

Neutrophil Extracellular Trap–related tissue biomarkers in Ulcerative Colitis: Emphasis on *Aquaporin-9*

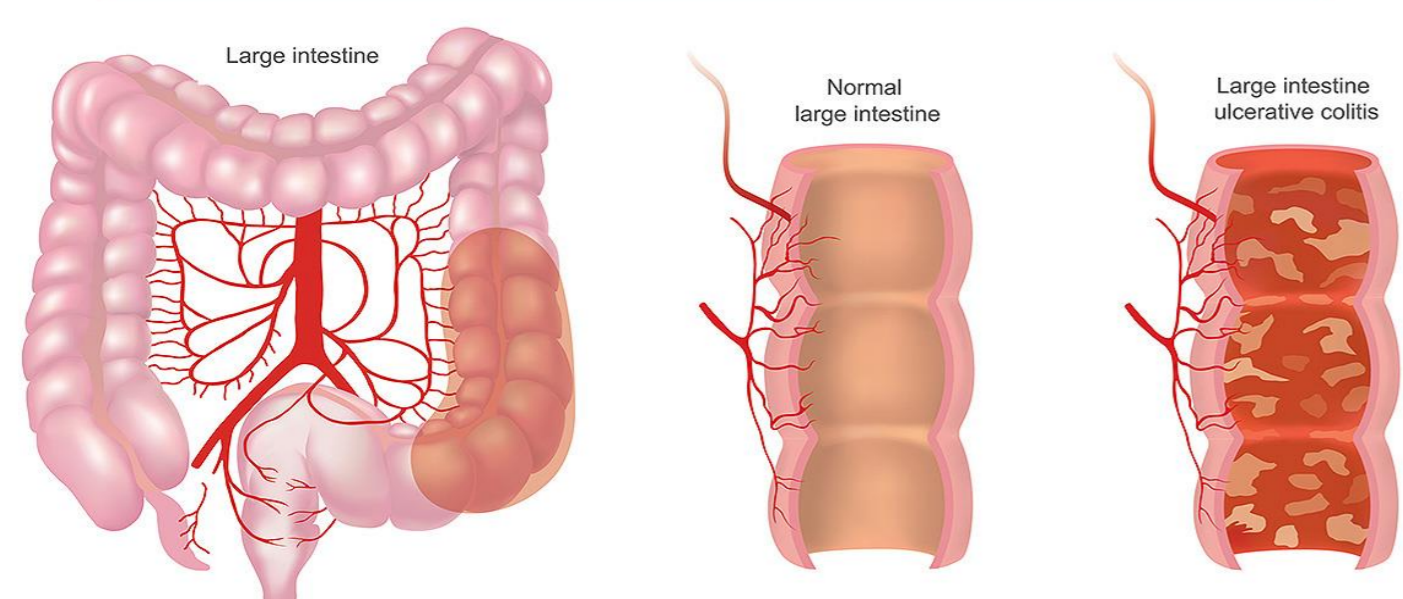
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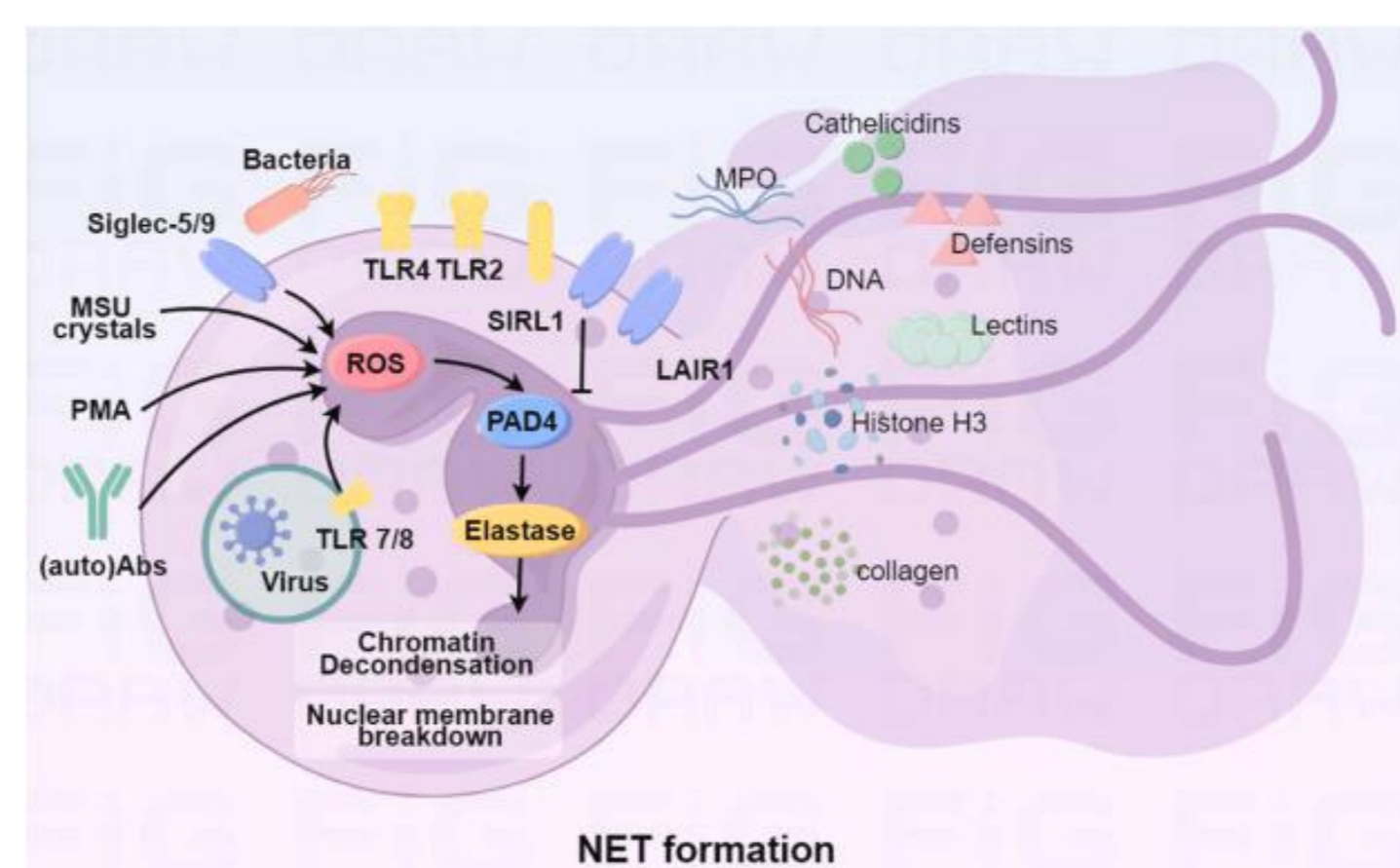
Aims

Ulcerative colitis (UC) is a chronic inflammatory bowel disease (IBD)

Ulcerative colitis (Inflammatory Bowel Disease : IBD)



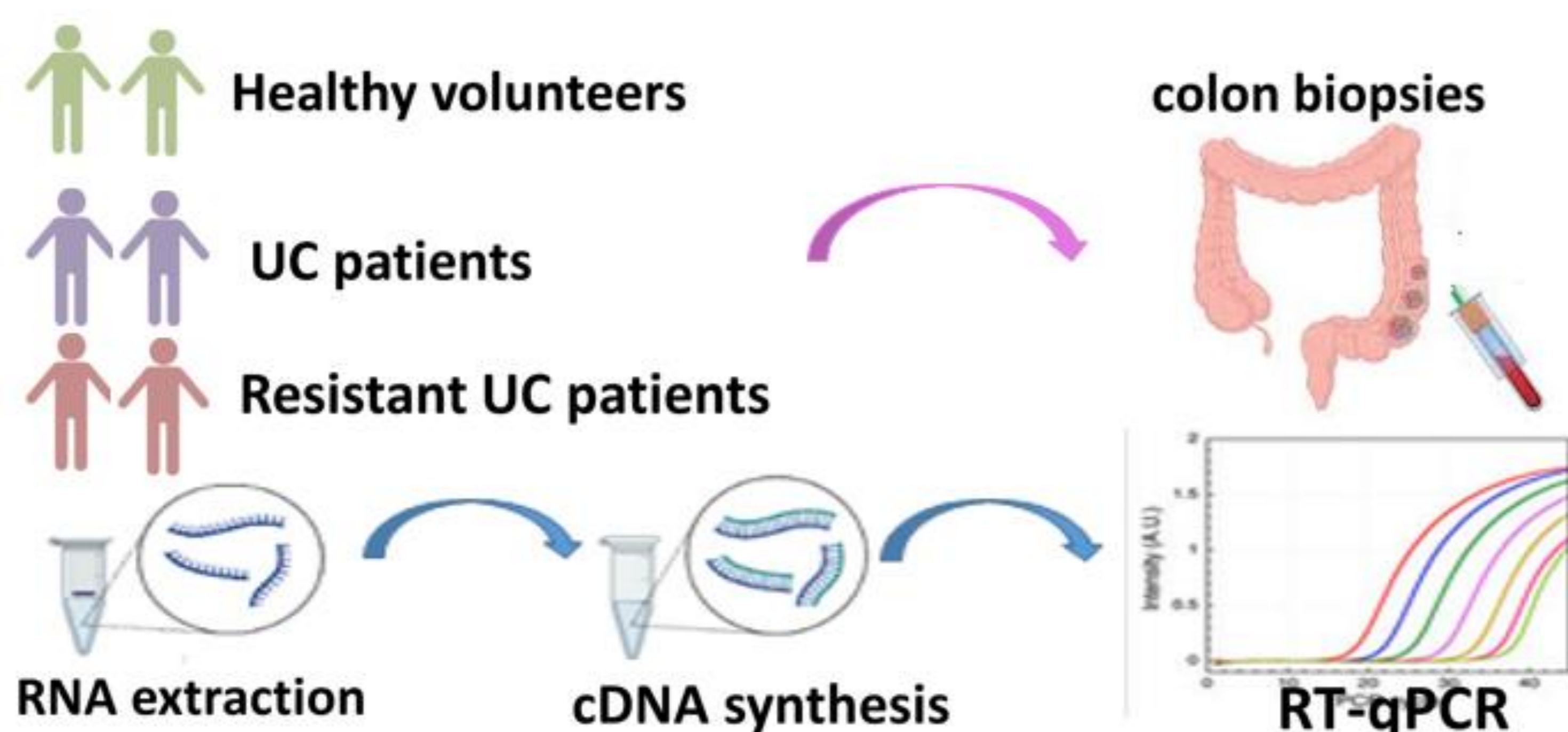
Neutrophil extracellular traps (NETs) have been recognized to UC progression



Identification of **NET-Related Genes** as Potential Biomarkers in UC

Methods

- Data acquisition**
Gene expression profiles (GSE224758) of colonic biopsies from UC patients & healthy controls were obtained from the GEO database
- Differential expression analysis**
Differentially expressed genes (DEGs) between UC and control samples were identified using GEO2R.
- Co-expression PPI network for DEGs that upregulated in UC group and Analysis with cytoscape**
- Detecting Gene modules**
- Selection of NET-related hub genes by pathway enrichment analysis for the largest gene module**
- Sample collection included 3 groups & RT-qPCR**

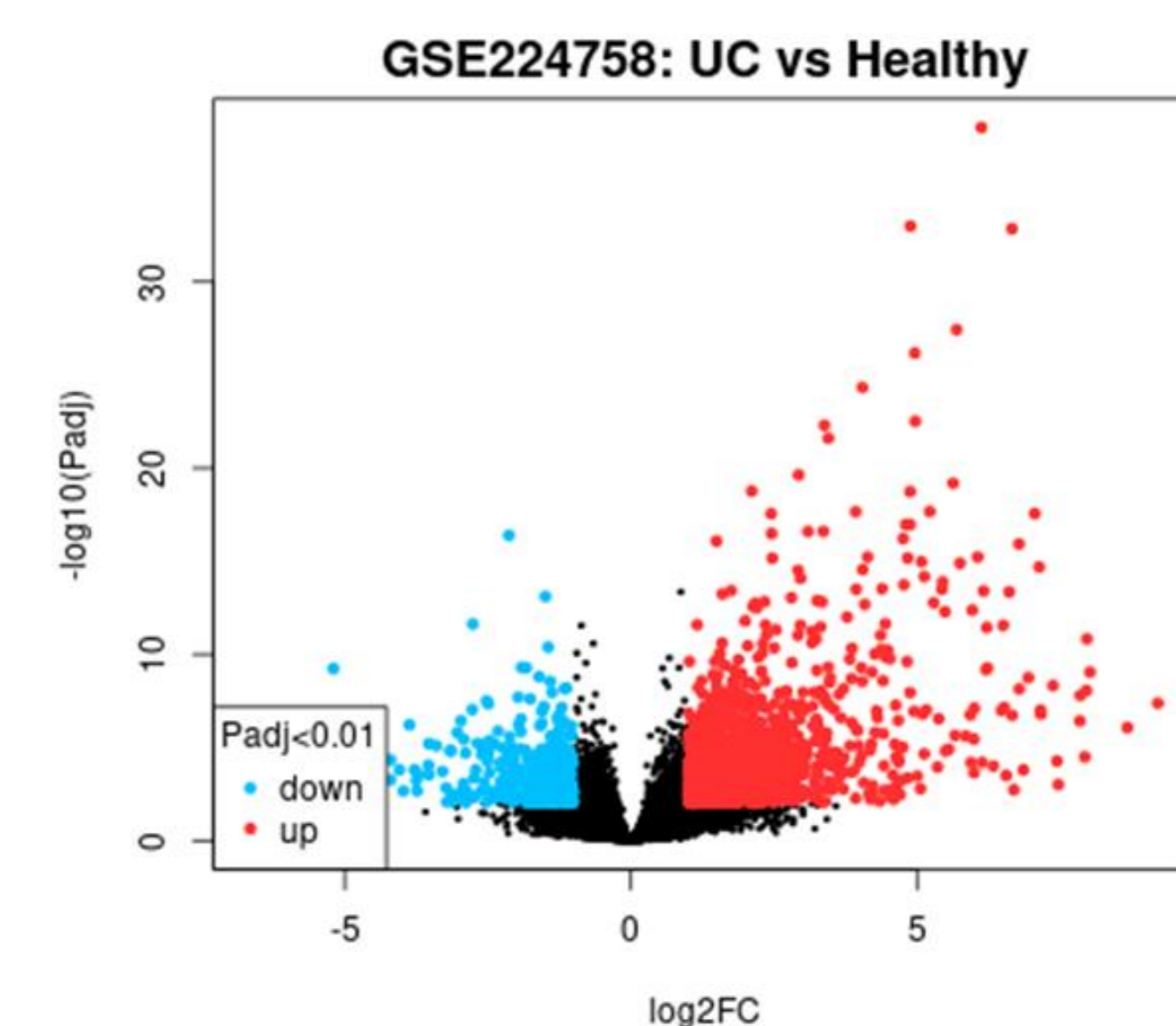


Results

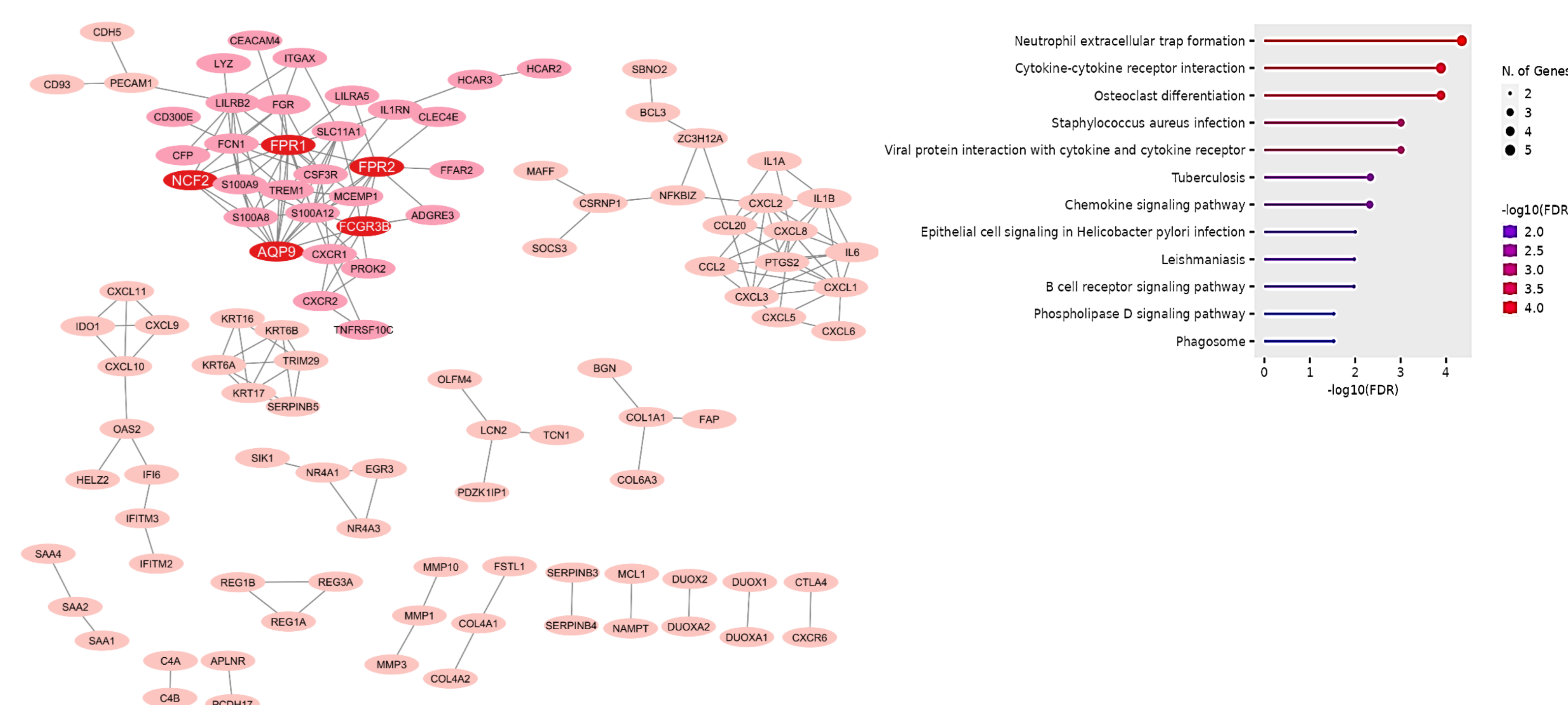
Identification of DEGs in UC

Volcano plot analysis of the GSE224758 dataset reveals **492 DEGs** between UC patients & healthy controls.

- ✓ **429 upregulated genes**
- ✓ **63 downregulated genes**

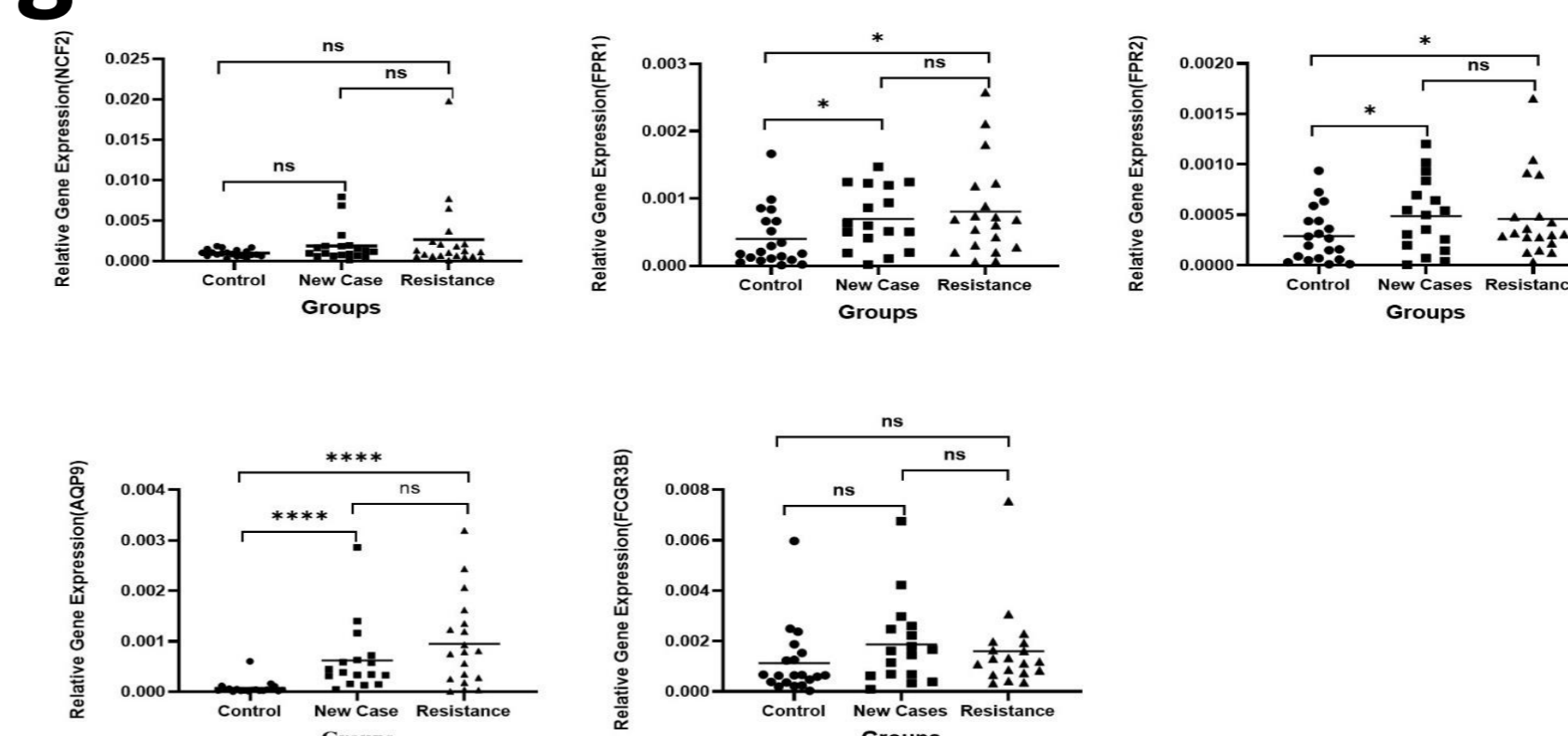


Co-expression PPI network of **upregulated DEGs (429)**
Pathway enrichment analysis

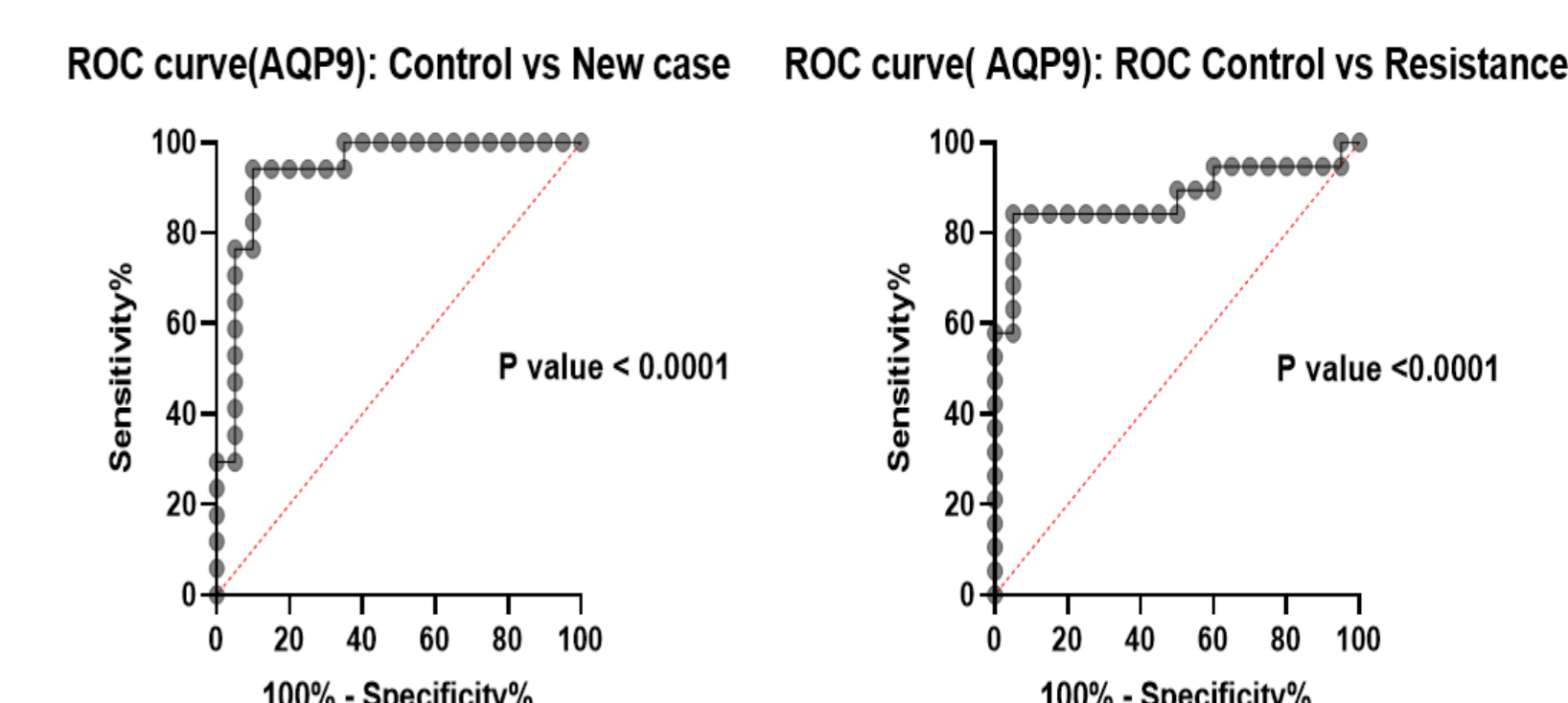


In the largest module, **red nodes** highlight the **5 key hub genes** (*FPR1*, *AQP9*, *FPR2*, *FCGR3B*, *NCF2*)

Validation of bioinformatics data by RT-qPCR for 5 Hub genes involved in NET formation pathway



ROC curve analysis of ***Aquaporin-9 (AQP9)*** demonstrates its ability to discriminate UC patients from healthy controls.



Conclusion

- NET-related genes, particularly ***AQP9***, ***FPR1*** & ***FPR2***, emerge as candidate tissue biomarkers for UC.
- Among these, ***AQP9*** exhibiting the strongest ability to distinguish patients from healthy controls.