#### Emergent Properties Common to both Stem Cells and Tumor Cells

Thea D. Tlsty University of California, San Francisco

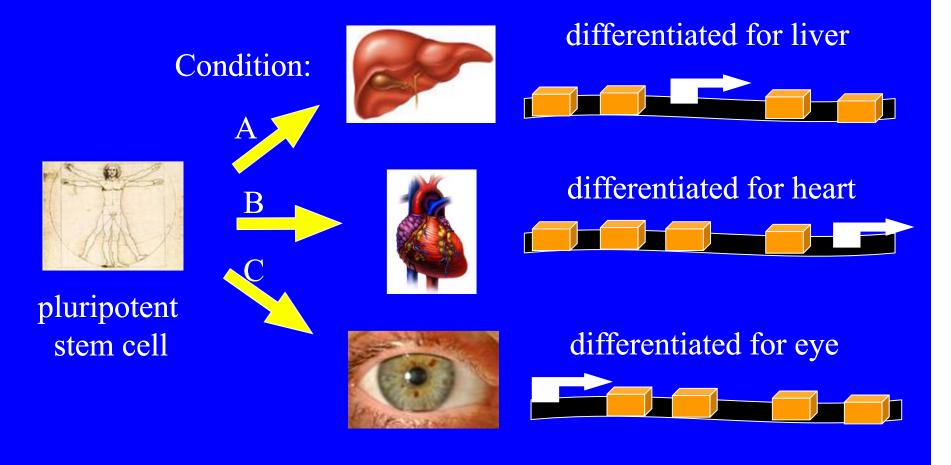
#### **Properties of Stem Cells**

Self-renewal

Multi-lineage potential

Response to injury

#### Cell fate decisions require <u>epigenetic plasticity</u> and <u>exogenous signals</u>





undifferentiated

# **Condition:** B stem cell **Condition**:

differentiated cell

distinct epigenomes

Epigenetic plasticity is a distinguishing characteristic of stem cells

identical epigenomes

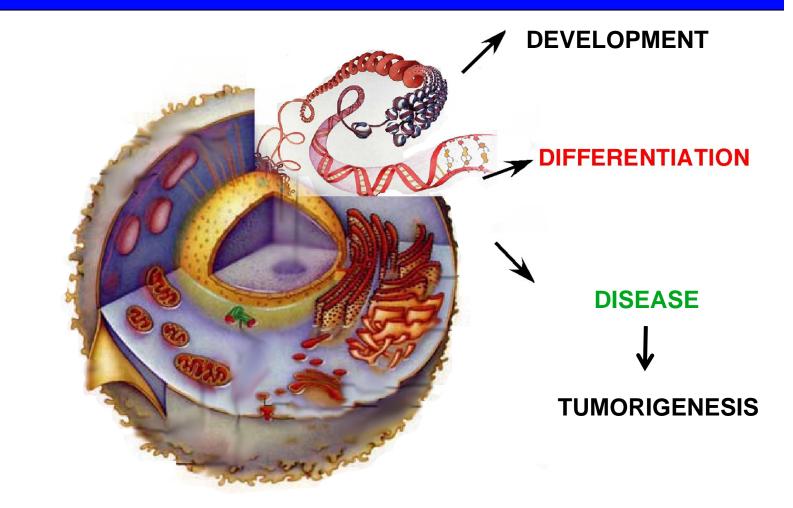
#### Acute Wounding — Healing

damage

In addition to Self-renewal and Multi-lineage potential, participation in wound healing is a key property of stem cells

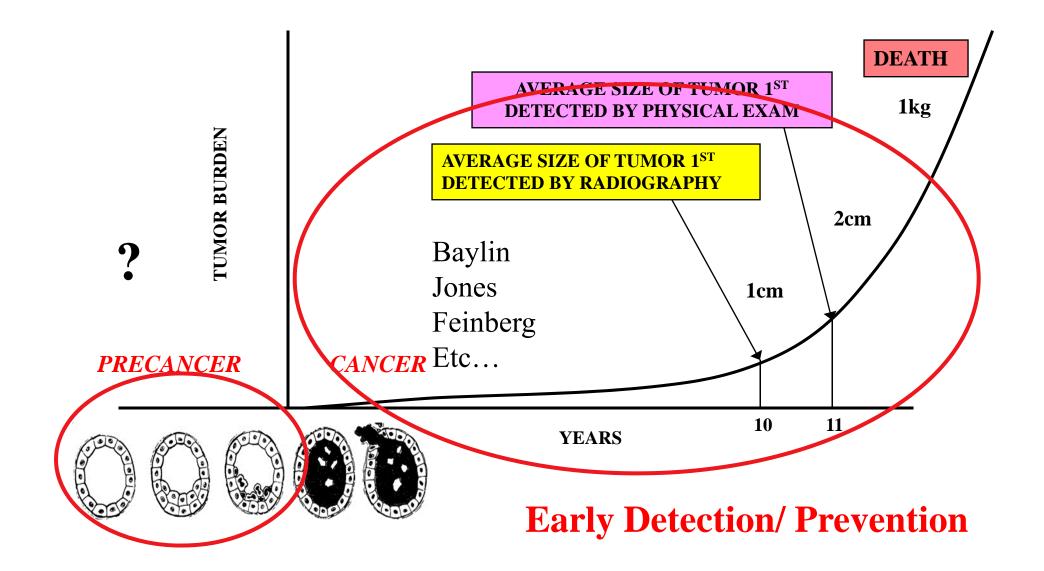
> Bypass arrest signals Home (migrate) to proper site Reprogram the genome Complete differentiation

The active acquisition of epigenetic changes is a poorly understood but important process in development, differentiation, and disease.



Both stem cells and cancer cells exhibit epigenetic plasticity - the ability to reprogram the genome in a heritable fashion.

#### **Epigenetic Changes are Frequent in Late Stage Cancer**

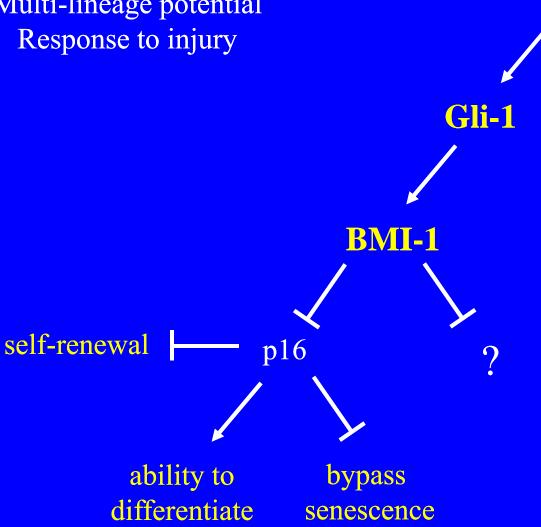


#### **Properties of Stem Cells**

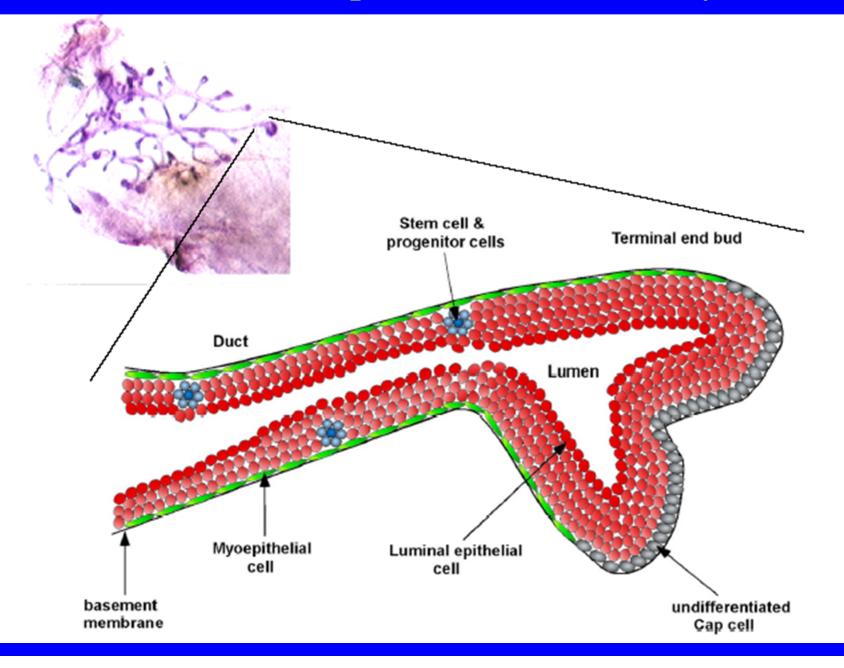
Self-renewal Multi-lineage potential Response to injury

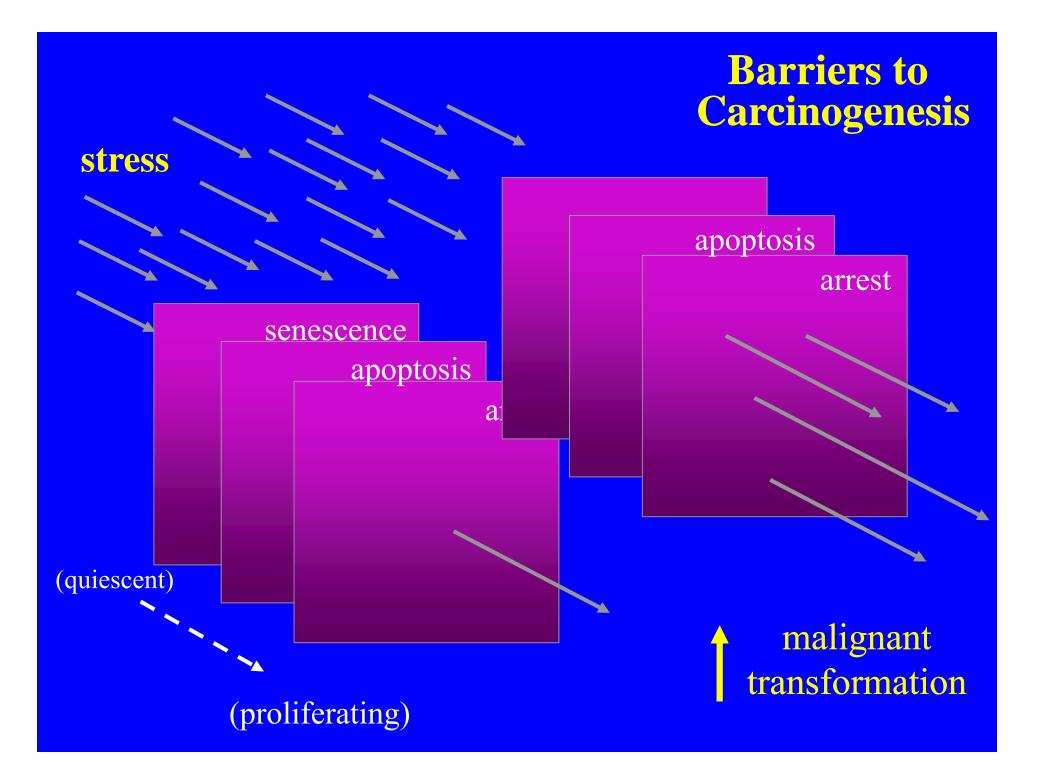
**Bmi-1** is required for maintenance of adult selfrenewinghaematopoietic stem cells In-kyung Park, et al. Nat 423, 302-305, 2003

Bmi-1 promotes neural stem cell self-renewal and neural development... by repressing the p16Ink4a and p19Arf senescence pathways Molofsky AV, et al. Genes Dev. 19,1432-7, 2005



#### Cellular Composition of Mammary Gland





#### Acute Wounding — Healing

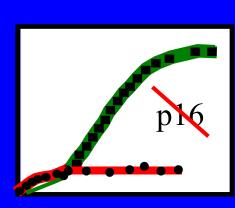
damage

In addition to Self-renewal and Multi-lineage potential, participation in wound healing is a key property of stem cells

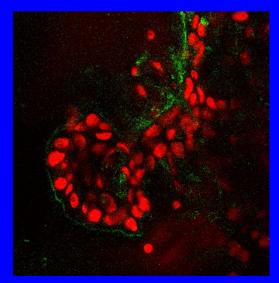
Bypass arrest signals- p16Home (migrate) to proper siteReprogram the genomeComplete differentiation

### Epithelial cells that can bypass stress signals are found in disease free women and can be propagated in culture

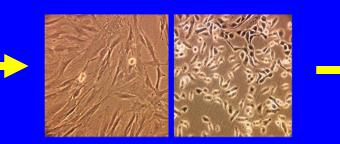
These cells provide an excellent opportunity to study precursors to cancer (and stem cells)



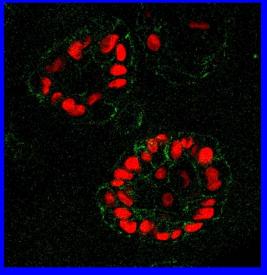




In vivo

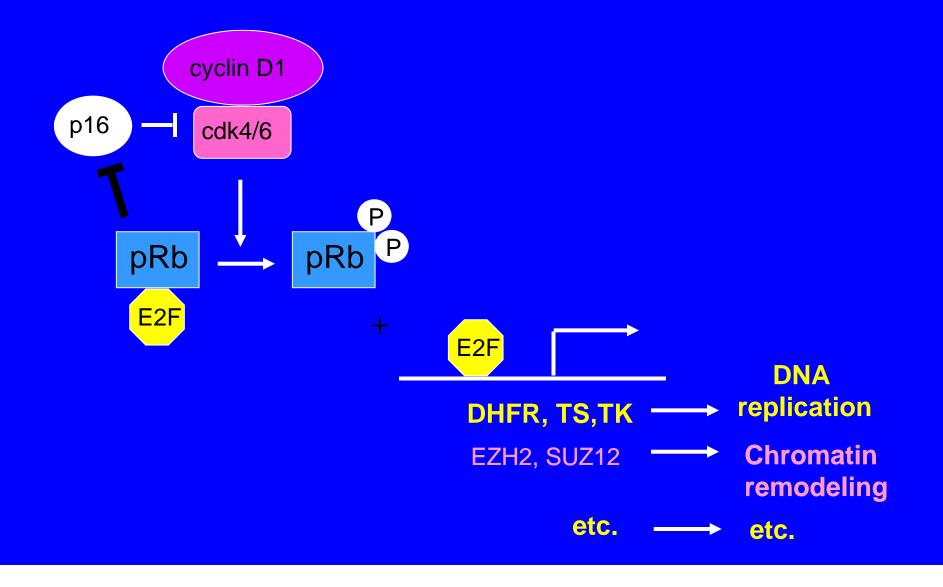


Fibroblasts Epithelial cells



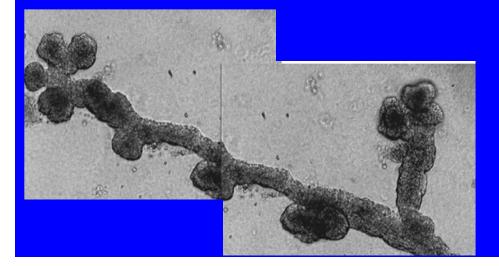


#### p16 Contributes to Cell Cycle Regulation and Negatively Regulates E2F Target Gene Expression



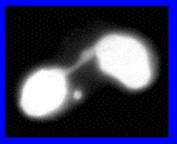
# This small distinctive subpopulation of cells exhibits several pre-malignant properties

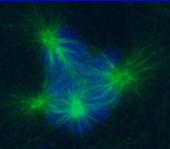
|              | By pass senescence | Genomic<br>instability | Apoptotic<br>resistant | Invasive | Etc. |
|--------------|--------------------|------------------------|------------------------|----------|------|
| Normal cell  | -                  | -                      | -                      | -        | _    |
| Precancerous | +                  | +                      | +                      | -        | _    |
| Cancer cell  | +                  | +                      | +                      | +        | +    |



#### Silencing of p16 confers several properties:

(1) Silencing of p16 provides cells with pre-malignant properties: allows the bypass of senescence





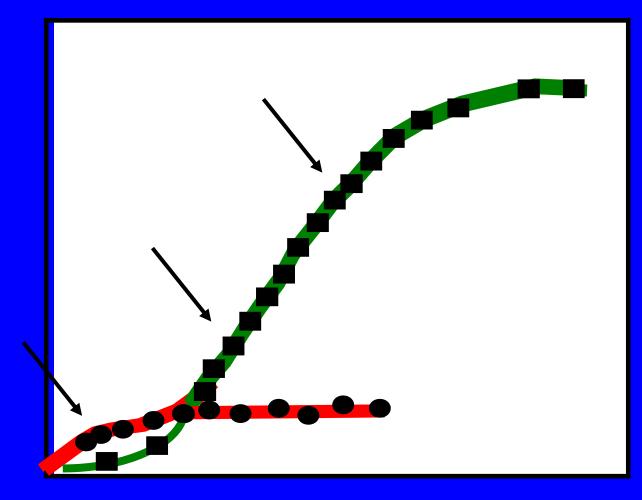
confers genetic plasticity activates and represses genes important for pre-malignant and stem/progenitor cell properties confers epigenetic plasticity Romanov et al., 2001

Holst et al., 2003 Crawford et al., 2004 Gauthier et al., 2005 McDermott et al., 2006 Reynolds et al., 2006 Dumont et al., 2009

 (2) Cells with these properties exist in healthy, disease-free individualsprobably serve as precursors to cancer, provide prognostic information.

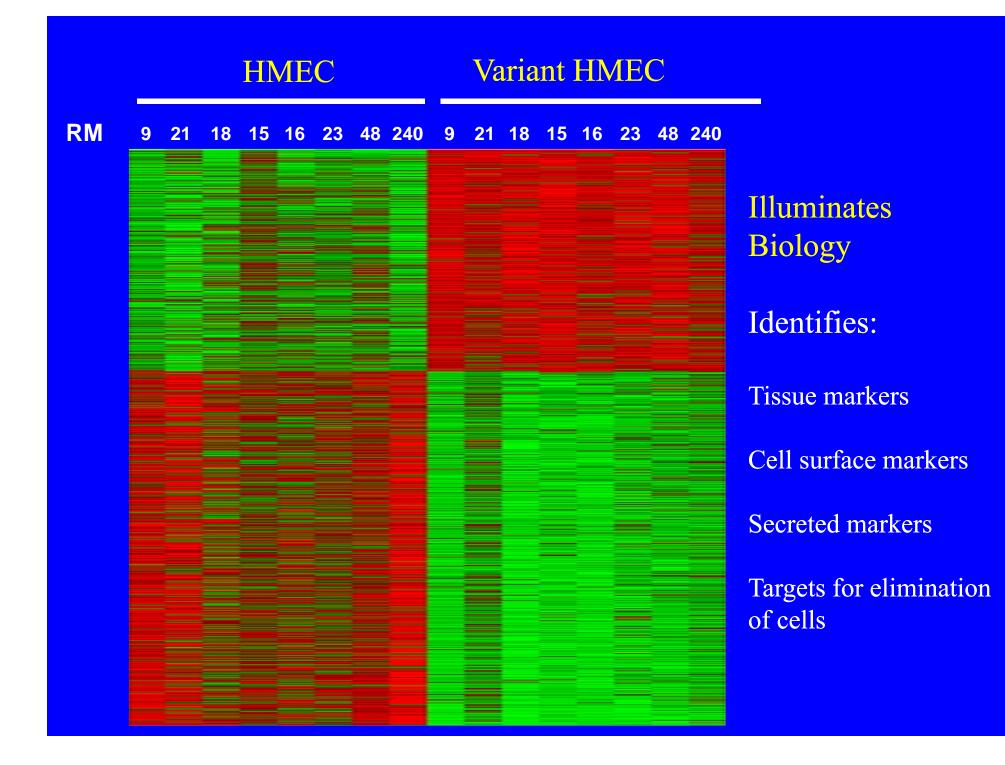
Holst et al., 2003 Crawford et al., 2004 Gauthier et al., 2007

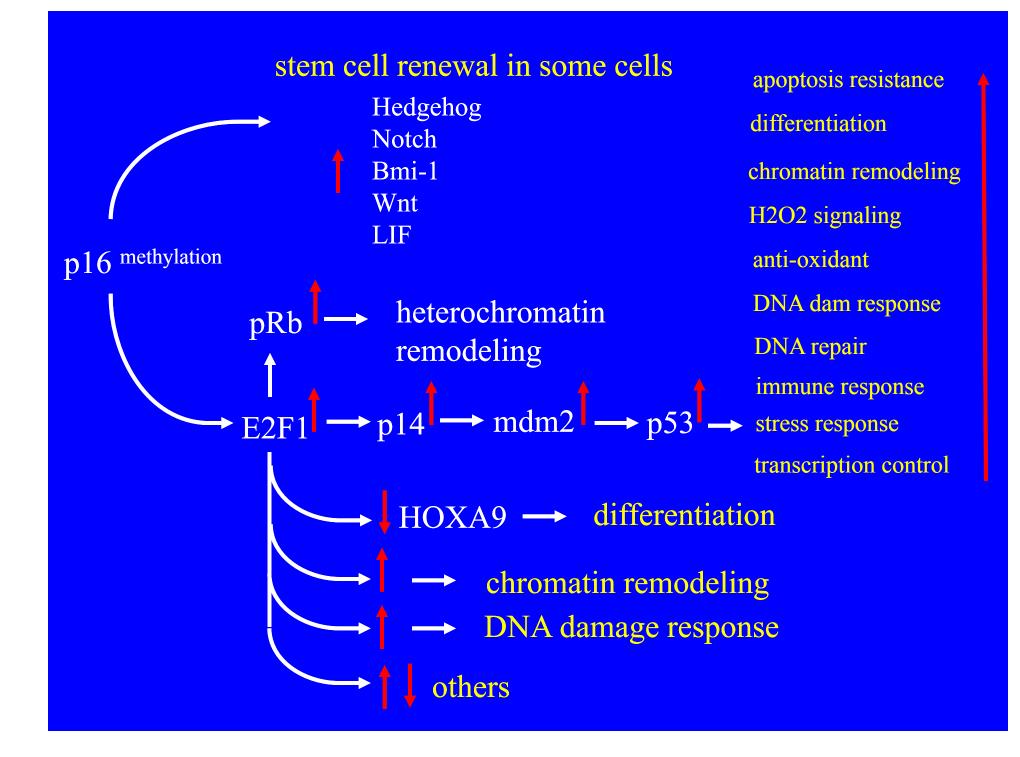
#### Clues to Early Cancer Phenotype: Use Expression Profiling



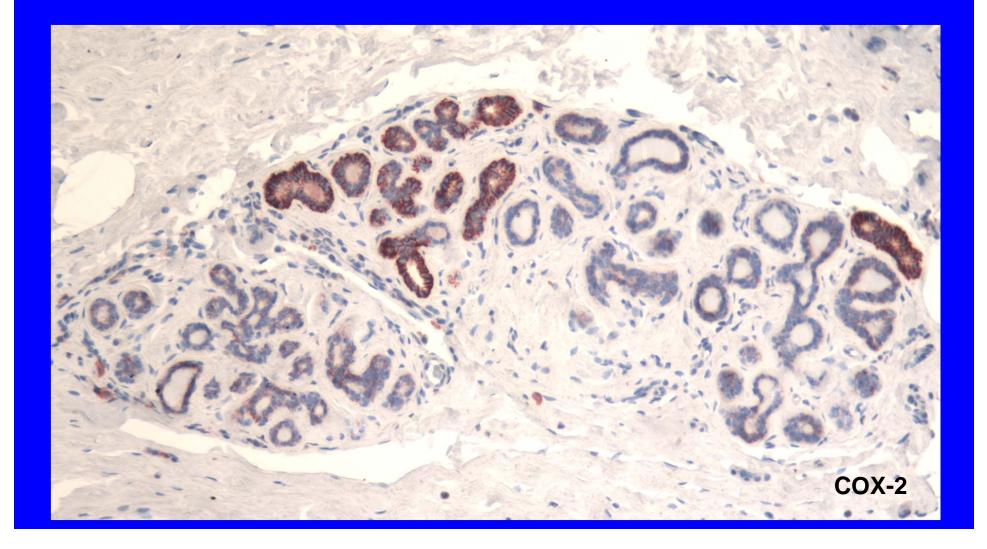
global analysis

candidate analysis

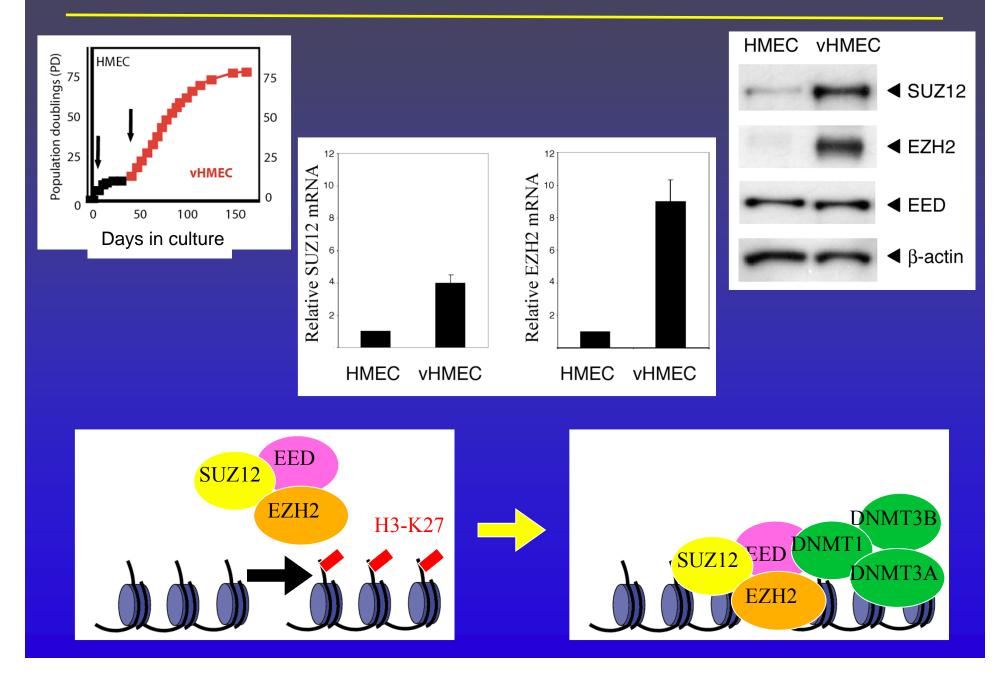




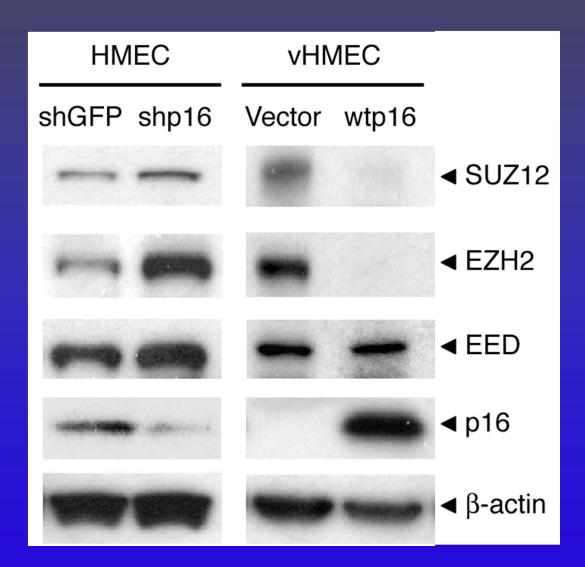
<u>Normal</u> tissue from healthy, cancer-free women contains foci that exhibit suppression of p16 and expression of a pre-malignant program



#### **PcG proteins are upregulated in PRIMED HMEC**

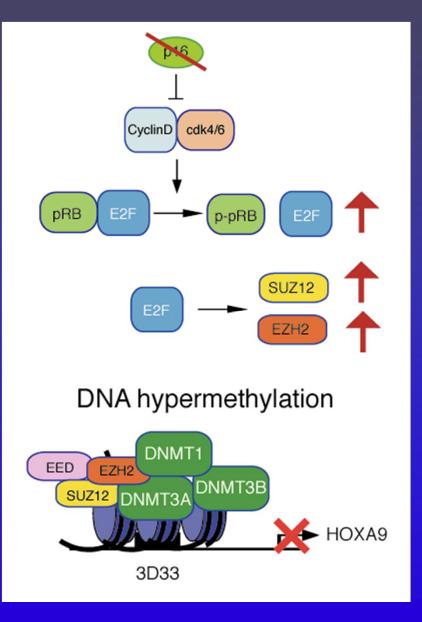


#### **PcG protein expression is p16-dependent**



#### How do stem cells and cancer cells acquire epigenetic plasticity? (ability to methylate and demethylate gene sequences)

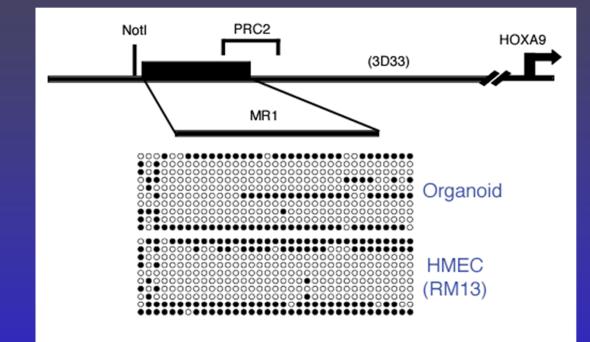
#### Loss of p16/pRb activity is necessary and sufficient for DNA hypermethylation at targeted loci

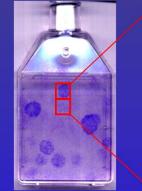


Repression of the p16/pRb pathway in human mammary epithelial cells activates an E2F-mediated increase in these proteins that remodel chromatin and causes targeted, *de novo* DNA methylation at a non-random collection of loci.

(Reynolds et al., J Biol Chem 281: 24790-24802, 2006).

#### Bisulfite validation of HOXA9 DNA hypermethylation

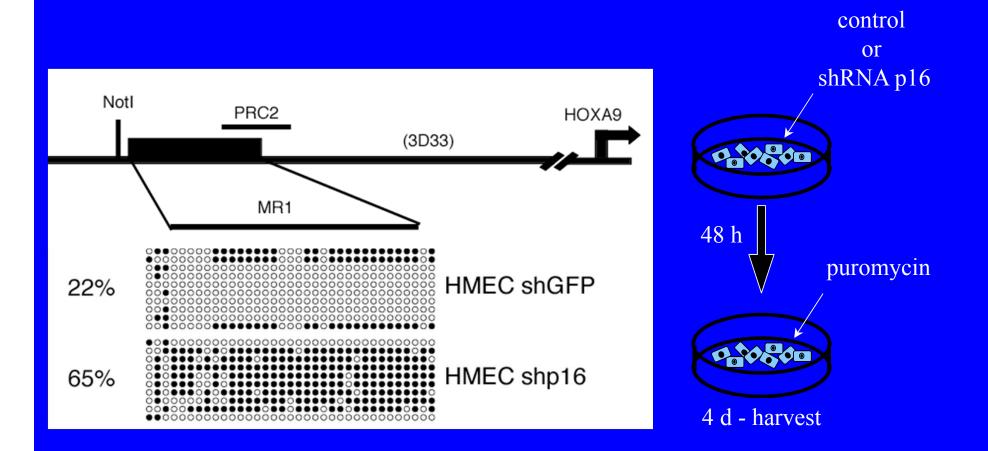






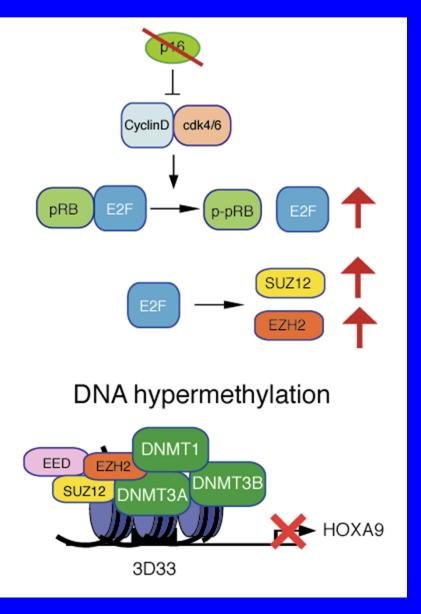


#### **Removal of p16 expression in HMEC induces rapid DNA hypermethylation**



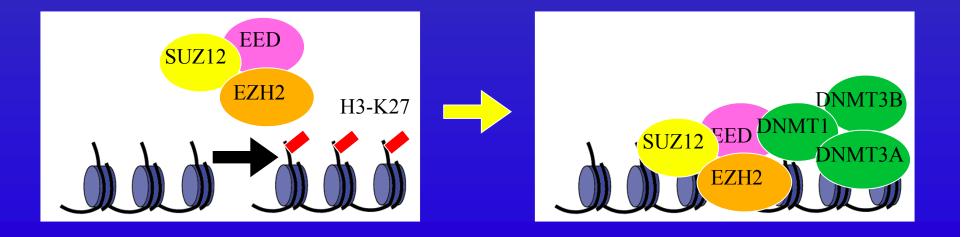
Paul Reynolds

## SUZ12/EZH2 are both necessary and sufficient for the activation of targeted DNA hypermethylation

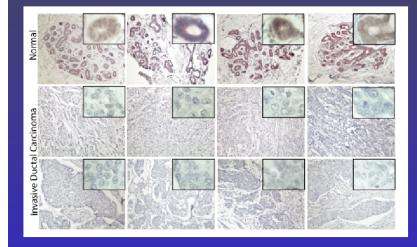


Removal of SUZ12/EZH2 prevents the methylation events. Exogenous addition of SUZ12/EZH2 activates the methylation events. Without histone methylation changes - DNA methylation changes cannot occur.

#### Transcriptional repression precedes DNA hypermethylaton



#### HOXA9 is silenced and undergoes DNA hypermethylation in a large proportion of primary breast tumors



| <u>T1</u><br>m u  | <u>T2</u><br>m u  | <u>T3</u><br>m u  | <u>T4</u><br>m u  | <u>T5</u><br>m u  | T6<br>mu          | <u>T7</u><br>m u  | <u></u>           | <u>T9</u><br>m u  | <u>T10</u><br>m u | <u>T11</u><br>m u                       |    |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---|----|
| <u>T12</u><br>m u | <u>T13</u><br>m u | <u>T14</u><br>m u | <u>T15</u><br>m u | <u>T16</u><br>m u | <u>T17</u><br>m u | <u>T18</u><br>m u | <u>T19</u><br>m u | <u>T20</u><br>m u | <u>T21</u><br>m u |   |    |
| <u>N1</u>         | <u>N2</u>         | <u>N3</u>         | +                 | -                 |                   |                   |                   | 00000000          | R1                | 000000000                               | 5  |
| mu                | mu                | mu                | mu                | mu                |                   |                   |                   |                   |                   | 000000000000000000000000000000000000000 | N2 |
|                   |                   |                   |                   |                   |                   |                   |                   |                   | ********          |   | 5  |

44%

T4

93%

#### **Summary and Conclusions - Part I**

• A commonly inactivated tumor suppressor, p16, regulates DNA methylation (epigenetic changes occur in preneoplastic cells)

• DNA methylation is an active and dynamic process (targeted) - chromatin remodeling and repression precedes and is necessary for subsequent DNA hypermethylation

 Loss of p16 confers epigenetic plasticity silencing genes important in differentiation (holds cells in a progenitor state)

#### p16 controls genetic and epigenetic plasticity

#### Genetic

- telomeric dysfunction chromosomal abnormalities
- centrosomes aneuploidy



Epigenetic - DNA hypermethylation

#### p16 controls genetic and epigenetic plasticity and specific stem cell characteristics

Genetic

- telomeric dysfunction chromosomal abnormalities
- centrosomes aneuploidy

Bypass signals that stop proliferation

Epigenetic - DNA hypermethylation (Regulates differentiation threshold)



Stem cell self-renewal

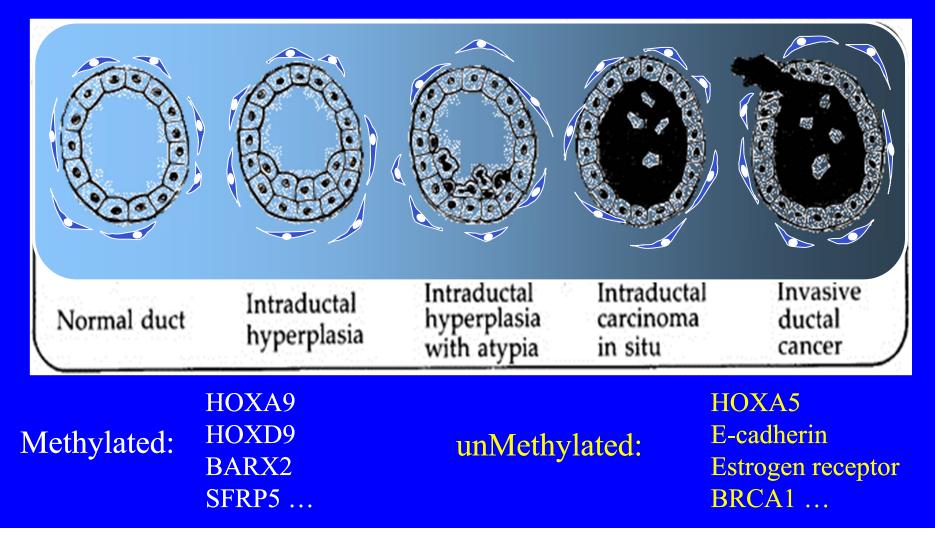
#### Targeting of Epigenetic Silencing

| Locus      | Expressed<br>HMEC | Expressed<br>vHMEC | Reactivated by<br>5-AZA | Epigentically<br>Silenced |                             |
|------------|-------------------|--------------------|-------------------------|---------------------------|-----------------------------|
|            |                   |                    |                         |                           |                             |
| HOXA9      | +                 | -                  | +                       | +                         | methylated in vHMEC         |
| HOXD9      | +                 | -                  | +                       | +                         |                             |
| BARX2      | +                 | -                  | +                       | +                         | Polycomb-assoc genes        |
| SFRP5      | +                 | -                  | +                       | +                         | involved in differentiation |
| FABP3      | +                 | _                  | +                       | +                         |                             |
| E-Cadherin | +                 | +                  |                         | -                         | unmethylated in vHMEC       |
| MLH1       | +                 | +                  |                         | -                         |                             |
| BRCA-1     | +                 | +                  |                         | -                         | But often methylated        |
| IGFBP3     | +                 | +                  |                         | -                         | in tumors                   |

Matt Wilson and Paul Reynolds

#### How do Cells Acquire Methylation of Genes Shown to be Silenced in Invasive Cancers?

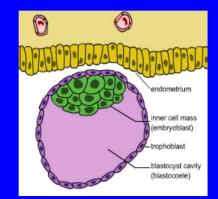
(random methylation events followed by selection or events programmed by signals that promote tumor progression)

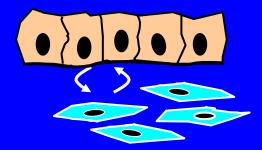


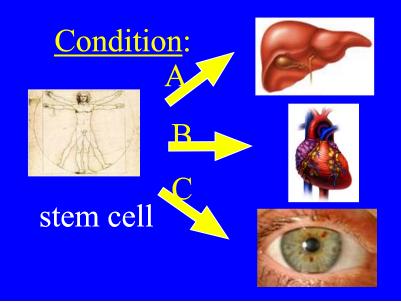
#### **Programming Stem Cell Units**

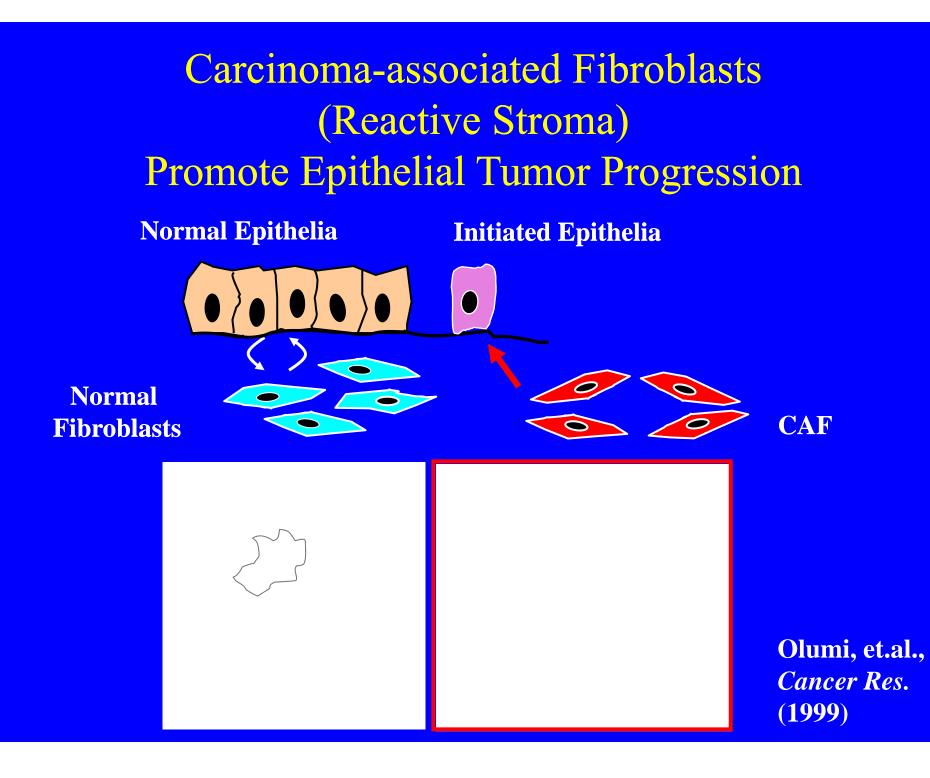
Tissue renewal whole organism - zygote (totipotent) embryonic stem cell (pluripotent)

specialized parts of the organism somatic stem cell

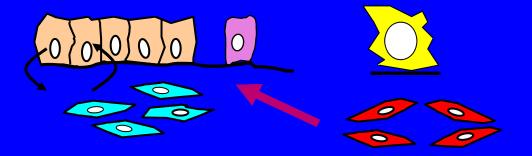






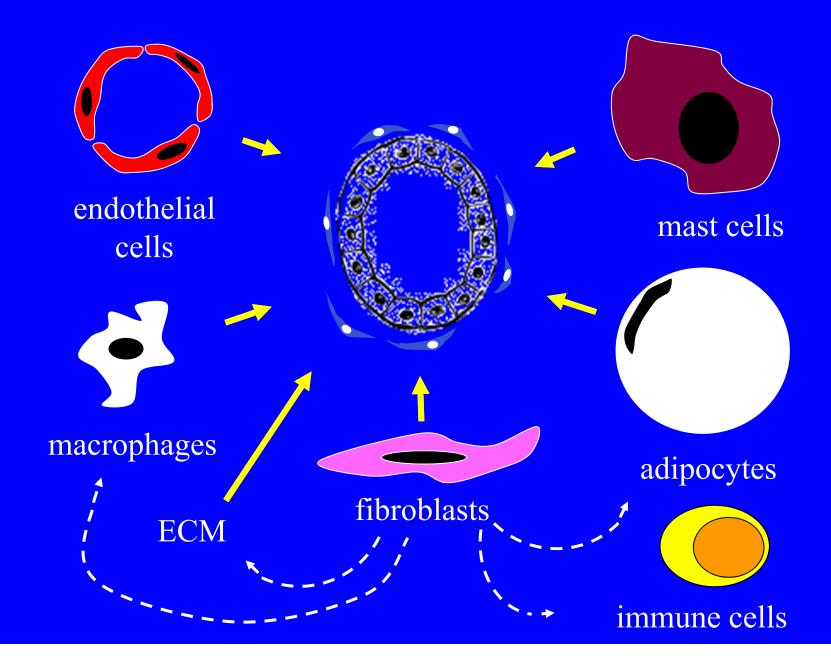


Carcinoma-associated Fibroblasts influence epithelial cells by causing:



Increased Cell Proliferation Decreased Cell Death Stimulation of Angiogenesis Alteration of Cell Adhesion Decreased genomic integrity

# **Stromal Contributions to Tumorigenesis**



#### **HYPOTHESIS**

We hypothesize that cells in an epigenetically-plastic state can be programmed by the microenvironment to acquire epigenetic changes that promote tumorigenesis.

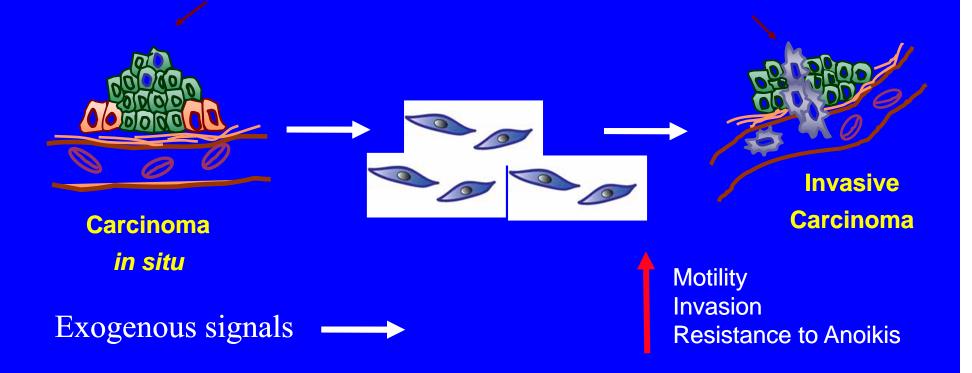
We use an *in vitro* model system where epigeneticallyplastic cells are placed in an environment that induces a malignant program.

# Epithelial to Mesenchymal Transition (EMT)

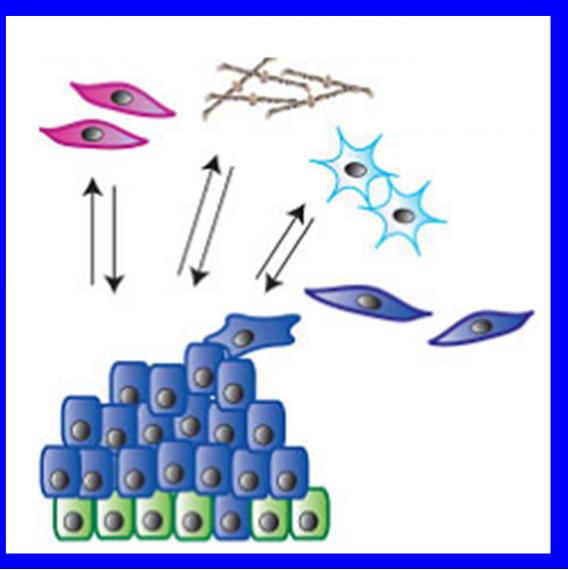
Used during:

(1) development to position cells for individual fates

(2) cancer progression

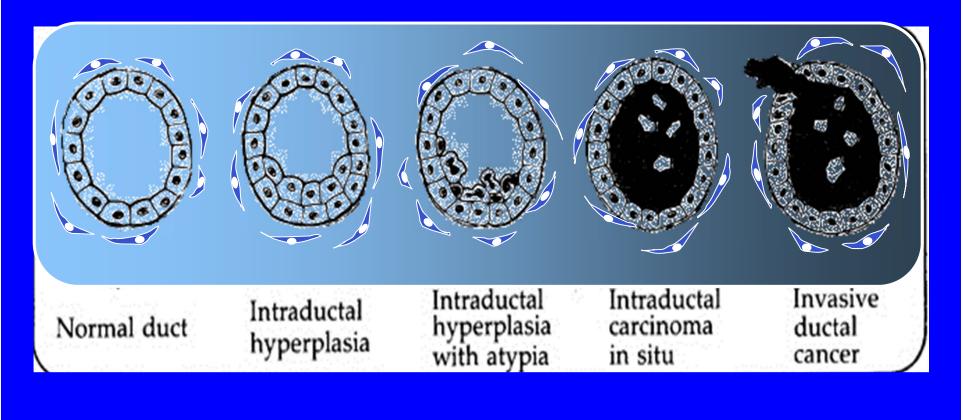


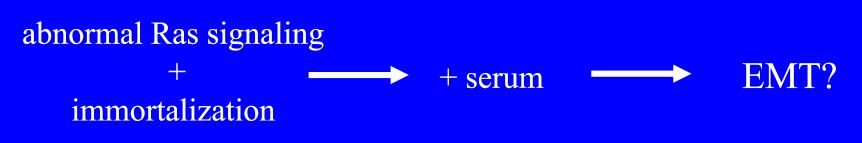
Oncogenic ras can cooperate with factors in serum to induce an Epithelial to Mesenchymal Transition and promote tumorigenesis in murine cells



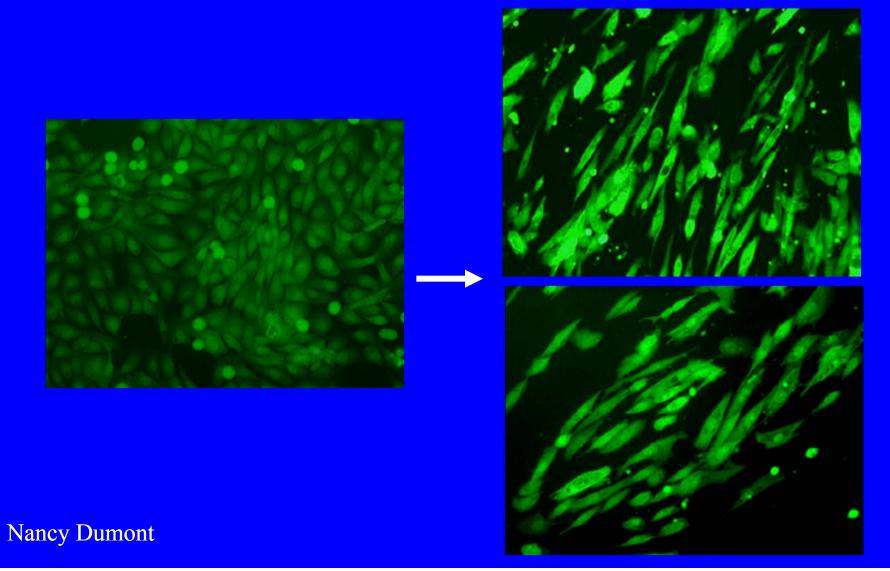
(Oft et al., Genes Dev 10: 2462-2477, 1996)

# Acquistion of Epithelial to Mesenchymal Transition





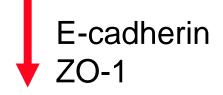
# **Epithelial to Mesenchymal Transition in Human Cells**

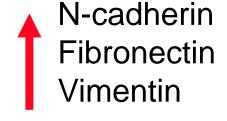


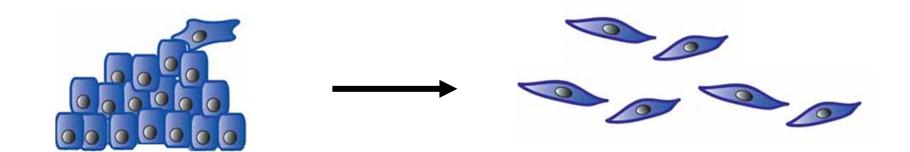
# **Epithelial Mesenchymal Transition** (EMT)

**Epithelial Markers** 

**Mesenchymal Markers** 

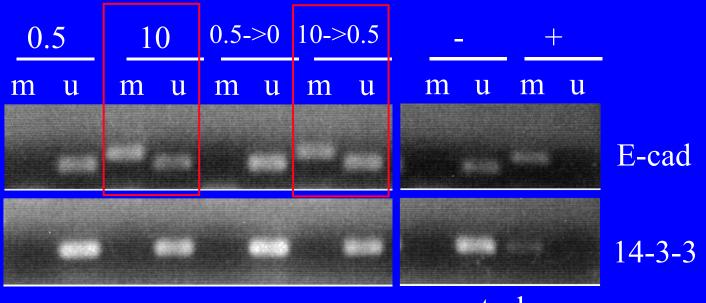






Phenotypes - increased motility

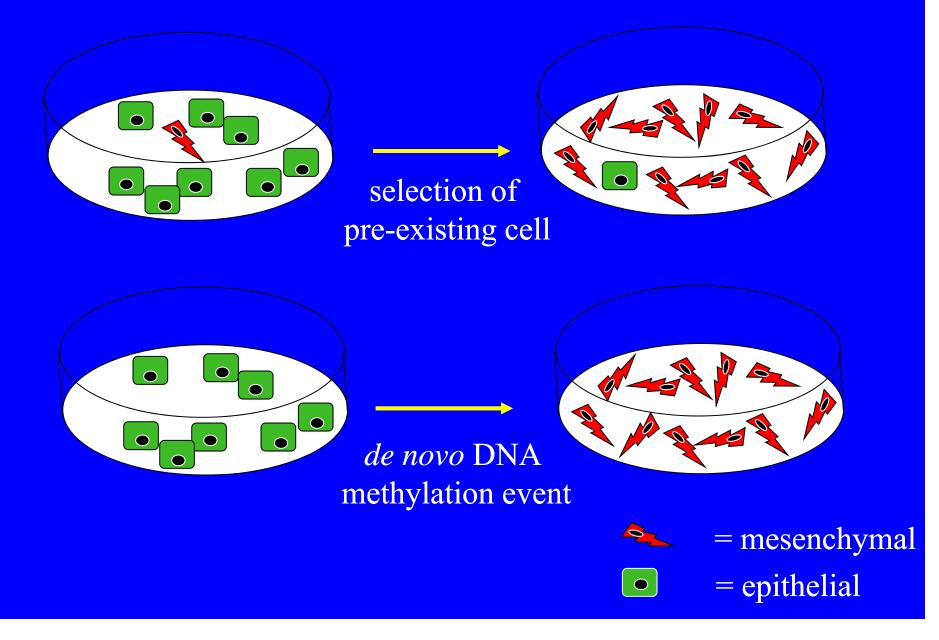
Using MS-PCR, we found that E-cadherin is silenced via Promoter DNA Methylation in vHMEC-ras with a Mesenchymal Morphology

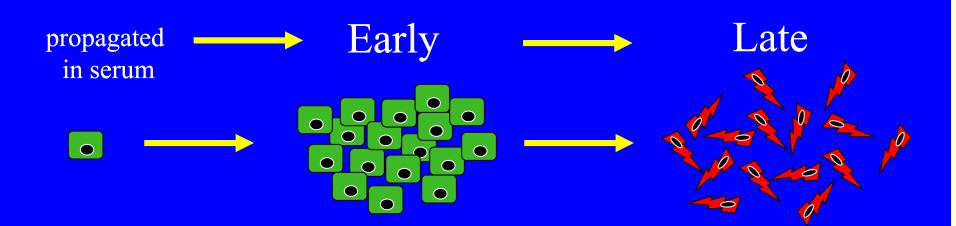


controls

Paul Reynolds

#### Selection or *de novo* DNA Methylation Event?

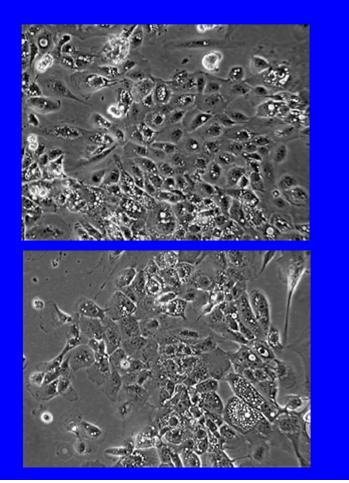


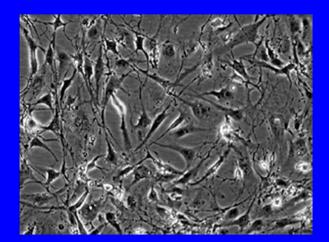


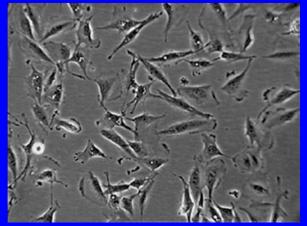
## Clone 1

#### Clone 2

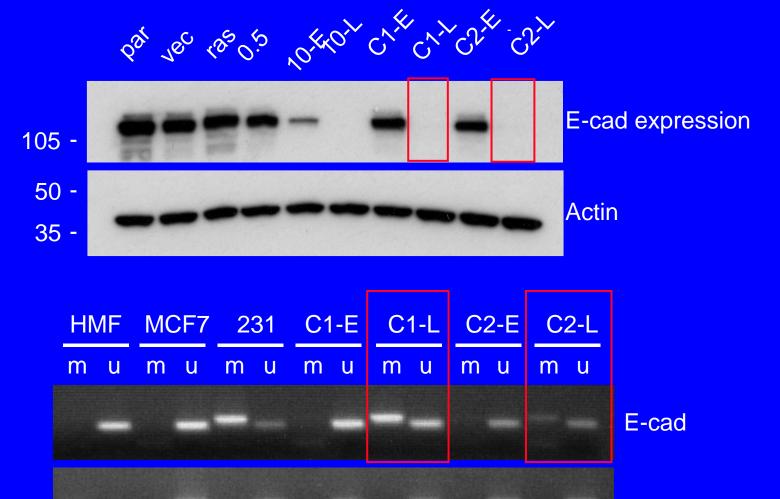
Nancy Dumont







### Methylation of the E-cadherin Promoter is a *de novo* Event



14-3-3σ

Nancy Dumont and Matt Wilson

# Panel of loci become hypermethylated:

E-cadherin Estrogen receptor α Twist CST6

This group of loci is part of a signature of loci that are only hypermethylated in <u>basal-like breast tumors</u> that exhibit mesenchymal phenotypes and poor prognosis. DNA Methylation Events in Cancer can be Deterministic Rather than Stocastic

In this system, methylation is not a random event.

Raises questions about common methylation events in cancer...

the methylation profile of a cell tells a story of where it's been and the cell's capacity to interact with the incoming information.

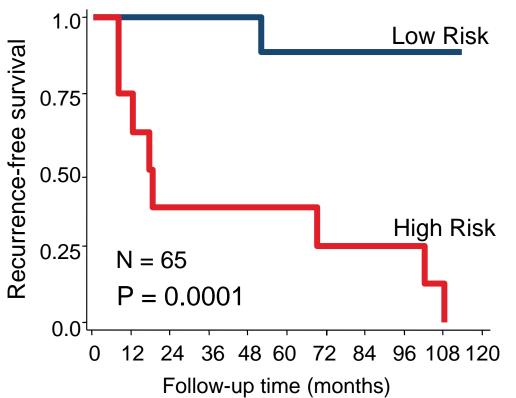
#### **Summary and Conclusions - Part II**

• Cells can be programmed by their microenvironment to undergo phenotypic and gene expression changes associated with targeted *de novo* epigenetic alterations important in tumor progression (and stem cell function?). other phenotypes - immortality, etc

 We can use this information to create tools that address clinical questions.
Prognostic biomarkers, novel therapeutic targets, etc.

#### New Assay Stratifies Risk for Subsequent Tumor Events in a Subset of DCIS Patients

Assay Signature



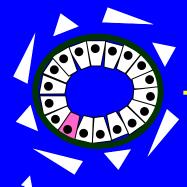
- 98% of biopsies that express the positive risk markers are associated with subsequent tumor events.
- 97% of biopsies that express negative risk markers are associated with NO subsequent tumor events.

How do cells acquire epigenetic plasticity (stemness)? Alter expression of key tumor suppressor and oncogene pathways

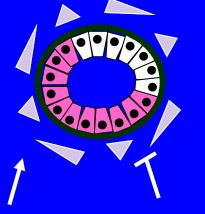
What determines which genes become hypermethylated during cancer progression? Process is deterministic - not random - guided by transcriptional co-regulators

Can we use this information to create tools that address clinical questions? Prognostic biomarkers, novel therapeutic targets, etc.

#### Mutual Reprogramming by Epithelial cells and their Adjacent Neighbors Generate Malignancies



methylation (aging, damage, diet, ?)



proliferation signals

CANCER

Centrosome abnormalities/ Methylation changes

telomeric dysfunction and altered gene expression

Stroma (inflammation, aging, etc.)

#### **<u>Tlsty Lab</u>**

Hal Berman Yongping Crawford Nancy Dumont

Paul Reynolds Mahvash Sigoradinia Matthew Wilson Jianmin Zhang

#### **Collaborators**

#### Joe Costello

Funding: NCI, DOD, Calif. State, Avon Foundation, Calif. Inst. of Regenerative Med., Cancer League