

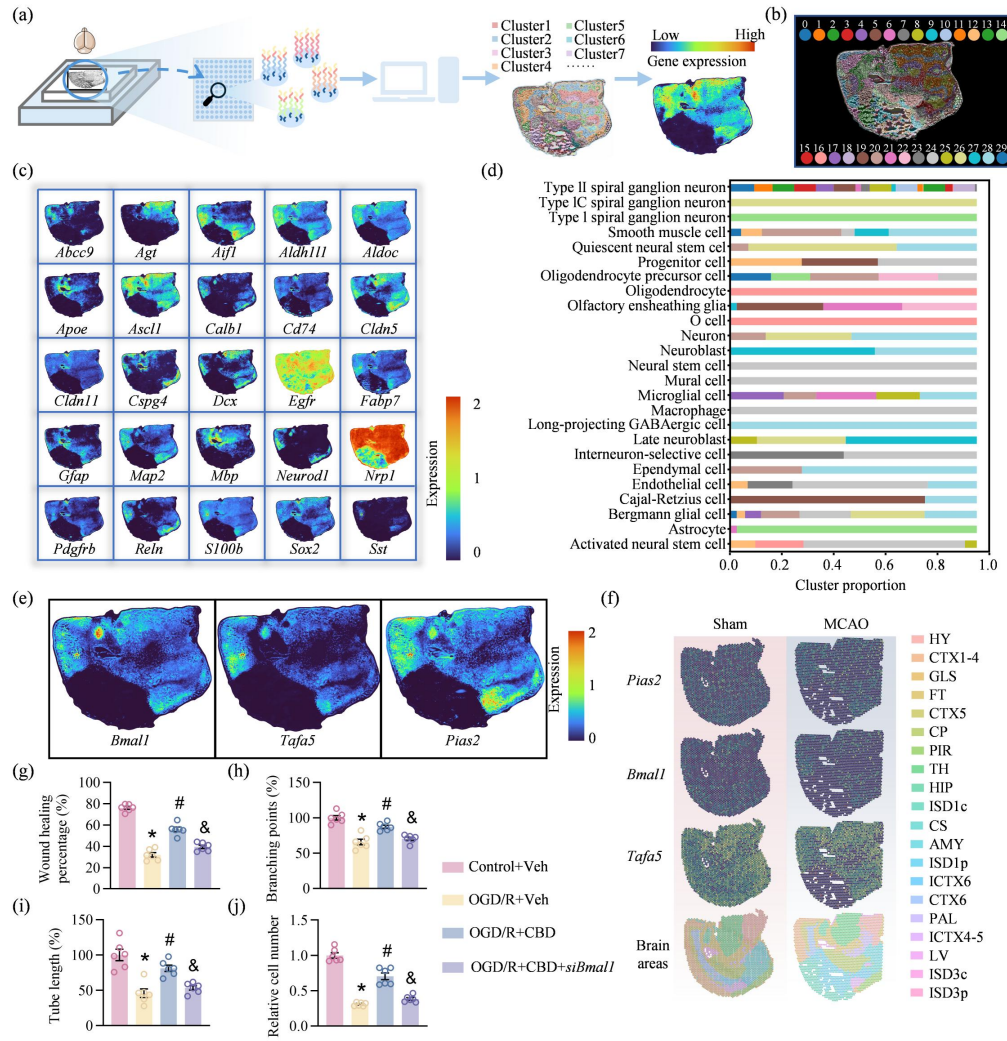


Fig. S12. Spatial transcriptomics highlights BMAL1 as a central NRF2-regulated target driving CBD-induced angiogenesis.

- (a) Workflow diagram for the collection and processing of spatial transcriptomics data.
- (b) Super-resolution structure of MCAO spatial transcriptomics data obtained through iSTAR.
- (c) The heatmap shows the super-resolution expression of marker genes for different cell types obtained through iSTAR computation, with brain slices as the background.
- (d) Cell type distribution across clusters in super-resolution spatial transcriptomics data.
- (e) Gene expression levels of *Tafa5*, *Pias2*, and *Bmal1* in MCAO mouse brain slices under super-resolution structure.
- (f) Gene expression levels of *Tafa5*, *Pias2*, and *Bmal1* in MCAO and Sham mouse brain slices under anatomical structure.
- (g) Statistical analysis of the percentage of HUVEC cells scratch healing ($n = 6$ per group).
- (h-i) Statistical analysis of the length and branches of capillary-like tubes formed by HUVEC cells ($n = 6$ per group).
- (j) Statistical analysis of relative migration number of HUVEC cells ($n = 6$ per group).

Data are presented as mean $\pm$ SEM. * $P < 0.05$ versus control group; # $P < 0.05$ versus OGD/R group; & $P < 0.05$ versus CBD-treated group.