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**Title: Plasma phosphorylated tau 217 detects amyloid- $\beta$  in neuronal synuclein disease**

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## Abstract

Multiple proteinopathies commonly coexist in neurodegenerative diseases, making it essential to evaluate plasma biomarker performance in these complex diseases. While plasma biomarkers accurately detect amyloid- $\beta$  pathology in Alzheimer's disease (AD), their performance is unknown in neuronal synuclein disease (NSD). We aimed to determine the accuracy of plasma pTau217, pTau181, A $\beta$ 42/40, GFAP, and NfL to detect amyloid- $\beta$  in NSD, then establish and validate cut points for the most promising marker. We included 253 participants (180 discovery; 73 validation). In the discovery cohort, NSD status was defined by CSF  $\alpha$ -synuclein seed amplification assay and amyloid- $\beta$  status by CSF A $\beta$ 42/40. Participants included individuals with clinical Lewy body disease (LBD), AD, and cognitively unimpaired. Validation cohorts consisted of clinically diagnosed LBD participants. In the discovery cohort, plasma pTau217, pTau181, A $\beta$ 42/40, and GFAP significantly differed by amyloid- $\beta$  status regardless of NSD status, while NfL was highest in NSD+/A $\beta$ + participants. Among all biomarkers, plasma pTau217 showed the best diagnostic performance (AUC=0.92, 95% CI=0.81-0.98). Applying plasma pTau217 cut points to pre-screen clinically diagnosed LBD participants reduced the need for confirmatory amyloid- $\beta$  PET or CSF in 41-56%. These findings support plasma pTau217 as a minimally-invasive tool for identifying pathological amyloid- $\beta$  in neuronal synucleinopathies with mixed Alzheimer's disease pathology.

## Introduction

In neurodegenerative diseases of aging, coexistence of pathological amyloid- $\beta$ , tau, and  $\alpha$ -synuclein is common and contributes to clinical heterogeneity, faster disease progression, and variable treatment response. Advances in biomarker technology now enable for accurate, scalable, and cost-effective detection of some of these proteinopathies. As these biomarkers move into clinical practice, it is essential to understand their performance in the context of mixed neurodegenerative diseases.

Lewy body disease (LBD), which includes Parkinson's disease (PD) and dementia with Lewy bodies (DLB), is characterized by the abnormal deposition of  $\alpha$ -synuclein ( $\alpha$ Syn). This diagnostic pathologic feature can be detected in cerebrospinal fluid (CSF) using the seed amplification assay (SAA), supporting the biologically-based definition of neuronal synuclein disease (NSD)(1). Concomitant amyloid- $\beta$  pathology is frequently found in both NSD and clinically diagnosed PD and DLB(2-7), and is associated with worse clinical outcomes(2), earlier dementia onset(8), faster cognitive decline(9,10) and shorter survival(11). These findings underscore the

importance of identifying NSD individuals with co-occurring amyloid- $\beta$  pathology, and the potential value of testing anti-amyloid therapies in this population.

CSF and positron emission tomography (PET) imaging A $\beta$  biomarkers are the gold standard for detecting amyloid- $\beta$  pathology in Alzheimer's disease (AD). However blood-based A $\beta$  biomarkers have emerged as promising tools with accuracy comparable to CSF and PET(12,13). Among them, plasma phosphorylated tau at threonine 217 (pTau217) has consistently outperformed other plasma biomarkers such as pTau181 and the A $\beta$ 42/40 ratio for detecting amyloid- $\beta$  in AD(12,14,15). Combinations of these markers, either with each other or with markers of neuroinflammation (i.e. glial fibrillary acidic protein, GFAP) and neurodegeneration (i.e. neurofilament light chain, NfL), have shown lower performance than pTau217 alone(12). Based on this evidence, pTau217 is now recommended for clinical and research use(16).

Multiple studies have evaluated plasma pTau181(10,15,17–27), pTau217(10,21,28,29), A $\beta$ 42/40 ratio(17,19,20,25), GFAP(17,19,20,25,26,30,31), and NfL(17,19,20,22,23,25–28) in clinically diagnosed LBD participants. However, their diagnostic accuracy for detecting amyloid- $\beta$  has not been evaluated in biologically defined NSD. This distinction is critical as A $\beta$  plasma biomarkers are being considered as a routine component of NSD staging(1), particularly since prior studies show A $\beta$  biomarker cut points can differ between “mixed” NSD plus AD pathology and “pure” AD pathology cases(32–34). Evaluating plasma biomarkers in NSD provides a closer approximation to underlying pathology than clinical diagnosis, which often does not predict the presence of Lewy bodies at autopsy(35–37).

As plasma biomarkers enter clinical use, their interpretation must align with the intended use population, as emphasized by the FDA-NIH Biomarker Working Group(38). In NSD, accurate interpretation of plasma biomarkers is crucial for their appropriate use as screening tools for patient selection and stratification in clinical trials, particularly as drug development begins to address mixed pathologies.

In this cross-sectional study, we assessed whether plasma pTau217, pTau181, A $\beta$ 42/40, GFAP, and NfL accurately detect amyloid- $\beta$  in individuals with biologically defined NSD. We calculated plasma biomarker cut points using one- and two-reference standard approaches in a discovery cohort, then validated these cut points in two independent clinical LBD cohorts to assess their generalizability. By establishing and validating plasma biomarker cut points for detecting amyloid- $\beta$  in NSD, this study addresses a critical gap in biomarker interpretation that currently limits their use in mixed pathology settings.

## Results

### Discovery cohort characteristics

This cross-sectional study included participants from two cohorts: Stanford University (SU) and the Sant Pau Initiative on Neurodegeneration (SPIN)(39). Participants were divided into one discovery cohort and two clinical validation cohorts. The discovery cohort consisted exclusively of SU participants, while SPIN participants contributed to one of the clinical validation cohorts. The discovery cohort included 180 SU participants with CSF  $\alpha$ Syn SAA and A $\beta$ 42/40 data: 86 cognitively unimpaired (CU), 30 LBD cognitively unimpaired (LBD-CU), 30 LBD cognitively impaired (LBD-CI), and 34 AD. CSF biomarkers were used to determine  $\alpha$ Syn status (NSD+/-) and A $\beta$  status (A $\beta$ +/-). Participants were classified into four biologically defined groups: NSD-/A $\beta$ - (n=69), NSD-/A $\beta$ + (n=44), NSD+/A $\beta$ - (n=39), and NSD+/A $\beta$ + (n=28). Median age was 69 years (min, max: 50-87), with 83 females (46.1%) and 97 males (53.9%). The NSD-/A $\beta$ - group was significantly younger than the NSD-/A $\beta$ + group ( $P=0.029$ ). Otherwise, the groups were similar in age, sex, and years of education (Table 1).

### Plasma biomarker levels stratified by CSF NSD and A $\beta$ status

In the SU discovery cohort, plasma levels of pTau217, pTau181, and GFAP were significantly higher, while A $\beta$ 42/40 was significantly lower in the A $\beta$ <sup>+</sup> compared to the A $\beta$ <sup>-</sup> groups, regardless of NSD status (all  $P < 0.001$ , Table 1 and Figure 1A-D). Plasma NfL levels were significantly higher in the NSD<sup>+</sup>/A $\beta$ <sup>+</sup> group than in all other groups (vs. NSD<sup>-</sup>/A $\beta$ <sup>-</sup>  $P < 0.001$ ; vs. NSD<sup>-</sup>/A $\beta$ <sup>+</sup>  $P = 0.045$ ; vs. NSD<sup>+</sup>/A $\beta$ <sup>-</sup>  $P = 0.012$ ), and significantly higher in the NSD<sup>-</sup>/A $\beta$ <sup>+</sup> than in the NSD<sup>-</sup>/A $\beta$ <sup>-</sup> group ( $P = 0.014$ ) (Figure 1E).

Visual inspection identified one outlier in the NSD<sup>+</sup>/A $\beta$ <sup>+</sup> group with a pTau181 level of 10.43 pg/mL (7.9 SDs above the mean). Removing this outlier in a sensitivity analysis did not change the results. In another sensitivity analysis, we excluded symptomatic participants (those with cognitive and/or motor symptoms) from the NSD<sup>-</sup>/A $\beta$ <sup>-</sup> group and asymptomatic participants from the NSD<sup>-</sup>/A $\beta$ <sup>+</sup>, NSD<sup>+</sup>/A $\beta$ <sup>+</sup>, and NSD<sup>+</sup>/A $\beta$ <sup>-</sup> groups. Findings were consistent except for plasma NfL (Supplementary Figure 1). In this analysis, asymptomatic NSD<sup>-</sup>/A $\beta$ <sup>-</sup> participants had lower plasma NfL levels than all other groups (vs. NSD<sup>-</sup>/A $\beta$ <sup>+</sup>  $P = 0.003$ ; vs. NSD<sup>+</sup>/A $\beta$ <sup>-</sup>  $P = 0.042$ ; vs. NSD<sup>+</sup>/A $\beta$ <sup>+</sup>  $P < 0.001$ ), and symptomatic NSD<sup>+</sup>/A $\beta$ <sup>+</sup> participants had higher plasma NfL levels than symptomatic NSD<sup>+</sup>/A $\beta$ <sup>-</sup> participants ( $P = 0.003$ ), suggesting that symptom severity might be associated with NfL levels.

To quantify plasma biomarker differences between A $\beta$ <sup>+</sup> and A $\beta$ <sup>-</sup> participants, we calculated median fold-change, standard deviation, and 95% confidence intervals (Figure 1F). Plasma pTau217 showed the largest median fold-change between A $\beta$ <sup>+</sup> and A $\beta$ <sup>-</sup> participants, with the highest value in the NSD<sup>+</sup> group (2.79 [SD: 0.33], 95% CI = 2.3-3.61; Supplementary Table 1).

### Association of plasma biomarkers with age, sex and APOE $\epsilon$ 4 carriership

Results from linear regression models examining the effects of age, sex, APOE  $\epsilon$ 4 carriership, CSF A $\beta$  and NSD status on plasma biomarker levels are shown in Supplementary Table 2. In both univariable and multivariable linear regression analyses, higher levels of pTau217 and pTau181 were associated with CSF A $\beta$  positivity ( $P < 0.001$ ). These results remained consistent after excluding the pTau181 outlier. Lower A $\beta$ 42/40 was associated with both APOE  $\epsilon$ 4 carriership ( $P = 0.012$ ) and CSF A $\beta$  positivity ( $P < 0.001$ ). Additionally, higher GFAP levels were associated with older age ( $P = 0.003$ ), CSF A $\beta$  positivity ( $P < 0.001$ ), and NSD positivity ( $P = 0.044$ ), while male sex ( $P = 0.013$ ) was associated with lower GFAP levels. Finally, higher NfL levels were associated with older age, CSF A $\beta$  positivity, and NSD positivity (all  $P < 0.001$ ).

### Diagnostic accuracy of plasma biomarkers for detecting amyloid- $\beta$

To determine diagnostic accuracy of plasma biomarkers for detecting amyloid- $\beta$  in NSD<sup>+</sup> and NSD<sup>-</sup>, we used Receiver Operating Characteristic (ROC) curves. In NSD<sup>+</sup> participants, plasma pTau217 and A $\beta$ 42/40 showed the highest accuracy for detecting A $\beta$  positivity (pTau217 AUC: 0.92, 95% CI: 0.85-1.00; A $\beta$ 42/40 AUC: 0.90, 95% CI: 0.81-0.98, Figure 2A). Their diagnostic performances outperformed NfL (AUC: 0.72, 95% CI: 0.59-0.84; vs. pTau217  $P = 0.003$ , vs. A $\beta$ 42/40  $P = 0.021$ ), but were comparable to pTau181 and GFAP (Supplementary Table 3). Including age, sex, and APOE  $\epsilon$ 4 carriership did not improve model accuracies. Sensitivity analyses confirmed that excluding the pTau181 outlier did not alter its diagnostic performance. However, pTau217 became significantly more accurate than pTau181 after this exclusion (pTau181 without outlier AUC: 0.79, 95% CI: 0.67-0.90; vs. pTau217  $P = 0.046$ ).

In NSD- participants, plasma pTau217 and A $\beta$ 42/40 again demonstrated the highest accuracies for detecting A $\beta$  positivity, with no significant difference between them (pTau217 AUC: 0.91, 95% CI: 0.86-0.97; A $\beta$ 42/40 AUC: 0.83, 95% CI: 0.75-0.92, Figure 2B). Plasma pTau217 outperformed pTau181 (AUC: 0.80, 95% CI: 0.72-0.88,  $P=0.03$ ), GFAP (AUC: 0.77, 95% CI: 0.69-0.86,  $P=0.01$ ), and NfL (AUC: 0.66, 95% CI: 0.56-0.76,  $P<0.001$ , Supplementary Table 4). Including age, sex, and *APOE*  $\epsilon$ 4 carriership significantly improved NfL's accuracy (AUC: 0.81, 95% CI: 0.72-0.89, vs. NfL alone  $P=0.031$ ), but was still less accurate than pTau217 alone ( $P=0.042$ ).

In both NSD+ and NSD- groups, models incorporating all biomarkers achieved the highest accuracy (AUC: 0.96, 95% CI: 0.92-1), but their performance was not significantly better than models using pTau217 or A $\beta$ 42/40 alone.

The above analysis used A $\beta$  PET positivity threshold of 36 centiloids (CL) as the gold standard to determine the CSF A $\beta$  status (A $\beta$  +/-, see Methods and Supplementary Figure 2). In an exploratory analysis using an A $\beta$  PET positivity threshold of 24 CL (Figures 2C and 2D), key differences emerged. In NSD+ participants, pTau217 remained the most accurate biomarker (AUC: 0.92, 95% CI: 0.84-0.99), significantly outperforming pTau181, GFAP, and NfL (Supplementary Table 5). In NSD-, all biomarkers performed similarly, except for NfL, which showed the lowest accuracy (AUC: 0.57, 95% CI: 0.47-0.68, Supplementary Table 6). Adding age, sex, and *APOE*  $\epsilon$ 4 carriership significantly improved NfL's performance (AUC: 0.80, 95% CI: 0.71-0.88) compared to NfL alone ( $P=0.002$ ), while other biomarkers showed no significant improvement. In combined biomarker models, the only difference from analyses using the 36 CL A $\beta$  PET positivity threshold was observed in NSD+ participants, in whom plasma pTau217 alone, but not A $\beta$ 42/40 alone ( $P=0.015$ ), performed comparably to all optimal biomarker combinations.

#### **Derivation and risk stratification of plasma pTau217 cut points for detecting amyloid- $\beta$**

Plasma pTau217 and A $\beta$ 42/40 demonstrated similar accuracy for detecting A $\beta$ ; however, pTau217 showed the best overall performance in both NSD+ and NSD- groups, with the largest median fold-change between A $\beta$ + and A $\beta$ - participants. Consequently, we selected pTau217 to determine the accuracy of reference cut points for detecting A $\beta$  in NSD.

In NSD+ participants from the SU discovery cohort, we established one-reference cut point for plasma pTau217 using the Youden Index ( $>0.54$  pg/mL). We then derived two-reference cut points: one at 90% sensitivity ( $<0.66$  pg/mL) and specificity ( $>0.69$  pg/mL), and another at 95% sensitivity ( $<0.47$  pg/mL) and specificity ( $>1.04$  pg/mL). These cut points differed in NSD- participants (Supplementary Table 7).

Figure 3, panel A shows predicted probabilities of A $\beta$  positivity under the two-reference model, stratifying participants into low, intermediate and high-risk categories. In the SU discovery cohort, NSD+ participants with a predicted probability  $<6\%$  had a 95% chance of being A $\beta$ -, and those with a predicted probability  $<36\%$  had a 90% chance of being A $\beta$ - (low probability). Conversely, NSD+ participants with predicted probabilities  $>94\%$  had a 95% chance of being A $\beta$ + and individuals with predicted probabilities  $>53\%$  had a 90% chance of being A $\beta$ + (high probability). Participants with predicted probabilities between 36% and 53% were classified as intermediate risk.

#### **Validation of plasma pTau217 cut points in two independent clinical LBD cohorts**

The two clinical validation cohorts included clinically-defined LBD participants without CSF  $\alpha$ Syn data from the Stanford University (LBD-SU,  $n=29$ ) and Sant Pau (LBD-SPIN,  $n=44$ ) cohorts. Amyloid- $\beta$  status (A $\beta$  +/-) was

determined by A $\beta$  PET in the LBD-SU cohort, and CSF A $\beta$ 42/40 in the LBD-SPIN cohort (Supplementary Figure 3). The LBD-SU clinical validation cohort (n=29) had a median age of 71 years (min, max: 57-81), with 6 females (20.7%), and 23 males (79.3%). The LBD-SPIN clinical validation cohort (n=44) had a median age of 78 years (min, max: 65-84), with 20 females (45.5%) and 24 males (54.5%) (Supplementary Table 8).

Application of reference cut points to the LBD-SU and LBD-SPIN clinical cohorts showed that the negative percentage agreement (NPA) was similar between the one- and two-reference cut point models at 90% sensitivity/specificity, ranging from 89.5% to 94.4% (Table 2). However, the two-reference cut point model significantly improved the positive percentage agreement (PPA) (two-reference cut point vs. one-reference cut point in LBD-SU: 100% vs. 72.7%, and in LBD-SPIN: 86.4% vs. 68.8%). At 95% sensitivity/specificity, the two-reference cut point model achieved perfect PPA (100%) in both cohorts while maintaining high NPA (LBD-SU: 93.8%, LBD-SPIN: 90.9%).

We then determined the number of people who would need confirmatory (CSF or PET) A $\beta$  testing at different cut points. In the one-reference cut point model, the high NPA but relatively low PPA suggests that plasma pTau217-positive individuals would require additional testing to confirm A $\beta$  positivity (Figure 3, Panel B). Using the two-reference cut point at 90% sensitivity/specificity, both intermediate- and high- risk individuals would require additional testing. In contrast, in the 95% sensitivity/specificity model, only the intermediate-risk group would require additional testing (Figure 3, Panel B).

In an exploratory analysis using a 24 CL threshold for A $\beta$  PET positivity, we observed both differences and similarities. The two-reference cut point models significantly improved PPA, reaching 100% in the LBD-SU cohort, while in LBD-SPIN, PPA remained moderate (83.3% in the 90% sensitivity/specificity model, and 81.3% in the 95% sensitivity/specificity model). NPAs remained consistently high across cohorts for both one- and two-reference cut point models (87.5% to 100%; Supplementary Table 9).

To assess the potential impact of using plasma pTau217 on clinical trial recruitment, we calculated the number needed to screen to identify 100 A $\beta$ + and/or 100 A $\beta$ - NSD participants under each model. The 95% sensitivity/specificity two-cut point model, while offering stringent accuracy, required screening the largest number of patients to identify 100 A $\beta$ + participants (see Figure 3, Panel B and C).

## Discussion

Our findings showed that plasma pTau217 accurately detects A $\beta$  positivity in individuals with NSD. To our knowledge, this is the first study analyzing A $\beta$ , neuroinflammation, and neurodegeneration plasma biomarkers in NSD. We identified plasma pTau217 as a reliable biomarker for A $\beta$  positivity and applied, for the first time in this population, a two-reference cut point approach similar to that proposed in AD(13,16,40). Since mixed pathologic  $\alpha$ Syn and amyloid- $\beta$  accumulation cannot be diagnosed clinically, accessible biomarkers are critically needed for accurate diagnosis and patient management. Plasma pTau217 provides a cost-effective, minimally-invasive alternative to A $\beta$  PET or CSF. This is particularly important as concomitant amyloid- $\beta$  mixed pathology is common in NSD and is associated with faster functional and cognitive decline(2,3,9,10). Thus, detecting A $\beta$  positivity in NSD could guide clinical decisions and inform clinical trial design.

In clinical trials targeting  $\alpha$ Syn-related cognitive impairment or dementia, excluding participants with amyloid- $\beta$  pathology may be necessary. Plasma pTau217 could serve as a prescreening tool reducing the need for additional tests. Furthermore, the high frequency of amyloid- $\beta$  pathology in NSD suggests that anti-amyloid therapies may

be appropriate for some individuals. A recent NIH RFA calls for phase 2 clinical trials testing the efficacy of anti-amyloid monoclonal antibodies in DLB with concomitant A $\beta$  positive biomarkers, expanding the application of targeting A $\beta$  in neurodegenerative diseases beyond AD. Validated tools like plasma pTau217 could efficiently identify eligible participants for such trials(41,42).

In this context, both one- and two-reference cut points at 90% sensitivity/specificity effectively identified individuals without A $\beta$  positivity, achieving high NPAs. The two-reference cut point method also demonstrated high PPA, allowing more individuals to avoid invasive or expensive testing compared to the one cut point approach. Additionally, the two-reference cut points were very close: 0.66 pg/mL at 90% sensitivity and 0.69 pg/mL at 90% specificity, reflecting a steep transition between A $\beta$  negative and positive participants. This narrow range reduces the effect of small measurement variations and suggests that either threshold could be used depending on whether sensitivity or specificity is prioritized.

Plasma pTau217 may also help stratify trial participants, potentially improving the detection of differential treatment responses. For example, a phase 2A trial of neflamapimod in DLB found that participants with abnormal plasma pTau181 levels did not respond to treatment, leading to the exclusion of biomarker-positive participants in the subsequent phase 2B trial(43,44). These findings suggest that amyloid- $\beta$  pathology may influence therapeutic responses in NSD and highlight the importance of accounting for mixed pathologies in drug development for neurodegenerative diseases.

In clinical practice, the goal may be ruling-in or ruling-out A $\beta$  positivity to guide prognosis and management. More stringent cut points at 95% sensitivity/specificity may be appropriate in this setting, helping clinicians provide better guidance to patients and families regarding prognosis and monitoring. This approach may also reduce the need for additional A $\beta$  testing. Potential false negative results, particularly in early or atypical cases, could be addressed by repeating plasma pTau217 when necessary, given that blood collection is minimally invasive and readily accessible.

Additionally, this study showed that different A $\beta$  PET positivity thresholds influence cut point calculations in NSD. Previous studies suggest that CSF AD biomarker levels in LBD are lower than in AD(32,33), indicating the need for disease-specific cut-points(45). Unlike AD, where amyloid- $\beta$  pathology burden is consistently high, people with NSD can show a broader spectrum of amyloid- $\beta$  accumulation, emphasizing a need for tailored biomarker thresholds(46).

Several studies have analyzed plasma pTau217, pTau181, A $\beta$ 42/40, GFAP and NfL in clinically diagnosed LBD patients (10,17–21,25,28). Using a biomarker-based definition, our findings demonstrated that pTau217, pTau181, and A $\beta$ 42/40 differed between A $\beta$ <sup>+</sup> and A $\beta$ <sup>-</sup> individuals, regardless of NSD status or symptom presence. This is important, as studies have suggested different CSF A $\beta$  and tau biomarker performance in those with and without LBD(41).

We also found elevated plasma GFAP levels in A $\beta$ <sup>+</sup> individuals regardless of NSD status, while NfL levels were highest in NSD participants with A $\beta$  positivity. Since NfL reflects neuroaxonal injury rather than pathology-specific processes, higher levels in individuals with both NSD and AD likely reflect the cumulative influence of multiple pathological processes on neuronal integrity(47). Consistent with this finding, the associations of both GFAP and NfL with NSD positivity and A $\beta$  positivity suggest that these markers reflect broader

neuroinflammatory or neurodegenerative processes rather than being specific to  $\alpha$ Syn or amyloid- $\beta$  pathology(48).

A key strength of this study is the use of a biologically defined discovery cohort of NSD and A $\beta$  status to assess biomarker performance, combined with external validation of plasma pTau217 in two clinical LBD cohorts. By establishing cut points in a cohort defined using the most validated biomarker for underlying  $\alpha$ Syn pathology, we provide thresholds that might be applicable in clinical practice and trials. This design bridges the gap between biomarker-based research frameworks and clinical settings where  $\alpha$ Syn status is often unknown, supporting the broader use of our findings. This study also has limitations. The clinical validation cohorts were relatively small. Additionally, all cohorts consisted of primarily non-Hispanic white individuals, which may limit the generalizability of our findings. Finally, future studies should evaluate whether longitudinal changes in plasma pTau217 reflect amyloid accumulation or disease progression, and whether comorbidities impact plasma biomarker levels in NSD.

In summary, this study supports the use of plasma pTau217 as a screening tool for amyloid- $\beta$  in NSD and in clinically-defined LBD, highlighting a critical mixed-pathology dimension within the biomarkers landscape. Our findings suggest that plasma pTau217 could be used for screening and stratification in NSD clinical trials. These results are important because they integrate clinical and biomarker data in a multi-etiology framework for the diagnosis of mixed neurodegenerative diseases of aging.

## Methods

### Participants

This cross-sectional study included participants from two cohorts: SU and SPIN(39), recruited between 2011 and 2023. All participants or their legally authorized representatives provided written informed consent for participation according to the Declaration of Helsinki. The Institutional Review Boards of each academic institution approved the study protocols: the Institutional Review Board of Stanford University granted approval of the study protocols IRB-33727 and IRB-37604, the Institutional Review Board of Hospital Sant Pau granted approval of the study protocol IIBSP-DOW-2014-30. This study followed the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) reporting guidelines.

All participants underwent comprehensive clinical evaluation involving medical history, physical and neurological examination, and neuropsychological assessment. Diagnoses were based on international consensus criteria, similar to our prior studies(10,49) and included: LBD without cognitive impairment (LBD-CU; i.e., PD diagnosis according to UK Brain Biobank criteria(50) without objective impairment on neuropsychological testing), LBD with cognitive impairment (LBD-CI; i.e., diagnosis of PD with mild cognitive impairment(51), prodromal DLB(52), PD dementia(53) or DLB(54)), AD(55), and cognitively unimpaired (CU) individuals (i.e., older adults without parkinsonian symptoms who performed within normal age- and sex-adjusted ranges on neuropsychological testing). In the SU cohort, global cognition was measured with the Montreal Cognitive Assessment (MoCA)(56) in 183 participants and the Mini-Mental State Examination (MMSE)(57) in 26 participants. MMSE scores were converted to MoCA scores according to age, sex, and education based on Monsell et al.(58) In the LBD-SPIN cohort, global cognition was measured with the MMSE. MoCA and MMSE scores were obtained within a 6-month window of plasma collection.

Participants were divided into one discovery and two clinical validation cohorts. The discovery cohort included 180 SU participants with CSF  $\alpha$ Syn SAA and A $\beta$ 42/40 data where we evaluated diagnostic accuracy of plasma biomarkers for detecting amyloid- $\beta$  in NSD+ and NSD- groups. The two clinical validation cohorts comprised

clinically-defined LBD-CU and LBD-CI participants (CSF  $\alpha$ Syn SAA data were not available) where we validated diagnostic accuracies of plasma biomarker cut points defined in the SU discovery cohort (Supplementary Figure 3).

### **Biomarkers**

All biomarker processing for plasma, CSF, and A $\beta$  PET imaging was performed blinded to clinical information. In the SU discovery cohort, CSF samples were obtained within six months of plasma collection. Most plasma and CSF samples were collected concurrently, with a median interval of 0.14 weeks (approximately 1 day; IQR: 0-4.9 weeks). A $\beta$  PET was performed within one year of plasma collection, with a median of 11.7 weeks (IQR: 4-23.3 weeks). CSF and A $\beta$  PET assessments occurred both before and after plasma collection, indicating no systematic ordering of biomarker acquisition relative to plasma collection. Given the slow longitudinal change of plasma, CSF, and A $\beta$  PET measures, these time differences are unlikely to meaningfully affect cross-sectional biomarker correlations. In the SPIN clinical validation cohort, CSF samples were obtained at time of plasma collection.

CSF A $\beta$ 42/40 was used to determine A $\beta$  status in all participants from the SU discovery cohort and the LBD-SPIN clinical validation cohort. A $\beta$  PET was used to determine A $\beta$  status in the LBD-SU clinical validation cohort and in an independent SU cohort, which was used to derive centiloid-based thresholds to calibrate CSF cut points.

### **Plasma**

SU research participants consented to donate blood samples during each annual research visit. Ethylenediaminetetraacetic acid (EDTA) plasma was collected by venipuncture, centrifuged for 10 minutes at 4°C at 2000 x g, aliquoted in polypropylene tubes, and stored at -80°C until biomarker measurement.

Plasma pTau181, A $\beta$ 42, and A $\beta$ 40 concentrations were measured by the Stanford Alzheimer's Disease Research Center (ADRC) Biomarker Core using the Lumipulse G1200 instrument. Detailed protocols have been published previously(10,59,60). Inter-batch variability was calculated by retesting six independent plasma aliquots one year after the initial analysis using different reagents batches and assay lot numbers. Plasma pTau181 was quantified using a modified version of the Lumipulse G CSF pTau181 assay (231654; Fujirebio Diagnostics)(60). The inter-batch coefficient of variation (CV) was 3.38%. All plasma samples were within the quantifiable range (0.16 to 10.43 pg/ml). Plasma A $\beta$ 42 and A $\beta$ 40 were measured using Lumipulse G assays(59). The inter-batch CV for the A $\beta$ 42/40 ratio was 2.93%, and values ranged from 0.0549 to 0.2031.

Plasma pTau217, GFAP, and NfL concentrations were measured at the University of Gothenburg Department of Psychiatry and Neurochemistry using the Single molecule array (Simoa®) HD-X platform (Quanterix, Billerica, MA), as detailed elsewhere(12). Plasma pTau217 for SU and SPIN participants was measured with the commercial ALZpath pTau217 assay (Quanterix, REF: 104371, LOT: 999024), in two independent batches. The batch-specific measurement range was 0.0072 to 30.0 pg/mL for SU plasma samples, and 0.0073-30.0 pg/mL for SPIN plasma samples. Plasma GFAP and NfL were measured with the commercial Neurology 4-plex E kit (Quanterix, REF: 103520, LOT: 503812). One SU participant's GFAP levels fell below the assay's lower limit of quantification and was excluded from statistical analysis.

### **CSF $\alpha$ Syn, A $\beta$ 42, and A $\beta$ 40**

CSF sample collection procedures were similar across SU and SPIN cohorts. The complete protocol for CSF collection and biomarker analysis (CSF  $\alpha$ Syn, A $\beta$ 42, A $\beta$ 40) in SU participants has been published

previously(10,61,62). CSF  $\alpha$ Syn status in the SU discovery cohort was determined at Amprion's CLIA Laboratory via  $\alpha$ Syn seed amplification assay (SYNTap® Biomarker Test)(61). CSF samples were classified as  $\alpha$ Syn "detected" (NSD+) or "not detected" (NSD-) based on a preestablished threshold for median maximum fluorescence of the triplicate wells within 150 hours. The complete protocol is published elsewhere(62). SU CSF A $\beta$ 42 and A $\beta$ 40 were quantified by the Stanford ADRC Biomarker Core using the Lumipulse G 1200 instrument, as previously described(63). SPIN cohort CSF A $\beta$ 42 and A $\beta$ 40 were quantified using the Lumipulse G600II at the Sant Pau Memory Unit laboratory, as previously described(64). A $\beta$  status in LBD-SPIN cohort was determined using a CSF A $\beta$ 42/40 cut point of  $<0.06220$ .

### **A $\beta$ PET**

We acquired  $^{18}$ F-florbetaben imaging on a PET/MRI scanner (Signa 3T, GE Healthcare) at the Stanford University Richard M. Lucas Center for Imaging. Emission data were acquired 90-110 minutes post-injection and processed as previously described(65). Global cortical SUVRs were calculated using the whole cerebellum as reference and converted to centiloids (CL)(66).

CSF A $\beta$  status was determined using A $\beta$  PET as the references standard in the SU discovery cohort. A $\beta$  PET positivity was defined using a threshold of 36 centiloids (CL) to maximize specificity (Supplementary Figure 2). This threshold was derived from a subset of SU participants (n=72) excluded from discovery and validation cohorts using a Gaussian Mixture Model. In an exploratory analysis, we used a 24 CL threshold(12) to maximize sensitivity (Supplementary Table 10).

Both 36 and 24 CL A $\beta$  PET thresholds were used to establish CSF A $\beta$ 42/40 cut points calculated with the Youden Index in ROC curve analyses, where abnormal CSF A $\beta$ 42/40 was defined as  $< 0.09$  for 36 CL (AUC = 0.98, 95% CI: 0.95-1) and  $< 0.11$  for 24 CL (AUC = 0.94, 95% CI: 0.84-1). With these CSF A $\beta$ 42/40 cut points, we classified 180 SU participants as either CSF A $\beta$ + or CSF A $\beta$ - for analysis.

### **APOE Genotyping**

For SU participants, *APOE* genotype was obtained from National Cell Repository for Alzheimer's Disease (NCRAD) using a Fluidigm fingerprint panel, or determined using PCR restriction fragment length polymorphism analysis within the Stanford ADRC(67). For SPIN participants, DNA was extracted from whole blood samples using the DNeasy® Blood & Tissue kit (Qiagen) at the Sant Pau Memory Unit laboratory. *APOE* genotyping was performed by direct DNA sequencing of exon 4 to identify the rs429358 and rs7412 polymorphisms that determine the *APOE* E2, E3, and E4 alleles.

### **Statistical analysis**

Plasma pTau217, pTau181, GFAP, and NfL data were log10-transformed due to skewed distributions. We summarized continuous variables using the mean (standard deviation) for normally distributed data, median (minimum, maximum) for non-normally distributed data, and proportions for categorical variables.

To assess group differences in continuous variables, we used either one-way ANOVAs or the Kruskal-Wallis tests, depending on data distribution. We performed post-hoc pairwise comparisons using *t*-tests or Mann-Whitney tests as appropriate. For categorical variables, we used either Pearson's  $\chi^2$  or Fisher's Exact tests depending on observed proportions. We corrected for multiple comparisons using the Holm method.

To quantify the differences in plasma biomarker levels between A $\beta$ <sup>+</sup> and A $\beta$ <sup>-</sup> participants in the SU discovery cohort, we calculated median fold-change, standard deviation, and 95% confidence intervals. With this cohort, we conducted univariable and multivariable linear regression analyses to evaluate associations between plasma biomarker levels and age, sex, *APOE*  $\epsilon$ 4 carriership (i.e.,  $\epsilon$ 4 homozygotes or heterozygotes), CSF A $\beta$ , and NSD status separately and jointly.

To determine diagnostic accuracy of plasma biomarkers for detecting A $\beta$  positivity in NSD<sup>+</sup> and NSD<sup>-</sup>, we used Receiver Operating Characteristic (ROC) curves. First, we analyzed each biomarker separately, incorporating age, sex, and *APOE*  $\epsilon$ 4 carriership in each model. Next, we combined multiple biomarkers into a single model. Model performance was compared with the DeLong test, and the best-performing biomarker was selected based on standard metrics. For this biomarker, we determined one-reference cut point using the Youden Index, as well as two-reference cut points based on 90% and 95% sensitivity and specificity. Then, we calculated the predicted probabilities for A $\beta$  positivity in the discovery and clinical validation cohorts using logistic regression under the two-reference models, and stratified participants into low, intermediate and high-risk. Finally, we calculated sensitivity, specificity, negative and positive percent agreement, as well as overall agreement.

Statistical analyses were performed using R version 4.3.0 (R Foundation for Statistical Computing). Two-sided *p*-values  $\leq 0.05$  were statistically significant and 95% confidence intervals were reported when applicable.

#### **Data availability**

The datasets generated and analyzed during the current study are not publicly available due to participant privacy and confidentiality constraints. However, anonymized data from the current study are available from the corresponding author on reasonable request, contingent upon completion of Stanford University's data use agreement approval.

#### **Code availability**

The underlying code for this study's statistical analysis is not publicly available but may be made available to qualified researchers upon reasonable request from the corresponding author.

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#### **Author contributions**

CA and AMS had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Concept and design: CA, KLP.

Acquisition, analysis or interpretation of data: CA, AMS, SAL, KLP, BA, LMG, NJA, ENW, DA, IRB, CBY, JRW, MSB, HV, MJP, TP, EVC, IS, JHM, KIA, VWH, TJM, LT, ECM, HZ.

Drafting of the manuscript: CA, AMS, SAL, KLP.

Critical review of the manuscript for important intellectual content: CA, KLP, AMS, SAL, BA, LMG, NJA, ENW, DA, IRB, JF, CBY, JRW, MSB, HV, MJP, TP, EVC, IS, JHM, VR, GAK, KIA, VWH, TJM, LT, ECM, HZ.

Statistical analysis: CA, AMS, SAL.

Obtained funding: CA, KLP.

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Supervision: CA, KLP.

#### **Competing interests**

These authors declare competing interests: LMG has received speaker fees from Quanterix and Esteve, and served as consultant for Quanterix. MJP is currently a full-time employee at Amprion Inc. DA has participated in advisory boards for Fujirebio-Europe, Roche Diagnostics, Grifols S.A. and Lilly, and received speaker honoraria from Fujirebio-Europe, Roche Diagnostics, Nutricia, Krka Farmacéutica S.L., Zambon S.A.U., Neuraxpharm, Alter Medica, Lilly and Esteve Pharmaceuticals S.A. DA holds a patent for markers of synaptopathy in neurodegenerative disease (licensed to ADx NeuroSciences N.V., WO2019175379 Markers of synaptopathy in neurodegenerative diseases). JF has served on advisory boards, adjudication committees, or speaker honoraria from AC Immune, Adamed, Alzheon, Biogen, Eisai, Esteve, Fujirebio, Ionis, Laboratorios Carnot, Life

Molecular Imaging, Lilly, Lundbeck, Novo Nordisk, Perha, Roche, Zambón, Spanish Neurological Society, T21 Research Society, Lumind foundation, Jérôme-Lejeune Foundation, Alzheimer's Association, National Institutes of Health USA, and Instituto de Salud Carlos III. JF also holds a patent for markers of synaptopathy in neurodegenerative disease (licensed to ADx NeuroSciences N.V., WO2019175379 Markers of synaptopathy in neurodegenerative diseases). HZ has served at scientific advisory boards and/or as a consultant for Abbvie, Acumen, Alector, Alzinova, ALZpath, Amylyx, Annexon, Apellis, Artery Therapeutics, AZTherapies, Cognito Therapeutics, CogRx, Denali, Eisai, Enigma, LabCorp, Merck Sharp & Dohme, Merry Life, Nervgen, Novo Nordisk, Optoceutics, Passage Bio, Pinteon Therapeutics, Prothena, Quanterix, Red Abbey Labs, reMYND, Roche, Samumed, ScandiBio Therapeutics AB, Siemens Healthineers, Triplet Therapeutics, and Wave, has given lectures sponsored by Alzecure, BioArctic, Biogen, Cellectricon, Fujirebio, LabCorp, Lilly, Novo Nordisk, Oy Medix Biochemica AB, Roche, and WebMD, is a co-founder of Brain Biomarker Solutions in Gothenburg AB (BBS), which is a part of the GU Ventures Incubator Program, and is a shareholder of MicThera (outside submitted work). KLP has been on the Scientific Advisory Board for Amprion and has been a consultant for Novartis, Lilly, BioArctic, Biohaven, Curasen and Neuron23. CA has received honoraria as a speaker from Hoffman-La Roche LTD, Nutricia, Schwabe Farma Ibérica SAU and Zambon; and is member of the Board of Directors of the Lewy Body Dementia Association, the Scientific Committee of Lewy Body España, and the Alzheimer's Association International Society to Advance Alzheimer's Research and Treatment (ISTAART) Advisory Council.

All other authors (AMS, SAL, BA, NJA, ENW, IRB, CBY, JRW, MSB, HV, TP, EVC, IS, JHM, VR, GAK, KIA, VWH, TJM, LT, and ECM) declare no financial or non-financial competing interests. No authors have pending patent applications related to the work described in this manuscript.

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### Figure Legends

**Figure 1. Plasma biomarker levels (pg/mL) across NSD/A $\beta$  groups.** Panel 1A-1E: Bars with asterisks represent significant differences between log-transformed plasma biomarker levels. Plasma pTau217, pTau181, A $\beta$ 42/40, and GFAP levels were abnormal in A $\beta$ + groups, regardless of NSD status. Plasma NfL levels were higher in the NSD+/A $\beta$ + group compared to the other groups; and in the NSD-/A $\beta$ + group compared to the NSD/A $\beta$ - group. Plasma pTau217 showed the largest median fold-change regardless of NSD status, with the highest median concentration observed in the NSD+ group (2.79 [SD: 0.33], 95% CI = 2.30-3.61; see Supplementary Table 1).

**Figure 2. ROC models for detecting amyloid- $\beta$  using individual plasma biomarkers in NSD+ and NSD- participants.** Figure 2 compares diagnostic accuracies of individual plasma biomarker receiver operating characteristic (ROC) models for detecting amyloid- $\beta$ . **Panels 2A** and **2C** show ROC area under the curve (AUC) results for NSD+ participants whereas **panels 2B** and **2D** show ROC AUC results for NSD- participants. **Panels 2A** and **2B** show models using a CSF A $\beta$ 42/40 cut point calculated based on A $\beta$  PET  $\geq$  36 centiloids (CL). **Panels 2C** and **2D** show models using a CSF A $\beta$ 42/40 cut point calculated based on A $\beta$  PET  $\geq$  24 CL. Plasma pTau217 outperforms other biomarkers for the detection of amyloid- $\beta$  in NSD+ participants. Individual

biomarker models performed similarly when detecting amyloid- $\beta$  in NSD- participants, with no biomarker significantly outperforming the other.

**Figure 3. Validation of plasma pTau217 in clinical LBD cohorts.** Panel 3A shows the predicted probability of amyloid- $\beta$  positivity based on a logistic regression model including z-transformed plasma pTau217 levels across cohorts. Each dot represents an individual participant, with blue dots indicating amyloid- $\beta$  negative and red dots indicating amyloid- $\beta$  positive. Predicted probabilities are shown for the NSD+ SU discovery cohort (left). Dashed lines indicate the probability thresholds corresponding to 90% (thick line) and 95% (thin line) sensitivity or specificity, demonstrating low- and high-risk cut points on the probability distribution, applying a similar approach as Brum et al. (doi: 10.1038/s43587-023-00471-5). Panel 3B shows a workflow of amyloid- $\beta$  detection with plasma pTau217 in the clinical validation cohorts. On the left, the flowchart presents the categorization of patients based on their plasma pTau217 levels: positive, intermediate, or negative results. The right panel presents the workflow using different reference cut points. The top section presents the number and percentage of patients that will require confirmatory testing (with PET or CSF), while the bottom section presents the number and percentage of patients that will not require additional testing. The color-coded boxes indicate a potential context of use (COU) for the different reference cut points: clinical trial (green) and clinical practice (yellow), assuming in clinical trials would bias towards more confirmatory testing for those suspected of being amyloid- $\beta$  positive. Panel 3C shows sample size estimates for hypothetical clinical trials, which are calculated using the NSD+ SU discovery cohort. In Scenario 1 the goal was to find 100 NSD who were amyloid- $\beta$  positive, versus Scenario 2 where the goal was to find 100 NSD who were amyloid- $\beta$  negative. The number of plasma pTau217 positives (or negatives) needed was calculated as 100 divided by the PPV (or NPV). The number to screen was calculated as plasma pTau217 positives (or negatives) needed divided by the percentage of plasma pTau217 positivity (or negativity).

**Table 1. Characteristics of the Stanford University discovery cohort**

	NSD-/A $\beta$ - (n=69)	NSD-/A $\beta$ + (n=44)	NSD+/A $\beta$ - (n=39)	NSD+/A $\beta$ + (n=28)	Total Cohort (n=180)	<i>p</i> value*
<b>Age, years</b> median (min, max)	66 (51, 87)	71 (54, 86)	69 (50, 82)	70 (57, 83)	69 (50, 87)	0.031
<b>Sex, male</b> No. (%)	38 (55.1)	20 (45.5)	22 (56.4)	17 (60.7)	97 (53.9)	0.589
<b>Years of education</b> median (min, max)	16 (5, 20)	16 (12, 20)	17.0 (12, 20)	16.0 (12, 20)	16.0 (5, 20)	0.935
<b>APOE <math>\epsilon</math>4 carrier</b> No. (%)	14 (20.3) <sup>b,d</sup>	29 (65.9) <sup>a,d</sup>	13 (33.3)	16 (57.1) <sup>a,b</sup>	72 (40.0)	< 0.001
<b>Clinical diagnosis, No. (%)</b>						
Cognitively Unimpaired	56 (81.2) <sup>b,c,d</sup>	20 (45.5) <sup>a,c,d</sup>	5 (12.8) <sup>a,b,d</sup>	5 (17.9) <sup>a,b,c</sup>	86 (47.8)	< 0.001
AD	8 (11.6)	22 (50.0)	0 (0.0)	4 (14.3)	34 (18.9)	
LBD Cognitively Impaired	2 (2.9)	1 (2.3)	10 (25.6)	17 (60.7)	30 (16.7)	
LBD Cognitively Unimpaired	3 (4.3)	1 (2.3)	24 (61.5)	2 (7.1)	30 (16.7)	
<b>Clinical status, No. (%)</b>						
Asymptomatic	56 (81.2) <sup>b,c,d</sup>	20 (45.5) <sup>a,c,d</sup>	5 (12.8) <sup>a,b</sup>	5 (17.9) <sup>a,b</sup>	86 (47.8)	< 0.001
Symptomatic	13 (18.8)	24 (54.5)	34 (87.2)	23 (82.1)	94 (52.2)	
<b>MoCA score</b> median (min, max)	27 (6, 30) <sup>b,d</sup>	25 (1, 30) <sup>a</sup>	26 (8, 30) <sup>d</sup>	22 (3, 30) <sup>a,c</sup>	26 (1, 30)	< 0.001
<b>CSF A<math>\beta</math>42/40</b> median (min, max)	0.13 (0.09, 0.15) <sup>b,d</sup>	0.06 (0.04, 0.09) <sup>a,c</sup>	0.12 (0.09, 0.15) <sup>b,d</sup>	0.07 (0.04, 0.09) <sup>a,c</sup>	0.11 (0.04, 0.15)	< 0.001

<b>Plasma pTau217, pg/mL</b> median (min, max)	0.34 (0.02, 1.88) <sup>b,d</sup>	0.84 (0.31, 3.87) <sup>a,c</sup>	0.35 (0.06, 2.41) <sup>b,d</sup>	0.96 (0.30, 3.29) <sup>a,c</sup>	0.47 (0.02, 3.87)	< 0.001
<b>Plasma pTau181, pg/mL</b> median (min, max)	1.43 (0.83, 3.52) <sup>b,d</sup>	1.99 (1.26, 5.41) <sup>a,c</sup>	1.47 (0.93, 4.39) <sup>b,d</sup>	1.92 (1.24, 10.43) <sup>a,c</sup>	1.60 (0.83, 10.43)	< 0.001
<b>Plasma GFAP, pg/mL</b> mean (SD)	128.45 (64.56) <sup>b,d</sup>	207.13 (92.14) <sup>a,c</sup>	140.89 (57.06) <sup>b,d</sup>	247.07 (121.46) <sup>a,c</sup>	168.84 (93.09)	< 0.001
<b>Plasma NfL, pg/mL</b> mean (SD)	20.85 (9.51) <sup>b,d</sup>	25.01 (9.12) <sup>a,d</sup>	23.67 (9.03) <sup>d</sup>	31.87 (12.85) <sup>a,b,c</sup>	24.18 (10.51)	0.001
<b>Plasma A<math>\beta</math>42/40</b> mean (SD)	0.10 (0.01) <sup>b,d</sup>	0.08 (0.01) <sup>a,c</sup>	0.10 (0.01) <sup>b,d</sup>	0.08 (0.01) <sup>a,c</sup>	0.09 (0.01)	<0.001

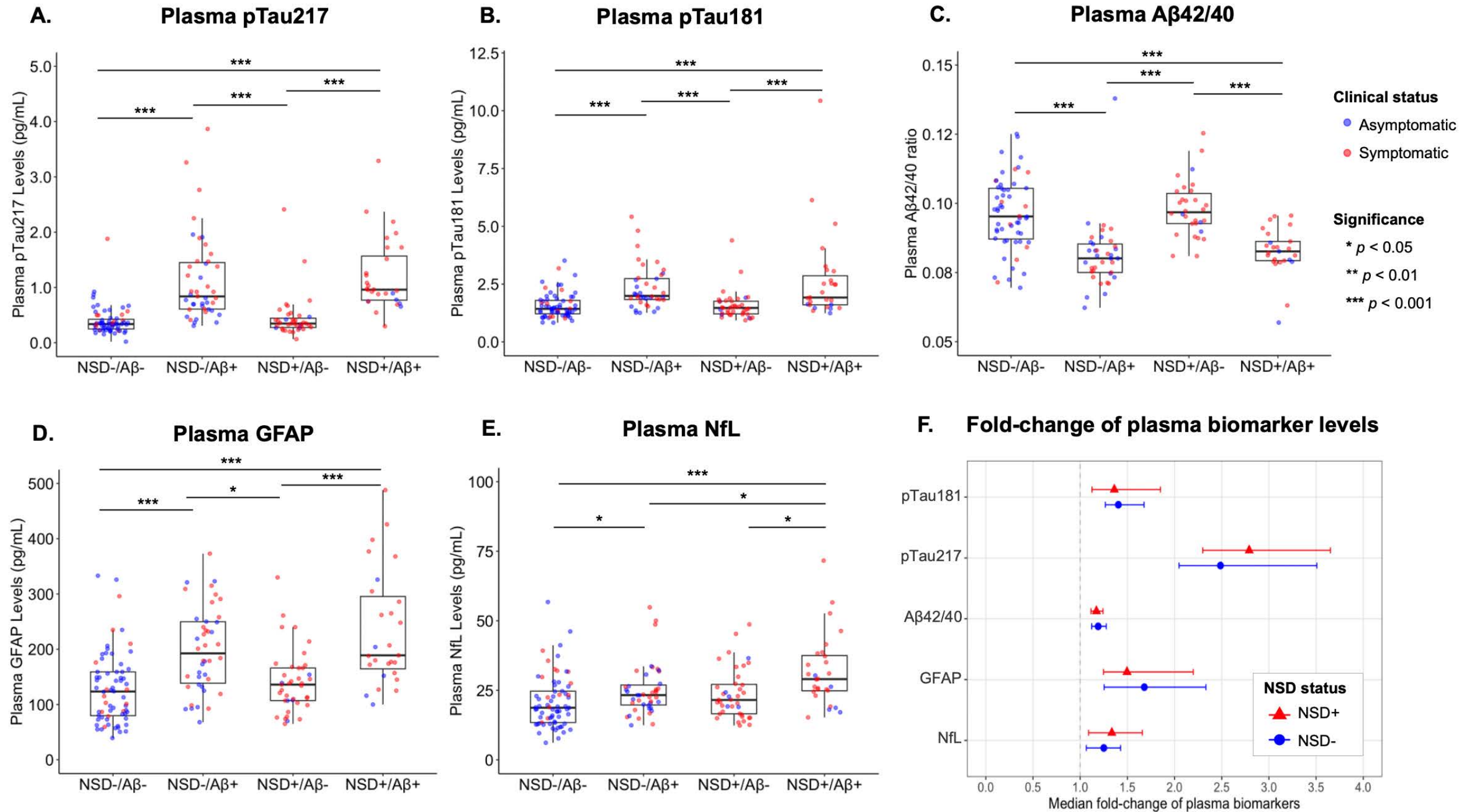
Note. NSD status was determined by CSF  $\alpha$ Syn SAA (not detected/detected); A $\beta$  status was determined by CSF A $\beta$ 42/40 (normal/abnormal). Clinical status = presence (i.e., symptomatic) or absence (i.e., asymptomatic) of cognitive and motor symptoms; \**p* values for descriptive comparisons are uncorrected; <sup>a</sup>*p*<0.05 compared with NSD-/A $\beta$ -; <sup>b</sup>*p*<0.05 compared with NSD-/A $\beta$ +; <sup>c</sup>*p*<0.05 compared with NSD+/A $\beta$ -; <sup>d</sup>*p*<0.05 compared with NSD+/A $\beta$ +. Abbreviations: NSD, Neuronal Synuclein Disease; A $\beta$ , amyloid- $\beta$ ; AD, Alzheimer's disease; LBD, Lewy body disease; MoCA, Montreal Cognitive Assessment; CSF, cerebrospinal fluid; pTau217, phosphorylated tau 217; pTau181, phosphorylated tau 181; GFAP, glial fibrillary acidic protein; NfL, neurofilament light chain. Missing data: APOE  $\epsilon$ 4 carriership: 15 (8.3%); MoCA: 2 (1.1%); Plasma pTau217: 3 (1.7%); Plasma pTau181: 7 (3.9%); Plasma GFAP and NfL: 1 (0.6%); Plasma A $\beta$ 42/40: 32 (17.8%).

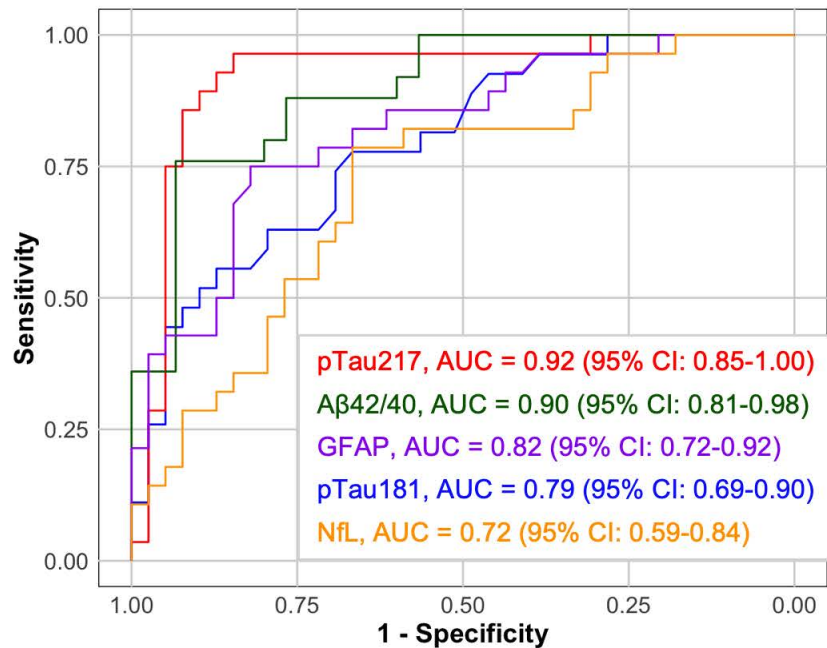
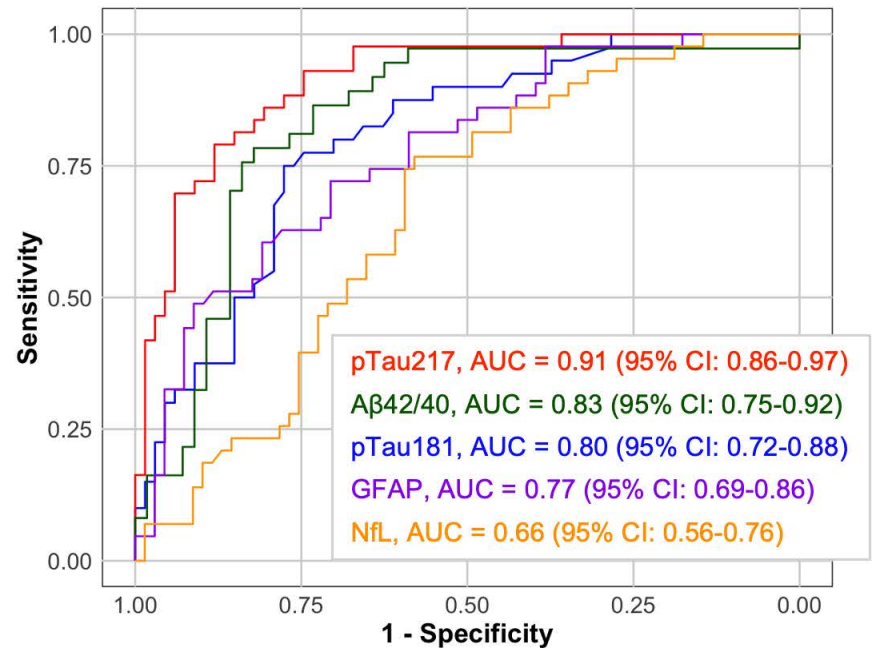
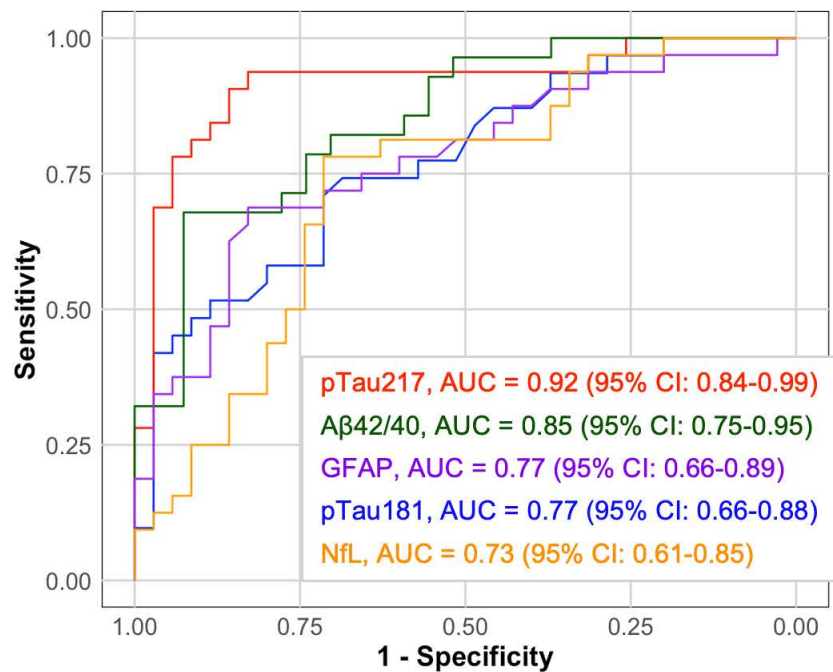
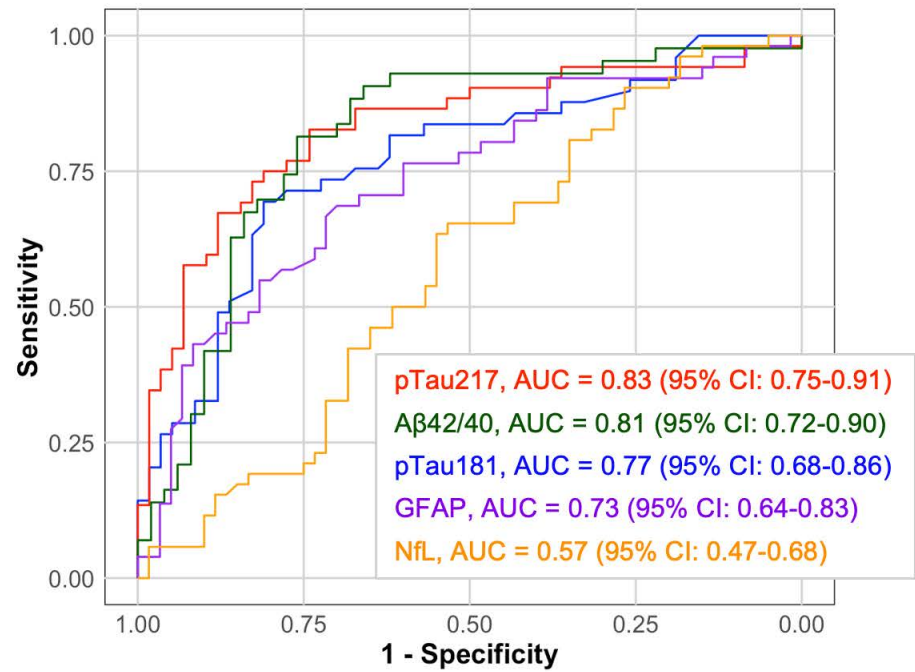
**Table 2. Plasma pTau217 one- and two-reference cut points for amyloid- $\beta$  positivity in discovery and clinical validation cohorts**

	One cut point (Youden Index)				Two cut points 90% Se/Sp			Two cut points 95% Se/Sp		
	pTau217 positive > 0.54 pg/mL				pTau217 positive >0.69 pg/mL pTau217 negative <0.66 pg/mL			pTau217 positive >1.04 pg/mL pTau217 negative <0.47 pg/mL		
Cohort	SU Discovery (NSD+)	LBD-SU	LBD-SPIN	Cohort	SU Discovery (NSD+)	LBD-SU	LBD-SPIN	SU Discovery (NSD+)	LBD-SU	LBD-SPIN
<b>Plasma A<math>\beta</math> positive, No. (%)</b>	33 (49.3)	11 (37.9)	32 (72.7)	<b>Plasma A<math>\beta</math> positive, No. (%)</b>	29 (43.4)	6 (20.7)	22 (50.0)	13 (19.4)	2 (6.9)	8 (18.2)
				<b>Plasma A<math>\beta</math> intermediate, No. (%)</b>	1 (1.5)	1 (3.4)	3 (6.8)	23 (34.3)	11 (37.9)	25 (56.8)
<b>Plasma A<math>\beta</math> negative, No. (%)</b>	34 (50.7)	18 (62.1)	12 (27.3)	<b>Plasma A<math>\beta</math> negative, No. (%)</b>	37 (55.2)	22 (75.9)	19 (43.2)	31 (46.3)	16 (55.2)	11 (25.0)
<b>Sensitivity, %</b>	96.4	88.9	95.7	<b>Sensitivity, lower cut point, %</b>	89.3	75.0	90.5	91.7	66.7	88.9
<b>Specificity, %</b>	84.6	85.0	52.4	<b>Specificity, upper cut point, %</b>	89.5	100.0	85.0	93.8	100.0	100.0

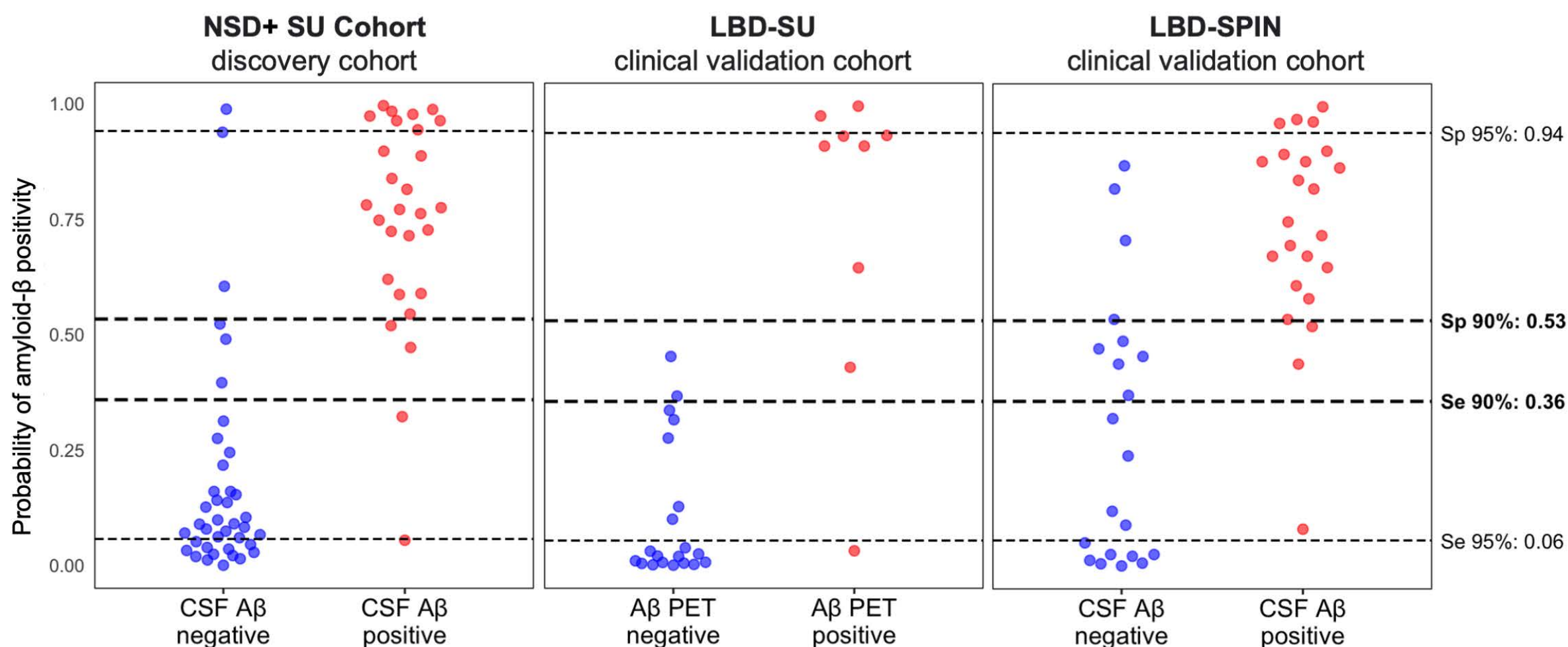
<b>PPA, %</b>	81.8	72.7	68.8	<b>PPA, upper cut point, %</b>	86.2	100.0	86.4	84.6	100.0	100.0
<b>NPA, %</b>	97.1	94.4	91.7	<b>NPA, lower cut point, %</b>	91.9	90.9	89.5	96.8	93.8	90.9
<b>OPA, %</b>	89.6	86.2	75.0	<b>OPA for plasma pTau217 positive and negative, %</b>	89.4	92.9	87.8	93.2	94.4	94.7

Note. The one-reference cut point for plasma pTau217 was calculated using the Youden Index. Two-reference cut points were calculated at 90% sensitivity/90% specificity, and at 95% sensitivity/95% specificity. Cut points were established in the biologically defined NSD+ SU Discovery cohort and applied to the clinically defined LBD-SU and LBD-SPIN cohorts. Amyloid- $\beta$  positivity was determined by CSF A $\beta$ 42/40 status (normal/abnormal) using a 36 centiloid A $\beta$  PET reference threshold. Abbreviations: Se, sensitivity; Sp, specificity; A $\beta$ , amyloid- $\beta$ ; SU, Stanford University; LBD, Lewy body disease; SPIN, Sant Pau Initiative on Neurodegeneration; pTau217, phosphorylated tau 217; PPA, positive percentage agreement; NPA, negative percentage agreement; OPA, overall percentage agreement; NSD+, individuals with Neuronal Synuclein Disease.

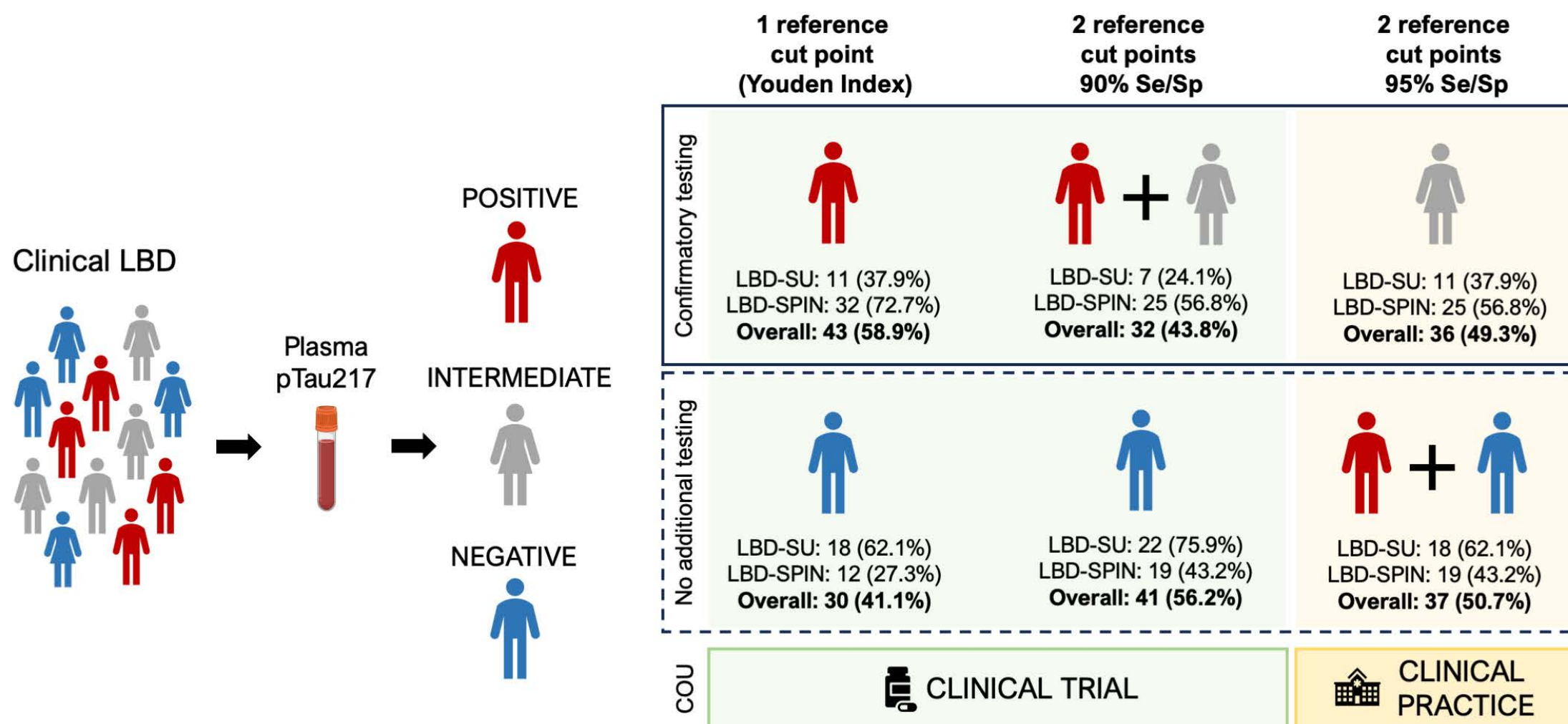


**A. NSD+ 36CL****B. NSD- 36CL****C. NSD+ 24CL****D. NSD- 24CL**

## A. Predicted probability of amyloid- $\beta$ positivity using plasma pTau217



## B. Workflow of amyloid- $\beta$ detection with plasma pTau217 in the clinical validation cohorts



## C. Sample size estimates for hypothetical clinical trials in NSD

SU discovery cohort	Scenario 1: To include 100 amyloid- $\beta$ positive LBD participants		
	1 reference cut point (Youden Index)	2 reference cut points 90% Se/Sp	2 reference cut points 95% Se/Sp
Plasma pTau217 positivity, %	49.3%	43.3%	19.4%
PPV, %	81.8%	86.2%	84.6%
Number of plasma pTau217 positives needed	~122	~116	~118
Number to screen	~248	~248	~610

SU discovery cohort	Scenario 2: To include 100 amyloid- $\beta$ negative LBD participants		
	1 reference cut point (Youden Index)	2 reference cut points 90% Se/Sp	2 reference cut points 95% Se/Sp
Plasma pTau217 negativity, %	50.7%	55.2%	46.3%
NPV, %	97.1%	91.9%	96.8%
Number of plasma pTau217 negatives needed	~103	~109	~103
Number to screen	~203	~197	~123