FIGURE S9.—Comparison of array analysis methods. The 090 SNP array data were analyzed for constitutional CNVs in parallel using VAMP (blue bars) and PennCNV (red bars) (WANG et al. 2007). PennCNV uses a hidden Markov model for CNV detection, an approach very different than VAMP. The graph shows the number of autosomal CNVs detected by each method according to the best percent match to CNVs called by the other method. Consistent with the notion that array event calling is principally a function of the sensitivity threshold, most CNVs showed either no match or a near-perfect match to the other method. There were many more VAMP-specific calls than PennCNV-specific calls so the latter cannot account for the large number of mate-pair-specific CNVs. Similar observations were made when VAMP was compared to the Illumina CNV calling algorithm (not shown).