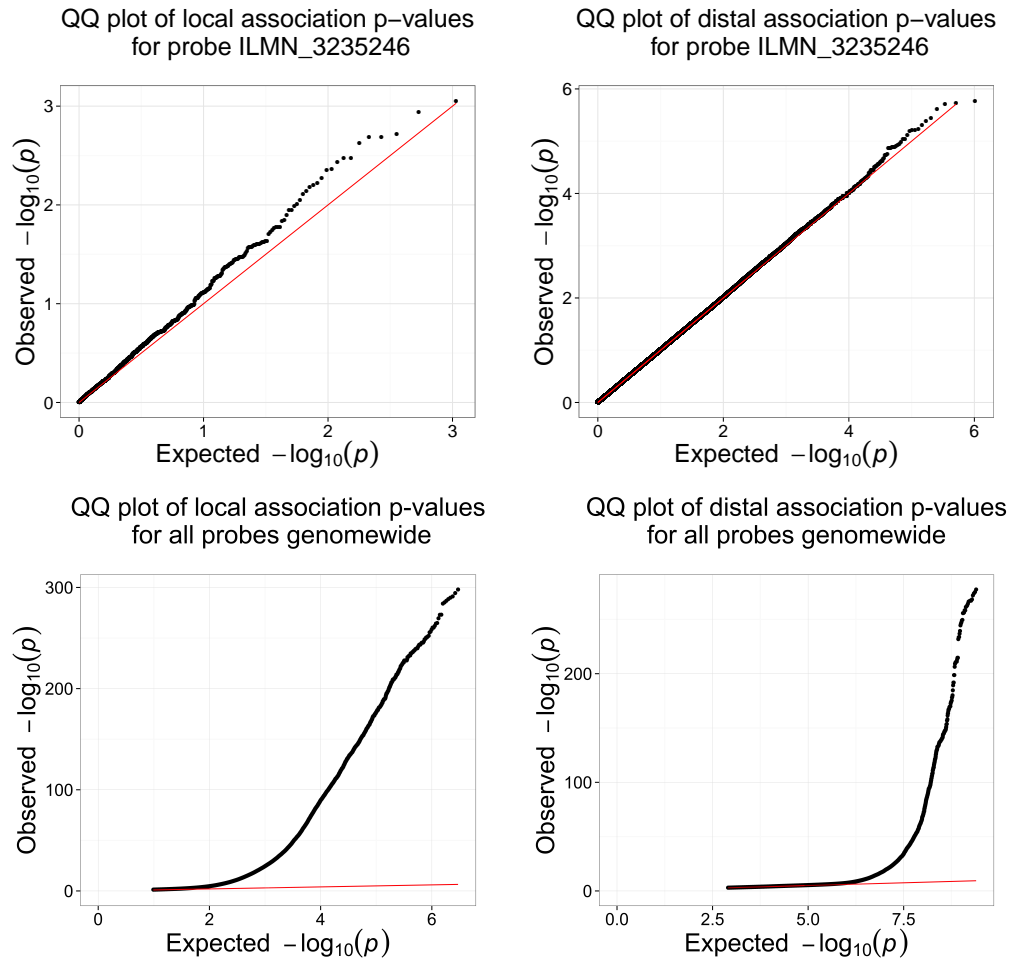


## Supporting Information.

**Characterization of expression quantitative trait loci in pedigrees from Colombia and Costa Rica ascertained for bipolar disorder.** C. B. Peterson, S. K. Service, A. J. Jasinska, F. Gao, I. Zelaya, T. M. Teshiba, C. E. Bearden, R. M. Cantor, V. I. Reus, G. Macaya, C. López-Jaramillo, M. Bogomolov, Y. Benjamini, E. Eskin, G. Coppola, N. B. Freimer, and C. Sabatti.



**S2 Fig. QQ plots.** QQ plots for local vs. distal association  $p$ -values obtained using Mendel for a randomly chosen probe and for all 34,030 probes genome-wide. Due to the large number of tests, in the genome-wide setting only  $p$ -values for local association  $< 0.05$  for distal association  $< 0.001$  were saved. For the local and distal association analyses across all probes, 7 and 13  $p$ -values respectively were recorded as exactly 0 due to limited precision in Mendel; these are omitted from the plots. The QQ plot for local association for a specific probe (upper left) shows enrichment of small  $p$ -values vs. what would be expected under the null ( $\lambda_{GC} = 1.15$ ); this deviation makes sense, however, given that most genes are subject to some form of local regulation. The QQ plot for distal association for a specific probe (upper right) shows that the distribution of test statistics is as expected under the null ( $\lambda_{GC} = 1.01$ ). The genome-wide distributions (lower left and right) suggest that there are a large number of non-null hypotheses for both local and distal regulation; the deviation from expected values takes place much earlier in the local regulation plot, however, suggesting that the proportion of non-null hypotheses is indeed higher among local vs. distal hypotheses.