NCRAD Biomarker Assay Lab

An Update to the Alzheimer's Disease Research Centers

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Keeping the End in Mind – Biomarker Assay Lab Goal

 Advance neurodegenerative disease research where standardization of processes and delivery of reliable and consistent research biomarker results can be achieved



Currently Available Assays

- Quanterix Simoa HD-X
 - Nf-Light Advantage Kit
 - pTau 181 v2 Advantage Kit
 - Neurology 2 Plex B Advantage Kit (NfL, GFAP)
 - Neurology 4 Plex E Advantage Kit (NfL, GFAP, Abeta 40, Abeta 42)
- Fujirebio Lumipulse
 - Lumipulse G β-Amyloid 1-42 Plasma Assay (January 2023)
 - Lumipulse G β-Amyloid 1-40 Plasma Assay (January 2023)
 - Lumipulse G pTau 181 Plasma Assay (January 2023)
- AlzPATH (Simoa HD-X)
 - pTau217 (July 2023)







ADCFB Initiative

- Participation
 - 24 ADRCs are providing samples prospectively
 - ~80 samples received per week
- Data Returns
 - Assays: N4PE (NfL, GFAP, Abeta 40, Abeta 42) and pTau 181
 - October 2022
 - 1846 samples
 - 16 Centers
 - April 2023 (just occurred)
 - 1023 samples
 - 19 Centers
- Data is returned via NACC
 - Working with NACC and the ADRC Biomarker Steering Committee to develop data return template compatible with the NACC "Data Front Door"
 - This will enable broader sharing of plasma biomarker data in the future and integrated with other data streams

ADRC Site PTID Specimen Barcode Specimen Quantity Unit of Measure LAB ID Lab Study ID Analysis Date INST ID Assay Platform Assay Name Assay Lot No. Avg NFL Conc Avg GFAP Conc Avg Abeta 40 Conc Avg Abeta 42 Conc Unit of Measure Notes

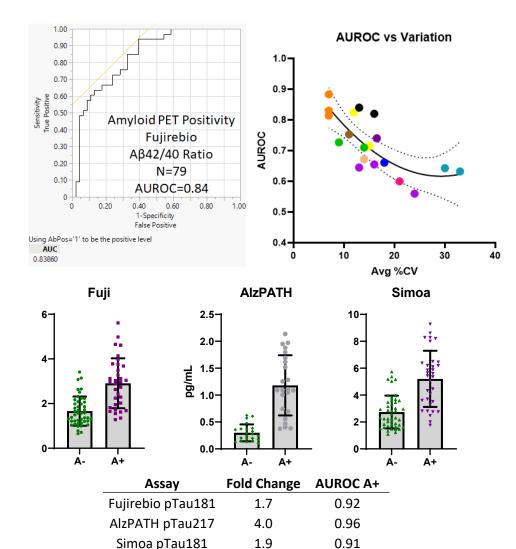




Changing Assays in ADCFB Initiative

Process of changing Assays for ADCFB

- First Example: Changing from A β 42/40 in N4PE with A β 42/40 on Lumipulse
 - Reason: improved analytical precision, improved AUROC
 - Bridge (analysis of some samples >=200 on both platforms)
 - Share harmonization methods within data description files
- Second Example: Changing from pTau181 to pTau217
 - Reason: Improved fold change and AUROC for amyloid
 - Bridge (analysis of some samples >=200 on both platforms)
 - Share harmonization methods within data description files







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