Supplemental Figure 3: Number of consistently differential ATAC-seq and ChIP-seq peaks across sample pairs. ATAC-seq and ChIP-seq peaks were called for all cases and controls. For each matched pair of samples, a MAnorm analysis identified shared peaks, control-specific peaks and AD-specific peaks (see Methods). Bar plots indicate the distributions of the number of control-specific (left) or case-specific peaks (right) for ATAC-seq (A,B) and ChIP-seq (C,D) . For example, there are approximately 10 ATAC-seq peaks in the genome that are control-specific in 4 of the 6 matched pairs (see panel A).