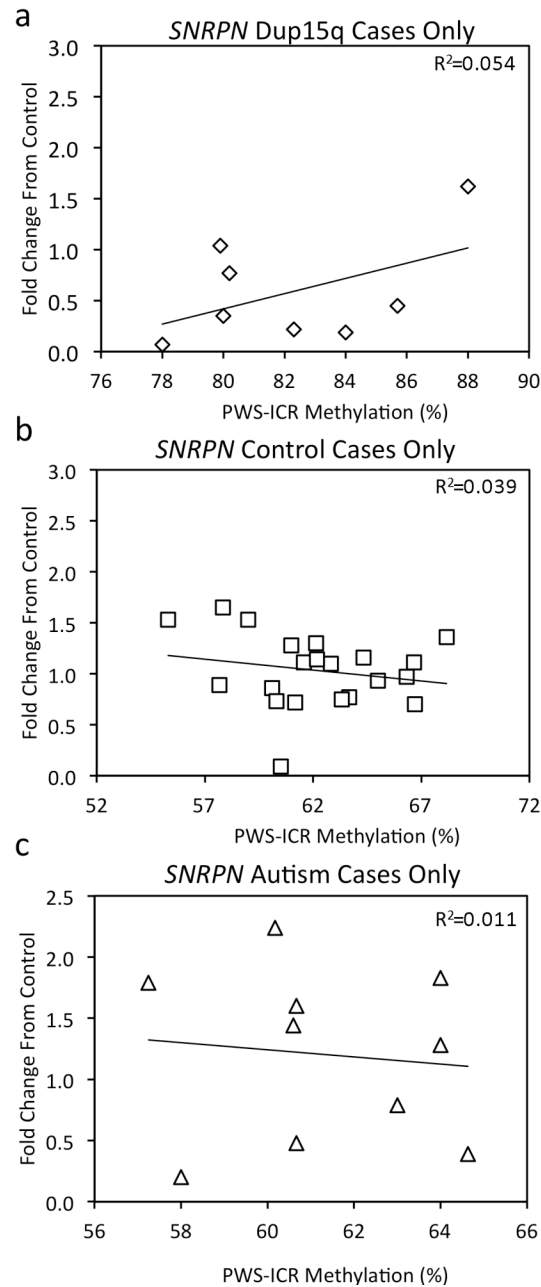




Correlation analyses of PWS-IC methylation and *SNRPN* transcript levels. The analysis was performed as explained in Figure 6d except only the Dup15q (a) controls (b) or autism (c) samples were correlated with PWS-ICR methylation. There was no significant correlation between percent maternal allele specific methylation at the PWS-IC and levels of *SNRPN* when separately grouping the cases. Significance was calculated by a simple regression analysis.