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Judging a Book by its Cover: Using Lectin Microarrays to Identify How Glycosylation is Regulated

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Judging a Book By Its Cover

Using Lectin Microarrays to Identify How Glycosylation is Regulated

John Rakus, Ph.D.
Department of Chemistry
Fort Lewis College
December 11, 2012



NEW YORK UNIVERSITY



Judging a Book By Its Cover

Using Lectin Microarrays to Identify How
Glycosylation is Regulated

John Rakus, Ph.D.

Advisor: Dr. Lara Mahal



Cells are primarily composed of three types of biomolecules

HeLa cell



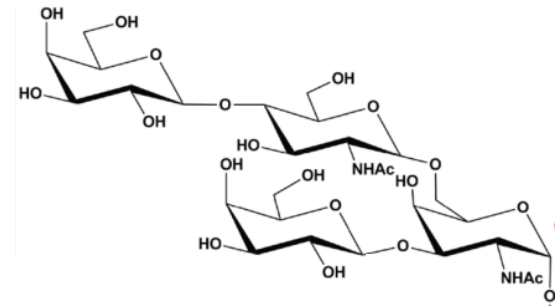
Protein (50% dry weight)



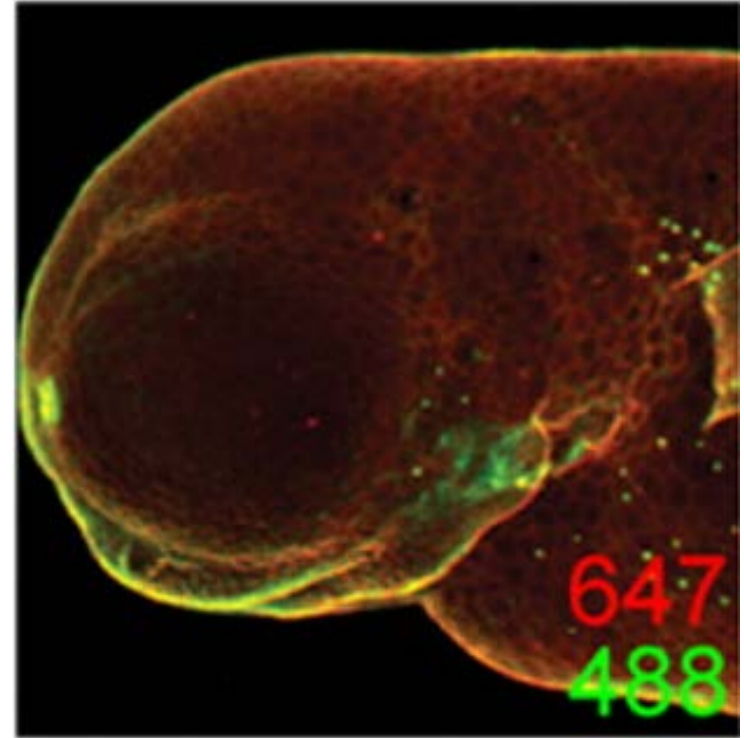
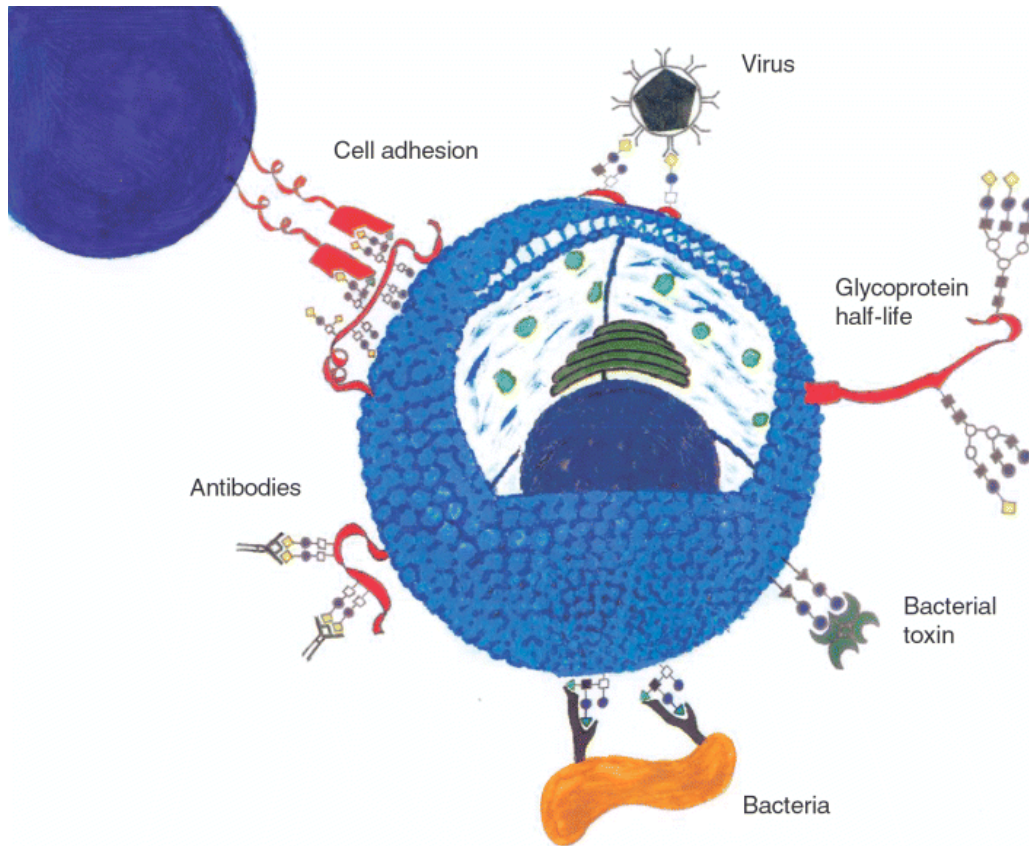
Nucleic acid (25% dry weight)



Carbohydrate (10% dry weight)



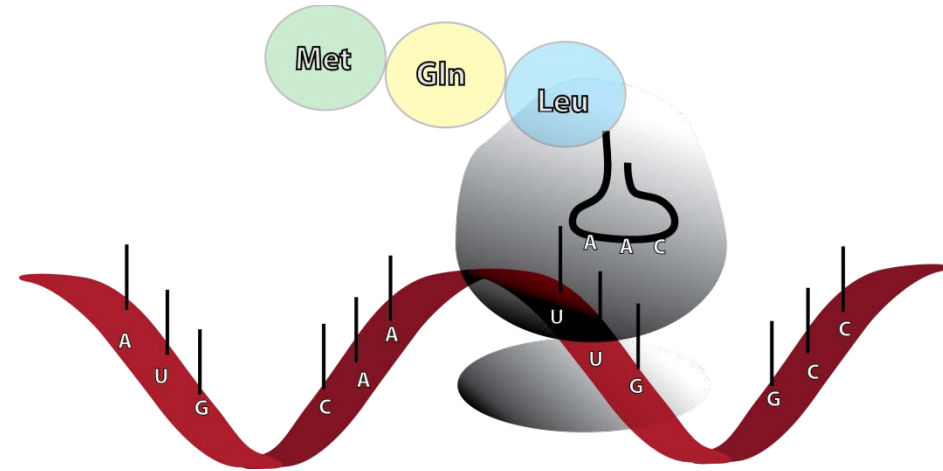
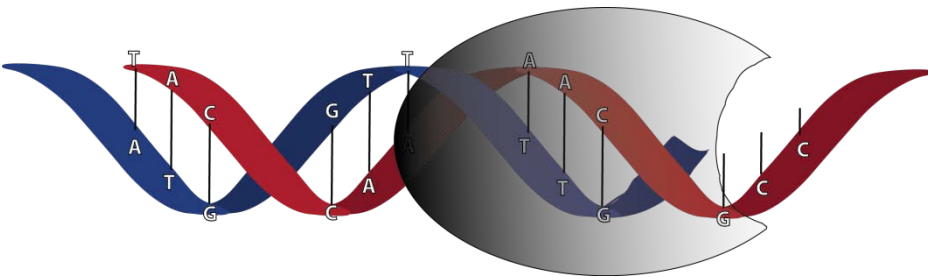
Carbohydrates are pervasive and involved in many cellular interactions



Holgerson et al, *Immuno Cell Biol*, 2005

Laughlin et al, *Science*, 2008

Nucleic acids and proteins are synthesized with a defined template and dedicated polymerases



Macromolecule: Nucleic acid

Macromolecule: polypeptide

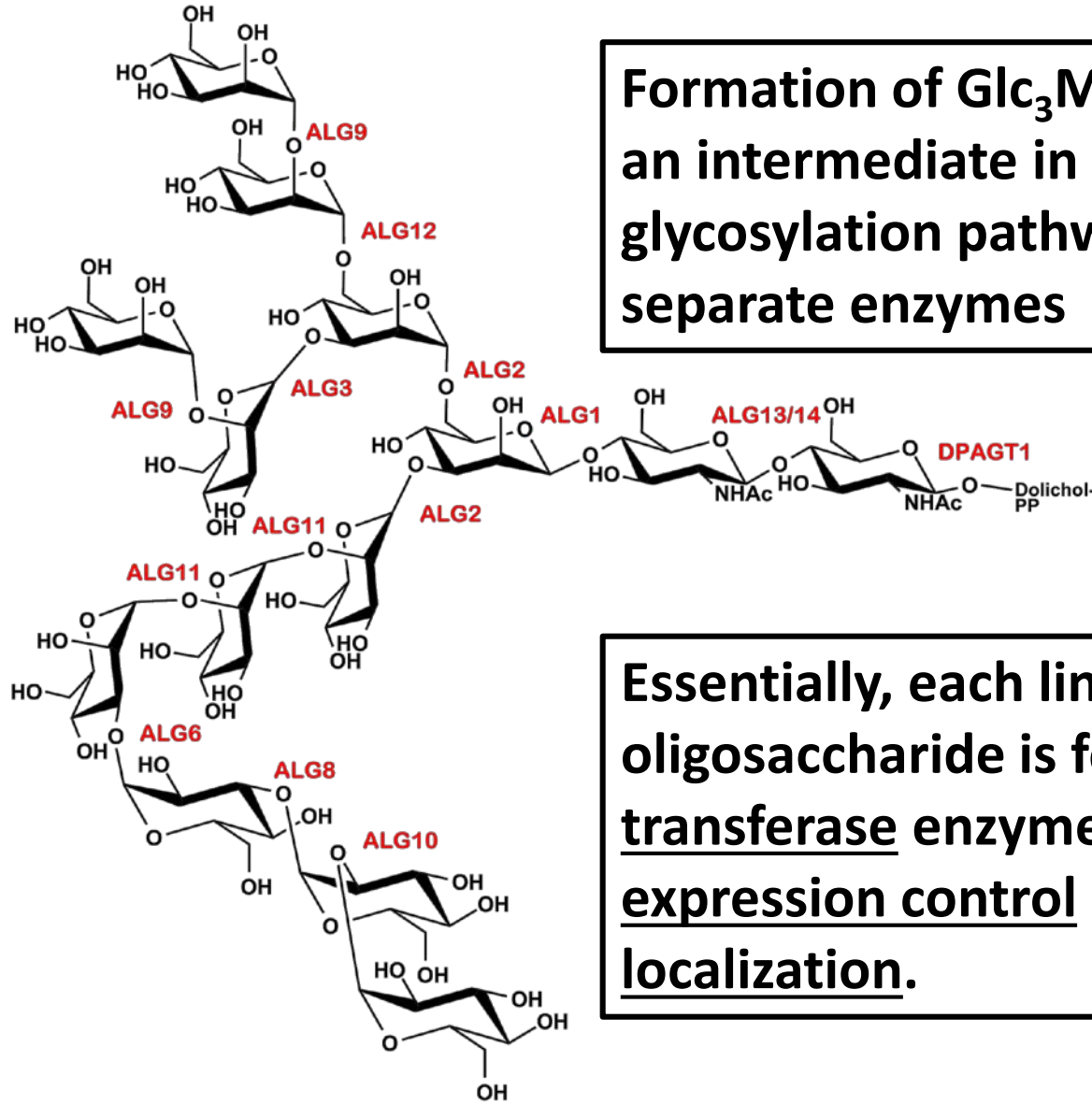
Polymerase: DNA Pol or RNA Pol

Polymerase: Ribosome

Template: DNA strand

Template: mRNA strand

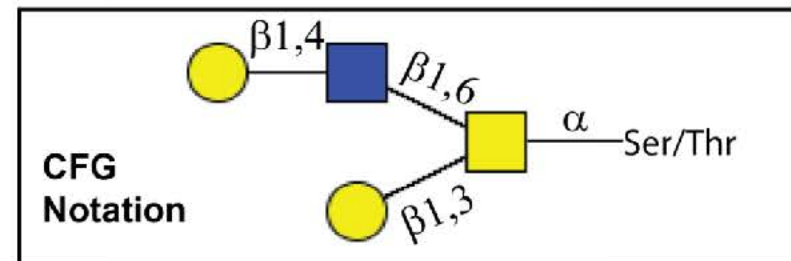
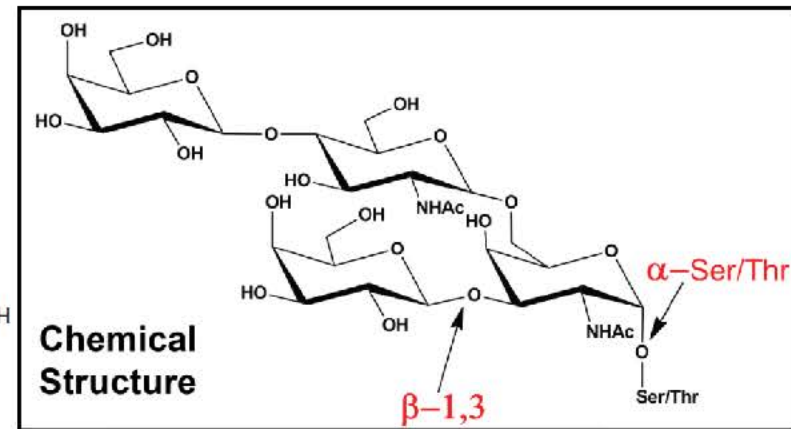
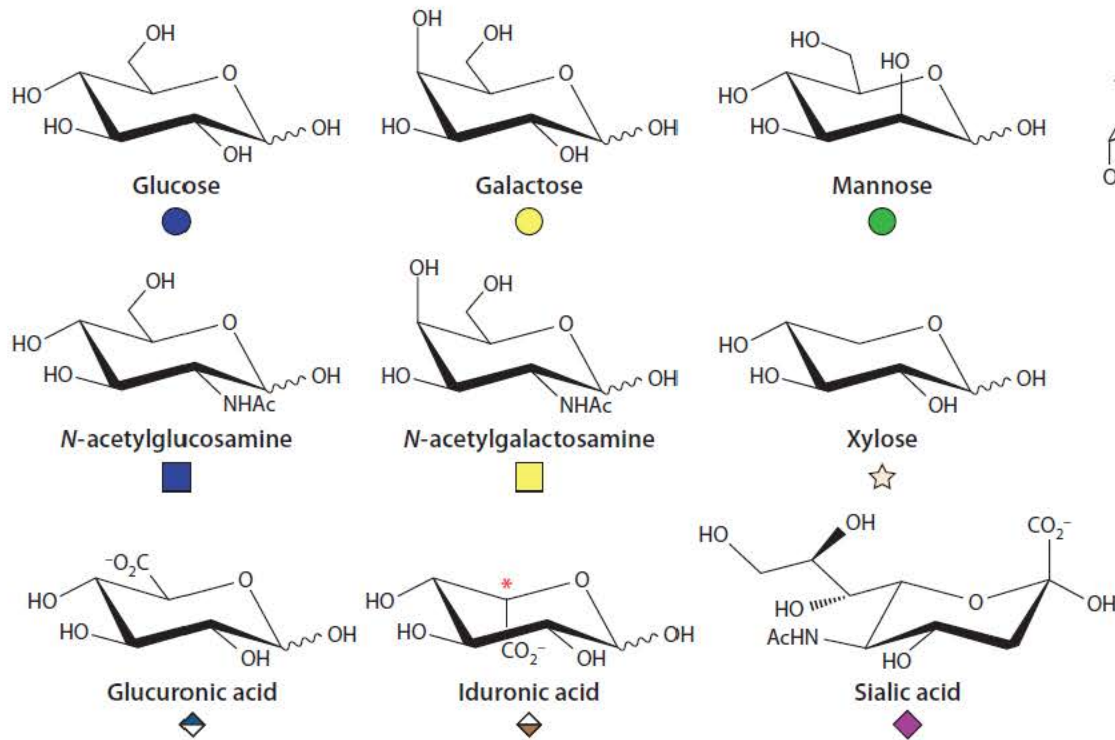
Glycan biosynthesis lacks a dedicated polymerase and genetic template



Formation of $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2\text{-DolPP}$, an intermediate in the *N*-linked glycosylation pathway, requires 12 separate enzymes

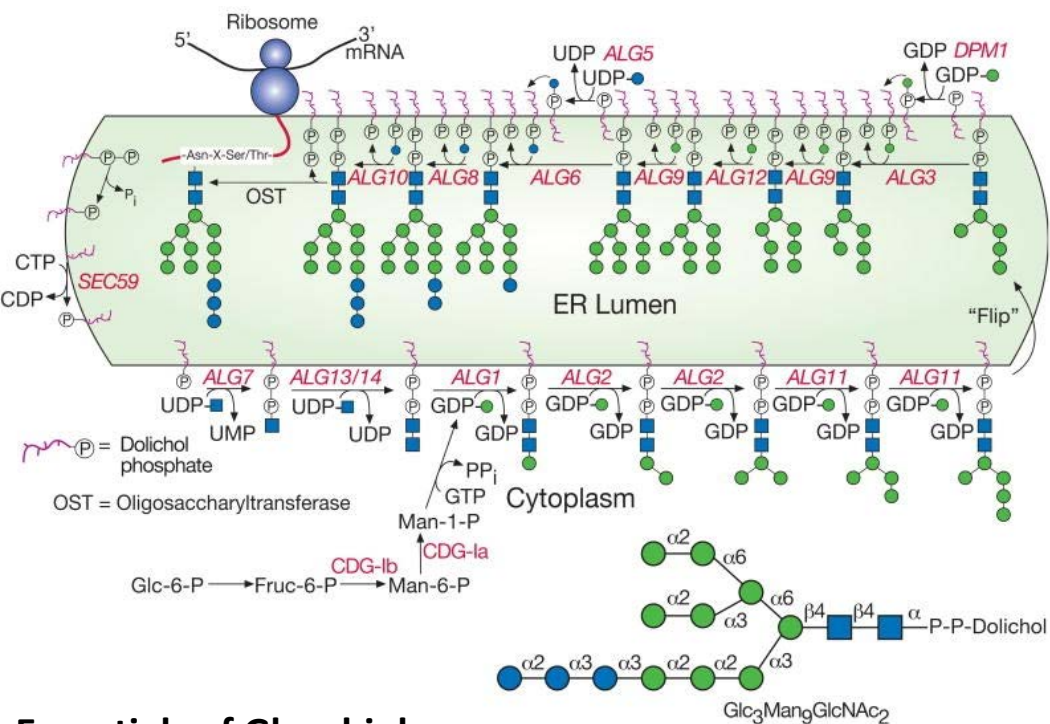
Essentially, each linkage in an oligosaccharide is formed by a specific transferase enzyme with specific expression control and subcellular localization.

Consortium for Functional Glycomics (CFG) Notation

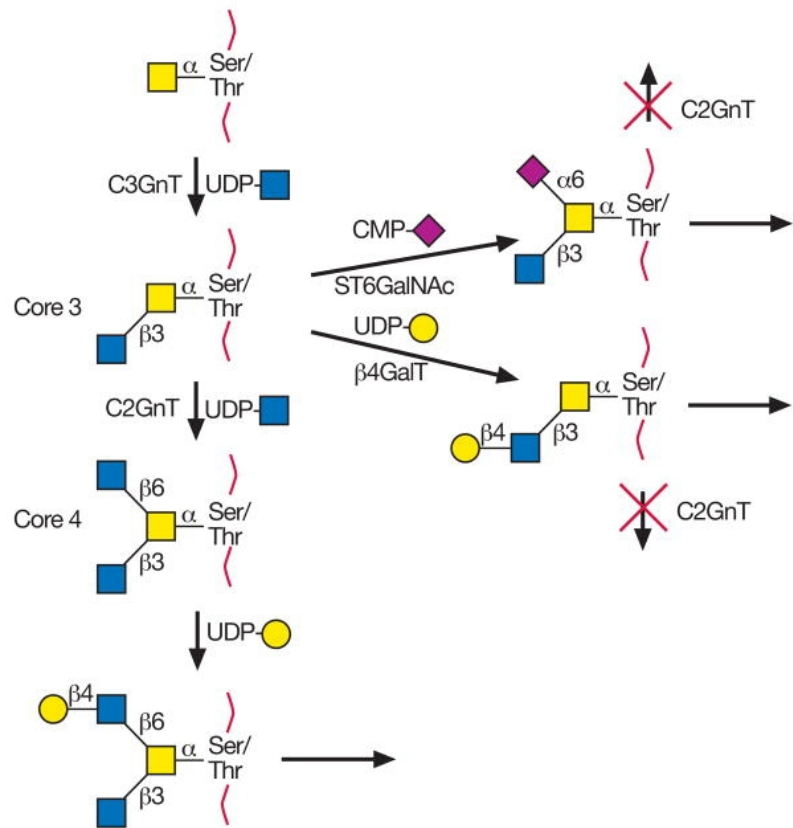


There are two primary glycosylation pathways

N-linked glycosylation occurs in the ER and Golgi and involves construction of a lipid-linked 14-mer precursor before being transferred to an Asn residue and further modified to form the final structure. Modified proteins have N-x-S/T consensus sequence

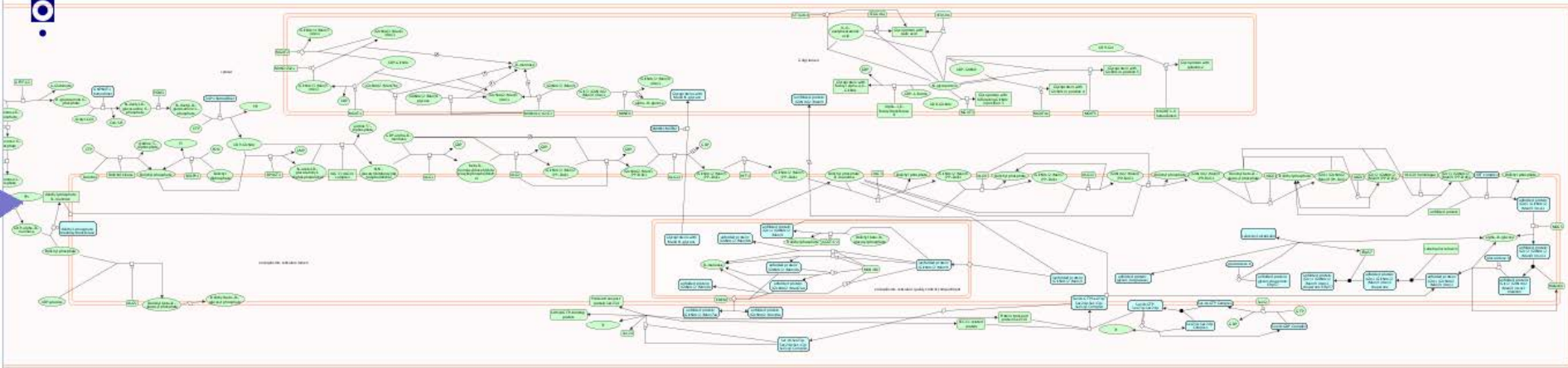


O-linked glycosylation occurs in the Golgi apparatus and involves transfer of a monosaccharide directly to a Ser/Thr residue by a specific ppGalNacT followed by further elaboration. No known consensus sequence



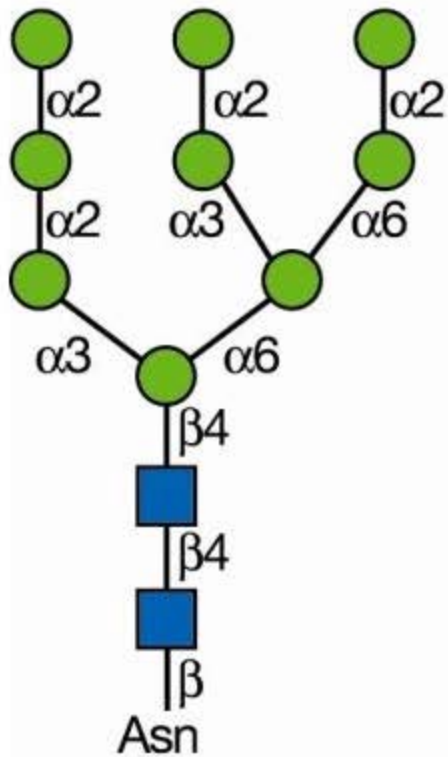
Carbohydrate synthetic regulation

N-linked glycosylation network (Reactome)

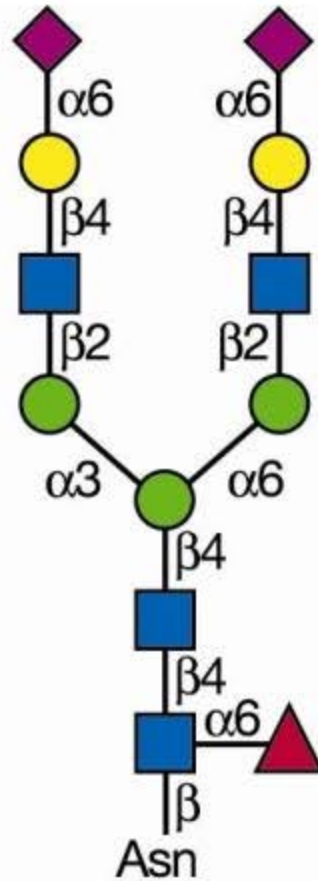


- **Synthesizing a glycome requires a large commitment of cellular resources**
- **Many glycosylation enzymes (glycosyltransferases and glycosidases), sugar transporter and metabolic proteins, and regulation elements (over 120 identified as of 2011)**

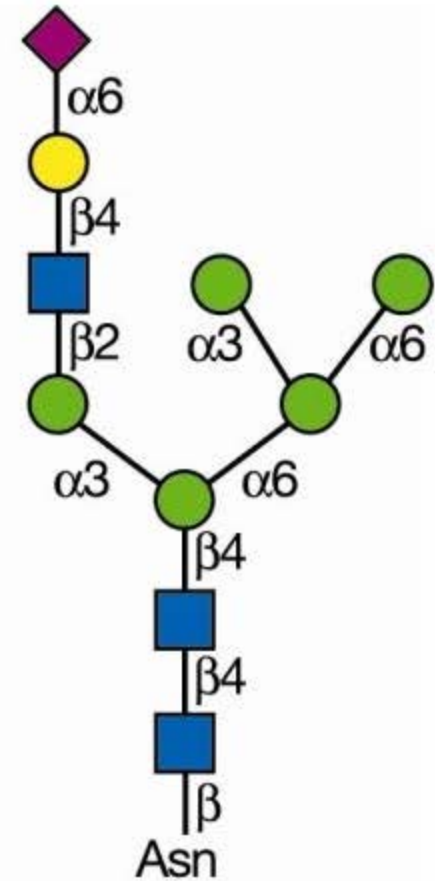
There are three types of N-linked glycans



Oligomannose



Complex



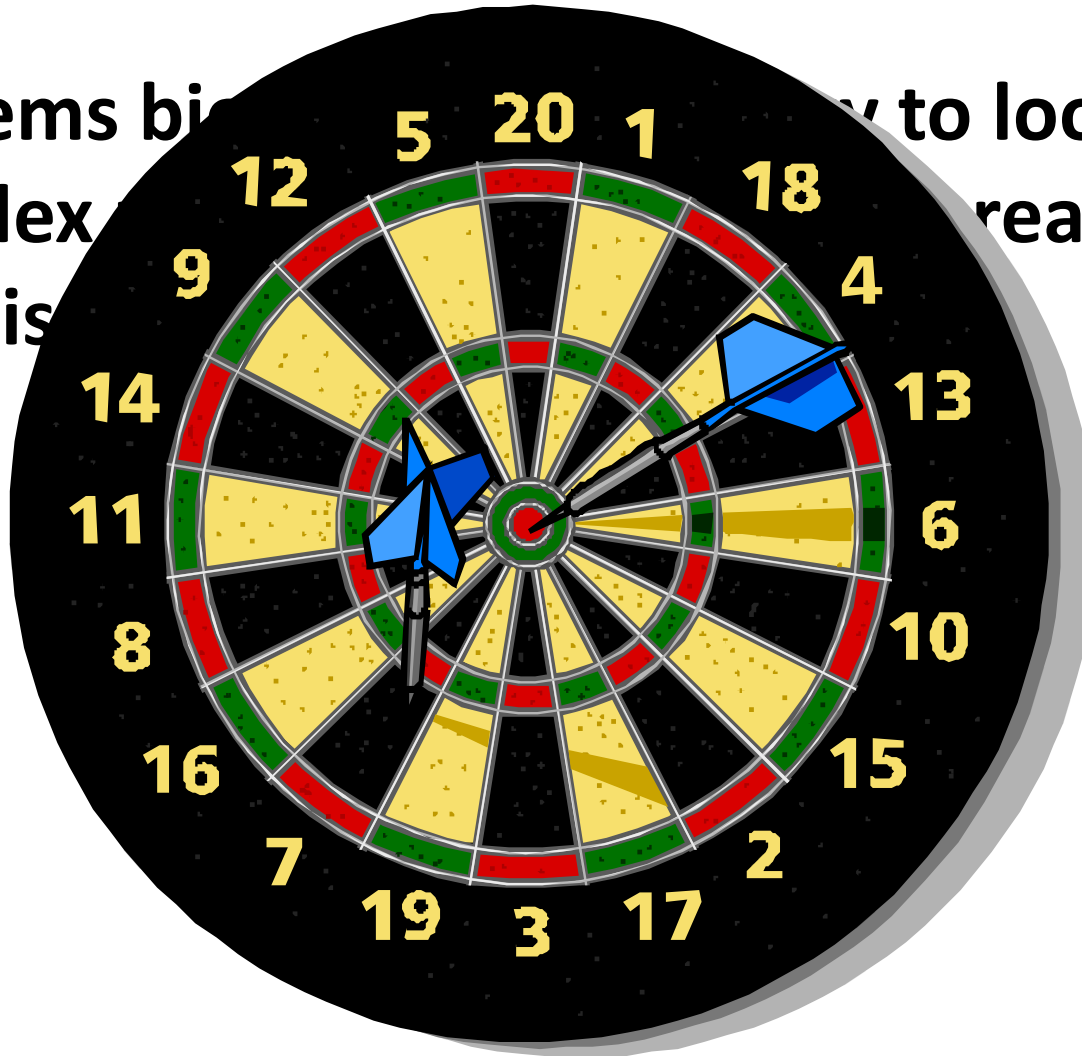
Hybrid

Glycosylation is complicated

- The structures are hard to discern
- The pathways are often redundant and overlapping
- The effects are subtle and, occasionally, conflicting

Systems Biology

“Systems biology is a new way to look at complex systems. It breaks them down into discrete parts and studies how they interact.”



The experiment

- 1. Look at the cell surface (glycome)**
- 2. See if different cells express different carbohydrates**
- 3. If so, try to explain why**

Model System: The NCI-60 Cell Panel

- **NCI-60: 60 cell lines for screening of potential cancer therapeutics**
- **Vary in tissue type, metastasis, individual of origin**
- **CellMiner.org: open source database containing mRNA, miRNA and protein array data, genetic mapping, pharmacological and mutational analysis**

The NCI-60 panel

LEUKEMIA

- CCRF-CRM
- HL-60
- K-562
- MOLT-4
- RPMI-8226
- SR

LUNG

- A549
- EKVX
- HOP-62
- HOP-92
- NCI-H226
- NCI-H23
- NCI-H322M
- NCI-H460
- NCI-H522

COLON

- COLO 205
- HCC-2998
- HCT-116
- HCT-15
- HT29
- KM12
- SW-620

CNS

- SF-268
- SF-295
- SF-539
- SNB-19
- SNB-75
- U251

MELANOMA

- LOX IMVI
- MALME-3M
- M14*
- MDA-MB-435*
- SK-MEL-2
- SK-MEL-28
- SK-MEL-5
- UACC-257
- UACC-62

OVARIAN

- IGR-OV1
- OVCAR-3
- OVCAR-4
- OVCAR-5
- OVCAR-8
- NCI/ADR-RES
- SK-OV-3

PROSTATE

- PC-3
- DU-145

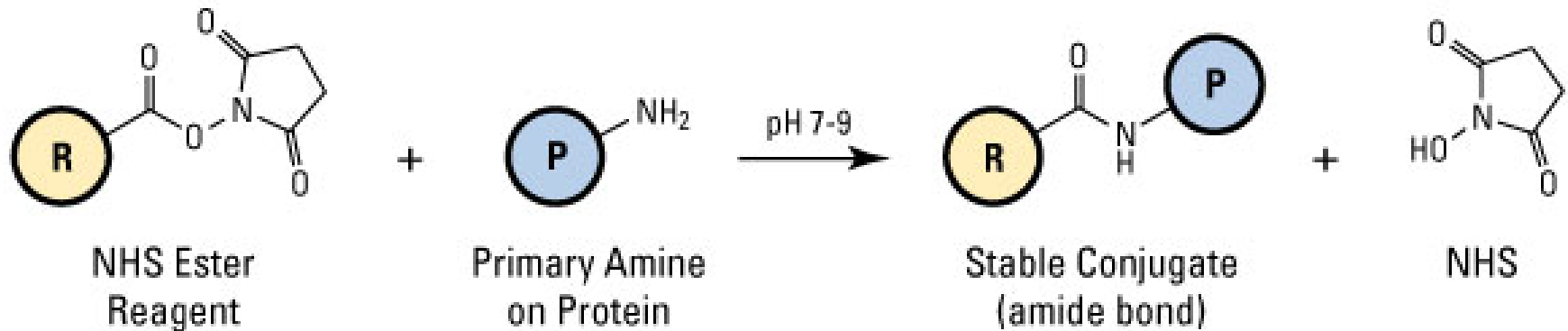
RENAL

- 786-0
- A498
- ACHN
- CAKI-1
- RXF 393
- SN12C
- TK-10
- UO-31

BREAST

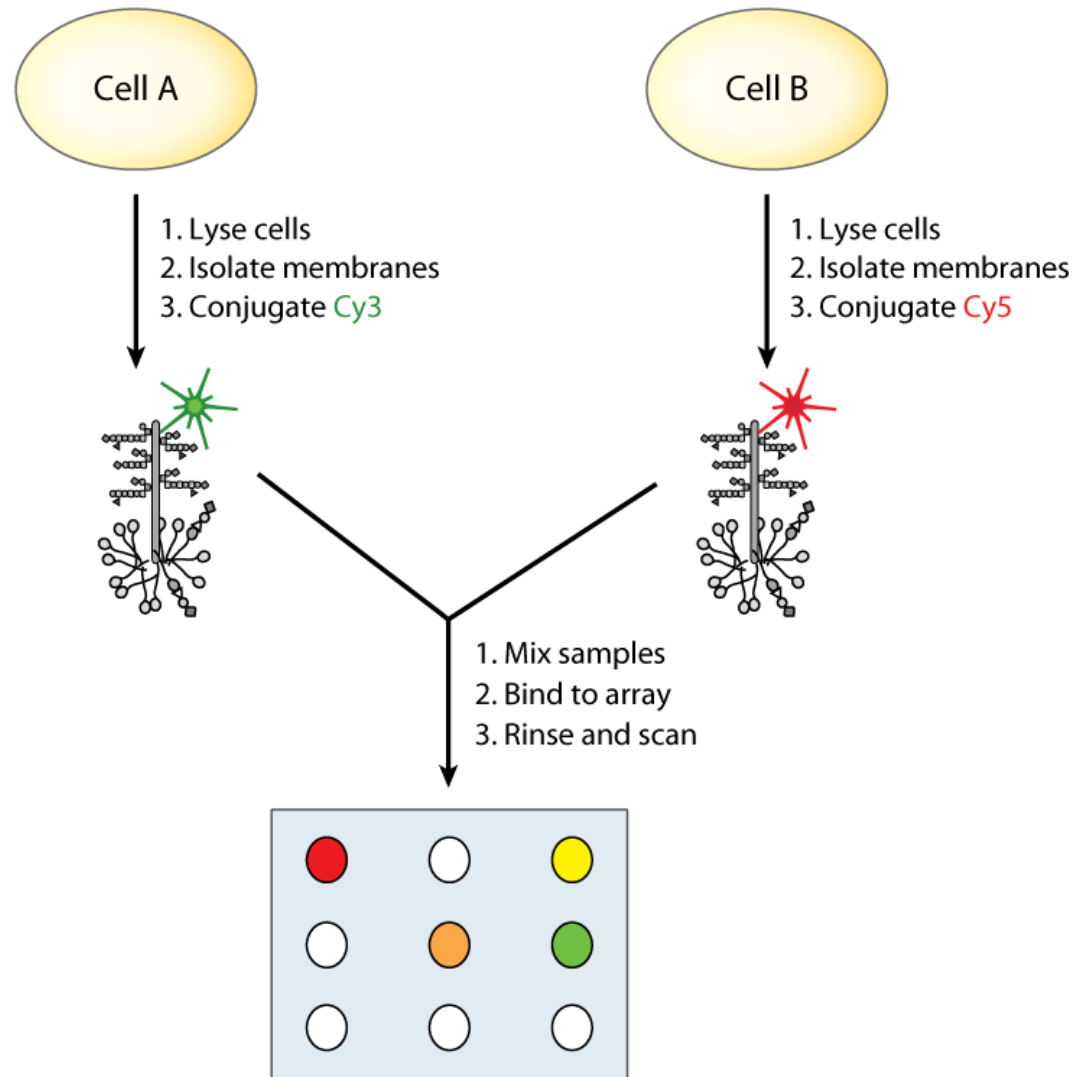
- MCF7
- MDA-MB-231
- MDA-MB-468
- HS 578T
- BT 549
- T-47D

Generation of Lectin Microarrays



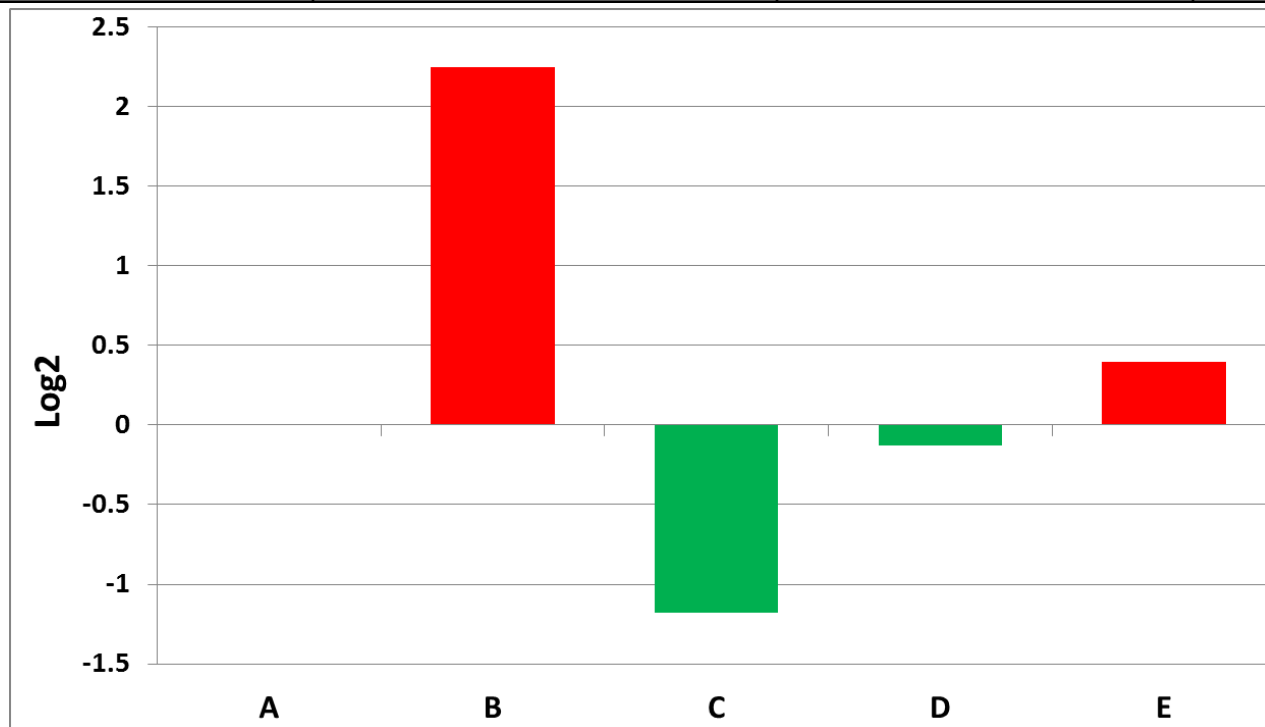
- Lectins are printed on NHS-ester coated glass slides in high spatial density at 10°C and ambient humidity
- Protein lysine residues react with esters to form amide-bound conjugates
- Unreacted esters are blocked with ethanolamine
- Slides can be stored for up to two months

Ratiometric lectin microarray analysis for semi-quantitative analysis of the dynamic glycome



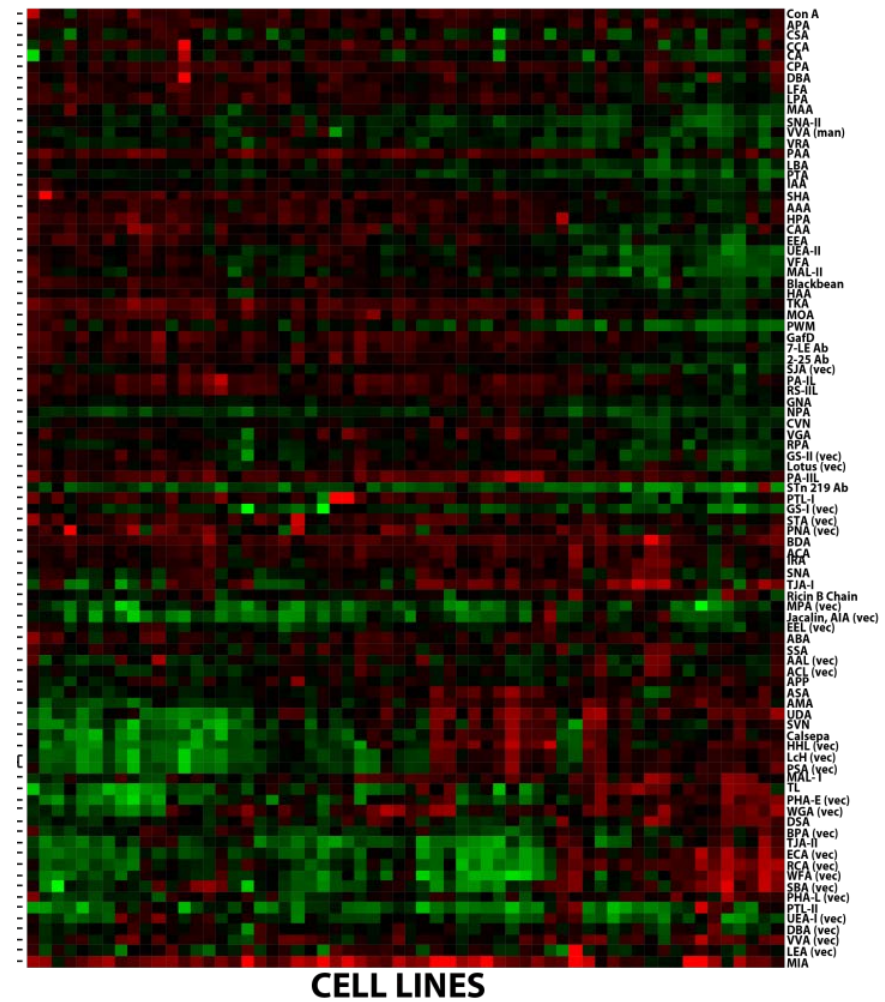
Interpreting a two-color experiment

Probe	Sample Fluorescence	Reference Fluorescence	Sample/Reference	$\text{Log}_2(S/R)$
A	500.00	500.00	1	0.00
B	2497.0	525.00	4.76	2.25
C	5500.0	12485	0.44	-1.18
D	125.20	137.23	0.91	-0.13
E	2545.0	1928.0	1.32	0.40



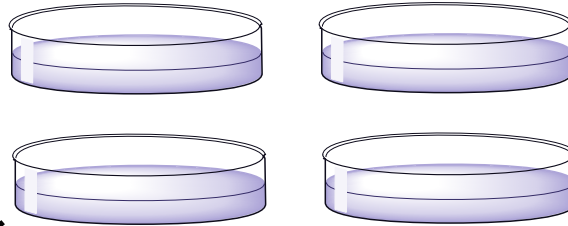
Interpreting a two-color experiment

When you have many samples and many probes, the data gets represented as a heat map



Experimental Strategy

Culture NCI-60 lines



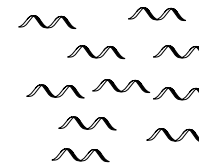
GLYCOMICS

GENOMICS

Isolate, label
membranes

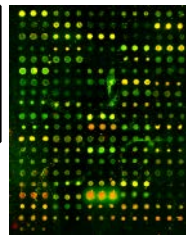


Fluorophore-labeled
cell sample

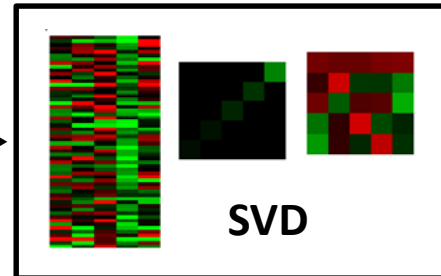


Isolate total
mRNA

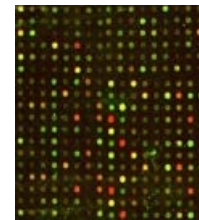
Analyze lectin
microarray



Combine and Integrate



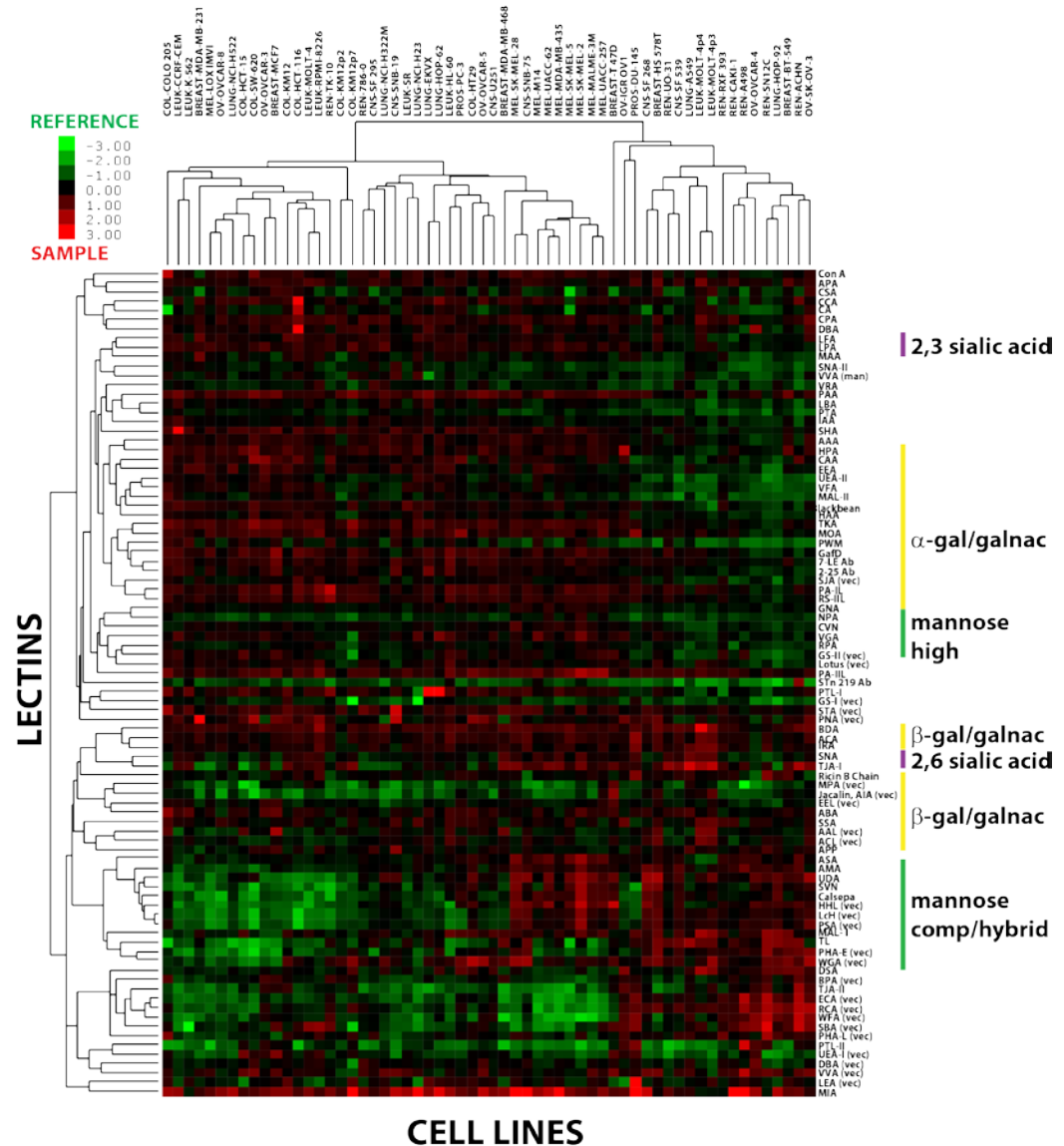
Analyze gene
microarray



Confirm
with whole
cell labeling

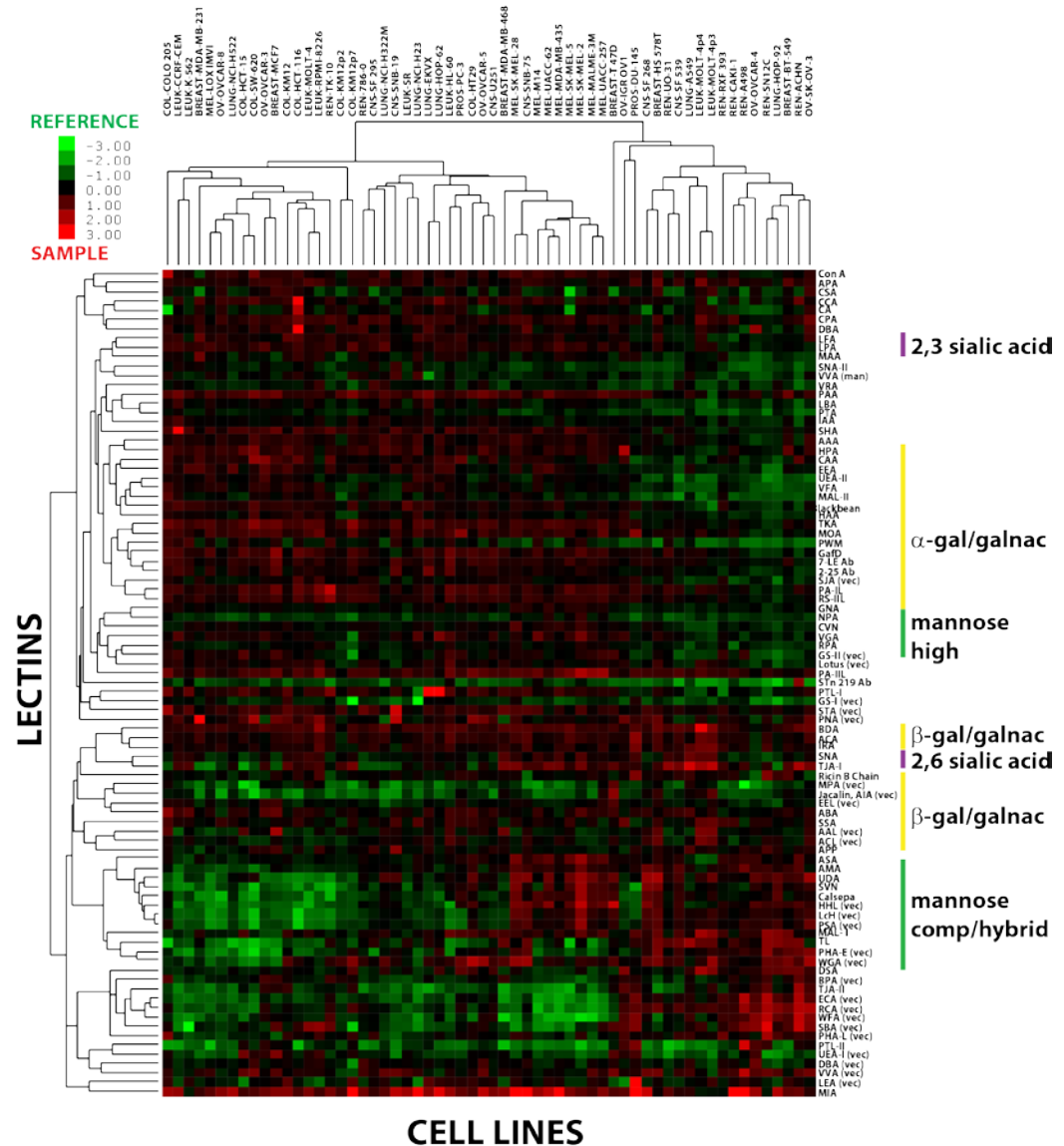
Lectin microarray analysis shows meaningful patterns

- 90 lectins
- 56 cell lines
- Biological replicates of two cell lines

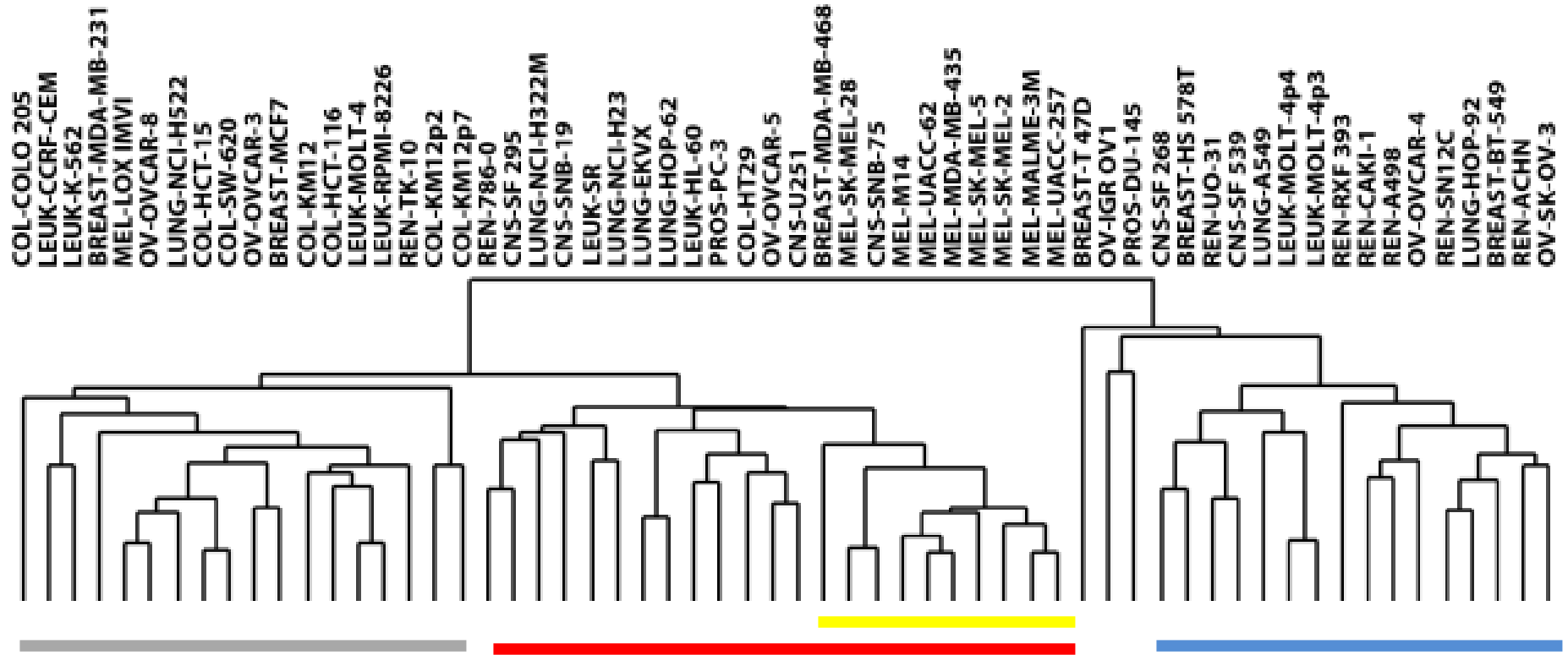


Lectin microarray analysis shows meaningful patterns

- Several clusters of lectins by carbohydrate specificity
- Cell lines cluster by tissue of origin



Cell lines cluster based on their glycosylation



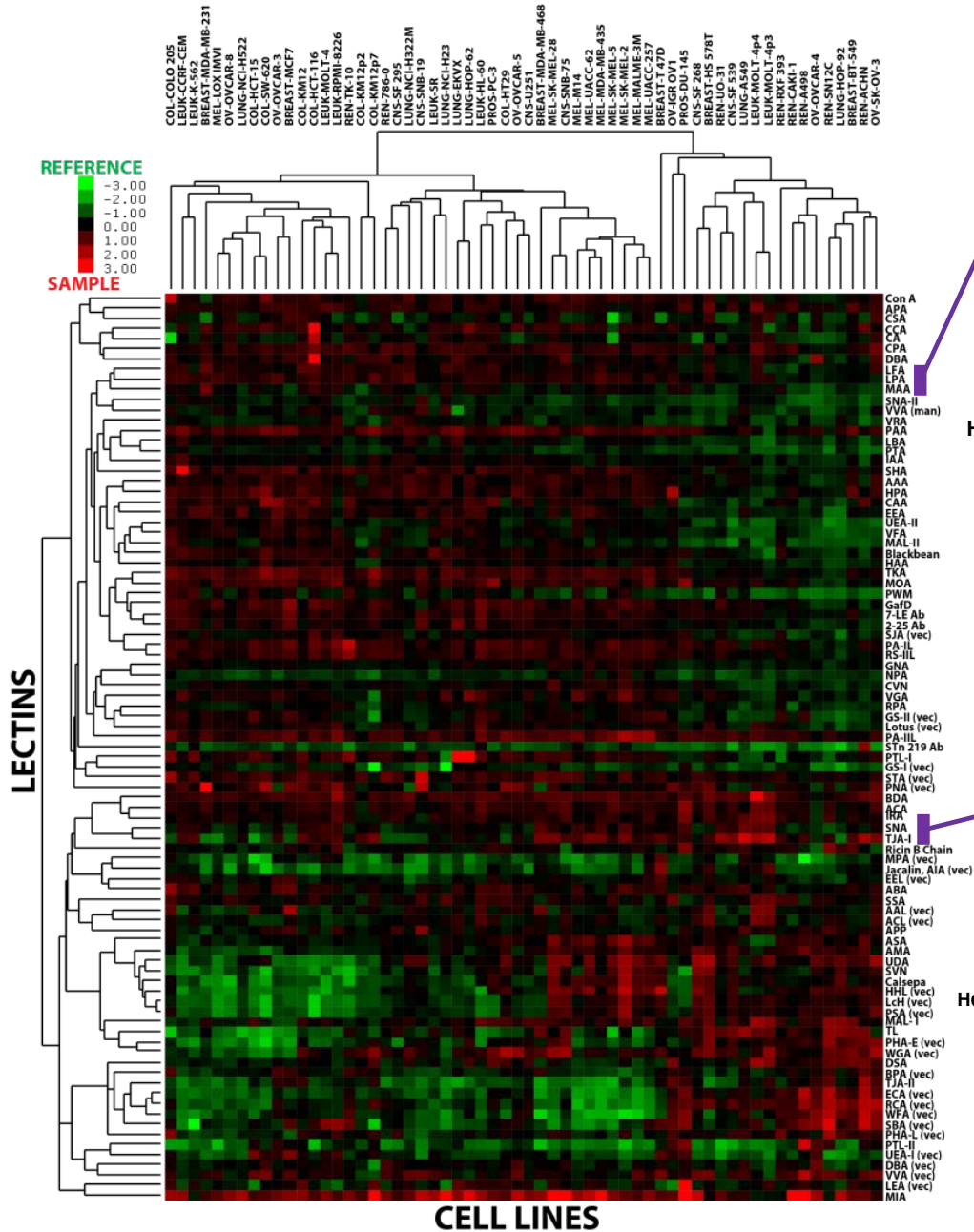
COLON (5/6, $p=0.39$)
LEUKEMIA (4/6, $p=0.39$)

CNS (4/5, $p=0.44$)
LUNG (4/7, $p=0.44$)

MELANOMA
(8/9, $p=0.60$)

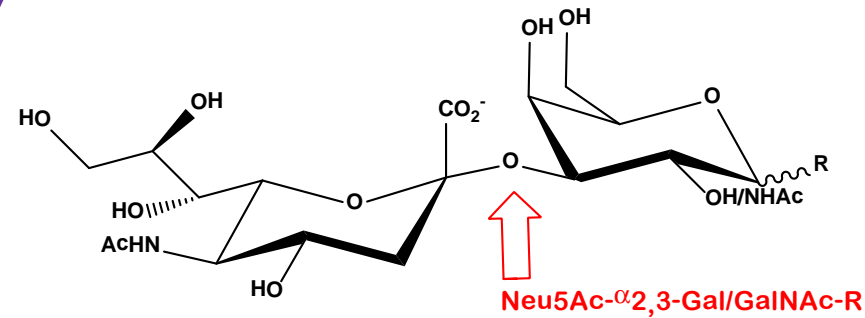
RENAL (6/8, $p=0.39$)

Glycosylation signatures: Sialic acid



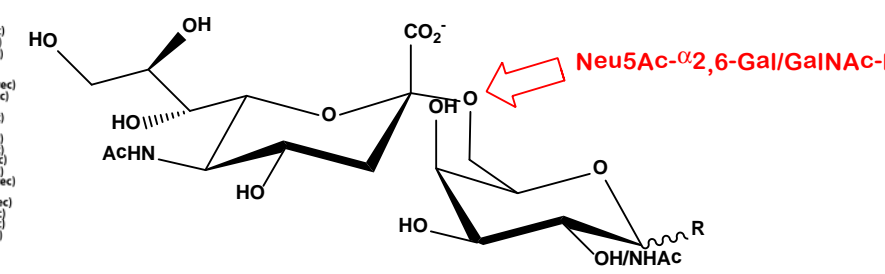
α2,3 sialic acid recognizing lectins
LFA, LPA, MAA

↓
in RENAL cell lines

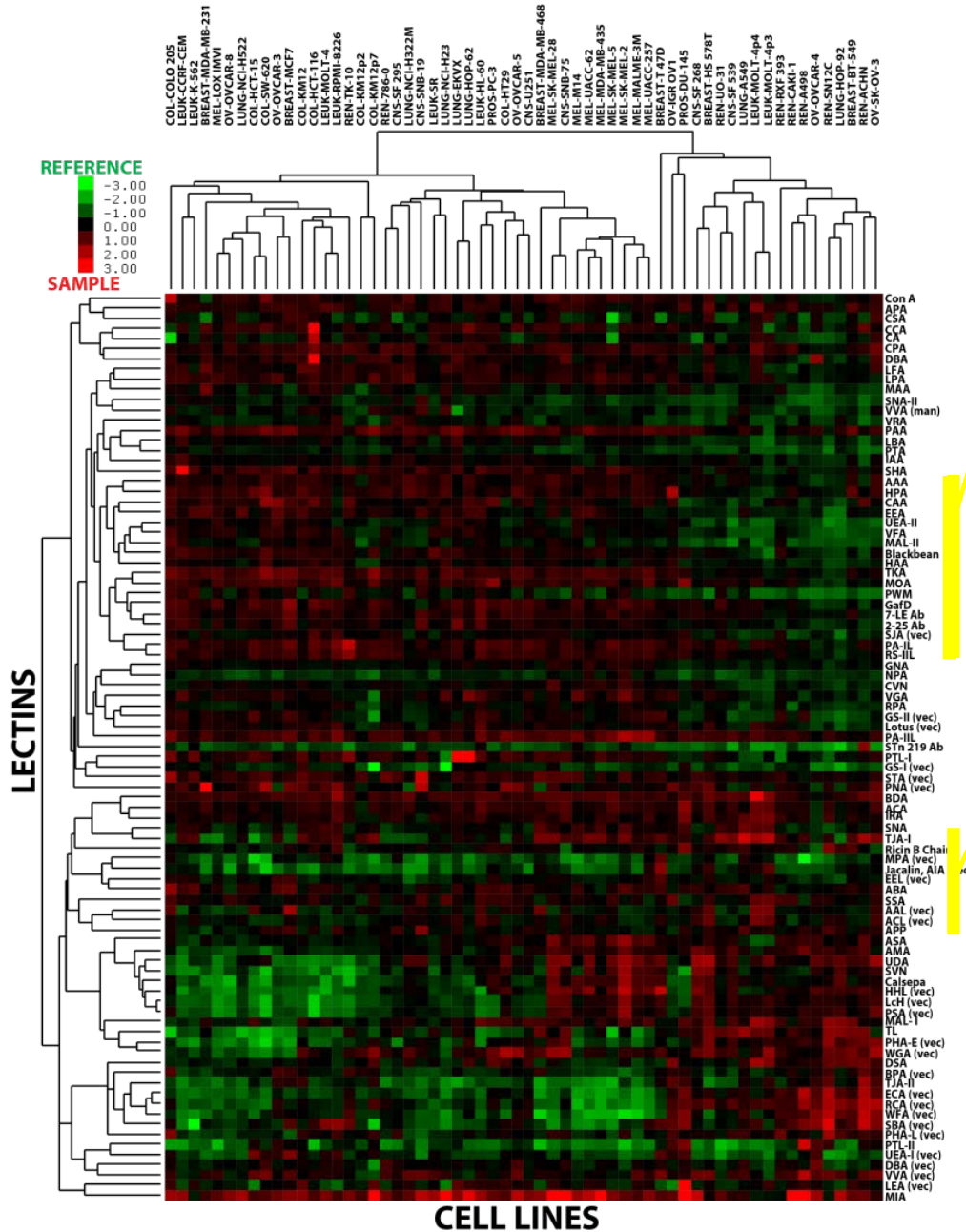


α2,6 sialic acid recognizing lectins
SNA, TJA-I

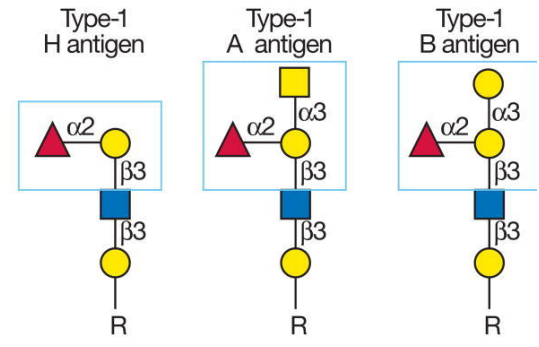
↑
in MELANOMA and LUNG cell lines



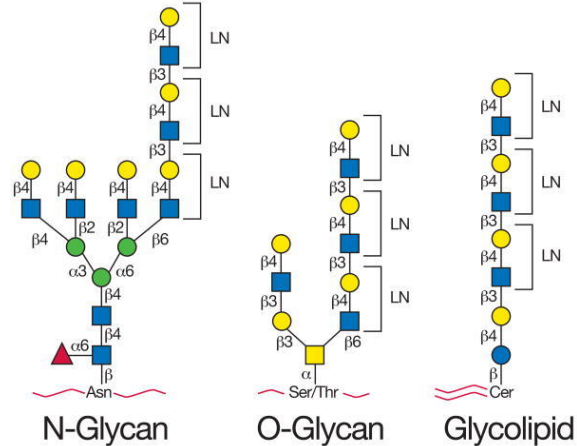
Glycosylation signatures: Gal/GalNAc



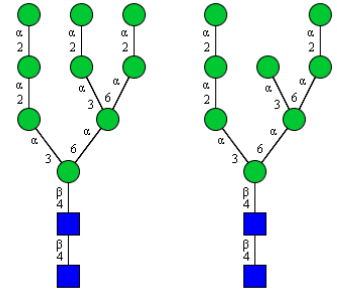
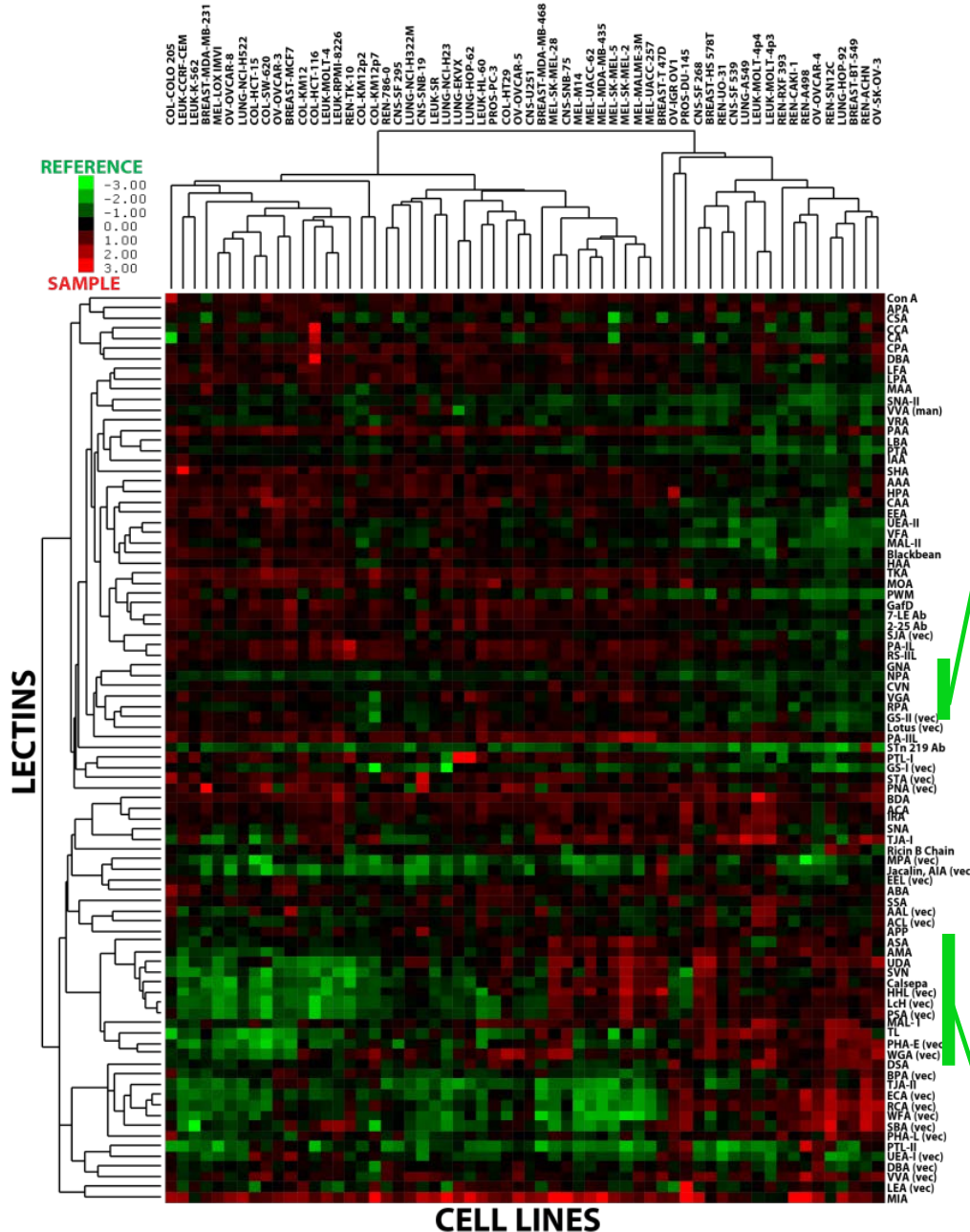
α-Gal/GalNAc; blood groups
MOA, EEA, LBA, VRA, IAA,
PTA, HPA



β-Gal/GalNAc
BDA, RICIN, ABA, AIA, AAL

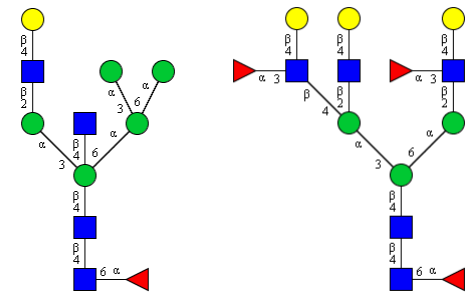


Glycosylation signatures: Mannose



Mannose (high)
GNA, NPA, CVN, RPA

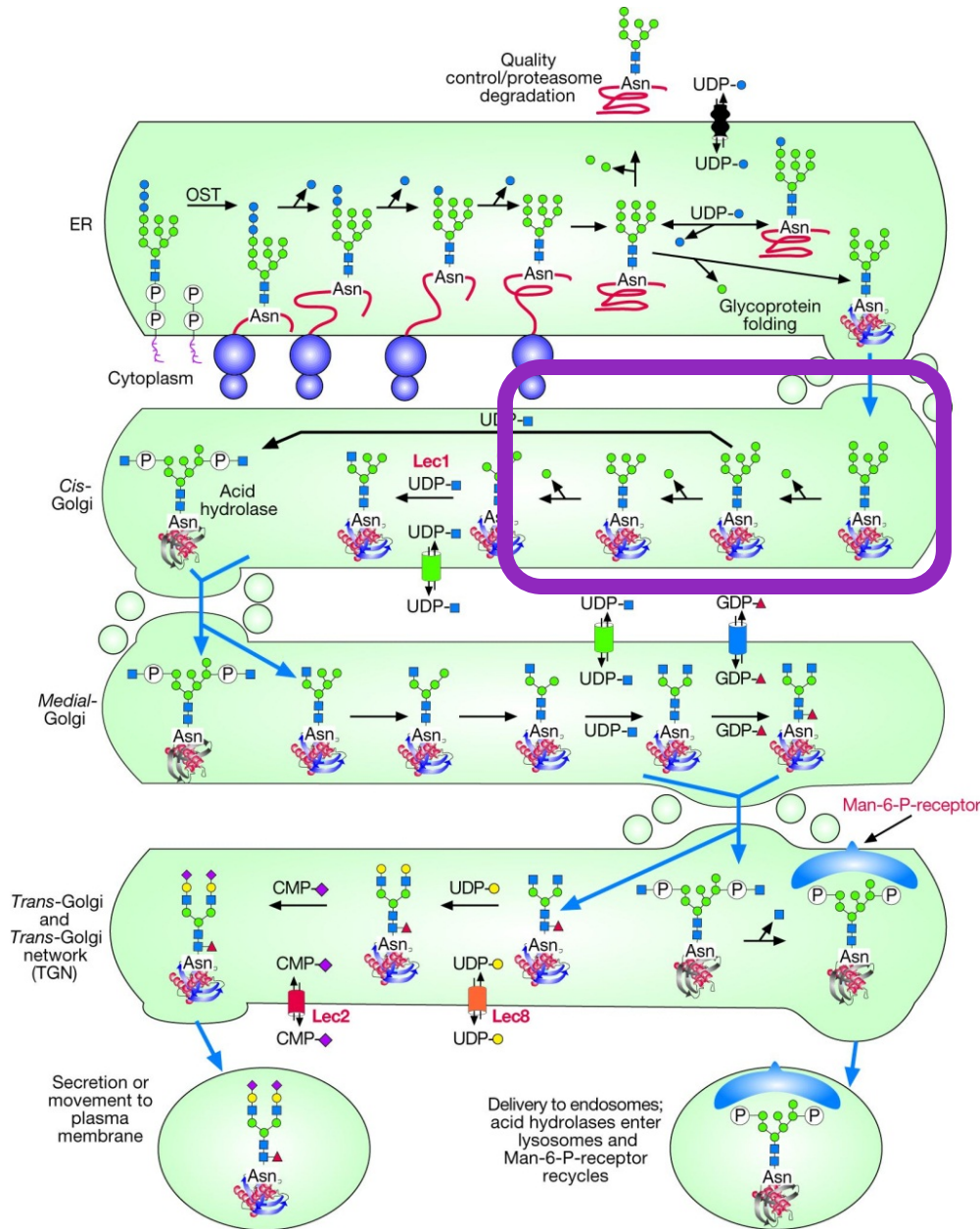
RENAL
MELANOMA
LUNG, COLON



Mannose (complex)
UDA, SVN, Calsepa,
HHL, LcH, PHA-E,
MAL-I, PSA

COLON,
LUNG
MELANOMA,
RENAL

Maturation of N-linked glycans



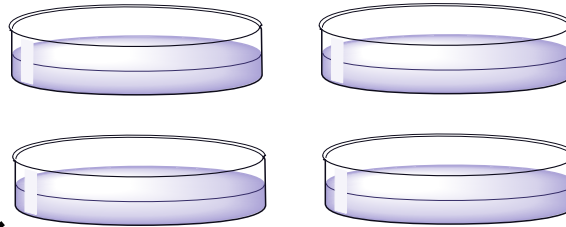
- Glc₃Man₉GlcNAc₂ precursor is transferred to nascent polypeptide in ER
- Upon proper folding, glycan is trimmed to high-mannose and, potentially further modified to hybrid/complex
- α-mannosidase I controls all hybrid/complex maturation steps

Conclusions (some)!

- **Human cells express different, specific carbohydrate patterns on their surfaces, based on their histological function**
- **What controls the glycome variation? (what does the interior of the house look like?)**

Experimental Strategy

Culture NCI-60 lines



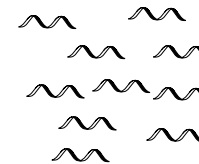
GLYCOMICS

GENOMICS

Isolate, label
membranes

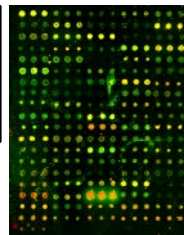


Fluorophore-labeled
cell sample

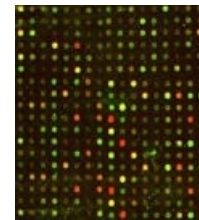
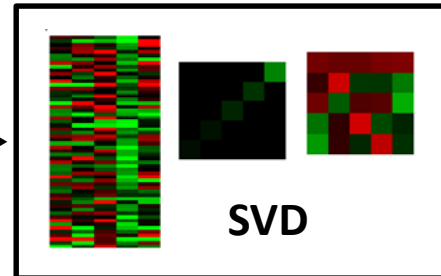


Isolate total
mRNA

Analyze lectin
microarray



Combine and Integrate



Analyze gene
microarray

Confirm
with whole
cell labeling

Patterns of NCI-60 Gene Expression Regulation

- mRNA and miRNA expression patterns investigated across entire NCI-60 (Liu et al, *Mol Biol Cell*, 2010)

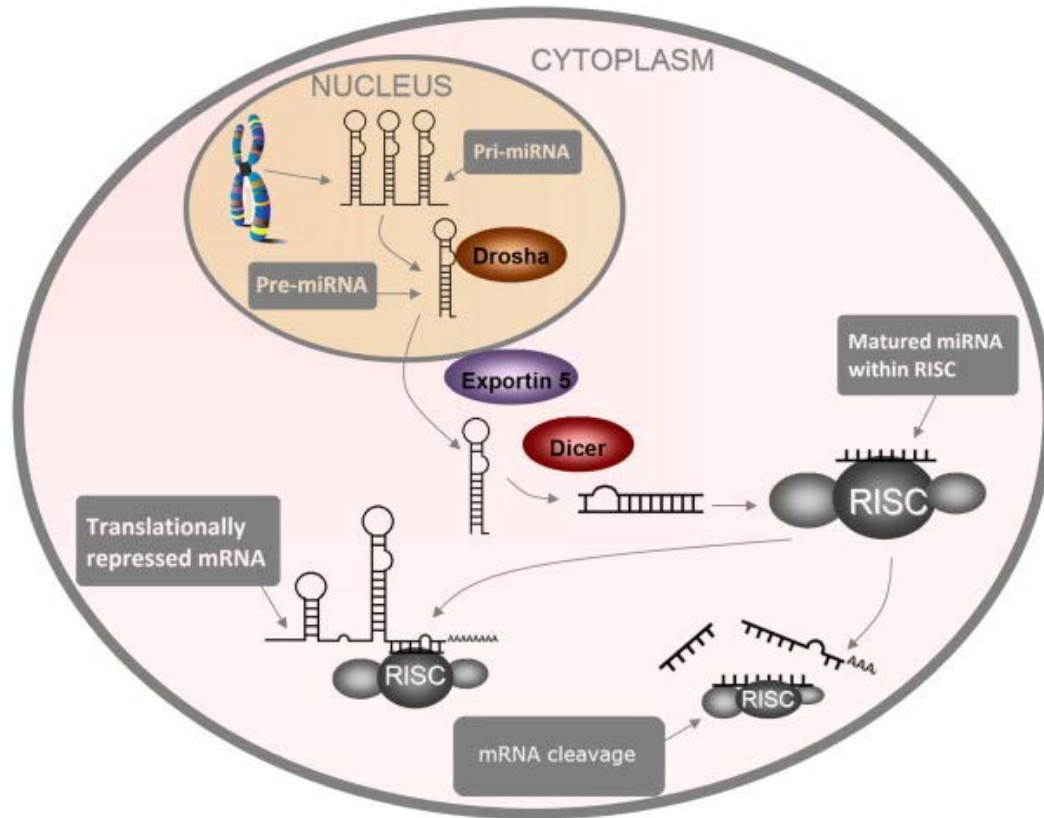
OBSERVATION OF HIGHLY EXPRESSED AND DIVERSE PROBES

-**Melanoma** (8/9 mRNA, 9/9 miRNA) and **leukemia** (6/6 mRNA and miRNA) lines cluster together based on expression patterns

-**Renal** (8/8 mRNA, 6/8 miRNA) and **colon** (6/7 mRNA and miRNA) also show strong correlation

-**CNS** and **lung cancer** show little correlation

microRNAs (miRNAs) regulate gene expression



- miRNA are genomically encoded short (~22 nt) molecules involved in repressing expression of mRNA
- Bind target miRNAs in a 6-10 bp seed region
- Upon processing, miRNAs recruit a post-transcriptional silencing complex to inhibit expression

How we make a cluster

$$r = \frac{1}{n} \sum_{i=1}^n \left(\frac{x_i - \bar{x}}{\sigma_x} \right) \left(\frac{y_i - \bar{y}}{\sigma_y} \right)$$

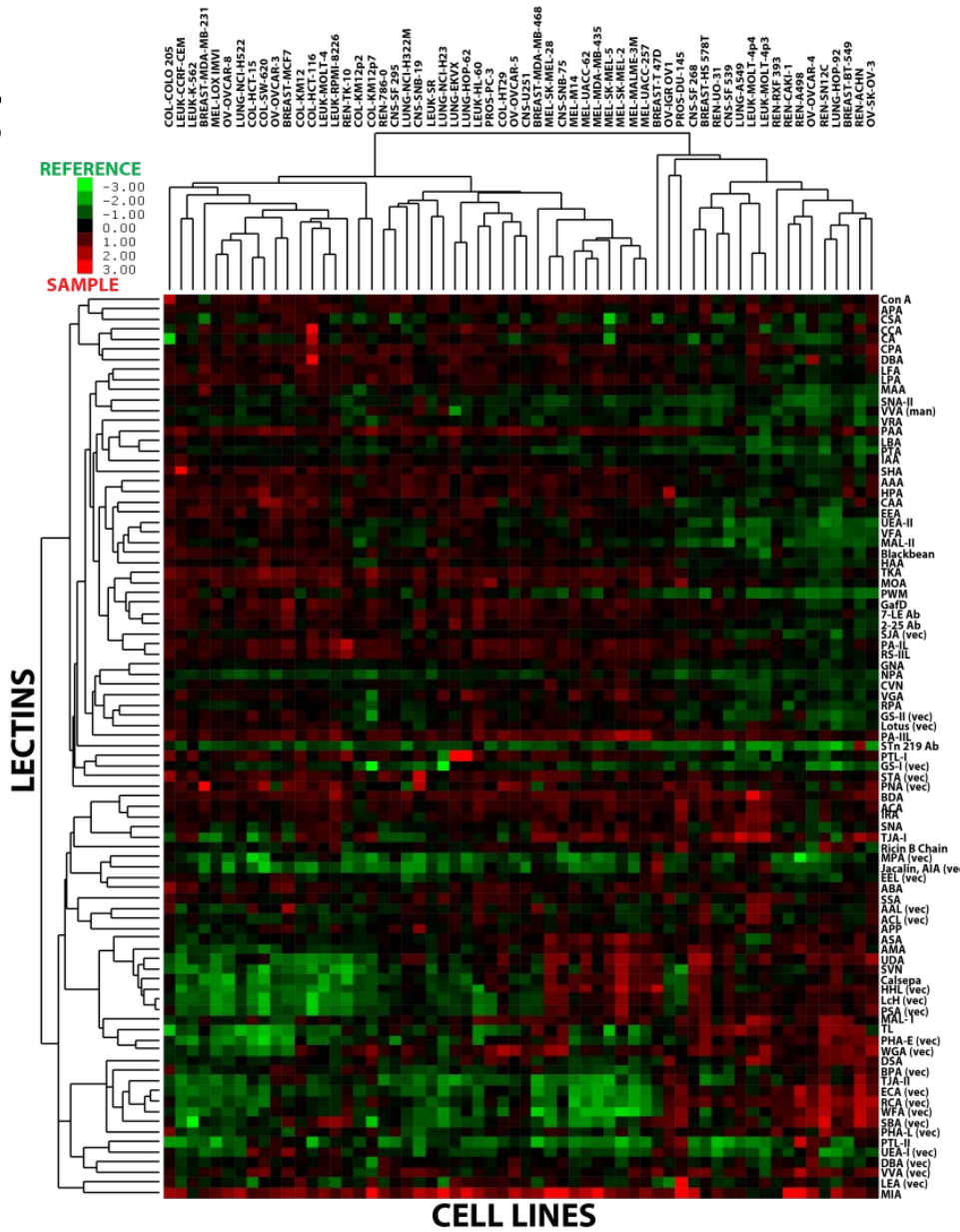
\bar{x} = average across all set of numbers

σ = standard deviation against all set of numbers

- This is a fancy way of saying I am working with vectors

- Probes vs cell line (horizontal) and cell line vs probe (vertical)

- The intensity for each point on a heat map has a distance from every other data point



Singular Value Decomposition

- Method to decompose a matrix into an orthogonally transformed set of variables
- Used to identify significant, co-varying patterns in large data sets. I.E. What signals account for the variation?
- Can be applied to any array individually or combined for SYSTEMS BIOLOGY examination of glycosylation pathways

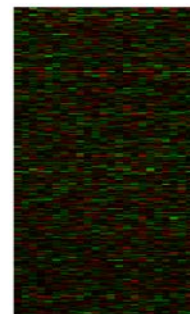
SVD Matrix

$$M = U \Sigma V^T$$

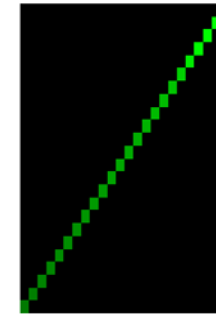
Eigenarrays vs genes/lectins

Arrays vs eigengenes/eigenlectins

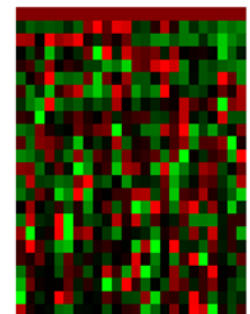
U



Σ



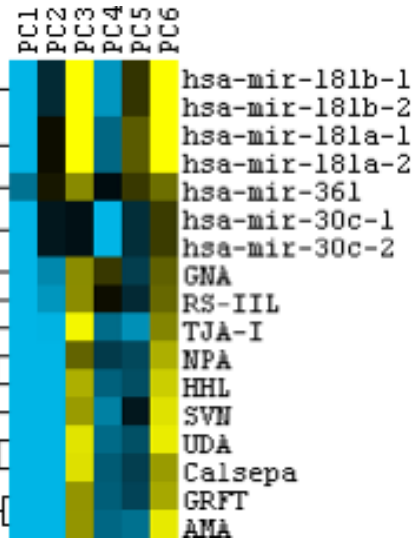
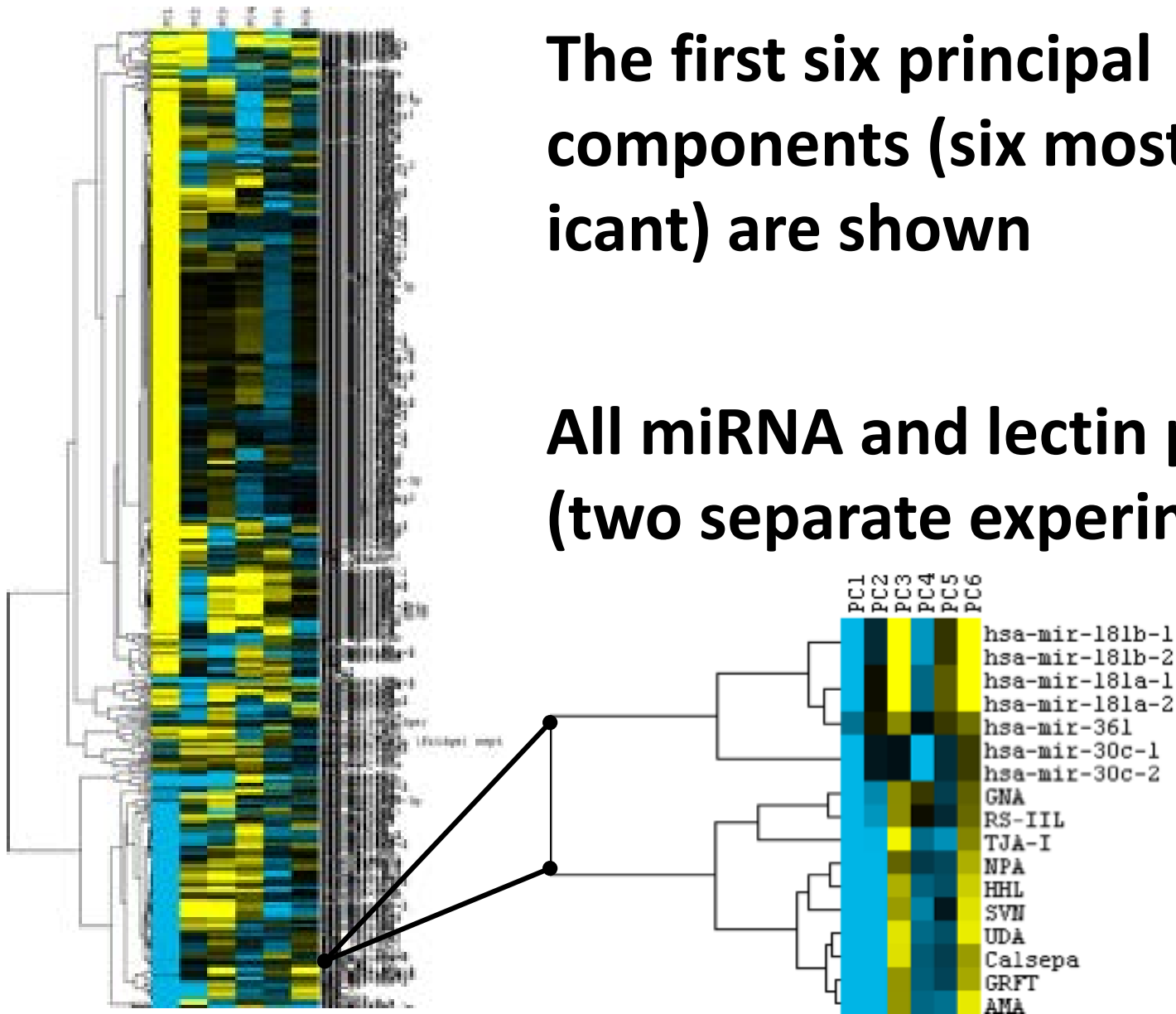
V^T



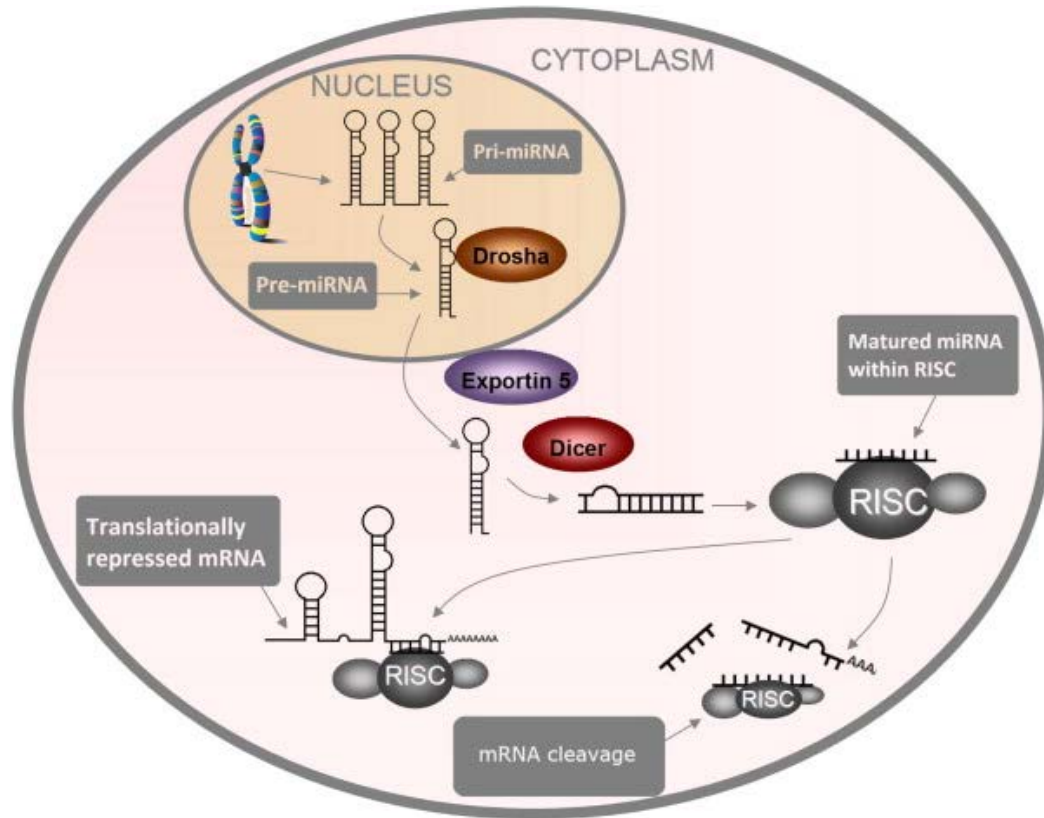
Lectin plus miRNA SVD Results

The first six principal components (six most significant) are shown

All miRNA and lectin probes (two separate experiments)

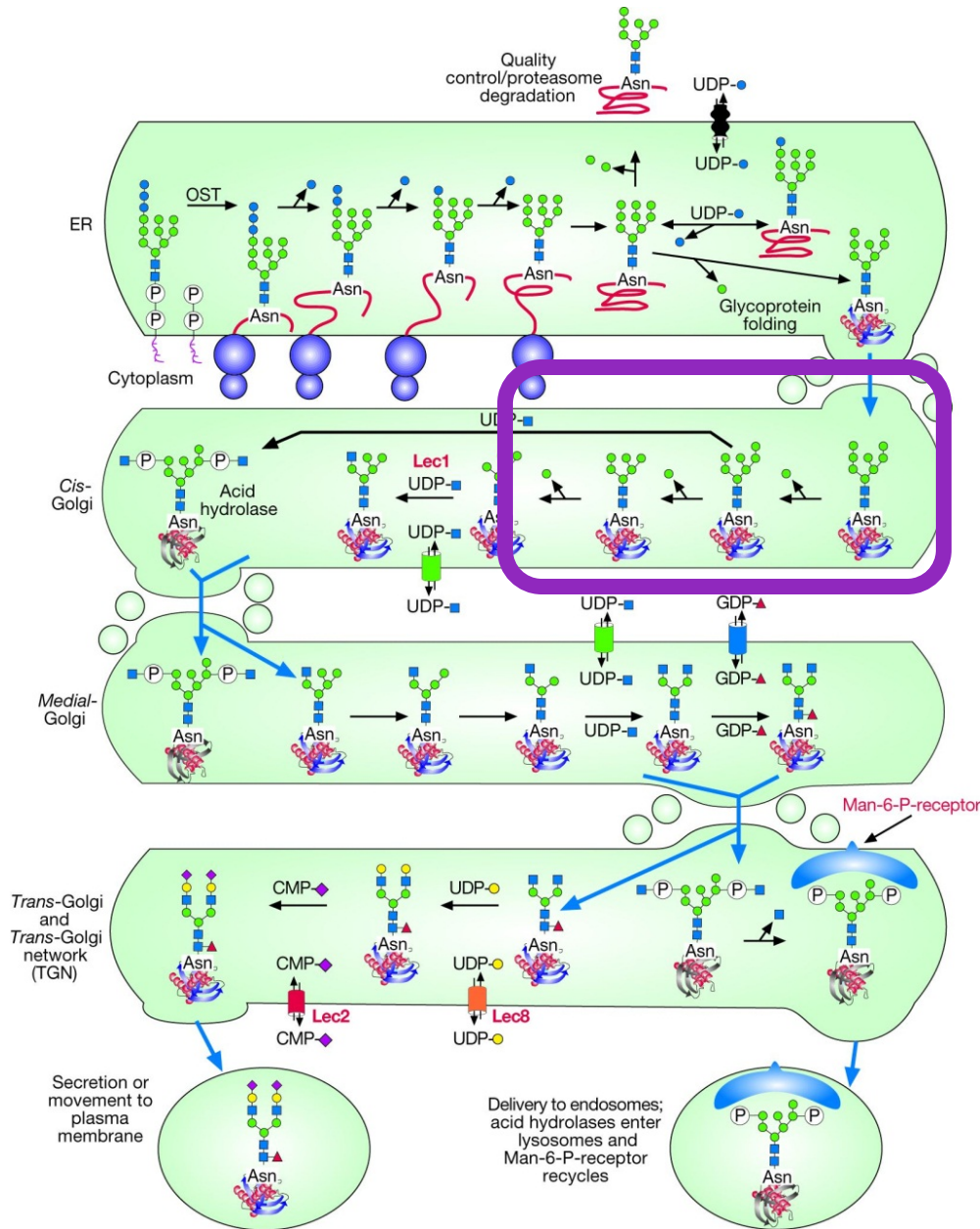


microRNAs (miRNA) regulate gene expression



- miRNA are genomically encoded short (~22 nt) molecules involved in repressing expression of mRNA
- Bind target miRNAs in a 6-10 bp seed region
- Upon processing, miRNAs recruit a post-transcriptional silencing complex to inhibit expression

Maturation of N-linked glycans



- Upon proper folding, glycan is trimmed to high-mannose and, potentially further modified to hybrid/complex
- α -mannosidase I controls all hybrid/complex maturation steps
- You cannot have complex and hybrid glycans if α -mannosidase I isn't expressed

We now have a hypothesis

- miRNA's regulate the *N*-linked maturation pathway
- miRNA expression controls *N*-linked glycome by repressing (or activating) α -mannosidase I
- High mannose cells have high miRNA expression which means low α -mannosidase I

We need evidence

Use high mannose (SN12C, SK-MEL-5) and complex (HCT-116, HT29) lines

Modulate miRNA expression in cells

Analyze mannosidase gene expression (RT-PCR)

Isolate total RNA

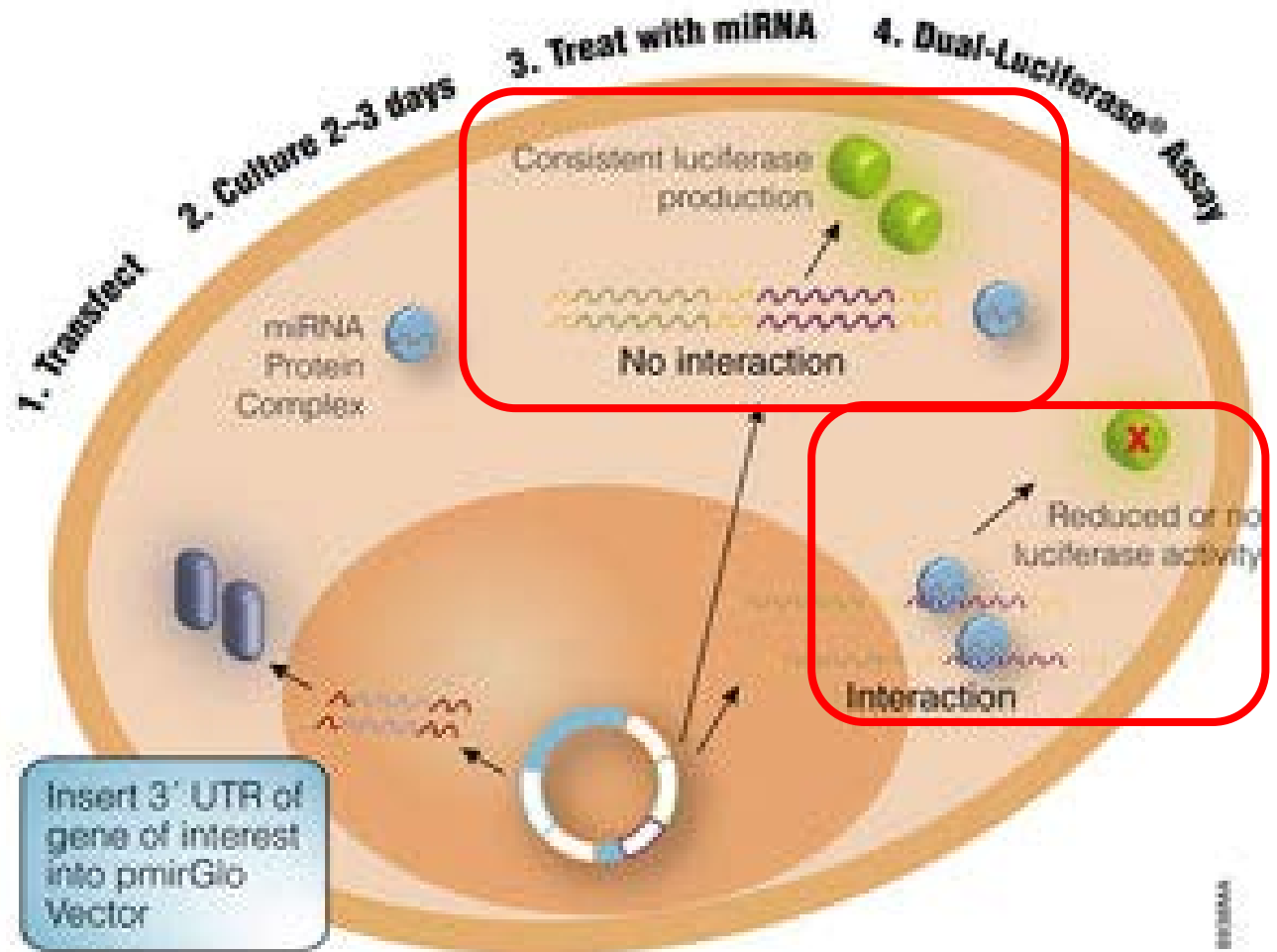
Isolate total protein

Analyze mannosidase protein expression (Western blot)

Analyze glycome (lectin microarray)

**Can the miRNAs bind the
mannosidase transcript?**

Luciferase read-through assay



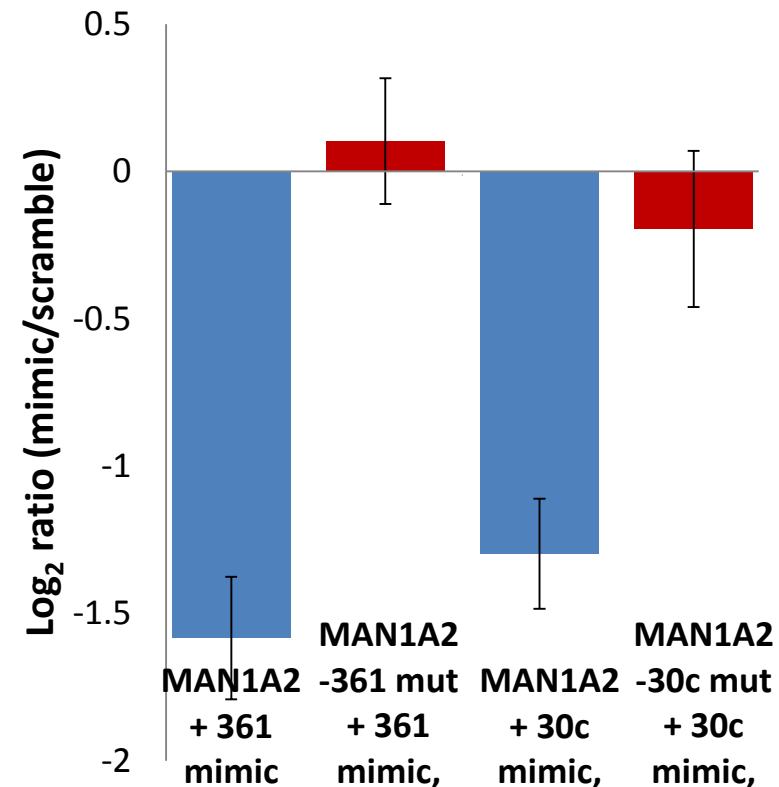
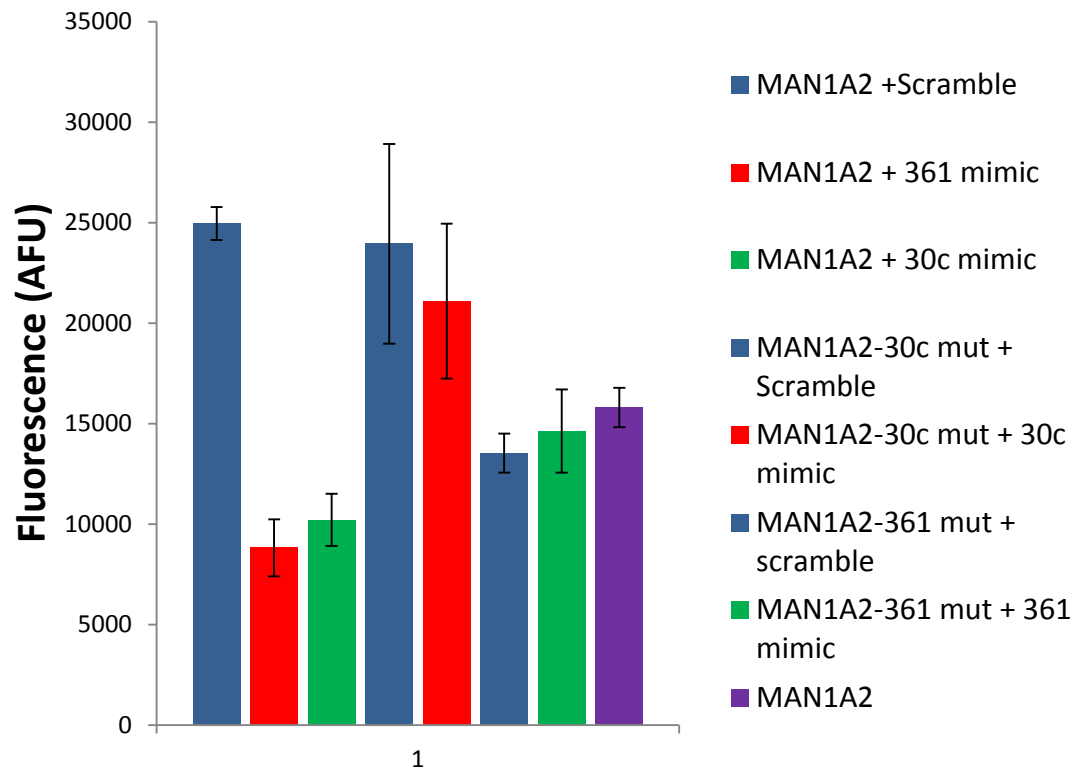
miR-30c and -361 bind the MAN1A2 3' UTR

MAN1A2.30cMut.stk<
MAN1A2.3UTR<

CCTGTGTTT**CGCTCAT**ATGGACCACTACAGAAATTAGTTTGAAGGGGCGGCTTTTGAAAA
CCTGTGTTT**TGTTTAC**ATGGACCACTACAGAAATTAGTTTGAAGGGGCGGCTTTTGAAAA
***** * * * *****

MAN1A2.361Mut.stk<
MAN1A2.3UTR<

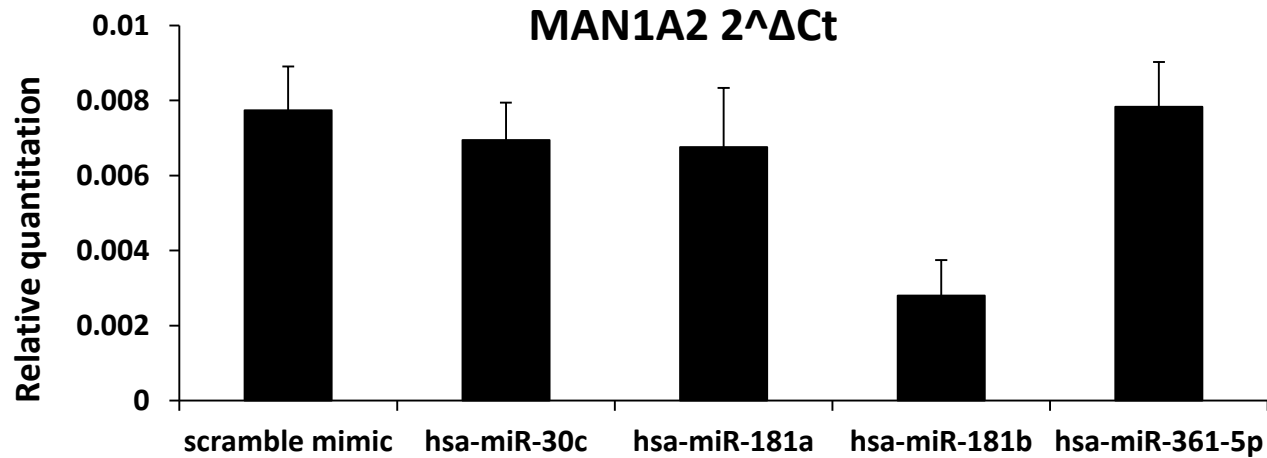
AAATTTCTTGGTTAAGTTTAATTTTCT**ATAGAG**CATGATCTCACAAAGAATACTCAAGT
AAATTTCTTGGTTAAGTTTAATTTTCT**CTGGGGC**ATGATCTCACAAAGAATACTCAAGT
***** . * . * *****



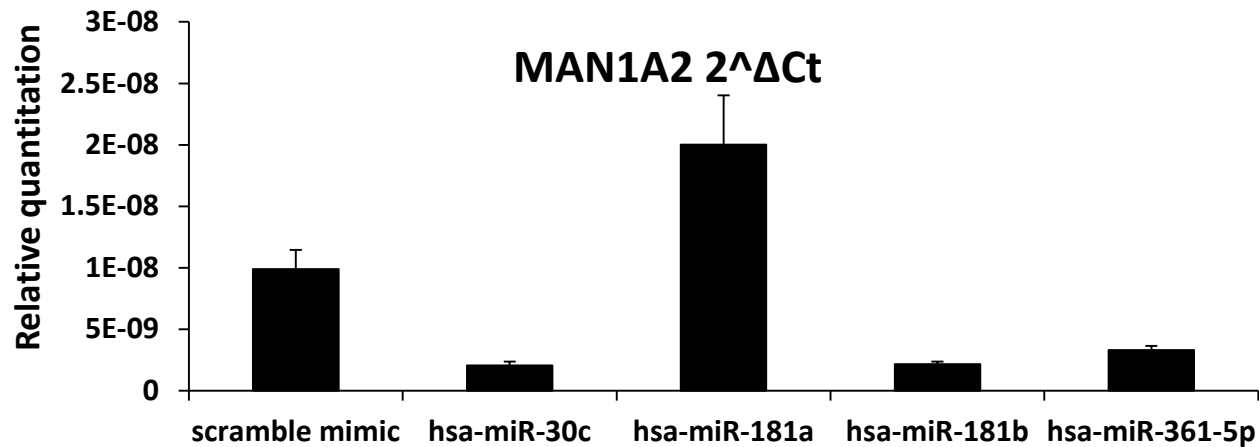
With Praveen Agrawal

**Do the miRNAs affect
mannosidase transcription?**

Transfection of cell lines with miRNA repress MAN1A2



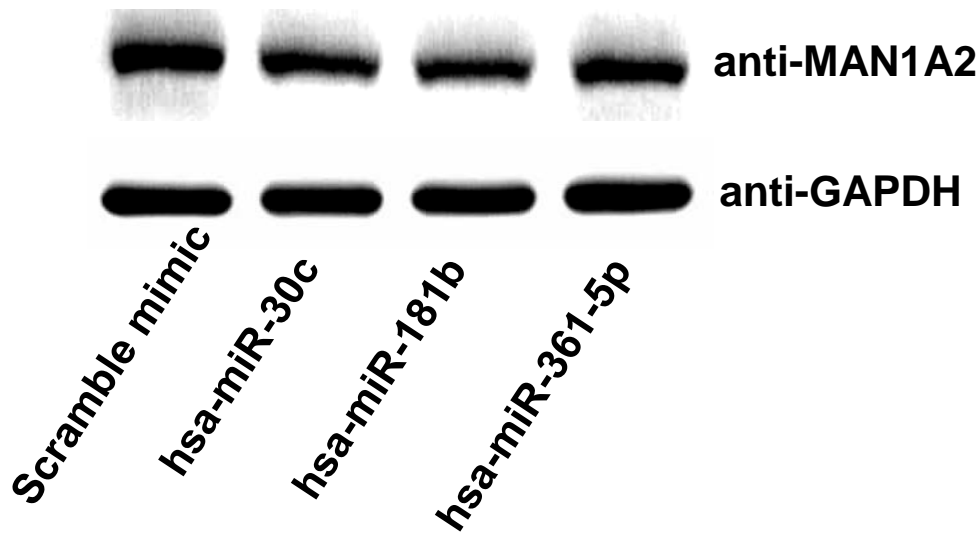
24 h post- transfection



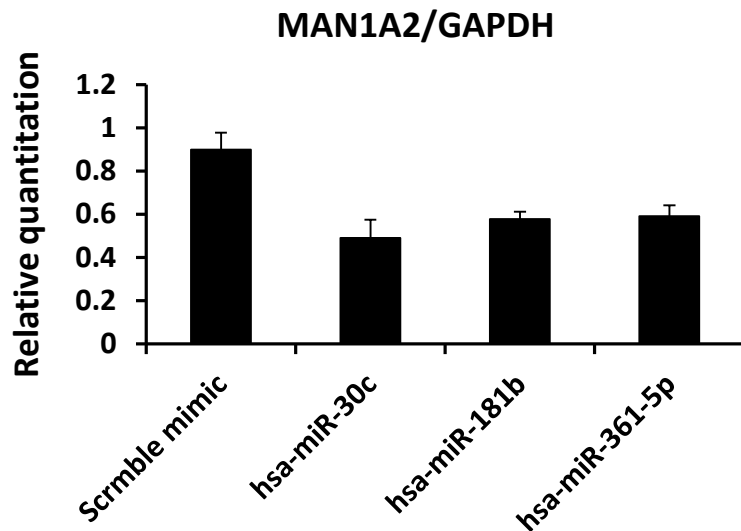
72 h post- transfection

**Do the miRNAs affect
mannosidase protein expression?**

72 h post- transfection

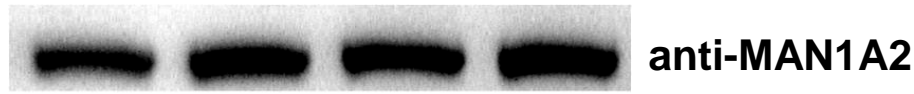


**Western Blot of MAN1A2
72 hrs after transfection
with miRNA**



**MAN1A2 expression
decreases ~50%**

72 h post- transfection



anti-MAN1A2

anti-GAPDH

Scramble inhibitor

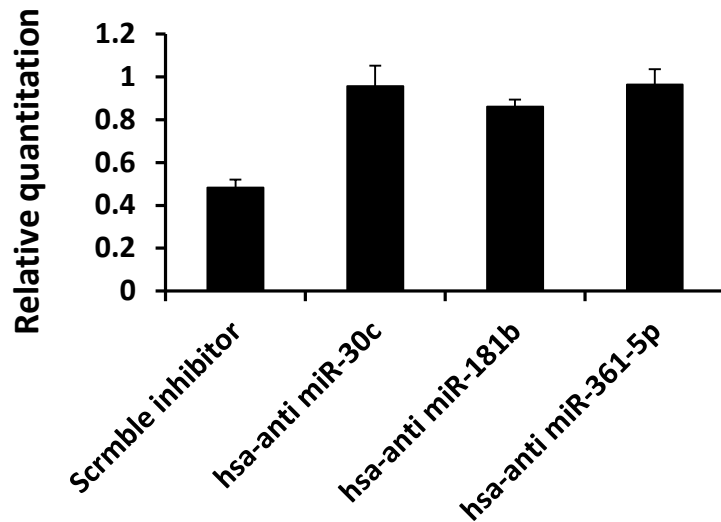
hsa-anti miR-30c

hsa-anti miR-181b

hsa-anti miR-361-5p

**Western Blot of MAN1A2
72 hrs after transfection
with miRNA inhibitor**

MAN1A2/GAPDH

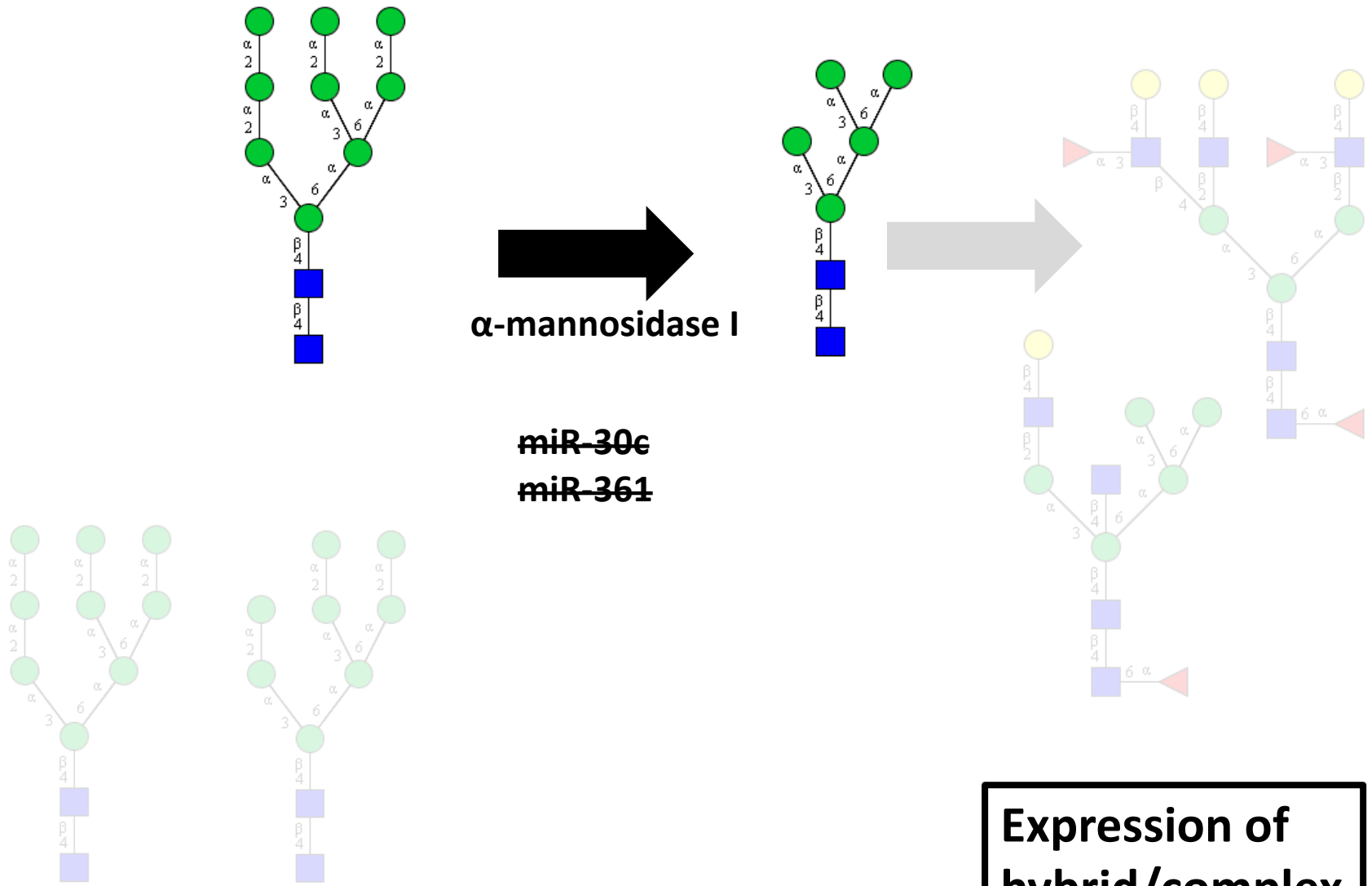


**MAN1A2 expression
increases ~50%**

Seeing inside the house

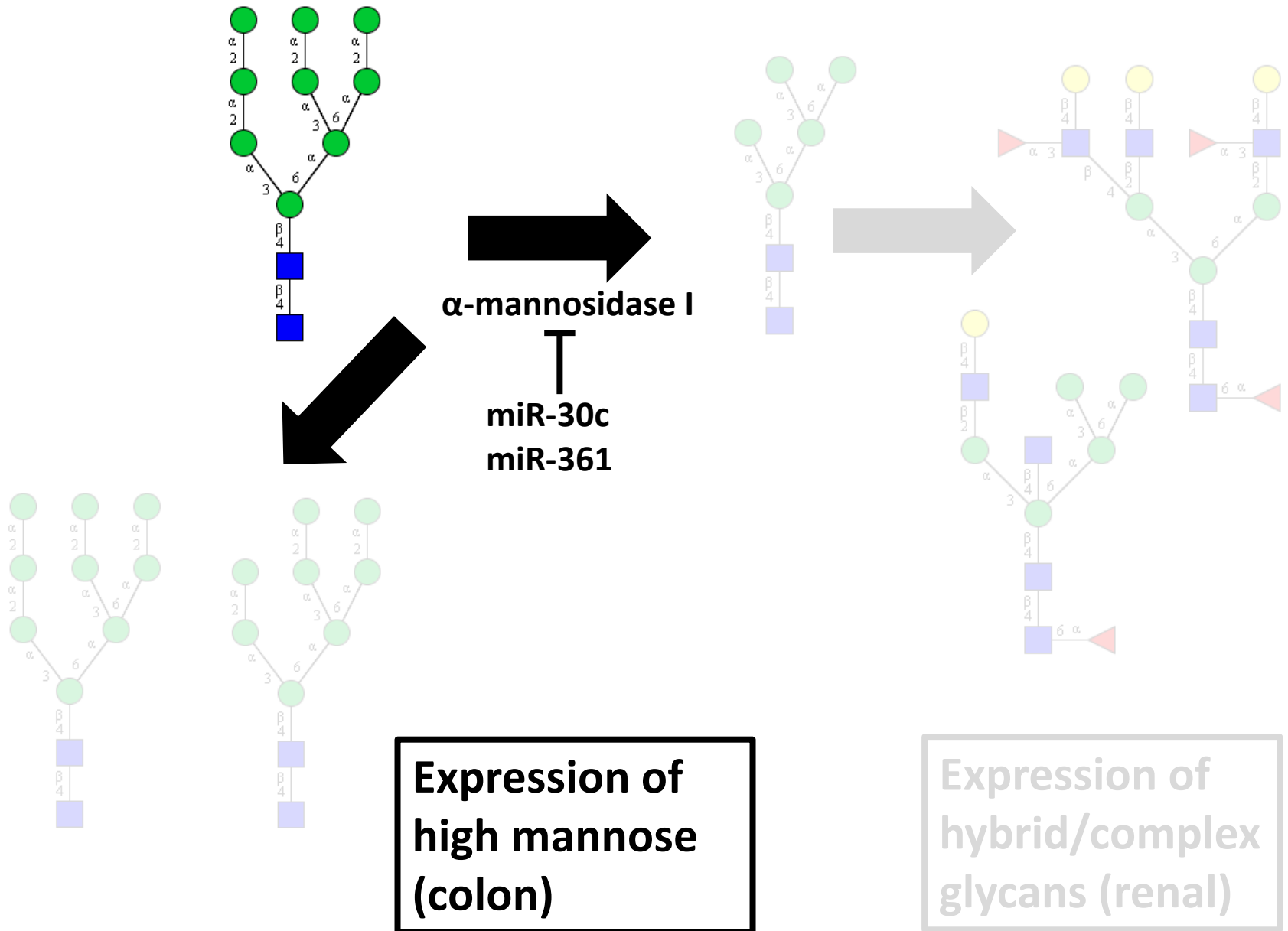
- **miRNA-30c and -361 affect expression of the enzyme α -mannosidase I (maybe -181b as well)**
- **Expression of α -mannosidase I determines the type of *N*-linked glycan expresses**
- **Cells differentially express miRNAs resulting in different glycomes**

A model for cell-type specific carbohydrate expression?



Expression of hybrid/complex glycans (renal)

A model for cell-type specific carbohydrate expression?



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