

Figure S1. (a) Percentage of area represented by blood vessels in hematoxylin-eosin paraffin-stained sections (representative images shown in **b** and **c**) from sham-injected hyh mice (*sham*, n = 13) and BM-MSC-transplanted (*BM-MSC*, n = 17) hydrocephalic hyh mice at P18.

Figure S2. Differential protein expression analysis in sham-injected hydrocephalic hyh mice (*sham*, n = 5) and BM-MSCs-transplanted (*BM-MSC*, n = 5) hydrocephalic hyh mice at P8. (a) Heatmaps and clusters of the two groups of mice. (b) Principal component analysis of hyh mice treated with BM-MSCs and hyh mice. (c) Volcano representation for overexpressed and underexpressed proteins in BM-MSC-treated mice compared with sham-injected hyh mice.

Figure S3. Overexpressed proteins analyzed and represented with STRING comparing BM-MSC-transplanted (*BM-MSC*, n = 5) hydrocephalic hyh mice with sham-injected hydrocephalic hyh mice (*sham*, n = 5) at P8. The results of Reactome pathways (MMU) are shown. *Strength* represents \log_{10} (observed/expected). This measure describes how large the enrichment effect is. It is the ratio between i) the number of proteins in your network that are annotated with a term and ii) the number of proteins that we expect to be annotated with this term in a random network of the same size. *False discovery rate* describes how significant the enrichment is. The p-values corrected for multiple testing within each category using the Benjamini–Hochberg procedure are shown.