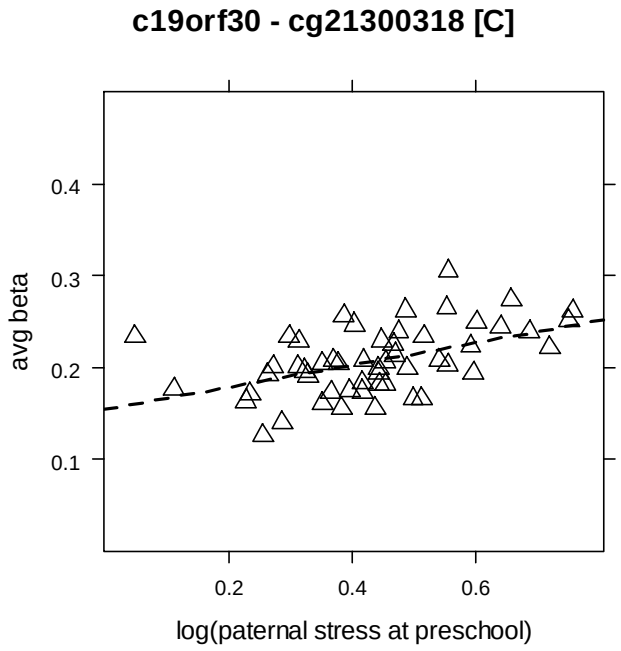
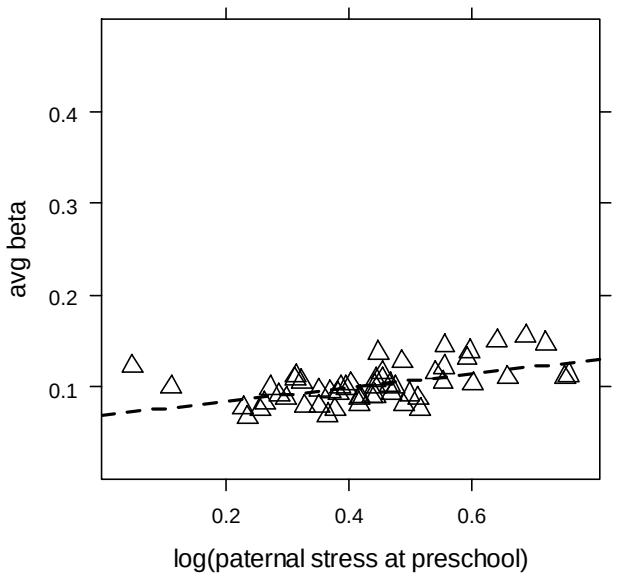
Sup. Fig.2:DNA methylation at two CpG sites in the first exon of the c19orf30 gene was correlated with paternal stress during preschool in girls only. In the set of 5 high confidence sites whose DNA methylation increased with paternal stress at preschool and had more than 5% change in DNA methylation, two CpG loci belonged to the c19orf30 gene, which is of unknown function. Specifically, these were cg21300318 (*rho*= .52, 8.7% DNA methylation change, slope = .12 (95% CI = .06 - .18),FDR = 0%) and cg20893022 (*rho* = .55, 5.3% DNA methylation change, slope = .07 (95% CI = .04 - .11),FDR = 0%). No statistically significant association was found in the full group or boys-only analysis. The average beta scale was restricted to show values between 0 - 0.5 rather than the full range of 0-1.0. Girls are represented as triangles with the regression line being wide-dashed. None of the other 4 CpG sites from the c19orf30 gene were associated with parental stress as judged by our criteria (FDR < 20%).




c19orf30 - cg20893022 [C]
avg beta
0.1
0.2
0.3
0.4
0.2
0.4
0.6
log(paternal stress at preschool)