

Supplemental Information

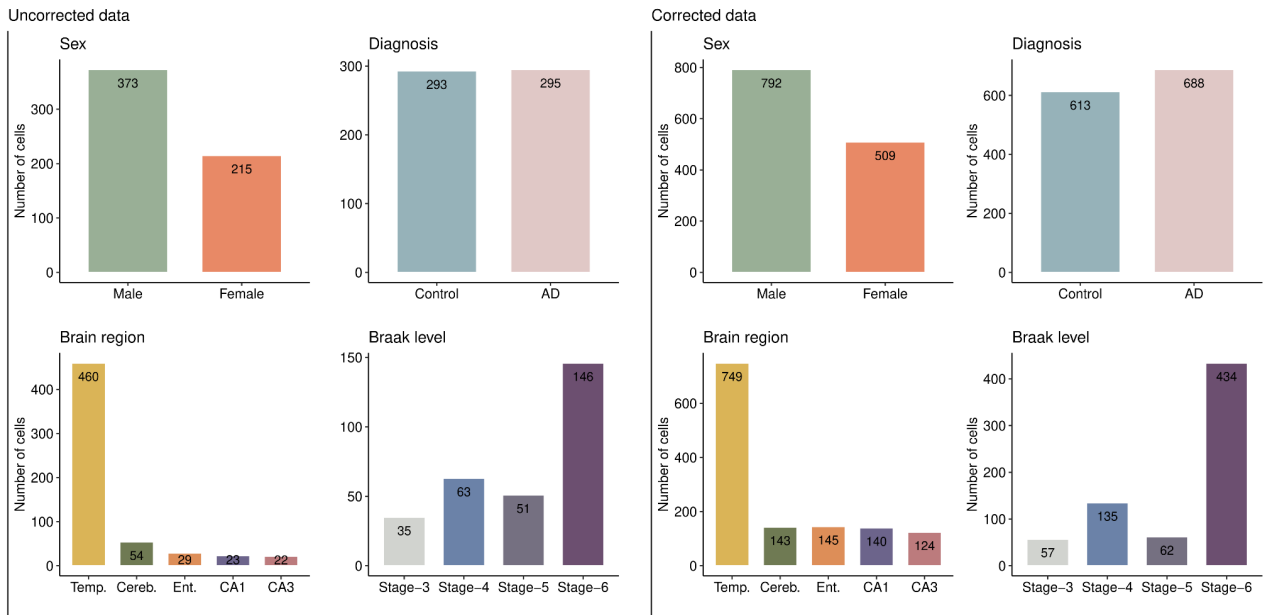


Figure S1. Information about the samples of uncorrected and PCA-corrected data. Distribution of samples according to sex (female, male) (A), diagnoses (Alzheimer's Disease, control) (B), brain regions (temporal cortex, cerebellum, entorhinal cortex, hippocampal subfields CA1, hippocampal subfields CA3) (C) and Braak level (stage 3, 4, 5 and 6) (D).

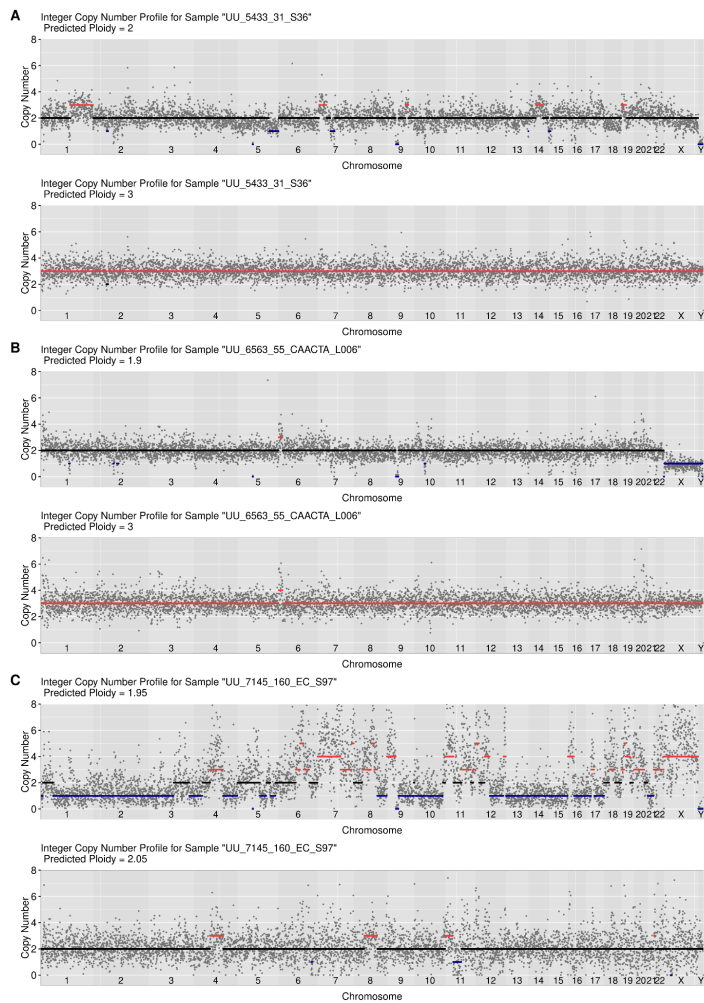


Figure S2. CN profiles of three cells deviating from the range of 1.9 and 2 after correction. The upper panels show the uncorrected data, and the lower panels show the corrected data. X-axes show chromosomes and Y-axes illustrate the CN profile of chromosomes estimated by *Ginkgo*. Each grey dot represents the scaled read counts per bin. Amplifications (CN>2) are shown in red; deletions (CN<2) in blue; disomy (CN=2) in black.

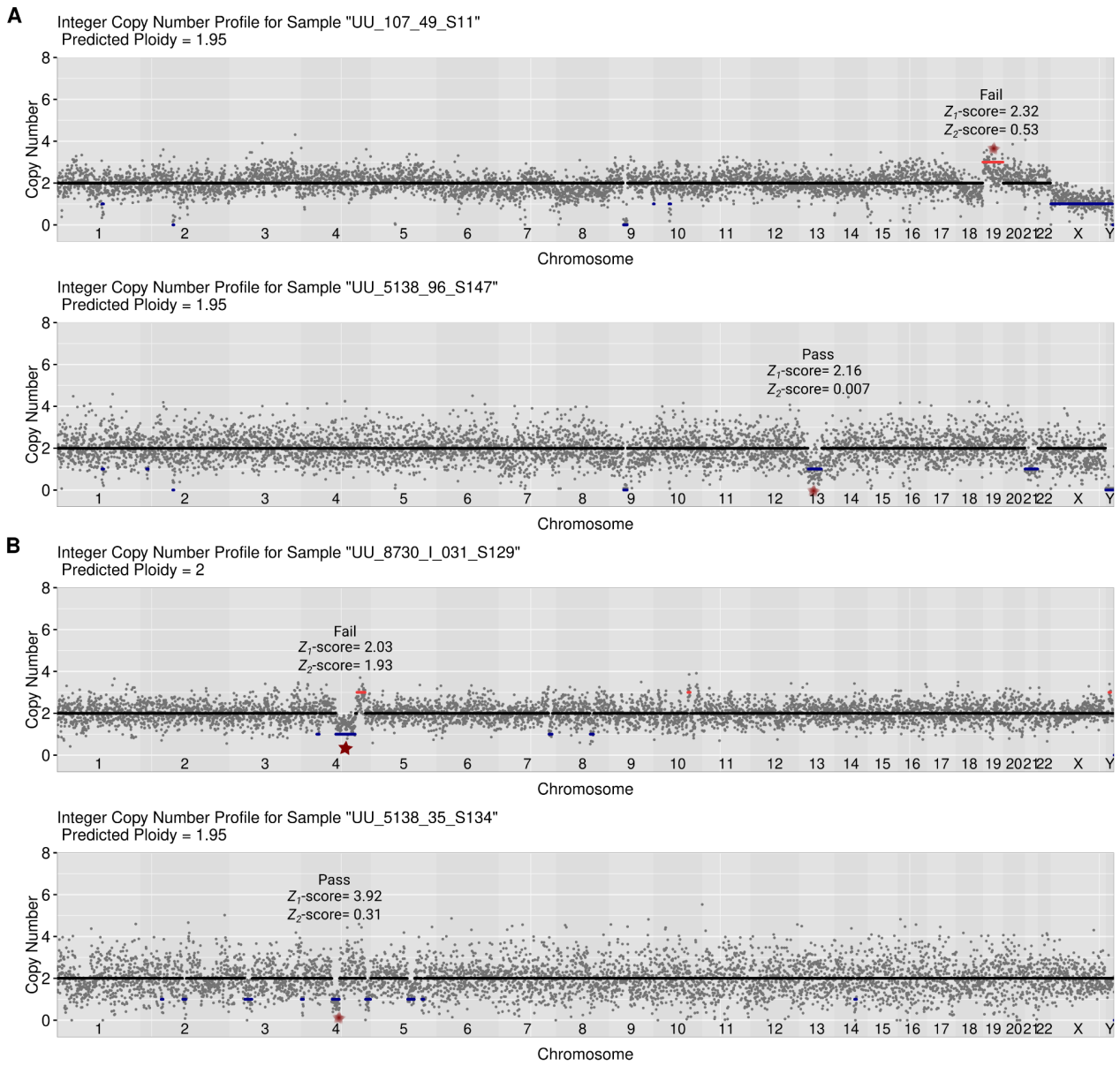


Figure S3. Examples of CNVs that (upper panels) failed to pass and (lower panels) passed the filtering criteria (Z_1 -scores ≥ 2 and Z_2 -scores ≤ 0.5) in the uncorrected-filtered data (A) and PCA-corrected data (B). Absolute values of the Z_1 - and Z_2 scores for the CNV are indicated on the plot. The CNVs in question (that failed or passed the filtering) are marked with red stars. X-axes show chromosomes and Y-axes illustrate the CN profile of chromosomes estimated by *Ginkgo*. Each grey dot represents the scaled read counts per bin. Amplifications (CN>2) are shown in red; deletions (CN<2) in blue; disomy (CN=2) in black.