ADNI PET Core Update

WW ADNI
Boston
July 2013

Current ADNI PET Data

Florbetapir

1011 Baseline scans (910 Processed)

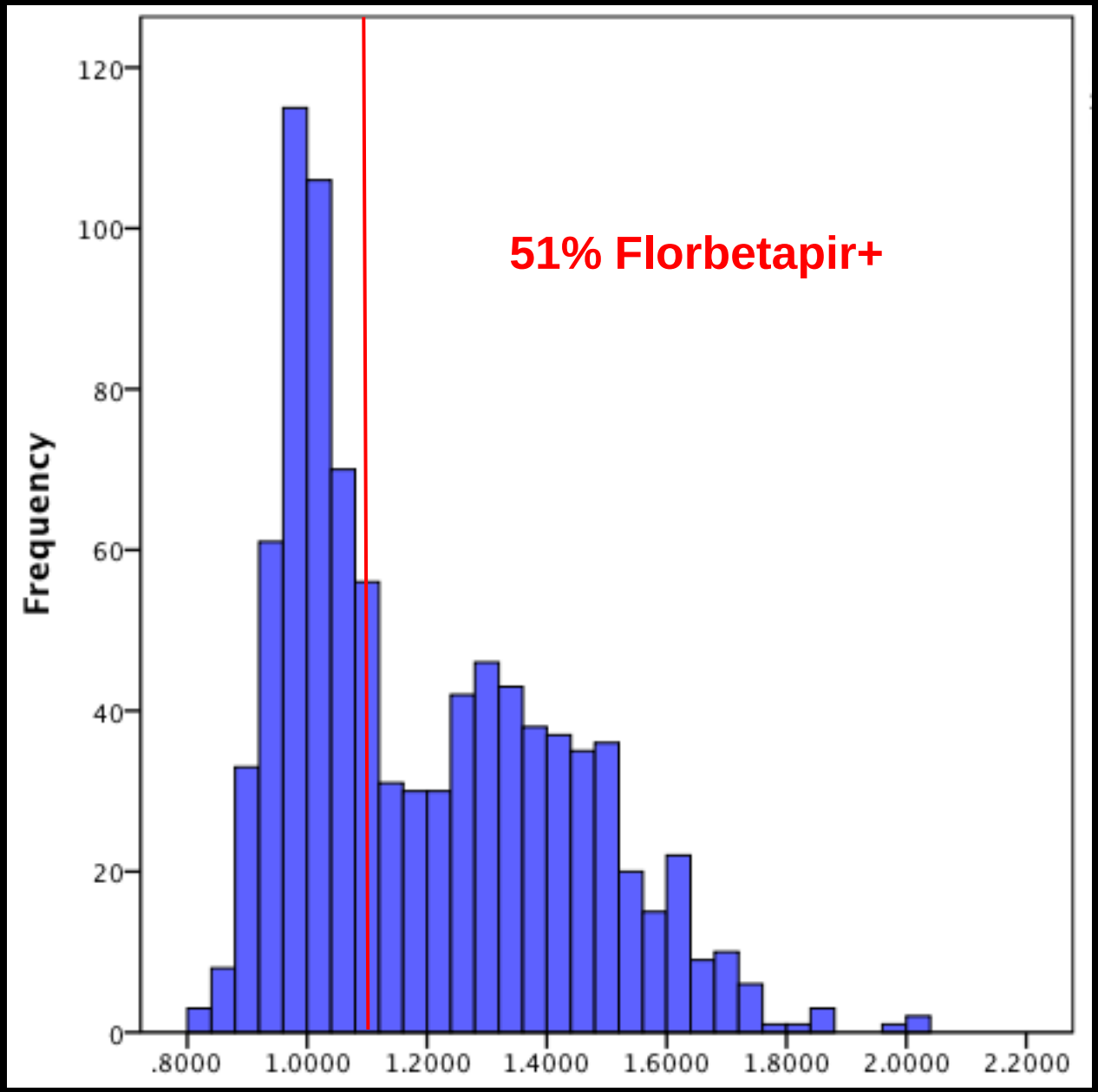
174 Follow-up scans (all processed)

39 “early frame” datasets

FDG (N = 2920)

	AD	EMCI	LMCI	N	SMC
Baseline	225	308	396	318	29
6 month	88		186	94	
12 month	76	64	202	130	
18 month			153		
24 month	62	4	149	100	
36 month			111	72	
48 month			58	57	
60 month			14	24	

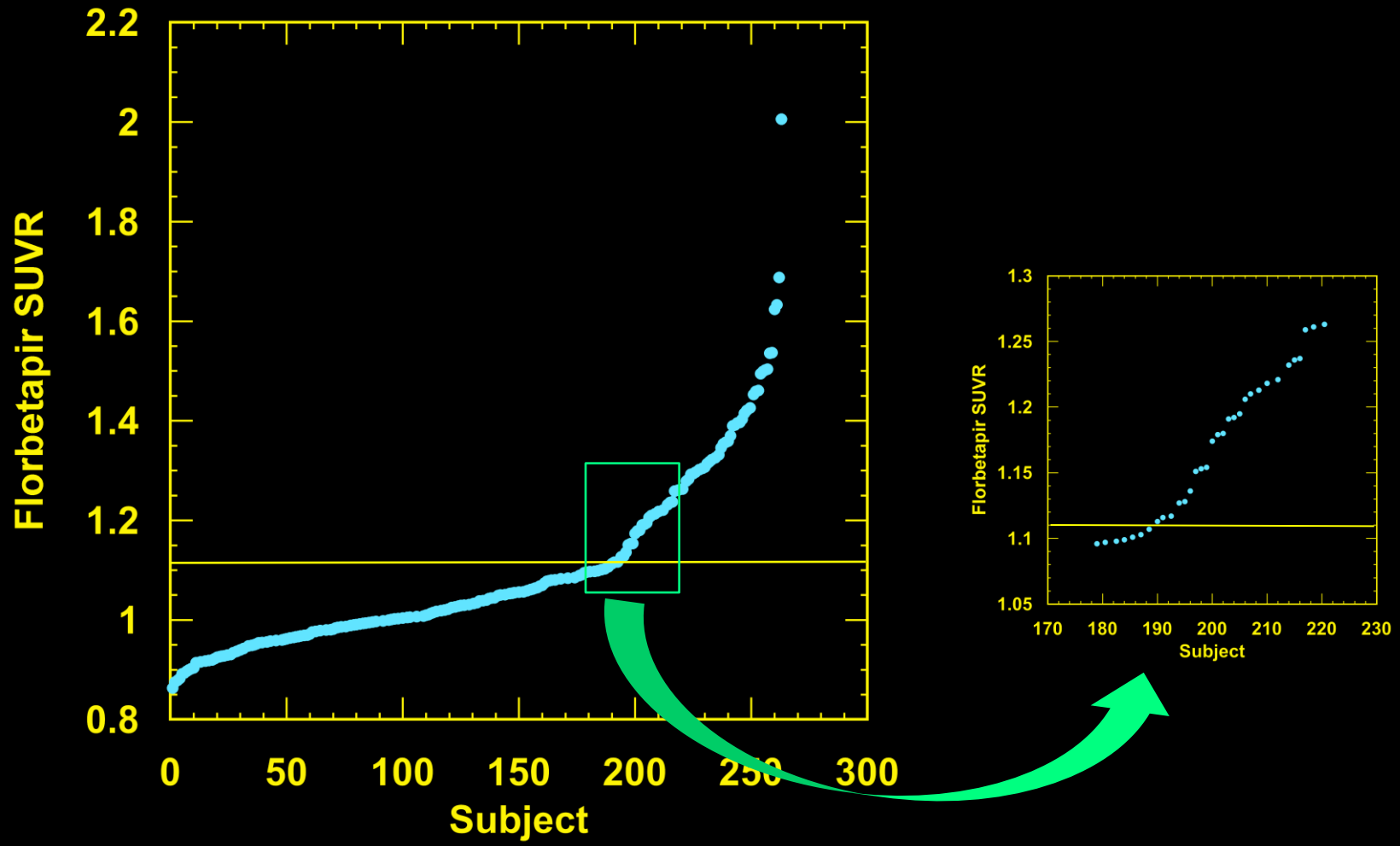
Florbetapir Frequency Distribution



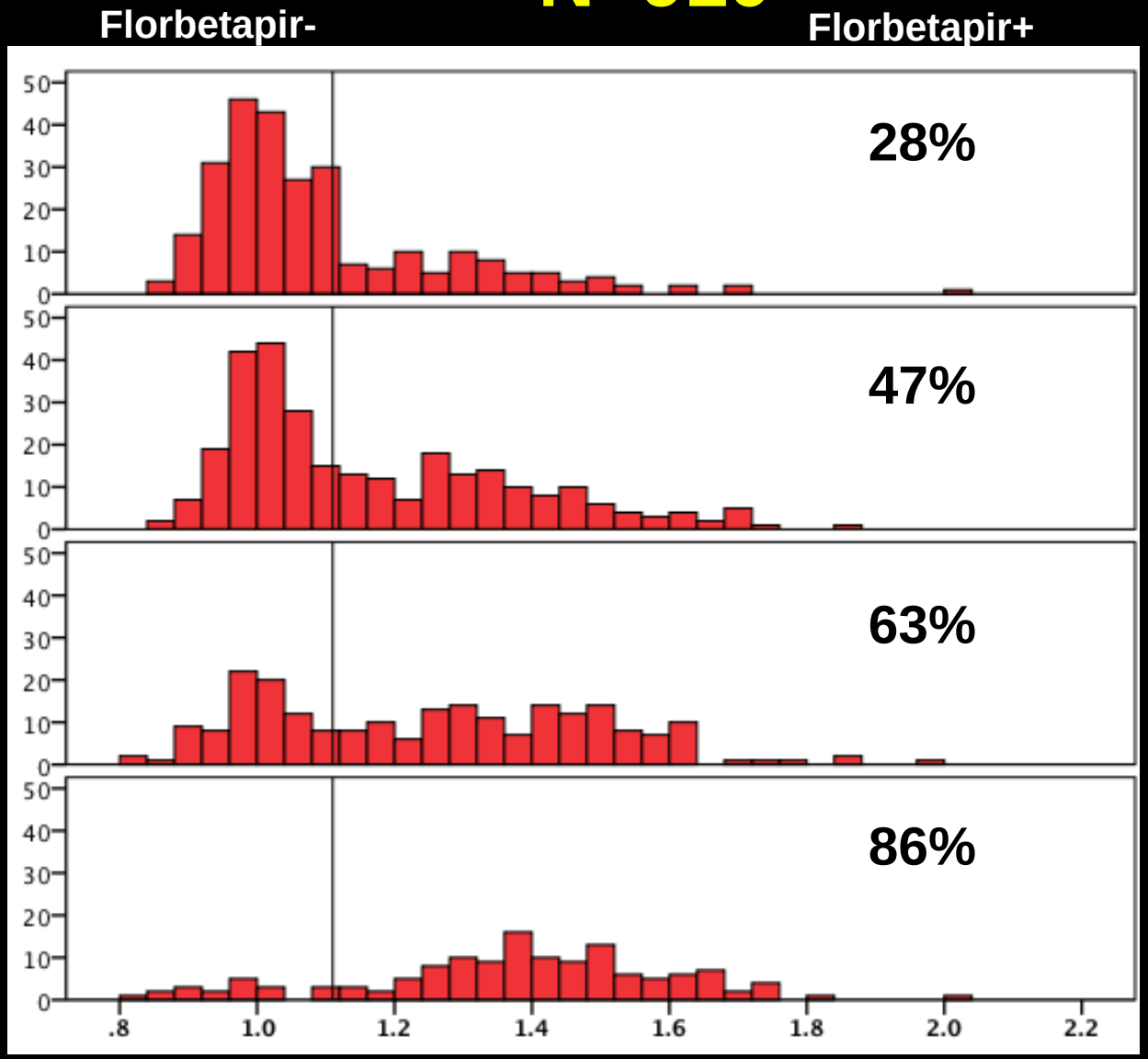
910 Subjects

263 Normals
289 EMCI
212 LMCI
146 AD

Florbetapir Threshold in Normals
1.11



ADNI Florbetapir summary March 2013 N=910



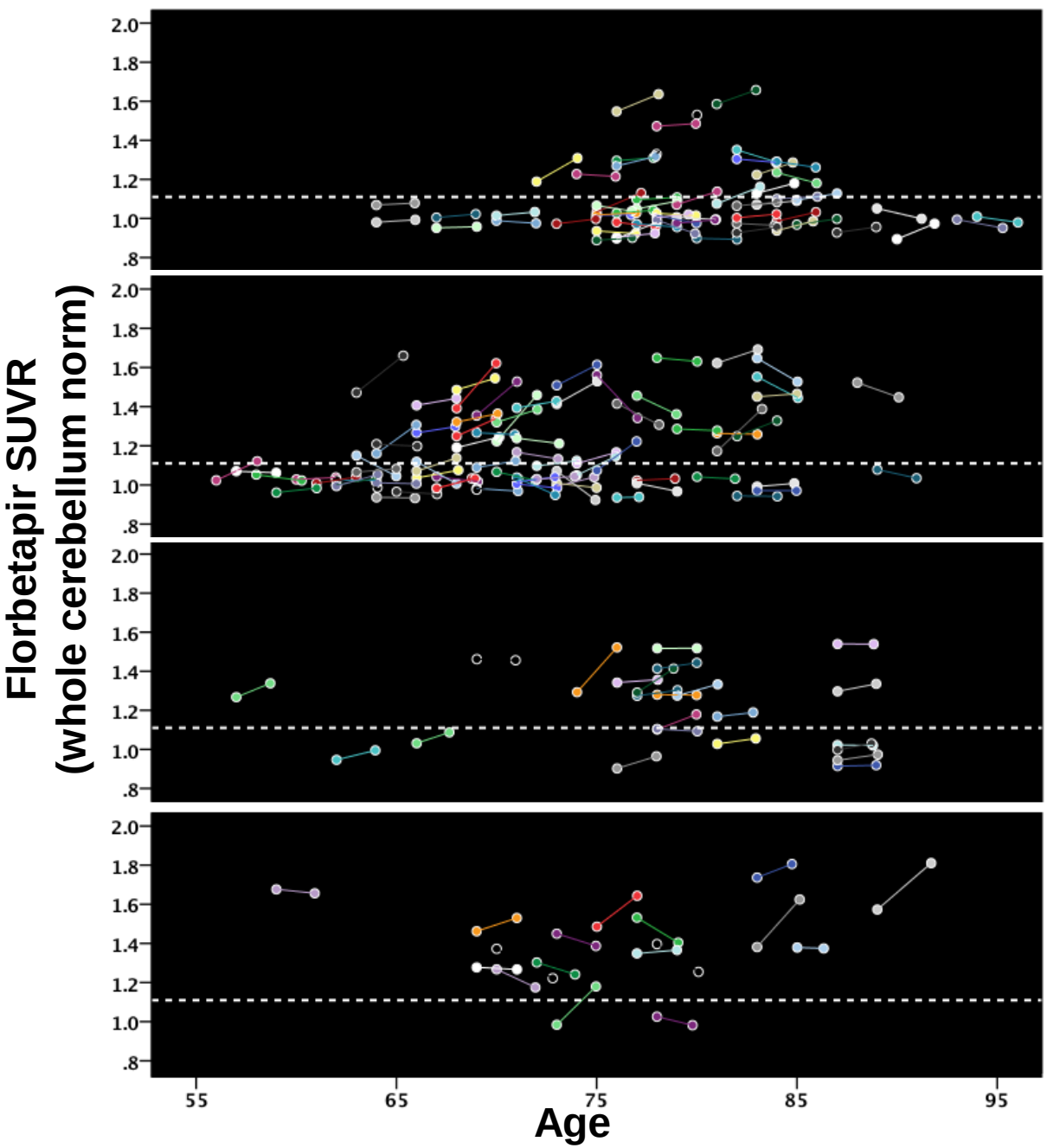
Normal
N=263

Early MCI
N=289

Late MCI
N=212

AD
N=146

Florbetapir 2 yr change



DX at first florbetapir

Normal N=58

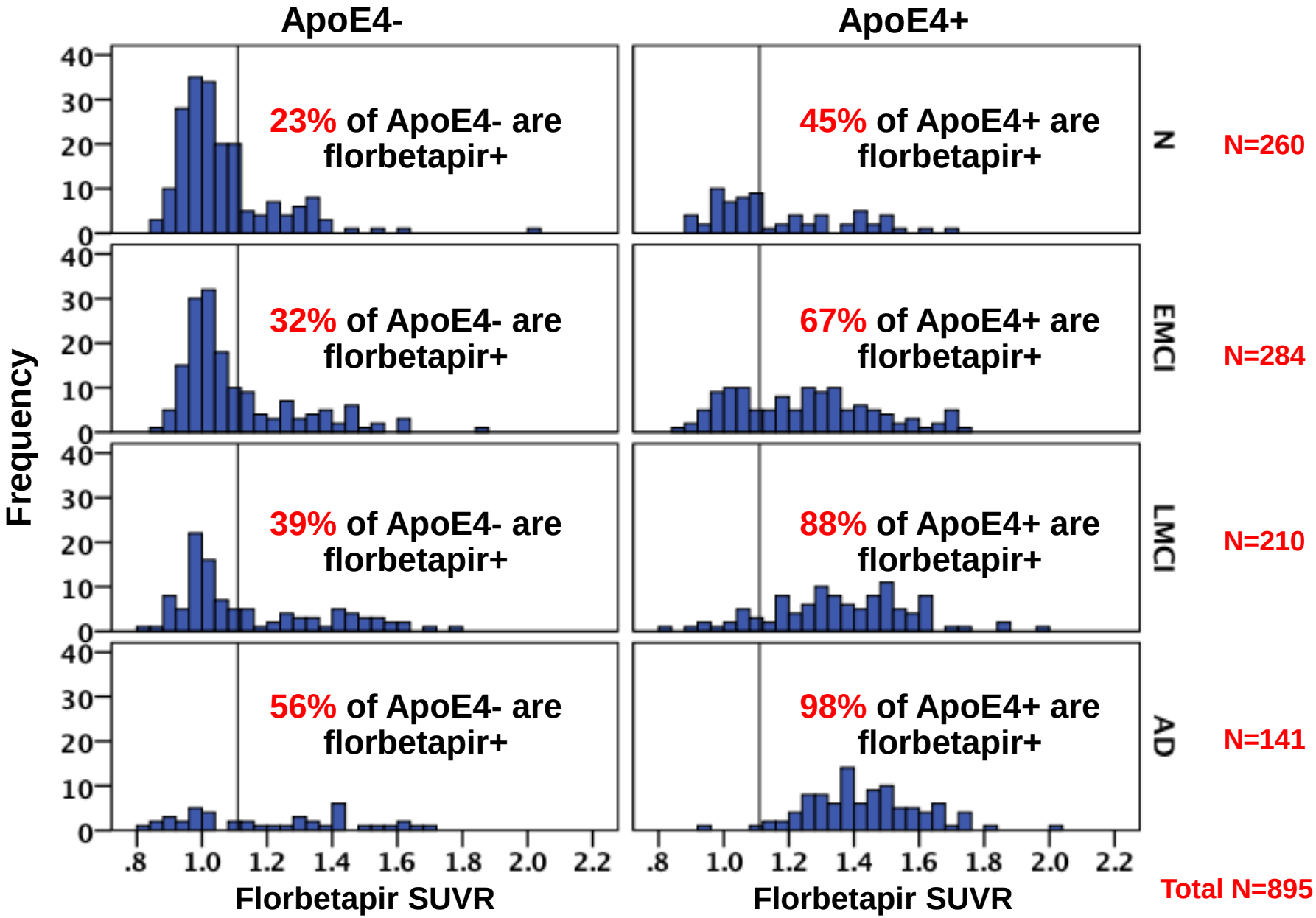
EMCI N=76

LMCI N=23

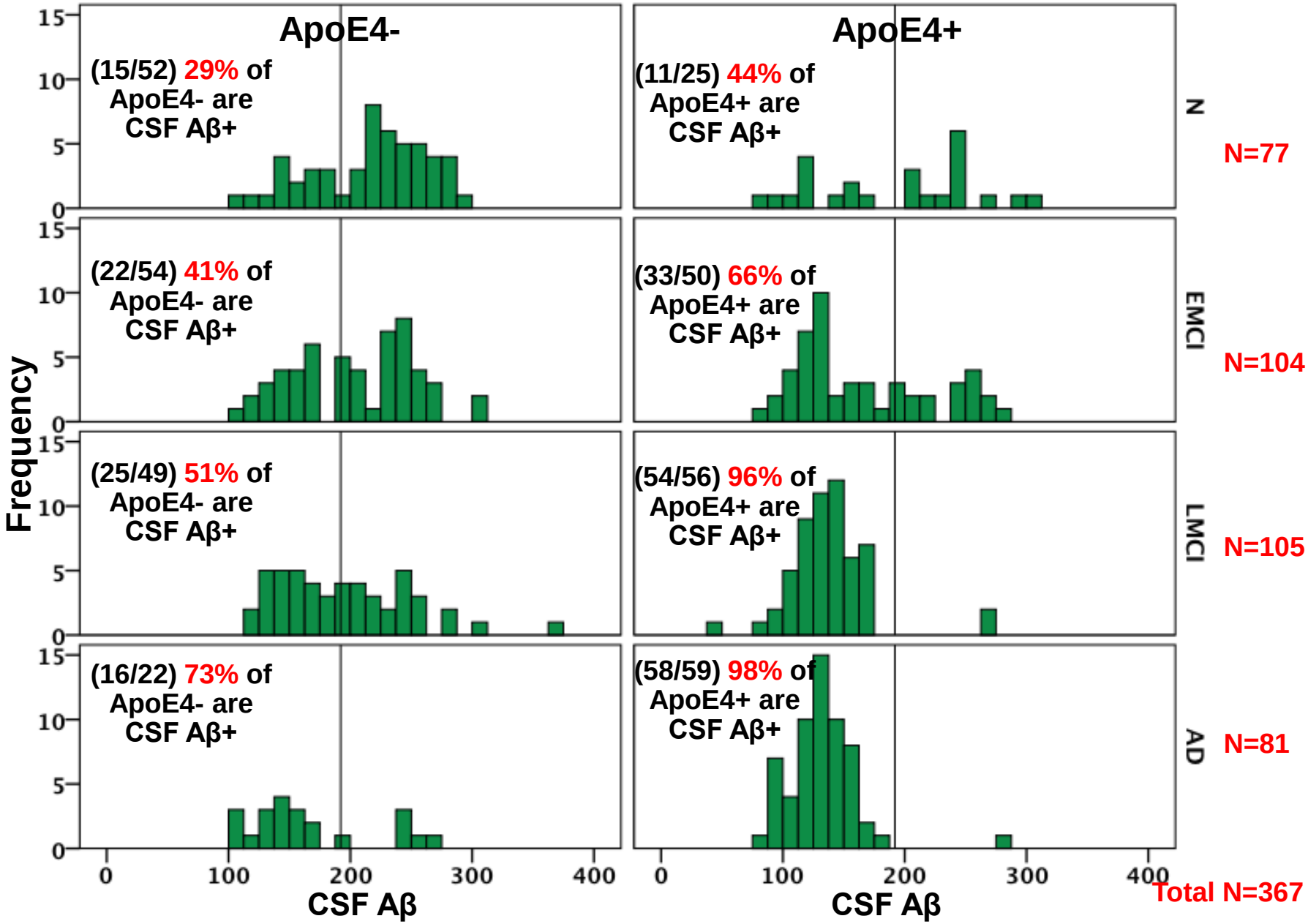
AD N=17

Total N=174

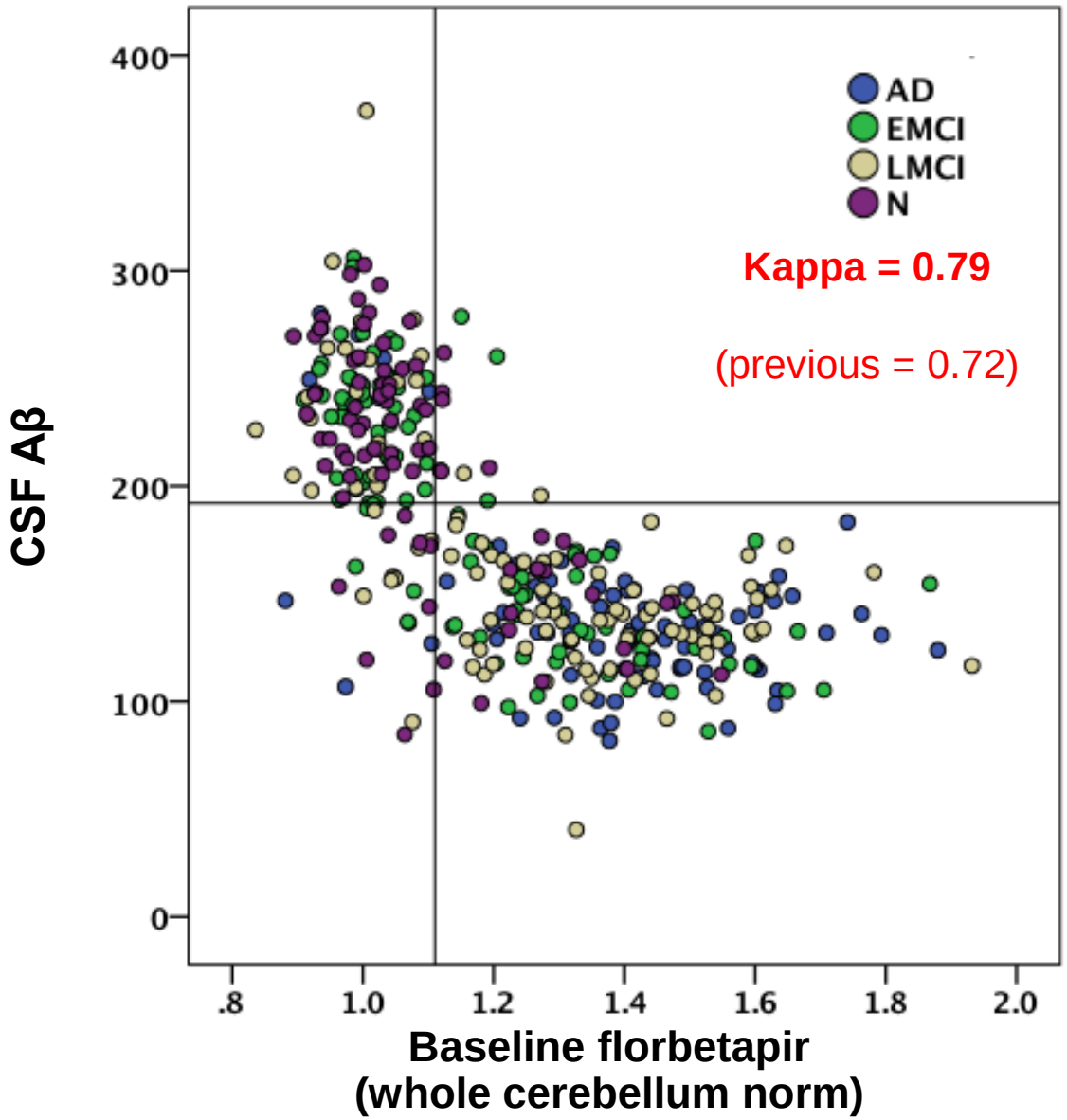
ADNI Florbetapir distribution stratified by ApoE4 status



ADNI CSF Aβ distribution stratified by ApoE4 status



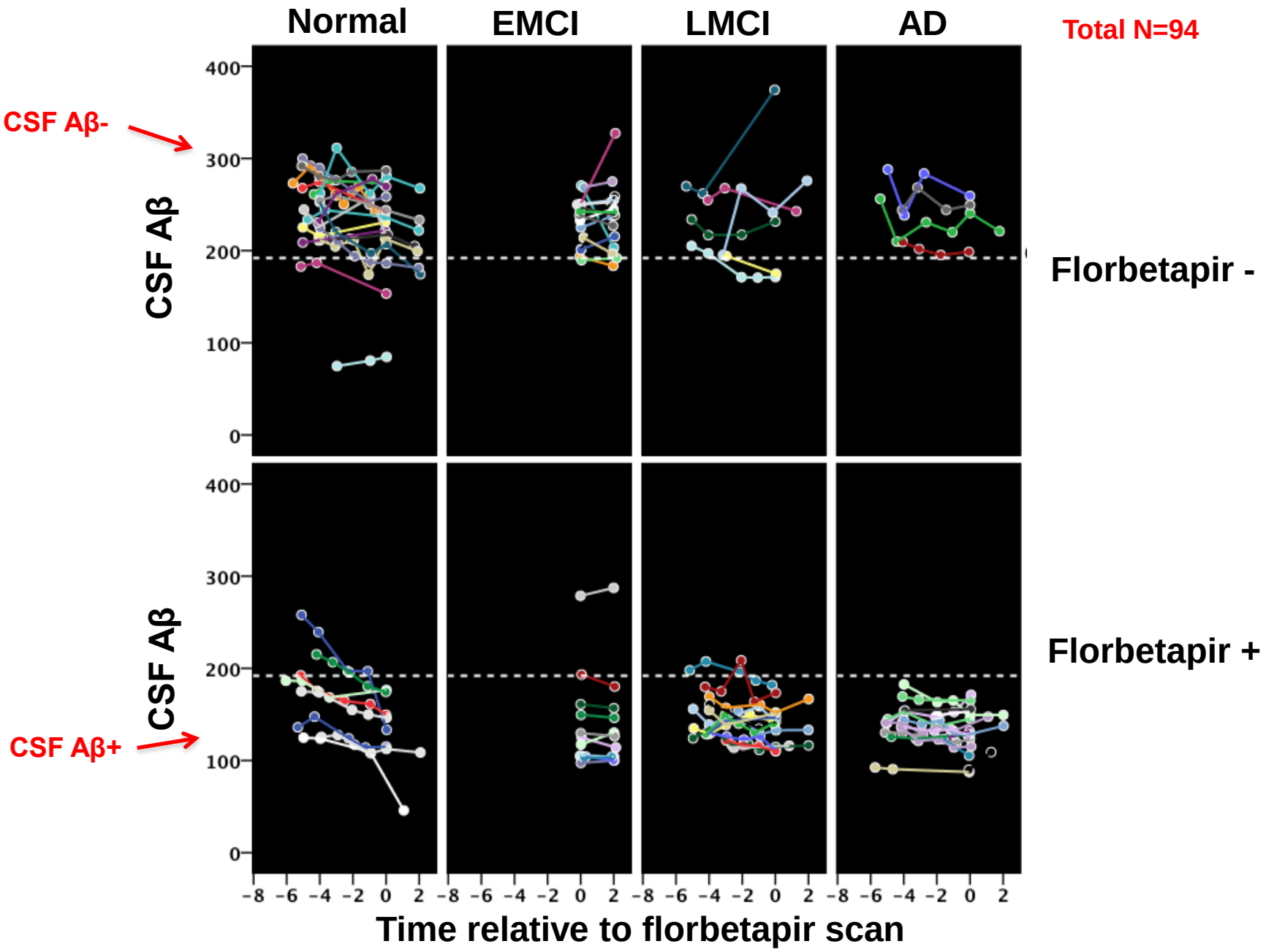
Florbetapir and CSF Aβ agreement

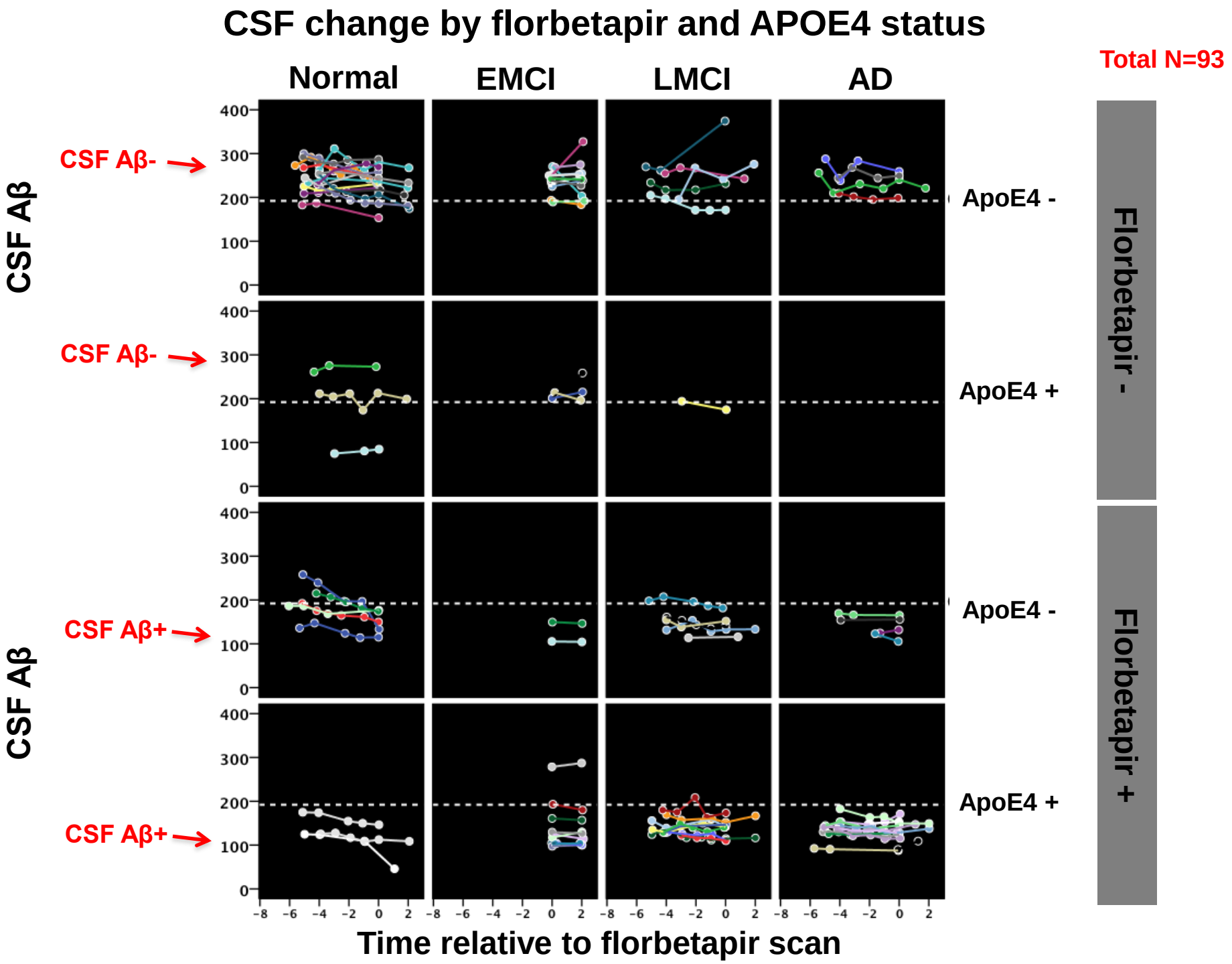


Total N=378

(previous = 374)

CSF change by florbetapir status




CSF change by florbetapir and APOE4 status
Total N=93
Normal
EMCI
LMCI
AD
CSF Aβ
CSF Aβ-
CSF Aβ+
ApoE4 -
ApoE4 +
Florbetapir -
Florbetapir +
400
300
200
100
0
-8
-6
-4
-2
0
2
Time relative to florbetapir scan

New Initiative: “Early Frames” Add on

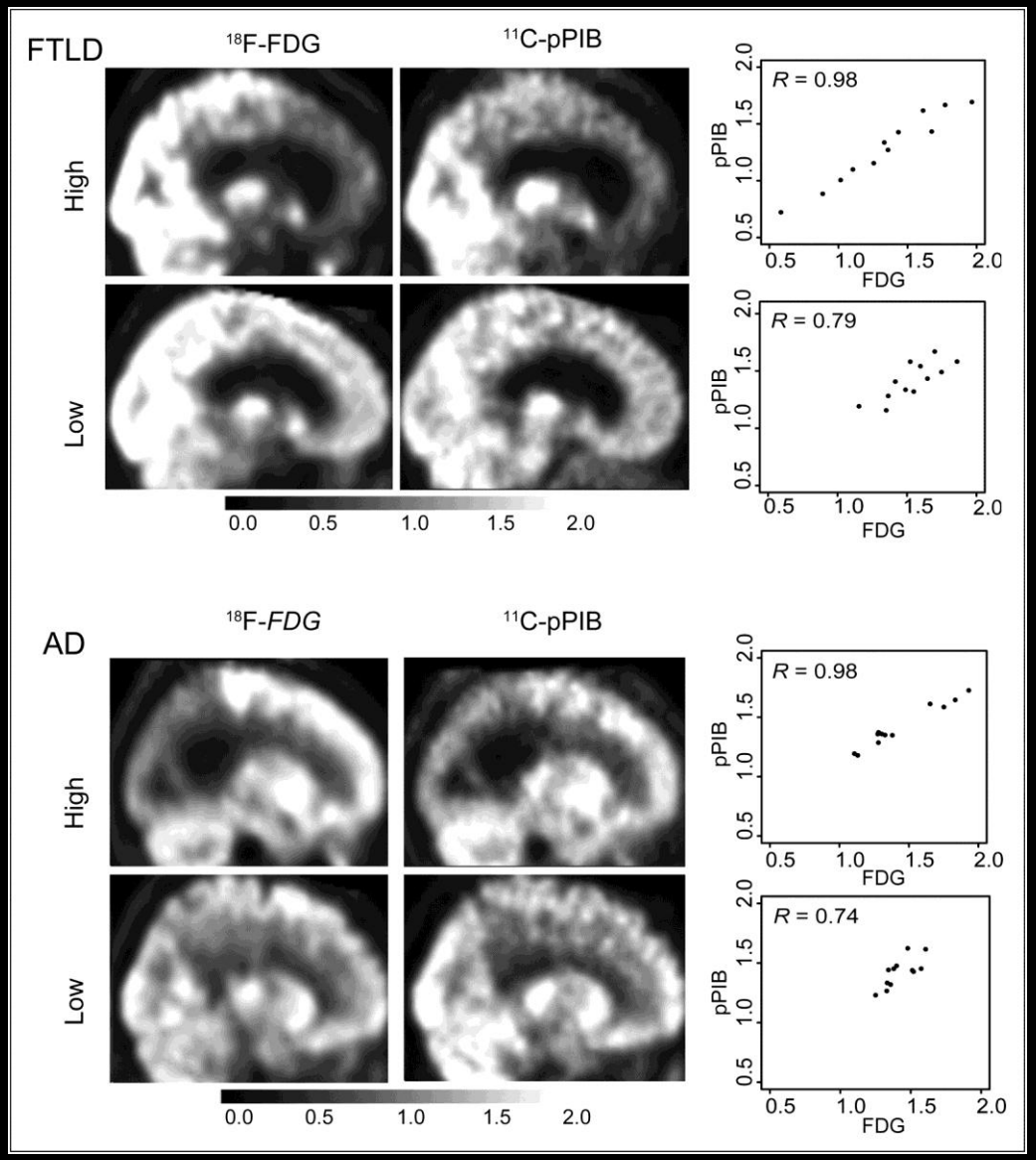
Initial uptake and clearance of highly permeable tracers reflect perfusion

Florbetapir data from injection to 50 min are not captured

Would Florbetapir data from 0-50 min provide functional information?

Compare early frame data to FDG-PET in a wide range of dementia severity/stages

Early PiB Frames vs FDG-PET



Minutes 1-8 after [^{11}C]PiB injection summed

Correlations between FDG and PiB data computed for 12 ROIs

Mean Pearson R = 0.91

(72 cases of AD or FTLD)

Rostomian et al, *J Nucl Med* 2011

Study Design

Approximately 20 sites

- **must be capable of dynamic scanning and simultaneous injection/scan start**

100 subjects: Normal, EMCI, LMCI, AD

Data collection 0-20 min, then back in scanner for the standard 50-70 min

All data treated identically to all other ADNI data

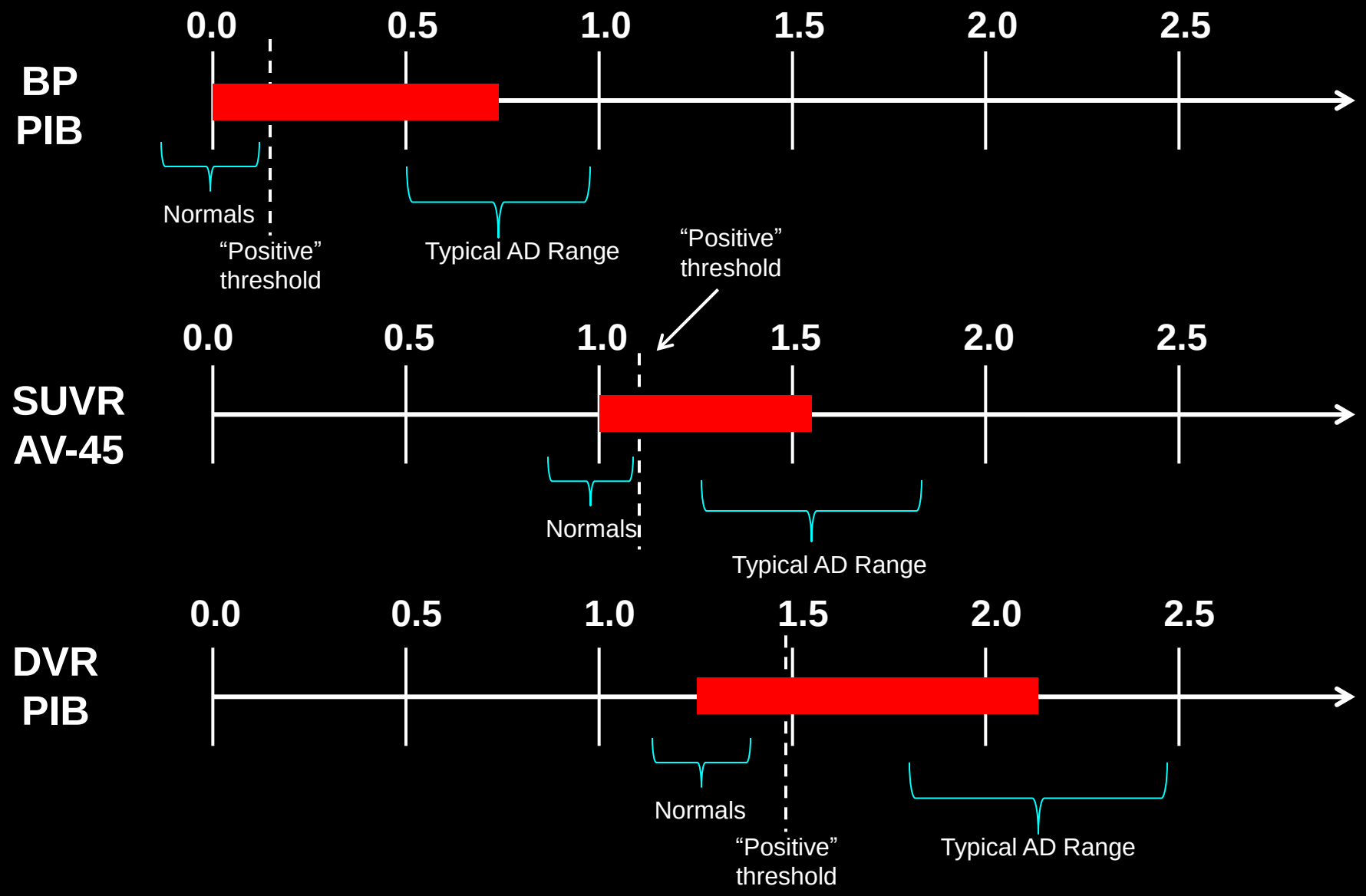
The “Centiloid’ Project

An effort to standardize the numerical reporting of PET amyloid tracer retention

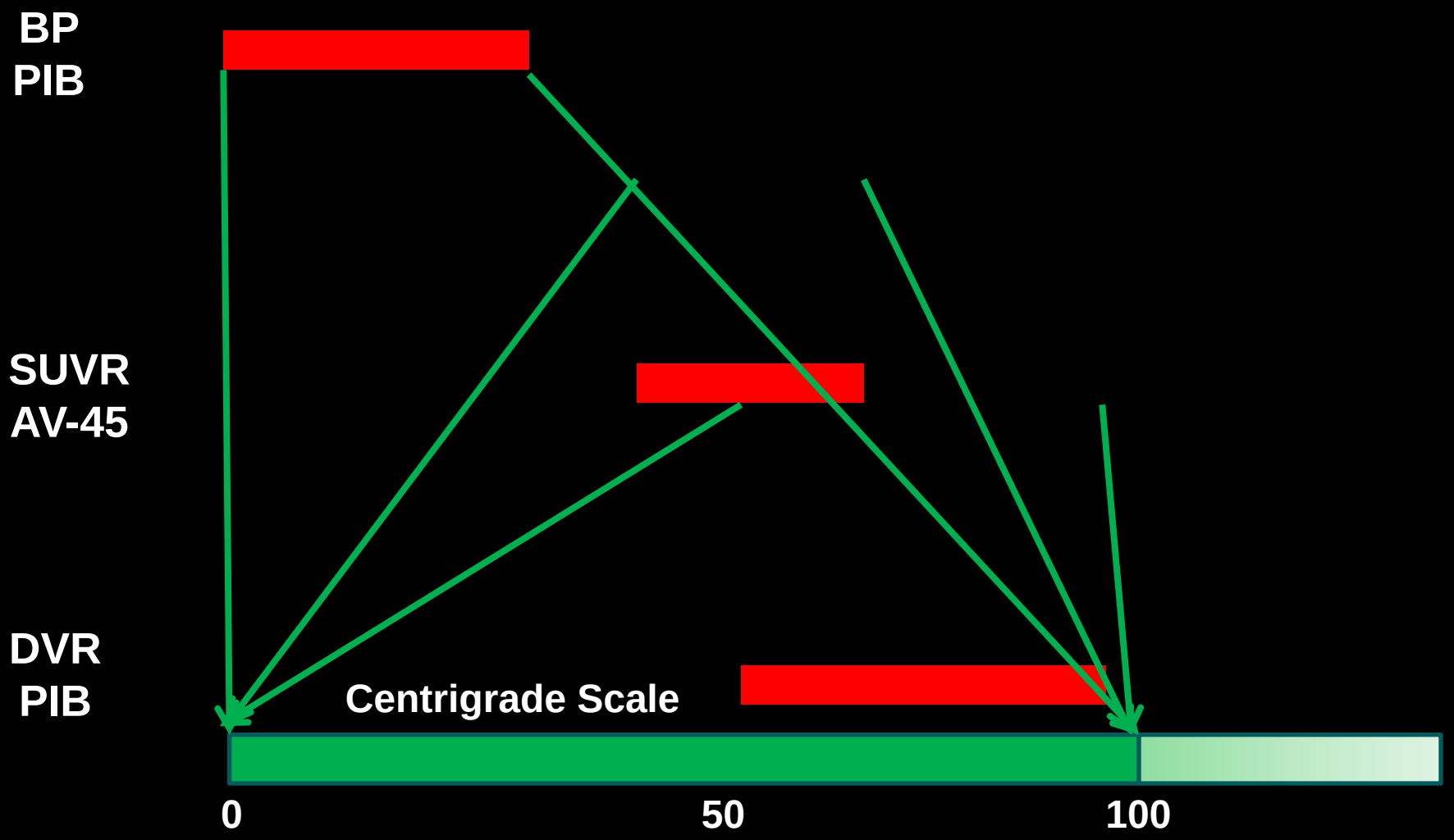
Goal: A numerical value reflects the same thing (ie, Aβ-, slightly Aβ+, very Aβ+, borderline) regardless of tracer

Participants: Bill Klunk, Mike Devous, Bill Jagust, Keith Johnson, Bob Koeppe, Chet Mathis, Mark Mintun, Mike Pontecorvo, Julie Price, Chris Rowe, Dan Skovronsky

Examples of Different Scales



Conversion of Scales



The Centiloid Scale is meant to:

Help standardize reporting across labs and tracers

Clearly define thresholds for amyloid positivity

Define range from “borderline” to “AD-like”

Consistent representation of longitudinal change

The Centiloid Scale is not meant to:

Solve all problems related to standardization

Represent an “industry standard” requirement

Constrain laboratories in how data are analyzed or reported

Ultimately, the amyloid imaging investigators will decide if this is a useful approach

A Brief Explanation of How it Works
Step 1: Standardization

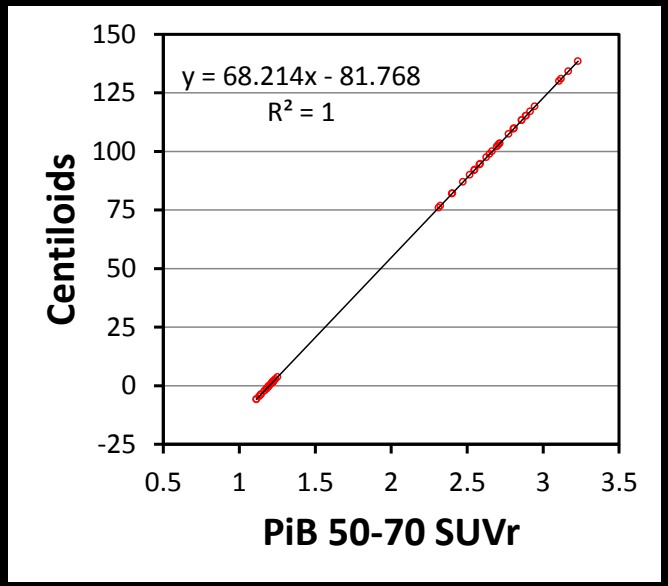
[^{11}C]PIB 50-70 min SUVR as the standard

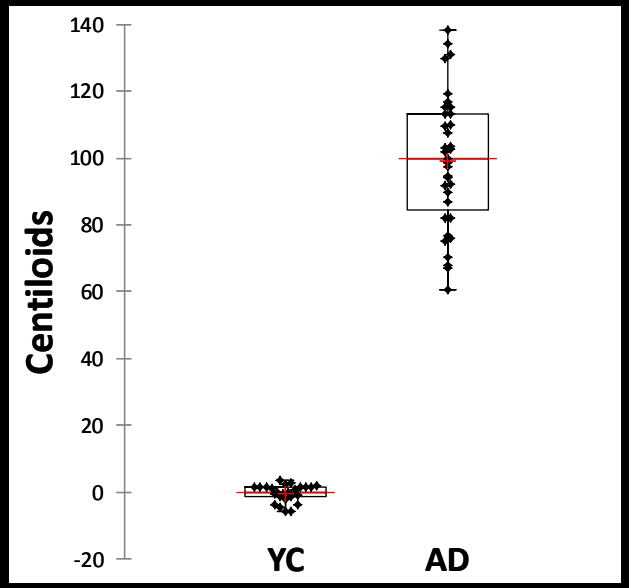
0 anchor: Young Subjects (median)

100 anchor: Probable AD patients (median)

Standard data analysis method

Conversion of SUVR to Centiloid (y = mx + b)





Step 2: Calibrate new Tracer (or method)

Collect PIB 50-70 SUVR data with new tracer data in same subjects (including young and AD)

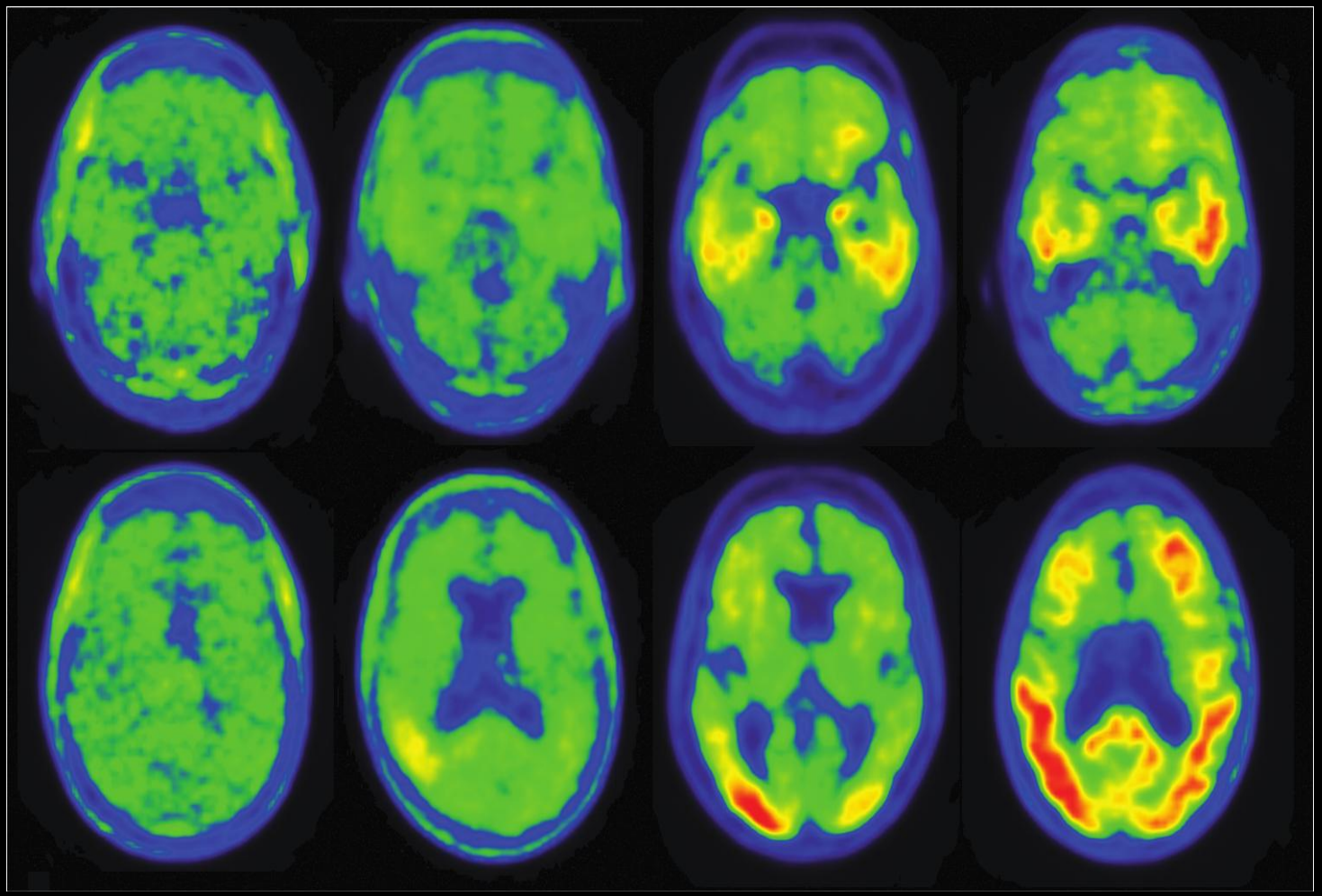
Verification that standard analysis method works by downloading and analyzing the standard dataset

Convert newly acquired PIB data to Centiloids

Convert new tracer data to Centiloids

Next Up: Tau Imaging

[18F]-T807 PET
(80-100 min p.i.)



HC (56y) | MCI (MMSE=26) | AD (MMSE=21) | AD (MMSE=7)

Chien et al, J Alz Disease 2012

Acknowledgements

Susan Landau, Suzanne Baker, Bob Koeppe, Eric Reiman, Kewei Chen, Norman Foster

Core Leaders

Site PIs

Participants