



Supplementary figure 1. Ingenuity Pathway Analysis of differentially expressed proteins. Differentially expressed proteins showing a 2-fold change or greater were selected and entered into IPA software to illustrate potential interactions. Differentially expressed proteins are shown in green (downregulated) or red (upregulated). Solid and dashed connecting lines indicate the presence of direct (a) and indirect (b) interactions, respectively.

Supplementary Table 1. Protein spots differentially expressed between control and resveratrol-treated cells					
Spot number	Protein name	Matched Peptides	Peptides sequence	Error ± ppm	
Spot 1	Dynactin subunit 1	4	R.AEITDAEGLGLK.L	- 61.54	
			R.AESLQQEVEALK.E	- 55.95	
			R.VDELTTDLEILK.A	- 61.23	
			K.DSPLLLQQISAMR.L	- 67.70	
Spot 3	Vinculin	5	R.SLGEISALTSK.L	- 64.26	
			K.MSAEINEIIR.V	- 50.33	
			K.ELLPVLISAMK.I	- 51.87	
			K.AQQVSQGLDVLTAQ.V	- 59.66	
			R.VDQLTAQLADLAAR.G	- 52.02	
Spot 7	60 kDa heat shock protein, mitochondrial	20	K.APGFGDNR.K	- 41.47	
			K.VGEVIVTK.D	- 49.47	
			K.LSDGVAVLK.V	- 46.18	
			K.VGLQVVAVK.A	- 66.66	
			R.VTDALNATR.A	- 52.90	
			K.EIGNIISDAMK.K	- 58.67	
			K.NAGVEGSLIVEK.I	- 54.67	
			K.VGGTSDVEVNEK.K	- 41.72	
			R.TVIIEQSWGSPK.V	- 50.21	
			R.GYISPYFINTSK.G	- 39.28	
R.GVMLAVDAVIAELK.K	- 53.59				

			K.TLNDELEIIEGMK.F	- 67.28
			K.CEFQDAYVLLSEK.K	- 44.01
			R.AAVEEGIVLGGGCALLR.C	- 60.18
			R.CIPALDSLTPANEDQK.I	- 49.89
			R.CIPALDSLTPANEDQK.I	- 46.16
			K.ISSIQSIVPALEIANHR.K	- 51.46
			R.IQEIIQLDVTTSEYEK.E	- 51.79
			R.ALMLQGVDLLADAVAVTMGPK.G	- 51.66
			K.LVQDVANNTNEEAGDGTTTATVLAR.S	- 40.44
			R.ESLIDGIK.R	- 43.60
			R.IILLAEGR.L	- 57.30
			R.ATDVMIAGK.V	- 45.94
			K.AGIPVYAWK.G	- 46.67
			K.YPQLLPGIR.G	- 65.84
			K.YPQLLPGIR.G	- 48.98
			K.VADIGLAAWGR.K	- 52.58
			K.VAVVAGYGDVGK.G	- 53.14
Spot 8	Adenosylhomocysteinase	16	K.VPAINVNDVTK.S	- 68.46
			K.KLDEAVAEHLGK.L	- 40.42
			K.ALDIAENEMPGLMR.M	- 48.15
			K.ALDIAENEMPGLM*R.M	- 44.69
			R.GISEETTTGVHNLYK.M	- 52.46
			R.GISEETTTGVHNLYK.M	- 41.97
			K.DGPLNMILDDGGDLTNLIHTK.Y	- 47.57
			K.DGPLNMILDDGGDLTNLIHTK.Y	- 45.97
			K.AAQASDLEK.I	- 39.07
Spot 12	Transaldolase	9	K.TIVMGASFR.N	- 42.31
			R.MESALDQLK.Q	- 37.66

			K.LLGELLQDNAK.L	- 37.21
			K.LLGELLQDNAK.L	805
			K.SYELEDPGVK.S	- 35.06
			K.LFVLFGAELK.K	- 32.94
			K.LSSTWEGIQAGK.E	- 42.69
			K.ALAGCDFLTISPK.L	- 55.21
Spot 13	G1/S-specific cyclin-D1	2	R.LQLLGATCMFVASK.M	- 40.97
			K.FISNPPSMVAAGSVVAAVQGLNLR.S	- 32.90
			K.VGVNGFGR.I	- 52.97
			K.QASEGPLK.G	- 44.50
			K.AGAHLQGGAK.R	- 30.99
			R.VVDLMAHMASK.E	- 44.01
			R.VVDLMAHMASK.E	-40.24
			R.VPTANVSVVDLTCR.L	-71.48
			K.LVINGNPITIFQER.D	566
			K.LISWYDNEFGYSNR.V	- 85.45
Spot 14	Glyceraldehyde-3-phosphate dehydrogenase/Alpha-soluble NSF attachment protein	14 / 9	K.IISNASCTTNCLAPLAK.V	- 36.98
			K.IISNASCTTNCLAPLAK.V	494
			R.VIISAPSADAPMFVMGVNHEK.Y	- 93.61
			K.WGDAGAEYVVESTGVFTTMEK.A	- 60.32
			K.WGDAGAEYVVESTGVFTTMEK.A	- 59.95
			K.VIHDNFGIVEGLMTTVHAITATQK.T	- 46.14
			/	/
			R.AIEIYTMGR.F	- 47.91
			K.TIQGDEEDLR.-	- 29.06
			K.IEEACEIYAR.A	- 40.95
			R.LDQWLTTMLLR.I	- 57.71
			K.EAEAMALLAEAER.K	- 67.24

			K.YEELFPAFSDSR.E	- 62.68
			K.NSQSFFSGLFGGSSK.I	- 62.79
			K.AIAHYEQSADYYK.G	- 32.39
			K.AALCHFCIDMLNAK.L	- 53.92
			R.GALQNIIPASTGAAK.A	-53.45
			R.VPTANVSVDLTCR.L	-59.32
			K.LVINGNPITIFQER.D	-60.03
			K.LISWYDNEFGYSNR.V	-48.35
			R.VIISAPSADAPMFVMGVNHEK.Y	-46.27
			/	/
Spot 15	Glyceraldehyde-3-phosphate dehydrogenase / Microtubule-associated protein RP	5 / 7	K.LTVEDLEK.E	-48.45
			K.FFDANYDGK.D	-48.00
			K.LEHEYIQNFK.I	-42.13
			K.FQDNFEFVQWFK.K	-46.70
			R.QGQETA VAPSLVAPALNKPK.K	-50.56
			R.NIELICQENEGENDPVLQR.I	-48.77
			R.NIELICQENEGENDPVLQR.I	-42.57
Spot 18	Dextrin	3	K.AVIFCLSADK.K	- 68.66
			R.YALYDASFETK.E	- 39.39
			K.EILVGDVGVTTITDPFK.H	- 55.40
* Oxidation				