

Supplementary Table 2. Demographic, clinical, and gene methylation levels of participants, compared to controls

| Variable | Parkinson's disease (<i>n</i> = 20) | | Control (<i>n</i> = 20) | | Test St. | <i>p</i> value |
|-------------|--------------------------------------|------------------|--------------------------|-------------------|----------|----------------|
| | Mean (SD) | Median (min-max) | Mean (SD) | Median (min-max) | | |
| Age | 62.05 (7.03) | 63 (50–75) | 58.75 (4.54) | 58 (52–68) | 138.5 | 0.096 |
| Sex F/M | 9/11 | N/A | 9/11 | N/A | N/A | 0.824 |
| UPDRS | 32.40 (14.47) | 30.50 (14–70) | N/A | N/A | N/A | N/A |
| <i>NBR1</i> | 0.22 (0.24) | 0.12 (0.01–0.65) | 3.6 (5.29) | 0.82 (0.05–16.42) | 339.0 | <0.001 |
| <i>GBA</i> | 0.66 (1.04) | 0.45 (0–4.54) | 2.34 (3.45) | 0.84 (0.08–12.93) | 291.0 | 0.013 |

Values are presented as mean \pm SD or median (min-max) unless otherwise indicated.

UPDRS, Unified Parkinson's Disease Rating Scale; *NBR1*, *BRCA1* neighbor for autophagy 1; *GBA*, glucocerebrosidase; SD, standard deviation; N/A, not applicable.