



Quanterix[®]

Discovery Fueled by Ultra-Sensitivity

Ultrasensitive biomarker detection to transform the future of healthcare

Danilo La Terra

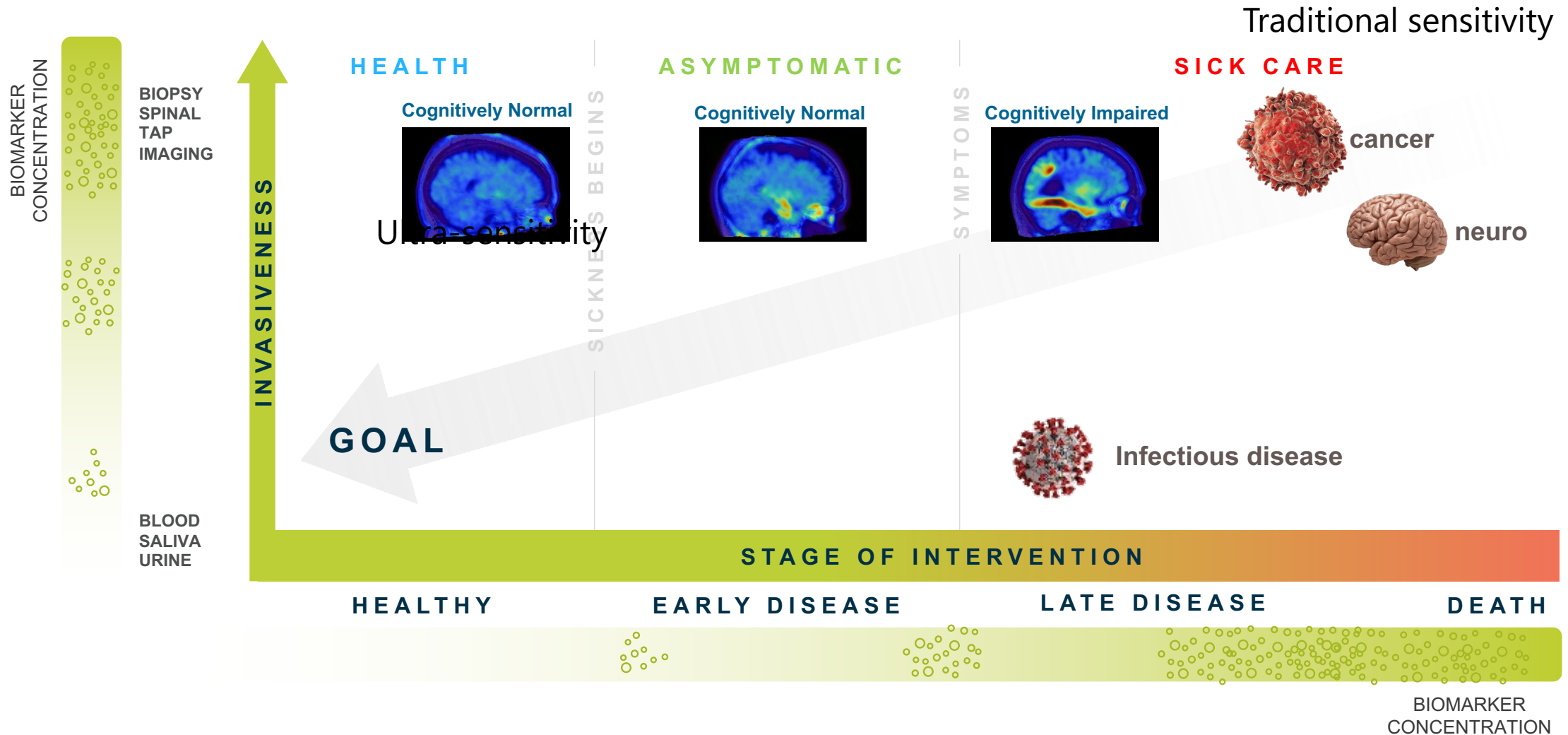
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Disclosure

Danilo La Terra is an employee at Quanterix corporation

Measurement of fluid biomarkers with ultra-sensitivity

Why it matters?



Simoa Bead Assay: Principle



Single-molecule enzyme-linked immunosorbent assay detects serum proteins at subfemtomolar concentrations

David M Rissin^{1,3}, Cheuk W Kan^{1,3}, Todd G Campbell¹, Stuart C Howes¹, David R Fournier¹, Linan Song¹, Tomasz Piech¹, Purvish P Patel¹, Lei Chang¹, Andrew J Rivnak¹, Evan P Ferrell¹, Jeffrey D Randall¹, Gail K Provuncher¹, David R Walt² & David C Duffy¹

The ability to detect single protein molecules^{1–2} in blood could accelerate the discovery and use of more sensitive diagnostic biomarkers. To detect low-abundance proteins in blood, we captured them on microscopic beads decorated with specific antibodies (one target protein molecule per bead) and then labeled the immunocomplexes with an enzymatic reporter capable of generating a fluorescent product. After isolating the beads in 50-fl reaction chambers designed to hold only a single bead, we used fluorescence imaging to detect single protein molecules. Our single-molecule enzyme-linked immunosorbent assay (digital ELISA) approach detected as few as ~10–20 enzyme-labeled complexes in 100 μ l of sample (~10⁻¹⁹ M) and routinely allowed detection of clinically relevant proteins in serum at concentrations (<10⁻¹⁵ M) much lower than conventional ELISA^{3–5}. Digital ELISA detected prostate-specific antigen (PSA) in sera from patients who have undergone radical prostatectomy at concentrations as low as 14 fg/ml (0.4 fM).

The clinical use of protein biomarkers to differentiate between healthy and disease states, and to monitor disease progression, requires the measurement of low concentrations of proteins in complex samples. Current immunoassays typically measure proteins at concentrations above 10⁻¹² M⁶. The serum concentrations of the majority of proteins important in cancer⁷, neurological disorders^{8,9}, and the early stages of infection¹⁰, however, are thought to range from 10⁻¹⁶ to 10⁻¹² M. For instance, a 1-mm³ tumor composed of a million cells that each secrete 5,000 proteins into 5 liters of circulating blood translates to a concentration of ~2 \times 10⁻¹⁵ M (or 2 fM). Moreover, serum from individuals recently infected with HIV contains 10–3,000 virions per ml, resulting in estimated concentrations of the p24 capsid antigen ranging from 50 \times 10⁻¹⁸ M (50 aM) to 15 \times 10⁻¹⁵ M (15 fM)¹¹. Attempts to develop methods capable of measuring these concentrations of proteins have focused on the replication of nucleic acid labels on proteins^{11,12}, or on measuring the bulk, ensemble properties of labeled protein molecules^{13–16}. The work of Mirkin *et al.*^{11,17} and others¹⁸ using labels based on gold nanoparticles and DNA biobarcode has pushed the detection of proteins into the low femtomolar range; a recent report

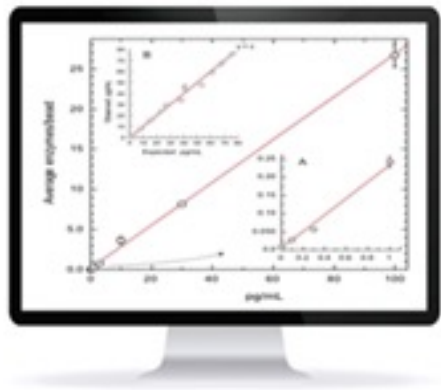
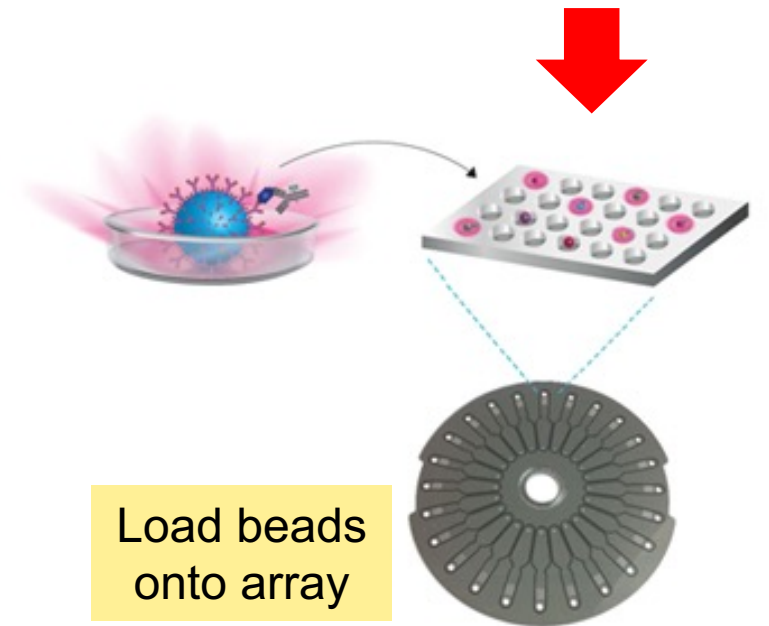
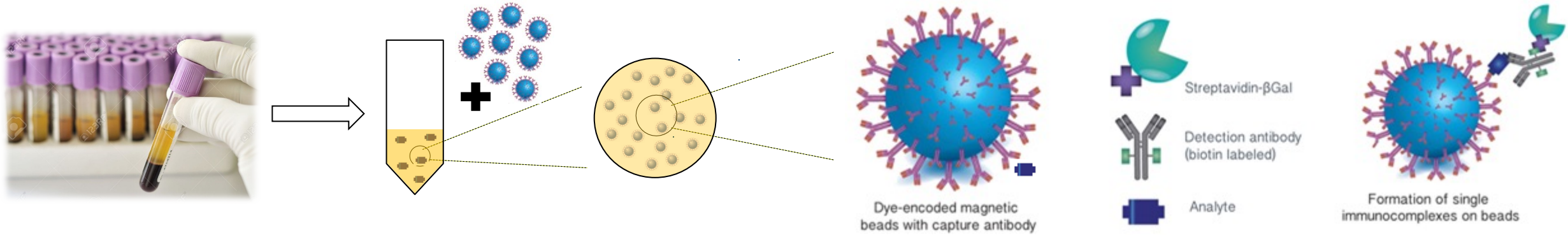
using this technology demonstrated the detection of 10 fM of PSA in serum¹⁷. Nonetheless, the sensitivities achieved by methods for detecting proteins still lag behind those for nucleic acids, such as PCR, limiting the number of gene products that have been detected in blood^{6,19}. The isolation and detection of single protein molecules provides a promising approach for measuring extremely low concentrations of proteins^{1,2}. For example, Todd *et al.*² have developed flow-based methods for serially detecting single fluorescently labeled detection antibodies that have been released from immunocomplexes formed on solid substrates. Here, we report an approach for detecting thousands of single protein molecules simultaneously using the same reagents as the gold standard for detecting proteins, namely, the ELISA. This method has been used to detect proteins in serum at subfemtomolar concentrations.

Our approach makes use of arrays of femtoliter-sized reaction chambers (Fig. 1)—which we term single-molecule arrays (SIMoAs)—that can isolate and detect single enzyme molecules^{20–24}. This approach builds from the work of Walt *et al.*^{20–23}, who used these arrays to study the kinetics²¹ and inhibition²⁰ of single enzymes. Our objective was to exploit the ability of SIMoAs to trap and detect single enzymes to detect single enzyme-labeled proteins. In the first step of this single-molecule immunoassay (Fig. 1a) a sandwich antibody complex is formed on microscopic beads (2.7 μ m diameter), and the bound complexes are labeled with an enzyme, as in a conventional bead-based ELISA. When assaying samples containing extremely low concentrations of protein, the ratio of protein molecules (and the resulting enzyme-labeled complex) to beads is small (typically <1:1) and, as such, the percentage of beads that contain a labeled immunocomplex follows a Poisson distribution. At low concentrations of protein, the Poisson distribution indicates that beads carry either a single immunocomplex or none. For example, if 50 aM of a protein in 0.1 ml (3,000 molecules) is captured and labeled on 200,000 beads, then 1.5% of the beads will carry one protein molecule and 98.5% will not carry any protein molecules (Fig. 1b)²². It is not possible to detect these low numbers of enzyme labels using standard detection technology (for example, a plate reader), because the fluorophores generated by each enzyme diffuse into a large assay volume (typically 0.1–1 ml), and it takes hundreds of thousands of enzyme labels to generate a

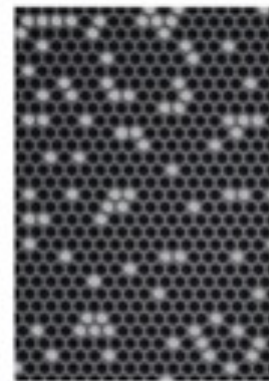
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Simoa Bead Assay: Principle

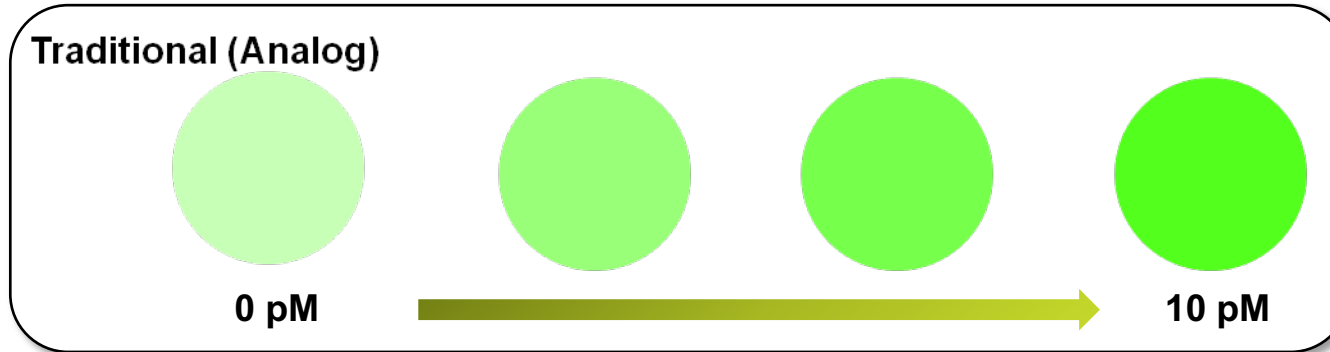


Analyze and Report



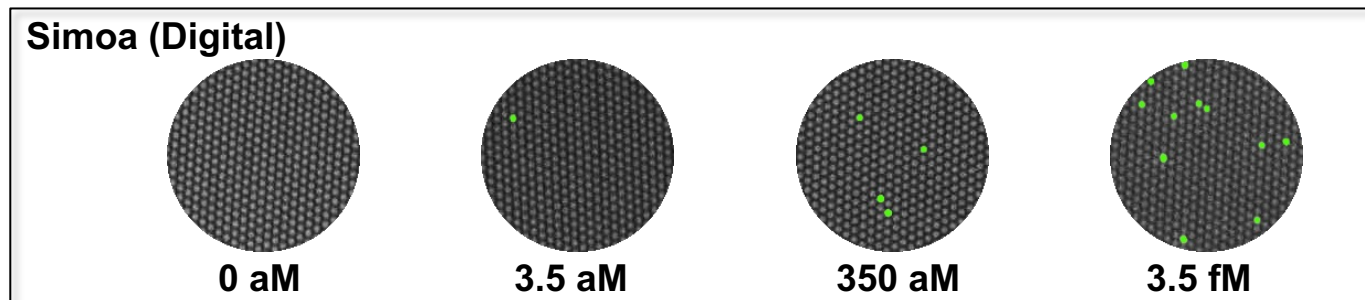
Image

Simoa Bead Assays: Digital vs. Analog Detection



- Reaction volume = 100×10^{-6} L
- Diffusion = dilution = low sensitivity
- Millions of molecules needed to reach detection limit

Microliters (μ L)

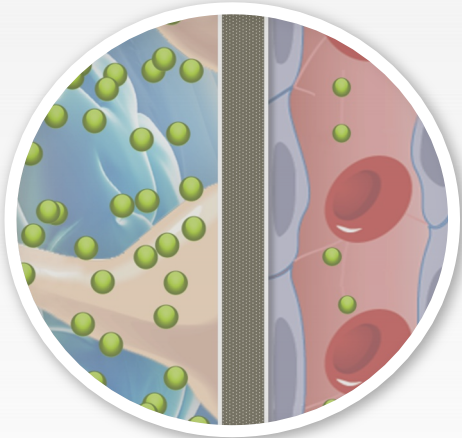


- Reaction volume = 50×10^{-15} L (**2 billion times smaller**)
- Diffusion defeated = single molecule resolution = ultimate sensitivity
- **One molecule needed to reach detection limit**

Femtoliters (fL)

Simoa sensitivity enables research across therapeutic and disease areas

Neurology



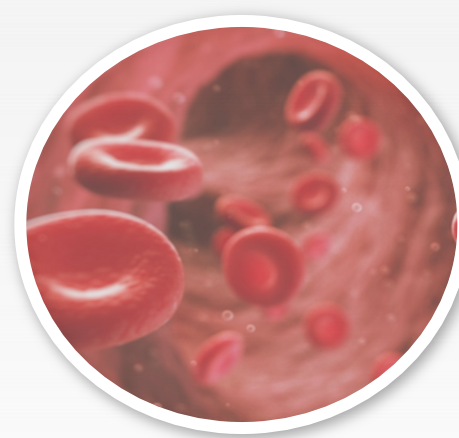
- Alzheimer's
- TBI/concussion
- MS
- Parkinson's
- ALS

Oncology



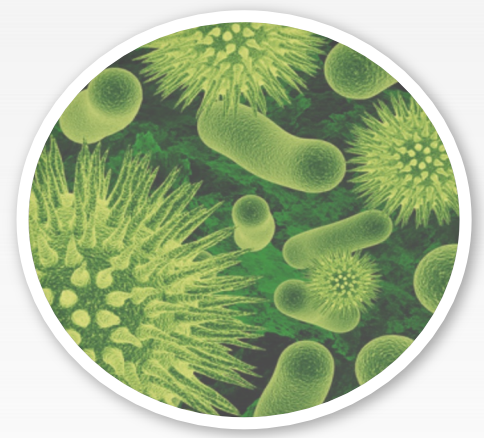
- Prostate Cancer
- Breast Cancer
- Pancreatic Cancer
- Cervical Cancer
- Lung Cancer

Inflammation



- Diabetes
- Celiac Disease
- Lupus
- Rheumatoid Arthritis
- Ulcerative Colitis

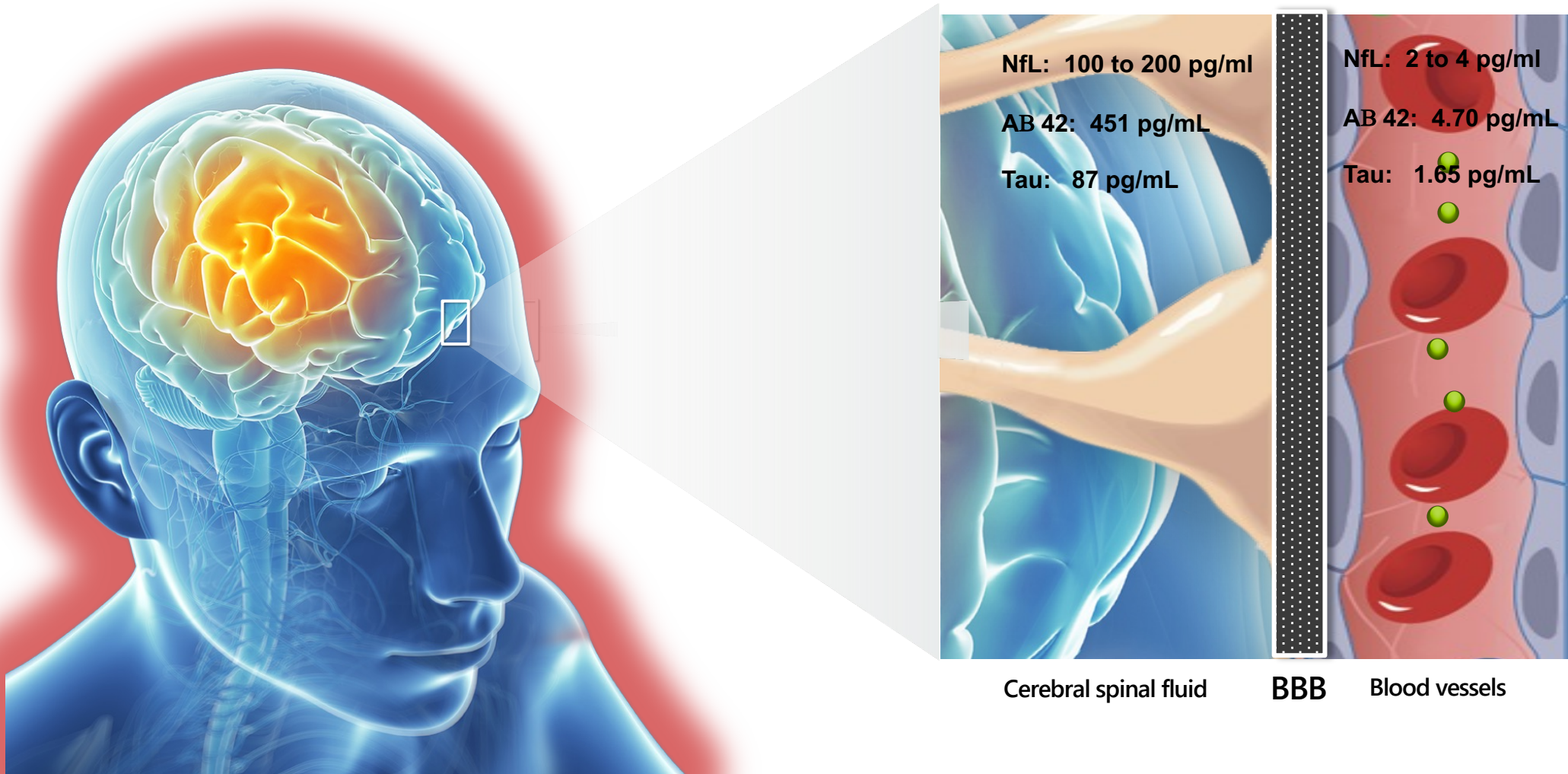
Infectious Disease



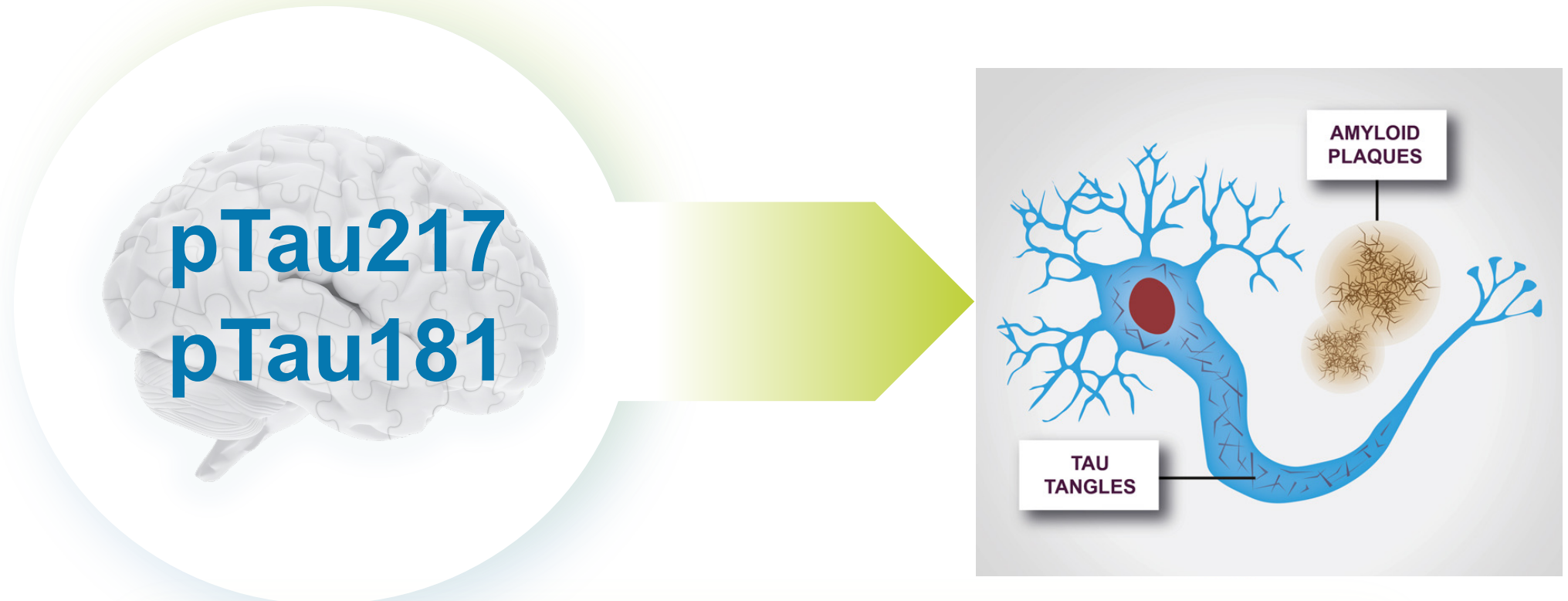
- HIV
- HCV
- *C. difficile*
- Tuberculosis
- COVID-19

Revolution in Neuronal Biomarkers Measurement: CSF & Blood

Brain Health with a non-invasive Blood Test



blood pTaus offer a crucial tool for the early detection and predictive assessment of Alzheimer's disease (AD)



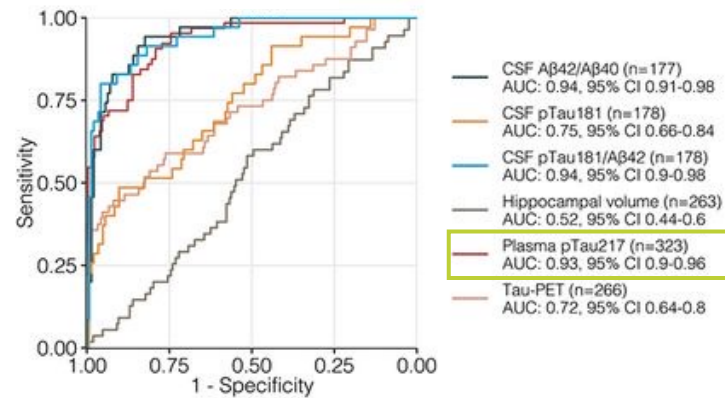
Highly accurate biomarker to assess Alzheimer's Disease

Plasma ALZpath pTau217 diagnostic accuracy in identifying Alzheimer's disease pathology

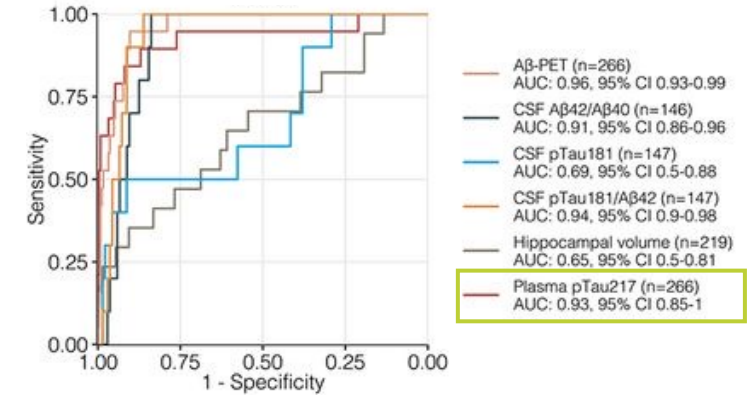
- Plasma pTau217 is comparable to CSF biomarkers in identifying AD pathology
- Plasma pTau217 accurately identifies the A T status in all cohorts, with highest levels in the A+T+ group.
- In the 8 years of longitudinal sampling in WRAP, the A+T+ group demonstrated a significantly higher annual increase in plasma pTau217 levels compared to the A-T-group.

Plasma pTau217 has similar accuracies to cerebrospinal fluid biomarkers and detects longitudinal changes.

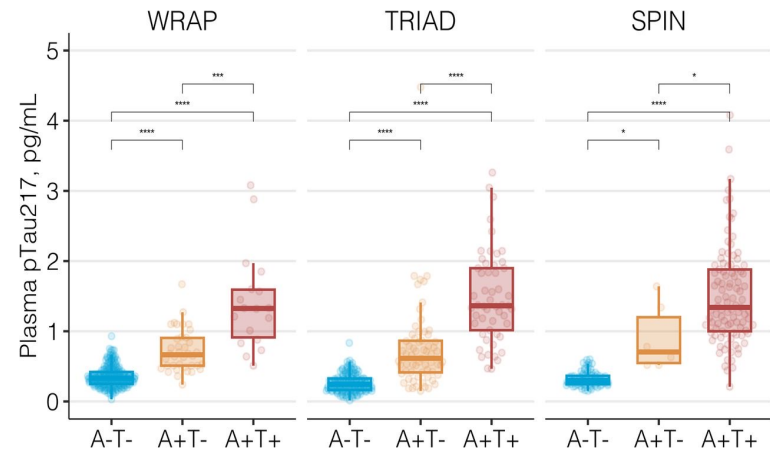
ROC curve to determine abnormal Aβ-PET (WRAP cohort)



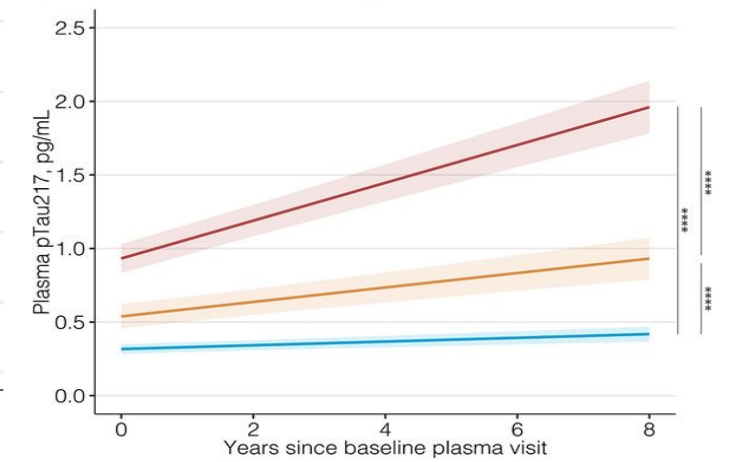
ROC curve to determine abnormal tau-PET (WRAP cohort)



Plasma p-tau217 according to amyloid and tau profiles in all the tested cohorts



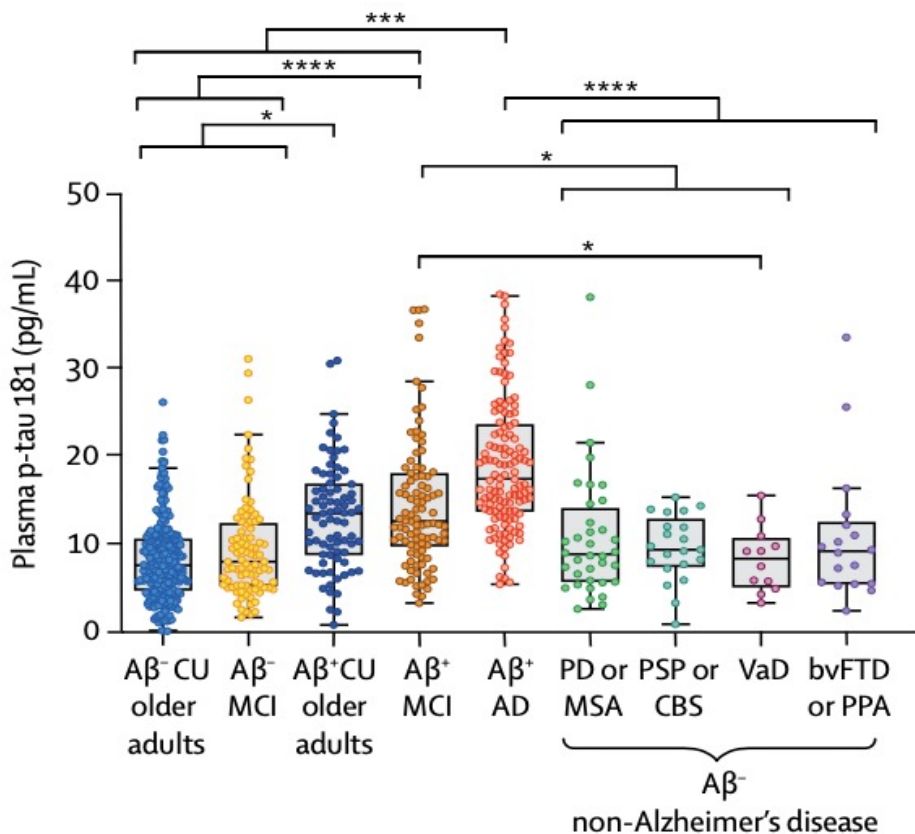
Longitudinal trajectories of plasma p-tau217 according to amyloid and tau PET (WRAP cohort)



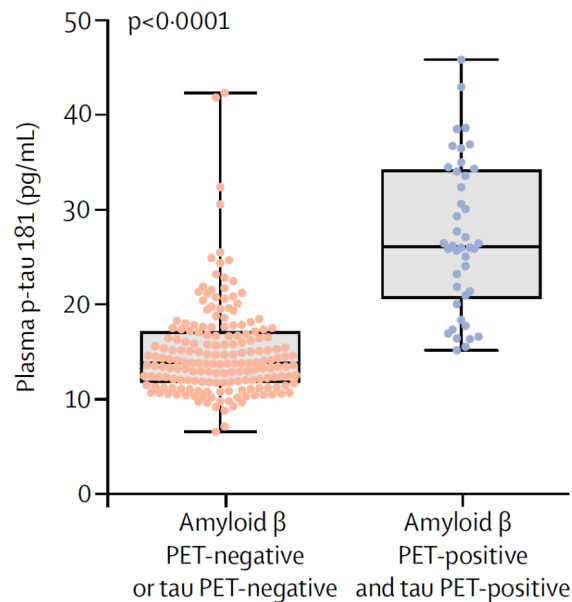
Blood phosphorylated tau 181 (p-tau181) as a specific biomarker for Alzheimer's disease

- Blood p-tau181 can predict tau and amyloid β pathologies, differentiate AD from other neurodegenerative disorders, and identify AD across the clinical continuum.

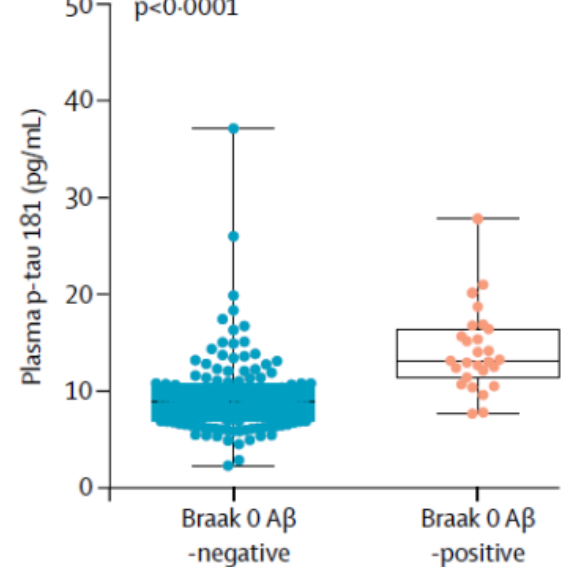
Blood p-tau181 may be used as a simple, accessible, and scalable test for screening and diagnosis of AD



Association with PET data for Amyloid and Tau pathology



Early amyloid pathology (no tau pathology)



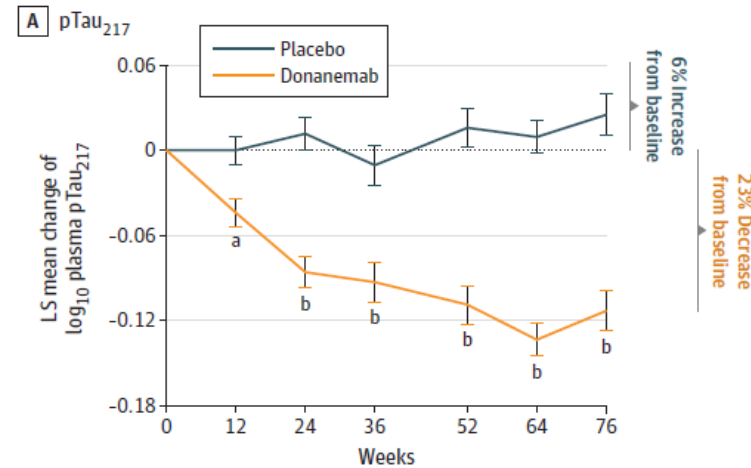
CU: Cognitively unimpaired PSP: Progressive supranuclear palsy
 MCI: Mild cognitive impairment CBS: Corticobasal syndrome
 AD: Alzheimer disease VaD: Vascular dementia.
 PD: Parkinson's disease bvFTD: Behavioural variant frontotemporal dementia
 MSA: Multiple systems atrophy PPA: Primary progressive aphasia.

Association of Donanemab Treatment With Plasma pTau217 and GFAP in early symptomatic AD

In the TRAILBLAZER-ALZ randomized, double-blind, placebo-controlled clinical trial: 272 participants received Donanemab or placebo and changes in plasma biomarkers pTau217, GFAP, NFL, Ab42/40 were measured.

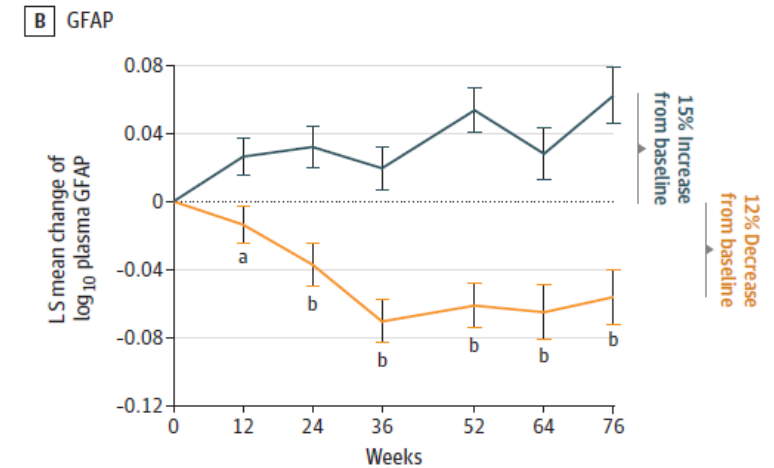
Mean plasma pTau217 and GFAP levels significantly decreased by 23% and 12% respectively after treatment.

Plasma pTau217 and GFAP reliably track treatment effectiveness and identify changes in AD pathology when using anti-amyloid therapy



No. at risk

Placebo	119	113	110	103	89	85	86
Donanemab	123	119	110	100	90	84	86



No. at risk

Placebo	104	87	91	85	71	69	67
Donanemab	106	93	84	79	70	63	69

NfL blood test - Key Biomarker to Assess Neural Damage



NfL is widely used in therapeutics trials with potential to become a standard for assessing brain health in clinical care

NfL and Multiple Sclerosis: Disease Activity and Treatment Response

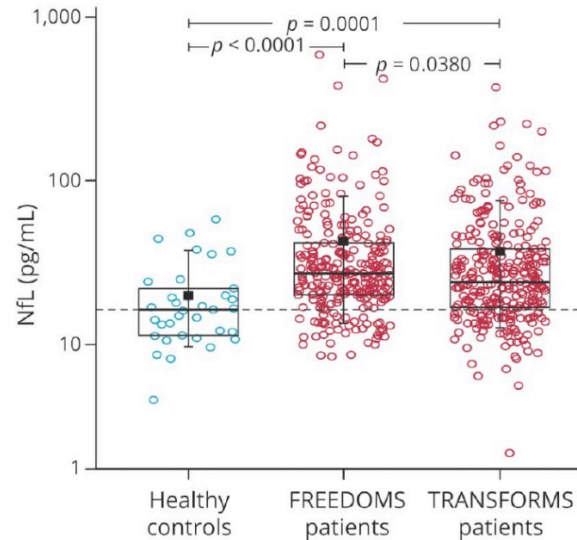
Blood NfL levels associate with clinical, MRI measures and treatment response in patients with RRMS in clinical trials

- Plasma NfL from 589 RRMS patients
- Baseline NfL higher in MS patients than in healthy controls and correlated with total lesion load, number of active lesions and treatment response

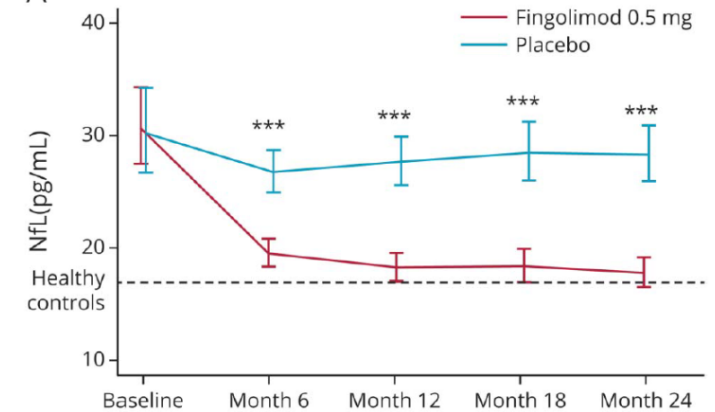
Blood NfL as an easily accessible biomarker of disease evolution and treatment response, also in a controlled clinical trial setting

RRMS: Relapsing Remitting Multiple Sclerosis
NfL: Neurofilament light

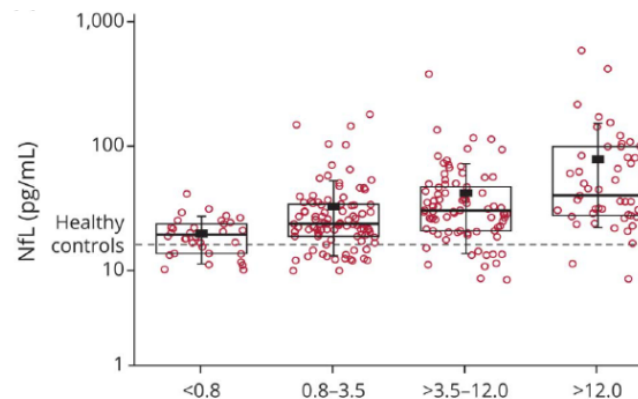
Combined FREEDOMS and TRANSFORMS



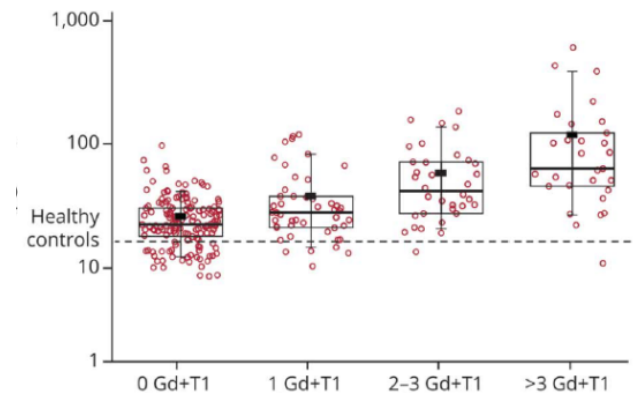
Effect of Fingolimod FREEDOMS



T2 lesion volume (total lesion load)
FREEDOMS

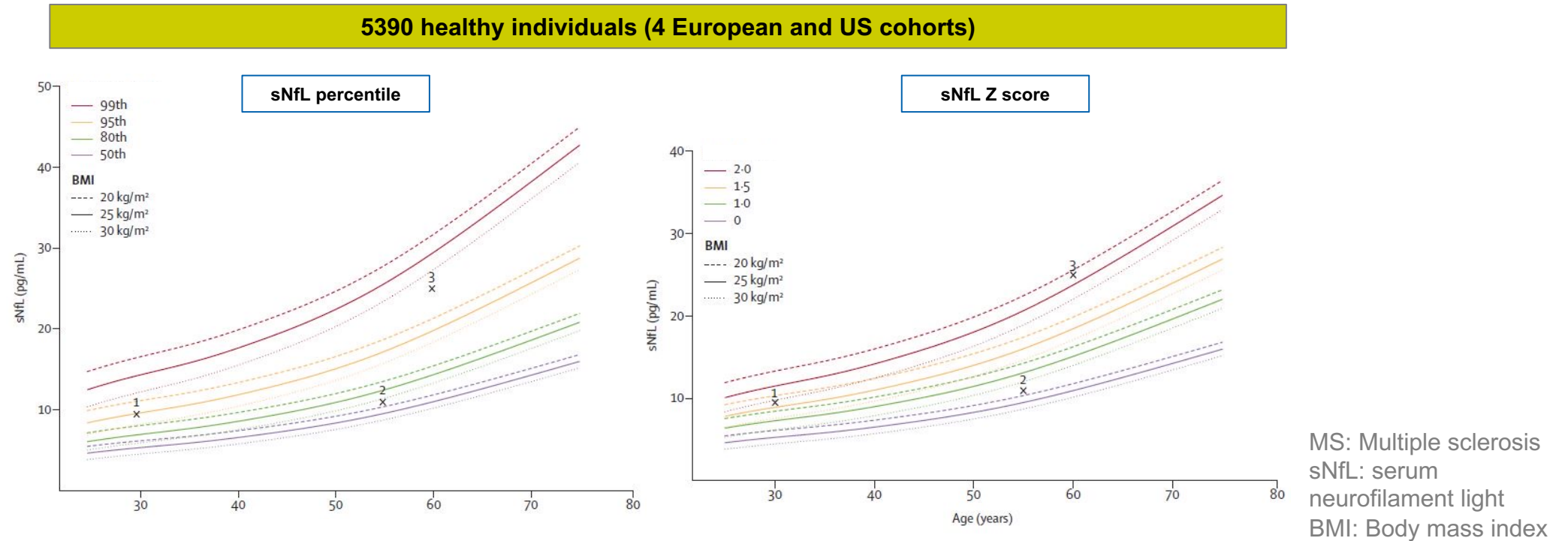


Gd+ T1 lesion count (active lesion)
FREEDOMS



Establishing sNfL normative ranges to aid identification of future MS risk

Seminal study defining sNfL reference values and development of online app







- Age related increase of sNfL in controls is not linear, but has a steeper increase after 50 years
- Increased Z scores outperformed absolute raw sNfL cutoff values for diagnostic accuracy

Easy identification and interpretation of elevated sNfL levels is more feasible in clinical practice

Clinical trial engagement

Non-invasive blood biomarker measurements empower pre- and post-market clinical trials

		 		
Donanemab Phase 2	JNJ-6373365 Phase 2	Lecanemab Phase 3	Ranibizumab Phase 4	Patisiran Phase 3
Simoa based pTau217	Simoa based pTau217+	Simoa pTau181 , GFAP, NfL	Simoa based VEGF assay	Simoa NfL assay
Collaboration of future multiplex biomarkers - AD	Analytical Validation - AD	Clinical trial support - AD	Clinical trial support - Macular Degeneration: Ranibizumag vs Aflibercept.	APOLLO study Polyneuropathy treatment Transthyretin- mediated (hATTR) amyloidosis

ELISA

ng/mL

pg/mL

fg/mL

900x
Sensitivity
increase

Simoa® Today

Simoa® innovation

Thanks!



Early disease
detection

