Supporting Information for the *International Journal of Mass Spectrometry*:

Protein Expression by Human Pulmonary Artery Smooth Muscle Cells Containing a *BMPR2* Mutation and the Action of ET-1 as Determined by Proteomic Mass Spectrometry

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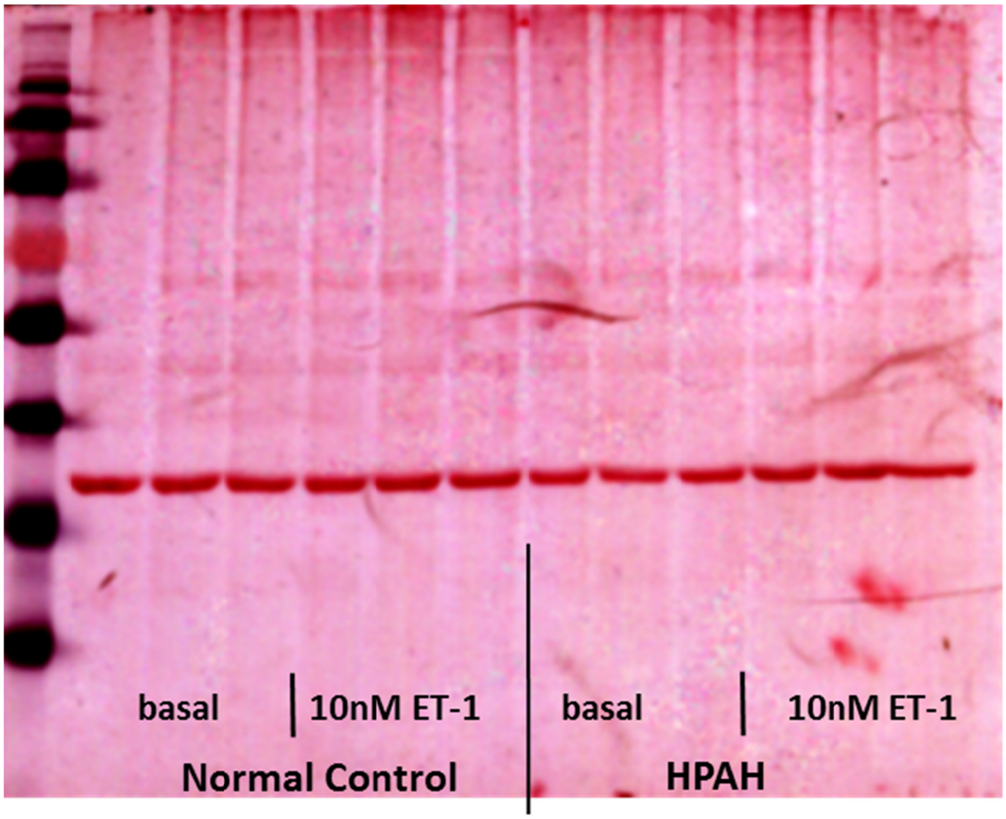
Page 2	**Supplementary Figure 1A.** The cultured human pulmonary smooth muscle cells were stained with antibodies against smooth muscle α-actin.
Page 3	**Supplementary Figure 1B.** The whole image of the Western blot after Ponceau S staining.
Page 4	**Supplementary Figure 2.** Differentially expressed proteins related to protein synthesis.
Page 8	**Supplementary Figure 3.** Differentially expressed proteins related with RhoA signaling, cytoskeleton organization and muscle contraction. The diagrams in 3A, 3B, and 3C present illustrations of the three comparisons.
Page 12	**Supplementary Table 1 (Separate Excel file).** Differentially expressed proteins in Control and PAH PASMC cells, in the absence and presence of ET-1.
Page 12	**Supplementary Table 2.** Detailed description of protein expression changes in described canonical pathways
Page 50	**Supplementary Table 3.** Meta data for Figure 5 and Supplementary Figure 2.
Page 53	**Supplementary Table 4.** Meta data for Figure 6 and Supplementary Figure 3.
Page 56	**Supplementary Table 5.** (a) CV% (or % RSD) based on summed intensity of respective proteins (b) T-test calculations indicated the significance of changes from replicate analyses in group comparison.

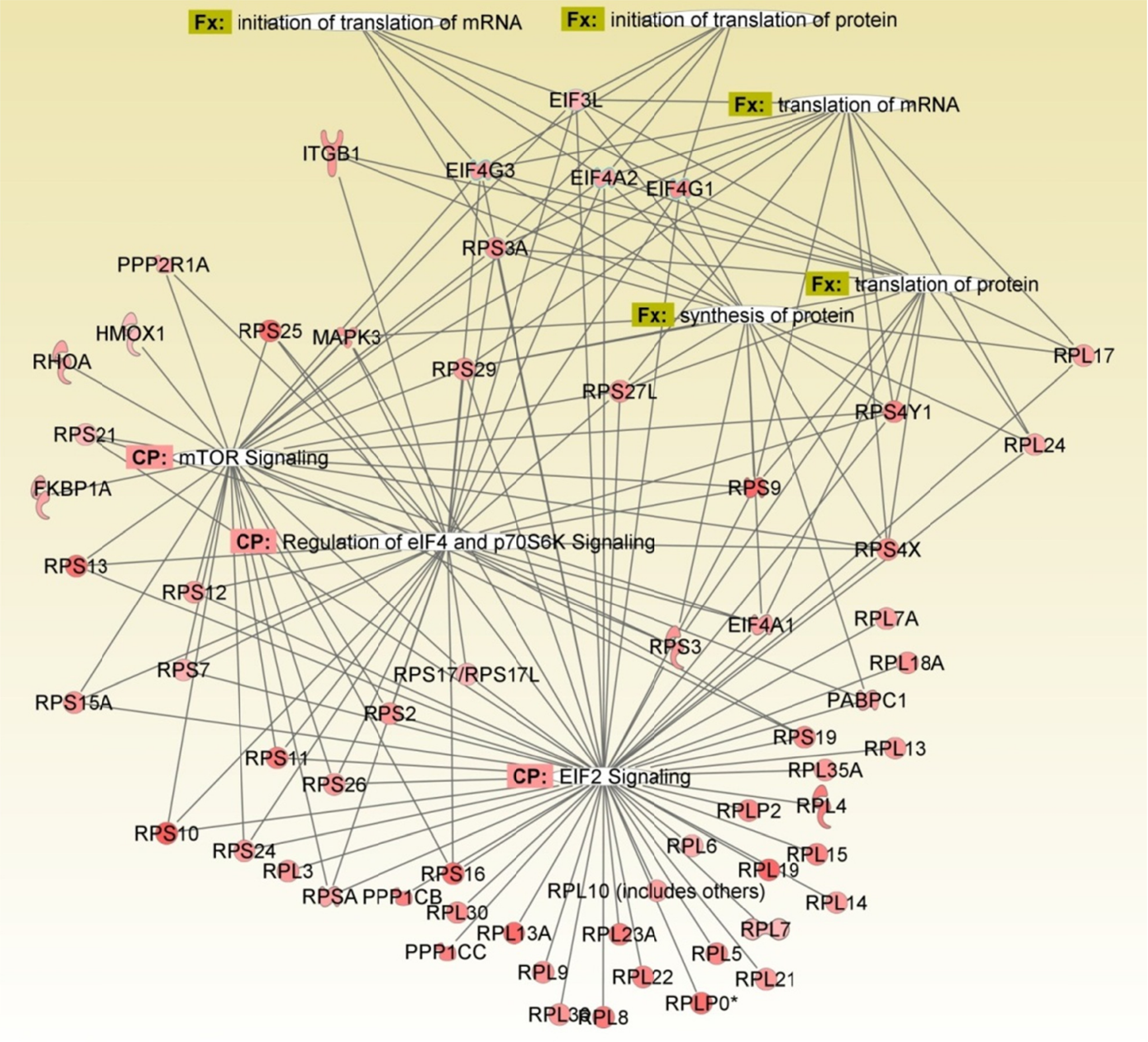
Supplementary Figure 1A. The cultured human pulmonary smooth muscle cells were stained with antibodies against smooth muscle α-actin.

Supplementary Figure 1B. The whole image of the Western blot after Ponceau S staining. After the transfer, the blot was stained for proteins using Ponceau S for 5 min, then, destained in 1% acetic acid until background is reduced. The stained blot was scanned for a permanent record. The blot was then rinsed with TBS-Tween to remove Ponceau S.

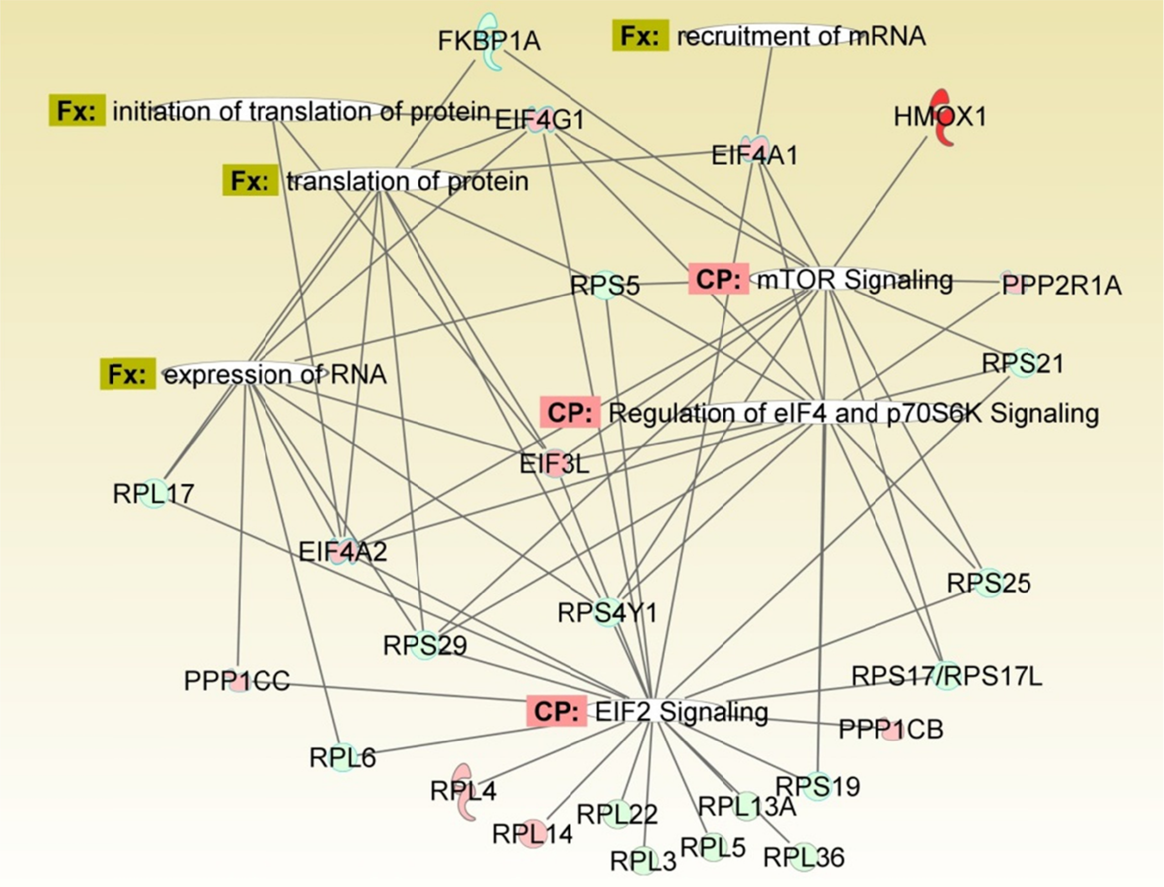


Supplementary Figure 2. Differentially expressed proteins related to protein synthesis. A, B, and C illustrate the diagram of the three comparisons. A. ET-1 treated *vs*. basal in PAH PASMC; B. PAH cells *vs*. Control cells under basal conditions; C. PAH *vs*. Control cells, both with ET-1 stimulation. The nodes represent different proteins. Green indicates downregulation, red indicates upregulation, and color intensity is proportional to fold change. The full name and fold changes of these proteins can be found in Supplementary Table 3. The annotations are supported by at least one reference from the literature, a textbook, or canonical information stored in the Ingenuity knowledge base.

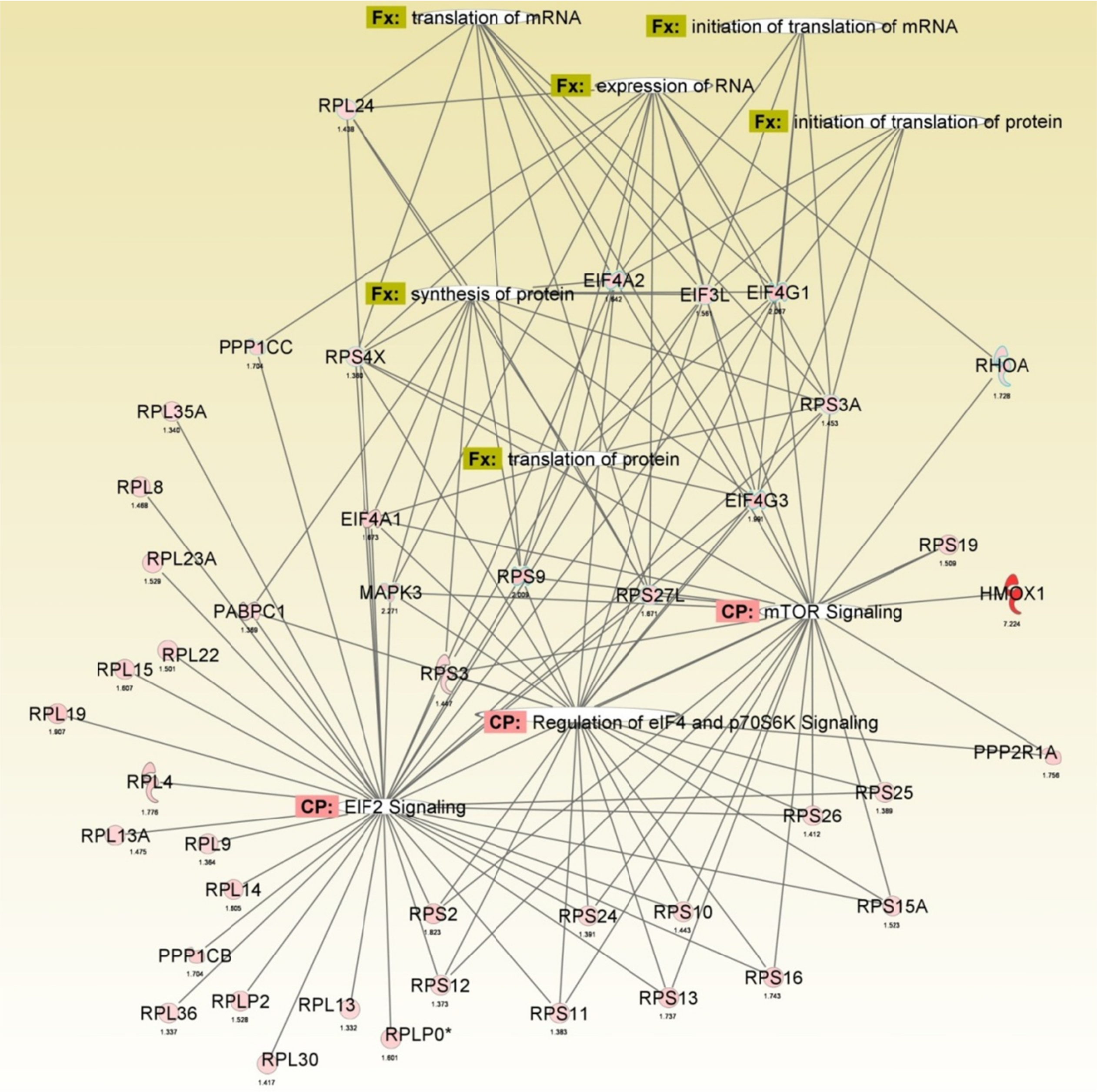
2A. Protein expression changes found in ET-1 treated PAH compared with basal.



2B. Protein expression changes found in PAH compared with CONTROL without ET-1 stimulation.

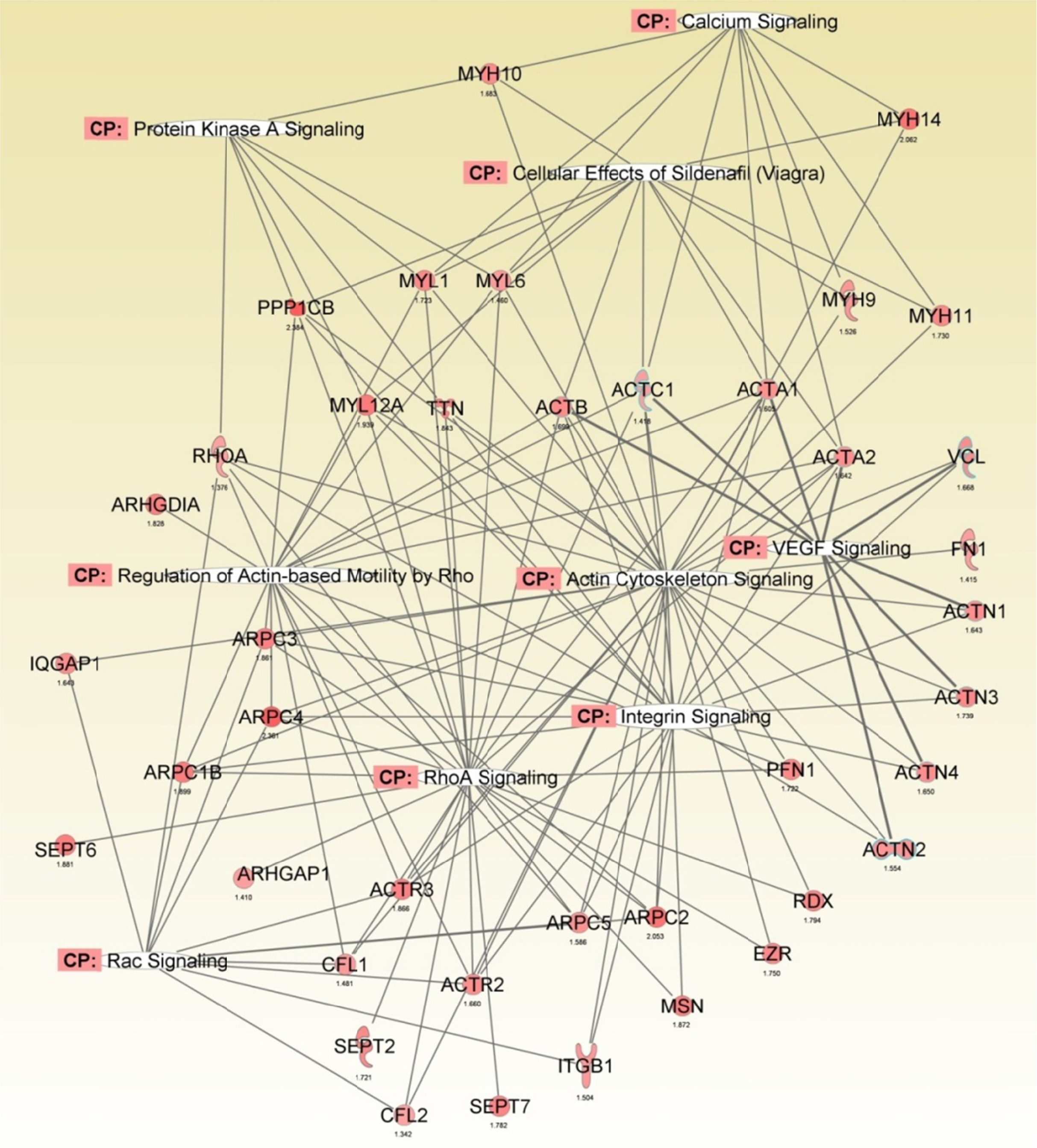


2C. Protein expression changes found in PAH compared with CONTROL both with ET-1 stimulation.

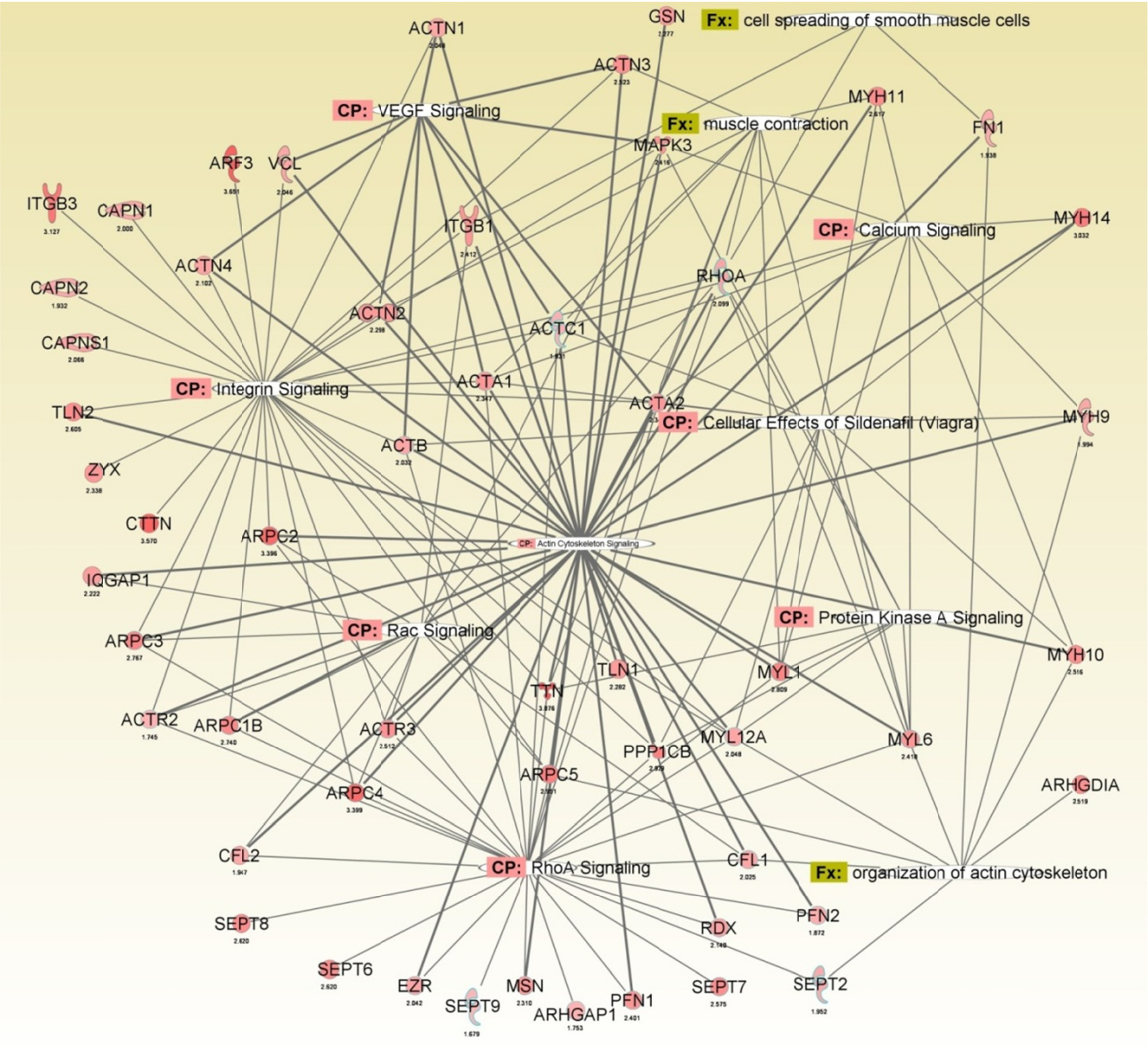


Supplementary Figure 3. Differentially expressed proteins related with RhoA signaling, cytoskeleton organization and muscle contraction. A, B, and C illustrate the diagram of the three comparisons. A. ET-1 treated *vs*. basal in PAH PASMC; B. PAH cells *vs*. Control cells under basal conditions; C. PAH *vs*. Control cells, both with ET-1 stimulation. The full name and fold changes of these proteins can be found in Supplementary Table 4.

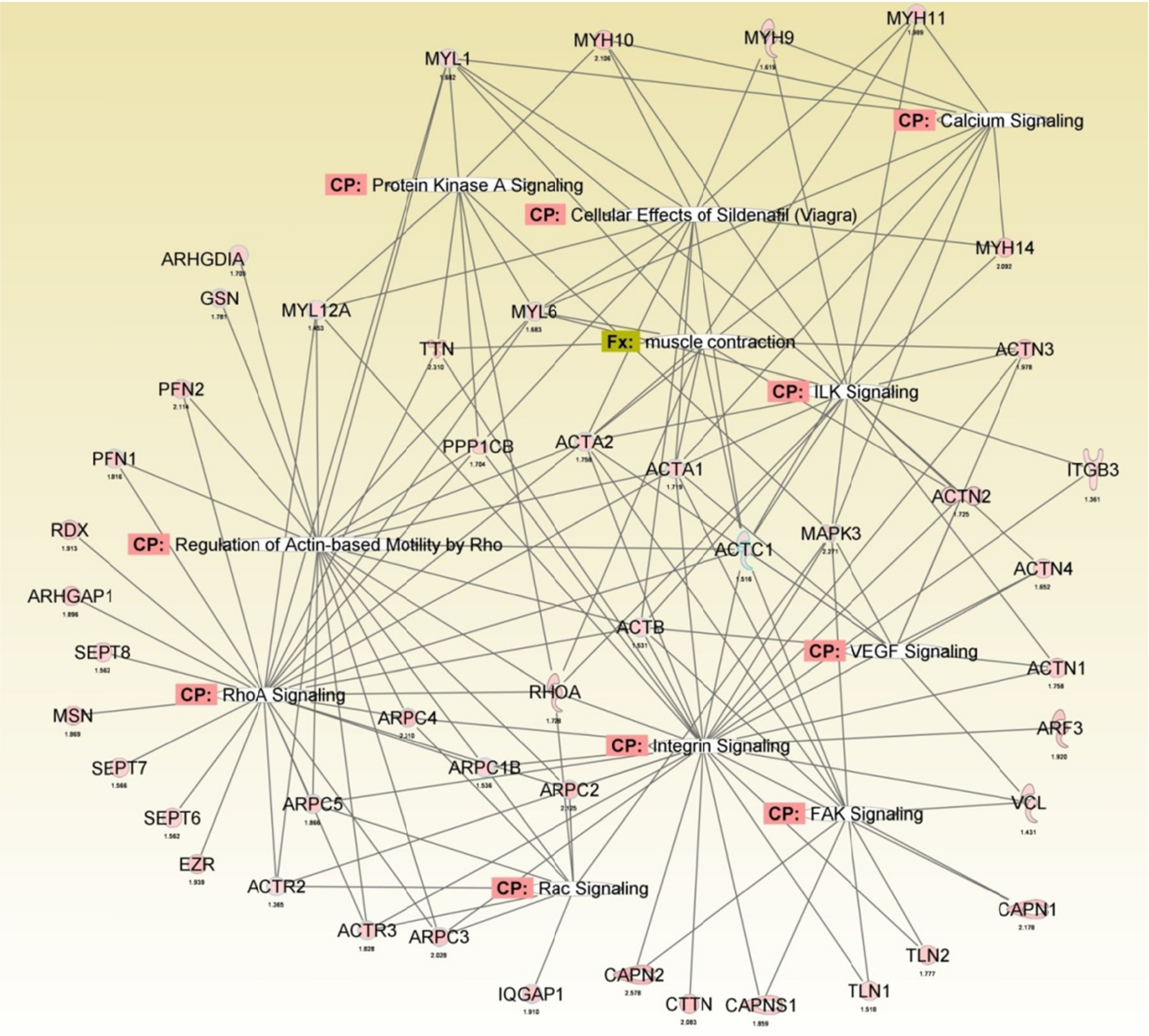
3A. protein expression changes found in ET-1 treated CONTROL compared with basal.



3B. Protein expression changes found in ET-1 treated PAH compared with basal.



3C. Protein expression changes found in PAH compared with CONTROL both with ET-1 stimulation.



Supplementary Table 1. Differentially expressed proteins in Control and PAH PASMC cells, in the absence and presence of ET-1. This table is presented as a separate Microsoft Excel file.

Supplementary Table 2. Detailed description of protein expression changes in described canonical pathways. The table shows the Symbol, Entrez Gene Name and Entrez Gene ID of the proteins. The fold changes of the proteins are shown for the four comparisons. A1: the change of protein expression in ET-1 treated *vs.* basal in Control PASMC; A2: the change of protein expression in ET-1 treated *vs.* basal in the PAH PASMC; A3: the change of protein expression in PAH cells *vs.* Control cells without ET-1 stimulation; A4: the change of protein expression in PAH cells *vs.* Control cells, both with ET-1 stimulation.

1. eIF2 (Eukaryotic Initiation Factor 2) signaling

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
EIF3L	eukaryotic translation initiation factor 3, subunit L	1.95	1.68	1.81	1.56
EIF4A1	eukaryotic translation initiation factor 4A1	1.80	2.20	1.37	1.67
EIF4A2	eukaryotic translation initiation factor 4A2	1.71	2.07	1.36	1.64
EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	1.79	2.52	1.47	2.07
EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	1.35	2.24	1.20	1.99
PABPC1	poly(A) binding protein, cytoplasmic 1	1.68	2.22	1.03	1.37
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.
PPP1CC	protein phosphatase 1,	2.38	2.93	1.39	1.70

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
	catalytic subunit, gamma isozyme				
RPL4	ribosomal protein L4	2.56	3.01	1.51	1.78
RPL5	ribosomal protein L5	1.50	2.73	-1.42	1.29
RPL7	ribosomal protein L7	1.38	1.60	-1.02	1.14
RPL8	ribosomal protein L8	1.68	3.06	-1.25	1.47
RPL9	ribosomal protein L9	1.99	2.49	1.09	1.36
RPL13	ribosomal protein L13	1.44	2.33	-1.21	1.33
RPL14	ribosomal protein L14	1.92	2.25	1.37	1.61
RPL15	ribosomal protein L15	1.41	2.80	-1.23	1.61
RPL19	ribosomal protein L19	1.50	3.47	-1.21	1.91
RPL21	ribosomal protein L21	1.68	2.26	-1.08	1.25
RPL22	ribosomal protein L22	1.36	2.86	-1.41	1.50
RPL24	ribosomal protein L24	1.60	2.03	1.13	1.44
RPL30	ribosomal protein L30	1.68	2.55	-1.07	1.42
RPL10 (includes others)	ribosomal protein L10	1.63	2.16	-1.02	1.30
RPL13A	ribosomal protein L13a	1.70	3.35	-1.34	1.48
RPL18A	ribosomal protein L18a	1.83	2.45	-1.05	1.27
RPL23A	ribosomal protein L23a	1.71	2.97	-1.13	1.53
RPL35A	ribosomal protein L35a	1.35	2.33	-1.29	1.34
RPL7A	ribosomal protein L7a	1.54	2.16	-1.12	1.25
RPLP0	ribosomal protein, large, P0	2.23	3.23	1.17	1.60
RPLP2	ribosomal protein, large, P2	2.28	2.72	1.28	1.53

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
RPS2	ribosomal protein S2	1.54	2.42	1.16	1.82
RPS3	ribosomal protein S3	1.66	2.40	1.00	1.45
RPS7	ribosomal protein S7	1.51	1.76	-1.07	1.10
RPS9	ribosomal protein S9	1.86	3.48	1.08	2.01
RPS10	ribosomal protein S10	2.31	3.75	-1.13	1.44
RPS11	ribosomal protein S11	1.83	3.01	-1.19	1.38
RPS13	ribosomal protein S13	2.40	3.28	1.27	1.74
RPS16	ribosomal protein S16	1.73	3.35	-1.11	1.74
RPS19	ribosomal protein S19	1.35	2.71	-1.33	1.51
RPS24	ribosomal protein S24	1.97	2.36	1.16	1.39
RPS25	ribosomal protein S25	1.82	3.37	-1.34	1.39
RPS26	ribosomal protein S26	1.81	2.32	1.10	1.41
RPS15A	ribosomal protein S15a	1.86	2.41	1.17	1.52
RPS27L	ribosomal protein S27-like	1.35	2.39	-1.06	1.67
RPS3A	ribosomal protein S3A	1.55	2.49	-1.11	1.45
RPS4X	ribosomal protein S4, X-linked	1.73	2.67	-1.13	1.36
RPS4Y1	ribosomal protein S4, Y-linked 1	1.60	2.77	-1.52	1.14
RPSA	ribosomal protein SA	1.46	2.10	-1.28	1.12

2. RhoA signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.77
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARHGAP1	Rho GTPase activating protein 1	1.41	1.75	1.53	1.90
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
CFL2	cofilin 2 (muscle)	1.34	1.95	-1.21	1.20
EZR	ezrin	1.75	2.04	1.66	1.94
MSN	moesin	1.87	2.31	1.51	1.87

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.63
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	1.94	2.05	1.38	1.45
PFN1	profilin 1	1.72	2.40	1.30	1.82
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70
RDX	radixin	1.79	2.14	1.60	1.91
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73
SEPT2	septin 2	1.72	1.95	1.17	1.32
SEPT6	septin 6	1.88	2.62	1.12	1.56
SEPT7	septin 7	1.78	2.58	1.08	1.57
SEPT8	septin 8	1.88	2.62	1.12	1.56
TTN	titin	1.84	3.88	1.10	2.31

3. Actin Cytoskeleton associated Signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ACTN1	actinin, alpha 1	1.64	2.05	1.41	1.76
ACTN2	actinin, alpha 2	1.55	2.30	1.17	1.73
ACTN3	actinin, alpha 3	1.74	2.52	1.36	1.98
ACTN4	actinin, alpha 4	1.65	2.10	1.30	1.65
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
CFL2	cofilin 2 (muscle)	1.34	1.95	-1.21	1.20
EZR	ezrin	1.75	2.04	1.66	1.94

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
FN1	fibronectin 1	1.42	1.94	-1.18	1.16
GSN	gelsolin	1.70	2.28	1.33	1.78
IQGAP1	IQ motif containing GTPase activating protein 1	1.64	2.22	1.41	1.91
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
MSN	moesin	1.87	2.31	1.51	1.87
MYH9	myosin, heavy chain 9, non-muscle	1.53	1.99	1.24	1.62
MYH10	myosin, heavy chain 10, non-muscle	1.68	2.52	1.41	2.11
MYH11	myosin, heavy chain 11, smooth muscle	1.73	2.62	1.32	1.99
MYH14	myosin, heavy chain 14, non-muscle	2.06	3.03	1.42	2.09
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	1.94	2.05	1.38	1.45
PFN1	profilin 1	1.72	2.40	1.30	1.82
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70
RDX	radixin	1.79	2.14	1.60	1.91
RHOA	ras homolog family member	1.38	2.10	1.13	1.73

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
	A				
TTN	titin	1.84	3.88	1.10	2.31
VCL	vinculin	1.67	2.05	1.17	1.431

4. Regulation of eIF4 and p70S6K Signaling

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
EIF3L	eukaryotic translation initiation factor 3, subunit L	1.95	1.68	1.81	1.56
EIF4A1	eukaryotic translation initiation factor 4A1	1.80	2.20	1.37	1.67
EIF4A2	eukaryotic translation initiation factor 4A2	1.71	2.07	1.36	1.64
EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	1.79	2.52	1.47	2.07
EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	1.35	2.24	1.20	1.99
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
PABPC1	poly(A) binding protein, cytoplasmic 1	1.68	2.22	1.03	1.37
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	1.54	1.97	1.37	1.76
RPS2	ribosomal protein S2	1.54	2.42	1.16	1.82

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
RPS3	ribosomal protein S3	1.66	2.40	1.00	1.45
RPS7	ribosomal protein S7	1.51	1.76	-1.07	1.10
RPS9	ribosomal protein S9	1.86	3.48	1.08	2.01
RPS10	ribosomal protein S10	2.31	3.75	-1.13	1.44
RPS11	ribosomal protein S11	1.83	3.01	-1.19	1.38
RPS13	ribosomal protein S13	2.40	3.28	1.27	1.74
RPS16	ribosomal protein S16	1.73	3.35	-1.11	1.74
RPS19	ribosomal protein S19	1.35	2.71	-1.33	1.51
RPS24	ribosomal protein S24	1.97	2.36	1.16	1.39
RPS25	ribosomal protein S25	1.82	3.37	-1.34	1.39
RPS26	ribosomal protein S26	1.81	2.32	1.10	1.41
RPS15A	ribosomal protein S15a	1.86	2.41	1.17	1.52
RPS27L	ribosomal protein S27-like	1.35	2.39	-1.06	1.67
RPS3A	ribosomal protein S3A	1.55	2.49	-1.11	1.45
RPS4X	ribosomal protein S4, X-linked	1.73	2.67	-1.13	1.36
RPS4Y1	ribosomal protein S4, Y-linked 1	1.60	2.77	-1.52	1.14
RPSA	ribosomal protein SA	1.46	2.10	-1.28	1.12

5. 14-3-3-mediated Signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
PDCD6IP	programmed cell death 6 interacting protein	1.47	2.02	1.433	1.966
PDIA3	protein disulfide isomerase family A, member 3	1.61	2.41	1.02	1.53
TUBA8	tubulin, alpha 8	1.68	2.12	1.17	1.48
TUBA1A	tubulin, alpha 1a	1.79	2.07	1.22	1.41
TUBA1B	tubulin, alpha 1b	1.46	1.80	1.05	1.29
TUBA1C	tubulin, alpha 1c	1.68	2.12	1.17	1.48
TUBA4A	tubulin, alpha 4a	1.62	2.00	1.76	2.17
TUBA4B	tubulin, alpha 4b (pseudogene)	2.21	2.11	1.39	1.32
TUBB1	tubulin, beta 1 class VI	2.01	2.45	1.16	1.41
TUBB3	tubulin, beta 3 class III	1.41	1.72	1.63	1.98
TUBB4	tubulin, beta 4A class IVa	1.62	1.91	1.43	1.68
TUBB6	tubulin, beta 6 class V	1.43	1.85	1.58	2.03
TUBB8	tubulin, beta 8 class VIII	2.03	2.52	1.08	1.34
TUBB	tubulin, beta class I	1.73	2.32	1.05	1.41
TUBB2A	tubulin, beta 2A class IIa	1.49	2.20	-1.18	1.25
TUBB2C	tubulin, beta 4B class IVb	1.43	2.75	-1.59	1.21
TUBB4Q	--	2.03	2.52	1.18	1.34
VIM	vimentin	1.56	2.12	1.25	1.69
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	1.80	2.68	1.13	1.68
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation	1.88	3.85	-1.04	1.97

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
	protein, epsilon polypeptide				
YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	1.68	2.40	-1.19	1.20
YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	1.63	2.14	-1.07	1.22
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	1.85	2.76	1.23	1.84

6. Integrin Signaling

Symbol	Entrez Gene Name	Fold Change (A1#)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.642	2.34	1.23	1.76
ACTB	actin, beta	1.69	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ACTN1	actinin, alpha 1	1.64	2.05	1.41	1.76
ACTN2	actinin, alpha 2	1.55	2.30	1.17	1.73
ACTN3	actinin, alpha 3	1.74	2.52	1.36	1.98
ACTN4	actinin, alpha 4	1.65	2.10	1.30	1.65
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARF3	ADP-ribosylation factor 3	2.87	3.65	1.511	1.92
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54

Symbol	**Entrez Gene Name**	**Fold Change (A1#)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
CAPN2	calpain 2, (m/II) large subunit	1.37	1.93	1.838	2.58
CAPNS1	calpain, small subunit 1	1.510	2.07	1.36	1.869
CTTN	cortactin	1.710	3.57	1.00	2.08
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1.46	3.13	-1.57	1.36
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	1.94	2.05	1.38	1.45
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73
TLN1	talin 1	1.54	2.28	1.02	1.52
TLN2	talin 2	1.44	2.61	-1.02	1.78
TTN	titin	1.84	3.88	1.10	2.31
VCL	vinculin	1.67	2.05	1.12	1.43
ZYX	zyxin	1.38	2.34	-1.42	1.19

7. Regulation of Actin-based Motility by Rho

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.729
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	1.83	2.52	1.24	1.71
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
GSN	gelsolin	1.70	2.28	1.33	1.78
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
MYL12A	myosin, light chain 12A,	1.94	2.05	1.38	1.45

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
	regulatory, non-sarcomeric				
PFN1	profilin 1	1.72	2.40	1.30	1.82
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73

8. Protein Ubiquitination Pathway

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	1.70	2.65	4.02	6.29
HLA-B	major histocompatibility complex, class I, B	1.64	2.53	1.69	2.60
HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	1.91	2.48	1.33	1.73
HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	1.91	2.40	1.31	1.65
HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	1.78	2.48	1.14	1.59
HSPA2	heat shock 70kDa protein 2	1.83	2.49	1.12	1.52
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	1.80	2.37	-1.02	1.29
HSPA6	heat shock 70kDa protein 6 (HSP70B')	1.85	2.16	1.53	1.79
HSPA8	heat shock 70kDa protein 8	1.65	2.34	-1.06	1.33
HSPA9	heat shock 70kDa protein 9 (mortalin)	1.35	1.59	1.44	1.70
HSPA1L	heat shock 70kDa protein 1-like	1.66	1.88	1.62	1.83
HSPD1	heat shock 60kDa protein 1 (chaperonin)	1.89	2.36	1.31	1.63
HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	1.73	2.51	1.24	1.80
PSMA1	proteasome (prosome, macropain) subunit, α type, 1	2.10	2.89	1.30	1.79
PSMA2	proteasome (prosome, macropain) subunit,α type, 2	1.72	1.97	1.32	1.51
PSMA3	proteasome (prosome, macropain) subunit, α type, 3	1.52	2.28	1.01	1.52

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
PSMA5	proteasome (prosome, macropain) subunit, α type, 5	1.99	2.45	1.36	1.68
PSMA6	proteasome (prosome, macropain) subunit, α type, 6	1.39	2.56	-1.13	1.63
PSMA7	proteasome (prosome, macropain) subunit, α type, 7	1.80	2.14	1.21	1.44
PSMB1	proteasome (prosome, macropain) subunit, β type, 1	1.60	1.92	1.21	1.45
PSMB2	proteasome (prosome, macropain) subunit, βtype, 2	1.42	2.57	-1.01	1.80
PSMB3	proteasome (prosome, macropain) subunit, β type, 3	2.02	2.38	1.40	1.65
PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	1.50	1.97	1.07	1.40
PSMD8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	1.91	1.68	1.88	1.65
PSME1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	2.56	3.69	1.56	2.24
PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	1.72	2.17	1.30	1.64
UBA1	ubiquitin-like modifier activating enzyme 1	1.67	2.05	1.01	1.24
UBE2N	ubiquitin-conjugating enzyme E2N	1.78	2.29	1.28	1.65
USO1	USO1 vesicle docking protein homolog (yeast)	1.97	3.58	-1.10	1.65
USP5	ubiquitin specific peptidase 5 (isopeptidase T)	1.52	1.72	1.58	1.78

9. Glycolysis/Gluconeogenesis

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	1.63	2.14	1.24	1.64
ALDH9A1	aldehyde dehydrogenase 9 family, member A1	1.55	2.27		2.62
ALDOA	aldolase A, fructose-bisphosphate	1.45	1.99	-1.16	1.19
ENO1	enolase 1, (alpha)	1.46	1.87	1.03	1.32
ENO2	enolase 2 (gamma, neuronal)	1.59	1.72	1.28	1.38
ENO3	enolase 3 (beta, muscle)	1.60	1.71	1.27	1.37
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	1.59	1.93	1.06	1.28
GPI	glucose-6-phosphate isomerase	1.57	1.98	1.31	1.66
HK1	hexokinase 1	1.43	1.62	1.69	1.92
LDHA	lactate dehydrogenase A	1.70	2.88	1.33	2.26
LDHAL6A	lactate dehydrogenase A-like 6A	1.41	2.70	1.11	2.13
LDHAL6B	lactate dehydrogenase A-like 6B	2.33	3.30	1.86	2.64
LDHB	lactate dehydrogenase B	1.49	2.59	1.17	2.05
PFKL	phosphofructokinase, liver	1.74	2.37	1.17	1.60
PGAM1	phosphoglycerate mutase 1 (brain)	1.33	2.12	-1.28	1.24
PGK1	phosphoglycerate kinase 1	1.64	2.40	-1.21	1.21
PGK2	phosphoglycerate kinase 2	1.75	2.42	-1.15	1.20
PGM1	phosphoglucomutase 1	2.09	1.92	1.97	1.81

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
PKM2	pyruvate kinase, muscle	1.69	1.74	1.107	1.13
TPI1	triosephosphate isomerase 1	1.43	2.36	-1.23	1.34

10. ILK (Integrin Linked Kinase) Signaling

Symbol	Entrez Gene Name	Fold Change (A1#)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.526
ACTN1	actinin, alpha 1	1.64	2.05	1.41	1.76
ACTN2	actinin, alpha 2	1.55	2.30	1.17	1.73
ACTN3	actinin, alpha 3	1.74	2.52	1.36	1.98
ACTN4	actinin, alpha 4	1.65	2.10	1.30	1.65
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
CFL2	cofilin 2 (muscle)	1.34	1.95	-1.21	1.20
FLNA	filamin A, alpha	1.57	2.04	1.49	1.94
FLNB	filamin B, beta	1.97	2.20	1.41	1.58
FLNC	filamin C, gamma	1.47	1.85	-1.58	-1.26
FN1	fibronectin 1	1.42	1.94	-1.18	1.16
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1.46	3.13	-1.57	1.36
MYH9	myosin, heavy chain 9, non-muscle	1.53	1.99	1.24	1.62
MYH10	myosin, heavy chain 10, non-muscle	1.68	2.52	1.41	2.11

Symbol	**Entrez Gene Name**	**Fold Change (A1#)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
MYH11	myosin, heavy chain 11, smooth muscle	1.73	2.62	1.32	1.99
MYH14	myosin, heavy chain 14, non-muscle	2.06	3.03	1.42	2.09
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	1.54	1.97	1.37	1.76
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73
VIM	vimentin	1.57	2.12	1.25	1.69

11. Protein Kinase A Signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
AKAP12	A kinase (PRKA) anchor protein 12	1.36	1.87	-3.80	-2.77
CAMK2A	calcium/calmodulin-dependent protein kinase II α	1.71	1.90	1.54	1.71
CAMK2B	calcium/calmodulin-dependent protein kinase II β	1.63	2.03	1.38	1.71
CAMK2D	calcium/calmodulin-dependent protein kinase II δ	1.72	2.22	1.42	1.83
CAMK2G	calcium/calmodulin-dependent protein kinase II γ	1.63	2.03	1.38	1.71
FLNA	filamin A, α	1.57	2.04	1.49	1.94
FLNB	filamin B, β	1.97	2.20	1.41	1.57
FLNC	filamin C, γ	1.47	1.85	-1.58	-1.26
GNB1	guanine nucleotide binding protein (G protein), β polypeptide 1	1.86	3.62	-1.06	1.83
GNB2	guanine nucleotide binding protein (G protein), β polypeptide 2	1.98	3.27	1.01	1.67
GNB3	guanine nucleotide binding protein (G protein), β polypeptide 3	2.59	4.64	1.20	2.15
GNB4	guanine nucleotide binding protein (G protein), β polypeptide 4	2.76	4.71	1.25	2.13
GNB2L1	guanine nucleotide binding protein (G protein), β polypeptide 2-like 1	2.39	3.54	1.01	1.49
HIST3H3	histone cluster 3, H3	1.66	3.41	-1.67	1.23
HLA-B	major histocompatibility complex, class I, B	1.64	2.53	1.69	2.60

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
MYH10	myosin, heavy chain 10, non-muscle	1.68	2.52	1.41	2.11
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	1.94	2.05	1.38	1.45
PDIA3	protein disulfide isomerase family A, member 3	1.61	2.41	1.02	1.53
PPP1CB	protein phosphatase 1, catalytic subunit, β isozyme	2.38	2.93	1.39	1.70
PPP1CC	protein phosphatase 1, catalytic subunit, γ isozyme	2.38	2.939	1.39	1.70
PYGB	phosphorylase, glycogen; brain	1.85	2.36	2.12	2.71
PYGL	phosphorylase, glycogen, liver	1.86	2.22	1.94	2.32
PYGM	phosphorylase, glycogen, muscle	1.86	2.22	1.94	2.32
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73
TTN	titin	1.84	3.88	1.10	2.31
YWHAB	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, β polypeptide	1.80	2.68	1.13	1.68
YWHAE	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, ε polypeptide	1.88	3.85	-1.04	1.97
YWHAG	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, γ polypeptide	1.68	2.40	-1.19	1.20
YWHAQ	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, θ polypeptide	1.63	2.14	-1.07	1.22
YWHAZ	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, ζ polypeptide	1.85	2.76	1.23	1.84

12. mTOR Signaling

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
EIF3L	eukaryotic translation initiation factor 3, subunit L	1.95	1.68	1.81	1.56
EIF4A1	eukaryotic translation initiation factor 4A1	1.80	2.20	1.37	1.67
EIF4A2	eukaryotic translation initiation factor 4A2	1.71	2.07	1.36	1.64
EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	1.79	2.52	1.47	2.07
EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	1.35	2.24	1.20	1.99
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	1.54	1.97	1.37	1.76
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73
RPS2	ribosomal protein S2	1.54	2.42	1.16	1.82
RPS3	ribosomal protein S3	1.66	2.40	1.00	1.45
RPS7	ribosomal protein S7	1.51	1.769	-1.07	1.10
RPS9	ribosomal protein S9	1.86	3.48	1.08	2.01
RPS10	ribosomal protein S10	2.31	3.75	-1.13	1.44
RPS11	ribosomal protein S11	1.83	3.01	-1.19	1.38
RPS13	ribosomal protein S13	2.40	3.28	1.27	1.74
RPS16	ribosomal protein S16	1.73	3.35	-1.11	1.74
RPS19	ribosomal protein S19	1.35	2.71	-1.33	1.51
RPS24	ribosomal protein S24	1.97	2.36	1.16	1.39
RPS25	ribosomal protein S25	1.82	3.37	-1.34	1.39

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
RPS26	ribosomal protein S26	1.81	2.32	1.10	1.41
RPS15A	ribosomal protein S15a	1.86	2.41	1.17	1.52
RPS27L	ribosomal protein S27-like	1.35	2.39	-1.06	1.67
RPS3A	ribosomal protein S3A	1.55	2.49	-1.11	1.45
RPS4X	ribosomal protein S4, X-linked	1.73	2.67	-1.13	1.36
RPS4Y1	ribosomal protein S4, Y-linked 1	1.60	2.77	-1.52	1.14
RPSA	ribosomal protein SA	1.46	2.10	-1.28	1.12

13. Clathrin-mediated Endocytosis Signaling

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
AP2A1	adaptor-related protein complex 2, alpha 1 subunit	1.87	2.07	1.49	1.65
AP2A2	adaptor-related protein complex 2, alpha 2 subunit	1.91	2.00	1.40	1.47
AP2B1	adaptor-related protein complex 2, beta 1 subunit	1.76	2.14	1.68	2.05
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CLTCL1	clathrin, heavy chain-like 1	1.35	1.89	1.65	2.31
CTTN	cortactin	1.71	3.57	1.00	2.08

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	1.57	2.01	2.18	2.79
HSPA8	heat shock 70kDa protein 8	1.65	2.34	-1.06	1.33
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1.46	3.13	-1.57	1.36
RAB7A	RAB7A, member RAS oncogene family	1.90	2.64	1.45	2.02

14. Caveolar-mediated Endocytosis Signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ARCN1	archain 1	1.58	2.07	1.18	1.54
COPB1	coatomer protein complex, subunit beta 1	1.51	2.10	1.37	1.91
FLNA	filamin A, alpha	1.57	2.04	1.49	1.94
FLNB	filamin B, beta	1.97	2.20	1.41	1.58
FLNC	filamin C, gamma	1.47	1.85	-1.58	-1.26
HLA-B	major histocompatibility complex, class I, B	1.64	2.53	1.69	2.60
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1.46	3.13	-1.57	1.36

15. Calcium Signaling

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
CALR	calreticulin	2.02	2.29	1.01	1.15
CAMK2A	calcium/calmodulin-dependent protein kinase II alpha	1.71	1.90	1.54	1.71
CAMK2B	calcium/calmodulin-dependent protein kinase II beta	1.63	2.03	1.38	1.71
CAMK2D	calcium/calmodulin-dependent protein kinase II delta	1.72	2.22	1.42	1.83
CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	1.63	2.03	1.38	1.71
MYH9	myosin, heavy chain 9, non-muscle	1.53	1.99	1.24	1.62
MYH10	myosin, heavy chain 10, non-muscle	1.68	2.52	1.41	2.11
MYH11	myosin, heavy chain 11, smooth muscle	1.73	2.62	1.32	1.99
MYH14	myosin, heavy chain 14, non-muscle	2.06	3.03	1.42	2.09
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
TPM2	tropomyosin 2 (beta)	1.77	1.64	1.41	1.30
TPM3	tropomyosin 3	1.73	1.53	1.39	1.24
TPM4	tropomyosin 4	1.68	1.66		1.18
TPM1 (includes EG:22003)	tropomyosin 1 (alpha)	1.75	1.56	1.32	1.18

16. Pentose Phosphate Pathway

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
ALDOA	aldolase A, fructose-bisphosphate	1.45	1.99	-1.16	1.19
G6PD	glucose-6-phosphate dehydrogenase	1.59	2.56	1.00	1.61
GPI	glucose-6-phosphate isomerase	1.57	1.98	1.31	1.66
PFKL	phosphofructokinase, liver	1.74	2.37	1.17	1.60
PGLS	6-phosphogluconolactonase	1.38	1.90	1.41	1.94
PGM1	phosphoglucomutase 1	2.09	1.92	1.97	1.81
PRPS1	phosphoribosyl pyrophosphate synthetase 1	1.80	2.44	1.17	1.58
PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	1.63	2.13	1.17	1.53
TALDO1	transaldolase 1	1.55	2.21	1.39	1.98
TKT	transketolase	1.52	1.67	1.33	1.46

17. Cdc42 Signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
CFL2	cofilin 2 (muscle)	1.34	1.95	-1.21	1.20
HLA-B	major histocompatibility complex, class I, B	1.64	2.53	1.69	2.60
IQGAP1	IQ motif containing GTPase activating protein 1	1.64	2.22	1.41	1.91
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	1.94	2.05	1.386	1.45

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70

18. Ephrin Receptor Signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
CFL2	cofilin 2 (muscle)	1.34	1.95	-1.21	1.20
GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	1.86	3.62	-1.06	1.83
GNB2	guanine nucleotide binding protein (G protein), beta polypeptide 2	1.98	3.27	1.01	1.67

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
GNB3	guanine nucleotide binding protein (G protein), beta polypeptide 3	2.59	4.64	1.20	2.15
GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	2.76	4.71	1.25	2.13
GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	2.39	3.54	1.01	1.49
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73

19. Rac Signaling

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.56	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
CFL2	cofilin 2 (muscle)	1.34	1.95	-1.21	1.20
IQGAP1	IQ motif containing GTPase activating protein 1	1.64	2.22	1.41	1.91
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73

20. Cellular Effects of Sildenafil (Viagra)

Symbol	**Entrez Gene Name**	**Fold Change (A1#)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
MYH9	myosin, heavy chain 9, non-muscle	1.53	1.99	1.24	1.62
MYH10	myosin, heavy chain 10, non-muscle	1.68	2.52	1.41	2.11
MYH11	myosin, heavy chain 11, smooth muscle	1.73	2.62	1.32	1.99
MYH14	myosin, heavy chain 14, non-muscle	2.06	3.03	1.42	2.09
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	1.94	2.05	1.38	1.45
PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)	1.63	2.12	1.03	1.34
PDIA3	protein disulfide isomerase family A, member 3	1.61	2.41	1.02	1.53
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70

21. FAK (Focal Adhesion Kinase) Signaling

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
CAPN2	calpain 2, (m/II) large subunit	1.37	1.93	1.83	2.58
CAPNS1	calpain, small subunit 1	1.51	2.07	1.36	1.86
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
TLN1	talin 1	1.54	2.28	1.02	1.52
TLN2	talin 2	1.44	2.61	-1.02	1.78
VCL	vinculin	1.67	2.05	1.17	1.43

22. VEGF (Vascular Endothelial Growth Factor) Signaling.

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.186	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ACTN1	actinin, alpha 1	1.64	2.05	1.41	1.76
ACTN2	actinin, alpha 2	1.55	2.30	1.17	1.73
ACTN3	actinin, alpha 3	1.74	2.52	1.36	1.98
ACTN4	actinin, alpha 4	1.65	2.10	1.30	1.65
VCL	vinculin	1.67	2.05	1.17	1.43
YWHAE	tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein, epsilon polypeptide	1.88	3.85	-1.04	1.97

Supplementary Table 3. Meta data for Figure 5 and supplementary Figure 1. Differentially expressed proteins related to protein synthesis in the four comparisons. Fold changes in four comparisons: A1: ET-1 treated vs. basal in CONTROL PASMC; A2. ET-1 treated vs. basal in PAH PASMC; A3. PAH cells vs. CONTROL cells under basal condition; A4. PAH *vs.* Control cells, both with ET-1 stimulation.

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
EIF3L	eukaryotic translation initiation factor 3, subunit L	1.95	1.68	1.81	1.56
EIF4A1	eukaryotic translation initiation factor 4A1	1.80	2.20	1.37	1.67
EIF4A2	eukaryotic translation initiation factor 4A2	1.71	2.07	1.36	1.64
EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	1.79	2.52	1.47	2.07
EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	1.35	2.24	1.20	1.99
PABPC1	poly(A) binding protein, cytoplasmic 1	1.68	2.22	1.03	1.37
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70
PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme	2.38	2.93	1.39	1.70
RPL4	ribosomal protein L4	2.56	3.01	1.51	1.78
RPL5	ribosomal protein L5	1.50	2.73	-1.42	1.29
RPL7	ribosomal protein L7	1.38	1.60	-1.02	1.14
RPL8	ribosomal protein L8	1.68	3.06	-1.25	1.47
RPL9	ribosomal protein L9	1.99	2.49	1.09	1.36
RPL13	ribosomal protein L13	1.44	2.33	-1.21	1.33
RPL14	ribosomal protein L14	1.92	2.25	1.37	1.61
RPL15	ribosomal protein L15	1.41	2.80	-1.23	1.61

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
RPL19	ribosomal protein L19	1.50	3.47	-1.21	1.91
RPL21	ribosomal protein L21	1.68	2.26	-1.08	1.25
RPL22	ribosomal protein L22	1.36	2.86	-1.41	1.50
RPL24	ribosomal protein L24	1.60	2.03	1.13	1.44
RPL30	ribosomal protein L30	1.68	2.55	-1.07	1.42
RPL10 (includes others)	ribosomal protein L10	1.63	2.16	-1.02	1.30
RPL13A	ribosomal protein L13a	1.70	3.35	-1.34	1.48
RPL18A	ribosomal protein L18a	1.83	2.45	-1.05	1.27
RPL23A	ribosomal protein L23a	1.71	2.97	-1.13	1.53
RPL35A	ribosomal protein L35a	1.35	2.33	-1.29	1.34
RPL7A	ribosomal protein L7a	1.54	2.16	-1.12	1.25
RPLP0	ribosomal protein, large, P0	2.23	3.23	1.17	1.60
RPLP2	ribosomal protein, large, P2	2.28	2.72	1.28	1.53
RPS2	ribosomal protein S2	1.54	2.42	1.16	1.82
RPS3	ribosomal protein S3	1.66	2.40	1.00	1.45
RPS7	ribosomal protein S7	1.51	1.76	-1.07	1.10
RPS9	ribosomal protein S9	1.86	3.48	1.08	2.01
RPS10	ribosomal protein S10	2.31	3.75	-1.13	1.44
RPS11	ribosomal protein S11	1.83	3.01	-1.19	1.38
RPS13	ribosomal protein S13	2.40	3.28	1.27	1.74
RPS16	ribosomal protein S16	1.73	3.35	-1.11	1.74
RPS19	ribosomal protein S19	1.35	2.71	-1.33	1.51
RPS24	ribosomal protein S24	1.97	2.36	1.16	1.39
RPS25	ribosomal protein S25	1.82	3.37	-1.34	1.39

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
RPS26	ribosomal protein S26	1.81	2.32	1.10	1.41
RPS15A	ribosomal protein S15a	1.86	2.41	1.17	1.52
RPS27L	ribosomal protein S27-like	1.35	2.39	-1.06	1.67
RPS3A	ribosomal protein S3A	1.55	2.49	-1.11	1.45
RPS4X	ribosomal protein S4, X-linked	1.73	2.67	-1.13	1.36
RPS4Y1	ribosomal protein S4, Y-linked 1	1.60	2.77	-1.52	1.14
RPSA	ribosomal protein SA	1.46	2.10	-1.28	1.12
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	1.54	1.97	1.37	1.76
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73

Supplementary Table 4. Meta data for Figure 6 and supplementary Figure 2. Differentially expressed proteins related to RhoA and cytoskeleton in the four comparisons. Fold changes in four comparisons: A1: ET-1 treated *vs.* basal in Control PASMC; A2. ET-1 treated *vs*. basal in PAH PASMC; A3. PAH cells *vs*. Control cells under basal condition; A4. PAH *vs*. Control cells, both with ET-1 stimulation.

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
ACTA1	actin, alpha 1, skeletal muscle	1.61	2.35	1.18	1.72
ACTA2	actin, alpha 2, smooth muscle, aorta	1.64	2.34	1.23	1.76
ACTB	actin, beta	1.70	2.03	1.28	1.53
ACTC1	actin, alpha, cardiac muscle 1	1.42	1.83	1.17	1.52
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.66	1.75	1.30	1.37
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	1.87	2.51	1.36	1.83
ARHGAP1	Rho GTPase activating protein 1	1.41	1.75	1.53	1.90
ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	2.05	3.40	1.28	2.13
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	1.86	2.77	1.36	2.03
ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa	2.36	3.40	1.60	2.31
ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa	1.59	2.95	1.00	1.87
ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa	1.90	2.74	1.07	1.54
CFL1	cofilin 1 (non-muscle)	1.48	2.03	-1.29	1.06
CFL2	cofilin 2 (muscle)	1.34	1.95	-1.21	1.20
EZR	ezrin	1.75	2.04	1.66	1.94
MSN	moesin	1.87	2.31	1.51	1.87

Symbol	**Entrez Gene Name**	**Fold Change (A1)**	**Fold Change (A2)**	**Fold Change (A3)**	**Fold Change (A4)**
MYL1	myosin, light chain 1, alkali; skeletal, fast	1.72	2.81	1.03	1.68
MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	1.46	2.42	1.02	1.68
MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	1.94	2.05	1.38	1.45
PFN1	profilin 1	1.72	2.40	1.30	1.82
PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	2.38	2.93	1.39	1.70
RDX	radixin	1.79	2.14	1.60	1.91
RHOA	ras homolog family member A	1.38	2.10	1.13	1.73
SEPT2	septin 2	1.72	1.95	1.17	1.32
SEPT6	septin 6	1.88	2.62	1.12	1.56
SEPT7	septin 7	1.78	2.58	1.08	1.57
SEPT8	septin 8	1.88	2.62	1.12	1.56
TTN	titin	1.84	3.88	1.10	2.31
ACTN1	actinin, alpha 1	1.64	2.05	1.41	1.76
ACTN2	actinin, alpha 2	1.55	2.30	1.17	1.73
ACTN3	actinin, alpha 3	1.74	2.52	1.36	1.98
ACTN4	actinin, alpha 4	1.65	2.10	1.30	1.65
FN1	fibronectin 1	1.42	1.94	-1.18	1.16
GSN	gelsolin	1.70	2.28	1.33	1.78
IQGAP1	IQ motif containing GTPase activating protein 1	1.64	2.22	1.41	1.91
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1.50	2.41	-1.24	1.29
MYH9	myosin, heavy chain 9, non-	1.53	1.99	1.24	1.62

Symbol	Entrez Gene Name	Fold Change (A1)	Fold Change (A2)	Fold Change (A3)	Fold Change (A4)
	muscle				
MYH10	myosin, heavy chain 10, non-muscle	1.68	2.52	1.41	2.11
MYH11	myosin, heavy chain 11, smooth muscle	1.73	2.62	1.32	1.99
MYH14	myosin, heavy chain 14, non-muscle	2.06	3.03	1.42	2.09
VCL	vinculin	1.67	2.05	1.17	1.43
ARF3	ADP-ribosylation factor 3	2.87	3.65	1.51	1.92
CAPN2	calpain 2, (m/II) large subunit	1.37	1.93	1.83	2.58
CAPNS1	calpain, small subunit 1	1.51	2.07	1.36	1.86
CTTN	cortactin	1.71	3.57	1.00	2.08
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1.46	3.13	-1.57	1.36
TLN1	talin 1	1.54	2.28	1.02	1.52
TLN2	talin 2	1.44	2.61	-1.02	1.78
ZYX	zyxin	1.38	2.34	-1.42	1.19
ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	1.83	2.52	1.24	1.71
FLNA	filamin A, alpha	1.57	2.04	1.49	1.94
FLNB	filamin B, beta	1.97	2.20	1.41	1.58
FLNC	filamin C, gamma	1.47	1.85	-1.58	-1.26
PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	1.54	1.97	1.37	1.76
VIM	vimentin	1.57	2.12	1.25	1.69

Supplementary Table 5A: CV% (or % RSD) based on summed intensity of respective proteins

	Control (-) ET-1	control (+) ET-1	PAH (-) ET-1	PAH (+) ET-1
	CV% distribution			
Average CV (%)	6.8	8.9	15.3	4.5
	protein counts (total: 1137)			
# proteins ≤ 20% CV	1125	1099	819	1112
	percent of proteins			
Percent of total ≤ 20% CV	98.9	96.7	72.0	97.8

Supplementary Table 5B: T-test calculations indicated the significance of changes from replicate analyses in group comparison.

	Control (+) ET-1 vs basal	PAH (+) ET-1 vs basal	PAH vs Control both basal	PAH vs Control both (+) ET-1
count(P<=0.05)	926	1114	602	1055