Supplementary Document for the Manuscript entitled "Estimating Time-Varying Directed Gene Regulation Networks"

Method	ρ	Mean	Standard Deviation
Locally sparse	1%	6.8%	1.0%
	5%	8.4%	2.9%
Smoothing spline	1%	100.0%	0.0%
	5%	100.0%	0.0%
Linear fSCAD	1%	24.3%	2.6%
	5%	30.5%	5.0%
Group Lasso	1%	17.9%	13.3%
	5%	16.0%	5.4%

Table S1: The mean and standard deviation of the specificities using four methods in 100 simulation replicates. Here ρ represents the noise-to-signal ratio in the simulated data.

Method	ρ	Mean	Standard Deviation
Locally Sparse	1%	0.23	0.15
	5%	0.96	1.27
Group Lasso	1%	6.72	0.60
	5%	6.80	2.97
AR1	1%	8.66	0.62
	5%	8.70	3.00
Constant Expression	1%	568.80	1.07
	5%	568.45	5.37

Table S2: The mean and standard deviation of squared prediction errors using four methods in 100 simulation replicates. Here ρ represents the noise-to-signal ratio in the simulated data.

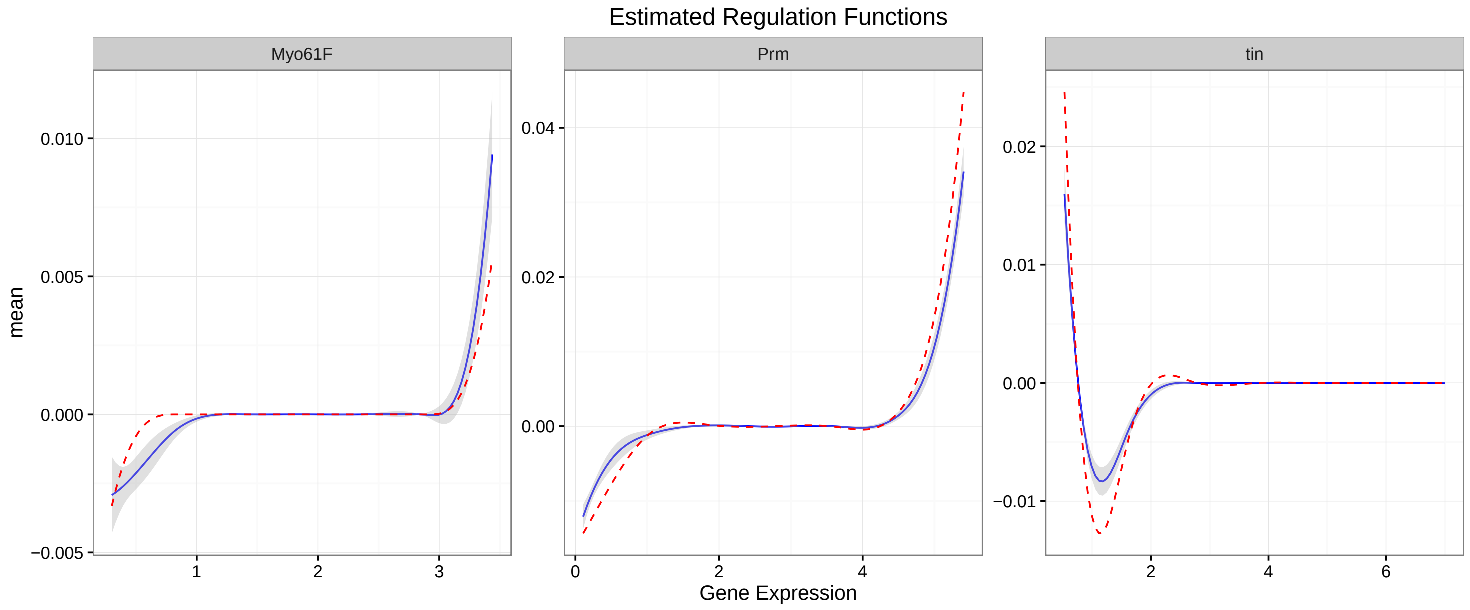

Figure S1: Estimated regulation functions from the simulated data with the noise-to-signal ratio of the simulated data $\rho = 1\%$ using the locally sparse method. The dashed red and solid blue lines represent the true regulation functions and the mean of the estimated regulation functions in 100 simulation replicates. The grey bands denote the pointwise 95% confidence interval of the estimated regulation functions.

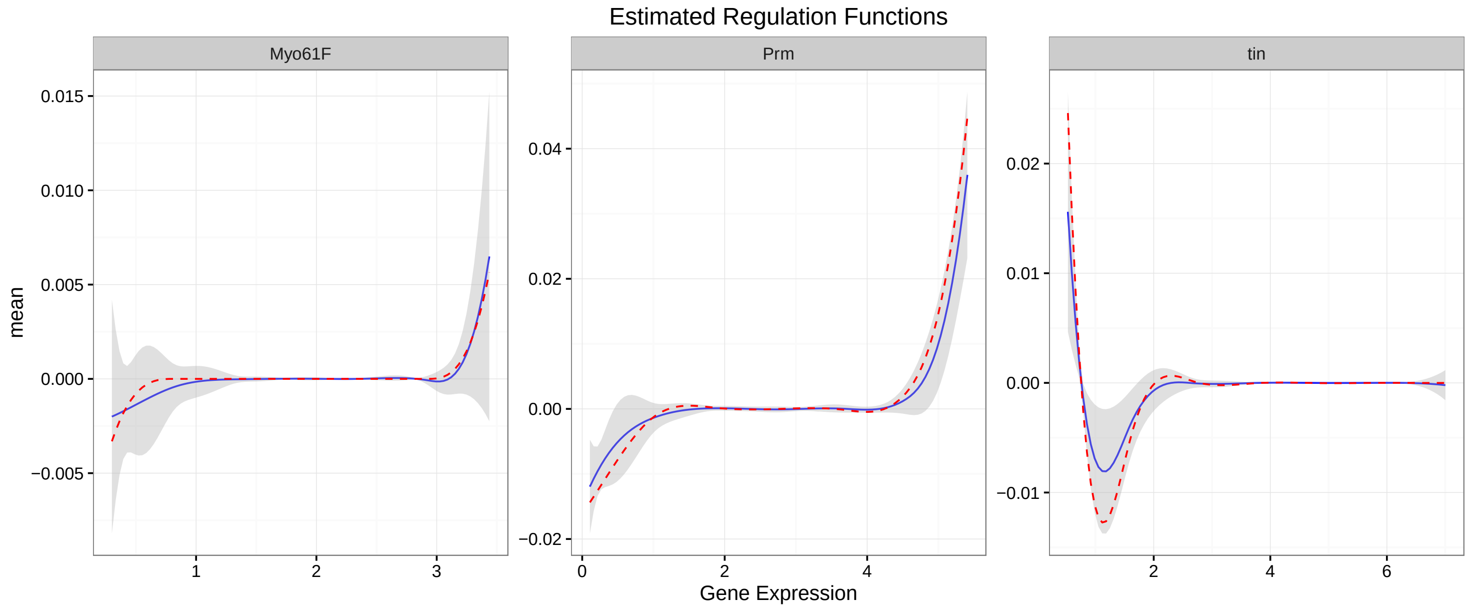

Figure S2: Estimated regulation functions from the simulated data with the noise-to-signal ratio of the simulated data $\rho = 5\%$ using the locally sparse method. The dashed red and solid blue lines represent the true regulation functions and the mean of the estimated regulation functions in 100 simulation replicates. The grey bands denote the pointwise 95% confidence interval of the estimated regulation functions.