



Transcriptional information on GBM from TCGA pilot project

Transcriptional subsets

Integrative approaches and opportunities

Transcription teams

Broad Institute of MIT and Harvard. Affymetrix U133A platform

Lawrence Berkeley National Laboratory and UC Berkeley. Affymetrix Exon 1.0 platform.

University of North Carolina. Agilent array platform

Johns Hopkins University and University of Southern California. Illumina Genotyping platform to detect changes in methylation

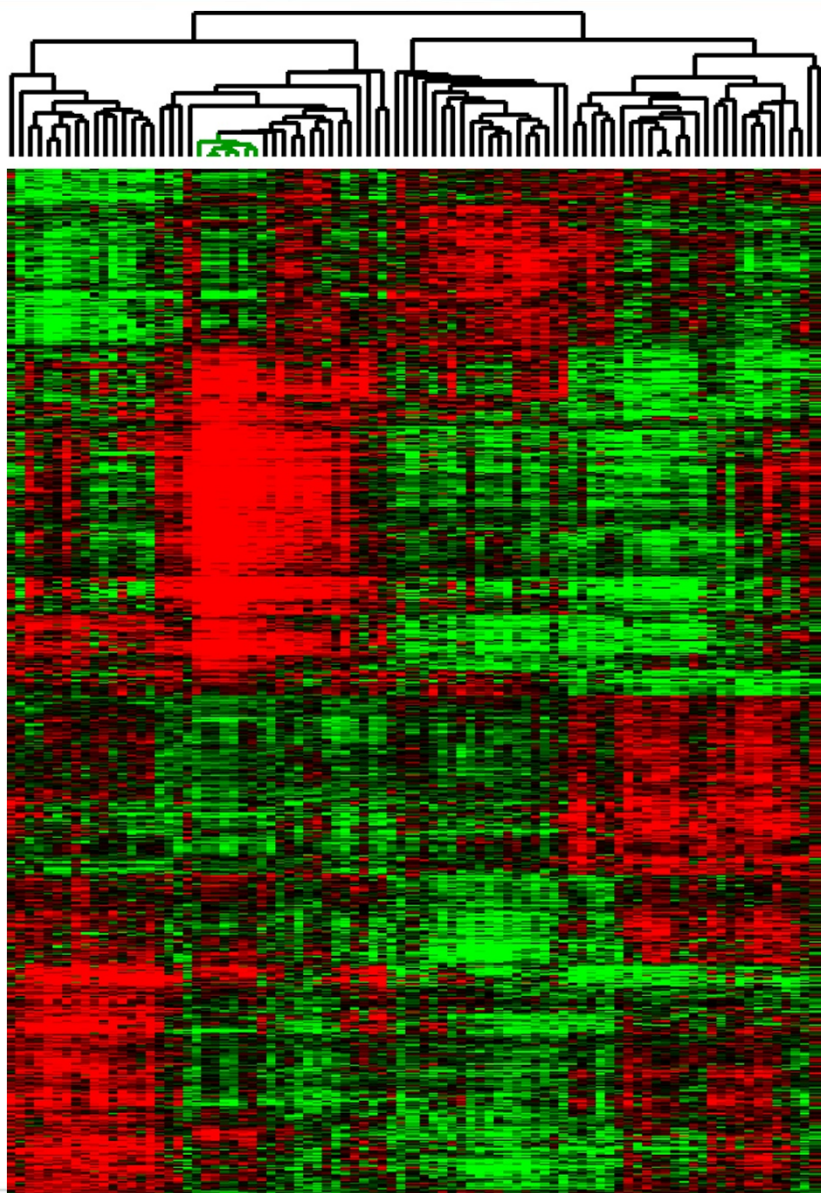


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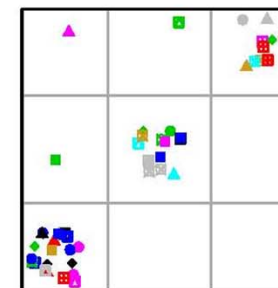
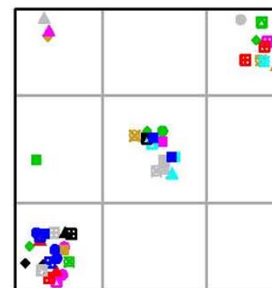
Transcriptional subsets

Integrative approaches and opportunities

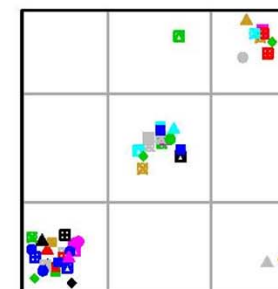
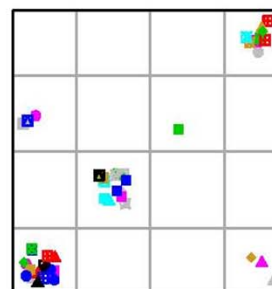
Consensus clusters



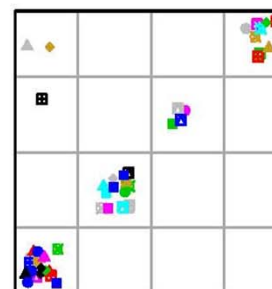
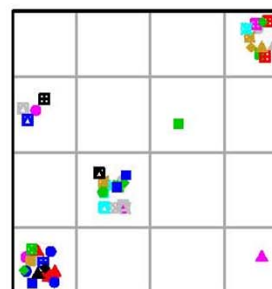
LBL



Broad



UNC



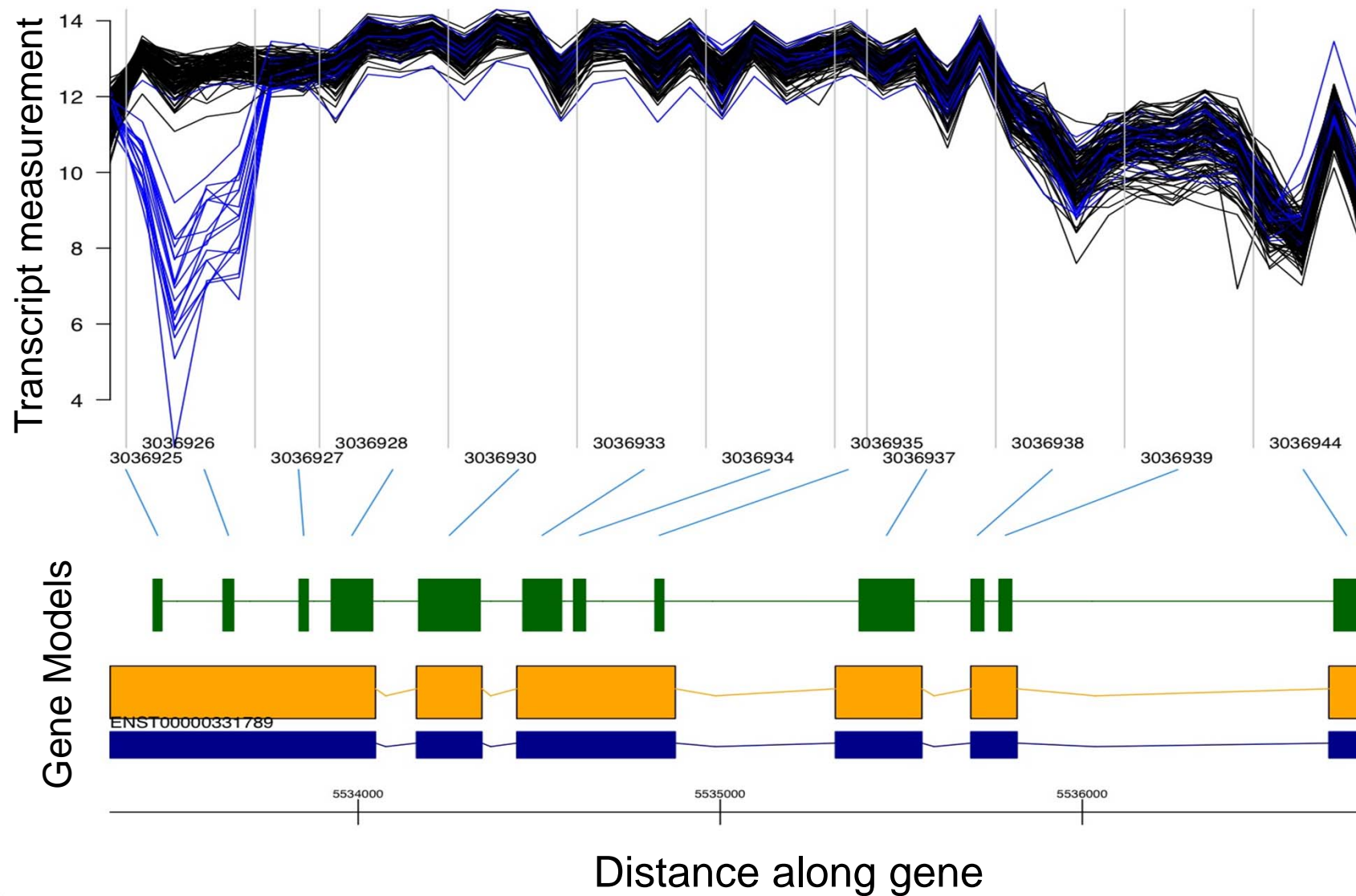
Comparison of Groupings by Gene Expression and microRNA



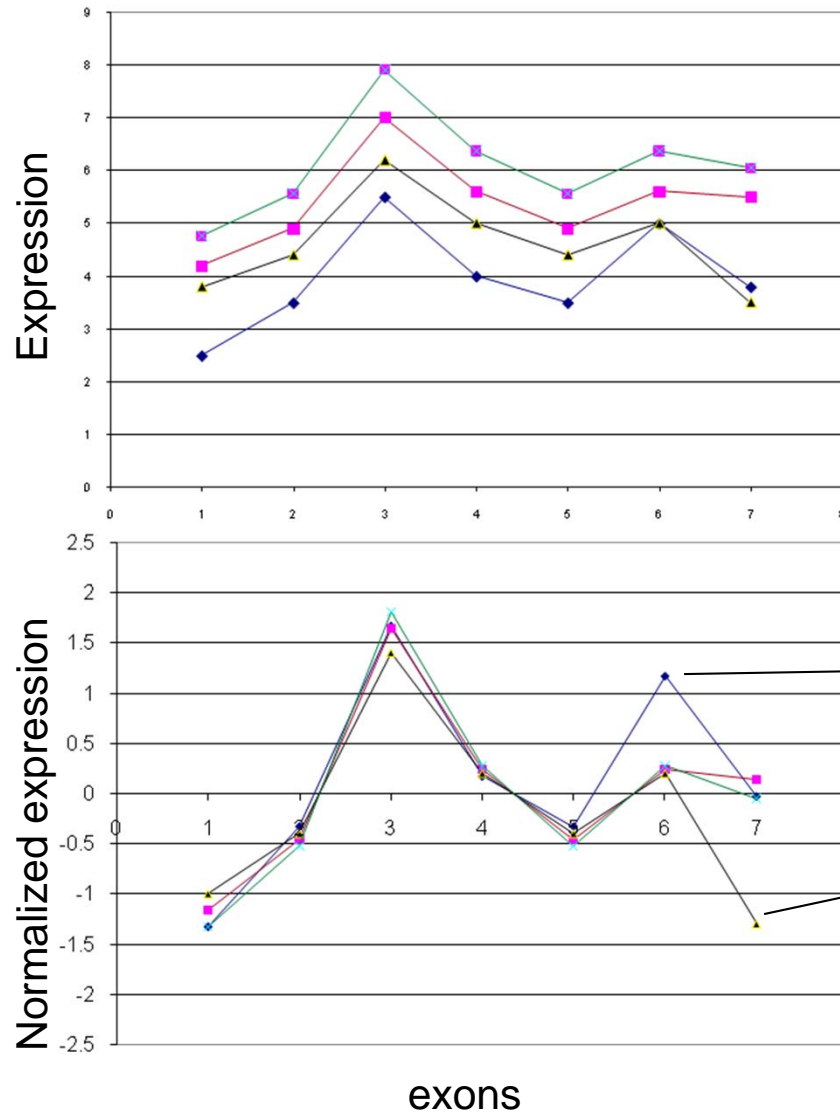
	Gene Expression			
microRNA	1	2	3	4
1	2	8	11	12
2	14	12	8	10

Alternative Transcript Subgroups Using Exon Arrays

THE CANCER GENOME ATLAS

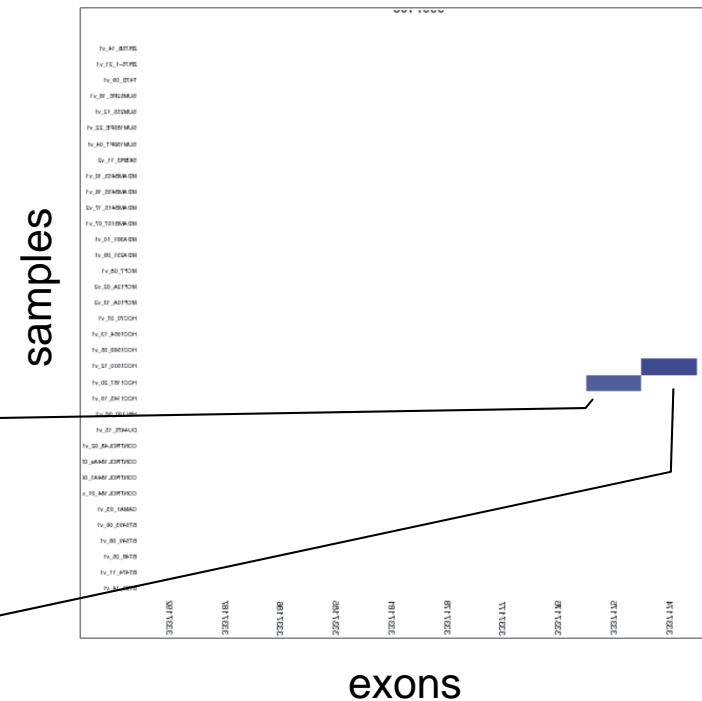


Statistical Approaches to Finding Splicing Isoforms



FIRMA - *F*inding *I*soforms using *R*obust *M*ultichip *A*veraging

Heatmap of FIRMA scores



E. Purdom, T. Speed,



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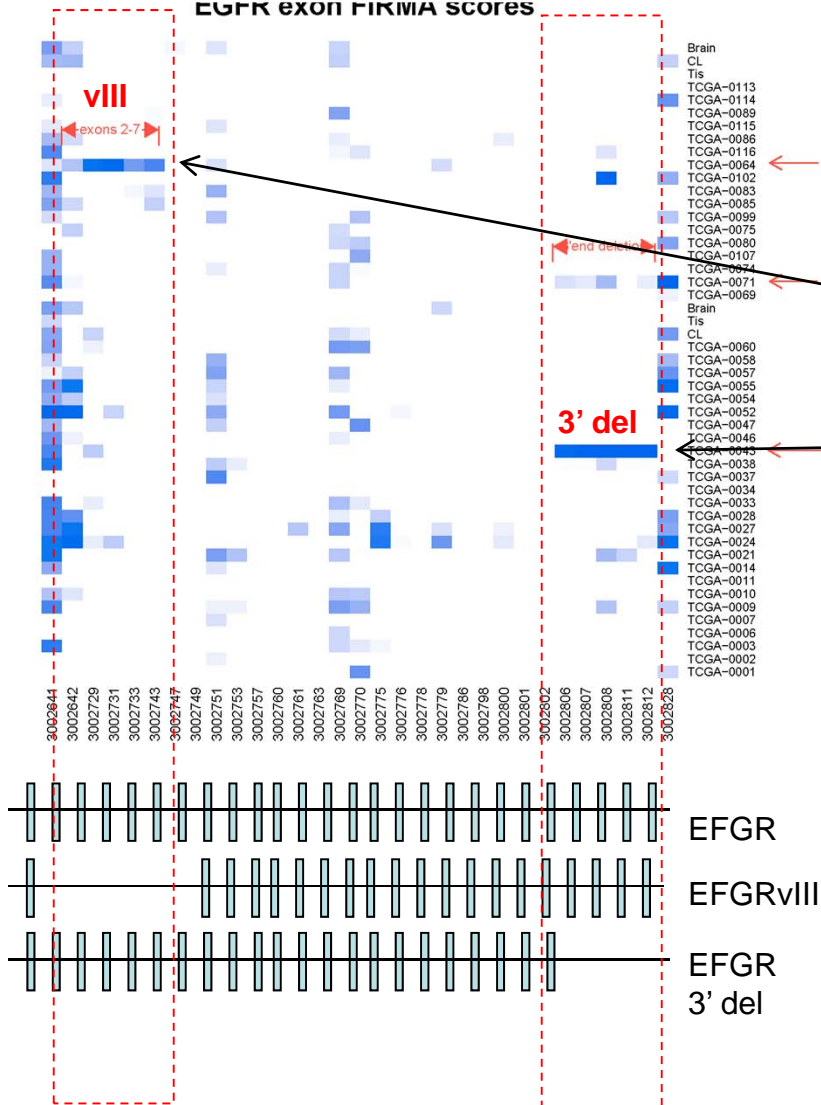
Integrative insights

EGFR Deletions in GBM Samples

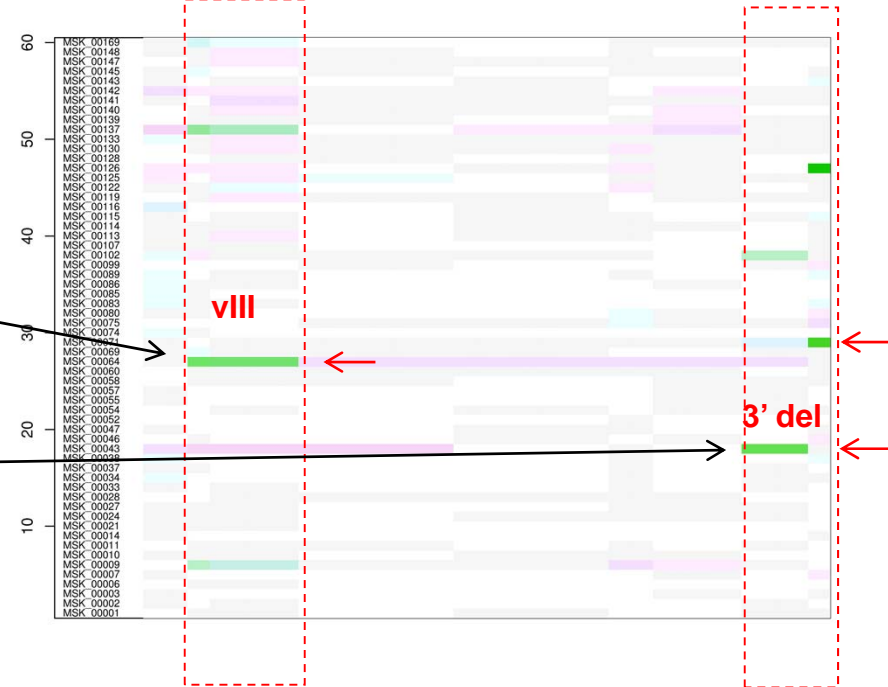


Human Exon data

EGFR exon FIRMA scores



Agilent 244K; MSK. Cameron Brennan



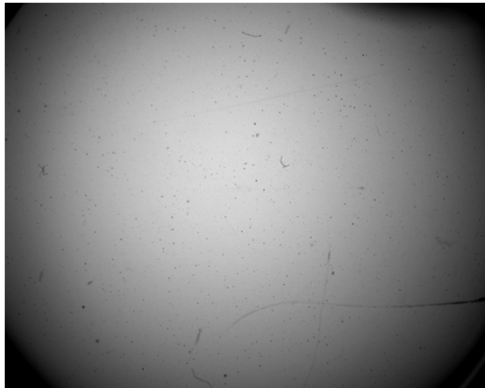
EGFRvIII and 3'deletions are detected in the samples showing transcriptional downregulation

EGFR C-terminal Deletions are Functional

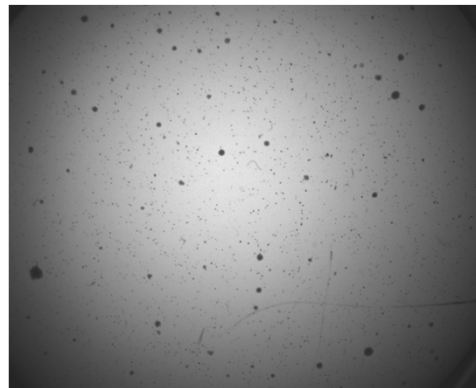


Increased NIH-3T3 cell colony formation in soft agar

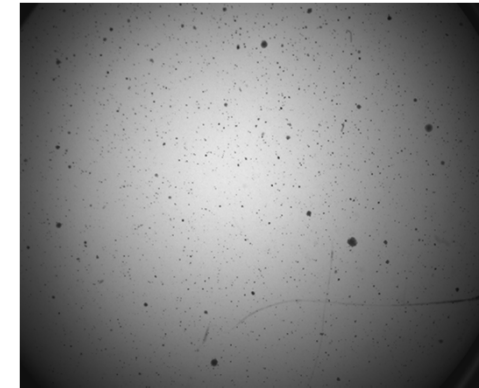
Wild-type EGFR



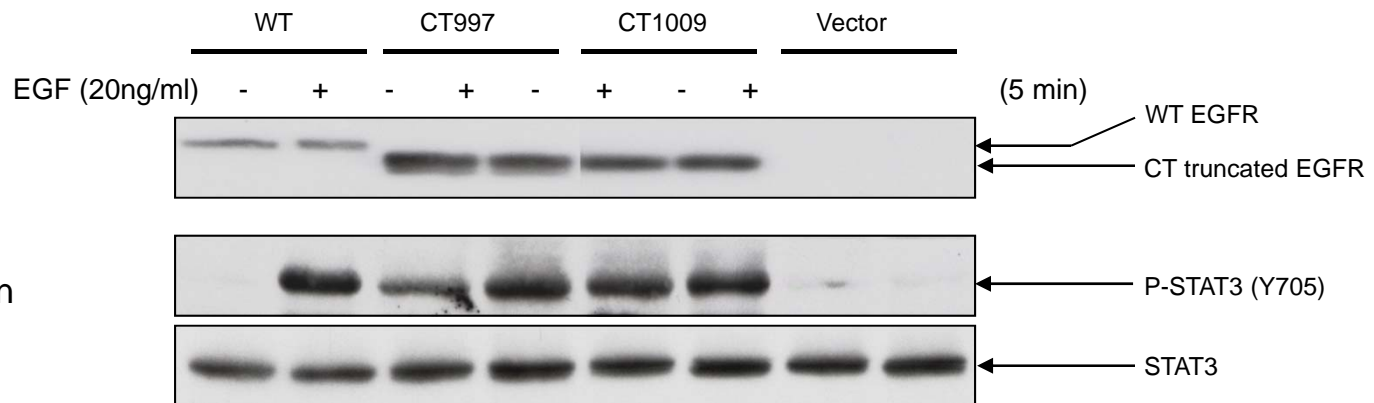
CT997 deletion



CT1009 deletion



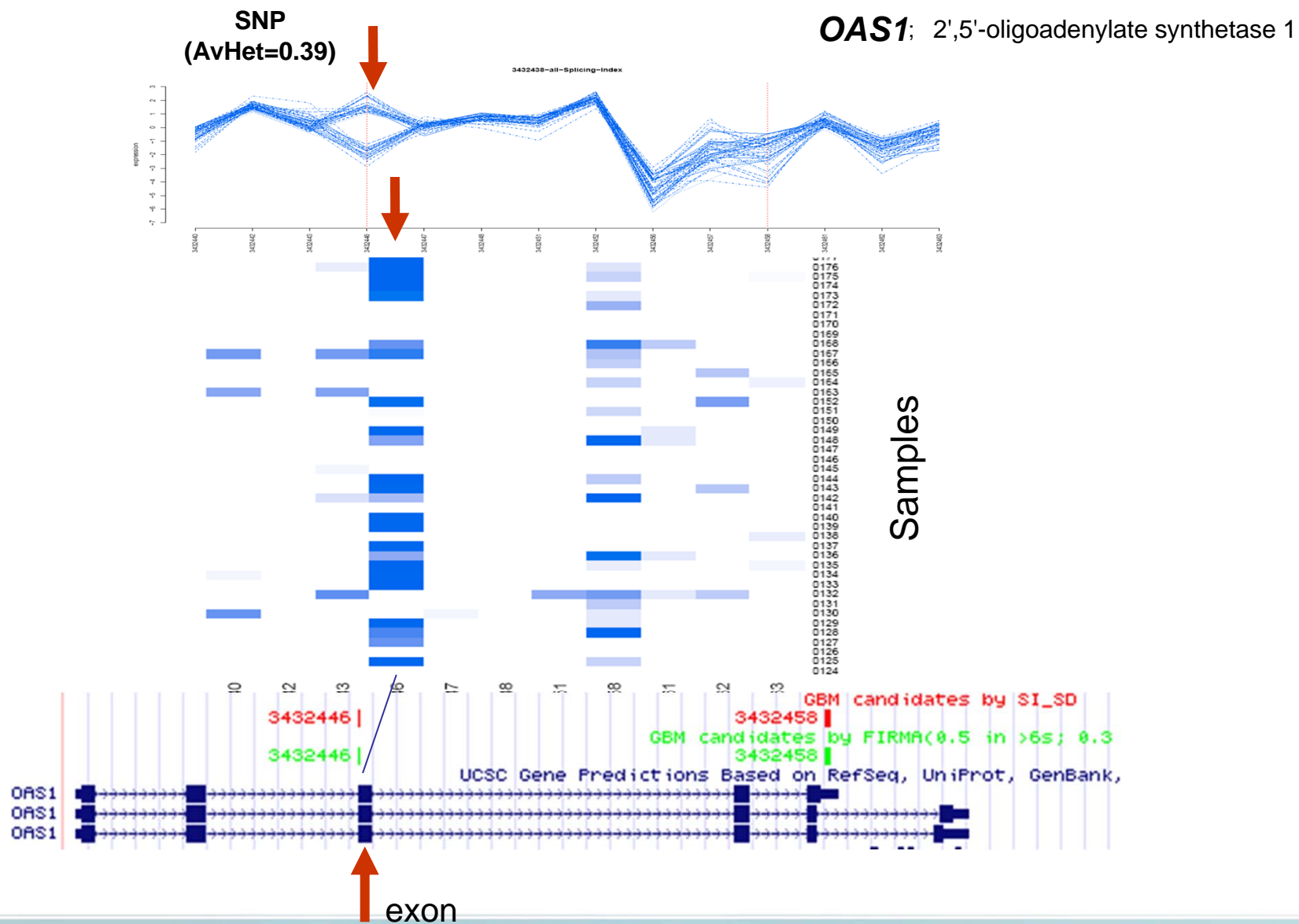
C-terminal EGFR deletions are biochemically active without added EGF



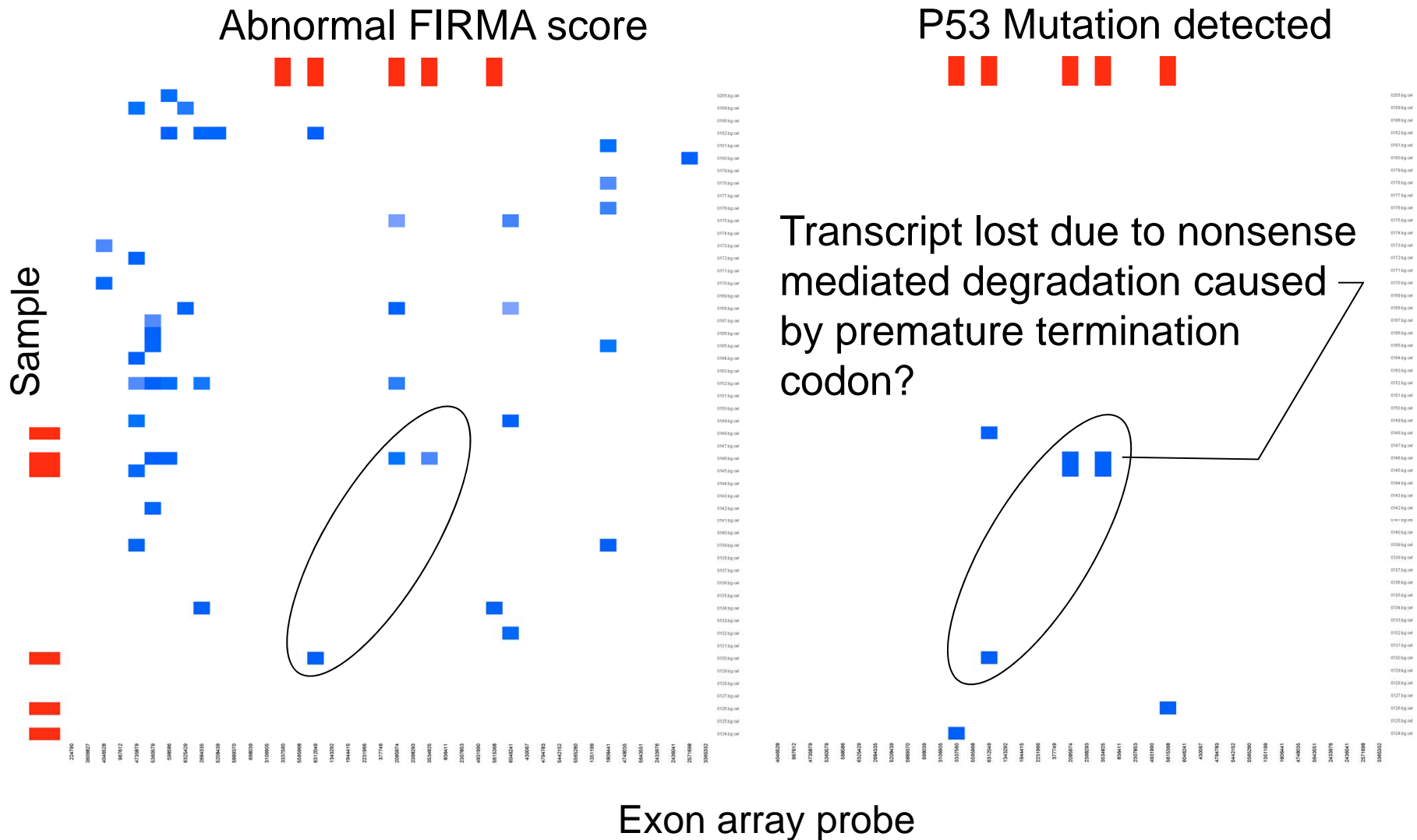
Jeonghee Cho
Matthew Meyerson

DNA Polymorphisms Influence Exon Level Expression Measurements

THE CANCER GENOME ATLAS



Mutation Mediated Transcription



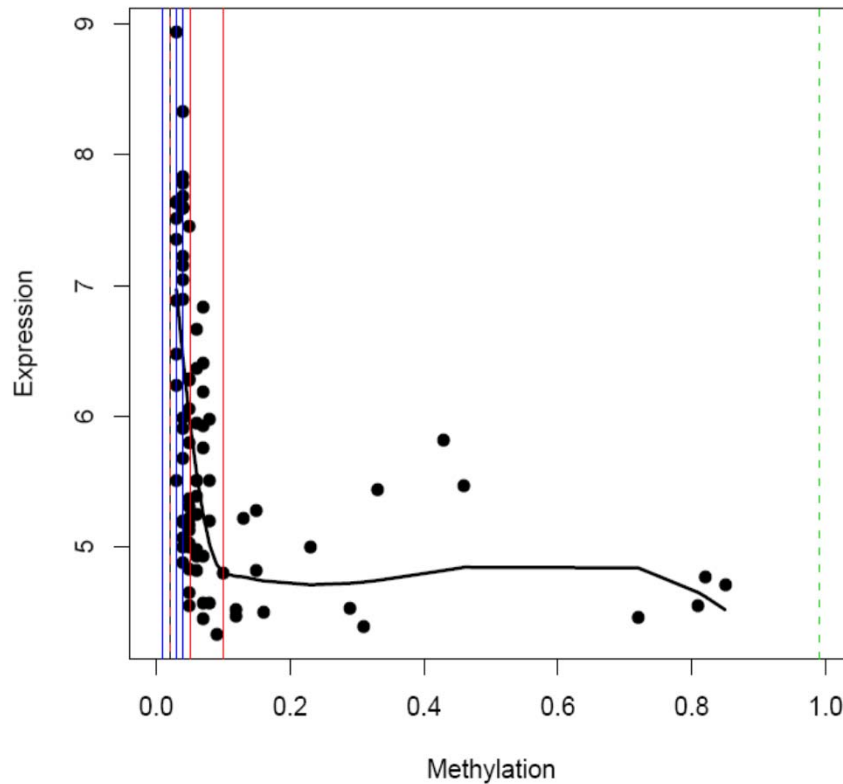
Note: Not yet validated experimentally

A. Lapuk and the TCGA

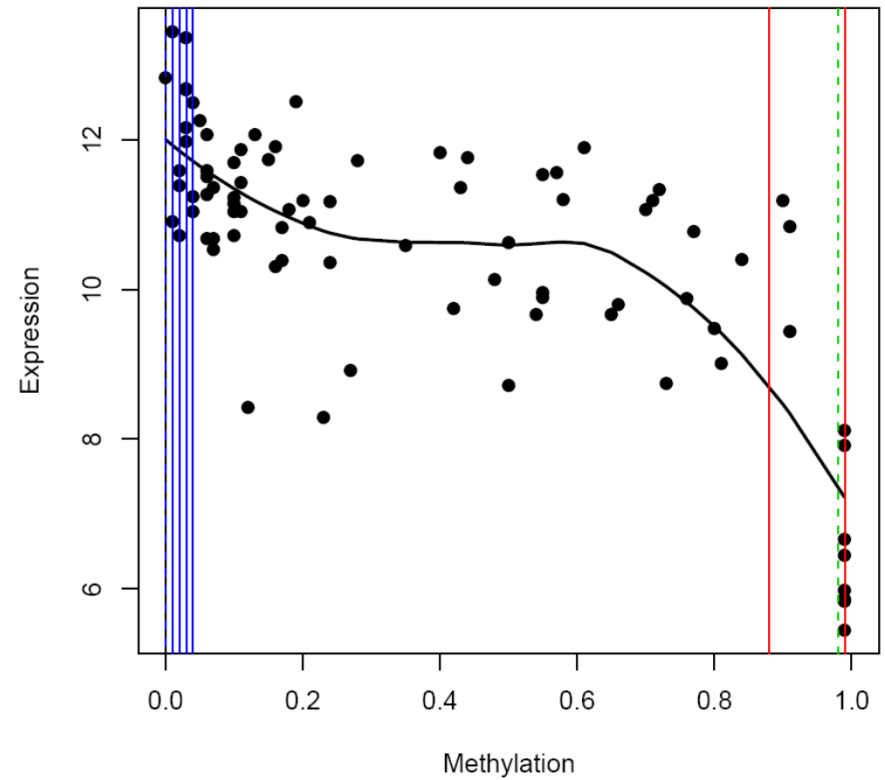
DNA Hypermethylation vs. Transcription



OMA2 EPHB1 -0.628



OMA2 RBP1 -0.648



Laird, Schuebel, Herman, Cope and the TCGA



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Transcription teams

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