

Supplemental note.

Global patterns of gene expression: comparison of two mutant lines.

Three indices were used to compare expression profiles of the two mutant lines. First, the direction of transcriptional changes in knock-out compared to wild type animals was estimated for each gene regardless of the degree or statistical significance of this change and then compared between the two mutant lines. Frequencies of common transcriptional changes were then compared to 50% chance using a χ^2 test. About 56-58% (for cortex and cerebellum respectively) of all genes examined were regulated in the same direction for the two mutant lines. These frequencies deviated from chance with a high level of statistical significance in both brain structures ($p < 0.001$). Second, we compared genes with statistically detectable differential expression ($p < 0.05$ detected by a two-tail t-test in each data set). A χ^2 test revealed that the number of significant genes common for the two mutant lines was greater than expected by chance (both brain regions $p < 0.01$). Finally, we compared directions of statistically significant transcriptional changes ($p < 0.05$ detected by a two-tail t-test) detected in both mutant lines. About 80-90% of these transcripts were regulated similarly in both lines, again showing significant deviation from chance (p values for both brain regions < 0.01). Thus, all three indices indicated similar global patterns of transcriptional regulation following a deletion of GABAA receptor $\alpha 1$ subunit gene in two independently created knock-out lines.