

Supplementary Materials: Comparison of
small n statistical tests of differential
expression applied to microarrays
Additional File 4

Carl Murie, Owen Woody, Anna Y. Lee , Robert Nadon

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- 1 pAUC scores: Calculated using a 5% false positive rate**

Table 1: Rankings from best to worst (1 to 5) of average pAUC scores (using a threshold of five percent of the false positives) of the six tests of differential expression. The average pAUC for each score is in parentheses. Differential tests are t-stat: t-statistic, LPE: LPE z-statistic, CyberT: CyberT t-statistic, limma: limma moderated t-statistic, BRB: BRB t-statistic, FC: Fold Change. The lmGene package was used to apply the Loess normalization and glog transformation to the cDNA data. BC indicates that background correction was applied to the data before normalization.

		t-stat	CyberT	LPE	BRB	limma	FC	median pAUC
HG133A	MAS 5.0	5 (.67)	1 (.72)	4 (.68)	2.5 (.69)	2.5 (.69)	6 (.18)	.69
	RMA	6 (.73)	3.5 (.84)	3.5 (.84)	3.5 (.84)	3.5 (.84)	1 (.86)	.84
	gcRMA	6 (.75)	2.5 (.84)	2.5 (.84)	4 (.79)	5 (.78)	1 (.86)	.82
	dChip	4.5 (.78)	3 (.80)	6 (.77)	1.5 (.81)	1.5 (.81)	4.5 (.78)	.79
	LMGene	6 (.73)	3.5 (.84)	3.5 (.84)	1.5 (.86)	5 (.82)	1.5 (.84)	.84
	VSN	6 (.73)	4 (.83)	4 (.83)	1.5 (.85)	4 (.83)	1.5 (.85)	.83
	avg. rank	5.6	2.9	3.9	2.4	3.6	2.6	
HG95	MAS 5.0	3 (.61)	1 (.73)	2 (.64)	4.5 (.46)	4.5 (.46)	6 (.10)	.54
	RMA	6 (.72)	1.5 (.87)	1.5 (.87)	3.5 (.85)	3.5 (.85)	5 (.84)	.85
	gcRMA	6 (.87)	1 (.95)	3 (.93)	3 (.93)	3 (.93)	5 (.92)	.93
	dChip	6 (.76)	3 (.84)	4 (.82)	1.5 (.86)	1.5 (.86)	5 (.81)	.83
	LMGene	6 (.76)	2 (.87)	1 (.89)	4 (.86)	4 (.86)	4 (.86)	.86
	VSN	6 (.61)	5 (.79)	3.5 (.82)	1.5 (.83)	3.5 (.82)	1.5 (.83)	.82
	avg. rank	5.5	2.3	2.5	3.0	3.3	4.4	
cDNA liver vs liver	Loess	5.5 (.97)	2.5 (.98)	2.5 (.98)	2.5 (.98)	2.5 (.98)	5.5 (.97)	.98
	Loess(BC)	5 (.96)	1 (.99)	2 (.98)	3.5 (.97)	3.5 (.97)	6 (.66)	.97
	glog Loess	6 (.94)	3 (.98)	3 (.98)	3 (.98)	3 (.98)	3 (.98)	.98
	glog Loess(BC)	6 (.93)	1.5 (.98)	1.5 (.98)	3.5 (.97)	3.5 (.97)	5 (.94)	.97
	VSN	6 (.95)	2.5 (.98)	2.5 (.98)	2.5 (.98)	2.5 (.98)	5(.97)	.98
	avg. rank	5.7	2.1	2.3	3.0	3.0	4.9	
cDNA liver vs pool	Loess	6 (.07)	5 (.08)	1 (.26)	3.5 (.09)	3.5 (.09)	2 (.17)	.09
	Loess(BC)	2(.03)	5 (.02)	5 (.02)	2 (.03)	2 (.03)	5 (.02)	.03
	glog Loess	1 (.16))	4 (.13)	2 (.14)	4 (.13)	4 (.13)	6 (.08)	.13
	glog Loess(BC)	1.5 (.15)	1.5 (.15)	3 (.14)	4.5 (.09)	4.5 (.09)	6 (.06)	.12
	VSN	3 (.10)	4 (.09)	5.5 (.05)	1.5 (.11)	1.5 (.11)	5.5 (.05)	.10
	avg. rank	2.7	3.9	3.3	3.1	3.1	4.9	
Simulated	Common	6 (.32)	3 (.54)	5 (.46)	3 (.54)	1 (.55)	3 (.54)	.54
	Local	6 (.16)	4 (.28)	5 (.21)	2 (.61)	1 (.62)	3 (.31)	.30
	Inverse	5 (.40)	3 (.53)	6 (.39)	1.5 (.54)	1.5 (.54)	4 (.48)	.50
	Gamma							
	avg. rank	5.7	3.3	5.3	2.2	1.1	3.3	
	total avg. rank	5.0	2.9	3.5	2.7	2.8	4.0	