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Summary information on specimens, neuropathology, and quantification of protein and isoprostane

The following information is available for download in tabular form as comma-separated values (csv) files:

- [De-identified clinical information \(including Alzheimer's disease, dementia, and TBI diagnoses\) for all donors included in the study.](#)
- [Values for Luminex protein quantification, isoprostane quantification and immunohistochemistry pathology metrics for tissue specimens.](#)
- [Brief description of stains used and values provided in the files listed above.](#)

RNA sequencing data

RNA sequencing datasets from 107 brains, including 377 samples from cortical grey (parietal and temporal) and white matter (parietal) and hippocampus.

The following files enable in-depth analysis of the available RNA-Seq data:

- [Normalized gene-level FPKM values for all samples \(as displayed in the RNA-Seq page heatmap\). \(zip\)](#)
- [URLs to data files for each sample, including un-normalized gene-level FPKM and TPM values, anonymized BAM files, and the corresponding bigWig file. \(csv\)](#)
- [Reference genome .gtf file used to process the RNA-Seq data. \(zip\)](#)

Supplemental Data

- [Subject and sampling weights calculated as described in the Weighted Analyses document. \(csv\)](#)