SUPPLEMENTAL MATERIAL

Supplemental Methods

UHPLC-MS Metabolomics

Control and HPAH BOECs were seeded in 6-well plates and grown to confluence in complete EGM-2MV. Cells were then washed with EBM2 containing 0.1% FBS (EBM2/0.1%) and then incubated in EBM2/0.1% to ensure that the cells were free of growth factors. The media were aspirated and 1.5 ml/well fresh EBM2/0.1% added for 24 hours. The media were removed and centrifuged at 14,000 x g for 10 minutes at 4 ^{o}C to remove any cell debris, then separated from the pellets, aliquoted and frozen immediately at -80 ^{o}C until they were shipped on dry ice to Metabolon Inc. (Morrisville, North Carolina, USA). The cells remaining in the wells were trypsinised and counted using a haemocytometer for normalization of analytes to cell number. Metabolomics analyses were performed on the conditioned media by Metabolon Inc., as previously described[1]. Briefly, the sample preparation process was carried out using the automated MicroLab STAR® system (Hamilton Company, Reno, North Virginia, USA). Recovery standards were added prior to the first step in the extraction process for quality control purposes. Sample preparation was conducted using a proprietary series of organic and aqueous extractions to remove the protein fraction while allowing maximum recovery of small molecules. The resulting extract was divided into two fractions; one for analysis by LC and one for analysis by GC. Samples were placed briefly on a TurboVap® (Zymark/Biotage, Uppsala, Sweden) to remove the organic solvent. Each sample was then frozen and dried under vacuum. Compounds were identified by comparison to library entries of purified standards or recurrent unknown entities. Identification of known chemical entities was based on comparison to metabolomic library entries of ~4000 in-house purified standards. Multivariate data analysis was performed on original scale data through the freely available software Metaboanalyst 3.0[2]. Data were processed for normalization to the median of values measured in the control group for each compound and auto-scaled. Statistical analysis (*t*-test) and multivariate analysis, including partial least square-discriminant analysis (PLS-DA) and hierarchical clustering analyses were performed as reported[2].

Human lung tissue

Tissues were obtained from the Papworth NHS Foundation Trust Hospital Tissue Bank (Papworth Everard, UK). Papworth Hospital ethical review committee approved the use of human tissues (Ethics Ref. 08/H0304/56+5) and informed consent was obtained from all subjects. Paraffin wax–embedded lung samples were isolated from patients with HPAH (n=4) and from control lung (n =4). *BMPR2* mutations were detected as previously described[3]. Control samples comprised tissue from pneumonectomy specimens resected for malignancy, but distant from the site of tumor.

Rat lung tissue

Tissue was obtained from the Sugen 5416-hypoxia rat model. Briefly, Male Sprague Dawley rats (12 weeks old, ~190-200g (Charles River, Saffron Walden, Essex, UK) were administered a single subcutaneous injection of Sugen 5416 (SU-5416; 20 mg/kg, Tocris, Bristol, UK) in vehicle (0.5% carboxyl methylcellulose sodium, 0.4% polysorbate 80, 0.9% benzyl alcohol, all Sigma-Aldrich, Poole, Dorset, UK). Subsequently, rats were placed into a 10% O_2 chamber for 3 weeks. After 3 weeks of hypoxia, animals were returned to a normoxic environment for 5 weeks. For terminal haemodynamic measurements rats were anaesthetized with xylazine (4.6

mg/kg) and ketamine (7 mg/kg). Body weight was recorded. Right ventricular function was assessed using a Millar SPR-869 pressure-volume catheter. Rats were then sacrificed and the hearts and lungs harvested. Right ventricular hypertrophy (RVH) was assessed by removing the heart and dissecting the right ventricle (RV) free wall from the left ventricle plus septum (LV+S), and weighing separately. The degree of right ventricular hypertrophy was determined for the ratio of the RV/LV+S (Futon Index). The right lung was then snap-frozen in liquid nitrogen. Animal studies were conducted in accordance with the UK Animals (Scientific Procedures) Act 1986 and approved under Home Office Project License 80/2460.

RNA extraction from cells and frozen lungs, and reverse transcription

Total RNA from tissues and cells was obtained using the miRNeasy kit (Qiagen, Hilden, Germany) following the manufacturer's instructions. Samples were treated with DNAse 1 (amplification grade; Sigma, St. Louis, MO, USA) to eliminate genomic DNA contamination and quantified using a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA). cDNA for miRNA analysis was synthesized from total RNA using stem-loop reverse transcription primers according to the TaqMan miRNA Assay protocol (Applied Biosystems, Foster City, CA, USA). Each reaction contained 50 ng of extracted total RNA, 50 nM stem-looped RT primer, 1X RT buffer, 0.25 mM each of dNTPs, 3.33 U/mL Multiscribe reverse transcriptase and 0.25 U/mL RNase inhibitor. The 15 μL reactions were incubated in a 96-well plate for 30 minutes at 16 °C, 30 minutes at 42 °C, 5 minutes at 85 °C and then held at 4 °C. Total cDNA for mRNA analysis was obtained from total RNA using the SuperScript II Reverse Transcriptase (Invitrogen, Paisley, UK). Each reaction contained 1 mg of total RNA, 1X SuperScript II buffer, 10 U/mL SuperScript II RT, 0.15 mg/mL of random hexamer primers (Invitrogen, Paisley, UK), 1 U/mL of RNase inhibitor (Promega, Madison, WI, USA) and 0.25 mM each of dNTPs. Cycling conditions were the following: 10 minutes at 25 °C, 30 minutes at 48 °C, 5 minutes at 95 °C. cDNA was stored at -20 °C. *RNU48*, *U6*, *B2M* and *HPRT* were selected as housekeeping genes for human miRNA, rat miRNA, human mRNA and rat mRNA analysis due to their stability across all the groups.

TaqMan qPCR analysis of mature miRNAs and mRNAs

For quantitative PCR (qPCR), 10 μL reactions were incubated in a 386-well optical plate at 95 °C for 10 minutes, followed by 40 cycles of 95 °C for 15 seconds and 60 °C for 1 minute. Results were normalized to *U6* or *RNU48* values for rat and human miRNAs respectively and to *B2M* or *HPRT* for gene expression in human and rat samples respectively. The fold change for every miRNA/gene of interest was obtained using the ΔΔCt method. The qPCRs for each miRNA/gene were run in triplicate and results are presented as the mean ± standard error of samples.

miRNA PCR array profiling of BOECs

Total RNA was extracted from ~400,000 BOECs per subject, using the miRNeasy mini kit according to manufacturer’s instructions, and including the optional on-column DNAase treatment step (Qiagen). The high quality of each extracted RNA sample was confirmed by evaluating both the purity (i.e., A260/A280 and A260/A230 ratios consistently between 1.9-2.1, as measured by NanoDrop 2000 spectrophotometer) and integrity (Agilent Bioanalyzer RIN numbers ranged between 9.7-10). miRNAs were measured using the complete integrated line of reagents from the miScript PCR system (Qiagen). Briefly, 750 ng of total RNA were reverse transcribed according to manufacturer's instructions in the miScript II RT kit (HiSpec option; Qiagen). Global miRNA profiling was performed with human miRNome miScript miRNA PCR arrays (V16.0, 384-well, Qiagen). The manufacturer's recommended PCR cycling conditions were followed for 40 cycles on a CFX384 real-time PCR machine (Biorad, Hercules, CA, USA), with a terminal melt curve. Raw PCR quantification cycles (Cq) were preprocessed prior to analysis by converting Cq values > 35 to the predefined detection limit of 35, in accordance with manufacturer's recommendations. Expression levels were normalized using a mean-centering restricted approach. Hierarchical clustering and statistical analysis were performed with Partek Genomics Suite (V6.6, Chesterfield, MO, USA).

Gene regulation of *BMPR2*, *PTBP1, SMAD1, SMAD5, PKM2* and *HIF1A* and miR-124 expression using siRNA or mimic sequences

BOECs were seeded in 6-well plates (2 x 10^5 cells/well) and grown for one day in normal medium (EGM-2 MV 10% FBS, Lonza, Workingham, UK). Prior to transfection, cells were incubated in Optimem I for 2 hours. BOECs were transfected on Day 0 with a final concentration of 10 nM siRNA with an On-TARGETplus siRNA for *BMPR2*, *SMAD1*, *SMAD5* and *PKM2* (Dharmacon^{TM}, Lafayette, CO, USA), a Silencer® for *PTBP1*, *LIMK1* and *HIF1A* (Thermo Fisher Scientific Inc., Waltham, MA, USA), or siScramble (Thermo Fisher Scientific Inc., Waltham, MA, USA) in complex with DharmaFECT1^{TM} (4 μl/well) diluted in Optimem I. For the up-regulation of miR-124, cells were transfected on Day 0 with a final concentration of 0.1 nM with a Pre-miR™ miRNA Precursor specific for miR-124 or with a Pre-miR™ miRNA scramble negative control (Applied Biosystems, Foster City, CA, USA). DharmaFECT1^{TM} was incubated in half the final volume (200 μl for 1 well) of

Optimem I for 5 minutes followed by addition of Optimem I (200 μl for 1 well) containing 10X final concentration of the relevant siRNA, making the final concentration of siRNA 5X. The mix was incubated for 20 minutes at room temperature to allow lipoplexes to form. The transfection mix (400 μl/well) was dropped onto cells in fresh Optimem I (1.6 ml/well), ensuring full coverage of the well. Cells were incubated with the complexes for 4 hours at 37 °C, followed by replacement with EGM-2 MV 10% FBS. RNA was extracted as indicated in the figure legends.

LIMK inhibition

To obtain specific inhibition of both LIMK1 and LIMK2, control BOECs were seeded in 6-well plates (2 x 10^5 cells/well) and grown for one day in normal medium (EGM-2 MV 10% FBS, Lonza). After 24 hours, EGM-2MV media was replaced with 10% FBS, growth factor-free EBM-2MV media (Lonza) and left overnight. Then cells were treated with DMSO vehicle or indicated concentration of LIMKi (3 or 10 μM) for 1 or 3 hours before RNA was extracted and examined for gene expression as previously reported[4].

Western blotting

Cultured human BOECs or frozen rat lung tissue were homogenized in lysis buffer (250 mmol/L Tris-HCl, pH 6.8, 4% SDS, 20% v/v glycerol, and 1X EDTA-free protease inhibitor cocktail, Roche, West Sussex, United Kingdom) and sonicated for ≈1 minute, and then centrifuged for 15 minutes at 15,000 x g. Protein concentration was determined using the Bio-Rad Lowry assay (Bio-Rad Laboratories, Hemel Hempstead, United Kingdom), using BSA as the standard. An equal amount of protein (10 µg) from each sample was diluted with 5X sample loading buffer and boiled for 5 minutes. The protein suspensions were separated by SDS-PAGE and transferred to a PVDF membrane and incubated with blocking buffer. Membranes were probed for PTBP1 (1:1000, goat polyclonal antibody, Abcam, Cambridge, United Kingdom). Blots were then incubated with an appropriate horseradish-peroxidase-conjugated antibody and enhanced chemiluminescence reagent (GE Bioscience, Little Chalfont, United Kingdom). To confirm equal loading blots were incubated with an anti-β-actin antibody (Sigma–Aldrich, Poole, United Kingdom).

BOECs protein extraction for the proteomic study

BOECs from 4 healthy controls and 4 HPAH patients with *BMPR2* mutations were plated at the same cell density and cultured in normal medium (EGM-2 MV 10% FBS, Lonza) until they reached confluence. BOECs were rinsed twice with cold PBS before being flash frozen on a bath of dry ice mixed with methanol for 30 seconds. The flask containing the BOECs were then removed from the dry ice bath and lysis buffer (50 mM Tris-HCl, pH 8, 150 mM NaCl, 1% IGEPAL CA-630, 0.5% deoxycholate, 0.1% SDS and 1X EDTA-free protease inhibitor cocktail) was added to the frozen monolayer of cells which was scraped for whole cell lysate collection. The whole cell protein lysates were then vortexed for 30 seconds, sonicated at 4 °C and centrifuged at 14,000 x g for 15 minutes at 4 °C. The supernatant was kept at -80 °C.

Protein digestion and peptide labelling with iTRAQ reagents

Protein samples (150 μg) obtained from BOECs were cleaned up by three stepwise additions of cold acetone (kept at -20 °C) to a final of 6 volumes added. The protein samples were incubated at -20 °C for 90 minutes and were vortexed every 15 minutes. Samples were centrifuged at 14,000 x g for 10 minutes at 4 °C to obtain a protein pellet. Acetone was decanted and once entirely evaporated, each protein pellet was suspended in iTRAQ TEAB buffer (1 M TEAB, 0.2% SDS, 6 M Urea, 1% NP-40). Thereafter, protein samples were quantified with the 2-D Quant Kit (GE Bioscience, Little Chalfont, UK) before being diluted at 2.5 mg/mL with TEAB buffer. Protein samples were quantified again with the 2-D Quant kit and 100 µg of protein from each BOEC sample were processed for further reduction, alkylation, digestion and iTRAQ labelling using iTRAQ Reagents Multiplex Kit (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's protocol. Briefly, protein samples were reduced with 5 mM tris-(2carboxyethyl)phosphine (TCEP) at 37 °C for 1 hour and the cysteine groups were blocked using a 10 mM methyl methanethiosulfonate (MMTS) solution at room temperature for 10 minutes. Protein samples were then digested with Lys-C (1:50, Promega, Madison, WI, USA) at 37 °C for 2 hours and the reaction was stopped with 10% trifluoroacetic acid (TFA). Proteins were further digested with trypsin (1:20, Applied Biosystems, Foster City, CA, USA) at 37 °C for 16 hours[5]. Digestion efficiency was performed by 1-D gel electrophoresis and Sypro Ruby gel staining. Peptide samples were dried completely before being suspended in TEAB for labelling. Each peptide sample was labelled at room temperature for 2 hours with one iTRAQ reagent vial (mass tag 113, 114, 115, 116, 117, 118, 119 and 121) previously reconstituted with 200 µl of isopropanol[6]. Samples from the 8 different conditions and labelled respectively with the different iTRAQ reagents were then combined. The volume of the combined sample was reduced using the speed vacuum for 2 hours or more until a brown pellet was obtained.

Peptide OFFGEL fractionation

For pI-based peptide separation, we used the 3100 OFFGEL Fractionator (Agilent Technologies, Santa Clara, CA, USA) with a 24-well set-up. The peptide sample was diluted to a final volume of respectively 3.6 ml using OFFGEL peptide sample solution (Agilent Technologies, Santa Clara, CA, USA). The IPG strip of 24 cm long with a 3–10 linear pH range (Agilent Technologies) was rehydrated in the IPG strip rehydration buffer according to the manufacturer’s protocol for 15 minutes. Then, 150 µl of peptide sample was loaded in each well. Electrofocusing of the peptides was performed at 20 °C and 50 µA until the 50 kVh level was reached. After focusing, the 24-peptide fractions were withdrawn and the wells rinsed with 150 µl of a solution of water/methanol/formic acid (49:50:1) for 15 minutes after which the rinsing solutions were pooled with their corresponding peptide fraction. All fractions were evaporated by centrifugation under vacuum and maintained at -20 °C until processed for mass spectrometry analysis. Proteomics analysis was performed at the OHRI Proteomics Core Facility (Ottawa, Canada).

2D LC-MS/MS

All HPLC solvents were Optima LC-MS grade from Fisher Scientific. The OFFGEL fractions were concentrated by vacufuge, purified by ZipTip (Millipore, Billerica, MA, USA), and diluted in 1% formic acid in water. Peptides were analyzed by two-dimensional liquid chromatography – tandem mass spectrometry (2D LC-MS/MS) using an UltiMate 3000 RSLC nano HPLC (Dionex) and an LTQ Orbitrap XL hybrid mass spectrometer with nanospray ionization source (Thermo Fisher Scientific Inc., Waltham, MA, USA). The system was controlled by Xcalibur software version 2.0.7

(Thermo Fisher Scientific Inc.). Peptides were loaded by autosampler onto an SCX column (POROS 10S, 300 µm x 10 cm; Dionex P/N 164565) and eluted by injections of 0, 10, 20, 50, 100, 500 and 1000 mM of ammonium acetate with 0.1% formic acid. Each eluted fraction was collected on a C18 trap column (Peptide CapTrap, Michrom Bioresources Inc., Auburn, CA, USA) for 5 minutes at a flow rate of 15 µl per minute and then eluted over a 60 minute gradient of 3% - 45% acetonitrile with 0.1% formic acid at a flow rate of 0.3 µl per minute onto a 10 cm long column with integrated emitter tip (Picofrit PF360-75-15-N-5 (New Objective) packed with Zorbax SB-C18 5 micron (Agilent Technologies, Santa Clara, CA)), and nanosprayed into the mass spectrometer. MS scans were acquired in FTMS mode at a resolution setting of 60,000. MS2 scans were acquired in both ion trap collisionally-induced dissociation (IT-CID) and Orbitrap high-energy collisional dissociation (FT-HCD) modes using data-dependent acquisition of the top 3 ions from each MS scan. Dynamic exclusion window was 30 seconds.

Peaklist generation

From each .raw file, a peak list in .mgf format was generated by using the computer program extract_msn (Thermo Fisher Scientific Inc.). Extract_msn parameters were -M0.1 -B800 -G1 -I10 -R2 -r8. The .mgf files from each HPLC fraction were concatenated to generate one peak list file per OFFGEL fraction. The computer program HCD_CID_merger.pl (http://web.expasy.org/HCD_CID_merger/HCD_CID_merger_doc.html) was used to generate a “merged” peak list in which the 112 – 122 m/z range was copied from each HCD scan and added into the corresponding IT-CID spectrum. As described in (http://dx.doi.org/10.1016/j.jprot.2009.10.015) this method is intended to combine the sensitivity of IT-CID for peptide identification with the ability of FT-HCD spectra to detect low mass iTRAQ reporter ions. Peak lists with only the HCD spectra and only the CID spectra were also generated using this software tool. The processed peak lists (HCD spectra only or merged spectra only) for each OFFGEL fraction were then concatenated to produce the final peak list. A total of 20,954 peptides were identified. Mascot's peptide significance threshold was set to the default value (5%). The false discovery rate was set at 1%.

Protein identification using Mascot

Mascot software version 2.4 (Matrix Science, Boston, MA, USA) was used to infer peptide and protein identities from the mass spectra. The peak lists representing the observed MS/MS spectra were matched against a custom database of protein sequences (human sequences from the 2011_07 version of uniprot_sprot.fasta.gz downloaded from ftp.uniprot.org concatenated with a Contaminants database downloaded from maxquant.org, June 9th 2011). Mass tolerance parameters were MS ± 10 ppm and MS/MS ± 0.6 Da. Reporter ion tolerance was 0.1 Da. Enzyme specificity was set to 'Trypsin/P' with <=3 miscuts. Methylthiolation of cysteine was set as a fixed modification (due to MMTS treatment). Oxidation of methionine, deamidation and iTRAQ modification of tyrosine were allowed as variable modifications. Quantitation mode was set to 'iTRAQ (8-plex)'. Note that Mascot does not quantify any peptides with iTRAQ modification of tyrosine because the labeling of tyrosine is assumed to be an incomplete reaction. To check for efficiency of iTRAQ labeling, searches were also conducted with iTRAQ (8-plex) modification as a variable modification on lysines and peptide N-termini.

Protein candidate selection

To select protein candidates that are more likely to be dysregulated in PAH, we analyzed the Mascot results obtained as above. We were able to quantify a total of 1176 proteins, although some of these have missing values for one channel or more. We then followed the ratio methods of the R package isobar[7] to select candidates for further analyses: first we fitted the log-ratios between replicates to a mixture of a Gaussian and a Cauchy probability distributions and used it to assign probabilities to the log-ratios between and HPAH cases and healthy control. Given a positive (negative) log-ratio, we used the right (left) tail of the fitted mixture distribution to assign to it a probability of having a higher (lower) value. The three *p*-values for the healthy/healthy log-ratios are combined into a single *p*-value. In the same way, the four *p*-values for the pah/healthy are also combined into one (Suppl. Table 4). As there are missing values, these calculations take into account the number of *p*-values that are used relative to the maximum possible number of *p*-values (i.e. 3 or 4). A good candidate to be deregulated in HPAH will have a low combined pah/healthy *p*-value and a high healthy/healthy combined *p*-value (Suppl.Table 3).

Mining of miRNA predicted protein targets

We investigated the candidates we obtained from microRNA PCR arrays (Suppl.Table 2) and iTRAQ for coordinated dysregulation of miRNA and their predicted target proteins by mining miRNA target prediction databases. We selected a total of 76 candidate proteins (39 downregulated and 37 upregulated) as the most likely to be dysregulated in HPAH by applying the liberal cut-offs of *p*-value <0.15 for PAH/healthy and *p*-value >0.35 for healthy/healthy. First, we obtained all the predicted targets for selected miRNAs that showed dysregulation in HPAH from available software and databases: miRDB (MirTarget2)[8], PicTar[9], miRanda[10]. Then we mapped the predicted targets to proteins, and we filtered the results to find pairs of miRNA and proteins that are dysregulated in opposing directions in our profiling experiments. For example, if a miRNA is upregulated in HPAH, the set of downregulated proteins are used to filter its predicted targets. The resulting pairs are displayed in Suppl.Table 5.

Glycolytic flux

Glycolytic flux of cells was measured by monitoring the conversion of 5-^{3}H-glucose to ^3H_2O as previously described[11]. Briefly, 2 x 10^5 cells/well (BOECs from HPAH or healthy controls, or control PAECs) were plated in a 48-well plate in normal medium (EGM-2 MV 10% FBS, Lonza). Twenty four hours after being seeded (or 48 to 72 hours post-transfection as indicated in figure legend) 5-^{3}H-glucose (PerkinElmer Life Sciences Inc., Boston, MA, USA) was added to each well to a final concentration of 0.5 μCi/well (0.0185 MBq/well) (0.1 μl/well). Samples were incubated for 2 hours at 37 °C in a humidified incubator under 5% CO_2. After that, 200 μl/well of supernatant were collected and placed into glass vials containing hanging wells carrying filter paper soaked with H_20. The vials were capped, sealed with rubber stoppers, and incubated for 2-3 days at 37 °C in the incubator to reach equilibrium. During the incubation, ^3H_2O generated by glycolysis diffused from the bottom of the glass vials to the filter paper carried by the hanging wells through evaporation, condensation and absorption. The filter paper was then transferred into scintillation vials containing 5 ml of scintillation liquid and counted in a scintillation counter. Appropriate ^{3}H-glucose-only and ^3H_2O-only controls were included, enabling the calculation of ^3H_2O in each sample and thus the rate of glycolysis as previously described[11].

Lactate detection

Lactate concentration in supernatants overlying culture cells was determined using the L-Lactate assay kit (Abcam, Cambridge, UK) following the manufacturer's instructions. Briefly, lactate was converted to pyruvate and hydrogen peroxide (H_2O_2) by lactate oxidase. H_2O_2 in the presence of a peroxidase subsequently catalyzes oxidative condensation of a precursor, producing a chromogen with an absorption maximum at 570 nm. This signal was then normalized to total protein content for each sample.

TCA cycle flux

TCA cycle flux of cells was measured by monitoring the conversion of D-[6-^{14}C]-glucose to $^{14}CO_2$. Briefly, 8 x 10^4 cells/well (BOECs from HPAH or healthy controls) were plated in a 12-well plate in normal medium (EGM-2 MV 10% FBS, Lonza). Twenty four hours after being seeded (or 48 to 72 hours post-transfection as indicated in figure legend) D-[6-^{14}C]-glucose (PerkinElmer Life Sciences Inc.) was added to each well to a final concentration of 0.55 μCi/well (0.02 MBq/well). Samples were incubated for 6 hours at 37 °C in a humidified incubator under 5% CO_2. After that, filter paper (2.7 x 2.7 cm), soaked in 1X hyamine was put on the lid of the 12-well plate to fully cover each well. 250 μl of 3 M perchloric acid were added to each well to lyse the cells and release CO_2, which was captured by the hyamine on the filter paper in the lid of the 12-well plates. This step was performed in a fume hood designated for radioactive substance use. Each plate was sealed with parafilm and left overnight at room temperature in a fume hood designated for radioactive substance use to ensure absorption of the $^{14}CO_2$. The filter paper was then transferred into scintillation vials containing 5 ml of scintillation liquid and counted in a scintillation counter. Appropriate D-[6-^{14}C]-glucose-only and blank controls were included, enabling the calculation of $^{14}CO_2$ in each sample and thus the TCA cycle flux.

Proliferation assay

BOECs were maintained in complete microvascular endothelial cell growth medium-2 (EGM-2MV 10% FBS, Lonza) and were used at passages 4–6. Cells were plated in 24-well plates at 10,000 cells per well, then quiesced in serum-free medium for 4 hours. Cells were counted on days 0, 2, 5 and 7 using trypan blue exclusion.

Migration assay

BOECs from control and *BMPR2* mutant lines were trypsinised and seeded into ibidi (Munich, Germany) culture inserts at 45,000 cells per chamber creating a uniform cell free gap. After 24 hours inserts were removed and cells were treated with EBM-2 (2% FBS, 20 mM HEPES and 2 μM Hydroxyurea). Time-lapse microscopy of duplicate wells was undertaken using a Leica SPE imaging system. Images were taken every 5 minutes for 18 hours at 37 °C. Images were imported into ImageJ and 10 cells per chamber were manually tracked using a plugin macro (rsbweb.nih.gov/ij/plugins/track/track.html). Distance was calculated using the manual tracking plugin. Furthest migrated was based on the largest X coordinate subtracted from the X coordinate at time 0.

Immunohistochemistry

Fixed sections of human or rat lung tissue (5 µm in thickness) were processed using

PT Link following the manufacturer's instructions (DakoCytomation, Ely, UK). Endogenous tissue peroxidase was quenched using hydrogen peroxidase (HP) blocking solution (DakoCytomation). Polyclonal rabbit-anti-human or rat PTBP1 (Abcam, Cambridge, UK), was labelled using an affinity purified anti-rabbit streptavidin biotin complex (StreptABC) peroxidase (Vector Laboratories, Peterborough, UK), visualised using 3-3' diaminobenzidine hydrochloride (DAB) substrate (DakoCytomation) and counterstained in Carrazzi's haematoxylin (DakoCytomation).

Immunofluorescence

BOECs were seeded onto BD Falcon™ glass chamberslides (BD Biosciences, Oxford, UK) coated with 0.1% gelatin solution and cultured for 48 hours prior to treatment. After treatment the chamberslides were washed with PBS, fixed with 4% paraformaldehyde and permeabilised with 0.5% Triton-X-100. Prior to staining cells were blocked with 0.5% BSA. PKM-2 was labelled with mouse anti-human-PKM2 (Schebo-Biotech UK, Basingstoke, UK) and a secondary goat anti-mouse Alexa-Fluor 488 (Life Technologies, Glasgow, UK). Chamberslides were counterstained with Phalloidin Alexa-Fluor 594 (Life Technologies) and mounted in glycerol/PBS solution containing DAPI (Vectashield, Vector Laboratories). Cells were viewed and photographed using a confocal microscope (Leica TCS SPE) and images captured using Leica LAS AF software.

Supplemental References

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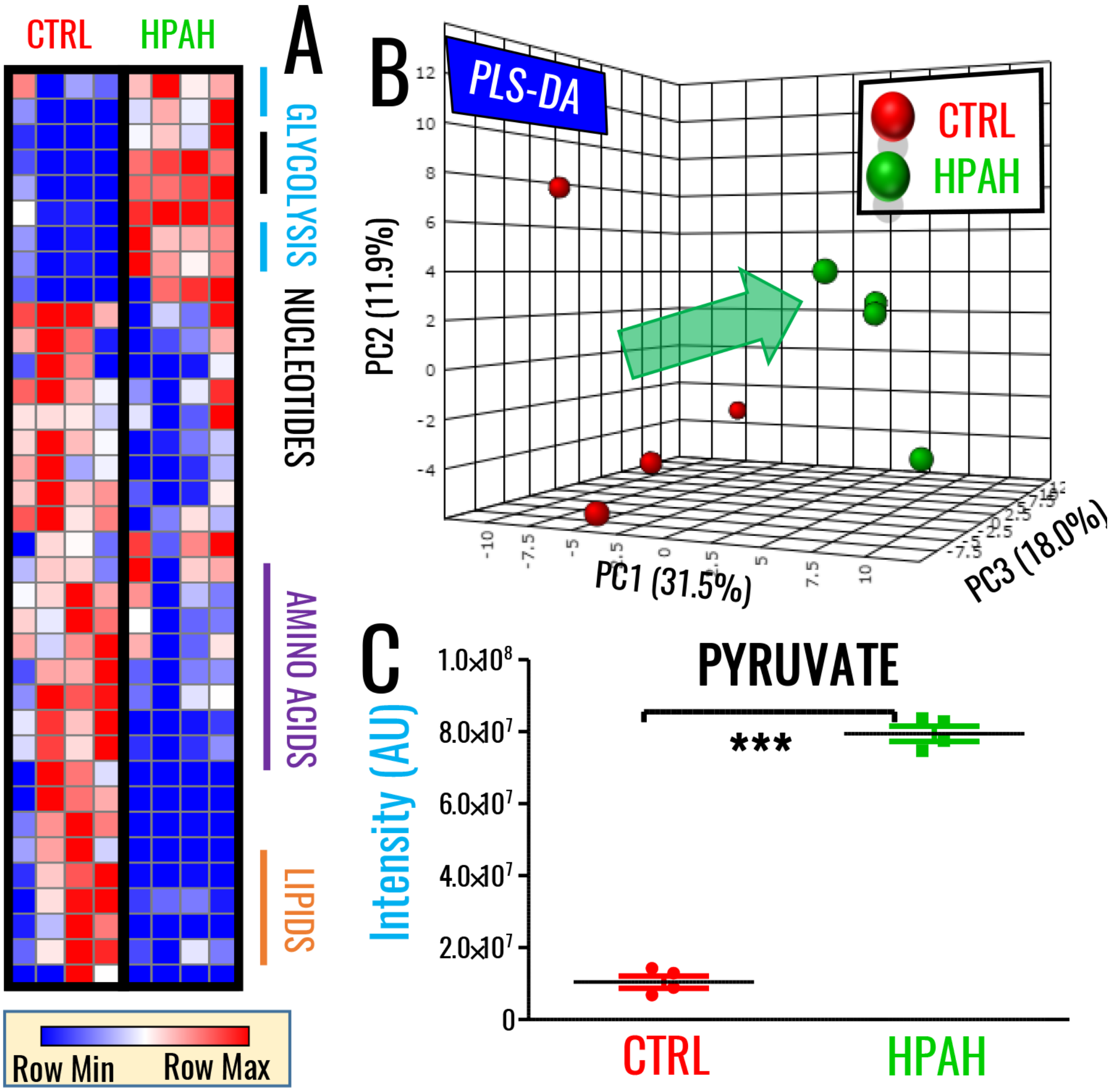
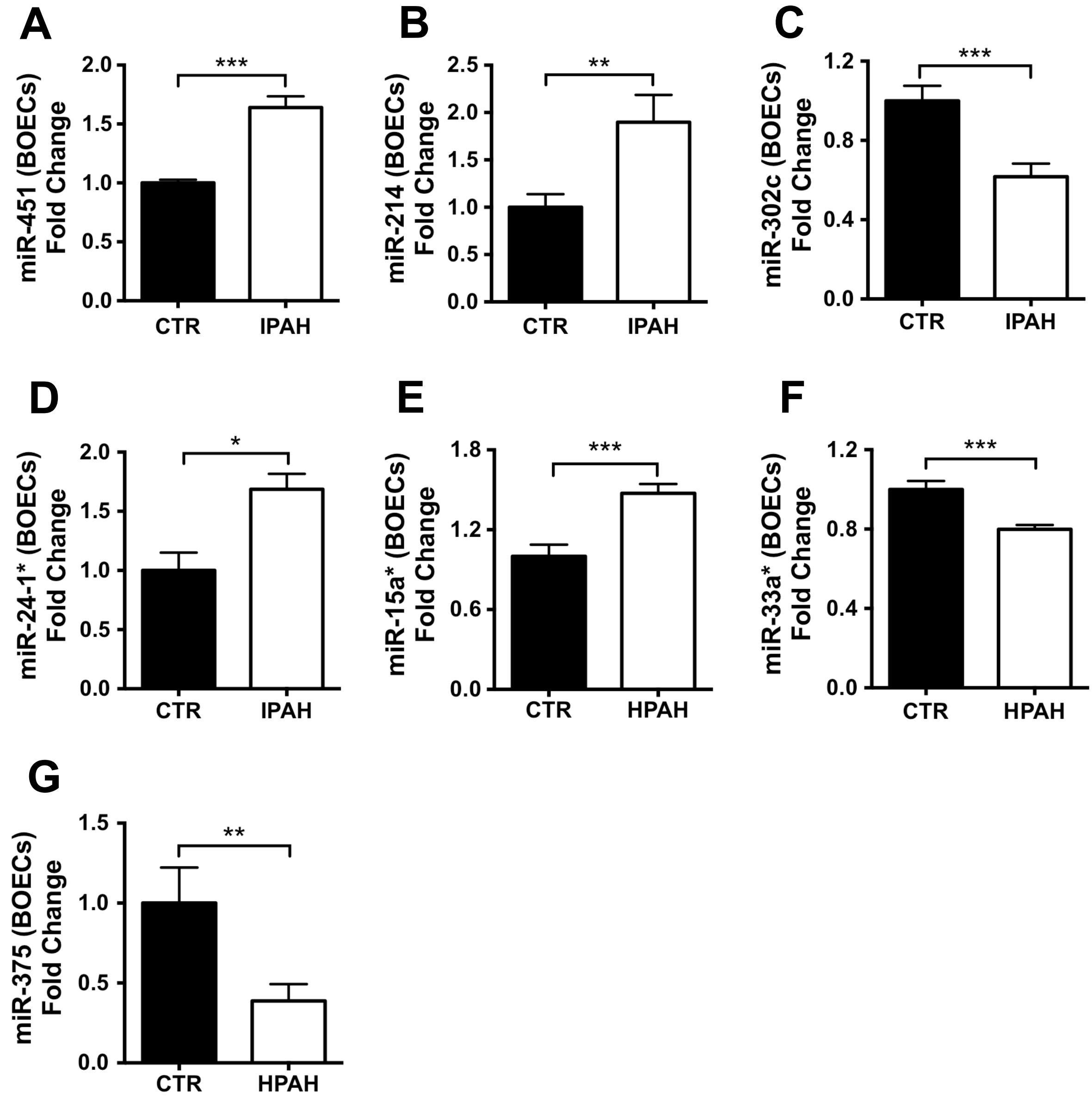
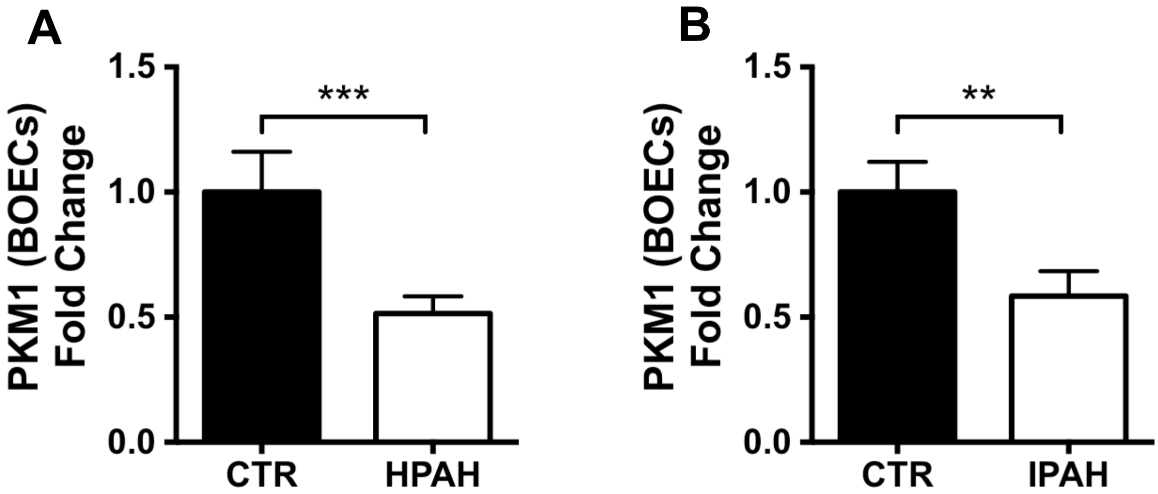
Supplemental Figures



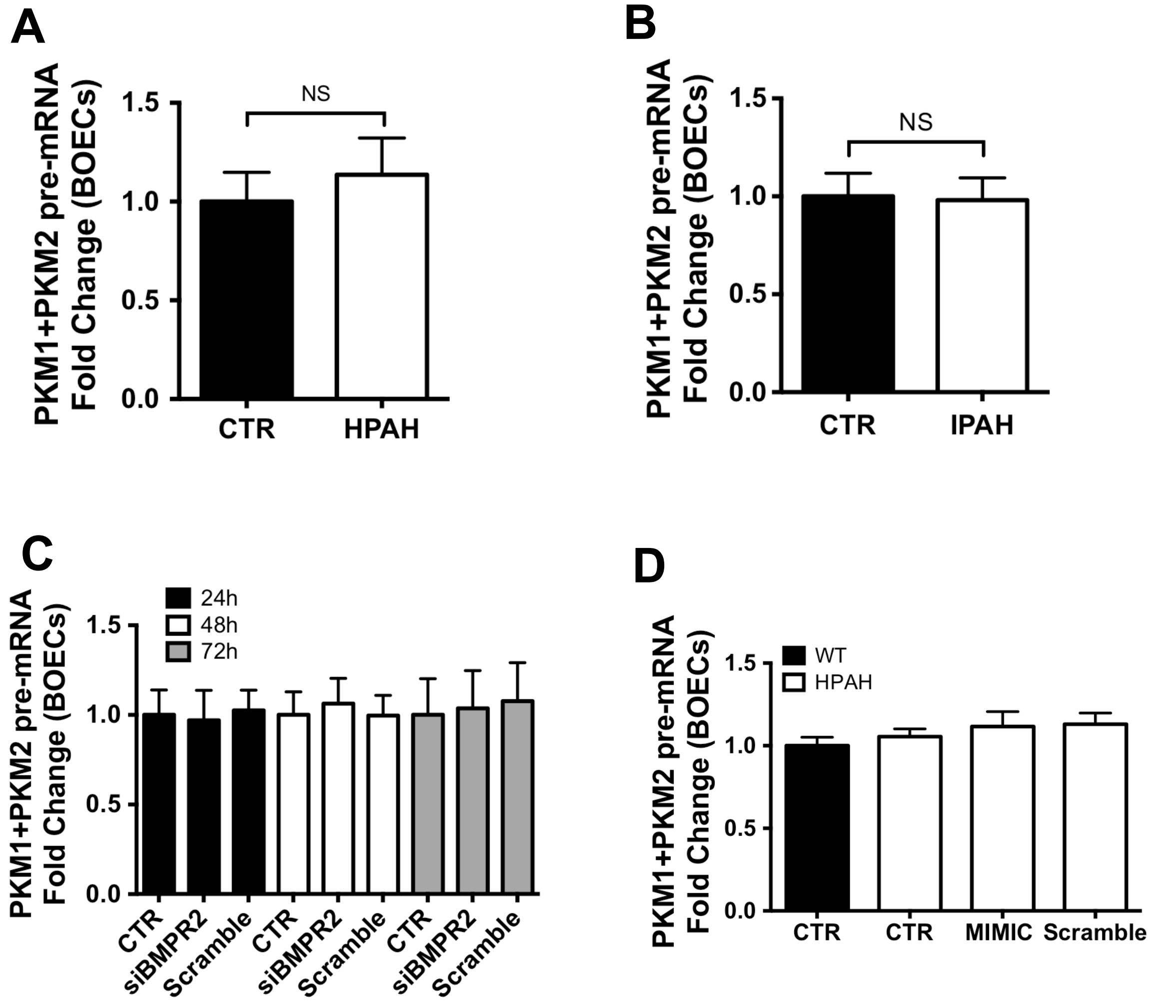
Suppl.Figure1. UHPLC-MS Metabolomics of HPAH and control BOECs. (A) Heat map showing a schematic representation of the top 50 metabolites (by lowest *p*-value, *t*-test) either increasing or decreasing in HPAH BOECs harboring a mutation in *BMPR2* (n=4) in comparison to control counterparts (n=4, blue: low; red: high). This group was enriched with metabolites from glycolysis, nucleotides, amino acids and lipids, as determined through Metaboanalyst 3.0. (B) Metabolic phenotypes were sufficiently different between the two groups to afford clustering of samples upon partial least square-discriminant analysis (PLS-DA). (C) Pyruvate was the most statistically significant metabolic change between the two groups (*** $p<0.001$).



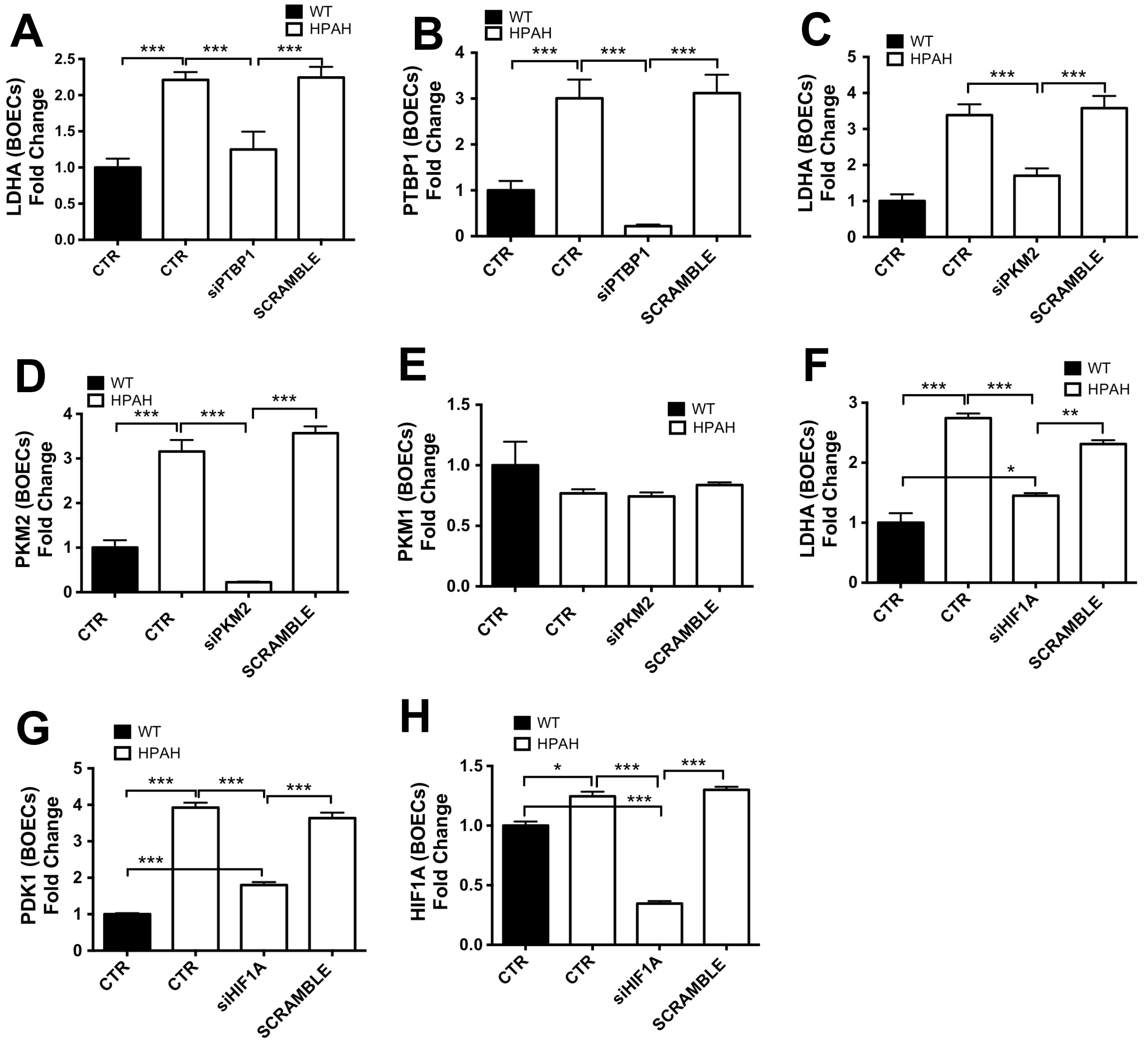
Suppl.Figure2. Validation of the expression of selected miRNAs dysregulated in the PCR-array study. (A-G) The expression of selected miRNAs, dysregulated in the PCR-array but not significantly after false rate discovery correction due to the relatively modest sample size, was validated in 7 HPAH, 5 IPAH and 8 control BOEC lines. In all cases, miRNA dysregulation followed the trend observed in the array as shown in Suppl.Table2, and in all cases the dysregulation was statistically significant. Data were analyzed using an unpaired *t*-test (***$p<0.001$, **$p<0.01$, *$p<0.05$).



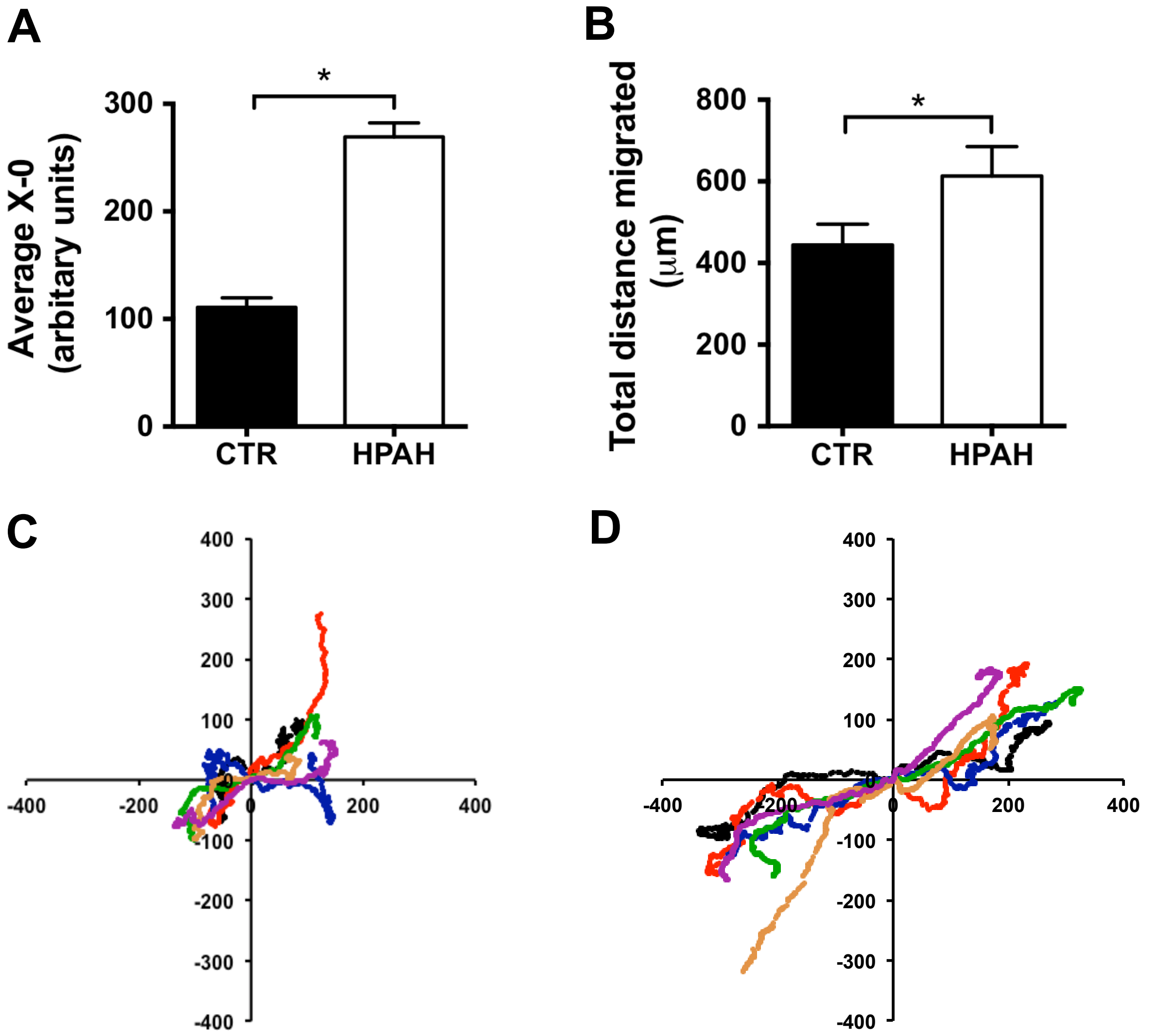
Suppl.Figure3. *PKM1* is downregulated in BOECs isolated from PAH patients. (A-B) The expression of *PKM1* was assessed by qPCR in BOECs isolated from HPAH (A, n=7) or IPAH (B, n=5) patients versus controls (n=8). Data were analyzed using an unpaired *t*-test (***p<0.001, **p<0.01).



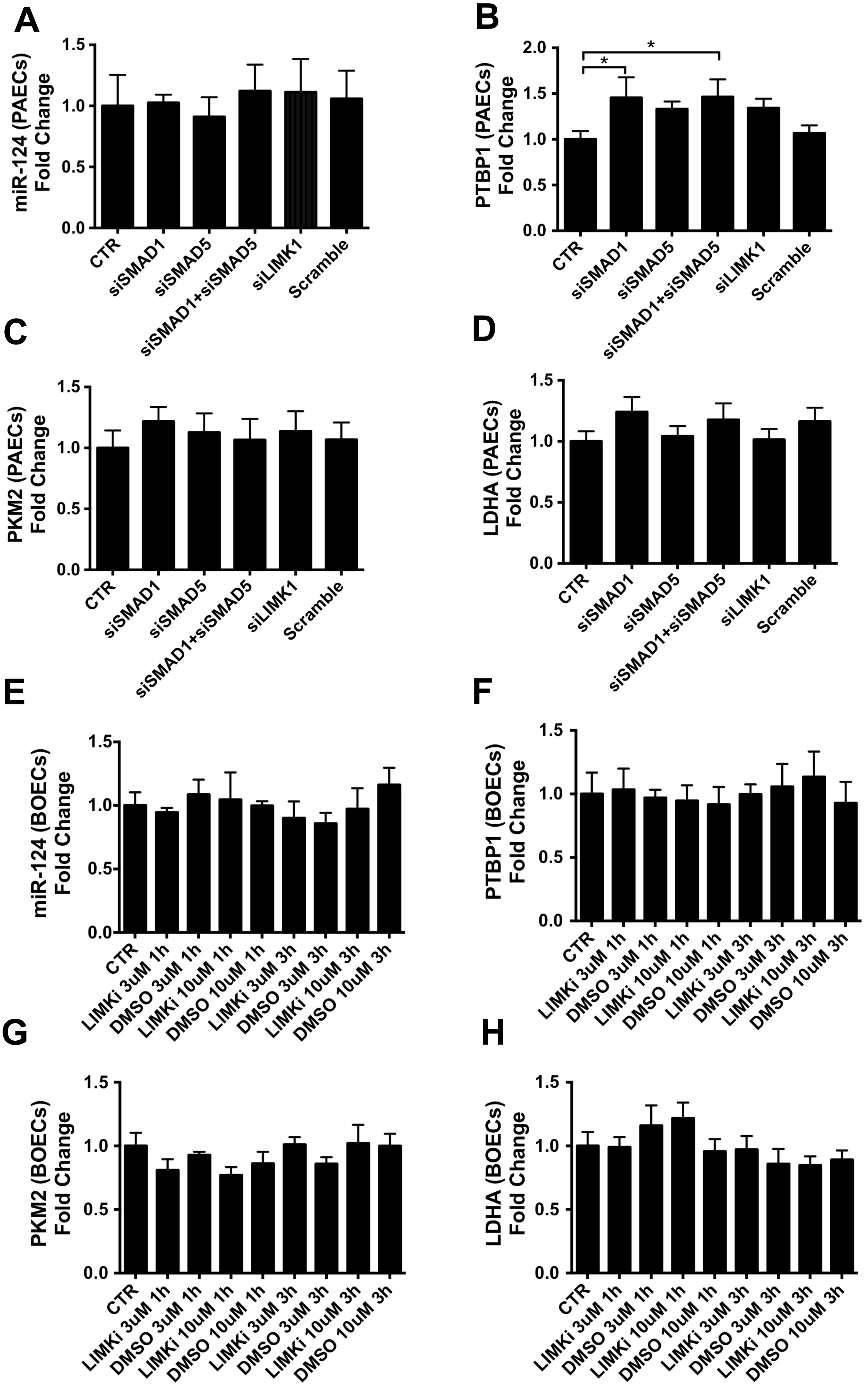
Suppl.Figure4. The precursor mRNA coding for both PKM1 and PKM2 is not dysregulated in BOECs isolated from PAH patients, in control cells treated with a si*BMPR2* or in miR-124 mimic-treated cells. (A-B) Total RNA was isolated from HPAH (A, n=7), IPAH (B, n=5) and control BOECs (n=8) and expression of the precursor mRNA was assessed by qPCR. (C) Control BOECs (n=3) were transfected in 6-well plates with a si*BMPR2* or a scramble-control or treated with the transfection reagent alone (CTR) and total RNA was isolated 24, 48 and 72 hours post-transfection. The expression of the *PKM1+PKM2* precursor was assessed by qPCR. (D) HPAH BOECs (n=3) were transfected in 6-well plates with a miR-124 mimic or a scramble sequence as negative control or treated with the transfection reagent alone (CTR). The expression of the precursor coding for PKM1 and PKM2 was assessed after 48 hours by qPCR. Every sample was tested in triplicate. Data are presented as the mean ± S.E.M. Data were analyzed using an unpaired *t*-test (A-B) or a 1-way ANOVA followed by Bonferroni post hoc test (C-D).



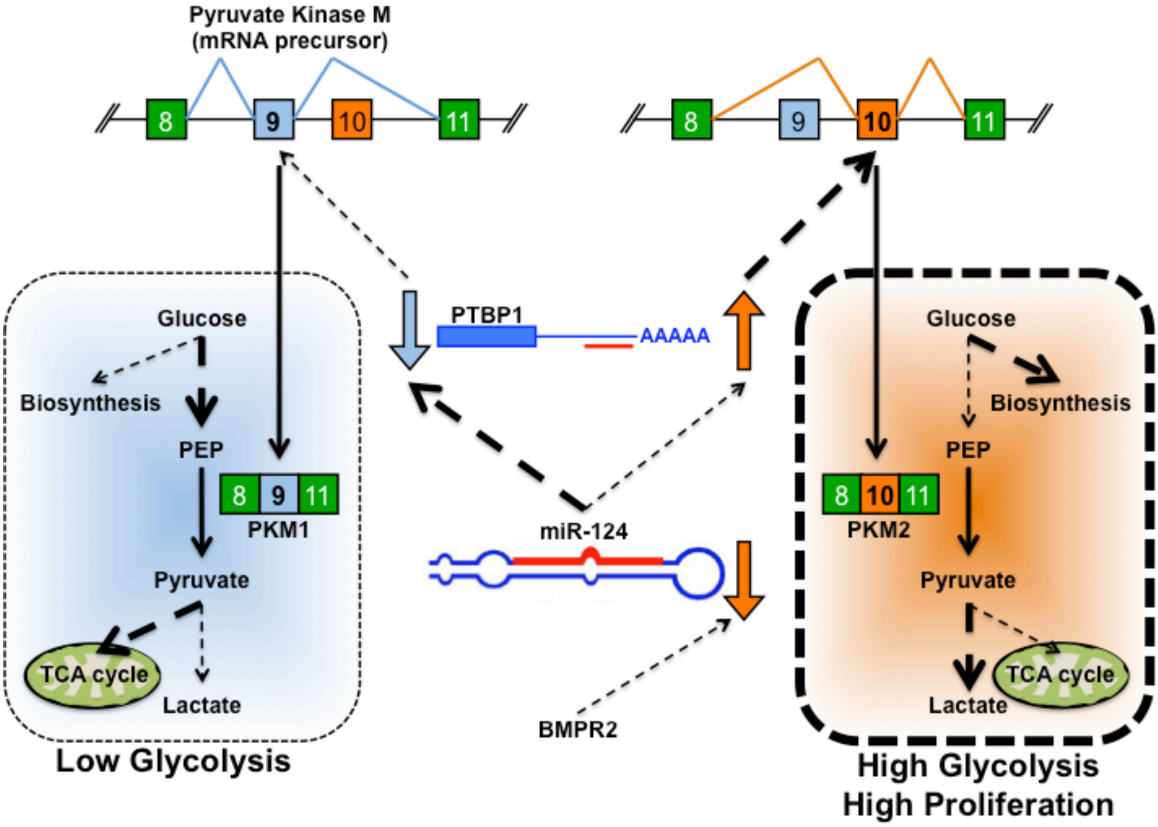
Suppl.Figure5. The downregulation of *PTBP1*, *PKM2* or *HIF1A* can reduce the expression of LDHA in BOECs. (A-H) HPAH BOECs (n=3) were transfected with si*PTBP1*, si*PKM2*, si*HIF1A* or with a scrambled control. Cells treated with the transfection reagent alone were used as a negative control (CTR). Total RNA was extracted 48 hours post-transfection and analyzed by qPCR for the expression of *LDHA* (A, C, F), *PTBP1* (B), *PKM2* (D) *PKM1* (E), *PDK1* (G) and *HIF1A* (H). Gene expression was also assessed in control BOECs (n=3) to establish the basal level of expression in unaffected subjects. Data are presented as the mean ± S.E.M. Samples were tested in triplicate. Data were analyzed using a 1-way ANOVA followed by Bonferroni post hoc test. (**p*<0.05, ***p*<0.01, ****p*<0.001).



Suppl.Figure6. BOECs isolated from HPAH patients exhibit abnormal migration. To assess migration, control or HPAH cells (n=3) were seeded in ibidi culture inserts. After 24 hours, inserts were removed and cells were treated with EBM-2 (2% FBS, 20 mM HEPES and 2 mM Hydroxyurea). Time-lapse microscopy of duplicate wells was undertaken using a Leica SPE imaging system. Images were taken every 5 minutes for 18 hours at 37 °C. (A-B) Ten cells were tracked per well from control and HPAH BOEC, respectively. Tracks were determined by cell nuclei position and migration origin was superimposed at the zero-cross point. (C) Quantification of BOEC migration using the distance migrated from zero-cross point (X-0) and (D) total distance migrated. Data are presented as the mean ± S.E.M. Data were analyzed using a paired *t*-test.


A
miR-124 (PAECs) Fold Change
1.5
1.0
0.5
0.0
CTR
siSMAD1
siSMAD5
siSMAD1+siSMAD5
siLIMK1
Scramble
B
PTBP1 (PAECs) Fold Change
2.0
1.5
1.0
0.5
0.0
*
*
CTR
siSMAD1
siSMAD5
siSMAD1+siSMAD5
siLIMK1
Scramble
C
PKM2 (PAECs) Fold Change
1.5
1.0
0.5
0.0
CTR
siSMAD1
siSMAD5
siSMAD1+siSMAD5
siLIMK1
Scramble
D
LDHA (PAECs) Fold Change
1.5
1.0
0.5
0.0
CTR
siSMAD1
siSMAD5
siSMAD1+siSMAD5
siLIMK1
Scramble
E
miR-124 (BOECs) Fold Change
1.5
1.0
0.5
0.0
CTR
LIMKi 3uM 1h
DMSO 3uM 1h
LIMKi 10uM 1h
DMSO 10uM 1h
LIMKi 3uM 3h
DMSO 3uM 3h
LIMKi 10uM 3h
DMSO 10uM 3h
F
PTBP1 (BOECs) Fold Change
1.5
1.0
0.5
0.0
CTR
LIMKi 3uM 1h
DMSO 3uM 1h
LIMKi 10uM 1h
DMSO 10uM 1h
LIMKi 3uM 3h
DMSO 3uM 3h
LIMKi 10uM 3h
DMSO 10uM 3h
G
PKM2 (BOECs) Fold Change
1.5
1.0
0.5
0.0
CTR
LIMKi 3uM 1h
DMSO 3uM 1h
LIMKi 10uM 1h
DMSO 10uM 1h
LIMKi 3uM 3h
DMSO 3uM 3h
LIMKi 10uM 3h
DMSO 10uM 3h
H
LDHA (BOECs) Fold Change
1.5
1.0
0.5
0.0
CTR
LIMKi 3uM 1h
DMSO 3uM 1h
LIMKi 10uM 1h
DMSO 10uM 1h
LIMKi 3uM 3h
DMSO 3uM 3h
LIMKi 10uM 3h
DMSO 10uM 3h

Suppl.Figure7. Manipulation of *SMAD1*, *SMAD5* or *LIMKs* does not regulate the expression of the miR-124/PTBP1 pathway. (A-D) Control PAECs were transfected with si*SMAD1*, si*SMAD5* or a si*LIMK1* and tested for the expression of miR-124 (A), *PTBP1* (B), *PKM2* (C), and *LDHA* (D) 48 hours post-transfection compared to transfection reagent alone (CTR) or scrambled siRNA (n=3). (E-H) Control BOECs were treated with 3 mM or 10 mM of a LIMK1 and 2 inhibitor (LIM Kinase Inhibitor I, LIMKi 3, Calbiochem) or DMSO as negative control or left untreated for comparison. Total RNA was then isolated after 1 and 3 hours for qPCR analysis. miR-124 (E), *PTBP1* (F), *PKM2* (G) and *LDHA* (H) expression were assessed as indicated in the different panels. Data are presented as the mean ± S.E.M. Samples were tested in triplicate. Data were analyzed using a 1-way ANOVA followed by Bonferroni post hoc test. None of the results were statistically significant.



Suppl.Figure8. Schematic diagram proposing the link between miR-124, PTBP1 and glycolysis via PKM2. In the center of the model, miR-124 is regulated by *BMPR2* expression and it directly targets *PTBP1*, which regulates *PKM1* and *PKM2* expression. In particular, binding of PTBP1 to the splice sites flanking exon 9 in PKM precursor transcript results in exon 9 exclusion and exon 10 inclusion, generating PKM2 (as shown on the right side of the model). The thickness of the arrows leading to the panel on the right indicates the high glycolytic efficiency of cells with low miR-124 and high PTBP1. Vice versa, when *PTBP1* expression is reduced (on the left), exon 9 of the PKM precursor is included in the final transcript and PKM1 is produced. This determines a low glycolytic level as symbolized by the thin arrows leading to the left side of the model.

Suppl.Table 1. Demographics of the HPAH and IPAH patients used for BOECs isolation

Subject ID	Age	Sex	Ethnicity	mPAP	CI	PVR	6 min walk	Treatment	PAH Classification	BMPR-II Mutation	microArray Study	qPCR Validation	Proteomic Study	Metabolon Study
BOEC-C1	45	F	Caucasian								✔	✔	✔	✔
BOEC-C2	20	M	Caucasian								✔	✔	✔	
BOEC-C3	40	M	Caucasian								✔	✔	✔	
BOEC-C4	30	M	Caucasian								✔	✔	✔	✔
BOEC-C6	37	F	Caucasian									✔		✔
BOEC-C7	41	M	Caucasian									✔		
BOEC-C8	38	M	Asian									✔		
BOEC-C15	35	F	Caucasian									✔		
BOEC-C24	34	F	Caucasian											✔
EPC-B1	45	M	Caucasian	46	1.75	9.7	381	ERA, PDEI	heritable	R320X	✔	✔	✔	✔
EPC-B2	21	M	Caucasian	71	1.8	16.4	360	PGI, PDEI	heritable	W9X	✔	✔	✔	✔
EPC-B4	35	F	Caucasian	65	1.9	n/a	459	ERA, PDEI	heritable	W9X	✔	✔	✔	✔
EPC-B9	79	F	Caucasian	52	2.25	10.96	124	PDEI	heritable	R584X		✔		✔
EPC-B10	36	F	Asian	40	1.36	19.6	482	ERA, PGI	heritable	R213X	✔	✔	✔	
EPC-B11	32	M	Caucasian	60	2.69	10.8	400	PGI, PDEI	heritable	C.*-944/5GC-AT		✔		
EPC-B14	49	F	Caucasian	56	1.4	?	not recorded	none	heritable	N903S		✔		
EPC-PAH8	37	M	Caucasian	97	1.9	20.99	550	PGI, PDEI	idiopathic		✔	✔		
EPC-PAH9	62	F	Caucasian	72	1.6	n/a	337	ERA, PDEI	idiopathic		✔	✔		
EPC-PAH7	45	F	Caucasian	n/a	n/a	n/a	388	ERA, PGI	idiopathic		✔	✔		
EPC-PAH15	24	F	Caucasian	n/a	n/a	n/a	310	not recorded	idiopathic			✔		
EPC-PAH17	49	F	Caucasian	56	1.4	n/a	not recorded	none	idiopathic			✔		

Suppl.Table 2: List of the miRNAs significantly dysregulated in the PCR array study with unadjusted p-value and corrispondent FDR adjusted p-value

Column ID	p-value (IPAH vs. CTR)	FDR adjusted p-value (IPAH vs. CTR)	FoldChange(IPAH vs. CTR)
hsa-miR-146a*	0.0008	0.5283	3.55
hsa-miR-451	0.0019	0.6505	2.68
hsa-miR-193a-3p	0.0053	0.6881	1.82
hsa-miR-1825	0.0053	0.6881	-2.58
hsa-miR-15a*	0.0056	0.6881	1.66
hsa-miR-124	0.0060	0.6881	-3.15
hsa-miR-214	0.0086	0.7788	3.46
hsa-miR-7	0.0108	0.7788	-2.24
hsa-miR-1827	0.0148	0.7788	1.78
hsa-miR-302c	0.0196	0.7788	-2.56
hsa-miR-1281	0.0200	0.7788	-1.69
hsa-miR-199b-3p	0.0207	0.7788	3.42
hsa-miR-622	0.0210	0.7788	-2.77
hsa-miR-4257	0.0220	0.7788	-1.75
hsa-miR-339-3p	0.0233	0.7788	1.41
hsa-miR-190b	0.0236	0.7788	3.25
hsa-miR-4300	0.0240	0.7788	-2.35
hsa-miR-3682-3p	0.0255	0.7788	-2.70
hsa-miR-199a-5p	0.0272	0.7788	3.64
hsa-miR-1255a	0.0276	0.7788	-2.15
hsa-miR-632	0.0289	0.7788	-2.90
hsa-miR-660	0.0305	0.7788	1.39
hsa-miR-4296	0.0323	0.7788	1.62
hsa-miR-548d-3p	0.0340	0.7788	-2.65
hsa-miR-1270	0.0344	0.7788	-2.17
hsa-miR-3200-5p	0.0369	0.7788	-1.61
hsa-miR-3913-5p	0.0372	0.7788	1.59
hsa-miR-24-1*	0.0383	0.7788	3.53
hsa-miR-3156-5p	0.0387	0.7788	1.98
hsa-miR-3907	0.0403	0.7788	-1.67
hsa-miR-148a*	0.0421	0.7788	1.59
hsa-miR-210	0.0466	0.7788	1.40
hsa-miR-34a*	0.0478	0.7788	1.62
hsa-miR-1184	0.0495	0.7788	-1.75

Column ID	p-value (FPAH vs. CTR)	FDR adjusted p-value (IPAH vs. CTR)	FoldChange (FPAH vs. CTR)
hsa-miR-15a*	0.0025	0.8886	1.70
hsa-miR-3680	0.0037	0.8886	1.44
hsa-miR-33a*	0.0046	0.8886	-1.40
hsa-miR-124	0.0056	0.8886	-2.78
hsa-miR-3934	0.0059	0.8886	2.03
hsa-miR-375	0.0068	0.8886	-1.84
hsa-miR-3139	0.0120	0.9988	1.79
hsa-miR-4279	0.0165	0.9988	-1.76
hsa-miR-3682-3p	0.0256	0.9988	-2.39
hsa-miR-4296	0.0273	0.9988	1.60
hsa-miR-129*	0.0294	0.9988	-2.77
hsa-miR-34c-3p	0.0351	0.9988	-1.49
hsa-miR-670	0.0388	0.9988	1.54
hsa-miR-3194-5p	0.0425	0.9988	1.87
hsa-miR-4330	0.0470	0.9988	1.52
hsa-miR-196b	0.0486	0.9988	-2.84
hsa-miR-3622a-5p	0.0490	0.9988	1.24

Suppl.Table 3. Partial list of the differently regulated proteins in HPAH identified by iTRAQ*

Disregulation in HPAH	Protein name	Accession	MS Score	Nomical Mass, Mr	Sig. Peptide Matches, n	H/H	HPAH/H	p-value
Up	Endophilin-A2	Q99961	52	52295	3	1.01	1.63	0.0321
	EH domain-containing protein 4	Q9H223	354	74097	26	1.02	1.31	0.0139
	Peroxisomal membrane protein PEX14	O75381	49	47038	2	1.05	1.30	0.0179
	DnaJ homolog subfamily A member 1	P31689	39	56693	11	0.96	1.28	0.0229
	Polypyrimidine tract-binding protein 1	P26599	64	67667	4	0.99	1.27	0.0331
	Splicing factor 3B subunit 3	Q15393	48	152488	2	1.03	1.26	0.0303
	10 kDa heat shock protein mitochondrial	P61604	1196	14575	74	0.98	1.25	0.0349
	GTP-binding nuclear protein Ran	P62826	267	30325	10	0.97	1.25	0.0301
	Threonyl-tRNA synthetase cytoplasmic	P26639	92	102978	3	1.01	1.25	0.0342
	Gamma-enolase	P09104	3690	55728	182	1.06	1.23	0.0444
	Tyrosyl-tRNA synthetase cytoplasmic	P54577	100	78243	11	0.99	1.23	0.0455
Down	LIM and senescent cell antigen-like-containing domain protein 1	P48059	69	47870	2	1.19	0.86	0.0273
	Protein disulfide-isomerase A5	Q14554	42	76885	4	1.19	0.83	0.0463
	Protein S100-A11	P31949	1722	15171	95	0.95	0.83	0.0333
	Deoxyribonucleoside 5'-monophosphate N-glycosidase	O43598	80	19797	2	1.04	0.80	0.0303
	A-kinase anchor protein 13	Q12802	27	368204	2	0.93	0.80	0.0322
	Lysosomal Pro-X carboxypeptidase	P42785	64	63479	4	0.96	0.79	0.0207
	UDP-N-acetylhexosamine pyrophosphorylase	Q16222	143	70614	37	1.09	0.76	0.0260
	Protein CYR61	O00622	73	52872	6	1.08	0.74	0.0059
	Uncharacterized protein C1orf167	Q5SNV9	22	178763	3	0.97	0.69	0.0018

*This is a partial list of protein candidates identifed by iTRAQ to be disregulated in HPAH (p-value < 0.05). HPAH vs. H. H indicates healthy and HPAH, hereditary pulmonary arterial hypertension. Accession, Uniprot identifier; MS Score, mass spectrometry score indicating the significance of protein identification from peptide mass fingerprint according to MASCOT software; Nominal Mass, Mr, theoretical molecular weight of the matching protein; Significant Peptide Matches, number of statistically significant peptide matches matching to the protein; H/H and HPAH/H: average of the fold changes for healthy vs healthy channels comparisons, and HPAH vs healthy, respectively (see Methods and supplementary table 1 for all fold values); p-value: p-value associated to HPAH/H fold changes (See Methods).

Suppl.Table 4. Full list of the differently regulated proteins in HPAH identified by iTRAQ

Protein Identity	Downregulation in HPAH		Upregulation in HPAH	
	"healthy/healthy p-value"	"HPAH/healthy pvalue"	"healthy/healthy pvalue"	"HPAH/healthy pvalue"
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1 mitochondrial	0.3516	0.1593	0.4717	0.9742
1 4-alpha-glucan-branching enzyme	0.8851	0.6627	0.3088	0.6459
10 kDa heat shock protein mitochondrial	0.5353	0.9844	0.6763	0.0349
116 kDa U5 small nuclear ribonucleoprotein component	0.9336	0.8092	0.1673	0.4297
14-3-3 protein beta/alpha	0.1484	0.6483	0.9665	0.7182
14-3-3 protein epsilon	0.1729	0.6697	0.9536	0.6777
14-3-3 protein gamma	0.1155	0.5555	0.9763	0.7909
14-3-3 protein theta	0.1024	0.5773	0.9791	0.7759
14-3-3 protein zeta/delta	0.1757	0.6670	0.9539	0.6895
182 kDa tankyrase-1-binding protein	0.8820	0.9677	0.1633	0.0917
2' 3'-cyclic-nucleotide 3'-phosphodiesterase	0.2040	0.4710	0.8958	0.8251
2' 5'-phosphodiesterase 12	0.3212	0.7980	0.8672	0.2060
26S protease regulatory subunit 10B	0.4035	0.6607	0.8147	0.6811
26S protease regulatory subunit 4	0.6607	0.9473	0.5801	0.1976
26S protease regulatory subunit 6A	0.1799	0.2918	0.9401	0.9210
26S protease regulatory subunit 6B	0.2464	0.6529	0.8962	0.7262
26S protease regulatory subunit 7	0.2537	0.1541	0.9150	0.9711
26S protease regulatory subunit 8	0.3749	0.5510	0.8490	0.7917
26S proteasome non-ATPase regulatory subunit 1	0.7664	0.8167	0.4729	0.5144
26S proteasome non-ATPase regulatory subunit 11	0.7593	0.7991	0.4293	0.4225
26S proteasome non-ATPase regulatory subunit 12	0.5230	0.5425	0.5207	0.7807
26S proteasome non-ATPase regulatory subunit 2	0.8935	0.7244	0.3219	0.6599
26S proteasome non-ATPase regulatory subunit 4	0.6155	0.9869	0.5860	0.1062
26S proteasome non-ATPase regulatory subunit 5	0.1296	0.3780	0.9445	0.7520
26S proteasome non-ATPase regulatory subunit 6	0.5461	0.8793	0.6279	0.3014
26S proteasome non-ATPase regulatory subunit 7	0.9367	0.9600	0.1970	0.1081
26S proteasome non-ATPase regulatory subunit 9	0.4733	0.7597	0.8036	0.6292
28S ribosomal protein S35 mitochondrial	0.0001	0.0000	1.0000	1.0000
39S ribosomal protein L1 mitochondrial	0.2406	0.6216	0.9124	0.3934
39S ribosomal protein L14 mitochondrial	0.9434	0.9422	0.1674	0.1354
39S ribosomal protein L38 mitochondrial	0.7047	0.9677	0.2325	0.0849
39S ribosomal protein L4 mitochondrial	0.7720	0.5408	0.4310	0.7116
39S ribosomal protein L43 mitochondrial	0.2060	0.5249	0.2254	0.4421
3-hydroxyacyl-CoA dehydrogenase type-2	0.0140	0.0193	0.9925	0.9979
3-ketoacyl-CoA thiolase mitochondrial	0.6381	0.0702	0.5564	0.9935
3-ketoacyl-CoA thiolase peroxisomal	0.6099	0.5530	0.5337	0.7826
3-mercaptopyruvate sulfurtransferase	0.8309	0.6470	0.4309	0.6591
40S ribosomal protein S10	0.1286	0.0258	0.9511	0.9889
40S ribosomal protein S12	0.1207	0.4787	0.9132	0.6994
40S ribosomal protein S13	1.0000	0.4704	0.0004	0.0296
40S ribosomal protein S14	0.9981	0.7745	0.0140	0.1668
40S ribosomal protein S15a	0.9997	0.5121	0.0027	0.1084
40S ribosomal protein S16	0.8537	0.2051	0.3211	0.8633
40S ribosomal protein S17-like	0.8339	0.3042	0.3175	0.6631
40S ribosomal protein S18	0.9981	0.6794	0.0144	0.4202
40S ribosomal protein S19	0.9998	0.7896	0.0027	0.1228
40S ribosomal protein S2	0.9359	0.3258	0.2056	0.5139
40S ribosomal protein S20	0.6589	0.2416	0.5445	0.7875
40S ribosomal protein S21	0.3027	0.7444	0.8726	0.4600

40S ribosomal protein S23	0.9842	0.5648	0.0441	0.2511
40S ribosomal protein S24	0.9553	0.9078	0.0998	0.2975
40S ribosomal protein S25	0.9999	0.9974	0.0014	0.0242
40S ribosomal protein S27	0.9794	0.6473	0.0929	0.3104
40S ribosomal protein S27-like	0.9842	0.6039	0.0792	0.3380
40S ribosomal protein S28	0.9692	0.8164	0.1058	0.4653
40S ribosomal protein S3	0.3729	0.3038	0.6945	0.8847
40S ribosomal protein S30	0.9998	0.5783	0.0012	0.0200
40S ribosomal protein S3a	0.9994	0.7044	0.0043	0.0913
40S ribosomal protein S4 X isoform	0.9998	0.6529	0.0020	0.0318
40S ribosomal protein S5	0.9745	0.3835	0.0646	0.6799
40S ribosomal protein S6	0.9998	0.6432	0.0012	0.0434
40S ribosomal protein S7	0.9882	0.5132	0.0689	0.4966
40S ribosomal protein S8	0.9991	0.8192	0.0088	0.1808
40S ribosomal protein S9	0.9999	0.5547	0.0010	0.0623
40S ribosomal protein SA	0.8223	0.7405	0.3442	0.5584
60 kDa heat shock protein mitochondrial	0.5981	0.9115	0.6178	0.1371
60S acidic ribosomal protein P0	0.9184	0.2853	0.1402	0.6164
60S acidic ribosomal protein P1	0.7890	0.5560	0.3836	0.5090
60S acidic ribosomal protein P2	0.9225	0.7279	0.2443	0.4364
60S ribosomal protein L10	0.9963	0.3710	0.0253	0.5201
60S ribosomal protein L10a	0.9996	0.8819	0.0044	0.1847
60S ribosomal protein L11	0.8425	0.3369	0.3994	0.8718
60S ribosomal protein L12	0.9942	0.1991	0.0293	0.5452
60S ribosomal protein L13	0.9999	0.4156	0.0008	0.4010
60S ribosomal protein L13a	0.9971	0.6815	0.0225	0.4100
60S ribosomal protein L14	0.9708	0.1613	0.0253	0.2496
60S ribosomal protein L15	0.9999	0.5984	0.0017	0.2839
60S ribosomal protein L17	0.9285	0.5014	0.0383	0.4542
60S ribosomal protein L18	0.9994	0.4849	0.0050	0.3202
60S ribosomal protein L18a	0.9482	0.7553	0.1892	0.4457
60S ribosomal protein L19	0.9997	0.9628	0.0017	0.0536
60S ribosomal protein L21	0.9940	0.4077	0.0286	0.3863
60S ribosomal protein L22	0.9957	0.6324	0.0295	0.2341
60S ribosomal protein L22-like 1	0.9822	0.7962	0.0418	0.0961
60S ribosomal protein L23	0.9212	0.5175	0.2448	0.4713
60S ribosomal protein L23a	0.9904	0.8628	0.0366	0.1335
60S ribosomal protein L24	0.9970	0.6672	0.0120	0.1448
60S ribosomal protein L26	0.9999	0.9002	0.0010	0.0614
60S ribosomal protein L27	0.9999	0.5319	0.0009	0.1799
60S ribosomal protein L27a	0.9999	0.9251	0.0020	0.1209
60S ribosomal protein L28	1.0000	0.5144	0.0005	0.0827
60S ribosomal protein L29	0.9966	0.8854	0.0062	0.0628
60S ribosomal protein L3	1.0000	0.7507	0.0004	0.0432
60S ribosomal protein L31	0.9999	0.7897	0.0014	0.0479
60S ribosomal protein L32	0.9657	0.5612	0.0400	0.3300
60S ribosomal protein L34	1.0000	0.9918	0.0002	0.0020
60S ribosomal protein L35	0.9999	0.8041	0.0005	0.0222
60S ribosomal protein L36	0.9943	0.5992	0.0074	0.0616
60S ribosomal protein L38	0.3996	0.6266	0.8157	0.6303
60S ribosomal protein L4	0.9985	0.6908	0.0085	0.1468
60S ribosomal protein L5	0.5735	0.5385	0.7142	0.6435
60S ribosomal protein L6	0.9976	0.4710	0.0052	0.1544
60S ribosomal protein L7	1.0000	0.6124	0.0005	0.1210
60S ribosomal protein L7a	0.9994	0.6906	0.0026	0.1449
60S ribosomal protein L8	1.0000	0.6366	0.0003	0.0449

60S ribosomal protein L9	0.9991	0.3097	0.0086	0.1989
6-phosphofructokinase liver type	0.3548	0.8255	0.3651	0.4658
6-phosphofructokinase type C	0.3163	0.6236	0.8325	0.6232
6-phosphogluconate dehydrogenase decarboxylating	0.2586	0.8678	0.7442	0.3438
6-phosphogluconolactonase	0.2277	0.0046	0.8889	0.9997
78 kDa glucose-regulated protein	0.6933	0.8426	0.5967	0.3443
Acetolactate synthase-like protein	0.2652	0.3405	0.9139	0.9107
Acetyl-CoA acetyltransferase cytosolic	0.0149	0.0217	0.9977	0.9966
Acetyl-CoA acetyltransferase mitochondrial	0.5222	0.2078	0.6647	0.9446
Acidic leucine-rich nuclear phosphoprotein 32 family member A	0.0667	0.5539	0.8317	0.6217
Aconitate hydratase mitochondrial	0.7767	0.9641	0.4659	0.1806
Actin aortic smooth muscle	0.5350	0.8893	0.7435	0.3260
Actin cytoplasmic 1	0.5236	0.8880	0.7541	0.3316
Actin-binding LIM protein 1	0.9124	0.8233	0.2067	0.1821
Actin-related protein 2	0.7424	0.8679	0.4933	0.4372
Actin-related protein 2/3 complex subunit 2	0.5032	0.8669	0.5284	0.3541
Actin-related protein 2/3 complex subunit 3	0.6652	0.7114	0.5792	0.5885
Actin-related protein 2/3 complex subunit 4	0.6122	0.9642	0.6836	0.1832
Actin-related protein 2/3 complex subunit 5	0.3627	0.2761	0.7004	0.8484
Actin-related protein 2/3 complex subunit 5-like protein	0.6488	0.9272	0.3271	0.2816
Actin-related protein 3	0.7746	0.6821	0.4010	0.7111
Activated RNA polymerase II transcriptional coactivator p15	0.6483	0.6553	0.4646	0.5732
Activator of 90 kDa heat shock protein ATPase homolog 1	0.9949	0.9927	0.0353	0.0264
Acyl-CoA-binding domain-containing protein 6	0.1509	0.0526	0.8280	0.9364
Acyl-CoA-binding protein	0.2736	0.5132	0.8835	0.4095
Acyl-coenzyme A thioesterase 9 mitochondrial	0.1794	0.2288	0.9324	0.9116
Acyl-protein thioesterase 2	0.6103	0.7897	0.5237	0.5132
Adapter molecule crk	0.9773	0.9397	0.0807	0.2497
Adenine phosphoribosyltransferase	0.4828	0.7765	0.7996	0.3925
Adenosylhomocysteinase	0.2100	0.8829	0.9145	0.1362
Adenylate kinase 2 mitochondrial	0.4572	0.4724	0.7627	0.8060
Adenylate kinase isoenzyme 1	0.3717	0.2903	0.8335	0.9323
Adenylosuccinate synthetase isozyme 2	0.9491	0.9679	0.1301	0.0757
Adenylyl cyclase-associated protein 1	0.2956	0.9269	0.8957	0.2925
ADP/ATP translocase 2	0.4904	0.9037	0.5945	0.2165
ADP/ATP translocase 3	0.6333	0.9105	0.5358	0.2220
ADP-ribosylation factor 3	0.9798	0.9744	0.0919	0.1407
ADP-ribosylation factor-like protein 3	0.0392	0.3760	0.9932	0.8988
ADP-sugar pyrophosphatase	0.4934	0.1503	0.6344	0.9801
AFG3-like protein 2	0.9572	0.9905	0.1265	0.0772
Aflatoxin B1 aldehyde reductase member 2	0.1625	0.1246	0.8961	0.8487
A-kinase anchor protein 12	0.0188	0.0921	0.9966	0.9782
A-kinase anchor protein 13	0.4477	0.0322	0.8019	0.9966
A-kinase anchor protein 17A	0.9592	0.2232	0.1232	0.9060
A-kinase anchor protein 2	0.8429	0.7995	0.3948	0.3793
Alanyl-tRNA synthetase cytoplasmic	0.1532	0.6579	0.9452	0.3252
Alcohol dehydrogenase [NADP+]	0.5369	0.4041	0.3413	0.6438
Aldehyde dehydrogenase mitochondrial	0.1660	0.0281	0.9342	0.9386
Alpha-1 3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	0.1116	0.0233	0.9759	0.9978
Alpha-2-macroglobulin receptor-associated protein	0.8371	0.2570	0.1413	0.9385
Alpha-actinin-1	0.2681	0.3895	0.9201	0.8500
Alpha-actinin-4	0.3289	0.7760	0.8805	0.5454
Alpha-centractin	0.2551	0.5232	0.9224	0.8024
Alpha-endosulfine	0.8939	0.9531	0.2820	0.2417
Alpha-enolase	0.7776	0.9870	0.5047	0.0880
Alpha-synuclein	0.9669	0.9973	0.0310	0.0186

Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	0.4495	0.9656	0.7996	0.1979
Aminopeptidase B	0.9020	0.9658	0.1836	0.1902
Aminopeptidase N	0.8088	0.7648	0.0089	0.1706
Amyloid-like protein 2	0.9058	0.4043	0.1689	0.7582
Anamorsin	0.2988	0.1307	0.6417	0.9702
Ankyrin repeat domain-containing protein 33	0.2386	0.1382	0.9177	0.9799
Annexin A1	0.5165	0.8151	0.7508	0.5094
Annexin A2	0.7928	0.8717	0.2999	0.3567
Annexin A3	0.0932	0.1703	0.8275	0.7119
Annexin A4	0.4118	0.7723	0.6915	0.3627
Annexin A5	0.3355	0.6289	0.3530	0.6399
Annexin A6	0.0349	0.2376	0.8835	0.7562
Annexin A7	0.7341	0.3485	0.5036	0.9020
AP-1 complex subunit beta-1	0.0740	0.7148	0.9868	0.2221
AP-2 complex subunit alpha-1	0.6450	0.4699	0.6050	0.8571
AP-2 complex subunit sigma	0.3194	0.1808	0.8323	0.9636
AP-3 complex subunit delta-1	0.7770	0.2889	0.1458	0.9137
Apoptosis regulator BAX	0.3784	0.2738	0.6943	0.9420
Apoptotic chromatin condensation inducer in the nucleus	0.0135	0.0449	0.9938	0.9205
Arginyl-tRNA synthetase cytoplasmic	0.8206	0.6829	0.3597	0.6417
Asparaginyl-tRNA synthetase cytoplasmic	0.4010	0.6968	0.8296	0.6546
Aspartate aminotransferase mitochondrial	0.7516	0.8495	0.3932	0.4679
Aspartyl/asparaginyl beta-hydroxylase	0.9749	0.1479	0.1193	0.8539
Aspartyl-tRNA synthetase cytoplasmic	0.6960	0.9072	0.4816	0.3713
Astrocytic phosphoprotein PEA-15	0.4947	0.2837	0.7155	0.8782
Ataxin-2	0.7758	0.8331	0.4115	0.4839
Ataxin-2-like protein	0.3206	0.5157	0.8503	0.8252
ATP synthase subunit alpha mitochondrial	0.8567	0.4038	0.2478	0.6703
ATP synthase subunit b mitochondrial	0.7605	0.4191	0.3657	0.7950
ATP synthase subunit beta mitochondrial	0.6602	0.5207	0.5305	0.6856
ATP synthase subunit delta mitochondrial	0.9269	0.4764	0.1572	0.2817
ATP synthase subunit gamma mitochondrial	0.5792	0.2366	0.6672	0.8703
ATP synthase subunit O mitochondrial	0.6101	0.2129	0.6084	0.7930
ATPase ASNA1	0.5356	0.9440	0.7600	0.1994
ATPase family AAA domain-containing protein 3A	0.4945	0.1547	0.6745	0.7473
ATP-binding cassette sub-family A member 1	0.7077	0.1426	0.1116	0.2609
ATP-binding cassette sub-family E member 1	0.6152	0.9690	0.5750	0.1047
ATP-citrate synthase	0.4911	0.8845	0.7910	0.4053
ATP-dependent DNA helicase Q4	0.0070	0.0019	0.9789	0.9923
ATP-dependent RNA helicase DDX1	0.5611	0.1855	0.5718	0.9238
ATP-dependent RNA helicase DDX3X	0.9892	0.8033	0.0558	0.3479
ATP-dependent zinc metalloprotease YME1L1	0.1378	0.5535	0.9682	0.6110
BAG family molecular chaperone regulator 3	0.9009	0.5053	0.0669	0.8123
Band 4.1-like protein 2	0.0919	0.6191	0.7395	0.2190
Band 4.1-like protein 3	0.2300	0.0230	0.1977	0.9968
Basement membrane-specific heparan sulfate proteoglycan core protein	0.2444	0.0440	0.8481	0.9960
Basic leucine zipper and W2 domain-containing protein 1	0.3876	0.5776	0.8271	0.5245
Basic leucine zipper and W2 domain-containing protein 2	0.0396	0.2607	0.9799	0.8795
B-cell receptor-associated protein 31	0.6725	0.8652	0.5014	0.3494
Bcl-2-associated transcription factor 1	0.8480	0.8324	0.0787	0.3833
BET1 homolog	0.0395	0.2226	0.9820	0.9133
Beta-2-microglobulin	0.0249	0.0303	0.9928	0.9938
Beta-2-syntrophin	0.3791	0.1221	0.8385	0.9660
Beta-catenin-like protein 1	0.0462	0.0292	0.9886	0.9967
Beta-enolase	0.9293	0.9913	0.2340	0.0720
BH3-interacting domain death agonist	0.0580	0.0227	0.4460	0.9968

Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	0.1326	0.0035	0.9073	0.9999
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	0.9915	0.9651	0.0149	0.0581
Bifunctional aminoacyl-tRNA synthetase	0.7533	0.9183	0.3970	0.2965
Bifunctional purine biosynthesis protein PURH	0.5855	0.9315	0.4007	0.2055
Biglycan	0.0038	0.0017	0.9983	0.9088
Biliverdin reductase A	0.3002	0.3360	0.8551	0.8975
BolA-like protein 2	0.2598	0.0989	0.1026	0.9524
Breakpoint cluster region protein	0.9075	0.8529	0.2373	0.3508
BTB/POZ domain-containing protein KCTD12	0.9864	0.8259	0.0358	0.1301
C-1-tetrahydrofolate synthase cytoplasmic	0.4365	0.6661	0.7324	0.4425
Cadherin-5	0.1598	0.4405	0.9485	0.8112
Calcium-binding mitochondrial carrier protein SCaMC-1	0.2901	0.2579	0.8981	0.9331
Calcium-binding protein p22	0.0905	0.5482	0.9569	0.8002
Calcyclin-binding protein	0.5865	0.7474	0.4407	0.5601
Caldesmon	0.0518	0.0233	0.9871	0.9927
Calmodulin	0.2803	0.8754	0.9095	0.3916
Calnexin	0.5954	0.7532	0.6340	0.5726
Calpain small subunit 1	0.7516	0.8917	0.3425	0.3182
Calpain-2 catalytic subunit	0.9400	0.9743	0.0600	0.1348
Calponin-2	0.1203	0.3465	0.9715	0.9165
Calponin-3	0.2354	0.6239	0.9242	0.7127
Calreticulin	0.1959	0.2971	0.9502	0.7960
Calumenin	0.2818	0.1523	0.7327	0.9793
cAMP-dependent protein kinase type I-alpha regulatory subunit	0.9188	0.9429	0.1294	0.2695
cAMP-dependent protein kinase type II-alpha regulatory subunit	0.9595	0.9498	0.1246	0.2533
CAP-Gly domain-containing linker protein 2	0.0532	NA	0.8349	NA
Carbonyl reductase [NADPH] 1	0.8637	0.9852	0.3200	0.1107
Carboxypeptidase A6	0.0707	0.0049	0.9840	0.9998
Carboxypeptidase D	0.3314	0.4479	0.8864	0.7517
Casein kinase II subunit alpha	0.3244	0.5991	0.7461	0.6395
Casein kinase II subunit beta	0.4692	0.2214	0.6284	0.8236
Caspase-4	0.4803	0.5367	0.2958	0.5033
Catalase	0.9597	0.9682	0.1435	0.0863
Catechol O-methyltransferase	0.3429	0.2918	0.8569	0.9392
Catenin alpha-1	0.3649	0.5695	0.8605	0.7845
Catenin alpha-2	0.7542	0.6573	0.5156	0.7288
Catenin beta-1	0.2466	0.4273	0.8609	0.8802
Catenin delta-1	0.6465	0.5558	0.5677	0.7850
Cathepsin B	0.7619	0.5793	0.3665	0.6584
Cathepsin D	0.1635	0.0782	0.9235	0.9900
Caveolin-1	0.8986	0.9988	0.1716	0.0069
CD166 antigen	0.2524	0.5460	0.6597	0.5429
CD44 antigen	0.8708	0.1955	0.1376	0.2275
CD59 glycoprotein	0.8993	0.9964	0.0400	0.0307
CD99 antigen	0.0065	0.0222	0.9979	0.9632
Cdc42-interacting protein 4	0.3090	0.7719	0.7329	0.5398
Cell division control protein 42 homolog	0.2273	0.6682	0.9274	0.7210
Cell surface glycoprotein MUC18	0.2619	0.5686	0.9024	0.6068
Cellular nucleic acid-binding protein	0.3756	0.4141	0.7555	0.5321
Charged multivesicular body protein 1b	0.5487	0.6459	0.6238	0.6961
Charged multivesicular body protein 3	0.0156	0.0022	0.9969	0.9999
Charged multivesicular body protein 4b	0.6131	0.8915	0.5205	0.3895
Chloride intracellular channel protein 1	0.5287	0.9839	0.6492	0.1277
Chloride intracellular channel protein 4	0.2745	0.9104	0.9120	0.3672
Choline transporter-like protein 2	0.6086	0.7637	0.4701	0.2721
Chromobox protein homolog 3	0.8319	0.4162	0.2441	0.8272

Citrate synthase mitochondrial	0.1797	0.5620	0.9558	0.8009
C-Jun-amino-terminal kinase-interacting protein 4	0.9608	0.7332	0.0517	0.5173
Clathrin heavy chain 1	0.6961	0.8658	0.6108	0.4139
Clathrin interactor 1	0.9738	0.9199	0.1210	0.0988
Clathrin light chain A	0.6495	0.8266	0.5805	0.5056
Cleavage and polyadenylation specificity factor subunit 5	0.5213	0.2257	0.2754	0.6749
Coatomer subunit alpha	0.0597	0.6790	0.9573	0.5701
Coatomer subunit beta'	0.1566	0.6609	0.9615	0.5409
Coatomer subunit delta	0.0613	0.0555	0.9898	0.9878
Coatomer subunit gamma	0.5617	0.2243	0.1707	0.9386
Cofilin-1	0.1270	0.7294	0.9570	0.6105
Cofilin-2	0.1293	0.6260	0.9605	0.7389
Coiled-coil domain-containing protein 124	0.8593	0.7666	0.1001	0.5092
Coiled-coil domain-containing protein 47	0.9936	0.9129	0.0202	0.3213
Coiled-coil domain-containing protein 50	0.0553	0.5499	0.9907	0.7569
Coiled-coil domain-containing protein 51	0.5636	0.1081	0.2657	0.9369
Coiled-coil domain-containing protein 93	0.8537	0.4049	0.2451	0.7207
Cold shock domain-containing protein E1	0.2163	0.0546	0.9402	0.9939
Collagen alpha-1(VI) chain	0.0805	0.0387	0.7025	0.8519
Constitutive coactivator of PPAR-gamma-like protein 1	0.9810	0.9706	0.0537	0.1107
COP9 signalosome complex subunit 8	0.6946	0.3155	0.6079	0.9285
Copine-1	0.9909	0.9938	0.0086	0.0586
Copine-2	0.0266	0.0000	0.9907	1.0000
Coronin-1C	0.4718	0.9082	0.3638	0.2418
CTP synthase 1	0.7712	0.3258	0.3016	0.9277
Cullin-4B	0.3734	0.7032	0.8410	0.6696
Cullin-associated NEDD8-dissociated protein 1	0.3704	0.6387	0.8418	0.5424
Cyclin-dependent kinase 1	0.3573	0.3463	0.7413	0.8358
Cyclin-dependent kinase 17	0.3756	0.3267	0.7652	0.8549
Cystatin-B	0.0030	0.0395	0.9997	0.9255
Cysteine and glycine-rich protein 1	0.0673	0.1193	0.9752	0.9381
Cysteine-rich protein 2	0.3870	0.3430	0.8512	0.8656
Cytochrome b-c1 complex subunit 1 mitochondrial	0.4329	0.8810	0.8308	0.3968
Cytochrome b-c1 complex subunit 2 mitochondrial	0.6397	0.3853	0.1911	0.8988
Cytochrome b-c1 complex subunit 6 mitochondrial	0.7985	0.8170	0.1925	0.4613
Cytochrome b-c1 complex subunit 7	0.9639	0.5673	0.1408	0.6697
Cytochrome c	0.0190	0.1569	0.9947	0.9654
Cytochrome c oxidase subunit 2	0.0249	0.0204	0.9844	0.9986
Cytochrome c oxidase subunit 4 isoform 1 mitochondrial	0.6530	0.9579	0.5376	0.2342
Cytochrome c oxidase subunit 5A mitochondrial	0.8128	0.8869	0.2934	0.4127
Cytochrome c oxidase subunit 5B mitochondrial	0.6183	0.9731	0.0644	0.1659
Cytochrome c oxidase subunit 6C	0.7698	0.5744	0.3733	0.6113
Cytoplasmic aconitate hydratase	0.3104	0.5980	0.8991	0.6144
Cytoplasmic dynein 1 heavy chain 1	0.5567	0.6432	0.6733	0.7182
Cytoplasmic dynein 1 intermediate chain 2	0.7747	0.5099	0.4228	0.7939
Cytoplasmic dynein 1 light intermediate chain 1	0.7016	0.8168	0.5996	0.5208
Cytoplasmic dynein 1 light intermediate chain 2	0.6466	0.2093	0.6586	0.9284
Cytoplasmic FMR1-interacting protein 1	0.9049	0.9805	0.2743	0.1189
Cytoskeleton-associated protein 4	0.4593	0.0837	0.5194	0.8504
Cytosol aminopeptidase	0.0946	0.4343	0.9532	0.7593
Cytosolic acyl coenzyme A thioester hydrolase	0.0416	0.1202	0.9929	0.8912
Cytosolic non-specific dipeptidase	0.4588	0.6433	0.5309	0.6037
DAZ-associated protein 1	0.9436	0.6210	0.1826	0.7045
dCTP pyrophosphatase 1	0.1515	0.8104	0.7546	0.1454
D-dopachrome decarboxylase	0.2727	0.2389	0.7891	0.8991
Death-associated protein kinase 1	0.0572	0.1086	0.9898	0.6921

Dedicator of cytokinesis protein 3	0.8609	0.7850	0.1338	0.4486
Dedicator of cytokinesis protein 4	0.1026	0.3682	0.9797	0.8374
Delta-1-pyrroline-5-carboxylate synthase	0.5496	0.3686	0.4967	0.8994
DENN domain-containing protein 4B	0.0013	0.0002	0.9999	1.0000
Deoxyribonucleoside 5'-monophosphate N-glycosidase	0.7541	0.0303	0.5019	0.9952
Deoxyuridine 5'-triphosphate nucleotidohydrolase mitochondrial	0.0912	0.5333	0.8645	0.3821
Destrin	0.1056	0.5211	0.9638	0.7954
Dihydrolipoyl dehydrogenase mitochondrial	0.7926	0.9457	0.3623	0.2742
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex mitochondrial	0.2635	0.3462	0.8506	0.8902
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex mitochondrial	0.7299	0.4839	0.5068	0.7873
Dihydropyrimidinase-related protein 2	0.2339	0.0120	0.8016	0.9639
Dihydropyrimidinase-related protein 3	0.2478	0.1470	0.8907	0.9595
Dipeptidyl peptidase 2	0.4436	0.1306	0.4985	0.9575
Disabled homolog 2	0.4566	0.0798	0.7286	0.9888
Disintegrin and metalloproteinase domain-containing protein 17	0.3145	0.2457	0.8559	0.9434
DNA fragmentation factor subunit alpha	0.9252	0.9873	0.2454	0.1006
DNA repair protein XRCC1	0.4068	0.0812	0.7857	0.9805
DNA replication licensing factor MCM2	0.9785	0.9926	0.0530	0.0120
DNA replication licensing factor MCM3	0.9365	0.9942	0.0626	0.0263
DNA replication licensing factor MCM7	0.9832	0.9950	0.0627	0.0545
DNA-(apurinic or apyrimidinic site) lyase	0.8136	0.7366	0.4076	0.5277
DNA-binding protein A	0.8907	0.9710	0.1728	0.1644
DNA-dependent protein kinase catalytic subunit	0.6716	0.8529	0.5613	0.4289
DNA-directed RNA polymerase II subunit RPB2	0.9557	0.9814	0.0248	0.0423
DNA-directed RNA polymerases I II and III subunit RPABC5	0.9062	0.8336	0.1075	0.4718
DnaJ homolog subfamily A member 1	0.4185	0.9967	0.6875	0.0229
DnaJ homolog subfamily A member 2	0.4239	0.5686	0.7541	0.5591
DnaJ homolog subfamily B member 1	0.9424	0.5272	0.2014	0.8245
DnaJ homolog subfamily B member 4	0.9270	0.9498	0.1653	0.1812
DnaJ homolog subfamily C member 11	0.9987	0.9984	0.0100	0.0196
DnaJ homolog subfamily C member 2	0.8903	0.6387	0.1646	0.7502
DnaJ homolog subfamily C member 3	0.8269	0.6276	0.1447	0.5472
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	0.5205	0.6746	0.5929	0.6511
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	0.4034	0.5516	0.8238	0.8076
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	0.7593	0.6077	0.0917	0.2111
Double-stranded RNA-specific adenosine deaminase	0.1733	0.0692	0.8647	0.7302
Drebrin	0.9736	0.9934	0.0938	0.0678
Drebrin-like protein	0.3090	0.1126	0.6809	0.9823
Dual specificity mitogen-activated protein kinase kinase 1	0.4563	0.8053	0.7353	0.5302
Dual specificity protein phosphatase 3	0.6891	0.3764	0.4440	0.8455
Dynactin subunit 1	0.2927	0.8899	0.9070	0.3107
Dynactin subunit 2	0.0150	0.0049	0.9978	0.9998
Dynactin subunit 6	0.3160	0.8142	0.8354	0.4729
Dynamin-1-like protein	0.7430	0.9662	0.5007	0.1857
Dynamin-2	0.4902	0.6733	0.5955	0.5659
Dynein heavy chain 17 axonemal	0.6880	0.7101	0.5329	0.4975
Dysferlin	0.8391	0.9627	0.3588	0.2125
Dystroglycan	0.9570	0.3711	0.1722	0.8901
E3 ubiquitin-protein ligase CHIP	0.0903	0.0026	0.9469	0.9998
E3 ubiquitin-protein ligase HUWE1	0.9894	0.9475	0.0536	0.2560
Early endosome antigen 1	0.2642	0.3643	0.6765	0.8450
EF-hand domain-containing protein D2	0.0403	0.1332	0.9431	0.9818
EGF-containing fibulin-like extracellular matrix protein 1	0.2219	0.0257	0.6534	0.7105
EH domain-containing protein 1	0.9638	0.9958	0.1435	0.0405
EH domain-containing protein 2	0.7269	0.9081	0.5305	0.3315
EH domain-containing protein 3	0.8525	0.9784	0.3672	0.1236

EH domain-containing protein 4	0.6306	0.9993	0.5081	0.0139
Electron transfer flavoprotein subunit alpha mitochondrial	0.0290	0.5411	0.9344	0.8024
Electron transfer flavoprotein subunit beta	0.8467	0.7457	0.2076	0.4932
ELKS/Rab6-interacting/CAST family member 1	0.6457	0.3839	0.4916	0.8874
Elongation factor 1-beta	0.2931	0.7912	0.8771	0.5506
Elongation factor 1-delta	0.4476	0.4726	0.7963	0.8407
Elongation factor 1-gamma	0.6894	0.7381	0.5842	0.4304
Elongation factor 2	0.5218	0.7198	0.7661	0.5789
Elongation factor Tu mitochondrial	0.7144	0.7745	0.5315	0.4318
Endoglin	0.0074	0.0210	0.9967	0.9767
Endophilin-A2	0.4959	0.4287	0.5133	0.0321
Endophilin-B1	0.5574	0.6923	0.6443	0.5621
Endoplasmic reticulum resident protein 29	0.1751	0.6996	0.9494	0.3805
Endoplasmic reticulum resident protein 44	0.9065	0.8449	0.2822	0.4148
Endoplasmin	0.9306	0.8702	0.2233	0.2688
Endothelial differentiation-related factor 1	0.2366	0.7443	0.9288	0.3638
Endothelin-converting enzyme 1	0.6509	0.7870	0.5316	0.3509
Enhancer of rudimentary homolog	0.4999	0.8321	0.7070	0.3357
Enoyl-CoA hydratase mitochondrial	0.3273	0.0968	0.4838	0.9897
Epididymal secretory protein E1	0.0005	0.1034	0.9998	0.7991
ERO1-like protein alpha	0.2710	0.5183	0.9147	0.5842
Erythrocyte band 7 integral membrane protein	0.6198	0.9347	0.4544	0.2198
ES1 protein homolog mitochondrial	0.8288	0.8604	0.3839	0.4170
Ester hydrolase C11orf54	0.5784	0.1397	0.6987	0.8534
Estradiol 17-beta-dehydrogenase 12	0.9579	0.4679	0.0978	0.4582
Eukaryotic initiation factor 4A-I	0.7943	0.9097	0.4398	0.2057
Eukaryotic initiation factor 4A-II	0.8379	0.9238	0.3926	0.1651
Eukaryotic initiation factor 4A-III	0.3165	0.7213	0.8828	0.5675
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	0.3399	0.7483	0.8860	0.2927
Eukaryotic translation initiation factor 1A X-chromosomal	0.8772	0.9904	0.2129	0.0494
Eukaryotic translation initiation factor 2 subunit 1	0.9595	0.8585	0.1319	0.3465
Eukaryotic translation initiation factor 3 subunit A	0.7479	0.5537	0.5437	0.7107
Eukaryotic translation initiation factor 3 subunit B	0.8033	0.6919	0.2531	0.5388
Eukaryotic translation initiation factor 3 subunit C	0.5010	0.5129	0.6414	0.7447
Eukaryotic translation initiation factor 3 subunit F	0.8255	0.6471	0.3666	0.6498
Eukaryotic translation initiation factor 3 subunit I	0.4191	0.0948	0.8293	0.9809
Eukaryotic translation initiation factor 3 subunit J	0.4730	0.7592	0.5593	0.5196
Eukaryotic translation initiation factor 4 gamma 1	0.3150	0.5307	0.7605	0.7833
Eukaryotic translation initiation factor 4B	0.8631	0.9138	0.2462	0.1881
Eukaryotic translation initiation factor 4H	0.9364	0.9590	0.2137	0.1680
Eukaryotic translation initiation factor 5	0.1879	0.3356	0.9385	0.7340
Eukaryotic translation initiation factor 5A-1	0.2403	0.9036	0.9071	0.1855
Eukaryotic translation initiation factor 5B	0.6782	0.6459	0.4799	0.5991
Exostosin-like 2	0.9512	0.9465	0.1525	0.2131
Exportin-1	0.5434	0.5497	0.3601	0.6586
Exportin-2	0.2992	0.7841	0.8625	0.2679
Exportin-4	0.0253	0.3298	0.9561	0.8261
Extended synaptotagmin-1	0.2449	0.4160	0.8956	0.8205
Ezrin	0.3762	0.6383	0.8526	0.5995
F-actin-capping protein subunit alpha-1	0.4675	0.5008	0.7384	0.8209
F-actin-capping protein subunit beta	0.1598	0.8082	0.9603	0.5361
Far upstream element-binding protein 1	0.6963	0.6906	0.4639	0.5359
Far upstream element-binding protein 2	0.7264	0.7874	0.4141	0.4317
Far upstream element-binding protein 3	0.6948	0.7256	0.5784	0.5498
Farnesyl pyrophosphate synthase	0.1194	0.3010	0.9577	0.8617
Fascin	0.3477	0.7450	0.8621	0.5552

Fatty acid desaturase 3	0.1366	0.0340	0.9483	0.9947
Fatty acid synthase	0.8422	0.9270	0.3538	0.3028
Fatty acid-binding protein epidermal	0.5857	0.9410	0.0052	0.0441
Ferritin heavy chain	0.0002	0.0349	1.0000	0.9870
FH1/FH2 domain-containing protein 1	0.3921	0.7994	0.2294	0.4224
Fibrillin-1	0.8553	0.5090	0.2614	0.6664
Fibrocystin	0.9619	0.9567	0.1014	0.2141
Fibronectin	0.8421	0.1522	0.3854	0.5691
Filamin-A	0.1724	0.3471	0.9487	0.9093
Filamin-B	0.1621	0.2913	0.9362	0.9363
Filamin-binding LIM protein 1	0.9744	0.9409	0.0826	0.2118
Filamin-C	0.9612	0.8703	0.1481	0.3699
Flavin reductase	0.2876	0.1673	0.8816	0.9239
Flotillin-2	0.8633	0.4584	0.0574	0.7872
Fructose-bisphosphate aldolase A	0.6266	0.8919	0.4751	0.2638
Fumarate hydratase mitochondrial	0.4452	0.7109	0.5386	0.6404
Fumarylacetoacetate hydrolase domain-containing protein 1	0.6591	0.6517	0.3976	0.5891
Fumarylacetoacetate hydrolase domain-containing protein 2A	0.6050	0.2354	0.4900	0.9589
FYVE RhoGEF and PH domain-containing protein 5	0.7601	0.8005	0.3242	0.5739
Galectin-1	0.2212	0.3199	0.8826	0.7194
Galectin-3	0.1212	0.3897	0.9305	0.5730
Gamma-enolase	0.8393	0.9932	0.4147	0.0444
Gamma-interferon-inducible protein 16	0.6461	0.5211	0.5278	0.5301
Gap junction alpha-1 protein	0.0133	0.0158	0.9974	0.9987
Gelsolin	0.0089	0.0216	0.9987	0.9297
General vesicular transport factor p115	0.7368	0.6731	0.5573	0.4246
Glucose-6-phosphate 1-dehydrogenase	0.2584	0.3573	0.8939	0.9122
Glucose-6-phosphate isomerase	0.9250	0.9278	0.2234	0.2634
Glucosidase 2 subunit beta	0.2694	0.3100	0.9051	0.8965
Glutamate dehydrogenase 1 mitochondrial	0.9622	0.9131	0.1006	0.2912
Glutaminase kidney isoform mitochondrial	0.7455	0.9930	0.2685	0.0113
Glutaminyl-tRNA synthetase	0.4487	0.7400	0.8143	0.6258
Glutaredoxin-3	0.3071	0.7852	0.8888	0.4097
Glutathione peroxidase 1	0.2392	0.3926	0.6883	0.7549
Glutathione S-transferase kappa 1	0.5420	0.8190	0.5453	0.3686
Glutathione S-transferase omega-1	0.0234	0.8001	0.4396	0.4691
Glutathione S-transferase P	0.3284	0.3854	0.8122	0.8730
Glutathione synthetase	0.0596	0.0182	0.9865	0.9990
Glyceraldehyde-3-phosphate dehydrogenase	0.6506	0.8901	0.6546	0.1913
Glycogen phosphorylase brain form	0.4061	0.6504	0.5763	0.6462
Glycogen phosphorylase liver form	0.9983	0.8740	0.0077	0.1085
Glycylpeptide N-tetradecanoyltransferase 1	0.0247	0.0107	0.9882	0.9995
Glycyl-tRNA synthetase	0.6142	0.9615	0.6830	0.1553
Glyoxalase domain-containing protein 4	0.3313	0.3525	0.8322	0.9170
Glyoxylate reductase/hydroxypyruvate reductase	0.0027	0.0007	0.9997	1.0000
Golgin subfamily A member 2	0.2046	0.6040	0.8287	0.7234
Golgin subfamily A member 3	0.1834	0.1724	0.7973	0.9623
Golgin subfamily B member 1	0.1138	0.1182	0.9703	0.9550
GTP:AMP phosphotransferase mitochondrial	0.8339	0.9746	0.0182	0.1201
GTPase IMAP family member 4	0.5950	0.8978	0.2587	0.0568
GTPase IMAP family member 8	0.3998	0.9156	0.5743	0.3321
GTP-binding nuclear protein Ran	0.4177	0.8984	0.6821	0.0301
GTP-binding protein SAR1a	0.0199	0.1472	0.9971	0.9579
Guanine nucleotide-binding protein G(i) subunit alpha-1	0.1069	0.3131	0.9532	0.8992
Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	0.4906	0.3957	0.2092	0.7899
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	0.7830	0.9572	0.3501	0.2317

Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	0.0304	0.0291	0.9903	0.9971
Guanine nucleotide-binding protein subunit alpha-13	0.0812	0.1553	0.9748	0.9724
Guanine nucleotide-binding protein subunit beta-2-like 1	0.3020	0.7096	0.8710	0.4464
Heat shock 70 kDa protein 1A/1B	0.7932	0.9731	0.2952	0.0990
Heat shock 70 kDa protein 4	0.8041	0.7998	0.2498	0.3702
Heat shock cognate 71 kDa protein	0.6424	0.9136	0.5895	0.2925
Heat shock protein 105 kDa	0.9621	0.9829	0.0623	0.0852
Heat shock protein beta-1	0.0155	0.2445	0.9948	0.9201
Heat shock protein beta-6	0.9999	0.9999	0.0003	0.0004
Heat shock protein HSP 90-alpha	0.3431	0.8733	0.8587	0.2349
Heat shock protein HSP 90-beta	0.4081	0.8419	0.8081	0.2952
Hedgehog-interacting protein	0.0476	0.0025	0.9312	0.9999
Hematological and neurological expressed 1 protein	0.3798	0.9349	0.7694	0.2591
Hematopoietic lineage cell-specific protein	0.0186	0.0606	0.9131	0.8256
Heme oxygenase 1	0.3551	0.8534	0.1104	0.0598
Heme oxygenase 2	0.7221	0.7931	0.5585	0.5586
Heme-binding protein 2	0.0009	0.0037	0.9999	0.9998
Hepatitis B virus X-interacting protein	0.1462	0.9033	0.9603	0.3572
Hepatoma-derived growth factor	0.0689	0.4475	0.9764	0.4932
Heterogeneous nuclear ribonucleoprotein A/B	0.6521	0.7318	0.4965	0.4084
Heterogeneous nuclear ribonucleoprotein A1	0.9913	0.9676	0.0483	0.1220
Heterogeneous nuclear ribonucleoprotein A3	0.9777	0.8854	0.1022	0.3299
Heterogeneous nuclear ribonucleoprotein D0	0.1598	0.0764	0.9307	0.9828
Heterogeneous nuclear ribonucleoprotein F	0.6797	0.6068	0.5384	0.6883
Heterogeneous nuclear ribonucleoprotein H	0.6783	0.6934	0.5580	0.5777
Heterogeneous nuclear ribonucleoprotein H2	0.6089	0.6800	0.6504	0.6005
Heterogeneous nuclear ribonucleoprotein H3	0.7939	0.8667	0.0626	0.3295
Heterogeneous nuclear ribonucleoprotein K	0.4498	0.8230	0.7032	0.2502
Heterogeneous nuclear ribonucleoprotein L	0.6862	0.1040	0.4677	0.6518
Heterogeneous nuclear ribonucleoprotein M	0.9536	0.3103	0.0931	0.6193
Heterogeneous nuclear ribonucleoprotein Q	0.9537	0.9187	0.1618	0.1570
Heterogeneous nuclear ribonucleoprotein R	0.9262	0.7947	0.2296	0.2089
Heterogeneous nuclear ribonucleoprotein U	0.9675	0.9703	0.0771	0.1383
Heterogeneous nuclear ribonucleoprotein U-like protein 1	0.8696	0.4287	0.0424	0.8015
Heterogeneous nuclear ribonucleoprotein U-like protein 2	0.4735	0.7908	0.6659	0.4843
Heterogeneous nuclear ribonucleoproteins A2/B1	0.9953	0.9147	0.0290	0.2692
Heterogeneous nuclear ribonucleoproteins C1/C2	0.9842	0.9193	0.0837	0.2853
Hexokinase-1	0.7105	0.5749	0.4837	0.6516
High mobility group protein B1	0.0118	0.2944	0.9935	0.3730
High mobility group protein B2	0.0105	0.2933	0.9924	0.3294
High mobility group protein HMG-I/HMG-Y	0.9998	0.9143	0.0006	0.0072
Hippocalcin-like protein 1	0.5582	0.3732	0.5928	0.8942
Histidine triad nucleotide-binding protein 1	0.9716	0.9658	0.0897	0.1928
Histidine triad nucleotide-binding protein 2 mitochondrial	0.2108	0.4134	0.8923	0.8152
Histidyl-tRNA synthetase cytoplasmic	0.4729	0.4584	0.6437	0.8456
Histone deacetylase complex subunit SAP18	0.9957	0.9983	0.0165	0.0122
Histone H1.3	0.9946	0.2965	0.0162	0.0848
Histone H1.5	0.9958	0.3305	0.0148	0.1089
Histone H2A type 1-C	1.0000	0.9917	0.0007	0.0116
Histone H2A.Z	0.9988	0.9959	0.0104	0.0286
Histone H2B type 1-K	1.0000	0.9970	0.0004	0.0035
Histone H3.2	1.0000	0.9457	0.0003	0.0083
Histone H4	1.0000	0.9689	0.0002	0.0044
HLA class I histocompatibility antigen A-68 alpha chain	0.0093	0.1667	0.9990	0.8774
HLA class I histocompatibility antigen B-7 alpha chain	0.0013	0.0001	0.9652	1.0000
Hsc70-interacting protein	0.5384	0.8729	0.7427	0.3680

Hsp90 co-chaperone Cdc37	0.6702	0.8160	0.6023	0.4367
Huntingtin-interacting protein 1-related protein	0.0097	0.0998	0.9975	0.9648
Hypoxanthine-guanine phosphoribosyltransferase	0.3554	0.1986	0.8351	0.9656
Hypoxia up-regulated protein 1	0.9472	0.7219	0.2014	0.4789
Importin subunit alpha-2	0.2708	0.0230	0.8604	0.9983
Importin subunit alpha-3	0.5136	0.9396	0.7415	0.0775
Importin subunit beta-1	0.7830	0.8236	0.4686	0.3395
Importin-5	0.5816	0.8774	0.5766	0.2131
Importin-8	0.4822	0.3695	0.6889	0.8336
Inhibitor of nuclear factor kappa-B kinase-interacting protein	0.9157	0.9925	0.2095	0.0730
Inorganic pyrophosphatase	0.4386	0.4119	0.8144	0.8462
Inosine-5'-monophosphate dehydrogenase 2	0.7448	0.0550	0.5106	0.8830
Inositol 1 4 5-trisphosphate receptor type 2	0.9999	0.9829	0.0011	0.0489
Inositol polyphosphate 1-phosphatase	0.1251	0.1707	0.9461	0.9574
Inositol-3-phosphate synthase 1	0.0079	0.0000	0.9798	1.0000
Insulin-like growth factor 2 mRNA-binding protein 1	0.8179	0.1640	0.0046	0.7039
Insulin-like growth factor 2 mRNA-binding protein 2	0.9980	0.4152	0.0104	0.5187
Insulin-like growth factor 2 mRNA-binding protein 3	0.9900	0.5886	0.0076	0.0871
Insulin-like growth factor-binding protein 7	0.0103	0.0197	0.9597	0.9971
Integrin alpha-2	0.0706	0.2950	0.9685	0.8013
Integrin alpha-5	0.8696	0.8542	0.2329	0.3677
Integrin alpha-6	0.9189	0.9933	0.0740	0.0130
Integrin alpha-V	0.5377	0.4383	0.7421	0.4235
Integrin beta-1	0.3050	0.7601	0.7838	0.5397
Integrin beta-3	0.0770	0.1782	0.9100	0.9576
Integrin-linked kinase-associated serine/threonine phosphatase 2C	0.0808	0.2401	0.8333	0.8338
Integrin-linked protein kinase	0.0610	0.0749	0.9899	0.9910
Intercellular adhesion molecule 2	0.7553	0.5100	0.2548	0.5502
Interleukin enhancer-binding factor 2	0.9985	0.9699	0.0117	0.0911
Interleukin enhancer-binding factor 3	0.9820	0.9783	0.0885	0.0873
Inverted formin-2	0.2675	0.8608	0.6275	0.4609
Isocitrate dehydrogenase [NADP] mitochondrial	0.0446	0.0218	0.9929	0.9985
Isocitrate dehydrogenase [NADP] cytoplasmic	0.4036	0.4873	0.7356	0.8526
Isoleucyl-tRNA synthetase cytoplasmic	0.3153	0.3391	0.8639	0.9049
Isovaleryl-CoA dehydrogenase mitochondrial	0.9811	0.9624	0.0364	0.1125
Junction plakoglobin	0.1732	0.2915	0.9580	0.8760
Keratin type I cytoskeletal 18	0.8860	0.8056	0.0471	0.0206
Kinectin	0.3900	0.4724	0.8459	0.7184
Kinesin-1 heavy chain	0.4182	0.4685	0.8372	0.8476
Lactoylglutathione lyase	0.4063	0.8563	0.8302	0.2139
LAG1 longevity assurance homolog 2	0.7460	0.6539	0.4819	0.7142
Lamina-associated polypeptide 2 isoforms beta/gamma	0.7424	0.8476	0.2688	0.0575
Lamin-B1	0.1746	0.1264	0.9366	0.5856
Lamin-B2	0.3627	0.1777	0.7765	0.5670
Laminin subunit gamma-1	0.0061	0.1118	0.9990	0.9765
L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0.8201	0.4283	0.2265	0.7538
Latent-transforming growth factor beta-binding protein 2	0.0070	0.0071	0.4427	0.9996
LETM1 and EF-hand domain-containing protein 1 mitochondrial	0.6887	0.7643	0.4483	0.3875
Leucine-rich PPR motif-containing protein mitochondrial	0.9394	0.9834	0.1975	0.0421
Leucine-rich repeat-containing protein 47	0.8419	0.8309	0.4133	0.4645
Leucine-rich repeat-containing protein 59	0.9023	0.8114	0.2825	0.3066
Leukocyte elastase inhibitor	0.3947	0.7908	0.5417	0.2896
Leukotriene A-4 hydrolase	0.5094	0.9748	0.7440	0.1322
LIM and senescent cell antigen-like-containing domain protein 1	0.8348	0.0273	0.2174	0.7389
LIM and SH3 domain protein 1	0.4162	0.6467	0.7282	0.6478
LIM domain and actin-binding protein 1	0.9903	0.9999	0.0218	0.0015

Liprin-alpha-1	0.6636	0.4804	0.0096	0.1926
Liprin-beta-1	0.7884	0.7935	0.1688	0.3558
LisH domain and HEAT repeat-containing protein KIAA1468	0.3517	0.2530	0.8369	0.8671
L-lactate dehydrogenase A chain	0.9713	0.9970	0.1016	0.0165
L-lactate dehydrogenase B chain	0.7376	0.9698	0.4092	0.0995
Lon protease homolog mitochondrial	0.0003	0.0000	1.0000	1.0000
Long-chain fatty acid transport protein 4	0.6524	0.9738	0.3750	0.1621
Long-chain-fatty-acid--CoA ligase 3	0.1776	0.9079	0.9559	0.2470
Lupus La protein	0.6560	0.7878	0.5851	0.3515
Lysosomal alpha-mannosidase	0.7929	0.6571	0.1556	0.5689
Lysosomal Pro-X carboxypeptidase	0.3974	0.0207	0.6865	0.9874
Macrophage migration inhibitory factor	0.4177	0.8180	0.6111	0.4599
Macrophage-capping protein	0.0028	0.0521	0.9899	0.9540
Major vault protein	0.8967	0.6695	0.0921	0.2696
Malate dehydrogenase cytoplasmic	0.7746	0.8461	0.4502	0.4355
Malate dehydrogenase mitochondrial	0.4410	0.4734	0.8013	0.8414
Mannose-1-phosphate guanyltransferase beta	0.0859	0.0337	0.9809	0.9805
Mannosyl-oligosaccharide glucosidase	0.8519	0.7647	0.2241	0.4936
MARCKS-related protein	0.0764	0.2451	0.9741	0.8568
Matrin-3	0.5151	0.1573	0.6976	0.7390
Membrane-associated progesterone receptor component 2	0.9900	0.9922	0.0301	0.0339
Metastasis-associated protein MTA2	0.9873	0.8098	0.0491	0.1989
Methionine adenosyltransferase 2 subunit beta	0.8215	0.6544	0.2120	0.7320
Methionyl-tRNA synthetase cytoplasmic	0.4422	0.6448	0.7968	0.6389
Methylmalonyl-CoA mutase mitochondrial	0.1746	0.4104	0.9528	0.7973
Microtubule-actin cross-linking factor 1 isoform 4	0.5476	0.3195	0.7273	0.9046
Microtubule-associated protein 1B	0.6398	0.5365	0.4893	0.7938
Microtubule-associated protein 1S	0.1247	0.2761	0.9615	0.9121
Microtubule-associated protein 2	0.0006	0.0170	1.0000	0.9983
Microtubule-associated protein 4	0.1918	0.4167	0.9476	0.8484
Microtubule-associated protein RP/EB family member 1	0.0910	0.1763	0.9785	0.9341
Mitochondrial fission 1 protein	0.0925	0.0528	0.9671	0.9946
Mitochondrial import inner membrane translocase subunit Tim13	0.0072	0.0006	0.9992	1.0000
Mitochondrial import inner membrane translocase subunit TIM44	0.3374	0.8119	0.8368	0.4464
Mitochondrial import inner membrane translocase subunit Tim8 A	0.0408	0.0705	0.9007	0.8414
Mitochondrial inner membrane protein	0.9052	0.9593	0.2420	0.2306
Mitochondrial inner membrane protein OXA1L	0.9531	0.9181	0.1203	0.2772
Mitochondrial-processing peptidase subunit alpha	0.3990	0.8321	0.7007	0.4743
Mitogen-activated protein kinase 1	0.4639	0.6921	0.7804	0.6643
Mitogen-activated protein kinase 14	0.4635	0.1069	0.6182	0.9711
Mitogen-activated protein kinase 3	0.4660	0.4733	0.7432	0.8490
Moesin	0.3154	0.6133	0.8846	0.5957
Monocarboxylate transporter 4	0.1048	0.8461	0.6922	0.4451
Mps one binder kinase activator-like 1A	0.6681	0.8212	0.5889	0.4086
Mucin-6	0.2708	0.0711	0.8973	0.8094
Multifunctional protein ADE2	0.6542	0.8786	0.6133	0.3614
Multimerin-1	0.9998	0.7954	0.0010	0.0456
Muscleblind-like protein 1	0.3475	0.3295	0.6069	0.8681
Myoferlin	0.9988	0.9912	0.0082	0.0237
Myosin light polypeptide 6	0.0139	0.0242	0.9940	0.9530
Myosin phosphatase Rho-interacting protein	0.9599	0.9837	0.0084	0.0177
Myosin regulatory light chain 12B	0.1072	0.0872	0.9606	0.8115
Myosin-10	0.2183	0.0513	0.9014	0.9128
Myosin-9	0.0225	0.0179	0.9923	0.9776
Myosin-Ic	0.8046	0.7251	0.3039	0.5881
Myosin-Ie	0.1689	0.0048	0.9076	0.9998

Myosin-Va	0.7383	0.5148	0.2658	0.7019
Myristoylated alanine-rich C-kinase substrate	0.3958	0.6981	0.7126	0.3260
Na(+)/H(+) exchange regulatory cofactor NHE-RF2	0.9718	0.9763	0.0165	0.0488
N-acetylglucosamine-6-sulfatase	0.7301	0.7678	0.3329	0.5644
NAD(P) transhydrogenase mitochondrial	0.5059	0.9096	0.6869	0.2430
NAD(P)H dehydrogenase [quinone] 1	0.8353	0.9978	0.0727	0.0037
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	0.7898	0.6574	0.4616	0.6414
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	0.6981	0.2713	0.4304	0.8998
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9 mitochondrial	0.0770	0.2599	0.8077	0.8943
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	0.9517	0.9155	0.1619	0.2854
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	0.7686	0.8926	0.2454	0.2643
NADH dehydrogenase [ubiquinone] flavoprotein 2 mitochondrial	0.0746	0.1227	0.9801	0.9782
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2 mitochondrial	0.0640	0.3689	0.9431	0.5462
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3 mitochondrial	0.8842	0.8638	0.1838	0.2338
NADH-cytochrome b5 reductase 3	0.6991	0.5942	0.3192	0.4945
NADH-ubiquinone oxidoreductase 75 kDa subunit mitochondrial	0.6984	0.6994	0.4930	0.6928
NADPH:adrenodoxin oxidoreductase mitochondrial	0.5586	0.7381	0.2092	0.4916
NADPH--cytochrome P450 reductase	0.5351	0.8241	0.3986	0.3964
Nardilysin	0.4825	0.9709	0.6956	0.1770
Nascent polypeptide-associated complex subunit alpha	0.3811	0.5845	0.8481	0.6669
NEDD8	0.7776	0.7375	0.4354	0.6492
NEDD8-activating enzyme E1 regulatory subunit	0.6042	0.2957	0.5391	0.8866
Neighbor of COX4	0.0452	0.4007	0.9848	0.8853
Nestin	0.4770	0.3376	0.7291	0.4855
Neuroblast differentiation-associated protein AHNAK	0.9587	0.9940	0.1705	0.0604
Neuroplastin	0.7840	0.8814	0.3017	0.1580
Neutral alpha-glucosidase AB	0.4566	0.3245	0.7303	0.9142
Neutral cholesterol ester hydrolase 1	0.2064	0.0627	0.1470	0.8151
NHP2-like protein 1	0.9318	0.9846	0.2208	0.0635
Niban-like protein 1	0.9109	0.8401	0.2461	0.3834
Nicalin	0.1613	0.0401	0.9508	0.9968
Nicotinamide N-methyltransferase	0.9648	0.4815	0.1418	0.7475
Nicotinamide phosphoribosyltransferase	0.6839	0.9279	0.2876	0.2641
Nidogen-1	0.0335	0.0011	0.9923	1.0000
Nitric oxide synthase-interacting protein	0.4227	0.9570	0.2037	0.0062
Nodal modulator 1	0.8933	0.8323	0.2342	0.4447
Non-histone chromosomal protein HMG-17	0.7280	0.8842	0.1973	0.0083
Non-POU domain-containing octamer-binding protein	0.5706	0.1042	0.6019	0.7319
Non-specific lipid-transfer protein	0.3217	0.8871	0.8956	0.2490
NSFL1 cofactor p47	0.9649	0.9168	0.0477	0.2741
Nuclear autoantigenic sperm protein	0.1662	0.7566	0.8437	0.1056
Nuclear migration protein nudC	0.7161	0.8304	0.5818	0.3668
Nuclear mitotic apparatus protein 1	0.5138	0.7313	0.6237	0.6240
Nuclear pore complex protein Nup133	0.7019	0.8364	0.4578	0.3549
Nuclear receptor subfamily 5 group A member 2	0.1482	0.0213	0.9343	0.9983
Nuclear transport factor 2	0.0936	0.1648	0.9797	0.9667
Nuclear ubiquitous casein and cyclin-dependent kinases substrate	0.7547	0.9152	0.5064	0.0798
Nuclease-sensitive element-binding protein 1	0.8900	0.9292	0.2017	0.2473
Nucleobindin-1	0.8670	0.4497	0.2963	0.8318
Nucleobindin-2	0.8330	0.8674	0.3491	0.2820
Nucleolin	0.9974	0.8973	0.0132	0.1748
Nucleolysin TIA-1 isoform p40	0.7071	0.7057	0.3916	0.5494
Nucleophosmin	0.9995	0.6627	0.0049	0.1566
Nucleoprotein TPR	0.7806	0.9214	0.3843	0.1967
Nucleoside diphosphate kinase B	0.7641	0.9237	0.4715	0.2675
Nucleosome assembly protein 1-like 1	0.2621	0.1558	0.9106	0.9732

Nucleosome assembly protein 1-like 4	0.4986	0.7143	0.7457	0.5751
Obg-like ATPase 1	0.3321	0.3882	0.8095	0.8847
Oligosaccharyltransferase complex subunit OSTC	0.0195	0.0010	0.9954	0.9999
Ornithine aminotransferase mitochondrial	0.3359	0.2729	0.8364	0.9278
Osteoclast-stimulating factor 1	0.0118	0.0115	0.9975	0.9886
Palladin	0.7097	0.1191	0.5875	0.8298
Parathymosin	0.3625	0.1847	0.7847	0.9478
PDZ and LIM domain protein 1	0.9923	0.9999	0.0279	0.0023
PDZ and LIM domain protein 4	0.7052	0.5247	0.5810	0.7344
PDZ and LIM domain protein 5	0.0205	0.4887	0.8979	0.7741
PDZ and LIM domain protein 7	0.0335	0.0257	0.9697	0.9656
Pentatricopeptide repeat-containing protein 3 mitochondrial	0.1489	0.0830	0.9211	0.9867
Peptidyl-prolyl cis-trans isomerase A	0.2901	0.6856	0.8782	0.4615
Peptidyl-prolyl cis-trans isomerase B	0.5856	0.7531	0.6463	0.3698
Peptidyl-prolyl cis-trans isomerase FKBP10	0.1042	0.2461	0.7935	0.9035
Peptidyl-prolyl cis-trans isomerase FKBP11	0.4285	0.6093	0.6492	0.6888
Peptidyl-prolyl cis-trans isomerase FKBP1A	0.5654	0.9488	0.5941	0.2506
Peptidyl-prolyl cis-trans isomerase FKBP3	0.9603	0.9336	0.1276	0.3002
Peptidyl-prolyl cis-trans isomerase FKBP4	0.3247	0.8447	0.0260	0.3066
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	0.4608	0.3990	0.8084	0.7480
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	0.1180	0.7478	0.9561	0.4457
Perilipin-3	0.3049	0.6270	0.8819	0.7044
Periostin	0.9907	0.8713	0.0029	0.0024
Peroxidasin homolog	0.2340	0.0858	0.9121	0.7894
Peroxiredoxin-1	0.5857	0.8142	0.6445	0.3844
Peroxiredoxin-2	0.7905	0.8667	0.4706	0.3521
Peroxiredoxin-4	0.1864	0.2368	0.7509	0.9435
Peroxiredoxin-5 mitochondrial	0.0933	0.0890	0.9492	0.9799
Peroxiredoxin-6	0.8603	0.9658	0.3566	0.1399
Peroxisomal membrane protein PEX14	0.6323	0.9973	0.4044	0.0179
Peroxisomal multifunctional enzyme type 2	0.8462	0.4633	0.1183	0.4823
PERQ amino acid-rich with GYF domain-containing protein 2	0.5542	0.3153	0.3250	0.8857
PHD finger-like domain-containing protein 5A	0.1159	0.0423	0.9538	0.9910
Phenylalanyl-tRNA synthetase beta chain	0.9218	0.8761	0.2494	0.2690
Phosphate carrier protein mitochondrial	0.5462	0.7620	0.7123	0.5552
Phosphatidylethanolamine-binding protein 1	0.4708	0.9507	0.8072	0.2057
Phosphatidylinositol transfer protein alpha isoform	0.8313	0.9564	0.1289	0.1576
Phosphatidylinositol transfer protein beta isoform	0.4023	0.5293	0.8386	0.7833
Phosphatidylinositol-binding clathrin assembly protein	0.0116	0.0563	0.9936	0.9822
Phosphoglycerate kinase 1	0.5737	0.8906	0.6621	0.3573
Phosphoglycerate mutase 1	0.7440	0.9193	0.4537	0.2915
Phosphoribosylformylglycinamidine synthase	0.8412	0.8353	0.0846	0.4310
Phosphoserine aminotransferase	0.9250	0.8343	0.0571	0.1354
Pirin	0.9694	0.9842	0.0429	0.0021
PITH domain-containing protein 1	0.1606	0.3505	0.4761	0.8695
Plasminogen activator inhibitor 1	0.8094	0.9929	0.0741	0.0481
Plasminogen activator inhibitor 1 RNA-binding protein	0.6593	0.8303	0.3840	0.4057
Plastin-3	0.5627	0.9629	0.6552	0.2124
Platelet endothelial cell adhesion molecule	0.6720	0.7268	0.6061	0.6218
Platelet-activating factor acetylhydrolase IB subunit alpha	0.6357	0.4420	0.5700	0.8695
Platelet-activating factor acetylhydrolase IB subunit beta	0.1534	0.2925	0.9575	0.9018
Platelet-activating factor acetylhydrolase IB subunit gamma	0.0001	0.0000	1.0000	1.0000
Plectin	0.8962	0.3926	0.2904	0.4885
PNMA-like protein 1	0.8634	0.9989	0.0042	0.0167
Poliovirus receptor	0.8606	0.3424	0.1048	0.4960
Poly [ADP-ribose] polymerase 1	0.0617	0.0244	0.9881	0.9954

Poly(rC)-binding protein 1	0.4572	0.8443	0.7809	0.3963
Poly(rC)-binding protein 2	0.3034	0.6007	0.8548	0.5709
Poly(U)-binding-splicing factor PUF60	0.6157	0.8042	0.5590	0.3088
Polyadenylate-binding protein 1	0.9961	0.9930	0.0262	0.0540
Polymerase delta-interacting protein 3	0.8788	0.8667	0.3483	0.1423
Polymerase I and transcript release factor	0.9765	0.8361	0.1155	0.2372
Polypeptide N-acetylgalactosaminyltransferase 2	0.8959	0.8262	0.2886	0.4661
Polypyrimidine tract-binding protein 1	0.5132	0.9238	0.6028	0.0331
POTE ankyrin domain family member E	0.6826	0.9078	0.6256	0.2637
Prefoldin subunit 1	0.1549	0.7030	0.9333	0.4253
Prefoldin subunit 2	0.5381	0.7460	0.6498	0.5723
Prefoldin subunit 3	0.2767	0.5769	0.9162	0.7471
Prefoldin subunit 5	0.4763	0.9641	0.7467	0.1293
Prefoldin subunit 6	0.5218	0.5103	0.7230	0.8266
Prelamin-A/C	0.7528	0.3352	0.3898	0.3091
Pre-mRNA-processing factor 19	0.9982	0.9777	0.0069	0.0754
Presequence protease mitochondrial	0.9002	0.9183	0.2727	0.3462
Proactivator polypeptide	0.2382	0.7322	0.8636	0.3462
Probable ATP-dependent RNA helicase DDX17	0.8298	0.7625	0.3388	0.3194
Probable ATP-dependent RNA helicase DDX5	0.8251	0.5859	0.2459	0.2952
Probable glutathione peroxidase 8	0.0965	0.5253	0.9644	0.5028
Procollagen galactosyltransferase 1	0.0180	0.0080	0.9966	0.9738
Procollagen-lysine 2-oxoglutarate 5-dioxygenase 1	0.0446	0.0048	0.9243	0.9587
Procollagen-lysine 2-oxoglutarate 5-dioxygenase 2	0.8389	0.9481	0.1613	0.1172
Procollagen-lysine 2-oxoglutarate 5-dioxygenase 3	0.0030	0.0061	0.9996	0.9572
Profilin-1	0.3039	0.6502	0.9041	0.7068
Programmed cell death 6-interacting protein	0.3370	0.5348	0.7525	0.7810
Programmed cell death protein 4	0.0009	0.0002	0.9999	1.0000
Programmed cell death protein 5	0.6807	0.8045	0.6068	0.5408
Programmed cell death protein 6	0.9593	0.9897	0.1079	0.0874
Prohibitin	0.6771	0.8633	0.5986	0.4126
Prohibitin-2	0.2776	0.6608	0.8456	0.6434
Proliferating cell nuclear antigen	0.2480	0.6798	0.8619	0.1275
Proliferation-associated protein 2G4	0.7493	0.7721	0.4529	0.3997
Proline synthase co-transcribed bacterial homolog protein	0.7377	0.8383	0.2144	0.2866
Proline-rich AKT1 substrate 1	0.9067	0.6954	0.1225	0.5871
Prolyl 4-hydroxylase subunit alpha-2	0.3413	0.6385	0.3900	0.6715
Prostaglandin E synthase 3	0.1170	0.7698	0.9445	0.1645
Prostaglandin G/H synthase 1	0.9505	0.9762	0.0255	0.0055
Proteasome activator complex subunit 1	0.0027	0.0796	0.9997	0.9861
Proteasome activator complex subunit 2	0.7335	0.9764	0.3174	0.0929
Proteasome subunit alpha type-1	0.5693	0.8101	0.7045	0.3847
Proteasome subunit alpha type-2	0.5497	0.5591	0.6898	0.7705
Proteasome subunit alpha type-3	0.3960	0.4233	0.6727	0.8280
Proteasome subunit alpha type-5	0.5856	0.7509	0.6219	0.5703
Proteasome subunit alpha type-6	0.8588	0.7625	0.3619	0.5924
Proteasome subunit alpha type-7	0.7527	0.9171	0.4936	0.3114
Proteasome subunit beta type-1	0.7796	0.6740	0.4577	0.6338
Proteasome subunit beta type-6	0.7198	0.9163	0.5594	0.1265
Proteasome subunit beta type-7	0.7307	0.2306	0.3664	0.9241
Protein AHNAK2	0.8836	0.9495	0.0233	0.1351
Protein BRICK1	0.9863	0.8600	0.0215	0.4505
Protein canopy homolog 3	0.0172	0.1525	0.9981	0.8567
Protein canopy homolog 4	0.6625	0.5361	0.3520	0.7280
Protein CDV3 homolog	0.9249	0.9830	0.1377	0.1068
Protein CutA	0.8282	0.7573	0.2003	0.6016

Protein CYR61	0.8626	0.0059	0.3417	0.9994
Protein diaphanous homolog 1	0.7630	0.6912	0.2402	0.3938
Protein diaphanous homolog 2	0.0073	0.1030	0.9992	0.9189
Protein disulfide-isomerase	0.5052	0.3661	0.6269	0.8810
Protein disulfide-isomerase A3	0.4528	0.5531	0.8168	0.7759
Protein disulfide-isomerase A4	0.6064	0.5091	0.6739	0.7013
Protein disulfide-isomerase A5	0.8551	0.0463	0.1076	0.9497
Protein disulfide-isomerase A6	0.3978	0.6484	0.8223	0.5503
Protein disulfide-isomerase TMX3	0.8626	0.7590	0.3376	0.3261
Protein DJ-1	0.3419	0.9516	0.8567	0.1525
Protein enabled homolog	0.8067	0.7930	0.0275	0.3294
Protein ERGIC-53	0.6593	0.5844	0.6229	0.5396
Protein FAM136A	0.9260	0.9814	0.2509	0.1249
Protein FAM43A	0.3951	0.1175	0.7968	0.9733
Protein flightless-1 homolog	0.9665	0.9613	0.1060	0.1954
Protein KIAA1967	0.7527	0.6602	0.5074	0.5880
Protein kinase C alpha type	0.3630	0.3746	0.2044	0.8375
Protein kinase C and casein kinase substrate in neurons protein 2	0.1464	0.8192	0.9665	0.4410
Protein kinase C delta-binding protein	0.8766	0.9600	0.1204	0.0061
Protein lin-7 homolog C	0.7890	0.6739	0.1923	0.6820
Protein LZIC	0.9169	0.8679	0.2157	0.3972
Protein NDRG1	0.8997	0.9993	0.1779	0.0094
Protein NOXP20	0.3449	0.6070	0.8836	0.6720
Protein phosphatase 1 regulatory subunit 7	0.7391	0.6852	0.4484	0.6938
Protein phosphatase 1F	0.8752	0.8531	0.2364	0.3756
Protein PML	0.7795	0.8676	0.3195	0.0926
Protein PRRC1	0.4486	0.4609	0.7985	0.7484
Protein PRRC2C	0.9687	0.8672	0.0474	0.4180
Protein Red	0.5418	0.7399	0.7180	0.5847
Protein S100-A10	0.6237	0.9820	0.5417	0.0687
Protein S100-A11	0.4077	0.0333	0.7934	0.9110
Protein S100-A13	0.3993	0.4029	0.4046	0.5946
Protein S100-A16	0.8460	0.4248	0.3677	0.7087
Protein S100-A6	0.9937	0.9519	0.0193	0.0647
Protein SEC13 homolog	0.1947	0.7772	0.9441	0.4888
Protein SET	0.2372	0.7550	0.8736	0.2890
Protein sprouty homolog 2	0.3136	0.0492	0.8546	0.9946
Protein TFG	0.4837	0.2768	0.4648	0.9418
Protein transport protein Sec23A	0.8164	0.9182	0.4337	0.3333
Protein transport protein Sec24C	0.2811	0.4015	0.9115	0.7653
Protein transport protein Sec31A	0.0688	0.0140	0.9864	0.9992
Protein unc-45 homolog A	0.7916	0.7777	0.3305	0.5868
Protein-glutamine gamma-glutamyltransferase 2	0.9778	0.9982	0.0251	0.0036
Protein-L-isoaspartate(D-aspartate) O-methyltransferase	0.3169	0.7011	0.8910	0.5253
Prothymosin alpha	0.2224	0.3152	0.8109	0.4537
Protocadherin-1	0.4269	0.1508	0.8331	0.9455
Protoporphyrinogen oxidase	0.5950	0.9251	0.4122	0.3244
Purine nucleoside phosphorylase	0.9936	0.6632	0.0106	0.4782
Puromycin-sensitive aminopeptidase	0.8892	0.8645	0.3026	0.3547
Putative 40S ribosomal protein S26-like 1	0.9999	0.4311	0.0010	0.3109
Putative elongation factor 1-alpha-like 3	0.3856	0.7363	0.8194	0.3642
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	0.7265	0.7899	0.5595	0.5753
Putative RNA-binding protein Luc7-like 2	0.8331	0.9643	0.2856	0.1505
Putative tropomyosin alpha-3 chain-like protein	0.4198	0.8256	0.7779	0.4680
Pyridoxal kinase	0.9845	0.9981	0.0783	0.0188
Pyridoxine-5'-phosphate oxidase	0.4890	0.9891	0.1540	0.0248

Pyrroline-5-carboxylate reductase 1 mitochondrial	0.5854	0.8004	0.3730	0.1788
Pyruvate dehydrogenase E1 component subunit beta mitochondrial	0.1234	0.0278	0.9642	0.9980
Pyruvate kinase isozymes M1/M2	0.5050	0.9360	0.7193	0.2414
Quinone oxidoreductase PIG3	0.0828	0.0300	0.9692	0.9970
Rab GDP dissociation inhibitor beta	0.4130	0.7187	0.8421	0.5841
Rab11 family-interacting protein 5	0.9262	0.9011	0.1575	0.2263
Radixin	0.3526	0.6411	0.8753	0.5996
Ran GTPase-activating protein 1	0.7293	0.9819	0.4476	0.1339
Rap1 GTPase-GDP dissociation stimulator 1	0.7121	0.7985	0.4497	0.5487
Ras GTPase-activating protein-binding protein 1	0.9870	0.9488	0.0399	0.0732
Ras GTPase-activating protein-binding protein 2	0.9900	0.9348	0.0548	0.0189
Ras GTPase-activating-like protein IQGAP1	0.6198	0.6818	0.6252	0.6839
Ras suppressor protein 1	0.1737	0.1880	0.9490	0.9599
Ras-interacting protein 1	0.8495	0.4640	0.3503	0.7876
Ras-related C3 botulinum toxin substrate 1	0.6319	0.8081	0.6210	0.5459
Ras-related C3 botulinum toxin substrate 2	0.7058	0.8824	0.4856	0.4137
Ras-related protein Rab-10	0.2057	0.5804	0.9353	0.7630
Ras-related protein Rab-11B	0.9054	0.8783	0.2738	0.3856
Ras-related protein Rab-1A	0.2522	0.6343	0.8981	0.6939
Ras-related protein Rab-1B	0.4059	0.8385	0.8396	0.4973
Ras-related protein Rab-2A	0.0767	0.0717	0.9862	0.9918
Ras-related protein Rab-5B	1.0000	0.6557	0.0005	0.6694
Ras-related protein Rab-5C	0.6239	0.2118	0.5370	0.9584
Ras-related protein Rab-7a	0.6090	0.7962	0.6751	0.4400
Ras-related protein Ral-A	0.0174	0.4380	0.9899	0.8534
Ras-related protein Ral-B	0.0263	0.5218	0.9837	0.8148
Ras-related protein Rap-1b	0.1152	0.1238	0.9748	0.9710
RELT-like protein 1	0.5982	0.9172	0.5663	0.2187
Reticulocalbin-1	0.3115	0.1022	0.8950	0.9046
Reticulocalbin-3	0.9998	0.9339	0.0006	0.0008
Reticulon-4	0.7248	0.1172	0.2304	0.5191
Retinal dehydrogenase 1	0.7428	0.7323	0.0022	0.0506
Rho GDP-dissociation inhibitor 1	0.8848	0.9438	0.3145	0.2851
Rho GDP-dissociation inhibitor 2	0.0437	0.7037	0.9910	0.6645
Rho GTPase-activating protein 1	0.1348	0.9132	0.9662	0.2850
Rho GTPase-activating protein 17	0.5655	0.6319	0.6529	0.7151
Rho-related GTP-binding protein RhoB	0.0713	0.4331	0.9799	0.7528
Rho-related GTP-binding protein RhoC	0.6709	0.7656	0.5740	0.6202
Ribonuclease inhibitor	0.6056	0.1956	0.4347	0.8424
Ribosome-binding protein 1	0.9625	0.7868	0.1121	0.4571
Ribulose-phosphate 3-epimerase	0.1713	0.3739	0.9339	0.8423
RNA-binding motif single-stranded-interacting protein 2	0.8910	0.3138	0.3251	0.8683
RNA-binding protein 10	0.5364	0.6443	0.5795	0.4593
RNA-binding protein 14	0.9934	0.9912	0.0188	0.0481
RNA-binding protein 39	0.7772	0.9569	0.3541	0.1845
RNA-binding protein FUS	0.5234	0.5763	0.3993	0.3242
Rootletin	0.7665	0.7544	0.2034	0.3856
rRNA 2'-O-methyltransferase fibrillarin	0.9999	0.9998	0.0015	0.0019
RuvB-like 1	0.0145	0.0461	0.9984	0.9919
S-adenosylmethionine synthase isoform type-2	0.2142	0.4272	0.9288	0.8235
SAP30-binding protein	0.5963	0.9621	0.6331	0.1580
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	0.5256	0.5361	0.6950	0.8025
Sec1 family domain-containing protein 1	0.5327	0.8719	0.7549	0.4358
SEC23-interacting protein	0.2458	0.5240	0.9209	0.6468
Secernin-1	0.0346	0.0904	0.9885	0.9801
Sepiapterin reductase	0.7526	0.9802	0.4993	0.1003

Septin-2	0.6808	0.7361	0.4265	0.6298
Septin-7	0.6845	0.8426	0.6029	0.3912
Septin-9	0.3494	0.0797	0.3148	0.8847
Serine hydroxymethyltransferase mitochondrial	0.4848	0.6548	0.6575	0.3229
Serine protease HTRA1	0.7418	0.5456	0.5296	0.7851
Serine/arginine repetitive matrix protein 1	0.5826	0.5590	0.3716	0.1614
Serine/arginine repetitive matrix protein 2	0.5596	0.7610	0.5890	0.6237
Serine/arginine-rich splicing factor 1	0.9602	0.4724	0.1320	0.8165
Serine/arginine-rich splicing factor 11	0.7478	0.9482	0.4861	0.2170
Serine/arginine-rich splicing factor 6	0.9513	0.6822	0.1466	0.3994
Serine/arginine-rich splicing factor 7	0.7284	0.5458	0.5362	0.6971
Serine/arginine-rich splicing factor 8	0.9355	0.7738	0.1611	0.4979
Serine/threonine-protein kinase 24	0.0881	0.3861	0.9769	0.9014
Serine/threonine-protein kinase N1	0.3733	0.1748	0.7979	0.9499
Serine/threonine-protein kinase PAK 2	0.2936	0.7831	0.8969	0.2122
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	0.1358	0.7647	0.8379	0.4370
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	0.5635	0.3763	0.6856	0.8777
Serine/threonine-protein phosphatase 2A activator	0.9001	0.9968	0.1469	0.0136
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	0.6403	0.6158	0.4686	0.6153
Serine/threonine-protein phosphatase 6 regulatory subunit 3	0.0273	0.4408	0.9862	0.4058
Serine/threonine-protein phosphatase PP1-beta catalytic subunit	0.9632	0.9937	0.1527	0.0373
Serpin B9	0.2217	0.6176	0.4536	0.1614
Serpin H1	0.9780	0.9880	0.0831	0.0386
Serrate RNA effector molecule homolog	0.2640	0.8705	0.8084	0.3602
Serum deprivation-response protein	0.8749	0.6001	0.0393	0.4004
Serum paraoxonase/arylesterase 2	0.0176	0.1427	0.9949	0.8107
Seryl-tRNA synthetase cytoplasmic	0.7876	0.8419	0.4989	0.4789
S-formylglutathione hydrolase	0.0792	0.4086	0.9804	0.8909
SH3 domain-binding glutamic acid-rich-like protein 3	0.7683	0.9012	0.3216	0.3404
SH3 domain-containing protein 19	0.2006	0.1065	0.9186	0.9746
Sialic acid synthase	0.9623	0.8463	0.0480	0.2490
Sideroflexin-1	0.7941	0.7654	0.3698	0.5783
Signal recognition particle 14 kDa protein	0.4509	0.3328	0.7460	0.8706
Signal recognition particle 68 kDa protein	0.8055	0.6248	0.4499	0.5438
Signal recognition particle 9 kDa protein	0.7455	0.6838	0.2645	0.6323
Signal recognition particle receptor subunit alpha	0.3891	0.5079	0.6055	0.7634
Signal transducer and activator of transcription 1-alpha/beta	0.1168	0.0585	0.7828	0.9445
Signal transducer and activator of transcription 3	0.9321	0.8616	0.1938	0.4429
Single-stranded DNA-binding protein mitochondrial	0.9438	0.8611	0.0552	0.2294
Small glutamine-rich tetratricopeptide repeat-containing protein alpha	0.7153	0.8302	0.3773	0.4035
Small nuclear ribonucleoprotein G	0.6368	0.7319	0.5489	0.5042
Small nuclear ribonucleoprotein Sm D1	0.8986	0.9505	0.2045	0.1523
Small nuclear ribonucleoprotein Sm D2	0.7612	0.8885	0.4782	0.3487
Small nuclear ribonucleoprotein Sm D3	0.8373	0.8295	0.3412	0.2855
Small ubiquitin-related modifier 2	0.4517	0.9389	0.8196	0.2325
Small ubiquitin-related modifier 3	0.4275	0.9185	0.8356	0.2858
Sodium/potassium-transporting ATPase subunit alpha-1	0.8596	0.8161	0.3167	0.3333
Sorcin	0.7371	0.6296	0.2841	0.6026
Sorting nexin-1	0.2653	0.6635	0.9222	0.6398
Sorting nexin-12	0.4176	0.4631	0.6377	0.8653
Sorting nexin-3	0.6338	0.5080	0.6374	0.7707
Sorting nexin-6	0.5817	0.6953	0.7161	0.5967
SPARC	0.0223	0.0234	0.8920	0.9978
Spectrin alpha chain brain	0.3252	0.3791	0.8936	0.9072
Spectrin beta chain brain 1	0.3827	0.3982	0.8586	0.8926
Spermidine synthase	0.9631	0.9630	0.1450	0.1609

Spliceosome RNA helicase DDX39B	0.6262	0.7870	0.5461	0.2848
Splicing factor proline- and glutamine-rich	0.7829	0.1258	0.3030	0.5297
Splicing factor 3B subunit 1	0.9764	0.9983	0.0312	0.0220
Splicing factor 3B subunit 2	0.6889	0.5275	0.5603	0.4698
Splicing factor 3B subunit 3	0.5727	0.9490	0.4421	0.0303
SRA stem-loop-interacting RNA-binding protein mitochondrial	0.9965	0.9999	0.0143	0.0009
Stabilin-1	0.7410	0.5204	0.4674	0.8358
Staphylococcal nuclease domain-containing protein 1	0.6704	0.5473	0.6217	0.7483
Stathmin	0.0735	0.5420	0.9696	0.5852
STE20-like serine/threonine-protein kinase	0.8551	0.9832	0.3850	0.1262
Stomatin-like protein 2	0.6529	0.5214	0.1117	0.4356
Stress-70 protein mitochondrial	0.9084	0.9714	0.1767	0.1010
Stress-induced-phosphoprotein 1	0.5253	0.9243	0.6517	0.2045
Structural maintenance of chromosomes protein 1A	0.6853	0.7779	0.6007	0.5236
Succinyl-CoA ligase [GDP-forming] subunit alpha mitochondrial	0.5025	0.7514	0.7545	0.5606
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1 mitochondrial	0.4653	0.5113	0.6776	0.7219
Sulfatase-modifying factor 2	0.0231	0.0070	0.9955	0.9984
Sulfide:quinone oxidoreductase mitochondrial	0.6057	0.1086	0.0135	0.1733
Sulfotransferase 1A3/1A4	0.9797	0.9990	0.0194	0.0050
Sulfotransferase family cytosolic 1B member 1	0.9779	0.0810	0.0998	0.6296
SUMO-activating enzyme subunit 2	0.0327	0.0007	0.9587	1.0000
SUN domain-containing protein 2	0.4216	0.3388	0.4721	0.8344
Superoxide dismutase [Cu-Zn]	0.5619	0.8408	0.7318	0.3366
Superoxide dismutase [Mn] mitochondrial	0.4419	0.5824	0.7011	0.4186
SWI/SNF complex subunit SMARCC1	0.5279	0.3103	0.4426	0.8836
SWI/SNF complex subunit SMARCC2	0.5816	0.5044	0.5473	0.5476
Switch-associated protein 70	0.8114	0.4235	0.3585	0.8637
Synaptic vesicle membrane protein VAT-1 homolog	0.4177	0.6645	0.7848	0.6795
Synaptojanin-2-binding protein	0.9836	0.8490	0.0880	0.4282
Synaptosomal-associated protein 23	0.9553	0.4529	0.0326	0.4998
Syntaxin-12	0.6159	0.8041	0.5002	0.4154
Syntaxin-4	0.7024	0.8453	0.4985	0.4702
Talin-1	0.5495	0.6445	0.7495	0.7165
Talin-2	0.2115	0.3578	0.9116	0.8988
T-complex protein 1 subunit alpha	0.7151	0.9694	0.4707	0.1307
T-complex protein 1 subunit beta	0.7046	0.8520	0.5365	0.3876
T-complex protein 1 subunit delta	0.6438	0.9211	0.5919	0.3268
T-complex protein 1 subunit epsilon	0.6340	0.8164	0.6651	0.4104
T-complex protein 1 subunit eta	0.5294	0.8909	0.6886	0.2816
T-complex protein 1 subunit gamma	0.5841	0.8346	0.6953	0.3643
T-complex protein 1 subunit theta	0.5818	0.8270	0.6634	0.3338
T-complex protein 1 subunit zeta	0.5064	0.8194	0.7101	0.4250
Thioredoxin	0.4181	0.9361	0.7852	0.2663
Thioredoxin domain-containing protein 12	0.4463	0.8376	0.6797	0.3184
Thioredoxin domain-containing protein 17	0.9941	0.9537	0.0107	0.0595
Thioredoxin domain-containing protein 5	0.0551	0.0023	0.9908	0.9995
Thioredoxin reductase 1 cytoplasmic	0.2829	0.9487	0.8795	0.1826
Thioredoxin-dependent peroxide reductase mitochondrial	0.9798	0.9150	0.0890	0.2951
Thioredoxin-like protein 1	0.3063	0.0869	0.8316	0.9911
Threonyl-tRNA synthetase cytoplasmic	0.5483	0.9139	0.5140	0.0342
Thrombospondin-1	0.0033	0.0051	0.9981	0.9932
Thymidylate kinase	0.4954	0.5047	0.7872	0.7270
Thymosin beta-10	0.0358	0.7043	0.6688	0.3180
Thymosin beta-4-like protein 3	0.0346	0.6549	0.8531	0.5214
Thyroid hormone receptor-associated protein 3	0.6734	0.5136	0.1250	0.8043
Tight junction protein ZO-1	0.4730	0.9477	0.7964	0.2137

Tight junction protein ZO-2	0.8324	0.9889	0.2728	0.0870
TLD domain-containing protein KIAA1609	0.4758	0.0619	0.5425	0.9421
Torsin-1A-interacting protein 1	0.6028	0.1123	0.6701	0.9791
TRAF2 and NCK-interacting protein kinase	0.9986	0.8941	0.0059	0.0380
Trans-2-enoyl-CoA reductase mitochondrial	0.7032	0.1939	0.3225	0.9568
Transaldolase	0.1885	0.1541	0.9440	0.9492
Transcription elongation factor A protein-like 5	0.9166	0.9506	0.0801	0.2631
Transcription elongation factor B polypeptide 1	0.3625	0.4152	0.8684	0.8560
Transcription factor BTF3	0.3072	0.7961	0.8504	0.4649
Transcription intermediary factor 1-beta	0.4987	0.5429	0.4004	0.6035
Transforming protein RhoA	0.7490	0.8550	0.4869	0.4887
Transgelin	0.0033	0.0002	0.6006	0.5557
Transgelin-2	0.2595	0.5071	0.7072	0.5829
Transitional endoplasmic reticulum ATPase	0.7182	0.6590	0.5780	0.7234
Transketolase	0.2180	0.7389	0.9242	0.4145
Translational activator GCN1	0.2088	0.2943	0.9430	0.8964
Translationally-controlled tumor protein	0.6546	0.7285	0.5488	0.5779
Translin-associated protein X	0.5063	0.5813	0.7332	0.6642
Translocator protein	0.9703	0.9021	0.0739	0.2281
Translocon-associated protein subunit alpha	0.9472	0.8480	0.0557	0.4021
Transmembrane emp24 domain-containing protein 10	0.5860	0.6628	0.6460	0.6655
Transmembrane emp24 domain-containing protein 9	0.4191	0.3249	0.6293	0.9042
Transmembrane protein 109	0.7268	0.9560	0.3749	0.2351
Transmembrane protein 43	0.5692	0.6054	0.7203	0.6762
Transportin-1	0.6302	0.9410	0.4739	0.2053
Trifunctional enzyme subunit alpha mitochondrial	0.8425	0.8138	0.3810	0.5169
Trifunctional enzyme subunit beta mitochondrial	0.6975	0.0828	0.3873	0.9529
Trifunctional purine biosynthetic protein adenosine-3	0.1186	0.8486	0.8097	0.0556
TRIO and F-actin-binding protein	0.6658	0.6556	0.3570	0.5365
Triosephosphate isomerase	0.4411	0.7306	0.7431	0.4891
Tripeptidyl-peptidase 1	0.5349	0.7544	0.2495	0.2151
Tripeptidyl-peptidase 2	0.5231	0.8144	0.6551	0.4533
tRNA-splicing ligase RtcB homolog	0.7074	0.5635	0.5838	0.7364
Tropomodulin-3	0.9805	0.9889	0.0860	0.0794
Tropomyosin alpha-1 chain	0.1248	0.2864	0.9687	0.9241
Tropomyosin alpha-3 chain	0.5905	0.9180	0.7031	0.3401
Tropomyosin alpha-4 chain	0.4406	0.7589	0.7844	0.5580
Tryptophanyl-tRNA synthetase cytoplasmic	0.8482	0.9316	0.1856	0.2365
Tubulin alpha-1C chain	0.1735	0.6937	0.9532	0.6770
Tubulin alpha-8 chain	0.1380	0.5222	0.9609	0.8117
Tubulin beta chain	0.3138	0.8206	0.8233	0.5417
Tubulin beta-2A chain	0.3508	0.8551	0.7844	0.4898
Tubulin beta-2C chain	0.3558	0.8402	0.7800	0.5114
Tubulin beta-3 chain	0.2750	0.8387	0.8537	0.5185
Tubulin beta-6 chain	0.4250	0.9056	0.7234	0.3826
Tubulin-folding cofactor B	0.4463	0.5780	0.5716	0.7261
Tubulin-specific chaperone A	0.5470	0.7414	0.7486	0.5825
Tumor protein D54	0.7781	0.7535	0.3647	0.3816
Tyrosine-protein phosphatase non-receptor type 1	0.9478	0.9863	0.0803	0.0738
Tyrosine-protein phosphatase non-receptor type 23	0.8920	0.7395	0.1918	0.4844
Tyrosyl-tRNA synthetase cytoplasmic	0.4059	0.9846	0.5310	0.0455
U1 small nuclear ribonucleoprotein 70 kDa	0.9890	0.5009	0.0469	0.7795
U2 small nuclear ribonucleoprotein A'	0.0050	0.1738	0.9992	0.9196
U6 snRNA-associated Sm-like protein LSm1	0.7648	0.9116	0.1149	0.1970
U6 snRNA-associated Sm-like protein LSm3	0.9716	0.9907	0.1060	0.0804
U8 snoRNA-decapping enzyme	0.7286	0.1235	0.5031	0.9595

Ubiquinone biosynthesis protein COQ9 mitochondrial	0.0024	0.0074	0.9734	0.1535
Ubiquitin carboxyl-terminal hydrolase 14	0.1382	0.4957	0.9266	0.7990
Ubiquitin carboxyl-terminal hydrolase 5	0.6917	0.7355	0.3571	0.5733
Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.2246	0.2825	0.0664	0.0111
Ubiquitin thioesterase OTUB1	0.2535	0.2283	0.8622	0.9465
Ubiquitin-40S ribosomal protein S27a	0.5835	0.8579	0.6493	0.0635
Ubiquitin-associated protein 2-like	0.0016	0.0019	0.9999	0.9998
Ubiquitin-conjugating enzyme E2 L3	0.5009	0.9160	0.7570	0.1127
Ubiquitin-conjugating enzyme E2 N	0.7780	0.9593	0.4785	0.1865
Ubiquitin-conjugating enzyme E2 variant 1	0.8677	0.8690	0.2722	0.4100
Ubiquitin-like modifier-activating enzyme 1	0.6409	0.7988	0.5951	0.4797
Ubiquitin-like-conjugating enzyme ATG3	0.1844	0.5424	0.9294	0.8001
UBX domain-containing protein 6	0.2885	0.7927	0.8593	0.4697
UDP-glucose 6-dehydrogenase	0.4520	0.2424	0.6332	0.9274
UDP-glucose:glycoprotein glucosyltransferase 1	0.2279	0.4857	0.9196	0.6300
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	0.1488	0.2221	0.9310	0.7641
UDP-N-acetylhexosamine pyrophosphorylase	0.8992	0.0260	0.3144	0.7819
UMP-CMP kinase	0.1164	0.0054	0.9689	0.9997
Uncharacterized glycosyltransferase AER61	0.0016	0.0009	0.9995	0.9999
Uncharacterized protein C1orf167	0.4863	0.0018	0.7146	0.9999
UPF0317 protein C14orf159 mitochondrial	0.6351	0.0883	0.6641	0.9723
UPF0366 protein C11orf67	0.9790	0.3581	0.0668	0.5718
UPF0568 protein C14orf166	0.6375	0.7681	0.3410	0.5308
UPF0585 protein C16orf13	0.4067	0.3938	0.8047	0.8752
UPF0765 protein C10orf58	0.9223	0.4882	0.2238	0.2469
Uridine 5'-monophosphate synthase	0.8966	0.9191	0.2370	0.3286
Uroporphyrinogen decarboxylase	0.4842	0.6810	0.7517	0.6665
Utrophin	0.7473	0.8246	0.5171	0.4451
UV excision repair protein RAD23 homolog B	0.0831	0.7543	0.9826	0.3602
Uveal autoantigen with coiled-coil domains and ankyrin repeats	0.9521	0.8054	0.1655	0.3128
Vacuolar protein sorting-associated protein 29	0.4420	0.9716	0.7556	0.1362
Vacuolar protein sorting-associated protein 33A	0.3311	0.4526	0.8031	0.8335
Vacuolar protein sorting-associated protein 35	0.4974	0.5476	0.4207	0.6991
Vacuolar protein sorting-associated protein 45	0.0145	0.0054	0.9970	0.9997
Vacuolar protein sorting-associated protein 4A	0.5442	0.5505	0.7204	0.7669
Vacuolar protein sorting-associated protein 4B	0.2753	0.2906	0.9160	0.9014
Vacuolar protein-sorting-associated protein 25	0.2863	0.6337	0.9106	0.5463
Valyl-tRNA synthetase	0.6777	0.8022	0.4139	0.5214
Vasodilator-stimulated phosphoprotein	0.1614	0.8257	0.9572	0.4974
Very long-chain specific acyl-CoA dehydrogenase mitochondrial	0.6805	0.2737	0.4563	0.9480
Vesicle-associated membrane protein-associated protein A	0.4013	0.7542	0.7230	0.4924
Vesicle-trafficking protein SEC22b	0.5657	0.0713	0.4727	0.9831
Vesicular integral-membrane protein VIP36	0.8285	0.9580	0.1451	0.1150
Vigilin	0.7790	0.4475	0.5044	0.8505
Vimentin	0.8453	0.1640	0.2154	0.3578
Vinculin	0.5259	0.6725	0.6723	0.6506
Voltage-dependent anion-selective channel protein 1	0.2789	0.7245	0.9076	0.6468
Voltage-dependent anion-selective channel protein 2	0.8247	0.8432	0.4411	0.4333
von Willebrand factor	0.0211	0.4564	0.3196	0.2415
V-type proton ATPase catalytic subunit A	0.7270	0.5851	0.2987	0.7427
V-type proton ATPase subunit B brain isoform	0.3476	0.0868	0.1437	0.9834
V-type proton ATPase subunit G 1	0.8445	0.5976	0.0915	0.6306
WD repeat-containing protein 1	0.4032	0.6363	0.8277	0.7492
WD40 repeat-containing protein SMU1	0.4002	0.1388	0.7875	0.6048
Xaa-Pro aminopeptidase 1	0.1797	0.2232	0.9517	0.9208
X-ray repair cross-complementing protein 5	0.0002	0.0000	1.0000	1.0000

X-ray repair cross-complementing protein 6	0.4484	0.6645	0.6354	0.2454
Zinc finger CCCH domain-containing protein 15	0.1426	0.1741	0.9546	0.7324
Zinc finger protein 185	0.8918	0.8028	0.0037	0.0230
Zinc finger protein ZPR1	0.4938	0.5414	0.6965	0.7714
Zyxin	0.0409	0.0493	0.9873	0.9067

Suppl.Table 5. Comparison between the proteomic and the miRNA microarray

Protein	Accesion	iTRAQ	miRNAs	Refseq	mirarray
MirTarget2					
cysteine-rich, angiogenic inducer, 61	O00622	down	hsa-miR-4330	NM_001554	up
ATP-binding cassette, sub-family A (ABC1), member 1	O95477	down	hsa-miR-4330	NM_005502	up
heat shock 60kDa protein 1 (chaperonin)	P10809	down	hsa-miR-3194-5p	NM_002156	up
PicTar					
SEC22B SEC22 vesicle trafficking protein homolog B	O75396	down	hsa-miR-4296	NM_004892	up
ATP-binding cassette, sub-family A (ABC1), member 1	O95477	down	hsa-miR-4330	NM_005502	up
ASPH aspartate beta-hydroxylase	Q12797	down	hsa-miR-670	NM_001164756	up
miRanda					
Dab, mitogen-responsive phosphoprotein, homolog 2	P98082	down	hsa-miR-15a	NM_001343	up
heterogeneous nuclear ribonucleoprotein L	P14866	down	hsa-miR-15a	NM_001533	up
reticulon 4	Q9NQC3	down	hsa-miR-15a	NM_020532	up
syntrophin, beta 2	Q13425	down	hsa-miR-15a	NM_006750	up
EH-domain containing 4	Q9H223	up	hsa-miR-124	NM_139265	down
SH3-domain GRB2-like 1	Q99961	up	hsa-miR-33a	NM_003025	down
polypyrimidine tract binding protein 1	P26599	up	hsa-miR-124	NM_002819	down
threonyl-tRNA synthetase	P26639	up	hsa-miR-33a	NM_152295	down
karyopherin alpha 3 (importin alpha 4)	O00505	up	hsa-miR-33a	NM_002267	down
karyopherin alpha 3 (importin alpha 4)	O00505	up	hsa-miR-124	NM_002267	down
nuclear casein kinase and cyclin-dependent kinase substrate 1	Q9H1E3	up	hsa-miR-33a	NM_022731	down
lactate dehydrogenase B	P07195	up	hsa-miR-375	NM_002300	down
ATP-binding cassette, sub-family E (OABP), member 1	P61221	up	hsa-miR-33a	NM_002940	down
EH-domain containing 3	Q9NZN3	up	hsa-miR-33a	NM_014600	down
proliferating cell nuclear antigen	P12004	up	hsa-miR-33a	NM_182649	down
t-complex 1	P17987	up	hsa-miR-33a	NM_030752	down
Ran GTPase activating protein 1	P46060	up	hsa-miR-196b	NM_002883	down
peroxiredoxin 6	P30041	up	hsa-miR-124	NM_004905	down
peroxiredoxin 6	P30041	up	hsa-miR-375	NM_004905	down
TargetScan					
EH-domain containing 4	Q9H223	up	miR-34ac/34bc-5p/449abc/449c-5p	NM_139265	down
polypyrimidine tract binding protein 1	P26599	up	miR-124/124ab/506	NM_002819	down
karyopherin alpha 3 (importin alpha 4)	O00505	up	miR-124/124ab/506	NM_002267	down

lactate dehydrogenase B	P07195	up	miR-375	NM_001174097	down
nuclear autoantigenic sperm protein (histone-binding)	P49321	up	miR-124/124ab/506	NM_152298	down
ubiquitin-conjugating enzyme E2L 3p	P68036	up	miR-34ac/34bc-5p/449abc/449c-5p	NM_003347	down
EH-domain containing 3	Q9NZN3	up	miR-124/124ab/506	NM_014600	down
peroxiredoxin 6	P30041	up	miR-124/124ab/506	NM_004905	down
LIM and senescent cell antigen-like domains 1	P48059	down	miR-15abc/16/16abc/195/322/424/497/1907	NM_001193482	up
A kinase (PRKA) anchor protein 13	Q12802	down	miR-125a-5p/125b-5p/351/670/4319	NM_006738	up
A kinase (PRKA) anchor protein 13	Q12802	down	miR-15abc/16/16abc/195/322/424/497/1907	NM_006738	up
mitogen-activated protein kinase 14	Q16539	down	miR-125a-5p/125b-5p/351/670/4319	NM_001315	up
reticulon 4	Q9NQC3	down	miR-15abc/16/16abc/195/322/424/497/1907	NM_007008	up
syntrophin, beta 2	Q13425	down	miR-15abc/16/16abc/195/322/424/497/1907	NM_006750	up
ASPH aspartate beta-hydroxylase	Q12797	down	miR-15abc/16/16abc/195/322/424/497/1907	NM_001164751	up

Suppl.Table 6. Demographics of the IPAH patients and controls used for PAEC isolation

Subject ID	Age	Sex	Ethnicity	mPAP
PAEC-C1	51	F	Caucasian	
PAEC-C2	50	F	Caucasian	
PAEC-C3	51	M	Caucasian	
PAEC-C4	36	F	Caucasian	
PAEC-IPAH1	32	F	Caucasian	70
PAEC-IPAH2	53	F	Caucasian	53
PAEC-IPAH3	27	M	Caucasian	68
PAEC-IPAH4	40	M	Caucasian	73
PAEC-IPAH5	32	F	Caucasian	49
PAEC-IPAH6	16	F	Caucasian	95