

We observed the natural recovery of stroke mice and identified two distinct recovery groups using an unbiased hierarchical cluster analysis of the rotating beam behavior data. A novel lesion mapping analysis indicated that both the spontaneously recovered and the non-recovered group exhibited comparable lesion profile. group RNA-sequencing transcriptome analysis of the ipsi- and contralesional primary motor cortices revealed a panel of recovery-related genes in the spontaneously-recovered mice and highlighted the involvement of contralesional motor cortex in spontaneous recovery, particularly Adora2a, Drd2 and Pde10a-mediated cAMP signaling pathway. Modulating these potential targets after stroke may be beneficial for stroke recovery outcome.