Supplemental Information

Contents

Supplementary Figures

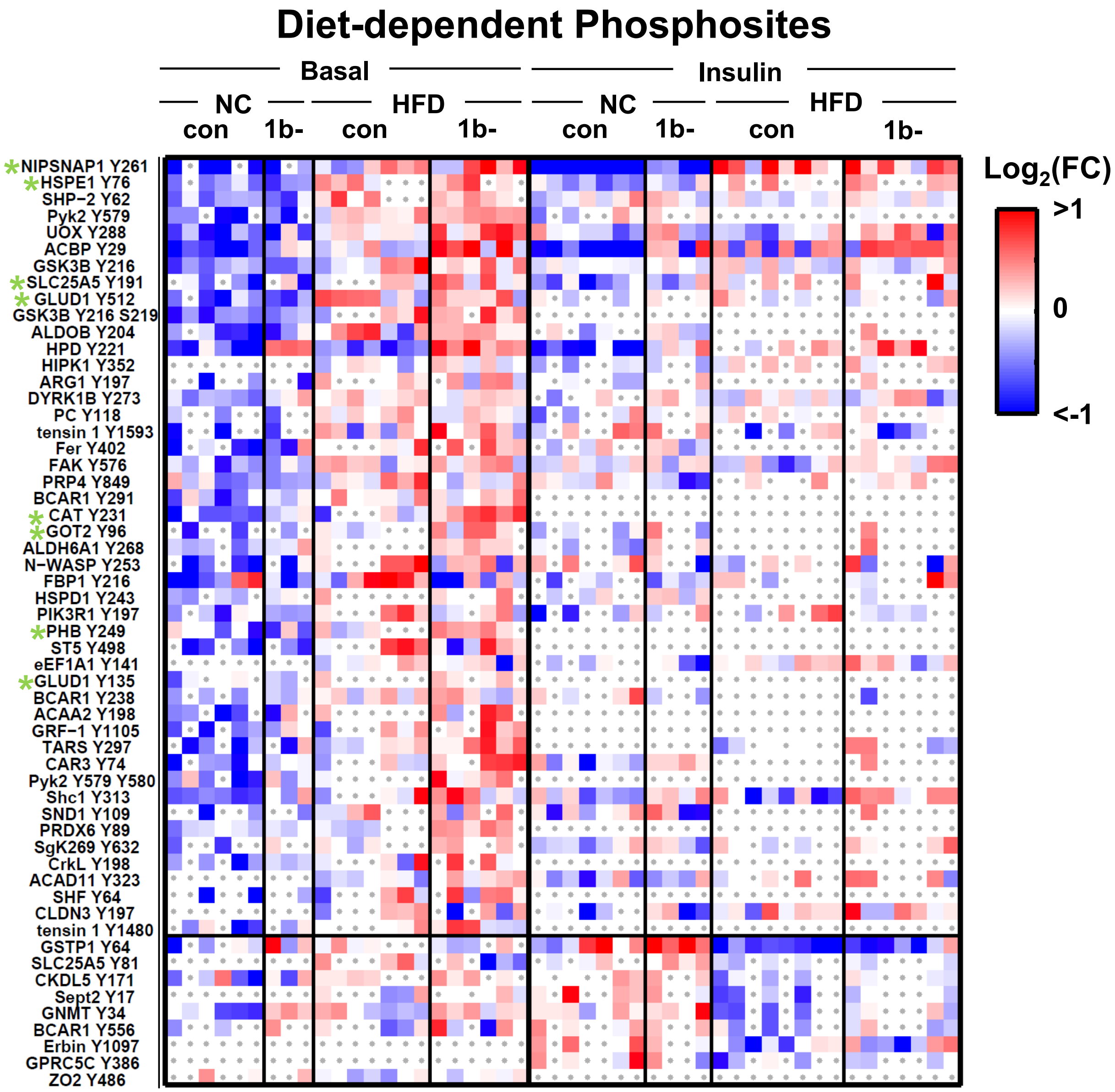

Figure S1. Diet-dependent Phosphosites
Heatmaps of those phosphorylation sites most significantly correlated to diet (raw, context-specific p-value < .025, see Methods). For basal or insulin datasets, the phosphorylation level of a phosphosite was normalized to the corresponding phosphosite mean (basal or insulin) and then log2-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.

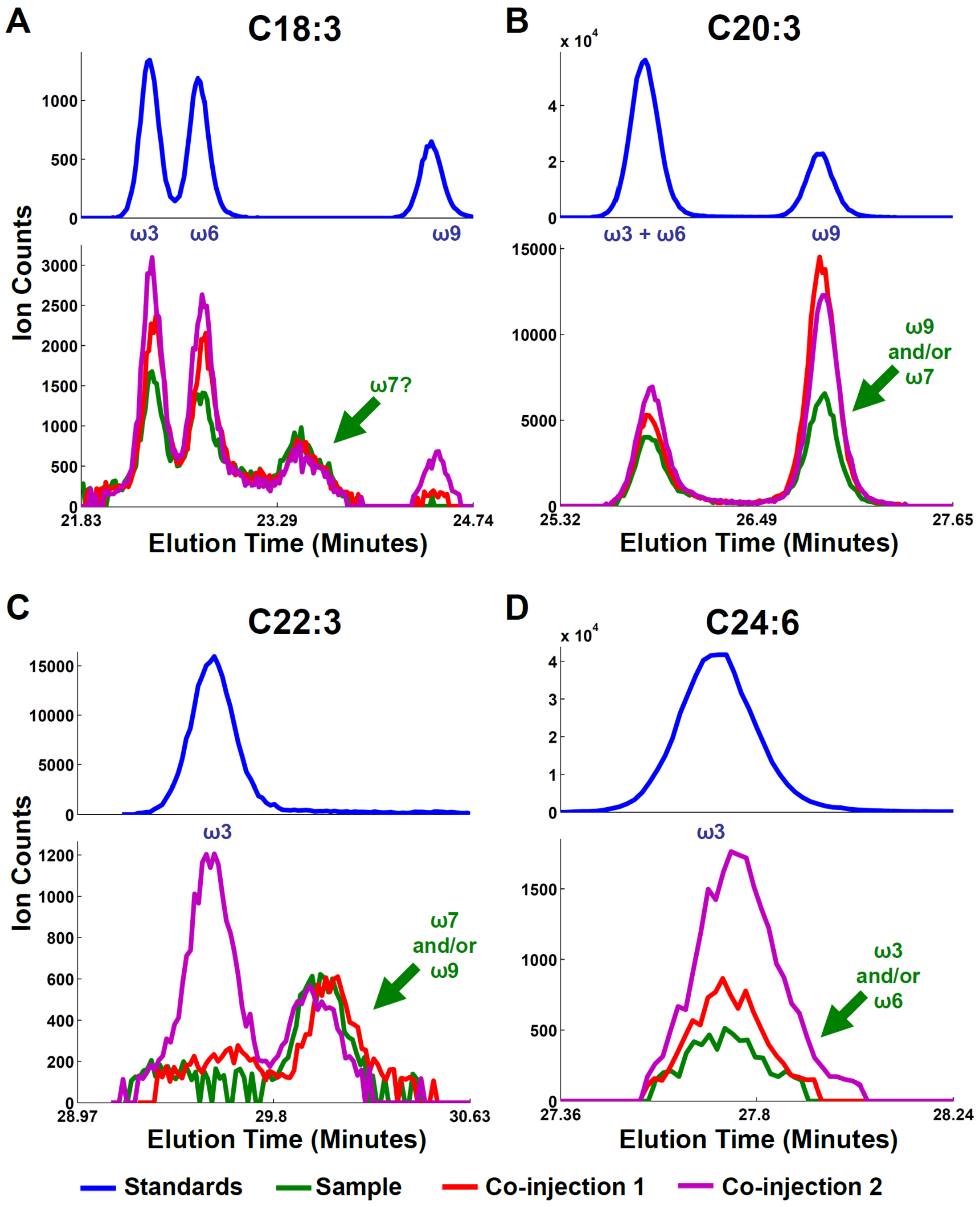

Figure S2. Co-elution to Determine PUFA Species
Blue and green curves correspond to ionchromatograms from standards and liver lipid samples analyzed in independent LC-MS experiments. Standards and lipid samples were co-injected (red and purple curves) in two additional experiments to determine the PTP1b-dependent isomer peak indicated by the green arrow. See text for discussion of results.

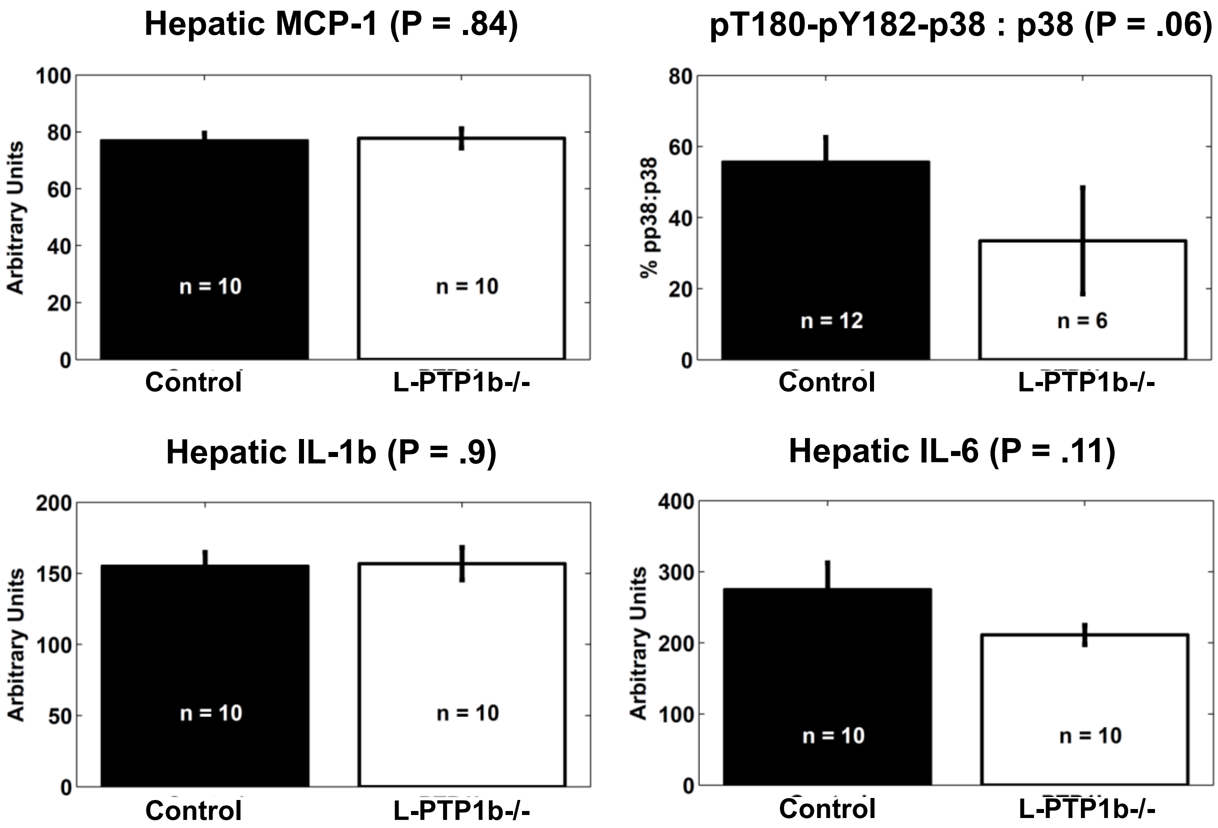

Figure S3. Measurements of Inflammation in HFD Liver
Bar graphs denote the mean and SEM associated with each of the measurements. Significance was determined with 2-sided Student t tests.

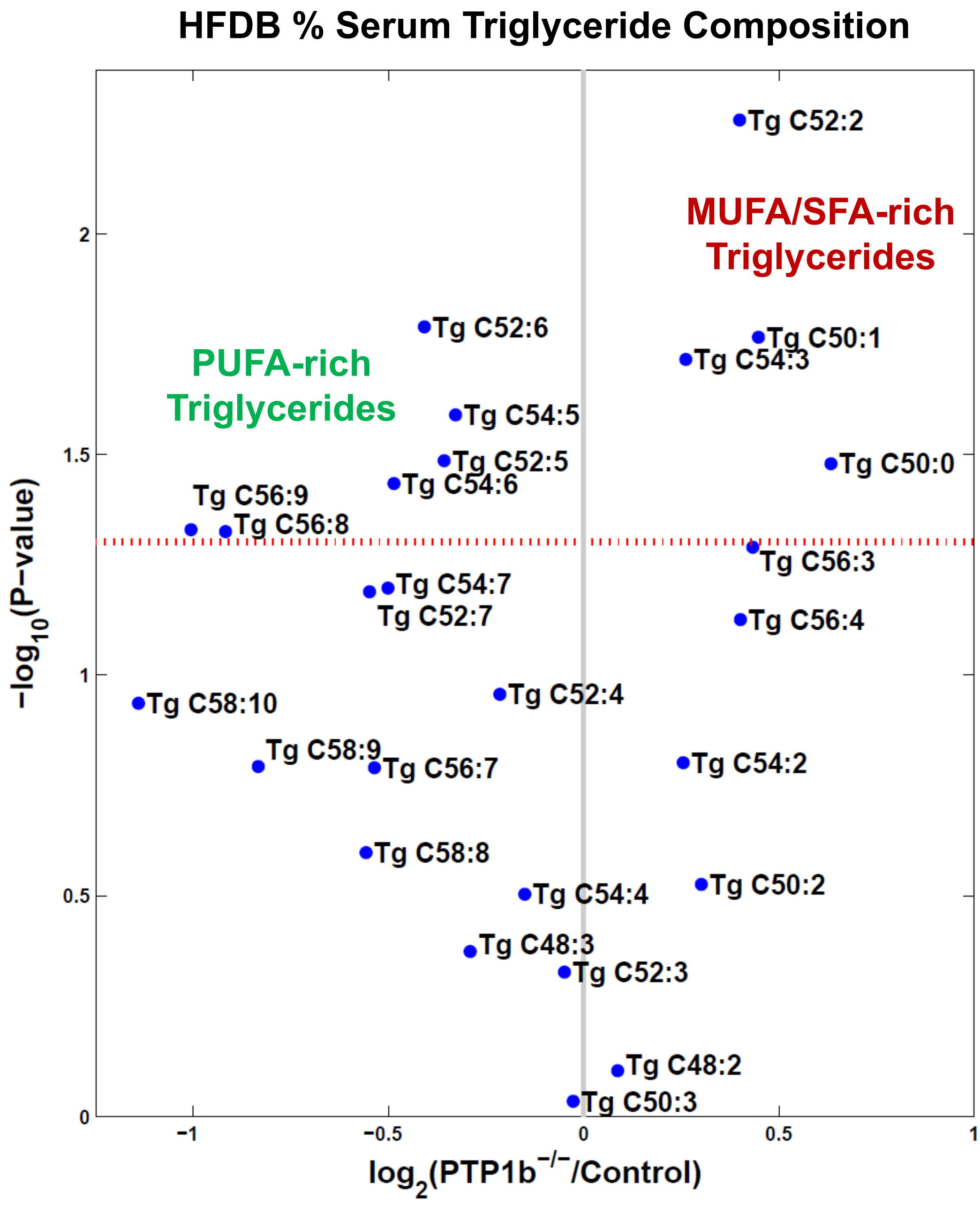

Figure S4. HFD Basal Serum Triglyceride Compositions
Volcano plot of percent serum triglyceride compositions on HFD: Each triglyceride is plotted as a function of $\log_2$-transformed, compositional fold-change (L-PTP1b-/- relative to control) and corresponding statistical significance, $-\log_{10}$(P-value), control, n = 10, L-PTP1b-/-, n = 6. The dotted, red line corresponds to P-value = .05. Significance was determined with 2-sided Student t tests.

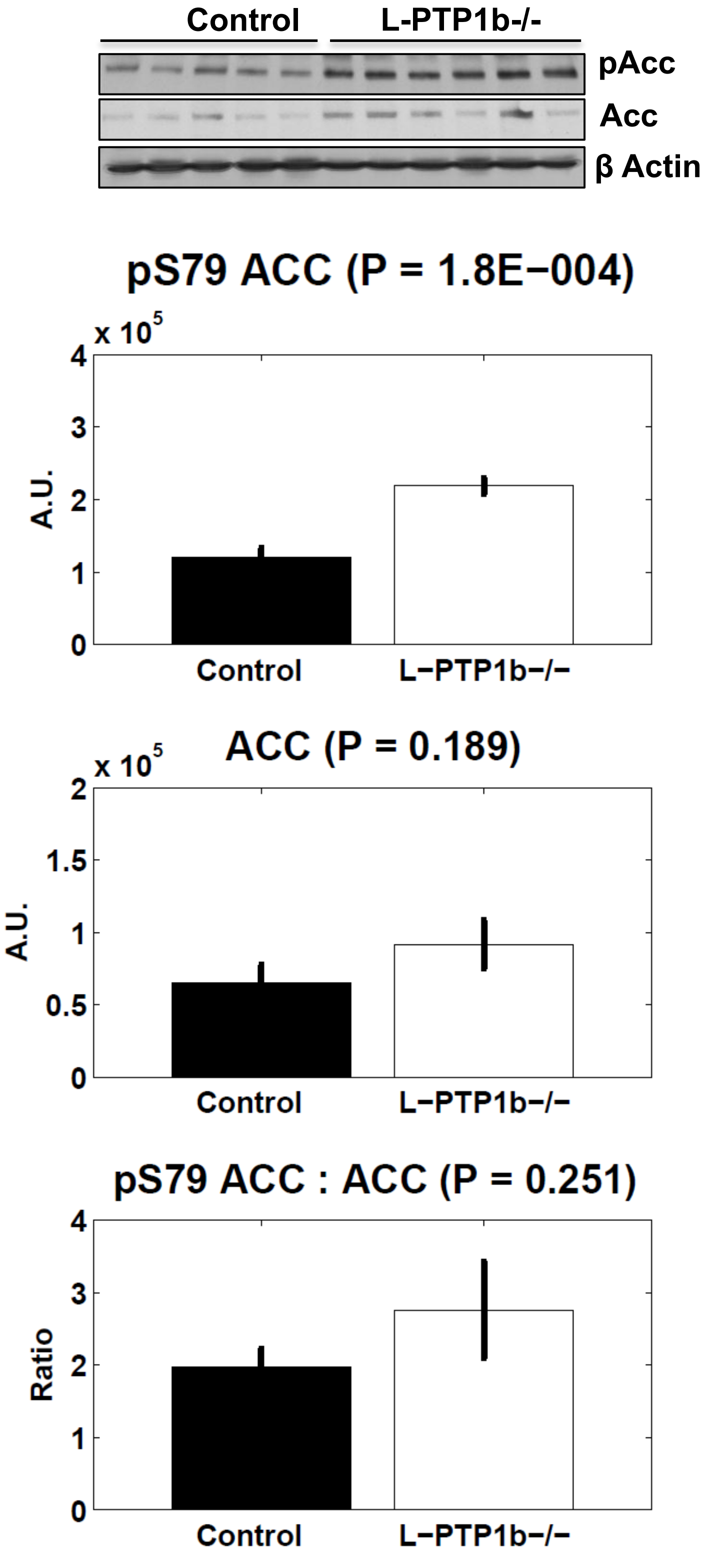

Figure S5. ACC phosphorylation
Western blots and quantification for pS79 ACC and total ACC. Significance was determined with 2-sided Student t tests.

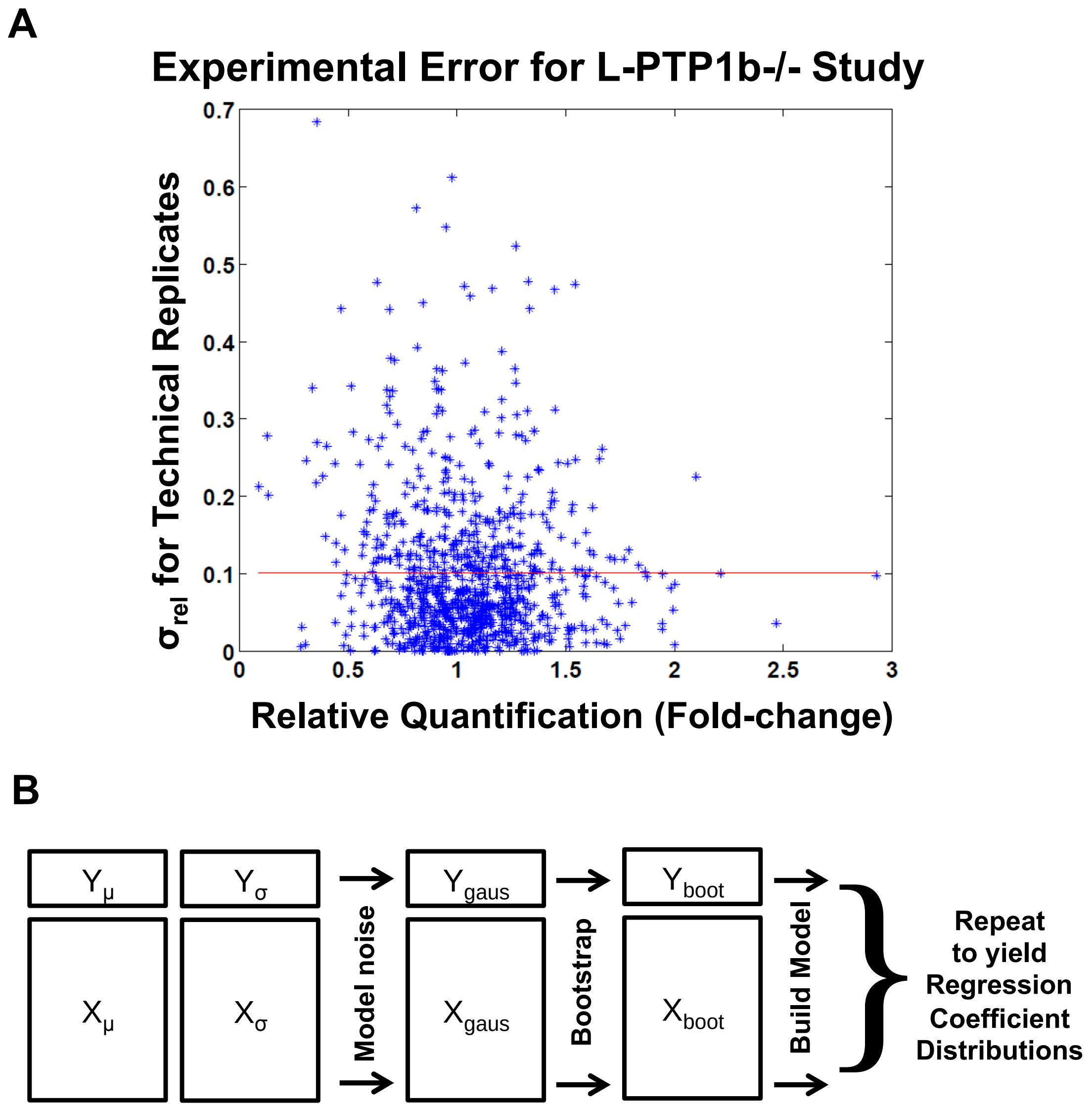

Figure S6. SMR

(A) A scatter plot of relative standard deviation, σ_{rel}, versus relative quantification, expressed as fold-change. The red line indicates mean σ_{rel} which is 10%.

(B) Stochastic multivariate regression (SMR) procedure. Predictor mean and standard deviation matrices are represented by X_μ, X_σ, dimensions [predictors × samples], and, response mean and standard deviation matrices are Y_μ, Y_σ, with dimesions [response × samples]. Noise is modeled via Monte Carlo sampling from Gaussian distributions whose means and standard deviations correspond to measurement means and error estimates, yielding X_{gaus} and Y_{gauss} matrices. The X_{gaus} and Y_{gauss} matrices are then sampled using bootstrapping to yield matrices X_{boot} and Y_{boot}, from which multivariate regression is performed to generate a sample of regression coefficients. This sampling procedure is repeated to yield distributions of regression coefficients from which coefficient significances can be estimated.

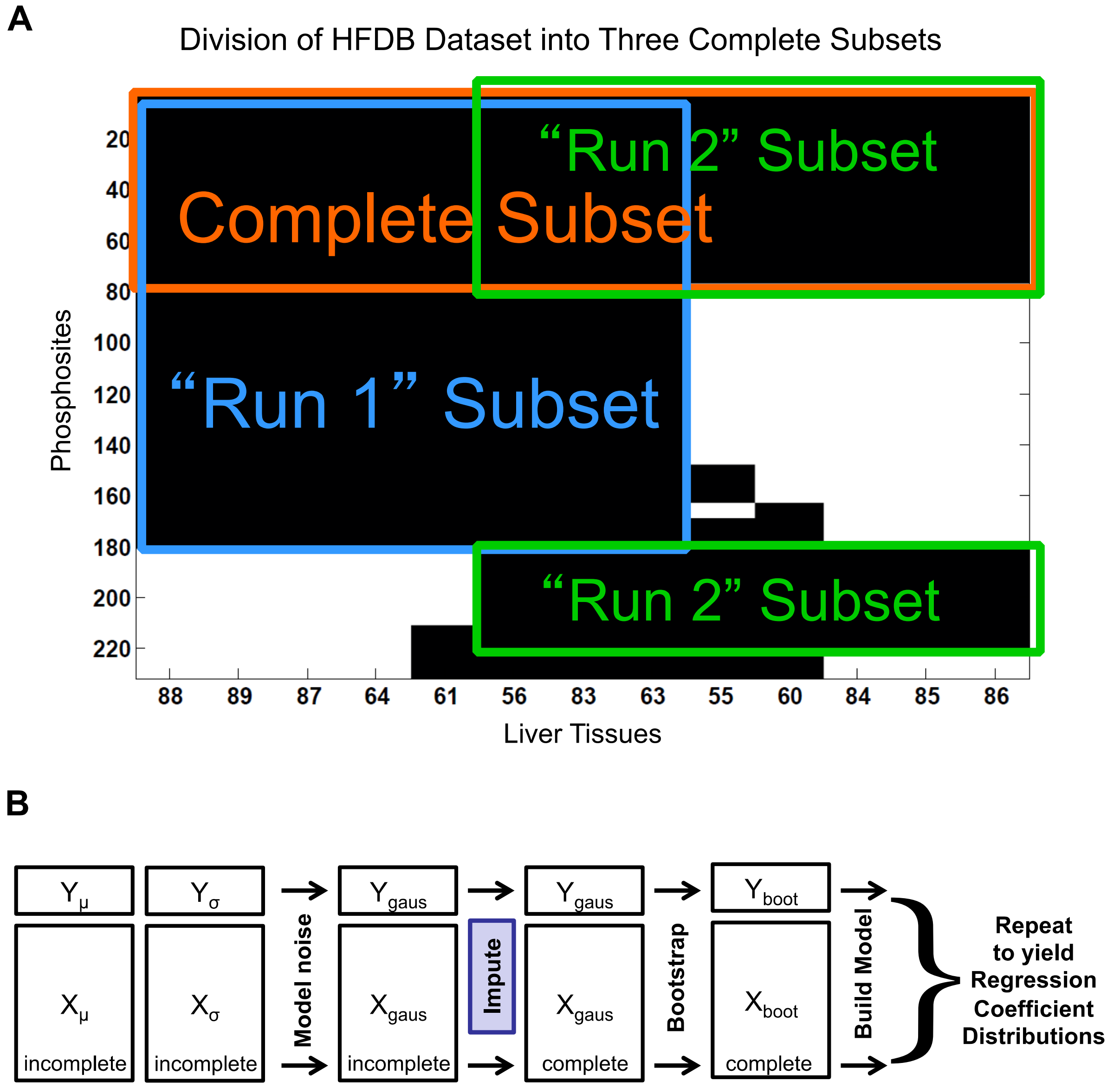

Figure S7. Missing Data Methods

(A) The three complete data subsets in the HFDB dataset, which are referred to in the "Merge complete subset models" missing-data methods.

(B) Adaptation of the SMR protocol for MRI of missing data. An imputation step is introduced between the Gaussian sampling and bootstrapping steps.

Supplemental Tables

Table S1: Animal weight and serum measurements

	NC		HFD	
	Control	**L-PTP1b$^{-/-}$**	**Control**	**L-PTP1b$^{-/-}$**
Weight (g)	25.4 +/- 1.0 (n = 13)	24.7 +/- 1.1 (n = 8)	32.8 +/- 1.4 (n = 19)***	30.3 +/- 0.8 (n = 17)
Fed Glucose (mg/dL)	192 +/- 6 (n = 13)	197 +/- 11 (n = 8)	236 +/- 7 (n = 15)***	223 +/- 11 (n = 13)
Fed Insulin (ng/mL)	0.89 +/- 0.13 (n = 7)	0.73 +/- 0.22 (n = 5)	3.47 +/- 0.91 (n = 7)*	2.92 +/- 0.94 (n = 5)
Fasting Glucose (mg/dL)	114 +/- 7 (n = 12)	160 +/- 11 (n = 8)**	120 +/- 8 (n = 15)	162 +/- 16 (n = 13)*
Fasted Insulin (pM)	56.42 +/- 10.24 (n = 6)	26.46 +/- 3.35 (n = 5)	63.3 +/- 13.14 (n = 8)	60.15 +/- 19.67 (n = 6)
Serum Triglycerides (mg/dL)	91.67 +/- 10.94 (n = 12)	78.38 +/- 8.22 (n = 8)	125.93 +/- 15.88 (n = 15)	91.85 +/- 7 (n = 13)
Cholesterol (mg/dL)	98.83 +/- 6.57 (n = 6)	83.6 +/- 12.52 (n = 5)	144.63 +/- 16.19 (n = 8)^	113.86 +/- 24.95 (n = 7)
HDL (mg/dL)	81.67 +/- 6.35 (n = 6)	69.4 +/- 11.53 (n = 5)	114.63 +/- 12.06 (n = 8)	88.43 +/- 19.37 (n = 7)
LDL (mg/dL)	4.33 +/- 0.78 (n = 6)	3.6 +/- 1.4 (n = 5)	10.63 +/- 1.93 (n = 8)*	14.86 +/- 4.29 (n = 7)
Adiponectin (pg/mL)	12.68 +/- 1.41 (n = 13)	11.45 +/- 1.05 (n = 8)	11.93 +/- 0.91 (n = 15)	15.03 +/- 1.48 (n = 11)
Leptin (pM)	54.24 +/- 19.56 (n = 5)	47.13 +/- 27.1 (n = 3)	168.97 +/- 89.5 (n = 7)	186.58 +/- 76.37 (n = 6)
Glucagon (pM)	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-/- mice to control on NC diet, (2) L-PTP1b-/- 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	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	RGWDENVyYTVPLVR/GWDENVyYTVPLVR	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	IAAFADAAVDPIDFPLAPAyAVPK	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	AANEAGyFNEEMAPIEVK	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	IESPEGYyEEAEPFDR	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	VAQQPLSLVGCDVLPDPSPDHLySFR	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	NNDLILyYFSDAK	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	YDGNVyENLFEWAK	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	DLGEAALNEyLR	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	ELGEHGLyEYTELK	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	AISFVGSNQAGEyIFER	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	YASICQQNGLVPIVEPEVLPDGDHDLEHCQyVSEK	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	IQSSAPQEEEEHPyELLLTAETK	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	LSLEGDHSTPPSAyGSVKPYTNFDAER	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	EGLYITEEIyK	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	VMEETFSyLLGR	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	yFSMTEVDK	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	DVDPGEHyIIK	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	FAELVyTGFWHSPECEFVR	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	EQGyDVIAYLANIGQK	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	TTDGVyEGVAIGGDR/TTDGVyEGVAIGGDRYPGSTFMDHVLR	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	SAVyIIENAK	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	IYNGDYyR	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	EAyNLGVR	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	MEDVyQTLVVHGQVLDSGR	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	GLLPNQYGQEVyDTPPMAVK	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	VLPPEVADGSVVDDGVyAVPPPAER	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	DPLLDVyDVPPSVEK/GPNGRDPLLDVyDVPPSVEK	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	HLLAPGPQDIyDVPPVR	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	RPGPGTLyDVPR	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	VGQGYVYEAAQTE	breast cancer anti-estrogen	gi|40254593	0.85 +/- 0.06 (n =	0.92 +/- 0.06 (n =	1.06 +/- 0.05 (n =	1.07 +/- 0.07 (n =	1.16 +/- 0.12 (n =	0.84 +/- 0.05 (n =	n.d.	0.67 (n = 1)	92, 57, 95, 82, 97

		QDEyDTPR	resistance 3		4)	3)	7)	6)	4)	2)			
BCAR3	Y424	TPPSPSPWLTSEANyCELNPAFAVGCDR	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	GPLDGSPyAQVQR	C1 domain-containing phosphatase and tensin-like protein	gi|119372288	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	LALPTAALyGLR	C1 domain-containing phosphatase and tensin-like protein	gi|119372288	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	VGEEGHEGCSyAVCSEGR	C1 domain-containing phosphatase and tensin-like protein	gi|119372288	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	DGNGyISAAELR/VFDKDGNGyISAAELR	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	SAyALGGLGSGICPNK	carbamoyl-phosphate synthetase 1	gi|124248512	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	VAGLLVLNySNDYNHWLATK	carbamoyl-phosphate synthetase 1	gi|124248512	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	VPAIyGVDTR	carbamoyl-phosphate synthetase 1	gi|124248512	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	Y1450	FVHDNyVIR	carbamoyl-phosphate synthetase 1	gi|124248512	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	yAAELHLVHWNTK	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	VVFDDTyDR	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	ATETVySEVK	carcinoembryonic 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

		LDIVNQFTTSQASR	protein 2				0.07 (n = 4)	0.1 (n = 4)					
CAT	Y231	LVNADGEAVyCK	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	GAGAFGyFEVTHDITR	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	NAGNEQDLGIQyK	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	LNGPQDHNHLLySTIPR	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	SLDNNySTLNER	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	yVDSEGHLyTVPIR	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	GSPGALSSDSELPENPySQVK	cingulin	gi|149251314	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	ENPyYDSR	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	Y1487	TSIDAyDNFDNISLAQR	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	Y1477	SVNESLNNLFITEEDyQALR	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(50)DGYQAQPLATR	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	IGEGTyGVVYK	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	NLSEGNNANYTEyVATR	cyclin-dependent kinase-like 5	gi|124244037	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	QDFPGQSSGFEySR	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	AGDEIICMDEVyGGTNR	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	yYTLEEIQK	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	YVLDDQyTSSSGAK	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	GRGDyDGIGGR	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	YEMTySGGGGGGGGGGGGTSR	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	TQPTDEEMLFIySHFK/LKTQPTDEEMLFIySHFK	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	DGLLFGPyESQEK	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	DyHFVTSR	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	GFSSDTALySQVQK	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	LTDSKEDPIyDEPEGLAPAPPR	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	LKEEGYELPYNPATDDyAVPPPR	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	NVyYELNDVR	enhancer trap locus 4	gi|124486588	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	GNPTVEVDLyTAK	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	AAVPSGASTGIyEALELR	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	TyVDPHTYEDPNQAVLK	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	VLEDDPEATyTTSGGK	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	FLEENSSDPTyTSSLGGK	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	Y1092	YSSDPTGAVTEDNIDDAFLPVPEyVNQSVPK	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	Y1172	GSHQMSLDNPDyQQDFFPK	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	Y1197	GPTAENAEyLR	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	Y1097	RTEGDyLSYR/TEGDyLSYR	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|126032329	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	EHALLAyTLGVK	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	GDDLLPAGTEDyIHIR	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	VIySQPSTR	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	HPEALDEETEHDyQNHI	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	yVGSMVADIHR	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	TLVYGGIFLyPANK/TLVYGGIFLyPANK	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	GNIYSLNEGyAKDFDPAINEYLQR/GNIYSLNEGyAKDFDPAINEYLQR/GNIYSLNEGyAK	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	LMNESLMLVTALNPHIGyDK	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	ETAIELGyLTAEQFDEWVKPK	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	ALSTANENDGyVDMSSFNAFESK	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	GPSEGAyDVILPR	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	SMSSSPWMPQDGFDPSDyAEPMDAVVKPR	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	NEEENIySVPHDSTQGK	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	RDDGSWEVIEGyR/DDGSWEVIEGyR	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	DIVHSGLAyTMER	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	NFGLyNER	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	IANDNSLNHEyLPILGLAEFR	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	NLDKEyLPIGGLAEFCK	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	NMGLyGER	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/KGyFEDR	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	yIIWSPVCR	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	MLLEyTDSSYDEK	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	YVTLIyTNYENGK	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	FEDGDLTLyQSNAILR	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	LISWYDNEyGYSNR	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	VVDLMAyMASK	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	SLGVAAEGLPDQyADGEAAR	glycine N-methyltransferase	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	AHMVTLDyTVQVPGTGR	glycine N-methyltransferase	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	VWQLyIGDTR	glycine N-methyltransferase	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	GEPNVSyICSR	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	GEPNVSyICsR	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	SSLTGSETDNEDVyTFK	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	SVLGNNFyEYYVNDPPR	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	VLLPEyGGTK	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	CEFQDAyVLLSEK	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	IQEITEQLDITTSEyEKEK	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	yIDQEELNK	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	APAAIGPySQAVQVDR	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,

		yGAEALER	alpha 1 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	LLVVyPWTQR	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	yFDSFGDLSSASAIMGNAK	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	VCEPCyEQLNK	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	MDyVEINIDHK	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	GGDyALAPGSQSSEMSLR	histocompatibility 2, D region locus 1	gi|133778955	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	GGDyALAPGSQTSDLSLPDCK	histocompatibility 2, K1, K region isoform 1	gi|133922588	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	AVCSTyLQSR	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	TVCSTyLQSR	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	GQNNPQVCPYNLyAEQLSGSAFTCPR	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	VPIVINPNAyDNLAIYK	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	TEVPyEELWLEEGKPSR	hypothetical protein LOC381126	gi|134288888	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	TSNSTSEESDLHyADIHVLR	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	IGIVGGCQEyTGAPYFAGISALK	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	YyKETSGLMLDVGGYMK	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	EIIVTDyTPQNLQELQK	indolethylamine N-methyltransferase	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	Y1136	TLSEVDyAPGPGR	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	Y1179/Y1175	DIy(50)ETDy(50)YR/DIy(50)ETDy(50)YRK	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	Y1175 Y1179	DIyETDyYRK	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	GEEELSNyICMGGK	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	EETGSEEyMNMDLGPGR	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	GDyMTMQIGCPR	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	SDDyMPMSPTSVSAPK	insulin receptor substrate 2	gi|124487073	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	APCSCSGDNDQyVLMSSPVGR	insulin receptor substrate 2	gi|124487073	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	SSSSNLGADDGyMPMTPGAALR	insulin receptor substrate 2	gi|124487073	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	ILGIPVIITEQyPK	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	SDyLNTFEFMDK	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	REVGDyGQLHK	Janus kinase 2	gi|114326478	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	STTFSTNyR	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	DVDEAyMNKVELESR	keratin complex 2, basic, gene 8	gi|114145561	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	Y1722	EGEyVVVGTNK	kinesin family member 13B	gi|124487163	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	QVVDSAyEVIK	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	SVDQDSQPVyCNLESLGR	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	SEGDTAyGQQVQPNTWK	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	GVNIGGAGSYIyEKPQTEAPQVTGPIEVPVVR	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	VDTDGNGyISCNELNDLFK	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	EVGVyEALKDDSWLK	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	IEDPVyGVYYVDHINRK/IEDPVyGVYYVDHINR	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	Y1001	SVSPTTEMVSNESVDyR	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	FVDLyGAQK	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	VADPDHDHTGFLTEyVATR	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/	VADPDHDHTGFLt(	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)EyVAt(50)R	kinase 1		6)	3)							24
p38-alpha	Y182	HTDDEMTGyVATR	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	HTDDEMtGyVATR	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	IADPEHDHTGFLt(50)EyVAt(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	IADPEHDHTGFLTEyVATR	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	Y1230	EyFTFPASK	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	Y1285	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	GIVVyTGDR	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	LyDLNMPAFVK	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	KTEQGPPSSEyIFER	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	KPEEVDDEVFySPR	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
PARD3	Y1123	EGHLMDTLyAQVK	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
PARD3	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	AGEEEHVySFPNK	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	DINAyNGETPTEK	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	QFADIAyNYR	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	LyEQLSGK	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	DQyLMWLTQK	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	HVEAIyIDIADR	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	IALyETPTGWK	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	HyGGLTGLNK	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	IGTAEPDyGALYEGR	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	ESDyESIGDLQQCR	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	QGIDHEyLSSVDLK	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	LKEQyQDLQMPEER/EQyQDLQMPEER	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	NNyALNTAATYAEPYRPVQYR	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	Y1166	STTNyVDFYSTK	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	ATETVySEIR	platelet/endothelial 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	SADDTyLQLK	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	DLEyLDLK	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	Y1051	IAEYSQLyDQIVFR	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	SIITYVSSLyDAMPR	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	EGEEPTVy(50)s(50)DDEEPKDETAR	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	KLEAAEDIAyQLSR	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	TFGENyVQELLEK	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	IQNTGDyYDLYGGEK	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	VyENVGLMQQQR	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	VVQEYIDAFSDyANFK	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	KLDTGGYyITTR	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	LCDFGSASHVADNDITPyLVSR	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	LDHHPEWFNVyNK	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	THAVSVSETDDyAEIIDEEDTYTMPSTR	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	EDGSFQGPTGNQHIyQPVGKPDPAAPPK	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	YMEDSTyYK	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	YIEDEDyYKASVTR	PTK2 protein tyrosine kinase 2	gi|27369678	0.64 +/- 0.08 (n =	0.67 +/- 0.13 (n =	1.1 +/- 0.05 (n =	1.23 +/- 0.03 (n =	0.96 +/- 0.11 (n =	1.09 +/- 0.04 (n =	n.d.	0.97 (n = 1)	33, 22, 22, 20, 30, 27,

		/YIEDEDyYK	beta		4)	2)	7)**	6)	4)	2)			19, 36, 31, 36
Pyk2	Y807	EAGyTEFTGPPQKPPR	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	YIEDEDyyKASVTR	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	ENGVDAVHPGyGFLSER	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	VFLLGEEVAQYDGAyK	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	NSQEAEVACPFIDSTySCPGK	RanBP-type and C3HC4-type zinc finger containing 1	gi|145046239	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
ARHGAP27	Y28	AQVDDPPEPVyANVER	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
ARHGAP42	Y342	LWLEAMDGKEPIyTLPAIISK	RIKEN cDNA 9030420J04 gene	gi|149259493	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
ARHGAP42	Y371	EPIyTLPAIISK	RIKEN cDNA 9030420J04 gene	gi|149259493	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	IEIPEyFNFAK	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	FDNLyGCR/SKFDNLyGCR	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	ADDyFLLR	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	FRENVQDVLPTLPNPDDyFLLR/ENVQDVLPTLPNPDDyFLLR	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	QQPTQFINPETPGyVGFANLP	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	ySEGYPGQR	serine hydroxymethyltransferase 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	DSDAEVySIIK	serine hydroxymethyltransferase 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	TAAELEAAGDyVK	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	GEPEALyAAVTK	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	yCRPESQEHPEADPGSAAPYLK	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	ALVPFLLDEDyEK	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	ENTIyLQVQTGK	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	AAyFGIYDTAK	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	yFPTQALNFAFK	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	SQPIDDEIyEELPEEEDTASVK	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	LPEDDERPPEEyDQPWEWK	Src homology 2 domain containing F	gi|111185924	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	LPQDDDRPADEyDQPWEWNR	src homology 2 domain-containing transforming protein B	gi|149252377	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	VTIADDySDPFDAK	src homology 2 domain-containing transforming protein B	gi|149252377	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	GESAGyMEPYEAQR	src homology 2 domain-containing	gi|149252377	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	ELFDDPSyVNIQNLDK	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	ADDADEFGySR	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	EyGMIYLGK	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	HSVNNTySQFQDEYSLEEVMK	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	ENPyEDVDLK	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	STLEENAyEDIVGGLPK	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	DNEVDGQDyHFVVSR/RDNEVDGQDyHFVVSR	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
talin 1	Y26	TMQFEPSTMVyDACR	talin 1	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
talin 1	Y1116	LLGEIAQGNENyAGIAAR	talin 1	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
talin 2	Y1665	ECDySIDGINR	talin 2	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	ySMPDNSPETR	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	HAAYGGySTPEDR	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	EDGMEEVVGHTQGPLDGSLyAK	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	AGSLPNyATINGK	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)ADGEVLHt(25)QGPVDGSLyAK	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	IyGISFPDPK	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	TRyEQLPR	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	YEVSSyTDQFSR	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	QyFDQYPR	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	QLSyFDRR	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	VFLRPSPEDEAIyGPNTK	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	SEGTyCCGPVSVR	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	yENVPLIGR	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	GEySPSVQK	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	EEVLLPLDNPyGK/MGLINKEEVLLPLDNPyGK	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	LMTGDTyTAHAGAK	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	VVETDPSPyCIVAPDTVIHCEGEPIKR	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

		TALALEVGELVK	virus CT10 oncogene homolog						0.07 (n = 4)	0.02 (n = 2)		1)	
CrkL	Y198	NSNSyGIPEPAHAYAQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK	v-crk 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	TLyDFPGNDAEDLPFK	v-crk 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	Y1325	SLEATDSAFDNPDyWHSR	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	NPGNQAAyEHFETMK	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	SFLDSGyR	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	KLDNGGYyITTR/LDNGGyYITTR	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	LIEDNEyTAR	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	TDEFQLHTNVNDGTEFGGSIyQK	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	LIyDFIEDQGGLEAVR	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	VIyDFIEK	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	MENCPDE	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	RGWDENVyYTVPLVR/GWDENVyYTVPLVR	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-/- mice to control on NC diet, (2) L-PTP1b-/- 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
Endoplasimic 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, PITPNA 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, PITPNA 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, CTNNB1 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 patway	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, ITSN2 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

P_{raw}	**NES**	**Category Label**	**N**	**Category Membership**	**Source**
<2E-05**	-3.47	**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
<2E-05**	-3.58	**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
<2E-05**	-3.10	**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
<2E-05**	-3.66	**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	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	**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
3.2E-05**	-2.40	**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
1.4E-04**	2.45	**Tight junction**	20	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*	KEGG
2.3E-04*	-2.30	**Fatty acid metabolism**	9	*HADHA Y724, ACAT1 Y328, ACAA2 Y198, ACOX1 Y629*, ACLY Y672*, PRDX6 Y89, ACSL5 Y69, ACBP Y29, CYB5A Y11	KEGG, Literature
4.5E-04*	-2.26	**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
4.5E-04*	-2.27	**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
5.2E-04*	-2.25	**Mitochondria**	35	*Lyn Y173, PC Y118, HADHA Y724, FH Y488, CPS1 Y140, HSPE1 Y76, SLC25A5 Y191, SLC25A5 Y81, ACAT1 Y328, FH Y462, GLUD1*	GO

				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	
6.5E-04*	-2.24	**Phenylalanine metabolism**	8	*GOT1 Y264, GOT2 Y96,* GOT1 Y71*, HPD Y232, GOT2 Y284, PAH Y166, PRDX6 Y89, HPD Y221	KEGG
7.1E-04*	-2.22	**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
1.1E-03^	-2.16	**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
1.1E-03^	-2.16	**Insulin-sensitive pYs in adipocytes**	33	*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	Schmelzle et al.
1.8E-03^	-2.09	**Cysteine and methionine metabolism**	9	*GOT1 Y264, BHMT Y289, CTH Y59, GOT2 Y96,* GOT1 Y71*, GOT2 Y284, CTH Y113, LDHA Y239, SAHH Y193	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-depedendent 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

P_{raw}	**NES**	**Category Label**	**N**	**Category Membership**	**Source**
2.2E-04**	2.28	**Mitochondria**	22	HSPE1 Y76, NIPSNAP1 Y261, SLC25A5 Y191, GOT2 Y96, GLUD1 Y512, CAT Y231*, *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*	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

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

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

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

C22:0	0.376 +/- 0.0337 (n = 7)	0.309 +/- 0.0557 (n = 3)	0.303 +/- 0.0828 (n = 19)	0.187 +/- 0.0188 (n = 17)
C24:6	0.0831 +/- 0.00985 (n = 7)	0.103 +/- 0.0206 (n = 3)	0.0128 +/- 0.00161 (n = 19)***	0.0205 +/- 0.00187 (n = 17)**
C24:5	0.0687 +/- 0.0117 (n = 7)	0.0841 +/- 0.0244 (n = 3)	0.0242 +/- 0.00293 (n = 19)***	0.0417 +/- 0.00487 (n = 17)**
C24:4	0.0127 +/- 0.00452 (n = 6)	0.0182 +/- 0.00691 (n = 3)	0.0193 +/- 0.00189 (n = 11)	0.0345 +/- 0.00435 (n = 10)**
C24:3	n.d.	n.d.	0.00349 +/- 0.0017 (n = 3)	0.0079 +/- 0.00284 (n = 4)
C24:2	0.0625 +/- 0.00539 (n = 7)	0.0571 +/- 0.00605 (n = 3)	0.0206 +/- 0.00366 (n = 11)***	0.0215 +/- 0.00223 (n = 10)
C24:1	0.358 +/- 0.0476 (n = 7)	0.295 +/- 0.0268 (n = 3)	0.14 +/- 0.032 (n = 11)**	0.113 +/- 0.0138 (n = 10)
C24:0	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-/- mice to control on NC diet, (2) L-PTP1b-/- 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

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

% Liver triglyceride composition

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

HFD Serum Triglyceride Compositions				
	Absolute Quantification (mg/dL)		Percent Composition	
	Control	L-PTP1b$^{-/-}$	Control	L-PTP1b$^{-/-}$
Tg C48:3	0.19 +/- 0.09 (n = 7)	0.18 +/- 0.17 (n = 6)	0.39 +/- 0.13 (n = 7)	0.32 +/- 0.18 (n = 6)
Tg C48:2	0.26 +/- 0.14 (n = 7)	0.3 +/- 0.25 (n = 6)	0.53 +/- 0.19 (n = 7)	0.56 +/- 0.24 (n = 6)
Tg C50:3	0.71 +/- 0.32 (n = 7)	0.75 +/- 0.61 (n = 6)	1.47 +/- 0.46 (n = 7)	1.44 +/- 0.54 (n = 6)
Tg C50:2	1.89 +/- 1.04 (n = 7)	2.45 +/- 1.81 (n = 6)	3.89 +/- 1.54 (n = 7)	4.8 +/- 1.43 (n = 6)
Tg C50:1	1.81 +/- 0.91 (n = 7)	2.31 +/- 1.29 (n = 6)	3.68 +/- 1.14 (n = 7)	5.01 +/- 0.27 (n = 6)*
Tg C50:0	0.27 +/- 0.14 (n = 7)	0.33 +/- 0.12 (n = 6)	0.54 +/- 0.15 (n = 7)	0.83 +/- 0.28 (n = 6)*
Tg C52:7	0.09 +/- 0.03 (n = 7)	0.06 +/- 0.03 (n = 6)	0.19 +/- 0.07 (n = 7)	0.13 +/- 0.02 (n = 6)^
Tg C52:6	0.4 +/- 0.08 (n = 7)	0.31 +/- 0.18 (n = 6)	0.87 +/- 0.17 (n = 7)	0.65 +/- 0.07 (n = 6)*
Tg C52:5	2.16 +/- 0.57 (n = 7)	1.79 +/- 1.25 (n = 6)	4.55 +/- 0.53 (n = 7)	3.56 +/- 0.92 (n = 6)*
Tg C52:4	8.4 +/- 2.42 (n = 7)	7.42 +/- 4.66 (n = 6)	17.67 +/- 2.36 (n = 7)	15.23 +/- 2.72 (n = 6)
Tg C52:3	8.26 +/- 2.38 (n = 7)	7.54 +/- 3.87 (n = 6)	17.3 +/- 1.55 (n = 7)	16.72 +/- 1.17 (n = 6)
Tg C52:2	6.92 +/- 2.62 (n = 7)	8.06 +/- 3.45 (n = 6)	14.2 +/- 1.94 (n = 7)	18.73 +/- 2.79 (n = 6)**
Tg C54:7	0.42 +/- 0.13 (n = 7)	0.29 +/- 0.16 (n = 6)	0.91 +/- 0.31 (n = 7)	0.64 +/- 0.08 (n = 6)^
Tg C54:6	1.6 +/- 0.48 (n = 7)	1.12 +/- 0.62 (n = 6)	3.46 +/- 0.98 (n = 7)	2.47 +/- 0.28 (n = 6)*
Tg C54:5	3.3 +/- 0.7 (n = 7)	2.6 +/- 1.44 (n = 6)	7.08 +/- 1.3 (n = 7)	5.64 +/- 0.44 (n = 6)*
Tg C54:4	2.5 +/- 0.65 (n = 7)	2.16 +/- 1.17 (n = 6)	5.34 +/- 1.1 (n = 7)	4.81 +/- 0.59 (n = 6)
Tg C54:3	4.29 +/- 1.06 (n = 7)	4.73 +/- 2.15 (n = 6)	9.05 +/- 1.17 (n = 7)	10.86 +/- 1.2 (n = 6)*
Tg C54:2	0.9 +/- 0.47 (n = 7)	0.94 +/- 0.44 (n = 6)	1.8 +/- 0.48 (n = 7)	2.15 +/- 0.32 (n = 6)
Tg C56:9	0.14 +/- 0.07 (n = 7)	0.07 +/- 0.04 (n = 6)*	0.32 +/- 0.17 (n = 7)	0.16 +/- 0.03 (n = 6)*
Tg C56:8	0.64 +/- 0.31 (n = 7)	0.32 +/- 0.17 (n = 6)^	1.4 +/- 0.7 (n = 7)	0.74 +/- 0.16 (n = 6)*
Tg C56:7	1.12 +/- 0.55 (n = 7)	0.7 +/- 0.3 (n = 6)	2.43 +/- 1.17 (n = 7)	1.68 +/- 0.39 (n = 6)
Tg C56:4	0.38 +/- 0.11 (n = 7)	0.42 +/- 0.14 (n = 6)	0.8 +/- 0.09 (n = 7)	1.06 +/- 0.33 (n = 6)^
Tg C56:3	0.37 +/- 0.17 (n = 7)	0.42 +/- 0.16 (n = 6)	0.75 +/- 0.18 (n = 7)	1.02 +/- 0.26 (n = 6)^
Tg C58:10	0.16 +/- 0.13 (n = 7)	0.06 +/- 0.02 (n = 6)^	0.36 +/- 0.27 (n = 7)	0.16 +/- 0.05 (n = 6)
Tg C58:9	0.25 +/- 0.17 (n = 7)	0.12 +/- 0.04 (n = 6)^	0.56 +/- 0.38 (n = 7)	0.32 +/- 0.13 (n = 6)
Tg C58:8	0.21 +/- 0.14 (n = 7)	0.12 +/- 0.03 (n = 6)	0.47 +/- 0.28 (n = 7)	0.32 +/- 0.12 (n = 6)
Total	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. ** = $P_{raw}<.01$, * = $P_{raw} < .05$, ^ = $P_{raw}<.1$.

Table S9: Enrichments for phosphosites predictive of the PTP1b-dependent ω3 / ω6 PUFA (C24:6, C24:5, C24:4, C22:3, C20:3)

P_{raw}	NES	Category Label	N	Category Membership	Source
1.1E-04**	2.44	**Metabolic process**	25	CYP2E1 Y426, CYB5A Y11, CAR2 Y114, LDHA Y239, PGM1 Y353, GAPDH Y316, PRDX6 Y89, CTH Y113, CPS1 Y162, TGM2 Y369*, *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*	GO
1.1E-04**	2.43	**Oxidation reduction**	24	CYP2E1 Y426, CYB5A Y11, SAHH Y193, HPD Y232, LDHA Y239, HPD Y221, HGD Y40, GAPDH Y316, PRDX6 Y89, FASN Y1248, ALDH1A7 Y484*, *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*	GO, SwissProt, Literature
1.4E-03^	2.13	**Endoplasimic Reticulum**	16	CYP2E1 Y426, CALM1 Y100, GLUL Y336, CYB5A Y11, PEBP1 Y181, HPD Y232*, *HPD Y221, VCP Y173, ASS1 Y133, CAV1 Y14 Y6, CAT Y231, ALDOB Y204, ACSL5 Y69, CAT Y84, HSPD1 Y385, ASS1 Y322,*	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 ω3 / ω6 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 ω7 / ω9 PUFA (C20:3, C22:3, C20:2, C18:3)

P_{raw}	NES	Category Label	N	Category Membership	Source
<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*, *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*	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*, *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*	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*, *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*	GO
1.3E-03^	2.23	Endoplasimic Reticulum	16	CYB5A Y11, CYP2E1 Y426, GLUL Y336, HPD Y221, CALM1 Y100, PEBP1 Y181, HPD Y232, VCP Y173, CAT Y231, ASS1 Y133*, *ALDOB Y204, CAV1 Y14 Y6, CAT Y84, ACSL5 Y69, HSPD1*	GO

				Y385, ASS1 Y322	

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 ω7 / ω9 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

P_{raw}	NES	Category Label	N	Category Membership	Source
1.1E-04**	2.55	**Oxidation reduction**	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*, *HPD Y232, CAT Y231, GLUD1 Y512, ALDH6A1 Y268, UOX Y288, UGDH Y108, GLUD1 Y135, GAPDH Y328, UOX Y230, HADHA Y724*	GO, SwissProt, Literature
4.9E-04*	2.37	**Metabolic process**	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	**Chemokine signaling pathway**	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	**Adherens junction**	23	*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	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.