SUPPLEMENTAL FIGURES

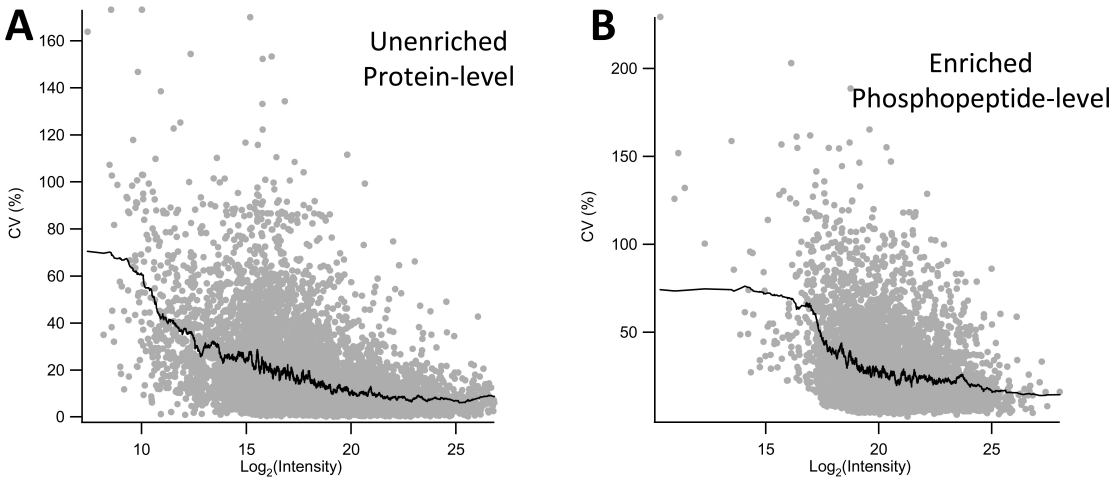

Figure S1. Moving average used in the calculations of Cohen's d for significance. Biological variation for each protein (A) and phosphopeptide (B) is plotted in gray. A 100-point moving average is plotted in black. This value was used for subsequent Cohen's d calculations.

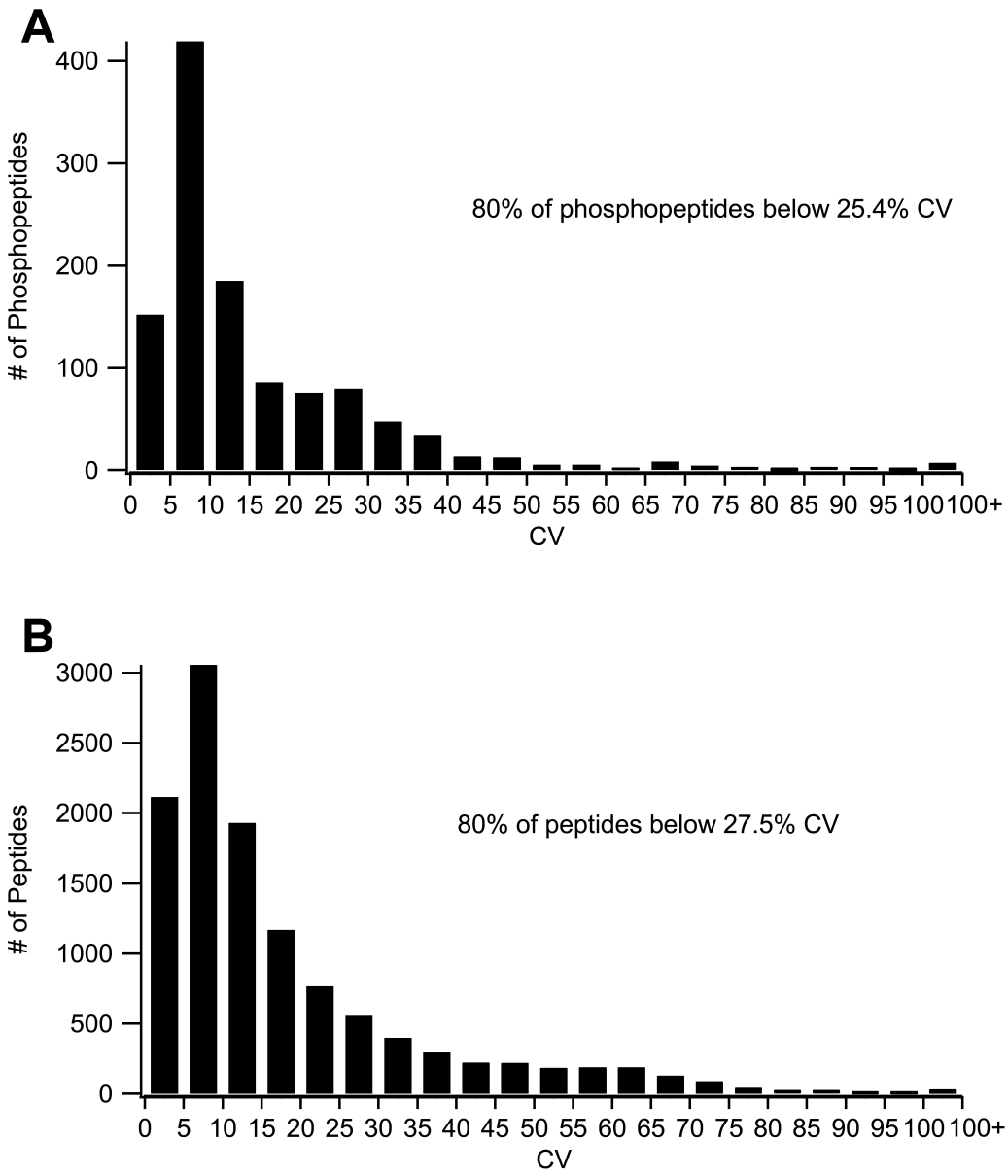

Figure S2. Distribution of Coefficient of variation (CV) values of identified phosphopeptides (A) and peptides (B) across the LC/MS analyses of pooled QC samples throughout each study.

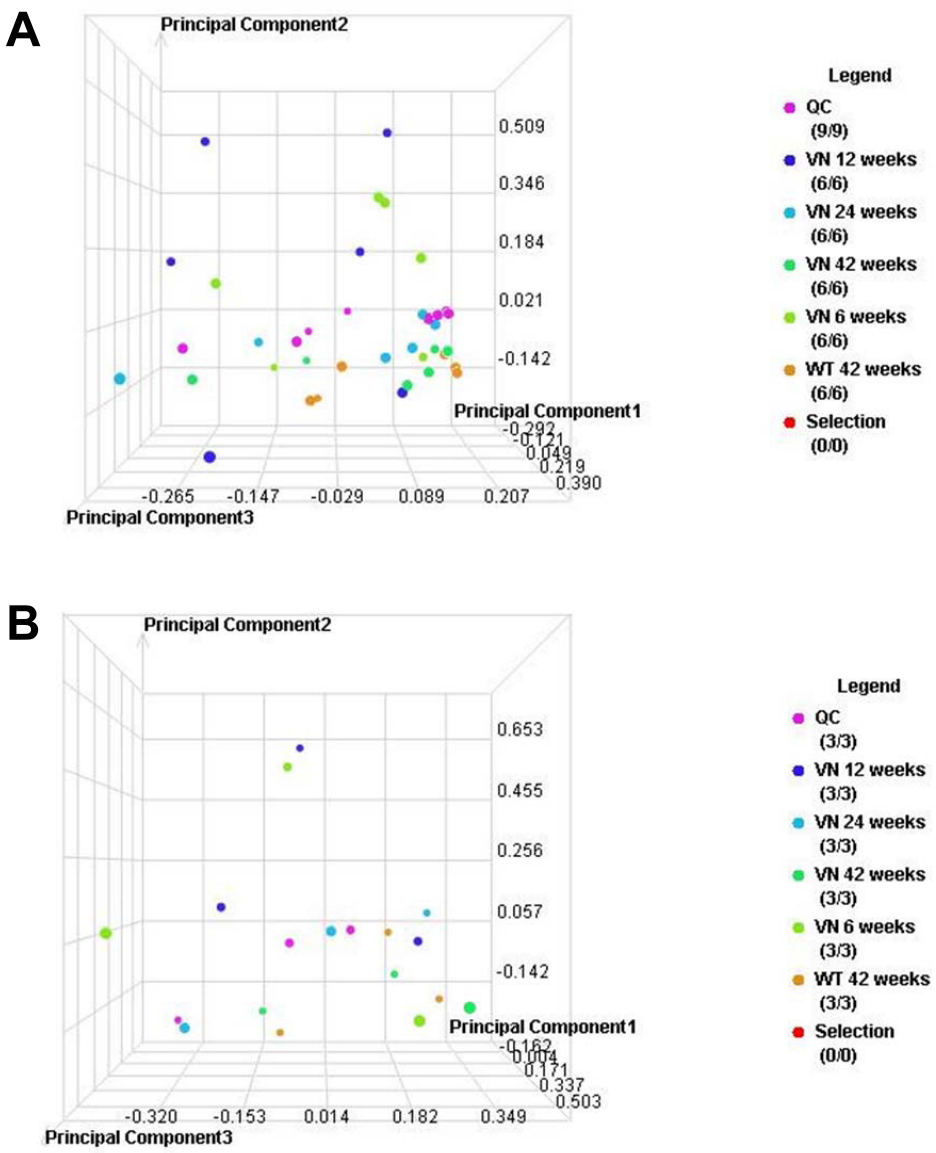

Figure S3. Principle component analysis using identified phosphopeptides (A) and isotope groups (B) in the enriched and unenriched analysis, respectively. This demonstrates a random distribution of the biological samples and does not indicate the presence of any potential outliers.

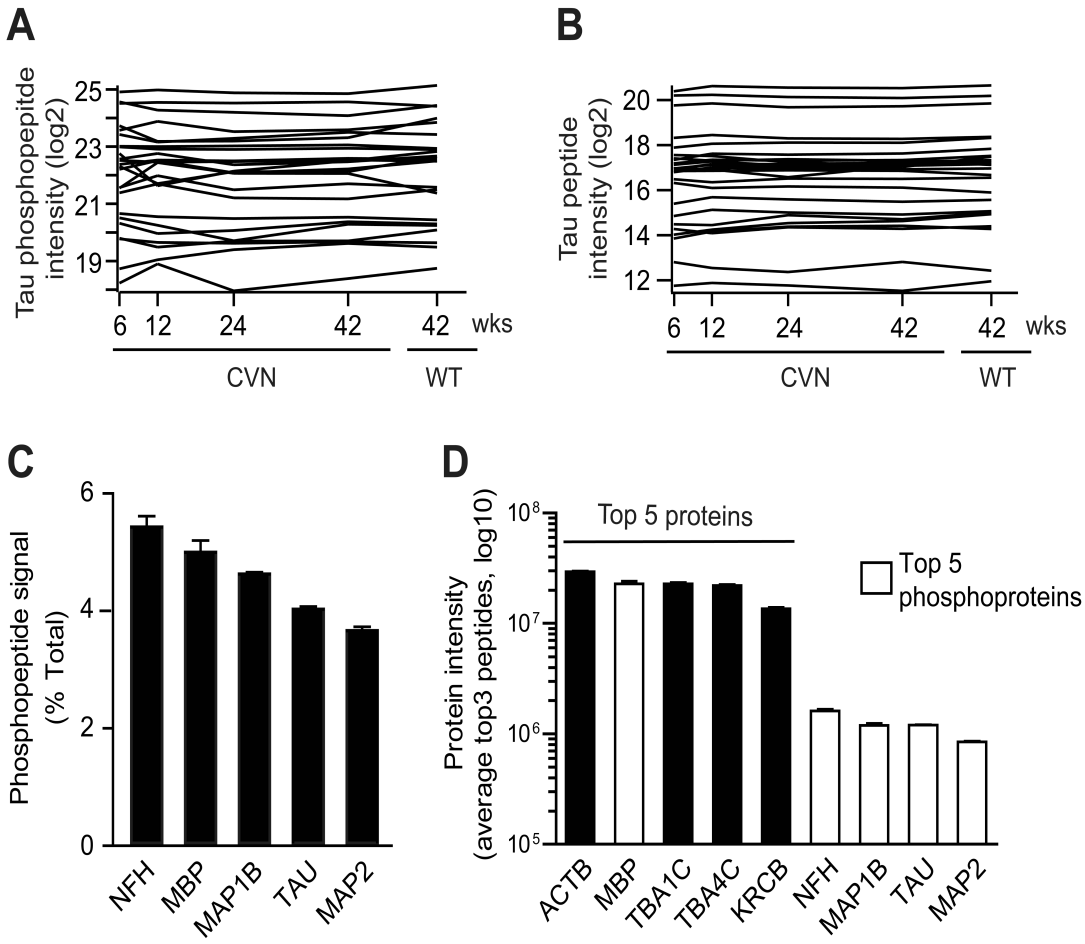

Figure S4. Phosphorylation of Tau in CVN-AD versus wild-type mice. A, Intensities of all tau phosphopeptides in the enriched samples from the proteomic data. B, Intensities of all tau peptides from the un-enriched proteomic data. C, The five most abundant phosphoproteins in terms of the percent of total phosphopeptide signal. D, The five most abundant proteins in terms of intensity, along with the top five phosphoproteins. Data in C and D are mean ± S.E.M. (n=18 analyses, un-enriched; n=39 analyses, phospho-enriched).