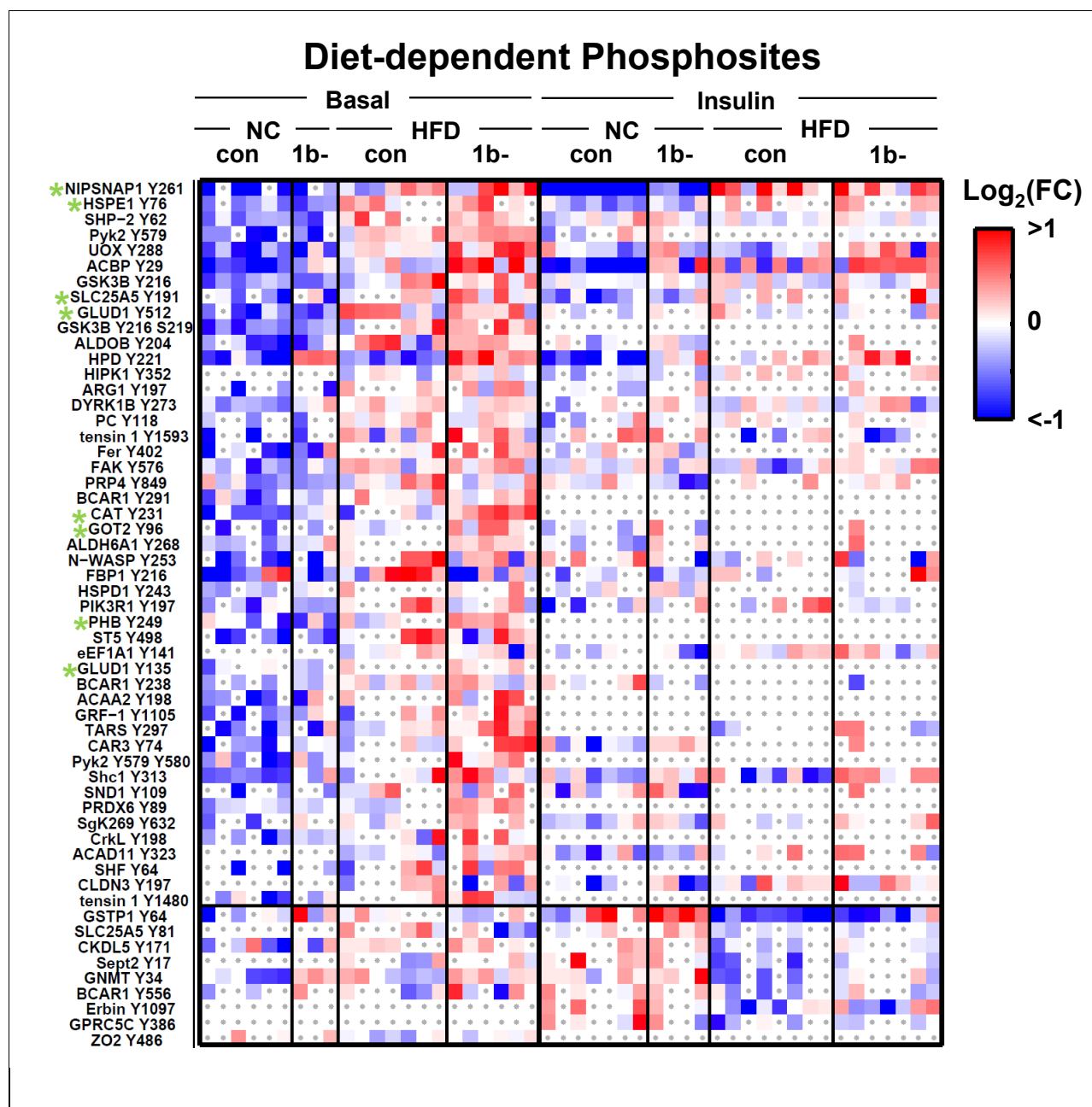


## Supplemental Information

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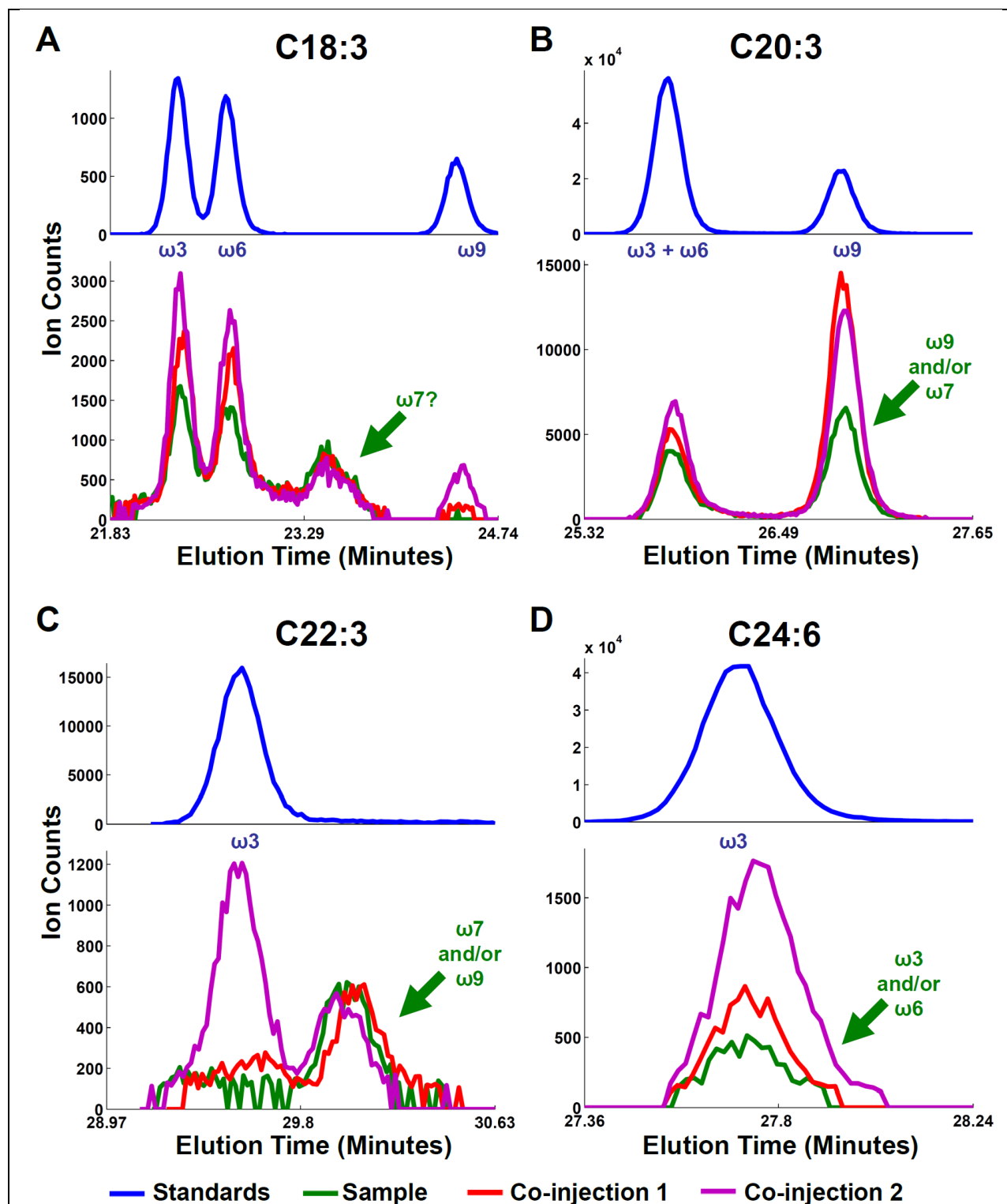
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Supplementary Figures



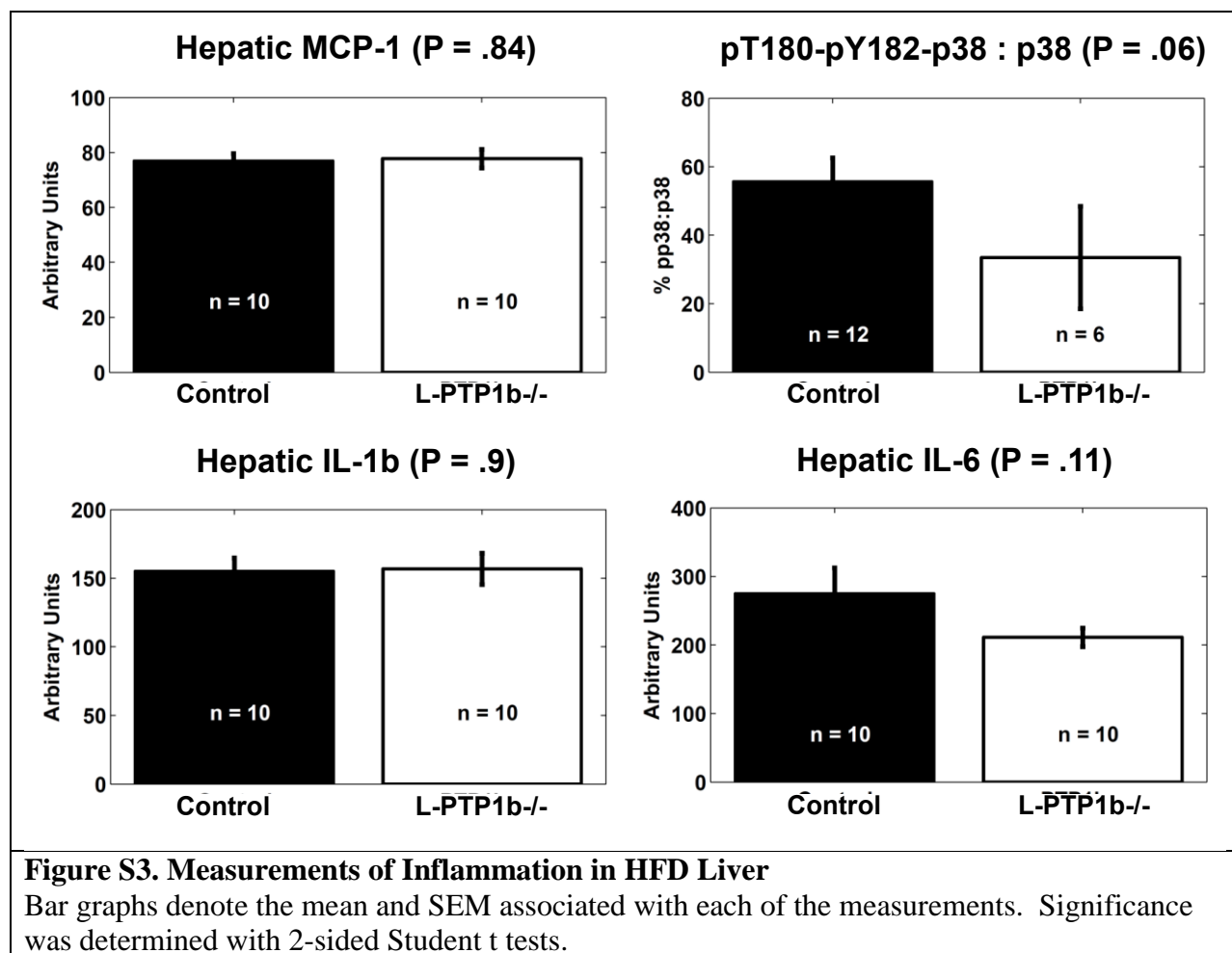
**Figure S1. Diet-dependent Phosphosites**

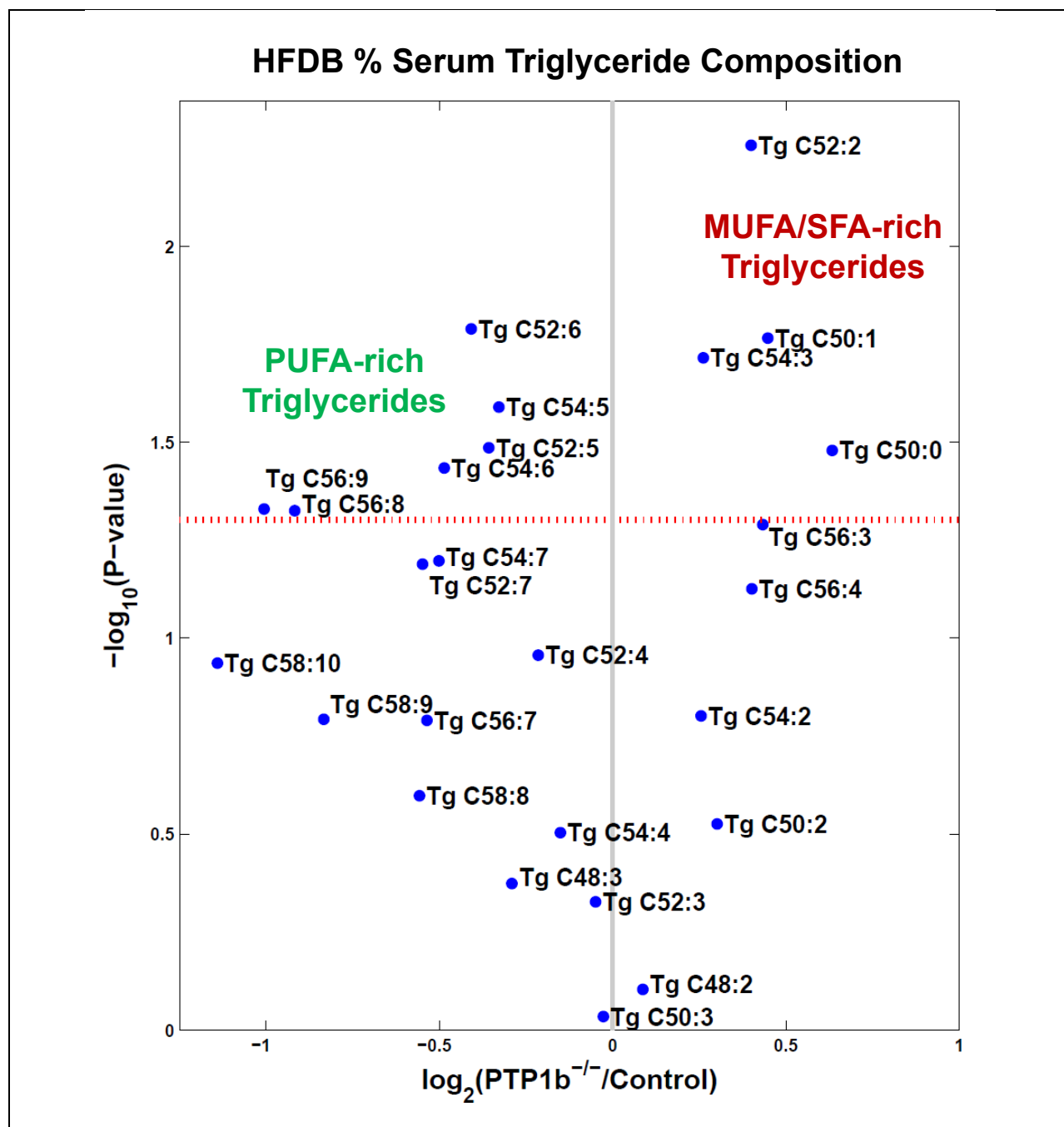
Heatmaps of those phosphorylation sites most significantly correlated to diet (raw, context-specific  $p$ -value  $< .025$ , see Methods). For basal or insulin datasets, the phosphorylation level of a phosphosite was normalized to the corresponding phosphosite mean (basal or insulin) and then  $\log_2$ -transformed. Missing data points are denoted by grey dots over white boxes. Negatively and positively correlated phosphosites are segregated. Green asterisks denote mitochondrial proteins. The phosphosites are separated into two clusters, dependent on whether HFD increases or decreases phosphorylation on the site.



**Figure S2. Co-elution to Determine PUFA Species**

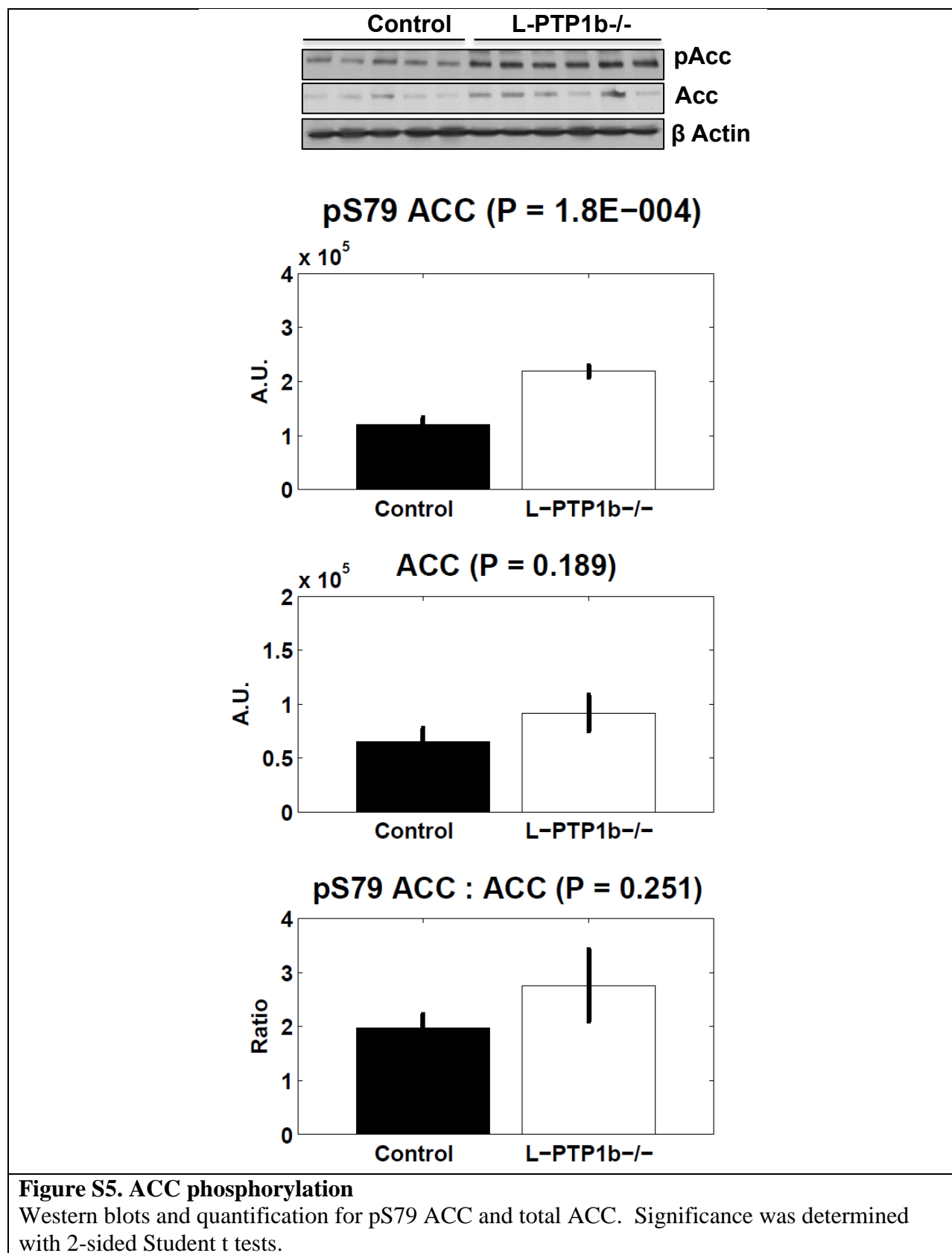
Blue and green curves correspond to ionchromatograms from standards and liver lipid samples analyzed in independent LC-MS experiments. Standards and lipid samples were co-injected (red and purple curves) in two additional experiments to determine the PTP1b-dependent isomer peak indicated by the green arrow. See text for discussion of results.

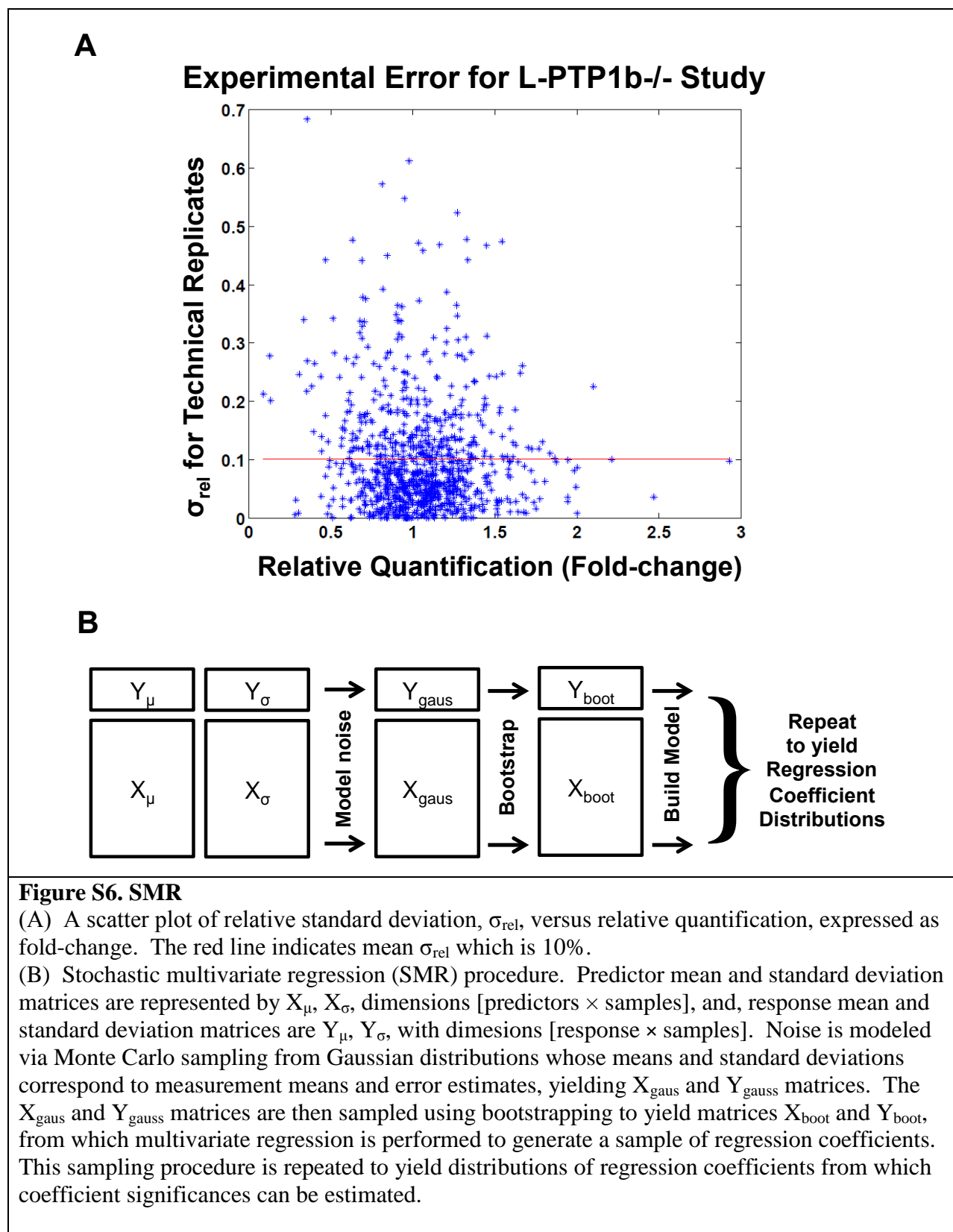


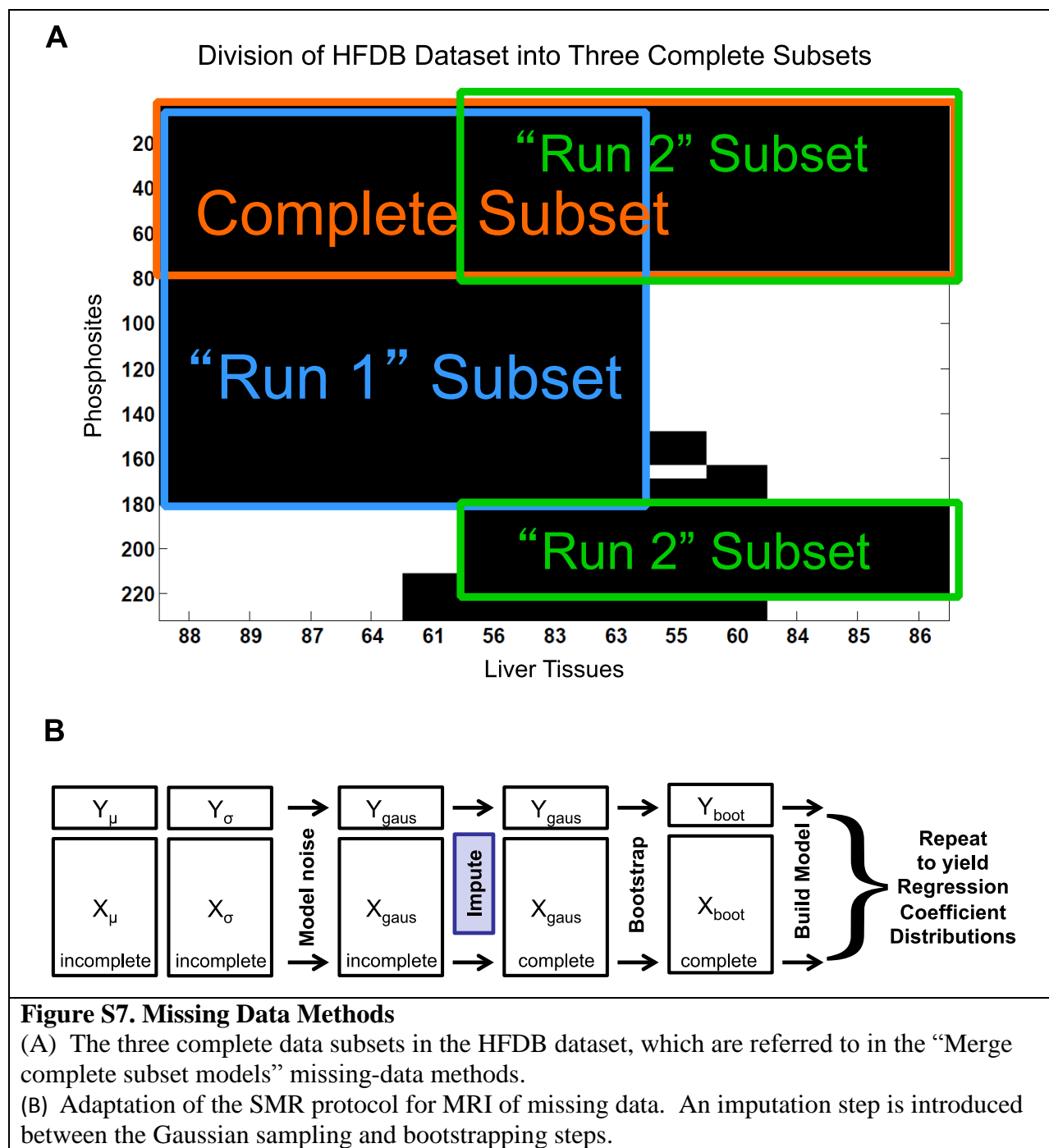


**Figure S4. HFD Basal Serum Triglyceride Compositions**

Volcano plot of percent serum triglyceride compositions on HFD: Each triglyceride is plotted as a function of log<sub>2</sub>-transformed, compositional fold-change (L-PTP1b<sup>-/-</sup> relative to control) and corresponding statistical significance, -log<sub>10</sub>(P-value), control, n = 10, L-PTP1b<sup>-/-</sup>, n = 6. The dotted, red line corresponds to P-value = .05. Significance was determined with 2-sided Student t tests.









## Supplemental Tables

**Table S1: Animal weight and serum measurements**

	NC		HFD	
	Control	L-PTP1b <sup>-/-</sup>	Control	L-PTP1b <sup>-/-</sup>
<b>Weight (g)</b>	25.4 +/- 1.0 (n = 13)	24.7 +/- 1.1 (n = 8)	32.8 +/- 1.4 (n = 19)***	30.3 +/- 0.8 (n = 17)
<b>Fed Glucose (mg/dL)</b>	192 +/- 6 (n = 13)	197 +/- 11 (n = 8)	236 +/- 7 (n = 15)***	223 +/- 11 (n = 13)
<b>Fed Insulin (ng/mL)</b>	0.89 +/- 0.13 (n = 7)	0.73 +/- 0.22 (n = 5)	3.47 +/- 0.91 (n = 7)*	2.92 +/- 0.94 (n = 5)
<b>Fasting Glucose (mg/dL)</b>	114 +/- 7 (n = 12)	160 +/- 11 (n = 8)**	120 +/- 8 (n = 15)	162 +/- 16 (n = 13)*
<b>Fasted Insulin (pM)</b>	56.42 +/- 10.24 (n = 6)	26.46 +/- 3.35 (n = 5)	63.3 +/- 13.14 (n = 8)	60.15 +/- 19.67 (n = 6)
<b>Serum Triglycerides (mg/dL)</b>	91.67 +/- 10.94 (n = 12)	78.38 +/- 8.22 (n = 8)	125.93 +/- 15.88 (n = 15)	91.85 +/- 7 (n = 13)
<b>Cholesterol (mg/dL)</b>	98.83 +/- 6.57 (n = 6)	83.6 +/- 12.52 (n = 5)	144.63 +/- 16.19 (n = 8)^	113.86 +/- 24.95 (n = 7)
<b>HDL (mg/dL)</b>	81.67 +/- 6.35 (n = 6)	69.4 +/- 11.53 (n = 5)	114.63 +/- 12.06 (n = 8)	88.43 +/- 19.37 (n = 7)
<b>LDL (mg/dL)</b>	4.33 +/- 0.78 (n = 6)	3.6 +/- 1.4 (n = 5)	10.63 +/- 1.93 (n = 8)*	14.86 +/- 4.29 (n = 7)
<b>Adiponectin (pg/mL)</b>	12.68 +/- 1.41 (n = 13)	11.45 +/- 1.05 (n = 8)	11.93 +/- 0.91 (n = 15)	15.03 +/- 1.48 (n = 11)
<b>Leptin (pM)</b>	54.24 +/- 19.56 (n = 5)	47.13 +/- 27.1 (n = 3)	168.97 +/- 89.5 (n = 7)	186.58 +/- 76.37 (n = 6)
<b>Glucagon (pM)</b>	25.04 +/- 6.98 (n = 7)	18.72 +/- 4.48 (n = 5)	21.88 +/- 4.34 (n = 8)	17.57 +/- 3.42 (n = 7)

Serum measurements and weight gain are written as mean +/- standard error for each of the diet and genotype conditions. The number of mice analyzed per condition is denoted in parentheses. Statistical analysis was performed using one-way ANOVA with sequential Sidak-Dunn method to adjust for multiple comparisons: (1) L-PTP1b<sup>-/-</sup> mice to control on NC diet, (2) L-PTP1b<sup>-/-</sup> mice to control on HFD, and (3) HFD control to NC control. \*\*\* = P<.001, \*\* = P<.01, \* = P < .05, ^ = P<.1.

**Table S2: Phosphotyrosine measurements**

Protein	Site	Peptide	Full Name	GI #	Basal				Insulin				Mascot Scores
					NC		HFD		NC		HFD		
					Con.	L-1b-	Con.	L-1b-	Con.	L-1b-	Con.	L-1b-	
HPD	Y232	SIVVTNyE ESIK	4-hydroxyphenylpyruvic acid dioxygenase	gi 33859486	0.84 +/- 0.08 (n = 5)	1.04 +/- 0.04 (n = 3)	0.98 +/- 0.02 (n = 7)	1.13 +/- 0.05 (n = 6)^	n.d.	n.d.	n.d.	n.d.	24, 64, 22, 49, 49
HPD	Y221	FWSVDDT QVHTEyS SLR	4-hydroxyphenylpyruvic acid dioxygenase	gi 33859486	0.66 +/- 0.09 (n = 6)	1.39 +/- 0.02 (n = 3)**	0.73 +/- 0.04 (n = 7)	1.46 +/- 0.13 (n = 6)***	0.62 +/- 0.07 (n = 7)	1.09 +/- 0.12 (n = 4)**	1.12 +/- 0.08 (n = 4)**	1.45 +/- 0.17 (n = 4)	58, 26, 42, 45, 64, 43, 32, 53, 48
NIPSNAP1	Y261	RGWDEN VyYTVPL VR/GWDE NVyYTVL LVR	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	gi 6679066	0.41 +/- 0.05 (n = 4)	0.67 +/- 0.16 (n = 2)	1.08 +/- 0.1 (n = 7)**	1.41 +/- 0.22 (n = 6)	0.38 +/- 0.05 (n = 7)	0.53 +/- 0.16 (n = 4)	1.46 +/- 0.19 (n = 8)***	1.36 +/- 0.15 (n = 7)	39, 63, 27, 41, 37, 49, 45, 41
NIPSNAP1	Y148	EyLEFR	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	gi 6679066	n.d.	n.d.	0.91 +/- 0.04 (n = 4)	1.09 +/- 0.1 (n = 4)	n.d.	n.d.	n.d.	n.d.	23
ACAT1	Y328	IAAFADA AVDPIDF PLAPAyA VPK	acetyl-Coenzyme A acetyltransferase 1 precursor	gi 21450129	n.d.	n.d.	0.96 +/- 0.07 (n = 4)	1.04 +/- 0.13 (n = 4)	0.84 +/- 0.15 (n = 4)	0.79 +/- 0.12 (n = 2)	1.29 +/- 0.17 (n = 4)	0.98 +/- 0.11 (n = 4)	26, 40, 38, 48
ACAA2	Y198	AANEAGy FNEEMAP IEVK	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	gi 29126205	0.68 +/- 0.07 (n = 4)	0.89 +/- 0.32 (n = 2)	1.17 (n = 1)	1.33 +/- 0.19 (n = 4)	n.d.	n.d.	n.d.	n.d.	42, 58
AFAP1L2	Y68	IESPEGYy EEAEPFD R	actin filament associated protein 1-like 2	gi 22122607	0.96 +/- 0.2 (n = 2)	0.97 (n = 1)	1.08 (n = 1)	1.01 +/- 0.02 (n = 3)	n.d.	n.d.	n.d.	n.d.	31
AFAP1L2	Y357	VAQQPLS LVGCDVL PDPSPDH LySFR	actin filament associated protein 1-like 2	gi 22122607	0.96 +/- 0.17 (n = 4)	0.94 +/- 0.15 (n = 3)	1.34 (n = 1)	n.d.	n.d.	n.d.	0.89 +/- 0.15 (n = 4)	1.11 +/- 0.1 (n = 4)	54, 56
ACSL5	Y69	NNDLILy YFSDAK	acyl-CoA synthetase long-chain family member 5	gi 58218988	0.73 +/- 0.06 (n = 6)	1.25 +/- 0.04 (n = 3)	0.75 (n = 1)	1.22 +/- 0.27 (n = 5)	n.d.	n.d.	n.d.	n.d.	28, 27, 20
ACAD11	Y323	LAGISQG	acyl-Coenzyme	gi 74271799	n.d.	n.d.	0.91 +/-	1.1 +/-	0.88 +/-	0.91 +/-	1.09 +/-	1.21 +/-	39, 30, 31,

		VyR	A dehydrogenase family, member 11				0.04 (n = 7)	0.05 (n = 6)	0.08 (n = 7)	0.1 (n = 4)	0.1 (n = 4)	0.15 (n = 4)	41, 62, 42
ACOX1	Y629	YDGNVye NLFWEA K	acyl-Coenzyme A oxidase 1, palmitoyl	gi 66793429	0.75 +/- 0.11 (n = 4)	1.11 +/- 0.21 (n = 2)	0.67 (n = 1)	1.28 +/- 0.15 (n = 4)	1.01 +/- 0.14 (n = 3)	0.96 +/- 0.06 (n = 4)	n.d.	1.15 (n = 1)	36, 48, 39
ALDH1L1	Y892	DLGEAAL NEyLR	aldehyde dehydrogenase 1 family, member L1	gi 27532959	0.81 +/- 0.04 (n = 4)	1.27 +/- 0.09 (n = 3)**	0.96 (n = 1)	n.d.	n.d.	n.d.	n.d.	n.d.	63
ALDH1L1	Y848	ALyVSDK	aldehyde dehydrogenase 1 family, member L1	gi 27532959	n.d.	n.d.	0.92 +/- 0.07 (n = 4)	1.08 +/- 0.06 (n = 4)	n.d.	n.d.	n.d.	n.d.	27
ALDH1A7	Y484	ELGEHGL yEYTELK	aldehyde dehydrogenase family 1, subfamily A7	gi 7106242	0.85 +/- 0.06 (n = 6)	1.39 +/- 0.08 (n = 3)**	0.6 +/- 0.06 (n = 7)*	1.42 +/- 0.05 (n = 6)***	0.82 +/- 0.07 (n = 7)	1.14 +/- 0.22 (n = 4)	0.94 +/- 0.08 (n = 8)	1.17 +/- 0.12 (n = 7)	41, 49, 37, 19, 30, 46, 16, 48, 46, 20, 23, 36, 44, 22, 48, 18
ALDH6A1	Y268	AISFVGS NQAGEyI FER	aldehyde dehydrogenase family 6, subfamily A1	gi 19527258	0.84 +/- 0.04 (n = 5)	1.03 +/- 0.09 (n = 3)	1.05 (n = 1)	1.13 +/- 0.02 (n = 5)	0.83 +/- 0.05 (n = 4)	1.13 +/- 0.02 (n = 2)	n.d.	1.41 (n = 1)	50, 53, 58, 68, 49
ALDOB	Y204	YASICQQ NGLVPIV EPEVLPD GDHDLH CQyVSEK	aldolase 2, B isoform	gi 21450291	0.69 +/- 0.08 (n = 5)	0.81 +/- 0.12 (n = 3)	1.17 +/- 0.13 (n = 7)^	1.15 +/- 0.04 (n = 6)	0.94 +/- 0.11 (n = 3)	0.97 +/- 0.07 (n = 4)	n.d.	1.29 (n = 1)	40, 21, 29, 74, 17, 70
ANKS1A	Y472	IQSSAPQE EEEHPyEL LLTAETK	ankyrin repeat and sterile alpha motif domain containing 1	gi 31088892	0.9 +/- 0.09 (n = 2)	1.11 (n = 1)	0.94 +/- 0.06 (n = 7)	1.08 +/- 0.07 (n = 6)	0.89 +/- 0.17 (n = 3)	1.15 +/- 0.14 (n = 4)	n.d.	0.73 (n = 1)	19, 18, 17, 44, 19
ANXA2	Y24	LSLEGDH STPPSAyG SVKPYTN FDAER	annexin A2	gi 6996913	n.d.	n.d.	1.02 +/- 0.15 (n = 7)	0.98 +/- 0.12 (n = 6)	n.d.	n.d.	0.83 +/- 0.06 (n = 4)	1.17 +/- 0.12 (n = 4)	26, 31, 31
ARG1	Y265	EGLYITEE IyK	arginase 1, liver	gi 7106255	0.69 +/- 0.04 (n = 4)	1 +/- 0.03 (n = 2)*	0.99 +/- 0.07 (n = 7)*	1.21 +/- 0.17 (n = 6)	0.76 +/- 0.08 (n = 7)	1.29 +/- 0.25 (n = 4)^	0.84 +/- 0.1 (n = 4)	1.28 +/- 0.16 (n = 4)^	32, 26, 31, 29, 26, 37, 40
ARG1	Y218	VMEETFS yLLGR	arginase 1, liver	gi 7106255	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.97 +/- 0.09 (n = 4)	1.03 +/- 0.14 (n = 4)	22
ARG1	Y197	yFSMTEV DK	arginase 1, liver	gi 7106255	0.66 +/- 0.14 (n = 2)	0.6 (n = 1)	1.11 +/- 0.05 (n = 4)^	1.12 +/- 0.11 (n = 5)	0.91 +/- 0.04 (n = 4)	1.1 +/- 0.11 (n = 2)	n.d.	1.17 (n = 1)	22, 21, 22
ARG1	Y188	DVDPGEH yIIK	arginase 1, liver	gi 7106255	n.d.	n.d.	0.88 +/- 0.05 (n = 4)	1.12 +/- 0.03 (n = 4)	n.d.	n.d.	n.d.	n.d.	20
ASS1	Y133	FELTCySL	argininosuccinate	gi 6996911	n.d.	n.d.	0.9 +/-	1.12 +/-	0.91 +/-	1.08 +/-	n.d.	1.32 (n =	24, 20, 16,

		APQIK	synthetase				0.06 (n = 7)	0.04 (n = 6)	0.09 (n = 7)	0.13 (n = 4)		1)	20
ASS1	Y322	FAELVvY GFVHSPE CEFVR	argininosuccinate synthetase	gi 6996911	0.95 +/- 0.14 (n = 4)	1.39 +/- 0.05 (n = 2)	1.05 +/- 0.11 (n = 4)	0.84 +/- 0.26 (n = 5)	0.85 +/- 0.11 (n = 7)	1.44 +/- 0.12 (n = 4)*	0.86 +/- 0.04 (n = 8)	1.06 +/- 0.14 (n = 7)	56, 66, 44, 65, 57, 59, 71
ASS1	Y29	EQGyDVI AYLANIG QK	argininosuccinate synthetase	gi 6996911	0.82 +/- 0.17 (n = 2)	1.24 (n = 1)	1.36 (n = 1)	0.92 +/- 0.13 (n = 3)	0.82 +/- 0.14 (n = 4)	1.28 +/- 0.04 (n = 2)	n.d.	1.18 (n = 1)	55, 29
ACLY	Y672	TTDGVyE GVAIGGD R/TTDGVy EGVAIGG DRYPGST FMDHVL R	ATP citrate lyase	gi 29293809	0.72 +/- 0.09 (n = 2)	0.89 (n = 1)	0.75 +/- 0.09 (n = 7)	1.4 +/- 0.14 (n = 6)**	n.d.	n.d.	0.9 +/- 0.12 (n = 8)	1.12 +/- 0.21 (n = 7)	21, 24, 51, 48, 51
ATP11C	Y126	SAVyIIE AK	Atpase, class VI, type 11C isoform b	gi 49355804	n.d.	n.d.	1.01 +/- 0.08 (n = 4)	0.99 +/- 0.09 (n = 4)	n.d.	n.d.	n.d.	n.d.	18
AXL	Y697	IYNGDy R	AXL receptor tyrosine kinase	gi 31542164	n.d.	n.d.	n.d.	n.d.	1.03 +/- 0.09 (n = 3)	0.88 +/- 0.07 (n = 4)	1.27 +/- 0.06 (n = 4)	0.83 +/- 0.1 (n = 4)*	22, 20
BHMT	Y289	EAYNLGV R	betaine-homocysteine methyltransferase	gi 7709990	n.d.	n.d.	0.93 +/- 0.05 (n = 4)	1.07 +/- 0.07 (n = 4)	n.d.	n.d.	1.05 +/- 0.09 (n = 4)	0.95 +/- 0.19 (n = 4)	26, 34
BCAR1	Y556	MEDVyQT LVVHGQ VLDSGR	breast cancer anti-estrogen resistance 1	gi 40254593	0.82 +/- 0.04 (n = 2)	1.29 (n = 1)	0.91 +/- 0.1 (n = 4)	1.08 +/- 0.19 (n = 5)	1.15 +/- 0.08 (n = 4)	1.16 +/- 0.01 (n = 2)	0.82 +/- 0.08 (n = 4)^	0.95 +/- 0.08 (n = 4)	42, 51, 34, 64
BCAR1	Y271	GLLPNQY GQEVyDT PPMAVK	breast cancer anti-estrogen resistance 1	gi 40254593	1.05 +/- 0.1 (n = 5)	1.14 +/- 0.05 (n = 3)	0.87 +/- 0.09 (n = 7)	1.04 +/- 0.11 (n = 6)	1.07 +/- 0.05 (n = 7)	0.92 +/- 0.07 (n = 4)	n.d.	0.85 (n = 1)	42, 24, 56, 70, 35, 63
BCAR1	Y414	VLPPEVA DGSVVD DGVyAVP PPAER	breast cancer anti-estrogen resistance 1	gi 40254593	n.d.	n.d.	1.1 +/- 0.29 (n = 4)	0.9 +/- 0.25 (n = 4)	n.d.	n.d.	n.d.	n.d.	33
BCAR1	Y291	DPLLDV yDVPPSVE K/GPNGR DPLLDV yDVPPSVE K	breast cancer anti-estrogen resistance 1	gi 40254593	0.82 +/- 0.08 (n = 6)	0.94 +/- 0.05 (n = 3)	1.09 +/- 0.07 (n = 7)^	1.1 +/- 0.07 (n = 6)	n.d.	n.d.	n.d.	n.d.	18, 55, 24, 17, 39
BCAR1	Y253	HLLAPGP QDIyDVPP VR	breast cancer anti-estrogen resistance 1	gi 40254593	0.86 +/- 0.06 (n = 5)	1.21 +/- 0.16 (n = 3)	0.97 +/- 0.05 (n = 7)	1.05 +/- 0.09 (n = 6)	1.06 +/- 0.07 (n = 7)	0.83 +/- 0.04 (n = 4)	1.03 +/- 0.09 (n = 4)	1.03 +/- 0.08 (n = 4)	70, 54, 36, 40, 54, 60, 55, 66, 42, 65
BCAR1	Y391	RPGPGTL yDVPR	breast cancer anti-estrogen resistance 1	gi 40254593	n.d.	n.d.	1 +/- 0.14 (n = 4)	1 +/- 0.22 (n = 4)	n.d.	n.d.	n.d.	n.d.	22, 44
BCAR1	Y238	VGQGYV YEAAQTE	breast cancer anti-estrogen	gi 40254593	0.85 +/- 0.06 (n = 2)	0.92 +/- 0.06 (n = 2)	1.06 +/- 0.05 (n = 2)	1.07 +/- 0.07 (n = 2)	1.16 +/- 0.12 (n = 2)	0.84 +/- 0.05 (n = 2)	n.d.	0.67 (n = 1)	92, 57, 95, 82, 97

		QDEyDTP R	resistance 3		4)	3)	7)	6)	4)	2)			
BCAR3	Y424	TPPSPSP WLTSEAN yCELNPA FAVGCDR	breast cancer anti-estrogen resistance 3	gi 7304925	0.87 +/- 0.11 (n = 6)	1.19 +/- 0.28 (n = 3)	1.1 (n = 1)	1.03 +/- 0.25 (n = 5)	n.d.	n.d.	n.d.	n.d.	36, 35, 35
TENC1	Y483	GPLDGSP yAQVQR	C1 domain- containing phosphatase and tensin-like protein	gi 11937228 8	0.98 +/- 0.05 (n = 6)	1.09 +/- 0.1 (n = 3)	0.96 +/- 0.05 (n = 7)	1.02 +/- 0.07 (n = 6)	0.94 +/- 0.03 (n = 4)	1.24 +/- 0.23 (n = 2)	0.77 +/- 0.06 (n = 8)	1.23 +/- 0.17 (n = 7)^	64, 67, 51, 72, 58, 35, 68, 33, 48, 60, 64, 29, 38, 70, 75
TENC1	Y705	LALPTAA LyGLR	C1 domain- containing phosphatase and tensin-like protein	gi 11937228 8	n.d.	n.d.	1.03 +/- 0.09 (n = 7)	0.97 +/- 0.05 (n = 6)	0.98 +/- 0.11 (n = 4)	1.03 +/- 0.01 (n = 2)	n.d.	1.03 (n = 1)	61, 33, 42, 52
TENC1	Y770	VGEEGHE GCSyAVC SEGR	C1 domain- containing phosphatase and tensin-like protein	gi 11937228 8	1 +/- 0.14 (n = 5)	1 +/- 0.04 (n = 3)	1.09 +/- 0.11 (n = 4)	0.93 +/- 0.08 (n = 5)	n.d.	n.d.	n.d.	n.d.	37, 54, 20
CALM1	Y100	DGNyIS AAELR/V FDKDG GyISAAEL R	calmodulin 2	gi 6680832	0.8 +/- 0.11 (n = 5)	1.51 +/- 0.13 (n = 3)*	0.84 +/- 0.1 (n = 7)	1.1 +/- 0.09 (n = 6)	0.82 +/- 0.04 (n = 7)	1.22 +/- 0.03 (n = 4)***	0.85 +/- 0.01 (n = 4)	1.24 +/- 0.09 (n = 4)**	59, 28, 24, 16, 16, 28, 16, 28, 23, 17
CPS1	Y590	SAyALGG LGSGICP NK	carbamoyl- phosphate synthetase 1	gi 12424851 2	n.d.	n.d.	1.02 +/- 0.13 (n = 4)	0.98 +/- 0.1 (n = 4)	0.97 +/- 0.07 (n = 4)	1.12 +/- 0.01 (n = 2)	n.d.	0.86 (n = 1)	19, 35
CPS1	Y140	VAGLLVL NySNDYN HWLGTK	carbamoyl- phosphate synthetase 1	gi 12424851 2	n.d.	n.d.	1.1 +/- 0.06 (n = 7)	0.88 +/- 0.12 (n = 6)	n.d.	n.d.	n.d.	n.d.	31, 38
CPS1	Y162	VPAIyGV DTR	carbamoyl- phosphate synthetase 1	gi 12424851 2	0.82 +/- 0.03 (n = 6)	1.22 +/- 0.14 (n = 3)*	0.89 +/- 0.05 (n = 4)	1.14 +/- 0.11 (n = 6)	n.d.	n.d.	n.d.	n.d.	60, 30, 26, 28, 19, 18, 38
CPS1	Y145 0	FVHDNyV IR	carbamoyl- phosphate synthetase 1	gi 12424851 2	n.d.	n.d.	1.14 +/- 0.07 (n = 7)	0.83 +/- 0.05 (n = 6)	0.81 +/- 0.06 (n = 4)	1 +/- 0.05 (n = 2)	1.15 +/- 0.09 (n = 4)	1.03 +/- 0.12 (n = 4)	35, 33, 40, 33, 37
CAR2	Y114	yAAELHL VHWNTK	carbonic anhydrase 2	gi 31981657	n.d.	n.d.	0.84 +/- 0.11 (n = 4)	1.16 +/- 0.16 (n = 4)	n.d.	n.d.	n.d.	n.d.	23
CAR3	Y74	VVFDDTy DR	carbonic anhydrase 3	gi 31982861	0.69 +/- 0.12 (n = 5)	0.95 +/- 0.03 (n = 3)	0.94 +/- 0.07 (n = 4)	1.39 +/- 0.14 (n = 5)^	0.88 +/- 0.09 (n = 7)	1.13 +/- 0.03 (n = 4)	n.d.	1.3 (n = 1)	28, 25, 34, 44, 37
CEACAM1	Y515	ATETVyS EVK	carcinoembryoni c antigen-related cell adhesion molecule 1 isoform 1	gi 85719299	0.89 +/- 0.29 (n = 4)	0.98 +/- 0.12 (n = 2)	1.07 +/- 0.11 (n = 7)	0.99 +/- 0.14 (n = 6)	1.2 +/- 0.13 (n = 7)	0.87 +/- 0.09 (n = 4)	0.78 +/- 0.04 (n = 4)	1.01 +/- 0.14 (n = 4)	27, 24, 26, 26, 29, 50, 21, 25, 19, 24
CASKIN2	Y253	NTyNQTA	cask-interacting	gi 31981530	n.d.	n.d.	1.01 +/-	0.99 +/-	n.d.	n.d.	n.d.	n.d.	47

		LDIVNQF TTSQASR	protein 2				0.07 (n = 4)	0.1 (n = 4)					
CAT	Y231	LVNADGE AVyCK	catalase	gi 6753272	0.7 +/- 0.07 (n = 6)	0.96 +/- 0.05 (n = 3)	0.88 +/- 0.1 (n = 4)	1.4 +/- 0.09 (n = 6)*	n.d.	n.d.	n.d.	n.d.	31, 48, 29, 38, 54
CAT	Y84	GAGAFGy FEVTHDI TR	catalase	gi 6753272	0.76 +/- 0.06 (n = 2)	1.03 (n = 1)	0.9 +/- 0.03 (n = 7)	1.19 +/- 0.04 (n = 6)***	0.99 +/- 0.12 (n = 3)	1.02 +/- 0.08 (n = 4)	n.d.	0.92 (n = 1)	30, 63, 63, 59
CTNNA1	Y619	LVyDGIR	catenin alpha 1	gi 6753294	n.d.	n.d.	1.06 +/- 0.1 (n = 4)	0.94 +/- 0.1 (n = 4)	n.d.	n.d.	n.d.	n.d.	26
CTNNA1	Y177	NAGNEQ DLGIQyK	catenin alpha 1	gi 6753294	n.d.	n.d.	1.11 +/- 0.1 (n = 4)	0.89 +/- 0.07 (n = 4)	n.d.	n.d.	n.d.	n.d.	19
CTNND1	Y96	LNGPQDH NHLLySTI PR	catenin, delta 1 isoform 1	gi 83745122	n.d.	n.d.	1.03 +/- 0.11 (n = 4)	0.97 +/- 0.04 (n = 4)	n.d.	n.d.	0.87 +/- 0.04 (n = 4)	1.13 +/- 0.09 (n = 4)	32, 45
CTNND1	Y904	SLDNNyS TLNER	catenin, delta 1 isoform 1	gi 83745122	n.d.	n.d.	1.02 +/- 0.06 (n = 4)	0.98 +/- 0.07 (n = 4)	1.19 +/- 0.05 (n = 4)	1 +/- 0.22 (n = 2)	0.87 +/- 0.09 (n = 8)	1.04 +/- 0.13 (n = 7)	68, 65, 66, 37, 56, 68
CAV1	Y14 Y6	yVDSEGH LyTVPIR	caveolin, caveolae protein 1	gi 6680854	n.d.	n.d.	1.17 +/- 0.37 (n = 4)	0.83 +/- 0.15 (n = 4)	n.d.	n.d.	n.d.	n.d.	18
CGN	Y229	GSPGALS SDELPE NPySQVK	cingulin	gi 14925131 4	n.d.	n.d.	0.98 +/- 0.08 (n = 7)	1.03 +/- 0.13 (n = 6)	n.d.	n.d.	n.d.	n.d.	26, 55
CLTC	Y899	ENPyYDS R	clathrin, heavy polypeptide (Hc)	gi 51491845	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	1.32 +/- 0.39 (n = 4)	0.68 +/- 0.17 (n = 4)	29
CLTC	Y148 7	TSIDAyD NFDNISL AQR	clathrin, heavy polypeptide (Hc)	gi 51491845	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.92 +/- 0.03 (n = 4)	1.08 +/- 0.09 (n = 4)	25
CLTC	Y147 7	SVNESLN NLFITEED yQALR	clathrin, heavy polypeptide (Hc)	gi 51491845	0.77 +/- 0.19 (n = 2)	1.59 (n = 1)	0.92 +/- 0.03 (n = 4)	1.05 +/- 0.05 (n = 4)	1.09 +/- 0.07 (n = 3)	1 +/- 0.03 (n = 4)	n.d.	0.73 (n = 1)	56, 71, 77, 64
CLDN2	Y194/ Y195	TNy(50)y(5 0)DGYQA QPLATR	claudin 2	gi 7710004	n.d.	n.d.	0.97 +/- 0.12 (n = 4)	1.03 +/- 0.06 (n = 4)	1 +/- 0.04 (n = 4)	0.86 +/- 0.03 (n = 2)	n.d.	1.29 (n = 1)	46, 35
CLDN3	Y197	ILySAPR	claudin 3	gi 6753438	n.d.	n.d.	1.09 +/- 0.12 (n = 4)	0.91 +/- 0.18 (n = 4)	0.74 +/- 0.19 (n = 3)	0.82 +/- 0.2 (n = 4)	1.06 +/- 0.08 (n = 8)	1.15 +/- 0.13 (n = 7)	26, 26, 24, 19
CDK2	Y15	IGEGTyG VYyK	cyclin-dependent kinase 2 isoform 2	gi 7949020	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.96 +/- 0.11 (n = 4)	1.04 +/- 0.12 (n = 4)	26
CKDL5	Y171	NLSEGNN ANYTEyV ATR	cyclin-dependent kinase-like 5	gi 12424403 7	0.82 +/- 0.15 (n = 5)	0.97 +/- 0.16 (n = 3)	1.08 +/- 0.01 (n = 4)	1.15 +/- 0.06 (n = 4)	1.1 +/- 0.06 (n = 4)	1.17 +/- 0.05 (n = 2)	0.84 +/- 0.06 (n = 4)^	0.98 +/- 0.03 (n = 4)	80, 25, 56, 53, 39
CTH	Y59	QDFPGQS SGFEySR	cystathionase	gi 22122387	0.94 +/- 0.06 (n = 4)	1.13 +/- 0.11 (n = 3)	0.86 (n = 1)	n.d.	n.d.	n.d.	n.d.	n.d.	48

CTH	Y113	AGDEIIC MDEVyG GTNR	cystathionase	gi 22122387	0.78 +/- 0.13 (n = 6)	1.13 +/- 0.19 (n = 3)	1.04 +/- 0.08 (n = 7)	1.11 +/- 0.08 (n = 6)	0.78 +/- 0.03 (n = 3)	1.14 +/- 0.04 (n = 4)**	0.76 +/- 0.05 (n = 4)	1.25 +/- 0.2 (n = 4)	55, 43, 43, 52, 76, 63, 64
CYB5A	Y11	yYTLLEIQ K	cytochrome b-5	gi 13385268	0.7 +/- 0.07 (n = 5)	1.54 +/- 0.14 (n = 3)**	0.59 +/- 0.04 (n = 4)	1.25 +/- 0.12 (n = 6)**	0.76 +/- 0.09 (n = 7)	1.35 +/- 0.06 (n = 4)**	0.63 +/- 0.06 (n = 8)	1.46 +/- 0.07 (n = 7)***	18, 36, 31, 22, 29, 25, 29, 31
CYP2E1	Y426	YSDyFK	cytochrome P450, family 2, subfamily e, polypeptide 1	gi 11276065	n.d.	n.d.	0.62 +/- 0.09 (n = 4)	1.38 +/- 0.14 (n = 4)	0.69 +/- 0.04 (n = 4)	1.5 +/- 0.12 (n = 2)	n.d.	1.23 (n = 1)	21, 19
TEC	Y415	YVLDDQy TSSSGAK	cytoplasmic tyrosine kinase, Dscr28C related	gi 7305569	n.d.	n.d.	n.d.	n.d.	1.12 +/- 0.06 (n = 4)	0.87 +/- 0.14 (n = 2)	n.d.	0.78 (n = 1)	25
DDX3X	Y104	GRGDyDG IGGR	DEAD/H (Asp- Glu-Ala- Asp/His) box polypeptide 3, X- linked	gi 6753620	n.d.	n.d.	0.91 +/- 0.16 (n = 4)	1.09 +/- 0.14 (n = 4)	n.d.	n.d.	n.d.	n.d.	39
DSP	Y32	YEMTySG GGGGGG GGGGGG TSR	desmoplakin isoform 1	gi 82950147	n.d.	n.d.	0.92 +/- 0.03 (n = 4)	1.08 +/- 0.05 (n = 4)	n.d.	n.d.	n.d.	n.d.	87
ACBP	Y29	TQPTDEE MLFySHF K/LKTQPT DEEMLFy SHFK	acyl-CoA binding protein / diazepam binding inhibitor isoform 2	gi 6681137	0.58 +/- 0.05 (n = 6)	0.97 +/- 0.1 (n = 3)**	0.95 +/- 0.06 (n = 7)**	1.48 +/- 0.2 (n = 6)*	0.49 +/- 0.05 (n = 7)	1.14 +/- 0.23 (n = 4)*	1.05 +/- 0.12 (n = 8)**	1.37 +/- 0.11 (n = 7)^	52, 43, 45, 29, 48, 41, 24, 64, 67, 18, 42, 49, 40, 31, 44, 32, 34
DMGDH	Y305	DGLLFGP yESQEK	dimethylglycine dehydrogenase precursor	gi 21311901	0.82 +/- 0.01 (n = 2)	1.2 (n = 1)	0.96 (n = 1)	1.07 +/- 0.07 (n = 3)	n.d.	n.d.	n.d.	n.d.	35
DLG1	Y783	DyHFVTS R	discs large homolog 1	gi 40254642	n.d.	n.d.	1.01 +/- 0.14 (n = 4)	0.99 +/- 0.02 (n = 4)	n.d.	n.d.	n.d.	n.d.	26
Dok1	Y450	GFSSDTA LySQVQK	docking protein 1	gi 31981796	n.d.	n.d.	1.1 +/- 0.08 (n = 7)	0.88 +/- 0.05 (n = 6)	n.d.	n.d.	n.d.	n.d.	20, 40
Dok1	Y361	LTDSKED PlyDEPEG LAPAPPR	docking protein 1	gi 31981796	n.d.	n.d.	1.11 +/- 0.07 (n = 7)	0.88 +/- 0.03 (n = 6)	0.98 +/- 0.07 (n = 4)	1.13 +/- 0.13 (n = 2)	n.d.	0.83 (n = 1)	60, 34, 60
Dok1	Y408	LKEEGYE LPYNPAT DDyAVPP PR	docking protein 1	gi 31981796	n.d.	n.d.	1.11 +/- 0.1 (n = 4)	0.89 +/- 0.07 (n = 4)	0.97 +/- 0.09 (n = 4)	1.1 +/- 0.05 (n = 2)	n.d.	0.91 (n = 1)	17, 33
DYRK1B	Y273	IYQyIQSR	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1b isoform a	gi 6753698	0.82 +/- 0.04 (n = 6)	1.06 +/- 0.09 (n = 3)*	1.08 +/- 0.04 (n = 7)**	1.06 +/- 0.04 (n = 6)	0.96 +/- 0.11 (n = 3)	1.05 +/- 0.06 (n = 4)	0.99 +/- 0.04 (n = 8)	1 +/- 0.08 (n = 7)	21, 34, 35, 30, 25, 31, 47, 26, 31, 34, 28, 32, 33, 29, 27
DYRK4	Y344	VYTyIQSR	dual-specificity	gi 46402173	n.d.	n.d.	1.04 +/-	0.96 +/-	1.08 +/-	0.97 +/-	0.98 +/-	0.91 +/-	40, 28, 26,

			tyrosine-(Y)- phosphorylation regulated kinase 4				0.08 (n = 4)	0.06 (n = 4)	0.07 (n = 7)	0.03 (n = 4)	0.08 (n = 4)	0.09 (n = 4)	22, 29
ETL4	Y295	NVYyELN DVR	enhancer trap locus 4	gi 12448658 8	n.d.	n.d.	n.d.	n.d.	1.01 +/- 0.06 (n = 4)	0.97 +/- 0.22 (n = 2)	n.d.	1.03 (n = 1)	58
ENO1	Y25	GNPTVEV DLyTAK	enolase 2, gamma neuronal	gi 7305027	0.68 +/- 0.03 (n = 4)	1.09 +/- 0.04 (n = 3)***	0.83 +/- 0.05 (n = 7)^	1.37 +/- 0.07 (n = 6)***	0.87 +/- 0.04 (n = 7)	1.17 +/- 0.13 (n = 4)	n.d.	1.22 (n = 1)	49, 24, 41, 37, 34, 44
ENO1	Y44	AAVPSGA STGIyEAL ELR	enolase 3, beta muscle	gi 6679651	0.35 +/- 0.04 (n = 2)	1.34 (n = 1)*	0.88 +/- 0.07 (n = 7)*	1.3 +/- 0.07 (n = 6)**	0.71 +/- 0.06 (n = 7)	1.31 +/- 0.06 (n = 4)***	1.03 +/- 0.09 (n = 4)*	1.17 +/- 0.07 (n = 4)	63, 98, 33, 48, 30, 79, 52, 53
EphA2	Y589	TyVDPHT YEDPNQA VLK	Eph receptor A2	gi 32484983	n.d.	n.d.	1.14 +/- 0.19 (n = 4)	0.86 +/- 0.13 (n = 4)	n.d.	n.d.	n.d.	n.d.	32, 32
EphA2	Y773	VLEDDPE ATyTTSG GK	Eph receptor A2	gi 32484983	0.91 +/- 0.24 (n = 4)	0.96 +/- 0.11 (n = 2)	1 +/- 0.03 (n = 4)	1.09 +/- 0.03 (n = 5)	1.06 +/- 0.1 (n = 7)	0.9 +/- 0.07 (n = 4)	0.96 +/- 0.05 (n = 8)	1.04 +/- 0.04 (n = 7)	46, 40, 28, 30, 25, 35, 49, 33, 38
EphB4	Y774	FLEENSS DPTyTSSL GGK	Eph receptor B4	gi 47059093	n.d.	n.d.	1.03 +/- 0.16 (n = 4)	0.97 +/- 0.04 (n = 4)	n.d.	n.d.	n.d.	n.d.	29
EGFR	Y109 2	YSSDPTG AVTEDNI DDAFLPV PEyVnQS VPK	epidermal growth factor receptor isoform 1	gi 46560582	1.02 +/- 0.33 (n = 2)	1.57 (n = 1)	1.45 (n = 1)	0.65 +/- 0.34 (n = 3)	1.04 +/- 0.18 (n = 3)	0.97 +/- 0.15 (n = 4)	n.d.	1.01 (n = 1)	24, 75
EGFR	Y117 2	GSHQMSL DNPdyQQ DFFPK	epidermal growth factor receptor isoform 1	gi 46560582	1.02 +/- 0.08 (n = 4)	1.07 +/- 0.18 (n = 3)	1.16 +/- 0.24 (n = 4)	0.81 +/- 0.19 (n = 5)	1.03 +/- 0.09 (n = 7)	0.93 +/- 0.07 (n = 4)	n.d.	1.09 (n = 1)	23, 26, 33, 58, 23, 28
EGFR	Y119 7	GPTAENA EyLR	epidermal growth factor receptor isoform 1	gi 46560582	0.87 +/- 0.05 (n = 6)	0.8 +/- 0.25 (n = 3)	1.37 +/- 0.23 (n = 7)	0.8 +/- 0.11 (n = 6)	1.02 +/- 0.12 (n = 7)	0.96 +/- 0.07 (n = 4)	n.d.	1 (n = 1)	60, 48, 27, 51, 60, 59, 46, 56, 55, 65, 55, 53, 67, 62
Erbin	Y109 7	RTEGDyL SYR/TEG DyLSYR	ErbB2 interacting protein isoform 2	gi 54607112	n.d.	n.d.	n.d.	n.d.	1.29 +/- 0.1 (n = 4)	1.08 +/- 0.11 (n = 2)	0.86 +/- 0.09 (n = 8)*	0.98 +/- 0.11 (n = 7)	26, 24, 21, 21
eEF1A1	Y177	EVSTyIK	eukaryotic translation elongation factor 1 alpha 1	gi 12603232 9	n.d.	n.d.	1.03 +/- 0.04 (n = 4)	0.97 +/- 0.08 (n = 4)	n.d.	n.d.	n.d.	n.d.	18
eEF1A1	Y141	EHALLAy TLGVK	eukaryotic translation elongation factor 1 alpha 2	gi 6681273	n.d.	n.d.	1.03 +/- 0.05 (n = 7)	0.97 +/- 0.09 (n = 6)	0.9 +/- 0.07 (n = 3)	0.81 +/- 0.12 (n = 4)	1.06 +/- 0.04 (n = 8)	1.08 +/- 0.09 (n = 7)	23, 47, 19, 53, 46, 31, 54
EIF1B	Y30	GDDLPA GTEDyIH R	eukaryotic translation initiation factor 1B	gi 21312159	0.79 +/- 0.09 (n = 4)	1.11 +/- 0.03 (n = 2)	0.92 (n = 1)	1.14 +/- 0.12 (n = 5)	n.d.	n.d.	n.d.	n.d.	21, 32



F11R	Y281	VlySQPSTR	F11 receptor	gi 27734847	n.d.	n.d.	1.29 +/- 0.14 (n = 4)	0.71 +/- 0.13 (n = 4)	n.d.	n.d.	1.08 +/- 0.11 (n = 4)	0.92 +/- 0.18 (n = 4)	22, 25
FASN	Y1248	VAEVLAGEGHLYSR	fatty acid synthase	gi 93102409	n.d.	n.d.	0.62 +/- 0.12 (n = 4)	1.38 +/- 0.21 (n = 4)	n.d.	n.d.	n.d.	n.d.	55
FcGR2B	Y289	HPEALDEETEHDyQNHl	Fc receptor, IgG, low affinity IIb isoform 2	gi 6857783	1.07 +/- 0.32 (n = 2)	1.11 (n = 1)	0.97 (n = 1)	0.93 +/- 0.19 (n = 3)	n.d.	n.d.	n.d.	n.d.	24
Fer	Y715	QEDGGVYSSSGLK	fer (fms/fps related) protein kinase, testis specific 2 isoform a	gi 83921584	1.06 +/- 0.16 (n = 5)	0.89 +/- 0.27 (n = 3)	1.01 +/- 0.05 (n = 7)	0.99 +/- 0.06 (n = 6)	n.d.	n.d.	n.d.	n.d.	27, 35, 40, 31
Fer	Y402	VQENDGKEPPPVVNYEEDAR	fer (fms/fps related) protein kinase, testis specific 2 isoform a	gi 83921584	0.62 +/- 0.11 (n = 4)	0.88 +/- 0.2 (n = 3)	1.16 +/- 0.15 (n = 4)^	1.32 +/- 0.1 (n = 4)	0.99 +/- 0.12 (n = 3)	0.98 +/- 0.09 (n = 4)	n.d.	1.11 (n = 1)	17, 56, 45, 37
FBP1	Y245	yVGSMVA DIHR	fructose bisphosphatase 1	gi 9506589	n.d.	n.d.	1.01 +/- 0.06 (n = 4)	0.99 +/- 0.08 (n = 4)	0.49 +/- 0.04 (n = 3)	0.73 +/- 0.08 (n = 4)	1.11 +/- 0.27 (n = 4)	1.55 +/- 0.73 (n = 4)	20, 57, 41
FBP1	Y265	TLVYGGI FLyPANK K/TLVYG GFLyPAN K	fructose bisphosphatase 1	gi 9506589	0.89 +/- 0.11 (n = 4)	0.56 +/- 0.09 (n = 2)	1.37 +/- 0.19 (n = 7)	0.8 +/- 0.12 (n = 6)^	0.88 +/- 0.12 (n = 4)	1.32 +/- 0.02 (n = 2)	0.95 +/- 0.07 (n = 4)	1.02 +/- 0.11 (n = 4)	23, 31, 23, 51, 36, 21, 38, 33, 22
FBP1	Y216	GNIYSLN EGyAKDF DPAINEY LQR/GNIY SLNEGyA KDFDPAI NEYLQR/ GNIYSLN EGyAK	fructose bisphosphatase 1	gi 9506589	0.93 +/- 0.2 (n = 6)	0.69 +/- 0.18 (n = 3)	1.35 +/- 0.17 (n = 7)	0.82 +/- 0.13 (n = 6)	0.83 +/- 0.09 (n = 3)	0.84 +/- 0.06 (n = 4)	1.03 +/- 0.08 (n = 4)	1.25 +/- 0.21 (n = 4)	20, 49, 52, 26, 45, 37, 49, 35, 48, 55
FH	Y462	LMNESL MLVTAL NPHIGyD K	fumarate hydratase 1	gi 33859554	n.d.	n.d.	1.03 +/- 0.1 (n = 4)	0.97 +/- 0.17 (n = 4)	n.d.	n.d.	n.d.	n.d.	20, 35
FH	Y488	ETAIELGy LTAEQFD EWVKPK	fumarate hydratase 1	gi 33859554	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	1.21 +/- 0.19 (n = 4)	0.79 +/- 0.1 (n = 4)	25
FGD5	Y713	ALSTANE NDGyVD MSSFNAF ESK	FYVE, RhoGEF and PH domain containing 5	gi 56699430	0.91 +/- 0 (n = 2)	1.48 (n = 1)	0.87 (n = 1)	0.95 +/- 0.15 (n = 3)	n.d.	n.d.	n.d.	n.d.	40
GPRC5C	Y386	GPSEGAY DVILPR	G protein-coupled receptor, family C, group	gi 22267464	n.d.	n.d.	n.d.	n.d.	1.27 +/- 0.19 (n = 4)	1.02 +/- 0.26 (n = 2)	0.82 +/- 0.09 (n = 4)	0.9 +/- 0.03 (n = 4)	53, 25

			5, member C										
GRF-1	Y1087	SMSSSPW MPQDGF DPSDyAE PMDAVV KPR	glucocorticoid receptor DNA binding factor 1	gi 75677442	n.d.	n.d.	1.06 +/- 0.14 (n = 4)	0.94 +/- 0.13 (n = 4)	n.d.	n.d.	n.d.	n.d.	42
GRF-1	Y1105	NEEENyS VPHDSTQ GK	glucocorticoid receptor DNA binding factor 1	gi 75677442	0.7 +/- 0.06 (n = 4)	0.96 +/- 0.09 (n = 3)	1.03 +/- 0.14 (n = 4)	1.3 +/- 0.15 (n = 4)	n.d.	n.d.	n.d.	n.d.	17, 26
GLUD1	Y135	RDDGSW EVIEGyR/ DDGSWE VIEGyR	glutamate dehydrogenase 1	gi 6680027	0.84 +/- 0.09 (n = 6)	0.92 +/- 0.04 (n = 3)	1.08 (n = 1)	1.23 +/- 0.09 (n = 5)	n.d.	n.d.	n.d.	n.d.	23, 36, 37
GLUD1	Y512	DIVHSG AyTMER	glutamate dehydrogenase 1	gi 6680027	0.7 +/- 0.09 (n = 5)	0.72 +/- 0.07 (n = 3)	1.21 +/- 0.11 (n = 7)*	1.15 +/- 0.09 (n = 6)	0.94 +/- 0.05 (n = 4)	1.06 +/- 0.01 (n = 2)	1.05 +/- 0.09 (n = 4)	0.98 +/- 0.1 (n = 4)	22, 32, 42, 52, 55, 51, 34
GOT1	Y264	NFGLyNE R	glutamate oxaloacetate transaminase 1, soluble	gi 6754034	n.d.	n.d.	1 +/- 0.07 (n = 4)	1 +/- 0.13 (n = 4)	n.d.	n.d.	n.d.	n.d.	21
GOT1	Y71	IANDNSL NHEyLPIL GLAEFR	glutamate oxaloacetate transaminase 1, soluble	gi 6754034	n.d.	n.d.	n.d.	n.d.	0.72 +/- 0.03 (n = 3)	1.24 +/- 0.15 (n = 4)	n.d.	0.88 (n = 1)	68
GOT2	Y96	NLDKEYL PIGGLAEF CK	glutamate oxaloacetate transaminase 2, mitochondrial	gi 6754036	0.63 +/- 0.03 (n = 2)	0.79 (n = 1)	0.96 +/- 0.04 (n = 4)*	1.22 +/- 0.11 (n = 5)	0.89 +/- 0.05 (n = 4)	1.06 +/- 0.29 (n = 2)	n.d.	1.31 (n = 1)	23, 32, 20
GOT2	Y284	NMGLyGE R	glutamate oxaloacetate transaminase 2, mitochondrial	gi 6754036	n.d.	n.d.	0.84 +/- 0.06 (n = 4)	1.16 +/- 0.07 (n = 4)	n.d.	n.d.	n.d.	n.d.	29
GLUL	Y336	GyFEDR/K GyFEDR	glutamine synthetase	gi 31982332	0.55 +/- 0.21 (n = 2)	0.65 (n = 1)	0.78 +/- 0.07 (n = 4)	1.43 +/- 0.12 (n = 5)*	n.d.	n.d.	n.d.	n.d.	20, 26
GPX1	Y147	yIIWSPVC R	glutathione peroxidase 1	gi 84871986	n.d.	n.d.	0.96 +/- 0.03 (n = 7)	1.05 +/- 0.03 (n = 6)	0.88 +/- 0.05 (n = 7)	1.04 +/- 0.03 (n = 4)	1 +/- 0.06 (n = 8)	1.1 +/- 0.08 (n = 7)	47, 42, 46, 44, 48, 24
GSTM1	Y23	MLLEyTD SSYDEK	glutathione S- transferase, mu 1	gi 6754084	0.88 +/- 0.08 (n = 6)	1.08 +/- 0.17 (n = 3)	0.89 +/- 0.05 (n = 4)	1.15 +/- 0.07 (n = 6)^	n.d.	n.d.	n.d.	n.d.	37, 23, 51, 30
GSTP1	Y109	YVTLyTN YEN GK	glutathione S- transferase, pi 1	gi 10092608	1.18 +/- 0.35 (n = 2)	1.39 (n = 1)	1.23 (n = 1)	0.67 +/- 0.03 (n = 3)	n.d.	n.d.	n.d.	n.d.	43
GSTP1	Y64	FEDGDLT LyQSNAIL R	glutathione S- transferase, pi 1	gi 10092608	0.79 +/- 0.13 (n = 4)	1.26 +/- 0.3 (n = 3)	1.07 +/- 0.08 (n = 4)	0.95 +/- 0.08 (n = 4)	1.24 +/- 0.21 (n = 7)	1.86 +/- 0.28 (n = 4)	0.6 +/- 0.05 (n = 8)*	0.72 +/- 0.11 (n = 7)	51, 50, 30, 37, 38, 34, 18, 45, 49
GAPDH	Y316	LISWYDN EyGYSNR	glyceraldehyde- 3-phosphate dehydrogenase	gi 6679937	n.d.	n.d.	0.72 +/- 0.06 (n = 4)	1.28 +/- 0.13 (n = 4)	0.91 +/- 0.07 (n = 4)	1.02 +/- 0.1 (n = 2)	n.d.	1.3 (n = 1)	57, 56

GAPDH	Y328	VVDLMA yMASK	glyceraldehyde- 3-phosphate dehydrogenase	gi 6679937	n.d.	n.d.	0.92 +/- 0.2 (n = 4)	1.08 +/- 0.19 (n = 4)	n.d.	n.d.	n.d.	n.d.	33
GNMT	Y22	SLGVAAE GLPDQyA DGEAAR	glycine N- methyltransferas e	gi 6754026	0.76 +/- 0.05 (n = 5)	1.21 +/- 0.12 (n = 3)*	0.83 (n = 1)	1.25 +/- 0.04 (n = 3)^	0.9 +/- 0.05 (n = 4)	1.16 +/- 0.09 (n = 2)	n.d.	1.05 (n = 1)	45, 58, 53, 37
GNMT	Y221	AHMVTL DyTVQVP GTGR	glycine N- methyltransferas e	gi 6754026	0.69 +/- 0.02 (n = 4)	1.12 +/- 0.2 (n = 3)	1 +/- 0.04 (n = 7)**	1.14 +/- 0.05 (n = 6)^	0.84 +/- 0.09 (n = 7)	1.2 +/- 0.08 (n = 4)*	0.9 +/- 0.02 (n = 4)	1.17 +/- 0.05 (n = 4)**	70, 61, 73, 76, 53, 72, 69
GNMT	Y34	VWQLyIG DTR	glycine N- methyltransferas e	gi 6754026	0.81 +/- 0.07 (n = 6)	1.18 +/- 0.05 (n = 3)*	0.98 +/- 0.07 (n = 7)	1.11 +/- 0.05 (n = 6)	1.04 +/- 0.05 (n = 7)	1.25 +/- 0.19 (n = 4)	0.69 +/- 0.01 (n = 4)**	0.99 +/- 0.07 (n = 4)*	50, 41, 34, 40, 44, 40, 60, 49, 41, 42, 47, 47, 34, 40, 42
GSK3B	Y216	GEPNVSI CSR	glycogen synthase kinase 3 beta	gi 9790077	0.78 +/- 0.04 (n = 6)	0.75 +/- 0.05 (n = 3)	1.16 +/- 0.14 (n = 7)^	1.16 +/- 0.08 (n = 6)	0.97 +/- 0.02 (n = 7)	1.01 +/- 0.04 (n = 4)	1 +/- 0.05 (n = 8)	1.02 +/- 0.06 (n = 7)	56, 59, 60, 36, 53, 58, 49, 53, 55, 49, 49, 62, 59, 51, 54, 50, 56, 51, 60
GSK3B	Y216 S219	GEPNVSI CsR	glycogen synthase kinase 3 beta	gi 9790077	0.72 +/- 0.05 (n = 6)	0.81 +/- 0.05 (n = 3)	1.21 +/- 0.2 (n = 4)^	1.28 +/- 0.1 (n = 5)	n.d.	n.d.	n.d.	n.d.	33, 37, 42, 20, 18
GAB2	Y290	SSLTGSET DNEDVYt FK	growth factor receptor bound protein 2- associated protein 2	gi 6753932	n.d.	n.d.	1.07 +/- 0.19 (n = 4)	0.93 +/- 0.05 (n = 4)	n.d.	n.d.	n.d.	n.d.	23
GCHFR	Y45	SVLGNNF yEYYVND PPR	GTP cyclohydrolase I feedback regulator	gi 28893139	n.d.	n.d.	n.d.	n.d.	0.92 +/- 0.07 (n = 3)	1.03 +/- 0.05 (n = 4)	n.d.	1.14 (n = 1)	31
HSPE1	Y76	VLLPEyG GTK	heat shock protein 1 (chaperonin 10)	gi 6680309	0.79 +/- 0.04 (n = 5)	0.75 +/- 0.06 (n = 3)	1.2 +/- 0.1 (n = 4)*	1.26 +/- 0.11 (n = 4)	0.82 +/- 0.05 (n = 7)	0.92 +/- 0.07 (n = 4)	1.16 +/- 0.09 (n = 4)*	1.23 +/- 0.04 (n = 4)	28, 24, 21, 38, 27, 24, 20
HSPD1	Y243	CEFQDAy VLLSEK	heat shock protein 1 (chaperonin)	gi 31981679	0.84 +/- 0.03 (n = 4)	0.98 +/- 0.05 (n = 2)	1.22 (n = 1)*	1.11 +/- 0.08 (n = 4)	0.96 +/- 0.07 (n = 3)	1.06 +/- 0.07 (n = 4)	n.d.	0.9 (n = 1)	16, 19, 27
HSPD1	Y385	IQEITEQL DITTSEyE KEK	heat shock protein 1 (chaperonin)	gi 31981679	0.62 +/- 0.11 (n = 4)	1.59 +/- 0.12 (n = 2)*	1.23 (n = 1)	1.02 +/- 0.14 (n = 5)	n.d.	n.d.	n.d.	n.d.	20, 24
HSP90A	Y285	yIDQEELN K	heat shock protein 1, alpha	gi 6754254	0.71 +/- 0.07 (n = 4)	1.1 +/- 0.1 (n = 2)^	0.74 (n = 1)	1.3 +/- 0.15 (n = 4)	n.d.	n.d.	n.d.	n.d.	31, 30
HRSP12	Y21	APAAIGPy SQAQVQV DR	heat-responsive protein 12	gi 40807498	0.98 +/- 0.1 (n = 6)	0.87 +/- 0.03 (n = 3)	1 +/- 0.03 (n = 7)	1.09 +/- 0.06 (n = 6)	0.9 +/- 0.05 (n = 7)	0.98 +/- 0.09 (n = 4)	1.03 +/- 0.05 (n = 8)	1.08 +/- 0.07 (n = 7)	73, 18, 46, 74, 87, 80, 64, 58, 48, 51, 91, 102
HBA	Y25	IGGHGAE	hemoglobin	gi 6680175	0.9 +/-	1.19 +/-	0.93 +/-	1.09 +/-	0.99 +/-	0.64 +/-	1.12 +/-	0.97 +/-	64, 59, 43,

		yGAEALE R	alpha I chain		0.13 (n = 6)	0.08 (n = 3)	0.16 (n = 7)	0.14 (n = 6)	0.16 (n = 4)	0.04 (n = 2)	0.09 (n = 8)	0.07 (n = 7)	37, 35, 102, 22, 34, 62, 61, 50, 42, 61
HBD	Y36	LLVVyPW TQR	hemoglobin, beta adult major chain	gi 31982300	n.d.	n.d.	0.9 +/- 0.1 (n = 4)	1.1 +/- 0.08 (n = 4)	n.d.	n.d.	0.94 +/- 0.08 (n = 4)	1.06 +/- 0.12 (n = 4)	29, 37, 26
HBD	Y42	yFDSFGD LSSASAI MGNAK	hemoglobin, beta adult major chain	gi 31982300	1.02 +/- 0.23 (n = 5)	1.23 +/- 0.39 (n = 3)	0.84 +/- 0.09 (n = 4)	0.96 +/- 0.35 (n = 4)	1.01 +/- 0.3 (n = 4)	0.81 +/- 0.13 (n = 2)	n.d.	1.33 (n = 1)	46, 61, 49, 54, 47
Hrs	Y216	VCEPCyE QLNK	HGF-regulated tyrosine kinase substrate	gi 31982286	n.d.	n.d.	0.9 +/- 0.1 (n = 4)	1.1 +/- 0.1 (n = 4)	n.d.	n.d.	n.d.	n.d.	25
vigilin	Y437	MDyVEINI DHK	high density lipoprotein binding protein	gi 19527028	0.5 +/- 0.08 (n = 6)	1.16 +/- 0.09 (n = 3)**	0.99 +/- 0.05 (n = 4)**	1.51 +/- 0.39 (n = 5)	0.84 +/- 0.07 (n = 7)	1.07 +/- 0.32 (n = 4)	0.97 +/- 0.04 (n = 4)	1.25 +/- 0.3 (n = 4)	41, 29, 29, 38, 41, 38, 49
HLAC	Y344	GGDyALA PGSQSSE MSLR	histocompatibilit y 2, D region locus 1	gi 13377895 5	n.d.	n.d.	n.d.	n.d.	1.02 +/- 0.1 (n = 4)	0.95 +/- 0.02 (n = 2)	n.d.	1.03 (n = 1)	43
H2-K1	Y342	GGDyALA PGSQTSD LSPDCK	histocompatibilit y 2, K1, K region isoform 1	gi 13392258 8	n.d.	n.d.	0.99 +/- 0.12 (n = 4)	1.01 +/- 0.17 (n = 4)	1.19 +/- 0.2 (n = 4)	1.11 +/- 0.25 (n = 2)	0.85 +/- 0.06 (n = 8)	1.03 +/- 0.1 (n = 7)	72, 49, 30, 46
HIPK1	Y352	AVCSTyL QSR	homeodomain interacting protein kinase 1	gi 6754196	n.d.	n.d.	0.97 +/- 0.05 (n = 7)	1.03 +/- 0.05 (n = 6)	0.86 +/- 0.04 (n = 4)	0.84 +/- 0.04 (n = 2)	1.1 +/- 0.06 (n = 4)*	1.12 +/- 0.06 (n = 4)	49, 42, 46, 44
HIPK3	Y359	TVCSTyL QSR	homeodomain interacting protein kinase 3	gi 6754200	n.d.	n.d.	1.01 +/- 0.04 (n = 4)	0.99 +/- 0.04 (n = 4)	n.d.	n.d.	n.d.	n.d.	40
HGD	Y40	GQNNPQ VCPYNly AEQLSGS AFTCPR	homogentisate 1, 2-dioxygenase	gi 7549763	n.d.	n.d.	0.9 +/- 0.05 (n = 4)	1.1 +/- 0.15 (n = 4)	n.d.	n.d.	n.d.	n.d.	68
SgK269	Y632	VPIVINPN AyDNLAI YK	Sugen kinase 269 / hypothetical protein LOC244895	gi 27370424	0.67 +/- 0.02 (n = 2)	1.11 (n = 1)	0.99 +/- 0.06 (n = 4)^	1.15 +/- 0.05 (n = 4)^	0.93 +/- 0.06 (n = 7)	0.95 +/- 0.1 (n = 4)	0.99 +/- 0.06 (n = 4)	1.18 +/- 0.08 (n = 4)	29, 41, 18, 26, 48
GAREM	Y453	TEVPyEEL WLEEGKP SR	hypothetical protein LOC381126	gi 13428888 8	n.d.	n.d.	0.84 +/- 0.12 (n = 4)	1.16 +/- 0.15 (n = 4)	0.66 +/- 0.06 (n = 4)	1.24 +/- 0.4 (n = 2)	n.d.	1.88 (n = 1)	44, 44
MGC14839	Y93	TSNSTSEE SDLHyAD IHVLR	hypothetical protein LOC66952	gi 13385350	0.97 +/- 0.36 (n = 2)	1.63 (n = 1)	0.74 (n = 1)	0.9 +/- 0.08 (n = 3)	n.d.	n.d.	n.d.	n.d.	29
CARKD	Y81	IGIVGGC QEyTGAP YFAGISA LK	hypothetical protein LOC69225	gi 21312234	1.07 +/- 0.09 (n = 6)	0.92 +/- 0.13 (n = 3)	1.14 +/- 0.03 (n = 7)	0.81 +/- 0.14 (n = 6)^	0.98 +/- 0.02 (n = 7)	1.04 +/- 0.05 (n = 4)	n.d.	0.98 (n = 1)	66, 74, 57, 71, 54, 68, 64, 47, 40, 33
LHPP	Y159	YyKETSG LMLDVG GYMK	hypothetical protein LOC76429	gi 70778744	n.d.	n.d.	0.73 +/- 0.08 (n = 4)	1.27 +/- 0.51 (n = 4)	n.d.	n.d.	n.d.	n.d.	34

INMT	Y87	EIIVTDyT PQNLQEL QK	indolethylamine N- methyltransferas e	gi 6678281	n.d.	n.d.	0.82 +/- 0.07 (n = 4)	1.18 +/- 0.11 (n = 4)	n.d.	n.d.	n.d.	n.d.	42
SHIP-2	Y113 6	TLSEVDy APGPGR	inositol polyphosphate phosphatase-like 1	gi 33859566	n.d.	n.d.	n.d.	n.d.	0.91 +/- 0.06 (n = 4)	1.33 +/- 0.22 (n = 2)	n.d.	0.71 (n = 1)	52
InsR	Y117 9/Y11 75	Dly(50)ET Dy(50)YR/ Dly(50)ET Dy(50)YR K	insulin receptor	gi 6754360	0.95 +/- 0.04 (n = 2)	1.21 (n = 1)	0.75 (n = 1)	1.05 +/- 0.32 (n = 3)	1.04 +/- 0.1 (n = 7)	1.08 +/- 0.15 (n = 4)	0.81 +/- 0.04 (n = 8)	1.13 +/- 0.13 (n = 7)	46, 24, 30, 36, 15, 23, 41, 23, 23
InsR	Y117 5 Y117 9	DlyETDyY RK	insulin receptor	gi 6754360	n.d.	n.d.	n.d.	n.d.	1.05 +/- 0.19 (n = 3)	1.04 +/- 0.14 (n = 4)	n.d.	0.7 (n = 1)	25
IRS1	Y460	GEEELSN yICMGGK	insulin receptor substrate 1	gi 29825829	n.d.	n.d.	n.d.	n.d.	0.92 +/- 0.05 (n = 7)	1.19 +/- 0.15 (n = 4)	n.d.	0.8 (n = 1)	25, 22
IRS1	Y935	EETGSEEy MNMDLG PGR	insulin receptor substrate 1	gi 29825829	n.d.	n.d.	n.d.	n.d.	0.85 +/- 0.07 (n = 4)	1.25 +/- 0.14 (n = 2)	n.d.	1.09 (n = 1)	42
IRS1	Y983	GDyMTM QIGCPR	insulin receptor substrate 1	gi 29825829	n.d.	n.d.	n.d.	n.d.	0.89 +/- 0.07 (n = 4)	1.32 +/- 0.19 (n = 2)	n.d.	0.8 (n = 1)	56
IRS2	Y671	SDDyMPM SPTSVSAP K	insulin receptor substrate 2	gi 12448707 3	0.51 +/- 0.04 (n = 4)	1.19 +/- 0.83 (n = 2)	1.14 +/- 0.07 (n = 4)***	1.2 +/- 0.1 (n = 5)	0.91 +/- 0.12 (n = 4)	1.35 +/- 0.26 (n = 2)	0.74 +/- 0.02 (n = 4)	1.18 +/- 0.11 (n = 4)*	26, 16, 17, 21, 25
IRS2	Y814	APCSCSG DNDQyVL MSSPVGR	insulin receptor substrate 2	gi 12448707 3	1.1 +/- 0.11 (n = 5)	0.97 +/- 0.07 (n = 3)	0.99 +/- 0.06 (n = 4)	0.93 +/- 0.06 (n = 5)	0.91 +/- 0.04 (n = 4)	1.22 +/- 0.09 (n = 2)	n.d.	0.91 (n = 1)	38, 43, 38, 41
IRS2	Y649	SSSNLG ADDGyMP MTPGAAL R	insulin receptor substrate 2	gi 12448707 3	0.72 +/- 0.4 (n = 2)	0.96 (n = 1)	1.01 +/- 0.05 (n = 7)	1.09 +/- 0.13 (n = 6)	0.98 +/- 0.05 (n = 4)	1.09 +/- 0.07 (n = 2)	0.92 +/- 0.05 (n = 4)	1.06 +/- 0.16 (n = 4)	64, 54, 44, 60, 58, 56, 57
ISOC1	Y159	ILGIPVIIT EQyPK	isochorismatase domain containing 1	gi 31541909	0.76 +/- 0.24 (n = 2)	1.03 (n = 1)	1.05 +/- 0.02 (n = 7)	1.02 +/- 0.13 (n = 6)	0.97 +/- 0.08 (n = 4)	0.89 +/- 0.08 (n = 2)	n.d.	1.33 (n = 1)	34, 21, 20, 20
IDH1	Y391	SDyLNTF EFMDK	isocitrate dehydrogenase 1 (NADP+), soluble	gi 58037546	0.69 +/- 0.09 (n = 4)	1.07 +/- 0.19 (n = 2)	0.88 (n = 1)	1.3 +/- 0.13 (n = 4)	n.d.	n.d.	n.d.	n.d.	31, 20
JAK2	Y570	REVGdYg QLHK	Janus kinase 2	gi 11432647 8	n.d.	n.d.	0.88 +/- 0.15 (n = 4)	1.12 +/- 0.05 (n = 4)	n.d.	n.d.	n.d.	n.d.	34
K18	Y14	STTFSTNy R	keratin 18	gi 6754482	n.d.	n.d.	0.8 +/- 0.05 (n = 7)	1.23 +/- 0.03 (n = 6)	1.08 +/- 0.08 (n = 4)	0.73 +/- 0.55 (n = 2)	n.d.	1.22 (n = 1)	37, 19, 26
K85	Y236	DVDCAYL	keratin complex	gi 31980832	n.d.	n.d.	n.d.	n.d.	0.49 +/-	2.2 +/-	n.d.	0.63 (n =	25

		R	2, basic gene 18						0.11 (n = 4)	0.45 (n = 2)		1)	
K8	Y210	DVDEAy MNKVEL ESR	keratin complex 2, basic, gene 8	gi 11414556 1	0.88 +/- 0.01 (n = 2)	1.1 (n = 1)^	0.66 +/- 0.16 (n = 4)	1.3 +/- 0.13 (n = 5)^	n.d.	n.d.	n.d.	n.d.	16, 20
KIF13B	Y172 2	EGEyVVV GTNK	kinesin family member 13B	gi 12448716 3	1.01 +/- 0.26 (n = 2)	0.8 (n = 1)	1.08 +/- 0.07 (n = 4)	0.98 +/- 0.07 (n = 5)	1.05 +/- 0.13 (n = 4)	0.92 +/- 0.06 (n = 2)	n.d.	0.95 (n = 1)	24, 23, 22
LDHA	Y239	QVVDsAy EVIK	lactate dehydrogenase A	gi 6754524	n.d.	n.d.	0.88 +/- 0.05 (n = 4)	1.12 +/- 0.07 (n = 4)	n.d.	n.d.	0.78 +/- 0.04 (n = 4)	1.22 +/- 0.1 (n = 4)	23, 32, 33
Lrrc25	Y289	SVDQDSQ PVyCNLE SLGR	leucine rich repeat containing 25	gi 23346481	0.82 +/- 0.11 (n = 6)	1.39 +/- 0.26 (n = 3)	0.96 +/- 0.11 (n = 7)	1.03 +/- 0.1 (n = 6)	1.12 +/- 0.13 (n = 4)	0.9 +/- 0.11 (n = 2)	n.d.	0.72 (n = 1)	37, 28, 55, 49, 49, 58
LPP	Y318	SEGDTAy GQQVQP NTWK	LIM domain containing preferred translocation partner in lipoma	gi 31982290	n.d.	n.d.	0.89 +/- 0.03 (n = 4)	1.11 +/- 0.06 (n = 4)	n.d.	n.d.	n.d.	n.d.	34
CRIP2	Y77	GVNIGGA GSYIyEKP QTEAPQV TGPIEVPV VR	LIM only protein HLP	gi 13195646	n.d.	n.d.	1.04 +/- 0.1 (n = 4)	0.96 +/- 0.16 (n = 4)	n.d.	n.d.	n.d.	n.d.	24
L-plastin	Y28	VDTDGN GyISCNEL NDLFK	lymphocyte cytosolic protein 1	gi 31543113	0.81 +/- 0.14 (n = 4)	1.13 +/- 0.08 (n = 2)	0.95 (n = 1)	1.13 +/- 0.07 (n = 4)	n.d.	n.d.	n.d.	n.d.	27, 61
MDH1	Y210	EVGVyEA LKDDSW LK	malate dehydrogenase 1, NAD (soluble)	gi 31982178	0.48 +/- 0.06 (n = 2)	0.79 (n = 1)	0.47 (n = 1)	1.6 +/- 0.09 (n = 3)^	n.d.	n.d.	n.d.	n.d.	17
MAGI1	Y361	IEDPVyG VYYVDHI NRK/IEDP VyGVYYV DHINR	membrane associated guanylate kinase, WW and PDZ domain containing 1 isoform a	gi 34328051	0.84 +/- 0.11 (n = 2)	0.82 (n = 1)	1.12 (n = 1)	1.12 +/- 0.15 (n = 3)	1.02 +/- 0.07 (n = 7)	0.98 +/- 0.04 (n = 4)	n.d.	0.93 (n = 1)	36, 83, 60
Met	Y100 1	SVSPTE MVSNEsV DyR	met proto- oncogene	gi 6678868	n.d.	n.d.	1.04 +/- 0.1 (n = 4)	0.96 +/- 0.09 (n = 4)	1.04 +/- 0.04 (n = 4)	0.99 +/- 0.2 (n = 2)	n.d.	0.87 (n = 1)	58, 50
HADHA	Y724	FVDLyGA QK	mitochondrial trifunctional protein, alpha subunit	gi 33859811	n.d.	n.d.	1.09 +/- 0.05 (n = 4)	0.91 +/- 0.07 (n = 4)	n.d.	n.d.	n.d.	n.d.	18
ERK2	Y185	VADPDH DHTGFLT EyVATR	mitogen activated protein kinase 1	gi 6754632	0.78 +/- 0.14 (n = 6)	1.14 +/- 0.05 (n = 3)	1.12 +/- 0.22 (n = 4)	1.08 +/- 0.16 (n = 5)	0.85 +/- 0.09 (n = 4)	0.88 +/- 0.16 (n = 2)	0.95 +/- 0.05 (n = 4)	1.25 +/- 0.1 (n = 4)^	61, 26, 47, 39, 28, 24, 28, 35, 30, 36, 59
ERK2	Y185 T188/	VADPDH DHTGFLt	mitogen activated protein	gi 6754632	0.7 +/- 0.14 (n =	1.05 +/- 0.12 (n =	1.71 (n = 1)	1.19 +/- 0.4 (n = 5)	n.d.	n.d.	n.d.	n.d.	37, 21, 35, 23, 31, 25,

	T183	50)EyVA(50)R	kinase 1		6)	3)							24
p38-alpha	Y182	HTDDEM TGyVATR	mitogen activated protein kinase 14	gi 10092590	0.93 +/- 0.16 (n = 6)	1.05 +/- 0.14 (n = 3)	0.9 +/- 0.26 (n = 7)	1.16 +/- 0.42 (n = 6)	0.95 +/- 0.09 (n = 3)	0.98 +/- 0.14 (n = 4)	0.92 +/- 0.12 (n = 8)	1.12 +/- 0.17 (n = 7)	80, 78, 72, 62, 33, 83, 64, 74, 77, 80, 81, 57, 66, 87, 75, 72
p38-alpha	Y182 T180	HTDDEMt GyVATR	mitogen activated protein kinase 14	gi 10092590	0.68 +/- 0.07 (n = 5)	1.17 +/- 0.27 (n = 3)	1.08 +/- 0.05 (n = 4)	1.13 +/- 0.26 (n = 6)	n.d.	n.d.	n.d.	n.d.	50, 69, 58, 62, 69, 38, 72, 62, 71
ERK1	Y205 T203/ T208	IADPEHD HTGFLt(50)EyVA(50)R	mitogen activated protein kinase 3	gi 21489933	0.79 +/- 0.11 (n = 4)	1.09 +/- 0.11 (n = 3)	1.58 (n = 1)	n.d.	n.d.	n.d.	n.d.	n.d.	27
ERK1	Y205	IADPEHD HTGFLTE yVATR	mitogen activated protein kinase 3	gi 21489933	0.83 +/- 0.08 (n = 5)	1.1 +/- 0.05 (n = 3)	1.06 +/- 0.1 (n = 4)	1.06 +/- 0.11 (n = 5)	1.01 +/- 0.08 (n = 7)	1.01 +/- 0.07 (n = 4)	0.88 +/- 0.08 (n = 4)	1.1 +/- 0.07 (n = 4)	62, 24, 67, 65, 70, 15, 22, 18, 38, 73
afadin	Y123 0	EyFTFPAS K	myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog isoform 1	gi 94401630	n.d.	n.d.	n.d.	n.d.	1 +/- 0.03 (n = 4)	1.1 +/- 0.19 (n = 2)	n.d.	0.81 (n = 1)	19
afadin	Y128 5	VyQLER	myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog isoform 1	gi 94401630	n.d.	n.d.	n.d.	n.d.	1.02 +/- 0.08 (n = 4)	1.13 +/- 0.1 (n = 2)	0.95 +/- 0.18 (n = 4)	0.97 +/- 0.07 (n = 4)	15, 15
ATP1A1	Y260	GIVVyTGD R	Na+/K+ -ATPase alpha 1 subunit	gi 21450277	n.d.	n.d.	1.54 +/- 0.92 (n = 4)	0.46 +/- 0.13 (n = 4)	n.d.	n.d.	n.d.	n.d.	37
Nck1	Y105	LyDLNMP AFVK	non-catalytic region of tyrosine kinase adaptor protein 1	gi 34328187	0.74 +/- 0.07 (n = 6)	1.16 +/- 0.06 (n = 3)*	1 +/- 0.09 (n = 7)^	1.18 +/- 0.18 (n = 6)	0.75 +/- 0.07 (n = 7)	1.08 +/- 0.17 (n = 4)	1.02 +/- 0.09 (n = 8)	1.18 +/- 0.12 (n = 7)	44, 21, 23, 25, 25, 37, 33, 43, 18, 31, 37, 23, 16
OAT	Y42	KTEQGPP SSEyIFER	ornithine aminotransferase	gi 8393866	1.04 +/- 0.16 (n = 2)	0.66 (n = 1)	1.02 (n = 1)	1.08 +/- 0.21 (n = 3)	n.d.	n.d.	n.d.	n.d.	30
OTC	Y317	KPEEVDD EVFySPR	ornithine transcarbamylase	gi 6679184	n.d.	n.d.	0.92 +/- 0.06 (n = 4)	1.08 +/- 0.09 (n = 4)	n.d.	n.d.	n.d.	n.d.	54
PAR3	Y112 3	EGHLM TLyAQVK	partitioning-defective protein 3 homolog isoform 3	gi 15809050	n.d.	n.d.	1.15 +/- 0.13 (n = 4)	0.85 +/- 0.09 (n = 4)	n.d.	n.d.	n.d.	n.d.	53
PAR3	Y107	ERDyAEI	partitioning-	gi 15809050	1.01 +/-	1.2 (n = 1)	1.13 +/-	0.85 +/-	n.d.	n.d.	n.d.	n.d.	52, 35

	6	QDFHR	defective protein 3 homolog isoform 3		0.07 (n = 2)		0.07 (n = 4)	0.07 (n = 5)^					
PXN	Y118	AGEEEHV ySFPNK	paxillin isoform alpha	gi 21281693	1.01 +/- 0.07 (n = 6)	0.95 +/- 0.03 (n = 3)	1.03 +/- 0.06 (n = 7)	0.99 +/- 0.07 (n = 6)	1.02 +/- 0.04 (n = 7)	1.03 +/- 0.08 (n = 4)	0.9 +/- 0.05 (n = 8)	1.08 +/- 0.09 (n = 7)	50, 36, 41, 53, 45, 44, 48, 54, 42, 24, 44, 42, 41, 54, 49, 26
PRDX6	Y89	DINAYNG ETPTEK	peroxiredoxin 6	gi 6671549	0.89 +/- 0.04 (n = 6)	0.95 +/- 0.03 (n = 3)	0.89 +/- 0.02 (n = 4)	1.25 +/- 0.05 (n = 5)**	n.d.	n.d.	n.d.	n.d.	17, 35, 39, 40
PAH	Y166	QFADIAY NYR	phenylalanine hydroxylase	gi 6679203	n.d.	n.d.	n.d.	n.d.	0.78 +/- 0.11 (n = 3)	1.16 +/- 0.03 (n = 4)	n.d.	1.01 (n = 1)	58
PEBP1	Y181	LyEQLSG K	phosphatidylethanolamine binding protein 1	gi 84794552	n.d.	n.d.	0.74 +/- 0.02 (n = 4)	1.26 +/- 0.27 (n = 4)	n.d.	n.d.	n.d.	n.d.	19
PIK3R1	Y197	LyEEYTR	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	gi 31712016	0.86 +/- 0.08 (n = 5)	0.81 +/- 0.01 (n = 3)	1.3 +/- 0.13 (n = 4)^	1.01 +/- 0.1 (n = 5)	0.77 +/- 0.13 (n = 4)	1.07 +/- 0.18 (n = 2)	1.27 +/- 0.16 (n = 4)	0.92 +/- 0.02 (n = 4)	22, 23, 22, 18, 26
PIK3R1	Y310	DQyLMW LTQK	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 isoform 1	gi 68299809	n.d.	n.d.	n.d.	n.d.	1.01 +/- 0.06 (n = 7)	1.08 +/- 0.05 (n = 4)	0.84 +/- 0.04 (n = 4)	1.06 +/- 0.05 (n = 4)*	18, 24, 17
PITPNA	Y141	HVEAIyID IADR	phosphatidylinositol transfer protein, alpha	gi 6679337	0.61 +/- 0.12 (n = 4)	1.38 +/- 0.09 (n = 2)*	0.95 +/- 0.06 (n = 7)*	1.19 +/- 0.06 (n = 6)*	0.86 +/- 0.04 (n = 4)	1.11 +/- 0.04 (n = 2)	n.d.	1.33 (n = 1)	46, 33, 52, 61, 40
PGM1	Y353	IALyETPT GWK	phosphoglucomutase 2	gi 31980726	0.86 +/- 0.15 (n = 4)	0.95 +/- 0.15 (n = 2)	0.92 +/- 0.03 (n = 7)	1.21 +/- 0.05 (n = 6)***	0.96 +/- 0.06 (n = 7)	1.03 +/- 0.03 (n = 4)	n.d.	1.19 (n = 1)	26, 17, 21, 32, 20, 23
PGK1	Y196	ELNyFAK	phosphoglycerate kinase 1	gi 70778976	n.d.	n.d.	0.97 +/- 0.04 (n = 4)	1.03 +/- 0.06 (n = 4)	n.d.	n.d.	n.d.	n.d.	22
PGAM2	Y92	HyGGLTG LNK	phosphoglycerate mutase 2	gi 9256624	n.d.	n.d.	0.97 +/- 0.04 (n = 4)	1.03 +/- 0.06 (n = 4)	n.d.	n.d.	n.d.	n.d.	28
PLCG1	Y771	IGTAEPDy GALYEGR	phospholipase C, gamma 1	gi 41393059	0.7 +/- 0.03 (n = 2)	1.06 (n = 1)	0.98 +/- 0.06 (n = 7)	1.11 +/- 0.07 (n = 6)	0.97 +/- 0 (n = 4)	0.85 +/- 0.08 (n = 2)	1.02 +/- 0.06 (n = 4)	1.09 +/- 0.07 (n = 4)	32, 31, 30, 16, 38
PAG	Y414	ESDyESIG DLQQR	phosphoprotein associated with glycosphingolipid microdomains 1	gi 31543456	0.79 +/- 0.03 (n = 2)	1.08 (n = 1)	0.99 (n = 1)	1.11 +/- 0.14 (n = 3)	n.d.	n.d.	n.d.	n.d.	35



PIPOX	Y119	QGIDHEy LSSVDLK	pipecolic acid oxidase	gi 6679507	0.75 +/- 0.13 (n = 2)	1.01 (n = 1)	0.56 (n = 1)	1.31 +/- 0.03 (n = 3)*	n.d.	n.d.	n.d.	n.d.	17
plakophilin 2	Y573	LKEQyQD LQMPEER /EQyQDL QMPEER	plakophilin 2	gi 21312960	0.83 +/- 0.1 (n = 4)	0.9 +/- 0.15 (n = 2)	1.01 +/- 0.19 (n = 4)	1.14 +/- 0.1 (n = 6)	n.d.	n.d.	n.d.	n.d.	30, 23, 19
plakophilin 4	Y469	NNyALNT AATYAEP YRPVQYR	plakophilin 4 isoform 1	gi 51491821	n.d.	n.d.	1.06 +/- 0.27 (n = 4)	0.94 +/- 0.16 (n = 4)	n.d.	n.d.	n.d.	n.d.	32
plakophilin 4	Y116 6	STTNyVD FYSTK	plakophilin 4 isoform 1	gi 51491821	n.d.	n.d.	n.d.	n.d.	1.02 +/- 0.09 (n = 3)	1 +/- 0.12 (n = 4)	n.d.	0.95 (n = 1)	18
PECAM-1	Y702	ATETVyS EIR	platelet/endotheli al cell adhesion molecule 1 isoform 1	gi 74024907	n.d.	n.d.	1.14 +/- 0.22 (n = 4)	0.86 +/- 0.12 (n = 4)	n.d.	n.d.	n.d.	n.d.	34
PLEKHA7	Y417	SADDTyL QLK	pleckstrin homology domain containing, family A member 7	gi 27370088	0.91 +/- 0.11 (n = 6)	0.83 +/- 0.17 (n = 3)	1.25 (n = 1)	1.16 +/- 0.12 (n = 5)	n.d.	n.d.	n.d.	n.d.	19, 19, 18
PLEKHA7	Y426	DLEyLDL K	pleckstrin homology domain containing, family A member 7	gi 27370088	1 +/- 0.25 (n = 2)	0.71 (n = 1)	1.22 (n = 1)	1.03 +/- 0.11 (n = 3)	n.d.	n.d.	n.d.	n.d.	32
PLEKHG1	Y105 1	IAEYSQLy DQIVFR	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	gi 84794546	n.d.	n.d.	1.03 +/- 0.03 (n = 4)	0.97 +/- 0.03 (n = 4)	0.84 +/- 0.14 (n = 4)	0.99 +/- 0.11 (n = 2)	1.1 +/- 0.09 (n = 4)	1.07 +/- 0.03 (n = 4)	42, 24, 24, 38
plectin 1	Y288	SIITYVSS LyDAMPR	plectin 1 isoform 1	gi 41322904	n.d.	n.d.	n.d.	n.d.	0.82 +/- 0.16 (n = 4)	1.29 +/- 0.05 (n = 2)	n.d.	1.16 (n = 1)	37
PGRMC1	S181 Y180	EGEPTV y(50)s(50) DDEEPPK DDEEPPK ETAR	progesterone receptor membrane component	gi 31980806	1.01 +/- 0.02 (n = 2)	0.89 (n = 1)	1.22 (n = 1)	0.96 +/- 0.11 (n = 3)	n.d.	n.d.	n.d.	n.d.	31
PHB	Y249	KLEAAED IAyQLSR	prohibitin	gi 6679299	0.89 +/- 0.08 (n = 6)	0.82 +/- 0.16 (n = 3)	1 +/- 0.08 (n = 4)	1.24 +/- 0.05 (n = 5)^	n.d.	n.d.	n.d.	n.d.	27, 49, 44, 39, 32
PROSC	Y69	TFGENyV QELLEK	proline synthetase co- transcribed isoform a	gi 16930823	0.89 +/- 0.06 (n = 6)	0.9 +/- 0.1 (n = 3)	1.05 +/- 0.05 (n = 7)	1.1 +/- 0.2 (n = 6)	n.d.	n.d.	n.d.	n.d.	33, 34, 29, 20, 30, 31

PSMA2	Y57	SILyDER	proteasome (prosome, macropain) subunit, alpha type 2	gi 134031994	n.d.	n.d.	0.92 +/- 0.05 (n = 4)	1.08 +/- 0.06 (n = 4)	0.87 +/- 0.05 (n = 4)	0.79 +/- 0.28 (n = 2)	1.03 +/- 0.07 (n = 4)	1.2 +/- 0.09 (n = 4)	37, 23, 24
SHP-2	Y62	IQNTGDy YDLYGGE K	protein tyrosine phosphatase, non-receptor type 11	gi 6755228	0.81 +/- 0.04 (n = 6)	0.78 +/- 0.1 (n = 3)	1.26 +/- 0.14 (n = 4)*	1.15 +/- 0.04 (n = 5)	1.01 +/- 0.06 (n = 7)	1.04 +/- 0.08 (n = 4)	0.97 +/- 0.03 (n = 8)	1 +/- 0.03 (n = 7)	46, 45, 46, 38, 50, 38, 57, 56, 60
SHP-2	Y584	VyENVGL MQQQR	protein tyrosine phosphatase, non-receptor type 11	gi 6755228	n.d.	n.d.	0.86 +/- 0.07 (n = 7)	1.16 +/- 0.07 (n = 6)	0.78 +/- 0.09 (n = 4)	1.15 +/- 0.27 (n = 2)	0.8 +/- 0.04 (n = 4)	1.35 +/- 0.13 (n = 4)*	43, 38, 53, 37
PTPRA	Y825	VVQEYID AFSDyAN FK	protein tyrosine phosphatase, receptor type, A	gi 6679557	0.73 +/- 0.09 (n = 5)	0.86 +/- 0.11 (n = 3)	1.32 +/- 0.19 (n = 7)^	0.93 +/- 0.13 (n = 6)	0.94 +/- 0.08 (n = 7)	0.99 +/- 0.15 (n = 4)	0.89 +/- 0.07 (n = 8)	1.2 +/- 0.17 (n = 7)	58, 81, 75, 51, 67, 66, 59, 69, 63, 64, 48
Fgr	Y197	KLDTGGY yITTR	proto-oncogene tyrosine-protein kinase Fgr	gi 31542816	n.d.	n.d.	1.11 +/- 0.07 (n = 4)	0.89 +/- 0.11 (n = 4)	n.d.	n.d.	n.d.	n.d.	27
PRP4	Y849	LCDFGSA SHVADN DITPyLVS R	PRP4 pre-mRNA processing factor 4 homolog B	gi 23956074	0.9 +/- 0.08 (n = 6)	0.8 +/- 0.02 (n = 3)	1.16 +/- 0.1 (n = 7)	1.01 +/- 0.07 (n = 6)	1.03 +/- 0.05 (n = 7)	0.77 +/- 0.09 (n = 4)^	1.1 +/- 0.07 (n = 4)	1.08 +/- 0.05 (n = 4)	24, 58, 74, 46, 33, 48, 62, 49, 57, 31, 71
PCBD1	Y70	LDHHPE WFNyN K	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	gi 13384608	n.d.	n.d.	0.98 +/- 0.1 (n = 4)	1.02 +/- 0.11 (n = 4)	n.d.	n.d.	n.d.	n.d.	17
FAK	Y397	THAVSVS ETDDyAEI IDEEDTY TMPSTR	PTK2 protein tyrosine kinase 2	gi 6679741	n.d.	n.d.	1.05 +/- 0.1 (n = 4)	0.95 +/- 0.1 (n = 4)	1.04 +/- 0.09 (n = 4)	1.01 +/- 0.07 (n = 2)	n.d.	0.85 (n = 1)	72, 44
FAK	Y861	EDGSFQG PTGNQHI yQPVGKP DPAAPPK	PTK2 protein tyrosine kinase 2	gi 6679741	n.d.	n.d.	1.01 +/- 0.16 (n = 4)	0.99 +/- 0.21 (n = 4)	n.d.	n.d.	n.d.	n.d.	18
FAK	Y576	YMEDSTy YK	PTK2 protein tyrosine kinase 2	gi 6679741	0.84 +/- 0.06 (n = 6)	0.88 +/- 0.08 (n = 3)	1.08 +/- 0.06 (n = 7)*	1.12 +/- 0.08 (n = 6)	0.97 +/- 0.04 (n = 7)	1.03 +/- 0.08 (n = 4)	0.9 +/- 0.07 (n = 8)	1.13 +/- 0.06 (n = 7)^	40, 32, 28, 35, 37, 40, 40, 33, 42, 34, 38, 21, 30
FAK	Y577 Y576/ T575/ S574	YMEDs(33)t(33)y(33)yKASK	PTK2 protein tyrosine kinase 2	gi 6679741	n.d.	n.d.	1.1 +/- 0.16 (n = 4)	0.9 +/- 0.09 (n = 4)	n.d.	n.d.	n.d.	n.d.	16
Pyk2	Y579	YIEDEDy YKASVTR	PTK2 protein tyrosine kinase 2	gi 27369678	0.64 +/- 0.08 (n = 6)	0.67 +/- 0.13 (n = 3)	1.1 +/- 0.05 (n = 4)	1.23 +/- 0.03 (n = 6)	0.96 +/- 0.11 (n = 7)	1.09 +/- 0.04 (n = 4)	n.d.	0.97 (n = 1)	33, 22, 22, 20, 30, 27,

		/YIEDEDy YK	beta		4)	2)	7)**	6)	4)	2)			19, 36, 31, 36
Pyk2	Y807	EAGyTEF TGPPQKP PR	PTK2 protein tyrosine kinase 2 beta	gi 27369678	n.d.	n.d.	0.86 +/- 0.05 (n = 4)	1.14 +/- 0.13 (n = 4)	n.d.	n.d.	n.d.	n.d.	32, 29
Pyk2	Y579 Y580	YIEDEDy KASVTR	PTK2 protein tyrosine kinase 2 beta	gi 27369678	0.75 +/- 0.11 (n = 5)	0.97 +/- 0.11 (n = 3)	0.98 (n = 1)	1.27 +/- 0.14 (n = 5)	n.d.	n.d.	n.d.	n.d.	20, 17, 23
PC	Y118	ENGVDA VHPGyGF LSER	pyruvate carboxylase	gi 6679237	0.83 +/- 0.06 (n = 2)	0.68 (n = 1)	1.08 +/- 0.04 (n = 7)^	1.01 +/- 0.04 (n = 6)	0.93 +/- 0.14 (n = 4)	1 +/- 0.06 (n = 2)	1.03 +/- 0.04 (n = 4)	1.04 +/- 0.02 (n = 4)	29, 28, 51, 38, 20
PDHB	Y67	VFLGEE VAQYDG AyK	pyruvate dehydrogenase (lipoamide) beta	gi 18152793	1.15 +/- 0.04 (n = 2)	0.87 (n = 1)	1.12 (n = 1)	0.9 +/- 0.08 (n = 3)	n.d.	n.d.	n.d.	n.d.	40
RBCK1	Y328	NSQEAEV ACPFIDST ySCPGK	RanBP-type and C3HC4-type zinc finger containing 1	gi 14504623 9	0.83 +/- 0.05 (n = 4)	1.18 +/- 0.04 (n = 3)*	1.01 +/- 0.08 (n = 4)	1.03 +/- 0.07 (n = 4)	n.d.	n.d.	n.d.	n.d.	65, 64
ARHGAP2 7	Y28	AQVDDPP EPVyANV ER	Rho GTPase activating protein 27 isoform 1	gi 83776555	n.d.	n.d.	0.9 +/- 0.11 (n = 4)	1.1 +/- 0.19 (n = 4)	n.d.	n.d.	n.d.	n.d.	35
RPL13A	Y137	FAyLGR	ribosomal protein L13a	gi 31981945	n.d.	n.d.	1.2 +/- 0.18 (n = 4)	0.8 +/- 0.18 (n = 4)	n.d.	n.d.	n.d.	n.d.	21
ARHGAP4 2	Y342	LWLEAM DGKEPIyT LPAISK	RIKEN cDNA 9030420J04 gene	gi 14925949 3	n.d.	n.d.	n.d.	n.d.	0.68 +/- 0.21 (n = 4)	1.52 +/- 0.14 (n = 2)	n.d.	1.26 (n = 1)	20
ARHGAP4 2	Y371	EPlyTLP AIISK	RIKEN cDNA 9030420J04 gene	gi 14925949 3	n.d.	n.d.	0.97 +/- 0.11 (n = 4)	1.03 +/- 0.2 (n = 4)	0.84 +/- 0.05 (n = 4)	1.17 +/- 0.08 (n = 2)	n.d.	1.31 (n = 1)	25, 30
ACSM3	Y51	IEIPEyFNF AK	SA hypertension- associated homolog	gi 85810988	n.d.	n.d.	0.96 +/- 0.06 (n = 4)	1.04 +/- 0.02 (n = 4)	n.d.	n.d.	n.d.	n.d.	28
SAHH	Y193	FDNlyGC R/SKFDNL yGCR	S- adenosylhomocysteine hydrolase	gi 61098092	0.78 +/- 0.07 (n = 6)	1.16 +/- 0.07 (n = 3)*	0.77 +/- 0.04 (n = 7)	1.41 +/- 0.1 (n = 6)***	0.78 +/- 0.06 (n = 7)	1.23 +/- 0.18 (n = 4)*	0.87 +/- 0.06 (n = 8)	1.24 +/- 0.09 (n = 7)*	20, 21, 21, 28, 26, 22, 24, 35, 15, 24, 15, 19
SEC14L4	Y36	ADDyFLL R	SEC14 (S. cerevisiae)-like 2	gi 22165368	1.08 +/- 0.12 (n = 4)	1.03 +/- 0.41 (n = 2)	1.08 +/- 0.09 (n = 4)	0.89 +/- 0.02 (n = 6)	0.91 +/- 0.05 (n = 3)	1.11 +/- 0.06 (n = 4)	n.d.	0.84 (n = 1)	29, 36, 29, 36
SEC14L2	Y36	FRENVQD VLPTLPN PDDyFLL R/ENVQD VLPTLPN PDDyFLL R	SEC14-like 2	gi 21362309	n.d.	n.d.	0.92 +/- 0.16 (n = 4)	1.08 +/- 0.21 (n = 4)	1.08 +/- 0.18 (n = 7)	1.36 +/- 0.14 (n = 4)	0.69 +/- 0.1 (n = 4)	0.8 +/- 0.2 (n = 4)	28, 20, 34, 21, 25
Sept2	Y17	QQPTQFI NPETPGy VGFANLP	septin 2	gi 6754816	n.d.	n.d.	0.97 +/- 0.11 (n = 4)	1.03 +/- 0.05 (n = 4)	1.31 +/- 0.17 (n = 4)	1.1 +/- 0.16 (n = 2)	0.71 +/- 0.06 (n = 4)*	0.93 +/- 0.04 (n = 4)^	36, 17, 23

		NQVHR											
SHMT1	Y67	ySEGYPG QR	serine hydroxymethyltr ansferase 1 (soluble)	gi 67846103	n.d.	n.d.	0.77 +/- 0.11 (n = 4)	1.23 +/- 0.21 (n = 4)	n.d.	n.d.	n.d.	n.d.	31
SHMT1	Y28	DSDAEVY SIK	serine hydroxymethyltr ansferase 1 (soluble)	gi 67846103	0.5 +/- 0.03 (n = 2)	0.87 (n = 1)	0.8 +/- 0.05 (n = 4)^	1.39 +/- 0.23 (n = 5)	0.72 +/- 0.09 (n = 4)	1.22 +/- 0.2 (n = 2)	n.d.	1.66 (n = 1)	19, 21, 29
SHEP1	Y178	TAAELEA AGDYVK	SH2 domain containing 3C	gi 7305329	1.12 +/- 0.14 (n = 4)	1.15 +/- 0.38 (n = 2)	0.96 +/- 0.08 (n = 4)	0.87 +/- 0.06 (n = 5)	n.d.	n.d.	n.d.	n.d.	24, 27, 20
ITSN2	Y922	GEPEALY AAVTK	SH3 domain protein 1B	gi 46560563	0.84 +/- 0.08 (n = 6)	1.02 +/- 0.39 (n = 3)	1.25 (n = 1)	1.13 +/- 0.16 (n = 5)	1.05 +/- 0.05 (n = 7)	1 +/- 0.08 (n = 4)	0.84 +/- 0.02 (n = 4)	1.07 +/- 0.17 (n = 4)	19, 27, 34, 19, 27, 24
STAT3	Y686	yCRPESQ EHPEADP GSAAPYL K	signal transducer and activator of transcription 3 isoform 3	gi 22094115	n.d.	n.d.	1.11 +/- 0.22 (n = 4)	0.89 +/- 0.29 (n = 4)	n.d.	n.d.	n.d.	n.d.	22
STAP2	Y250	ALVPFLL DEDYEK	signal- transducing adaptor protein-2	gi 22122357	0.88 +/- 0.13 (n = 4)	1.03 +/- 0.11 (n = 2)	1.23 +/- 0.14 (n = 4)	0.9 +/- 0.44 (n = 5)	0.9 +/- 0.09 (n = 4)	1.17 +/- 0.28 (n = 2)	n.d.	1.04 (n = 1)	43, 50, 37, 46
SLC22A1	Y545	ENTLYLQV QTGK	solute carrier family 22 member 1	gi 31982010	n.d.	n.d.	n.d.	n.d.	1.07 +/- 0.09 (n = 4)	1 +/- 0.13 (n = 2)	n.d.	0.71 (n = 1)	21
SLC25A5	Y191	AAyFGIY DTAK	solute carrier family 25, member 5	gi 22094075	0.71 +/- 0.12 (n = 4)	0.84 +/- 0.27 (n = 2)	1.05 +/- 0.08 (n = 4)	1.21 +/- 0.11 (n = 6)	0.79 +/- 0.07 (n = 7)	0.92 +/- 0.11 (n = 4)	1.12 +/- 0.08 (n = 4)^	1.34 +/- 0.28 (n = 4)	29, 25, 23, 36, 17, 19
SLC25A5	Y81	yFPTQAL NFAFK	solute carrier family 25, member 5	gi 22094075	n.d.	n.d.	1.2 +/- 0.1 (n = 4)	0.8 +/- 0.13 (n = 4)	1.02 +/- 0.07 (n = 3)	1.14 +/- 0.06 (n = 4)	0.9 +/- 0.02 (n = 4)	0.94 +/- 0.03 (n = 4)	25, 30, 37, 38
SCAP2	Y260	SQPIDDEI yEELPEEE EDTASVK	src family associated phosphoprotein 2	gi 9055324	0.88 +/- 0.16 (n = 4)	1.14 +/- 0.22 (n = 2)	1.17 +/- 0.16 (n = 4)	0.91 +/- 0.14 (n = 5)	1.1 +/- 0.35 (n = 3)	1.05 +/- 0.21 (n = 4)	n.d.	0.5 (n = 1)	29, 37, 50, 40
SHF	Y64	LPEDDER PPEEYDQP WEWK	Src homology 2 domain containing F	gi 11118592 4	0.39 +/- 0.04 (n = 2)	0.84 (n = 1)	1.07 +/- 0.19 (n = 4)	1.22 +/- 0.14 (n = 5)	n.d.	n.d.	n.d.	n.d.	18, 18
Shb	Y432	LPQDDDR PADEYDQ PWEWNR	src homology 2 domain- containing transforming protein B	gi 14925237 7	0.76 +/- 0.2 (n = 5)	0.96 +/- 0.25 (n = 3)	1.07 +/- 0.11 (n = 4)	1.17 +/- 0.12 (n = 6)	1.13 +/- 0.19 (n = 3)	0.86 +/- 0.24 (n = 4)	n.d.	1.17 (n = 1)	20, 54, 36, 28, 43, 53
Shb	Y342	VTIADY SDPFDK	src homology 2 domain- containing transforming protein B	gi 14925237 7	0.77 +/- 0.21 (n = 4)	1.13 +/- 0.42 (n = 2)	1.02 +/- 0.09 (n = 7)	1.09 +/- 0.06 (n = 6)	1.11 +/- 0.16 (n = 3)	0.92 +/- 0.12 (n = 4)	n.d.	0.97 (n = 1)	40, 48, 36, 19, 30, 43
Shb	Y364	GESAGyM EPYEAQR	src homology 2 domain- containing	gi 14925237 7	0.85 +/- 0.21 (n = 2)	1.06 (n = 1)	1.01 (n = 1)	1.08 +/- 0.12 (n = 3)	n.d.	n.d.	n.d.	n.d.	32

			transforming protein B										
Shc1	Y313	ELFDDPSy VNIQNLD K	src homology 2 domain-containing transforming protein C	gi 15778828	0.7 +/- 0.02 (n = 6)	1.01 +/- 0.13 (n = 3)*	1.14 +/- 0.23 (n = 4)^	1.2 +/- 0.14 (n = 6)	0.89 +/- 0.07 (n = 7)	1.12 +/- 0.07 (n = 4)	0.83 +/- 0.1 (n = 8)	1.23 +/- 0.07 (n = 7)*	38, 40, 41, 53, 56, 27, 39, 43, 47, 46
SND1	Y908	ADDADEF GySR	staphylococcal nuclease domain containing 1	gi 77404392	0.58 +/- 0.04 (n = 4)	1.07 +/- 0.14 (n = 3)*	0.83 +/- 0.1 (n = 4)^	1.55 +/- 0.08 (n = 4)**	n.d.	n.d.	n.d.	n.d.	65, 37
SND1	Y109	EyGMIYL GK	staphylococcal nuclease domain containing 1	gi 77404392	0.58 +/- 0.21 (n = 2)	0.75 (n = 1)	1.13 +/- 0.12 (n = 4)	1.15 +/- 0.14 (n = 4)	0.99 +/- 0.08 (n = 7)	0.93 +/- 0.21 (n = 4)	n.d.	1.36 (n = 1)	17, 24, 20, 19
SCP2	Y197	HSVNNTy SQFQDEY SLEEVMK	sterol carrier protein 2, liver	gi 45476581	n.d.	n.d.	0.93 +/- 0.05 (n = 4)	1.07 +/- 0.12 (n = 4)	n.d.	n.d.	n.d.	n.d.	50
ST5	Y498	ENPyEDV DLK	suppression of tumorigenicity 5 isoform 1	gi 47679093	0.62 +/- 0.06 (n = 4)	0.69 +/- 0.09 (n = 2)	1.41 +/- 0.16 (n = 4)*	1.08 +/- 0.15 (n = 6)	n.d.	n.d.	n.d.	n.d.	43, 33, 35
ST5	Y485	STLEENA yEDIVGG LPK	suppression of tumorigenicity 5 isoform 1	gi 47679093	0.69 +/- 0.07 (n = 2)	1.19 (n = 1)	0.87 (n = 1)	1.19 +/- 0.2 (n = 3)	n.d.	n.d.	n.d.	n.d.	32
DLG3	Y705	DNEVDG QDyHFVV SR/RDNE VDGQDyH FVVSr	synapse-associated protein 102	gi 7949129	0.91 +/- 0.35 (n = 2)	1.21 (n = 1)	1.2 +/- 0.18 (n = 4)	0.83 +/- 0.09 (n = 5)	1.11 +/- 0.16 (n = 4)	0.93 +/- 0.05 (n = 2)	n.d.	0.71 (n = 1)	38, 61, 51
tal1	Y26	TMQFEPS TMVyDAC R	tal1	gi 6755809	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.93 +/- 0.09 (n = 4)	1.07 +/- 0.07 (n = 4)	28
tal1	Y1116	LLGEIAQ GNENyAG IAAR	tal1	gi 6755809	0.65 +/- 0 (n = 2)	0.93 (n = 1)	1.15 +/- 0.17 (n = 4)	1.05 +/- 0.05 (n = 4)	1.07 +/- 0.13 (n = 4)	1.39 +/- 0.15 (n = 2)	0.83 +/- 0.15 (n = 4)	0.91 +/- 0.03 (n = 4)	55, 34, 48, 65
tal1	Y1665	ECDySIDG INR	tal1	gi 124486957	0.98 +/- 0.12 (n = 4)	1.04 +/- 0.07 (n = 3)	0.97 (n = 1)	n.d.	n.d.	n.d.	n.d.	n.d.	47
tensin 1	Y1593	ySMPDNS PETR	tensin 1	gi 94363487	0.45 +/- 0.09 (n = 2)	0.64 (n = 1)	1.02 +/- 0.09 (n = 7)*	1.22 +/- 0.14 (n = 6)	1.22 +/- 0.12 (n = 4)	1.3 +/- 0.06 (n = 2)	0.88 +/- 0.17 (n = 4)	0.75 +/- 0.12 (n = 4)	49, 60, 38, 46, 26
tensin 1	Y1480	HAAyGGy STPEDR	tensin 1	gi 94363487	0.72 +/- 0.15 (n = 4)	0.93 +/- 0.12 (n = 2)	1.09 +/- 0.08 (n = 4)	1.15 +/- 0.13 (n = 6)	n.d.	n.d.	n.d.	n.d.	64, 61, 57
tensin 1	Y537	EDGMEE VVGHTQ GPLDGSL yAK	tensin 1	gi 94363487	0.67 +/- 0.16 (n = 4)	0.99 +/- 0.46 (n = 2)	0.99 +/- 0.22 (n = 4)	1.27 +/- 0.24 (n = 5)	1.04 +/- 0.15 (n = 7)	0.91 +/- 0.08 (n = 4)	1.03 +/- 0.1 (n = 4)	1 +/- 0.03 (n = 4)	34, 42, 37, 25, 60, 39, 17
tensin 1	Y1558	AGSLPNy ATINGK	tensin 1	gi 94363487	1.08 +/- 0.06 (n = 4)	1.13 +/- 0.08 (n = 3)	0.92 +/- 0.04 (n = 7)	0.98 +/- 0.07 (n = 6)	1.08 +/- 0.06 (n = 4)	0.96 +/- 0.07 (n = 2)	n.d.	0.76 (n = 1)	34, 22, 34, 36

tensin 3	Y354 S332/ Y333/ S337/ T345	WDs(25)y(25)ENMs(25)ADGEV LHT(25)QG PVDGSLy AK	tensin 3	gi 134152676	0.72 +/- 0.1 (n = 4)	1.44 +/- 0.2 (n = 2)	1.17 (n = 1)	1.01 +/- 0.16 (n = 5)	n.d.	n.d.	n.d.	n.d.	30, 29
TARS	Y297	IyGISFPDP K	threonyl-tRNA synthetase	gi 27229277	0.64 +/- 0.11 (n = 4)	0.87 +/- 0.3 (n = 2)	0.99 +/- 0.05 (n = 7)*	1.29 +/- 0.11 (n = 6)*	n.d.	n.d.	0.91 +/- 0.06 (n = 4)	1.09 +/- 0.15 (n = 4)	27, 23, 21, 31, 26
ZO1	Y1145	TRyEQLP R	tight junction protein 1	gi 6678355	n.d.	n.d.	1.07 +/- 0.02 (n = 4)	0.93 +/- 0.08 (n = 4)	n.d.	n.d.	n.d.	n.d.	19
ZO1	Y1066	YEVSSyT DQFSR	tight junction protein 1	gi 6678355	n.d.	n.d.	0.9 +/- 0.05 (n = 4)	1.1 +/- 0.08 (n = 4)	n.d.	n.d.	n.d.	n.d.	25
ZO1	Y1190	QyFDQYP R	tight junction protein 1	gi 6678355	n.d.	n.d.	n.d.	n.d.	0.96 +/- 0.04 (n = 4)	1.08 +/- 0.05 (n = 2)	n.d.	0.99 (n = 1)	21
ZO1	Y1360	QLSyFDR R	tight junction protein 1	gi 6678355	n.d.	n.d.	0.99 +/- 0.08 (n = 4)	1.01 +/- 0.09 (n = 4)	n.d.	n.d.	n.d.	n.d.	31
ZO2	Y486	VFLRPSPE DEAIyGP NTK	tight junction protein 2	gi 7549795	1.16 +/- 0.13 (n = 2)	1.18 (n = 1)	0.93 +/- 0.04 (n = 7)	1 +/- 0.03 (n = 6)	n.d.	n.d.	n.d.	n.d.	19, 20, 22
TGM2	Y369	SEGTyCC GPVSVR	transglutaminase 2, C polypeptide	gi 6678329	n.d.	n.d.	0.7 +/- 0.07 (n = 7)	1.35 +/- 0.1 (n = 6)	0.6 +/- 0.11 (n = 4)	1.04 +/- 0.03 (n = 2)	0.84 +/- 0.05 (n = 4)^	1.54 +/- 0.27 (n = 4)	44, 44, 51, 42
TTYH2	Y494	yENVPLIG R	tweety 2	gi 68989251	n.d.	n.d.	1.16 +/- 0.08 (n = 4)	0.84 +/- 0.16 (n = 4)	n.d.	n.d.	n.d.	n.d.	22
UGDH	Y108	yIEACAR	UDP-glucose dehydrogenase	gi 6678499	n.d.	n.d.	1 +/- 0.01 (n = 4)	1 +/- 0.04 (n = 4)	n.d.	n.d.	n.d.	n.d.	21
UOX	Y230	GEySPSV QK	urate oxidase	gi 6678509	n.d.	n.d.	0.74 +/- 0.16 (n = 4)	1.26 +/- 0.5 (n = 4)	n.d.	n.d.	n.d.	n.d.	17
UOX	Y288	EEVLLPL DNPYgK/ MGLINKE EVLLPLD NPyGK	urate oxidase	gi 6678509	0.7 +/- 0.07 (n = 6)	0.73 +/- 0.2 (n = 3)	1.03 +/- 0.03 (n = 7)**	1.4 +/- 0.13 (n = 6)*	0.94 +/- 0.07 (n = 7)	1.04 +/- 0.13 (n = 4)	0.91 +/- 0.06 (n = 8)	1.14 +/- 0.12 (n = 7)	29, 34, 28, 18, 24, 26, 38, 23, 32, 47, 42, 31, 24, 31, 47, 35, 29, 33, 40, 23, 21
Abl	Y393	LMTGDyT AHAGA K	v-abl Abelson murine leukemia oncogene 1	gi 33859504	n.d.	n.d.	0.95 +/- 0.1 (n = 4)	1.05 +/- 0.13 (n = 4)	n.d.	n.d.	n.d.	n.d.	24
VCP	Y173	VVETDPS PyCIVAPD TVIHCEG EPIKR	valosin containing protein	gi 30023842	n.d.	n.d.	0.71 +/- 0.03 (n = 4)	1.29 +/- 0.1 (n = 4)	n.d.	n.d.	n.d.	n.d.	40
Crk	Y251	VPNAyDK	v-crk sarcoma	gi 31559995	n.d.	n.d.	n.d.	n.d.	1.05 +/-	0.89 +/-	n.d.	1.03 (n =	24

		TALALEV GELVK	virus CT10 oncogene homolog						0.07 (n = 4)	0.02 (n = 2)		1)	
CrkL	Y198	NSNSyGIP EPAHAYA QPQTTP LPTVAST PGAAINP LPSTQNG PVFAK	v-crck sarcoma virus CT10 oncogene homolog (avian)- like	gi 31542421	0.7 +/- 0.11 (n = 4)	0.89 +/- 0.02 (n = 3)	1.12 +/- 0.22 (n = 4)	1.26 +/- 0.16 (n = 4)	n.d.	n.d.	n.d.	n.d.	70, 83
CrkL	Y132	TLyDFPG NDAEDLP FK	v-crck sarcoma virus CT10 oncogene homolog (avian)- like	gi 31542421	0.93 +/- 0.08 (n = 6)	1.08 +/- 0.04 (n = 3)	1.13 (n = 1)	1.01 +/- 0.08 (n = 5)	0.9 +/- 0.06 (n = 7)	1.08 +/- 0.06 (n = 4)	1.03 +/- 0.07 (n = 4)	1.06 +/- 0.07 (n = 4)	32, 20, 36, 31, 35, 55, 32
HER3	Y132 5	SLEATDS AFDNPdy WHSR	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3	gi 61098019	0.92 +/- 0.31 (n = 2)	0.86 (n = 1)	0.76 (n = 1)	1.18 +/- 0.15 (n = 3)	1.1 +/- 0.06 (n = 4)	1.12 +/- 0.34 (n = 2)	0.81 +/- 0.07 (n = 4)	1.03 +/- 0.12 (n = 4)	74, 21, 43
vinculin	Y692	NPGNQA AyEHFET MK	vinculin	gi 31543942	n.d.	n.d.	0.98 +/- 0.13 (n = 4)	1.02 +/- 0.14 (n = 4)	n.d.	n.d.	n.d.	n.d.	21
vinculin	Y822	SFLDSGy R	vinculin	gi 31543942	0.88 +/- 0.05 (n = 4)	0.94 +/- 0.05 (n = 3)	1.06 +/- 0.06 (n = 7)	1.03 +/- 0.05 (n = 6)	1.16 +/- 0.07 (n = 3)	0.9 +/- 0.08 (n = 4)	n.d.	0.93 (n = 1)	33, 30, 28, 21, 24
Yes	Y220	KLDNGG YyITR/L DNGGyYI TTR	viral oncogene yes homolog	gi 6678617	n.d.	n.d.	1.08 +/- 0.07 (n = 7)	0.91 +/- 0.07 (n = 6)	1.08 +/- 0.11 (n = 4)	1.16 +/- 0.07 (n = 2)	0.89 +/- 0.05 (n = 4)	0.95 +/- 0.07 (n = 4)	33, 40, 18, 29, 29
Yes	Y424	LIEDNEyT AR	viral oncogene yes homolog	gi 6678617	0.98 +/- 0.04 (n = 6)	0.92 +/- 0.05 (n = 3)	1.06 +/- 0.07 (n = 7)	0.98 +/- 0.09 (n = 6)	0.98 +/- 0.22 (n = 7)	1.07 +/- 0.19 (n = 4)	0.86 +/- 0.03 (n = 8)	1.14 +/- 0.15 (n = 7)	52, 56, 52, 34, 49, 46, 60, 60, 58, 58, 56, 52, 61, 56, 56, 56, 57
Yes	Y192	GAySLSIR	viral oncogene yes homolog	gi 6678617	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	1 +/- 0.04 (n = 4)	1 +/- 0.07 (n = 4)	21
VDAC1	Y195	TDEFQLH TNVNDGT EFGGSlyQ K	voltage- dependent anion channel 1	gi 6755963	n.d.	n.d.	n.d.	n.d.	0.95 +/- 0.03 (n = 4)	1.09 +/- 0.08 (n = 2)	n.d.	1.01 (n = 1)	35
WASP	Y293	LlyDFIED QGGLEAV R	Wiskott-Aldrich syndrome homolog	gi 6678581	n.d.	n.d.	n.d.	n.d.	0.86 +/- 0.1 (n = 7)	0.9 +/- 0.07 (n = 4)	0.93 +/- 0.08 (n = 4)	1.43 +/- 0.23 (n = 4)	69, 25, 71
N-WASP	Y253	VlyDFIEK	Wiskott-Aldrich syndrome-like	gi 58037309	0.6 +/- 0.05 (n = 4)	0.72 +/- 0.31 (n = 2)	1.47 +/- 0.16 (n = 4)**	1.05 +/- 0.11 (n = 6)	1.27 +/- 0.09 (n = 4)	0.63 +/- 0.48 (n = 2)	0.98 +/- 0.08 (n = 4)	0.93 +/- 0.3 (n = 4)	21, 18, 24, 18, 16
Lyn	Y452	MENCPE	Yamaguchi	gi 33859588	0.52 +/-	1.58 (n =	0.9 (n = 1)	1.16 +/-	n.d.	n.d.	n.d.	n.d.	26

		LyDIMK	sarcoma viral (v-yes-1) oncogene homolog		0.01 (n = 2)	1)		0.4 (n = 3)					
Lyn	Y173	SLDNGGYyISPR	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	gi 33859588	n.d.	n.d.	1.06 +/- 0.07 (n = 7)	0.93 +/- 0.07 (n = 6)	1.04 +/- 0.06 (n = 4)	1.05 +/- 0.28 (n = 2)	1.02 +/- 0.03 (n = 4)	0.92 +/- 0.07 (n = 4)	68, 56, 47, 52, 22
Lyn	Y376	VIEDNEyTAR	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	gi 33859588	0.95 +/- 0.1 (n = 5)	1.35 +/- 0.32 (n = 3)	0.88 +/- 0.08 (n = 4)	0.93 +/- 0.11 (n = 5)	1.15 +/- 0.19 (n = 7)	1.07 +/- 0.11 (n = 4)	0.76 +/- 0.12 (n = 8)	1.09 +/- 0.18 (n = 7)	59, 56, 42, 29, 30, 50, 62, 69, 52, 42
ZAP	Y508	EAVySGVQSLR	zinc finger CCCH type, antiviral 1	gi 21746169	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.72 +/- 0.06 (n = 4)	1.28 +/- 0.13 (n = 4)	41
ZDHHC8	S534 Y538	EPsPVRyDNLSR	zinc finger, DHHC domain containing 8	gi 84619699	0.93 +/- 0.11 (n = 2)	0.89 (n = 1)	1.12 (n = 1)	1.05 +/- 0.08 (n = 3)	n.d.	n.d.	n.d.	n.d.	20
HPD	Y232	SIVVTNyEESIK	4-hydroxyphenylpyruvic acid dioxygenase	gi 33859486	0.84 +/- 0.08 (n = 5)	1.04 +/- 0.04 (n = 3)	0.98 +/- 0.02 (n = 7)	1.13 +/- 0.05 (n = 6)^	n.d.	n.d.	n.d.	n.d.	24, 64, 22, 49, 49
HPD	Y221	FWSVDDTQVHTEySSLR	4-hydroxyphenylpyruvic acid dioxygenase	gi 33859486	0.66 +/- 0.09 (n = 6)	1.39 +/- 0.02 (n = 3)**	0.73 +/- 0.04 (n = 7)	1.46 +/- 0.13 (n = 6)***	0.62 +/- 0.07 (n = 7)	1.09 +/- 0.12 (n = 4)**	1.12 +/- 0.08 (n = 4)**	1.45 +/- 0.17 (n = 4)	58, 26, 42, 45, 64, 43, 32, 53, 48
NIPSNAP1	Y261	RGWDEN VyYTVPL VR/GWDE NVyYTVPLVR	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	gi 6679066	0.41 +/- 0.05 (n = 4)	0.67 +/- 0.16 (n = 2)	1.08 +/- 0.1 (n = 7)**	1.41 +/- 0.22 (n = 6)	0.38 +/- 0.05 (n = 7)	0.53 +/- 0.16 (n = 4)	1.46 +/- 0.19 (n = 8)***	1.36 +/- 0.15 (n = 7)	39, 63, 27, 41, 37, 49, 45, 41

Phosphotyrosine measurements are written as mean +/- standard error for each of the diet and genotype conditions. The number of mice analyzed per condition is denoted in parentheses. For each dataset (basal or insulin-stimulated) statistical analysis was performed using one-way ANOVA with sequential Sidak-Dunn method to adjust for multiple comparisons (1) L-PTP1b<sup>-/-</sup> mice to control on NC diet, (2) L-PTP1b<sup>-/-</sup> mice to control on HFD, and (3) HFD control to NC control. \*\*\* = P<.001, \*\* = P<.01, \* = P < .05, ^ = P<.1.

**Table S3: Sets tested in phosphosite-set enrichment analysis**

Set	Size	Phosphosites	Source
Golgi apparatus	17	Lyn Y173, ZO1 Y1145, DYRK4 Y344, CAV1 Y14 Y6, ZO1 Y1360, Lyn Y376, ZO1 Y1190, HSPD1 Y243, PEBP1 Y181, ZO1 Y1066, FASN Y1248, HPD Y232, HSPD1 Y385, GLUL Y336, CAT Y231, CAT Y84, HPD Y221	GO
Lysosome	8	GOT1 Y264, ALDOB Y204, ASS1 Y29, GOT1 Y71, ASS1 Y133, ASS1 Y322, CAT Y231,	GO



		CAT Y84	
Mitochondria	35	Lyn Y173, PC Y118, HADHA Y724, FH Y488, CPS1 Y140, HSPE1 Y76, SLC25A5 Y191, SLC25A5 Y81, ACAT1 Y328, FH Y462, GLUD1 Y135, CPS1 Y1450, GLUD1 Y512, ACAA2 Y198, ACSM3 Y51, Lyn Y376, OTC Y317, NIPSNAP1 Y148, GOT2 Y96, NIPSNAP1 Y261, CPS1 Y590, VDAC1 Y195, HSPD1 Y243, PEBP1 Y181, ASS1 Y29, PHB Y249, ASS1 Y133, ASS1 Y322, GOT2 Y284, CPS1 Y162, HSPD1 Y385, CAT Y231, CAT Y84, ACSL5 Y69, CYB5A Y11	GO
Endoplasmic Reticulum	18	CAV1 Y14 Y6, ALDOB Y204, HSPD1 Y243, PEBP1 Y181, ASS1 Y29, ASS1 Y133, HPD Y232, ASS1 Y322, HSPD1 Y385, GLUL Y336, CAT Y231, CAT Y84, VCP Y173, ACSL5 Y69, CYP2E1 Y426, CALM1 Y100, HPD Y221, CYB5A Y11	GO
Endosome	15	EGFR Y1172, Crk Y251, ATP1A1 Y260, CAV1 Y14 Y6, EGFR Y1197, EGFR Y1092, InsR Y1175 Y1179, CDK2 Y15, ARHGAP27 Y28, Hrs Y216, InsR Y1179/Y1175, HSPD1 Y243, ANXA2 Y24, HSPD1 Y385, Shc1 Y313	GO
Cytosol	108	Lyn Y173, Dok1 Y450, BCAR1 Y238, FBP1 Y216, Yes Y220, Fgr Y197, RPL13A Y137, p38-alpha Y182, Crk Y251, afadin Y1285, PIK3R1 Y197, Dok1 Y408, BCAR1 Y291, SHP-2 Y62, BCAR1 Y556, FAK Y577 T575, Dok1 Y361, vinculin Y822, BCAR1 Y271, SEC14L4 Y36, FBP1 Y265, PLCG1 Y771, CAV1 Y14 Y6, eEF1A1 Y177, IRS2 Y649, GRF-1 Y1087, STAT3 Y686, BCAR1 Y414, DLG1 Y783, Yes Y192, FAK Y861, InsR Y1175 Y1179, BCAR1 Y391, GOT1 Y264, vinculin Y692, UGDH Y108, CDK2 Y15, Abl Y393, GSK3B Y216 S219, afadin Y1230, CTNND1 Y904, talin 1 Y1116, BCAR1 Y253, Yes Y424, CTNNB1 Y654, PGAM2 Y92, CrkL Y198, PGK1 Y196, ALDOB Y204, LHPP Y159, SCAP2 Y260, FAK Y397, FAK Y576, WASP Y293, talin 1 Y26, CrkL Y132, p38-alpha Y182 T180, Hrs Y216, Lyn Y376, OTC Y317, JAK2 Y570, CAR2 Y114, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, SEC14L4 Y36, GSK3B Y216, FBP1 Y245, InsR Y1179/Y1175, plectin 1 Y288, IRS2 Y814, HSPD1 Y243, SHMT1 Y67, IDH1 Y391, CTNND1 Y96, TARS Y297, GRF-1 Y1105, IRS1 Y983, IRS1 Y460, IRS1 Y935, ERK2 Y185, PIK3R1 Y310, GPX1 Y147, GOT1 Y71, HSP90A Y285, IRS2 Y671, SHMT1 Y28, FASN Y1248, HPD Y232, Nck1 Y105, ERK1 Y205, ACLY Y672, HSPD1 Y385, PGM1 Y353, GNMT Y22, CAT Y231, CAT Y84, LDHA Y239, Shc1 Y313, VCP Y173, PRDX6 Y89, GNMT Y34, SHP-2 Y584, PTPNA Y141, GNMT Y221, TGM2 Y369, CALM1 Y100, HPD Y221, SAHH Y193	GO
Peroxisome	10	UOX Y230, SCP2 Y197, ISOC1 Y159, ACOX1 Y629, IDH1 Y391, ACAD11 Y323, UOX Y288, CAT Y231, CAT Y84, PRDX6 Y89	GO

Plasma Membrane	36	CLDN2 Y194/Y195, TTYH2 Y494, EGFR Y1172, CLDN3 Y197, EphA2 Y589, FAK Y577 T575, PECAM-1 Y702, CEACAM1 Y515, CAV1 Y14 Y6, EGFR Y1197, SLC22A1 Y545, HLAC Y344, EphB4 Y774, EGFR Y1092, FAK Y861, InsR Y1175 Y1179, HER3 Y1325, EphA2 Y773, H2-K1 Y342, FAK Y397, FAK Y576, OTC Y317, Sept2 Y17, ERK2 Y185 T188/T183, GOT2 Y96, InsR Y1179/Y1175, plectin 1 Y288, HSPD1 Y243, PEBP1 Y181, PHB Y249, ERK2 Y185, HSP90A Y285, GOT2 Y284, HSPD1 Y385, PIPNA Y141, CALM1 Y100	GO
Cytoskeleton related	42	PARD3 Y1076, CTNNA1 Y177, PARD3 Y1123, p38-alpha Y182, CLTC Y899, SHP-2 Y62, FAK Y577 T575, N-WASP Y253, vinculin Y822, KIF13B Y1722, CTNNA1 Y619, GRF-1 Y1087, DLG1 Y783, FAK Y861, vinculin Y692, CGN Y229, talin 2 Y1665, Abl Y393, talin 1 Y1116, CTNNB1 Y654, PXN Y118, Pyk2 Y579, FAK Y397, FAK Y576, WASP Y293, talin 1 Y26, Pyk2 Y579 Y580, p38-alpha Y182 T180, JAK2 Y570, CLTC Y1477, Sept2 Y17, CLTC Y1487, plectin 1 Y288, Pyk2 Y807, SHIP-2 Y1136, GRF-1 Y1105, ANXA2 Y24, K8 Y210, K85 Y236, SHP-2 Y584, K18 Y14, CALM1 Y100	GO
Membrane organization and vesicle-mediated transport	9	CLTC Y899, CAV1 Y14 Y6, DLG1 Y783, CTNNB1 Y654, ITSN2 Y922, ARHGAP27 Y28, WASP Y293, CLTC Y1477, CLTC Y1487	GO
Cell death	13	Shb Y432, EphA2 Y589, Shb Y342, HIPK3 Y359, SHF Y64, CTNNB1 Y654, EphA2 Y773, JAK2 Y570, VDAC1 Y195, GPX1 Y147, K8 Y210, VCP Y173, K18 Y14	GO, SwissProt
Ion transport	6	TTYH2 Y494, ATP1A1 Y260, CAV1 Y14 Y6, SLC22A1 Y545, CDK2 Y15, VDAC1 Y195	GO, SwissProt
PDZ	13	PARD3 Y1076, PARD3 Y1123, ZO1 Y1145, DLG3 Y705, afadin Y1285, Erbin Y1097, MAGI1 Y361, DLG1 Y783, ZO1 Y1360, afadin Y1230, ZO2 Y486, ZO1 Y1190, ZO1 Y1066	PFAM
S/T kinase	15	p38-alpha Y182, PRP4 Y849, DYRK4 Y344, HIPK3 Y359, CDK2 Y15, GSK3B Y216 S219, HIPK1 Y352, CKDL5 Y171, p38-alpha Y182 T180, DYRK1B Y273, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, ERK2 Y185, ERK1 Y205	PFAM
Y kinase	29	Lyn Y173, AXL Y697, TEC Y415, EGFR Y1172, Yes Y220, Fgr Y197, EphA2 Y589, FAK Y577 T575, EGFR Y1197, EphB4 Y774, EGFR Y1092, Yes Y192, FAK Y861, InsR Y1175 Y1179, Abl Y393, Yes Y424, HER3 Y1325, Met Y1001, EphA2 Y773, Pyk2 Y579, FAK Y397, FAK Y576, Pyk2 Y579 Y580, Lyn Y376, Fer Y715, JAK2 Y570, InsR Y1179/Y1175, Fer Y402, Pyk2 Y807	PFAM
SH3	26	Lyn Y173, BCAR1 Y238, TEC Y415, Yes Y220, Fgr Y197, Crk Y251, DLG3 Y705, BCAR1	PFAM

		Y291, BCAR1 Y556, BCAR1 Y271, PLCG1 Y771, BCAR1 Y414, DLG1 Y783, Yes Y192, BCAR1 Y391, Abl Y393, BCAR1 Y253, Yes Y424, ITSN2 Y922, CrkL Y198, SCAP2 Y260, CrkL Y132, Lyn Y376, ARHGAP42 Y371, ARHGAP42 Y342, Nck1 Y105	
Variant SH3	10	ZO1 Y1145, Crk Y251, CASKIN2 Y253, ZO1 Y1360, ITSN2 Y922, CrkL Y198, ZO2 Y486, CrkL Y132, ZO1 Y1190, ZO1 Y1066	PFAM
SH2	35	Lyn Y173, SHEP1 Y178, TEC Y415, Yes Y220, Fgr Y197, Crk Y251, tensin 1 Y1558, Shb Y432, PIK3R1 Y197, Shb Y342, SHP-2 Y62, tensin 1 Y1480, TENC1 Y705, PLCG1 Y771, tensin 1 Y1593, STAT3 Y686, Yes Y192, Abl Y393, SHF Y64, Yes Y424, tensin 1 Y537, CrkL Y198, CrkL Y132, BCAR3 Y424, Lyn Y376, Fer Y715, Fer Y402, TENC1 Y770, SHIP-2 Y1136, TENC1 Y483, PIK3R1 Y310, tensin 3 Y354 S332/Y333/S337/T345, Nck1 Y105, Shc1 Y313, SHP-2 Y584	PFAM
SAM	6	EphA2 Y589, EphB4 Y774, CASKIN2 Y253, EphA2 Y773, ANKS1A Y472, SHIP-2 Y1136	PFAM
PH	16	Dok1 Y450, Dok1 Y408, Dok1 Y361, PLCG1 Y771, PLEKHG1 Y1051, IRS2 Y649, GAB2 Y290, ITSN2 Y922, ARHGAP27 Y28, SCAP2 Y260, IRS2 Y814, AFAP1L2 Y357, IRS1 Y983, IRS1 Y460, IRS1 Y935, IRS2 Y671	PFAM
FERM domain	11	FAK Y577 T575, FAK Y861, talin 2 Y1665, talin 1 Y1116, Pyk2 Y579, FAK Y397, FAK Y576, talin 1 Y26, Pyk2 Y579 Y580, JAK2 Y570, Pyk2 Y807	Interpro
Adherens junction	32	PARD3 Y1076, CTNNA1 Y177, PARD3 Y1123, EGFR Y1172, Yes Y220, ZO1 Y1145, afadin Y1285, N-WASP Y253, vinculin Y822, CTNNA1 Y619, EGFR Y1197, EGFR Y1092, Yes Y192, InsR Y1175 Y1179, ZO1 Y1360, vinculin Y692, afadin Y1230, CTNND1 Y904, Yes Y424, CTNNB1 Y654, Met Y1001, WASP Y293, Fer Y715, ERK2 Y185 T188/T183, ZO1 Y1190, ERK1 Y205 T203/T208, InsR Y1179/Y1175, ZO1 Y1066, Fer Y402, CTNND1 Y96, ERK2 Y185, ERK1 Y205	KEGG
Leukocyte transendothelial migration	37	CLDN2 Y194/Y195, BCAR1 Y238, CTNNA1 Y177, F11R Y281, p38-alpha Y182, CLDN3 Y197, afadin Y1285, PIK3R1 Y197, BCAR1 Y291, SHP-2 Y62, BCAR1 Y556, FAK Y577 T575, PECAM-1 Y702, vinculin Y822, BCAR1 Y271, PLCG1 Y771, CTNNA1 Y619, GRF-1 Y1087, BCAR1 Y414, FAK Y861, BCAR1 Y391, vinculin Y692, afadin Y1230, CTNND1 Y904, BCAR1 Y253, CTNNB1 Y654, PXN Y118, Pyk2 Y579, FAK Y397, FAK Y576, Pyk2 Y579 Y580, p38-alpha Y182 T180, Pyk2 Y807, CTNND1 Y96, GRF-1 Y1105, PIK3R1 Y310, SHP-2 Y584	KEGG
ErbB signaling pathway	23	EGFR Y1172, Crk Y251, PIK3R1 Y197, FAK Y577 T575, PLCG1 Y771, EGFR Y1197, EGFR Y1092, FAK Y861, Abl Y393, GSK3B Y216 S219, HER3 Y1325, CrkL Y198, FAK Y397, FAK Y576, CrkL Y132, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B	KEGG

		Y216, ERK2 Y185, PIK3R1 Y310, Nck1 Y105, ERK1 Y205, Shc1 Y313	
Chemokine signaling pathway	36	Lyn Y173, PARD3 Y1076, BCAR1 Y238, PARD3 Y1123, Fgr Y197, Crk Y251, PIK3R1 Y197, BCAR1 Y291, BCAR1 Y556, FAK Y577 T575, N-WASP Y253, BCAR1 Y271, STAT3 Y686, BCAR1 Y414, FAK Y861, BCAR1 Y391, GSK3B Y216 S219, BCAR1 Y253, CrkL Y198, PXN Y118, Pyk2 Y579, FAK Y397, FAK Y576, WASP Y293, Pyk2 Y579 Y580, CrkL Y132, Lyn Y376, JAK2 Y570, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, Pyk2 Y807, ERK2 Y185, PIK3R1 Y310, ERK1 Y205, Shc1 Y313	KEGG
Focal adhesion	37	BCAR1 Y238, EGFR Y1172, Crk Y251, PIK3R1 Y197, BCAR1 Y291, BCAR1 Y556, FAK Y577 T575, vinculin Y822, BCAR1 Y271, CAV1 Y14 Y6, EGFR Y1197, GRF-1 Y1087, BCAR1 Y414, EGFR Y1092, FAK Y861, BCAR1 Y391, vinculin Y692, talin 2 Y1665, GSK3B Y216 S219, talin 1 Y1116, BCAR1 Y253, CTNNA1 Y654, CrkL Y198, Met Y1001, PXN Y118, FAK Y397, FAK Y576, talin 1 Y26, CrkL Y132, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, GRF-1 Y1105, ERK2 Y185, PIK3R1 Y310, ERK1 Y205, Shc1 Y313	KEGG
Neurotrophin signaling pathway	25	p38-alpha Y182, Crk Y251, PIK3R1 Y197, SHP-2 Y62, PLCG1 Y771, IRS2 Y649, Abl Y393, GSK3B Y216 S219, CrkL Y198, CrkL Y132, p38-alpha Y182 T180, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, IRS2 Y814, IRS1 Y983, IRS1 Y460, IRS1 Y935, ERK2 Y185, PIK3R1 Y310, IRS2 Y671, ERK1 Y205, Shc1 Y313, SHP-2 Y584, CALM1 Y100	KEGG
Arginine and proline metabolism	19	CPS1 Y140, GOT1 Y264, ARG1 Y218, GLUD1 Y135, CPS1 Y1450, GLUD1 Y512, ARG1 Y197, OTC Y317, GOT2 Y96, CPS1 Y590, ASS1 Y29, GOT1 Y71, ASS1 Y133, ASS1 Y322, GOT2 Y284, ARG1 Y188, CPS1 Y162, GLUL Y336, ARG1 Y265	KEGG
Glycolysis / Gluconeogenesis	12	FBP1 Y216, FBP1 Y265, GAPDH Y328, PGAM2 Y92, PGK1 Y196, ALDOB Y204, FBP1 Y245, GAPDH Y316, PGM1 Y353, LDHA Y239, ENO1 Y44, ENO1 Y25	KEGG
Insulin signaling pathway	25	FBP1 Y216, Crk Y251, PIK3R1 Y197, FBP1 Y265, IRS2 Y649, InsR Y1175 Y1179, GSK3B Y216 S219, CrkL Y198, CrkL Y132, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, FBP1 Y245, InsR Y1179/Y1175, IRS2 Y814, IRS1 Y983, IRS1 Y460, IRS1 Y935, ERK2 Y185, PIK3R1 Y310, IRS2 Y671, FASN Y1248, ERK1 Y205, Shc1 Y313, CALM1 Y100	KEGG
Fc gamma R-mediated phagocytosis	15	Lyn Y173, Crk Y251, PIK3R1 Y197, N-WASP Y253, PLCG1 Y771, GAB2 Y290, CrkL Y198, WASP Y293, CrkL Y132, Lyn Y376, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, ERK2 Y185, PIK3R1 Y310, ERK1 Y205	KEGG
Tight junction	20	PARD3 Y1076, CLDN2 Y194/Y195, CTNNA1 Y177, PARD3 Y1123, Yes Y220, F11R	KEGG

		Y281, ZO1 Y1145, CLDN3 Y197, afadin Y1285, CTNNA1 Y619, MAGI1 Y361, Yes Y192, ZO1 Y1360, CGN Y229, afadin Y1230, Yes Y424, CTNNB1 Y654, ZO2 Y486, ZO1 Y1190, ZO1 Y1066	
Alanine, aspartate and glutamate metabolism	14	CPS1 Y140, GOT1 Y264, GLUD1 Y135, CPS1 Y1450, GLUD1 Y512, GOT2 Y96, CPS1 Y590, ASS1 Y29, GOT1 Y71, ASS1 Y133, ASS1 Y322, GOT2 Y284, CPS1 Y162, GLUL Y336	KEGG
Nitrogen metabolism	11	CPS1 Y140, GLUD1 Y135, CPS1 Y1450, GLUD1 Y512, CTH Y59, CAR2 Y114, CPS1 Y590, CAR3 Y74, CPS1 Y162, GLUL Y336, CTH Y113	KEGG
Signal transduction	20	Lyn Y173, SHEP1 Y178, EGFR Y1172, Crk Y251, Shb Y432, Shb Y342, CEACAM1 Y515, PLCG1 Y771, EGFR Y1197, EGFR Y1092, HER3 Y1325, Met Y1001, Lyn Y376, Fer Y715, JAK2 Y570, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, Fer Y402, ERK2 Y185, ERK1 Y205	GO
Metabolic process	29	HADHA Y724, CPS1 Y140, ACAT1 Y328, PCBD1 Y70, ARG1 Y218, GAPDH Y328, GLUD1 Y135, CPS1 Y1450, GLUD1 Y512, PGAM2 Y92, ARG1 Y197, CTH Y59, CAR2 Y114, CPS1 Y590, IDH1 Y391, GPX1 Y147, GAPDH Y316, PAH Y166, ARG1 Y188, CPS1 Y162, PGM1 Y353, CTH Y113, LDHA Y239, PRDX6 Y89, ARG1 Y265, TGM2 Y369, CYP2E1 Y426, ENO1 Y44, CYB5A Y11	GO
Lipid localization	6	CAV1 Y14 Y6, ATP11C Y126, SCP2 Y197, GOT2 Y96, vigilin Y437, GOT2 Y284	GO
Lipid transport	6	ATP11C Y126, SCP2 Y197, GOT2 Y96, vigilin Y437, GOT2 Y284, ACBP Y29	GO, SwissProt, literature
Glycerolipid metabolic process	8	PIK3R1 Y197, SHP-2 Y62, CAV1 Y14 Y6, PIK3R1 Y310, GPX1 Y147, CAT Y231, CAT Y84, SHP-2 Y584	GO
Lipid metabolism	11	HADHA Y724, ACAT1 Y328, ACAA2 Y198, ACSM3 Y51, ACOX1 Y629, vigilin Y437, ACLY Y672, PRDX6 Y89, ACSL5 Y69, ACBP Y29, CYB5A Y11	KEGG, SwissProt, Literature
Fatty acid metabolism	9	HADHA Y724, ACAT1 Y328, ACAA2 Y198, ACOX1 Y629, ACLY Y672, PRDX6 Y89, ACSL5 Y69, ACBP Y29, CYB5A Y11	KEGG, Literature
Glycine, serine, threonine	8	BHMT Y289, CTH Y59, SHMT1 Y67, SHMT1 Y28, GNMT Y22, CTH Y113, GNMT Y34, GNMT Y221	KEGG

metabolism			
Cysteine and methionine metabolism	9	GOT1 Y264, BHMT Y289, CTH Y59, GOT2 Y96, GOT1 Y71, GOT2 Y284, CTH Y113, LDHA Y239, SAHH Y193	KEGG
Phenylalanine metabolism	8	GOT1 Y264, GOT2 Y96, GOT1 Y71, HPD Y232, GOT2 Y284, PAH Y166, PRDX6 Y89, HPD Y221	KEGG
Tryptophan metabolism	5	HADHA Y724, ACAT1 Y328, INMT Y87, CAT Y231, CAT Y84	KEGG
Pathways in cancer	28	FH Y488, CTNNA1 Y177, EGFR Y1172, Crk Y251, PIK3R1 Y197, FAK Y577 T575, PLCG1 Y771, CTNNA1 Y619, EGFR Y1197, STAT3 Y686, EGFR Y1092, FAK Y861, CDK2 Y15, Abl Y393, GSK3B Y216 S219, CTNNB1 Y654, CrkL Y198, Met Y1001, FAK Y397, FAK Y576, CrkL Y132, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, ERK2 Y185, PIK3R1 Y310, HSP90A Y285, ERK1 Y205	KEGG
Fc epsilon RI signaling pathway	12	Lyn Y173, p38-alpha Y182, PIK3R1 Y197, PLCG1 Y771, GAB2 Y290, p38-alpha Y182 T180, Lyn Y376, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, ERK2 Y185, PIK3R1 Y310, ERK1 Y205	KEGG
Regulation of actin cytoskeleton	28	BCAR1 Y238, EGFR Y1172, Crk Y251, PIK3R1 Y197, BCAR1 Y291, BCAR1 Y556, FAK Y577 T575, N-WASP Y253, vinculin Y822, BCAR1 Y271, EGFR Y1197, BCAR1 Y414, EGFR Y1092, FAK Y861, BCAR1 Y391, vinculin Y692, BCAR1 Y253, CrkL Y198, PXN Y118, FAK Y397, FAK Y576, WASP Y293, CrkL Y132, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, ERK2 Y185, PIK3R1 Y310, ERK1 Y205	KEGG
Tyrosine metabolism	7	GOT1 Y264, HGD Y40, GOT2 Y96, GOT1 Y71, HPD Y232, GOT2 Y284, HPD Y221	KEGG
Oxidation reduction	29	HADHA Y724, UGDH Y108, GAPDH Y328, GLUD1 Y135, GLUD1 Y512, UOX Y230, HGD Y40, ACOX1 Y629, ALDH1L1 Y848, VDAC1 Y195, IDH1 Y391, ACAD11 Y323, UOX Y288, GPX1 Y147, GAPDH Y316, FASN Y1248, HPD Y232, PAH Y166, ALDH6A1 Y268, ALDH1L1 Y892, CAT Y231, CAT Y84, LDHA Y239, PRDX6 Y89, CYP2E1 Y426, HPD Y221, SAHH Y193, ALDH1A7 Y484, CYB5A Y11	GO, SwissProt, Literature
GTPase-related	11	SHEP1 Y178, N-WASP Y253, PLEKHG1 Y1051, GRF-1 Y1087, ITS2N2 Y922, ARHGAP27 Y28, WASP Y293, BCAR3 Y424, ARHGAP42 Y371, ARHGAP42 Y342, GRF-1 Y1105	GO, PFAM
Protein biosynthesis	5	RPL13A Y137, eEF1A1 Y141, eEF1A1 Y177, EIF1B Y30, TARS Y297	GO, SwissProt
Cytoskeletal	21	BCAR1 Y238, BCAR1 Y291, BCAR1 Y556, FAK Y577 T575, N-WASP Y253, BCAR1	GO

organization		Y271, BCAR1 Y414, DLG1 Y783, FAK Y861, BCAR1 Y391, talin 2 Y1665, Abl Y393, talin 1 Y1116, BCAR1 Y253, PXN Y118, FAK Y397, FAK Y576, WASP Y293, talin 1 Y26, Nck1 Y105, Shc1 Y313	
Response to oxidatitive stress	5	IDH1 Y391, GPX1 Y147, CAT Y231, CAT Y84, PRDX6 Y89	GO
Catalytic Site S/T Kinase	15	p38-alpha Y182, PRP4 Y849, DYRK4 Y344, HIPK3 Y359, CDK2 Y15, GSK3B Y216 S219, HIPK1 Y352, CKDL5 Y171, p38-alpha Y182 T180, DYRK1B Y273, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, ERK2 Y185, ERK1 Y205	PTMScout
Catalytic Site Y Kinase	15	AXL Y697, TEC Y415, FAK Y577 T575, EphB4 Y774, InsR Y1175 Y1179, Abl Y393, Yes Y424, EphA2 Y773, Pyk2 Y579, FAK Y576, Pyk2 Y579 Y580, Lyn Y376, Fer Y715, JAK2 Y570, InsR Y1179/Y1175	PTMScout
PTP1b interactors	39	Dok1 Y450, BCAR1 Y238, EGFR Y1172, ZO1 Y1145, ST5 Y498, Dok1 Y408, BCAR1 Y291, BCAR1 Y556, FAK Y577 T575, Dok1 Y361, BCAR1 Y271, PLCG1 Y771, CAV1 Y14 Y6, EGFR Y1197, BCAR1 Y414, EGFR Y1092, FAK Y861, InsR Y1175 Y1179, BCAR1 Y391, ZO1 Y1360, CTNND1 Y904, BCAR1 Y253, PXN Y118, FAK Y397, FAK Y576, JAK2 Y570, ERK2 Y185 T188/T183, ZO1 Y1190, ERK1 Y205 T203/T208, InsR Y1179/Y1175, ZO1 Y1066, CTNND1 Y96, SHIP-2 Y1136, IRS1 Y983, IRS1 Y460, IRS1 Y935, ERK2 Y185, LPP Y318, ERK1 Y205	MINT & Ren et al.
PTP1b substrate sites	7	PLCG1 Y771, CAV1 Y14 Y6, EGFR Y1197, InsR Y1175 Y1179, InsR Y1179/Y1175, SHIP-2 Y1136, LPP Y318	Ren et al.
Insulin-sensitive pYs in adipocytes	33	PARD3 Y1076, p38-alpha Y182, DLG3 Y705, SHP-2 Y62, Dok1 Y361, N-WASP Y253, GPRC5C Y386, IRS2 Y649, BCAR1 Y414, PTPRA Y825, talin 1 Y1116, BCAR1 Y253, DDX3X Y104, Met Y1001, PXN Y118, FAK Y397, CrkL Y132, ANKS1A Y472, Sgk269 Y632, IRS2 Y814, IRS1 Y983, IRS1 Y460, ANXA2 Y24, IRS1 Y935, ERK2 Y185, vigilin Y437, Nck1 Y105, ERK1 Y205, Shc1 Y313, SHP-2 Y584, ACBP Y29, ENO1 Y44, CALM1 Y100	Schmelzle et al.

**Table S4: Enrichment analysis of genotype-dependent phosphosites**

<b>P<sub>raw</sub></b>	<b>NES</b>	<b>Category Label</b>	<b>N</b>	<b>Category Membership</b>	<b>Source</b>
<2E-05**	-3.47	<b>Metabolic process</b>	29	<i>HADHA Y724, CPS1 Y140, ACAT1 Y328, PCBD1 Y70, ARG1 Y218, GAPDH Y328, GLUD1 Y135, CPS1 Y1450, GLUD1 Y512, PGAM2 Y92, ARG1 Y197, CTH Y59, CAR2 Y114, CPS1 Y590, IDH1 Y391, GPX1 Y147, GAPDH Y316, PAH Y166*, ARG1 Y188, CPS1 Y162, PGM1 Y353, CTH Y113, LDHA Y239, PRDX6 Y89, ARG1 Y265, TGM2 Y369, CYP2E1 Y426, ENO1 Y44, CYB5A Y11</i>	GO
<2E-05**	-3.58	<b>Oxidation reduction</b>	29	<i>HADHA Y724, UGDH Y108, GAPDH Y328, GLUD1 Y135, GLUD1 Y512, UOX Y230, HGD Y40, ACOX1 Y629, ALDH1L1 Y848, VDAC1 Y195, IDH1 Y391, ACAD11 Y323, UOX Y288, GPX1 Y147*, GAPDH Y316, FASN Y1248, HPD Y232, PAH Y166, ALDH6A1 Y268, ALDH1L1 Y892, CAT Y231, CAT Y84, LDHA Y239, PRDX6 Y89, CYP2E1 Y426, HPD Y221, SAHH Y193, ALDH1A7 Y484, CYB5A Y11</i>	GO, SwissProt, Literature
<2E-05**	-3.10	<b>Endoplasmic Reticulum</b>	18	<i>CAVI Y14 Y6, ALDOB Y204, HSPD1 Y243, PEBP1 Y181, ASS1 Y29, ASS1 Y133, HPD Y232*, ASS1 Y322, HSPD1 Y385, GLUL Y336, CAT Y231, CAT Y84, VCP Y173, ACSL5 Y69, CYP2E1 Y426, CALM1 Y100, HPD Y221, CYB5A Y11,</i>	GO
<2E-05**	-3.66	<b>Cytosol</b>	108	<i>Lyn Y173, Dok1 Y450, BCAR1 Y238, FBP1 Y216, Yes Y220, Fgr Y197, RPL13A Y137, p38-alpha Y182, Crk Y251, afadin Y1285, PIK3R1 Y197, Dok1 Y408, BCAR1 Y291, SHP-2 Y62, BCAR1 Y556, FAK Y577 T575, Dok1 Y361, vinculin Y822, BCAR1 Y271, SEC14L4 Y36, FBP1 Y265, PLCG1 Y771, CAVI Y14 Y6, eEF1A1 Y177, IRS2 Y649, GRF-1 Y1087, STAT3 Y686, BCAR1 Y414, DLG1 Y783, Yes Y192, FAK Y861, InsR Y1175 Y1179, BCAR1 Y391, GOT1 Y264, vinculin Y692, UGDH Y108, CDK2 Y15, Abl Y393, GSK3B Y216 S219, afadin Y1230, CTNND1 Y904, talin 1 Y1116, BCAR1 Y253, Yes Y424, CTNNB1 Y654, PGAM2 Y92, CrkL Y198, PGK1 Y196, ALDOB Y204, LHPP Y159, SCAP2 Y260, FAK Y397, FAK Y576, WASP Y293, talin 1 Y26, CrkL Y132, p38-alpha Y182 T180, Hrs Y216, Lyn Y376, OTC Y317, JAK2 Y570, CAR2 Y114, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208*, SEC14L4 Y36, GSK3B Y216, FBP1 Y245, InsR Y1179/Y1175, plectin 1 Y288, IRS2 Y814, HSPD1 Y243, SHMT1</i>	GO



				Y67, IDH1 Y391, CTNND1 Y96, TARS Y297, GRF-1 Y1105, IRS1 Y983, IRS1 Y460, IRS1 Y935, ERK2 Y185, PIK3R1 Y310, GPX1 Y147, GOT1 Y71, HSP90A Y285, IRS2 Y671, SHMT1 Y28, FASN Y1248, HPD Y232, Nck1 Y105, ERK1 Y205, ACLY Y672, HSPD1 Y385, PGM1 Y353, GNMT Y22, CAT Y231, CAT Y84, LDHA Y239, Shc1 Y313, VCP Y173, PRDX6 Y89, GNMT Y34, SHP-2 Y584, PITPNA Y141, GNMT Y221, TGM2 Y369, CALM1 Y100, HPD Y221, SAHH Y193	
3.2E-05**	-2.41	<b>Insulin signaling pathway</b>	25	<i>FBP1 Y216, Crk Y251, PIK3R1 Y197, FBP1 Y265, IRS2 Y649, InsR Y1175 Y1179, GSK3B Y216 S219, CrkL Y198, CrkL Y132, ERK2 Y185 T188/T183*, ERK1 Y205 T203/T208, GSK3B Y216, FBP1 Y245, InsR Y1179/Y1175, IRS2 Y814, IRS1 Y983, IRS1 Y460, IRS1 Y935, ERK2 Y185, PIK3R1 Y310, IRS2 Y671, FASN Y1248, ERK1 Y205, Shc1 Y313, CALM1 Y100</i>	KEGG
3.2E-05**	-2.40	<b>Lipid metabolism</b>	11	<i>HADHA Y724, ACAT1 Y328, ACAA2 Y198, ACSM3 Y51, ACOX1 Y629, vigilin Y437*, ACLY Y672, PRDX6 Y89, ACSL5 Y69, ACBP Y29, CYB5A Y11</i>	KEGG, SwissProt, Literature
1.4E-04**	2.45	<b>Tight junction</b>	20	<i>PARD3 Y1076, CLDN2 Y194/Y195, CTNNA1 Y177, PARD3 Y1123, Yes Y220, F11R Y281, ZO1 Y1145, CLDN3 Y197, afadin Y1285*, CTNNA1 Y619, MAGI1 Y361, Yes Y192, ZO1 Y1360, CGN Y229, afadin Y1230, Yes Y424, CTNNB1 Y654, ZO2 Y486, ZO1 Y1190, ZO1 Y1066</i>	KEGG
2.3E-04*	-2.30	<b>Fatty acid metabolism</b>	9	<i>HADHA Y724, ACAT1 Y328, ACAA2 Y198, ACOX1 Y629, ACLY Y672*, PRDX6 Y89, ACSL5 Y69, ACBP Y29, CYB5A Y11</i>	KEGG, Literature
4.5E-04*	-2.26	<b>Neurotrophin signaling pathway</b>	25	<i>p38-alpha Y182, Crk Y251, PIK3R1 Y197, SHP-2 Y62, PLCG1 Y771, IRS2 Y649, Abl Y393, GSK3B Y216 S219, CrkL Y198, CrkL Y132, p38-alpha Y182 T180, ERK2 Y185 T188/T183, ERK1 Y205 T203/T208, GSK3B Y216, IRS2 Y814, IRS1 Y983*, IRS1 Y460, IRS1 Y935, ERK2 Y185, PIK3R1 Y310, IRS2 Y671, ERK1 Y205, Shc1 Y313, SHP-2 Y584, CALM1 Y100</i>	KEGG
4.5E-04*	-2.27	<b>Arginine and proline metabolism</b>	19	<i>CPS1 Y140, GOT1 Y264, ARG1 Y218, GLUD1 Y135, CPS1 Y1450, GLUD1 Y512, ARG1 Y197, OTC Y317, GOT2 Y96, CPS1 Y590, ASS1 Y29, GOT1 Y71*, ASS1 Y133, ASS1 Y322, GOT2 Y284, ARG1 Y188, CPS1 Y162, GLUL Y336, ARG1 Y265</i>	KEGG
5.2E-04*	-2.25	<b>Mitochondria</b>	35	<i>Lyn Y173, PC Y118, HADHA Y724, FH Y488, CPS1 Y140, HSPE1 Y76, SLC25A5 Y191, SLC25A5 Y81, ACAT1 Y328, FH Y462, GLUD1</i>	GO

				<i>Y135, CPS1 Y1450, GLUD1 Y512, ACAA2 Y198, ACSM3 Y51, Lyn Y376, OTC Y317, NIPSNAP1 Y148, GOT2 Y96, NIPSNAP1 Y261, CPS1 Y590, VDAC1 Y195, HSPD1 Y243, PEBP1 Y181, ASS1 Y29, PHB Y249, ASS1 Y133, ASS1 Y322*, GOT2 Y284, CPS1 Y162, HSPD1 Y385, CAT Y231, CAT Y84, ACCL5 Y69, CYB5A Y11</i>	
6.5E-04*	-2.24	<b>Phenylalanine metabolism</b>	8	<i>GOT1 Y264, GOT2 Y96, GOT1 Y71*, HPD Y232, GOT2 Y284, PAH Y166, PRDX6 Y89, HPD Y221</i>	KEGG
7.1E-04*	-2.22	<b>Glycolysis / Gluconeogenesis</b>	12	<i>FBP1 Y216, FBP1 Y265, GAPDH Y328, PGAM2 Y92, PGK1 Y196, ALDOB Y204, FBP1 Y245, GAPDH Y316, PGM1 Y353*, LDHA Y239, ENO1 Y44, ENO1 Y25</i>	KEGG
1.1E-03^	-2.16	<b>Golgi apparatus</b>	17	<i>Lyn Y173, ZO1 Y1145, DYRK4 Y344, CAV1 Y14 Y6, ZO1 Y1360, Lyn Y376, ZO1 Y1190, HSPD1 Y243, PEBP1 Y181, ZO1 Y1066, FASN Y1248*, HPD Y232, HSPD1 Y385, GLUL Y336, CAT Y231, CAT Y84, HPD Y221</i>	GO
1.1E-03^	-2.16	<b>Insulin-sensitive pYs in adipocytes</b>	33	<i>PROSC Y69, Lyn y173, PARD3 Y1076, Dok1 Y450, CLDN2 Y194/Y195, HADHA Y274, FBP1 Y216, FH Y488, TEC Y415, PARD3 Y1123, CPS1 Y140, EGFR Y1172, Yes Y220, RPL13A Y137, p38-alpha Y182, CLTC Y899, Crk Y251, afadin Y1285, tensin 1 Y1558, PRP4 Y849, Shb Y432, Eef1a1 y141, DYRK4 Y344, PIK3R1 Y197, Dok1 Y408, ATP1A1 Y260*, HBD Y42, CARKD Y81, BCAR1 Y556, FAK Y577 T575, tensin 1 Y1480, PECAM-1 Y702, TENC1 Y705</i>	Schmelzle et al.
1.8E-03^	-2.09	<b>Cysteine and methionine metabolism</b>	9	<i>GOT1 Y264, BHMT Y289, CTH Y59, GOT2 Y96, GOT1 Y71*, GOT2 Y284, CTH Y113, LDHA Y239, SAHH Y193</i>	KEGG

NES stands for normalized enrichment scores as described in Methods. \*\* = FDR = .01, \* = FDR = .05, ^ = FDR = .1. NES > 0 indicates that phosphorylation on sites in pathway significantly decrease with PTP1b deletion, while NES < 0 indicates that phosphorylation on sites in the pathway are hyperphosphorylated upon PTP1b deletion. The phosphosites in each category membership are ordered from most PTP1b-dependent decreased phosphorylation to most PTP1b-dependent increased phosphorylation. Those phosphosites that contributed most to the enrichment (compose the “leading edge”) appear in regular font, while the other sites in that category are italicized.

**Table S5: Enrichment of diet-dependent phosphosites**

<b>P<sub>raw</sub></b>	<b>NES</b>	<b>Category Label</b>	<b>N</b>	<b>Category Membership</b>	<b>Source</b>
2.2E-04**	2.28	<b>Mitochondria</b>	22	HSPE1 Y76, NIPSNAP1 Y261, SLC25A5 Y191, GOT2 Y96, GLUD1 Y512, CAT Y231*, <i>GLUD1 Y135, PHB Y249, ACAT1 Y328, CAT Y84, PC Y118, CPS1 Y162, Lyn Y173, ACAA2 Y198, HSPD1 Y243, ACSL5 Y69, CPS1 Y1450, CYB5A Y11, ASS1 Y322, HSPD1 Y385, Lyn Y376, SLC25A5 Y81</i>	GO

NES stands for normalized enrichment scores. \*\* = FDR = .01, \* = FDR = .05, ^ = FDR = .1. NES > 0 indicates that phosphorylation on sites in pathway significantly increase upon HFD, while NES < 0 indicates that phosphorylation on sites in the pathway have reduced phosphorylation under HFD. The phosphosites in each category membership are ordered from most positively HFD-dependent to most negatively HFD-dependent phosphorylation. Those phosphosites that contributed most to the enrichment (compose the “leading edge”) appear in regular font, while the other sites in that category are italicized.

**Table S6: Quantification of hepatic free fatty acids**

<b>Absolute quantification of hepatic free fatty acids (pmol FFA / mg liver tissue)</b>				
	<b>NC</b>		<b>HFD</b>	
	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>
<b>C16:3</b>	0.0537 +/- 0.00785 (n = 7)	0.0626 +/- 0.0162 (n = 3)	0.0515 +/- 0.00988 (n = 10)	0.044 +/- 0.0127 (n = 9)
<b>C16:2</b>	0.135 +/- 0.017 (n = 7)	0.134 +/- 0.0253 (n = 3)	0.442 +/- 0.0556 (n = 11)**	0.64 +/- 0.212 (n = 10)
<b>C16:1</b>	3.35 +/- 0.349 (n = 9)	3.11 +/- 0.427 (n = 7)	8.4 +/- 1.27 (n = 19)*	8.32 +/- 1.38 (n = 17)
<b>C16:0</b>	43.6 +/- 2.89 (n = 9)	43.2 +/- 2.04 (n = 7)	76.4 +/- 15.2 (n = 19)	59.3 +/- 4.78 (n = 17)
<b>C18:3 ω3 + ω6</b>	1.06 +/- 0.174 (n = 7)	1.11 +/- 0.155 (n = 3)	0.441 +/- 0.103 (n = 19)*	0.47 +/- 0.142 (n = 17)
<b>C18:3 ω7*</b>	n.d.	n.d.	0.112 +/- 0.0135 (n = 19)	0.175 +/- 0.0247 (n = 17)
<b>C18:2</b>	13.1 +/- 2.09 (n = 9)	11.5 +/- 2.22 (n = 7)	16.9 +/- 3.36 (n = 19)	14.2 +/- 1.9 (n = 17)
<b>C18:1</b>	16.8 +/- 1.42 (n = 9)	17.7 +/- 2.89 (n = 7)	64.3 +/- 12.4 (n = 19)*	57.5 +/- 6.89 (n = 17)
<b>C18:0</b>	23.7 +/- 1.95 (n = 9)	23.6 +/- 1.84 (n = 7)	36.4 +/- 5.63 (n = 19)	28.6 +/- 2.02 (n = 17)
<b>C20:5</b>	2.03 +/- 0.32 (n = 9)	3.14 +/- 1.49 (n = 7)	0.0894 +/- 0.0138 (n = 19)***	0.0865 +/- 0.0145 (n = 17)
<b>C20:4</b>	3.28 +/- 0.828 (n = 9)	2.33 +/- 0.528 (n = 7)	4.59 +/- 1.2 (n = 19)	4.42 +/- 0.68 (n = 17)
<b>C20:3 ω3 + ω6</b>	0.37 +/- 0.0503 (n = 7)	0.544 +/- 0.129 (n = 3)	0.43 +/- 0.0575 (n = 19)	0.5 +/- 0.0484 (n = 17)
<b>C20:3 ω9 + ω7*</b>	0.076 +/- 0.00841 (n = 7)	0.0893 +/- 0.0122 (n = 3)	0.328 +/- 0.0571 (n = 19)*	0.631 +/- 0.0768 (n = 17)**
<b>C20:2</b>	0.351 +/- 0.0396 (n = 7)	0.477 +/- 0.0783 (n = 3)	0.693 +/- 0.143 (n = 19)	1.04 +/- 0.133 (n = 17)
<b>C20:1</b>	1.04 +/- 0.159 (n = 9)	1.03 +/- 0.228 (n = 7)	2.92 +/- 0.635 (n = 19)	2.83 +/- 0.258 (n = 17)
<b>C20:0</b>	0.762 +/- 0.0862 (n = 7)	0.721 +/- 0.0948 (n = 3)	1.15 +/- 0.327 (n = 19)	0.6 +/- 0.085 (n = 17)
<b>C22:6</b>	7.25 +/- 1.27 (n = 9)	5.47 +/- 1.07 (n = 7)	1.38 +/- 0.233 (n = 19)***	1.2 +/- 0.132 (n = 17)
<b>C22:5</b>	0.91 +/- 0.119 (n = 7)	1.22 +/- 0.27 (n = 3)	0.429 +/- 0.0723 (n = 19)**	0.457 +/- 0.0319 (n = 17)
<b>C22:4</b>	0.221 +/- 0.0234 (n = 7)	0.303 +/- 0.0817 (n = 3)	0.279 +/- 0.0424 (n = 19)	0.308 +/- 0.0292 (n = 17)
<b>C22:3 ω3 + ω6*</b>	0.0159 +/- 0.00434 (n = 6)	0.0307 +/- 0.00698 (n = 3)	0.0177 +/- 0.00297 (n = 18)	0.0256 +/- 0.00281 (n = 17)
<b>C22:3 ω9* + ω7*</b>	n.d.	n.d.	0.0489 +/- 0.00942 (n = 19)	0.0889 +/- 0.01 (n = 17)**
<b>C22:2</b>	0.0352 +/- 0.00529 (n = 7)	0.0436 +/- 0.00468 (n = 3)	0.0586 +/- 0.0205 (n = 11)	0.0641 +/- 0.0065 (n = 10)
<b>C22:1</b>	0.232 +/- 0.0338 (n = 7)	0.263 +/- 0.0191 (n = 3)	0.406 +/- 0.115 (n = 19)	0.313 +/- 0.0346 (n = 17)
<b>C22:0</b>	0.446 +/- 0.039 (n = 7)	0.407 +/- 0.0248 (n = 3)	0.705 +/- 0.256 (n = 19)	0.36 +/- 0.0555 (n = 17)
<b>C24:6</b>	0.103 +/- 0.0145 (n = 7)	0.141 +/- 0.0334 (n = 3)	0.0269 +/- 0.00412 (n = 19)***	0.0377 +/- 0.0028 (n = 17)^
<b>C24:5</b>	0.0822 +/- 0.0124 (n = 7)	0.118 +/- 0.0403 (n = 3)	0.0495 +/- 0.00695 (n = 19)*	0.0753 +/- 0.00682 (n = 17)*
<b>C24:4</b>	0.0146 +/- 0.00438 (n = 6)	0.0254 +/- 0.0105 (n = 3)	0.047 +/- 0.00757 (n = 11)*	0.0735 +/- 0.0103 (n = 10)^
<b>C24:3</b>	n.d.	n.d.	0.0124 +/- 0.00715 (n = 3)	0.0124 +/- 0.0045 (n = 4)

<b>C24:2</b>	0.0739 +/- 0.00409 (n = 7)	0.0768 +/- 0.00994 (n = 3)	0.0481 +/- 0.0112 (n = 11)	0.0432 +/- 0.00423 (n = 10)
<b>C24:1</b>	0.415 +/- 0.0435 (n = 7)	0.397 +/- 0.0449 (n = 3)	0.332 +/- 0.0987 (n = 11)	0.225 +/- 0.0244 (n = 10)
<b>C24:0</b>	0.461 +/- 0.049 (n = 7)	0.472 +/- 0.0639 (n = 3)	0.559 +/- 0.26 (n = 11)	0.503 +/- 0.252 (n = 10)
<b>Total</b>	130 +/- 6 (n = 7)	137 +/- 17 (n = 3)	218 +/- 40 (n = 19)	183 +/- 17 (n = 17)

<b>% Composition of hepatic free fatty acids pool</b>				
	<b>NC</b>		<b>HFD</b>	
	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>
<b>C16:3</b>	0.0412 +/- 0.00432 (n = 7)	0.0453 +/- 0.00846 (n = 3)	0.0196 +/- 0.00271 (n = 10)***	0.0171 +/- 0.00219 (n = 9)
<b>C16:2</b>	0.108 +/- 0.0075 (n = 7)	0.0976 +/- 0.00876 (n = 3)	0.189 +/- 0.0138 (n = 11)***	0.244 +/- 0.0351 (n = 10)
<b>C16:1</b>	2.85 +/- 0.182 (n = 7)	3.07 +/- 0.0928 (n = 3)	3.86 +/- 0.182 (n = 19)*	3.98 +/- 0.17 (n = 17)
<b>C16:0</b>	40.7 +/- 4.02 (n = 7)	33.3 +/- 1.18 (n = 3)	36.9 +/- 1.32 (n = 19)	34.6 +/- 1.02 (n = 17)
<b>C18:3 ω3 + ω6</b>	0.84 +/- 0.077 (n = 7)	0.819 +/- 0.0571 (n = 3)	0.232 +/- 0.0133 (n = 19)***	0.323 +/- 0.0742 (n = 17)
<b>C18:3 ω7*</b>	n.d.	n.d.	0.0542 +/- 0.0038 (n = 19)	0.0844 +/- 0.00497 (n = 17)**
<b>C18:2</b>	11.6 +/- 1.11 (n = 7)	12.1 +/- 1.21 (n = 3)	7.22 +/- 0.38 (n = 19)***	6.94 +/- 0.31 (n = 17)
<b>C18:1</b>	14.7 +/- 0.851 (n = 7)	17.9 +/- 0.654 (n = 3)^	27.7 +/- 1.58 (n = 19)***	28.7 +/- 1.29 (n = 17)
<b>C18:0</b>	22.8 +/- 2.98 (n = 7)	18.5 +/- 2.07 (n = 3)	21 +/- 1.31 (n = 19)	18.9 +/- 0.904 (n = 17)
<b>C20:5</b>	1.94 +/- 0.202 (n = 7)	1.85 +/- 0.211 (n = 3)	0.0435 +/- 0.00367 (n = 19)***	0.0418 +/- 0.00408 (n = 17)
<b>C20:4</b>	2.93 +/- 0.551 (n = 7)	2.52 +/- 0.507 (n = 3)	1.98 +/- 0.234 (n = 19)	2.27 +/- 0.337 (n = 17)
<b>C20:3 ω3 + ω6</b>	0.305 +/- 0.0316 (n = 7)	0.399 +/- 0.0769 (n = 3)	0.203 +/- 0.014 (n = 19)**	0.254 +/- 0.00879 (n = 17)**
<b>C20:3 ω9 + ω7*</b>	0.0626 +/- 0.00406 (n = 7)	0.0658 +/- 0.00267 (n = 3)	0.154 +/- 0.0135 (n = 19)***	0.322 +/- 0.0285 (n = 17)***
<b>C20:2</b>	0.295 +/- 0.0336 (n = 7)	0.35 +/- 0.0205 (n = 3)	0.304 +/- 0.0328 (n = 19)	0.535 +/- 0.0589 (n = 17)**
<b>C20:1</b>	0.954 +/- 0.13 (n = 7)	1.19 +/- 0.0775 (n = 3)	1.2 +/- 0.13 (n = 19)	1.5 +/- 0.133 (n = 17)
<b>C20:0</b>	0.651 +/- 0.0893 (n = 7)	0.541 +/- 0.0869 (n = 3)	0.453 +/- 0.0812 (n = 19)	0.308 +/- 0.0256 (n = 17)
<b>C22:6</b>	6.54 +/- 0.744 (n = 7)	5.74 +/- 0.928 (n = 3)	0.648 +/- 0.0555 (n = 19)***	0.644 +/- 0.0787 (n = 17)
<b>C22:5</b>	0.77 +/- 0.0994 (n = 7)	0.903 +/- 0.176 (n = 3)	0.204 +/- 0.0229 (n = 19)***	0.25 +/- 0.021 (n = 17)
<b>C22:4</b>	0.187 +/- 0.023 (n = 7)	0.223 +/- 0.0531 (n = 3)	0.133 +/- 0.0137 (n = 19)	0.159 +/- 0.0119 (n = 17)
<b>C22:3 ω3 + ω6*</b>	0.0131 +/- 0.00746 (n = 5)	0.0161 +/- 0.00299 (n = 3)	0.00829 +/- 0.00129 (n = 18)	0.0139 +/- 0.00166 (n = 17)*
<b>C22:3 ω9* + ω7*</b>	n.d.	n.d.	0.0247 +/- 0.00274 (n = 19)	0.0514 +/- 0.00524 (n = 17)**
<b>C22:2</b>	0.0311 +/- 0.00653 (n = 7)	0.0323 +/- 0.00092 (n = 3)	0.0223 +/- 0.00626 (n = 11)	0.0324 +/- 0.00388 (n = 10)
<b>C22:1</b>	0.199 +/- 0.0337 (n = 7)	0.198 +/- 0.027 (n = 3)	0.179 +/- 0.0367 (n = 19)	0.164 +/- 0.0117 (n = 17)

<b>C22:0</b>	0.376 +/- 0.0337 (n = 7)	0.309 +/- 0.0557 (n = 3)	0.303 +/- 0.0828 (n = 19)	0.187 +/- 0.0188 (n = 17)
<b>C24:6</b>	0.0831 +/- 0.00985 (n = 7)	0.103 +/- 0.0206 (n = 3)	0.0128 +/- 0.00161 (n = 19)***	0.0205 +/- 0.00187 (n = 17)**
<b>C24:5</b>	0.0687 +/- 0.0117 (n = 7)	0.0841 +/- 0.0244 (n = 3)	0.0242 +/- 0.00293 (n = 19)***	0.0417 +/- 0.00487 (n = 17)**
<b>C24:4</b>	0.0127 +/- 0.00452 (n = 6)	0.0182 +/- 0.00691 (n = 3)	0.0193 +/- 0.00189 (n = 11)	0.0345 +/- 0.00435 (n = 10)**
<b>C24:3</b>	n.d.	n.d.	0.00349 +/- 0.0017 (n = 3)	0.0079 +/- 0.00284 (n = 4)
<b>C24:2</b>	0.0625 +/- 0.00539 (n = 7)	0.0571 +/- 0.00605 (n = 3)	0.0206 +/- 0.00366 (n = 11)***	0.0215 +/- 0.00223 (n = 10)
<b>C24:1</b>	0.358 +/- 0.0476 (n = 7)	0.295 +/- 0.0268 (n = 3)	0.14 +/- 0.032 (n = 11)**	0.113 +/- 0.0138 (n = 10)
<b>C24:0</b>	0.392 +/- 0.0439 (n = 7)	0.364 +/- 0.097 (n = 3)	0.223 +/- 0.0865 (n = 11)	0.195 +/- 0.0474 (n = 10)

Quantification of liver free fatty acids is written as mean +/- standard error for each of the diet and genotype conditions. The number of mice analyzed per condition is denoted in parentheses. Statistical analysis was performed using one-way ANOVA with sequential Sidak-Dunn method to adjust for multiple comparisons: (1) L-PTP1b<sup>-/-</sup> mice to control on NC diet, (2) L-PTP1b<sup>-/-</sup> mice to control on HFD, and (3) HFD control to NC control. \*\*\* = P<.001, \*\* = P<.01, \* = P < .05, ^ = P<.1. An asterick by fatty acid species indicates that the fatty acid measurement likely corresponds to that species, but its identification was not rigorously confirmed with a standard.

**Table S7: Quantification of hepatic triglycerides and total cholesterol**

<b>Absolute quantification of triglycerides and cholesterol (nmol lipid / mg liver tissue)</b>				
	<b>NC</b>		<b>HFD</b>	
	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>
<b>Tg C48:3</b>	0.126 +/- 0.0434 (n = 7)	0.104 +/- 0.0477 (n = 3)	0.0848 +/- 0.0237 (n = 10)	0.116 +/- 0.0218 (n = 7)
<b>Tg C48:2</b>	0.305 +/- 0.107 (n = 7)	0.25 +/- 0.114 (n = 3)	0.167 +/- 0.0473 (n = 10)	0.36 +/- 0.0767 (n = 7) <sup>^</sup>
<b>Tg C48:1</b>	n.d.	n.d.	0.0942 +/- 0.0235 (n = 6)	0.362 +/- 0.0605 (n = 5)
<b>Tg C50:4</b>	0.373 +/- 0.12 (n = 7)	0.398 +/- 0.187 (n = 3)	0.252 +/- 0.0751 (n = 10)	0.551 +/- 0.112 (n = 7) <sup>^</sup>
<b>Tg C50:3</b>	1.74 +/- 0.597 (n = 7)	2.14 +/- 1.02 (n = 3)	1.15 +/- 0.349 (n = 10)	3 +/- 0.645 (n = 7) <sup>*</sup>
<b>Tg C50:2</b>	3.15 +/- 1.06 (n = 7)	3.64 +/- 1.62 (n = 3)	1.92 +/- 0.636 (n = 10)	5.98 +/- 1.27 (n = 7) <sup>*</sup>
<b>Tg C50:1</b>	0.953 +/- 0.284 (n = 7)	1.08 +/- 0.431 (n = 3)	0.754 +/- 0.238 (n = 10)	2.28 +/- 0.476 (n = 7) <sup>*</sup>
<b>Tg C52:5</b>	1.67 +/- 0.51 (n = 7)	0.946 +/- 0.579 (n = 3)	0.674 +/- 0.184 (n = 10)	1.25 +/- 0.236 (n = 7)
<b>Tg C52:4</b>	10.8 +/- 2.93 (n = 7)	14 +/- 5.61 (n = 3)	4.75 +/- 1.38 (n = 10) <sup>^</sup>	9.53 +/- 1.78 (n = 7)
<b>Tg C52:3</b>	16.7 +/- 4.06 (n = 7)	24.9 +/- 9.58 (n = 3)	13.1 +/- 3.95 (n = 10)	33.4 +/- 7.29 (n = 6) <sup>*</sup>
<b>Tg C52:2</b>	5.49 +/- 1.2 (n = 7)	9.44 +/- 3.21 (n = 3)	11 +/- 3.73 (n = 10)	35.6 +/- 8.6 (n = 6) <sup>*</sup>
<b>Tg C54:7</b>	1.21 +/- 0.345 (n = 7)	1.32 +/- 0.517 (n = 3)	0.111 +/- 0.043 (n = 4) <sup>^</sup>	0.0857 +/- 0.0159 (n = 6)
<b>Tg C54:6</b>	2.63 +/- 0.713 (n = 7)	2.97 +/- 1.46 (n = 3)	0.628 +/- 0.157 (n = 10) <sup>*</sup>	0.67 +/- 0.126 (n = 7)
<b>Tg C54:5</b>	3.84 +/- 0.996 (n = 7)	4.97 +/- 2.31 (n = 3)	2.57 +/- 0.586 (n = 10)	3.62 +/- 0.682 (n = 7)
<b>Tg C54:4</b>	3.56 +/- 0.891 (n = 7)	5.1 +/- 2.13 (n = 3)	5.76 +/- 1.32 (n = 10)	10.7 +/- 2.04 (n = 7)
<b>Tg C54:3</b>	1.62 +/- 0.337 (n = 7)	2.36 +/- 0.898 (n = 3)	5.78 +/- 1.47 (n = 10) <sup>^</sup>	14.2 +/- 3.19 (n = 7) <sup>*</sup>
<b>Tg C54:2</b>	0.243 +/- 0.0419 (n = 7)	0.304 +/- 0.087 (n = 3)	0.762 +/- 0.302 (n = 10)	2.2 +/- 0.535 (n = 7) <sup>^</sup>
<b>Tg C56:10</b>	0.0396 +/- 0.011 (n = 7)	0.037 +/- 0.0186 (n = 3)	n.d.	n.d.
<b>Tg C56:9</b>	0.437 +/- 0.113 (n = 7)	0.471 +/- 0.208 (n = 3)	0.0175 +/- 0.00452 (n = 8) <sup>**</sup>	0.0118 +/- 0.00195 (n = 6)
<b>Tg C56:8</b>	4.47 +/- 1.1 (n = 7)	5.23 +/- 2.12 (n = 3)	0.115 +/- 0.0274 (n = 10) <sup>***</sup>	0.0768 +/- 0.0146 (n = 7)
<b>Tg C56:7</b>	3.25 +/- 0.695 (n = 7)	4.48 +/- 1.84 (n = 3)	0.385 +/- 0.105 (n = 10) <sup>***</sup>	0.323 +/- 0.0551 (n = 7)
<b>Tg C56:6</b>	0.626 +/- 0.135 (n = 7)	0.829 +/- 0.345 (n = 3)	0.408 +/- 0.122 (n = 10)	0.546 +/- 0.0985 (n = 7)
<b>Tg C56:5</b>	0.264 +/- 0.0485 (n = 7)	0.367 +/- 0.144 (n = 3)	0.374 +/- 0.109 (n = 10)	0.801 +/- 0.154 (n = 7) <sup>^</sup>
<b>Tg C56:4</b>	0.179 +/- 0.033 (n = 7)	0.235 +/- 0.0954 (n = 3)	0.36 +/- 0.133 (n = 10)	1.1 +/- 0.254 (n = 7) <sup>*</sup>
<b>Tg C56:3</b>	n.d.	n.d.	0.162 +/- 0.0391 (n = 6)	1.33 +/- 0.373 (n = 5)
<b>Tg C56:2</b>	n.d.	n.d.	0.0304 +/- 0.0112 (n = 6)	0.0941 +/- 0.0314 (n = 5)
<b>Total Triglycerides</b>	62 +/- 16 (n = 7)	84 +/- 33 (n = 3)	58 +/- 7.5 (n = 19)	110 +/- 15 (n = 16) <sup>**</sup>
<b>Total Cholesterol</b>	3 +/- 0.19 (n = 7)	3 +/- 0.29 (n = 3)	5.6 +/- 0.16 (n = 10) <sup>***</sup>	5.5 +/- 0.2 (n = 7)

% Liver triglyceride composition				
	NC		HFD	
	Control	L-PTP1b <sup>-/-</sup>	Control	L-PTP1b <sup>-/-</sup>
<b>Tg C48:3</b>	0.192 +/- 0.0161 (n = 7)	0.116 +/- 0.0242 (n = 3)^	0.17 +/- 0.0187 (n = 10)	0.103 +/- 0.0164 (n = 6)*
<b>Tg C48:2</b>	0.467 +/- 0.0411 (n = 7)	0.281 +/- 0.0398 (n = 3)^	0.339 +/- 0.0346 (n = 10)*	0.297 +/- 0.0333 (n = 6)
<b>Tg C48:1</b>	n.d.	n.d.	0.338 +/- 0.105 (n = 6)	0.223 +/- 0.023 (n = 4)
<b>Tg C50:4</b>	0.572 +/- 0.0342 (n = 7)	0.446 +/- 0.0569 (n = 3)	0.476 +/- 0.0361 (n = 10)	0.461 +/- 0.0495 (n = 6)
<b>Tg C50:3</b>	2.58 +/- 0.205 (n = 7)	2.44 +/- 0.264 (n = 3)	2.16 +/- 0.192 (n = 10)	2.34 +/- 0.153 (n = 6)
<b>Tg C50:2</b>	4.83 +/- 0.363 (n = 7)	4.26 +/- 0.313 (n = 3)	3.54 +/- 0.265 (n = 10)*	4.71 +/- 0.185 (n = 6)*
<b>Tg C50:1</b>	1.57 +/- 0.138 (n = 7)	1.3 +/- 0.0544 (n = 3)	1.53 +/- 0.192 (n = 10)	1.85 +/- 0.15 (n = 6)
<b>Tg C52:5</b>	2.53 +/- 0.179 (n = 7)	1.42 +/- 0.728 (n = 3)*	1.31 +/- 0.0628 (n = 10)***	1.02 +/- 0.0926 (n = 6)*
<b>Tg C52:4</b>	17 +/- 0.465 (n = 7)	16.6 +/- 0.225 (n = 3)	9.07 +/- 0.515 (n = 10)***	7.58 +/- 0.455 (n = 6)
<b>Tg C52:3</b>	27 +/- 0.887 (n = 7)	29.9 +/- 0.308 (n = 3)	25.4 +/- 1.46 (n = 10)	26.4 +/- 0.702 (n = 6)
<b>Tg C52:2</b>	9.25 +/- 0.543 (n = 7)	11.8 +/- 0.839 (n = 3)*	20.5 +/- 1.15 (n = 10)***	27.5 +/- 1.04 (n = 6)**
<b>Tg C54:7</b>	1.89 +/- 0.126 (n = 7)	1.63 +/- 0.222 (n = 3)	0.164 +/- 0.0204 (n = 4)***	0.0763 +/- 0.0158 (n = 6)*
<b>Tg C54:6</b>	4.17 +/- 0.141 (n = 7)	3.37 +/- 0.417 (n = 3)*	1.34 +/- 0.223 (n = 10)***	0.563 +/- 0.0562 (n = 6)*
<b>Tg C54:5</b>	6.2 +/- 0.218 (n = 7)	5.55 +/- 0.795 (n = 3)	5.42 +/- 0.65 (n = 10)	2.94 +/- 0.193 (n = 6)*
<b>Tg C54:4</b>	5.83 +/- 0.216 (n = 7)	5.88 +/- 0.718 (n = 3)	12.2 +/- 0.999 (n = 10)***	8.7 +/- 0.217 (n = 6)*
<b>Tg C54:3</b>	2.83 +/- 0.217 (n = 7)	2.82 +/- 0.307 (n = 3)	12 +/- 1.36 (n = 10)***	11.4 +/- 0.547 (n = 6)
<b>Tg C54:2</b>	0.47 +/- 0.078 (n = 7)	0.402 +/- 0.0861 (n = 3)	1.45 +/- 0.164 (n = 10)***	1.81 +/- 0.31 (n = 6)
<b>Tg C56:10</b>	0.0646 +/- 0.00706 (n = 7)	0.0424 +/- 0.00595 (n = 3)	n.d.	n.d.
<b>Tg C56:9</b>	0.715 +/- 0.0648 (n = 7)	0.559 +/- 0.0516 (n = 3)	0.0357 +/- 0.00307 (n = 8)***	0.0101 +/- 0.00242 (n = 5)***
<b>Tg C56:8</b>	7.37 +/- 0.656 (n = 7)	6.51 +/- 1.04 (n = 3)	0.246 +/- 0.015 (n = 10)***	0.0696 +/- 0.0113 (n = 6)***
<b>Tg C56:7</b>	5.47 +/- 0.313 (n = 7)	5.44 +/- 0.518 (n = 3)	0.816 +/- 0.0643 (n = 10)***	0.3 +/- 0.0566 (n = 6)***
<b>Tg C56:6</b>	1.07 +/- 0.0777 (n = 7)	0.978 +/- 0.0304 (n = 3)	0.799 +/- 0.034 (n = 10)**	0.49 +/- 0.0744 (n = 6)**
<b>Tg C56:5</b>	0.48 +/- 0.0548 (n = 7)	0.434 +/- 0.0447 (n = 3)	0.758 +/- 0.0514 (n = 10)**	0.688 +/- 0.069 (n = 6)
<b>Tg C56:4</b>	0.332 +/- 0.0448 (n = 7)	0.278 +/- 0.0585 (n = 3)	0.657 +/- 0.0466 (n = 10)***	0.944 +/- 0.129 (n = 6)*
<b>Tg C56:3</b>	n.d.	n.d.	0.484 +/- 0.0557 (n = 6)	0.874 +/- 0.153 (n = 4)
<b>Tg C56:2</b>	n.d.	n.d.	0.0892 +/- 0.023 (n = 6)	0.0606 +/- 0.015 (n = 4)

Quantification of liver triglycerides and cholesterol is written as mean +/- standard error for each of the diet and genotype conditions. Number of mice analyzed per condition is denoted in parentheses. Statistical analysis was performed using one-way ANOVA with



sequential Sidak-Dunn method to adjust for multiple comparisons: (1) L-PTP1b<sup>-/-</sup> mice to control on NC diet, (2) L-PTP1b<sup>-/-</sup> mice to control on HFD, and (3) HFD control to NC control. \*\*\* =  $P < .001$ , \*\* =  $P < .01$ , \* =  $P < .05$ , ^ =  $P < .1$ .

**Table S8: HFD Serum Triglyceride Compositions**

<b>HFD Serum Triglyceride Compositions</b>				
	<b>Absolute Quantification (mg/dL)</b>		<b>Percent Composition</b>	
	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>	<b>Control</b>	<b>L-PTP1b<sup>-/-</sup></b>
<b>Tg C48:3</b>	0.19 +/- 0.09 (n = 7)	0.18 +/- 0.17 (n = 6)	0.39 +/- 0.13 (n = 7)	0.32 +/- 0.18 (n = 6)
<b>Tg C48:2</b>	0.26 +/- 0.14 (n = 7)	0.3 +/- 0.25 (n = 6)	0.53 +/- 0.19 (n = 7)	0.56 +/- 0.24 (n = 6)
<b>Tg C50:3</b>	0.71 +/- 0.32 (n = 7)	0.75 +/- 0.61 (n = 6)	1.47 +/- 0.46 (n = 7)	1.44 +/- 0.54 (n = 6)
<b>Tg C50:2</b>	1.89 +/- 1.04 (n = 7)	2.45 +/- 1.81 (n = 6)	3.89 +/- 1.54 (n = 7)	4.8 +/- 1.43 (n = 6)
<b>Tg C50:1</b>	1.81 +/- 0.91 (n = 7)	2.31 +/- 1.29 (n = 6)	3.68 +/- 1.14 (n = 7)	5.01 +/- 0.27 (n = 6)*
<b>Tg C50:0</b>	0.27 +/- 0.14 (n = 7)	0.33 +/- 0.12 (n = 6)	0.54 +/- 0.15 (n = 7)	0.83 +/- 0.28 (n = 6)*
<b>Tg C52:7</b>	0.09 +/- 0.03 (n = 7)	0.06 +/- 0.03 (n = 6)	0.19 +/- 0.07 (n = 7)	0.13 +/- 0.02 (n = 6)^
<b>Tg C52:6</b>	0.4 +/- 0.08 (n = 7)	0.31 +/- 0.18 (n = 6)	0.87 +/- 0.17 (n = 7)	0.65 +/- 0.07 (n = 6)*
<b>Tg C52:5</b>	2.16 +/- 0.57 (n = 7)	1.79 +/- 1.25 (n = 6)	4.55 +/- 0.53 (n = 7)	3.56 +/- 0.92 (n = 6)*
<b>Tg C52:4</b>	8.4 +/- 2.42 (n = 7)	7.42 +/- 4.66 (n = 6)	17.67 +/- 2.36 (n = 7)	15.23 +/- 2.72 (n = 6)
<b>Tg C52:3</b>	8.26 +/- 2.38 (n = 7)	7.54 +/- 3.87 (n = 6)	17.3 +/- 1.55 (n = 7)	16.72 +/- 1.17 (n = 6)
<b>Tg C52:2</b>	6.92 +/- 2.62 (n = 7)	8.06 +/- 3.45 (n = 6)	14.2 +/- 1.94 (n = 7)	18.73 +/- 2.79 (n = 6)**
<b>Tg C54:7</b>	0.42 +/- 0.13 (n = 7)	0.29 +/- 0.16 (n = 6)	0.91 +/- 0.31 (n = 7)	0.64 +/- 0.08 (n = 6)^
<b>Tg C54:6</b>	1.6 +/- 0.48 (n = 7)	1.12 +/- 0.62 (n = 6)	3.46 +/- 0.98 (n = 7)	2.47 +/- 0.28 (n = 6)*
<b>Tg C54:5</b>	3.3 +/- 0.7 (n = 7)	2.6 +/- 1.44 (n = 6)	7.08 +/- 1.3 (n = 7)	5.64 +/- 0.44 (n = 6)*
<b>Tg C54:4</b>	2.5 +/- 0.65 (n = 7)	2.16 +/- 1.17 (n = 6)	5.34 +/- 1.1 (n = 7)	4.81 +/- 0.59 (n = 6)
<b>Tg C54:3</b>	4.29 +/- 1.06 (n = 7)	4.73 +/- 2.15 (n = 6)	9.05 +/- 1.17 (n = 7)	10.86 +/- 1.2 (n = 6)*
<b>Tg C54:2</b>	0.9 +/- 0.47 (n = 7)	0.94 +/- 0.44 (n = 6)	1.8 +/- 0.48 (n = 7)	2.15 +/- 0.32 (n = 6)
<b>Tg C56:9</b>	0.14 +/- 0.07 (n = 7)	0.07 +/- 0.04 (n = 6)*	0.32 +/- 0.17 (n = 7)	0.16 +/- 0.03 (n = 6)*
<b>Tg C56:8</b>	0.64 +/- 0.31 (n = 7)	0.32 +/- 0.17 (n = 6)^	1.4 +/- 0.7 (n = 7)	0.74 +/- 0.16 (n = 6)*
<b>Tg C56:7</b>	1.12 +/- 0.55 (n = 7)	0.7 +/- 0.3 (n = 6)	2.43 +/- 1.17 (n = 7)	1.68 +/- 0.39 (n = 6)
<b>Tg C56:4</b>	0.38 +/- 0.11 (n = 7)	0.42 +/- 0.14 (n = 6)	0.8 +/- 0.09 (n = 7)	1.06 +/- 0.33 (n = 6)^
<b>Tg C56:3</b>	0.37 +/- 0.17 (n = 7)	0.42 +/- 0.16 (n = 6)	0.75 +/- 0.18 (n = 7)	1.02 +/- 0.26 (n = 6)^
<b>Tg C58:10</b>	0.16 +/- 0.13 (n = 7)	0.06 +/- 0.02 (n = 6)^	0.36 +/- 0.27 (n = 7)	0.16 +/- 0.05 (n = 6)
<b>Tg C58:9</b>	0.25 +/- 0.17 (n = 7)	0.12 +/- 0.04 (n = 6)^	0.56 +/- 0.38 (n = 7)	0.32 +/- 0.13 (n = 6)
<b>Tg C58:8</b>	0.21 +/- 0.14 (n = 7)	0.12 +/- 0.03 (n = 6)	0.47 +/- 0.28 (n = 7)	0.32 +/- 0.12 (n = 6)
<b>Total</b>	47.64 +/- 12.19 (n = 7)	45.55 +/- 24.01 (n = 6)		

Quantification of serum triglycerides is written as mean +/- standard error for HFD conditions. Number of mice analyzed per condition is denoted in parentheses. Statistical analysis was performed using two-tailed Student's T-tests. L-PTP1b-/- mice were compared to control. \*\* =  $P_{\text{raw}} < .01$ , \* =  $P_{\text{raw}} < .05$ , ^ =  $P_{\text{raw}} < .1$ .

**Table S9: Enrichments for phosphosites predictive of the PTP1b-dependent  $\omega 3$  /  $\omega 6$  PUFA (C24:6, C24:5, C24:4, C22:3, C20:3)**

$P_{\text{raw}}$	NES	Category Label	N	Category Membership	Source
1.1E-04**	2.44	<b>Metabolic process</b>	25	CYP2E1 Y426, CYB5A Y11, CAR2 Y114, LDHA Y239, PGM1 Y353, GAPDH Y316, PRDX6 Y89, CTH Y113, CPS1 Y162, TGM2 Y369*, <i>ARG1 Y188, GPX1 Y147, ARG1 Y197, PCBD1 Y70, ENO1 Y44, GAPDH Y328, ACAT1 Y328, HADHA Y724, PGAM2 Y92, CPS1 Y140, GLUD1 Y135, CPS1 Y590, GLUD1 Y512, ARG1 Y265, CPS1 Y1450</i>	GO
1.1E-04**	2.43	<b>Oxidation reduction</b>	24	CYP2E1 Y426, CYB5A Y11, SAHH Y193, HPD Y232, LDHA Y239, HPD Y221, HGD Y40, GAPDH Y316, PRDX6 Y89, FASN Y1248, ALDH1A7 Y484*, <i>UOX Y288, GPX1 Y147, ALDH1L1 Y848, CAT Y231, ALDH6A1 Y268, UGDH Y108, GAPDH Y328, CAT Y84, UOX Y230, HADHA Y724, GLUD1 Y135, GLUD1 Y512, ACAD11 Y323</i>	GO, SwissProt, Literature
1.4E-03^	2.13	<b>Endoplasmic Reticulum</b>	16	CYP2E1 Y426, CALM1 Y100, GLUL Y336, CYB5A Y11, PEBP1 Y181, HPD Y232*, <i>HPD Y221, VCP Y173, ASS1 Y133, CAV1 Y14 Y6, CAT Y231, ALDOB Y204, ACSL5 Y69, CAT Y84, HSPD1 Y385, ASS1 Y322,</i>	GO

NES stands for normalized enrichment scores. \*\* = FDR = .01, \* = FDR = .05, ^ = FDR = .1. NES > 0 indicates that increased phosphorylation on sites in the pathway are positively predictive of proportion of  $\omega 3$  /  $\omega 6$  PUFA, while NES < 0 indicates that increased phosphorylation on sites in the pathway are negatively predictive. The phosphosites in each category membership are ordered from most positively to most negatively predictive. Those phosphosites that contributed most to the enrichment (compose the “leading edge”) appear in regular font, while the other sites in that category are italicized.

**Table S10: Enrichments for phosphosites predictive of PTP1b-dependent  $\omega 7 / \omega 9$  PUFA (C20:3, C22:3, C20:2, C18:3)**

<b>P<sub>raw</sub></b>	<b>NES</b>	<b>Category Label</b>	<b>N</b>	<b>Category Membership</b>	<b>Source</b>
<2E-05**	2.53	Oxidation reduction	24	CYB5A Y11, ALDH1A7 Y484, CYP2E1 Y426, GAPDH Y316, SAHH Y193, FASN Y1248, HPD Y221, LDHA Y239, HPD Y232, PRDX6 Y89, CAT Y231*, <i>GPX1 Y147, HGD Y40, UOX Y288, ALDH1L1 Y848, ALDH6A1 Y268, GLUD1 Y135, CAT Y84, GAPDH Y328, ACAD11 Y323, UGDH Y108, UOX Y230, HADHA Y724, GLUD1 Y512</i>	GO, SwissProt, Literature
7.4E-04*	2.31	Metabolic process	25	CYB5A Y11, CYP2E1 Y426, GAPDH Y316, TGM2 Y369, CAR2 Y114, LDHA Y239, PGM1 Y353, PRDX6 Y89, CPS1 Y162, ARG1 Y188, GPX1 Y147, ENO1 Y44*, <i>GLUD1 Y135, CTH Y113, PCBD1 Y70, GAPDH Y328, PGAM2 Y92, CPS1 Y590, HADHA Y724, ARG1 Y197, ACAT1 Y328, ARG1 Y265, GLUD1 Y512, CPS1 Y140, CPS1 Y1450</i>	GO
1.1E-03^	2.25	Cytosol	88	ACLY Y672, SAHH Y193, SHP-2 Y584, FASN Y1248, HPD Y221, TGM2 Y369, TARS Y297, CALM1 Y100, CAR2 Y114, LDHA Y239, PGM1 Y353, HPD Y232, PRDX6 Y89, VCP Y173, CAT Y231, BCAR1 Y271, PITPNA Y141, GRF-1 Y1105*, <i>OTC Y317, GNMT Y221, CrkL Y198, GPX1 Y147, Hrs Y216, PLCG1 Y771, LHPP Y159, GSK3B Y216 S219, ALDOB Y204, p38-alpha Y182 T180, ERK2 Y185 T188/T183, ERK1 Y205, vinculin Y822, PGK1 Y196, ERK2 Y185, IRS2 Y671, BCAR1 Y391, CAV1 Y14 Y6, CAT Y84, GSK3B Y216, CTNND1 Y904, vinculin Y692, Shc1 Y313, Abl Y393, SHMT1 Y28, BCAR1 Y238, JAK2 Y570, CTNND1 Y96, BCAR1 Y414, FAK Y576, Yes Y220, GNMT Y34, SHMT1 Y67, IRS2 Y649, GRF-1 Y1087, BCAR1 Y556, Lyn Y173, SEC14L4 Y36, BCAR1 Y253, BCAR1 Y291, PGAM2 Y92, IRS2 Y814, UGDH Y108, Lyn Y376, FBP1 Y245, Yes Y424, Dok1 Y408, SHP-2 Y62, FAK Y397, CTNNB1 Y654, p38-alpha Y182, FAK Y861, GOT1 Y264, Nck1 Y105, RPL13A Y137, DLG1 Y783, eEF1A1 Y177, talin 1 Y1116, Fgr Y197, FAK Y577 T575, SCAP2 Y260, HSPD1 Y385, FBP1 Y216, SEC14L4 Y36, STAT3 Y686, CrkL Y132, Dok1 Y361, PIK3R1 Y197, Dok1 Y450, FBP1 Y265</i>	GO
1.3E-03^	2.23	Endoplasmic Reticulum	16	CYB5A Y11, CYP2E1 Y426, GLUL Y336, HPD Y221, CALM1 Y100, PEBP1 Y181, HPD Y232, VCP Y173, CAT Y231, ASS1 Y133*, <i>ALDOB Y204, CAV1 Y14 Y6, CAT Y84, ACSL5 Y69, HSPD1</i>	GO

				<i>Y385, ASS1 Y322</i>	
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NES stands for normalized enrichment scores. \*\* = FDR = .01, \* = FDR = .05, ^ = FDR = .1. NES > 0 indicates that increased phosphorylation on sites in pathway are positively predictive of proportion of  $\omega 7 / \omega 9$  PUFA, while NES < 0 indicates that increased phosphorylation on sites in the pathway are negatively predictive. The phosphosites in each category membership are ordered from most positively to most negatively predictive of phenotype. Those phosphosites that contributed most to the enrichment (compose the “leading edge”) appear in regular font, while the other sites in that category are italicized.

**Table S11: Enrichments for phosphosites predictive of steatosis**

<b>P<sub>raw</sub></b>	<b>NES</b>	<b>Category Label</b>	<b>N</b>	<b>Category Membership</b>	<b>Source</b>
1.1E-04**	2.55	<b>Oxidation reduction</b>	24	GAPDH Y316, ALDH1A7 Y484, HPD Y221, CYP2E1 Y426, CYB5A Y11, FASN Y1248, CAT Y84, GPX1 Y147, HGD Y40, SAHH Y193, PRDX6 Y89, ALDH1L1 Y848, ACAD11 Y323, LDHA Y239*, <i>HPD Y232, CAT Y231, GLUD1 Y512, ALDH6A1 Y268, UOX Y288, UGDH Y108, GLUD1 Y135, GAPDH Y328, UOX Y230, HADHA Y724</i>	GO, SwissProt, Literature
4.9E-04*	2.37	<b>Metabolic process</b>	25	GAPDH Y316, TGM2 Y369, CYP2E1 Y426, PGM1 Y353, ENO1 Y44, CYB5A Y11, GPX1 Y147, ARG1 Y188, PRDX6 Y89*, LDHA Y239, CAR2 Y114, PGAM2 Y92, GLUD1 Y512, ARG1 Y265, ARG1 Y197, PCBD1 Y70, CPS1 Y162, CTH Y113, CPS1 Y590, GLUD1 Y135, GAPDH Y328, HADHA Y724, ACAT1 Y328, CPS1 Y140, CPS1 Y1450	GO
7.8E-04*	-2.17	<b>Chemokine signaling pathway</b>	32	JAK2 Y570, Pyk2 Y807, Pyk2 Y579 Y580, CrkL Y198, Shc1 Y313, BCAR1 Y238, BCAR1 Y556, BCAR1 Y271, FAK Y576, Pyk2 Y579, GSK3B Y216 S219, FAK Y397, FAK Y861, BCAR1 Y391, BCAR1 Y414, CrkL Y132*, N-WASP Y253, FAK Y577 T575, PXN Y118, GSK3B Y216, Lyn Y376, STAT3 Y686, BCAR1 Y291, PARD3 Y1076, BCAR1 Y253, ERK2 Y185 T188/T183, PIK3R1 Y197, Fgr Y197, PARD3 Y1123, ERK2 Y185, ERK1 Y205, Lyn Y173	KEGG
8.2E-04^	-2.17	<b>Adherens junction</b>	23	<i>vinculin Y822, ZO1 Y1066, Fer Y402, CTNND1 Y904, CTNNB1 Y654, ZO1 Y1360, Met Y1001, vinculin Y692, CTNND1 Y96, Fer Y715, CTNNA1 Y619, N-WASP Y253, PARD3 Y1076*, ERK2 Y185 T188/T183, EGFR Y1172, CTNNA1 Y177, Yes Y220, PARD3 Y1123, ERK2 Y185, ERK1 Y205, ZO1 Y1145, Yes Y424, EGFR Y1197</i>	KEGG

NES stands for normalized enrichment scores. \*\* = FDR = .01, \* = FDR = .05, ^ = FDR = .1. NES > 0 indicates that phosphorylation on sites in pathway most significantly increase with steatosis, while NES < 0 indicates that phosphorylation on sites in the pathway decrease with steatosis. The phosphosites in each category membership are ordered from most positively-predictive of steatosis to most negatively-predictive of steatosis. Those phosphosites that contributed most to the enrichment (compose the “leading edge”) appear in regular font, while the other sites in that category are italicized.

