

Supplementary results

Figure1.

Schematic of the animal experiment design.

Figure2.

(a) Total ion chromatograms of mass spectrometry analysis of the proteins. (b) Secondary mass spectrum of *P. gingivalis*-Rgp . (c) The binding sites of RgpA and Cav-1.

Figure3.

To demonstrate the molecular mechanism of *P. gingivalis*-enhanced BBB permeability, high-throughput sequencing of BMECs infected with *P. gingivalis* (MOI 100) was performed. According to the differential gene screening ($|\text{Log}_2\text{FC}| \geq 1$, $P < 0.05$, $\text{FDR} < 0.05$), there were 1661 differential genes, including 983 upregulated and 678 downregulated genes after *P. gingivalis* treatment compared with control group (Fig. 2a). Gene Ontology (GO) assignments were used to assign functional classifications to the differentially expressed genes (DEGs) . All DEGs were annotated with 20 functional terms and categorized as biological process, cellular component, or molecular function (Fig. 2b). Cluster of orthologous group function annotation analysis showed that the DEGs were mainly enriched in intracellular transport, secretion, and vesicle transport pathways (Fig. 2c). To analyze the specific molecular regulating permeability, cluster analysis showed that transcytosis-related gene *Mfsd2a* expression was downregulated significantly (Fig. 1D).

Figure4.

To confirm the role of Mfsd2a in BMECs permeability and Cav-1 expression, overexpressed plasmids and siRNA of Mfsd2a were transfected into BMECs. Compared with the control group, Mfsd2a protein expressions in the BMECs^{pcMfsd2a} (Fig.2a) and BMECs^{SiMfsd2a} groups (Fig.2b) were significantly higher and lower at 24 h, respectively.

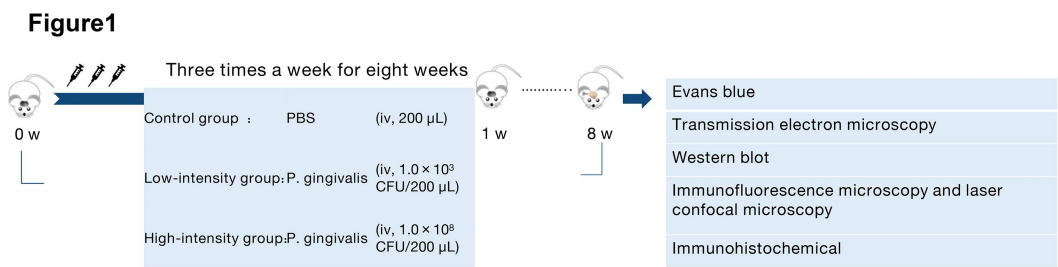


Figure2

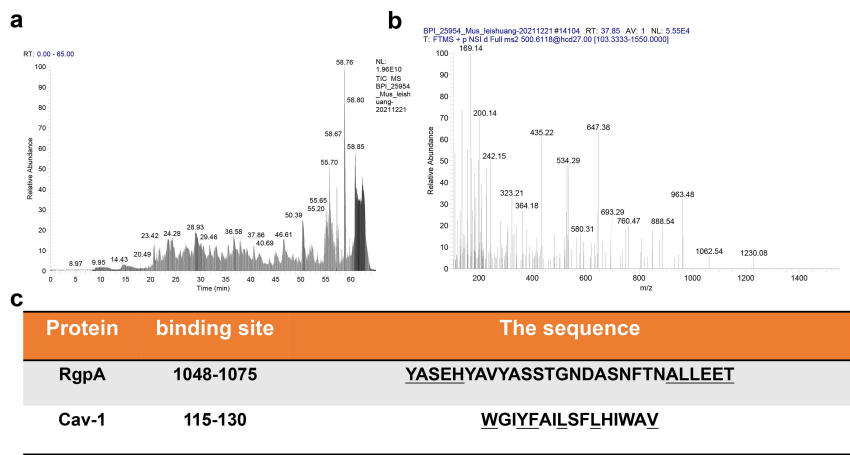


Figure3

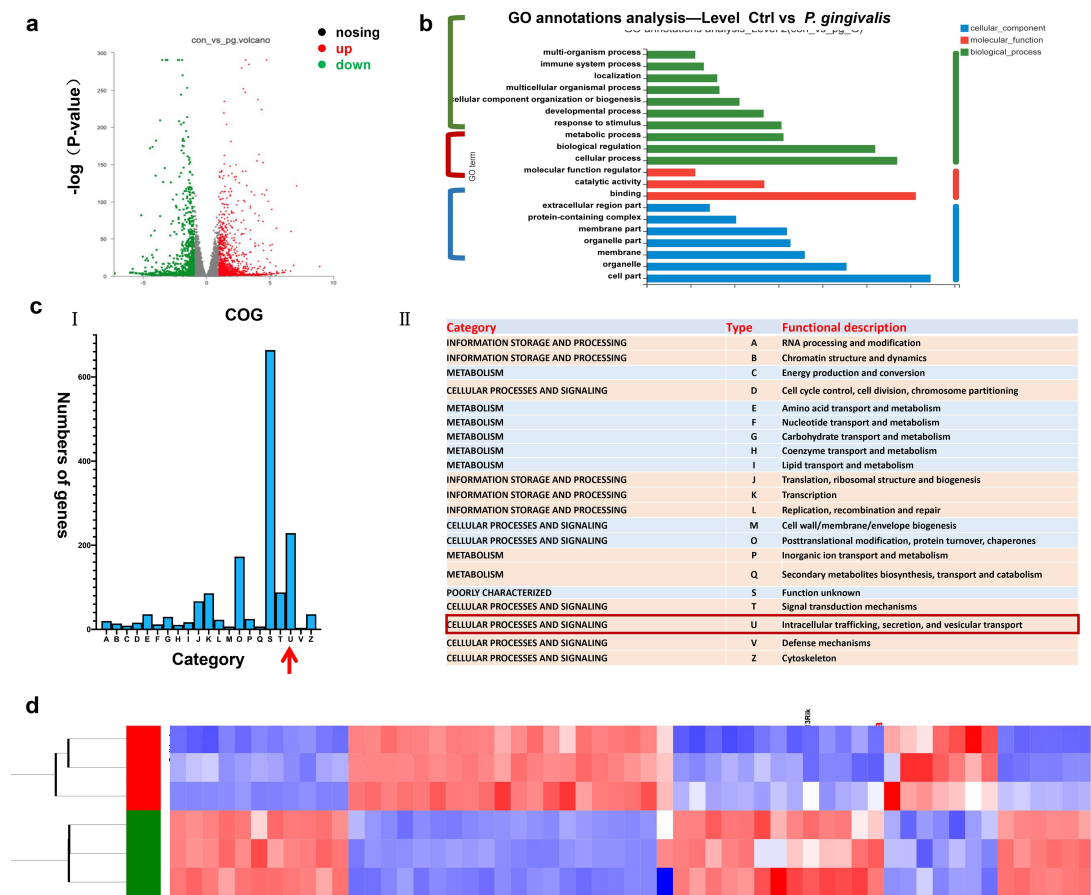


Figure4

