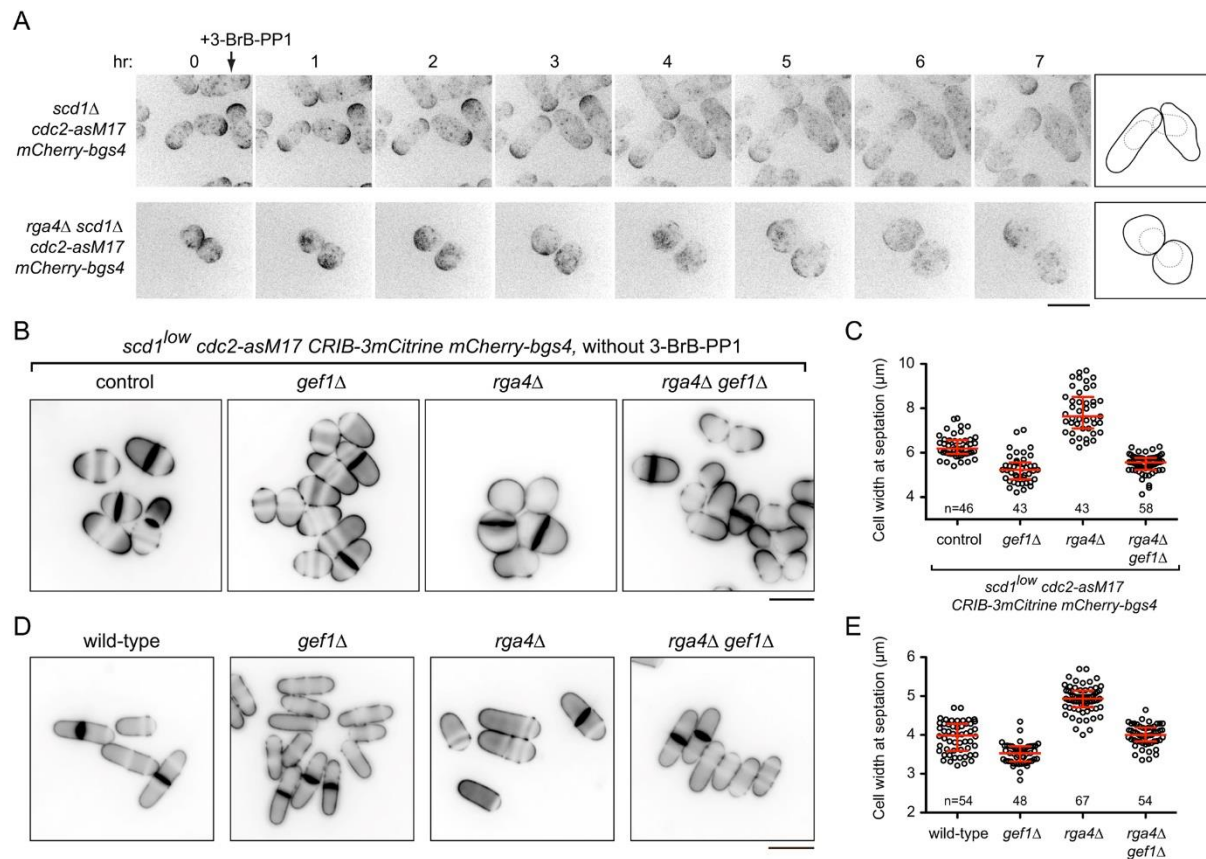


Figure 7. *scd1* Δ *rga4* Δ cells show PORTLI growth, and *gef1* Δ rescues the short/wide-cell phenotypes associated with *rga4* Δ .

(A) Movie time-points showing cell morphology and mCherry-Bgs4 distribution in indicated genotypes after 3-BrB-PP1 treatment (added just after the 0 hr time-point). Diagrams show outlines at beginning and end of movies. Outlines are more obvious in movies (Movie 9). (B) Calcofluor staining of actively cycling cells for the indicated genotypes. *scd1* expression was repressed 24 hr before imaging. Although *cdc2-asM17* is present, 3-BrB-PP1 was not added to cultures. (C) Cell width at septation for genotypes in B. Median and interquartile ranges are shown. All pairwise comparisons were highly significant (Mann-Whitney test; $p < 0.0001$ for all except *gef1* Δ vs. *rga4* Δ *gef1* Δ , for which $p = 0.004$). n indicates number of cells scored. (D) Calcofluor staining of actively cycling wild-type cells and mutants indicated, in wild-type background. (E) Cell width at septation for genotypes in D. Median and interquartile ranges are shown. All pairwise comparisons were highly significant (Mann-Whitney test; $p < 0.0001$), except wild-type vs. *rga4* Δ *gef1* Δ ($p = 0.57$). Bars, 10 μ m. See also Figure S8 and Movie 9.

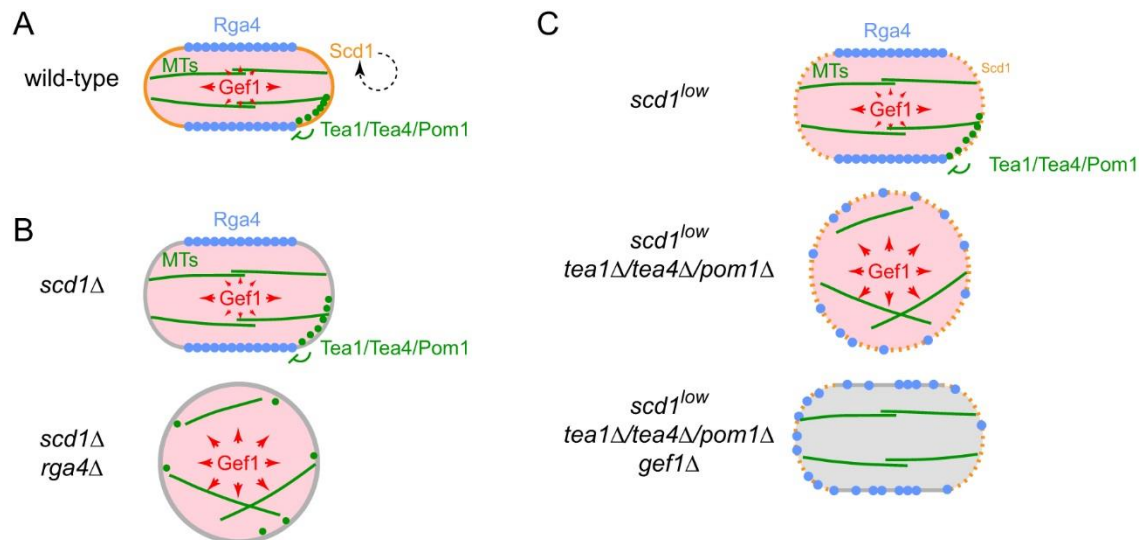


Figure 8. Simplified schematic model for polarized growth via microtubule-dependent coordination of local and global Cdc42 GEF activities.

(A) In wild-type cells, five main features of the model lead to normal polarized growth: 1) Scd1 (orange) is a plasma membrane-associated “local” Cdc42 GEF at cell tips and maintains a focused polarity zone via positive feedback. 2) Gef1 (pink) is a cytosolic, “global” Gdc42 GEF. 3) Microtubules (MTs; green) target the Tea1/Tea4/Pom1 axis (green) to cell tips. 4) This restricts Cdc42 GAP Rga4 (blue) to the plasma membrane at cell sides. 5) Rga4 on the membrane locally counters cytosolic Gef1 activity, preventing net GEF activity at cell sides (different-sized red arrows). (B) The model as applied to *scd1Δ* and *scd1Δ rga4Δ* cells. In *scd1Δ* cells, there is no strong focused polarity zone, but Rga4 can still locally counter global Gef1 activity, leading to greater “net” Gef1 activity in the region of cell tips, as in wild-type cells. Cells are therefore polarized but wider than wild-type. In *scd1Δ rga4Δ* cells, absence of Rga4 means that Gef1 is not locally countered anywhere and thus can promote PORTLI growth. Distribution of MTs and Tea1/Tea4/Pom1 will also be abnormal, due to round cell shape. (C) The model as applied to the genotypes indicated. In *scd1^{low}* cells, only a very limited amount of local Cdc42 GEF Scd1 is present at cell tips, and thus the polarity zone is not focused as in wild-type. However, “net” Gef1 activity remains greater in region of cell tips, and Gef1 cooperates with Scd1. In *scd1^{low} tea1Δ/tea4Δ/pom1Δ* cells, Rga4 is no longer spatially restricted, and therefore “net” Gef1 activity is not spatially controlled. This competes with (low) Scd1 and overwhelms its contribution to polarized growth. In *scd1^{low} tea1Δ/tea4Δ/pom1Δ gef1Δ* cells, competition from Gef1 is alleviated, allowing the low Scd1 to support polarized growth.

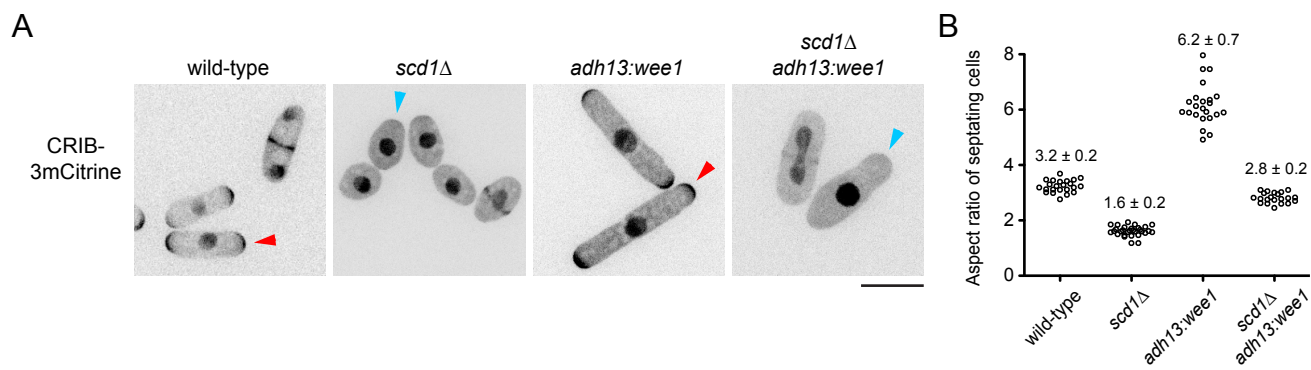


Figure S1. Overexpression of mitotic inhibitory kinase Wee1 reveals polarized growth of *scd1Δ* cells. **(A)** Cell morphology and distribution of Cdc42-GTP reporter CRIB-3mCitrine in cells of the indicated genotypes. Polarized shape of *scd1Δ* cells is seen upon *wee1* overexpression. Arrowheads indicate detection (red) or no significant detection (blue) of CRIB at cell tips. **(B)** Aspect ratio (cell length divided by cell width) of septating cells of the indicated genotypes, with mean and SD. Wild-type and *scd1Δ adh13:wee1* cells have similar ratios. Numbers of cells scored were: 23 (wild-type), 30 (*scd1Δ*), 23 (*adh13:wee1*), and 21 (*scd1Δ adh13:wee1*). Bar, 10 μ m.

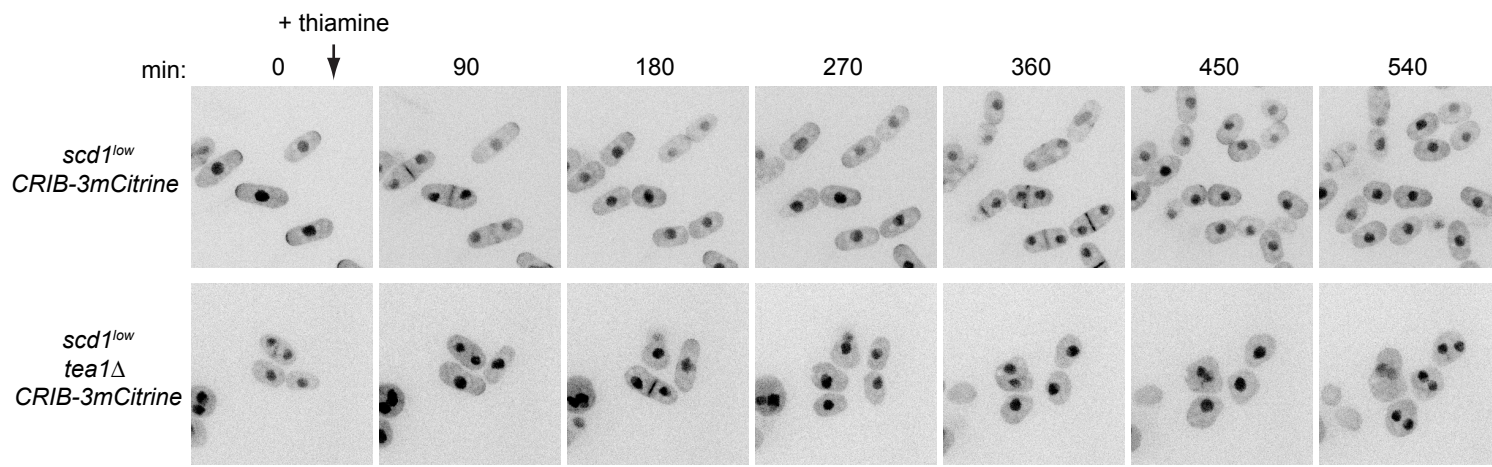


Figure S2. Growth of *scd1*^{low} and *scd1*^{low} *tea1*Δ cells expressing wild-type Cdc2.

Cell morphology and CRIB-3mCitrine localization in the indicated genotypes. These cells also express Lifeact-mCherry (not shown). Thiamine was added to repress *nmt81:3HA-scd1* expression just after the 0 min time-point; therefore at early time-points, cells have relatively higher levels of Scd1 and thus more detectable CRIB at cell tips (see also Fig. 3A). Effects of *scd1* repression are apparent from 270 min onwards. Note increased wide/round cell shape in *scd1*^{low} cells over time (top panels), and isotropic-like growth and extremely round shape in *scd1*^{low} *tea1*Δ cells (bottom panels). Binucleate cells in *scd1*^{low} *tea1*Δ are likely related to defects in cytokinesis caused by round shape. Some *scd1*^{low} *tea1*Δ cells are binucleate even before repression, but not all *scd1*^{low} *tea1*Δ cells become binucleate after repression (see also Fig. S3A and Methods). Bar, 10 μm. See also Movie 3.

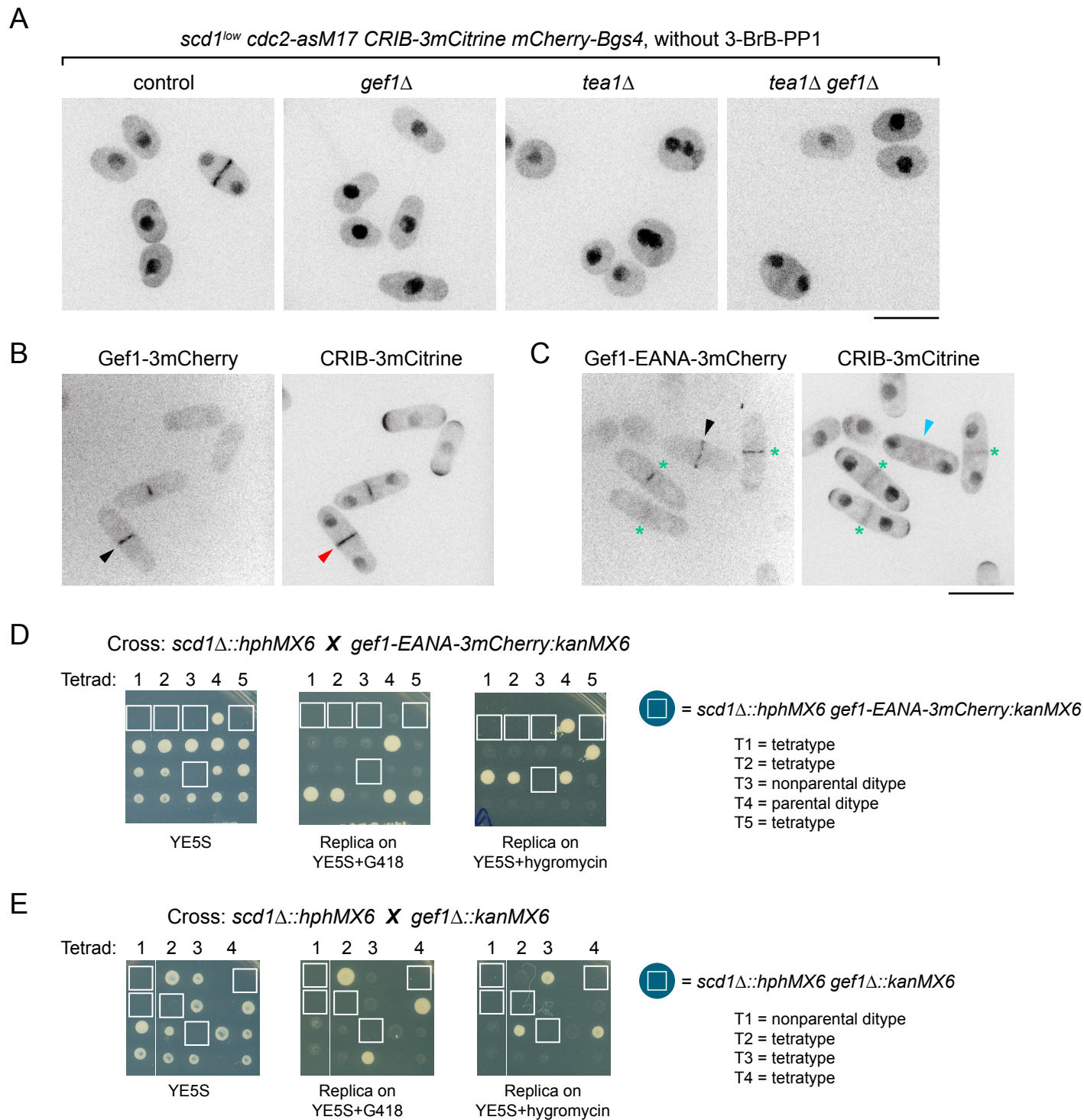


Figure S3. Supporting data for restoration of polarized growth in *scd1^{low} tea1Δ* cells after further loss of *gef1* function

(A) Cell morphology in the indicated genotypes during exponential growth, after 24 hr *scd1* repression. 3-BrB-PP1 was not added to cultures, and thus *cdc2-asM17* was not inhibited. CRIB-3mCitrine signal is shown here as a marker for cell volume and cell nuclei. Note that *tea1Δ* cells are round and often binucleate (see Methods), while *tea1Δ gef1Δ* cells are more similar to *gef1Δ* and control cells. (B,C) *Gef1-EANA-mCherry* is a loss-of-function mutation. In septating cells, both wild-type *Gef1-3mCherry* (B) and mutant *Gef1-EANA-3mCherry* (C) localize to the division site (black arrowheads). Wild-type *Gef1-3mCherry* promotes Cdc42-GTP (CRIB-3mCitrine) accumulation at the division site during early stages of septation (red arrowhead), but *Gef1-EANA-3mCherry* does not (blue arrowhead). In later stages of septation, CRIB-3mCitrine at the division site is more diffuse and weak and does not correlate with *Gef1-EANA-3mCherry* (green asterisks); this later localization is known to be independent of *Gef1* (Wei et al., 2016). (D, E) Tetrad analyses showing synthetic lethality of *gef1-EANA-3mCherry* with *scd1Δ* (D) and confirming synthetic lethality of *gef1Δ* with *scd1Δ* (E) (Coll et al., 2003). Spores were germinated on YE5S and replica-plated as indicated. Boxes indicate inferred position of non-viable double mutants. Bars, 10 μm.

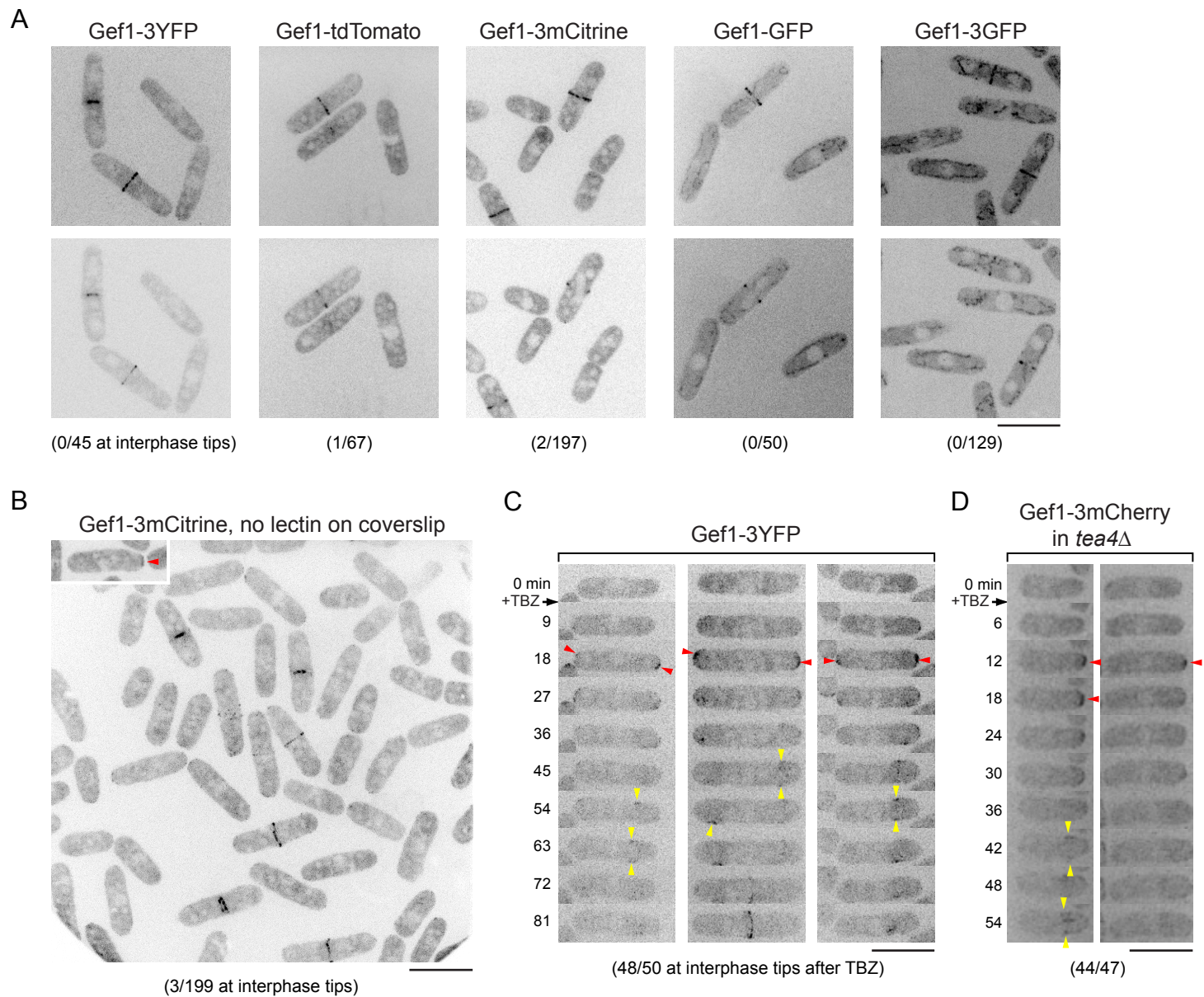


Figure S4. Gef1 is cytosolic during interphase but transiently localizes to cell tips after TBZ treatment.

(A) Still images of Gef1 fused to different fluorescent proteins. Top panels show maximum projections, and bottom panels show corresponding central Z-section or two adjacent central Z-sections. During interphase, Gef1 is cytosolic, and during cell division, Gef1 localizes to the division site. In all cases, cells were grown in YE5S to mid-log phase and imaged under conditions that minimize stress (Mutavchiev et al., 2016; see Methods). In some cases, high exposures were used to confirm absence of Gef1 from cell tips; as a result, mitochondrial autofluorescence is apparent in images of Gef1-GFP and Gef1-3GFP. Numbers of cells with detectable Gef1 at interphase tips are shown below the representative images. **(B)** Gef1-3mCitrine localization in cells imaged within 10 min after adding to uncoated glass-coverslip dishes. Under these conditions, Gef1 is also cytosolic during interphase. This demonstrates that pretreatment of coverslips with soybean lectin (normally used for longer-term imaging; see Methods) does not alter Gef1 localization. Inset shows one interphase cell with Gef1 at cell tips (arrowhead). **(C)** Recruitment of Gef1-3YFP from the cytosol to cell tips after treatment with the microtubule depolymerizing drug thiabendazole (TBZ; 150 μ g/ml). TBZ has off-target effects that lead to cell depolarization independently of disrupting microtubules (Sawin and Snaith, 2004). TBZ was added just after imaging the 0 min time-point. After TBZ treatment, Gef1-3YFP transiently localizes to cell tips (red arrowheads) and later localizes more weakly to patches on cell sides (yellow arrowheads), which move towards cell middle. **(D)** Recruitment of Gef1-3mCherry from the cytosol to cell tips after TBZ treatment in *tea4Δ* cells. This demonstrates that Tea4 is not required for TBZ-induced Gef1 cell-tip localization. In (C) and (D), numbers below images indicate number of cells with Gef1 at interphase cell tips within 20 min after TBZ treatment. Bars, 10 μ m. See also Movie 5.

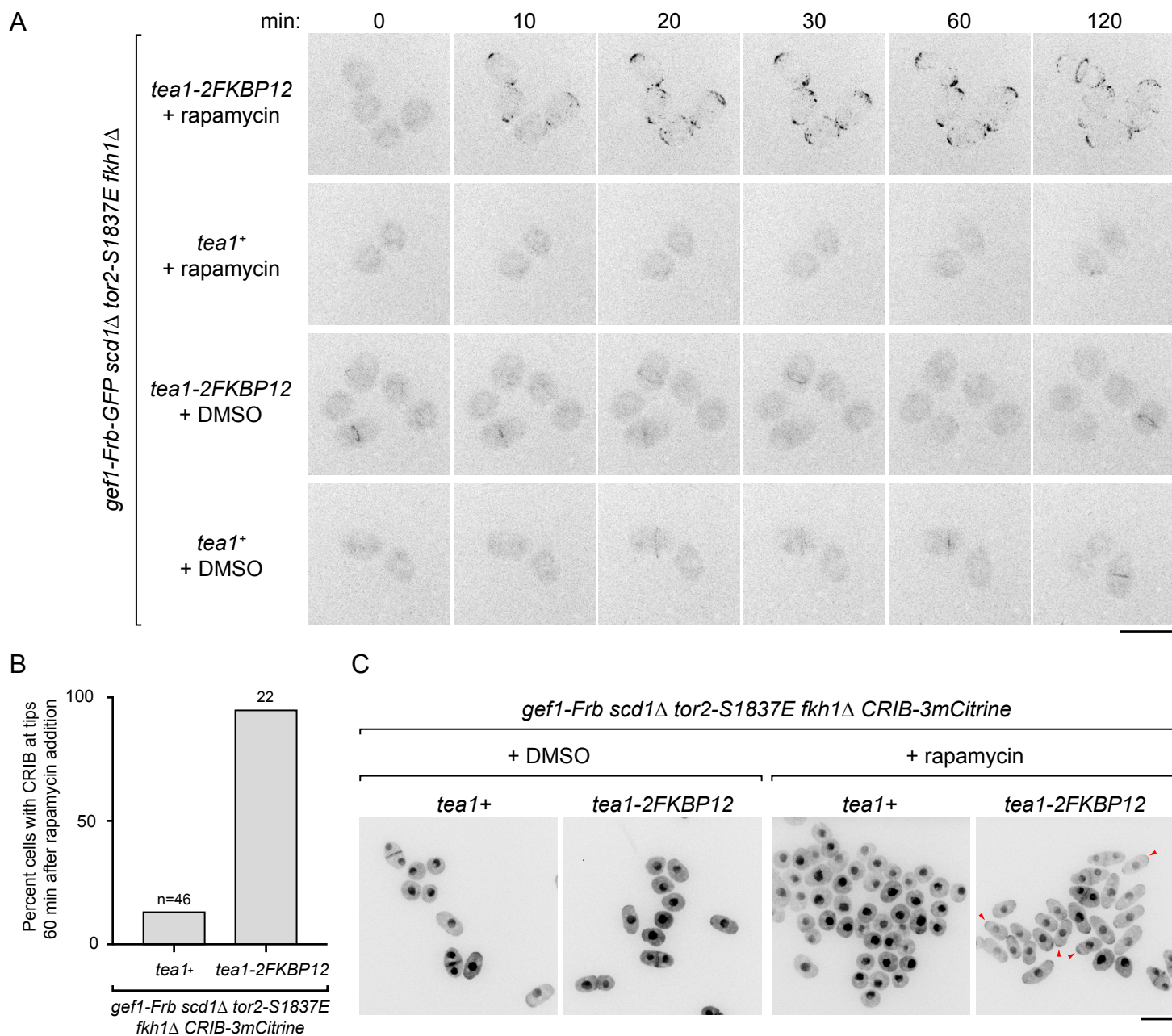


Figure S5. Targeting Gef1 to cell tips via rapamycin-induced dimerization with Tea1.

(A) Movie time-points showing Gef1-Frb-GFP localization and cell morphology in the indicated genotypes after rapamycin or control DMSO treatment. Gef1-Frb-GFP recruitment to cell tips requires both rapamycin and Tea1-2FKBP12 and leads to increased polarized cell shape. (B) Quantification of CRIB-3mCitrine localization at cell tips in the indicated genotypes 60 min after rapamycin addition to target Gef1 to cell tips, from movies of the type shown in Fig. 5D. A small percentage of *tea1+* cells have detectable CRIB at cell tips, but this is much lower than in *tea1-2FKBP12* cells (see also panels in (C)). Differences were highly significant ($p < 0.0001$; Fisher's exact test). (C) Cell morphology and CRIB-3mCitrine localization in the indicated genotypes after 16 hr treatment with rapamycin or DMSO. Note polarized cell shape and CRIB localization to cell tips in rapamycin-treated *tea1-2FKBP12* cells (examples indicated by arrowheads). Bars, 10 μ m. See also Movie 6.

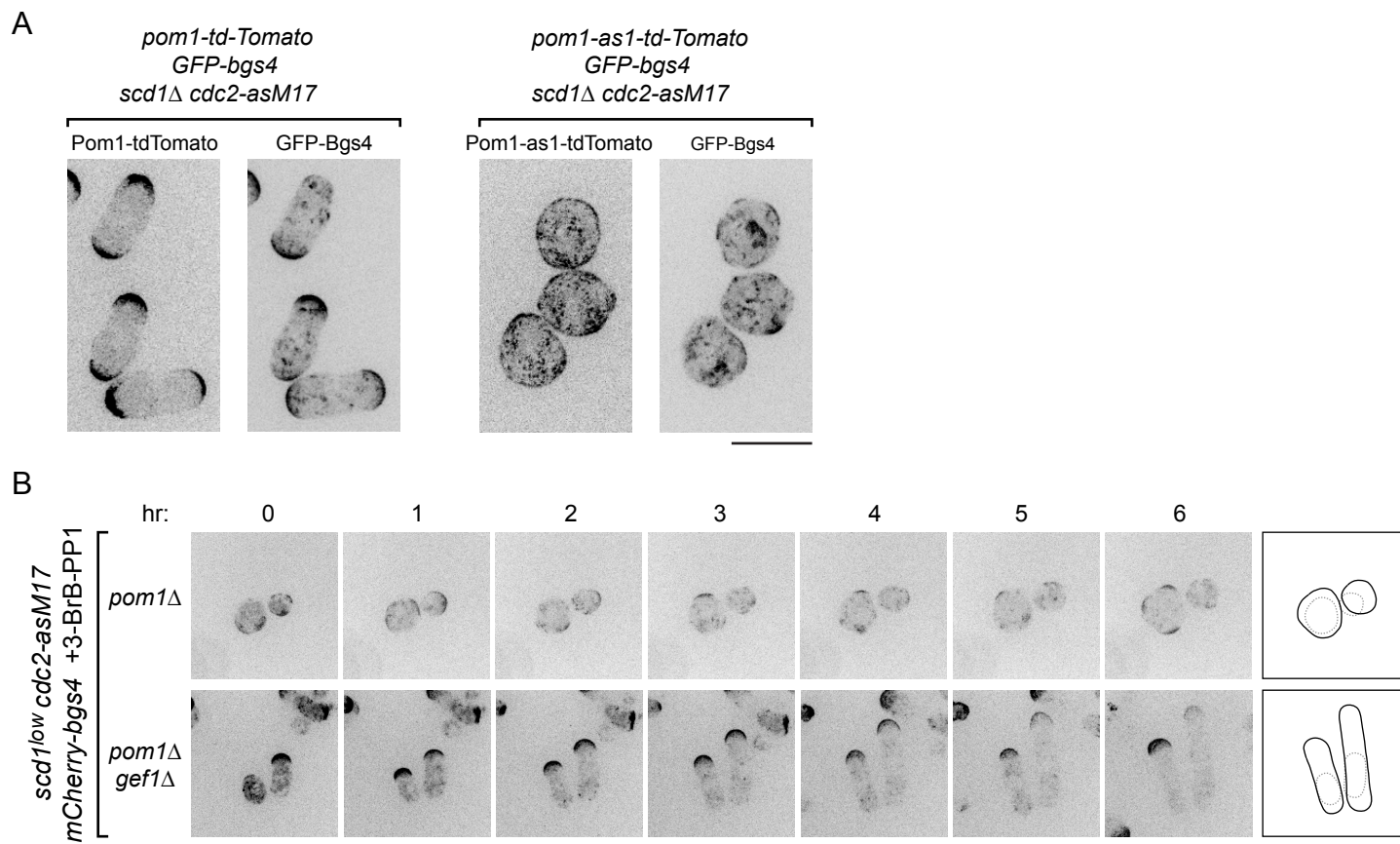


Figure S6. Supporting data for the role of Pom1 in PORTLI growth.

(A) Single time-point images (i.e. not from movies) of Pom1-tdTomato and GFP-Bgs4, and Pom1-as1-tdTomato and GFP-Bgs4, in the indicated genotypes after 4 hr 3-BrB-PP1 treatment. Experiment was as in Figure 6, but to avoid photobleaching, no images were acquired prior to those shown here. This demonstrates that membrane-associated Pom1-as1-tdTomato is much more homogeneously distributed after inhibition by 3-BrB-PP1 in these cells and that loss of signal from cell tips is not simply due to photobleaching. **(B)** Deletion of *gef1* restores polarized growth to *scd1^{low} pom1Δ* cells. Movie time-points showing cell morphology and mCherry-Bgs4 distribution in indicated genotypes. *scd1* expression was repressed 24 hr before imaging. 3-BrB-PP1 was added 30 min before imaging. Diagrams show cell outlines at beginning and end of movies; outlines were aligned slightly to account for limited cell movement. Bars, 10 μ m. See also Movie 8.

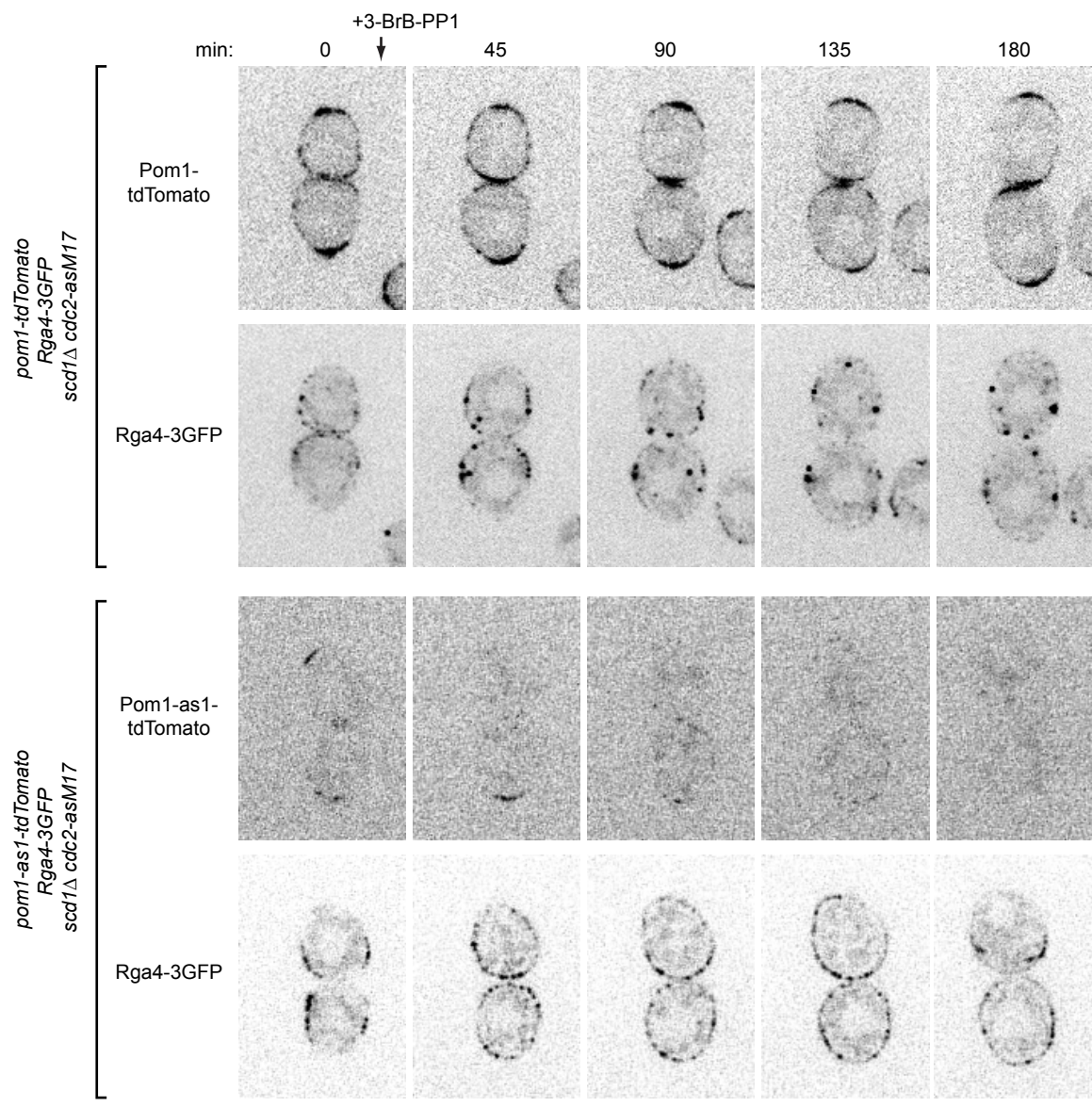


Figure S7. Single-channel images of Pom1-tdTomato, Pom1-as1-tdTomato and Rga4-3GFP after 3-BrB-PP1 addition.

Single-channel images corresponding to the merged images shown in Figure 6C. Note that at some time-points, some Rga4-GFP signal appears to internal (i.e. not on the plasma membrane). Bars, 10 μ m.

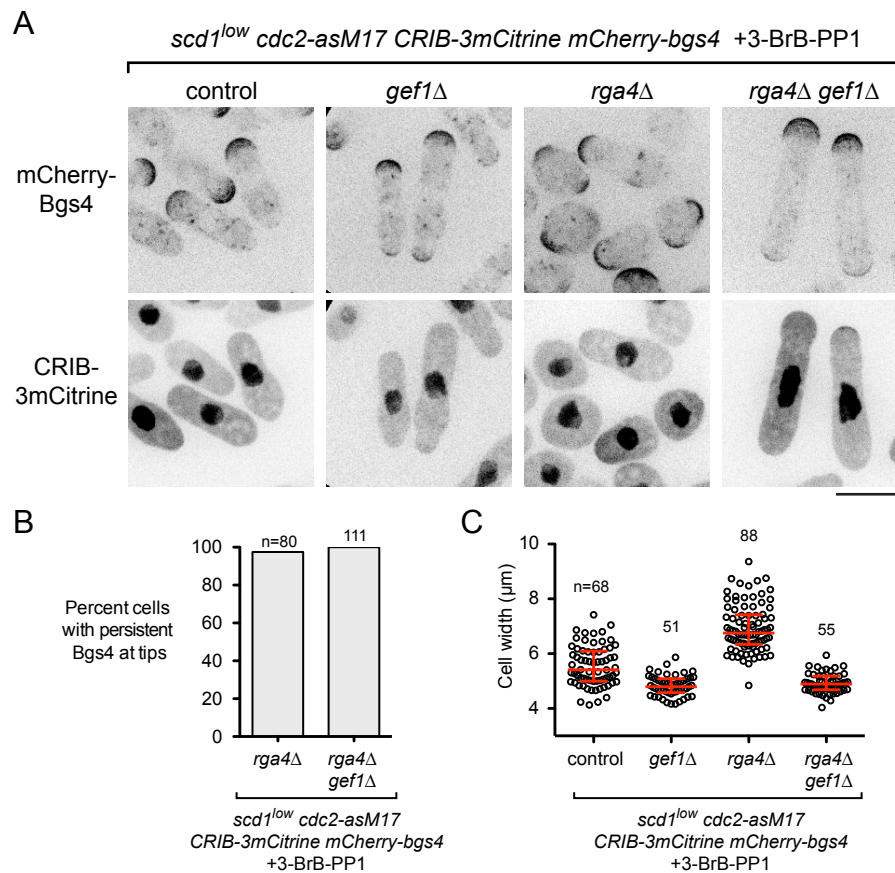
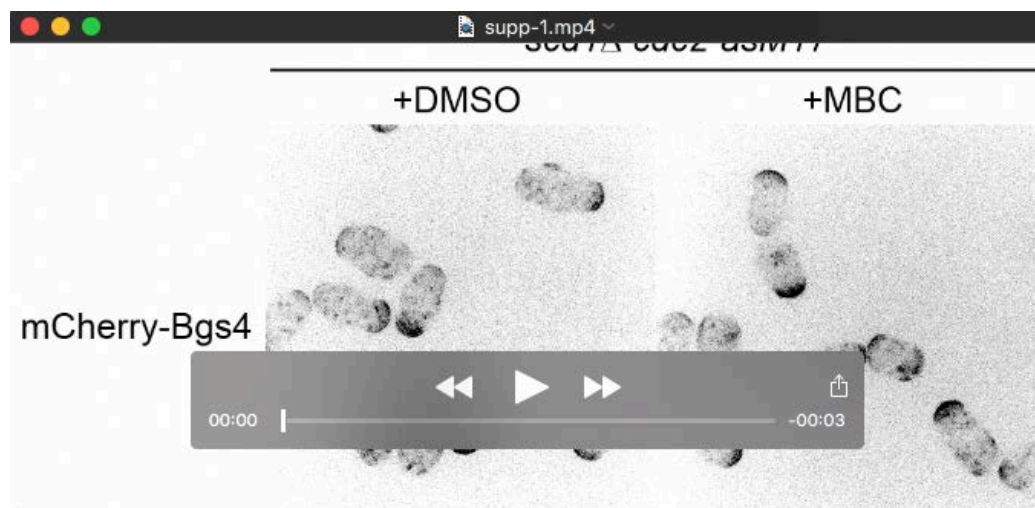


Figure S8. Polarity defects in *rga4Δ scd1^{low}* cells during extended interphase are rescued by *gef1Δ*.

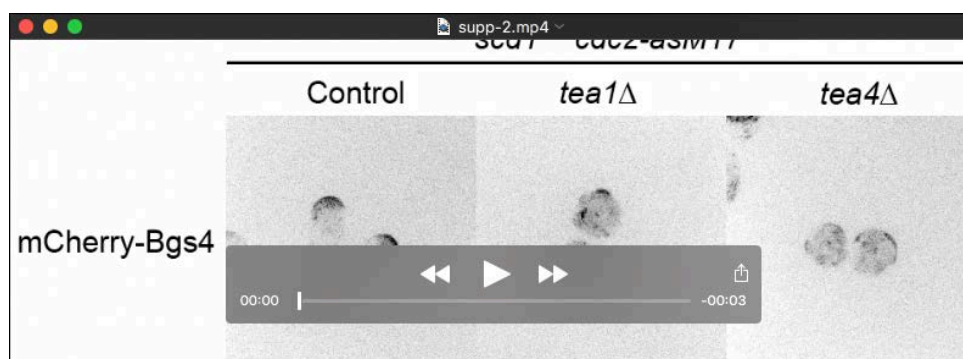
(A) Cell morphology, mCherry Bgs4-localization and CRIB-3mCitrine distribution in the indicated genotypes after 3-BrB-PP1 treatment. *scd1* expression was repressed for 24 hr before addition of 3-BrB-PP1. Cells were imaged 5 hr after addition of 3-BrB-PP1. CRIB-3mCitrine signal shows cell dimensions and was used to measure cell width in C. Note that *rga4Δ* cells in *scd1^{low}* background are wider/rounder than other genotypes, although polarity defects are not as strong as in *scd1Δ* background (see Figure 7A). **(B)** Quantification of mCherry-Bgs4 at cell tips in the indicated genotypes, from experiments in A. **(C)** Cell width for the indicated genotypes from images as in A, 5 hr after addition of 3-BrB-PP1. Median and interquartile ranges are shown. All pairwise differences were highly significant ($p < 0.0001$; Mann-Whitney test), except *gef1Δ* vs. *rga4Δ gef1Δ* ($p = 0.20$). n indicates number of cells scored. Bar, 10 μ m.

MOVIES



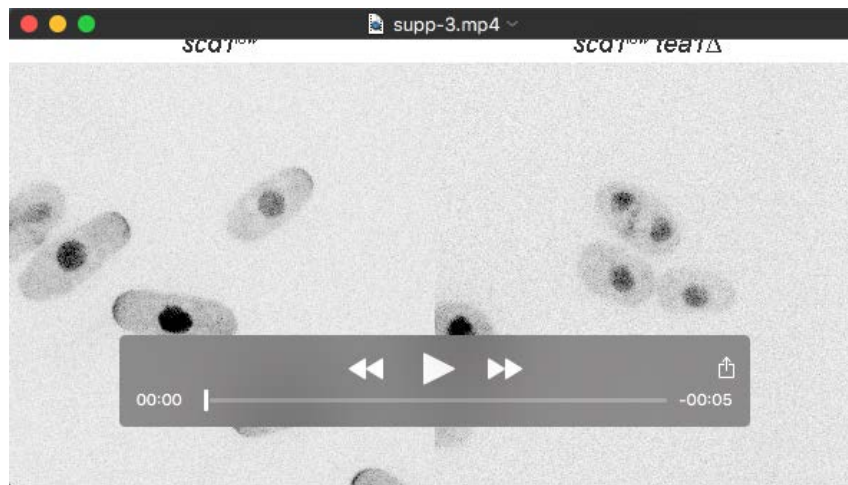
Movie 1. Microtubule depolymerization in *scd1* Δ cells leads to PORTLI growth.

mCherry-Bgs4 distribution and cell morphology of *scd1* Δ *cdc2-asM17* *mCherry-bgs4* cells. Bgs4 on the plasma membrane indicates sites of growth. Cells were pretreated with 3-BrB-PP1 60 min prior to start of imaging, to inhibit Cdc2 kinase activity, and then treated with either DMSO or MBC at start of imaging (still in presence of 3-BrB-PP1). For DMSO treatment, cell at lower right corresponds to cell shown in Fig. 2A. For MBC treatment, cell at mid-lower center corresponds to cell shown in Fig. 2A. Time interval during acquisition, 10 min; total elapsed time, 420 min; time compression at 15 frames per second playback, 9000X.



Movie 2. When *scd1* is expressed at very low levels, *tea1* Δ and *tea4* Δ cells show PORTLI growth.

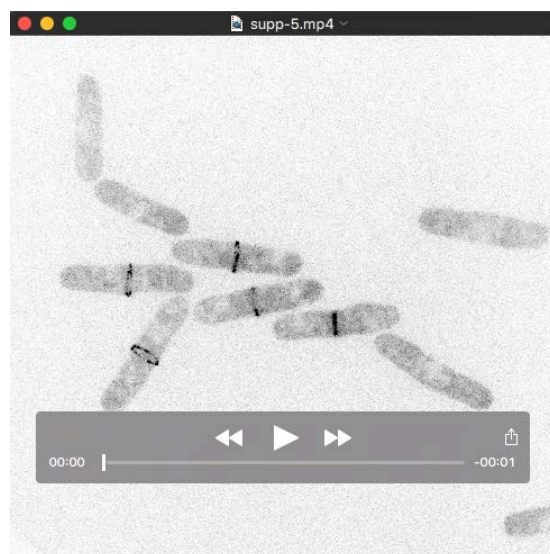
mCherry-Bgs4 distribution and cell morphology in control cells, *tea1* Δ , and *tea4* Δ cells, all in a *scd1*^{low} *cdc2-asM17* *mCherry-bgs4* genetic background. Bgs4 on the plasma membrane indicates sites of growth. Cells correspond to those shown in Fig. 3B. *scd1* expression was repressed by thiamine addition 24 hr prior to start of imaging. Cdc2 kinase activity was inhibited by 3-BrB-PP1 addition 30 min before imaging. Time interval during acquisition, 10 min; total elapsed time, 420 min; time compression at 15 frames per second playback, 9000X.



Movie 3. Growth of *scd1^{low}* and *scd1^{low} tea1 Δ* cells expressing wild-type Cdc2. CRIB-3mCitrine distribution and cell morphology in exponentially-growing *scd1^{low}* and *scd1^{low} tea1 Δ* cells expressing wild-type Cdc2. Thiamine was added to repress *scd1* expression just after the first time-point, which is paused in the movie. Cells correspond to those shown in Fig. S2. Effects of *scd1* repression, including isotropic-like growth of *scd1^{low} tea1 Δ* cells, become apparent about half-way through the movie. See Fig. S2 legends and Methods for further details. Time interval during acquisition, 9 min; total elapsed time, 540 min; time compression at 15 frames per second playback, 8100X.



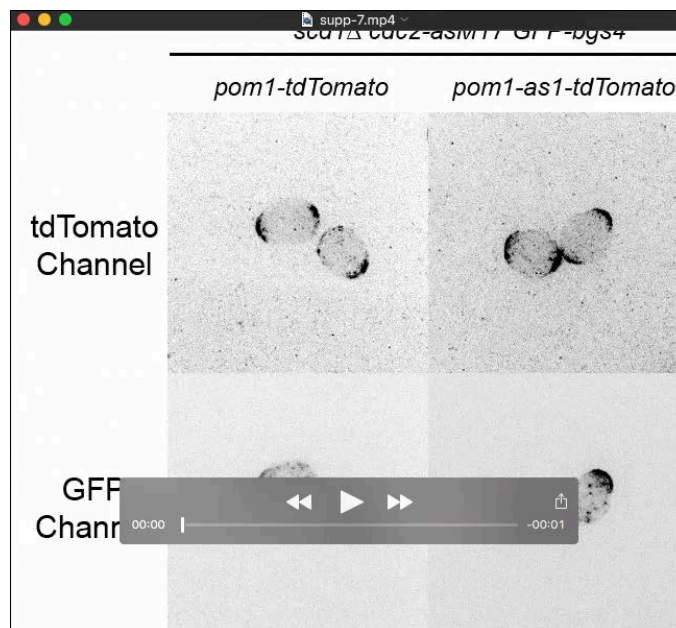
Movie 4. Loss of *gef1* function restores polarized growth to *scd1^{low} tea1 Δ* cells. mCherry-Bgs4 distribution and cell morphology in *tea1 Δ* , *gef1 Δ* , *tea1 Δ gef1 Δ* and *tea1 Δ gef1-EANA* cells, all in a *scd1^{low} cdc2-asM17 mCherry-bgs4* genetic background. Bgs4 on the plasma membrane indicates sites of growth. Cells correspond to those shown in Fig. 4A. *scd1* expression was repressed by thiamine addition 24 hr prior to start of imaging. Cdc2 kinase activity was inhibited by 3-BrB-PP1 addition 30 min before imaging. A transient loss of Bgs4 from cell tips is seen in some *scd1^{low} gef1* mutant cells (~20%), including some of the examples shown in the movie; the reasons for this are not completely clear. Time interval during acquisition, 10 min; total elapsed time, 420 min; time compression at 15 frames per second playback, 9000X.



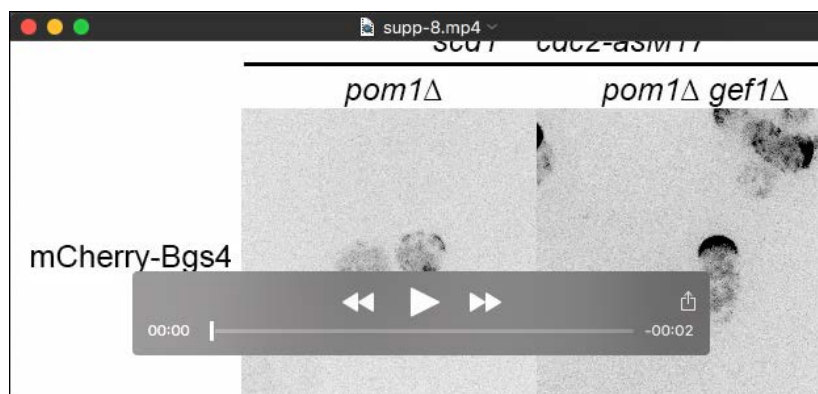
Movie 5. Gef1-3YFP is transiently recruited to the cell tips upon TBZ treatment. TBZ was added just after the first time-point, which is paused in the movie. Prior to TBZ addition, Gef1-3YFP in dividing cells is present at the division site and in the cytoplasm, and Gef1-3YFP in interphase cells is uniformly distributed in the cytoplasm, without any visible enrichment at the cell tips. Upon TBZ addition, interphase Gef1-3YFP signal is transiently observed at cell tips and later appears to move along the cell cortex towards the cell middle. Three of the cells in the movie correspond to those shown in Fig. S4C. Time interval during acquisition, 9 min; total elapsed time, 81 min; time compression at 15 frames per second playback, 8100X.



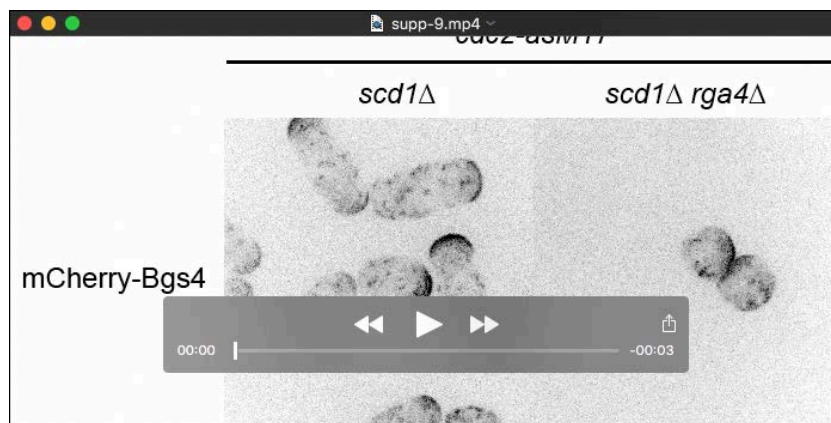
Movie 6. Rapamycin addition to *gef1-Frb-GFP tea1-2FKBP12* cells leads to recruitment of Gef1-Frb-GFP to cell tips and increased cell polarization. Gef1-Frb-GFP localization and cell morphology in *tea1-2FKBP12* cells and in control cells expressing untagged Tea1 (*tea1+*), all in *scd1Δ tor2-S1837E fkh1Δ* genetic background, after addition of rapamycin or control DMSO. Cells correspond to those shown in Fig. S5A. Rapamycin or DMSO were added just after the sixth time point. Time interval during acquisition, 5 min; total elapsed time, 150 min; time compression at 15 frames per second playback, 4500X



Movie 7. Inhibition of Pom1 kinase activity in *scd1* Δ cells leads to PORTLI growth. Cell morphology and distribution of Pom1-tdTomato and GFP-Bgs4, or Pom1-as1-tdTomato and GFP-Bgs4, in *scd1* Δ *cdc2-asM17* genetic background after 3-BrB-PP1 treatment. Bgs4 on the plasma membrane indicates sites of growth. Cells correspond to those shown in Fig. 6A. 3-BrB-PP1 inhibits activity of both Cdc2-asM17 and Pom1-as1-tdTomato and was added just after the first time-point. Note that 3-BrB-PP1 treatment depolarizes Pom1-as1-tdTomato, and this leads to PORTLI growth. Time interval during acquisition, 20 min; total elapsed time, 240 min; time compression at 15 frames per second playback, 18,000X.



Movie 8. Deletion of *gef1* restores polarized growth to *scd1*^{low} *pom1* Δ cells. mCherry-Bgs4 distribution and cell morphology of *pom1* Δ and *pom1* Δ *gef1* Δ mutants in *scd1*^{low} *cdc2-asM17* *mCherry-bgs4* genetic background. Bgs4 on the plasma membrane indicates sites of growth. Cells correspond to those shown in Fig. S6B. *scd1* expression was repressed by thiamine addition 24 hr prior to start of imaging. Cdc2 kinase activity was inhibited by 3-BrB-PP1 addition 30 min before imaging. Time interval during acquisition, 10 min; total elapsed time, 350 min; time compression at 15 frames per second playback, 9000X.



Movie 9. Deletion of *rga4* leads to PORTLI growth in *scd1Δ* cells. mCherry-Bgs4 distribution and cell morphology of *scd1Δ* and *scd1Δ rga4Δ* mutants in *cdc2-asM17 mCherry-bgs4* background. Bgs4 on the plasma membrane indicates sites of growth. Cells correspond to those shown in Fig. 7A, with slightly larger fields. Cdc2 kinase activity was inhibited by 3-BrB-PP1 addition 30 min before imaging. Time interval during acquisition, 12 min; total elapsed time, 480 min; time compression at 15 frames per second playback, 10,800X.

Table S1: Yeast strains used in this work, listed by figure

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