Supplemental Data

Note: Tables S1 and S2 are Excel Spreadsheets

Table S1: Table of pPeptides Identified by PhosphoScan Mass Spectrometry

Shown are all the peptides identified by SpectrumMill with their quantification across all the samples, obtained as described in Materials and Methods. Each peak represents an occurrence of a peptide with unique sequence and charge. Lowercase s,t, and y represent phosphorylated residues while unmodified residues are written in uppercase. Also shown is average Log 2 intensity for all peaks from all the samples and their differences. “t” and “p” values for each peak differences derived from ANOVA analysis are shown.

Table S2: Table of Pathway Studio Interactions

This table shows the relations that are obtained in pathway analysis using Pathway Studio (Ariadne Genomics, Inc) shown in Fig. 1F by. It shows molecules for which a given relation is found, type of relation, limited quote from literature and medline references that supports a particular relation.

	U251		LN428		LNZ308		U87	
Locus	1	2	1	2	1	2	1	2
AMEL	111.29	106.09	111.5	106.43	105.83	0.00	106.26	0.00
D3s1358	134.75	130.92	134.61	130.92	126.74	0.00	134.75	130.85
TH01	177.82	0.00	177.04	170.26	177.67	0.00	177.40	0.00
D13s317	188.72	184.86	176.51	0.00	196.75	188.86	188.49	176.74
D8s1179	233.90	225.73	224.61	220.60	225.57	205.35	217.12	213.08
D7s820	237.82	229.56	236.7	220.47	237.57	229.47	225.04	220.97
TPOX	268.82	0.00	280.49	267.83	273.31	269.04	268.34	0.00
D16s539	294.86	0.00	280.91	0.00	294.94	282.09	294.38	0.00
D18s51	305.82	0.00	321.09	305.01	329.73	305.75	305.44	0.00
CSF1PO	344.95	340.60	336.07	0.00	345.18	340.95	340.55	336.31
Penta D	422.84	0.00	428.12	0.00	418.31	408.41	433.07	408.32
Penta E	412.09	396.06	444.4	433.69	412.53	396.32	433.78	396.07

Table S3: STR Fingerprinting consensus results of the lines used.

Shown are the allele sizes obtained by analysis of genomic DNA from the three cell lines used in this manuscript, and analyzed using the GenomeLab Human STR Primer set from Beckman Coulter, according to the manufacturer's instructions. 0.00 indicates that no second allele was observed for this marker. While we do not claim that our isolates of these cell lines are their definitive instances, these data allow specific identification of our lines, and potentially comparison to the lines from other laboratories using this analysis.