

Supplementary Materials: A Proteomic Approach for the Identification of Up-Regulated Proteins Involved in the Metabolic Process of the Leiomyoma

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Table S1. Spots and list of peptides identified by MALDI-TOF/TOF.

Spot N	Protein Description	Molecular Weight	Isoelectric Point	Peptides
1	Protein disulfide isomerase A3	54.9	6.86	FLQDYFDGNLK TFSHELSDFGLESTAGEIPVVAIR
6	Myosin regulatory light polypeptide 9	19.8	4.92	LNGTDPEDVIR FTDEEVDEmYR
7	Desmin	53.4	5.27	FASEASGYQDNIAR INLPIQTYSALNFR
12	Four and a half LIM domains protein 1	24.7	8.6	FDCHYCR FWHDTCFR QVIGTGSFFPK CLHPLANETFVAK
13	Keratin, type II cytoskeletal 1	66.2	8.15	LALDLEIATYR SLNNQFASFIDKVR
20	Immunoglobulin heavy constant alpha 1	38.5	6.08	WLQGSQELPR QEPSQGTITTFVTSILR
22	isoform 5 of Prelamin-A/C	63.1	6.84	SSFSQHAR NIYSEELR NIYSEELR LADALQELR TQSPQNCSIM TQSPQNCSIM TLEGELHDLR LRDLEDLAR AQNTWGCNSLR NIYSEELRETK TALINSTGEEVAMR AQHEDQVEQYKK VAVEEVDEEGKFVR VAVEEVDEEGKFVR TLEGELHDLRGQVAK IRIDSLSAQLSQLQK IRIDSLSAQLSQLQK NSNLVGAAHEELQQSR NSNLVGAAHEELQQSR AGQVVTIWAAGAGATHSPPTDLVWK
16	AP-1 complex subunit mu-2	48.1	8.23	RDPAMPLPK SASAVFILDVK MSASAVFILDVK SASAVFILDVKGK
15	LIM and SH3 domain protein 1 fragment	19.0	9.04	GFSVVADTPELQR LKQQSELQSQVR LKQQSELQSQVR
17	T-complex protein 1 subunit epsilon	57.6	5.37	NLIRDNR NLIRDNR NSSLGPTIEK GGNKMIEEAK MLVIEQCKNSR DVSFELIKVEGK QMAEIAVNAVLTVADMERR DGDVTVTNDGATILSMDVDHQIAK

Table S1. *Cont.*

Spot N	Protein Description	Molecular Weight	Isoelectric Point	Peptides
19	Malate dehydrogenase cytoplasmic	23.2	6.9	GEFVTTVQQR GEFVTTVQQR FVEGLPINDFSR SAPSIPKENFSCLTR LSSAMSAAKAICDHVR MVIVVGNPANTNCLTASK
23	Actin, alpha cardiac muscle 1	42.3	5.23	AGFAGDDAPR GYSFVTTAER AVFPSIVGRPR QEYDEAGPSIVHR IWHHTFYNELR
24	Alpha-1-antitrypsin	46.7	5.47	DTEEDFHVDQVTTVK VFSNGADLSGVTEEAPLK ITPNLAEFASFSLYR TDTSHHDQDHPTFNK SVLQQLGITK LSITGTYDLK
21	Serum albumin	53.0	6.62	YLYEIAR RHPDYSVLLLR

Table S2. Spots and list of peptides identified by LTQ-Orbitrap XL.

Spot N	Protein Description	Molecular Weight	Isoelectric Point	Peptides
2	Tubulin beta chain	47.7	4.81	TAVcDIPPR EVDEQmLNVQNK ISVYYNEATGGK ImNTFSVVPSPK ISEQFTAmFR
3	L-lactate dehydrogenase B chain	36.6	6.05	VIGSGcNLD SAR IVVVTAGVR IVADKDYSVTANSK SADTLWDIQQ LKDDEVAQLK LIAPVAEEEEATVPNNK GLTSVINQK mVVESAYEVIK DYSVTANSK LNLVQR KSADTLWDIQQ MVVESAYEVIK NVNVFK YLmAEK LSGLPK
4	Annexin A4	35.5	5.86	AASGFNA mEDAQTLR GLGTDDNTLIR QDAQDLYEAGEKK DEGNYLDDALVR AEIDmLDIR VLVSLSAGGR QDAQDLYEAGEK VLLVLcGGDD SDTSFmFQR ISQTYQQQYGR GLGTDEDAIISVLAYR AASGFNA mEDAQTLRK SDTSFMFQR AEIDMLDIR SAYFAEK FLTVLcSR TPEEIR DIEQSIK SLEDDIR RISQTYQQQYGR
5	isoform 2 of Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta	36.3	6	LLVSASQDGK LFVSGAcDASAK AGVLAGHDNR
10	Cellular retinoic acid-binding protein 2	15.7	5.4	PNFSGNWK VGEEFEEQTVDGRpK LLKGEGPK IAVAAASKPAVEIK VLGVNVmLR QEGDTFYIK VYVRE
8	Calmodulin 1	16.8	4.22	DTDSEEEIR mKDTDSEEEIR ELGTVmR
9	isoform3 of Polymerase I and transcript release factor	22.6	7.56	EGQVEVLK ATEmVEVGADDDEGGAER ATEMVEVGADDDEGGAER

Table S2. Cont.

Spot N	Protein Description	Molecular Weight	Isoelectric Point	Peptides
11	Fatty acid binding protein, epidermal	15.2	7.01	FEETTADGR LVVEcVmNNVTcTR ELGVGIALR TTQFScTLGEK GFDEYmK FEETTADGRK ATVQQLEGR
18	Aspartate aminotransferase, cytoplasmic	46.2	7.01	LALGDDSPALK VGGVQSLGGTGALR IGADFLAR LALGDDSPALK INVSGLTTK VGGVQSLGGTGALR LALGDDSPALKEK ITWSNPPAQGAR INVSGLTTK ITWSNPPAQGAR VNLGVGAYR VGGVQSLGGTGALR NLDYVATSIHEAVTK
14	Keratin, type I cytoskeletal 9	62.0	5.24	SGGGGGGGLSGGSIR SGGGGGGGLSGGSIR GSGGSYGGGSGGGYGGGSGSR SGGGGGGGLSGGSIR GSGGSHGGGSGFGGESGGSYGGG EEASGSGGYGGGSGK GSGGSYGGGSGGGYGGGSGSR FSSSSGYGGGSSR GSGGSHGGGSGFGGESGGSYGGG EEASGSGGYGGGSGK GSGGSYGGGSGGGYGGGSGSR

Comparative proteomic analysis was performed between uterine leiomyoma and myometrium tissues in order to generate 2-DE reference maps and to identify up-regulated proteins. An average of 2000 spots was detected on gels for both types of proteomes. Analyses indicate that 24 protein spots were significantly up-regulated in leiomyoma samples if compared to the myometrium ($p < 0.05$; in terms of expression, all 24 with a fold change ≥ 1.5 -fold) (Figure 1) (Figures S1 and S2). We also identified four down-regulated proteins (transgelin, lamin A/C, α -1-actinin, and carbonic anhydrase 1), but differences were not significant and were thus not further investigated.

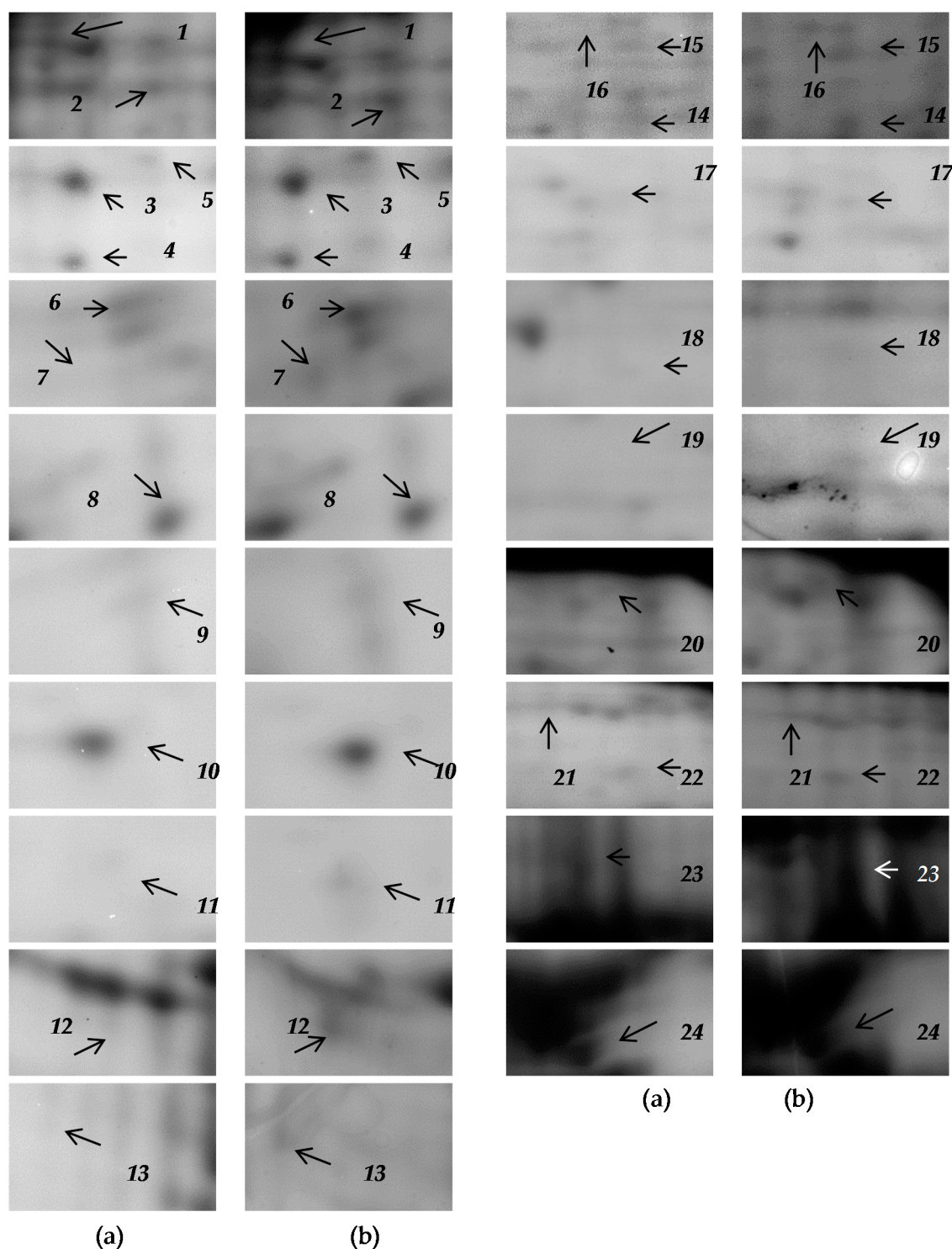


Figure S1. Visualization of spots for up-regulated proteins; (a) Myometrium; (b) Leiomyoma. 1. Protein disulfide isomerase A3; 2. Tubulin β chain; 3. L-lactate dehydrogenase B chain; 4. Annexin A4; 5. isoform 2 of Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit β ; 6. Myosin regulatory light polypeptide 9; 7. Desmin; 8. Calmodulin 1; 9. Isoform3 of Polymerase I and transcript; 10. Cellular retinoic acid-binding protein 2; 11. Fatty acid binding protein, epidermal; 12. Four and a half LIM domains protein 1; 13. Keratin, type II cytoskeletal 1; 14. Keratin, type I cytoskeletal 9; 15. LIM and SH3 domain protein 1 fragment; 16. AP-1 complex subunit mu-2; 17. T-complex protein 1 subunit epsilon; 18. Aspartate aminotransferase cytoplasmic; 19. Malate dehydrogenase cytoplasmic; 20. Immunoglobulin heavy constant α 1; 21. Serum albumin; 22. isoform 5 of Prelamin-A/C; 23. Actin, α cardiac muscle 1; 24. α -1-antitrypsin.

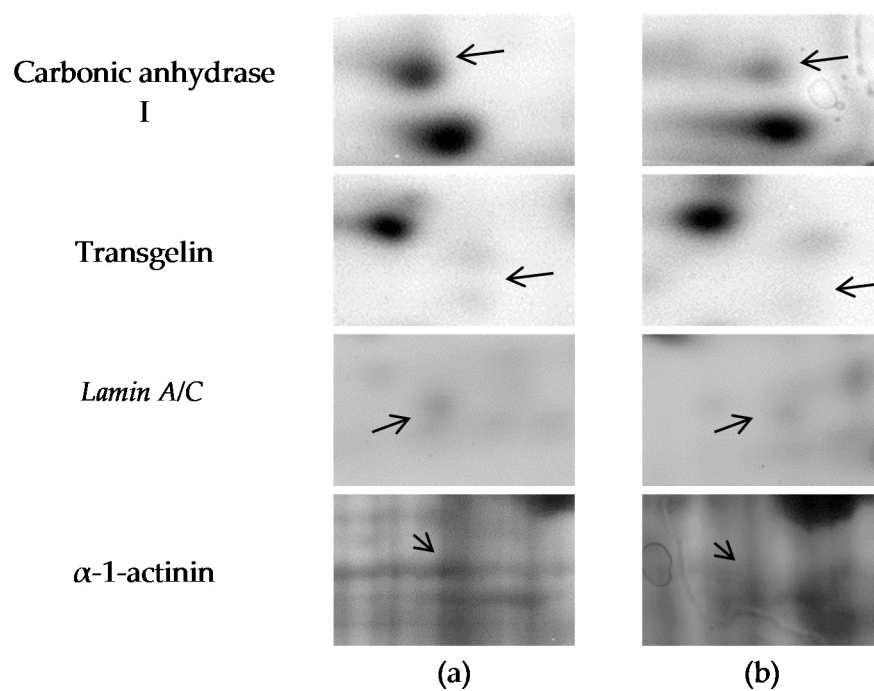


Figure S2. Visualization of spots for down-regulated proteins: (a) Myometrium; (b) Leiomyoma.