

Supplementary Figures

Trendy Visualization

This shiny app is designed to explore the output from Trendy. First the .RData object output from Trendy must be uploaded.

Input .Rdata from trendy() run:

Browse... trendyForShiny.RData

Upload complete

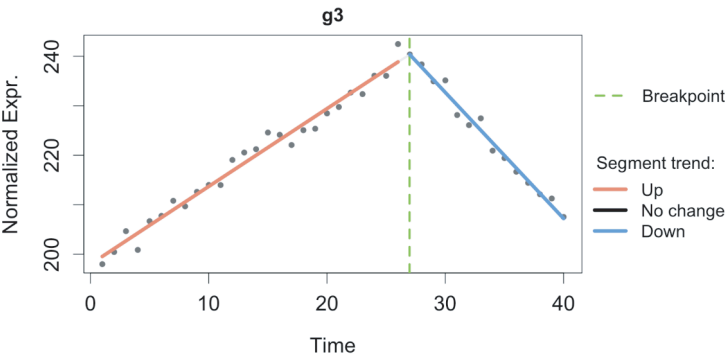
Upload File

To visualize gene trends one by one, use the 'Visualize genes' tab.
To obtain a list of genes according to a specific pattern use the 'Obtain gene patterns' tab.

Visualize genes

Obtain gene patterns

Select a row in the table to update the trend visualization.



Show 10 entries

Search:

Feature	AdjustedR2	Segment1 Trend	Segment2 Trend	Segment3 Trend	Breakpoint1	Breakpoint2
g3	0.979	1	-1		26.977	
g1	0.978	-1	0		13.765	
g28	0.975	0	1		19.007	
g20	0.974	-1	0		12.8	
g15	0.973	1	-1		26.318	

Figure S1: Screenshot of Trendy R/Shiny application The trendy() function outputs an .RData object which can be uploaded to the Trendy R/Shiny application available within the Trendy R package via the function trendyShiny(). Users can explore the data, fitted trends, and easily extract lists of genes with specific patterns of interest.

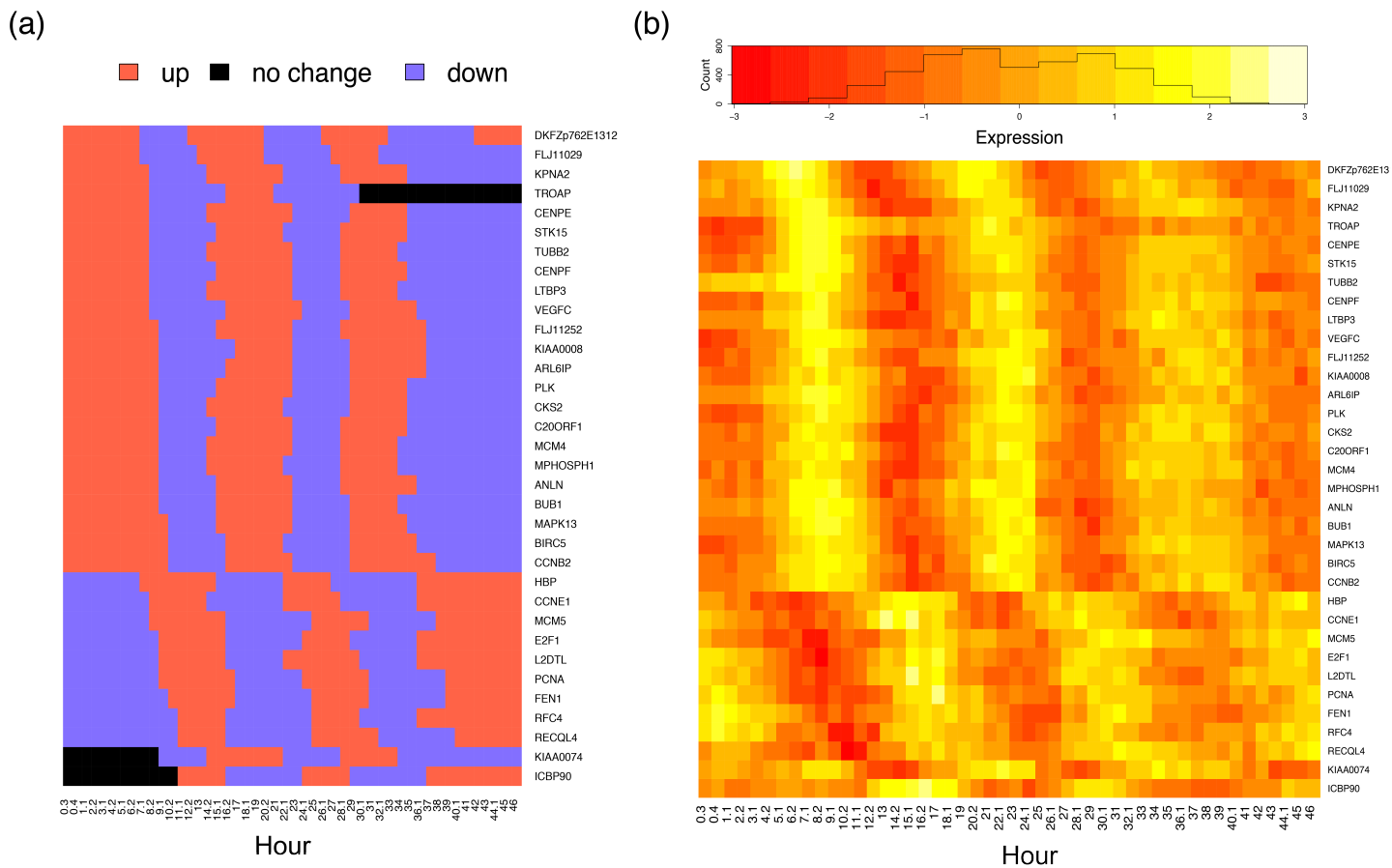
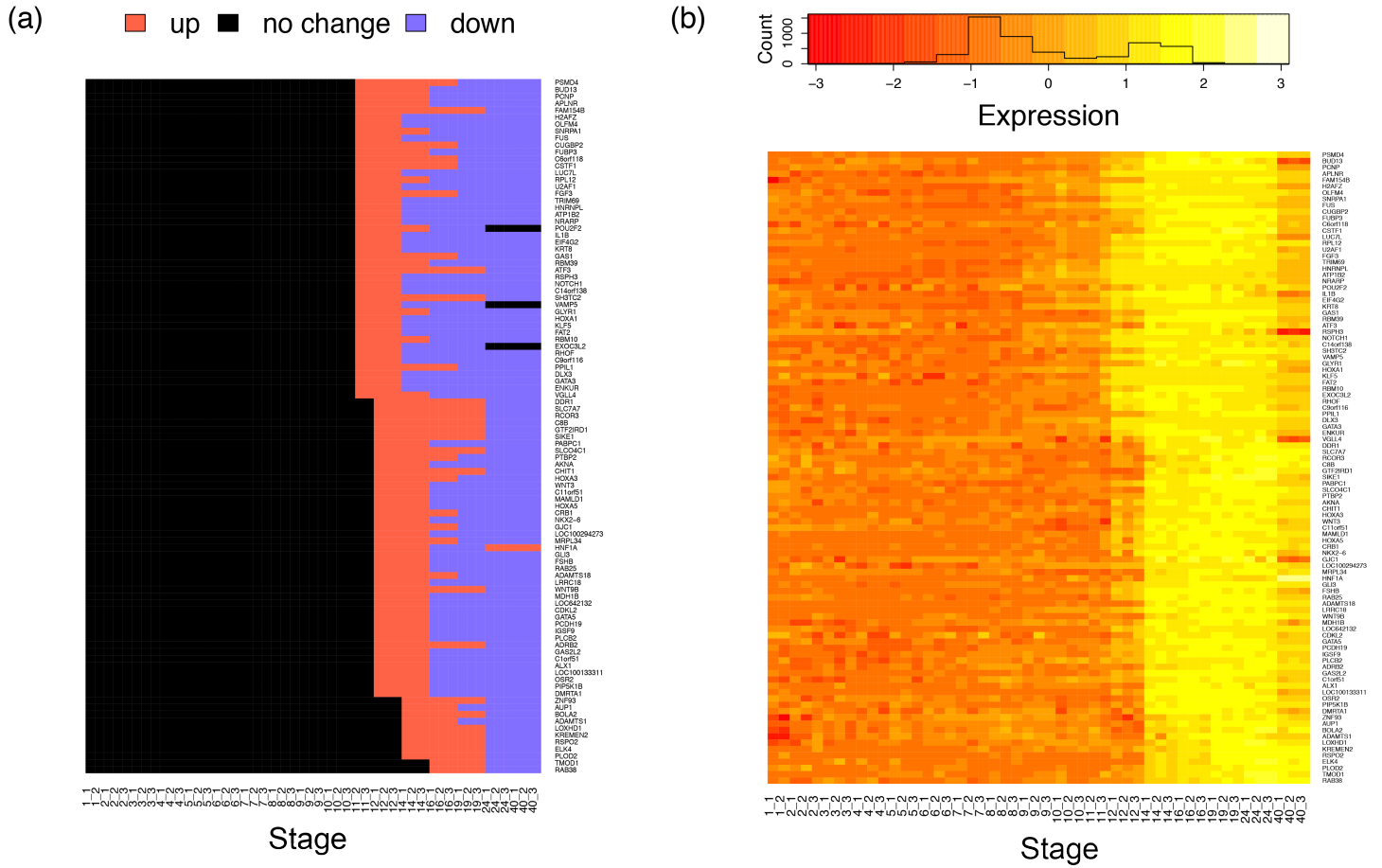
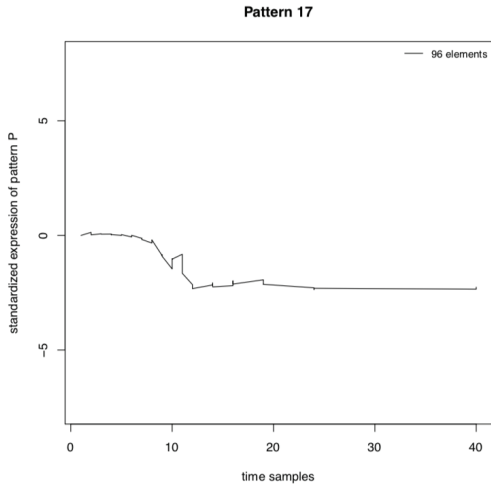


Figure S2: Expression dynamics for cycling genes in Whitfield dataset Panel (a) shows the fitted trends for the 34 top genes having pattern “up-down-up-down” and Panel (b) is an expression heatmap for the same set of genes.



FunPat Output Example:



Element_ID	Score	Cluster	t1	t2
MTMR6	8.25E-05	17	-0.002788929	0.131623627
MPPED2	9.91E-05	17	-0.002788929	0.131623627
ZNF347	0.00076847	17	-0.002788929	0.131623627

Trendy Output Example:

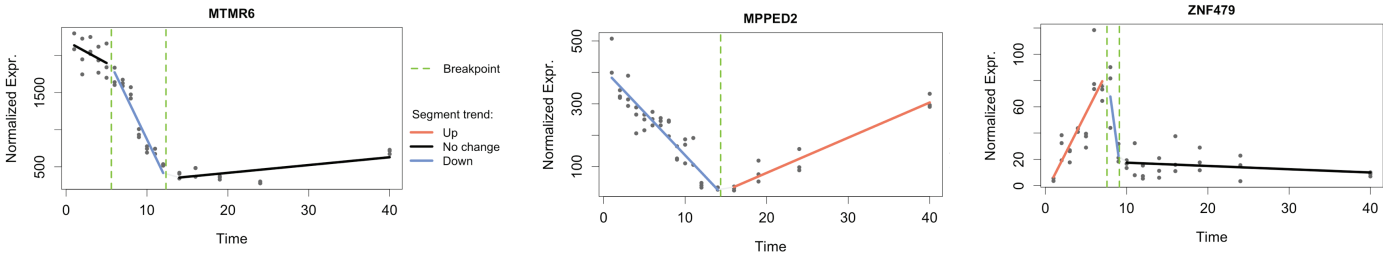


Figure S4: Comparison to FunPat The output of FunPat for one example cluster is shown. Specifically, Pattern 17 found in the Axolotl data contains a total of 96 genes. Three of those genes are shown with their respective Trendy fits.