

## DNA Microarray Analysis

Sample 1 □ Normal strain; labeled with green fluor

Sample 2 □ Deletion strain; labeled with red fluor

### Microarray analysis of strain deleted for gene E

Gene A – yellow

Gene B – green

Gene C – green

Gene D – yellow

Gene E – green

Gene F – red

Gene G – yellow

Gene H – yellow

Gene I – yellow

Gene J – green

Gene K – yellow

Gene L – yellow

Gene M – yellow

Gene N – yellow

Gene O – yellow

Gene P – green

Gene Q – yellow

Gene R – green

Gene S – red

Gene T – yellow

Gene U – yellow

Gene V – yellow

Gene W – yellow

Gene X – yellow

Gene Y – red

Gene Z – red

### Microarray analysis of strain deleted for gene T

Gene A – yellow

Gene B – green

Gene C – green

Gene D – yellow

Gene E – yellow

Gene F – red

Gene G – yellow

Gene H – yellow

Gene I – yellow

Gene J – green  
Gene K – yellow  
Gene L – yellow  
Gene M – yellow  
Gene N – yellow  
Gene O – yellow  
Gene P – green  
Gene Q – yellow  
Gene R – green  
Gene S – red  
Gene T – green  
Gene U – yellow  
Gene V – yellow  
Gene W – yellow  
Gene X – yellow  
Gene Y – red  
Gene Z – red

#### Microarray analysis of strain deleted for gene I

Gene A – yellow  
Gene B – yellow  
Gene C – yellow  
Gene D – yellow  
Gene E – yellow  
Gene F – yellow  
Gene G – yellow  
Gene H – yellow  
Gene I – green  
Gene J – yellow  
Gene K – yellow  
Gene L – red  
Gene M – yellow  
Gene N – yellow  
Gene O – yellow  
Gene P – yellow  
Gene Q – yellow  
Gene R – yellow  
Gene S – yellow  
Gene T – yellow  
Gene U – yellow  
Gene V – yellow  
Gene W – yellow  
Gene X – yellow  
Gene Y – yellow  
Gene Z – yellow

Microarray analysis of strain deleted for gene Y

Gene A – yellow  
Gene B – yellow  
Gene C – yellow  
Gene D – yellow  
Gene E – yellow  
Gene F – green  
Gene G – yellow  
Gene H – yellow  
Gene I – yellow  
Gene J – yellow  
Gene K – yellow  
Gene L – yellow  
Gene M – yellow  
Gene N – yellow  
Gene O – yellow  
Gene P – yellow  
Gene Q – yellow  
Gene R – yellow  
Gene S – green  
Gene T – yellow  
Gene U – yellow  
Gene V – yellow  
Gene W – yellow  
Gene X – yellow  
Gene Y – green  
Gene Z – green

Microarray analysis of strain deleted for gene R

Gene A – yellow  
Gene B – yellow  
Gene C – yellow  
Gene D – yellow  
Gene E – yellow  
Gene F – red  
Gene G – yellow  
Gene H – yellow  
Gene I – yellow  
Gene J – yellow  
Gene K – yellow  
Gene L – yellow  
Gene M – yellow  
Gene N – yellow

Gene O – yellow  
Gene P – yellow  
Gene Q – yellow  
Gene R – green  
Gene S – red  
Gene T – yellow  
Gene U – yellow  
Gene V – yellow  
Gene W – yellow  
Gene X – yellow  
Gene Y – red  
Gene Z – red

Microarray analysis of strain deleted for gene B

Gene A – yellow  
Gene B – green  
Gene C – green  
Gene D – yellow  
Gene E – yellow  
Gene F – red  
Gene G – yellow  
Gene H – yellow  
Gene I – yellow  
Gene J – green  
Gene K – yellow  
Gene L – yellow  
Gene M – yellow  
Gene N – yellow  
Gene O – yellow  
Gene P – green  
Gene Q – yellow  
Gene R – green  
Gene S – red  
Gene T – yellow  
Gene U – yellow  
Gene V – yellow  
Gene W – yellow  
Gene X – yellow  
Gene Y – red  
Gene Z – red

Microarray cluster analysis:

R, J, C, P – cluster 1

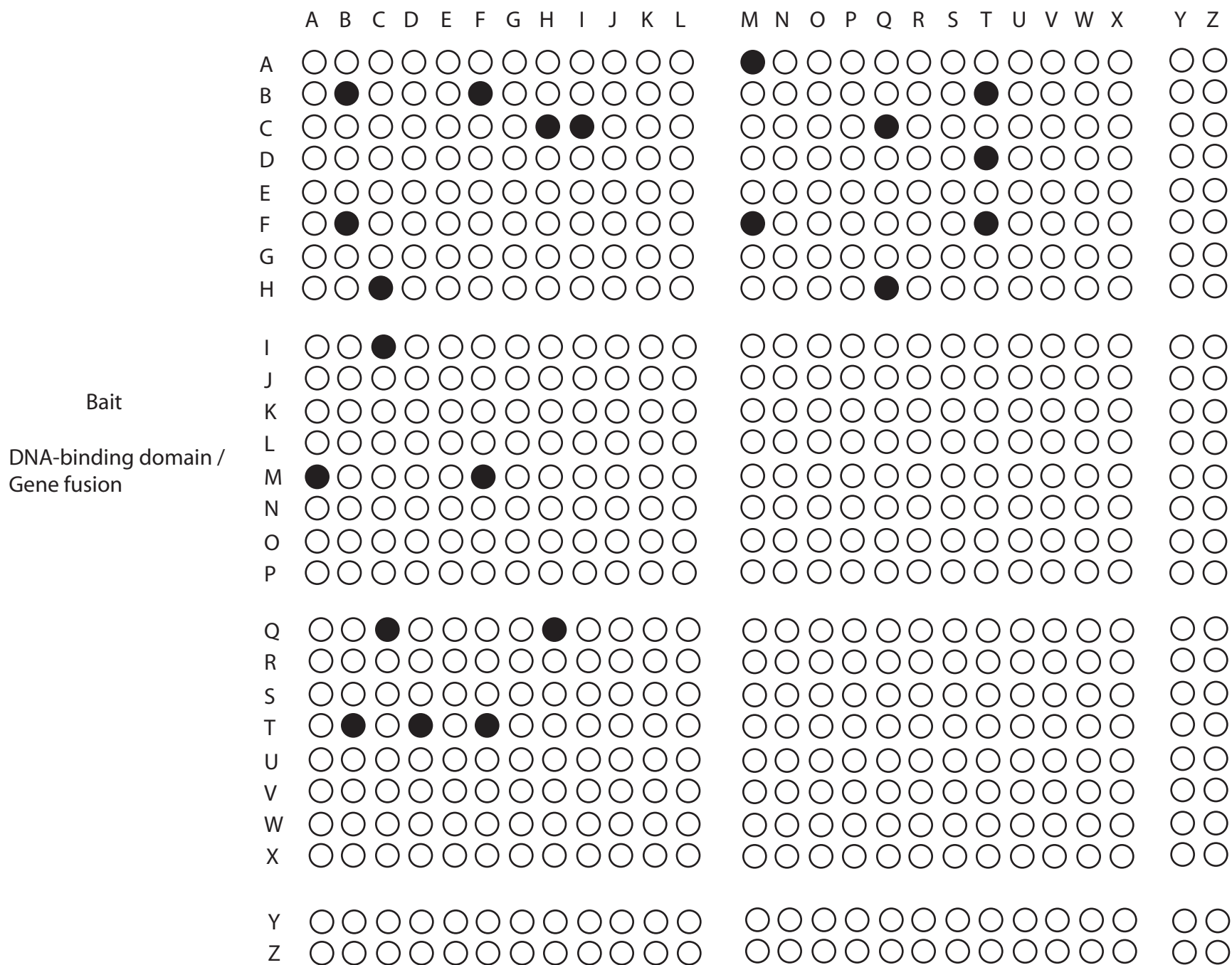
Z, F, S – cluster 2

Considering the microarray data listed above (deletion strain analysis and cluster analysis), do your best to propose a model (diagram) of the pathway we're studying.

Two-Hybrid Analysis (-His)  
(His3 reporter)

Prey

Transcriptional activation domain / gene fusion



Bait

DNA-binding domain /  
Gene fusion

Mass spectrometry analysis:

T, B, and F are phosphorylated

I is ubiquitinated

Considering the two-hybrid data and the mass spec analysis above, do your best to propose a model (diagram) of the pathway we're studying:

Homology-Searching:

By searching each of the 26 genes against databases of known proteins, you find significant matches for the following genes:

Gene B  
Gene C  
Gene D  
Gene F  
Gene H  
Gene Q

Based on the alignments, draw conclusions regarding the functions of these genes. Also, consider whether these alignments may help suggest potential genetic, protein, and regulatory interactions.