Supplementary material

Human Umbilical MSC-Derived Exosomes Improve Intracerebral Hemorrhage Recovery via SIRT1-Driven Suppression of NF-κB/NOS2 Signaling: Coordinating Microglial Homeostasis and Neuroprotection

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Fig.S1 Nanoparticle Tracking Analysis (NTA) of hUMSC-Exos showing size distribution, concentration, and median diameter.

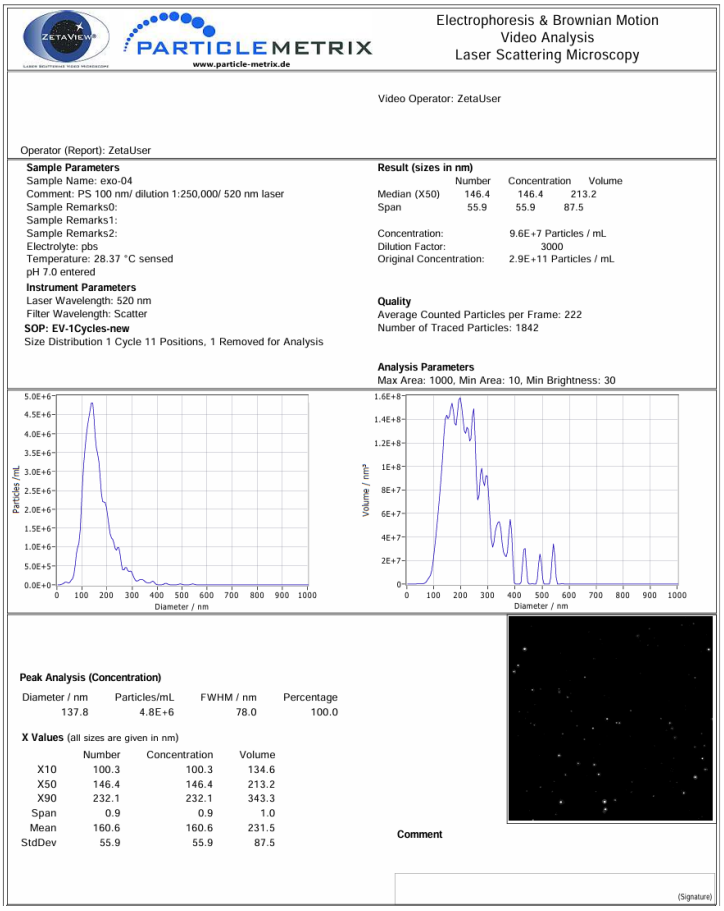

Fig.S2 hUMSC-Exos enhance microglial phagocytosis of myelin debris during the chronic phase after ICH. Representative immunofluorescence images show co-localization of Iba1 and dMBP (a marker for degenerated myelin debris) in brain tissues from Sham, ICH, and ICH+exosomes (ICH+EXO) groups at 35 days post-ICH (chronic phase). The right panel presents quantitative analysis of the percentage of Iba1^{+}dMBP^{+} double-positive area relative to the total dMBP^{+} area. Data are shown as mean ± SD (one-way ANOVA with Bonferroni's post hoc test; ***$p < 0.001$).

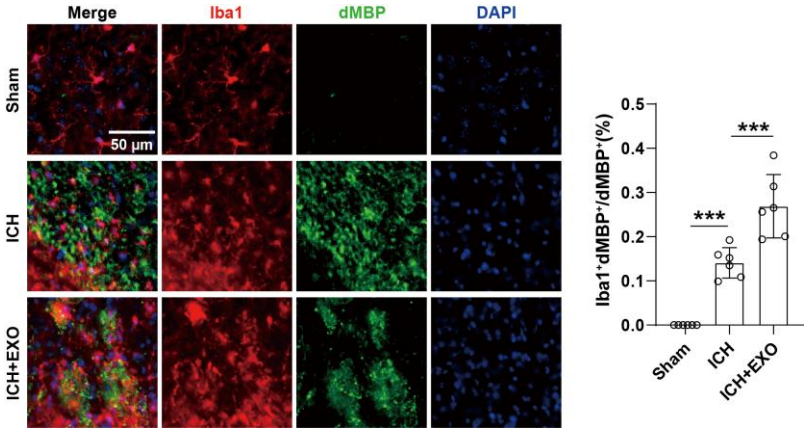

Fig.S3 RT-qPCR analysis of marker gene expression for distinct neural cell populations. Markers represent: oligodendrocytes (Mbp), neurons (Grin2b, Rbfox3, Map2), astrocytes (S100β, Gfap, Slc1a3), and microglia (Aif1, Itgam, Cx3cr1, Hexb, P2ry12). The Log10 (Fold change) shows differential expression patterns of these markers, reflecting cellular composition differences, with positive values indicating up-regulation and negative values down-regulation relative to a reference (implied by the 0 baseline).

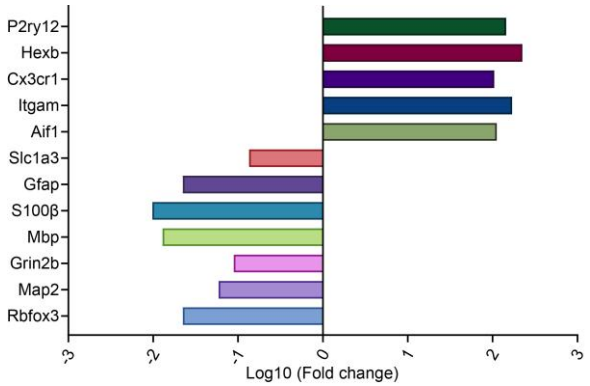

Fig.S4 RNA-seq saturation analysis of different experimental groups. Plots show the relationship between the number of sequenced reads (x - axis, in millions) and the number of detected genes (y - axis, as a percentage) for Sham (Sham_1, Sham_2, Sham_3), ICH (ICH_1, ICH_2, ICH_3), and ICH + Exo (ICH + Exo_1, ICH + Exo_2, ICH + Exo_3) groups. These saturation curves help evaluate the adequacy of sequencing depth for gene detection across samples, ensuring that the sequencing effort is sufficient to capture the transcriptomic complexity in each experimental condition.

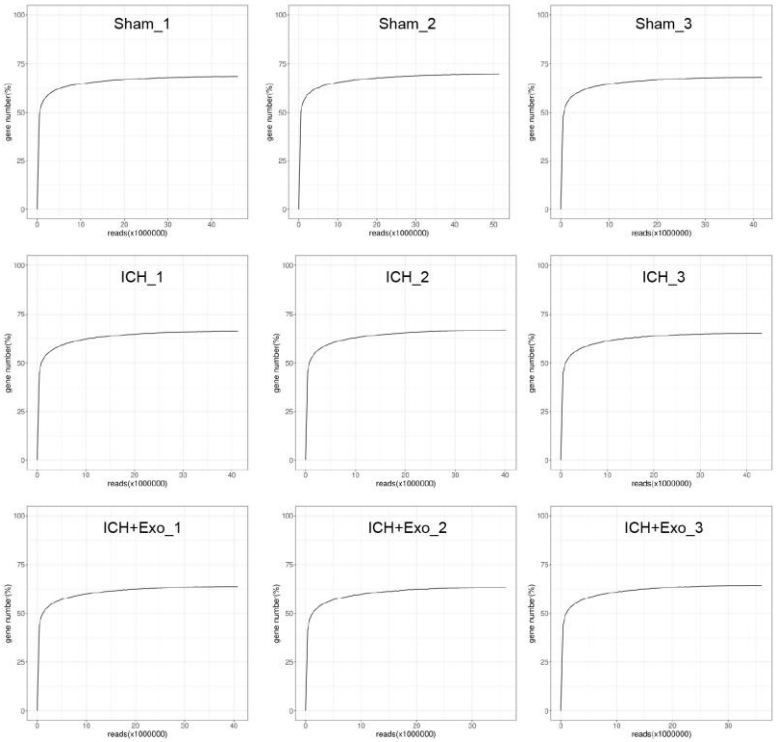

Fig.S5 Transcriptomic profiling of Sham, ICH, and ICH+Exo groups. (A) Violin plot illustrating the distribution of gene expression levels (Log10(TPM)) across samples. Each violin represents a sample. The plot shows the density and spread of transcript abundance, reflecting overall gene expression patterns within and between groups. (B) Venn diagram depicting the overlap of expressed genes among Sham, ICH, and ICH+Exo groups. Numbers in each segment indicate the count of unique and shared genes, highlighting commonalities and differences in the transcriptomes across experimental conditions. TPM, transcripts per million.