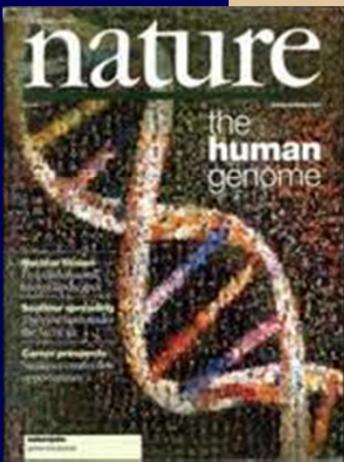


# Functional Oncogenomics: A Tool for Identification and Validation of Targeted Therapies in Multiple Myeloma

Wee Joo Chng, MB, PhD  
National University Cancer Institute of Singapore  
Singapore, Singapore

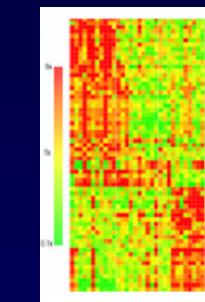
# Molecular Abnormalities in Cancer



## Sequencing

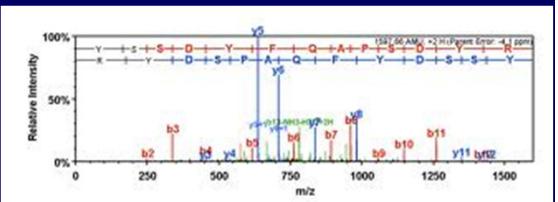


## Microarray

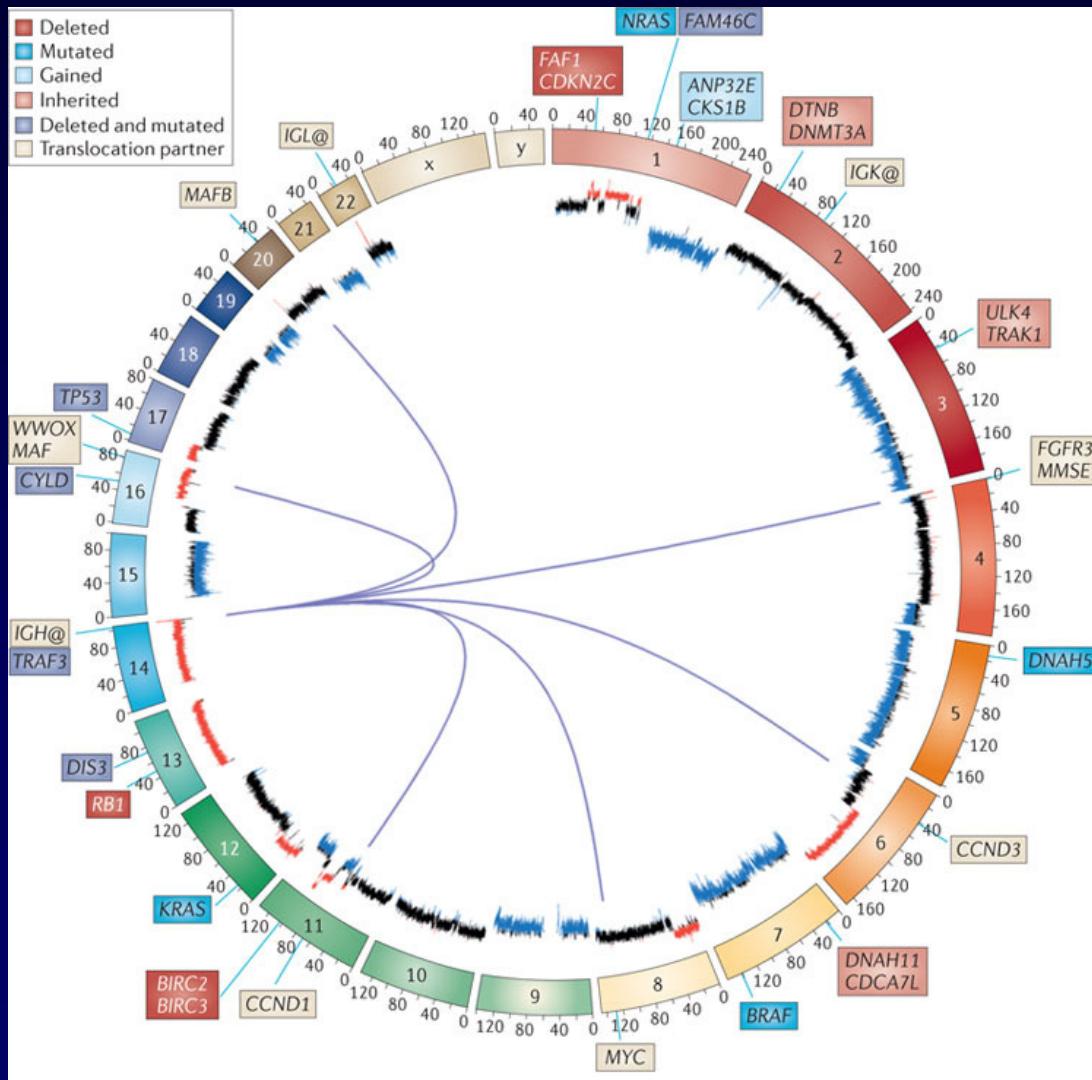


mRNA  
miRNA  
Methylation  
Protein

## Proteomics



# Genomic Landscape in Multiple Myeloma (MM)

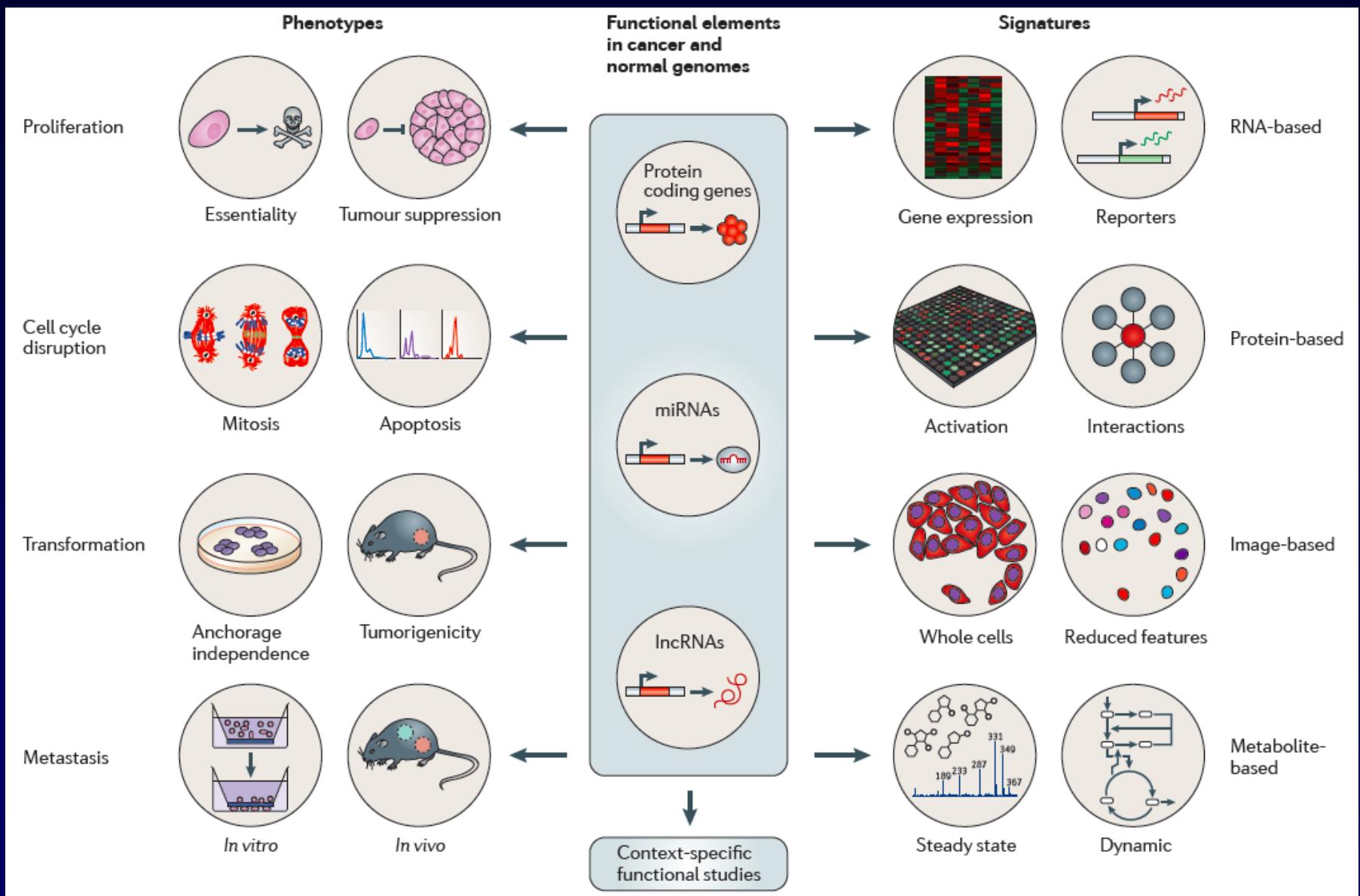


Morgan GJ, et al. *Nat Rev Cancer*. 2012;12(5):335-348.

# Functional Genomics

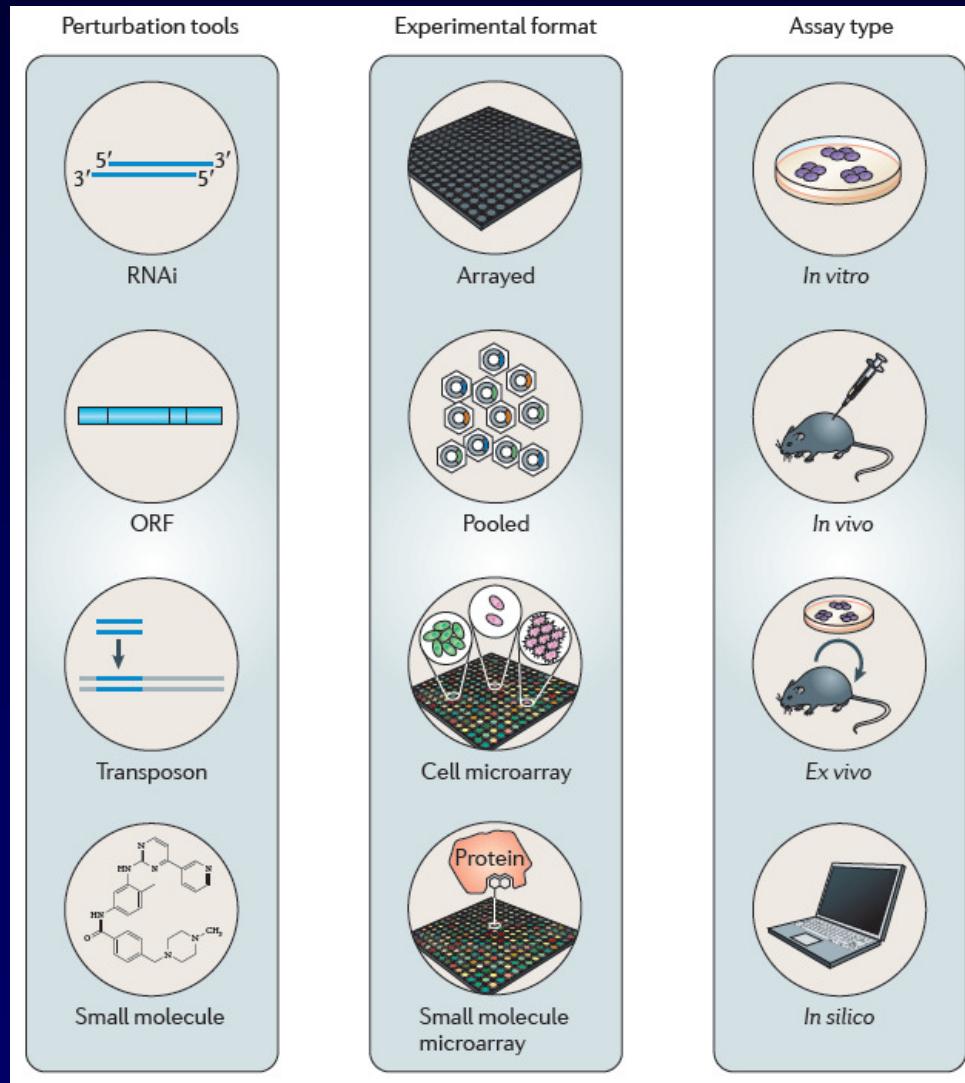
- The large-scale manipulation of gene expression or function using high-throughput approaches
- Basic tenet: Perturbation of gene function and assessment of phenotypic effects can provide insights into its biological function
- Allow establishment of causal relationship between genotype and phenotype

# Overview of Cancer Functional Genomics



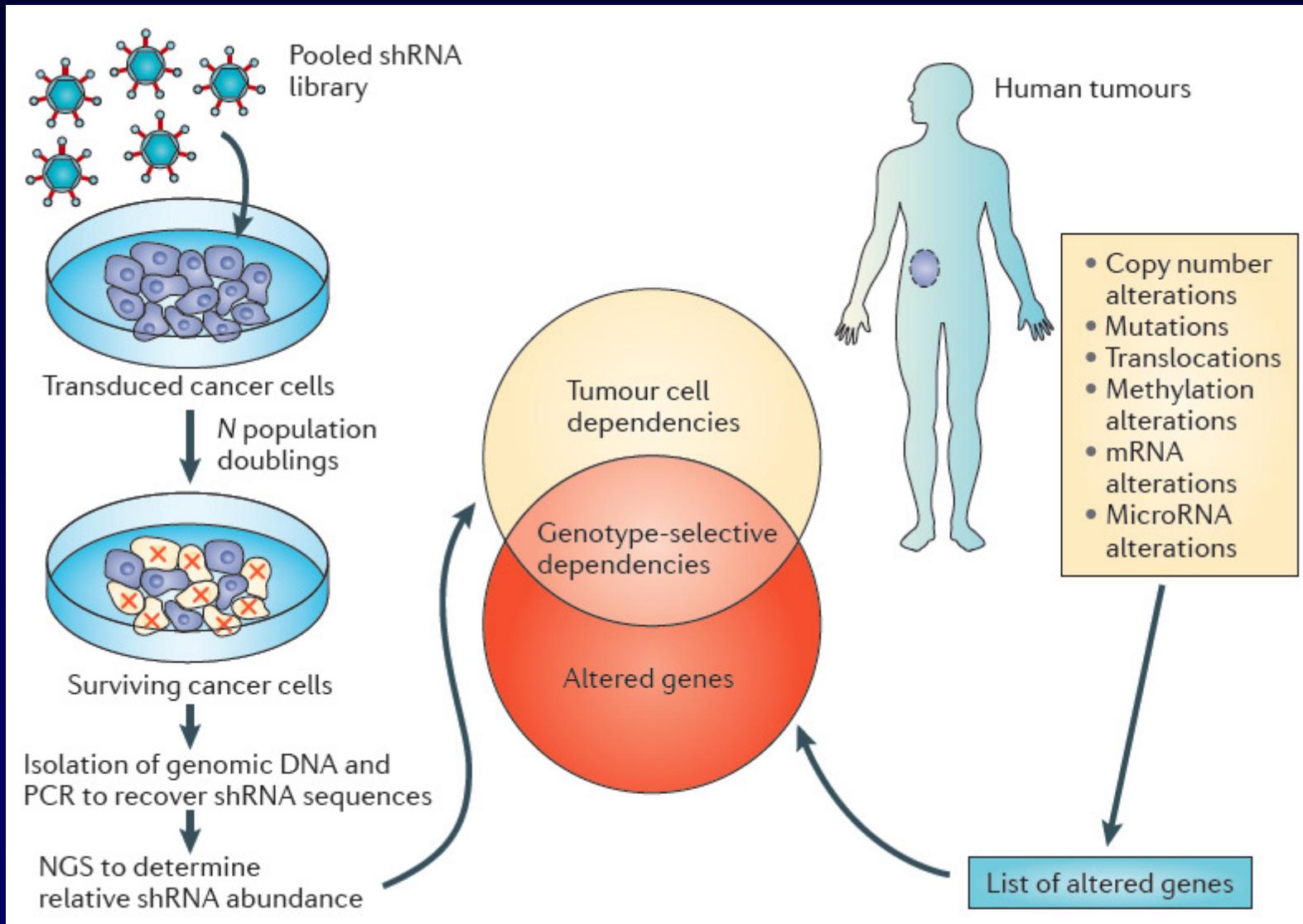
Boehm JS, et al. *Nat Rev Genet*. 2011;12(7):487-498.

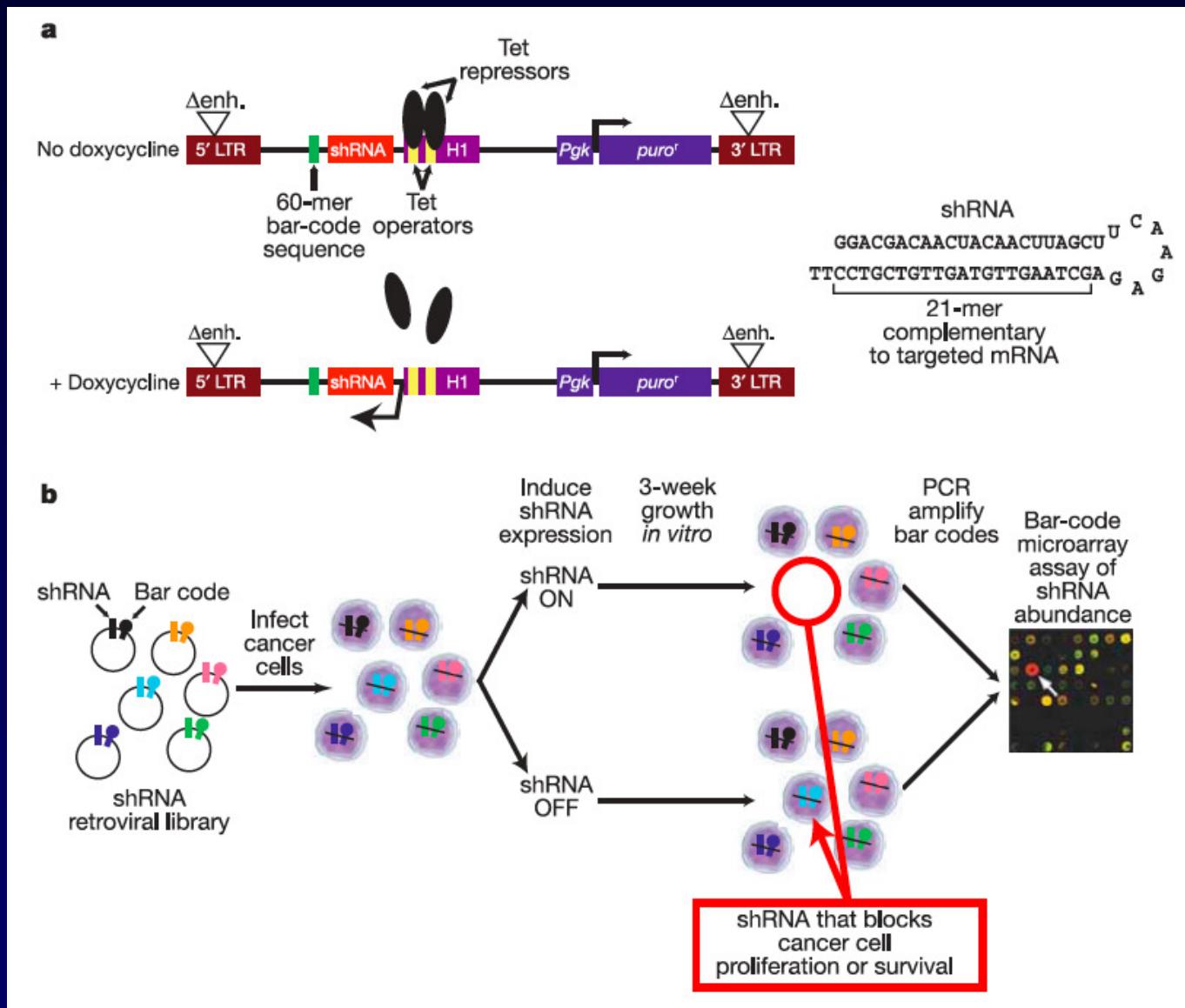
# Tools and Formats for Cancer Functional Genomics



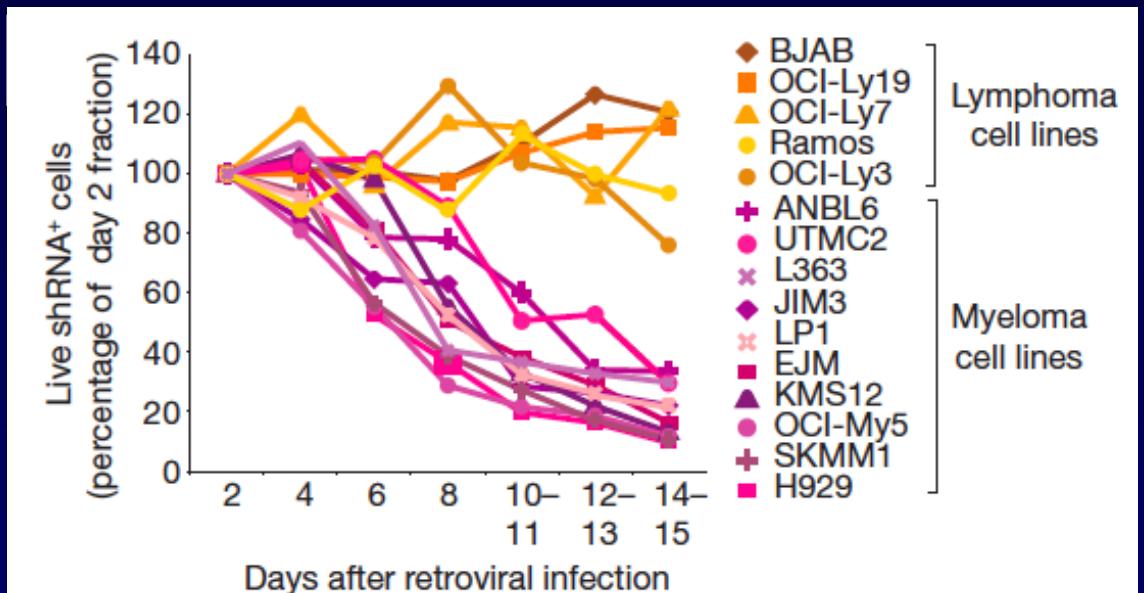
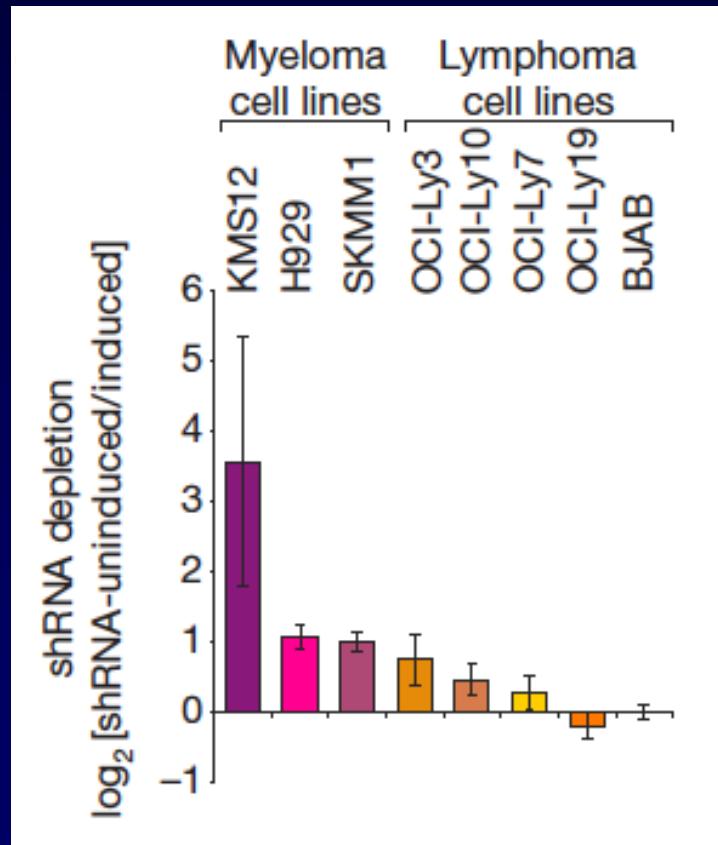
Boehm JS, et al. *Nat Rev Genet.* 2011;12(7):487-498.

# RNAi Screen

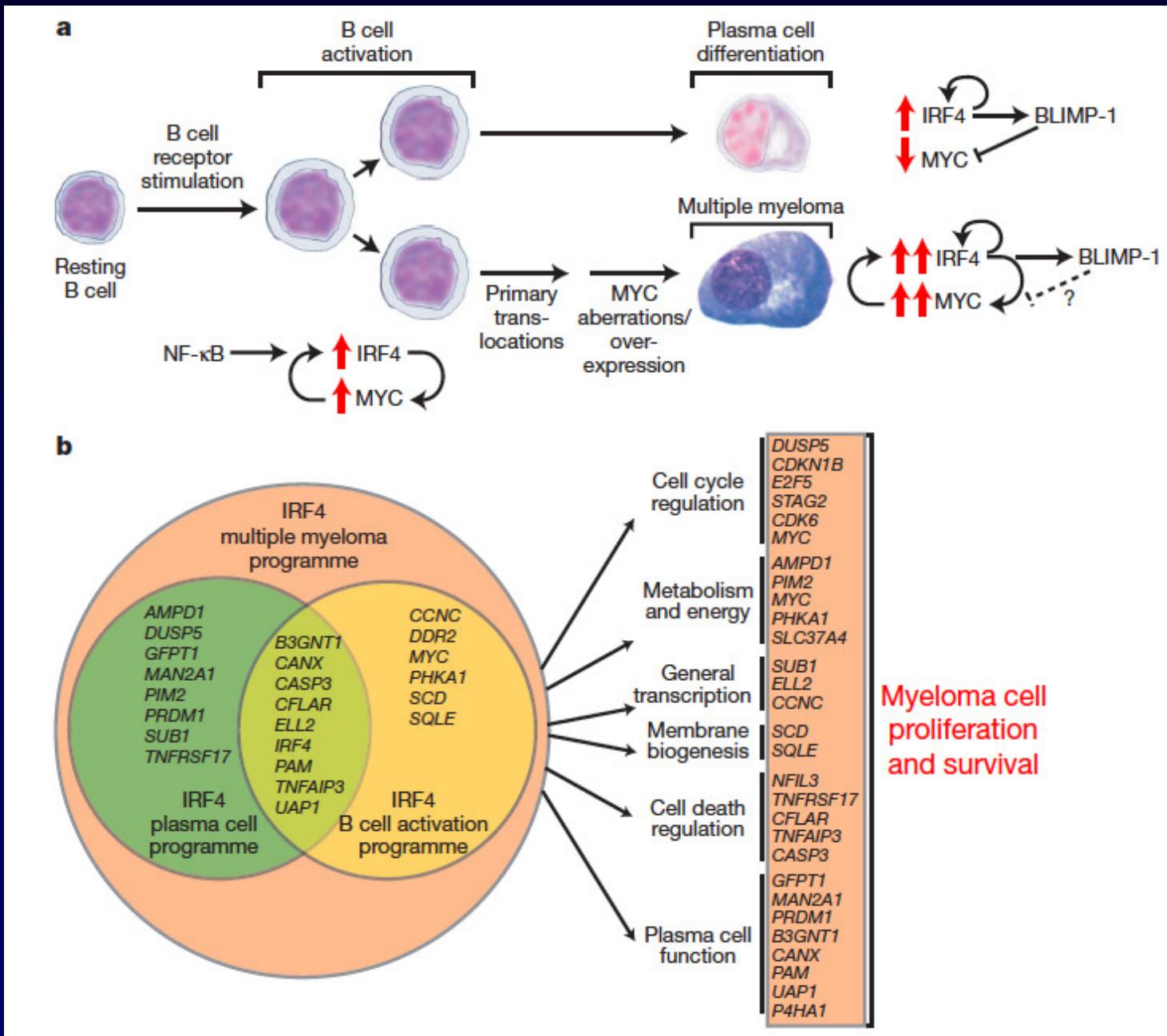




# IRF4 Addiction in MM

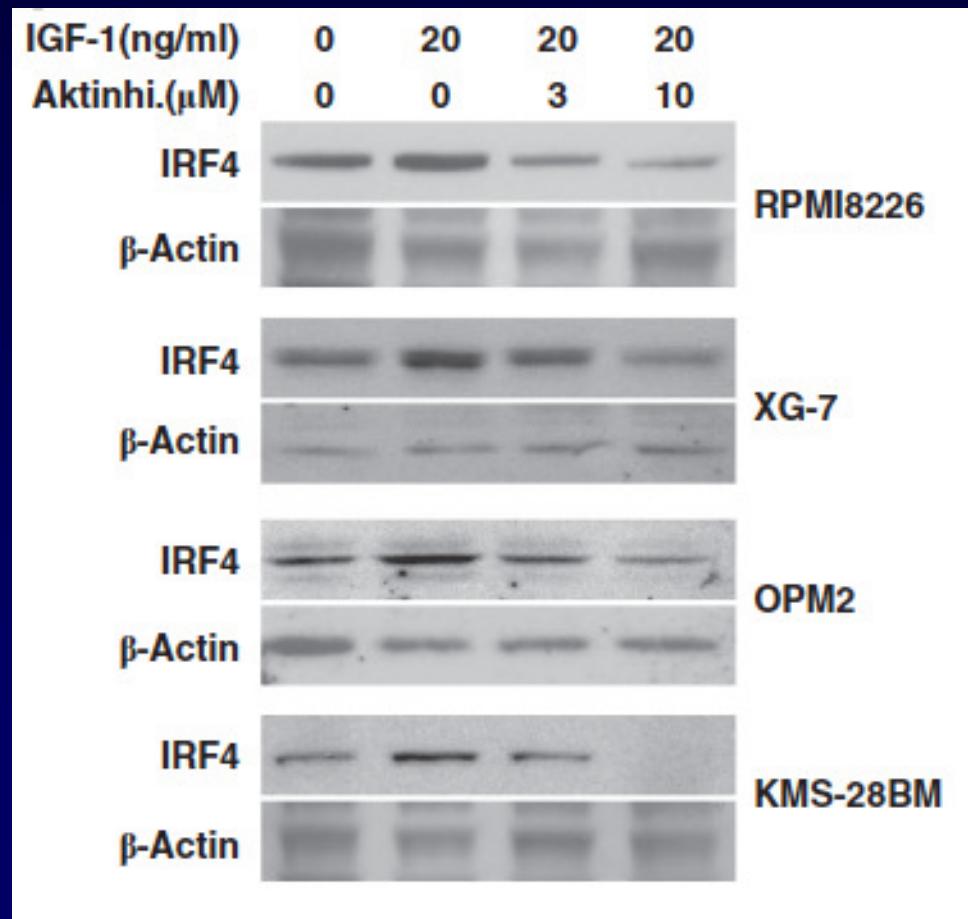
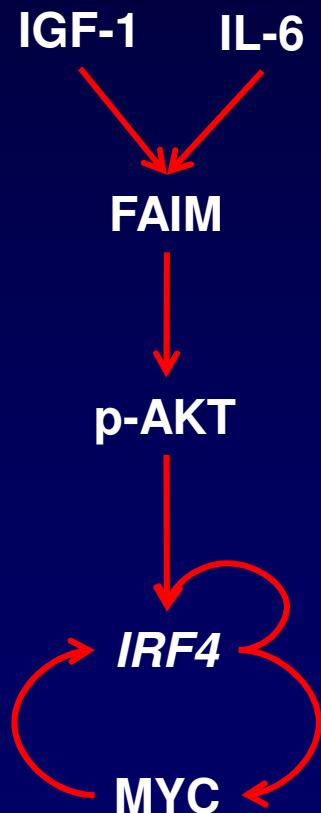


Shaffer AL, et al. *Nature*. 2008;454(7201):226-231.



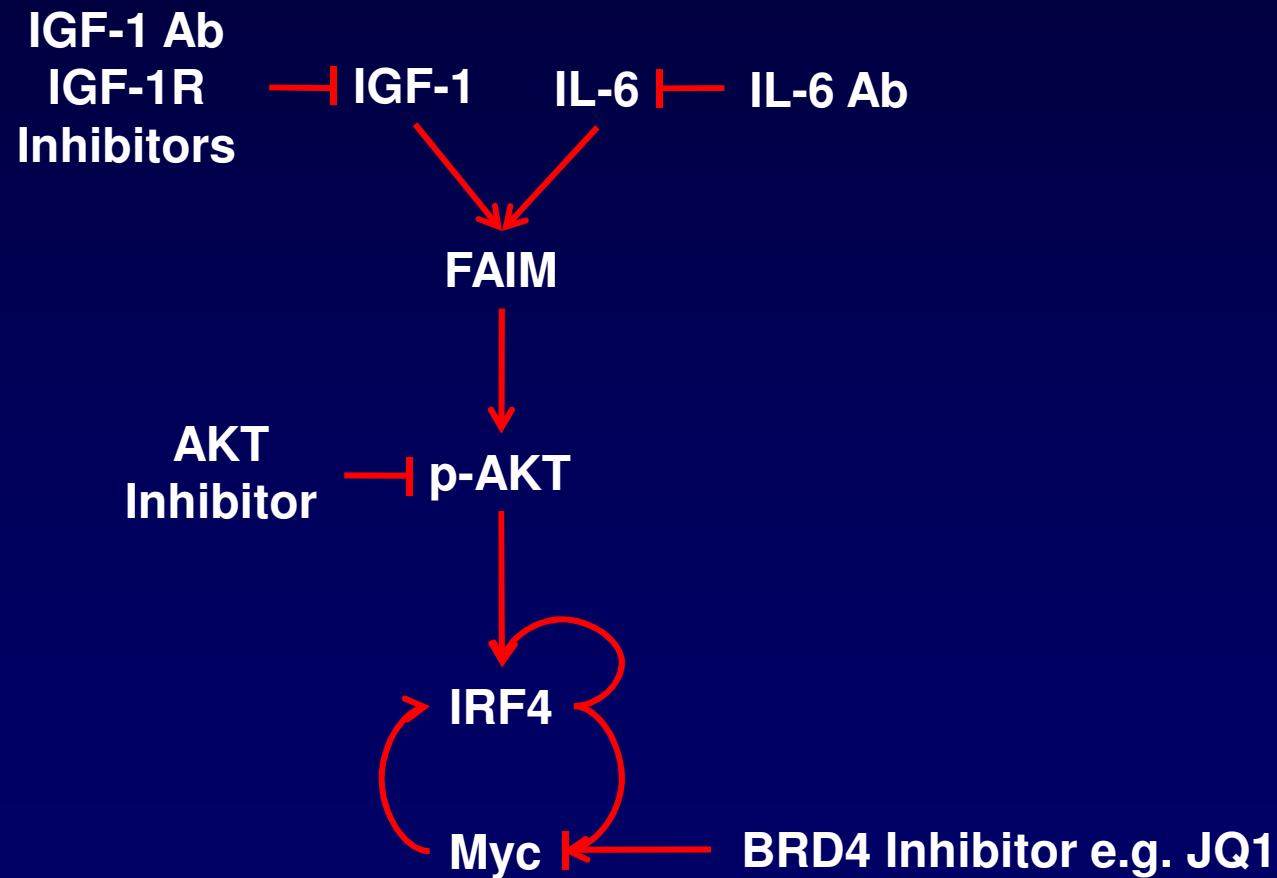
Shaffer AL, et al. *Nature*. 2008;454(7201):226-231.

# Fas Apoptosis Inhibitory Molecule Is Upregulated by IGF-1 Signaling and Modulates Akt Activation and *IRF4* Expression in MM

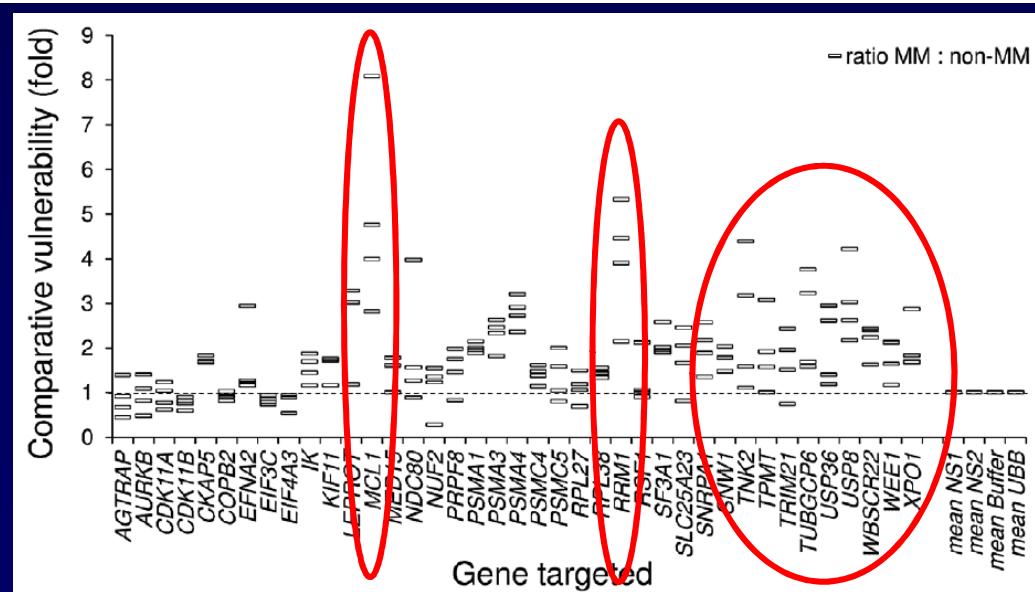
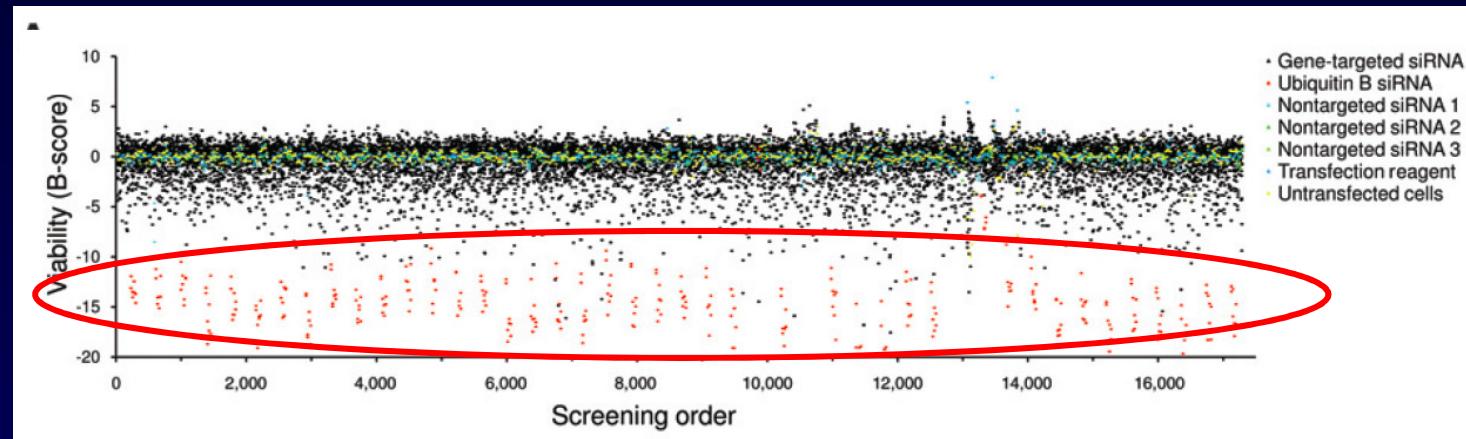


Huo J, et al. *Leukemia*. 2012 Nov 9. [Epub ahead of print].

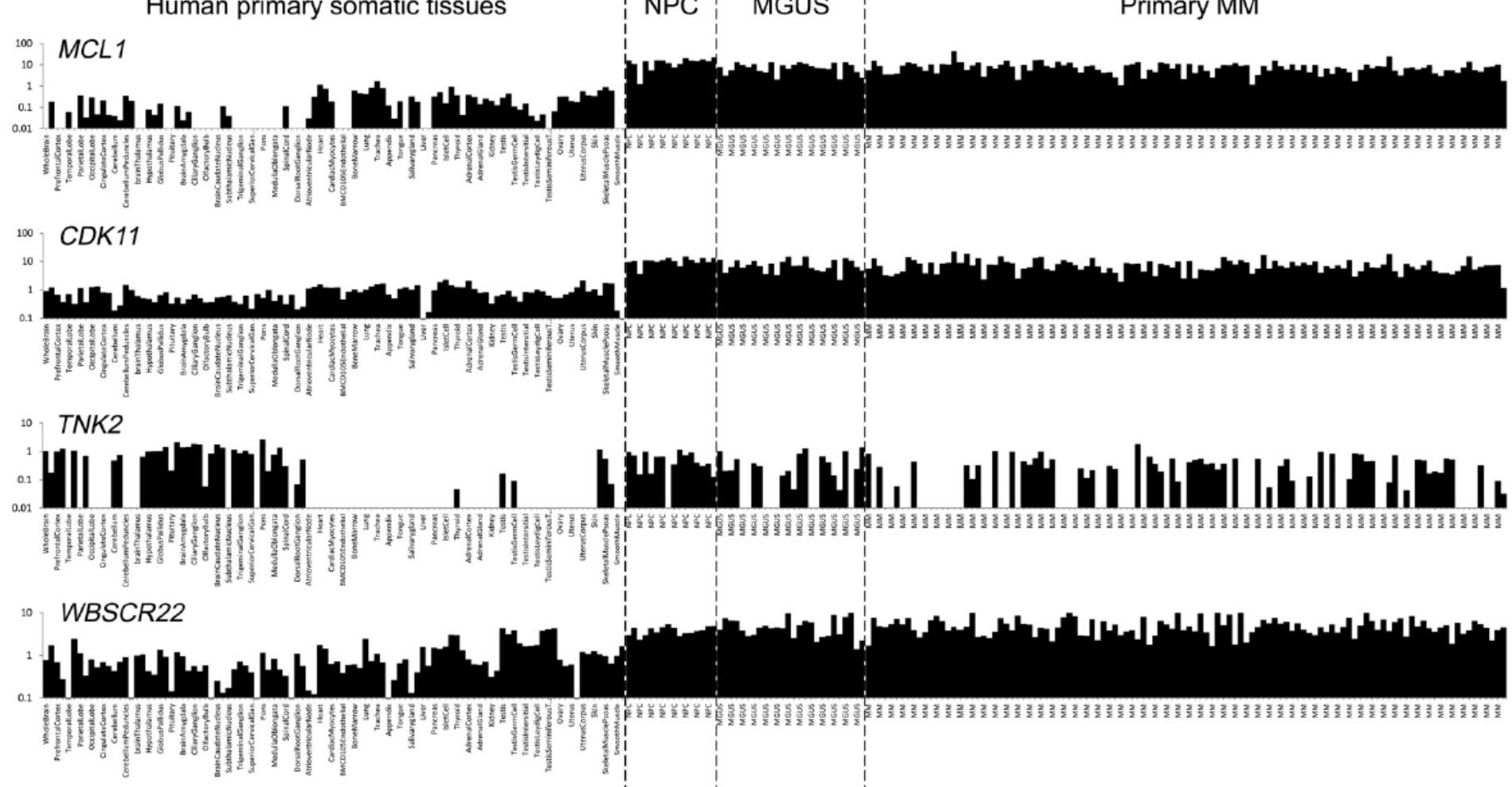
# Potential Strategies to Target IRF4



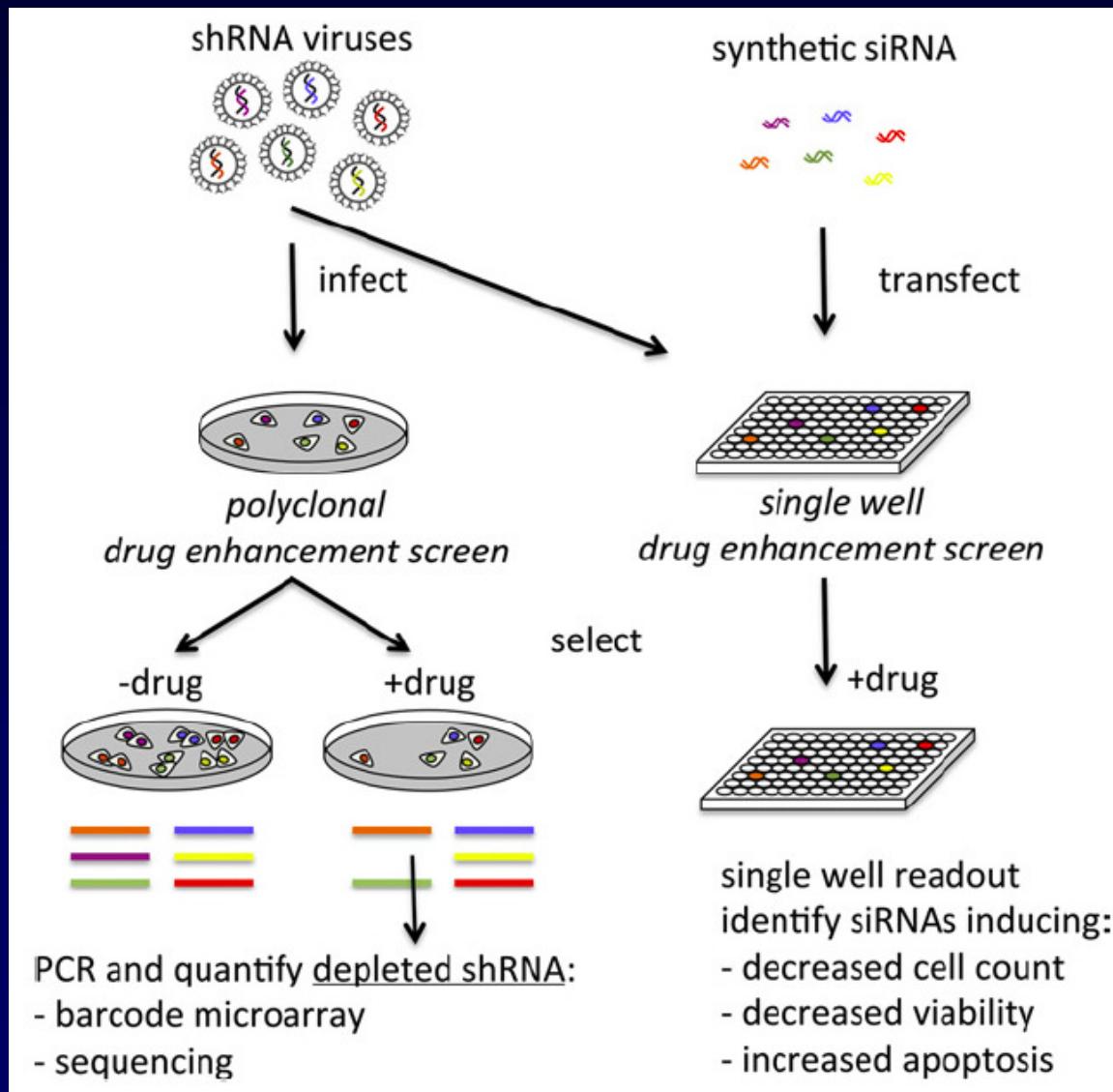
# Identification of Molecular Vulnerabilities in Human MM Cells by RNA Interference Lethality Screening of the Druggable Genome



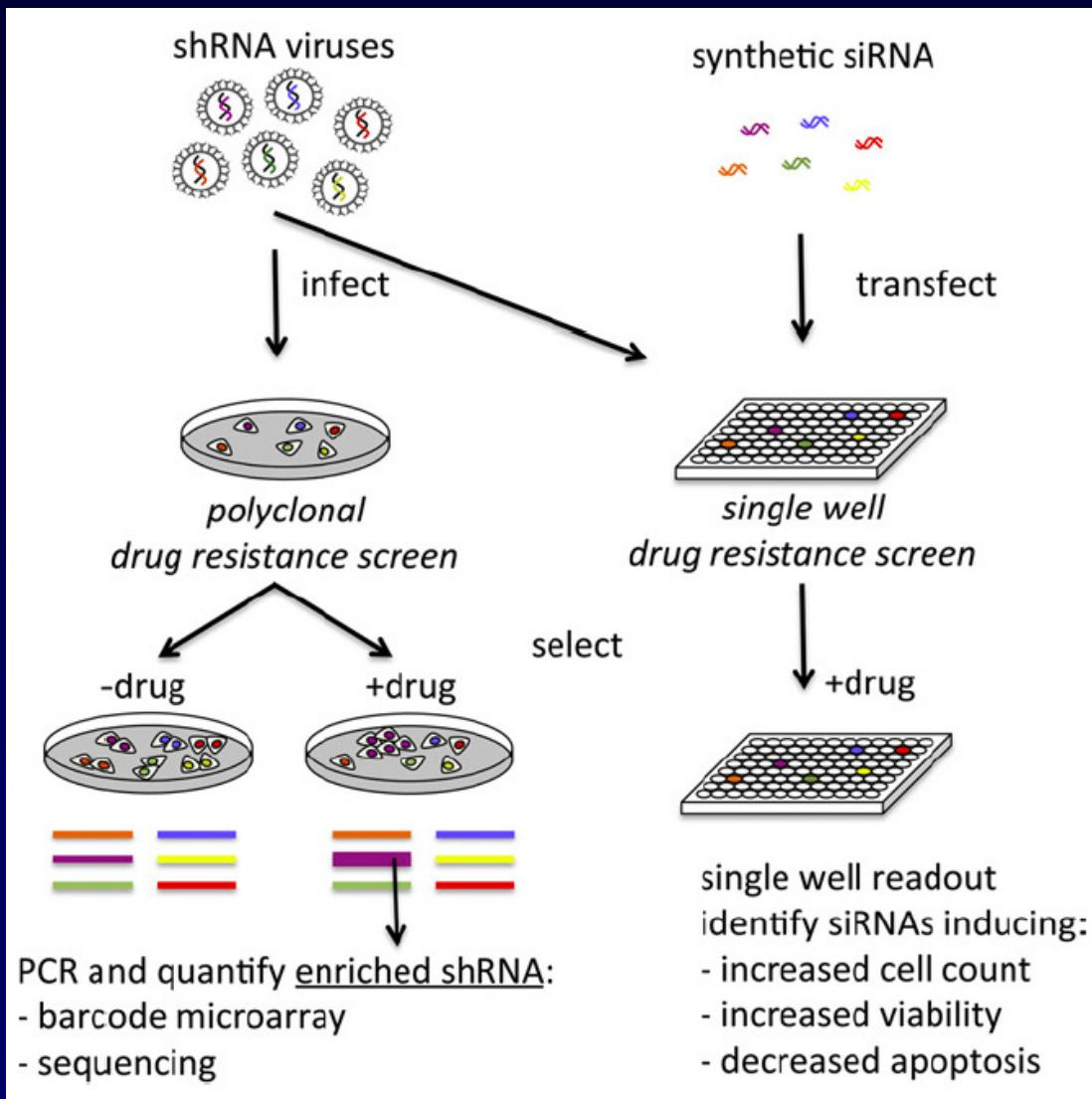
Tiedemann RE, et al. *Cancer Res.* 2012;72(3):757-768.



# RNAi Screen for Drug Enhancer

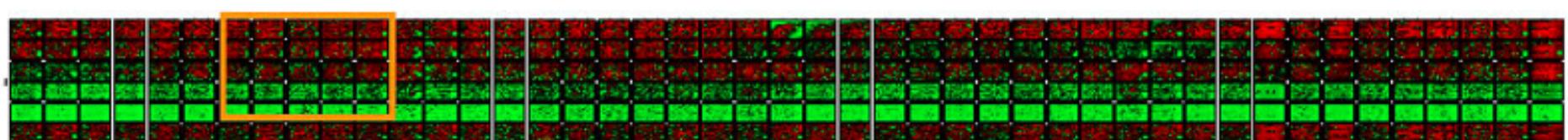
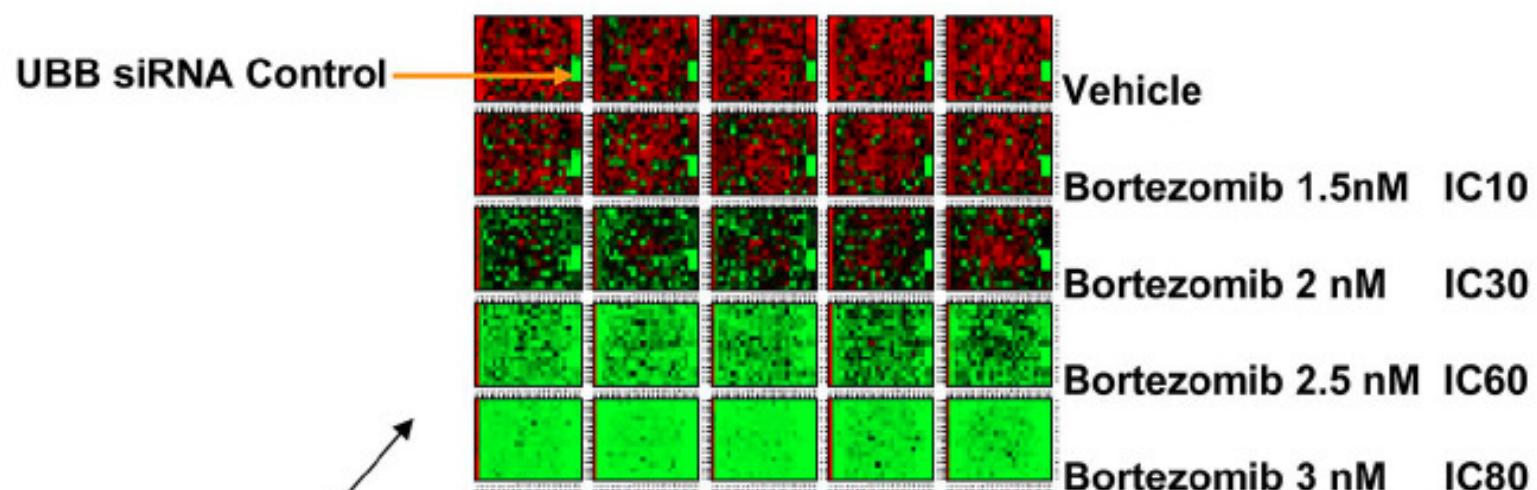


# RNAi Screen for Drug Resistance



# Rnai Screen of the Druggable Genome Identifies Modulators of Proteasome Inhibitor Sensitivity in Myeloma Including *CDK5*

A



# Primary Screen

Bortezomib sensitizers identified in KMS11

Gene ID	No. of siRNA	GEP	Gene ID	No. of siRNA	GEP
<i>BAZ1B</i>	2	P	<i>PSMB7</i>	3	P
<i>CCNK</i>	2	ND	<i>RAB8B</i>	3	P
<i>CDC42SE2</i>	3	P	<i>RB1CC1</i>	2	P
<i>CDK5</i>	2	P	<i>STK6</i>	2	P
<i>CEBPA</i>	2	P	<i>TFAP4</i>	2	P
<i>CHD4</i>	2	P	<i>TFE3</i>	2	P
<i>CRKL</i>	3	P	<i>TNFAIP3</i>	4	P
<i>CTNNB1</i>	2	P	<i>TNK1</i>	2	P
<i>DCAMKL1</i>	2	ND	<i>TOP1</i>	2	P
<i>ENC1</i>	2	P	<i>USP8</i>	2	P
<i>MAST2</i>	2	P	<i>VAMP2</i>	3	P
<i>MDM4</i>	2	P	<i>VBP1</i>	2	P
<i>MIF</i>	2	P	<i>VDAC3</i>	2	P
<i>NCOR1</i>	2	P	<i>WTAP</i>	3	P
<i>NM37</i>	2	P	<i>XOC</i>	2	P
<i>OGT</i>	2	P	<i>XRCC5</i>	2	P
<i>PSMA5</i>	3	P	<i>YY1</i>	3	P
<i>PSMB2</i>	4	P	<i>ZNF197</i>	2	P
<i>PSMB3</i>	4	P			

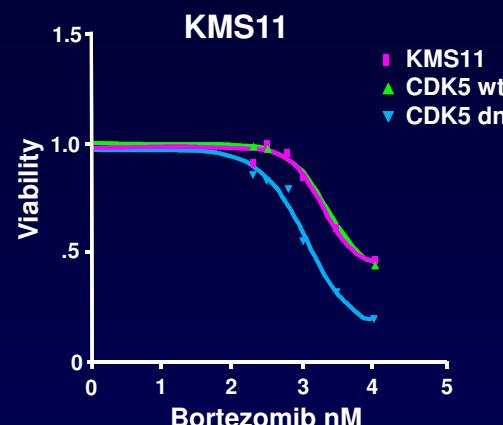
# Validation

Top ranking sensitizers from KMS11 HTS

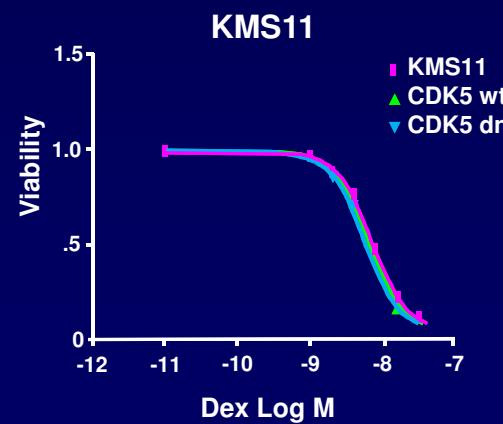
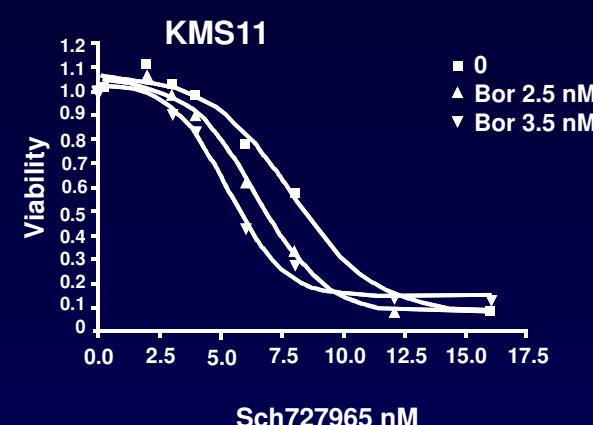
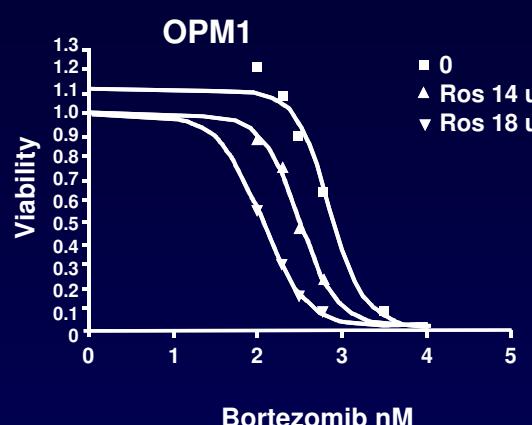
Sample ID	No. of siRNA	Mean EC50
<i>BAZ1B</i>	2	1.4
<i>CDC42SE2</i>	3	1.5
<i>CDK5</i>	2	0.8
<i>MDM4</i>	2	1.2
<i>NME7</i>	2	1.3
<i>PSMA5</i>	3	0.8
<i>PSMB2</i>	4	1.1
<i>PSMB3</i>	4	0.9
<i>PSMB7</i>	3	1.2
<i>RAB8B</i>	2	1.4
<i>TFE3</i>	2	1.6
<i>TNFAIP3</i>	2	1.5
<i>TNK1</i>	2	1.5
<i>TOP1</i>	2	1.6
<i>VAMP2</i>	3	1.7
<i>YY1</i>	2	1.5

Control EC50 = 2.2

## Sensitizing effect is specific to Bortezomib



## Synergism Between Bortezomib and CDK Inhibitors

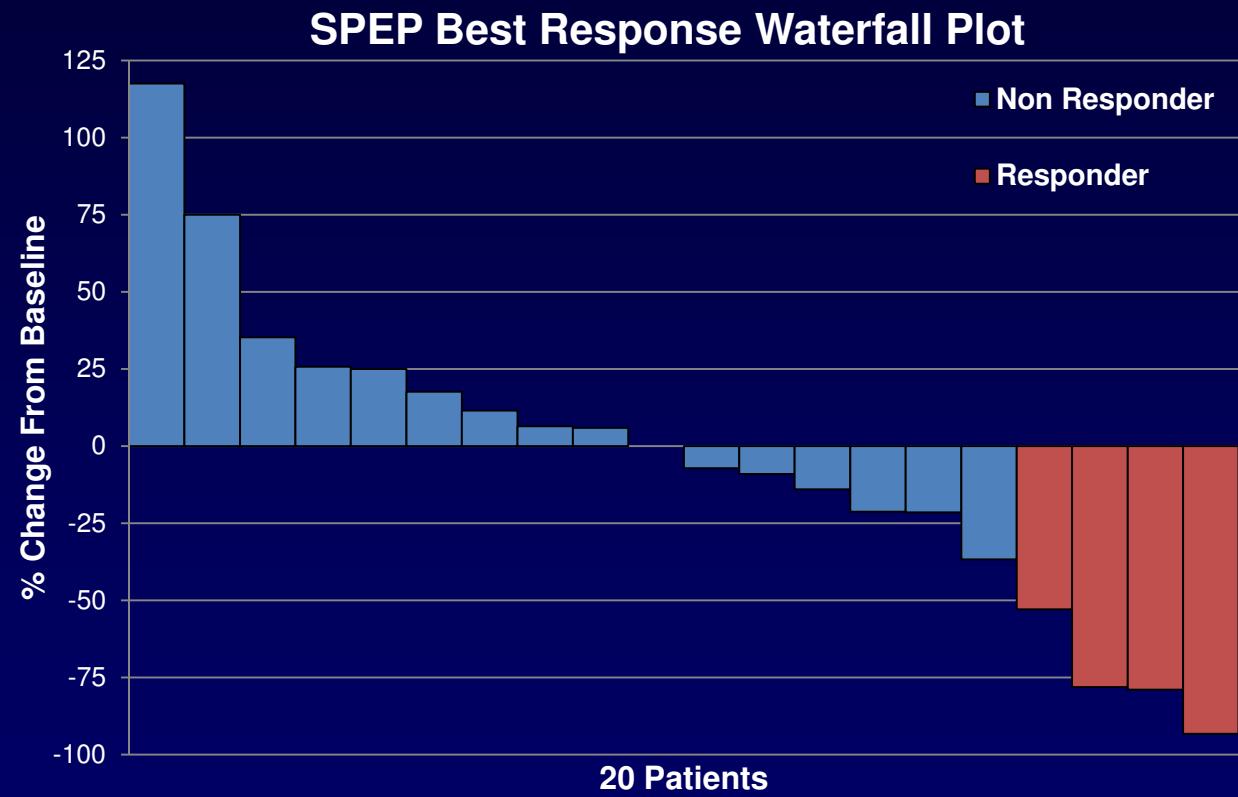


	Bortezomib 2.5 nM		Bortezomib 3.5 nM	
	OPM1	KMS11	OPM1	KMS11
SCH 727965 4 nM	-0.05	-0.14	-0.11	-0.24
SCH 727965 6 nM	-0.14	-0.32	-0.46	-0.88
SCH 727965 8 nM	-0.29	-0.80	-1.03	-1.06
SCH 727965 12 nM	-0.53	-0.77	-1.05	-0.23
SCH 727965 16 nM	-0.39	-0.04	-0.08	-0.60

# **Phase 1/2 Trial of a Novel CDK Inhibitor Dinaciclib (SCH727965) in Patients With Relapsed Multiple Myeloma Demonstrates Encouraging Single Agent Activity**

**Shaji Kumar, Betsy LaPlant, Wee Joo Chng, Jeffrey Zonder, Natalie Callander, Vivek Roy, Briant Fruth, Charles Erlichman, A. Keith Stewart  
Phase 2 Consortium (P2C)**

# Serum M-Protein Responses



# Conclusions

- Functional genomics approaches complement current structural genomics efforts and can greatly help identify critical genes in different context
- In the coming years, the results of these studies will greatly increase our understanding of biology and identify therapeutic targets in myeloma
- Some of the results have already identified actionable targets that are currently being tested in clinical trials

# Acknowledgements

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Rafael Fonseca

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Esteban Braggio

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NRF RCE Grant

NMRC Center Grant

MOE AcRF

# Thank You