Multiplexing: Measure more than cytokines!



AGENDA

- Module 1: xMAP technology based genomic and proteomic applications
- ✓ Module 2: Lab demo of SNP typing assay.
- ☐ Module 3: Milliplex MAP phospho-signaling
- Module 4: Lab demo of a signaling assay
- ☐ Module 5: Wrap up, additional questions/review

Ramsey McIntire, PhD

Multiplex & Cytometry Specialist

EMD Millipore

MILLIPLEX MAP - Market Leader!



Human

Cytokine/chemokine
T lymphocytes
Cytokine receptors
Immunoglobulin
Cardiovascular

Cancer IGFBPs

Angiogenesis Metastasis

Neurodegenerative

Neuropeptide

Adipokine/Adipocyte Metabolic hormone

Metabolic

Liver

Pituitary

Thyroid

Bone

Skin

Kidney Toxicity

Signaling

Y/S/T phosphorylation

Apoptosis

RTK

OxPhos Fatty Acid Ox Glycolysis



Primate

Cytokine/chemokine Metabolic hormone

Rat

Cytokine/chemokine Immunoglobulin Adipokine/Adipocyte Metabolic hormone Pituitary Stress hormone Thyroid Bone Cardiovascular Neuropeptide Kidney toxicity Vascular injury



Assays



Mouse

Cytokine/chemokine
T lymphocytes
Immunoglobulin
Adipokine/adipocyte
Metabolic hormone
Pituitary
Thyroid
Bone
Cardiovascular
Angiogenesis
Neuropeptide

Canine

Cytokine/chemokine

Metabolism Pituitary

Kidney Toxicity



Cytokine/chemokine

The Challenges of Cell Signaling

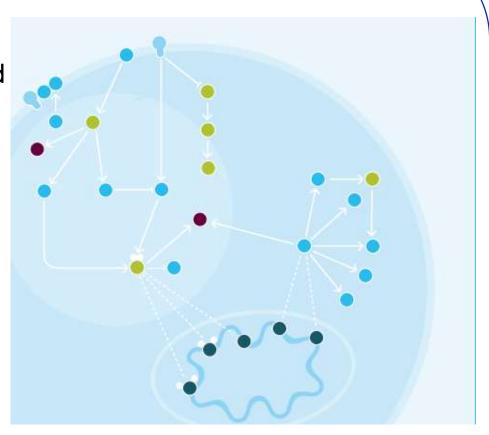


Cell signaling is part of a complex system of communication that dictates basic activities in the cell and coordinates cellular functions.

Protein targets of interest are often transient and low expression.

Why multiplex?

- Analyze multiple proteins in a pathway simultaneously
- Analyze multiple pathways in one cell/tissue lysate simultaneously
- Save samples and time!



Milliplex vs. Western Blot



10 proteins40 samples

Number of assays required

Total time to result

Results per assay

Total sample used

Internal controls possible?

xMAP® Technology

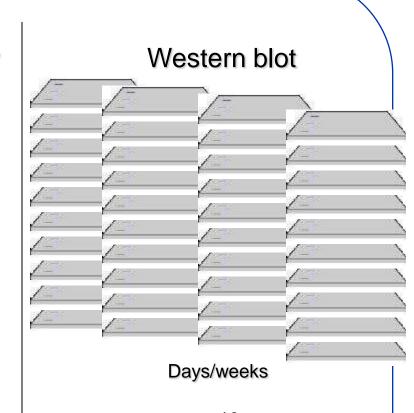


18 hours

400

50 μl (1-25 μg)

YES



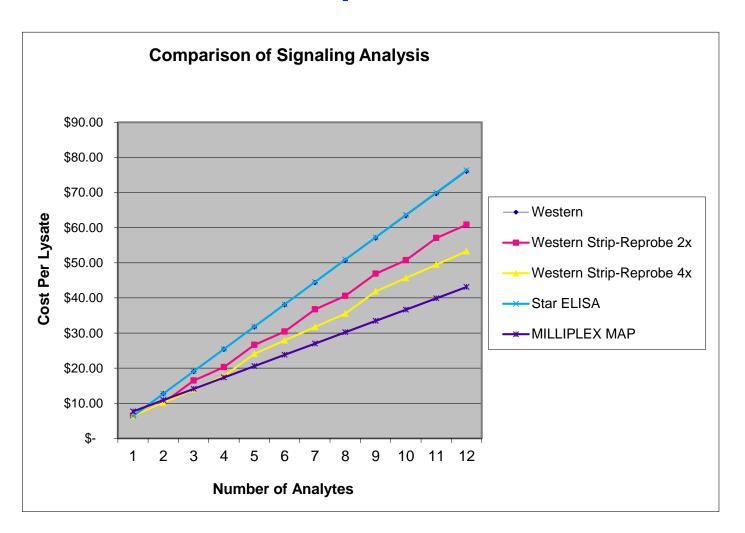
~10

~200 µl (~100-500 µg)

NO

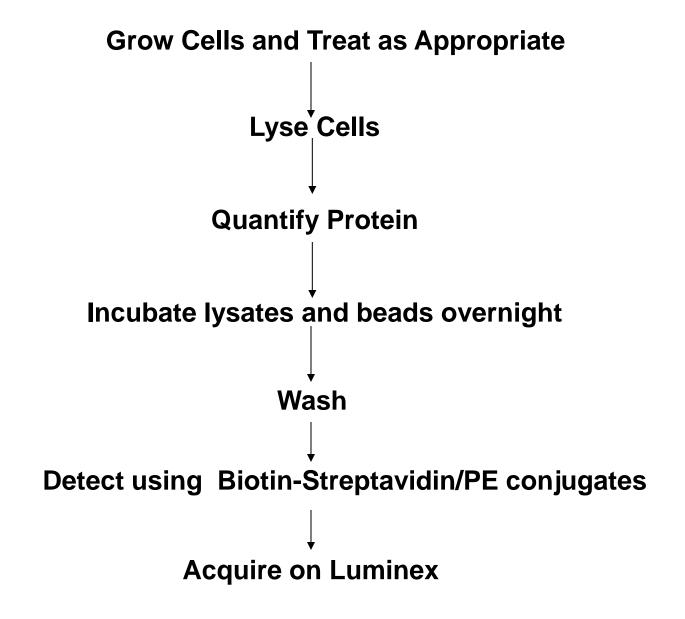


Western Blot Comparison



Milliplex Intracellular Assay Procedure





Akt/mTOR Panel: 11-plex



Analytes: p70S6K (Thr412)

IRS1 (Ser312)

GSK3 α (Ser21)

GSK3b (Ser9)

Akt (Ser473)

PTEN (Ser380)

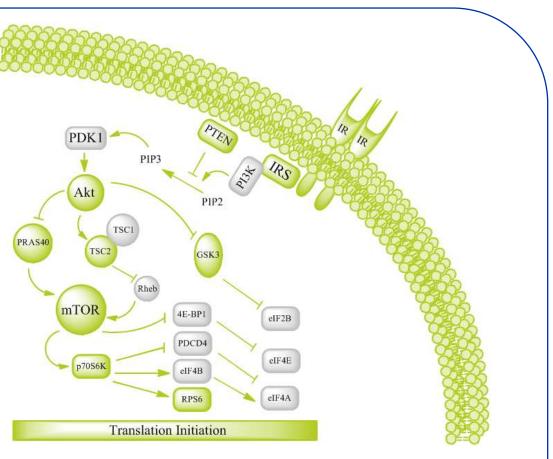
IR (Tyr1162/Tyr1163)

IGF1R (Tyr1135/Tyr1136)

RPS6 (Ser235/Ser236)

TSC2 (Ser939)

mTOR (Ser2448)



The MILLIPLEX MAP Human Akt/mTOR Phosphoprotein Magnetic Bead Panel 11-plex, is used to detect changes in phosphorylated p70S6K (Thr412), IRS1 (Ser312), GSK3a (Ser21), GSK3b (Ser9), Akt (Ser473), PTEN (Ser380), IR Tyr1162/Tyr1163), IGF1R (Tyr1135/Tyr1136), RPS6 (Ser235/Ser236), TSC2 (Ser939), and mTOR (Ser2448) in cell lysates using the Luminex® system. The detection assay is a rapid, convenient alternative to Western Blotting and immunoprecipitation procedures. Each kit has sufficient reagents for one 96-well plate assay.

Akt/mTOR Panel



11-plex Akt/mTOR Panel Analysis of Insulin Treated HepG2 and IGF-1 Treated MCF-7 Cells

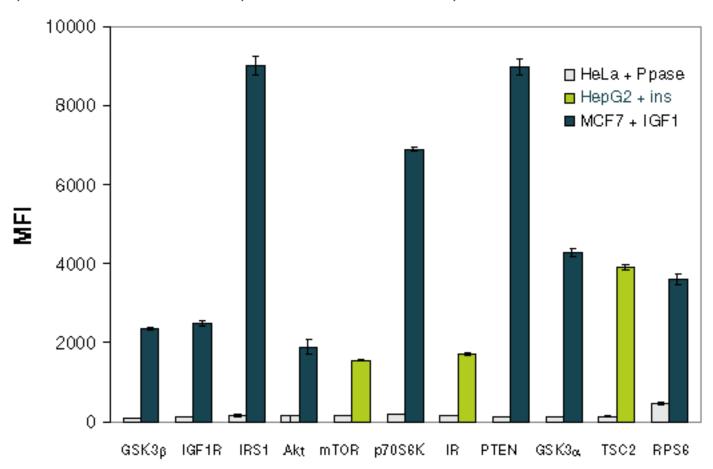
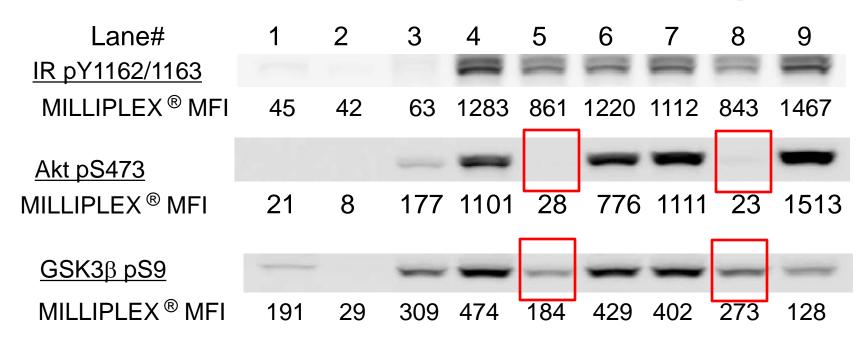


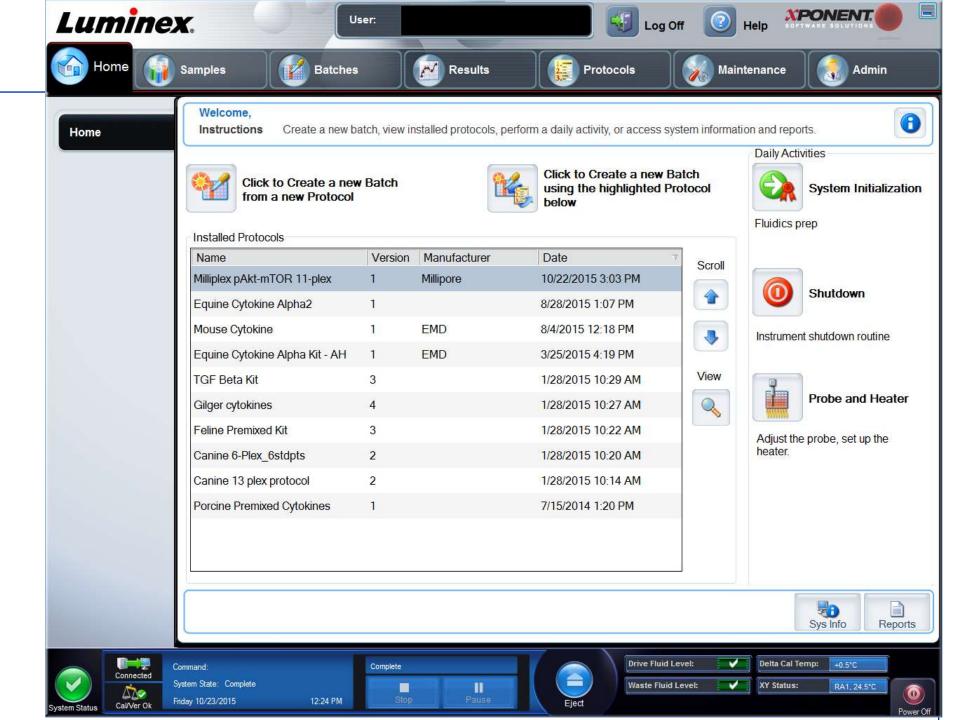
Figure 1. Multiplex analysis of HepG2 and MCF-7 cells treated with insulin or IGF-1. HepG2 cells stimulated with 10 μg/mL of insulin (15 min) or MCF-7 cells stimulated with 50 ng/mL IGF-1 (10 min) were assayed. The cells were lysed in MILLIPLEX MAP Lysis Buffer containing protease inhibitors. 20 μg total protein of each lysate diluted in MILLIPLEX MAP Assay Buffer 2 were analyzed according the Assay protocol (lysate incubation at 4°C overnight). The Median Fluorescence Intensity (MFI) was measured with the Luminex system. The figures represent the average and standard deviation of three replicate

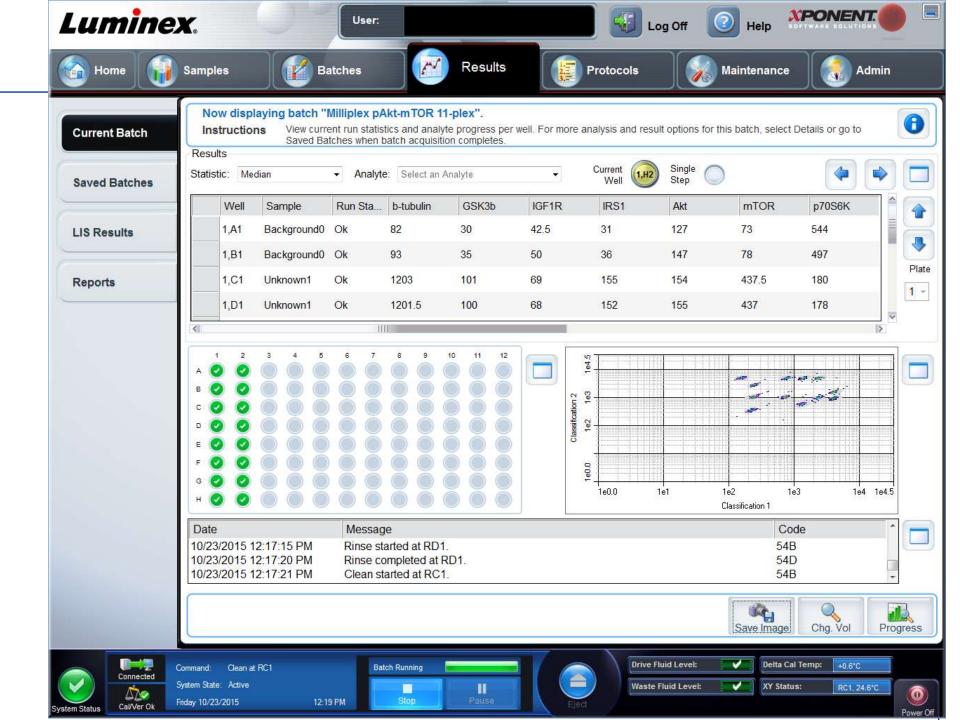


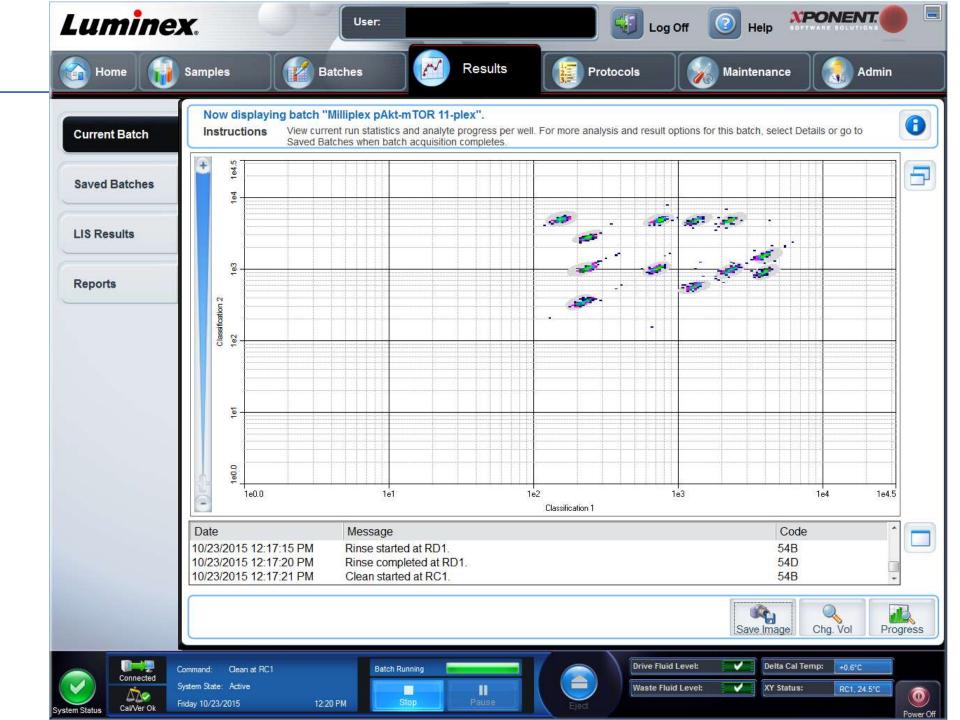
Akt/mTOR Panel: Western to Panel Comparison

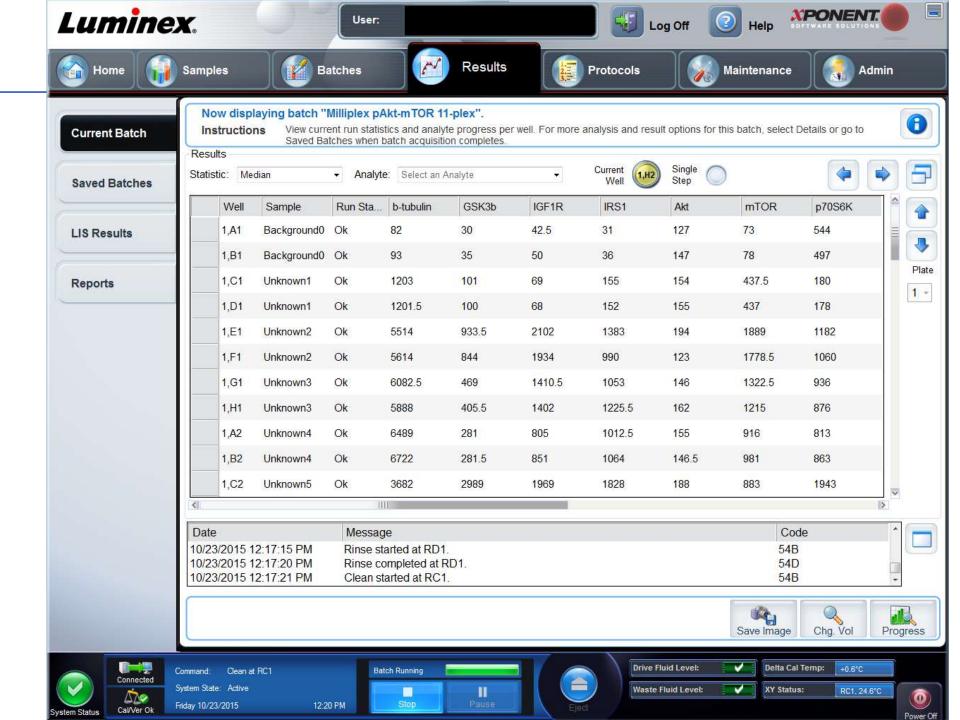


- 1. HeLa untreated
- 2. HeLa treated with lambda phosphatase
- 3. HepG2 untreated
- 4. HepG2 + insulin
- 5. HepG2 + 0.1 μM wortmannin + insulin *PI3K inh.
- 6. HepG2 + 0.1 μ M rapamycin + insulin
- 7. HepG2 + 10 μ M U0126 + insulin
- 8. HepG2 + 50 μM LY-294-002 + insulin *PI3K Inh.
- 9. HepG2 + 1 μM Ro-31-8220 + insulin *Rsk2 inh.









Akt/mTOR Panel



OPEN & ACCESS Freely available online



Tissue-Specific Responses of IGF-1/Insulin and mTOR Signaling in Calorie Restricted Rats

Naveen Sharma¹, Carlos M. Castorena¹, Gregory D. Cartee^{1,2,3}*

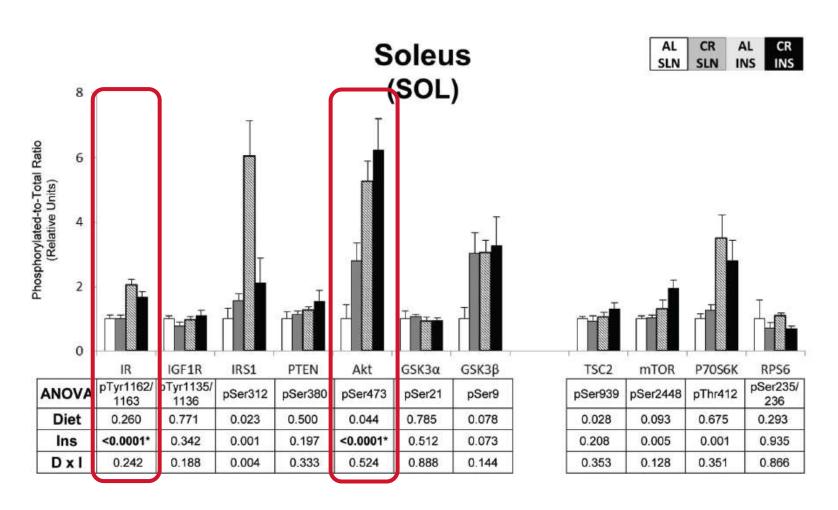
1 Muscle Biology Laboratory, School of Kinesiology, University of Michigan, Ann Arbor, Michigan, United States of America, 2 Department of Molecular and Integrative Physiology, University of Michigan, Ann Arbor, Michigan, United States of America, 3 Institute of Gerontology, University of Michigan, Ann Arbor, Michigan, United States of America

Abstract

Moderate calorie restriction (CR) (~60% of ad libitum, AL, intake) has been associated with numerous favorable physiological outcomes in many species, and the insulin/IGF-1 and mTOR signaling pathways have each been proposed as potential mediators for many of CR's bioeffects. However, few studies have assessed the widely held idea that CR induces the down-regulation of the insulin/IGF-1 and/or mTOR pathways in multiple tissues. Accordingly, we analyzed the phosphorylation status of 11 key signaling proteins from the insulin/IGF-1 (IR^{1y+162/1163}, IGF-1R^{1y+135/1136}, IRS-1^{Ser312}, PTEN^{Ser380}, Akt^{Ser473}, GSK3α^{Ser21}, GSK3β^{Ser9}) and mTOR (TSC2^{Ser939}, mTOR^{Ser2448}, P70S6K^{Thr412}, RPS6^{Ser235/236}) pathways in 11 diverse tissues [liver, kidney, lung, aorta, two brain regions (cortex and cerebellum), and two slow-twitch and three fast-twitch skeletal muscles] from 9-month-old male AL and CR Fischer 344 x Brown Norway rats. The rats were studied under two conditions: with endogenous insulin levels (i.e., AL>CR) and with insulin infused during a hyperinsulinemic-euglycemic clamp so that plasma insulin concentrations were matched between the two diet groups. The most striking and consistent effect of CR was greater pAkt in 3 of the 5 skeletal muscles of CR vs. AL rats. There were no significant CR effects on the mTOR signaling pathway and no evidence that CR caused a general attenuation of mTOR signaling across the tissues studied. Rather than supporting the premise of a global downregulation of insulin/IGF-1 and/or mTOR signaling in many tissues, the current results revealed clear tissue-specific CR effects for the insulin signaling pathway without CR effects on the mTOR signaling pathway.

Measured effects of Calorie Restriction and Insulin treatment in multiple skeletal muscles, brain, liver, kidney, heart, and lung





Overall finding: Calorie restriction showed tissue-specific effects, but more consistently impacted insulin/IGF rather than mTOR

Src Family Kinase Panel





Integrative Genomic and Proteomic Analyses Identify Targets for *Lkb1*-Deficient Metastatic Lung Tumors

Julian Carretero, ^{1,2,13} Takeshi Shimamura, ^{1,3,13} Klarisa Rikova, ⁴ Autumn L. Jackson, ⁵ Matthew D. Wilkerson, ⁵ Christa L. Borgman, ¹ Matthew S. Buttarazzi, ^{1,7} Benjamin A. Sanofsky, ^{1,7} Kate L. McNamara, ^{1,7} Kathleyn A. Brandstetter, ^{1,7} Zandra E. Walton, ^{1,7} Ting-Lei Gu, ⁴ Jeffrey C. Silva, ⁴ Katherine Crosby, ⁴ Geoffrey I. Shapiro, ^{1,3} Sauveur-Michel Maira, ⁸ Hongbin Ji, ⁹ Diego H. Castrillon, ¹⁰ Carla F. Kim, ¹¹ Carlos García-Echeverria, ⁸ Nabeel Bardeesy, ¹² Norman E. Sharpless, ^{5,6} Neil D. Haves, ⁵ William Y. Kim, ^{5,6} Jeffrey A. Engelman, ¹² and Kwok-Kin Wong^{1,3,7,*}

SUMMARY

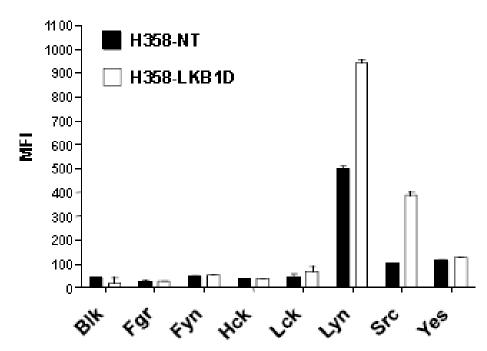
In mice, *Lkb1* deletion and activation of *Kras^{G12D}* results in lung tumors with a high penetrance of lymph node and distant metastases. We analyzed these primary and metastatic de novo lung cancers with integrated genomic and proteomic profiles, and have identified gene and phosphoprotein signatures associated with *Lkb1* loss and progression to invasive and metastatic lung tumors. These studies revealed that SRC is activated in *Lkb1*-deficient primary and metastatic lung tumors, and that the combined inhibition of SRC, PI3K, and MEK1/2 resulted in synergistic tumor regression. These studies demonstrate that integrated genomic and proteomic analyses can be used to identify signaling pathways that may be targeted for treatment.

Src Family Kinase Panel



Because Phosphoscan and western blot analyses detect a phosphorylation site (Y416) that is common to all SRC family kinases (SFKs) including SRC, FYN, LYN, LCK, HCK FGR, and YES, we interrogated the phosphorylation status of SFKs affected by LKB1 loss in NCI-H358 and A549 cell lines using a Luminex bead assay.

These changes in SRC and FAK suggest impaired adhesion and increased cellular motility (Yeatman, 2004).

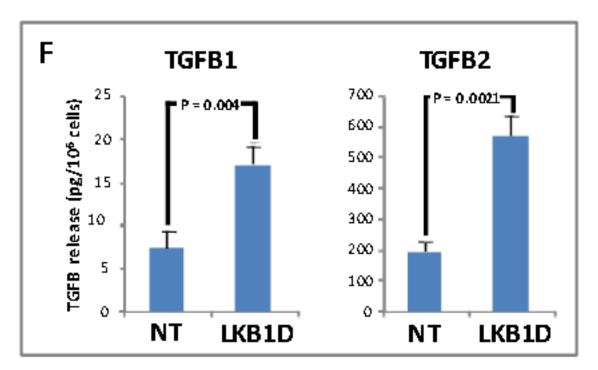


D. Phosphoprotein profile of NCI-H358 cells analyzed by protein arrays.

NCI-H358 cells stably expressing shRNA to *LKB1* (LKB1D) or a non-specific shRNA (NT) were subjected to a kinase array as described in materials in methods.

Increased TGFbeta secretion: EMT?





F. TGF- β release analyzed by multiplex bead assay. *In vitro* secretion of TGFB1, TGFB2 and TGFB3 (below detection limit, not shown) were carried out in NO-H358 cells stably expressing shRNA to *LKB1* (LKB1D) or a non-specific shRNA (NT). Conditioned media were collected after 24h of cell culture and incubated with beads coated with specific antibodies for TGFB1, TGFB2 and TGFB3 as described in Methods. Data is graphed as mean of 3 replicates (pg/10⁶ cells ± SD).

MILLIPLEX MAP Cell Signaling Portfolio



Pathway Panels:

Glycolysis

Oxidative Phosphorylation

Oxidative Stress

Pyruvate Dehydrogenase

Akt/mTOR

Early Apoptosis

Late Apoptosis

DNA Damage

Heat Shock Protein

MAPK/SAPK

Mitogenesis RTK

Multi-Pathway

NFkB

Src Kinase

STAT

Human T Cell Receptor

TGFbeta

Phospho-Total 2 Plexes:

Akt/PKB

CREB

Erk/MAPK ½

IRS1

JNK

mTOR

p38

STAT3

(all of above can be plexed)

Individual MapMates:

46 and counting!



Thank you!

Ramsey McIntire: Multiplex & Cytometry

Karen Tamul: Field Application Scientist

Michelle Dennis: All things EMD Millipore!