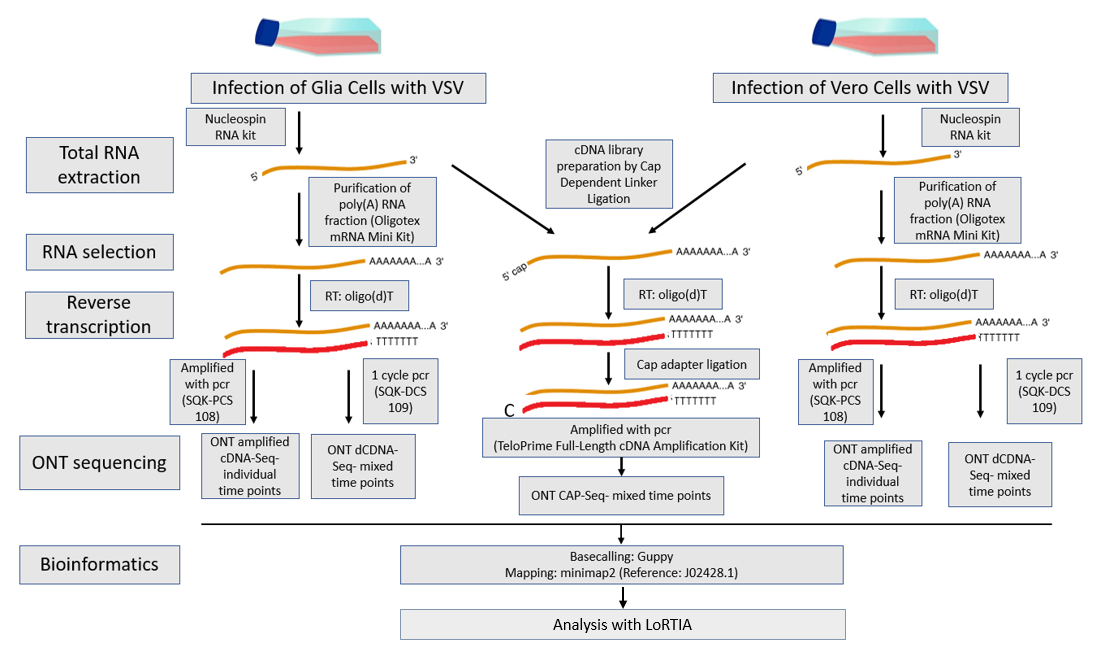
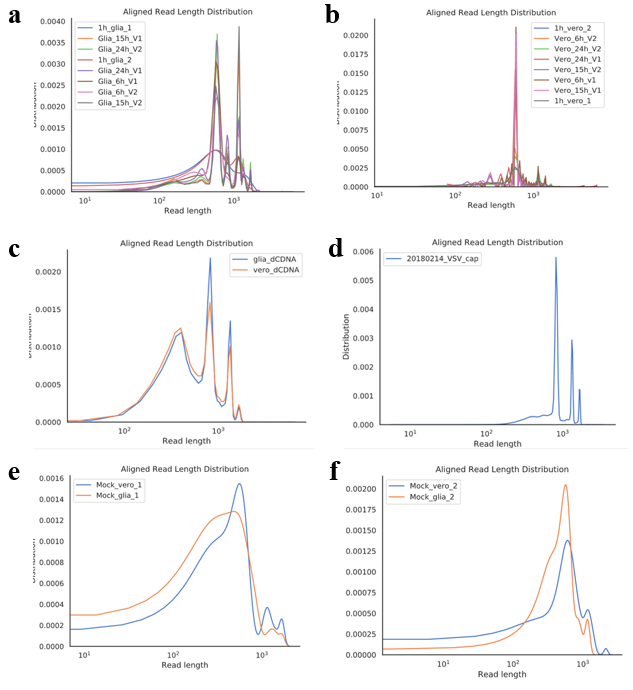
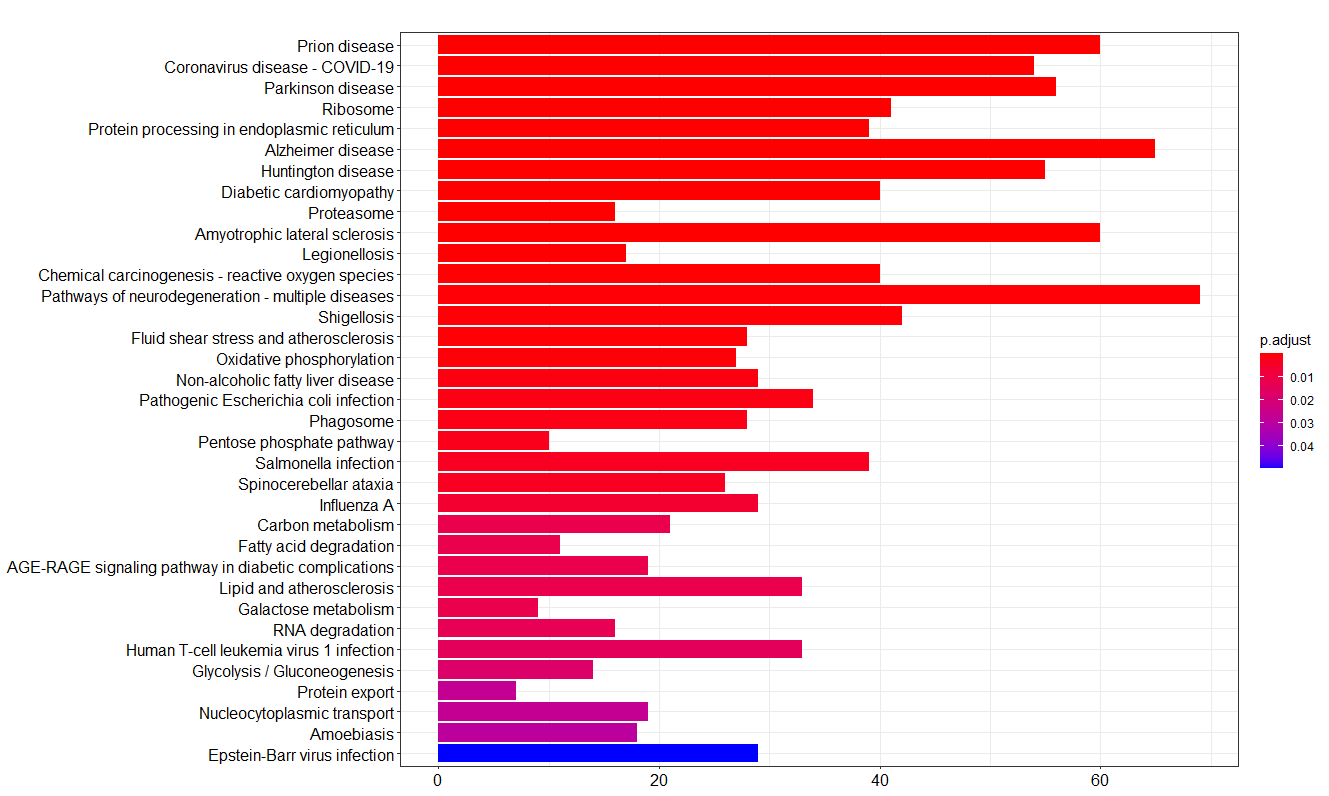
****

**Additional File 1, Figure S1 The flowchart diagram shows the MinION (ONT) sequencing methodologies and the bioinformatic analysis that we use.**

*Sequencing libraries were generated by three different methods (amplified cDNA (for individual time points), dcDNA (for mixed time points), and dcDNA by Cap-selection (for mixed time points)). The basecalling was done with the Guppy program. The resulting reads were mapped with minimap2. Further analyzes were performed using the Lortia program.*

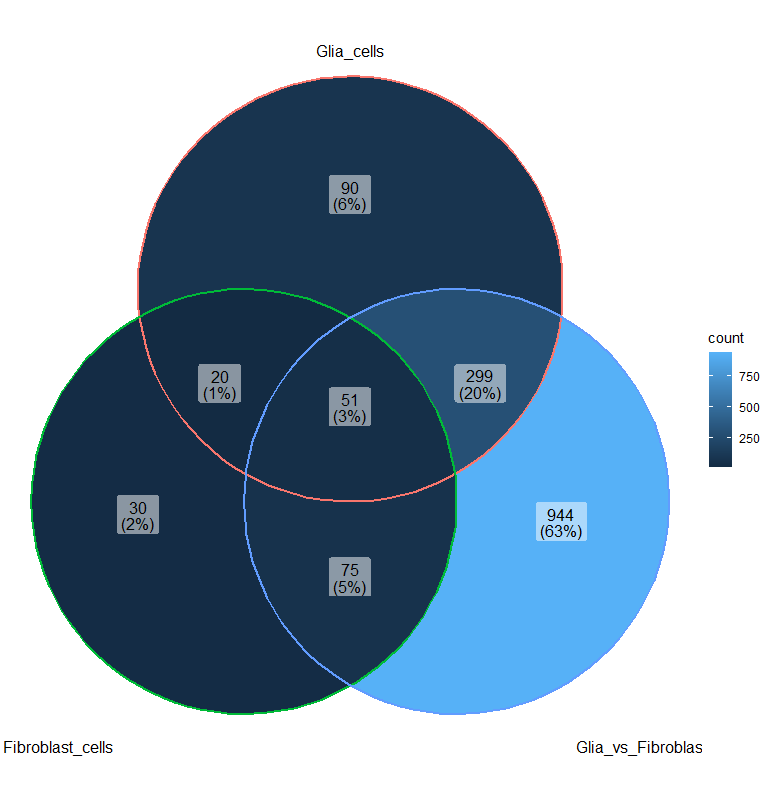


**Additional File 1, Figure S2.** **Aligned read length density distribution in the two cell lines, obtained by ONT MinION sequencing.** Amplified cDNA sequencing from glial (a) and fibroblast (b) cell types at different time points. Direct cDNA sequencing from glial and fibroblast cell types (c). cDNA sequencing of a mixture of samples obtained by Cap selection (d). cDNA sequencing of a mix of Mock 1 and 2 (e, f).



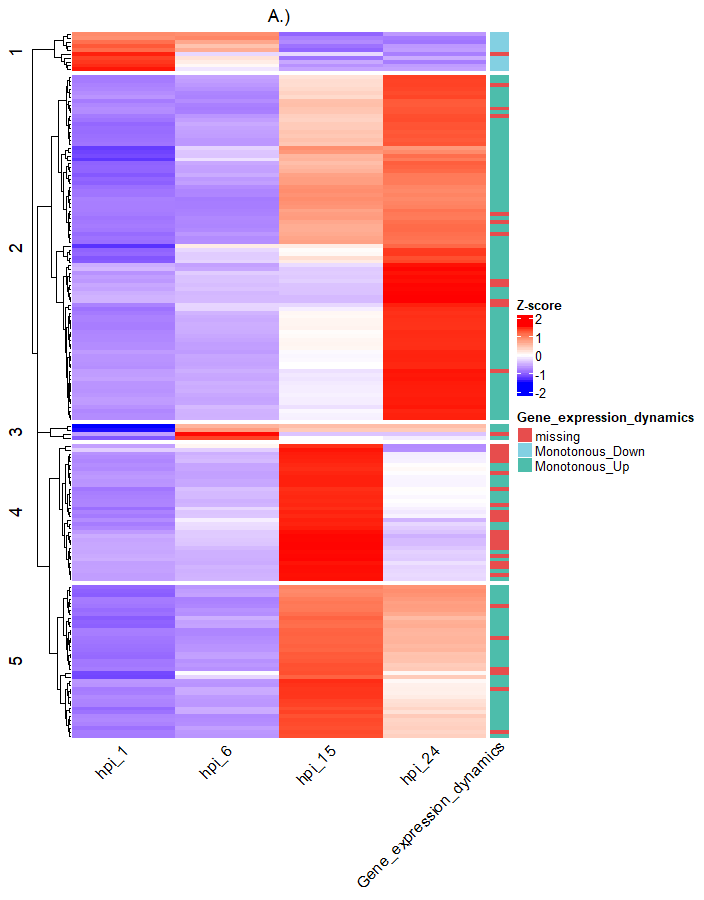
**Additional File 1, Figure S3.**

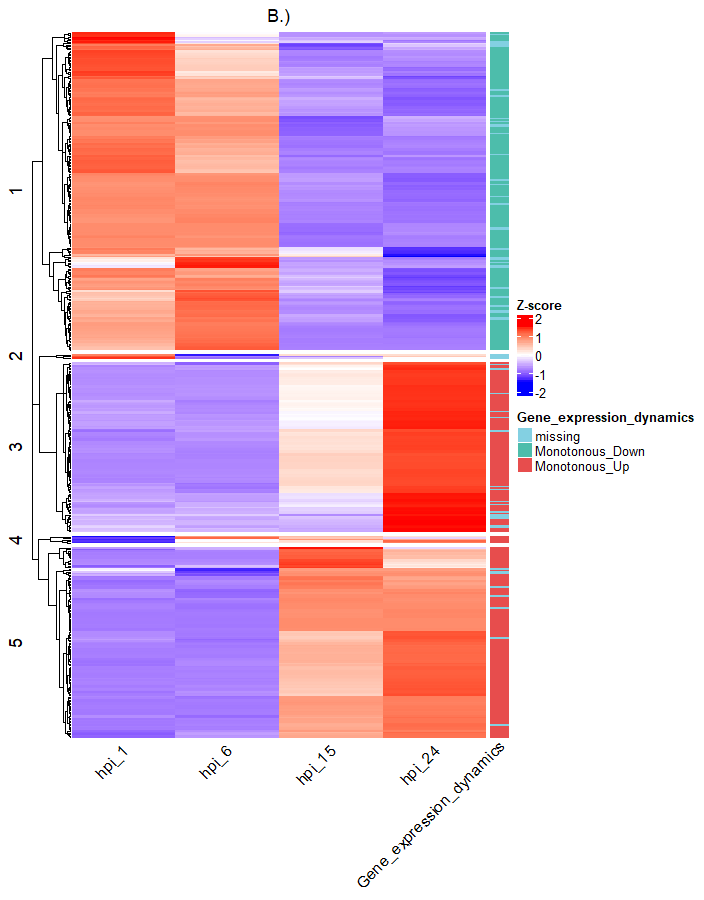
Differentially expressed KEGG pathways between the two cell lines. X-axis showa the number of differentially expressed genes (DEGs) in each pathway, while the colors of the bars correspond to the adjusted *p*-values of the test results.



**Additional File 1, Figure S4.**

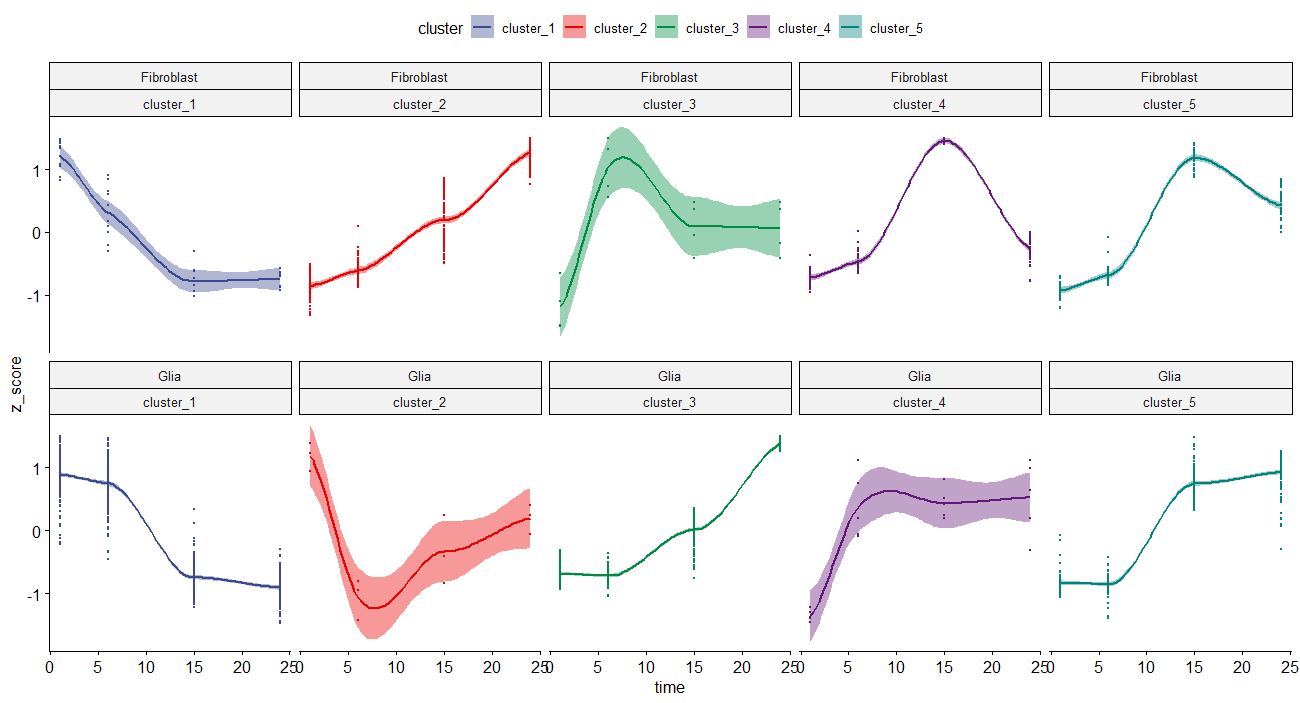
The number of differentially expressed genes (DEGs) in each comparison.

****



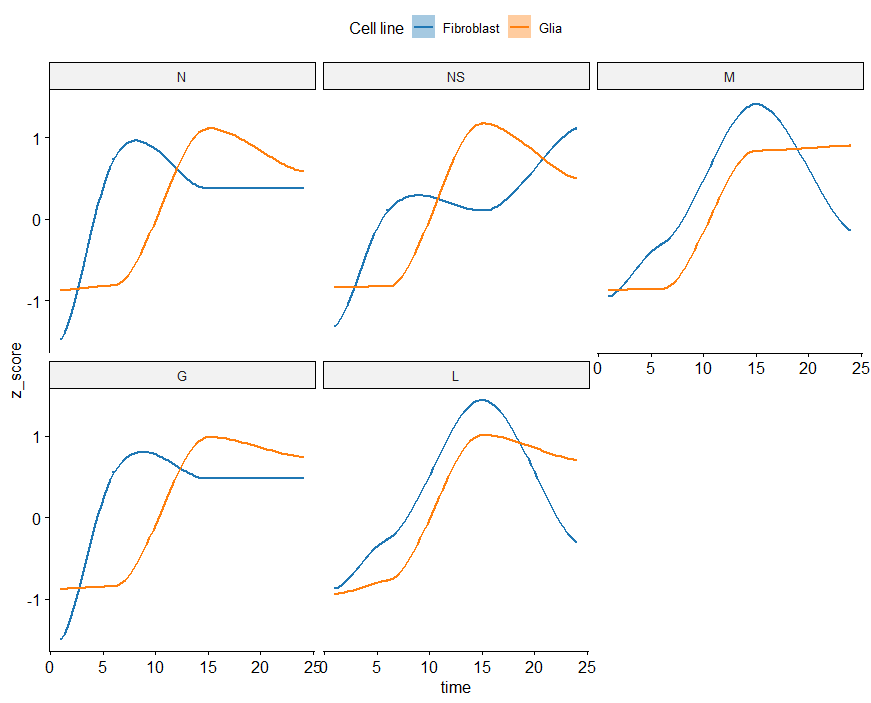
**Additional File 1,** **Figure S5/A-B.**

Heatmap of the z-score normalized gene expression kinetics in the two cell lines: **A:** Fibroblast; **B:** Glia. The annotation column on the right (gene expression dynamics) shows whether ImpulseDE2 characterized the given genes expression as either monotonously decreasing or increasing.



**Additional File 1, Figure S6.**

Z-score normalized host gene-expression values in each gene cluster in the two cell lines. The genes were clustered with k-means clustering. Shaded areas represent 95% confidence intervals.



**Additional File 1, Figure S7.**

Z-score normalized viral gene-expression values in the two cell lines.