Second-generation tau PET tracer *in situ* binding assessed with fluorescence imaging –

Supplementary information

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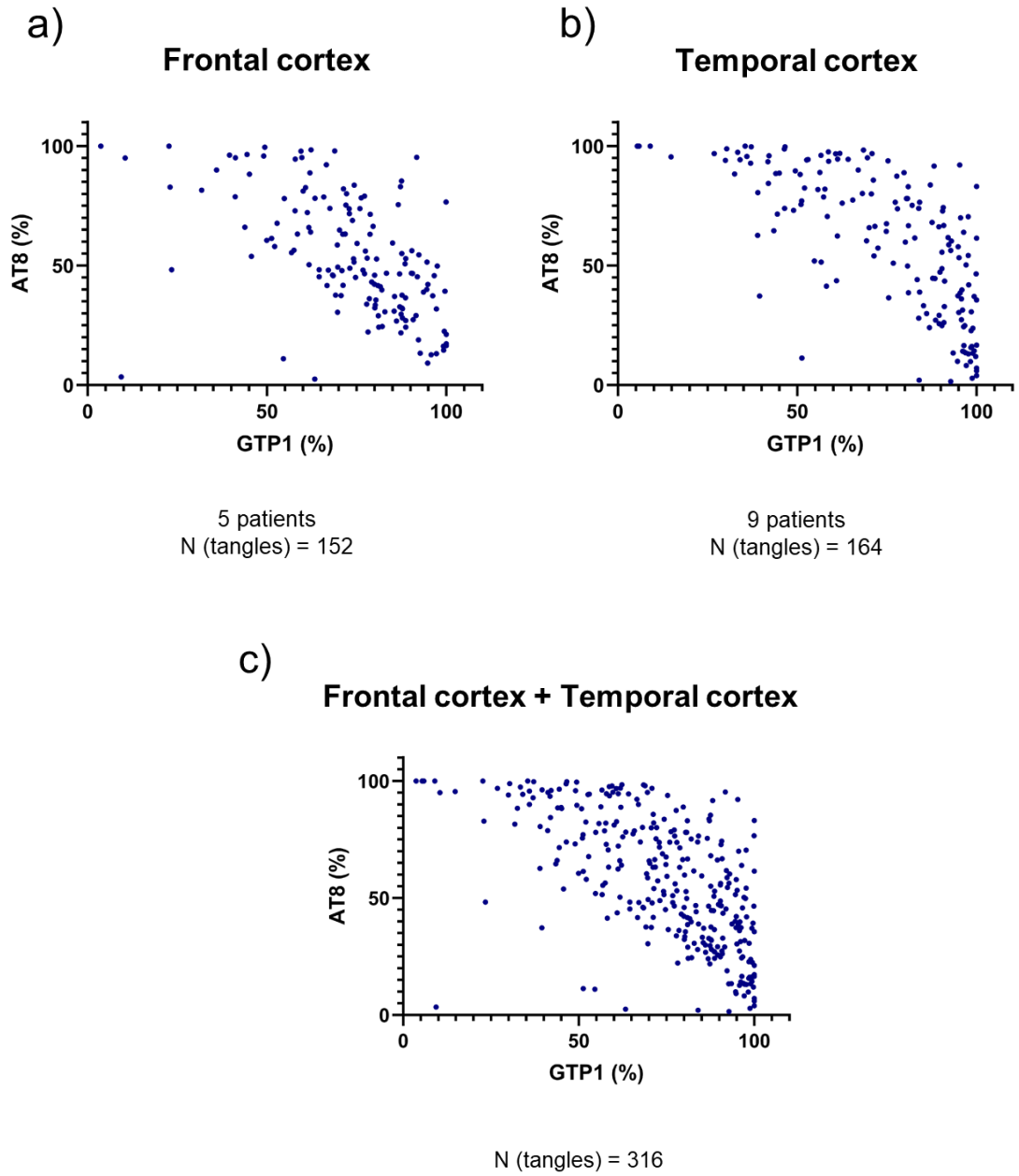

Fig. S1 GTP1 and AT8 cover different area size within the same tangle Each data point corresponds to a single tangle that is double positive for GTP1 and AT8. Its position along the x-axis shows how much of the tangle area is captured by GTP1, and its position along the y-axis how much of its area is captured by AT8. a) Double positive tangles in frontal cortex (5 patients), b) Double positive tangles in temporal cortex (9 patients), c) Double positive tangles in frontal cortex and temporal cortex (data from a) and b) combined). The given values represent fractions within the total area of the tangle.

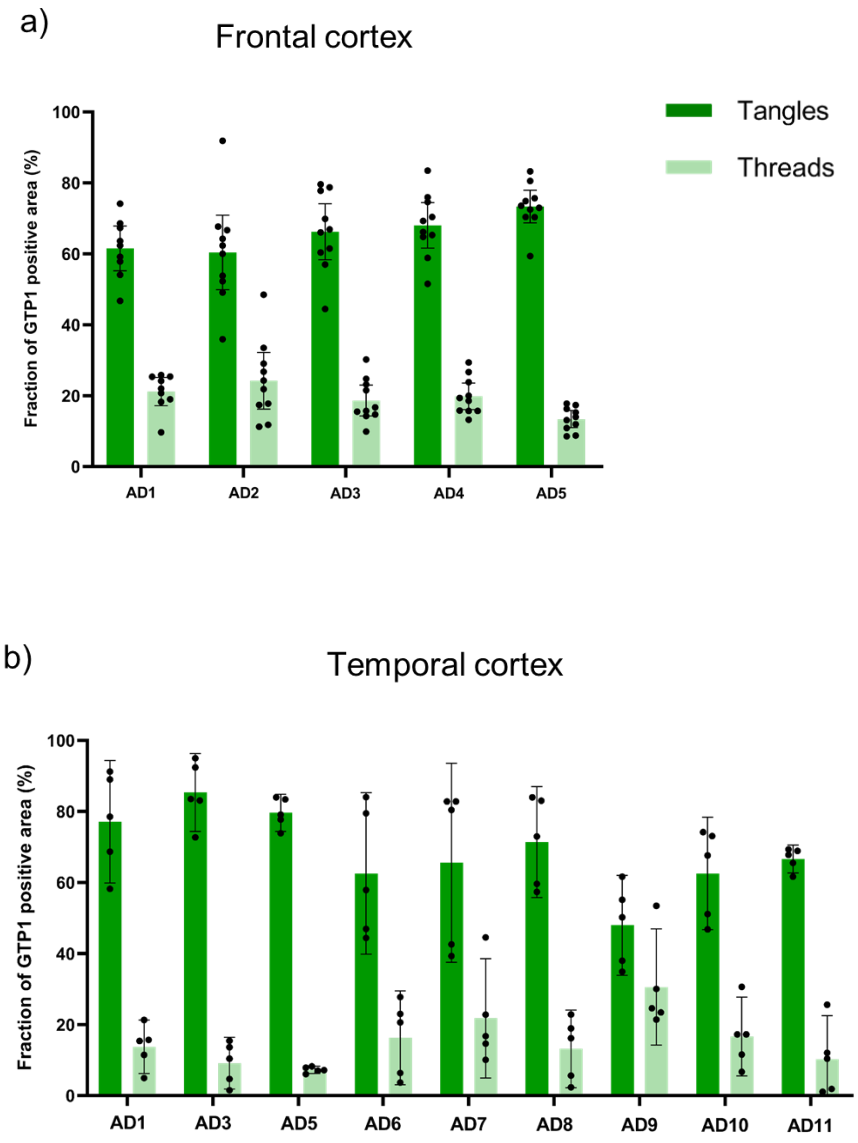

Fig. S2 The majority of GTP1-positive area consists of tau tangles and neuropil threads across all patients, both in frontal and temporal cortex A) In frontal cortex (five patients: AD1-5), the majority of GTP1-positive area was recognized as tangles. Mean GTP1-positive area occupied by tangles ranges from 60,39% (AD2) to 73,35% (AD5) of the area, while mean GTP1-positive area occupied by threads ranges from 13,39% (AD5) to 24,20% (AD2 of the area). B) In the frontal cortex (nine patients: AD1, AD3, AD5, AD6-AD11), mean GTP1-positive area occupied by tangles ranges from 47,98% (AD9) to 85,35% (AD3) of the area, while mean GTP1-positive area occupied by threads ranges from 7,26% (AD5) to 30,58% (AD9) of the area. Each data point corresponds to a single field of view. Error bars represent 95% confidence interval.

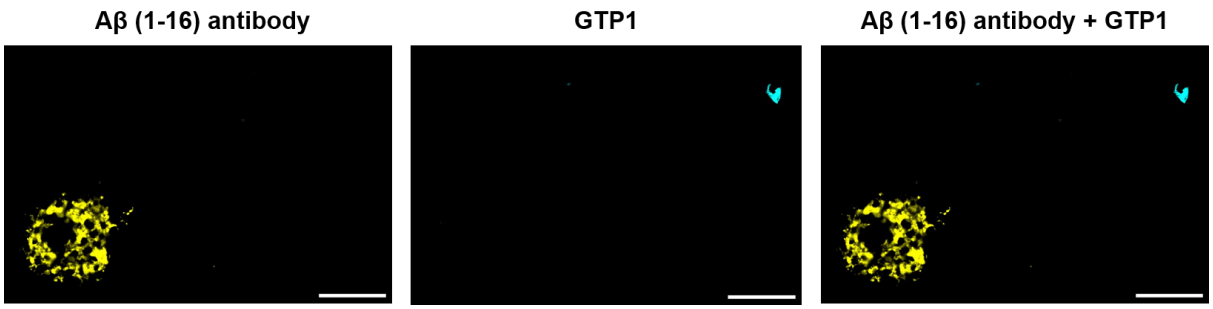

Fig. S3 GTP1 does not stain amyloid-β plaques GTP1 does not co-localize with the amyloid-β plaque labeled with Aβ (1-16) antibody. GTP1 stains the tau tangle in the same field of view. Scale bar: 50 μm.