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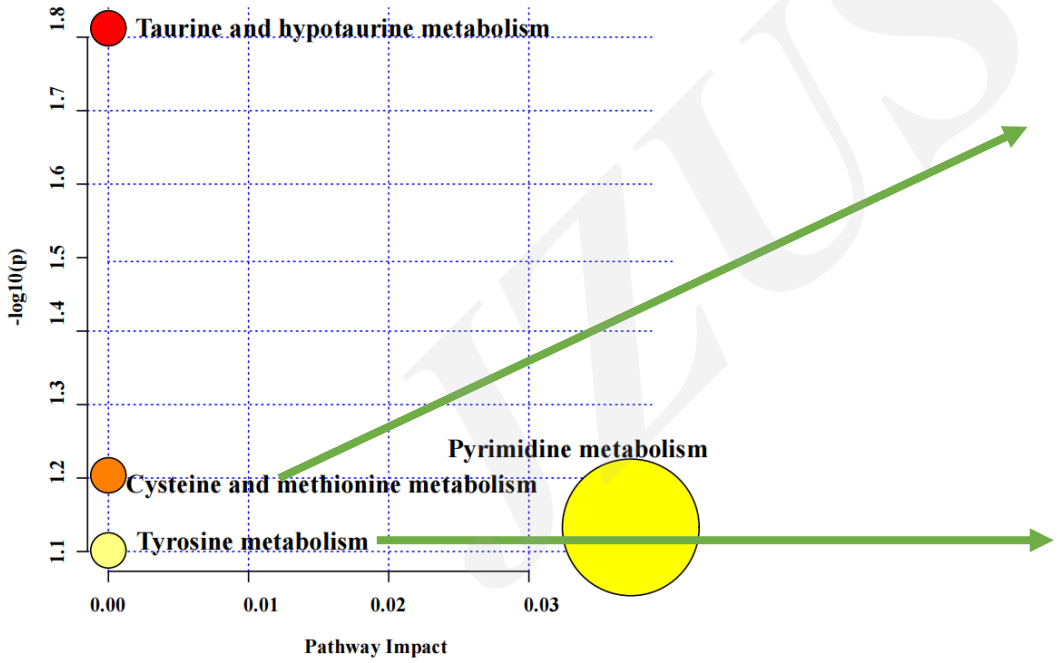
Adrenal pheochromocytoma impacts three main pathways: cysteine-methionine, pyrimidine, and tyrosine metabolism

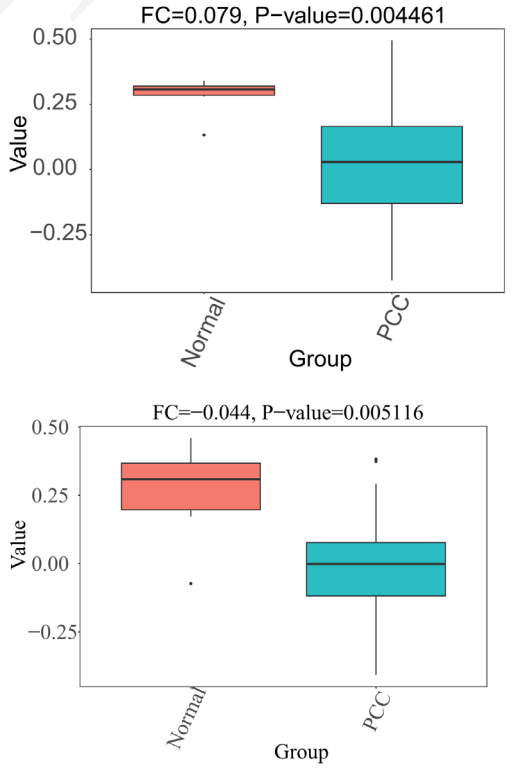
Key words: pheochromocytoma and paraganglioma (PPGL), metabolomics, gene set variation analysis, L-dihyroorotic acid, vanylglycol

Research Summary

This study focused on the joint analysis of metabolomics and transcriptomics of pheochromocytoma and found that the cysteine-methionine metabolic pathway, the tyrosine metabolic pathway and the pyrimidine metabolic pathway were three main metabolic pathways altered in PCC.



Metabolomics



Transcriptomics (GSVA score)

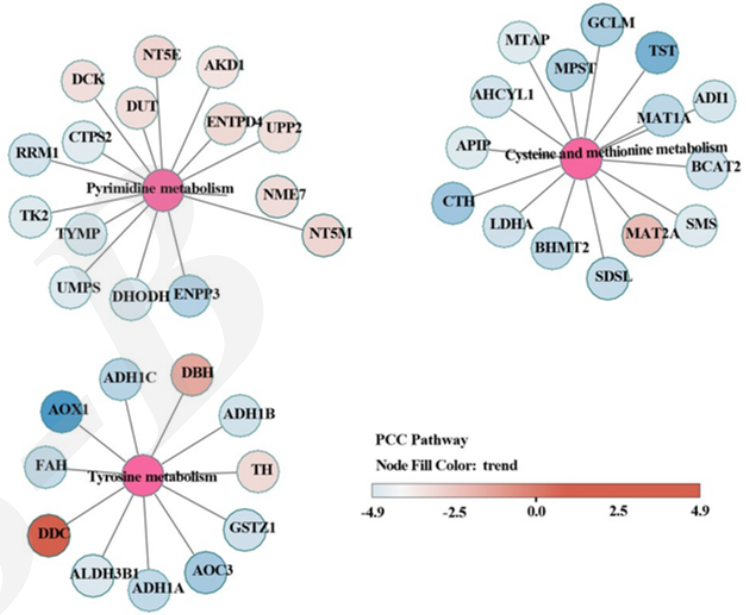
Innovation points

Combine metabolomic and transcriptomic analysis of PCC.

Find that the cysteine-methionine metabolic pathway, the tyrosine metabolic pathway and the pyrimidine metabolic pathway were three main metabolic pathways altered in PCC.

Develop the optimized diagnostic model of L-dihyrorotic acid and vanylglycol.

(a) Network of relationship between differential genes and pathways.



(b) ROC curve for the discovery set. (c) ROC curve for the validation set.

