Supporting information for Tudor *et al.* (2002) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.242566899

Table 3. Mean (SD in parentheses) power and false-positive rate per gene (false pos) across the four MG-U74A experiments examined in this paper when analyzed with different statistical methods

Method:	**t test**		**Neighborhood**		**PaGE**		**t test, BY corrected**		**WY**		**SAM**	
Fold-change:	**1.5**	**2**	**1.5**	**2**	**1.5**	**2**	**1.5**	**2**	**1.5**	**2**	**1.5**	**2**
Power: mean (SD)	0.96 (0.03)	1 (0.01)	0.71 (0.17)	0.9 (0.11)	0.3 (0.09)	0.3 (0.13)	0.66 (0.18)	0.88 (0.1)	0.61 (0.16)	0.85 (0.08)	0.97 (0.04)	1 (0.01)
False pos: mean (SD)	2.4e-4 (1.1e-4)	1.1e-5 (4.6e-6)	1.9e-5 (1.5e-5)	0 (0)	3.8e-4 (3.0e-4)	1.1e-5 (1.3e-5)	5.0e-6 (4.1e-6)	0 (0)	1.4e-5 (2.4e-5)	1.5e-6 (3.0e-6)	5.9e-4 (2.6e-4)	3.3e-5 (1.5e-5)

The methods used are as follows: *t* test (parametric unpaired two-tailed *t* test with $P < 0.05$), Neighborhood (signal-to-noise neighborhood analysis (2), $P < 0.05$), PaGE (patterns of gene expression, (3), confidence >50%), *t* test, BY corrected (Benjamini-Yekutieli method for false discovery rate control (6), $q < 0.05$), WY (Westfall-Young method for family-wise error rate control (4, 5), $P < 0.05$), SAM (VERA/SAM error model (7), $P < 0.05$ assuming distribution is $\sim\chi^2$(1 d.o.f)), SAM, BY corrected (same as SAM, but Benjamini-Yekutieli multiple testing correction applied to *P* values generated by SAM algorithm). The false-positive rates are calculated by comparing the number of false positives to the size of the entire dataset. It should be pointed out that these power simulations provide an upper limit to the power since they do not take into account the ability of steps upstream of the data analysis (e.g., cRNA amplification, scanning, etc.) to reliably detect small fold-changes. In addition, the sample size analysis did not take into consideration data analysis steps upstream of statistical analysis such as scaling and outlier detection/elimination which would be expected to vary with samples size.