Regulation of Platelet Derived Growth Factor Signaling by Leukocyte Common Antigen-related (LAR) Protein Tyrosine Phosphatase: A Quantitative Phosphoproteomics Study*[S]

Adil R. Sarhan‡, Trushar R. Patel‡¶, Andrew J. Creese‡, Michael G. Tomlinson‡, Carina Hellberg‡, John K. Heath‡, Neil A. Hotchin‡, and Debbie L. Cunningham‡§

Intracellular signaling pathways are reliant on protein phosphorylation events that are controlled by a balance of kinase and phosphatase activity. Although kinases have been extensively studied, the role of phosphatases in controlling specific cell signaling pathways has been less so. Leukocyte common antigen-related protein (LAR) is a member of the LAR subfamily of receptor-like protein tyrosine phosphatases (RPTPs). LAR is known to regulate the activity of a number of receptor tyrosine kinases, including platelet-derived growth factor receptor (PDGFR). To gain insight into the signaling pathways regulated by LAR, including those that are PDGF-dependent, we have carried out the first systematic analysis of LAR-regulated signal transduction using SILAC-based quantitative proteomic and phosphoproteomic techniques. We have analyzed differential phosphorylation between wild-type mouse embryo fibroblasts (MEFs) and MEFs in which the LAR cytoplasmic phosphatase domains had been deleted (LARΔP), and found a significant change in abundance of phosphorylation on 270 phosphosites from 205 proteins because of the absence of the phosphatase domains of LAR. Further investigation of specific LAR-dependent phosphorylation sites and enriched biological processes reveal that LAR phosphatase activity impacts on a variety of cellular processes, most notably regulation of the actin cytoskeleton. Analysis of putative upstream kinases that may play an intermediary role between LAR and the identified LAR-dependent phosphorylation events has revealed a role for LAR in regulating mTOR and JNK signaling. ***Molecular & Cellular Proteomics 15: 10.1074/mcp.M115.053652, 1823–1836, 2016.***

‡From the School of Biosciences, College of Life and Environmental Sciences, University of Birmingham, Edgbaston, Birmingham, B15 2TT, United Kingdom

Received July 15, 2015, and in revised form, March 23, 2016
Published, MCP Papers in Press, April 13, 2016, DOI 10.1074/mcp.M115.053652
Author contributions: A.R.S., T.R.P., M.G.T., C.H., J.K.H., N.A.H., and D.L.C. designed research; A.R.S., T.R.P., and D.L.C. performed research; A.R.S., T.R.P., A.J.C., J.K.H., N.A.H., and D.L.C. analyzed data; T.R.P., A.J.C., M.G.T., J.K.H., N.A.H., and D.L.C. wrote the paper.

Phosphorylation is a key post-translational modification involved in the regulation of cell signaling. Control of phosphorylation is vital in maintaining normal biological processes, and dysregulation is implicated in many diseases. Kinases and phosphatases have opposing roles in modulating levels of phosphorylation, acting in a coordinated manner within cells to maintain cellular homeostasis via their regulation of cell signaling pathways. Historically phosphatases were viewed as being promiscuous enzymes whose role was simply to dephosphorylate their substrates in order to terminate signal transduction pathways. It is now evident that phosphatases display selectivity and are not simply 'off switches' but can contribute to both deactivation and activation of signaling pathways (1). Although the role of kinases has been extensively studied, much less is known about phosphatases and their specific contributions to cell signaling.

Leukocyte common antigen-related protein (LAR)[1] belongs to the LAR subfamily of receptor-like protein tyrosine phosphatases (RPTPs). It is composed of an extracellular domain containing three immunoglobulin domains (Ig), a fibronectin type III domain (FNIII), and cytoplasmic domains, D1 and D2, that are essential for phosphatase activity (2–4). LAR is widely expressed in a variety of cell types, such as neuronal cells, epithelial cells and fibroblasts (5). Several disorders are associated with LAR including defective development of mammary glands, abnormal neuronal development and function, diabetes and cancer (6, 7). Signal transduction regulated by LAR has thus far predominantly been studied in neuronal cells, where it participates in axonal outgrowth, nerve regeneration and orchestration of synapse development (6, 8). LAR regulates tyrosine kinase receptor growth factor signaling by either dephosphorylating negative regulatory tyrosine residues to enhance receptor activation (9), or by dephosphorylating activating tyrosine residues to deactivate the receptor (10, 11).

[1] The abbreviations used are: LAR, leukocyte common antigen-related protein; PDGF, platelet derived growth factor; RPTP, receptor protein tyrosine phosphatase; SILAC, stable isotope labelling with amino acids in cell culture; WCL, whole cell lysate; WT, wild-type.

LAR localizes to integrin-based focal adhesion complexes (12) and adherens junctions (13).

Platelet-derived growth factor (PDGF) signaling is involved in many cellular processes such as cell growth, survival and motility (14). Overexpression of the PDGF receptor is associated with diseases such as atherosclerosis and cancer, signifying it as a target for therapeutic interventions (15–17). PDGF isoforms act as dimers composed of interacting A, B, C, and D polypeptide chains. These can be homodimeric or heterodimeric isoforms that can interact with PDGF α and PDGF β receptors leading to receptor dimerization and activation of kinase activity via autophosphorylation (18). This results in the recruitment and activation of signaling pathways that culminate in transcriptional responses and the promotion of cell proliferation and survival (18, 19).

Phosphatases are generally considered as negative regulators of signaling pathways. A number of protein tyrosine phosphatases (PTPs) have been reported to dephosphorylate tyrosine residues (Tyr) on PDGFRβ thereby deactivating the receptor and inhibiting downstream signaling. For example, dephosphorylation of Tyr^{857} on PDGFRβ by low molecular weight protein tyrosine phosphatase (LMW-PTP) inhibits the receptor kinase activity and subsequent downstream signaling via PI-3 kinase (20). T-cell protein tyrosine phosphatase (TC-PTP) has been shown to inhibit binding of phospholipase C γ1 (PLC γ1) through dephosphorylation of Tyr^{1021} that results in altered cell migration in response to PDGF (21). SHP-2 can inhibit binding of Ras-GAP to PDGFRβ by dephosphorylation of PDGFRβ Tyr^{771}, which results in enhanced activity of the Ras signaling pathway (22). By contrast, LAR promotes PDGF signaling by inhibiting activity of the cytoplasmic tyrosine kinase, c-Abl (23). In the absence of LAR phosphatase activity c-Abl inhibits PDGFRβ signaling by phosphorylating and inhibiting the receptor (23).

In this study, we set out to gain insight into the landscape of cell signaling events regulated by LAR. In the first systematic analysis of LAR-regulated signal transduction we have used stable isotope labeling by amino acids in cell culture (SILAC) (24, 25) to analyze differential phosphorylation in wild-type (WT) mouse embryo fibroblasts (MEFs) and MEFs in which the LAR cytoplasmic phosphatase domains had been deleted (LARΔP) (26). Although LAR is known to promote PDGFR activation in fibroblasts (23), the signaling consequences of this regulation have not been fully studied, thus we carried out these studies in the absence and presence of PDGF. We identified 270 LAR-dependent phosphorylation events on 205 proteins, including known LAR interactors, kinases, guanine nucleotide exchange factors (GEFs), and GTPase activating proteins (GAPs). Subsequent functional classification revealed an enrichment of LAR-mediated phosphorylation events on proteins involved in cytoskeletal organization. Further kinase prediction analysis revealed a role for LAR in regulating both mTOR and JNK signaling pathways, both of which play a role in regulation of the actin cytoskeleton.

These results significantly expand our understanding of signaling events downstream of LAR. This approach has enabled us to identify LAR-dependent changes in phosphorylation within the entire signaling network, highlighting the role of LAR as a key regulator of growth factor-dependent cell signaling pathways.

EXPERIMENTAL PROCEDURES

Reagents and Antibodies—Antibodies were purchased from Cell Signaling Technologies (SAPK/JNK, SAPK/JNK Thr183/Tyr185, mTOR, mTOR Ser2448, P70S6K Thr389, c-Jun, c-Jun Ser63, MKK7, MKK7 Ser271/Thr275; Danvers, MA), Santa Cruz (ERK1/2 and ERK Thr202/Tyr204; Dallas, TX), and Sigma-Aldrich (Flag; Dorset, UK). Recombinant human PDGF-BB was obtained from Cell Signaling Technologies. Rabbit polyclonal Alix has been previously described (27). The secondary goat anti-mouse and goat anti-rabbit IgG IRDye conjugated antibodies were from LI-COR Biosciences (Cambridge, UK).

Cell Culture—Mouse embryonic fibroblasts (MEFs) from mice where the LAR phosphatase domains had been deleted (LARΔP) and from littermate wild-type (WT) (26), were used in the study (both cell types are kind gifts from Wiljan J.A.J. Hendriks, Radboud University Medical Center, Nijmegen, Netherlands). Cells were grown in DMEM supplemented with 10% fetal bovine serum (FBS), 100 U/ml penicillin, 0.1 mg/ml streptomycin, and 250 μg/ml amphotericin B. For SILAC labeling, cells were cultured in SILAC DMEM (Thermo Fisher Scientific, Loughborough, UK) supplemented with either "light" isotopically normal L-Lysine and L-Arginine (R0K0) (Sigma-Aldrich), "medium" $^{13}C_6$ L-Arginine and 4,4,5,5-D4 L-Lysine (R6K4), or "heavy" $^{13}C_6$ $^{15}N_4$ L-Arginine and $^{13}C_6$ $^{15}N_2$ L-Lysine (R10K8) (Goss Scientific, Crewe, UK), with 0.5 mg/ml proline (Sigma), 0.1 mg/ml streptomycin, 100 U/ml penicillin, 250 μg/ml amphotericin B and 10% v/v dialyzed fetal bovine serum (Labtech International, East Sussex, UK). Cells were grown in SILAC media for seven doubling times before being analyzed for incorporation efficiency of the SILAC amino acids (see supplemental Fig. S1).

Transfection—The FLAG-LAR expression vector was kindly provided by Ruey-Hwa Chen (National Taiwan University, Taipei, Taiwan). LARΔP cells were transfected using Lipofectamine 2000 (Thermo Fisher Scientific) according to manufacturer's instructions.

Cell Stimulation, Cell Lysis, and Immunoblotting—Cells were serum starved for 16 h prior to stimulation with 20 ng/ml PDGF-BB for the indicated times. Treated cells were placed on ice and washed twice with ice-cold phosphate buffered saline (PBS). Cells were then lysed with lysis buffer (20 mM Tris-HCl, pH 7.5, 0.5% Triton X-100, 0.5% deoxycholate, 150 mM NaCl, 10 mM EDTA, 0.5 mM Na_3VO_4, and 1% Trasylol) for 15 min on ice. Lysed cells were centrifuged at 15,000 $\times$ *g* for 15 min at 4 °C and the supernatant (WCL) was collected. Protein concentrations were determined using the BCA protein assay (Thermo Fisher Scientific) as per the manufacturer's instructions. An equal volume of 2$\times$ sample buffer (1.0 M Tris-HCl pH 8.8, 0.5% Bromphenol blue, 43.5% glycerol, 10% SDS, 1.3% β-mercaptoethanol) was added to the WCL, and the sample was boiled at 95 °C for 6 min. Samples were run on SDS-PAGE gels and transferred to nitrocellulose membranes. The membranes were blocked with 5% bovine serum albumin (BSA) (Sigma-Aldrich) at room temperature for one hour and incubated in 5% BSA in TBS-T (20 mM Tris-HCl, pH 7.5, 0.1% Tween 20, 150 mM NaCl) containing primary antibody overnight at 4 °C. Following 3 $\times$ 10 min washes in TBS-T, the membrane was incubated in TBS-T containing IRDye conjugated secondary antibody (LI-COR Biosciences) for 1 h at room temperature. The membranes were washed again as above and proteins were visualized using fluorescence detection on the Odyssey Infrared Imaging System (LI-COR Biosciences). Following quantitation of immunoblots (n = 3)

statistical analysis was performed using a two-way ANOVA, Sidak's multiple comparison test.

Trypsin Digestion, Sample Fractionation, and Phosphopeptide Enrichment of Samples—For the proteome analysis, 5 μg of light, medium, and heavy lysates were mixed, run on a 10% SDS-PAGE gel, and Coomassie stained. Each lane was cut into 10 bands. In-gel digestion using Trypsin Gold (Promega, Southampton, UK) was carried out as previously described (28). For the phosphoproteome analysis, 10 mg of light, medium, and heavy lysates were pooled prior to trypsin digestion. Proteins were reduced with 8 mM DTT, alkylated with 20 mM iodoacetamide in 50 mM ammonium bicarbonate and digested with Trypsin Gold (1:100 enzyme/protein ratio) at 37 °C overnight. Digested samples were acidified by addition of 0.5% TFA. Peptides were desalted using Sep-Pak C18 Cartridges (Waters, Milford, MA) according to manufacturer's instructions. Desalted and dried peptides were resuspended in 100 μl mobile phase A (10 mM KH_3PO_4, 20% acetonitrile, pH 3) and loaded onto a 100 × 4.6 mm polysulfoethyl A column (5 μm particle size, 200 nm pore size, PolyLC, Columbia, MD). Separation used a gradient elution profile that started with 100% mobile phase A, increased from 0 to 50% mobile phase B (10 mM KH_3PO_4, 20% acetonitrile, 500 mM KCl, pH 3) over 30 min, increased to 100% B over 5 min, and then returned to 100% A. Each of the 20 resulting fractions was desalted using a C8 macrotrap cartridge (Michrom BioResources, Auburn, CA) according to manufacturer's instructions. Phosphopeptides were enriched using TiO_2 tips (Titansphere™ Phos-TiO kit, GL Sciences, Torrance, CA). Tips were washed in buffer A (0.5% (v/v) TFA, 80% (v/v) ACN) and equilibrated in buffer B (0.38% (v/v) TFA, 60% (v/v) ACN, 25% (v/v) lactic acid). Phosphopeptides were resuspended in buffer B and loaded onto the tips, washed once in buffer B and twice in buffer A before being eluted sequentially in 5% ammonia solution followed by 5% pyrrolidine. Phosphopeptide-enriched samples were desalted on reverse-phase C18 ZipTips (Millipore, Nottingham, UK). Peptides were eluted in 50% (v/v) ACN, 0.1% (v/v) formic acid (FA), dried to completion and resuspended in 0.1% FA. All resulting peptide mixtures were analyzed in duplicate by liquid chromatography tandem mass spectrometry (LC-MS/MS).

Mass Spectrometry—On-line liquid chromatography was performed by use of a Dionex Ultimate 3000 NSLC system (Thermo Fisher Scientific). Peptides were loaded onto an Acclaim PepMap 100 C18 resolving column (15 cm length; 75 μm internal diameter; LC Packings Sunnyvale, CA) and separated over a 30 min gradient from 3.2% to 44% acetonitrile (J.T. Baker (Avantor Performance Materials), Deventer, The Netherlands). Peptides were eluted directly (350 nL/min) via a Triversa nanospray source (Advion Biosciences, Ithaca, NY) into a LTQ Orbitrap Elite mass spectrometer (Thermo Fisher Scientific). The mass spectrometer alternated between a full FT-MS scan (m/z 380–1600) and subsequent CID MS/MS scans of the seven most abundant ions. Survey scans were acquired in the Orbitrap cell with a resolution of 60,000 at m/z 200. Precursor ions were isolated and subjected to CID in the linear ion trap. Isolation width was 2 Th and only multiply charged precursor ions were selected for MS/MS. The MS1 maximum ion inject time was 1000 ms with an AGC target of $1e^6$ charges. The MS2 ion inject time was 50ms with an AGC target of $2e^5$ charges. Dynamic exclusion was utilized, fragmented ions were excluded for 60 s with an exclusion list size of 500. CID was performed with helium gas at a normalized collision energy of 35%. Precursor ions were activated for 10 ms. Data acquisition was controlled by Xcalibur 3.0.63 software.

Identification and Quantification of Peptide and Proteins—Mass spectra were processed using the MaxQuant software (version 1.5.3.8) (29). Data were searched, using the Andromeda search engine within MaxQuant (30), against the mouse Swiss-Prot database (downloaded 6.10.15). The mouse database contained 16,719 reviewed protein entries. The search parameters were: minimum peptide length 7, peptide tolerance 20 ppm (first search) and 6 ppm (second search), mass tolerance 0.5 Da, cleavage enzyme trypsin/P, and 2 missed cleavages were allowed. Carbamidomethyl (C) was set as a fixed modification. Oxidation (M), acetylation (Protein N-term), and phospho (STY) were set as variable modifications. The appropriate SILAC labels were selected and the maximum labeled amino acids was set to 3. All experiments were filtered to have a peptide and protein false-discovery rate (FDR) below 1% and the match between runs featured was enabled. All raw files from both the phosphoproteome and proteome pipeline were analyzed together in MaxQuant. Within the MaxQuant output, phosphorylation sites were considered to be localized correctly if the localization probability was at least 0.75 (75%) and the score difference at least 5. Bioinformatics analysis was performed in the Perseus software environment, which is part of MaxQuant (Perseus version 1.5.0.15; www.perseus.framework.org). Significance testing was carried out using a Student's *t* test on log 2 transformed ratios and controlled with a Benjamini-Hochberg FDR threshold of 0.05. Peptides quantified in three or more experimental repeats were deemed significantly changed and regulated by LAR phosphatase activity if they had a p value of < 0.05 and a ratio of < 0.667 or > 1.5 (at least a 1.5-fold change in abundance).

The mass spectrometry proteomics data, including the MaxQuant output, have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the data set identifier PXD002545 (31).

Cluster Analysis, GO Analysis, and Kinase Motif Analysis—GProX software (32) was used to perform clustering of log2 transformed ratios from the MaxQuant output. Unsupervised fuzzy *c*-means clustering was used with an upper regulation threshold of 1 and a lower regulation threshold of −1. Overrepresentation of GO terms in the clusters was performed within GProX using a binomial statistical test with a Benjamini-Hochberg p value adjustment, a p value threshold of 0.05, and a minimum occurrence of 2. DAVID (Database for Annotation, Visualization and Integrated Discovery) (33) was used to identify over-represented GO terms in the phosphoproteome data set. The background list comprised of all of the proteins identified across our experiments. The threshold count and EASE score were set to 2 and 0.05 respectively. Phosphopeptides containing well localized phosphosites were analyzed for predicted kinase motifs using GPS (34) with a high stringency setting. Protein network visualization was performed using Cytoscape (35) with WordCloud plugin (36).

RESULTS

Absence of LAR Phosphatase Activity Leads to Alterations in the Global Phosphoproteome and Proteome—Our aim was to gain insight into the protein signaling networks downstream of LAR. We utilized SILAC (24, 25) to quantitatively compare levels of protein expression (proteome analysis) and phosphorylation (phosphoproteome analysis) in PDGF-stimulated wild-type (WT) and LARΔP (lacking cytoplasmic phosphatase domains) MEFs. Three populations of WT and LARΔP cells were SILAC-labeled by culturing them in light R0K0, medium R6K4, or heavy R10K8 SILAC media. Cells were left untreated or stimulated with PDGF-BB for 7 min as indicated in Fig. 1*A*. Within the phosphoproteome data set, 2559 unique phosphosites from 1311 proteins were identified with high localization scores (localization probability >0.75; score difference >5) in one or more experimental replicates. These phosphosites were comprised of 2125 (83%) serine, 260 (10%) threonine, and 174 (7%) tyrosine phosphorylation sites. Of these, 266

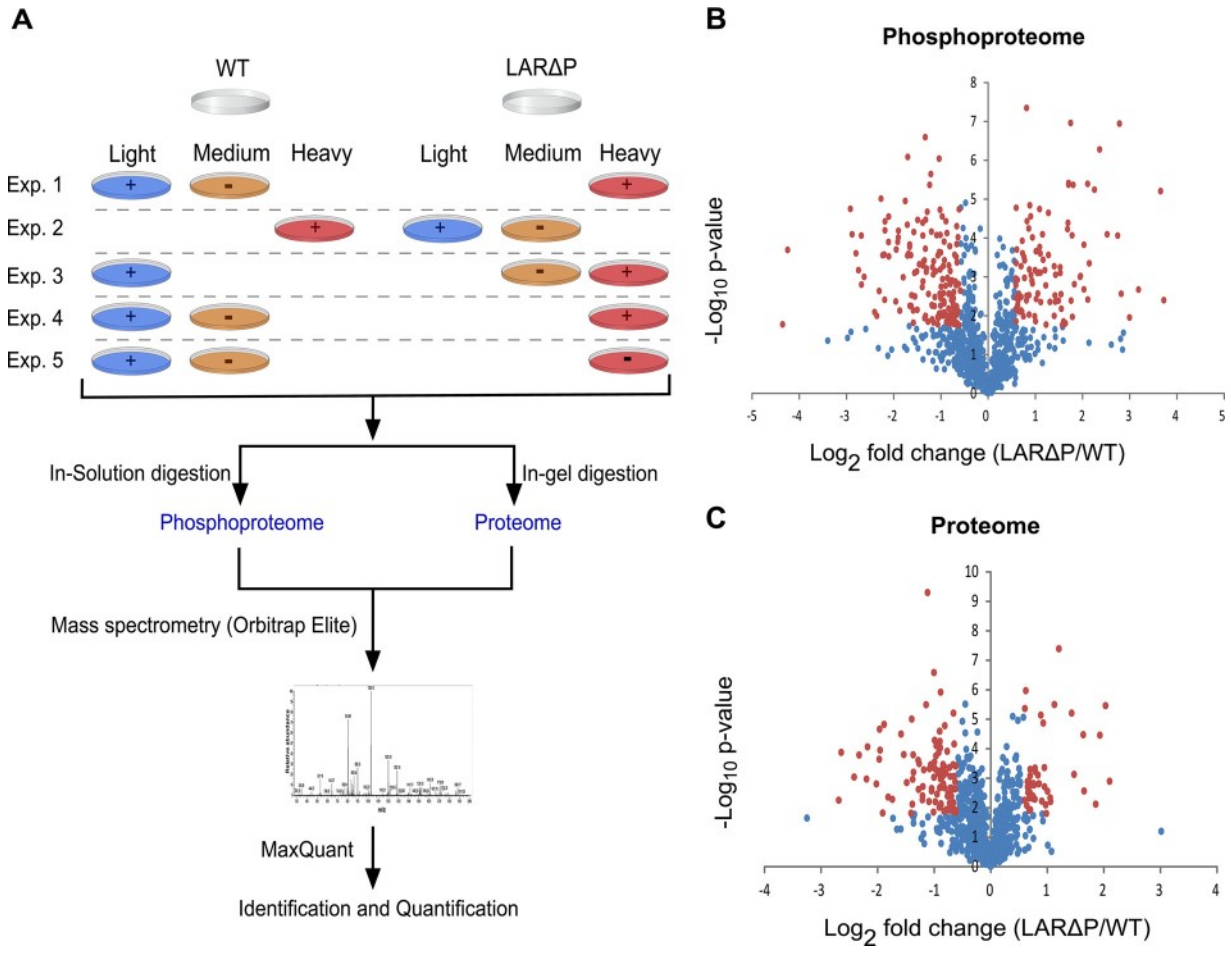

FIG. 1. **Global phosphoproteomics and proteomics to measure contribution of phosphatase activity of LAR to PDGF signaling.** *A*, Schematic overview of experimental design. Volcano plots showing the magnitude (log2 fold-change) and significance (–log10 Benjamini-Hochberg adjusted *p* value) of differential phosphopeptide (*B*) and protein (*C*) abundance in PDGF-stumulated WT *versus* LARΔP cells. Significantly up-regulated phosphopeptides and proteins are marked in red (adjusted *p* value < 0.05; > 1.5 fold-change).

(10%) are not listed in PhosphoSitePlus (37) and are considered novel.

To compare the phosphoproteome of PDGF stimulated WT and LARΔP cells four biological replicates, including a label swap control, were incorporated into the experimental design (Fig. 1*A*). The overlap between the four biological replicates is shown in supplemental Fig. S2*A*: 54% of the phosphopeptides were identified in two or more replicates, and 27% were identified in three or more replicates. The Pearson's correlation coefficient for the peptide ratios measured across the four biological replicates, including the label swap experiment, ranged from 0.64–0.86 indicating good biological reproducibility (supplemental Fig. S2*B*). In cells lacking LAR phosphatase activity, a total of 270 phosphopeptides from 205 proteins showed a significant change in abundance ($p < 0.05$; > 1.5-fold change) (Fig. 1*B*; supplemental Table S1). Of these, 255 (95%) contained serine phosphorylation sites, 9 (3%) threonine, and 6 (2%) tyrosine. A total of 103 phosphosites were up-regulated and 167 down-regulated. Within our phosphoproteome data set we identified serine, threonine, and tyrosine phosphorylation events mediated by LAR allowing us to gain an understanding of the global signaling landscape. LAR could contribute to the regulation of phosphorylation on these sites via modulation of the activity of specific kinases and phosphatases, or in the case of tyrosine, via direct dephosphorylation, given that LAR is a tyrosine phosphatase.

These LAR-dependent changes in phosphopeptide abundance could be caused by alterations in regulation of specific phosphorylation events or changes in protein abundance, hence our combined proteomic and phosphoproteomic approach. Within the proteomic data set (comparing PDGF treated WT cells and LARΔP cells) a total of 2939 proteins were identified; 1150 with associated quantitation data in two or more biological replicates. Of these, 147 proteins (47 up-regulated; 100 down-regulated) showed a significant change ($p < 0.05$; > 1.5-fold change) in abundance in the LARΔP cells compared with the WT cells (Fig. 1*C*; supplemental Table S2). This is a significant finding as 13% of the quantified proteome was changed because of the absence of LAR phos-

phatase activity, suggesting that LAR may be involved in regulating protein turnover. Merging the phosphoproteome and proteome data sets resulted in a measure of corresponding protein abundance for 23% of the quantified phosphorylation sites. Of the 270 LAR-dependent phosphorylation events, 11% changed significantly at the level of the proteome indicating regulation at the protein level rather than the peptide level.

Tyrosine Phosphorylation Regulated by LAR—Considering potential direct LAR substrates, a loss of LAR phosphatase activity would lead to an increase in tyrosine phosphorylation of these proteins, hence we looked for tyrosine phosphorylated peptides within the data set that increased in LARΔP cells. Only one tyrosine phosphorylated peptide, belonging to the protein Lcp2 (SLP76), increased in abundance in the absence of LAR activity (LARΔP cells) (supplemental Table S1). SLP76 is an adaptor protein, mostly studied in T cells, that relays signals from activated receptors to the cytoskeleton (38). We have identified an increase in Tyr^{465} phosphorylation which is a tyrosine residue located in the C-terminal SH2 domain of SLP76. The remainder of the tyrosine phosphopeptides decrease in abundance in LARΔP cells, which suggests that the regulation of phosphorylation on these sites is via an indirect LAR-regulated mechanism.

Biological Processes Regulated by LAR—Gene Ontology (GO) analysis of the phosphoproteins regulated by LAR revealed a number of enriched GO biological processes, molecular functions, and cellular components. The most significantly enriched terms are shown in Figs. 2*A*, 2*B*, and 2*C* (for full DAVID output see supplemental Table S3). The dominant enriched GO terms were associated with cytoskeletal organization and cell adhesion. LAR has been shown to regulate the cytoskeleton in conjunction with TRIO, a guanine nucleotide exchange factor for small GTPases (39). Here we have identified a 3-fold increase in the phosphorylation of TRIO on Ser^{2458} and Ser^{2462} in LARΔP cells, indicating that LAR dependent signaling networks are regulating its phosphorylation status. Despite this link to cytoskeletal organization, the extent of the LAR-dependent cytoskeletal regulatory network has not been previously studied. It is evident from our phosphoproteome data set that a large number of cytoskeletal proteins are dependent upon LAR phosphatase activity to regulate their phosphorylation (Fig. 2*D*). LAR has also been shown to interact with cadherin, β-catenin, and plakoglobin to regulate adherens junctions and desmosomes (40–42). Here, we have identified specific LAR-dependent phosphorylation sites on these proteins and discovered additional LAR regulated cell junction proteins (Fig. 2*D*). In LARΔP cells we have identified a decrease in phosphorylation on cadherin-11 (Ser^{714}), α-catenin (Ser^{641}), β-catenin (Ser^{191}; Ser^{675}), δ-catenin (Ser^{864}), and plakoglobin (Ser^{665}), all proteins present at sites of cell-cell adhesion. β-catenin is a reported substrate for LAR, and tyrosine dephosphorylation has been linked to inhibition of epithelial cell migration (43). Here, we have not identified specific tyrosine phosphorylation sites on β-catenin that may be directly dephosphorylated by LAR, but instead we identified two serine residues with altered phosphorylation. Phosphorylation of one of these, Ser^{191}, by JNK2 has been shown to be essential for nuclear accumulation of β-catenin in response to Wnt (44). It is possible that LAR is capable of regulating β-catenin phosphorylation indirectly by regulating the activity of kinases that phosphorylate β-catenin, such as JNK2, as well as directly by dephosphorylating specific tyrosine residues (43). In addition, we have evidence that LAR also regulates tight junctions with phosphorylation of two key proteins, ZO-1 (Tjp1) and ZO-2 (Tjp2), decreased in LARΔP cells (ZO-1 Ser^{1614}; ZO-2 Ser^{107}; Ser^{239}; Ser^{1136}).

LAR-regulated Phosphorylation Events Downstream of PDGF—In order to identify differential changes in abundance within the phosphoproteome data set, phosphopeptides were clustered according to their response to PDGF stimulation *versus* unstimulated cells. The comparison of PDGF stimulated WT and LARΔP cells *versus* unstimulated WT cells allowed the evaluation of the comparative end point of phosphopeptide abundance. This is the phosphorylation signal that the cells would ultimately respond to in the presence of PDGF. This may be due to a differential response to PDGF or constitutive down- or up-regulation in unstimulated LARΔP cells, hence we also included a comparison of PDGF stimulated LARΔP cells *versus* unstimulated LARΔP cells. Our experimental design included three biological replicates for the ratio between PDGF treated and unstimulated WT cells, and two biological replicates for the ratios between PDGF treated LARΔP cells and unstimulated WT or LARΔP cells (Fig. 1*A*). We obtained ratios for 375 peptides, each of which had been quantified in two biological replicates. Six clusters were identified (Fig. 3*A* and supplemental Table S4). Clusters 2, 3, 4, and 6 contained those phosphopeptides that, in the presence of PDGF, showed a LAR phosphatase-dependent alteration in relative abundance when compared with basal levels in WT cells. This is not true for those phosphopeptides in clusters 1 and 5 where similar levels were observed in both PDGF stimulated WT and LARΔP cells when compared with unstimulated WT cells. Phosphopeptides in clusters 2 and 3 exhibited similar fold changes in phosphopeptide abundance because of PDGF stimulation in both WT and LARΔP cells compared with their basal levels, however, the abundance in PDGF stimulated LARΔP cells compared with unstimulated WT cells was significantly different. This indicated that the absence of LAR phosphatase activity causes changes in basal levels of phosphorylation on these phosphoproteins. Phosphopeptides in clusters 4 and 6 have a similar fold change in LARΔP cells in response to PDGF, whether this is compared with unstimulated WT or LARΔP cells. However, the fold change is different to that observed in WT cells.

Enrichment analysis for GO terms over-represented in each cluster showed a clear distinction between the biological roles

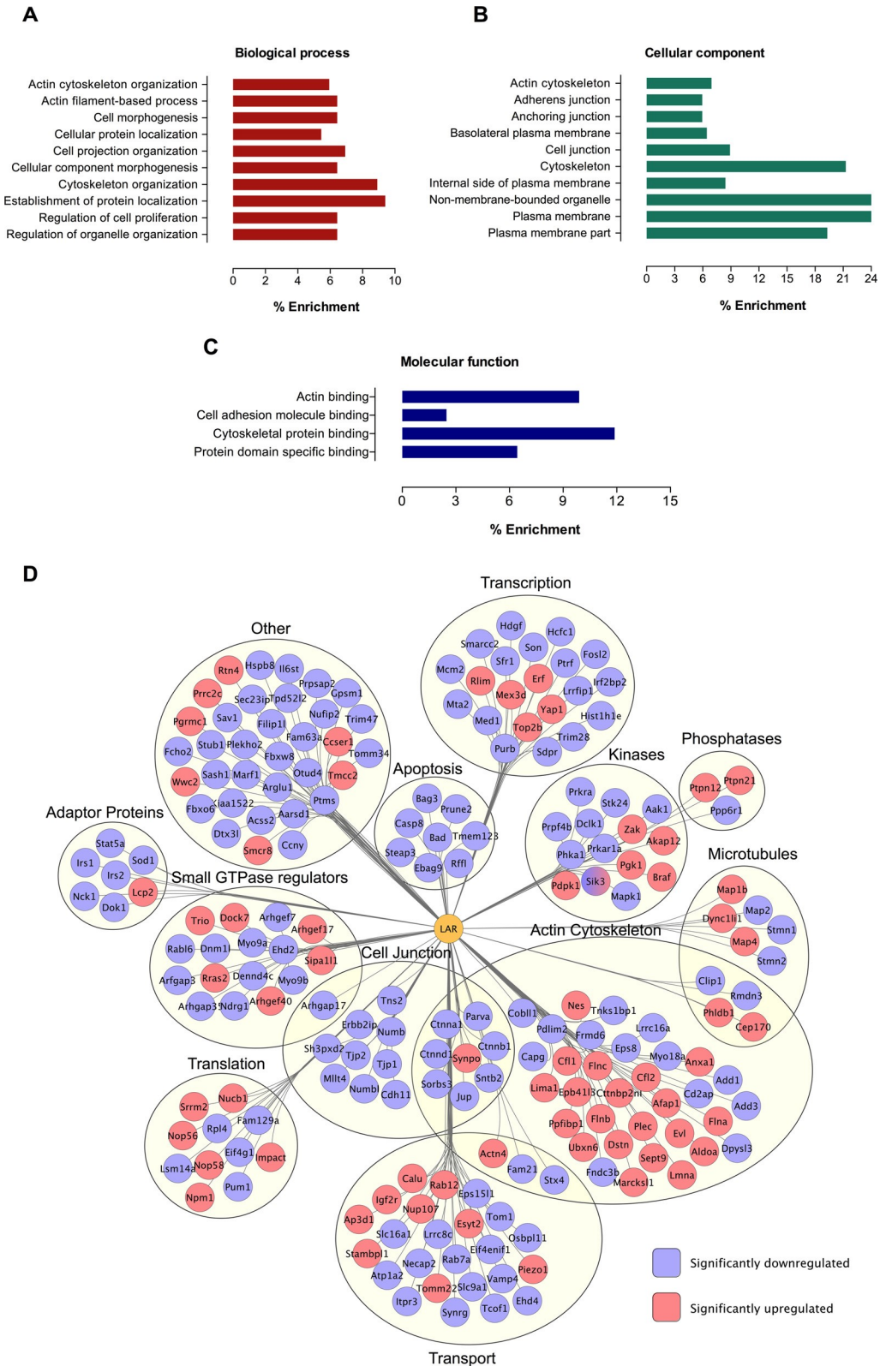

FIG. 2. **LAR regulated distinct biological processes.** Proteins containing the 270 LAR regulated phosphosites were analyzed in DAVID to identify enriched GO Terms and keywords. The top (≤ 10) enriched categories for GO Biological Processes (*A*), GO Molecular Function (*B*) and GO Cellular Component (*C*) are plotted as bar charts. *D,* Proteins were clustered according to their keywords. Blue indicates that the protein contained a phosphosite(s) that was down-regulated in LARΔP cells and red indicates up-regulation.

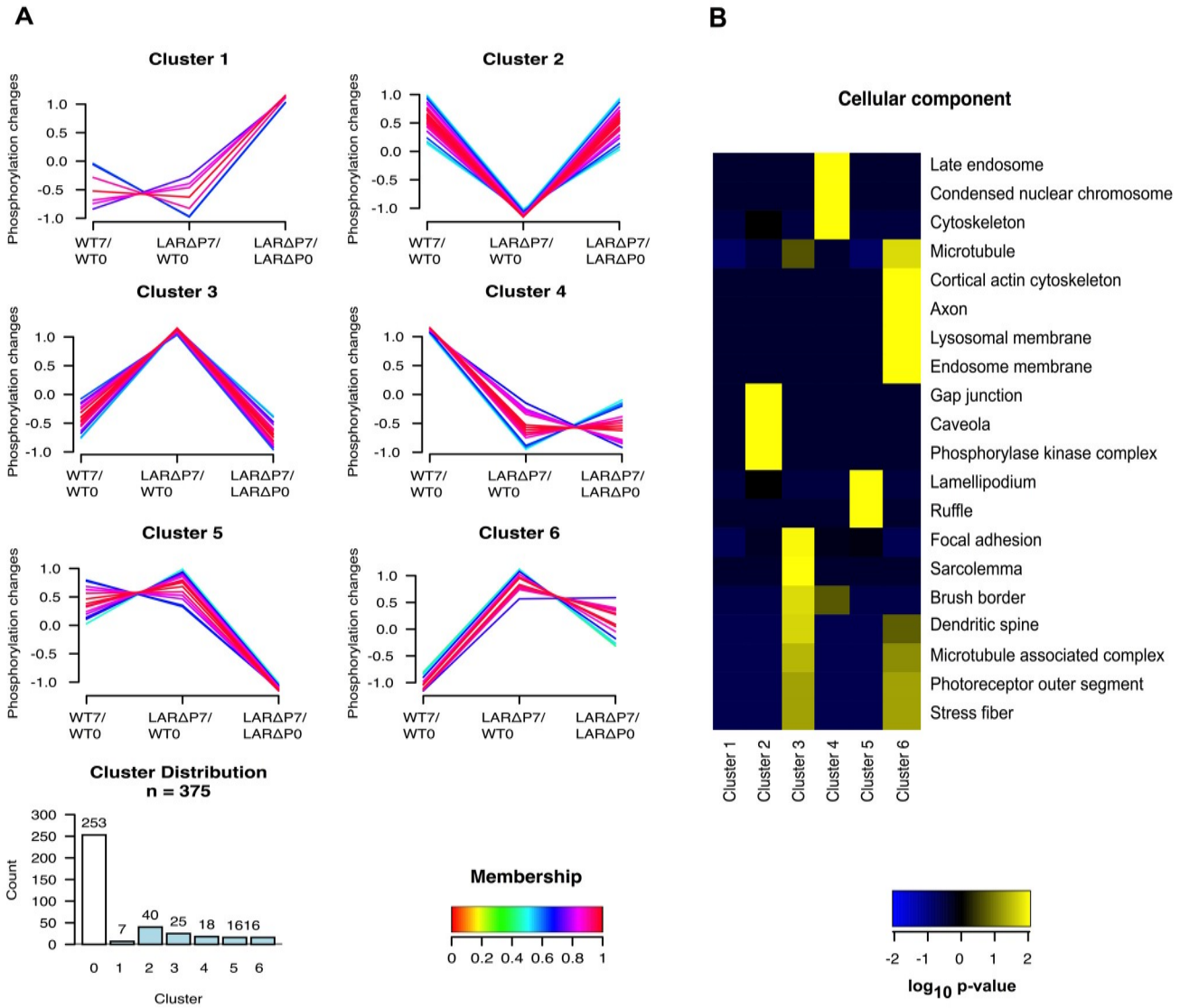

FIG. 3. **Phosphorylation events in WT and LARΔP cells show clusters of regulation correlated to distinct biological processes.** *A,* GProX clustering of phosphopeptide abundance changes. Ratios of PDGF (7 min) stimulated WT and LARΔP cells over WT unstimulated cells and PDGF (7 min) stimulated LARΔP cells over LARΔP unstimulated cells were subjected to unsupervised clustering using the fuzzy c means alogrithm. The number of phosphopeptides in each cluster is indicated. *B,* Overrepresentation of GO terms in the clusters was performed within GProX using a binomial statistical test with a Benjamini-Hochberg *p* value adjustment (*p* value threshold 0.05). Enriched categories for GO Cellular Components are represented as a heat map.

regulated by these groups of phosphoproteins (supplemental Fig. S3; supplemental Table S4). This is highlighted in Fig. 3*B* which is focused on Cellular Component GO Terms. There is a clear distinction between the discrete cellular components within which the differentially regulated phosphopeptides reside. The majority of the enriched terms are cytoskeletal and vesicular compartments. With regards to PDGF stimulation, cluster 4 is perhaps the most interesting as these proteins contain phosphosites that are rapidly phosphorylated in response to PDGF; however, this is not the case when LAR phosphatase activity is reduced. These responses are not caused by constitutive down-regulation in LARΔP cells. One of the enriched components in this cluster is the late endosome compartment (GO:0005770), which contains a Rab7a peptide phosphorylated on Ser^{72}. Phosphorylation of this residue on Rab7a plays a regulatory role in late endosome maturation (45) and our data revealed a 14-fold increase in response to PDGF in WT cells; however, this was reduced over 2-fold in LARΔP cells (supplemental Table S4). Within cluster 4 there was also an enrichment of cytoskeletal proteins (GO: 0005856) including Sorbs3 (vinexin), a protein involved in regulation of actin stress fiber formation (46), and Add3 (gamma-adducin), a protein that promotes assembly of the spectrin-actin network which plays a role in regulating both adhe-

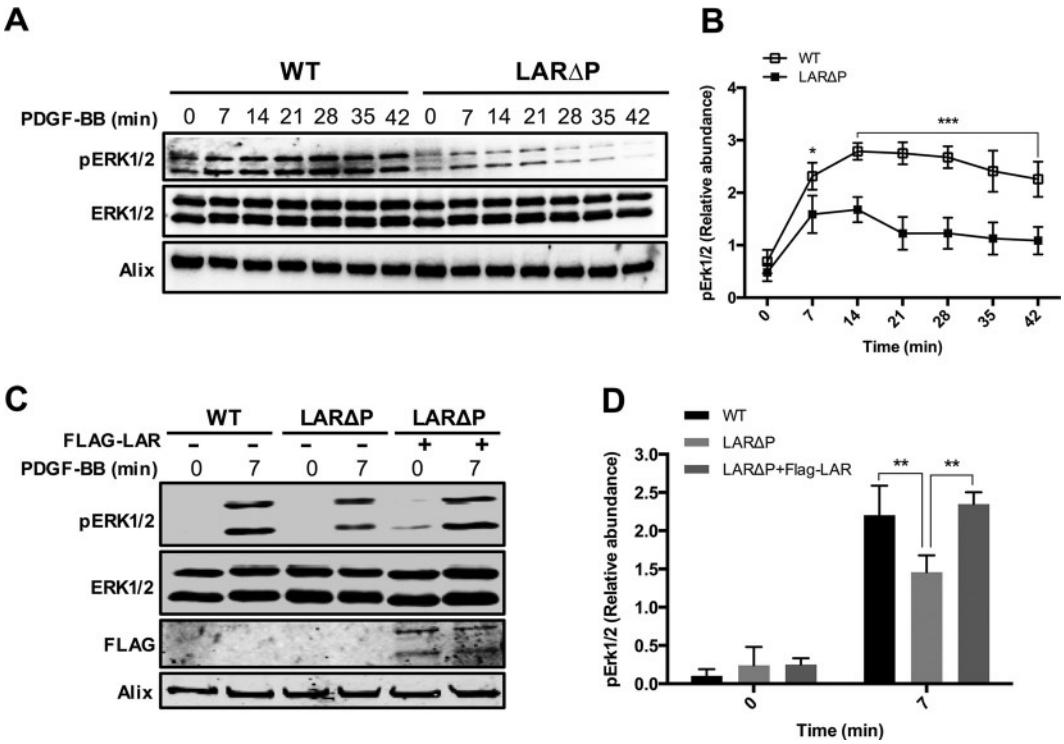

FIG. 4. **LAR Regulates the ERK signaling pathway.** *A,* WT and LARΔP cells were stimulated with 20 ng/ml PDGF for differing periods of time as indicated. Levels of ERK 1/2 Thr^{202}/Tyr^{204}, total ERK and Alix in whole cell lysates were analyzed by Western blotting. *B,* Western blots ($n = 3$) were quantified and ratios of pERK to Alix were plotted over time (***, $p < 0.001$; *, $p < 0.05$). *C,* WT, LARΔP, and LARΔP cells transfected with Flag-WT-LAR were stimulated with 20 ng/ml PDGF for the indicated time periods. Levels of pERK 1/2, total ERK and Alix in whole cell lysates were analyzed by Western blotting. *D,* Western blots ($n = 3$) from the rescue experiments were quantified and ratios of pERK to Alix were plotted (**, $p < 0.01$).

rens and tight junctions (47). We have identified phosphorylation events on both Sorbs3 and Add3 that are reduced by up to 3-fold in the absence of LAR activity, hence this activity is a requirement for PDGF-regulated phosphorylation of these proteins (supplemental Table S4). These data highlight the interplay between LAR and PDGF in regulation of the cytoskeleton and protein transport.

Regulation of Kinase Activity by LAR—LAR-dependent phosphorylation of several kinases has been identified (Fig. 2*D*). These include Braf (B-Raf) and Mapk1 (ERK2), both members of the Ras-MAPK signaling pathway. An increase in B-Raf Ser^{484} and a decrease in ERK2 Tyr^{185} was observed in LARΔP cells. Phosphorylation of ERK1 and 2 on Thr^{183} and Tyr^{185} (Thr^{202}/Tyr^{204} in human) occurs during MAPK signaling and activates the ERK kinases, which in turn can phosphorylate their many substrates. PDGF-dependent ERK1/2 phosphorylation at these activating sites has previously been shown to be reduced in the absence of LAR phosphatase activity (23) and this was verified here. Analysis of PDGF-dependent ERK phosphorylation in WT and LARΔP cells confirms that ERK activity is significantly reduced in LARΔP cells treated with PDGF when compared with WT cells (Figs. 4*A* and 4*B*). Re-expression of WT LAR in LARΔP cells increased ERK phosphorylation to levels resembling those observed in WT cells, confirming that LAR phosphatase activity is required for ERK activation (Figs. 4*C* and 4*D*).

With an aim to delineate further signaling pathways regulated by LAR we sought to identify those kinases which may be responsible for inducing phosphorylation of substrates within our phosphoproteomic data set. The kinase prediction tool GPS (34) was used to identify predicted kinases upstream of substrate motifs containing a phosphorylation site showing differential abundance between WT and LARΔP (270 phosphopeptides). Our proteome data set allowed the identification of instances where phosphopeptide abundance was a result of proteome regulation rather than control of specific phosphorylation sites by regulatory kinases and phosphatases. In order to control for these effects, any proteins found to have a similar fold change in expression to the change in phosphopeptide abundance were not included in our analysis. Of the remaining 240 LAR-regulated phosphorylation sites, 223 were identified as putative substrates for a particular kinase (supplemental Table S5). Members of the CMGC family (includes Cyclin-dependent kinases, Mitogen-activated protein kinases, Glycogen synthase kinases and CDK-like kinases) were predicted to phosphorylate the majority of sites (Fig. 5). The most predominant predicted kinase subfamily was the CMGC/CDK family followed by the CMGC/MAPK

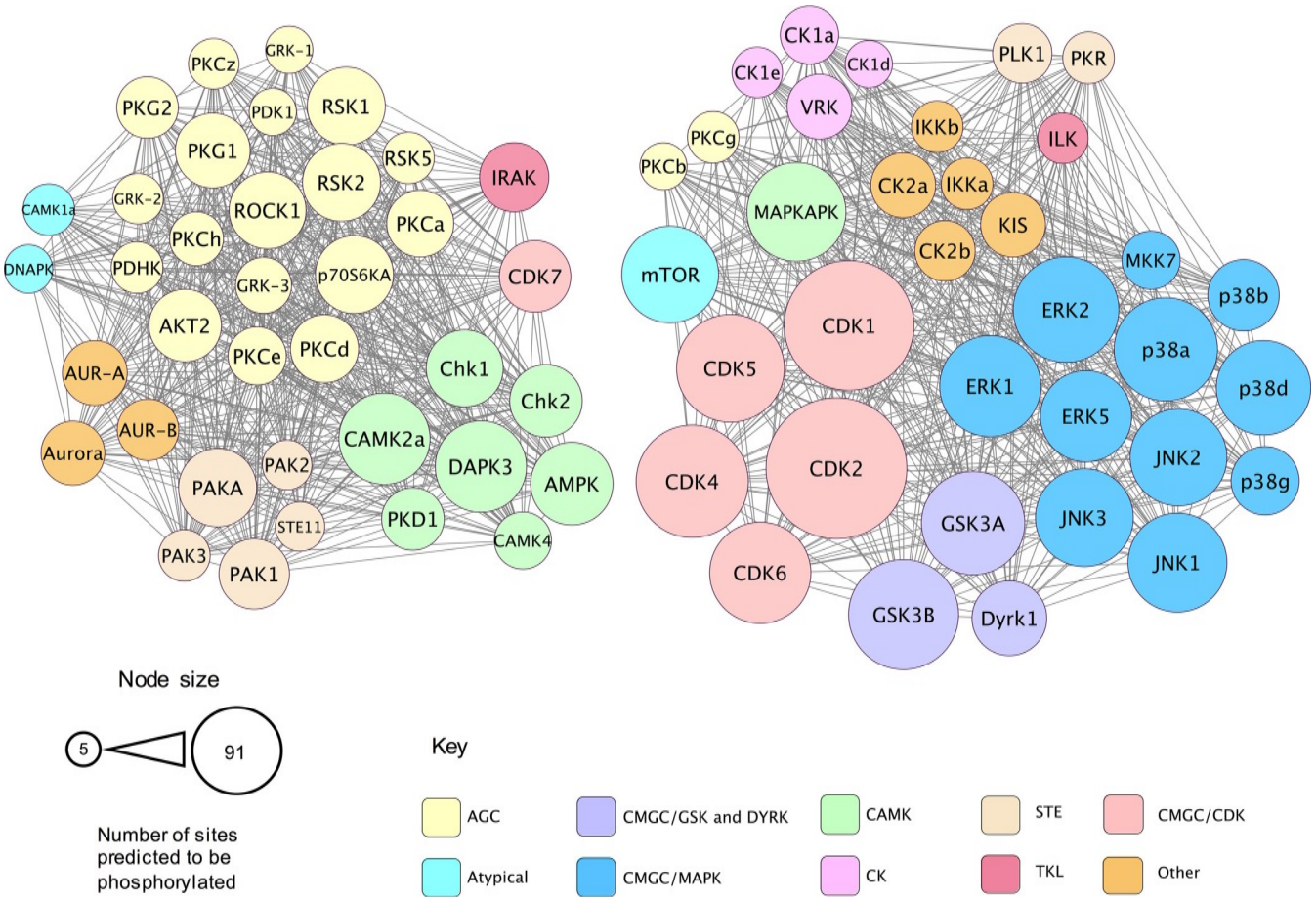

FIG. 5. **LAR Regulates Distinct Kinase Nodes.** Phosphorylation sites regulated by LAR were searched using the kinase prediction tool GPS. All kinases predicted to phosphorylate at least five identified phosphorylation sites are displayed. Each node represents an individual kinase, and nodes are colored according to kinase group (see key for details). An edge connecting two nodes indicates that the corresponding kinase groups were predicted to phosphorylate at least one common residue. Node size corresponds to the total number of LAR regulated phosphorylation sites that were predicted to be phosphorylated by the corresponding kinase.

subfamily, including ERK, JNK, and p38 kinases. Other predominant kinases were MAPKAPK and mTOR (Fig. 5).

LAR Regulates mTOR Signaling—Our kinase prediction analysis revealed mTOR as a prominent node of regulation (Fig. 5). The mTOR signaling pathway is known to regulate protein synthesis via the mTORC1 complex and cytoskeletal organization via the mTORC2 complex (48). Considering the significant changes in protein abundance in LARΔP cells and also the number of LAR-regulated cytoskeletal proteins identified it was hypothesized that LAR may be regulating the mTOR pathway. In order to further analyze the role of LAR in regulating the activity of mTOR we used antibodies recognizing Ser^{2448} phosphorylated mTOR and Thr^{389} phosphorylated P70S6 kinase, both of which are indicators of active mTOR signaling. In WT cells, phosphorylation of mTOR on Ser^{2448} increased following stimulation with PDGF (Figs. 6*A* and 6*B*). However, the absence of LAR phosphatase activity in LARΔP cells resulted in a significant decrease in PDGF-dependent phosphorylation of this residue establishing a role for LAR in mTOR signaling (Figs. 6*A* and 6*B*). Analysis of P70S6 kinase Thr^{389} phosphorylation revealed a similar response to PDGF to that seen with mTOR Ser^{2448} in WT cells and reduced phosphorylation in LARΔP cells (Figs. 6*A* and 6*C*). Re-expression of WT LAR in LARΔP cells resulted in an increase in mTOR Ser^{2448} phosphorylation to levels resembling those observed in WT cells (Fig. 6*D* and 6*E*). Taken together, these results confirm a novel role for LAR phosphatase in the regulation of mTOR signaling.

JNK is a Key Node of Kinase Regulation by LAR—JNK kinases are involved in regulation of the actin cytoskeleton, a role also played by LAR. Predicted substrates for JNK kinases were found enriched within our phosphoproteomic data set (Fig. 5). Using GPS (34), predicted JNK targets identified in our data set of LAR-dependent phosphosites included: Eps8, a highly phosphorylated signaling adaptor protein that regulates actin dynamics and architecture (49–53); Stathmin1 and Stathmin2, both involved in microtubule disassembly (54); Tjp1, involved in tight junction assembly (55); and Tenc1 (Tns2), a focal adhesion protein that binds actin

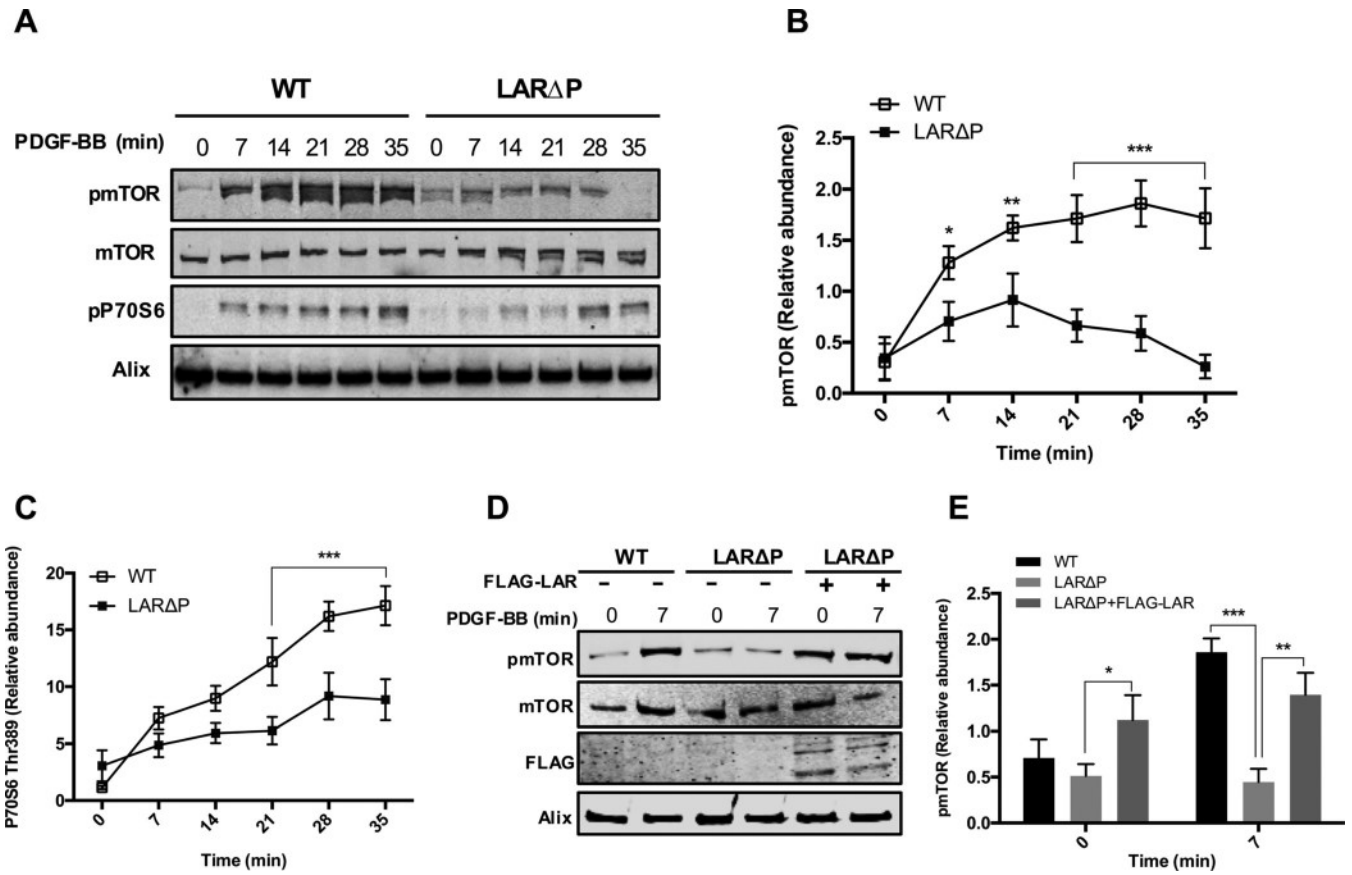

FIG. 6. **LAR Regulates the mTOR signaling pathway.** *A,* WT and LARΔP cells were stimulated with 20 ng/ml PDGF for differing periods of time as indicated. Levels of mTOR Ser^{2448}, total mTOR, P70S6 Thr^{389}, and Alix in whole cell lysates were analyzed by Western blotting. *B, C,* Western blots ($n = 3$) were quantified and ratios of phospho-proteins to Alix were plotted over time (***, $p < 0.001$; **, $p < 0.01$; *, $p < 0.05$). *D,* WT, LARΔP, and LARΔP cells transfected with Flag-WT-LAR were stimulated with 20 ng/ml PDGF for the indicated time periods. Levels of mTOR Ser^{2448}, total mTOR, FLAG-LAR and Alix in whole cell lysates were analyzed by Western blotting. *E,* Western blots ($n = 3$) from the rescue experiments were quantified and ratios of mTOR Ser^{2448} to Alix were plotted (***, $p < 0.001$; **, $p < 0.01$; *, $p < 0.05$).

filaments (56). JNK is known to phosphorylate Ser^{62} of Stathmin 2 (57) and phosphorylation of this residue was significantly reduced in LARΔP cells compared with WT. These data prompted us to investigate whether LAR phosphatase regulates JNK phosphorylation. In the absence of LAR phosphatase activity, we observed significantly reduced JNK activity upon stimulation with PDGF (Figs. 7*A* and 7*B*). Consistent with this, we also observed a significant decrease in activity of MKK7, an upstream kinase known to activate JNK (Figs. 7*A* and 7*C*), and also a JNK downstream effector, c-Jun (Fig. 7*A* and 7*D*), in LARΔP cells. Re-expression of WT LAR in LARΔP cells restored JNK phosphorylation (Figs. 7*E* and 7*F*) demonstrating that LAR phosphatase domains are required for regulation of JNK activity. These data show LAR plays a role in regulating PDGF-mediated activation of the JNK signaling pathway.

DISCUSSION

Phosphorylation events are crucial for the regulation of cell signaling networks and, consequently, the cells response to a biological outcome. The regulatory role of kinases in specific cell signaling pathways has been long established. In more recent years it has been realized that phosphatases can be viewed in a similar manner and can regulate specific cell signaling events rather than acting as generic dephosphorylation enzymes as was once thought (1). The breadth of cell signaling pathways regulated by LAR has not previously been investigated. Using combined global quantitative phosphoproteomics and proteomics we have provided a comprehensive analysis of signaling events regulated by LAR phosphatase. The phosphorylation of 270 sites on 205 proteins was significantly up or down-regulated in LARΔP cells compared with WT cells. Our data establish that LAR phosphatase activity is essential for the regulation of many phosphorylation events within the cell that impact on a variety of cellular processes, particularly regulation of the cytoskeleton and cell-cell interactions. Our data set significantly expands the number of proteins regulated by LAR that are involved in these biological functions, and identifies specific regulatory phos-

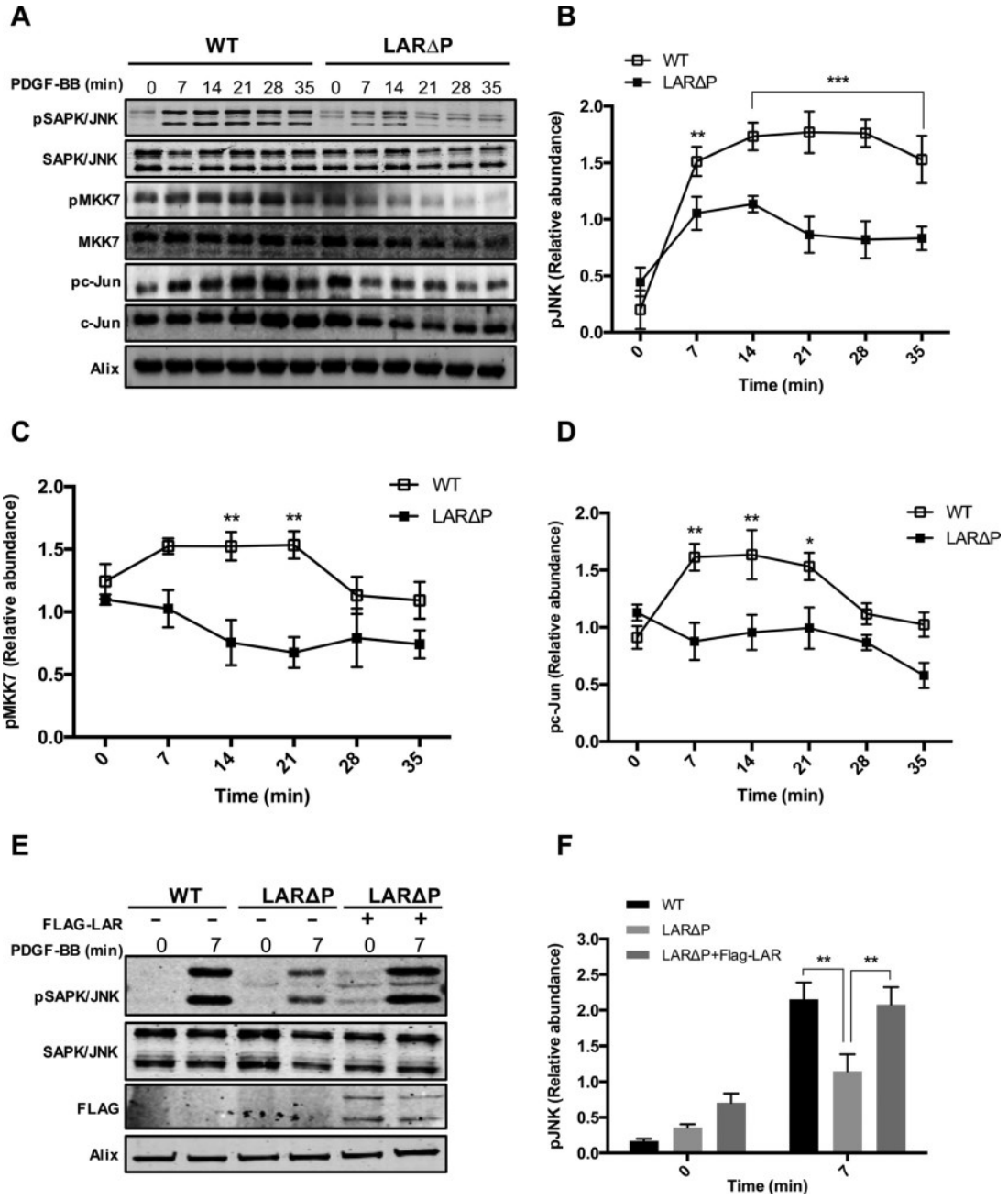

FIG. 7. **LAR Regulates the JNK signaling pathway.** *A,* WT and LARΔP cells were stimulated with 20 ng/ml PDGF for differing periods of time as indicated. Levels of JNK Thr[183]/Tyr[185], total JNK, MKK7 Ser[271]/Thr[275], total MKK7, c-Jun Ser[63], c-Jun and Alix in whole cell lysates were analyzed by Western blotting. *B–D,* Western blots ($n = 3$) were quantified and ratios of phospho-protein to total protein were plotted over time (***, $p < 0.001$; **, $p < 0.01$; *, $p < 0.05$). *E*, WT, LARΔP, and LARΔP cells transfected with Flag-WT-LAR were stimulated with 20 ng/ml PDGF for the indicated time periods. Levels of JNK Thr[183]/Tyr[185], total JNK, Flag-LAR and Alix in whole cell lysates were analyzed by Western blotting. *F,* Western blots ($n = 3$) from the rescue experiments were quantified and ratios of JNK Thr[183]/Tyr[185] to total JNK were plotted (**, $p < 0.01$).

phosites for future scrutiny. It is likely that LAR regulates phosphorylation via a number of mechanisms; via direct dephosphorylation, via regulation of activity of other phosphatases or kinases that can directly modulate the specific site, or via alterations in protein abundance.

As well as regulation at the phosphoproteome level, the absence of LAR also caused considerable changes to the identified proteome. These results highlight a possible role for LAR phosphatase activity in maintaining levels of proteins within the cell, either via regulation of protein degradation or protein synthesis. We have evidence that LAR may be regulating both processes. Protein degradation is controlled via two major pathways: lysosomal proteolysis and the ubiquitin-proteasome pathway. A number of proteins with roles in these two pathways

have significant changes in phosphorylation levels because of the inactivity of LAR. The phosphorylation of Ser^{72} on Rab7a, a small GTPase, was decreased in LARΔP cells. Dephosphorylation of this residue is necessary for late endosome maturation in preparation for lysosomal fusion and protein degradation (45). This is one example of LAR-dependent regulation of a serine residue that is likely to occur indirectly via modulation of the activity of critical serine/threonine kinases or phosphatases upstream of Rab7a phosphorylation. Evidence for LARs involvement in protein ubiquitination is the identification of LAR-regulated phosphorylation sites on three E3 ubiquitin-protein ligases: Rffl (Ser^{254}), Rlim (Ser^{229}), and Dtx3l (Ser^{9}). It is possible that the ubiquitin ligase activity of these proteins is regulated via these phosphorylation events. We have also identified LAR as a regulator of mTOR signaling. mTOR is a serine/threonine protein kinase that regulates numerous cellular functions including protein synthesis and consequently, cell growth (58). Additionally, LAR-regulated phosphoproteins include those involved in translation of mRNA and protein synthesis. Hence, LAR may contribute to the maintenance of protein levels via the regulation of protein synthesis and mTOR signaling.

Within the data set are TRIO, and β-catenin, proteins known to interact with, and in the case of β-catenin be a substrate for LAR (13, 39, 43, 59–61). TRIO is a multi-domain protein that acts as a guanine-nucleotide exchange factor for Rac and Rho small GTPases (39) and β-catenin an important protein involved in regulation of cell-cell junctions (62). In addition to localizing LAR-regulated sites of phosphorylation on these proteins, we have also expanded the protein networks around these two proteins that also contain LAR-regulated phosphosites. For each of these proteins we identified LAR-mediated changes in serine phosphorylation which could result from an alteration in activity of a serine/threonine kinase or a serine/threonine phosphatase. These proteins may need to be localized in the vicinity of LAR via a direct interaction with TRIO or β-catenin in order to be regulated by these intermediate regulatory kinases or phosphatases.

Also within our data set are IRS1 and IRS2, adaptor proteins that bind to the insulin receptor and regulate insulin sensitivity (63). Both proteins are reported to interact with LAR (59, 60). LAR is known to regulate insulin dependent signaling, however, there is some debate in the literature as to whether this is because of direct dephosphorylation of the insulin receptor or a consequence of regulation of the pathway further downstream of the receptor (64, 65). IRS1 has been reported to be direct substrate for LAR, however, there is some controversy over whether this is the case (64, 65). Despite evidence that serine and threonine phosphorylation of IRS1 and IRS2 is important for regulation of insulin sensitivity (63) previous work has concentrated on identifying LAR-dependent tyrosine phosphorylation of IRS proteins. To date there has been no analysis of indirect, LAR-mediated, phosphorylation events on IRS1 or IRS2 that contribute to modulation of the cells response to insulin. Here, we have identified a reduction in serine phosphorylation of both IRS1 (Ser^{265}) and IRS2 (Ser^{362}) in LARΔP cells. Significantly, both phosphorylation events are reported to be insulin dependent (63).

Grouping the phosphopeptides according to their relative abundance in PDGF stimulated cells resulted in six distinct clusters. These clusters can be differentiated on their response to PDGF and also on their functional subclasses. There are three possible scenarios that may cause relative changes in abundance of the phosphopeptides between PDGF-stimulated LARΔP cells and unstimulated WT cells: (1) the levels of phosphorylation in unstimulated WT and LARΔP are similar, however, the response to PDGF is altered; (2) the basal level of phosphorylation of the specific residue in unstimulated LARΔP cells has changed, coupled with an absence of PDGF response or a similar fold response to wild-type cells; or (3) there is a change at the level of the proteome, *i.e.* a change in protein abundance in LARΔP cells. In each case the result would still be differential phosphorylation in PDGF-stimulated cells because of the absence of the phosphatase domains of LAR, which would ultimately lead to changes in signaling pathways reliant on the specific phosphorylation events. Using cluster analysis, we have identified those phosphoproteins regulated by both LAR and PDGF, and these include Rab7a and a number of cytoskeletal proteins.

c-Jun N-terminal kinase (JNK) is serine/threonine kinase that is activated by a broad range of external stimuli including PDGF, transforming growth factor-β, and environmental stress (66). Signaling via JNK regulates cell migration and enhances chemotaxis in response to PDGF stimulation (67). Several strands of evidence supporting a role for LAR in regulating JNK signaling are present within our data. First, a member of the JNK signaling pathway, Zak, is present within the LAR-regulated phosphoproteomic data set. JNK can be activated via phosphorylation of Thr^{183} and Tyr^{185} via the action of MKK4 and MKK7 kinases (68, 69). Zak is a stress-activated kinase upstream of both MKK4 and MKK7 (70) and phosphorylation of Ser^{638} of Zak was increased 3.9-fold in LARΔP cells. This is the first strand of evidence that links LAR to JNK signaling. The second piece of evidence is the fact that we have identified specific JNK regulated phosphosites within the data that are regulated by LAR, including Ser^{191} of β-catenin, and Ser^{62} of Stathmin 2 (44, 57). In addition to this, using kinase motif predictions, we have identified JNK as a key node of regulation of a number of additional phosphosites within the LAR-regulated phosphoproteomics data set. LAR-regulated PDGF-dependent phosphorylation of JNK on Thr^{183} and Tyr^{185} has been verified by Western blotting. This demonstrates the strength of our approach in identifying novel signaling pathways regulated by LAR and has highlighted a novel role for LAR in regulating JNK signaling.

CONCLUSIONS

We have employed a global quantitative phosphoproteomics approach for the interrogation of LAR-mediated cell sig-

naling events. We have focused on obtaining information pertaining to both direct and indirect phosphorylation events to increase our knowledge of the complete landscape of LAR-regulated signaling. The study has identified LAR as a regulator of key signaling pathways, including mTOR and JNK, and has significantly expanded the number of proteins regulated downstream of LAR phosphatase activity.

Acknowledgments—We thank Cleidiane Zampronio and Jinglei Lu (Functional Genomics, Proteomics and Metabolomics Facility, University of Birmingham) for technical support.

* ARS is supported by a scholarship from the Higher Committee for Education Development in Iraq (HCED) (D11000650). TRP is supported by the Marie Skłodowska-Curie Fellowship program. AJC is funded by EPSRC (EP/L023490/1).

S This article contains supplemental Figs. S1 to S3 and Tables S1 to S5.

§ To whom correspondence should be addressed: School of Biosciences, College of Life and Environmental Sciences, University of Birmingham, Edgbaston, Birmingham B15 2TT, United Kingdom. Tel.: +44 (0)121 414 2652; Fax: +44 (0)121 414 5925; E-mail: d.cunningham@bham.ac.uk.

¶ Current address: Alberta RNA Research and Training Institute, Department of Chemistry and Biochemistry, University of Lethbridge, 4401 University Drive, Lethbridge, Alberta T1K 3M4, Canada.

DLC and NAH are joint senior authors.

REFERENCES

1. Tonks, N. K. (2013) Protein tyrosine phosphatases–from housekeeping enzymes to master regulators of signal transduction. *FEBS J.* **280,** 346–378
2. Nam, H. J., Poy, F., Krueger, N. X., Saito, H., and Frederick, C. A. (1999) Crystal structure of the tandem phosphatase domains of RPTP LAR. *Cell* **97,** 449–457
3. Tonks, N. K. (2006) Protein tyrosine phosphatases: from genes, to function, to disease. *Nat. Rev. Mol. Cell Biol.* **7,** 833–846
4. Ostman, A., Hellberg, C., and Bohmer, F. D. (2006) Protein-tyrosine phosphatases and cancer. *Nat. Rev. Cancer* **6,** 307–320
5. Streuli, M., Krueger, N. X., Ariniello, P. D., Tang, M., Munro, J. M., Blattler, W. A., Adler, D. A., Disteche, C. M., and Saito, H. (1992) Expression of the receptor-linked protein tyrosine phosphatase LAR: proteolytic cleavage and shedding of the CAM-like extracellular region. *EMBO J.* **11,** 897–907
6. Chagnon, M. J., Uetani, N., and Tremblay, M. L. (2004) Functional significance of the LAR receptor protein tyrosine phosphatase family in development and diseases. *Biochem. Cell Biol.* **82,** 664–675
7. Pulido, R., Serra-Pages, C., Tang, M., and Streuli, M. (1995) The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma isoforms are expressed in a tissue-specific manner and associate with the LAR-interacting protein LIP.1. *Proc. Natl. Acad. Sci. U.S.A.* **92,** 11686–11690
8. Um, J. W., and Ko, J. (2013) LAR-RPTPs: synaptic adhesion molecules that shape synapse development. *Trends Cell Biol.* **23,** 465–475
9. Yang, T., Massa, S. M., and Longo, F. M. (2006) LAR protein tyrosine phosphatase receptor associates with TrkB and modulates neurotrophic signaling pathways. *J. Neurobiol.* **66,** 1420–1436
10. Niu, X. L., Li, J., Hakim, Z. S., Rojas, M., Runge, M. S., and Madamanchi, N. R. (2007) Leukocyte antigen-related deficiency enhances insulin-like growth factor-1 signaling in vascular smooth muscle cells and promotes neointima formation in response to vascular injury. *J. Biol. Chem.* **282,** 19808–19819
11. Machide, M., Hashigasako, A., Matsumoto, K., and Nakamura, T. (2006) Contact inhibition of hepatocyte growth regulated by functional association of the c-Met/hepatocyte growth factor receptor and LAR protein-tyrosine phosphatase. *J. Biol. Chem.* **281,** 8765–8772
12. Serra-Pages, C., Kedersha, N. L., Fazikas, L., Medley, Q., Debant, A., and Streuli, M. (1995) The LAR transmembrane protein tyrosine phosphatase and a coiled-coil LAR-interacting protein co-localize at focal adhesions. *EMBO J.* **14,** 2827–2838
13. Kypta, R. M., Su, H., and Reichardt, L. F. (1996) Association between a transmembrane protein tyrosine phosphatase and the cadherin-catenin complex. *J. Cell Biol.* **134,** 1519–1529
14. Andrae, J., Gallini, R., and Betsholtz, C. (2008) Role of platelet-derived growth factors in physiology and medicine. *Genes Dev.* **22,** 1276–1312
15. Heldin, C. H. (2013) Targeting the PDGF signaling pathway in tumor treatment. *Cell Communication Signaling* **11,** 97
16. Heldin, C. H. (2014) Targeting the PDGF signaling pathway in the treatment of non-malignant diseases. *J. Neuroimmune Pharmacol.* **9,** 69–79
17. Ostman, A., and Heldin, C. H. (2001) Involvement of platelet-derived growth factor in disease: development of specific antagonists. *Adv. Cancer Res.* **80,** 1–38
18. Heldin, C. H., Ostman, A., and Ronnstrand, L. (1998) Signal transduction via platelet-derived growth factor receptors. *Biochim. Biophys. Acta* **1378,** F79–113
19. Cao, Y. (2013) Multifarious functions of PDGFs and PDGFRs in tumor growth and metastasis. *Trends Mol. Med.* **19,** 460–473
20. Chiarugi, P., Cirri, P., Taddei, M. L., Giannoni, E., Fiaschi, T., Buricchi, F., Camici, G., Raugei, G., and Ramponi, G. (2002) Insight into the role of low molecular weight phosphotyrosine phosphatase (LMW-PTP) on platelet-derived growth factor receptor (PDGF-r) signaling. LMW-PTP controls PDGF-r kinase activity through TYR-857 dephosphorylation. *J. Biol. Chem.* **277,** 37331–37338
21. Persson, C., Savenhed, C., Bourdeau, A., Tremblay, M. L., Markova, B., Bohmer, F. D., Haj, F. G., Neel, B. G., Elson, A., Heldin, C. H., Ronnstrand, L., Ostman, A., and Hellberg, C. (2004) Site-selective regulation of platelet-derived growth factor beta receptor tyrosine phosphorylation by T-cell protein tyrosine phosphatase. *Mol. Cell. Biol.* **24,** 2190–2201
22. Ekman, S., Kallin, A., Engstrom, U., Heldin, C. H., and Ronnstrand, L. (2002) SHP-2 is involved in heterodimer specific loss of phosphorylation of Tyr771 in the PDGF beta-receptor. *Oncogene* **21,** 1870–1875
23. Zheng, W., Lennartsson, J., Hendriks, W., Heldin, C. H., and Hellberg, C. (2011) The LAR protein tyrosine phosphatase enables PDGF beta-receptor activation through attenuation of the c-Abl kinase activity. *Cell Signal* **23,** 1050–1056
24. Ong, S. E., Blagoev, B., Kratchmarova, I., Kristensen, D. B., Steen, H., Pandey, A., and Mann, M. (2002) Stable isotope labeling by amino acids in cell culture, SILAC, as a simple and accurate approach to expression proteomics. *Mol. Cell. Proteomics* **1,** 376–386
25. Cunningham, D. L., Sweet, S. M., Cooper, H. J., and Heath, J. K. (2010) Differential phosphoproteomics of fibroblast growth factor signaling: identification of Src family kinase-mediated phosphorylation events. *J. Proteome Res.* **9,** 2317–2328
26. Schaapveld, R. Q., Schepens, J. T., Robinson, G. W., Attema, J., Oerlemans, F. T., Fransen, J. A., Streuli, M., Wieringa, B., Hennighausen, L., and Hendriks, W. J. (1997) Impaired mammary gland development and function in mice lacking LAR receptor-like tyrosine phosphatase activity. *Developmental Biol.* **188,** 134–146
27. Lennartsson, J., Wardega, P., Engstrom, U., Hellman, U., and Heldin, C. H. (2006) Alix facilitates the interaction between c-Cbl and platelet-derived growth factor beta-receptor and thereby modulates receptor down-regulation. *J. Biol. Chem.* **281,** 39152–39158
28. Shevchenko, A., Tomas, H., Havlis, J., Olsen, J. V., and Mann, M. (2006) In-gel digestion for mass spectrometric characterization of proteins and proteomes. *Nat. Protoc.* **1,** 2856–2860
29. Cox, J., and Mann, M. (2008) MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. *Nat. Biotechnol.* **26,** 1367–1372
30. Cox, J., Neuhauser, N., Michalski, A., Scheltema, R. A., Olsen, J. V., and Mann, M. (2011) Andromeda: a peptide search engine integrated into the MaxQuant environment. *J. Proteome Res.* **10,** 1794–1805
31. Vizcaino, J. A., Cote, R. G., Csordas, A., Dianes, J. A., Fabregat, A., Foster, J. M., Griss, J., Alpi, E., Birim, M., Contell, J., O'Kelly, G., Schoenegger, A., Ovelleiro, D., Perez-Riverol, Y., Reisinger, F., Rios, D., Wang, R., and Hermjakob, H. (2013) The PRoteomics IDEntifications (PRIDE) database and associated tools: status in 2013. *Nucleic Acids Res.* **41,** D1063–1069
32. Rigbolt, K. T., Vanselow, J. T., and Blagoev, B. (2011) GProX, a user-friendly platform for bioinformatics analysis and visualization of quantitative proteomics data. *Mol. Cell. Proteomics* **10,** O110 007450
33. Huang da, W., Sherman, B. T., and Lempicki, R. A. (2009) Systematic and integrative analysis of large gene lists using DAVID bioinformatics re-

sources. *Nat. Protoc.* **4,** 44–57
34. Xue, Y., Ren, J., Gao, X., Jin, C., Wen, L., and Yao, X. (2008) GPS 2.0, a tool to predict kinase-specific phosphorylation sites in hierarchy. *Mol. Cell. Proteomics* **7,** 1598–1608
35. Shannon, P., Markiel, A., Ozier, O., Baliga, N. S., Wang, J. T., Ramage, D., Amin, N., Schwikowski, B., and Ideker, T. (2003) Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res.* **13,** 2498–2504
36. Oesper, L., Merico, D., Isserlin, R., and Bader, G. D. (2011) WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. *Source code for biology and medicine* **6,** 7
37. Hornbeck, P. V., Kornhauser, J. M., Tkachev, S., Zhang, B., Skrzypek, E., Murray, B., Latham, V., and Sullivan, M. (2012) PhosphoSitePlus: a comprehensive resource for investigating the structure and function of experimentally determined post-translational modifications in man and mouse. *Nucleic Acids Res.* **40,** D261–270
38. Zeng, R., Cannon, J. L., Abraham, R. T., Way, M., Billadeau, D. D., Bubeck-Wardenberg, J., and Burkhardt, J. K. (2003) SLP-76 coordinates Nck-dependent Wiskott-Aldrich syndrome protein recruitment with Vav-1/Cdc42-dependent Wiskott-Aldrich syndrome protein activation at the T cell-APC contact site. *J. Immunol.* **171,** 1360–1368
39. Debant, A., Serra-Pages, C., Seipel, K., O'Brien, S., Tang, M., Park, S. H., and Streuli, M. (1996) The multidomain protein Trio binds the LAR transmembrane tyrosine phosphatase, contains a protein kinase domain, and has separate rac-specific and rho-specific guanine nucleotide exchange factor domains. *Proc. Natl. Acad. Sci. U.S.A.* **93,** 5466–5471
40. Symons, J. R., LeVea, C. M., and Mooney, R. A. (2002) Expression of the leucocyte common antigen-related (LAR) tyrosine phosphatase is regulated by cell density through functional E-cadherin complexes. *Biochem. J.* **365,** 513–519
41. Srinivasan, S., Mahowald, A. P., and Fuller, M. T. (2012) The receptor tyrosine phosphatase Lar regulates adhesion between Drosophila male germline stem cells and the niche. *Development* **139,** 1381–1390
42. Aicher, B., Lerch, M. M., Muller, T., Schilling, J., and Ullrich, A. (1997) Cellular redistribution of protein tyrosine phosphatases LAR and PTP-sigma by inducible proteolytic processing. *J. Cell Biol.* **138,** 681–696
43. Muller, T., Choidas, A., Reichmann, E., and Ullrich, A. (1999) Phosphorylation and free pool of beta-catenin are regulated by tyrosine kinases and tyrosine phosphatases during epithelial cell migration. *J. Biol. Chem.* **274,** 10173–10183
44. Wu, X., Tu, X., Joeng, K. S., Hilton, M. J., Williams, D. A., and Long, F. (2008) Rac1 activation controls nuclear localization of beta-catenin during canonical Wnt signaling. *Cell* **133,** 340–353
45. Shinde, S. R., and Maddika, S. (2016) PTEN modulates EGFR late endocytic trafficking and degradation by dephosphorylating Rab7. *Nat. Commun.* **7,** 10689
46. Kioka, N., Sakata, S., Kawauchi, T., Amachi, T., Akiyama, S. K., Okazaki, K., Yaen, C., Yamada, K. M., and Aota, S. (1999) Vinexin: a novel vinculin-binding protein with multiple SH3 domains enhances actin cytoskeletal organization. *J. Cell Biol.* **144,** 59–69
47. Naydenov, N. G., and Ivanov, A. I. (2011) Spectrin-adducin membrane skeleton: A missing link between epithelial junctions and the actin cytoskeleton? *Bioarchitecture* **1,** 186–191
48. Laplante, M., and Sabatini, D. M. (2012) mTOR signaling in growth control and disease. *Cell* **149,** 274–293
49. Cunningham, D. L., Creese, A. J., Auciello, G., Sweet, S. M., Tatar, T., Rappoport, J. Z., Grant, M. M., and Heath, J. K. (2013) Novel binding partners and differentially regulated phosphorylation sites clarify Eps8 as a multi-functional adaptor. *PLoS ONE* **8,** e61513
50. Disanza, A., Carlier, M. F., Stradal, T. E., Didry, D., Frittoli, E., Confalonieri, S., Croce, A., Wehland, J., Di Fiore, P. P., and Scita, G. (2004) Eps8 controls actin-based motility by capping the barbed ends of actin filaments. *Nat. Cell Biol.* **6,** 1180–1188
51. Provenzano, C., Gallo, R., Carbone, R., Di Fiore, P. P., Falcone, G., Castellani, L., and Alema, S. (1998) Eps8, a tyrosine kinase substrate, is recruited to the cell cortex and dynamic F-actin upon cytoskeleton remodeling. *Exp. Cell Res.* **242,** 186–200
52. Roffers-Agarwal, J., Xanthos, J. B., and Miller, J. R. (2005) Regulation of actin cytoskeleton architecture by Eps8 and Abi1. *BMC Cell Biol.* **6,** 36
53. Yap, L. F., Jenei, V., Robinson, C. M., Moutasim, K., Benn, T. M., Threadgold, S. P., Lopes, V., Wei, W., Thomas, G. J., and Paterson, I. C. (2009) Upregulation of Eps8 in oral squamous cell carcinoma promotes cell migration and invasion through integrin-dependent Rac1 activation. *Oncogene* **28,** 2524–2534
54. Wittmann, T., Bokoch, G. M., and Waterman-Storer, C. M. (2004) Regulation of microtubule destabilizing activity of Op18/stathmin downstream of Rac1. *J. Biol. Chem.* **279,** 6196–6203
55. Anderson, J. M., Stevenson, B. R., Jesaitis, L. A., Goodenough, D. A., and Mooseker, M. S. (1988) Characterization of ZO-1, a protein component of the tight junction from mouse liver and Madin-Darby canine kidney cells. *J. Cell Biol.* **106,** 1141–1149
56. Davis, S., Lu, M. L., Lo, S. H., Lin, S., Butler, J. A., Druker, B. J., Roberts, T. M., An, Q., and Chen, L. B. (1991) Presence of an SH2 domain in the actin-binding protein tensin. *Science* **252,** 712–715
57. Tararuk, T., Ostman, N., Li, W., Bjorkblom, B., Padzik, A., Zdrojewska, J., Hongisto, V., Herdegen, T., Konopka, W., Courtney, M. J., and Coffey, E. T. (2006) JNK1 phosphorylation of SCG10 determines microtubule dynamics and axodendritic length. *J. Cell Biol.* **173,** 265–277
58. Hay, N., and Sonenberg, N. (2004) Upstream and downstream of mTOR. *Genes Dev.* **18,** 1926–1945
59. Keshava Prasad, T. S., Goel, R., Kandasamy, K., Keerthikumar, S., Kumar, S., Mathivanan, S., Telikicherla, D., Raju, R., Shafreen, B., Venugopal, A., Balakrishnan, L., Marimuthu, A., Banerjee, S., Somanathan, D. S., Sebastian, A., Rani, S., Ray, S., Harrys Kishore, C. J., Kanth, S., Ahmed, M., Kashyap, M. K., Mohmood, R., Ramachandra, Y. L., Krishna, V., Rahiman, B. A., Mohan, S., Ranganathan, P., Ramabadran, S., Chaerkady, R., and Pandey, A. (2009) Human Protein Reference Database–2009 update. *Nucleic Acids Res.* **37,** D767–772
60. Prasad, T. S., Kandasamy, K., and Pandey, A. (2009) Human Protein Reference Database and Human Proteinpedia as discovery tools for systems biology. *Methods Mol. Biol.* **577,** 67–79
61. Dunah, A. W., Hueske, E., Wyszynski, M., Hoogenraad, C. C., Jaworski, J., Pak, D. T., Simonetta, A., Liu, G., and Sheng, M. (2005) LAR receptor protein tyrosine phosphatases in the development and maintenance of excitatory synapses. *Nat. Neurosci.* **8,** 458–467
62. Harris, T. J., and Tepass, U. (2010) Adherens junctions: from molecules to morphogenesis. *Nat. Rev. Mol. Cell Biol.* **11,** 502–514
63. Copps, K. D., and White, M. F. (2012) Regulation of insulin sensitivity by serine/threonine phosphorylation of insulin receptor substrate proteins IRS1 and IRS2. *Diabetologia* **55,** 2565–2582
64. Goldstein, B. J., Bittner-Kowalczyk, A., White, M. F., and Harbeck, M. (2000) Tyrosine dephosphorylation and deactivation of insulin receptor substrate-1 by protein-tyrosine phosphatase 1B. Possible facilitation by the formation of a ternary complex with the Grb2 adaptor protein. *J. Biol. Chem.* **275,** 4283–4289
65. Mander, A., Hodgkinson, C. P., and Sale, G. J. (2005) Knock-down of LAR protein tyrosine phosphatase induces insulin resistance. *FEBS Lett.* **579,** 3024–3028
66. Kyosseva, S. V. (2004) Mitogen-activated protein kinase signaling. *Int. Rev. Neurobiol.* **59,** 201–220
67. Amagasaki, K., Kaneto, H., Heldin, C. H., and Lennartsson, J. (2006) c-Jun N-terminal kinase is necessary for platelet-derived growth factor-mediated chemotaxis in primary fibroblasts. *J. Biol. Chem.* **281,** 22173–22179
68. Davis, R. J. (2000) Signal transduction by the JNK group of MAP kinases. *Cell* **103,** 239–252
69. Lawler, S., Fleming, Y., Goedert, M., and Cohen, P. (1998) Synergistic activation of SAPK1/JNK1 by two MAP kinase kinases in vitro. *Current Biol.* **8,** 1387–1390
70. Gallo, K. A., and Johnson, G. L. (2002) Mixed-lineage kinase control of JNK and p38 MAPK pathways. *Nat. Rev. Mol. Cell Biol.* **3,** 663–672