

Study	Analysis	Samples	Statistical Approach
1 – Description: To utilize standard differential gene expression analysis and WGCNA to explore transcriptome changes associated with neurocognitive impairment and antiretroviral regimen, and to further interrogate extant transcriptome data using WGCNA	Differential gene expression analysis of NCI and CPE	15 HIV+ brains	Pearson Correlation of individual gene expression levels with NCI (GDS score) and CPE. Those with highest correlations ($>.70$ or $<-.70$) were then examined using GNCPro, a bioinformatics tool.
	Enrichment analysis of genes significantly correlated with NCI or CPE	15 HIV+ brains	Enrichment analyses were performed on all differentially expressed genes ($p<0.05$) using Expression Analysis Systematic Explorer [33].
	WGCNA of groups previously defined by Gelman et al, 2012	6 HIV- 4 HIV+ 7 HAND 4 HAND/HIVE	ANOVA used to compare module eigengenes across four groups
	WGCNA of NCI and CPE	15 HIV+ brains	Correlated modules discovered through WGCNA with NCI and CPE
2–Description: To identify genes and pathways associated with NCI in both HIV and Alzheimer’s disease.	Identify genes that are commonly associated with NCI in HIV and Alzheimer’s disease	15 HIV+ brains 8 HIV-/normal controls 20 HIV-/AD	In each sample (HIV+ and control/AD), correlated all gene probes with NCI. Impairment genes were defined as those whose expression either increased ($R>0.25$) or decreased ($R<-0.25$) with impairment.