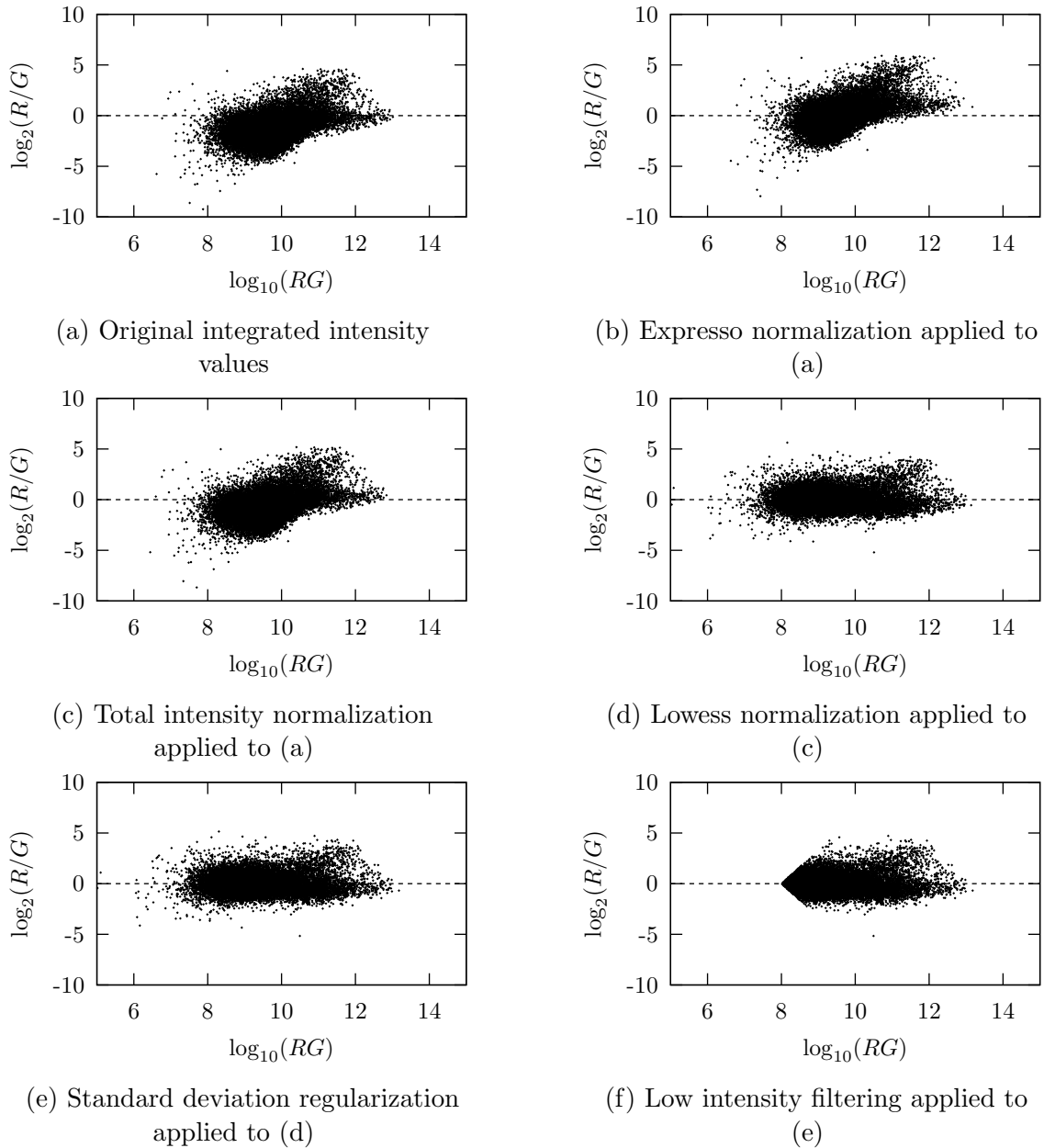


## RI Plots

**Additional File 1.** Supplement to BMC Bioinformatics paper *The statistics of identifying differentially expressed genes in *Expresso* and *TM4*: a comparison*, by Allan A. Sioson, Shrinivasrao P. Mane, Pinghua Li, Wei Sha, Lenwood S. Heath, Hans J. Bohnert, and Ruth Grene, 2006.



**Supplementary Figure 1:** RI-plots illustrating specific intensity-dependent dye bias as microarray data is processed. (a) The original data (IIV) for the Experiment 1, WT plant samples, and second replicate microarray. The intensity-dependent dye bias is apparent in the RI-plot of this

unnormalized data set. (b) Espresso normalization ( $IIV_E$ , where E signifies Espresso normalization) applied to IIV. This shifts the plot up so that the points are evenly distributed above and below the  $x$ -axis, though it does not correct the intensity-dependent bias. (c) MIDAS total intensity normalization ( $IIV_T$ ) applied to IIV. This makes little difference in the RI-plot and certainly does not correct the intensity-dependent bias. (d) MIDAS lowess normalization ( $IIV_{TL}$ ) applied to  $IIV_T$ . Visually, this appears to remove some of the intensity-dependent bias, though the result does not appear as good as that in Figure 2 of Quackenbush [14]. (e) MIDAS standard deviation regularization ( $IIV_{TLS}$ ) applied to  $IIV_{TL}$ . There is little effect. (f) MIDAS low intensity filtering ( $IIV_{TLSF}$ ) applied to  $IIV_{TLS}$ . This eliminates spots with  $RG$  values below 10,000. Again, there is little effect.