

Synthetic gene expression perturbation systems with rapid, tunable, single-gene specificity in yeast

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Benjamin L.
Oakes, Xin Wang,
Krysta A.
Dummit, David
Botstein and
Marcus B. Noyes

Background

Results

Conclusions

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Carles Boix

Background

- ▶ System to perturb the expression of a single gene only.

Journal Club 1

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- ▶ System to perturb the expression of a single gene only.
- ▶ Tool to understand complex regulatory networks.

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- ▶ System to perturb the expression of a single gene only.
- ▶ Tool to understand complex regulatory networks.
- ▶ Nutritional perturbation, such as GAL or MET promoters.

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- ▶ Nutritional perturbation, such as GAL or MET promoters.
- ▶ Use inducers that don't have any other influence on the system.
- ▶ Use DBDs that do not have multiple locations in the genome (~ 9 bp)

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Create a system which is:

Fast

Tightly regulated

Gratuitous (no effect on other genes)

Gradable

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Create a system which is:

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This is the β -estradiol system which we are using.

DNA-binding domain (DBD)

Human estrogen receptor (ER)

VP16 activation domain

Use specific zinc fingers (Z_3 and Z_4)

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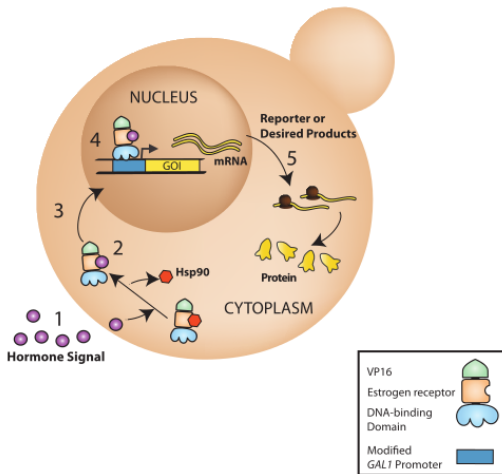


Figure : Synthesized ATF system

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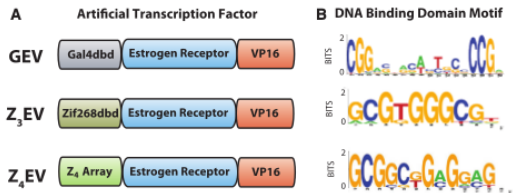


Figure : Constructed ATFs and Binding Motifs

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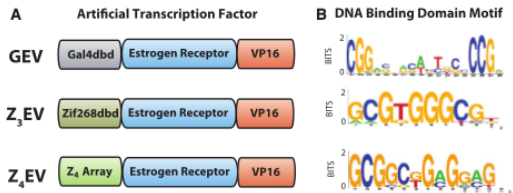


Figure : Constructed ATFs and Binding Motifs

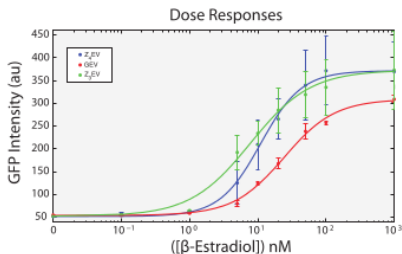


Figure : GFP level with reporter plasmid.

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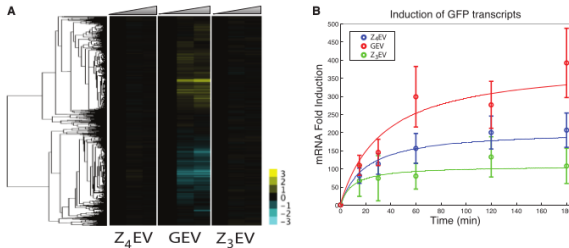


Figure : Gene expression levels and GFP mRNA levels.

More than 50-fold induction in 15 minutes.

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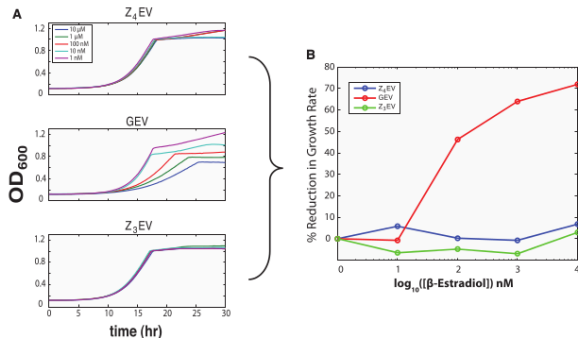


Figure : Growth defect present in GEV strains.

Increasing β -estradiol decreases GEV growth rate.

70% Growth rate decrease from 10nM to 10 μ M.

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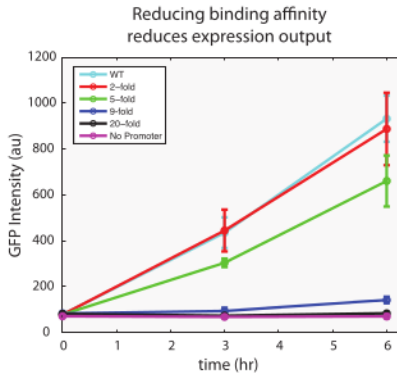


Figure : Grading output by binding affinity

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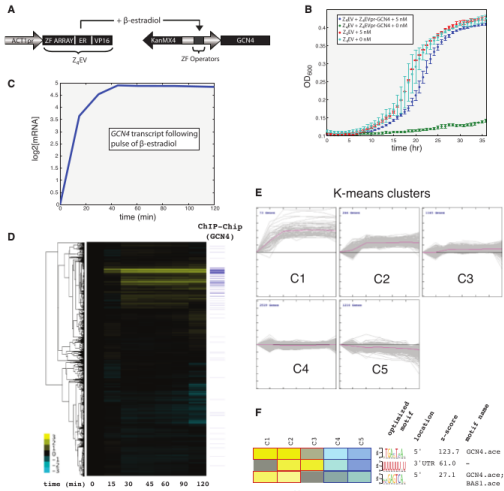


Figure : *GCN4* (GOI) is a transcriptional activator of enzymes required for production of *aa*.

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The β -estradiol system:

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- ▶ Gratuitous
- ▶ Fast (50 fold in 15 min)
- ▶ Does not have a growth defect
- ▶ Can be moderated by binding affinity

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Have shown utility with a case study: *GCN4*. Authors find ~ 200 – 300 genes repressed and enriched (116 genes known before from ChIP data).

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