

Antibodies

TCTP (1:10000, Abcam #ab133568, Waltham, MA USA), GNAQ (1:1000, St John's laboratory # STJ43766, London, UK), Bid (1:1000, Abcam #ab32060, Waltham, MA USA), tBid (1:1000, Abcam #ab108293, Waltham, MA USA), β -Actin (1:5000, Millipore #MAB1501, Darmstadt, Germany), Anti-rabbit IgG (1:10000, GE Healthcare #NA934, Wauwatosa, WI, USA), Anti-mouse IgG (1:10000, GE Healthcare #N931, Wauwatosa, WI, USA), Phospho-ASK1 (Ser83) (1:1000, Cell Signaling #3761, St. Louis, MO, USA), Phospho-ASK1 (Thr845) (1:1000, Cell Signaling #3765, St. Louis, MO, USA), ASK1 (1:2000, Abcam #ab45178, Waltham, MA USA), Phospho-STAT3 (Tyr705) (1:10000, Abcam #ab76315, Waltham, MA USA), STAT3 (1:1000, Abcam #ab109085, Waltham, MA USA), Phospho-JNK (T183/Y185) (1:1000, Signaling #4671, St. Louis, MO, USA)

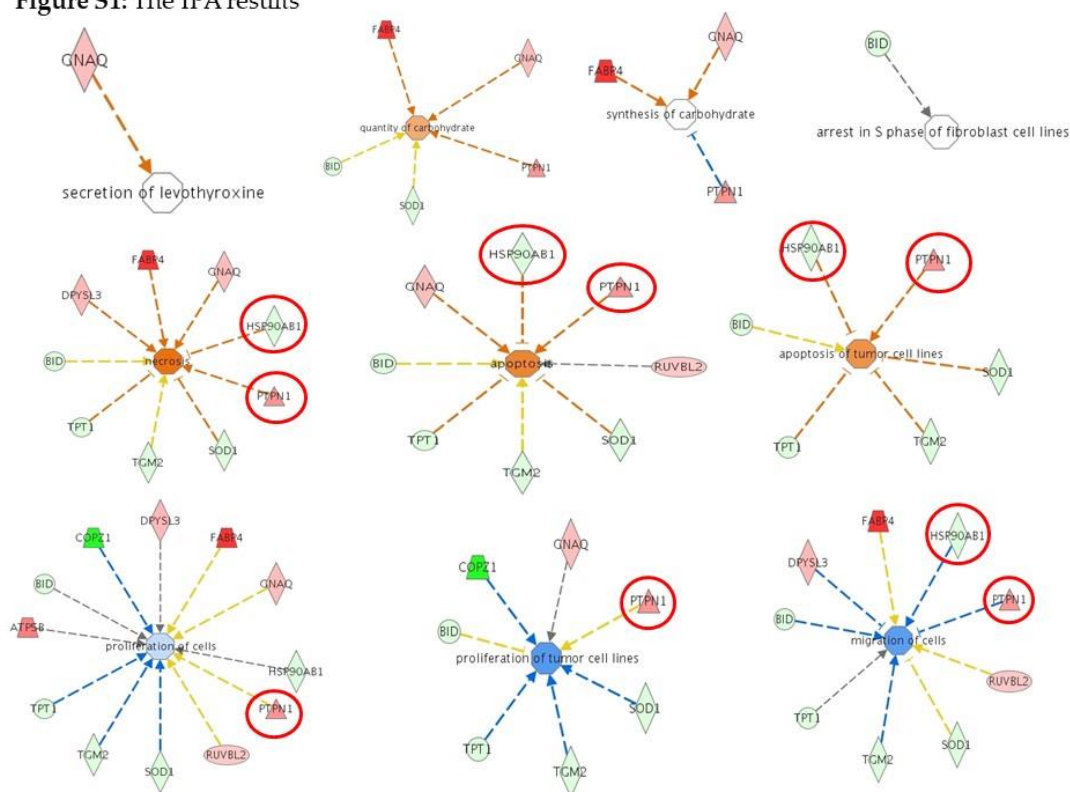
Collection and Identification of Plant Materials

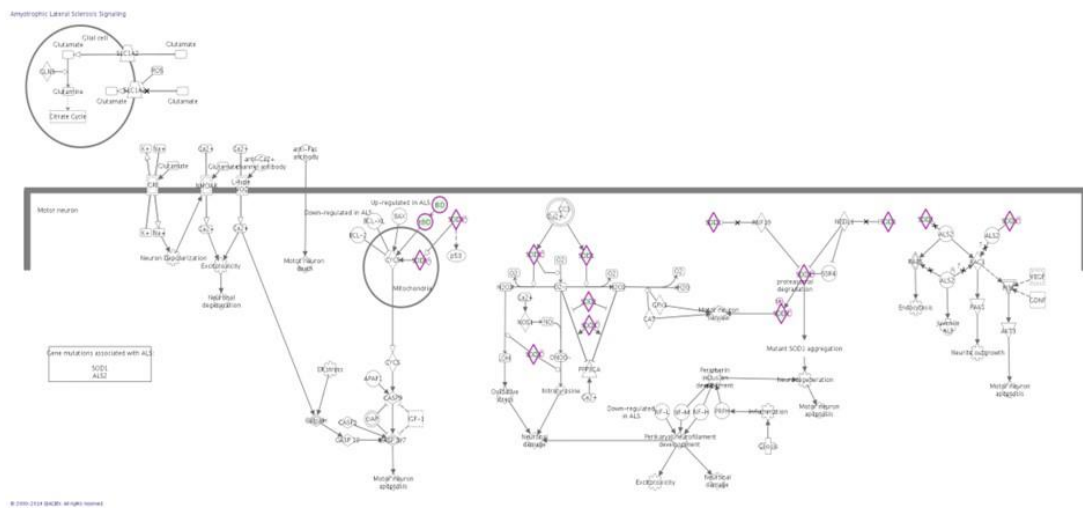
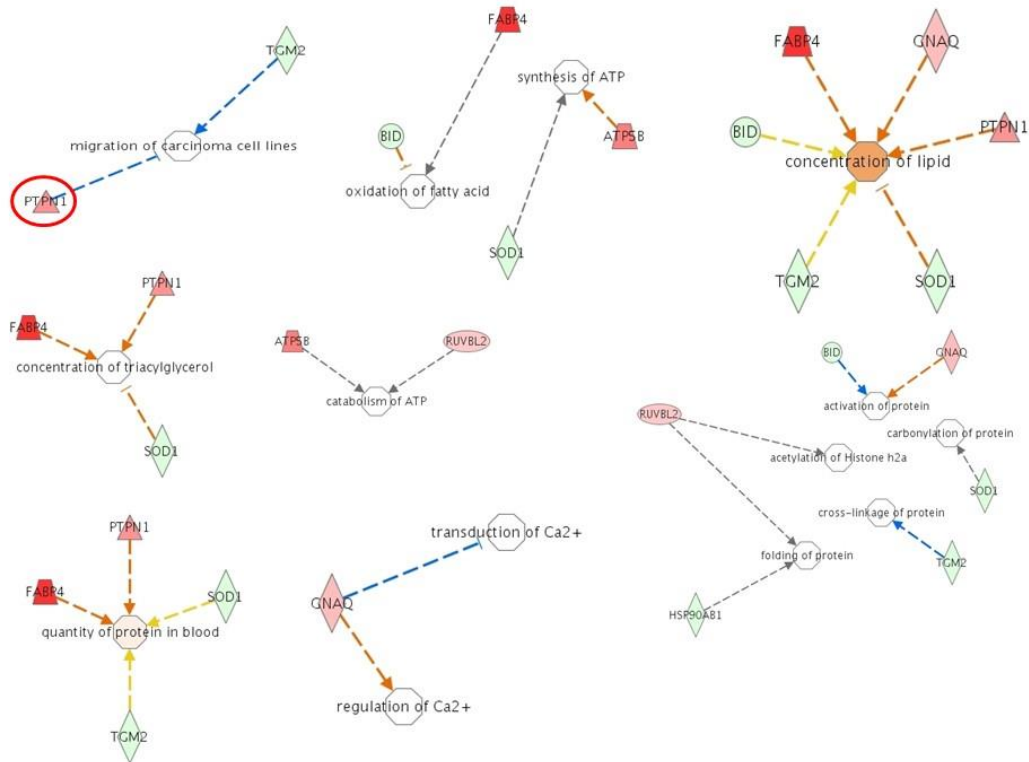
Please refer to Nutrients 2018, 10, 543.

Preparation of the Ethanol Extracts from Pulps and Peels of Pomegranates

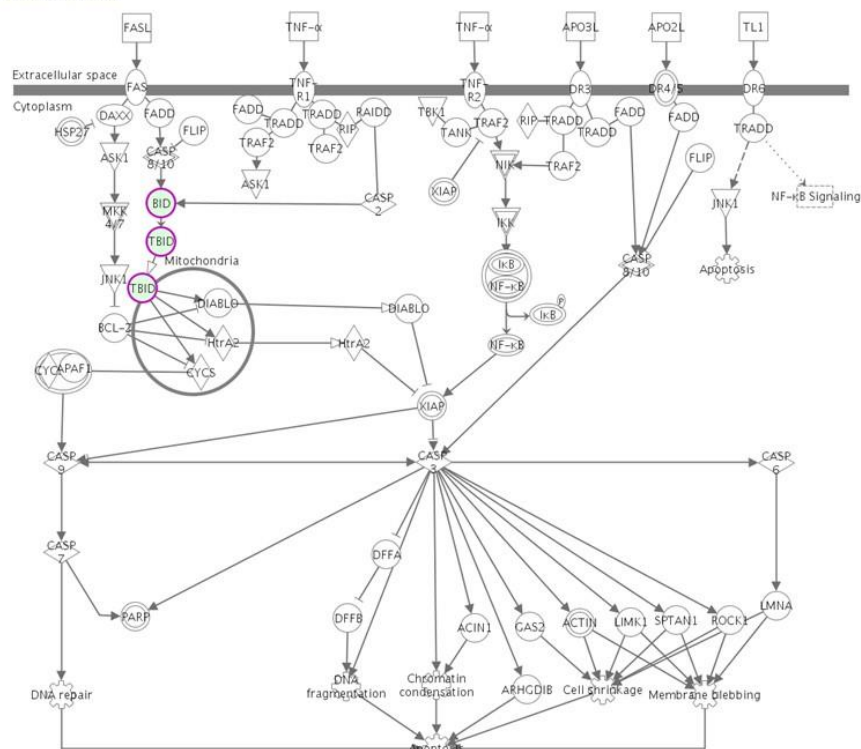
Please refer to Nutrients 2018, 10, 543.

Figure S1: The IPA results



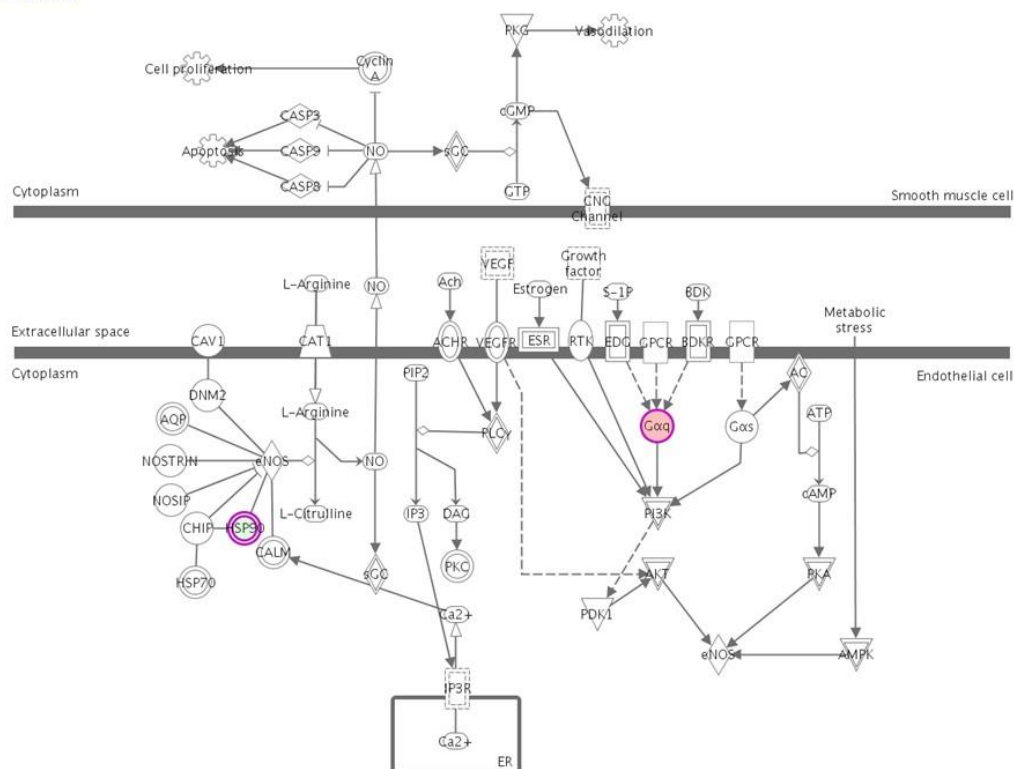


Death Receptor Signaling



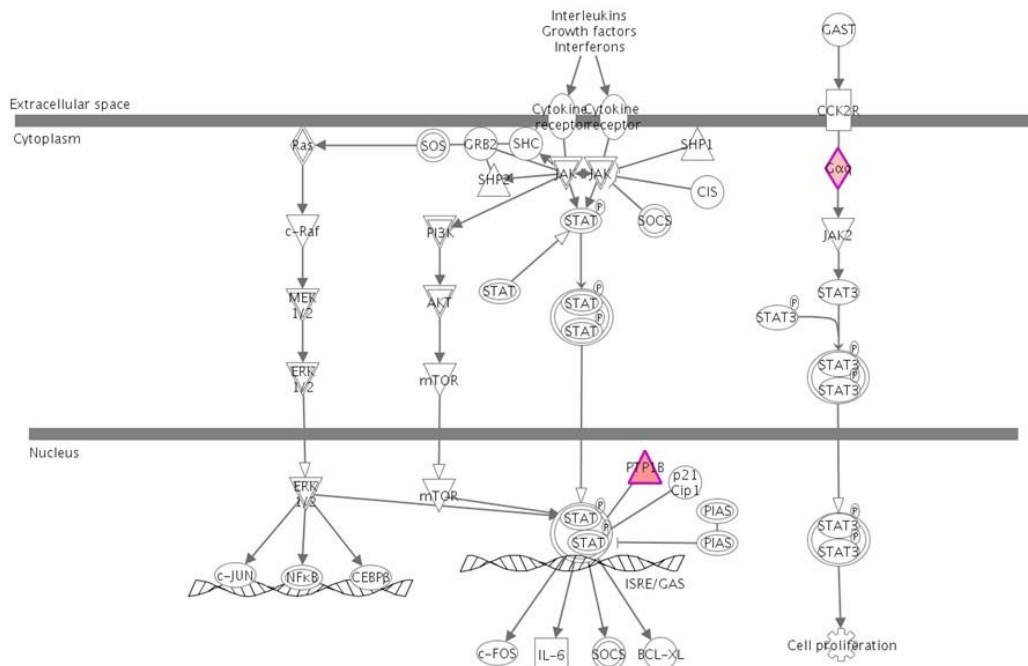
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eNOS Signaling



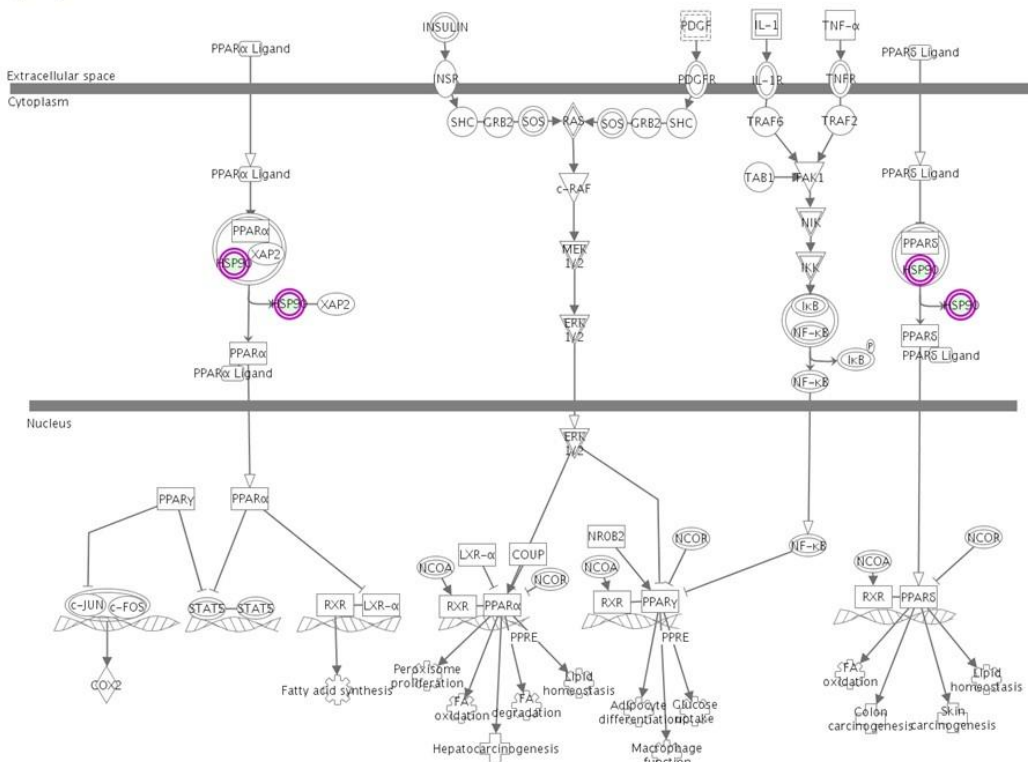
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JAK/Stat Signaling

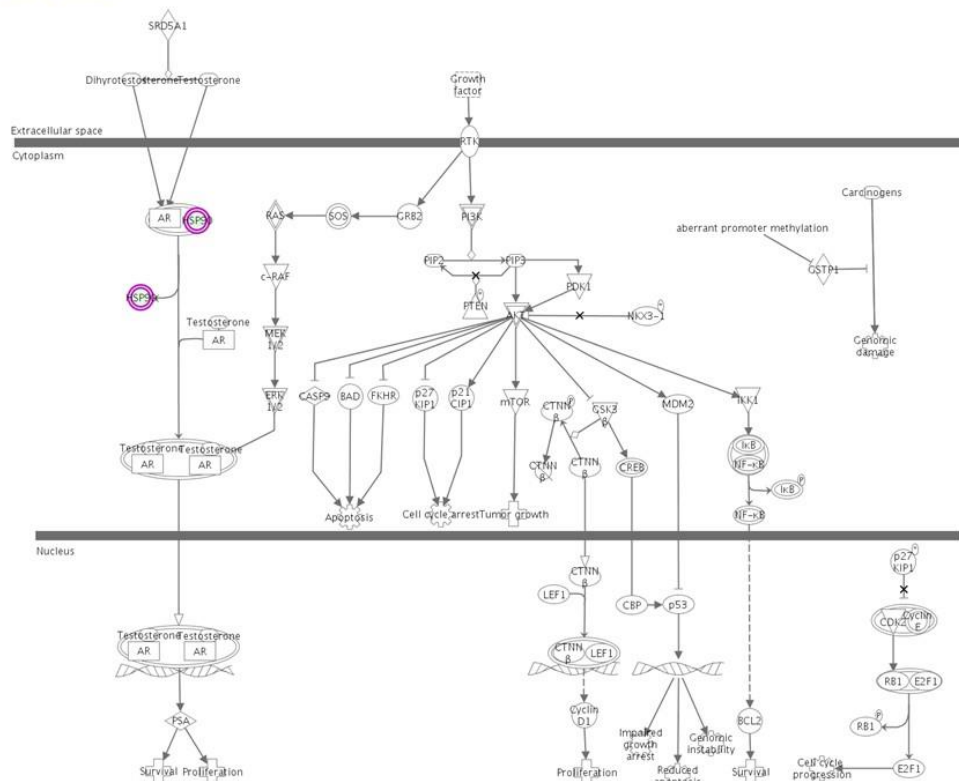


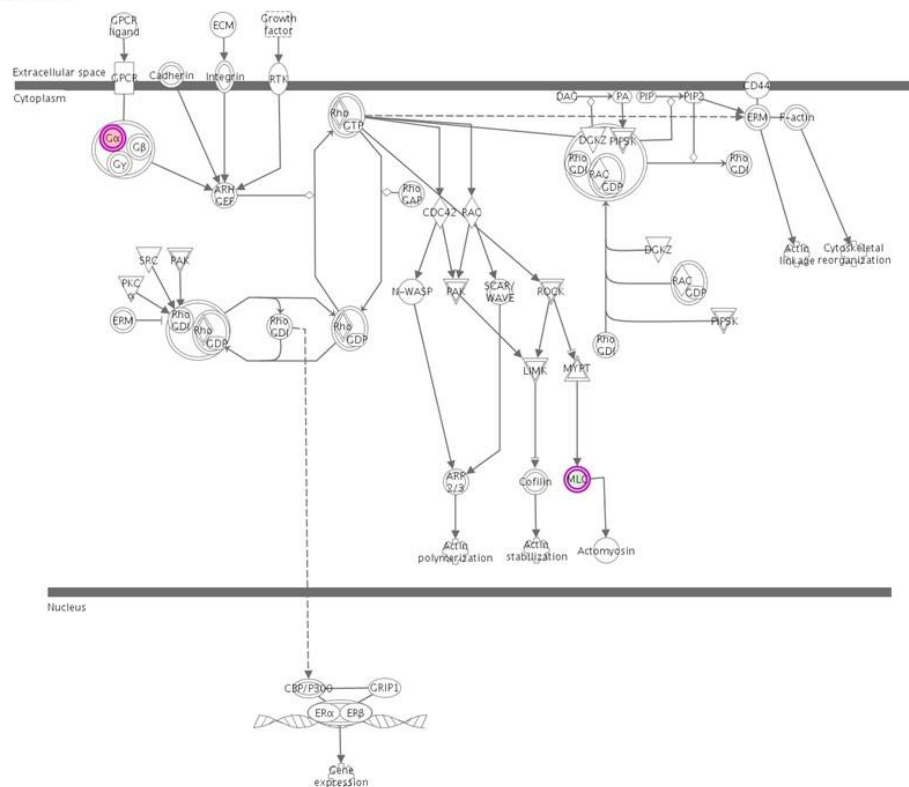
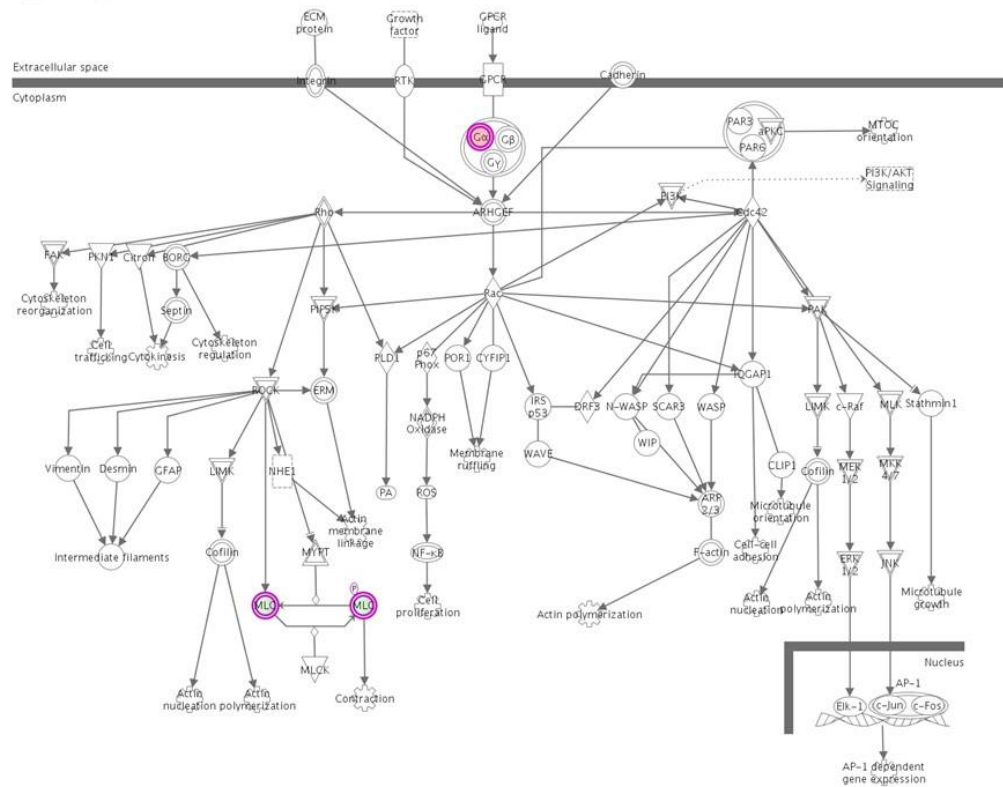
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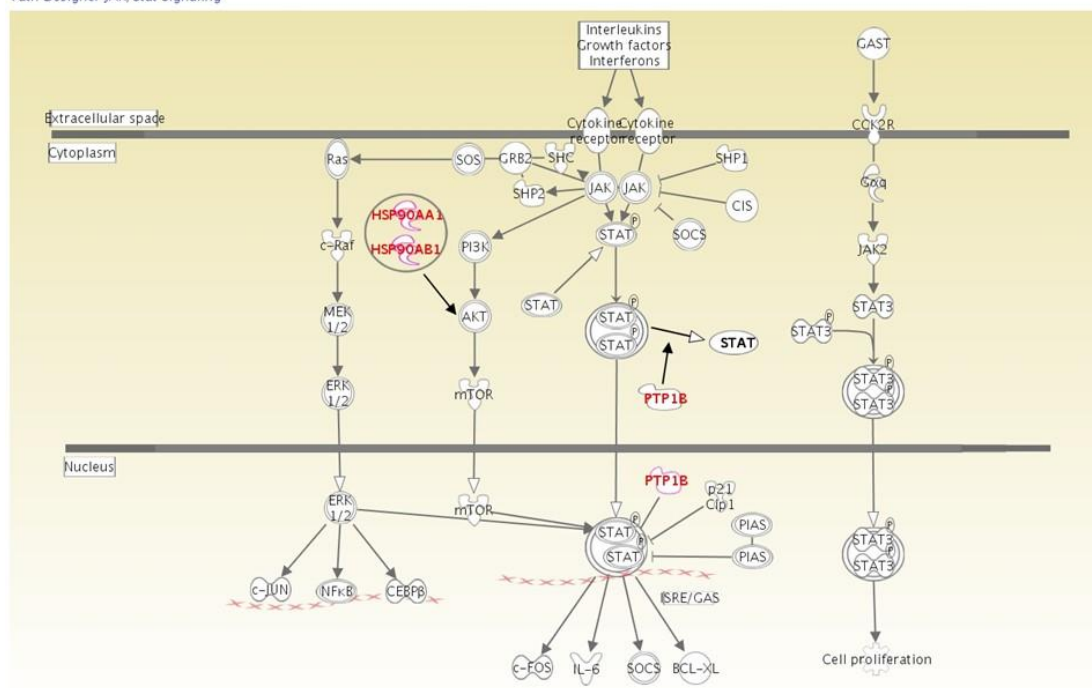
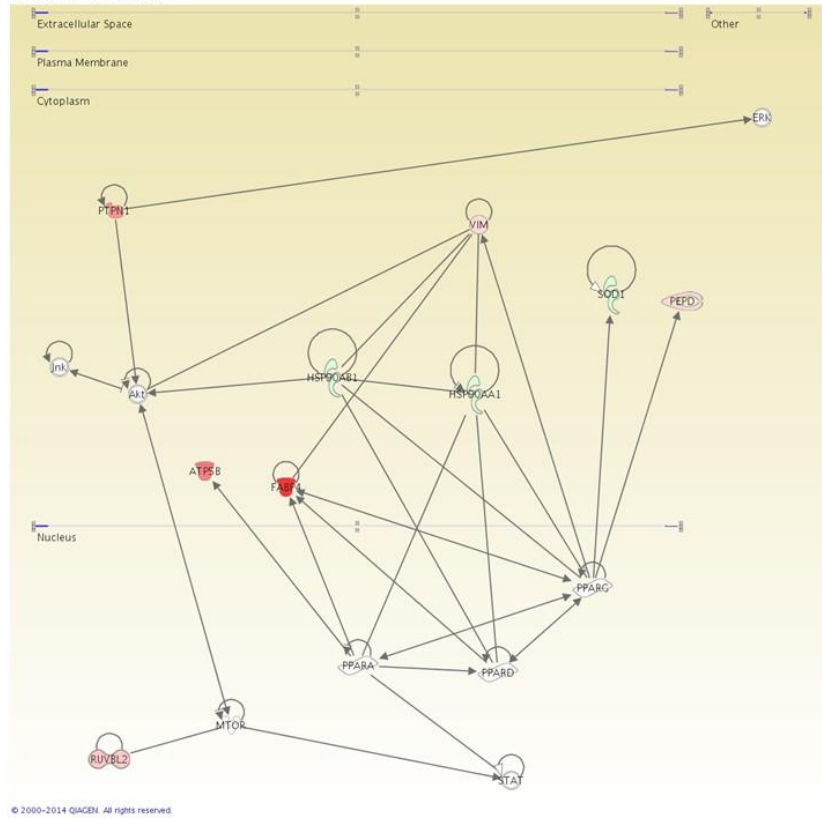
PPAR Signaling

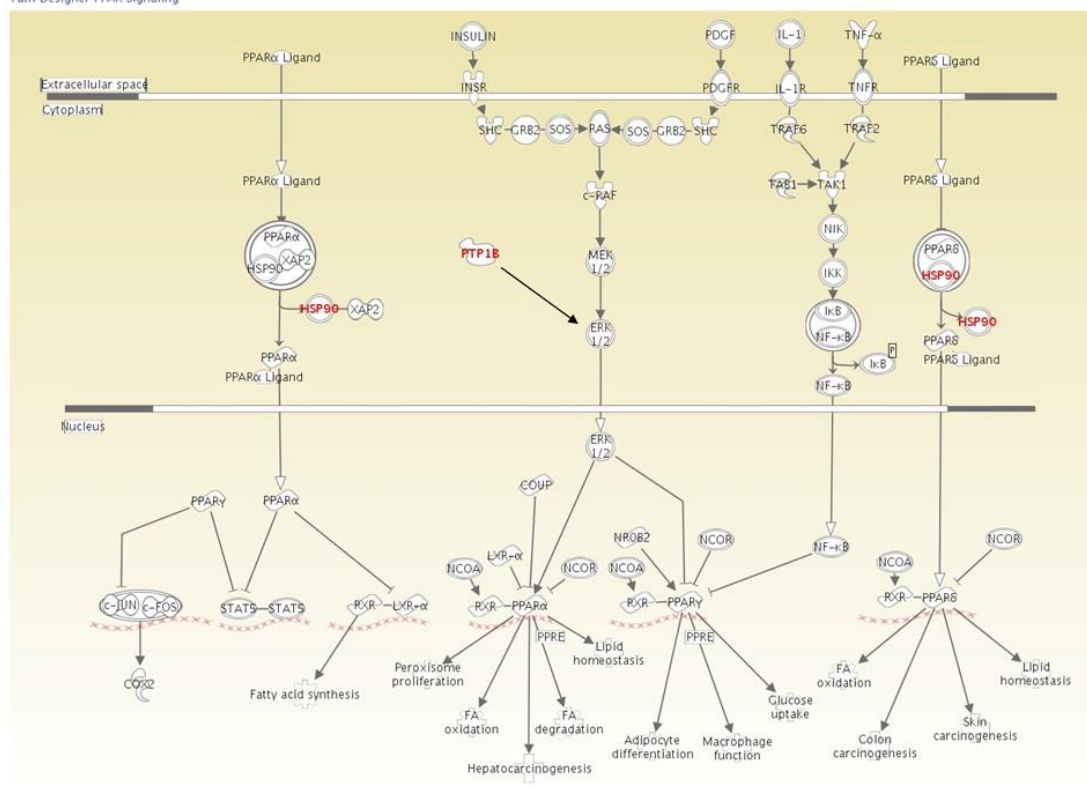


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**Table S1.** The volumes of each de-regulated protein spot.

Spot number	Control (ppm±S.D.)	Treatment (ppm±S.D.)	P value
Spot 1	260.25±145.48	29.27±12.12	0.0153
Spot 2	421.65±85.72	51.90±32.67	0.0024
Spot 3	316.60±71.50	6.24±2.28	0.0025
Spot 4	221.94±41.62	59.60±19.99	0.0079
Spot 5	669.22±131.03	91.52±21.28	0.0024
Spot 6	138.46±50.49	34.42±11.12	0.0465
Spot 7	229.62±58.18	55.38±15.82	0.0202
Spot 8	255.98±70.35	102.12±32.49	0.0824
Spot 9	102.73±14.71	263.52±40.56	0.0039
Spot 10	12.20±4.33	111.22±20.80	0.0016
Spot 11	187.06±92.95	13.26±9.61	0.0086

Spot 12	242.74±73.76	38.22±9.02	0.0250
Spot 13	9.92±2.71	46.00±8.50	0.0037
Spot 14	43.64±9.03	165.88±25.06	0.0018
Spot 15	586.52±196.74	119.22±25.01	0.0462
Spot 16	95.30±19.74	252.78±45.11	0.0126
Spot 17	28.56±8.79	416.14±63.14	0.0003
Spot 18	19.58±7.99	148.18±30.13	0.0033
Spot 19	30.38±13.21	152.36±38.50	0.0172

Table S2. The detailed mass spectrometry data of matched peptides

Spot	Protein I.D.	Matched ² peptide number	Sequence ¹
1	myosin light polypeptide 6 (MYL6)	3	NKDQGTIEDYVEGLR (2,4.12,0.48,1) ALGQNPTNAEVLK (2,3.28,0.31,1) VLGNPKSDEMNVK (2,3.18,0.32,1)
2	myosin regulatory light chain MRLC2 (MYL2)	7	ATSNVFAMFDQSQIQEFK (2,6.33,0.57,1) FTDEEVDELYREAPIDKK (3,3.90,0.14,1) ELLTTMGDRFTDEEVDELYREAPIDK (3,3.43,0.43,3) KGNFNYIEFTR (2,3.31,0.36,1) GNFNYIEFTR (2,3.26,0.16,1) DGFIDKEDLHDMLASLGK (3,3.06,0.40,2) LNGTDPEDVIR (2,2.77,0.18,1)
3	coatomer protein complex, subunit zeta 1 (COPZ1)	3	VALRGEDVPLTEQTVSQVLQSAK (3,5.53,0.54,1) AILILDNDGDRLFAK (2,4.28,0.54,1) YYDDTYPVKEQK (2,2.89,0.24,4)
4	Chromobox protein homolog 3 (CBX3)	6	KVEEAEPEEFVVEKVLDR (3,5.40,0.55,1) IIGATDSSGELMFLMK (2,5.32,0.65,1) WKDSDEADLVLAKE (3,3.89,0.36,1) SKKVEEAEPEEFVVEK (2,3.60,0.40,1) DSDEADLVLAKE (2,3.22,0.36,1) LTWHSCPEDEAQ (2,2.66,0.31,1)
5	Human Translationally Controlled Tumor Protein (TCTP)	3	MIYRDLISHDEMFSDIYK (3,3.37,0.13,2) DLISHDEMFSDIYKIR (3,2.96,0.42,1) YIKDYMK (2,2.18,0.22,1)
6	Ran GTPase-activating protein 1 (RanGAP1)	14	SSVLIAQQTDTSDPEKVVSAFLK (3,5.19,0.59,1) MAVQDAVDALMQK (2,4.95,0.46,1)

			DAALAVAEAMADKAELEK (2,4.76,0.55,1) NRLENDGATALAEAFR (2,4.51,0.48,1) VINLNDNTFTEK (2,4.15,0.47,1) HSLLQTLYKV (2,3.7,0.48,1) VINLNDNTFTEKGAVAMAETLK (3,3.48,0.33,1) SKGAVAIADAIR (3,3.31,0.44,1) EIEDFDSLEALRLEGNTVGVEAAR (3,3.25,0.26,1) TQVAGGQLSFK (2,3.16,0.44,2) KSSAQGKPLALK (2,3.03,0.34,2) VSSVFKDEATVR (2,2.73,0.41,1) SSAQGKPLALK (2,2.64,0.32,4) GAVAMAETLKTLR (2,2.51,0.38,2)
7	Heat shock protein HSP 90-beta (HSP90- β)	10	NPDDITQEEYGEFYK (2,5.63,0.58,1) HLEINPDHPIVETLR (2,4.43,0.54,1) GVVDSEDLPLNISR (2,4.03,0.4,1) YHTSQSGDEMTSLSEYVSR (3,3.87,0.56,1) ELISNASDALDKIR (2,3.57,0.52,1) ADLINNLGTIAK (2,3.42,0.46,1) VILHLKEDQTEYLEER (3,3.27,0.44,1) TLTLVDTGIGMTK (2,3.09,0.55,1) EQVANSFAVER (2,2.83,0.44,3) YIDQEELNKTPIWTR (3,2.71,0.43,3)
8	Heat shock protein HSP 90-alpha (HSP90- α)	6	KHLEINPDHSIETLR (4,4.18,0.40,1) HLEINPDHSIETLR (3,3.65,0.47,1) NPDDITNEEYGEFYK (2,3.54,0.50,1) ELISNSSDALDKIR (2,2.85,0.35,5) DNSTMGYMAAK (2,2.79,0.38,1) LGIHEDSQNR (2,2.64,0.42,1)
9	vimentin (VIM)	13	LQDEIQNMKEEMAR (2,4.23,0.53,1) ILLAELEQLKGQ GK (2,4.19,0.39,1) LQEEMLQREEAENTLQSFR (3,4.12,0.50,1) TNEKVELQELNDR (2,3.85,0.43,1) FADLSEAANR (2,3.65,0.43,1) KVESLQEEIAFLK (2,3.48,0.32,1) NLQEAEEWYKSK (2,3.44,0.42,1) NLQEAEEWYK (2,3.40,0.32,1) LGDLYEEEMR (2,3.16,0.30,1) QDVDNASLAR (2,3.11,0.37,1) DGQVINETSQHDDLE (2,3.04,0.34,2) ISLPLPNFSSLNLR (2,2.56,0.36,1) ETNLDSLPLVDTHSKR (2,2.47,0.43,4)
10	Mitochondrial ATP synthase subunit beta (ATP5B)	18	EGNLDLYHEMIESGVINLK (2,5.53,0.51,1) TREGNDLYHEMIESGVINLKDATSK (3,5.26,0.35,1) LVLEVAQH LGESTVR (2,4.99,0.61,1) FTQAGSEVSALLGR (2,4.95,0.53,1) VALVYGQMNEPPGAR (2,4.90,0.57,1) FLSQPFQVAEVFTGHMGK (2,4.85,0.56,1) TVLIMELINNVAK (2,4.73,0.43,1)

			IMDPNIVGSEHYDVAR (2,4.68,0.56,1) SLQDIILGMDDELSEEDKLTCSR (3,4.57,0.60,1) GQKVLDSGAPIKIPVGPETLGR (3,4.57,0.55,1) AIAELGIYPAVDPLDSTSR (2,4.33,0.58,1) VLDSGAPIKIPVGPETLGR (3,4.25,0.47,1) EGNDLYHEMIESGVINLK (3,4.11,0.17,6) IMNVIGEPIDERGPIKTK (2,3.63,0.46,1) IPSAVGYQPTLATDMGTMQER (3,3.63,0.40,1) IGLFGGAGVGK (2,3.30,0.47,1) ETRLVLEVAQHLGESTVR (3,3.08,0.33,12) TIAM*DGTEGLVR (2,2.32,0.23,2)
11	Coactosin-Like Protein-1 (COTL1)	7	TGTDKTLVKEVVQNFAK (3,5.32,0.61,1) ELEEDFIKSELKK (2,4.26,0.32,1) TLVKEVVQNFAK (2,3.81,0.42,1) SKFALITWIGENVSGLQR (3,3.38,0.34,1) EFVISDRKELEEDFIK (3,3.25,0.11,1) FTTGDAMSKR (2,2.76,0.45,1) AKTGTDKTLVK (2,2.38,0.25,2)
12	Pro-Apoptotic Protein Bid (Bid)	2	LGRIEADSESQEDIIR (3,4.98,0.48,1) HLAQVGDSMDR (2,3.42,0.46,1)
13	Guanine nucleotide-binding protein alpha-q (GNAQ)	6	YYLNDLDRVADPAYLPTQQDVLR (3,6.13,0.47,1) VSAFENPYVDAIK (2,4.29,0.40,1) VADPAYLPTQQDVLR (2,3.78,0.44,1) IIHSGSGYSEDEK (2,3.53,0.1,1) LLLLGTGESGK (2,2.87,0.24,1) RINDEIER (2,2.46,0.15,3)
14	RuvB-like 2 ; 48 kDa TATA box-binding protein interacting protein (RUVBL2)	12	ALESDFMAPVLIMATNR (2,4.58,0.58,1) TQGFALFSGDTGEIKSEVR (3,4.12,0.55,1) IRGTSYQSPHGIPIDLLDR (3,3.48,0.42,1) LLIVSTTPYSEKDTK (2,3.42,0.41,2) DKVQAGDVITIDKATGK (2,3.36,0.60,1) EVVHTVSLHEIDVINSR (3,3.26,0.43,1) GLGLDDALEPR (2,3.26,0.43,1) AVLIAGQPGTGK (2,3.20,0.50,1) QASQGMVGQLAAR (2,3.15,0.46,1) ARDYDAMGSQTK (2,3.01,0.48,1) RAAGVVLEMIR (2,2.94,0.28,16) VYSFLDES (2,2.58,0.33,1)
15	Superoxide dismutase 1 (SOD1)	4	TLVVHEKADDLGKGGNEESTK (3,5.69,0.26,1) GDGPVQGIINFEQK (2,4.28,0.50,1) HVGDLGNVTADK (2,3.09,0.50,1) LACGVIGIAQ (2,2.65,0.25,1)
16	Human Prolidase (PEPD)	6	NPAVQAGSIVVLQGGEETQR (2,6.21,0.60,1) YTNKISSEAHR (3,3.81,0.59,1)

			VFKTDMELEVL (2,3.53,0.47,1) TDMELEVL (2,3.00,0.38,1) LPASHATWMGK (2,2.94,0.53,1) AVYEAVL (2,2.04,0.30,5)
17	Fatty acid-binding protein 4 (FABP4)	2	LVSENFDDYMKEVGVGFATRK (3,4.05,0.56,1) NTEISFILGQEFDEVTADDRK (3,3.92,0.57,1)
18	protein-tyrosine phosphatase 1B (PTP1B)	7	IKLHQEDNDYINASLIKMEEAQR (4,4.66,0.51,1) QLELENLTTQETR (2,4.30,0.27,1) FSYLAVIEGAK (2,4.24,0.51,1) FIMGDSSVQDQWK (2,3.80,0.49,1) GSPLNAAPYGIESMSQDTEVR (3,3.66,0.44,1) SGSWAAIYQDIR (2,3.44,0.39,1) EMIFEDTNLK (2,2.67,0.24,4)
19	dihydropyrimidinase-related protein 3 (DPYSL3)	10	MDENQFVAVTSTNAAK (2,5.27,0.11,1) NLHQSGFSLSGTQVDEGVR (2,5.16,0.64,1) ISVGSDSLVIWDPDAVK (2,5.02,0.55,1) IMLEDGNLHVTQGAGR (2,4.86,0.59,1) GMYDGPVFDLTTTPK (2,4.12,0.63,1) TLDFDALSVGQR (2,3.90,0.54,1) EESREPAPASPAGVEIR (3,3.41,0.20,9) GMTTVDDFFQGTK (2,3.29,0.48,2) SAADLISQAR (2,2.54,0.21,1) IFNLYPR (2,2.41,0.29,4)

¹The numbers in parentheses correspond to z, Xcorr, dCn, Rsp parameters of TurboSequest respectively.

²Matched peptide number: number of peptides matched with protein in MS/MS query.