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Temporal Changes of Recovery-related Transcriptome in Stroke

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Objective
The endogenous remodeling post stroke, such as angiogenesis, neurogenesis and axonal sprouting is restrictive to induce complete restoration of neurological function. To identify the therapeutic targets to evoke endogenous restorative mechanism for stroke recovery, we investigated temporal alteration of endogenous recovery-related genes at different time points post stroke.

Methods
Photothrombotic stroke was induced in wistar rats. Peri-infarct tissues were collected at different time points (1w, 4w and 8w) and RNA sequencing was conducted. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis and Gene Ontology (GO) analysis were conducted to analyze the profiles of the genes involved in axonal sprouting, growth factor and angiogenesis categories (FDR<0.05 and |fc|>2)

Results
KEGG pathway analysis revealed that inflammatory response was dominant at 1 week and downregulated afterwards. ECM-receptor interaction was facilitated to support recovery until late stages. GO analysis discovered that endogenous recovery process was active until 4 weeks and the change was not completed even at 8 weeks, Nefh, Syt2 and Robo3 were downregulated and conversely, C3, Gfap, Igf2, Aqp1, Spp1, Anaxa1, Cd44, Bmp6, Dcn, Crabp2, Dab2, Vim, Lgals1, Lgals3, Aprnr, Col1a1, Col3a1, Foxd1, Foxc2, Efemp1, sfrp1, Aldh1a2, Cdkn1c were upregulated.

Conclusion
These gene profile alterations may identify new therapeutic target to prompt recovery post stroke at various time points.

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