The majority of CNVs were seen in the telomeres and centromeres as predicted, however, many differences were identified in the discordant twin pairs not seen in either the concordant for AP or concordant control pairs. When compared to the Affymetrix CNV standard, 98% of the novel CNVs found in the discordant pairs were associated with gains in CNVs (in some cases very large 22454 KB). A one-way ANOVA revealed a trend suggesting that the mean number of total CNVs was not equal across MZ groups ($F(2,94) = 2.98, p = .055$). Collapsing across MZ groups, number of CNVs did not significantly differ as a function of affection status ($F(1,95) = .016, p = .90$). Prior to analyses, a square root transformation was performed on total CNV data in order to correct for positive skew.

Individual CNVs associated with specific genes will be presented. These CNVs were found in association with both known and novel candidate regions for attention problems.

In a sample of 50 MZ pairs and their parents we will determine the concordance and discordance of inherited CNVs in cross twin and cross standard (using Affymetrix cross baseline data set) comparisons in twins who both have longitudinal persistent CBCL attention problems (AP) ($N= 17$), in pairs in which neither have attention problems ($N= 22$) and in discordant pairs in which one member of the pair has AP ($N= 11$). Parental CNV scans will be used to determine whether or not conservation of CNVs across pedigree is found.