

Supplemental table 1: Proteins differently expressed among comparison of B16-F10 control, B16-F10 treated, Melan-a control and Melan-a treated

Spot	Protein	GI	Mr/pI	Score	Coverage (%)	Peptides	Abundance
1	phosphoglycerate kinase	gi 202423	/44508 /7.53	658	22	K.LGDVYVNDAFGTAHR.A K.ALESPERPFLAILGGAK.V K.ITLPVDFVTADKFDENAK.T K.QIVWNGPVGVFWEAFAR.G K.QIVWNGPVGVFWEAFAR.G K.DCVGPEVENACANPAAGTVILLENLR.F	BC<BT 1.26 MC<BC 2.33 MC<BT 2.92
2	Enolase 1, (alpha)	gi 59808815	/47128 /6.16	667	23	R.IGAEVYHNLK.N R.GNPTVEVDLYTAK.G R.YITPDQLADLYK.S K.LAQSNWGVVMVSHR.S R.AAVPSGASTGIYEALRL.D K.LAMQEFMILPVGASSFR.E K.AGYTDQVVIGMDVAASEFYR.S	BC>BT 2.61 MC=BC MC>BT 3.54
3	heat shock protein 65	gi 51455	/60903 /5.91	871	16	R.TVIEQSWGSPK.V R.AAVEEGIVLGGGCALLR.C K.ISSVQSIVPALEIA N AHR.K R.KPLVIIAEDVDGEALSTLVLR.L K.LVQDVANNTNEEAGDGT T TATVLAR.S	BC>BT 1.14 MC=BC MC=BT
	put. beta-actin (aa 27-375)	gi 49868	/39161 /5.78	629	22	R.AVFPSIVGR.S R.GYSFTTTAER.E K.QEYDESGPSIVHR.K K.IWHHTFYNELR.V K.SYELPDGQVITIGNER.F K.DLYANTVLSGGT T MYPGIADR.M K.DLYANTVLSGGT T MYPGIADR.M	
4	heat shock protein 70 cognate	gi 309319	70793 5.37	646	14	K.FELTGIPPAPR.G K.VEIANDQGNR.T R.FEELNADLFR.G R.RFDDAVVQSDMK.H R.TTPSYVAFTDTER.L K.STAGDTHLGGEDFDNR.M K.TVTNAVVTVPAYFNDSQR.Q	BC>BT 1.34 MC=BC MC=BT

5	phosphoglycerate mutase 1	gi 114326546	28814 6.67	824	54	R.VLIAAHGNSLR.G R.HGESAWNLENR.F R.DAGYEFDIQFTSVQK.R R.FSGWYDADLSPAGHEEAK.R K.NLKPIKPMQFLGDEETVR.K K.NLKPIKPMQFLGDEETVR.K R.SYDVPPPPMEPDHPFYSNISK.D R.SYDVPPPPMEPDHPFYSNISK.D	BC<BT 1.22 MC<BC 1.27 MC<BT 1.55
6	gamma-actin	gi 809561	40992 5.56	691	25	K.AGFAGDDAPR.A R.GYSFTTTAER.E R.AVFPSIVGRPR.H K.QEYDESGPSIVHR.K K.IWHHTFYNELR.V K.SYELPDGQVITIGNER.F K.DLYANTVLSGGTMYPGIADR.M K.DLYANTVLSGGTMYPGIADR.M	BC>BT 1.13 MC=BC MC=BT
	put. beta-actin (aa 27-375)	gi 49868	39161 5.78	629	22	R.AVFPSIVGR.S R.GYSFTTTAER.E K.QEYDESGPSIVHR.K K.IWHHTFYNELR.V K.SYELPDGQVITIGNER.F K.DLYANTVLSGGTMYPGIADR.M K.DLYANTVLSGGTMYPGIADR.M	
7	triosephosphate isomerase	gi 54855	26679 6.90	516	25	K.IAVAAQNQCYK.V K.SNVNDGVAQSTR.I R.HVFGESDELIGQK.V K.TATPQQAQEVHEK.L K.DLGATWVVLGHSER.R R.RHVFGESDELIGQK.V	BC<BT 1.42 MC=BC MC<BT 1.56
	1-Cys peroxiredoxin protein	gi 4139186	24825 5.98	94	8	R.NFDEILR.V K.LSILYPATTGR.N	

8	phosphoglycerate mutase 1	gil114326546	28814 6.67	824	54	R.HYGGLTGLNK.A R.VLIAAHGNSLR.G R.HGESAWNLENR.F R.ALPFWNEEIVPQIK.E R.DAGYEFDICFTSVQK.R R.FSGWYDADLSPAGHEEAK.R K.NLKPIKPMQFLGDEETVR.K K.NLKPIKPMQFLGDEETVR.K R.YADLTEDQLPSCESLKDTIAR.A	BC<BT 1.25 MC=BC MC<BT 1.37
9	cofilin-1	gil6680924	18548 8.22	519	40	K.MLPDKDCR.Y K.AVLFCLEDKK.N K.LGGSAVISLEGKPL.- K.HELQANCYEEVK.D K.HELQANCYEEVKDR.C K.EILVGDVGGTVDDPYTTTFVK.M	BC>BT 1.35 MC=BC MC>BT 1.50
10	pyruvate kinase M	gil551295	57824 7.58	687	24	K.GDYPLEAVR.M R.LDIDSAPITAR.N R.NTGIICTIGPASR.S K.IYVDDGLISLQVK.E K.DAVLNAWAEDVDLR.V R.FDEILEASDGIMVAR.G R.LNFSHGTHEYHAETIK.N R.EAEAAIYHLQLFEELR.R R.EATESFASDPILYRPVAVALDTK.G	BC<BT 1.12 MC=BC MC=BT
11	heat shock protein 70 cognate	gil309319	70793 5.37	646	14	K.FELTGIPPAPR.G K.VEIIANDQG NR.T R.FEELNADLFR.G R.RFDDAVVQSDMK.H R.TTPSYVAFTDTER.L K.STAGDTHLGGEDFDNR.M K.TVTNAVVTVPAYFNDSQR.Q	BC>BT 1.12 MC>BC 1.16 MC>BT 1.30

	Rho GDP dissociation inhibitor (GDI) alpha	gi 13435747	23377 5.12	566	26	K.YIQHTYR.K K.TDYMVGSYGPR.A K.IDKTDYMVGSYGPR.A R.VAVSADPNVPNVIVTR.L K.SIQEIQLDKDDESLR.K K.SIQEIQLDKDDESLRK.Y	
12	nucleophosmin isoform 1	gi 6679108	32540 4.62	417	19	K.DLKPSTPR.S K.VDNDENEHQLSLR.T R.MTDQEAIQDLWQWR.K R.MTDQEAIQDLWQWR.K K.MSVQPTVSLGGFEITPPVVLRL.L K.MSVQPTVSLGGFEITPPVVLRL.L	BC>BT 1.30 MC<BC 1.40 MC=BT
13	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLT <u>C</u> R.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC<BT 1.26 MC=BC MC<BT 1.23
	glutathione S-transferase P 1	gi 10092608	23594 7.68	216	12	-.PPYTIVYFPVR.G K.FEDGDLTLYQSNAILR.H	
14	heat shock protein 65	gi 51455	60903 5.91	871	16	R.TVIEQSWGSPK.V R.AAVEEGIVLGGGC <u>A</u> LLR.C K.ISSVQSIVPALEIANAHR.K R.KPLVIIAEDVDGEALSTLVNLRL.L K.LVQDVANNTNEEAGDGTTTATVLAR.S	BC>BT 1.14 MC<BC 1.18 MC=BT
	chaperonin subunit 8 (theta), isoform CRA_b	gi 148665922	54021 5.19	96	4	R.FAEAFEAIPIR.- -.LFTVNDAAITLR.F	
15	Sui1 homolog	gi 4868333	12668 6.04	208	26	K.TLTTVQGIADDYDK.K K.GDDLLPAGTEDYIHIR.I	BC>BT 1.23

	serine (or cysteine) peptidase inhibitor, clade H, member 1, isoform CRA_a	gi 148684430	44954 9.01	94	2	R.DNQSGSLLFIGR.L	MC=BC MC>BT 1.38
16	Stathmin	gi 9789995	17264 5.76	208	22	K.DKHVEEVR.K K.DKHVEEVRK.N K.ESVPDFPLSPPK.K R.ASGQAFELILSPR.S	BC>BT 1.20 MC>BC 1.56 MC>BT 1.87
18	calcyclin binding protein	gi 3142331	28301 7.78	175	17	K.TDTVILCR.K K.ISNYGWDQSDK.F K.IYITLTGVHQVPTENVQVHFTER.S	BC>BT 1.16 MC<BC 1.21
	eukaryotic translation initiation factor 4H	gi 15808988	27324 6.67	110	5	K.EALTYDGALLGDR.S	MC=BT
19	phosphoglycerate kinase	gi 202423	44508 7.53	658	22	K.LGDVYVNDAFGTAHR.A K.ALESPERPFLAILGGAK.V K.ITLPVDFVTADKFDENAK.T K.QIVWNGPVGVFWEAFAR.G K.QIVWNGPVGVFWEAFAR.G K.DCVGPEVENACANPAAGTVILLENLR.F	BC<BT 1.28 MC<BC 2.21 MC<BT 2.83
20	Prohibitin	gi 6679299	29802 5.57	265	16	R.FDAGELITQR.E K.DLQNVNITLR.I R.IYTSIGEDYDER.V R.KLEAAEDIAYQLSR.S	BC<BT 1.13 MC=BC MC=BT

	glyoxalase domain-containing protein 4	gi 255003777	33296 5.28	110	11	K.SDEWFATR.N R.FQTVHFFR.D K.LELQGIQGAVDHAAAFGR.I	
22	translationally-controlled tumor protein	gi 6678437	19450 4.76	146	13	K.GKLEEQKPER.V R.DLISHDELFSDIYK.I	BC>BT 1.26 MC>BC 1.39 MC>BT 1.75
	prostaglandin E synthase 3	gi 9790017	18709 4.36	140	18	R.SILCCLR.K R.KGESGQSWPR.L K.LTFSC_LGGSDNFK.H	
	eukaryotic translation initiation factor 3 subunit K isoform 1	gi 21312044	25070 4.81	87	5	R.YNPENLATLER.Y	
23	histidine triad nucleotide-binding protein 1	gi 33468857	13768 6.36	533	71	K.IIFEDDR.C K.AQVAQPGGDTIFGK.I R.C_LAFHDISPQAPTHFLVIPK.K R.MVVNEGADGGQSVYHIHLHVLGGR.Q R.MVVNEGADGGQSVYHIHLHVLGGR.Q K.KHISQISVADDDDESLLGHLMIVGK.K K.KHISQISVADDDDESLLGHLMIVGK.K	BC=BT MC<BC 1.68 MC<BT 1.50
24	protein disulfide-isomerase A3 precursor	gi 112293264	56643 5.88	690	20	K.QAGPASVPLR.T K.DASVVGFFR.D K.FVMQEEFSR.D R.LAPEYEEAATR.L R.FAHTNIESLVK.E R.ELNDFISYLQR.E K.EYDDNGEGITIFRPLHLANK.F K.TFSHELSDFGLESTTGEVPVVAIR.T	BC=BT MC<BC 1.36 MC<BT 1.31
25	fatty acid-binding protein, epidermal isoform 1	gi 6754450	15127 6.14	320	32	K.ELGVGLALR.K K.FDETTADGR.K R.LMESHGFEEYMK.E R.LMESHGFEEYMK.E K.MIVECVMNNATCTR.V K.MIVECVMNNATCTR.V	BC=BT MC<BC 1.35 MC<BT 1.36

26	10 kDa heat shock protein, mitochondrial	gi 6680309	10956 7.93	330	43	K.FLPLFDR.V R.KFLPLFDR.V K.VLLPEYGGTK.V K.VLQATVVAVGSGGK.G K.VVLDDKDYFLFR.D	BC=BT MC<BC 1.57 MC<BT 1.53
27	Enolase 1, (alpha)	gi 59808815	47128 6.16	667	23	R.IGAEVYHNLK.N R.GNPTVEVDLYTAK.G R.YITPDQLADLYK.S K.LAQSNWGVVMVSHR.S R.AAVPSGASTGIYEALRL.D K.LAMQEFMILPVGASSFR.E K.AGYTDQVVIGMDVAASEFYR.S	BC=BT MC<BC 1.33 MC=BT
28	cytochrome b5	gi 13385268	15232 4.96	426	41	K.STWVILHHK.V K.TYIIGELHPDDR.S K.FLEEHPPGEEVLR.E R.EQAGGDATENFEDVGHSTDAR.E	BC=BT MC<BC 5.28 MC<BT 5.03
29	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVDLTQR.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC<BC 1.21 MC<BT 1.29
	L-lactate dehydrogenase A chain isoform 1	gi 6754524	36475 7.62	151	9	K.LVIITAGAR.Q K.VTLTPEEEAR.L R.VIGSGCNLDSAR.F	
30	protein disulfide-isomerase A3 precursor	gi 112293264	56643 5.88	690	20	K.QAGPASVPLR.T K.DASVVGFFR.D K.FVMQEEFSR.D R.LAPEYAAAATR.L R.FAHTNIESLVK.E R.ELNDFISYLQR.E K.EYDDNGEGITIFRPLHLANK.F K.TFSHELSDFGLESTTGEVPVVAIR.T	BC=BT MC<BC 1.29 MC=BT
	alpha-fetoprotein, partial	gi 191765	47195 5.47	212	9	K.APQVSTPTLVEAAR.N K.LGEYGFQNAILVR.Y K.DVFLGTFLYEYSR.R	

31	Elongation factor 1-delta	gi 13124192	31274 4.91	272	17	R.ITSLEVENQNLR.G R.FYEQMNGPVTSGSR.Q K.SLAGSSGPGASSGPGGDHSELIVR.I	BC=BT MC>BC 1.19 MC=BT
32	phosphoglycerate kinase	gi 202423	44508 7.53	658	22	K.LGDVYVNDAFGTAHR.A K.ALESPERPFLAILGGAK.V K.ITLPVDFVTADKFDENAK.T K.QIVWNGPVGVFWEAFAR.G K.QIVWNGPVGVFWEAFAR.G K.DCVGPEVENACANPAAGTVILLENLR.F	BC=BT MC<BC 1.80 MC<BT 1.94
	long-chain acyl-CoA dehydrogenase	gi 726095	48052 8.34	154	8	R.IFSSEHDIFR.E K.AQDTAELFFEDVR.L K.GFYLLMQELPQER.L	
	heparin binding protein 44	gi 220434	42058 7.49	104	6	K.LIHNLNVILAR.Y K.IQEYNVLLDTLSR.A	
33	beta-galactoside binding protein	gi 193442	14796 5.32	341	33	K.LPDGHEFK.F K.EDGTWGTEHR.E K.DSNNLC_LHFNPR.F R.FNAHGDANTIVC_NTK.E	BC=BT MC<BC 1.99 MC<BT 1.97
35	10 kDa heat shock protein, mitochondrial	gi 6680309	10956 7.93	330	43	K.FLPLFDR.V R.KFLPLFDR.V K.VLLPEYGGTK.V K.VLQATVVAVGSGGK.G K.VVLDDKDYFLFR.D	BC=BT MC<BC 1.56 MC<BT 1.69
	macrophage migration inhibitory fator	gi 6754696	12496 6.79	166	17	K.LLCGLLSDR.L M.PMFIVNTNVPR.A M.PMFIVNTNVPR.A	
36	D-dopachrome decarboxylase	gi 6753618	13069 6.09	68	11	M.PFVELETNLPASR.I	BC=BT MC<BC 2.05 MC=BT

38	Stress-induced phosphoprotein 1	gil13277819	62528 6.40	201	5	K.AAALEFLNR.F K.LMDVGLIAIR.- R.KAAALEFLNR.F K.LDPQNHVLYSNR.S	BC=BT MC>BC 1.30 MC>BT 1.46
	Matricin	gil347839	60450 6.23	73	4	R.AVAQALEVIPR.T K.TAVETAVLLLR.I	
40	guanosine diphosphate (GDP) dissociation inhibitor 2	gil148700276	52911 8.66	98	4	K.MLLFTEVTR.Y K.DLGTDSQIFISR.A	BC=BT MC<BC 1.19 MC=BT
41	glyceraldehyde-3-phosphate dehydrogenase	gil6679937	35787 8.44	442	19	R.VPTPNVSVDLT C R.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC<BC 1.27 MC=BT
43	cytochrome b5	gil13385268	15232 4.96	426	41	K.STWVILHHK.V K.TYIIGELHPDDR.S K.FLEEHPGGEEVLR.E R.EQAGGDATENFEDVGHSTDAR.E	BC=BT MC>BC 1.40 MC>BT 1.72
	eukaryotic translation initiation factor 5a	gil148680531	18356 5.08	62	7	K.VHLVGIDIFTGK.K	
44	phosphoglycerate kinase	gil202423	44508 7.53	658	22	K.LGDVYVND A FGTAHR.A K.ALESPERPFLAILGGAK.V K.ITLPVDFVTADKFDENAK.T K.QIVWNGPVG V FEWEAFAR.G K.QIVWNGPVG V FEWEAFAR.G K.DC V GP E VENACANPAAGTVILLENLR.F	BC=BT MC<BC 1.73 MC<BT 2.09

45	macrophage migration inhibitory factor	gi 6754696	12496 6.79	166	17	K.LLCGLLSDR.L M.PMFIVNTNVPR.A M.PMFIVNTNVPR.A	BC=BT MC<BC 1.50 MC<BT 1.68
46	heat shock protein 70 cognate	gi 309319	70793 5.37	646	14	K.FELTGIPPAPR.G K.VEIIANDQGNR.T R.FEELNADLFR.G R.RFDDAVVQSDMK.H R.TTPSYVAFTDTER.L K.STAGDTHLGGEDFDNR.M K.TVTNAVVTVPAYFNDSQR.Q	BC=BT MC>BC 2.05 MC=BT
	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLTQR.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	
48	protein disulfide-isomerase A3 precursor	gi 112293264	56643 5.88	690	20	K.QAGPASVPLR.T K.DASVVGFFR.D K.FVMQEEFSR.D R.LAPEYEEAATR.L R.FAHTNIESLVK.E R.ELNDFISYLQR.E K.EYDDNGEGITIFRPLHLANK.F K.TFSHELSDFGLESTTGEVPVVAIR.T	BC=BT MC<BC 1.35 MC<BT 1.32
53	nucleophosmin isoform 1	gi 6679108	32540 4.62	417	19	K.DLKPSTPR.S K.VDNDENEHQLSLR.T R.MTDQEIQDLWQWR.K R.MTDQEIQDLWQWR.K K.MSVQPTVSLGGFEITPPVVL.R.L K.MSVQPTVSLGGFEITPPVVL.R.L	BC=BT MC<BC 1.47 MC=BT
56	phosphoglycerate kinase	gi 202423	44508 7.53	658	22	K.LGDVYVNDAFGTAHR.A K.ALESPERPFLAILGGAK.V K.ITLPVDFVTADKFDENAK.T K.QIVWNGPVGVFWEAFAR.G K.QIVWNGPVGVFWEAFAR.G K.DCVGPEVENACANPAAGTVILLENLR.F	BC=BT MC<BC 1.80 MC<BT 2.22

58	peptidyl-prolyl cis-trans isomerase A	gi 6679439	17960 7.74	394	37	R.VSFELFADK.V K.FEDENFILK.H K.EGMNIVEAMER.F R.IIPGFMCQGGDFTR.H R.IIPGFMCQGGDFTR.H M.VNPTVFFDITADDEPLGR.V	BC=BT MC<BC 1.26 MC=BT
59	Stress-induced phosphoprotein 1	gi 13277819	62528 6.40	201	5	K.AAALEFLNR.F K.LMDVGLIAIR.- R.KAAALEFLNR.F K.LDPQNHVLYSNR.S	BC=BT MC>BC 1.40 MC>BT 1.47
61	protein disulfide isomerase-related protein 5	gi 1710248	46170 4.95	107	7	K.GSFSEQGINEFLR.E -.LYSSDDVIELTPSNFNR.E	BC=BT MC>BC 1.47 MC>BT 1.59
62	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLTQR.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC<BC 1.22 MC<BT 1.30
	peroxiredoxin-1	gi 6754976	22162 8.26	218	20	K.IGYPAPNFK.A R.TIAQDYGVLK.A R.LVQAFQFTDK.H R.QITINDLPVGR.S R.QITINDLPVGR.S	
	peroxiredoxin-4 precursor	gi 7948999	31033 6.67	82	4	R.QITLNDLPVGR.S R.QITLNDLPVGR.S	
63	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLTQR.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC<BC 1.26 MC<BT 1.25
64	glutathione S-transferase P 1	gi 10092608	23594 7.68	216	12	-.PPYTIVYFPVR.G K.FEDGDLTLYQSNAILR.H	BC=BT MC>BC

	thioredoxin-dependent peroxide reductase, mitochondrial precursor	gil6680690	28109 7.15	173	9	K.HLSVNDLPVGR.S R.DYGVLLSAGIALR.G	1.30 MC>BT 1.35
	PEST proteolytic signal-containing nuclear protein	gil71480098	18951 6.86	83	6	K.FGFAIGSQATAR.K	
67	Stress-induced phosphoprotein 1	gil13277819	62528 6.40	201	5	K.AAALEFLNR.F K.LMDVGLIAIR.- R.KAAALEFLNR.F K.LDPQNHVLYSNR.S	BC=BT MC>BC 1.41 MC>BT 1.45
68	Chain E, Cytochrome C Oxidase At The Fully Oxidized State	gil1942990	12428 5.01	178	21	R.LNDFASAVR.I -.SHGSHTDEEFDAR.W	BC=BT MC<BC 1.59 MC=BT
70	aldolase C	gil229506	38993 9.06	195	14	K.ELSDIAHR.I R.QLLLTADDR.V K.ADDGRPFPQVIK.S K.GVVPLAGTDGETTTQGLDGLSER.C	BC=BT MC<BC 1.42 MC<BT 1.67
71	phosphoglycerate kinase	gil202423	44508 7.53	658	22	K.LGDVYVNDAFGTAHR.A K.ALESPERPFLAILGGAK.V K.ITLPVDFVTADKFDENAK.T K.QIVWNGPVGVFWEAFAR.G K.QIVWNGPVGVFWEAFAR.G K.DCVGPEVENACANPAAGTVILLENLR.F	BC=BT MC<BC 1.41 MC=BT
76	heat shock protein 70 cognate	gil309319	70793 5.37	646	14	K.FELTGIPPAPR.G K.VEIIANDQGNR.T R.FEELNADLFR.G R.RFDDAVVQSDMK.H R.TTPSYVAFTDTER.L K.STAGDTHLGGEDFDNR.M K.TVTNAVVTVPAYFNDSQR.Q	BC=BT MC>BC 1.69 MC>BT 1.98
	mitochondrial stress-70 protein	gil407341	73483 5.91	313	8	K.VQQTVDLFR.A K.SDIGEVILVGGMTR.M K.LLGQFTLIGIPPAPR.G K.NAVITVPAYFNDSQR.Q	

77	Prostaglandina E synthase 3	gi 9790017	18709 4.36	140	18	R.SILCCLR.K R.KGESGQSWPR.L K.LTFSC ₂ LGGSDFK.H	BC=BT MC>BC 1.33 MC>BT 1.63
79	pyruvate kinase M	gi 551295	57824 7.58	687	24	K.GDYPLEAVR.M R.LDIDSAPITAR.N R.NTGIICTIGPASR.S K.IYVDDGLISLQVK.E K.DAVLNAWAEDVDLR.V R.FDEILEASDGIMVAR.G R.LNFSHGTHEYHAETIK.N R.EAEAAIYHLQLFEELR.R R.EATESFASDPILYRPVAVALDTK.G	BC=BT MC>BC 1.19 MC=BT
80	nucleophosmin isoform 1	gi 6679108	32540 4.62	417	19	K.DLKPSTPR.S K.VDNDENEHQLSLR.T R.MTDQEAIQDLWQWR.K R.MTDQEAIQDLWQWR.K K.MSVQPTVSLGGFEITPPVVLR.L K.MSVQPTVSLGGFEITPPVVLR.L	BC=BT MC<BC 1.35 MC=BT
	calreticulin precursor	gi 6680836	47965 4.33	249	9	K.EQFLDGDWNTNR.W K.HEQNIDCGGGYVK.L K.IKDPDAAKPEDWDER.A	
81	mCG13235	gi 148684097	15406 9.82	188	25	K.EGLPPDQQR.L K.ESLHLVLR.L K.TITLEVEPSDTIENVK.A	BC=BT MC>BC 1.64 MC=BT
	polyubiquitin, partial	gi 1675359	4605 4.72	118	39	K.TITLEVEPSDTIENVK.A K.TITLEVEPDDTIENVK.A	
	NEDD8 precursor	gi 6679034	8967 6.59	106	34	K.ILGGSVLHLVLALR.G K.EIEIDIEPTDKVER.I	
83	alpha-fetoprotein, partial	gi 191765	47195 5.47	212	9	K.APQVSTPTLVEAAR.N K.LGEYGFQNAILVR.Y K.DVFLGTFLYEYSR.R	BC=BT MC>BC 1.38 MC>BT 1.26

84	gamma-actin	gi 809561	40992 5.56	691	25	K.AGFAGDDAPR.A R.GYSFTTTAER.E R.AVFPSIVGRPR.H K.QEYDESGPSIVHR.K K.IWHHTFYNELR.V K.SYELPDGQVITIGNER.F K.DLYANTVLSSGGTTMYPGIADR.M K.DLYANTVLSSGGTTMYPGIADR.M	BC=BT MC<BC 1.05 MC=BT
	put. beta-actin (aa 27-375)	gi 49868	39161 5.78	629	22	R.AVFPSIVGR.S R.GYSFTTTAER.E K.QEYDESGPSIVHR.K K.IWHHTFYNELR.V K.SYELPDGQVITIGNER.F K.DLYANTVLSSGGTTMYPGIADR.M K.DLYANTVLSSGGTTMYPGIADR.M	
	Eukaryotic translation initiation factor 3, subunit F	gi 47682703	37857 5.33	175	16	K.YAYYDTER.I R.VIGLSSDLQQVGGASAR.I R.LHPVILASIVDSYER.R R.EAPNPIHLTVDTGLQHGR.M	
85	Vimentin	gi 55408	53689 5.06	455	17	R.DNLAEDIMR.L K.FADLSEAANR.N K.VELQELNDR.F R.LGDLYEEEMR.D K.MALDIEIATYR.K R.ISLPLPTFSSLNLR.E R.EMEENFALEAANYQDTIGR.L	BC=BT MC>BC 1.30 MC=BT
87	glyceraldehyde-3- phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLTQR.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC=BC MC<BT 1.20
88	annexin A5	gi 6753060	35730 4.83	267	18	K.FITIFGTR.S R.SEIDLFNIR.K R.GTVTDFPGFDGR.A K.GLGTDEDSILNLLTSR.S K.YMTISGFQIEETIDR.E	BC=BT MC=BC MC>BT 1.33

91	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLT C R.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC=BC MC<BT 1.45
	aldolase C	gi 229506	38993 9.06	195	14	K.ELSDIAHR.I R.QLLLTADDR.V K.ADDGRPFPQVIK.S K.GVVPLAGTDGETTTQGLDGLSER.C	
92	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLT C R.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC=BC MC<BT 1.41
	alcohol dehydrogenase [NADP(+)]	gi 10946870	36564 6.90	75	6	K.ALGLSNFNSR.Q K.HHPEDVEPALR.K	
93	beta-galactoside binding protein	gi 193442	14796 5.32	341	33	K.LPDGHEFK.F K.EDGTWGTEHR.E K.DSNNL C LHFNPR.F R.FNAHGDANTIV C NTK.E	BC=BT MC=BC MC<BT 1.40
94	T-complex protein 1 subunit zeta	gi 6753324	57968 6.63	95	2	K_QADLYISEGLHPR.I K.QADLYISEGLHPR.I	BC=BT MC=BC MC>BT 1.23
95	phosphoglycerate kinase	gi 202423	44508 7.53	658	22	K.LGDVYVNDAFGTAHR.A K.ALESPERPFLAILGGAK.V K.ITLPVDFVTADKFDENAK.T K_QIVWNGPVGVFWEAFAR.G K.QIVWNGPVGVFWEAFAR.G K.DC V VGPEVENACANPAAGTVILLENLR.F	BC=BT MC=BC MC<BT 1.59
96	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	gi 19527270	21510 5.31	92	6	R.YILEGSGYFDVR.D	BC=BT MC=BC MC>BT 1.21
	39S ribosomal protein L12, mitochondrial precursor	gi 22164792	21695 9.34	78	5	K.NYVQGINLVQAK.K	

98	heat shock protein 70 cognate	gij309319	70793 5.37	646	14	K.FELTGIPPAPR.G K.VEIIANDQGNR.T R.FEELNADLFR.G R.RFDDAVVQSDMK.H R.TTPSYVAFTDTER.L K.STAGDTHLGGEDFDNR.M K.TVTNAVVTVPAYFNDSQR.Q	BC=BT MC=BC MC>BT 1.70
	mitochondrial stress-70 protein	gij407341	73483 5.91	313	8	K.VQQTVDLFR.A K.SDIGEVILVGGMTR.M K.LLGQFTLIGIPPAPR.G K.NAVITVPAYFNDSQR.Q	
100	vacuolar protein-sorting-associated protein 25 isoform 2	gij25092662	20735 5.97	192	17	K.SSFLIMWR.R K.LIYQWVSR.S R.FPPFFTLQPNVDTR.Q	BC=BT MC=BC MC<BT 1.28
101	pyruvate kinase M	gij551295	57824 7.58	687	24	K.GDYPLEAVR.M R.LDIDSAPITAR.N R.NTGIICTIGPASR.S K.IYVDDGLISLQVK.E K.DAVLNAWAEDVDLR.V R.FDEILEASDGIMVAR.G R.LNFSGHGTHEYHAETIK.N R.EAEAAIYHLQLFEELR.R R.EATESFASDPILYRPVAVALDTK.G	BC=BT MC=BC MC<BT 1.35
	tubulin beta-5 chain	gij7106439	49639 4.78	90	6	R.FPGQLNADLR.K K.GHYTEGAELVDSVLDVVR.K	
102	peptidyl-prolyl cis-trans isomerase A	gij6679439	17960 7.74	394	37	R.VSFELFADK.V K.FEDENFILK.H K.EGMNIVEAMER.F R.IIPGFMCGGDFTR.H R.IIPGFMCGGDFTR.H M.VNPTVFFDITADDEPLGR.V	BC=BT MC=BC MC<BT 1.13
103	thioredoxin-dependent peroxide reductase, mitochondrial precursor	gij6680690	28109 7.15	173	9	K.HLSVNDLPVGR.S R.DYGVLLSESAGIALR.G	BC=BT MC=BC MC>BT

	trafficking protein particle complex subunit 4	gi 11140825	24370 5.83	135	17	K.FVVLADPR.Q K.AGGLIYQWDSYSPR.A K.EVLEYLGNPANYPVSIR.F	1.54
	ER membrane protein complex subunit 8	gi 6754870	23333 5.72	106	7	R.SYETLVDFDNHLDDIR.N	
104	beta-galactoside binding protein	gi 193442	14796 5.32	341	33	K.LPDGHEFK.F K.EDGTWGTEHR.E K.DSNNLCLHFNPR.F R.FNAHGDANTIVCNTK.E	BC=BT MC=BC MC<BT 1.62
105	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLT <u>C</u> R.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC=BC MC<BT 1.46
106	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLT <u>C</u> R.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC=BC MC<BT 1.37
107	glyceraldehyde-3-phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLT <u>C</u> R.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC=BC MC<BT 1.18
108	Destrin	gi 9790219	18509 8.14	95	7	K.HEYQANGPEDLNR.T	BC=BT MC=BC MC>BT 1.30
110	14-3-3 protein epsilon	gi 13928824	29103 4.55	360	20	K.DSTLIMQLLR.D K.DSTLIMQLLR.D R.YLAEFATGNDR.K R.YLAEFATGNDRK.E K.VAGMDVELTVEER.N K.AASDIAMTELPPTHPIR.L K.AASDIAMTELPPTHPIR.L	BC=BT MC=BC MC<BT 1.16

113	phosphoglycerate mutase 1	gi 114326546	28814 6.67	824	54	R.VLIAAHGNSLR.G R.HGESAWNLENR.F R.ALFWNEEIVPQIK.E R.DAGYEFDICFTSVQK.R R.FSGWYDADLSPAGHEEAK.R K.NLKPIKPMQFLGDEETVR.K K.NLKPIKPMQFLGDEETVR.K R.SYDVPPPPMEPDHPFYSNISK.D	BC=BT MC=BC MC<BT 1.32
	calcyclin binding protein	gi 3142331	28301 7.78	175	18	K.TDTVILCR.K K.ISNYGWDQSDK.F K.IYITLTGVHQVPTENVQVHFTER.S	
114	Enolase 1, (alpha)	gi 59808815	47128 6.16	667	23	R.IGAEVYHNLK.N R.GNPTVEVDLYTAK.G R.YITPDQLADLYK.S K.LAQSNWGVMSHR.S R.AAVPSGASTGIYEALER.D K.LAMQEFMILPVGASSFR.E K.AGYTDQVVIGMDVAASEFYR.S	BC=BT MC=BC MC<BT 1.29
116	alpha-fetoprotein, partial	gi 191765	47195 5.47	212	9	K.APQVSTPTLVEAAR.N K.LGEYGFQNAILVR.Y K.DVFLGTFLYEYSR.R	BC=BT MC=BC MC<BT 1.40
	F-actin-capping protein subunit beta isoform a	gi 83649737	31326 5.47	84	5	K.LEVEANNAFDQYR.D R.KLEVEANNAFDQYR.D	
117	glyceraldehyde-3- phosphate dehydrogenase	gi 6679937	35787 8.44	442	19	R.VPTPNVSVVDLTQR.L K.LVINGKPITIFQER.D K.LISWYDNEYGYSNR.V K.VIHDNFGIVEGLMTTVHAITATQK.T	BC=BT MC=BC MC<BT 1.46
	macrophage migration inhibitory factor	gi 6754696	12496 6.79	166	17	K.LLCGLLSDR.L M.PMFIVNTNVPR.A M.PMFIVNTNVPR.A	

GI: GenInfo code; pI: isoelectric point; BC: B16-F10 control; BT: B16-F10 treated; MC: Melan-a control and MT: Melan-a treated.

Supplemental table 2: Functional categories of the identified proteins.

Functional category	Spot #
01. Metabolism	
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	96
Alcohol dehydrogenase [nadp(+)]	92
Aldolase c	70; 91
Alpha-fetoprotein, partial	30; 83; 116
Cytochrome b5	28; 43
D-dopachrome decarboxylase	36
Enolase 1, (alpha)	2; 27; 114
Fatty acid-binding protein, epidermal isoform 1	25
Glutathione s-transferase p 1	13; 64
Glyceraldehyde-3-phosphate dehydrogenase	13; 29; 41; 46; 62; 63; 87; 91; 92; 105; 106; 107; 117
L-lactate dehydrogenase a chain isoform 1	29
Long-chain acyl-coa dehydrogenase	32
Macrophage migration inhibitory factor	35; 45; 117
Phosphoglycerate kinase	1; 19; 32; 44; 56; 71; 95
Phosphoglycerate mutase 1	5; 8; 113
Prostaglandin e synthase 3	22
Pyruvate kinase m	10; 79; 101
Triosephosphate isomerase	7
Tubulin beta-5 chain	101
02. Energy	
Aldolase c	70; 91
Enolase 1, (alpha)	2; 27; 114
L-lactate dehydrogenase a chain isoform 1	29
Long-chain acyl-coa dehydrogenase	32
Phosphoglycerate kinase	1; 19; 32; 44; 56; 71; 95
Phosphoglycerate mutase 1	5; 8; 113
Pyruvate kinase m	10; 79; 101
Triosephosphate isomerase	7
10. Cell cycle and DNA processing	
Calreticulin precursor	80
Cofilin-1	9
Destrin	108
Heat shock protein 70 cognate	4; 11; 46; 76; 98
Prohibitin	20
Stathmin	16
Tubulin beta-5 chain	101
Vacuolar protein-sorting-associated protein 25 isoform 2	100
11. Transcription	
Nedd8 precursor	81
Vacuolar protein-sorting-associated protein 25 isoform 2	100
12. Protein synthesis	
39s ribosomal protein l12, mitochondrial precursor	96
Elongation factor 1-delta	31
Eukaryotic translation initiation factor 3 subunit k isoform 1	22
Eukaryotic translation initiation factor 3, subunit f	84
Eukaryotic translation initiation factor 4h	18
Eukaryotic translation initiation factor 5a	43
Sui1 homolog	15
14. Protein fate (folding, modification, destination)	
10 kda heat shock protein, mitochondrial	26; 35
14-3-3 protein epsilon	110

Calcyclin binding protein	18; 113
Calreticulin precursor	80
Heat shock protein 65	3; 14
Heat shock protein 70 cognate	4; 11; 46; 76; 98
Mitochondrial stress-70 protein	76; 98
Nedd8 precursor	81
Nucleophosmin isoform 1	12; 53; 80
Phosphoglycerate kinase	1; 19; 32; 44; 56; 71; 95
Protein disulfide-isomerase a3 precursor	24; 30; 48
T-complex protein 1 subunit zeta	94
Tubulin beta-5 chain	101
16. Protein with binding function or cofactor requirement (structural or catalytic)	
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	96
10 kda heat shock protein, mitochondrial	26; 35
14-3-3 protein epsilon	110
39s ribosomal protein l12, mitochondrial precursor	96
Aldolase c	70; 91
Alpha-fetoprotein, partial	30; 83; 116
Annexin a5	88
Beta-galactoside binding protein	33; 93; 104
Calreticulin precursor	80
Cofilin-1	9
Cytochrome b5	28; 43
Destrin	108
Elongation factor 1-delta	31
Enolase 1, (alpha)	2; 27; 114
Eukaryotic translation initiation factor 4h	18
F-actin-capping protein subunit beta isoform a	116
Fatty acid-binding protein, epidermal isoform 1	25
Guanosine diphosphate (gdp) dissociation inhibitor 2	40
Heat shock protein 70 cognate	4; 11; 46; 76; 98
L-lactate dehydrogenase a chain isoform 1	29
Long-chain acyl-coa dehydrogenase	32
Mitochondrial stress-70 protein	76; 98
Nedd8 precursor	81
Nucleophosmin isoform 1	12; 53; 80
Phosphoglycerate kinase	1; 19; 32; 44; 56; 71; 95
Pyruvate kinase m	10; 79; 101
Stathmin	16
Stress-induced phosphoprotein 1	38; 59; 67
T-complex protein 1 subunit zeta	94
Thioredoxin-dependent peroxide reductase, mitochondrial precursor	64; 103
Trafficking protein particle complex subunit 4	103
Translationally-controlled tumor protein	22
Tubulin beta-5 chain	101
Vimentin	85
18. Regulation of metabolism and protein function	
Elongation factor 1-delta	31
Guanosine diphosphate (gdp) dissociation inhibitor 2	40
Rho gdp dissociation inhibitor (gdi) alpha	11
20. Cellular transport, transport facilities and transport routes	
1-cys peroxiredoxin protein	7
Alpha-fetoprotein, partial	30; 83; 116
Cytochrome b5	28; 43
Fatty acid-binding protein, epidermal isoform 1	25
Long-chain acyl-coa dehydrogenase	32
Mitochondrial stress-70 protein	76; 98

Peroxisredoxin-1	62
Trafficking protein particle complex subunit 4	103
Tubulin beta-5 chain	101
Vacuolar protein-sorting-associated protein 25 isoform 2	100
30. Cellular communication/signal transduction mechanism	
Beta-galactoside binding protein	33; 93; 104
Rho gdp dissociation inhibitor (gdi) alpha	11
Stathmin	16
32. Cell rescue, defense and virulence	
1-cys peroxiredoxin protein	7
Glutathione s-transferase p 1	13; 64
Heat shock protein 70 cognate	4; 11; 46; 76; 98
Macrophage migration inhibitory fator	35; 45; 117
Mitochondrial stress-70 protein	76; 98
Nucleophosmin isoform 1	12; 53; 80
Peroxisredoxin-1	62
Peroxisredoxin-4 precursor	62
Thioredoxin-dependent peroxide reductase, mitochondrial precursor	64; 103
34. Interaction with the environment	
Cofilin-1	9
Destrin	108
Heat shock protein 70 cognate	4; 11; 46; 76; 98
Mitochondrial stress-70 protein	76; 98
Stathmin	16
36. Systemic interaction with the environment	
Annexin a5	88
Macrophage migration inhibitory fator	35; 45; 117
40. Cell fate	
Cofilin-1	9
Eukaryotic translation initiation factor 5a	43
F-actin-capping protein subunit beta isoform a	116
Macrophage migration inhibitory fator	35; 45; 117
Protein disulfide-isomerase a3 precursor	24; 30; 48
Translationally-controlled tumor protein	22
41. Development (Systemic)	
Cofilin-1	9
Stathmin	16
Trafficking protein particle complex subunit 4	103
42. Biogenesis of cellular components	
Calreticulin precursor	80
Cofilin-1	9
Destrin	108
F-actin-capping protein subunit beta isoform a	116
Stathmin	16
Tubulin beta-5 chain	101
Vacuolar protein-sorting-associated protein 25 isoform 2	100
Vimentin	85
43. Cell type differentiation	
Stathmin	16
Trafficking protein particle complex subunit 4	103
45. Tissue differentiation	
Alpha-fetoprotein, partial	30; 83; 116
Stathmin	16
47. Organ differentiation	
Alpha-fetoprotein, partial	30; 83; 116
Cofilin-1	9
Stathmin	16