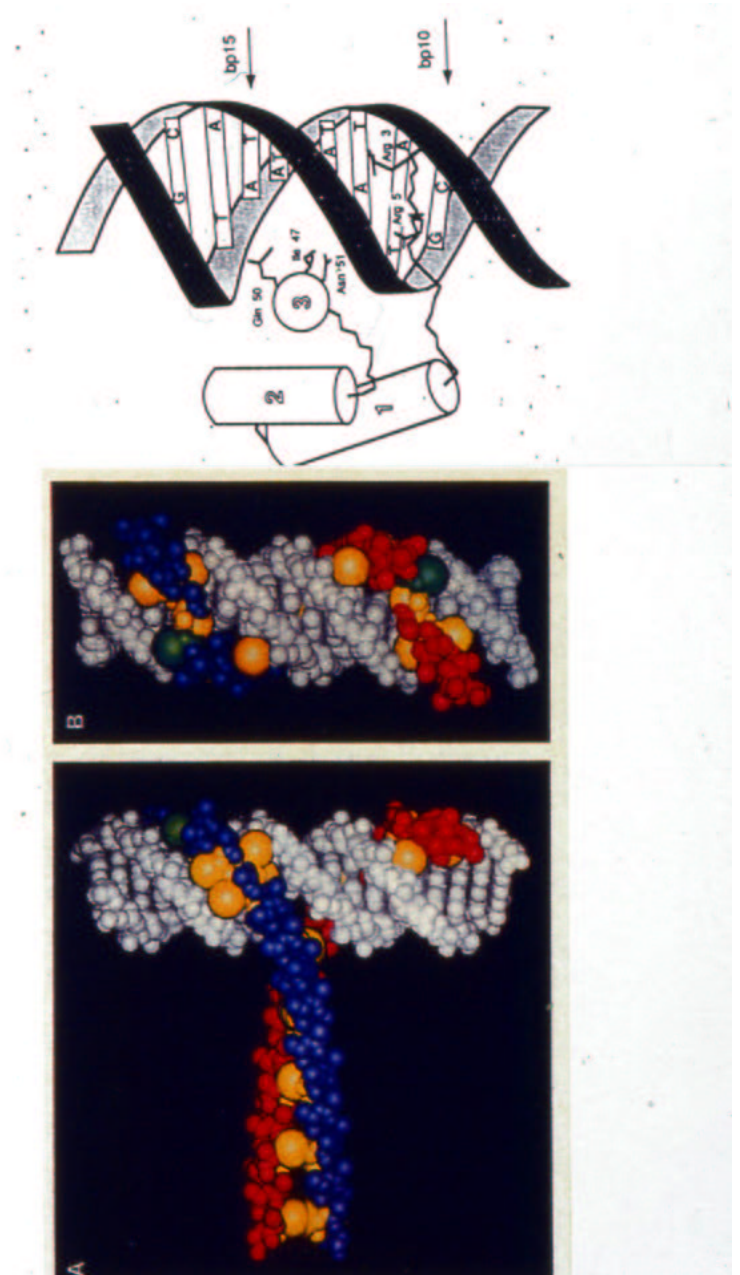
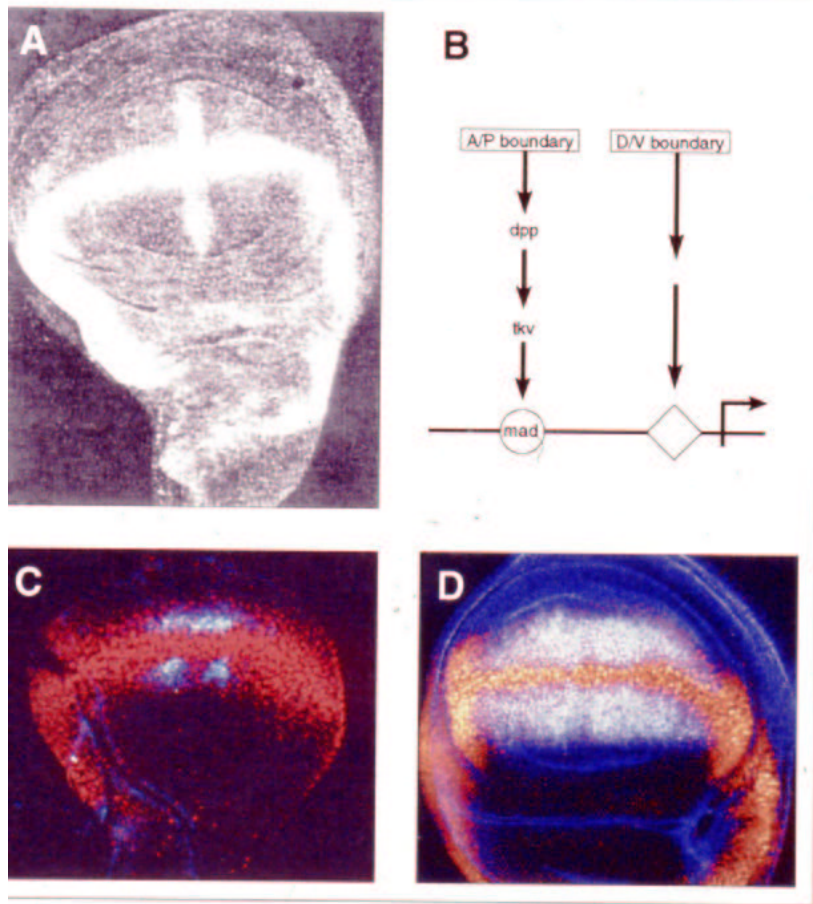
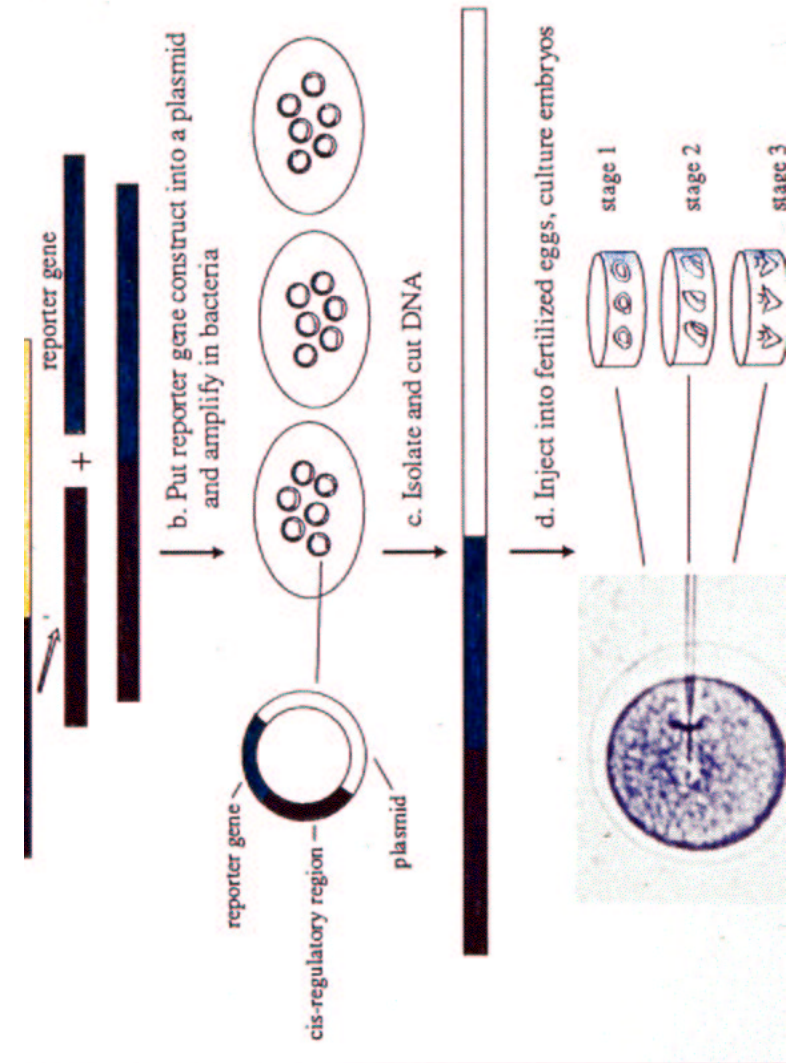
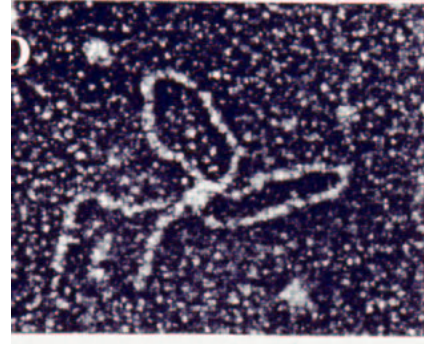
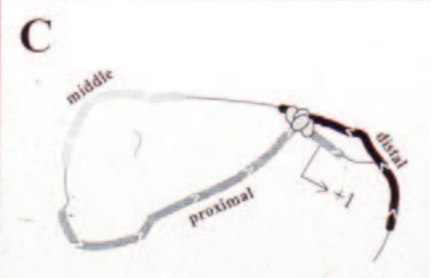
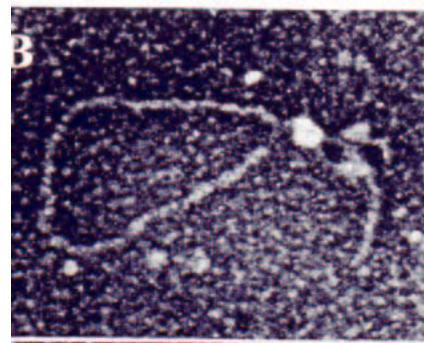
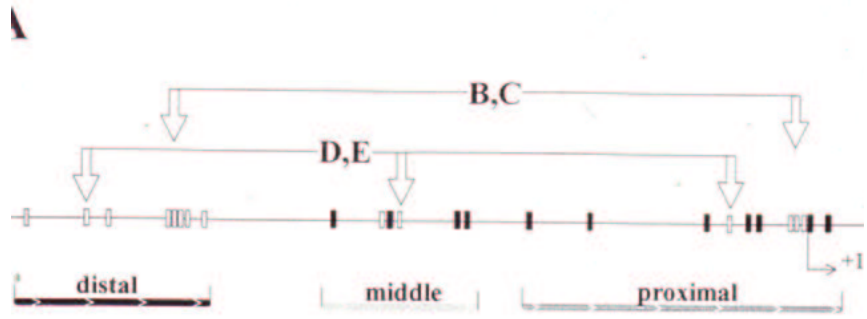


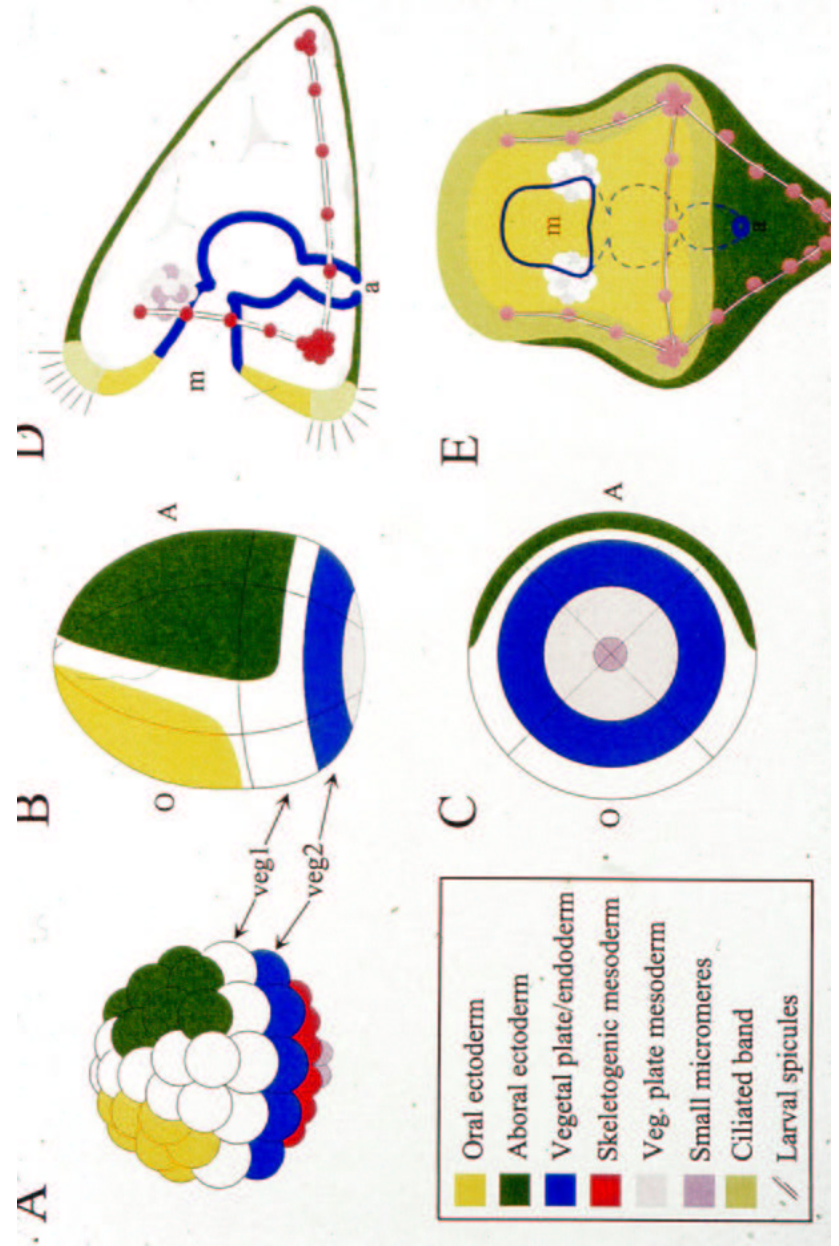
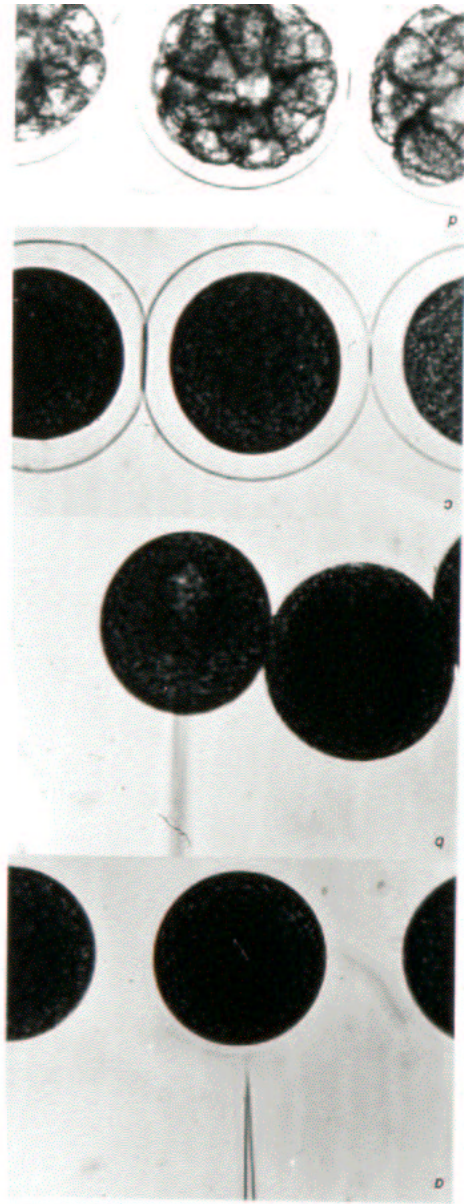
9:18:12 AM

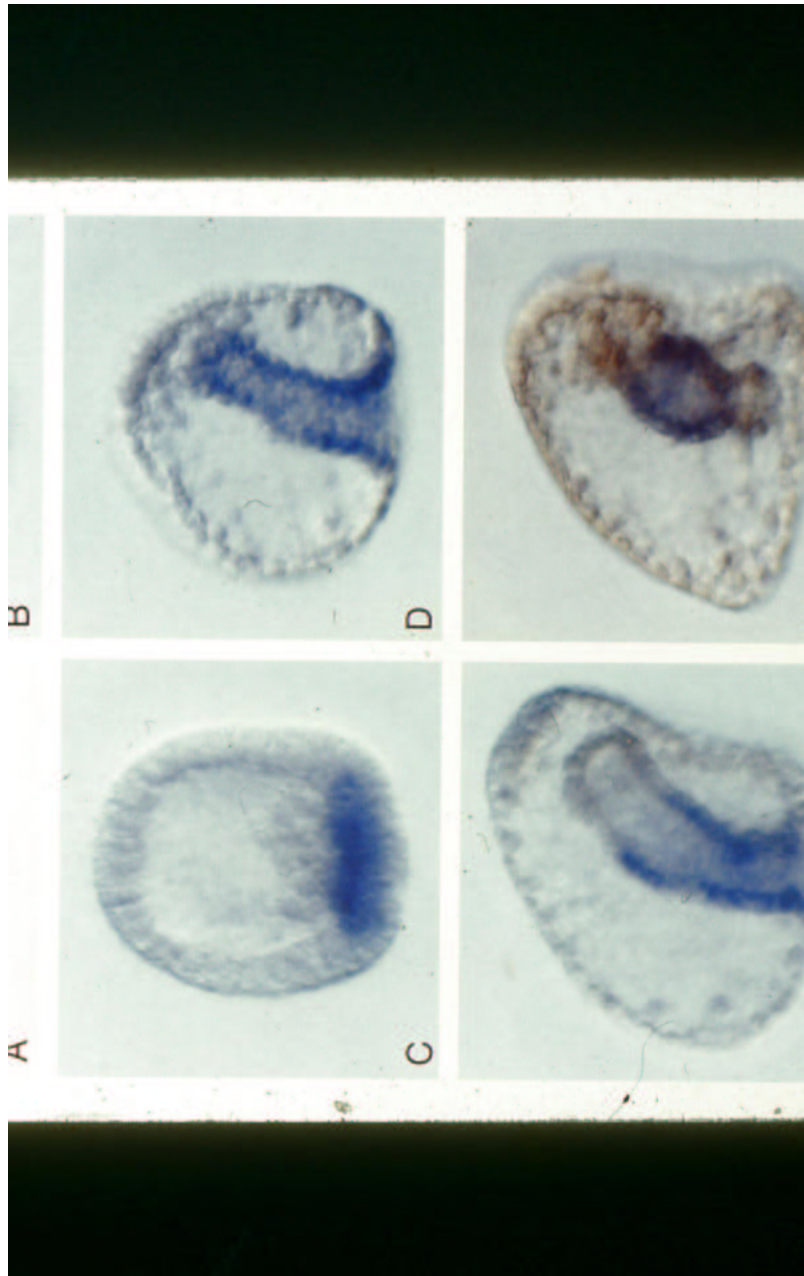
Some Principles of Developmental *Cis* Regulation

- Developmental specification depends on *cis*-regulatory information processing.
- *Cis*-regulatory modules always consist of assemblages of diverse target sites.
- For any given developmental *cis*-regulatory module, the output is novel with respect to any of the inputs.
- *Cis*-regulatory specification functions usually depend on negative as well as positive input.
- High specificity DNA/protein interactions within *cis*-regulatory modules always indicate regulatory function, and these individual functions are of many different kinds.









spatial inputs of ENDO-16

Veg2 Lineage

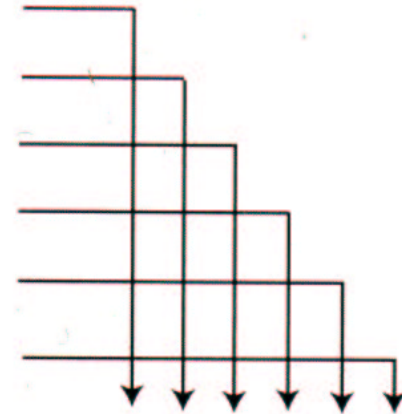
Ectoderm Boundary

Skel. mesenchyme
Boundary

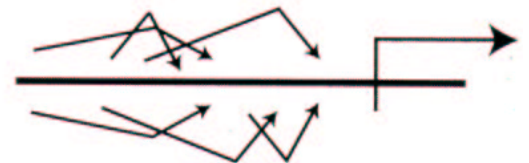
Archenteron

Late Veg2 ectoderm
Component

Midgut



temporal Intermodule
inputs and Outputs

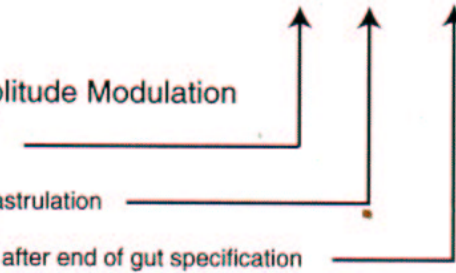


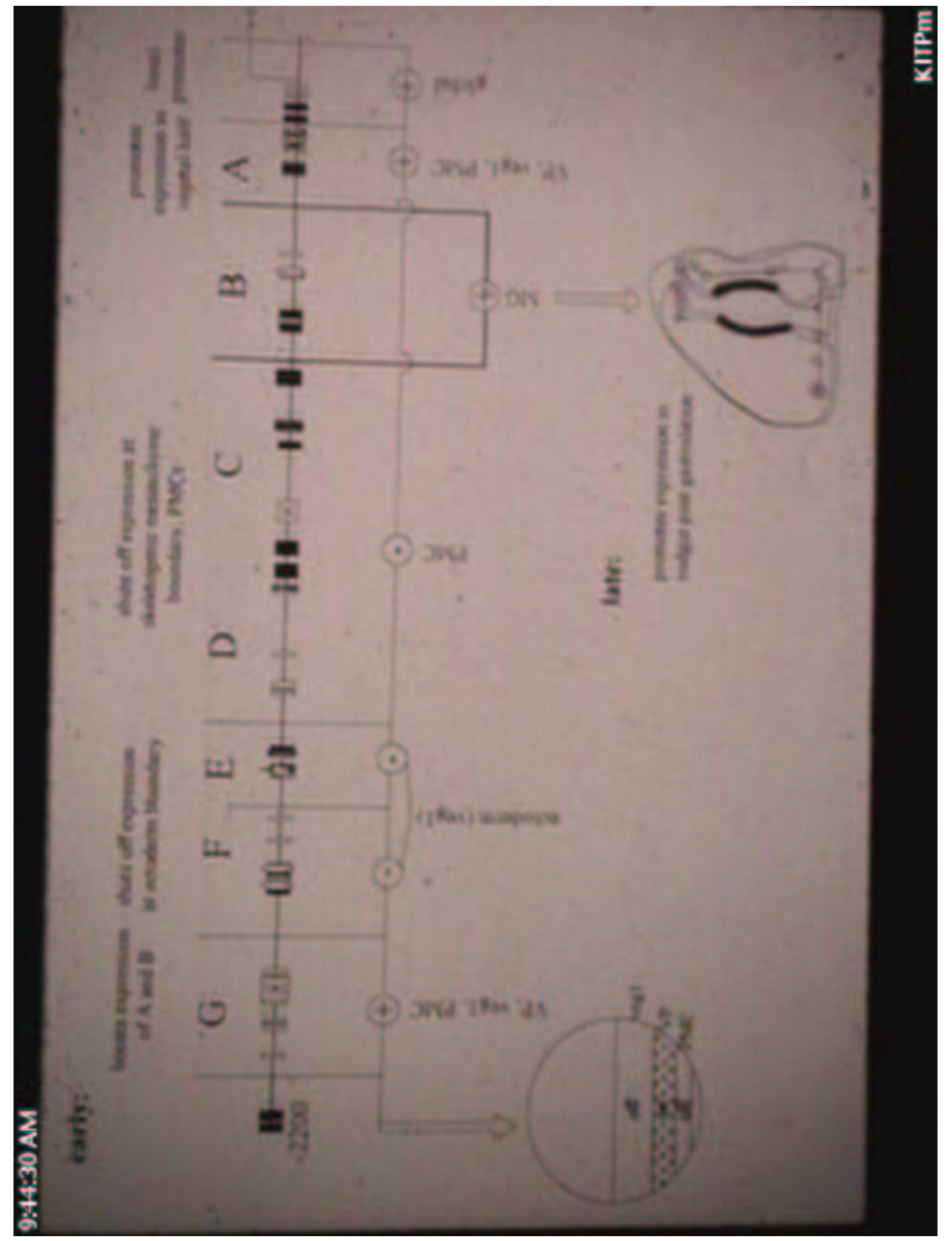
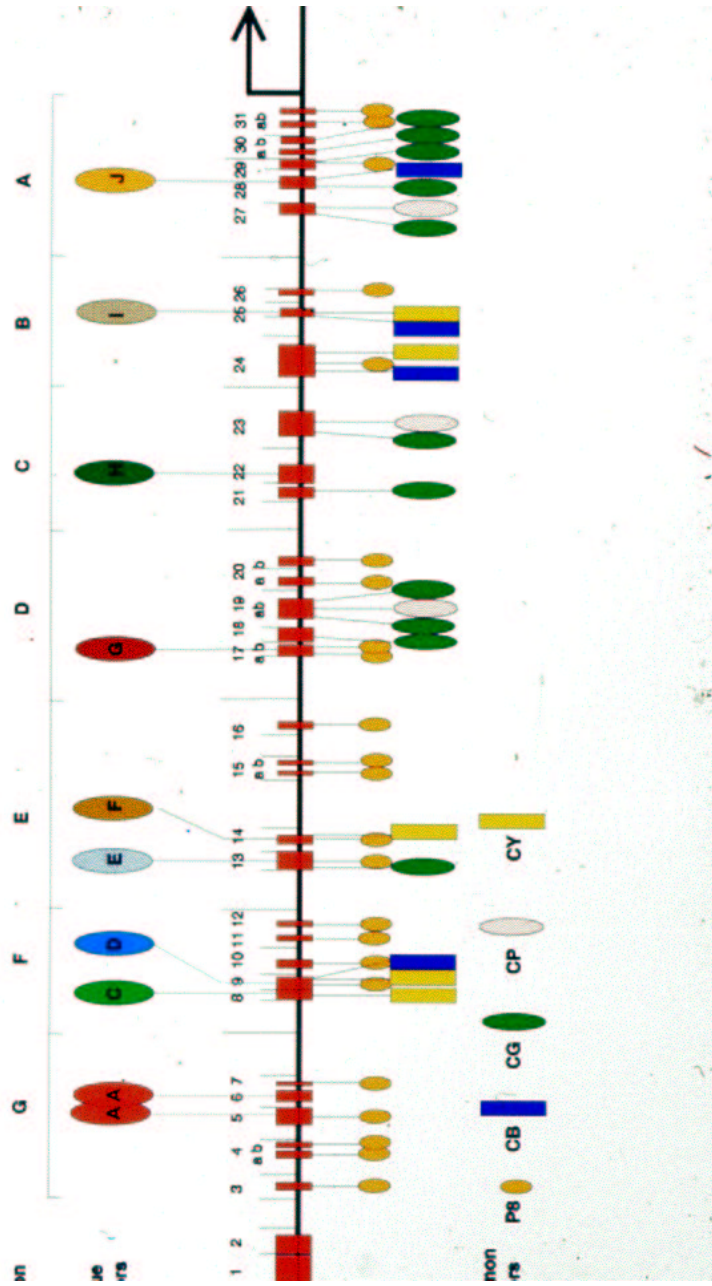
temporal Amplitude Modulation

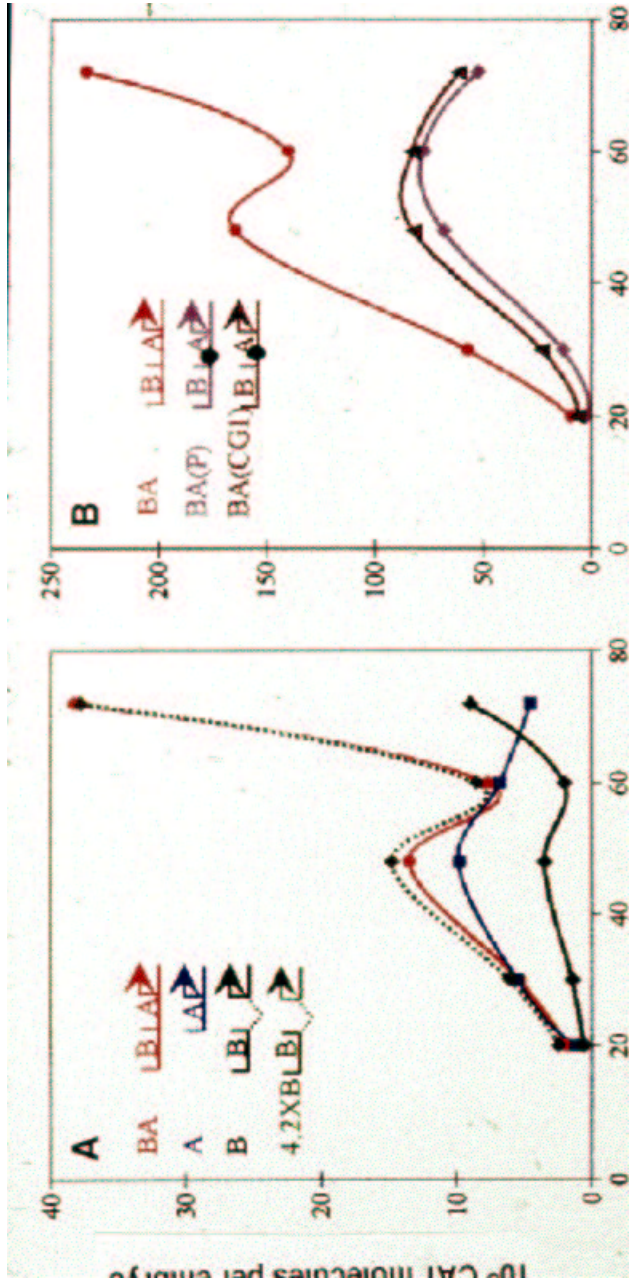
Low, early

Increases on gastrulation

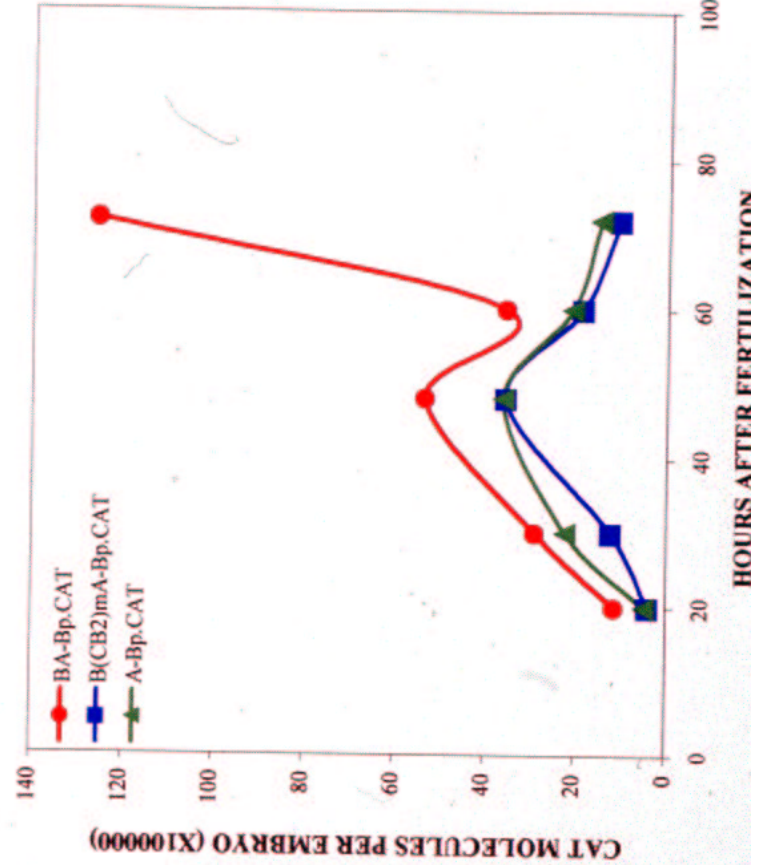
Sharp increase after end of gut specification







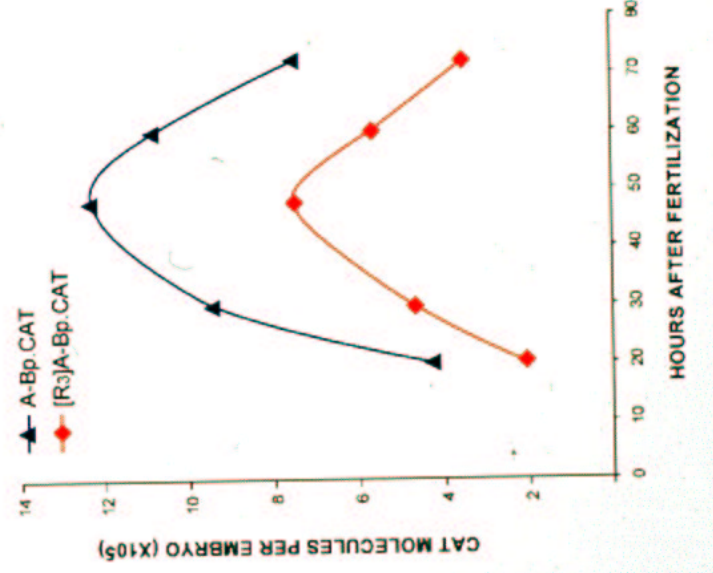
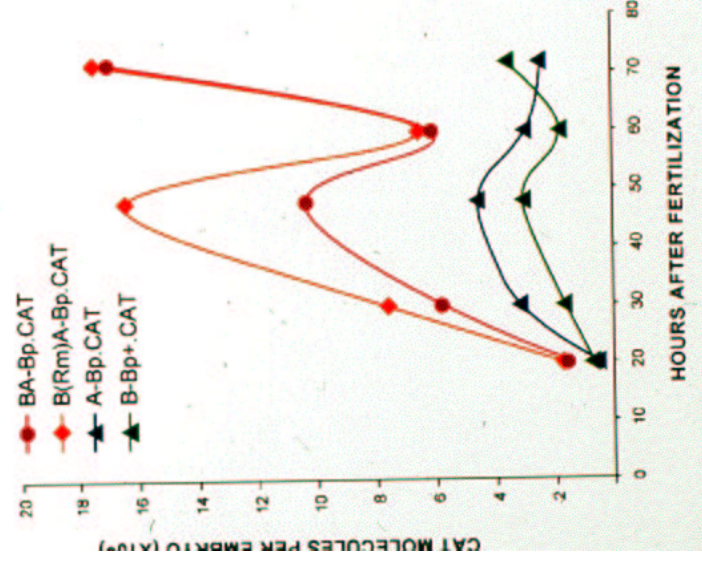
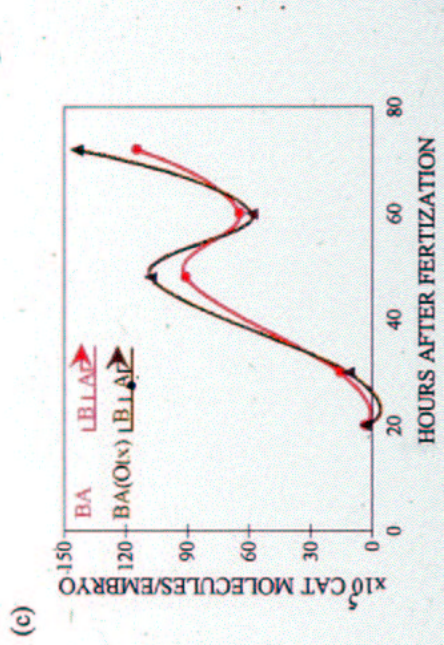
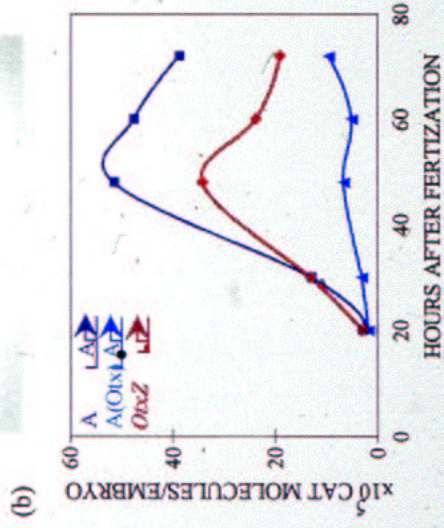
THE CASE OF MODULE B IS ESSENTIAL FOR MODULE B interaction with module A





(a)

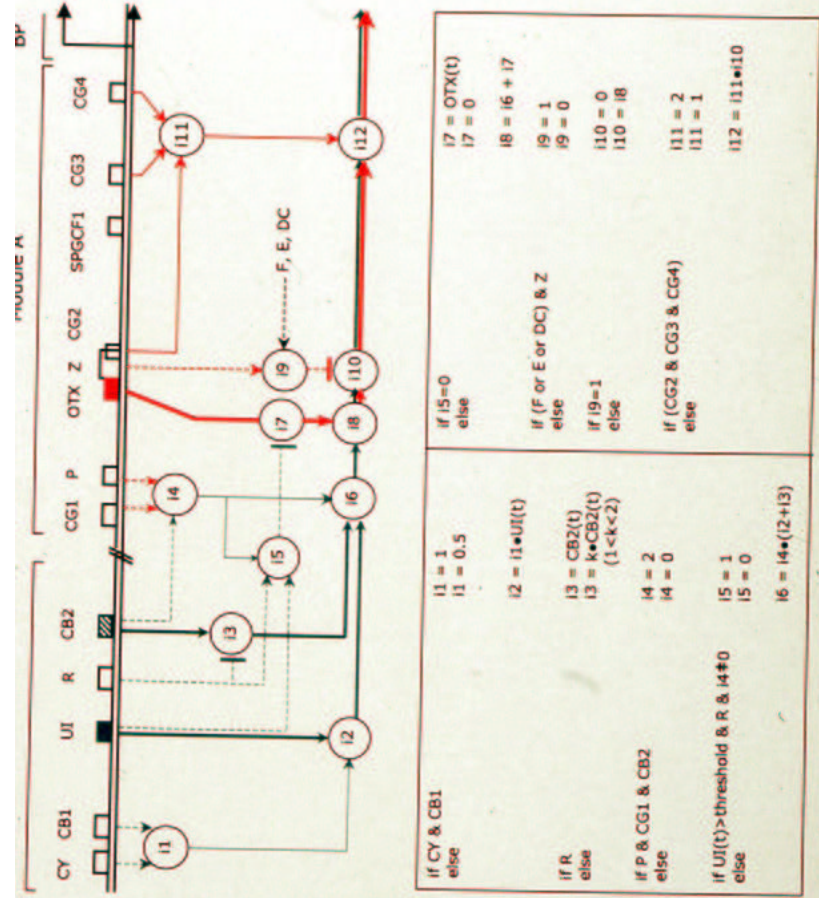
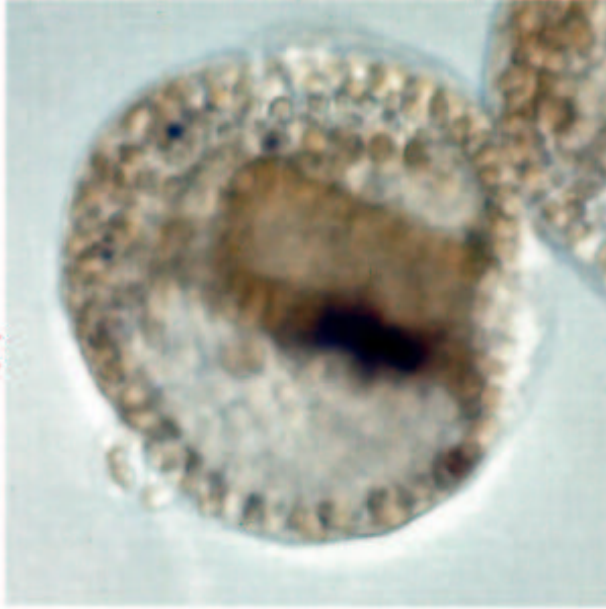
Constructs	Endoderm
<i>OtxZ</i>	56.5%
<i>(Otx)Z</i>	3.6%
<i>Otx(Z)</i>	72.0%
A	78.9%
A(<i>Otx</i>)	5.1%
ENDO16	97.0%



(J)-(CG3&4)mBp



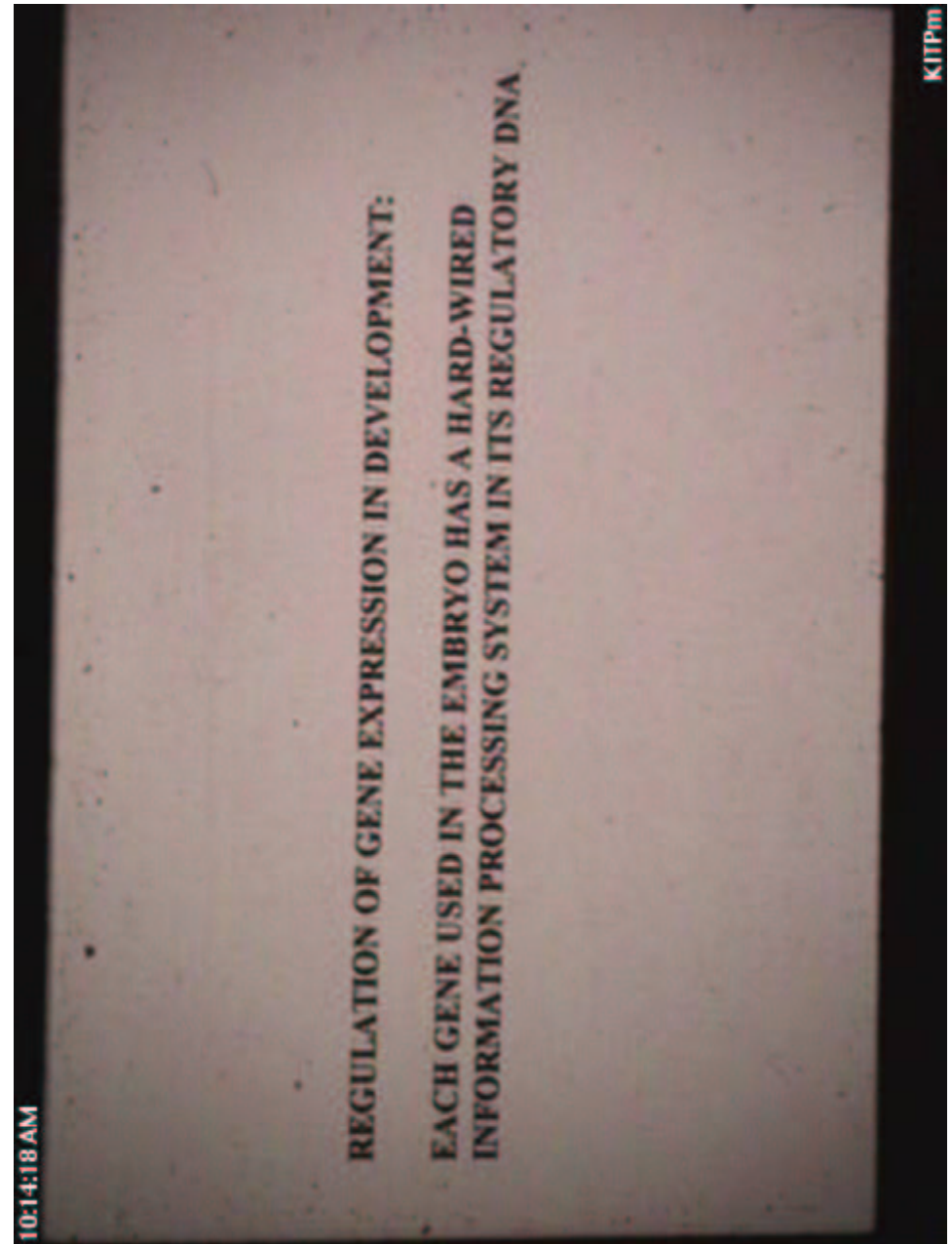
(J)-SM50



... output produced by given module B mutations

$\{$	$= [CB2(t) + UI(t)]$
$\{$ (CYm)	$= 0.5 \times UI(t) + CB2(t) = 0.5B + 0.5 \times CB2(t)$
$\{$ (CB1m)	$= 0.5 \times UI(t) + CB2(t) = 0.5B + 0.5 \times CB2(t)$
$\{$ (CYm,CB1m)	$= 0.5 \times UI(t) + CB2(t) = 0.5B + 0.5 \times CB2(t)$
$\{$ (Rm,CB2m)	$= UI(t) = B - CB2(t)$
$\{$ (UIm)	$= CB2(t)$
for $UI(t) > \text{threshold}$	
$\{$ A	$= 4 \times [CB2(t) + UI(t)]$
$\{$ A(CYm)	$= 4 \times [CB2(t) + 0.5 \times UI(t)] = 0.5BA + 2CB2(t)$
$\{$ A(CB1m)	$= 4 \times [CB2(t) + 0.5 \times UI(t)] = 0.5BA + 2CB2(t)$
$\{$ A(CYm,CB1m)	$= 4 \times [CB2(t) + 0.5 \times UI(t)] = 0.5BA + 2CB2(t)$
$\{$ A(UIm)	$= 4 \times CB2(t) + A$
$\{$ A(CB2m)	$= A$
$\{$ A(Rm)	$= 4 \times [UI(t) + k \times CB2(t)] + A$ $= BA + A + 4 \times (k-1) \times CB2(t)$
$\{$ A(Rm,Otxm)	$= 4 \times [UI(t) + k \times CB2(t)]$ $= BA + 4 \times (k-1) \times CB2(t)$
$\{$ A(UIm,CB2m)	$= A$
$\{$ A(Rm,CB2m)	$= A$
$\{$ A(UIm,Otxm)	$= 4 \times CB2(t) + A(Otxm)$
$\{$ A(UIm,Otxm,CB2m)	$= A(Otxm) = BP(t)$
$\{$ A(Pm)	$= A$
$\{$ A(CG1m)	$= A$

*Blue expressions consist of components that can be perceived directly from genetic data (as illustrated in Figs 3-7).



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WHAT IS A DEVELOPMENTAL GENE NETWORK? GENOMIC DEFINITION:

DNA ELEMENTS

All genes transcriptional regulation of which is required to execute the developmental process, including:

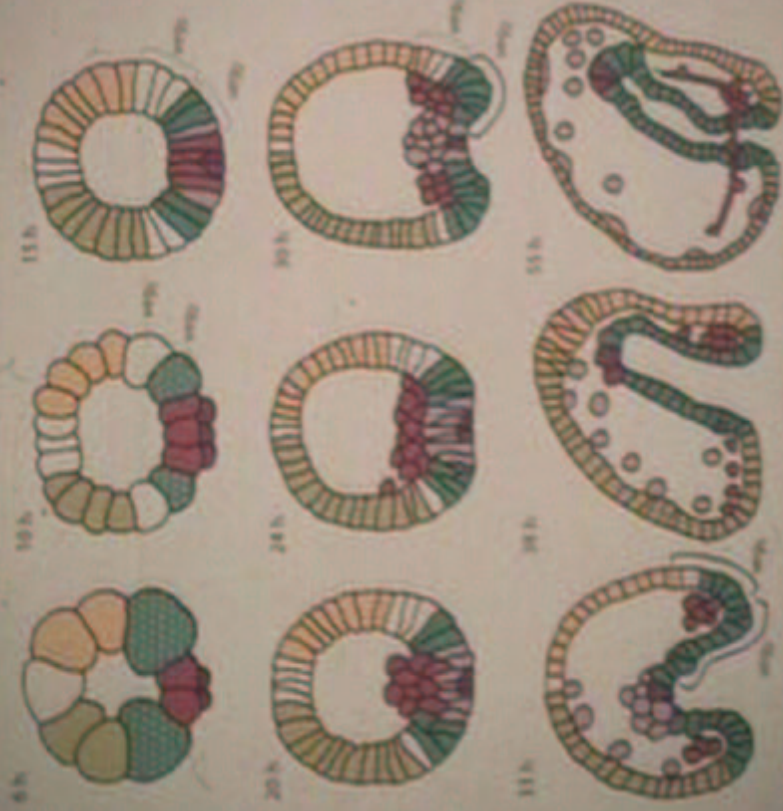
- Genes encoding transcription factors
- Genes encoding signal components that provide inputs into relevant *cis*-regulatory systems
- Genes encoding downstream differentiation proteins
- All relevant *cis*-regulatory control elements for these genes

ARCHITECTURE

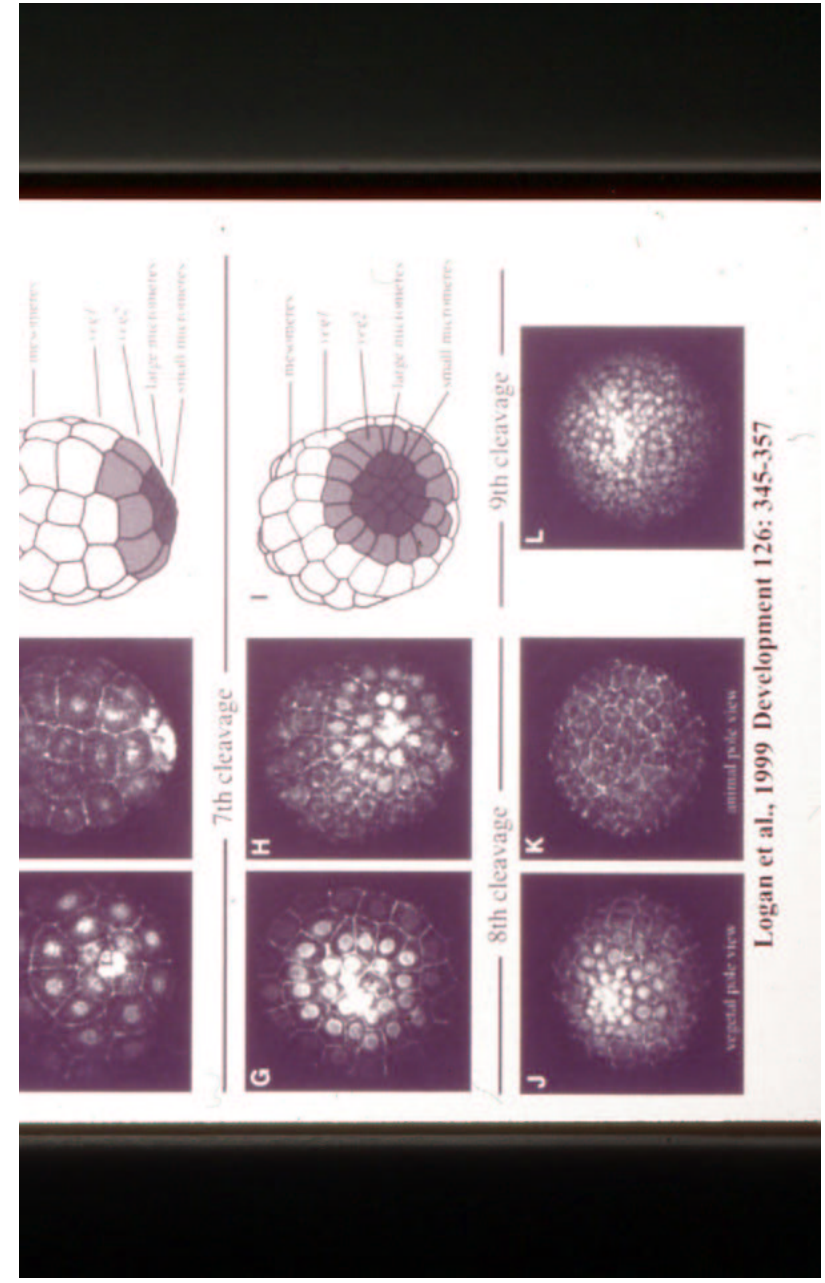
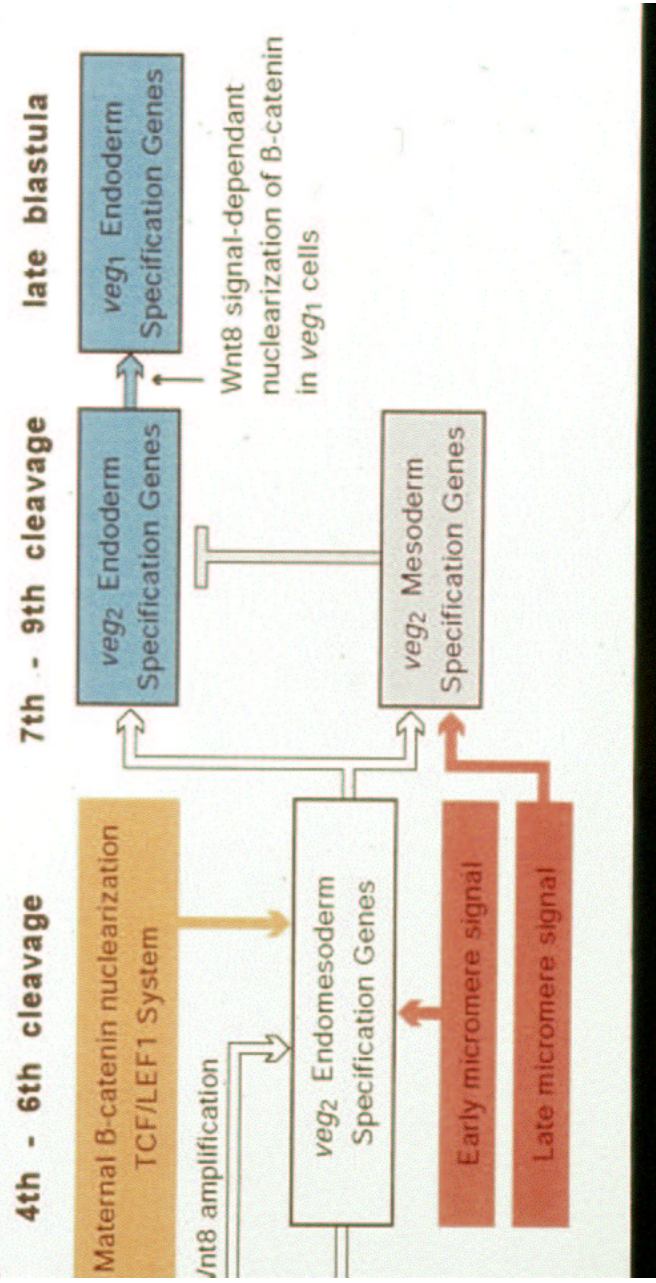
Functional linkages connecting these *cis*-regulatory elements

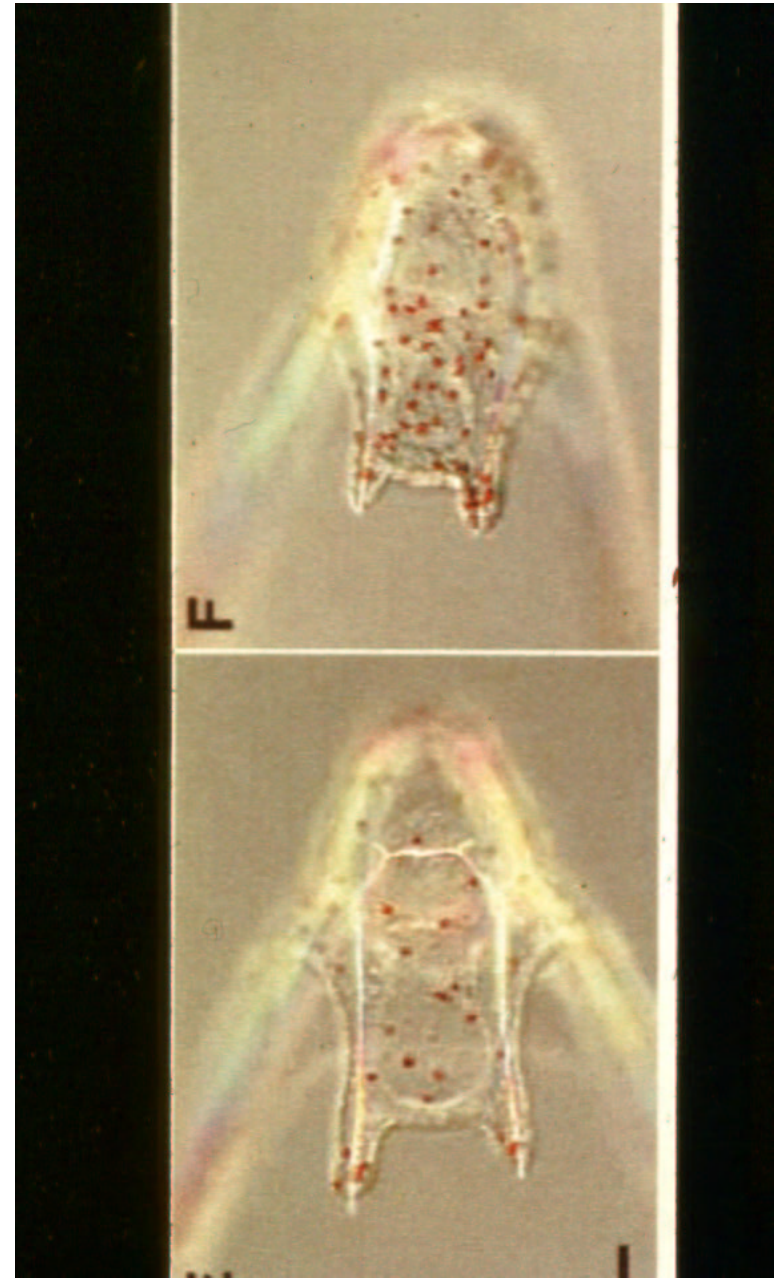
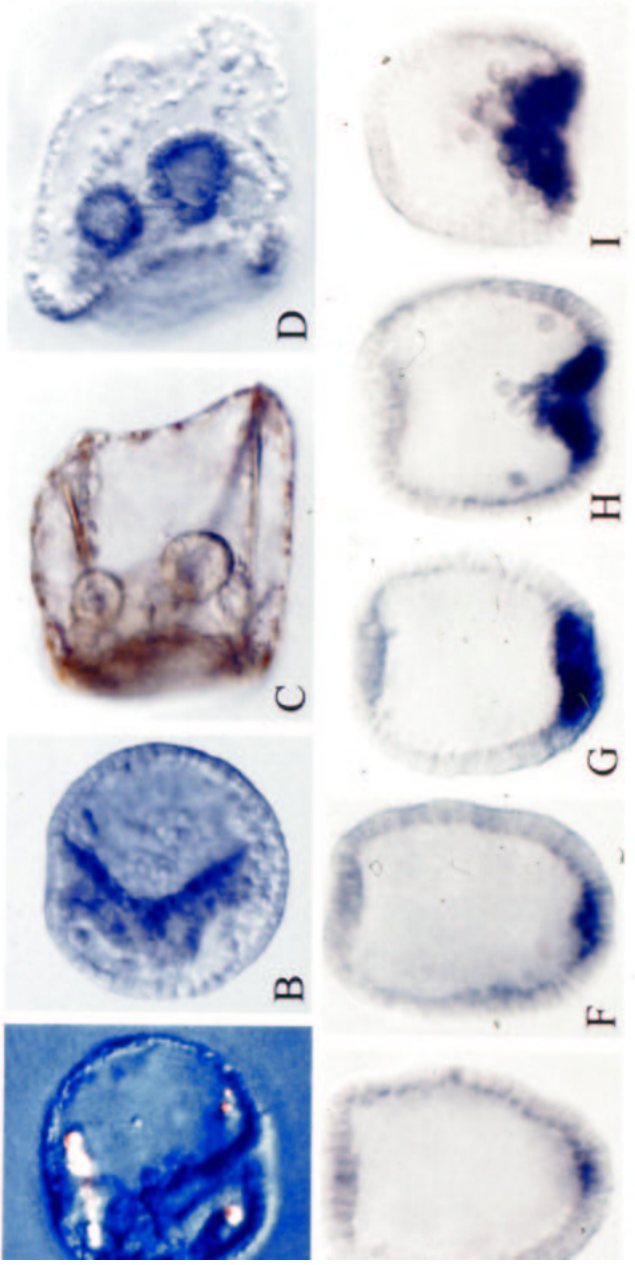
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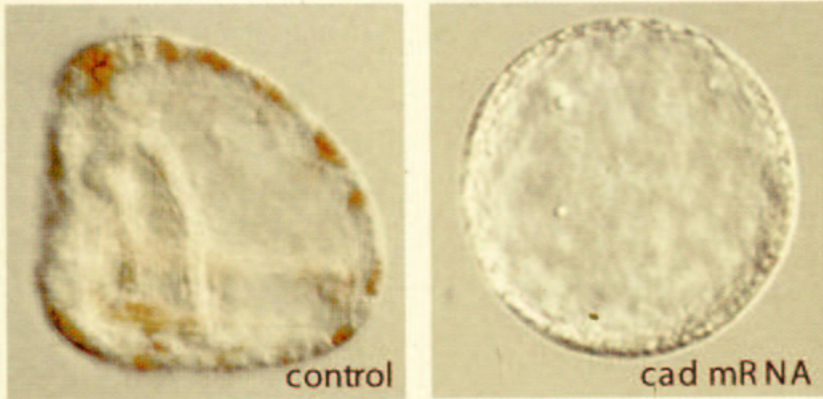
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Perturbation: Cadherin mRNA injection

Effect: Blocks activation of Wnt/Tcf signaling pathway

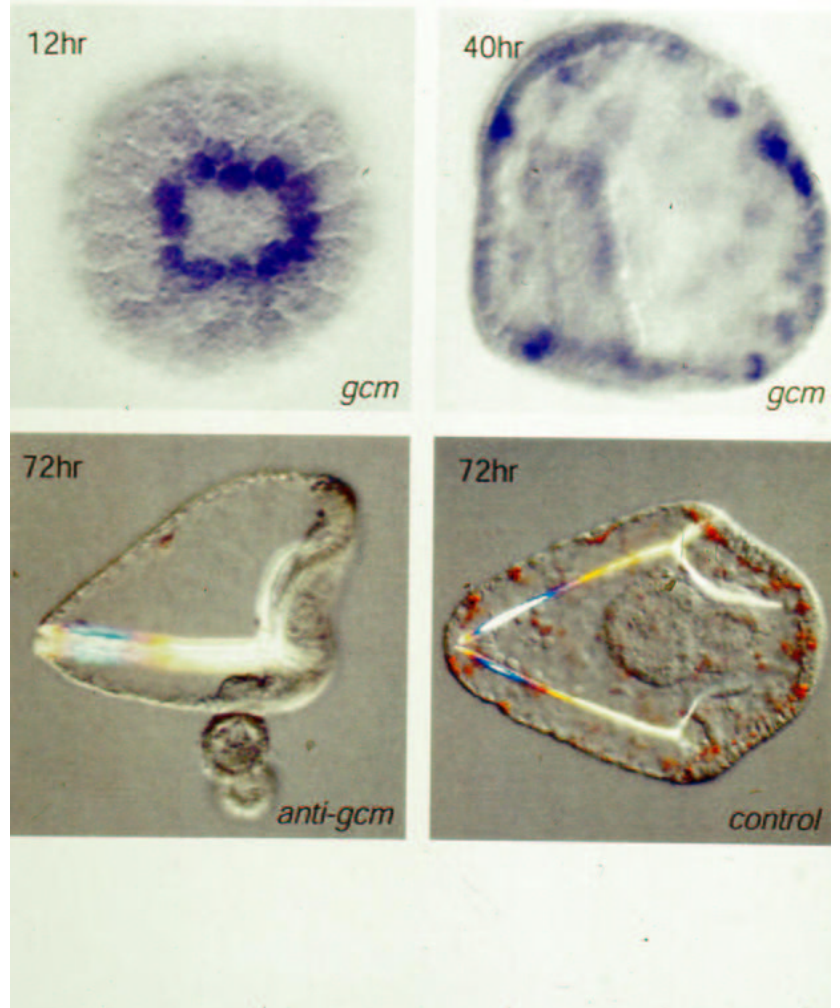


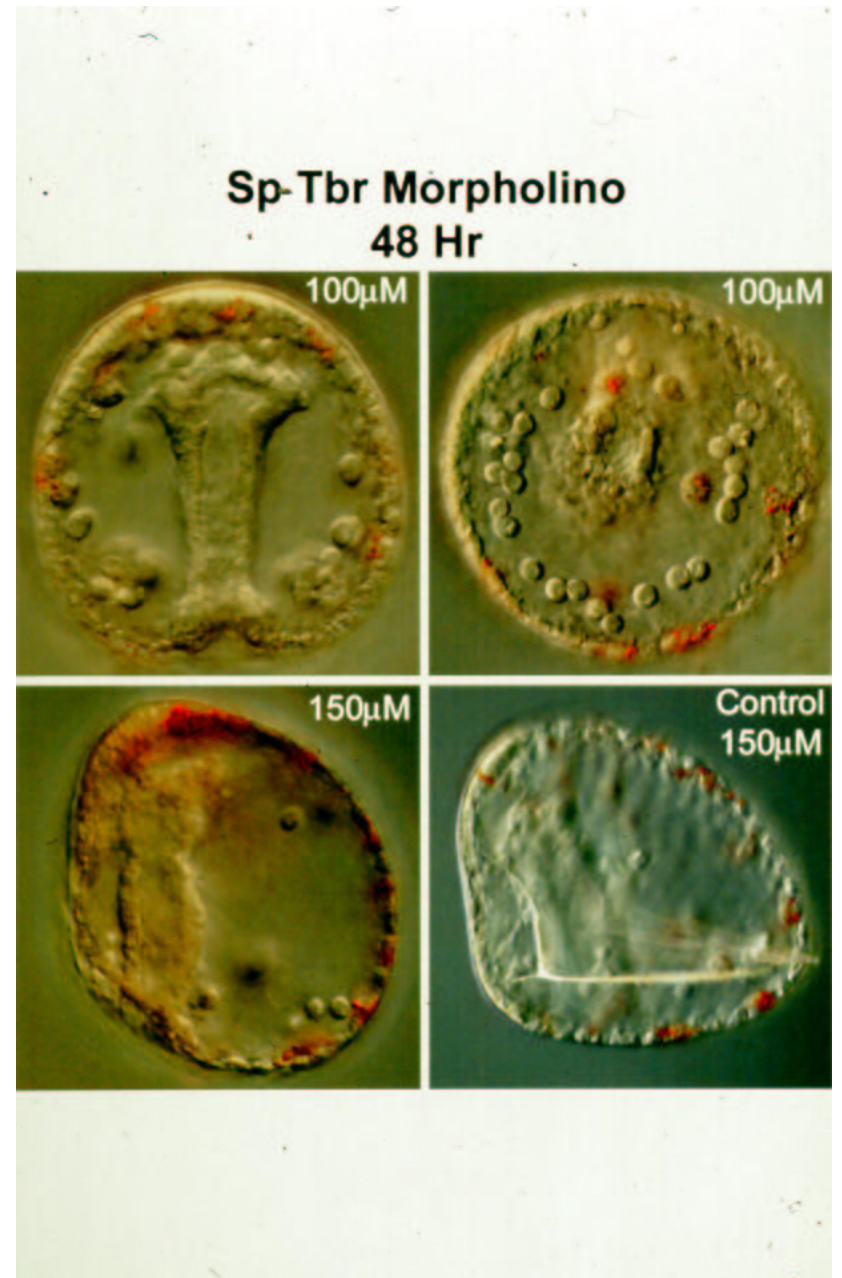
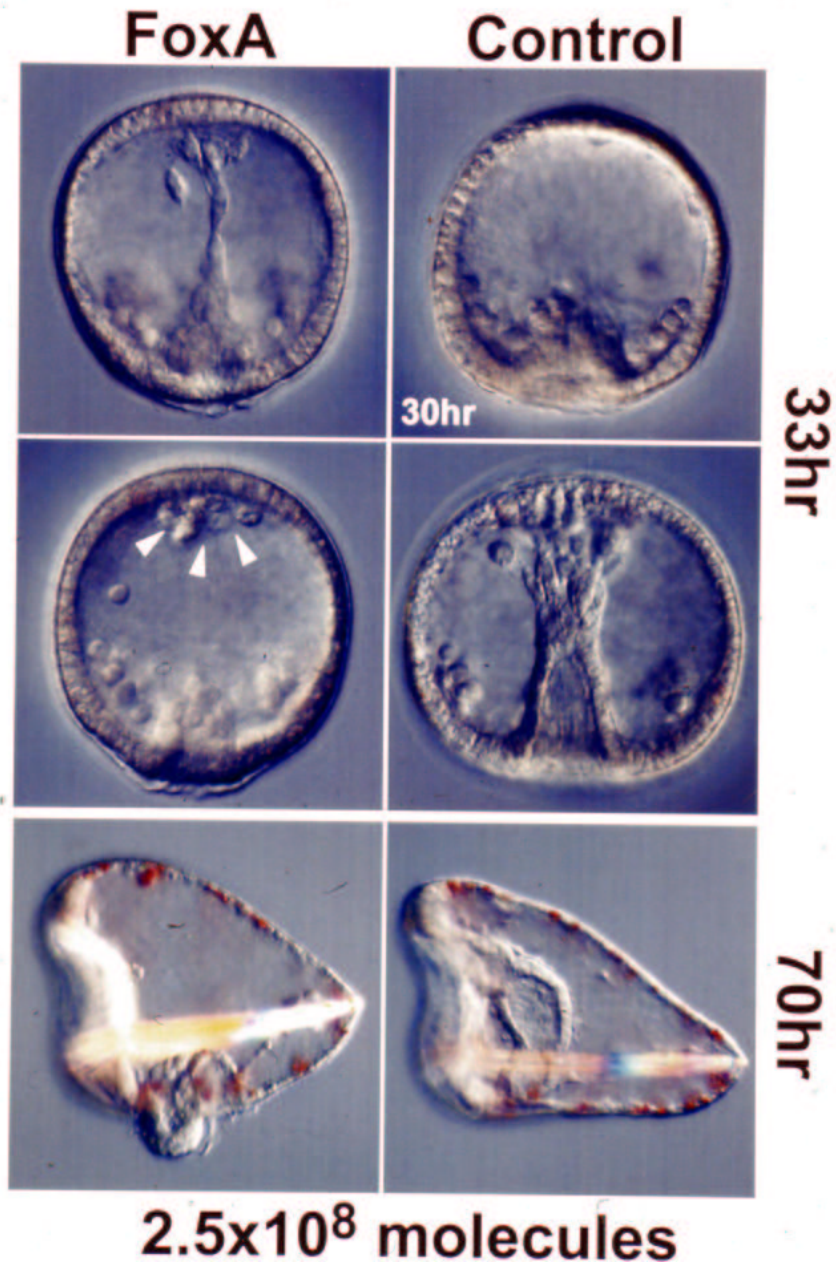
Perturbation: Negative Notch mRNA injection

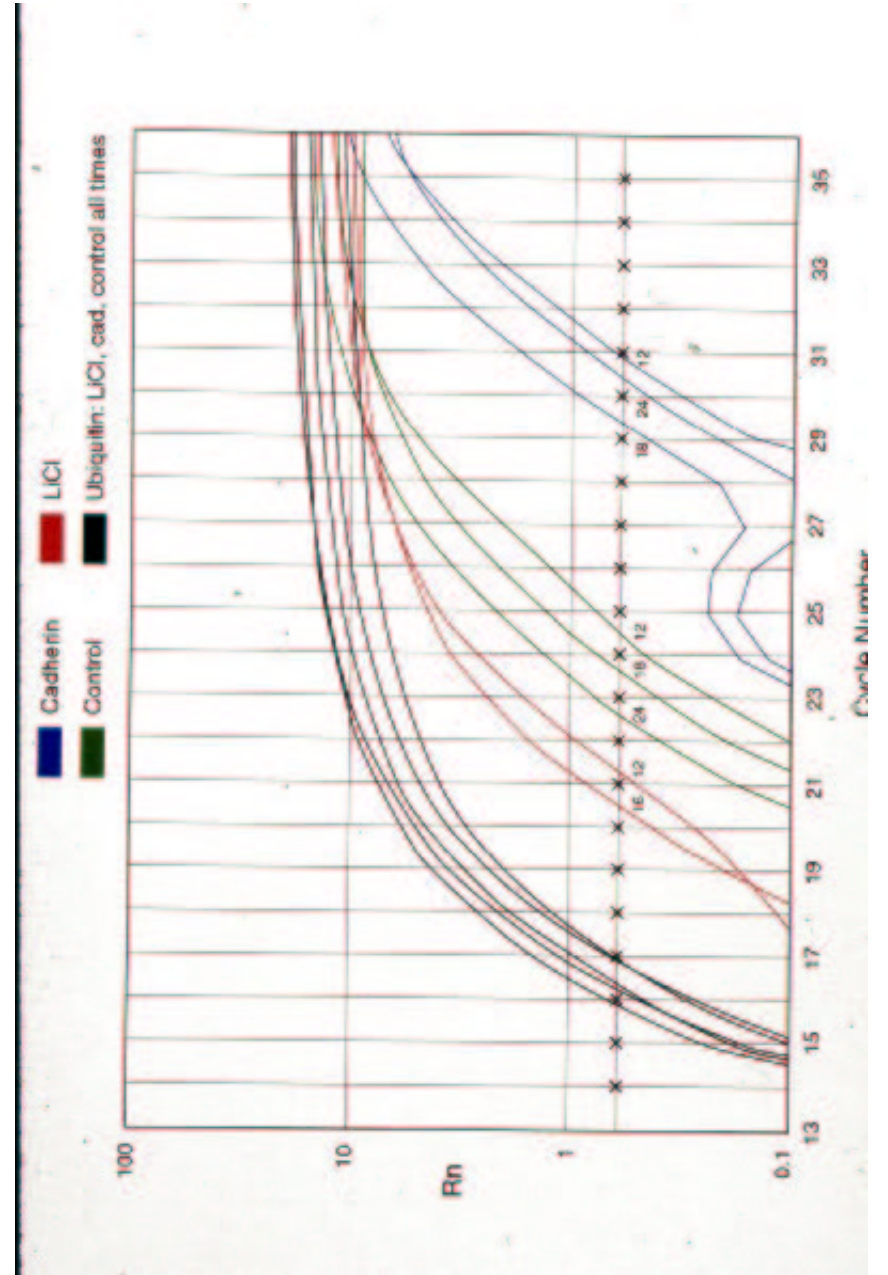
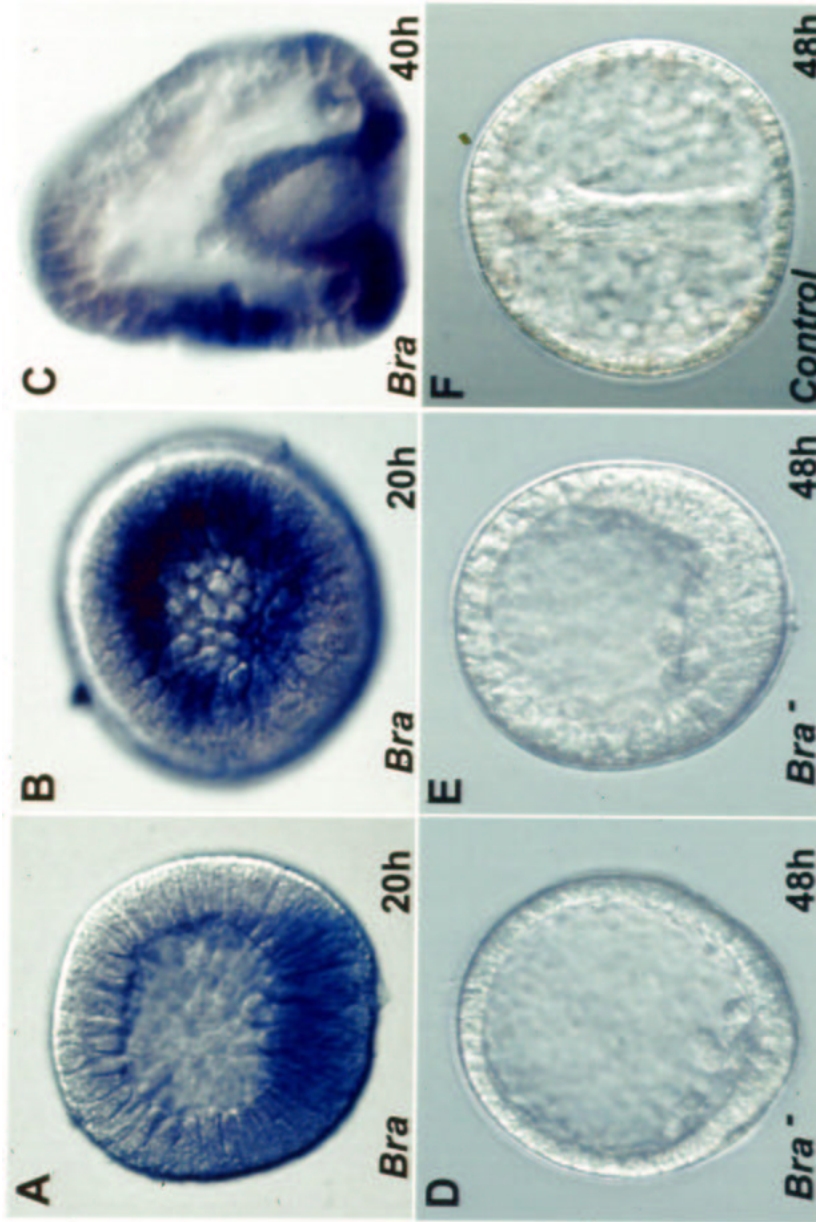
Effect: Blocks Notch signaling pathway



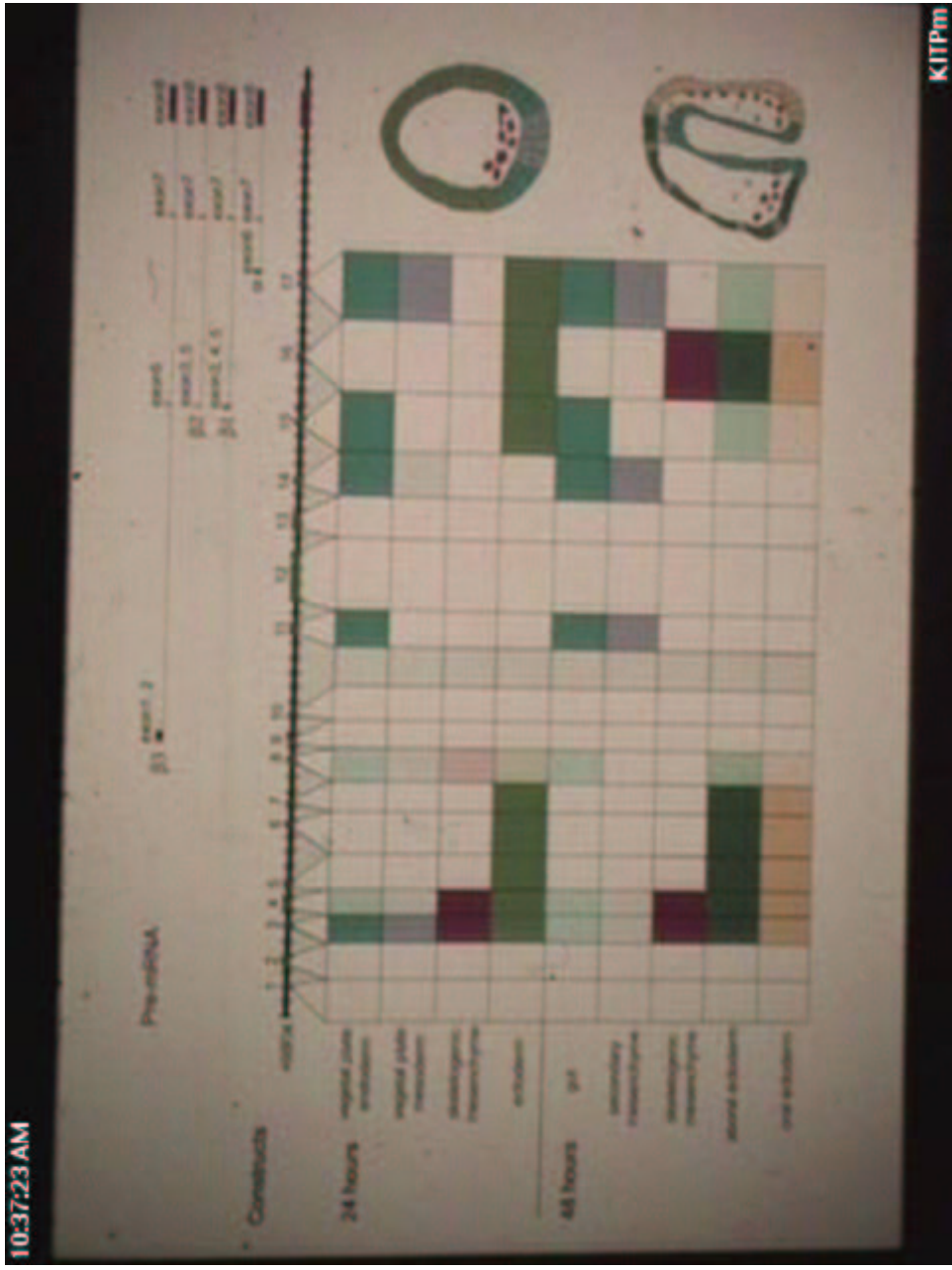
Spgcm, a Transcriptional Regulator of Pigment Cell Specification







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