Calcium Dependent Protein Kinases are key effectors of calcium signaling in malaria parasite. PfCDPK1 is critical for asexual development of Plasmodium falciparum, but its precise function and substrates remain largely unknown. Using a conditional knockdown strategy, we here establish that this kinase is critical for the invasion of host erythrocytes. Furthermore, using a multidisciplinary approach involving comparative phosphoproteomics we gain insights into the underlying molecular mechanisms. We identify substrates of PfCDPK1, which includes proteins of Inner Membrane Complex and glideosome-actomyosin motor assembly. Interestingly, PfCDPK1 phosphorylates PfPKA regulatory subunit (PfPKA-R) and regulates PfPKA activity in the parasite, which may be relevant for the process of invasion. This study delineates the signaling network of PfCDPK1 and sheds light on mechanisms via which it regulates invasion.
Plasmodium falciparum is a major causative agent of pernicious human malaria, which infects the mosquito and the human host. Plasmodium infects two different cell types in the human host: hepatocytes and the erythrocytes and encounters diverse host environments, which it successfully survives to propagate. The asexual development of the parasite involves invasion of host RBCs by the parasite followed by its intraerythrocytic development, multiplication and egress to invade fresh RBCs, which results in clinical manifestations and pathogenesis of disease. While it has become increasingly clear that parasite involves invasion of host RBCs by the parasite followed by invasion and motility was found to be significantly enriched (Supplementary Data 1). The S-curve for one of the replicates is provided and some of the significantly altered phosphorylation sites belonging to key proteins (Supplementary Data 2) are indicated. Two key proteins that were marginally higher than the cut-off in the replicate represented here but were significantly altered in two other replicates (Supplementary Data 2) are lettered in red. PfPKA-R-S149, which was altered in only one replicate (Supplementary Data 1), is indicated by *. Proteins that exhibited reduced phosphorylation upon PfCDPK1 depletion were subjected to Gene Ontology enrichment analysis. Biological process of "entry into host cell" that consists of proteins involved in invasion and motility was found to be significantly enriched (Supplementary Data 2). Distribution of amino acids surrounding the S/T in proteins that exhibited significantly altered phosphorylation in two other replicates (Supplementary Data 2) are indicated by *.
CDPKs possess a Calmodulin Like Domain at their C-terminus via which calcium dependent activation of the enzyme occurs. PbCDPK4 regulates sexual differentiation of the rodent parasite P. berghei and PbCDPK5 guides the egress of merozoites from the host erythrocyte. CDPKs regulate important processes in T. gondii as well. For instance, TgCDPK1 is involved in microneme secretion triggered by calcium. While PbCDPK1 is not essential for P. berghei asexual development, independent reports have suggested that PictCDPK1 is refractory to gene disruption, indicating that it may be indispensable for asexual blood stage development of P. falciparum. Insights into the putative role of PictCDPK1 in P. falciparum have come from studies using a pharmacological inhibitor purfalcamine, and peptide inhibitors which have suggested that PictCDPK1 may be involved in egress from the RBC and/or invasion. Since these inhibitors and other tools are likely to “hit” other targets, the specific function of CDPK1 in P. falciparum life cycle remains unknown and a genetic approach was needed to specifically determine its role in parasite biology.

We have used a conditional “knockdown” approach to dissect the role of PictCDPK1 in the process of host RBC invasion. Quantitative phosphoproteomics was employed for the identification of potential PictCDPK1 targets in the parasite to gain insights into its putative role in this process. PictCDPK1 may contribute to the process of invasion by regulating key parasite proteins, which include proteins of the inner membrane complex (IMC) and cAMP signaling module. Present studies also identify molecular interactions via which calcium and cAMP pathways may cross-talk in the parasite.

Results

Conditional knockdown of PictCDPK1 in P. falciparum. To elucidate the function of PictCDPK1 and identify its putative...
substrates, we generated parasites in which PfCDPK1 expression was down regulated. Since PfCDPK1 is refractory to gene disruption11, 12, a FKBP destabilization domain (DD) strategy was used to conditionally regulate its expression in *P. falciparum*13. The DD-fusion proteins are unstable in the absence of the DD ligand Shld-1 (Shld-1), which allows conditional knockdown of fused proteins. Using a single crossover strategy, PfCDPK1 was fused to the triple HA-tag followed by a DD domain at its C-terminus (Fig. 1a, Supplementary Fig. 1) to obtain PfCDPK1-3HA-DD parasites, which were cultured in the presence of Shld-1. The removal of Shld-1 resulted in ~70% reduction of PfCDPK1 expression as quantified by western blotting (Fig. 1b).

**Identification of potential PfCDPK1 substrates.** In order to elucidate the mechanism via which PfCDPK1 interplays with cellular processes of the parasite, it was important to globally identify proteins that undergo PfCDPK1-dependent phosphorylation in the parasite to unravel CDPK signaling pathways. The phosphoproteome of PfCDPK1-3HA-DD parasites was compared in the presence or absence of Shld-1. During asexual blood stage reproduction, PfCDPK1 exhibits maximum expression in late schizont stages and merozoites15. Therefore, it was pertinent to use these stages for phosphoproteomics. Shld-1 was removed at the ring stage and late schizont lysates were prepared for phosphoproteomic analysis. A mass spectrometry-based quantitative phosphoproteomic and proteomic approach involving iTRAQ labeling to measure differences in the phosphorylation state of proteins upon PfCDPK1 knockdown was employed (Fig. 1c). These studies resulted in identification of 2057 unique phosphosites from 1233 *P. falciparum* proteins (Fig. 1d, Supplementary Data 1). Several of these peptides exhibited differential phosphorylation upon PfCDPK1 knockdown achieved by Shld-1 removal (Fig. 1d, Supplementary Data 1).

Proteins that exhibited >0.75 fold change in phosphorylation in at least two replicates at specific residues upon PfCDPK1 ablation were considered as significant (Supplementary Data 1). This cutoff range was defined by using the PfCDPK1-dependent phosphorylation of S103 in PfGAP45 as an internal standard, as this protein was previously demonstrated to be phosphorylated by PfCDPK1 in vitro15. This glososome-associated protein is expressed in late stage parasites and showed a ~0.75 fold reduction in phosphorylation at S103 upon PfCDPK1 knockdown, which could be detected using a S103 specific phospho-antibody (Fig. 2a, see below).

Since PfCDPK1 is a kinase, the proteins that exhibited significant reduced phosphorylation upon its depletion were of specific interest. In all, 79 sites from 64 proteins exhibited significant decrease in phosphorylation in at least two replicates (Fig. 1d, Supplementary Data 2). Motif analysis of hypophosphorylated peptides showed overrepresentation of certain conserved amino acid sequences spanning the altered phosphorylation sites. Interestingly, most represented motifs comprised of basic amino acids with a preference for an R (or K) preceding the target S/T (Fig. 1f, Supplementary Data 2). These data agree well with previously identified preferred motifs for CDPK phosphorylation16. In addition, motifs in which target S/T were followed by acidic D/E residues were also found to be modulated (Fig. 1f, Supplementary Data 2).

Gene Ontology (GO) analysis suggested that a number of differentially phosphorylated proteins may be involved in invasion and/or motility (Fig. 1e, Supplementary Data 2). Several ribosomal proteins, proteins involved in RNA metabolism and processing, were also part of this group, but they are unlikely to be a direct PfCDPK1 targets. Surprisingly, the low molecular weight rhoptry complex containing RAMA and RAP1 also appeared to be modulated by PfCDPK1.

The regulatory subunit of cAMP dependent Protein Kinase (PKA-R) exhibited a change in its phosphorylation status at S149, which was just above the indicated threshold in phosphoproteomic analysis (Fig. 1d, Supplementary Data 1). Importantly, this phosphorylation site was part of a motif closely related to PfCDPK1 target motifs mentioned above. Since PKA-R is a key signaling molecule of the cAMP pathway, which our preliminary studies had implicated in PfCDPK1 function, it was also validated and pursued for further studies (described below).

Interestingly, a large number of putative target proteins were predicted or known to be associated with the IMC and the parasite pellicle (Fig. 1e, Supplementary Fig. 2, Supplementary Data 2), a membranous structure that underlies the plasma membrane. Given the membrane localization of PfCDPK1, which is facilitated by its N-terminus lipid modification and its previously reported interaction with IMC proteins in the membrane17, 18, these findings corroborate well and raised the possibility of these targets in close proximity of PfCDPK1.

We predicted the likelihood of protein–protein interactions (PPI) among the differentially phosphorylated proteins identified in our study from STRING database (Fig. 1g, Supplementary Data 3), which is a resource of PPI that have emerged either from direct experiments reported in the literature and predicted on the basis of co-expression and gene arrangement in the genome19. STRING has been used successfully to predict PPI in *Plasmodium*20. STRING analysis demonstrated a confident clustering PPI among the candidate proteins, which supports the results obtained by comparative phosphoproteomic analysis (Fig. 1g). Importantly, PfCDPK1 was predicted to be involved intimately with several of its targets identified by phosphoproteomics such as GAP45 and IMC1g that were validated during the course of these studies.

**PfCDPK1 is involved in the phosphorylation of IMC proteins.** Several IMC proteins, which are part of the actomyosin motor like GAP45 and Myosin A, or other IMC proteins such as IMC1c (ALV5), IMC1g (ALV4) associated with the IMC protein meshwork exhibited reduced phosphorylation upon PfCDPK1 knockdown (Fig. 1d). Previous studies have indicated that PfCDPK1 co-localizes with the Myosin Tail Interacting Protein, as well as Merozoite Surface Protein 1 (MSPI) in both schizonts and free merozoites17 suggesting that it is in close proximity to the IMC and plasma membrane. As mentioned above, PfGAP45- which was previously demonstrated to be an in vitro substrate of PfCDPK115, 21- exhibited differential phosphorylation at S89 and S103 (Fig. 1d, Supplementary Data 2). Using an antibody which recognizes S103 phosphorylated PfGAP4515, we were able to demonstrate that PfGAP45 phosphorylation at this site is indeed reduced upon PfCDPK1 knockdown (Fig. 2a) and supported the phosphoproteomics data (Fig. 1d). In addition, two other IMC proteins PfIMC1g (PF3D7_1003600) and PfIMC1c (PF3D7_0525800) were differentially phosphorylated (Fig. 1d). PfCDPK1 phosphorylated IMC1g in vitro (Fig. 2c). Importantly, metabolic labeling revealed that PfCDPK1 depletion resulted in reduced phosphorylation of PfIMC1g (Fig. 2d). These data strongly suggested that PfCDPK1 is a major kinase that phosphorylates IMC1g in the parasite. Moreover, PfCDPK1 exhibited localization in close proximity with IMC1g (Fig. 2e) in the parasite, which was reflected by overlapping fluorescence in IFA. In addition, the fact that IMC1g immunoprecipitated with PfCDPK1 suggested its interaction with the kinase in the parasite (Fig. 2f).
Regulation of PfPKA by PfCDPK1. Recently published reports have hinted at a cross talk between cAMP and calcium signaling during invasion. However, the underlying molecular mechanisms are poorly understood. cAMP mediates signaling via cAMP-dependent protein kinase (PKA) in most organisms including the malaria parasite. Therefore, we investigated the possibility of PfPKA regulation by PfCDPK1. To this end, PfPKA-C was immunoprecipitated and its activity was assayed upon PfCDPK1 knockdown. Interestingly, a significant decrease in its activity upon PfCDPK1 knockdown suggested that PfCDPK1 regulates PfPKA-C in the parasite (Fig. 3a).

As mentioned above, analyses of phosphoproteomic data revealed that the phosphorylation of PfPKA-R was down regulated at S149 upon PfCDPK1 knockdown in one of the replicates (Supplementary Data 1, Fig. 3b). It was worth noting that S149 belongs to K/RxxS/S motif (Fig. 3d), which is very closely related to one of the major PfCDPK1 target motifs indicated above (Fig. 1f) that were enriched among significantly altered phosphopeptides. In order to confirm if PfPKA-R is a substrate of PfCDPK1, in vitro kinase assays were performed using recombinant PfPKA-R. Indeed, PfCDPK1 phosphorylated PfPKA-R in vitro (Fig. 3c, Supplementary Fig. 3a). Western blotting was performed on lysates from PfCDPK1-3HA-DD parasites treated with Shld-1 or left untreated. An antibody, which recognizes both unphosphorylated and phosphorylated PfPKA-R, was used as a control for Western blotting (bottom panel). Shld-1 was removed from PfCDPK1-3HA-DD parasite cultures as described above and schizont lysates were prepared after ~44 h. PfPKA-C was immunoprecipitated and PfPKA-C-IP was used for Western blotting to detect PfPKA-R. Western blotting with indicated antibodies was also performed on total parasite lysates. Right Panel, Fold change in PfPKA-R associated with PfPKA-C was quantitated by densitometry after normalization with respect to PfPKA-R present in total parasite lysate (Mean ± s.e.m., *n=4, p<0.05, t-test).
Fig. 4 cAMP-dependent PIPKA-signaling may prevent PFCDPK1 activation via a negative feedback loop. a 3D7 schizonts were treated with DMSO, BAPTA-AM, IBMX or 8Br-cAMP for 3 h following which parasite lysates were prepared and PFCDPK1 was immunoprecipitated. PFCDPK1-IP was used to assess the kinase activity as described above using PIGAP45 as phosphoacceptor substrate. Fold change in activity was determined with respect to DMSO control (Mean ± s.e.m., *n=3, p<0.05, t-test). b PIPKA-R-GFP parasites were left untreated (−) or treated with 8Br-cAMP (+) followed by immunoprecipitation with PFCDPK1 or PIPKA-C antisera and kinase assays were performed with the IP, as described above using recombinant PIGAP45 or Histone H1 as phosphoacceptor substrate and phosphorylation was detected by phosphorimaging and quantified by densitometry of the bands from the phosphorimage (right panel) (Mean ± s.e.m., *n=3, p<0.05, t-test). c 3D7 schizont-infected red blood cells were treated with 20 μM myristoylated PKI followed by immunoprecipitation of PFCDPK1 and kinase assay was performed as described above followed by quantitation of CDPK1 activity by densitometry of radiolabeled Histone H1 (Mean ± s.e.m., *n=3, p<0.05, t-test). d To assess the effect of PIPKA on PFCDPK1 activity a two step assay was used. Step 1: PIPKA-C-HA was immunoprecipitated from PIPKA-C-HA parasites using anti-HA antibody. PIPKA-C-HA-IP (lane 2 and 3) or a control unrelated IP (lane 1) was incubated with recombinant PFCDPK1 in a kinase assay reaction in the presence (lane 2) or absence (lane 3) of unlabelled ATP. Step 2: Kinase assays were performed for PFCDPK1 obtained after Step 1 by using MBP as the phosphoacceptor substrate and radiolabelled ATP. The phosphorimage of the SDS-PAGE gel revealed that PIPKA-C-HA-IP inhibited PFCDPK1 activity when incubated with ATP (lane 2 vs. lane 3). Lower Panel, Densitometry was performed on radiolabeled bands to quantitate the phosphorylation and fold change in activity with respect to control (lane 1) is indicated. Data presented is Mean ± s.e.m. of three independent experiments, *n=3, ANOVA, p<0.05)

co-localized in late schizont parasites. PFCDPK1 exhibited co-localization with PIPKA-R (Supplementary Fig. 4c). In addition, co-immunoprecipitation of PIPKA-R with PFCDPK1 indicated their association in the parasite (Fig. 3b). PIPKA-R-PFCDPK1 interaction was also observed in parasites that overexpress PIPKA-R (Supplementary Fig. 4b).

S149, which is the target site of PFCDPK1 in the parasite, resides in the Inhibitory Segment (IS) of PIPKA-R (Fig. 3d). While cAMP binding to PKA-R is essential for dissociation of the R and the C subunits, subsequent phosphorylation of the IS contributes to this process and catalytic activation of the C subunit in the case of mammalian PKA. The IS sequence is reasonably well conserved in mammalian and Plasmodium PKA-R and S149 aligns with corresponding site in PKA-R from other species (Fig. 3d). The impact of PFCDPK1 knockdown on PIPKA-R/PFKC-PKA-C interaction was analyzed by performing co-immunoprecipitation experiments. PIPKA-R was pulled down with PKA-C in the presence of Shld-1 (Fig. 3g). Upon Shld-1 removal, there was a significant increase (Fig. 3g) in binding of these proteins, which suggested that PFCDPK1 may prevent interaction between the R and the C subunits of PIPKA. PFCDPK1 is activated by calcium, which induces conformational change that facilitates this process. Co-IP experiments revealed that chelating intracellular calcium by BAPTA-AM resulted in a loss of PIPKA-R-PFCDPK1 interaction (Fig. 3h) suggesting that modulation of cAMP levels impacted PFCDPK1 activity. Strikingly, phosphodiesterase inhibitor IBMX, which sustains
cAMP levels in the parasite\textsuperscript{22} and addition of 8Br-cAMP to parasites caused a significant decrease in PfCDPK1 activity (Fig. 4a). These data indicated that cAMP signaling may negatively regulate PfCDPK1 activity. The next logical step was to investigate the involvement of PiPKA in this process. We used parasites that overexpressed PiPKA-R as GFP fusion protein under AMA-1 promoter, which ensured its expression in schizont and segmenter stages. The overexpression of PfPKA-R sequesters PiPKA-C, which results in suppression of its activity and increasing cellular cAMP by addition of 8Br-cAMP to parasites resulted in elevation of the activity (Fig. 4a, red bars). In contrast, PfCDPK1 activity was significantly reduced (Fig. 4a, blue bars). A reverse experiment was also performed in which parasites were treated with a PKA inhibitor peptide PKI, which directly inhibits PiPKA-C\textsuperscript{25, 26}. This inhibitor caused a significant increase in PfCDPK1 activity (Fig. 4c). Collectively, these data suggested that PiPKA-C may negatively regulate PfCDPK1 in the parasite.

Next, the direct effect of PiPKA-C on PfCDPK1 activity was assessed by performing in vitro kinase assays using recombinant PfCDPK1. Since recombinant PiPKA-C is catalytically inactive, a parasite line that over expresses PiPKA-C fused to 3xHA tag was used to immunoprecipitate PiPKA-C-HA and IP was used as a source of active PiPKA-C\textsuperscript{27}. PiPKA-C-IP was incubated with PfCDPK1 in the absence or presence of unlabelled ATP, which was added to facilitate possible phosphorylation of PfCDPK1 by PiPKA-C. Subsequently, PfCDPK1 was separated from PiPKA-C-HA-IP. The activity of PiPKA-phosphorylated PfCDPK1 (+ATP, Fig. 4d, lane 2), or the unphosphorylated (-ATP, Fig. 4d, lane 3) was compared by performing assays using \textsuperscript{32}P-labelled ATP and MBP, which was used as a phosphoacceptor substrate for PfCDPK1. A significant decrease in PfCDPK1 activity was
detected when PiPKA-C-HA-IP was added along with cold ATP (Fig. 4d, lane 2) in comparison to the reaction in which cold ATP was excluded from the first step of the assay (Fig. 4d, lane 3). In addition, a control IP of an unrelated protein failed to alter PiCDPK1 activity (lane 1). These results indicated that PiPKA-C may inhibit PiCDPK1 activity. The observed negative feedback loop may be mechanism via which PiPKA may down regulate or shut down PiCDPK1 in the parasite.

**PiCDPK1 may regulate RBC invasion by the parasite.** PiCDPK1 seems to regulate a variety of parasite proteins, which possibly explains its importance for blood stage development11, 12. Efforts were made to understand the process it may regulate during blood stage development. To this end, the effect of PiCDPK1 knockdown on parasite growth was assessed by culturing parasites in the absence of Shld-1. A decrease in parasitemia was observed after each cycle, which was even more accentuated after the second cycle (~2 fold, Fig. 5a). Since decrease in parasitemia was observed mainly after each cycle and because PiCDPK1 is expressed mainly in schizonts33, a defect in egress or invasion was suspected. Next, we tested if the knockdown of PiCDPK1 had an impact on the invasion of host RBCs. To achieve this, Shld-1 was removed from ring stage parasites and schizonts were used for the invasion assays. Schizonts ruptured normally in the absence or presence of Shld-1 and were rarely observed after ~6 h of incubation with fresh erythrocytes suggesting that PiCDPK1 knockdown did not cause an apparent defect on egress. However, a significant decrease in the invasion, which was indicated by reduction in freshly formed rings, was observed in the case of Shld-1 deprived parasites (Fig. 5b). The invasion of RBCs by merozoites is a multi-step process initiated by the attachment to the RBC28. We tested if PiCDPK1 may regulate invasion by regulating the process of attachment. For this purpose, cytochalasin D (Cyt D) an inhibitor of actin polymerization, which allows attachment but prevents invasion, was used. Cyt D treated parasites from Shld-1+/− of actin polymerization, which allows attachment but prevents invasion. For this purpose, cytochalasin D (Cyt D) was treated with neuraminidase, it resulted in a significant decrease in invasion of control (Shld-1+) parasites (Fig. 5c, 1st bar vs. 3rd bar). While Shld-1 removal ablated invasion of untreated RBCs (1st bar vs. 2nd bar, Shld-1), the effect was less significant in the case of RBCs treated with Nm (3rd vs. 4th bar). These data suggested that PiCDPK1 may regulate invasion via a sialic acid-dependent receptor. While glycophrin A is resistant to chymotrypsin, there are several receptors for other parasite adhesins that are sensitive to chymotrypsin31. There was almost no difference in invasion efficiency of PiCDPK1-3HA-DD (Fig. 5f, 1st bar vs. 3rd bar) upon chymotrypsin treatment, which is consistent with parental D10 line being refractory to chymotrypsin treatment36, 37. PiCDPK1 depletion caused a similar defect in invasion of chymotrypsin-treated RBCs, as was the case with untreated RBCs (Fig. 5f, 1st bar vs. 2nd bar and 3rd bar vs. 4th bar). These data suggested that the observed invasion defects might be mainly due to the inability of the parasites to use the EBA-175/glycophrin A pathway.

**Regulation of invasion by PiCDPK1 and PiPKA.** Previously, CAMP and PiPKA were implicated in microneme secretion22. Our studies suggested that PiPKA activity is regulated by PiCDPK1 (Fig. 3), therefore, attempts were made to see if this cross-talk may contribute to invasion. First, PiPKA-R-GFP parasites were used to confirm the role of PiPKA in invasion22. An increase in the formation of rings was observed upon an increase in CAMP levels and schizont rupture remained almost unaltered (Fig. 6a), which was indicative of enhanced invasion and was consistent with a previous report22. The PKA-inhibitor PKI was also used to inhibit PiPKA in PiCDPK1-3HA-DD parasite-infected red blood cells. A marked reduction in invasion by PKI was observed (Fig. 6b, 1st bar vs. 3rd bar) in control Shld-1 treated parasites with normal PiCDPK1 expression implicating PiPKA in this process. While PiCDPK1 depletion (Shld-1) reduced invasion (Fig. 6b, 1st bar vs. 2nd bar), PKI was unable to cause an additional defect (4th bar vs. 2nd and 3rd bar). The significantly decreased sensitivity to invasion by the PKA-inhibitor when PiCDPK1 was depleted suggested that PiCDPK1-mediated regulation of PiPKA may contribute to the invasion process.

In summary, the present studies suggest PiCDPK1 may regulate invasion via phosphorylation and interaction with key proteins involved in IMC and glideosome function. Since PiCDPK1 and PiPKA regulate RBC invasion and PiCDPK1 is an upstream activator of PiPKA, it is reasonable to propose that their cross talk may contribute to the process of invasion (Fig. 6c).

**Discussion**

While PbCDPK1 was considered to be non-essential for the growth of P. berghei10, conditional knockdown of PbCDPK1 resulted in severe defects in ookinete differentiation and mosquito transmission38. Previous studies suggested that PiCDPK1 may be a critical enzyme, as its gene-disruption was not possible in P. falciparum11, 12. Despite these studies, the function of PiCDPK1 in blood stage development of the human parasite had remained elusive. The present studies indicate that PiCDPK1 may regulate the invasion of host RBCs by P. falciparum, which corroborated well with its ability to regulate EBA-175 secretion. Interestingly, PiCDPK1 can complement TgCDPK3, which is its closest Toxoplasma homologue, and salvages the egress phenotype in T. gondii39. The sialic acid -dependent invasion pathway, which involves interaction between DBL domain containing proteins like EBA-175 and the sialic acid moiety of glycophorins, was impaired upon PiCDPK1 depletion. However, invasion via chymotrypsin-resistant receptors like basigin35, 40 was not
affected significantly. It will be surprising if PfCDPK1 specifically inhibits the sialic acid-dependent invasion events as it seems to target substrates, which may ubiquitously regulate the invasion process. It is possible that residual 30–40% expression of PfCDPK1 after Shld-1 removal may be sufficient for other pathways to operate. A recent study reported that knockdown of PfCDPK1 using the DD-FKBP domain did not alter parasite growth13. However, the knockdown obtained in these studies was nominal. GFP along with the DD domain was fused to PfCDPK1 instead of a HA-tag in these studies, which may have a bearing on the extent of PfCDPK1 degradation. In addition, the background parasites used were 3D7 in this case, which are largely insensitive to neuraminidase treatment and predominantly use the sialic acid-independent pathway31. The J-domain of PfCDPK1, which is inhibitory for kinase activity, caused parasite arrest in early schizogony and egress from parasites. It was rightly concluded that the J-Domain may also target proteins from these studies that the J-Domain may also target proteins other than PfCDPK113.

PfCDPK1 seems to regulate several proteins of the actomyosin motor and glideosome assembly, which connects the motor to the IMC. One of the features of network analysis was the connectivity exhibited by PfCDPK1 to proteins belonging to these complexes. Out of these, only PfGAP4515, 18 was previously implicated in PfCDPK1 signaling. Since almost all previous studies have been based on in vitro phosphorylation experiments, their association with and regulation by PfCDPK1 in the parasite remained to be established, which was possible by using PfCDPK1-3HA-DD parasites. PfGAP45 is phosphorylated at several sites other than S89 and S103. While mutation of some of these sites to A/D residues and overexpression of mutants did not alter glideosome function15, 21 it is likely that the cumulative effect of phosphorylation of these and other sites by kinases like PfPKG41 may regulate its function in Plasmodium. Other IMC proteins such as IMC1g/PfALV4 (PF3D7_0525800) and IMC1c/PfALV5 (PF3D7_10003600), which are alveolins42, were differentially phosphorylated upon PfCDPK1 knockdown. Both proteins are known to be heavily phosphorylated41, 43 and it will be interesting to dissect the role of their phosphorylation on IMC assembly and function. Interestingly, low molecular weight complex proteins RAMA-RAP1 were differentially phosphorylated upon PfCDPK1 depletion. Since PfCDPK1 does not seem to reside in rhoptries, it is possible that it may interact with these proteins in lipid rafts during trafficking, which was supported by a previous proteomics study that indicated44 the presence of these proteins in lipid rafts.

While a cross-talk between cAMP and calcium pathways has been reported in Plasmodium22, 25, molecular interactions that guide it have largely remained unclear. We identified PfPKA-R as a substrate for PfCDPK1. The major phosphorylation site-S149, which is phosphorylated by PfCDPK1, resides in the inhibitory sequence, which lies upstream of the nucleotide binding domain (Fig. 3c). The crystal structure of the mammalian PKA complex

Fig. 6 Regulation of invasion by PfCDPK1 and PfPKA. a The invasion of PKA-R-GFP schizonts in the absence (squares) or presence (triangles) of 8Br-cAMP was assessed by counting the number of rings and schizonts on Giemsa smears after indicated time as described above. A representative of three independent experiments is shown. b Shld-1 was withdrawn from the parasites and invasion assays were performed using schizonts as described above. In one set of experiments PKI was added for 3 h before addition of fresh RBCs for invasion. The number of rings formed were counted from Giemsa stained thin blood smears, which reflected successful invasion. Data represents % invasion with respect to Shld-1 treated parasites (100%) (Mean ± s.e.m., n=2 ± , ANOVA, p<0.05, **p<0.01, NS). c Model of PfCDPK1 mediated signaling in malaria parasite: PLC-mediated calcium release results in the activation of PfCDPK1 (Pushkar Sharma, unpublished results), which triggers phosphorylation of key substrates like IMC-glideosome proteins that include IMC1g, IMC1c, and PfGAP45. PfCDPK1 facilitates the activation of PfPKA-C by promoting its dissociation from PfPKA-R. PfCDPK1 may be turned off in the parasite via a negative feedback loop regulated by PfPKA. These events and the regulation of exocytosis of EBA-175 by PfCDPK1 signaling may contribute to the process of invasion.
indicates that IS docks into the active site of PKA-C rendering it to be inactive by engaging key residues. Indeed, S149 phosphorylation of PIPKA-R was mediated by PfCDPK1 in the parasite, as suggested by use of a specific anti-pS149 antibody and co-immunoprecipitation of PIPKA-R and PfCDPK1 established their interaction in the parasite. PfCDPK1 knockdown results in enhanced interaction between R and C subunits of PIPKA-R, which corroborated well with the decrease in PIPKA-C catalytic activity. Therefore, it is reasonable to conclude that the phosphorylation and/or binding with PfCDPK1 promote the dissociation of PIPKA-R from PIPKA-C, which results in PIPKA-C activation. Given that K/RXXS motif that encompasses S149, may also be targeted by other kinases like AGC kinases and therefore, may be a key nodal site for cross talk of cAMP signaling with other signaling pathways as well. A negative feedback loop via which PfCDPK1 activity can be turned off by PIPKA-C also emerged from present studies. Even though, we have not identified a PIPKA target site on PfCDPK1, it appears that PIPKA-C activity may contribute towards PfCDPK1 down regulation. A recent study suggested that PIPK may phosphorylate Psrhodopseudomonas acidophila, which may be the reason for the development of a new method for the detection of Psrhodopseudomonas acidophila. Our present work demonstrated that S64 can be autophosphorylated by PfCDPK1 and mutation of this site does not cause a major change in its activity. Therefore, the mechanism of PfCDPK1 regulation by PIPKA and PIPK may be distinct, which will be interesting to elucidate. While this manuscript was under review, it was reported that the replacement of the gatekeeper residue in ATP-binding site attenuated PfCDPK1 activity and parasites expressing the gatekeeper mutant-PfCDPK1 were more sensitive to PIPK inhibiting C2. Although direct demonstration was not provided, it was suggested that PIPK or its downstream kinases might compensate for the loss of PfCDPK1 activity which will be an interesting proposition to test.

Previous reports have also suggested that PIPKA may regulate the secretion of microneme proteins like AMA-1 and EBA-175. We found mainly a defect in EBA-175 exocytosis and not in AMA-1, although, the possibility of residual ~30% PfCDPK1 being sufficient for AMA-1 release cannot be ruled out. Present studies highlight a novel hub involving PfCDPK1-PIPKA interaction for the cross-talk between calcium and cAMP pathways. Like PfCDPK1, PIPKA is also critical for blood stage development of P. falciparum. Inhibition with generic PKA inhibitors like H89 and PKI27, 28 implicated it as essential development and invasion. Using PKI and transgenic PKA-R overexpressing parasites, we confirmed a role of PIPKA in RBC invasion. While PKI blocked invasion, its addition did not result in an additive effect upon PfCDPK1 knockdown, which hinted that PfCDPK1-mediated activation of PIPKA may be critical for invasion. While it is largely a correlation, it is indeed possible that PfCDPK1 may mediate EBA-175 secretion via PIPKA, as both these kinases regulate this process. Collectively, the present studies demonstrate the involvement of PfCDPK1 in regulating key modules like the IMC and cAMP signaling in the parasite, which might shed light on the mechanism via which it regulates host RBC invasion.

Methods

Reagents and antibodies. All the molecular biology reagents were purchased from Sigma-Aldrich. Oligonucleotides were procured from Sigma-Aldrich, restriction enzymes were obtained from New England Biolabs, USA. Commercially available antibodies were obtained from Santa Cruz Biotechnology (mouse anti-β-Actin (1:500), C6, sc-4778 HRP), rabbit anti-HA (1:500, Y-11, sc-805) and rabbit anti-GAPDH (1:500, FL 335, sc-25778). Protein A/G plus agarose beads (sc-2003) were obtained from Santa Cruz Biotechnology. Anti-EBA-175 antibody was obtained from MR4 (1:1000, MRA-2). Other antibodies were kindly gifted by Dr. Chetan Chitnis, Institute Pasteur, Paris (1:1000, rabbit anti-AMA1).

Prof. Alan Cowman, Walter & Eliza Hall Institute (1:2500, rabbit anti-RH5), Dr. Anthony A. Holder (1:2000 rabbit anti-GAP45). Shld-1 was purchased from Cytoskeleton, LLC, USA. PfPKA inhibitor PKI was obtained from Enzo life sciences (PKI4d, amide, myristoylated), 8Br-cAMP, BAPTA-AM, Neuraminidase, trypsin, cryptotyrosin were obtained from Sigma-Aldrich.

Generation of transgenic parasites. For C-terminal tagging of PfCDPK1 locus with 3HA-DD, ~1.1 kb of the 3’ end of the PfCDPK1 ORF (PlasmodiobDB ID PF3D7_0217500) without the stop codon was PCR amplified from P. falciparum genomic DNA (strain D10) with primers oJDD40 (5’TAGGGGCGCCCTCTAGTTACCATTTATGAAGGTGGGG) and oJDD62 (5’TAGCTCGAGGAAAGATTATTTCAAAATTTTGTCATCACTG). The amplicon was ligated into 3HA-DD plasmid between the restriction sites NotI and XhoI, upstream and in-frame with the coding sequence of the 3HA and DD-tags.52 The PfCDPK1-3HA-DD plasmid, which has the human DHFR selection cassette, was prepared by using Quagen Maxi prep kit. Approximately 100 µg plasmid DNA was transfected into D10 strain (WEHI) and selected using 5 nM WR99210 (gifted by Jacobus Pharmaceuticals). Integration of the plasmid was promoted by several cycles of drug treatment (~1 week) followed by culturing parasites without drug (~3 weeks). When parasites became resistant to WR99210 after a prolonged period of drug, parasites were cloned by limiting dilution in a 96 well plate (nominal density, 3 parasites per 10 well). The integration of 3HA-DD at the PfCDPK1 locus was confirmed by genotyping PCR, for which PCR primers were designed to amplify the endogenous locus, the 3’ integration and the epoie (see Supplementary Fig. 1). Furthermore, the 3’-integration amplicon was cloned and sequenced to confirm the integration at the locus.

The PfPKA-R overexpressing cell line was designed using the pARL-GFP vector. The full length gene (PF3D7_1223100) was PCR amplified using Phusion DNA polymerase and PIPKA-RGGF_F and PIPKA-RGGF_R, KpnI AvrII digested and cloned into the digested pARL-GFP plasmid. The chimeric gene containing the open reading frame of PIPKA and GFP is driven by the late stage specific AMA1 promoter mimicking the expression profile of the endogenous PIPKA-R gene. The construct was sequenced and analyzed for accuracy.

Parasite culture and transfections. P. falciparum sexual stages were cultured in O2 erythrocytes according to standard procedures.58 In addition, 3D7 (MRA) were transfected with 100 µg of purified plasmid DNA, as described previously. Positive selection of transfected parasites was achieved by addition of 10 µg/ml WR99210, an antifolate that selects for the presence of human DHFR gene. P. falciparum lines were cultured in complete RPMI 1640 medium with 0.5% albumax and gassed with 7% CO2, 1% O2 and 88% N2 at 37 °C. Synchronization of parasites was achieved by treatment with 5% sorbitol.50. P. falciparum CDPK1-3HA-DD parasites were cultured in the presence of 2.5 nM WR99210 and 0.25 µM Shld-1. PIPKA-R-GFP and PIPKA-C-HA27 overexpressing parasite cultures were supplemented with 10 nM WR99210. PfCDPK1-3HA-DD parasites were generated in D10 background by transfecting plasmids for single cross-over homologous recombination. PIPKA-R-GFP overexpressing parasites were generated by transfection of 3D7 strain.

Treatment of parasites with pharmacological reagents. Typically, schizont-infected RBCs were treated with IBMX (250 µM), BAPTA-AM (40 µM), 8Br-cAMP (100 µM), PKI (20 µM) unless indicated otherwise.

Growth rate and invasion assays. For comparison of growth rate of the PfCDPK1-3HA-DD parasites in the presence or absence of Shld-1, parasites were synchronized using 5% sorbitol. The effect of Shld-1 removal on PfCDPK1-3HA-DD parasites was studied by splitting synchronized parasite cultures into two halves at ring stage. Shld-1 was withdrawn for one half and plating was done at equal parasitemia at the schizont stage. Parasite growth was quantified for 2–3 life cycles.

The parasite invasion assays were performed, as described earlier.39, 40 with minor modifications. Invasion assays were performed by using schizonts from which Shld-1 was withdrawn for one cycle, as described above. Schizonts (~38–40 h.p.i.) at 0.5–1% parasitemia were incubated with fresh RBCs and formed new rings was monitored by examining Giemsa stained smears after 3–4 h and/or by performing FACS of SYBR Green stained parasites, which were fixed 30 h post invasion. FACS assay was performed using a slightly modified previous published protocol. Briefly, ~300 µl parasite infected RBCs were washed thrice with PBS and were fixed with 4% paraformaldehyde for 30 min. After fixation, parasites were washed twice with PBS and stained with SYBR Green (1:5000 in PBS) for 1 h. Imaging of transfected parasites was performed at 250X magnification by using Fluo software after exciting the autofluorescence from unstained cells by gating. To study the effect of Neuraminidase (Nn), ring infected RBCs were treated with 66 nM nN. Neuraminidase and SYBR Green stained parasites were resuspended in 800 µl of PBS and used for FACS by using BD Accuri C6 Plus machine. Data were analyzed using Flowjo software after excluding the autofluorescence from unstained cells by gating. To study the effect of Chymotrypsin (CT), RBCs were treated with 1 mg ml−1 CT for 1 h at 37 °C, as described previously. For
performing invasion assays with PPIKA-R-GFP parasites, parasites were treated with 100 µM 8Br-cAMP 3 h prior to performing invasion assays.

Parasite attachment assay. The attachment assays were performed as described earlier with slight modifications. Briefly, CDPCKD3-1HA-DD parasites were tightly synchronized, split into 2 × 15 ml (5% parasitemia, 5% hematocrit) and from one half Shld-1 was withdrawn. The parasites were allowed to mature to schizonts synchronized, split into 2 × 15 ml (5% parasitemia, 5% hematocrit) and from one NATURE COMMUNICATIONS | DOI: 10.1038/s41467-017-00053-1 ARTICLE

analyzed on Orbitrap Fusion Tribrid mass spectrometer interfaced with Proxeon minute for over 60 min. A total of 96 fractions were concatenated into 12 fractions complete RPMI1640 along with fresh RBCs and treated with 1

were then washed with 80% ACN in 3% TFA and eluted using 4% ammonia Basic RPLC and phosphopeptide enrichment were again analyzed as two technical replicates. 

Technical replicates with 114 and 115 iTRAQ reporter ions and peptides from CDPCKD1 knockdown parasites were labeled with 116 and 117 reporter ions. Labeling of the peptides was checked and the four samples were pooled in equal amount and dried. One more biological replicate was processed in the same way, which was again analyzed as two biological replicates. 

Basic RPLC and phosphopeptide enrichment. The lyophilized peptides were reconstituted in RPLC solvent A (10 mM triethylammonium bicarbonate, pH 8.5) and fractionated on Xbridge C18 5 um 250 × 4.6 mm column (Waters Corporation, Milford, MA, USA) using Agilent 1100 binary pump (Agilent Technologies, Santa Clara, CA, USA). The sample was resolved through reverse-phase liquid chromatography method using a gradient of 5 to 60% solvent B (10 mM triethylammonium bicarbonate, pH 8.5 in 95% Acetonitrile) in a ratio of 1 unit of trypsin per 20 unit of sample and kept for overnight digestion at 37 °C. Buffer exchange was done using Sep-Pak C18 columns (Waters Corporation, Milford, MA, USA) and peptides were lyophilized. iTRAQ labeling of the peptides was carried out as per manufacturer’s instructions. Peptides from wild type parasites were labeled in technical replicates with 114 and 115 iTRAQ reporter ions and peptides from CDPCKD1 knockdown parasites were labeled with 116 and 117 reporter ions. Labeling of the peptides was checked and the four samples were pooled in equal amount and dried. One more biological replicate was processed in the same way, which was again analyzed as two technical replicates. 

LC-MS/MS analysis. Each fraction was reconstituted in 0.1% formic acid and analyzed on Orbitrap Fusion Trivibrid mass spectrometer interfaced with Proxeme Easy-nLC 1000 system (Thermo Scientific, Bremen, Germany). The sample was first loaded onto a 2 cm long pre-column packed in-house with magic C18 AQ (MichromBioresources, Auburn, CA, USA). Peptides were resolved on an analytical column (75 µm i. x 15 cm, 3 µm particle and 100 Å pore size) using a linear gradient of 7 to 30% of solvent B (0.1% formic acid in 95% Acetonitrile) over 120 min. Both MS and MS/MS was acquired using Orbitrap mass analyzer and full scans were acquired with scan range of 350–1800 m/z and at a resolution of 120,000 at 200 m/z. The data were acquired in top speed mode with 3 s cycles, which would allow the instrument to continuously perform MS scans until the list of precursors diminish to zero or 3 s. Most intense precursor ions were selected and fragmented using higher energy collisional dissociation (HCD) with 35% normalized (HCD) energy. Fragment ions were detected in Orbitrap with mass resolution of 30,000 and AGC target value was set to 50,000 with maximum ion injection time of 200 ms. Singly charged ions were rejected and dynamic exclusion was set to 30 s. Internal calibration was carried out using lock mass option (m/z 445.1200025) from ambient air.

MS data analysis. The mass spectrometry derived data were searched using Mascot and Sequest search engines using Proteome Discoverer 1.4 (Thermo Fisher Scientific, Bremen, Germany). Phosphopeptides enriched fractions and total proteome data from each replicate were searched against a combined Human and P. falciparum NCBI RefSeq protein database (version 65) with carbamidomethylation of cysteine residues, peptide N-terminal and lysine side chain of iTRAQ as fixed modification. Oxidation of methionine and phosphorylation of serine, threonine and tyrosine were selected as dynamic modifications. Trypsin was set as the protease and maximum of one missed cleavage was allowed. Precursor mass tolerance was set to 20 ppm and fragment mass tolerance of 0.1 Da was allowed. All PSMs were identified at 1% FDR. An error threshold, 0.1 Da, was used for individual PSM using percolator, providing statistical confidence for each spectral match. If a given spectrum was assigned to different peptides by Mascot and Sequest, they were discarded and not considered for further analysis. The probability of phosphorylation for each site was calculated by the phosphorylation node in Proteome Discoverer. Only the phosphopeptides with >75% site localization were considered for further analysis. Phosphorylation fold change for each peptide was normalized with the total proteome level change and a normalized phosphorylation change of >0.75 fold was considered as significantly regulated.

Gene ontology analysis. The gene ontologies for Plasmodium falciparum proteins were downloaded from PlasmoDB database. Hypophosphorylated proteins that lacked appropriate GO annotation were assigned with relevant GO terminologies based on manual curation of the available literature. We merged our manually curated information with the available ontologies and carried out GO enrichment analysis on the list of hypophosphorylated proteins using FunRich tool. The list of proteins identified in our analysis was selected as background and the hypophosphorylated proteins were provided as input. The fold enrichment and P values associated with biological processes, molecular functions and cellular localizations are provided in Supplementary Data 2.

Motif analysis. The list of hypophosphorylated sites with a width of 15 amino acids was subjected to motif analysis using motif-X tool. A background of P. falciparum protein database was used for the analysis and occurrences threshold was set to default i.e. 20. A P value threshold of ≤ 1e-6 was used to identify enriched motifs.

Protein–protein interaction networks prediction. The list of differentially phosphorylated proteins upon CDPK1 knockdown was submitted to STRING database (version 10.0) for protein–protein interaction analysis. Interactions with high confidence and score of >0.7 were considered as significant and considered for the study.

Expression of recombinant proteins. For expression of PPIKA-C (PlasmoDB ID PF3D7_0934800), PPIKA-R (PlasmoDB ID PF3D7_1223100) and their mutants as GST fusion proteins, their ORFs were cloned in pGEXTK1 vector (GE Healthcare) using PCR primers PPIKA-C_R and PPIKA-R_R (PPIKA-C_R and PPIKA-C_C-R_PPIKA-C). Primer sequences are provided in Supplementary Table 1. The list of proteins identified in our analysis was selected as background and the hypophosphorylated proteins were provided as input. The fold enrichment and P values associated with biological processes, molecular functions and cellular localizations are provided in Supplementary Data 2.

Generation of antisera. Antisera was raised against PPIKA-C and PPIKA-R using KLH-conjugated synthetic peptides designed from their C-terminus following standard procedures in rabbits (2–3 months old, New Zealand) and mice (Balb/c, 4–6 week old) (Supplementary Fig. 6). PPIKA-C_R (KLH) cys-VYPPKRKLKNKFEDSSNFEOH; PPIKA-R (KLH) cys-CDLHRRNVENYKKVLNE-OH. Antisera against PfPKA-C1g was raised in mice using full length 6His PfPKA-C1g recombinant protein, which was expressed using standard procedures. Antibody against PPIKA-R phosphorylated at S149 was custom generated by Antagene, Inc. (USA) for this purpose, a synthetic peptide with sequence Cys- HFIQKKRL(p)SVSAEAYGDWNK or a control without phosphoserine was used. Cysteine at the N-terminus was added for KLH-conjugation. The phosphorylated and non-phosphorylated peptides were used to immunize rabbits over 2 weeks schedule. Antiserum was collected after 10 days and fourfold immunization and antibody titers were determined by performing ELISA against the phosphorylated and the non-phosphorylated peptides. The antisera were enriched following a two-step phospho-peptide antibody purification method.

Kinase assays. Protein kinase assays were performed using recombinant 6xHis-PCDK1 in a reaction buffer containing 50 mM Tris pH 7.4, 10 mM MgCl₂, 1 mM Dithiothreitol, 100 µM CaCl₂ and 100 µM 8Br-cAMP [32P]ATP 15µCi/ reaction using recombinant substrates like PAGAP45, PPIKA-R, I2M, and C1g. Reactions were carried out at 30°C for 45 min and stopped by boiling them in SDS-PAGE loading buffer. The reaction mixture was electrophoresed on SDS-PAGE and
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separate merozoite and secreted proteins released in the supernatant. The supernatant containing merozoites was further centrifuged at 3300×g for 5 min to separate the free merozoites from the infected and uninfected RBCs. The culture media was added to schizont/segmenters, which were allowed to burst to release merozoites.

Metabolic labeling of parasites. PCDPK1-3HA-DD parasites were synchronized twice at the ring stage. Parasites were split in two halves after washing with complete RPMI 1640 media and Shld-1 was withdrawn from one of them. ~40 h post-invasion, parasites were washed twice with phosphate deficient RPMI 1640 media (Hyclone) supplemented with 0.5% albumin (Gibco, Life Tech). These parasites were incubated with 32P orthophosphoric acid (1–2 mCi ml−1) till segments were formed. Parasite lysate was prepared in complete lysis buffer described below and immunoprecipitation was done using specific antibodies. The immunoprecipitate was electrophoresed on SDS-PAGE and labeled proteins were detected by phosphorimaging using a Fujifilm FLA-5000 scanner.

Immunoblotting and immunoprecipitation. After various treatments with various pharmacological inhibitors, parasites were harvested by 0.05% saponin lysis at 4 °C in 1× SDS-PAGE loading buffer for western blotting. Immunoblots were cropped for presentation in main figures. For assaying PfPKA-C activity, a parasite line overexpressing PfPKA-C-HA was used.

Immunoprecipitation was done using specific antisera and blots were developed using SuperSignal West Pico, or Dura Chemiluminescence Substrate (Thermo Scientific) following manufacturer’s instructions. For immunoprecipitation, 60–100 µg of lysate protein was typically used and incubated with relevant antibodies at 4 °C for 12 h followed by incubation with protein A+G plus agarose beads for 5 h. The beads were washed with cold complete lysis buffer and resuspended in 50 µl 1× kinase assay buffer for kinase assay and in 30 µl 1× SDS-PAGE loading buffer for western blotting. Immunoblotting was performed using specific antisera and blots were developed using SuperSignal West Pico, or Dura Chemiluminescence Substrate (Thermo Scientific) following manufacturer’s instructions.

Densitometry and statistical analysis. Image J (NIH) software was used to perform densitometry of western blots. The band intensity of the loading control was normalized. Statistical analysis was performed using Prism (Graph Pad software Inc USA). Data are represented as mean ± SEM from three independent experiments, unless indicated otherwise and p<0.05 was taken as statistically significant.

Data availability. The mass spectrometry-based proteomics data has been deposited to the ProteomeXchange Consortium (http://proteomecentral.proteomexchange.org) and can be accessed via the PRIDE partner repository with the data set identifier PXD000207.

All other relevant data are available from the authors upon request.

Received: 1 November 2016 Accepted: 26 April 2017
Published online: 05 July 2017

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Acknowledgements
We thank Divya Thomas and Gourav Dey for assistance with some of the experiments. Studies were supported by grants BT/COE/34/SP15138/2015 and BT/PR/7976/BRB/10/1223/2013 from Department of Biotechnology, India and funds from NII core. S.K. is a recipient of Junior Research Fellowship from the Council of Scientific and Industrial Research (CSIR), India. P.S. is a J.C. Bose fellow.

Author contributions
S.K., M.K., R.E., A.S.P., A.K.M., J.D.D.: Planned and performed experiments, analyzed the data and contributed to manuscript writing and preparation of figures. P.S., M.T.D., T.G., H.G., T.S.K.P.: Provided scientific oversight and guided the studies. P.S. Also contributed to manuscript writing and preparation of some figures.

Additional information
Supplementary Information accompanies this paper at http://dx.doi.org/10.1038/s41467-017-00053-1.

Competing interests: The authors declare no competing financial interests.

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