Table S3. SILAC-based quantification of pTyr peptides recovered from nontransformed vs. Src-transformed cells

					Number of identifications in label-free analysis [b]			
					nontransformed		Src-transformed	
Protein name	**UniProt #**	**pY site**	**Peptide**	**Ratio (H/L)[a]**	**peptide**	**total**	**peptide**	**total**
Src	Q80XU2	Y418	LIEDNEY@TAR	32	11	11	20	27
		Y438	WTAPEAALY@GR	H only	0	0	9	21
p190RhoGAP	Q91YM2	Y943	NEEENIY@SVPHDSTQGK	2.8	28	28	20	20
RIN1	Q921Q7	Y35	EKPSTDPLY@DTPDTR	5.0	4	4	4	4
p130cas	Q61140	Y253	HLLAPGPQDIY@DVPPVR	4.0	31	32	10	10
Talin 1	P26039	Y26	TMQFEPSTMVY@DAC*R	6.2	5	8	10	11
		Y70	ALDY@YMLR	6.5	5	12	9	9
VASP	P70460	Y39	VQIY@HNPTANSFR	9.0	4	5	5	7
p120ctn	P30999	Y96	LNGPQDHNHLLY@STIPR	10.5	12	12	15	15
Alpha enolase	P17182	Y43	AAVPSGASTGIY@EALELR	H only	6	6	51	81
			AAVPSGASTGIY@EALELRDNDKTR	8.9	0		0	
GAPDH	P16858	Y315	LISWYDNEY@GYSNR	12.5	8	8	34	41
eEF1A-1	P10126	Y29	STTTGHLIY@K	9.0	11	11	18	18
CDK1	P11440	Y15	IEKIGEGTY@GVVYK	0.51	7	132	0	9
			IGEGTY@GVVYK	0.55	39		8	
GSK-3	Q9WV60	Y216	GEPNVSY@IC*SR	1.11	25	92	2	5
Vimentin	P20152	Y52	SLY@SSSPGGAYVTR	H only	2	2	11	17
Proteasome subunit alpha type 2 -- PSMA2	P49722	Y56	SILY@DER	5.8	0	0	0	1
		Y75	HIGLVY@SGMGPDYR	6.4	1	1	24	72
Heat shock protein HSP 90-beta	P11499	Y483	SIY@YITGESK	5.5	2	2	11	11
Eukaryotic translation initiation factor 3 subunit 6-interacting protein -- Eif3s6ip	Q91YE4	Y72	TVSDLIDQKVY@ELQASR	12.3	0	0	23	27
Thioredoxin reductase 1, cytoplasmic	Q9JMH6	Y131	KVVYENAY@GR	H only	0	0	9	15
			VVYENAY@GR	H only	0		6	
Eukaryotic translation initiation factor 3, subunit 8	Q8R1B4	Y879	QGTY@GGYFR	26.7	0	0	0	14
			VFDHKQGTY@GGYFR	10	0		1	
Polymerase I and transcript release factor -- PTRF	O54724	Y310	KSFTPDHVVY@AR	85	2	7	2	3
			SFTPDHVVY@AR	6.8	3		1	
		Y158	VMIY@QDEVKLPAK	2	1	3	1	2
Histone H4	P62806	Y51	ISGLIY@EETR	12.4	0	0	11	12
Plectin 1	Q6S394	Y3250	ARQEEVY@SELQAR	H only	0	0	17	17
Glucose-6-phosphate 1-dehydrogenase X	Q00612	Y400	VQPNEAVY@TK	35	0	0	2	14
Actin, alpha skeletal muscle (Beta-actin) (Gamma-actin)	P68134	Y93	IWHHTFY@NELR	6.7	3	3	12	12
Regulator of nonsense transcripts 1 -- RENT1	Q9EPU0	Y930	FMTTAMY@DAR	14.8	0	0	7	7
Proteasome subunit beta type 5 precursor	O55234	Y165	AIY@QATYR	H only	0	0	7	7

OTU domain containing 4 protein -- Otud4; PREDICTED: HIV-1 induced protein HIN-1 isoform 1	UPI0000218B34	Y458	LLY@EIQNR	11.5	0	0	10	16
Double-stranded RNA-binding protein Staufen homolog	Q9Z108	Y404	TRPSEQLY@YLSR	H only	0	0	18	18
Prolyl endopeptidase	Q9QUR6	Y71	MTELY@DYPK	8.8	1	1	7	14
Clathrin heavy chain	Q68FD5	Y899	FLRENPY@YDSR	H only	0	0	5	5
Anaphase promoting complex subunit 2	Q8BZQ7	Y825	DQQLIY@SAGVYRLPK	H only	0	0	10	30
Ubiquitin associated protein 2-like -- UBAP2L	Q80X50	Y878	DGSLASNPY@SGDLTK	12.9	0	0	9	16
Splicing factor, arginine/serine-rich 3	P84104	Y32	AFGY@YGPLR	3.9	0	0	8	8
Annexin A2	P07356	Y237	SYSPY@DMLESIKK	10.0	0	0	9	10
Alpha-1 catenin	P26231	Y619	LVY@DGIR	8.0	0	0	0	0
			LVY@DGIRDIR	9.9	0		0	
Tight junction protein ZO-1	P39447	Y1521	TITPVY@NR	7.2	0	0	0	0
Elongation complex protein 3	Q9CZX0	Y329	GTGLY@ELWK	H only	0	0	0	0
DNA damage-binding protein 1	Q9QYK0	Y718	TVPLY@ESPR	5.1	0	0	0	0
U1 snRNP 70 kDa	Q62376	Y126	EFEVY@GPIKR	H only	0	0	0	0

Footnotes:

a Nontransformed cells were grown in regular DMEM and Src-transformed cells were adapted for growth in DMEM containing "heavy" amino acids 13C6-arginine and 13C6-lysine. The heavy/light ratio (H/L) indicates the fraction of a given pTyr-containing peptide in the Src-transformed cell poplation relative to the same peptide in the nontransformed cells. "H only", indicates the peptide peak was clearly evident only in the Src-transformed cells.

b Shown for comparision are the numbers of times the specific peptides were identified and the total pTyr site identifications from the lavel-free analysis.