

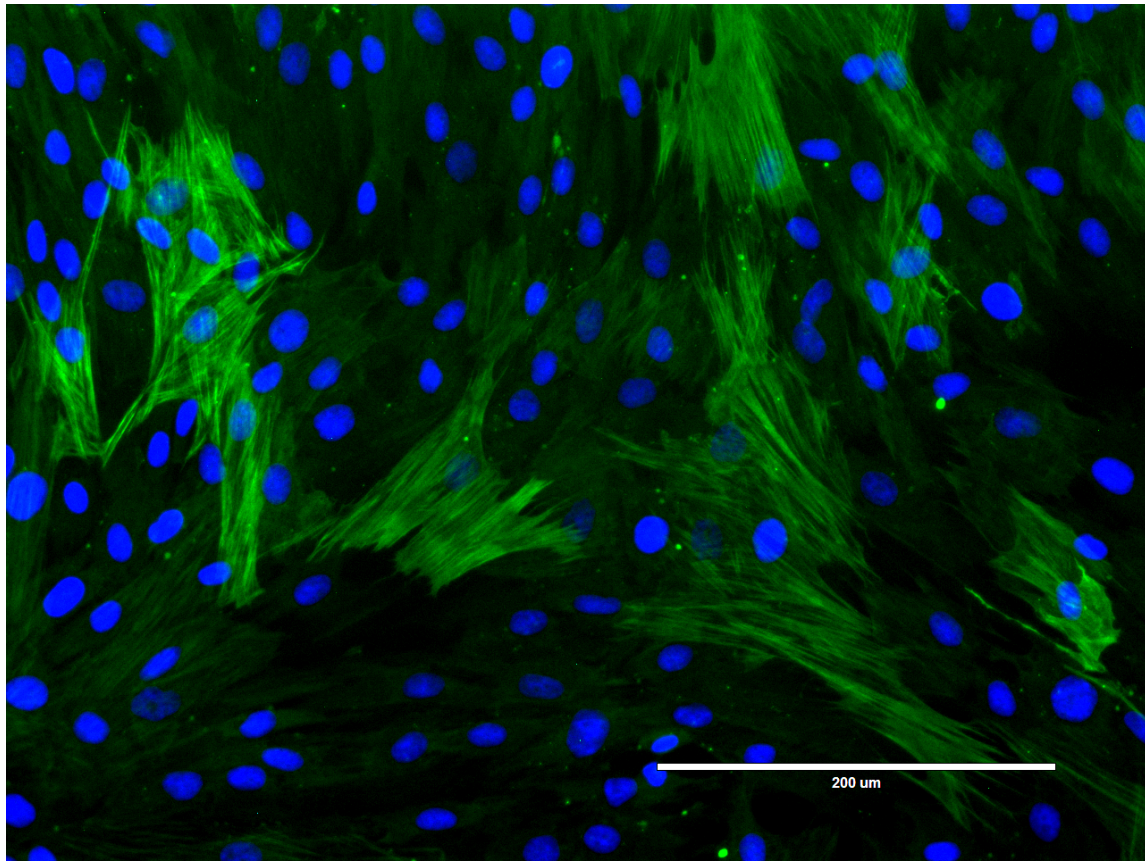
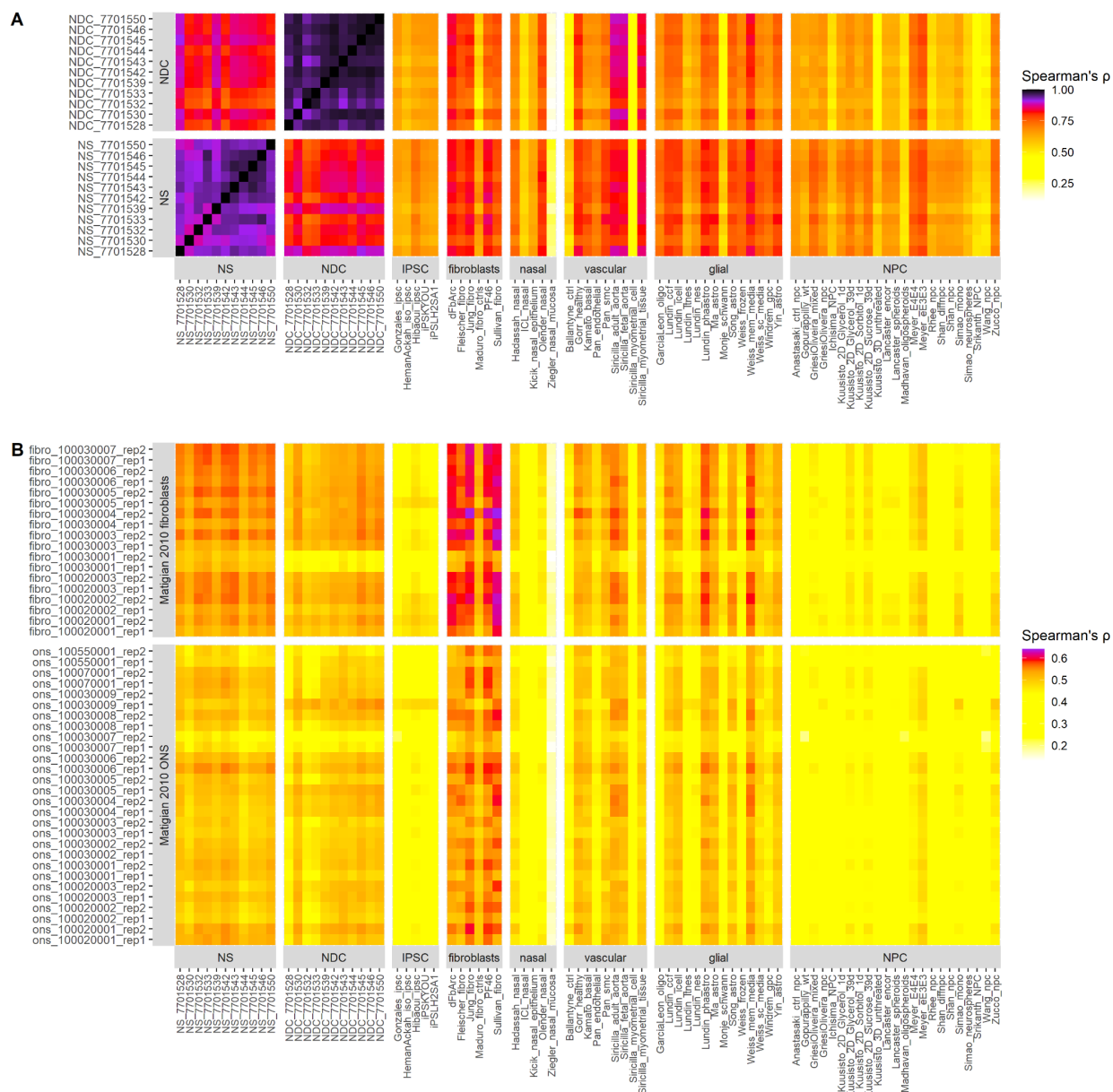


Figure S1. Heterogeneity of SMA in NDC. NDC were stained with SMA (green) and DAPI (blue).



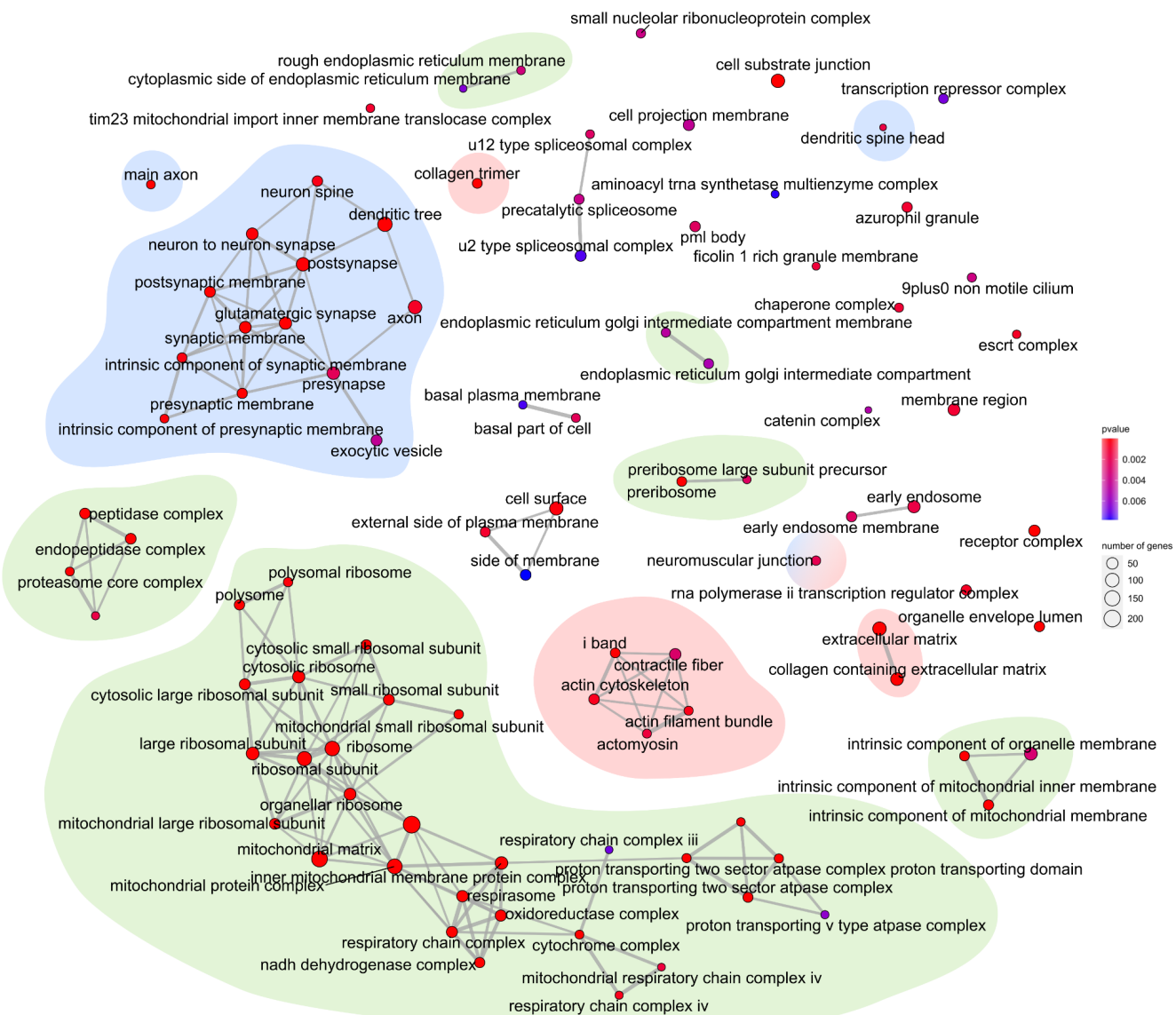


Figure S3. Map of mutually overlapping gene sets, enriched in GSEA analysis of gene ontologies of cellular components (GO:CC). The colored areas represent groups of enriched ontologies: structures involved in cell metabolism, like mitochondria and proteasome (green), neuronal structures (blue) and cytoskeleton and extracellular matrix (red). The colour corresponds to the p-value; the size of the node is proportional to the size of the gene set. Not every node is signed due to lack of drawing space, the complete list of enriched ontologies could be found in Supplementary Table S3.

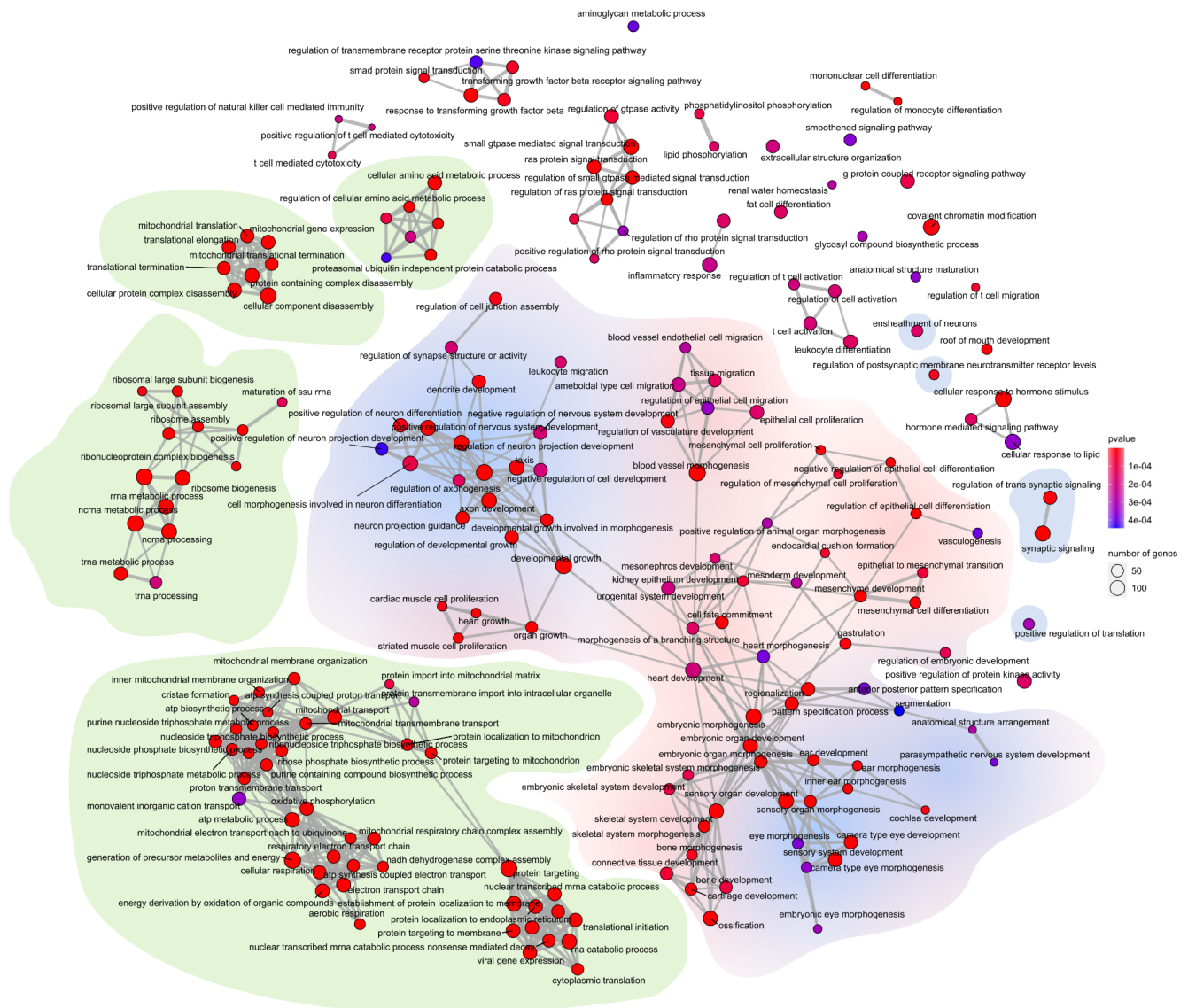


Figure S4. Graph of mutually overlapping gene sets, enriched in GSEA analysis of gene ontologies of biological processes (GO:BP). The colored areas represent three major groups of enriched ontologies: metabolic (green), neuronal and sensory (blue) and non-neuronal, mainly vascular and stromal cell development (red). The most expansive set of ontologies is dyed with blue and red gradients since it could be assigned to both neuronal and non-neuronal areas. The colour of nodes corresponds to the p-value; the size of the node is proportional to the size of the gene set. Not every node is signed due to lack of drawing space, the complete list of enriched ontologies could be found in Supplementary Table S4.

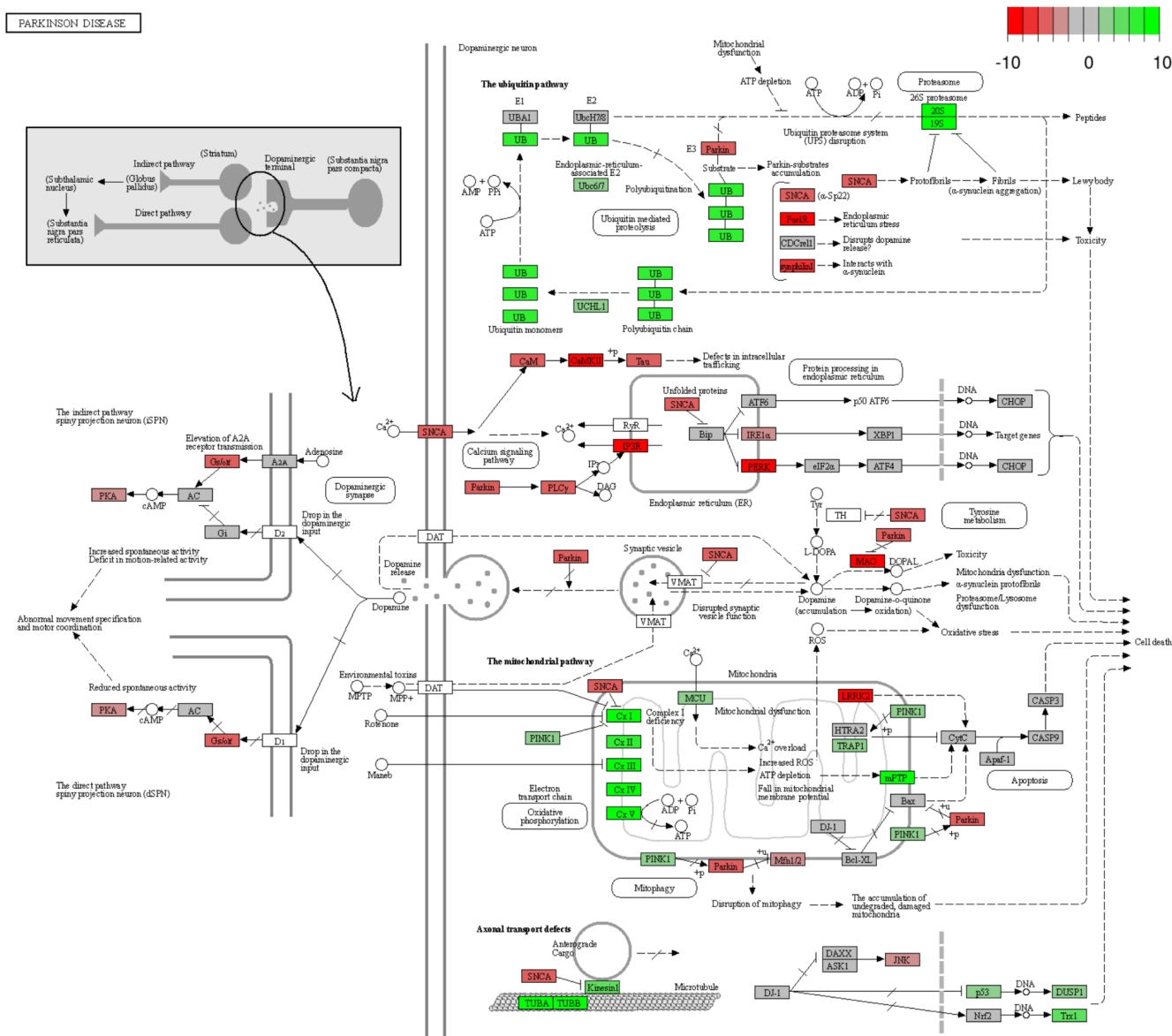


Figure S5. Pathview visualisation of fold change (NDC vs NS) of genes involved in Parkinson's disease. The shades of coloured boxes represent fold change of underlying genes in NDC compared to NS. Green corresponds to upregulated genes, red to downregulated ones.