Table 4. Estimated power and false positive rate per gene for several different sizes of samples (e.g. $N = 4$ means a simulated experiment containing two control and two experimental samples)

	Sample size	*t* test		SAM		*t* test, BY corrected		SAM, BY corrected		method fold change
		1.5	2	1.5	2	1.5	2	1.5	2	
power: mean (sd)	N = 4	0.68 (0.09)	0.82 (0.06)	0.85 (0.07)	0.98 (0.03)	0.11 (0.03)	0.11 (0.03)	0.34 (0.16)	0.88 (0.09)	
false pos: mean (sd)		6.6e-4 (8.3e-5)	2.2e-5 (9.8e-6)	4.9e-3 (5.6e-4)	3.7e-4 (1.8e-4)	3.7e-4 (1.3e-4)	1.2e-5 (7.3e-6)	7.1e-4 (4.7e-4)	1.9e-4 (6.1e-5)	
power: mean (sd)	N = 8	0.94 (0.04)	0.98 (0.02)	0.98 (0.02)	1 (0)	0.23 (0.1)	0.5 (0.1)	0.77 (0.13)	0.96 (0.05)	
false pos: mean (sd)		4.1e-4 (2.2e-4)	2.4e-5 (1.7e-5)	1.6e-3 (4.9e-4)	1.1e-4 (5.4e-5)	4.4e-5 (5.1e-5)	4.9e-6 (9.8e-6)	7.1e-4 (2.1e-4)	5.4e-5 (2.9e-5)	
power: mean (sd)	N = 12	0.97 (0.02)	1 (0.01)	0.98 (0.01)	0.99 (0.01)	0.51 (0.07)	0.81 (0.08)	0.86 (0.06)	0.97 (0.04)	
false pos: mean (sd)		2.5e-4 (8.1e-5)	1.2e-5 (9.8e-5)	7.1e-4 (2.0e-4)	3.7e-4 (2.7e-5)	1.7e-5 (2.4e-5)	2.4e-6 (2.4e-6)	3.6e-4 (1.5e-4)	3.4e-5 (9.8e-6)	

The methods used are the same as those for Table 3.