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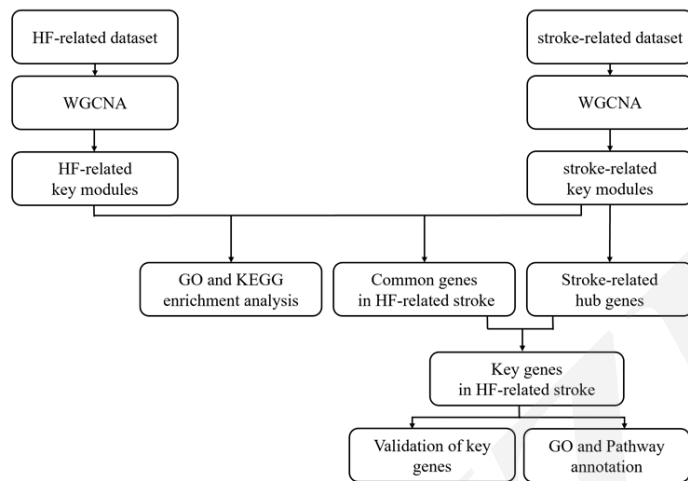
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Bioinformatic analysis for potential biological processes and key targets of heart failure-related stroke

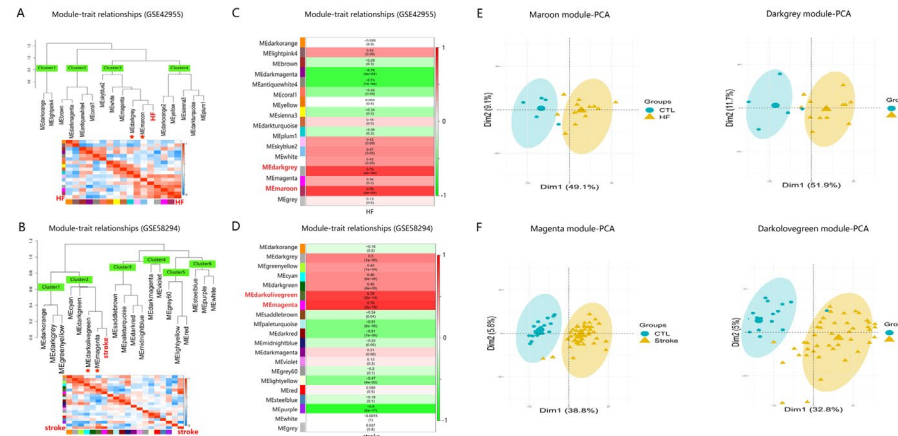
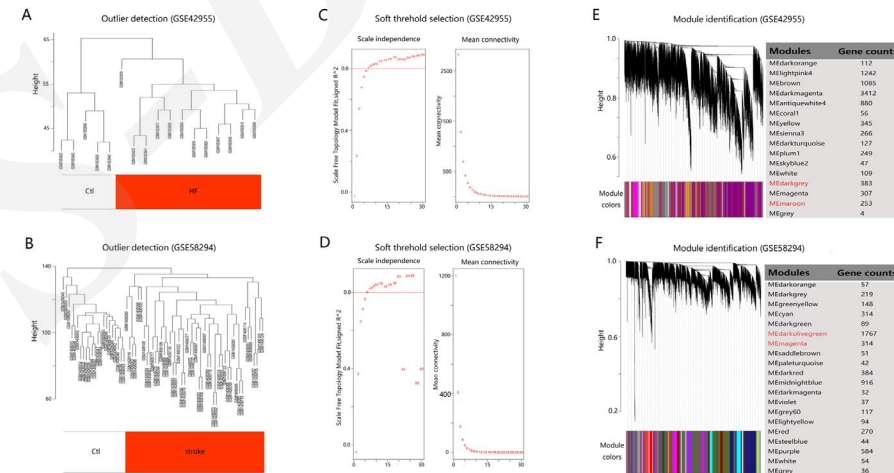
Key words: Cardioembolic stroke, Heart failure, Bioinformatics, Weighted gene co-expression network analysis (WGCNA)

Research Summary

This study aimed to uncover underlying mechanisms and promising intervention targets of heart failure (HF)-related stroke.



WGCNA was performed to identify two HF-related and two stroke-related key modules. Functional enrichment analysis of these key modules identified the underlying biological processes in HF-related stroke, including protein ubiquitination, Wnt signaling, and extracellular exosome. In addition, 155 genes were identified as common genes in both HF-related and stroke-related key modules, and are thus the top possibilities for genes that play a biological role in HF-related stroke. Most importantly, among these common genes, OTULIN and NFIL3 were identified as the hub genes of stroke-related key modules, indicating their key roles in HF-related stroke. Functional annotation revealed that key genes acted in HF-related stroke by participating in or regulating the biological processes identified above. Finally, NFIL3 and OTULIN were validated to be up-regulated in HF and stroke groups, supporting the importance of OTULIN and NFIL3 in HF-related stroke.



Innovation points

● **Protein ubiquitination, Wnt signaling and exosomes** are involved in HF-related stroke.

● **155 common genes** are likely to act in the mechanism of HF-related stroke.

● **OTULIN** and **NFIL3** play a more critical role in HF-related stroke by participating in or regulating protein ubiquitination and Wnt signaling.

