

Supplemental material for “A Benchmark for Affymetrix GeneChip Expression Measures” by Cope, L.M., Irizarry, R.A., Jaffee, H., Wu, Z., and Speed, T.P.

**Table 1.** Updated Affymetrix’s spike-in Latin square design. New spike-in probesets are shown in bold. All probeset IDs end in `_at`, but we have removed it to save space. The design consists of 16 probesets spiked-in in 14 array groups. The concentration in array group *A* are 0, 0.25, 0.5, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, and 1024 picoMolar. Each subsequent array group rotates the spike-in concentrations; i.e. array group *B* begins with 0.25 picoMolar and ends at 0 picoMolar, on up to the last array group, which begins with 1024 picoMolar and ends with 512 picoMolar. There are three replicates in each array group except *C* for which there are 2 and the two array groups denoted with *M, N, O, P* and *Q, R, S, T* for which we have 12 replicates.

Array type	Probeset Identifier													
	37777 407	684	1597	38734	39058	36311	36889	1024	36202 <b>546</b>	36085	40322	<b>33818</b>	1091	1708
<i>A</i>	0	0.25	0.5	1	2	4	8	16	32	64	128	256	512	1024
<i>B</i>	0.25	0.5	1	2	4	8	16	32	64	128	256	512	1024	0
<i>C</i>	0.5	1	2	4	8	16	32	64	128	256	512	1024	0	0.25
<i>D</i>	1	2	4	8	16	32	64	128	256	512	1024	0	0.25	0.5
<i>E</i>	2	4	8	16	32	64	128	256	512	1024	0	0.25	0.5	1
<i>F</i>	4	8	16	32	64	128	256	512	1024	0	0.25	0.5	1	2
<i>G</i>	8	16	32	64	128	256	512	1024	0	0.25	0.5	1	2	4
<i>H</i>	16	32	64	128	256	512	1024	0	0.25	0.5	1	2	4	8
<i>I</i>	32	64	128	256	512	1024	0	0.25	0.5	1	2	4	8	16
<i>J</i>	64	128	256	512	1024	0	0.25	0.5	1	2	4	8	16	32
<i>K</i>	128	256	512	1024	0	0.25	0.5	1	2	4	8	16	32	64
<i>L</i>	256	512	1024	0	0.25	0.5	1	2	4	8	16	32	64	128
<i>M, N, O, P</i>	512	1024	0	0.25	0.5	1	2	4	8	16	32	64	128	256
<i>Q, R, S, T</i>	1024	0	0.25	0.5	1	2	4	8	16	32	64	128	256	512

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**Fig. 1.** Using the replicates from the dilution data, we calculate the mean predicted variance for each gene, tissue and dilution by squaring the estimated standard error. The usual sample variance  $s_{tdg}^2 = \sum_r (y_{tdrg} - y_{td\cdot g})^2 / 4$  are calculated as well. These boxplots are of the log ratios of the predicted and observed variance.

