Supplement Figure 2. Case/control pairwise differential ATAC-seq analysis and transcription factor motif enrichment. (**Left plots**). For each of the six matched sample pairs, differential ATAC-seq peak analysis was performed. ATAC-seq peaks that are equally strong between case and controls (“shared”), significantly stronger in the control (“control-specific”), or significantly stronger in the case (“AD-specific”) were identified using MAnorm (see Methods). The percent of peaks falling within each category is indicated to the left of each heatmap. Heatmap color indicates the normalized strength of the ATAC-seq signal. (**Right plots**). Transcription factor motif enrichment analysis was performed for each sample pair (see Methods). Each dot represents a transcription factor motif. The X-axis and Y-axis indicate the p-value of enrichment within control-specific and AD-specific ATAC-seq peaks, respectively. Motif family color key is provided at the top of each plot.