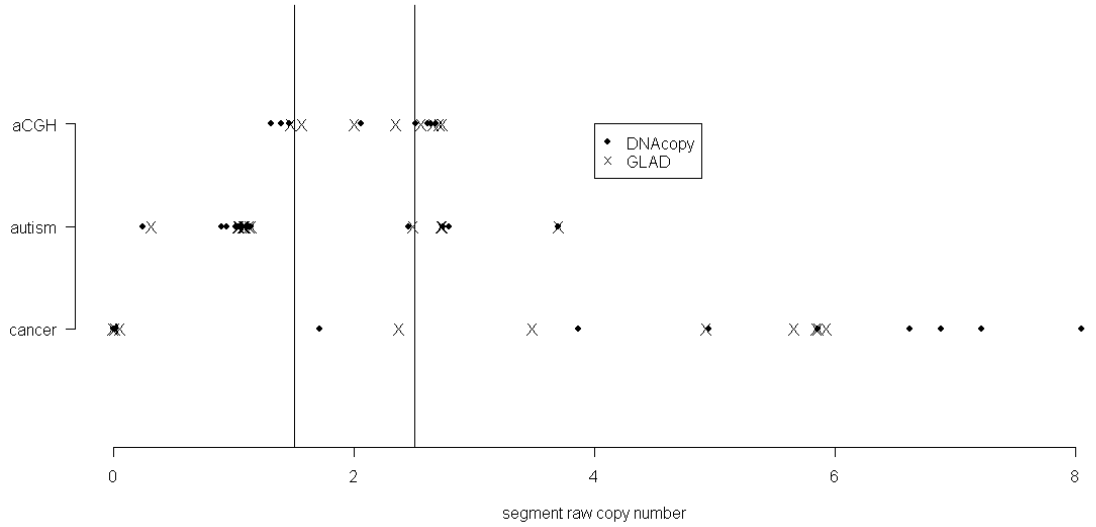
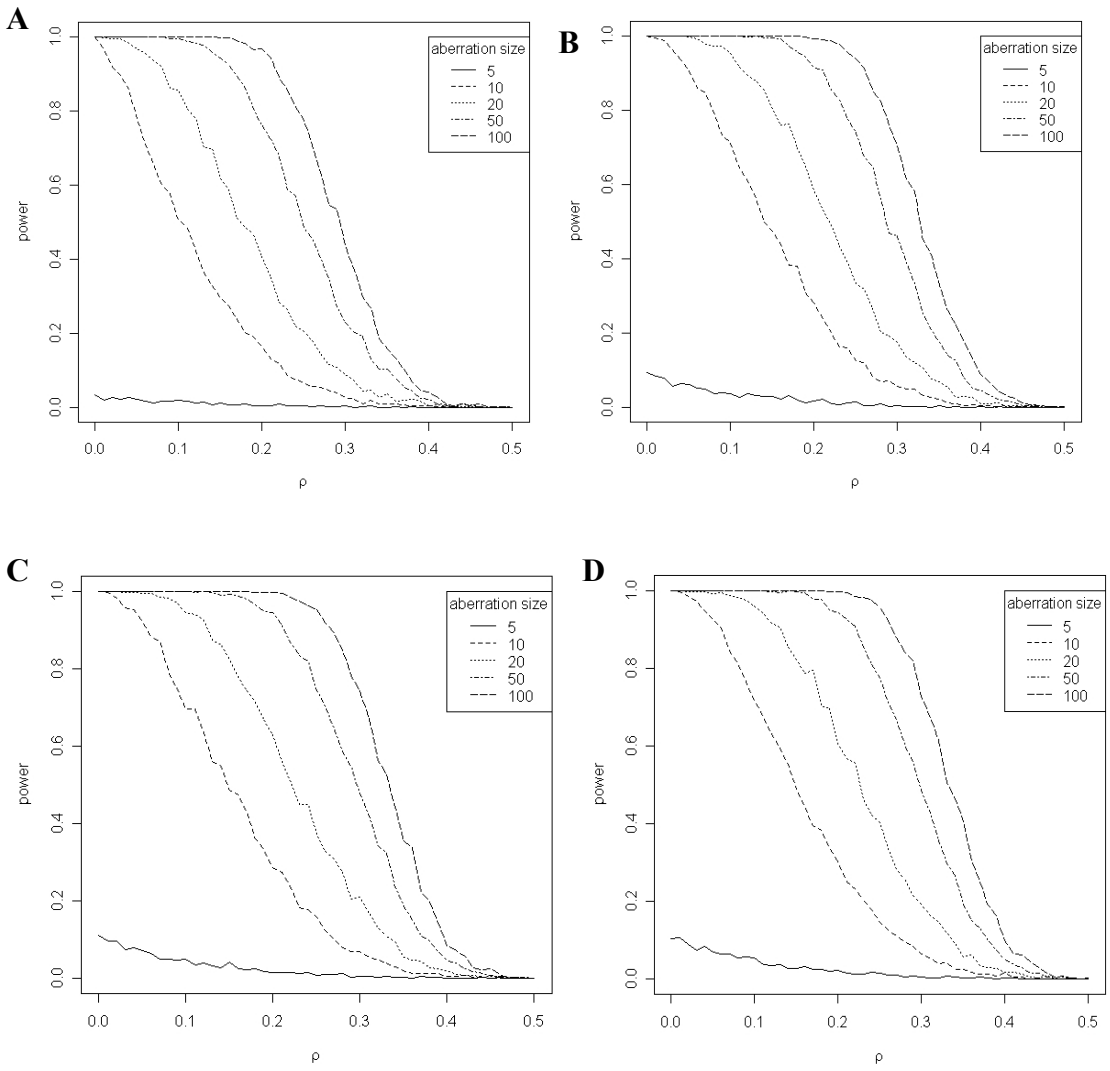
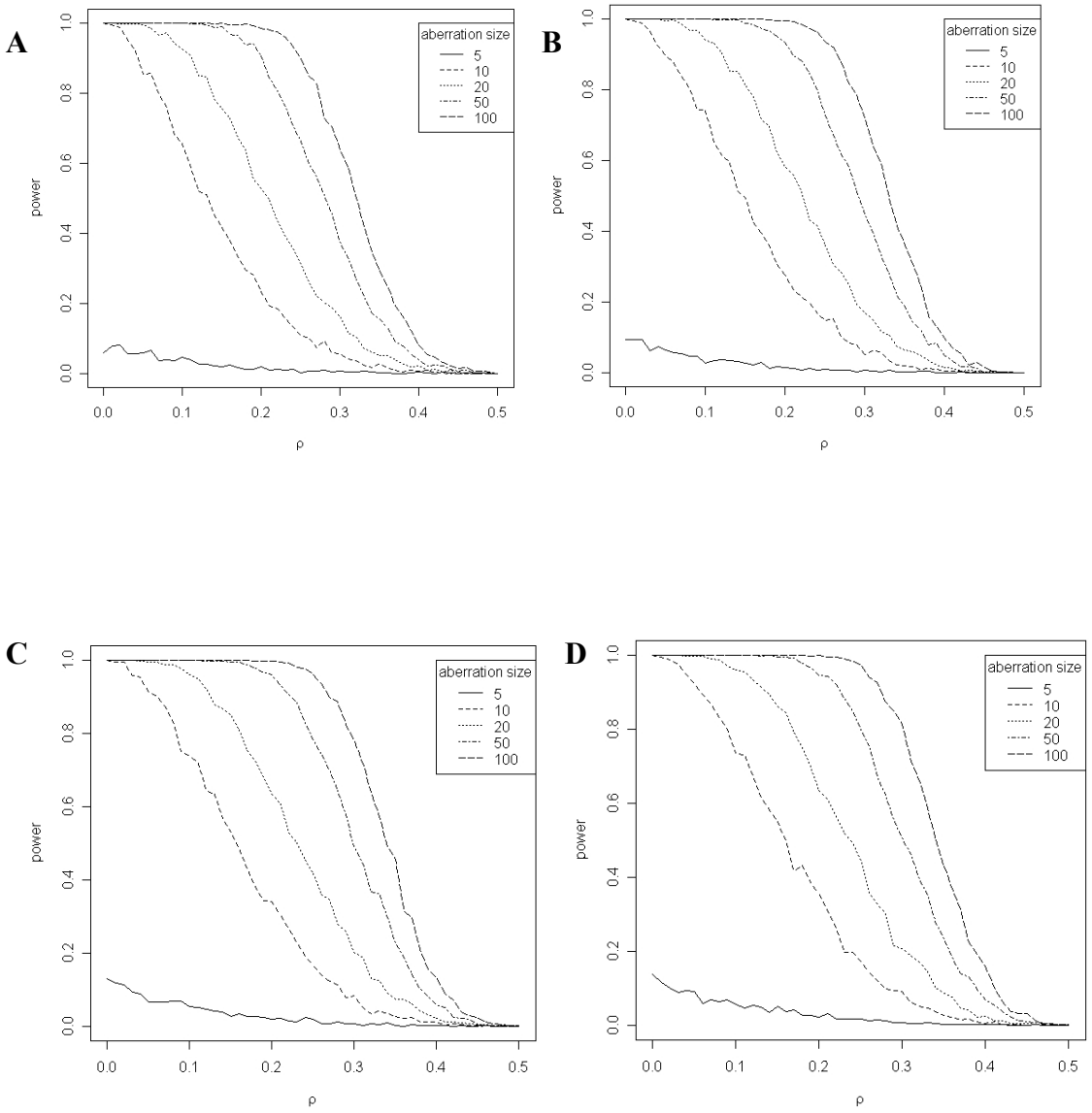


Supplementary Figure 1: Results of applying DNAcopy and GLAD to raw data. For each of the three data sets reported in Tables 1, 2, and 3 (cancer, autism, and aCGH, respectively), we segmented the raw copy number data using DNAcopy (Venkantraman and Olshen, 2007) and GLAD (Hupé et al., 2004). Plotted here are the mean (for DNAcopy) and median (for GLAD) values of the segment most concordant with the CNV call reported by the producers of the data sets. Vertical lines are drawn at 1.5 and 2.5. Log_2 ratios from aCGH data was converted to raw copy number using the formula: raw copy number = $2 \times 2^{\log 2 \text{ ratio}}$.



Supplementary Figure 2. Power simulation study for *RS* statistic.
Power (using a threshold that would yield an expected two false positives per sample, genome-wide across 400,000 markers) to detect deletions in a sample as part of a study with sample sizes (A) 10, (B) 50, (C) 100, and (D) 200. Aberration sizes are given in terms of number of markers, and ρ is a measure of probe fidelity (see Methods).



Supplementary Figure 3. Power simulation study for min*RS* statistic.
Power (using a threshold that would yield an expected two false positives per sample, genome-wide across 400,000 markers) to detect deletions in a sample as part of a study with sample sizes (A) 10, (B) 50, (C) 100, and (D) 200. Aberration sizes are given in terms of number of markers, and ρ is a measure of probe fidelity (see Methods).