

## Supplementary Tables

**Supplementary Table 1.** Source of clinical variables for each cohort

| <b>Clinical Variable</b>           | <b>CCNA/COMPASS-ND</b>                                                              | <b>Newcastle – AMPLE</b>                           | <b>Newcastle – CATFIELD</b>                        | <b>Newcastle – TMSS</b>                                                  |
|------------------------------------|-------------------------------------------------------------------------------------|----------------------------------------------------|----------------------------------------------------|--------------------------------------------------------------------------|
| <b>Literature references</b>       | 1-4                                                                                 | 5                                                  | 6                                                  | 7                                                                        |
| <b>Global cognitive function</b>   | MoCA <sup>8</sup>                                                                   | MMSE <sup>9</sup>                                  | MMSE <sup>9</sup>                                  | MMSE <sup>9</sup>                                                        |
| <b>Cognitive fluctuations</b>      | Mayo Fluctuation Scale <sup>10</sup>                                                | Dementia Cognitive Fluctuation Scale <sup>11</sup> | Dementia Cognitive Fluctuation Scale <sup>11</sup> | Dementia Cognitive Fluctuation Scale <sup>11</sup>                       |
| <b>Visual hallucinations</b>       | NPI-Q <sup>12</sup>                                                                 | Lewy Body Symptom Questionnaire <sup>13</sup>      | Lewy Body Symptom Questionnaire <sup>13</sup>      | NEVHI <sup>14</sup>                                                      |
| <b>REM sleep behavior disorder</b> | Screening question:<br>Moves in their sleep or<br>acts out their dreams<br>(yes/no) | Lewy Body Symptom Questionnaire <sup>13</sup>      | Lewy Body Symptom Questionnaire <sup>13</sup>      | Screening question:<br>evidence of REM<br>behavior disorder?<br>(yes/no) |
| <b>Parkinsonism</b>                | Spontaneous features of<br>parkinsonism                                             | Lewy Body Symptom Questionnaire <sup>13</sup>      | Lewy Body Symptom Questionnaire <sup>13</sup>      | UPDRS, part III <sup>15, 16</sup>                                        |

CCNA, Canadian Consortium for Neurodegeneration in Aging; COMPASS-ND, Comprehensive Assessment of Neurodegeneration and Dementia; MMSE, Mini-Mental State Examination; MoCA, Montreal Cognitive Assessment; NEVHI, North-East Visual Hallucinations Interview; NPI-Q, Neuropsychiatric Inventory Questionnaire; UPDRS, Unified Parkinson's Disease Rating Scale

**Supplementary Table 2.** GTEx list of tissues analyzed.

| <b>Tissue category (brain versus body)</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| <p><b><i>Brain tissue (N=13):</i></b></p> <ul style="list-style-type: none"> <li>- Amygdala</li> <li>- Anterior cingulate cortex (BA24)</li> <li>- Caudate</li> <li>- Cerebellar hemisphere</li> <li>- Cerebellum</li> <li>- Cortex</li> <li>- Frontal cortex (BA9)</li> <li>- Hippocampus</li> <li>- Hypothalamus</li> <li>- Nucleus accumbens</li> <li>- Putamen</li> <li>- Spinal cord, cervical C1</li> <li>- Substantia nigra</li> </ul>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <p><b><i>Peripheral body tissue (N=55):</i></b></p> <ul style="list-style-type: none"> <li>- Adipose tissue (subcutaneous)</li> <li>- Adipose tissue (visceral, omentum)</li> <li>- Adrenal gland</li> <li>- Artery (aorta)</li> <li>- Artery (coronary)</li> <li>- Artery (tibial)</li> <li>- Bladder</li> <li>- Cervix (ectocervix)</li> <li>- Cervix (endocervix)</li> <li>- Colon (sigmoid)</li> <li>- Colon (transverse)</li> <li>- Colon (transverse, mixed cell)</li> <li>- Colon (transverse, mucosa)</li> <li>- Colon (transverse, muscularis)</li> <li>- Cultured fibroblasts</li> <li>- EBV-transformed lymphocytes</li> <li>- Esophagus (gastroesophageal junction)</li> <li>- Esophagus (mucosa)</li> <li>- Esophagus (muscularis)</li> <li>- Fallopian tube</li> <li>- Heart (atrial appendage)</li> <li>- Heart (left ventricle)</li> <li>- Kidney (cortex)</li> <li>- Kidney (medulla)</li> <li>- Liver</li> <li>- Liver (hepatocytes)</li> <li>- Liver (mixed cells)</li> <li>- Liver (portal tract)</li> <li>- Lung</li> <li>- Mammary gland (breast tissue)</li> <li>- Minor salivary gland</li> <li>- Muscle (skeletal)</li> <li>- Nerve (tibial)</li> <li>- Ovary</li> <li>- Pancreas</li> <li>- Pancreas (acini)</li> <li>- Pancreas (islets)</li> <li>- Pancreas (mixed cell)</li> <li>- Pituitary gland</li> <li>- Prostate</li> <li>- Skin (not sun-exposed, suprapubic)</li> </ul> |

- Skin (sun-exposed, lower leg)
- Small intestine (terminal ileum)
- Small intestine (terminal ileum, lymphoid aggregate)
- Small intestine (terminal ileum, mixed cell)
- Spleen
- Stomach
- Stomach (mixed cell)
- Stomach (mucosa)
- Stomach (muscularis)
- Testis
- Thyroid gland
- Uterus
- Vagina
- Whole blood

BA, Brodmann area; EBV, Epstein-Barr virus; GTEx, Genotype-Tissue Expression.

**Supplementary Table 3.** List of the imaging studies used to generate neuromaps maps

| Neurotransmitter system                                                                                                                                                                                                                           | Imaging modality                                                                                                                                                                                                                                                                                                                                                                                                         | Study                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>GABA:</b> GABA <sub>A</sub>                                                                                                                                                                                                                    | [ <sup>11</sup> C]flumazenil PET                                                                                                                                                                                                                                                                                                                                                                                         | Norgaard et al, 2021 <sup>17, 18</sup><br>Hansen et al, 2022 <sup>18</sup>                                                                                                                                                                                                                                                                                                                                                                                   |
| <b>Glutamate:</b> mGluR5                                                                                                                                                                                                                          | [ <sup>11</sup> C]ABP688 PET                                                                                                                                                                                                                                                                                                                                                                                             | DuBois et al, 2016 <sup>19</sup><br>Smart et al, 2019 <sup>20</sup><br>Hansen et al, 2022 <sup>18</sup>                                                                                                                                                                                                                                                                                                                                                      |
| <b>Acetylcholine</b> <ul style="list-style-type: none"> <li>• α4β2</li> <li>• M1</li> <li>• vesicular acetylcholine transporter [VACHT]</li> </ul>                                                                                                | <ul style="list-style-type: none"> <li>• [<sup>18</sup>F]flubatine PET</li> <li>• [<sup>11</sup>C]LSN3172176 PET</li> <li>• [<sup>18</sup>F]FEOBV PET</li> </ul>                                                                                                                                                                                                                                                         | Hillmer et al, 2016 <sup>21</sup><br>Naganawa et al, 2021 <sup>22</sup><br>Aghourian et al, 2017 <sup>23</sup><br>Bedard et al, 2019 <sup>24</sup><br>Hansen et al, 2022 <sup>18</sup>                                                                                                                                                                                                                                                                       |
| <b>Dopamine</b> <ul style="list-style-type: none"> <li>• D1 receptor</li> <li>• D2 receptor</li> <li>• dopamine transporter [DAT]</li> </ul>                                                                                                      | <ul style="list-style-type: none"> <li>• [<sup>11</sup>C]SCH23390 PET</li> <li>• [<sup>18</sup>F]fallypride PET</li> <li>• [<sup>11</sup>C]FLB457 PET</li> <li>• [<sup>11</sup>C]raclopride PET</li> <li>• [<sup>18</sup>F]FE-PE2I PET</li> <li>• [123I]FP-CIT SPECT</li> </ul>                                                                                                                                          | Kaller et al, 2017 <sup>25</sup><br>Jaworska et al, 2020 <sup>26</sup><br>Smith et al, 2019 <sup>27</sup><br>Sandiego et al, 2015 <sup>28</sup><br>Alakurtti et al, 2015 <sup>29</sup><br>Sasaki et al, 2012 <sup>30</sup><br>Marek et al, 2018 <sup>31</sup><br>Hansen et al, 2022 <sup>18</sup>                                                                                                                                                            |
| <b>Noradrenaline:</b> noradrenaline transporter [NET]                                                                                                                                                                                             | [ <sup>11</sup> C]MRB PET                                                                                                                                                                                                                                                                                                                                                                                                | Hesse et al, 2017 <sup>32</sup><br>Ding et al, 2010 <sup>33</sup><br>Hansen et al, 2022 <sup>18</sup>                                                                                                                                                                                                                                                                                                                                                        |
| <b>Serotonin</b> <ul style="list-style-type: none"> <li>• 5-HT<sub>1A</sub></li> <li>• 5-HT<sub>1B</sub></li> <li>• 5-HT<sub>2A</sub></li> <li>• 5-HT<sub>4</sub></li> <li>• 5-HT<sub>6</sub></li> <li>• serotonin transporter [5-HTT]</li> </ul> | <ul style="list-style-type: none"> <li>• [<sup>11</sup>C]CUMI-101 PET</li> <li>• [<sup>11</sup>C]WAY-100635 PET</li> <li>• [<sup>11</sup>C]AZ10419369</li> <li>• [<sup>11</sup>C]P943</li> <li>• [<sup>18</sup>F]ALTANSERIN</li> <li>• [<sup>11</sup>C]CIMBI-36</li> <li>• [<sup>11</sup>C]MDL100907</li> <li>• [<sup>11</sup>C]SB207145</li> <li>• [<sup>11</sup>C]GSK215083</li> <li>• [<sup>11</sup>C]DASB</li> </ul> | Beliveau et al, 2017 <sup>34</sup><br>Savli et al, 2012 <sup>35</sup><br>Beliveau et al, 2017 <sup>34</sup><br>Gallezot et al, 2010 <sup>36</sup><br>Savli et al, 2012 <sup>35</sup><br>Beliveau et al, 2017 <sup>34</sup><br>Talbot et al, 2012 <sup>37</sup><br>Beliveau et al, 2017 <sup>34</sup><br>Radhakrishnan et al, 2018 <sup>38</sup><br>Beliveau et al, 2017 <sup>34</sup><br>Savli et al, 2012 <sup>35</sup><br>Hansen et al, 2022 <sup>18</sup> |
| <b>Endocannabinoids:</b> CB1                                                                                                                                                                                                                      | <ul style="list-style-type: none"> <li>• [<sup>18</sup>F]FMPEP-D2 PET</li> <li>• [<sup>11</sup>C]OMAR PET</li> </ul>                                                                                                                                                                                                                                                                                                     | Laurikainen et al, 2019 <sup>39</sup><br>Normandin et al, 2015 <sup>40</sup><br>Hansen et al, 2022 <sup>18</sup>                                                                                                                                                                                                                                                                                                                                             |
| <b>Opioids:</b> μ                                                                                                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                          | Hansen et al, 2022 <sup>18</sup>                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <b>Histamine:</b> H <sub>3</sub>                                                                                                                                                                                                                  | [ <sup>11</sup> C]GSK189254 PET                                                                                                                                                                                                                                                                                                                                                                                          | Gallezot et al, 2017 <sup>41</sup><br>Hansen et al, 2022 <sup>18</sup>                                                                                                                                                                                                                                                                                                                                                                                       |
| <b>Synaptic density:</b> SV2A                                                                                                                                                                                                                     | [ <sup>11</sup> C]UCB-J PET                                                                                                                                                                                                                                                                                                                                                                                              | Mecca et al, 2020 <sup>42</sup>                                                                                                                                                                                                                                                                                                                                                                                                                              |

|  |  |                                                                                                                                             |
|--|--|---------------------------------------------------------------------------------------------------------------------------------------------|
|  |  | Holmes et al, 2019 <sup>43</sup><br>Finnema et al, 2019 <sup>44</sup><br>Chen et al, 2018 <sup>45</sup><br>Hansen et al, 2022 <sup>18</sup> |
|--|--|---------------------------------------------------------------------------------------------------------------------------------------------|

**Supplementary Table 4.** Clinical characteristics of DLB patients and controls across cohorts

| Clinical Assessment                        | Controls | DLB       | P-value                     |
|--------------------------------------------|----------|-----------|-----------------------------|
| <b>Newcastle Dataset (N = 69 DLB)</b>      |          |           |                             |
| <b><i>TMSS cohort (N = 16 DLB)</i></b>     |          |           |                             |
| Non-visual hallucinations, n (%)           | 0 (0%)   | 6 (43%)   | < <b>0.0001<sup>a</sup></b> |
| Delusions, n (%)                           | 0 (0%)   | 8 (53%)   | < <b>0.0001<sup>a</sup></b> |
| Fluctuations:                              | 0 (0%)   | 16 (100%) | < <b>0.0001<sup>a</sup></b> |
| - Impaired alertness n (%)                 | -        | 15 (94%)  | NA                          |
| - Confusion, n (%)                         | -        | 13 (87%)  | NA                          |
| - Total score                              | -        | 8.9 ± 4.2 | NA                          |
| <b><i>CATFIELD cohort (N = 21 DLB)</i></b> |          |           |                             |
| Fluctuations:                              | -        | 13 (68%)  | NA                          |
| - Impaired alertness, n (%)                | -        | 13 (68%)  | NA                          |
| - Confusion, n (%)                         | -        | 12 (63%)  | NA                          |
| - Total score                              | -        | 4.1 ± 4.2 | NA                          |
| <b><i>AMPLE cohort (N = 32 DLB)</i></b>    |          |           |                             |
| Parkinsonian motor features:               |          |           |                             |
| - Rigidity, n (%)                          | 2 (12%)  | 12 (39%)  | < <b>0.0001<sup>a</sup></b> |
| - Shuffling gait, n (%)                    | 0 (0%)   | 26 (84%)  | < <b>0.0001<sup>a</sup></b> |
| - Tremor, n (%)                            | 3 (18%)  | 25 (81%)  | < <b>0.0001<sup>a</sup></b> |
| - Slowness, n (%)                          | 0 (0%)   | 24 (80%)  | < <b>0.0001<sup>a</sup></b> |
| - Hypomimia, n (%)                         | 0 (0%)   | 16 (53%)  | < <b>0.0001<sup>a</sup></b> |
| - Balance problems, n (%)                  | 2 (15%)  | 22 (73%)  | < <b>0.0001<sup>a</sup></b> |
| Loss of smell, n (%)                       | 3 (18%)  | 18 (58%)  | < <b>0.0001<sup>a</sup></b> |
| Fluctuations:                              | -        | 26 (81%)  | NA                          |
| - Impaired alertness, n (%)                | -        | 22 (69%)  | NA                          |
| - Confusion, n (%)                         | -        | 20 (63%)  | NA                          |
| - Total score                              | -        | 6.6 ± 4.3 | NA                          |
| Auditory hallucinations, n (%)             | 0 (0%)   | 8 (28%)   | < <b>0.0001<sup>a</sup></b> |
| Sleep abnormalities:                       |          |           |                             |
| - Dream enactment behaviors, n (%)         | 1 (6%)   | 16 (55%)  | < <b>0.0001<sup>a</sup></b> |

|                                             |            |             |                                |
|---------------------------------------------|------------|-------------|--------------------------------|
| - Restless legs syndrome, n (%)             | 1 (6%)     | 5 (16%)     | <b>0.04<sup>a</sup></b>        |
| <b>CCNA/COMPASS-ND Dataset (N = 14 DLB)</b> |            |             |                                |
| PDQ-39 score                                | -          | 27.5 ± 15.5 | NA                             |
| MBI-C score                                 | 0.1 ± 0.4  | 18.5 ± 9.7  | <b>&lt; 0.0001<sup>b</sup></b> |
| NPI-Q score:                                |            |             |                                |
| - Severity score                            | 0.7 ± 1.2  | 8.9 ± 6.8   | <b>&lt; 0.0001<sup>b</sup></b> |
| - Distress score                            | 0.5 ± 1.2  | 10.0 ± 8.9  | <b>&lt; 0.0001<sup>b</sup></b> |
| GAD-7 anxiety scale                         | 3.2 ± 4.0  | 6.8 ± 5.0   | <b>0.01</b>                    |
| GDS score                                   |            |             |                                |
| CDR scale score, median (IQR)               | 0 (0)      | -           | NA                             |
| Cognitive testing:                          |            |             |                                |
| - RAVLT, trial A5, z-score                  | 0.9 ± 0.8  | -1.4 ± 1.5  | <b>&lt; 0.0001<sup>b</sup></b> |
| - RAVLT, trial A7, z-score                  | 1.4 ± 1.8  | -1.0 ± 1.3  | <b>&lt; 0.0001<sup>b</sup></b> |
| - Trail Making Test, part A, z-score        | -0.7 ± 0.6 | 2.5 ± 1.7   | <b>&lt; 0.0001<sup>b</sup></b> |
| - Trail Making Test, part B, z-score        | -0.3 ± 1.1 | 3.1 ± 1.5   | <b>&lt; 0.0001<sup>b</sup></b> |
| - Letter fluency, sum of words              | 46 ± 10    | 21 ± 9      | <b>&lt; 0.0001<sup>b</sup></b> |
| - Judgement of Line Orientation, score      | 26 ± 4     | 15 ± 8      | <b>&lt; 0.0001<sup>b</sup></b> |

Data are presented as mean ± standard deviation unless otherwise indicated. Bold values represent significant differences. <sup>a</sup> Fisher's exact test; <sup>b</sup> Student's t-test

CCNA, Canadian Consortium for Neurodegeneration in Aging; CDR, Clinical Dementia Rating; COMPASS-ND, Comprehensive Assessment of Neurodegeneration and Dementia; DLB, dementia with Lewy bodies; GAD-7, Generalized Anxiety Disorder; GDS, Geriatric Depression Scale; IQR, interquartile range; MBI-C, Mild Behavioral Impairment Checklist; MMSE, Mini-Mental State Examination; MoCA, Montreal Cognitive Assessment; NA not available; NPI-Q, Neuropsychiatric Inventory Questionnaire; PDQ-39, 39-item Parkinson's Disease Questionnaire; RAVLT, Rey Auditory Verbal Learning Test.

**Supplementary Table 5.** Region-wise cortical thickness comparisons between DLB patients and controls

| Region                      | Controls  | DLB       | P-value  | P <sub>FDR</sub> -value | W-score DLB |
|-----------------------------|-----------|-----------|----------|-------------------------|-------------|
| <b>Left hemisphere</b>      |           |           |          |                         |             |
| banks superior temp. sulcus | 2.38±0.11 | 2.27±0.16 | <0.00001 | <b>0.00001</b>          | -1.026      |
| caudal anterior cingulate   | 2.34±0.19 | 2.30±0.24 | 0.46859  | 0.47558                 | -0.102      |
| caudal middle frontal       | 2.46±0.11 | 2.38±0.18 | 0.00234  | <b>0.00370</b>          | -0.681      |
| cuneus                      | 1.84±0.13 | 1.80±0.16 | 0.17945  | 0.19682                 | -0.278      |
| entorhinal                  | 3.04±0.27 | 2.73±0.37 | <0.00001 | <b>&lt;0.00001</b>      | -1.127      |
| fusiform                    | 2.57±0.14 | 2.40±0.24 | <0.00001 | <b>&lt;0.00001</b>      | -1.239      |
| inferior parietal           | 2.34±0.09 | 2.24±0.12 | <0.00001 | <b>&lt;0.00001</b>      | -1.090      |
| inferior temporal           | 2.62±0.13 | 2.46±0.19 | <0.00001 | <b>&lt;0.00001</b>      | -1.170      |
| isthmus cingulate           | 2.13±0.13 | 2.05±0.17 | 0.00270  | <b>0.00418</b>          | -0.590      |
| lateral occipital           | 2.16±0.11 | 2.08±0.14 | 0.00011  | <b>0.00026</b>          | -0.693      |
| lateral orbitofrontal       | 2.54±0.11 | 2.49±0.21 | 0.11895  | 0.13481                 | -0.416      |
| lingual                     | 1.88±0.12 | 1.82±0.16 | 0.02015  | <b>0.02586</b>          | -0.423      |
| medial orbitofrontal        | 2.26±0.14 | 2.17±0.19 | 0.00086  | <b>0.00151</b>          | -0.658      |
| middle temporal             | 2.66±0.12 | 2.53±0.17 | <0.00001 | <b>&lt;0.00001</b>      | -1.108      |
| parahippocampal             | 2.58±0.26 | 2.45±0.28 | 0.00348  | <b>0.00504</b>          | -0.469      |
| paracentral                 | 2.24±0.17 | 2.14±0.25 | 0.00592  | <b>0.00805</b>          | -0.578      |
| pars opercularis            | 2.47±0.10 | 2.42±0.15 | 0.08042  | 0.09429                 | -0.393      |
| pars orbitalis              | 2.60±0.15 | 2.50±0.19 | 0.00026  | <b>0.00056</b>          | -0.685      |
| pars triangularis           | 2.34±0.10 | 2.30±0.12 | 0.04465  | 0.05327                 | -0.388      |
| pericalcarine               | 1.60±0.13 | 1.57±0.15 | 0.28816  | 0.30462                 | -0.210      |
| postcentral                 | 2.04±0.12 | 1.95±0.14 | 0.00006  | <b>0.00016</b>          | -0.731      |
| posterior cingulate         | 2.27±0.15 | 2.19±0.21 | 0.01936  | <b>0.02531</b>          | -0.471      |
| precentral                  | 2.43±0.14 | 2.30±0.23 | 0.00006  | <b>0.00016</b>          | -0.931      |
| precuneus                   | 2.27±0.12 | 2.15±0.17 | <0.00001 | <b>0.00001</b>          | -0.955      |
| rostral anterior cingulate  | 2.57±0.21 | 2.48±0.25 | 0.02296  | <b>0.02892</b>          | -0.441      |
| rostral middle frontal      | 2.34±0.10 | 2.27±0.12 | 0.00074  | <b>0.00132</b>          | -0.610      |
| superior frontal            | 2.56±0.12 | 2.48±0.17 | 0.00181  | <b>0.00293</b>          | -0.641      |
| superior parietal           | 2.18±0.11 | 2.09±0.13 | 0.00001  | <b>0.00004</b>          | -0.795      |
| superior temporal           | 2.57±0.12 | 2.43±0.18 | <0.00001 | <b>&lt;0.00001</b>      | -1.163      |
| supramarginal               | 2.42±0.10 | 2.31±0.13 | <0.00001 | <b>&lt;0.00001</b>      | -1.162      |
| frontal pole                | 2.73±0.25 | 2.66±0.26 | 0.10146  | 0.11694                 | -0.310      |
| temporal pole               | 3.41±0.28 | 3.15±0.45 | 0.00010  | <b>0.00025</b>          | -0.875      |
| transverse temporal         | 2.30±0.22 | 2.10±0.27 | 0.00001  | <b>0.00002</b>          | -0.834      |
| insula                      | 2.73±0.15 | 2.61±0.24 | 0.00034  | <b>0.00070</b>          | -0.796      |
| <b>Right hemisphere</b>     |           |           |          |                         |             |
| banks superior temp. sulcus | 2.46±0.13 | 2.34±0.16 | 0.00001  | <b>0.00004</b>          | -0.842      |
| caudal anterior cingulate   | 2.26±0.19 | 2.21±0.20 | 0.18525  | 0.19995                 | -0.232      |
| caudal middle frontal       | 2.46±0.12 | 2.37±0.15 | 0.00037  | <b>0.00074</b>          | -0.650      |
| cuneus                      | 1.84±0.12 | 1.81±0.16 | 0.12367  | 0.13786                 | -0.299      |
| entorhinal                  | 3.00±0.30 | 2.76±0.38 | 0.00005  | <b>0.00013</b>          | -0.779      |
| fusiform                    | 2.57±0.13 | 2.38±0.24 | <0.00001 | <b>&lt;0.00001</b>      | -1.492      |
| inferior parietal           | 2.36±0.09 | 2.27±0.15 | 0.00003  | <b>0.00008</b>          | -0.900      |
| inferior temporal           | 2.64±0.13 | 2.47±0.20 | <0.00001 | <b>&lt;0.00001</b>      | -1.280      |
| isthmus cingulate           | 2.12±0.16 | 2.02±0.18 | 0.00053  | <b>0.00098</b>          | -0.600      |
| lateral occipital           | 2.21±0.12 | 2.14±0.14 | 0.00108  | <b>0.00184</b>          | -0.581      |
| lateral orbitofrontal       | 2.47±0.11 | 2.38±0.19 | 0.00135  | <b>0.00224</b>          | -0.775      |
| lingual                     | 1.90±0.11 | 1.84±0.17 | 0.02641  | <b>0.03207</b>          | -0.462      |
| medial orbitofrontal        | 2.31±0.14 | 2.23±0.21 | 0.00708  | <b>0.00944</b>          | -0.592      |
| middle temporal             | 2.70±0.10 | 2.57±0.18 | <0.00001 | <b>&lt;0.00001</b>      | -1.211      |
| parahippocampal             | 2.52±0.22 | 2.36±0.27 | 0.00038  | <b>0.00074</b>          | -0.647      |
| paracentral                 | 2.23±0.16 | 2.13±0.24 | 0.00454  | <b>0.00643</b>          | -0.622      |

|                            |           |           |          |                    |        |
|----------------------------|-----------|-----------|----------|--------------------|--------|
| pars opercularis           | 2.46±0.13 | 2.39±0.19 | 0.02372  | <b>0.02933</b>     | -0.480 |
| pars orbitalis             | 2.56±0.17 | 2.45±0.24 | 0.00339  | <b>0.00501</b>     | -0.647 |
| pars triangularis          | 2.35±0.13 | 2.27±0.19 | 0.00556  | <b>0.00772</b>     | -0.589 |
| pericalcarine              | 1.62±0.13 | 1.59±0.17 | 0.45280  | 0.46652            | -0.176 |
| postcentral                | 2.04±0.12 | 1.93±0.15 | 0.00001  | <b>0.00002</b>     | -0.862 |
| posterior cingulate        | 2.28±0.13 | 2.18±0.20 | 0.00045  | <b>0.00085</b>     | -0.779 |
| precentral                 | 2.40±0.14 | 2.28±0.24 | 0.00021  | <b>0.00045</b>     | -0.882 |
| precuneus                  | 2.28±0.11 | 2.14±0.16 | <0.00001 | <b>&lt;0.00001</b> | -1.210 |
| rostral anterior cingulate | 2.65±0.20 | 2.64±0.27 | 0.79213  | 0.79213            | -0.093 |
| rostral middle frontal     | 2.32±0.13 | 2.25±0.13 | 0.00304  | <b>0.00459</b>     | -0.538 |
| superior frontal           | 2.56±0.11 | 2.47±0.16 | 0.00012  | <b>0.00028</b>     | -0.858 |
| superior parietal          | 2.18±0.11 | 2.08±0.14 | 0.00002  | <b>0.00007</b>     | -0.798 |
| superior temporal          | 2.62±0.13 | 2.45±0.20 | <0.00001 | <b>&lt;0.00001</b> | -1.335 |
| supramarginal              | 2.43±0.11 | 2.32±0.14 | <0.00001 | <b>&lt;0.00001</b> | -0.970 |
| frontal pole               | 2.68±0.24 | 2.63±0.27 | 0.29118  | 0.30462            | -0.183 |
| temporal pole              | 3.41±0.28 | 3.12±0.51 | 0.00007  | <b>0.00016</b>     | -0.972 |
| transverse temporal        | 2.32±0.21 | 2.13±0.26 | 0.00001  | <b>0.00002</b>     | -0.855 |
| insula                     | 2.74±0.16 | 2.58±0.26 | 0.00003  | <b>0.00008</b>     | -0.917 |

Mean ± standard deviation cortical thickness values are shown for the DLB and control groups across each cortical region following data harmonization using ComBAT. Group differences were assessed using analysis of variance (ANOVA) adjusted for age and sex. FDR-corrected P-values ( $P_{FDR}$ ) are reported, with statistical significance set at  $P_{FDR} < 0.05$ . W-scores represent standardized deviations in cortical thickness for DLB patients relative to age- and sex-matched controls as reference; negative values indicate regional cortical thinning. Regions are listed by hemisphere and anatomical label according to the Desikan-Killiany atlas.

DLB, dementia with Lewy bodies; FDR, false discovery rate.

**Supplementary Table 6.** Region-wise cortical volume comparisons between DLB patients and controls

| Region                      | Controls           | DLB                | P-value  | P <sub>FDR</sub> -value | W-score<br>DLB |
|-----------------------------|--------------------|--------------------|----------|-------------------------|----------------|
| <b>Left hemisphere</b>      |                    |                    |          |                         |                |
| banks superior temp. sulcus | 2198.39 ± 367.88   | 2045.42 ± 373.57   | 0.00035  | <b>0.00059</b>          | -0.487         |
| caudal anterior cingulate   | 1561.96 ± 379.13   | 1544.24 ± 490.17   | 0.32185  | 0.33670                 | -0.053         |
| caudal middle frontal       | 5752.86 ± 908.43   | 5447.13 ± 1036.44  | 0.00198  | <b>0.00274</b>          | -0.351         |
| cuneus                      | 2777.84 ± 2767.37  | 2767.37 ± 561.42   | 0.38215  | 0.39373                 | -0.066         |
| entorhinal                  | 1802.56 ± 350.46   | 1560.44 ± 374.36   | <0.00001 | <b>&lt;0.00001</b>      | -0.755         |
| fusiform                    | 8756.32 ± 1111.07  | 7982.31 ± 1419.31  | <0.00001 | <b>&lt;0.00001</b>      | -0.891         |
| inferior parietal           | 10724.97 ± 1567.56 | 9689.82 ± 1574.99  | <0.00001 | <b>&lt;0.00001</b>      | -0.756         |
| inferior temporal           | 10039.56 ± 1305.62 | 9161.56 ± 1472.28  | <0.00001 | <b>&lt;0.00001</b>      | -0.856         |
| isthmus cingulate           | 2405.87 ± 335.37   | 2300.95 ± 430.40   | 0.00072  | <b>0.00114</b>          | -0.444         |
| lateral occipital           | 11446.38 ± 1472.07 | 10713.24 ± 1495.44 | <0.00001 | <b>&lt;0.00001</b>      | -0.562         |
| lateral orbitofrontal       | 7104.23 ± 852.21   | 6880.17 ± 1012.89  | 0.00002  | <b>0.00004</b>          | -0.408         |
| lingual                     | 5759.99 ± 958.69   | 5493.39 ± 1004.88  | 0.00701  | <b>0.00860</b>          | -0.293         |
| medial orbitofrontal        | 4707.62 ± 618.34   | 4578.81 ± 746.12   | 0.00403  | <b>0.00527</b>          | -0.315         |
| middle temporal             | 9702.73 ± 1314.31  | 8972.94 ± 1325.81  | <0.00001 | <b>&lt;0.00001</b>      | -0.690         |
| parahippocampal             | 1940.88 ± 344.57   | 1799.90 ± 359.86   | 0.00045  | <b>0.00072</b>          | -0.429         |
| paracentral                 | 3196.96 ± 382.78   | 3036.32 ± 512.86   | 0.00115  | <b>0.00177</b>          | -0.412         |
| pars opercularis            | 4292.37 ± 760.29   | 4063.72 ± 702.29   | 0.00287  | <b>0.00382</b>          | -0.408         |
| pars orbitalis              | 2201.96 ± 290.84   | 2043.49 ± 327.57   | <0.00001 | <b>&lt;0.00001</b>      | -0.705         |
| pars triangularis           | 3254.94 ± 474.46   | 3140.26 ± 539.74   | 0.00564  | <b>0.00710</b>          | -0.380         |
| pericalcarine               | 1870.63 ± 326.89   | 1910.62 ± 451.67   | 0.82524  | 0.83756                 | 0.107          |
| postcentral                 | 9196.90 ± 1115.75  | 8717.50 ± 1294.13  | 0.00002  | <b>0.00004</b>          | -0.497         |
| posterior cingulate         | 2796.80 ± 418.83   | 2541.51 ± 576.20   | 0.00001  | <b>0.00002</b>          | -0.729         |
| precentral                  | 12550.04 ± 1524.54 | 11705.86 ± 1785.43 | <0.00001 | <b>&lt;0.00001</b>      | -0.618         |
| precuneus                   | 8792.49 ± 1101.44  | 8117.16 ± 1234.69  | <0.00001 | <b>&lt;0.00001</b>      | -0.773         |
| rostral anterior cingulate  | 2432.15 ± 507.87   | 2371.58 ± 564.84   | 0.02505  | <b>0.02989</b>          | -0.176         |
| rostral middle frontal      | 13559.13 ± 1722.91 | 13526.60 ± 2073.53 | 0.07051  | 0.07991                 | -0.041         |
| superior frontal            | 20614.95 ± 2324.36 | 20167.58 ± 2768.83 | 0.00120  | <b>0.00181</b>          | -0.270         |
| superior parietal           | 12267.58 ± 1349.25 | 11401.96 ± 1651.01 | <0.00001 | <b>&lt;0.00001</b>      | -0.790         |
| superior temporal           | 11356.18 ± 1281.80 | 10713.88 ± 1586.83 | <0.00001 | <b>&lt;0.00001</b>      | -0.605         |
| supramarginal               | 10293.77 ± 1554.89 | 9883.23 ± 1647.49  | 0.00025  | <b>0.00046</b>          | -0.374         |
| frontal pole                | 1004.79 ± 162.76   | 946.31 ± 172.46    | 0.00708  | <b>0.00860</b>          | -0.460         |
| temporal pole               | 2544.93 ± 350.89   | 2354.55 ± 495.54   | 0.00147  | <b>0.00212</b>          | -0.550         |
| transverse temporal         | 1183.14 ± 228.00   | 1051.67 ± 250.60   | <0.00001 | <b>0.00001</b>          | -0.591         |
| insula                      | 6781.53 ± 821.50   | 5369.40 ± 998.65   | <0.00001 | <b>&lt;0.00001</b>      | -0.660         |
| <b>Right hemisphere</b>     |                    |                    |          |                         |                |
| banks superior temp. sulcus | 1995.05 ± 159.50   | 1783.17 ± 287.39   | <0.00001 | <b>&lt;0.00001</b>      | -0.849         |
| caudal anterior cingulate   | 1813.58 ± 436.32   | 1741.89 ± 436.45   | 0.09864  | 0.10819                 | -0.168         |
| caudal middle frontal       | 5414.61 ± 817.71   | 5333.69 ± 1118.88  | 0.04969  | 0.05727                 | -0.092         |
| cuneus                      | 3008.05 ± 406.70   | 3982.31 ± 580.68   | 0.25711  | 0.27318                 | -0.083         |
| entorhinal                  | 1647.16 ± 393.60   | 1469.64 ± 365.99   | 0.00133  | <b>0.00197</b>          | -0.414         |
| fusiform                    | 8471.71 ± 1168.03  | 7518.18 ± 1425.77  | <0.00001 | <b>&lt;0.00001</b>      | -0.971         |
| inferior parietal           | 13102.84 ± 1967.61 | 11768.20 ± 1909.55 | <0.00001 | <b>&lt;0.00001</b>      | -0.802         |
| inferior temporal           | 9591.39 ± 1254.19  | 8794.38 ± 1563.81  | <0.00001 | <b>&lt;0.00001</b>      | -0.732         |
| isthmus cingulate           | 2164.67 ± 349.76   | 2060.17 ± 429.04   | 0.00555  | <b>0.00710</b>          | -0.370         |
| lateral occipital           | 11667.40 ± 1495.83 | 11176.67 ± 1868.71 | 0.00015  | <b>0.00028</b>          | -0.385         |
| lateral orbitofrontal       | 6872.25 ± 798.16   | 6642.13 ± 1009.91  | 0.00001  | <b>0.00002</b>          | -0.424         |
| lingual                     | 6069.13 ± 937.40   | 5923.23 ± 1076.43  | 0.08567  | 0.09550                 | -0.170         |
| medial orbitofrontal        | 5230.08 ± 664.45   | 5021.89 ± 840.39   | 0.00006  | <b>0.00012</b>          | -0.440         |
| middle temporal             | 10668.87 ± 1151.51 | 9888.43 ± 1570.56  | <0.00001 | <b>&lt;0.00001</b>      | -0.919         |
| parahippocampal             | 1777.14 ± 252.29   | 1661.88 ± 322.37   | 0.00014  | <b>0.00028</b>          | -0.507         |

|                            |                    |                    |          |                    |        |
|----------------------------|--------------------|--------------------|----------|--------------------|--------|
| paracentral                | 3509.08 ± 492.70   | 3334.08 ± 598.98   | 0.00149  | <b>0.00212</b>     | -0.411 |
| pars opercularis           | 3513.36 ± 571.92   | 3298.93 ± 545.99   | 0.00009  | <b>0.00018</b>     | -0.486 |
| pars orbitalis             | 2516.43 ± 309.74   | 2386.70 ± 418.47   | 0.00031  | <b>0.00055</b>     | -0.556 |
| pars triangularis          | 3854.28 ± 663.92   | 3580.09 ± 619.03   | 0.00003  | <b>0.00006</b>     | -0.546 |
| pericalcarine              | 2138.98 ± 361.14   | 2194.08 ± 528.18   | 0.89068  | 0.89068            | 0.095  |
| postcentral                | 8819.50 ± 1187.47  | 8316.13 ± 1378.42  | 0.00001  | <b>0.00002</b>     | -0.484 |
| posterior cingulate        | 2809.69 ± 412.55   | 2633.60 ± 633.96   | 0.00264  | <b>0.00359</b>     | -0.479 |
| precentral                 | 12409.06 ± 1398.83 | 11615.66 ± 1931.38 | <0.00001 | <b>&lt;0.00001</b> | -0.644 |
| precuneus                  | 9201.89 ± 1139.97  | 8447.43 ± 1335.48  | <0.00001 | <b>&lt;0.00001</b> | -0.825 |
| rostral anterior cingulate | 1820.10 ± 349.45   | 1738.27 ± 433.41   | 0.03128  | <b>0.03668</b>     | -0.296 |
| rostral middle frontal     | 14178.55 ± 2003.91 | 13724.47 ± 2212.94 | 0.00036  | <b>0.00059</b>     | -0.327 |
| superior frontal           | 19796.37 ± 2279.32 | 19252.58 ± 2653.23 | 0.00024  | <b>0.00045</b>     | -0.324 |
| superior parietal          | 12105.47 ± 1246.29 | 11234.78 ± 1581.68 | <0.00001 | <b>&lt;0.00001</b> | -0.833 |
| superior temporal          | 10796.56 ± 1202.26 | 10023.39 ± 1487.86 | <0.00001 | <b>&lt;0.00001</b> | -0.744 |
| supramarginal              | 9229.47 ± 1288.52  | 8731.52 ± 1441.15  | <0.00001 | <b>0.00001</b>     | -0.529 |
| frontal pole               | 1199.55 ± 197.45   | 1160.29 ± 237.62   | 0.10306  | 0.11124            | -0.240 |
| temporal pole              | 2446.62 ± 374.74   | 2158.83 ± 474.74   | <0.00001 | <b>0.00001</b>     | -0.777 |
| transverse temporal        | 888.61 ± 163.52    | 789.11 ± 159.10    | <0.00001 | <b>&lt;0.00001</b> | -0.645 |
| insula                     | 6587.56 ± 795.24   | 6121.98 ± 962.01   | <0.00001 | <b>&lt;0.00001</b> | -0.776 |

Mean ± standard deviation cortical volume values are shown for the DLB and control groups across each cortical region following data harmonization using ComBAT. Group differences were assessed using analysis of variance (ANOVA) adjusted for age, sex, and eTIV. FDR-corrected P-values ( $P_{FDR}$ ) are reported, with statistical significance set at  $P_{FDR} < 0.05$ . W-scores represent standardized deviations in cortical volume for DLB patients relative to age- and sex-matched controls as reference; negative values indicate reduced cortical volume. Regions are listed by hemisphere and anatomical label according to the Desikan-Killiany atlas.

DLB, dementia with Lewy bodies; eTIV, estimated total intracranial volume; FDR = false discovery rate.

**Supplementary Table 7. Region-wise cortical surface area comparisons**  
between DLB patients and controls

| Region                      | Controls       | DLB            | P-value  | P <sub>FDR</sub> -value | W-score<br>DLB |
|-----------------------------|----------------|----------------|----------|-------------------------|----------------|
| <b>Left hemisphere</b>      |                |                |          |                         |                |
| banks superior temp. sulcus | 957.28±136.80  | 945.28±149.81  | 0.19168  | 0.33421                 | -0.152         |
| caudal anterior cingulate   | 621.44±131.32  | 631.47±180.81  | 0.57657  | 0.75398                 | 0.034          |
| caudal middle frontal       | 2124.51±309.20 | 2115.50±385.00 | 0.33717  | 0.48831                 | 0.003          |
| cuneus                      | 1416.19±206.07 | 1432.40±236.89 | 0.75496  | 0.86795                 | 0.030          |
| entorhinal                  | 431.26±90.66   | 439.99±96.41   | 0.76584  | 0.86795                 | 0.074          |
| fusiform                    | 3003.81±379.10 | 2960.95±438.95 | 0.00646  | <b>0.03447</b>          | -0.227         |
| inferior parietal           | 4195.83±581.72 | 3994.85±564.14 | 0.00016  | <b>0.00363</b>          | -0.438         |
| inferior temporal           | 3255.48±476.54 | 3234.17±511.54 | 0.07939  | 0.16359                 | -0.145         |
| isthmus cingulate           | 1023.31±144.92 | 1038.80±185.23 | 0.38733  | 0.53752                 | -0.016         |
| lateral occipital           | 4750.93±603.78 | 4660.02±655.09 | 0.03224  | 0.10440                 | -0.181         |
| lateral orbitofrontal       | 2616.58±280.83 | 2600.72±361.52 | 0.04719  | 0.12394                 | -0.106         |
| lingual                     | 2877.57±390.60 | 2832.44±378.53 | 0.10936  | 0.21872                 | -0.132         |
| medial orbitofrontal        | 1908.49±191.39 | 1952.80±251.54 | 0.81028  | 0.87459                 | 0.187          |
| middle temporal             | 3043.59±379.80 | 2985.88±412.03 | 0.01270  | 0.05134                 | -0.258         |
| parahippocampal             | 642.82±86.17   | 631.42±87.75   | 0.01640  | 0.05869                 | -0.170         |
| paracentral                 | 1329.61±150.81 | 1368.16±177.14 | 0.74376  | 0.86795                 | 0.238          |
| pars opercularis            | 1564.44±263.59 | 1521.32±262.49 | 0.04403  | 0.12394                 | -0.273         |
| pars orbitalis              | 685.99±90.84   | 669.42±98.98   | 0.00659  | <b>0.03447</b>          | -0.258         |
| pars triangularis           | 1268.52±192.70 | 1250.41±195.37 | 0.04415  | 0.12394                 | -0.240         |
| pericalcarine               | 1292.58±224.62 | 1325.76±243.14 | 0.60812  | 0.78023                 | 0.145          |
| postcentral                 | 4067.11±415.68 | 4095.70±521.07 | 0.17309  | 0.30974                 | -0.010         |
| posterior cingulate         | 1137.50±164.07 | 1095.12±220.87 | 0.01347  | 0.05134                 | -0.354         |
| precentral                  | 4817.64±523.66 | 4865.52±523.78 | 0.32784  | 0.48831                 | 0.051          |
| precuneus                   | 3671.07±458.34 | 3599.96±444.95 | 0.00055  | <b>0.00622</b>          | -0.281         |
| rostral anterior cingulate  | 842.57±178.21  | 867.26±201.28  | 0.54186  | 0.72248                 | 0.077          |
| rostral middle frontal      | 5098.91±662.22 | 5260.56±839.09 | 0.79739  | 0.87456                 | 0.301          |
| superior frontal            | 7027.73±785.72 | 7155.17±876.77 | 0.48992  | 0.66629                 | 0.150          |
| superior parietal           | 5119.60±547.97 | 4982.86±639.43 | 0.00031  | <b>0.00527</b>          | -0.365         |
| superior temporal           | 3909.90±433.72 | 3944.19±458.42 | 0.26367  | 0.41697                 | 0.037          |
| supramarginal               | 3906.26±590.96 | 3970.62±601.63 | 0.33751  | 0.48831                 | 0.037          |
| frontal pole                | 271.27±35.18   | 258.12±28.92   | 0.00064  | <b>0.00622</b>          | -0.456         |
| temporal pole               | 497.07±60.39   | 505.49±79.89   | 0.93162  | 0.94552                 | 0.086          |
| transverse temporal         | 456.11±63.35   | 454.79±76.09   | 0.20167  | 0.34284                 | -0.047         |
| insula                      | 2450.83±274.20 | 2428.01±253.46 | 0.00451  | <b>0.03067</b>          | -0.172         |
| <b>Right hemisphere</b>     |                |                |          |                         |                |
| banks superior temp. sulcus | 856.19±99.57   | 801.94±115.53  | 0.00011  | <b>0.00363</b>          | -0.600         |
| caudal anterior cingulate   | 712.17±158.49  | 710.74±165.95  | 0.37015  | 0.52438                 | -0.041         |
| caudal middle frontal       | 1989.90±260.96 | 2065.08±404.10 | 0.67494  | 0.84272                 | 0.311          |
| cuneus                      | 1513.91±196.07 | 1538.70±257.98 | 0.97694  | 0.97694                 | 0.116          |
| entorhinal                  | 394.87±81.95   | 403.41±86.47   | 0.89538  | 0.93671                 | 0.142          |
| fusiform                    | 2903.60±382.39 | 2842.48±404.58 | 0.00225  | <b>0.01700</b>          | -0.232         |
| inferior parietal           | 5023.82±747.21 | 4692.54±667.08 | <0.00001 | <b>0.00007</b>          | -0.544         |
| inferior temporal           | 3094.49±426.58 | 3066.63±522.51 | 0.05211  | 0.13124                 | -0.138         |
| isthmus cingulate           | 913.72±142.13  | 930.09±175.55  | 0.70640  | 0.84272                 | 0.047          |
| lateral occipital           | 4722.49±589.47 | 4678.01±758.22 | 0.07335  | 0.16199                 | -0.107         |
| lateral orbitofrontal       | 2640.75±314.26 | 2676.76±358.97 | 0.25216  | 0.40826                 | 0.075          |
| lingual                     | 2998.92±404.06 | 3025.76±415.41 | 0.79400  | 0.87456                 | 0.047          |
| medial orbitofrontal        | 2051.63±248.65 | 2071.26±253.88 | 0.16595  | 0.30499                 | 0.037          |
| middle temporal             | 3316.82±355.46 | 3268.08±474.87 | 0.00936  | <b>0.04546</b>          | -0.245         |
| parahippocampal             | 610.10±82.10   | 608.60±77.93   | 0.03677  | 0.11365                 | -0.135         |

|                            |                |                |         |                |        |
|----------------------------|----------------|----------------|---------|----------------|--------|
| paracentral                | 1493.06±188.35 | 1531.16±200.96 | 0.68642 | 0.84272        | 0.118  |
| pars opercularis           | 1315.68±201.39 | 1281.29±196.31 | 0.01079 | <b>0.04891</b> | -0.288 |
| pars orbitalis             | 812.64±101.59  | 819.46±127.02  | 0.27646 | 0.42726        | -0.002 |
| pars triangularis          | 1482.77±238.63 | 1440.02±213.39 | 0.00529 | <b>0.03270</b> | -0.300 |
| pericalcarine              | 1440.65±218.39 | 1475.67±280.59 | 0.84038 | 0.89290        | 0.111  |
| postcentral                | 3926.35±458.50 | 3955.00±512.20 | 0.06952 | 0.16199        | -0.023 |
| posterior cingulate        | 1125.94±168.13 | 1112.19±240.91 | 0.21566 | 0.35768        | -0.097 |
| precentral                 | 4842.46±490.95 | 4864.68±556.25 | 0.12956 | 0.25172        | -0.004 |
| precuneus                  | 3845.45±483.28 | 3769.53±507.95 | 0.00049 | <b>0.00622</b> | -0.276 |
| rostral anterior cingulate | 601.60±109.86  | 583.93±138.27  | 0.07504 | 0.16199        | -0.180 |
| rostral middle frontal     | 5401.56±817.91 | 5415.89±815.74 | 0.07623 | 0.16199        | -0.007 |
| superior frontal           | 6716.78±752.37 | 6864.73±894.21 | 0.69582 | 0.84272        | 0.195  |
| superior parietal          | 5025.60±548.57 | 4874.97±656.40 | 0.00074 | <b>0.00629</b> | -0.372 |
| superior temporal          | 3647.26±370.73 | 3672.65±469.85 | 0.15813 | 0.29869        | -0.028 |
| supramarginal              | 3514.06±468.35 | 3502.43±530.51 | 0.04739 | 0.12394        | -0.128 |
| frontal pole               | 332.11±40.57   | 323.94±43.02   | 0.01359 | 0.05134        | -0.307 |
| temporal pole              | 483.04±73.35   | 488.81±75.23   | 0.91225 | 0.93989        | 0.064  |
| transverse temporal        | 335.40±47.10   | 334.64±47.50   | 0.07416 | 0.16199        | -0.134 |
| insula                     | 2360.57±306.92 | 2360.33±300.16 | 0.02567 | 0.08728        | -0.126 |

Mean ± standard deviation cortical surface area values are shown for the DLB and control groups across each cortical region following data harmonization using ComBAT. Group differences were assessed using analysis of variance (ANOVA) adjusted for age, sex, and eTIV. FDR-corrected P-values ( $P_{FDR}$ ) are reported, with statistical significance set at  $P_{FDR} < 0.05$ . W-scores represent standardized deviations in cortical surface area for DLB patients relative to age- and sex-matched controls as reference; negative values indicate decreased surface area. Regions are listed by hemisphere and anatomical label according to the Desikan-Killiany atlas.

DLB, dementia with Lewy bodies; eTIV, estimated total intracranial volume; FDR = false discovery rate.

**Supplementary Table 8.** Biological processes and cellular components enriched in regions with cortical thinning in DLB within latent variable 3

| GO identifier                                                          | GO term                                                                   | Gene set size | Number of leading edge IDs | ES    | NES   | P-value (FDR)   |
|------------------------------------------------------------------------|---------------------------------------------------------------------------|---------------|----------------------------|-------|-------|-----------------|
| <b>Biological processes</b>                                            |                                                                           |               |                            |       |       |                 |
| <i>Negatively weighted genes (associated with decreased thickness)</i> |                                                                           |               |                            |       |       |                 |
| GO:0099003 <sup>§</sup>                                                | vesicle-mediated transport in synapse                                     | 205           | 83                         | -0.48 | -2.61 | < <b>0.0001</b> |
| GO:0010257 <sup>§</sup>                                                | NADH dehydrogenase complex assembly                                       | 54            | 38                         | -0.56 | -2.39 | 0.0005          |
| GO:0048499                                                             | synaptic vesicle membrane organization                                    | 27            | 15                         | -0.65 | -2.33 | 0.001           |
| GO:0022900 <sup>§</sup>                                                | electron transport chain                                                  | 146           | 88                         | -0.46 | -2.33 | 0.0008          |
| GO:0099177 <sup>§</sup>                                                | regulation of trans-synaptic signalling                                   | 425           | 152                        | -0.38 | -2.26 | 0.0009          |
| GO:0099565 <sup>§</sup>                                                | chemical synaptic transmission, postsynaptic                              | 94            | 42                         | -0.46 | -2.22 | 0.001           |
| GO:0099072 <sup>§</sup>                                                | regulation of postsynaptic membrane neurotransmitter receptor levels      | 82            | 36                         | -0.45 | -2.14 | 0.002           |
| GO:1902414 <sup>§</sup>                                                | protein localization to cell junction                                     | 103           | 47                         | -0.43 | -2.13 | 0.002           |
| GO:0070585 <sup>§</sup>                                                | protein localization to mitochondrion                                     | 122           | 57                         | -0.42 | -2.12 | 0.002           |
| GO:0015980 <sup>§</sup>                                                | energy derivation by oxidation of organic compounds                       | 280           | 134                        | -0.36 | -2.02 | 0.005           |
| GO:0002209 <sup>§</sup>                                                | behavioral defense response                                               | 41            | 24                         | -0.50 | -2.01 | 0.007           |
| GO:0050803 <sup>§</sup>                                                | regulation of synapse structure or activity                               | 225           | 93                         | -0.36 | -1.98 | 0.008           |
| GO:0035249                                                             | synaptic transmission, glutamatergic                                      | 97            | 36                         | -0.41 | -1.97 | 0.008           |
| GO:0098664                                                             | G protein-coupled serotonin receptor signaling pathway                    | 19            | 8                          | -0.61 | -1.97 | 0.008           |
| GO:0050808 <sup>§</sup>                                                | synapse organization                                                      | 440           | 172                        | -0.33 | -1.93 | 0.010           |
| GO:0070050 <sup>§</sup>                                                | neuron cellular homeostasis                                               | 55            | 26                         | -0.45 | -1.92 | 0.010           |
| GO:0007005 <sup>§</sup>                                                | mitochondrion organization                                                | 439           | 200                        | -0.32 | -1.87 | 0.015           |
| GO:0051703 <sup>§</sup>                                                | biological process involved in intraspecies interaction between organisms | 45            | 17                         | -0.46 | -1.86 | 0.016           |
| GO:1901293 <sup>§</sup>                                                | nucleoside phosphate biosynthetic process                                 | 240           | 102                        | -0.33 | -1.84 | 0.019           |
| GO:0051648 <sup>§</sup>                                                | vesicle localization                                                      | 203           | 71                         | -0.34 | -1.83 | 0.019           |
| GO:1902600 <sup>§</sup>                                                | proton transmembrane transport                                            | 114           | 67                         | -0.37 | -1.81 | 0.023           |
| GO:0042391 <sup>§</sup>                                                | regulation of membrane potential                                          | 364           | 133                        | -0.31 | -1.81 | 0.023           |
| GO:0072522 <sup>§</sup>                                                | purine-containing compound biosynthetic process                           | 216           | 93                         | -0.33 | -1.80 | 0.023           |

|                                                                               |                                                               |     |     |       |       |          |
|-------------------------------------------------------------------------------|---------------------------------------------------------------|-----|-----|-------|-------|----------|
| GO:0018210                                                                    | peptidyl-threonine modification                               | 79  | 24  | -0.38 | -1.80 | 0.023    |
| GO:0050890 <sup>§</sup>                                                       | cognition                                                     | 277 | 124 | -0.32 | -1.79 | 0.022    |
| GO:0009141 <sup>§</sup>                                                       | nucleoside triphosphate metabolic process                     | 223 | 98  | -0.33 | -1.79 | 0.021    |
| GO:0048857 <sup>§</sup>                                                       | neural nucleus development                                    | 58  | 26  | -0.41 | -1.79 | 0.021    |
| GO:0006836 <sup>§</sup>                                                       | neurotransmitter transport                                    | 178 | 57  | -0.33 | -1.77 | 0.024    |
| GO:0031644 <sup>§</sup>                                                       | regulation of nervous system process                          | 96  | 34  | -0.36 | -1.76 | 0.027    |
| GO:0106027                                                                    | neuron projection organization                                | 81  | 37  | -0.37 | -1.73 | 0.035    |
| GO:0001963                                                                    | synaptic transmission, dopaminergic                           | 23  | 10  | -0.51 | -1.73 | 0.034    |
| GO:1990089                                                                    | response to nerve growth factor                               | 44  | 14  | -0.42 | -1.72 | 0.035    |
| GO:0019693 <sup>§</sup>                                                       | ribose phosphate metabolic process                            | 396 | 163 | -0.29 | -1.72 | 0.035    |
| GO:0023019                                                                    | signal transduction involved in regulation of gene expression | 15  | 6   | -0.55 | -1.69 | 0.041    |
| GO:0090150 <sup>§</sup>                                                       | establishment of protein localization to membrane             | 244 | 83  | -0.30 | -1.68 | 0.045    |
| GO:0009308                                                                    | amine metabolic process                                       | 90  | 36  | -0.35 | -1.66 | 0.048    |
| GO:0006887 <sup>§</sup>                                                       | exocytosis                                                    | 289 | 76  | -0.29 | -1.66 | 0.048    |
| GO:0015844                                                                    | monoamine transport                                           | 70  | 25  | -0.37 | -1.66 | 0.047    |
| <b><i>Positively weighted genes (associated with increased thickness)</i></b> |                                                               |     |     |       |       |          |
| GO:0070828                                                                    | heterochromatin organization                                  | 88  | 40  | 0.47  | 2.12  | 0.009    |
| <b>Cellular components</b>                                                    |                                                               |     |     |       |       |          |
| <b><i>Negatively weighted genes (associated with decreased thickness)</i></b> |                                                               |     |     |       |       |          |
| GO:0070469                                                                    | respirasome                                                   | 86  | 62  | -0.54 | -2.60 | < 0.0001 |
| GO:0098798 <sup>§</sup>                                                       | mitochondrial protein-containing complex                      | 273 | 164 | -0.43 | -2.41 | < 0.0001 |
| GO:1990204 <sup>§</sup>                                                       | oxidoreductase complex                                        | 107 | 66  | -0.49 | -2.41 | < 0.0001 |
| GO:0098984 <sup>§</sup>                                                       | neuron to neuron synapse                                      | 339 | 123 | -0.40 | -2.30 | < 0.0001 |
| GO:0098978 <sup>§</sup>                                                       | glutamatergic synapse                                         | 390 | 159 | -0.40 | -2.29 | < 0.0001 |
| GO:0099572 <sup>§</sup>                                                       | postsynaptic specialization                                   | 320 | 111 | -0.38 | -2.16 | 0.0004   |
| GO:0070069 <sup>§</sup>                                                       | cytochrome complex                                            | 33  | 24  | -0.56 | -2.14 | 0.0006   |
| GO:0097060 <sup>§</sup>                                                       | synaptic membrane                                             | 354 | 122 | -0.37 | -2.12 | 0.001    |
| GO:0005743 <sup>§</sup>                                                       | mitochondrial inner membrane                                  | 431 | 215 | -0.35 | -2.10 | 0.001    |
| GO:0060076 <sup>§</sup>                                                       | excitatory synapse                                            | 62  | 26  | -0.47 | -2.06 | 0.001    |
| GO:0098685 <sup>§</sup>                                                       | Schaffer collateral - CA1 synapse                             | 90  | 45  | -0.42 | -1.99 | 0.002    |
| GO:0048786 <sup>§</sup>                                                       | presynaptic active zone                                       | 71  | 30  | -0.45 | -1.98 | 0.002    |
| GO:0043198 <sup>§</sup>                                                       | dendritic shaft                                               | 40  | 24  | -0.48 | -1.97 | 0.002    |
| GO:0150034 <sup>§</sup>                                                       | distal axon                                                   | 242 | 96  | -0.34 | -1.90 | 0.004    |
| GO:0044309 <sup>§</sup>                                                       | neuron spine                                                  | 165 | 60  | -0.36 | -1.86 | 0.006    |
| GO:1990351 <sup>§</sup>                                                       | transporter complex                                           | 368 | 113 | -0.31 | -1.82 | 0.004    |
| GO:0044306 <sup>§</sup>                                                       | neuron projection terminus                                    | 111 | 40  | -0.37 | -1.80 | 0.010    |
| GO:0030133 <sup>§</sup>                                                       | transport vesicle                                             | 376 | 110 | -0.30 | -1.77 | 0.012    |
| GO:0030427 <sup>§</sup>                                                       | site of polarized growth                                      | 153 | 59  | -0.34 | -1.77 | 0.012    |
| GO:0071782                                                                    | endoplasmic reticulum tubular network                         | 26  | 13  | -0.47 | -1.74 | 0.015    |
| GO:0005759 <sup>§</sup>                                                       | mitochondrial matrix                                          | 451 | 199 | -0.29 | -1.71 | 0.018    |
| GO:0098982 <sup>§</sup>                                                       | GABA-ergic synapse                                            | 74  | 23  | -0.37 | -1.70 | 0.019    |
| GO:0043025 <sup>§</sup>                                                       | neuronal cell body                                            | 433 | 151 | -0.28 | -1.66 | 0.026    |
| GO:0099568 <sup>§</sup>                                                       | cytoplasmic region                                            | 223 | 86  | -0.30 | -1.66 | 0.025    |

|                         |                    |     |    |       |       |       |
|-------------------------|--------------------|-----|----|-------|-------|-------|
| GO:0031045              | dense core granule | 34  | 9  | -0.43 | -1.62 | 0.031 |
| GO:0048770 <sup>s</sup> | pigment granule    | 103 | 32 | -0.34 | -1.62 | 0.031 |
| GO:0099522 <sup>s</sup> | cytosolic region   | 19  | 14 | -0.47 | -1.56 | 0.047 |
| GO:1905368 <sup>s</sup> | peptidase complex  | 111 | 45 | -0.31 | -1.56 | 0.047 |

List of genes significantly enriched in biological processes and cellular components within the third latent variable for cortical thickness based on gene enrichment analyse within the third latent variable using WebGestalt.

**Supplementary Table 9.** Gene set enrichment analysis: biological processes enriched in genes associated with cortical volume and cortical surface area in DLB

| GO identifier                                                            | GO term                                                              | Gene set size | Number of leading edge IDs | ES    | NES   | P-value (FDR) |
|--------------------------------------------------------------------------|----------------------------------------------------------------------|---------------|----------------------------|-------|-------|---------------|
| <b>Cortical Volume</b>                                                   |                                                                      |               |                            |       |       |               |
| <b>Negatively weighted genes (associated with lower cortical volume)</b> |                                                                      |               |                            |       |       |               |
| GO:0099003                                                               | vesicle-mediated transport in synapse                                | 205           | 77                         | -0.47 | -2.52 | < 0.0001      |
| GO:0010257                                                               | NADH dehydrogenase complex assembly                                  | 54            | 39                         | -0.56 | -2.39 | < 0.0001      |
| GO:0099565                                                               | chemical synaptic transmission, postsynaptic                         | 94            | 39                         | -0.49 | -2.32 | < 0.0001      |
| GO:0022900                                                               | electron transport chain                                             | 146           | 87                         | -0.45 | -2.27 | < 0.0001      |
| GO:0099177                                                               | regulation of trans-synaptic signaling                               | 425           | 159                        | -0.38 | -2.25 | 0.0002        |
| GO:0007005                                                               | mitochondrion organization                                           | 439           | 197                        | -0.37 | -2.15 | 0.002         |
| GO:0070585                                                               | protein localization to mitochondrion                                | 122           | 56                         | -0.43 | -2.15 | 0.002         |
| GO:0099072                                                               | regulation of postsynaptic membrane neurotransmitter receptor levels | 82            | 37                         | -0.45 | -2.10 | 0.002         |
| GO:0070050                                                               | neuron cellular homeostasis                                          | 55            | 24                         | -0.49 | -2.08 | 0.003         |
| GO:0071867                                                               | response to monoamine                                                | 61            | 24                         | -0.47 | -2.06 | 0.003         |
| GO:0002209                                                               | behavioral defense response                                          | 41            | 17                         | -0.52 | -2.05 | 0.004         |
| GO:0098664                                                               | G protein-coupled serotonin receptor signaling pathway               | 19            | 9                          | -0.62 | -2.04 | 0.004         |
| GO:1901293                                                               | nucleoside phosphate biosynthetic process                            | 240           | 99                         | -0.37 | -2.03 | 0.004         |
| GO:0001963                                                               | synaptic transmission, dopaminergic                                  | 23            | 11                         | -0.59 | -2.02 | 0.004         |
| GO:0015980                                                               | energy derivation by oxidation of organic compounds                  | 280           | 115                        | -0.36 | -2.00 | 0.005         |
| GO:0035249                                                               | synaptic transmission, glutamatergic                                 | 97            | 38                         | -0.41 | -1.98 | 0.006         |
| GO:0072522                                                               | purine-containing compound biosynthetic process                      | 216           | 89                         | -0.37 | 1.97  | 0.006         |
| GO:1902600                                                               | proton transmembrane transport                                       | 114           | 56                         | -0.40 | -1.96 | 0.006         |
| GO:0009141                                                               | nucleoside triphosphate metabolic process                            | 223           | 101                        | -0.36 | -1.96 | 0.006         |
| GO:0048499                                                               | synaptic vesicle membrane organization                               | 27            | 10                         | -0.53 | -1.94 | 0.006         |
| GO:0019693                                                               | ribose phosphate metabolic process                                   | 396           | 158                        | -0.32 | -1.88 | 0.010         |
| GO:0050808                                                               | synapse organization                                                 | 440           | 163                        | -0.31 | -1.86 | 0.011         |
| GO:0042391                                                               | regulation of membrane potential                                     | 364           | 138                        | -0.32 | -1.83 | 0.014         |

|                                                                                  |                                                                   |     |     |       |       |          |
|----------------------------------------------------------------------------------|-------------------------------------------------------------------|-----|-----|-------|-------|----------|
| GO:0043161                                                                       | proteasome-mediated ubiquitin-dependent protein catabolic process | 412 | 153 | -0.30 | -1.79 | 0.018    |
| GO:0072594                                                                       | establishment of protein localization to organelle                | 400 | 140 | -0.30 | -1.75 | 0.021    |
| GO:001605                                                                        | vesicle organization                                              | 323 | 132 | -0.30 | -1.71 | 0.028    |
| <b>Positively weighted genes (associated with higher cortical volume)</b>        |                                                                   |     |     |       |       |          |
| GO:0070828 †                                                                     | heterochromatin organization                                      | 88  | 47  | 0.050 | 2.36  | < 0.0001 |
| GO:0070269 †                                                                     | pyroptosis                                                        | 25  | 16  | 0.57  | 2.01  | 0.025    |
| GO:0035329                                                                       | hippo signaling                                                   | 35  | 15  | 0.49  | 1.96  | 0.031    |
| GO:0072337 †                                                                     | modified amino acid transport                                     | 35  | 14  | 0.50  | 1.94  | 0.029    |
| GO:0007606                                                                       | sensory perception of chemical stimulus                           | 107 | 55  | 0.38  | 1.89  | 0.038    |
| <b>Cortical surface area</b>                                                     |                                                                   |     |     |       |       |          |
| <b><i>Positively weighted genes (associated with increased surface area)</i></b> |                                                                   |     |     |       |       |          |
| GO:0022900                                                                       | electron transport chain                                          | 146 | 87  | 0.46  | 2.28  | 0.001    |
| GO:0042060                                                                       | wound healing                                                     | 310 | 126 | 0.38  | 2.11  | 0.008    |
| GO:1901657                                                                       | glycosyl compound metabolic process                               | 59  | 20  | 0.48  | 2.08  | 0.006    |
| GO:0019882                                                                       | antigen processing and presentation                               | 92  | 34  | 0.45  | 2.06  | 0.006    |
| GO:0002396                                                                       | MHC protein complex assembly                                      | 18  | 11  | 0.65  | 2.03  | 0.007    |
| GO:0036314                                                                       | response to sterol                                                | 26  | 12  | 0.56  | 1.96  | 0.016    |
| GO:0002347                                                                       | response to tumour cell                                           | 35  | 13  | 0.52  | 1.95  | 0.015    |
| GO:0050866                                                                       | negative regulation of cell activation                            | 139 | 67  | 0.40  | 1.95  | 0.014    |
| GO:0044282                                                                       | small molecule catabolic process                                  | 292 | 120 | 0.36  | 1.94  | 0.014    |
| GO:0048010                                                                       | vascular endothelial growth factor receptor signaling pathway     | 50  | 21  | 0.47  | 1.92  | 0.018    |
| GO:0045785                                                                       | positive regulation of cell adhesion                              | 362 | 153 | 0.34  | 1.90  | 0.020    |
| GO:0042063                                                                       | gliogenesis                                                       | 292 | 110 | 0.35  | 1.89  | 0.023    |
| GO:0034109                                                                       | homotypic cell-cell adhesion                                      | 67  | 32  | 0.44  | 1.88  | 0.024    |
| GO:0050817                                                                       | coagulation                                                       | 161 | 62  | 0.37  | 1.83  | 0.037    |
| GO:0032637                                                                       | interleukin-8 production                                          | 55  | 35  | 0.44  | 1.83  | 0.037    |
| GO:1901342                                                                       | regulation of vasculature development                             | 223 | 75  | 0.35  | 1.82  | 0.036    |
| GO:0090594                                                                       | inflammatory response to wounding                                 | 18  | 14  | 0.57  | 1.81  | 0.038    |
| GO:0007229                                                                       | integrin-mediated signaling pathway                               | 91  | 47  | 0.39  | 1.80  | 0.040    |
| GO:0050900                                                                       | leukocyte migration                                               | 264 | 104 | 0.34  | 1.80  | 0.039    |
| GO:0002181                                                                       | cytoplasmic translation                                           | 148 | 63  | 0.36  | 1.80  | 0.037    |
| GO:0072593                                                                       | reactive oxygen species metabolic process                         | 166 | 69  | 0.35  | 1.77  | 0.048    |
| GO:0060840                                                                       | artery development                                                | 85  | 38  | 0.39  | 1.76  | 0.049    |
| GO:0006882                                                                       | intracellular zinc ion homeostasis                                | 28  | 13  | 0.49  | 1.76  | 0.049    |

|            |                                                                  |     |    |      |      |       |
|------------|------------------------------------------------------------------|-----|----|------|------|-------|
| GO:0035924 | cellular response to vascular endothelial growth factor stimulus | 53  | 29 | 0.42 | 1.75 | 0.048 |
| GO:0050673 | epithelial cell proliferation                                    | 319 | 92 | 0.32 | 1.75 | 0.049 |
| GO:0010463 | mesenchymal cell proliferation                                   | 34  | 14 | 0.46 | 1.74 | 0.049 |

List of genes significantly enriched in biological processes within the first latent variable for cortical volume and surface area based on gene enrichment analyse within the third latent variable using WebGestalt. † Result not found with Panther.

DLB, dementia with Lewy bodies; GO, gene ontology; FDR, false-discovery rate; ES, enrichment score; NES, normalized enrichment score.

**Supplementary Table 10.** Over-representation results of unique and shared genes in pathway enrichment of cortical atrophy in DLB

[illegible]

|                                        |                                                        |     |      |   |        |                 |
|----------------------------------------|--------------------------------------------------------|-----|------|---|--------|-----------------|
| GO:0001963                             | synaptic transmission, dopaminergic                    | 23  | 0.04 | 5 | 124.40 | <b>2.62E-07</b> |
| GO:0098780                             | response to mitochondrial depolarisation               | 20  | 0.03 | 3 | 85.84  | <b>4.76E-04</b> |
| GO:0015844                             | monoamine transport                                    | 70  | 0.12 | 5 | 40.88  | <b>2.99E-05</b> |
| GO:0018958                             | phenol-containing compound metabolic process           | 81  | 0.14 | 4 | 28.26  | <b>7.25E-04</b> |
| GO:0030534                             | adult behavior                                         | 121 | 0.21 | 5 | 23.65  | <b>2.07E-04</b> |
| GO:0070585                             | protein localization to mitochondrion                  | 122 | 0.21 | 5 | 23.45  | <b>2.07E-04</b> |
| GO:0018209                             | peptidyl-serine modification                           | 175 | 0.31 | 6 | 19.62  | <b>6.39E-05</b> |
| GO:0051235                             | maintenance of location                                | 265 | 0.46 | 7 | 15.12  | <b>4.14E-05</b> |
| GO:0097193                             | intrinsic apoptotic signaling pathway                  | 264 | 0.46 | 6 | 13.01  | <b>4.41E-04</b> |
| GO:0042391                             | regulation of membrane potential                       | 364 | 0.64 | 8 | 12.58  | <b>2.99E-05</b> |
| <b>Shared AD- and PD-pathway genes</b> |                                                        |     |      |   |        |                 |
| GO:0006882                             | intracellular zinc ion homeostasis                     | 28  | 0.01 | 2 | 136.25 | <b>0.0282</b>   |
| GO:1990000                             | amyloid fibril formation                               | 34  | 0.02 | 2 | 112.21 | <b>0.0282</b>   |
| GO:0002269                             | leukocyte activation involved in inflammatory response | 38  | 0.20 | 2 | 100.39 | <b>0.0282</b>   |
| GO:0019755                             | one-carbon compound transport                          | 39  | 0.02 | 2 | 97.82  | <b>0.0282</b>   |
| GO:0000041                             | transition metal ion transport                         | 80  | 0.04 | 3 | 71.53  | <b>0.0054</b>   |
| GO:0150076                             | neuroinflammatory response                             | 57  | 0.03 | 2 | 66.93  | <b>0.0303</b>   |
| GO:0051347                             | positive regulation of transferase activity            | 273 | 0.14 | 3 | 20.96  | <b>0.0303</b>   |
| GO:0051345                             | positive regulation of hydrolase activity              | 287 | 0.15 | 3 | 19.94  | <b>0.0303</b>   |
| GO:0010563                             | negative regulation of phosphorus metabolic process    | 292 | 0.15 | 3 | 19.60  | <b>0.0303</b>   |
| GO:0010038                             | response to metal ion                                  | 299 | 0.16 | 3 | 19.14  | <b>0.0303</b>   |

Bold values represent significantly enriched biological process terms for every pathway enrichment analysis. Only the top 10 genes are shown when significant. Genes are ordered per analysis by decreasing enrichment scores.

AD, Alzheimer's disease; DLB, dementia with Lewy bodies; ER, enrichment ratio; FDR, false discovery rate; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; PD = Parkinson's disease.

**Supplementary Table 11.** Over-representation results of biological processes enriched in the genes not part of KEGG AD and PD pathways

| GO identifier | GO term                               | Gene set size | Expected value | Overlap | ER    | P <sub>FDR</sub> -value |
|---------------|---------------------------------------|---------------|----------------|---------|-------|-------------------------|
| GO:0007214    | GABA signaling pathway                | 25            | 0.19           | 5       | 26.62 | <b>1.05E-04</b>         |
| GO:0070050    | neuron cellular homeostasis           | 55            | 0.41           | 11      | 26.62 | <b>5.70E-11</b>         |
| GO:1902600    | proton transmembrane transport        | 114           | 0.86           | 17      | 19.85 | <b>5.16E-15</b>         |
| GO:0006885    | regulation of pH                      | 81            | 0.61           | 10      | 16.3  | <b>8.57E-08</b>         |
| GO:0099003    | vesicle-mediated transport in synapse | 205           | 1.54           | 20      | 12.98 | <b>1.24E-14</b>         |
| GO:0006820    | monoatomic anion transport            | 124           | 0.93           | 8       | 8.59  | <b>3.32E-04</b>         |
| GO:0006898    | receptor-mediated endocytosis         | 206           | 1.55           | 11      | 7.11  | <b>4.91E-05</b>         |
| GO:0021700    | developmental maturation              | 255           | 1.92           | 12      | 6.26  | <b>4.91E-05</b>         |
| GO:0016050    | vesicle organization                  | 323           | 2.43           | 15      | 6.18  | <b>2.48E-06</b>         |
| GO:0042391    | regulation of membrane potential      | 364           | 2.74           | 13      | 4.75  | <b>2.73E-04</b>         |

Bold values represent significantly enriched biological process terms. Only the top 10 genes are shown when significant. Genes are ordered by decreasing enrichment scores.

AD, Alzheimer's disease; ER, enrichment ratio; FDR, false discovery rate; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; PD, Parkinson's disease.

**Supplementary Table 12.** Comparisons between enrichment in brain vs. body tissues of genes enriched in DLB-related atrophy independent from AD and PD pathways.

| Gene ID            | Gene name       | Mean brain TPM | Mean body TPM | log <sub>2</sub> fold change brain vs. body | P-value    | FDR-adjusted q-values |
|--------------------|-----------------|----------------|---------------|---------------------------------------------|------------|-----------------------|
| ENSG00000104888.10 | <i>SLC17A7</i>  | 246.57         | 2.21          | 6.27                                        | 0.00629149 | <b>0.01415585</b>     |
| ENSG00000213760.11 | <i>ATP6V1G2</i> | 286.00         | 2.92          | 6.19                                        | 0.00000001 | <b>0.00000018</b>     |
| ENSG00000162728.5  | <i>KCNJ9</i>    | 63.81          | 0.17          | 5.79                                        | 0.00000001 | <b>0.00000018</b>     |
| ENSG00000162188.6  | <i>GNG3</i>     | 108.31         | 1.28          | 5.58                                        | 0.00000001 | <b>0.00000018</b>     |
| ENSG00000126583.12 | <i>PRKCG</i>    | 40.03          | 0.47          | 4.80                                        | 0.00000002 | <b>0.00000018</b>     |
| ENSG00000079841.19 | <i>RIMS1</i>    | 21.22          | 0.40          | 3.99                                        | 0.00000002 | <b>0.00000018</b>     |
| ENSG00000163285.8  | <i>GABRG1</i>   | 14.90          | 0.10          | 3.85                                        | 0.00000001 | <b>0.00000018</b>     |
| ENSG00000155511.18 | <i>GRIA1</i>    | 29.72          | 1.19          | 3.81                                        | 0.00000002 | <b>0.00000018</b>     |
| ENSG00000152578.13 | <i>GRIA4</i>    | 15.93          | 0.54          | 3.46                                        | 0.00000002 | <b>0.00000018</b>     |
| ENSG00000148408.14 | <i>CACNA1B</i>  | 15.79          | 0.76          | 3.25                                        | 0.00000007 | <b>0.00000036</b>     |
| ENSG00000125675.20 | <i>GRIA3</i>    | 21.63          | 1.75          | 3.04                                        | 0.00000004 | <b>0.00000026</b>     |
| ENSG00000132535.22 | <i>DLG4</i>     | 77.70          | 9.00          | 2.98                                        | 0.00000014 | <b>0.00000065</b>     |
| ENSG00000011677.13 | <i>GABRA3</i>   | 7.29           | 0.08          | 2.94                                        | 0.00000000 | <b>0.00000018</b>     |
| ENSG00000152822.14 | <i>GRM1</i>     | 7.02           | 0.07          | 2.91                                        | 0.00000002 | <b>0.00000018</b>     |
| ENSG00000171130.19 | <i>ATP6V0E2</i> | 88.34          | 11.41         | 2.85                                        | 0.00000002 | <b>0.00000018</b>     |
| ENSG00000078295.17 | <i>ADCY2</i>    | 20.26          | 2.55          | 2.58                                        | 0.00000004 | <b>0.00000026</b>     |
| ENSG00000154654.15 | <i>NCAM2</i>    | 11.23          | 1.14          | 2.51                                        | 0.00000004 | <b>0.00000026</b>     |
| ENSG00000166206.15 | <i>GABRB3</i>   | 10.29          | 1.04          | 2.47                                        | 0.00000012 | <b>0.00000058</b>     |
| ENSG00000106089.12 | <i>STX1A</i>    | 67.45          | 12.69         | 2.32                                        | 0.00007538 | <b>0.00021200</b>     |
| ENSG00000168243.11 | <i>GNG4</i>     | 18.88          | 3.73          | 2.07                                        | 0.00000067 | <b>0.00000273</b>     |
| ENSG00000107902.14 | <i>LHPP</i>     | 54.67          | 12.72         | 2.02                                        | 0.00000005 | <b>0.00000029</b>     |
| ENSG00000171867.18 | <i>PRNP</i>     | 277.61         | 103.23        | 1.42                                        | 0.00000084 | <b>0.00000330</b>     |
| ENSG00000163288.14 | <i>GABRB1</i>   | 1.85           | 0.10          | 1.38                                        | 0.00000002 | <b>0.00000018</b>     |
| ENSG00000033627.17 | <i>ATP6V0A1</i> | 101.03         | 38.38         | 1.37                                        | 0.00000010 | <b>0.00000052</b>     |
| ENSG00000185386.15 | <i>MAPK11</i>   | 50.15          | 19.17         | 1.34                                        | 0.00008542 | <b>0.00022612</b>     |
| ENSG00000069966.19 | <i>GNB5</i>     | 13.57          | 5.81          | 1.10                                        | 0.00077279 | <b>0.00187976</b>     |
| ENSG00000114573.10 | <i>ATP6V1A</i>  | 51.76          | 24.45         | 1.05                                        | 0.00008025 | <b>0.00021887</b>     |
| ENSG00000047249.18 | <i>ATP6V1H</i>  | 53.06          | 27.10         | 0.94                                        | 0.00000780 | <b>0.00002599</b>     |
| ENSG00000204843.13 | <i>DCTN1</i>    | 122.86         | 66.79         | 0.87                                        | 0.00006645 | <b>0.00019292</b>     |
| ENSG00000185883.12 | <i>ATP6V0C</i>  | 388.13         | 220.40        | 0.81                                        | 0.00016720 | <b>0.00041800</b>     |
| ENSG00000176697.20 | <i>BDNF</i>     | 1.43           | 0.42          | 0.77                                        | 0.01049381 | <b>0.02303519</b>     |

|                    |                 |        |        |      |            |                   |
|--------------------|-----------------|--------|--------|------|------------|-------------------|
| ENSG00000100554.12 | <i>ATP6V1D</i>  | 43.57  | 25.49  | 0.75 | 0.00000156 | <b>0.00000560</b> |
| ENSG00000128524.5  | <i>ATP6V1F</i>  | 230.08 | 141.10 | 0.70 | 0.00000353 | <b>0.00001223</b> |
| ENSG00000105258.9  | <i>POLR2I</i>   | 99.43  | 61.91  | 0.67 | 0.00000020 | <b>0.00000086</b> |
| ENSG00000007174.18 | <i>DNAH9</i>    | 0.96   | 0.25   | 0.65 | 0.00000098 | <b>0.00000369</b> |
| ENSG00000131100.13 | <i>ATP6V1E1</i> | 207.39 | 131.89 | 0.65 | 0.00009672 | <b>0.00024870</b> |
| ENSG00000078369.18 | <i>GNB1</i>     | 248.32 | 164.20 | 0.59 | 0.00144673 | <b>0.00342647</b> |
| ENSG00000006125.18 | <i>AP2B1</i>    | 75.82  | 55.28  | 0.45 | 0.00365359 | <b>0.00843136</b> |
| ENSG00000188130.14 | <i>MAPK12</i>   | 12.61  | 8.97   | 0.45 | 0.01902725 | <b>0.03982448</b> |
| ENSG00000183914.15 | <i>DNAH2</i>    | 0.82   | 0.37   | 0.41 | 0.00001791 | <b>0.00005558</b> |
| ENSG00000179520.11 | <i>SLC17A8</i>  | 0.46   | 0.16   | 0.33 | 0.00001477 | <b>0.00004746</b> |
| ENSG00000100246.13 | <i>DNAL4</i>    | 17.87  | 15.88  | 0.16 | 0.01902725 | <b>0.03982448</b> |

Bold values represent significant differences in the proportion of brain/CNS tissues (N=13) overexpressing the gene compared to non-brain tissues (N=55).

AD, Alzheimer's disease; DLB, dementia with Lewy bodies; ER, enrichment ratio; FDR, false discovery rate; PD, Parkinson's disease; TPM, transcripts per million.

**Supplementary Table 13.** Over-representation results of biological processes enriched in the genes preferentially expressed in brain tissues based on GTEx

| GO identifier | GO term                                     | Gene set size | Expected value | Overlap | ER   | P <sub>FDR</sub> -value |
|---------------|---------------------------------------------|---------------|----------------|---------|------|-------------------------|
| GO:0099177    | regulation of trans-synaptic signaling      | 11            | 5.37           | 11      | 2.05 | <b>0.0089</b>           |
| GO:0042391    | regulation of membrane potential            | 13            | 6.35           | 11      | 1.73 | 0.13                    |
| GO:0035249    | synaptic transmission, glutamatergic        | 6             | 2.93           | 6       | 2.05 | 0.14                    |
| GO:0050808    | synapse organization                        | 6             | 2.93           | 6       | 2.05 | 0.14                    |
| GO:0006836    | neurotransmitter transport                  | 5             | 2.44           | 5       | 2.05 | 0.14                    |
| GO:0007215    | glutamate receptor signaling pathway        | 5             | 2.44           | 5       | 2.05 | 0.14                    |
| GO:0050803    | regulation of synapse structure or activity | 5             | 2.44           | 5       | 2.05 | 0.14                    |
| GO:0098739    | import across plasma membrane               | 5             | 2.44           | 5       | 2.05 | 0.14                    |
| GO:0006820    | monoatomic anion transport                  | 8             | 3.91           | 7       | 1.79 | 0.14                    |
| GO:0007033    | vacuole organization                        | 7             | 3.42           | 6       | 1.76 | 0.22                    |

Bold values represent significantly enriched biological process terms. Only the top 10 genes are shown.

DLB, dementia with Lewy bodies; ER, enrichment ratio; FDR, false discovery rate; GO, Gene Ontology; GTEx, Genotype-Tissue Expression.

**Supplementary Table 14.** Results of spatial mapping between neurochemical maps and cortical thickness in DLB

| Transmitter          | Spearman correlation coefficient | P-value  | P <sub>FDR</sub> -corrected value | P-value test against random null model | P-value test against spatial null model |
|----------------------|----------------------------------|----------|-----------------------------------|----------------------------------------|-----------------------------------------|
| 5-HT <sub>1A</sub>   | -0.35                            | 0.0034   | <b>0.014</b>                      | <b>0.0001</b>                          | <b>0.0169</b>                           |
| 5-HT <sub>1B</sub>   | 0.43                             | 0.00026  | <b>0.002</b>                      | <b>0.0003</b>                          | <b>0.0041</b>                           |
| 5-HT <sub>2A</sub>   | -0.01                            | 0.91     | 0.96                              | -                                      | -                                       |
| 5-HT <sub>4</sub>    | -0.48                            | 0.00004  | <b>0.0004</b>                     | <b>0.0001</b>                          | <b>0.0002</b>                           |
| 5-HT <sub>6</sub>    | 0.01                             | 0.89     | 0.96                              | -                                      | -                                       |
| 5-HTT                | 0.20                             | 0.095    | 0.24                              | -                                      | -                                       |
| $\alpha$ 4 $\beta$ 2 | 0.21                             | 0.081    | 0.23                              | -                                      | -                                       |
| CB <sub>1</sub>      | -0.17                            | 0.161    | 0.36                              | -                                      | -                                       |
| D <sub>1</sub>       | 0.15                             | 0.22     | 0.44                              | -                                      | -                                       |
| D <sub>2</sub>       | -0.52                            | 0.000007 | <b>&lt;0.0001</b>                 | <b>0.0001</b>                          | <b>0.0003</b>                           |
| DAT                  | 0.09                             | 0.456    | 0.70                              | -                                      | -                                       |
| GABA <sub>A</sub>    | 0.36                             | 0.0025   | <b>0.013</b>                      | <b>0.0014</b>                          | <b>0.012</b>                            |
| H <sub>3</sub>       | 0.23                             | 0.054    | 0.18                              | -                                      | -                                       |
| M <sub>1</sub>       | -0.12                            | 0.34     | 0.62                              | -                                      | -                                       |
| mGluR5               | -0.01                            | 0.97     | 0.97                              | -                                      | -                                       |
| $\mu$                | 0.02                             | 0.86     | 0.96                              | -                                      | -                                       |
| NET                  | 0.08                             | 0.50     | 0.72                              | -                                      | -                                       |
| NMDA                 | 0.04                             | 0.73     | 0.96                              | -                                      | -                                       |
| VACHT                | 0.109                            | 0.37     | 0.62                              | -                                      | -                                       |
| SV2A                 | -0.01                            | 0.91     | 0.96                              | -                                      | -                                       |

Empirical Spearman correlation coefficients for the associations between receptors, transporters, and receptor binding sites of different neurotransmitter systems and cortical thickness W-scores in DLB. P-values were corrected for FDR correction. Significant correlations were further tested against distributions of correlations from sets of random and spatial null models.

DLB, dementia with Lewy bodies; FDR, false discovery rate.

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