Heatmap:

The visual representations presented seem to be associated with heatmaps and tables that aggregate the values of gene expression datasets. The images appear to be related to this information.

The first image is a **heatmap**, which is a data visualization technique used to represent the levels of gene expression across various conditions or samples. Here's a breakdown of what you're seeing:

Vertical Axis (Rows): Each row represents a different gene. Probe set IDs are unique numbers for certain sequences of DNA or RNA that are used to measure how much a gene is expressed. We use these IDs to talk about genes (for example, "200706_s_at").

Horizontal Axis (Columns): These likely represent different experimental samples or conditions, with the percentages possibly indicating different time points, treatment concentrations, or patient groups.

Color Scale: The colors in the heatmap correspond to the expression level of each gene in each sample or condition. Typically, colors towards one end of the spectrum (like red) indicate higher expression, and colors towards the other end (like blue) indicate lower expression. In this heatmap, it seems that a range of colors from blue, yellow, to red are used, which could represent a gradient from low to high expression levels.

The second image is a list of values, specifically the **sum of GSM values**. "GSM" stands for "Geo Sample," which is a term from the GEO (Gene Expression Omnibus) database that refers to individual samples for which gene expression is measured.

Values: Each value in the list represents the sum of the expression levels of all genes within a particular sample (GSM ID). This might be used to get an overall sense of the gene activity within each sample or to normalize the data.

Researchers can figure out which genes are differentially expressed under different conditions by using these kinds of visualizations and summaries along with statistical tests. This may help us understand diseases like Parkinson's, as the title of the paper suggests. The
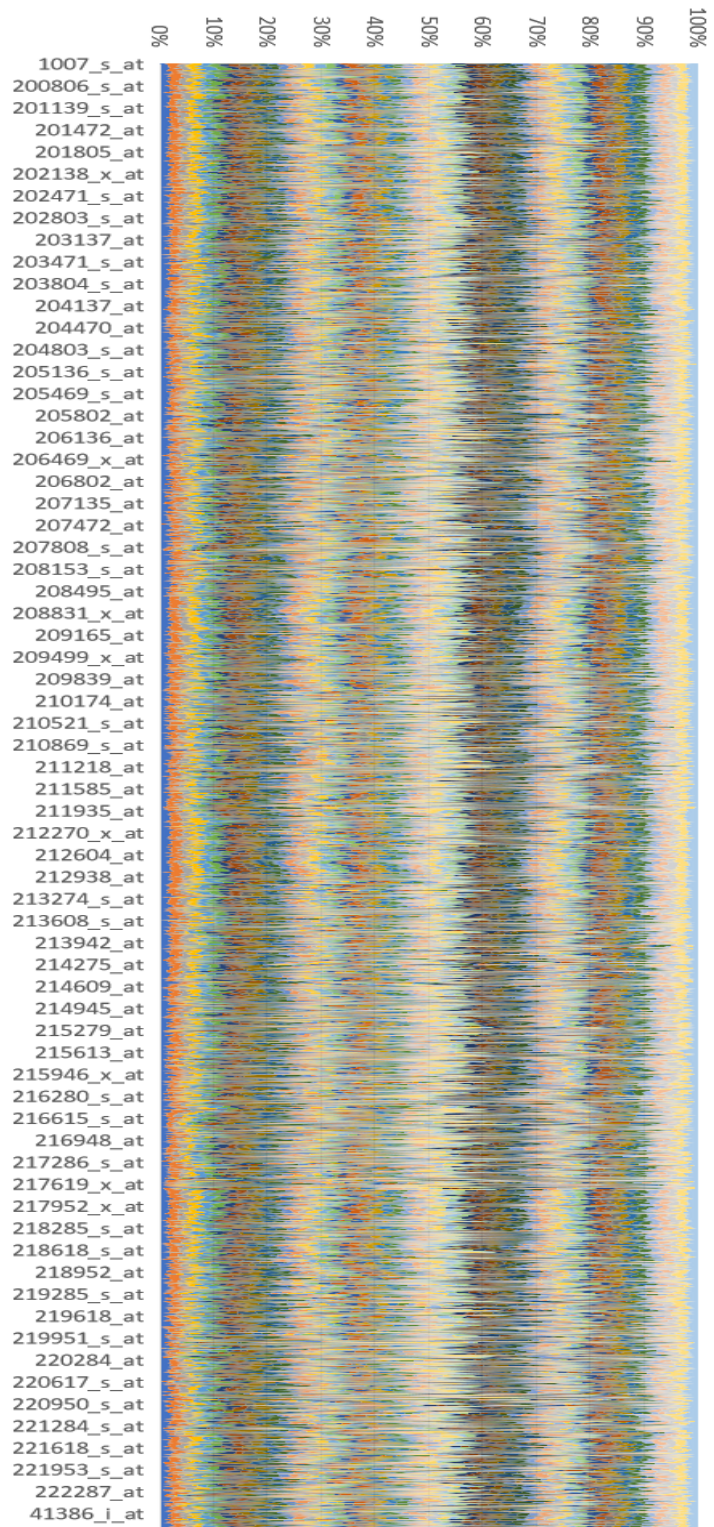

Fig. Heatmap

heatmap provides a quick visual comparison across all genes and samples, while the summed values might be a step in preprocessing the data for further analysis.

Values

■ Sum of GSM153449	■ Sum of GSM153453	■ Sum of GSM153454	■ Sum of GSM153455
■ Sum of GSM153462	■ Sum of GSM153465	■ Sum of GSM153481	■ Sum of GSM153482
■ Sum of GSM153483	■ Sum of GSM153485	■ Sum of GSM153489	■ Sum of GSM153457
■ Sum of GSM153450	■ Sum of GSM153456	■ Sum of GSM153447	■ Sum of GSM153490
■ Sum of GSM153491	■ Sum of GSM153492	■ Sum of GSM153493	■ Sum of GSM153494
■ Sum of GSM153440	■ Sum of GSM153438	■ Sum of GSM153431	■ Sum of GSM153426
■ Sum of GSM153409	■ Sum of GSM153508	■ Sum of GSM153503	■ Sum of GSM153500
■ Sum of GSM153497	■ Sum of GSM153496	■ Sum of GSM153488	■ Sum of GSM153484
■ Sum of GSM153479	■ Sum of GSM153477	■ Sum of GSM153452	■ Sum of GSM153451
■ Sum of GSM153444	■ Sum of GSM153448	■ Sum of GSM153433	■ Sum of GSM153495
■ Sum of GSM153498	■ Sum of GSM153501	■ Sum of GSM153502	■ Sum of GSM153505
■ Sum of GSM153506	■ Sum of GSM153429	■ Sum of GSM153428	■ Sum of GSM153427
■ Sum of GSM153425	■ Sum of GSM153423	■ Sum of GSM153419	■ Sum of GSM153406
■ Sum of GSM153405			

Fig. GSM Values selected for the heatmap