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# Elucidating the Comorbidity Trajectory subsequent to AD: The Cluster patterns and Genetic Contributions

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**Study Background**

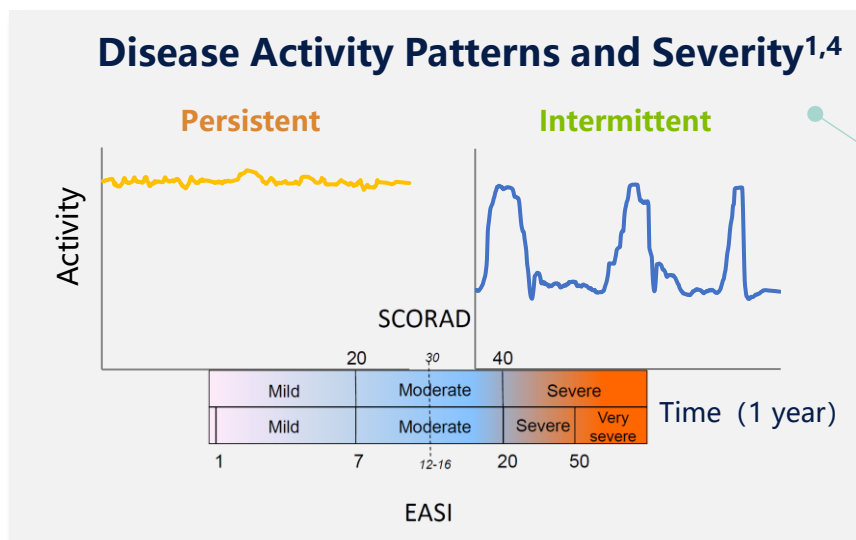
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**Study Design and Results**

**Content**

# Study Background

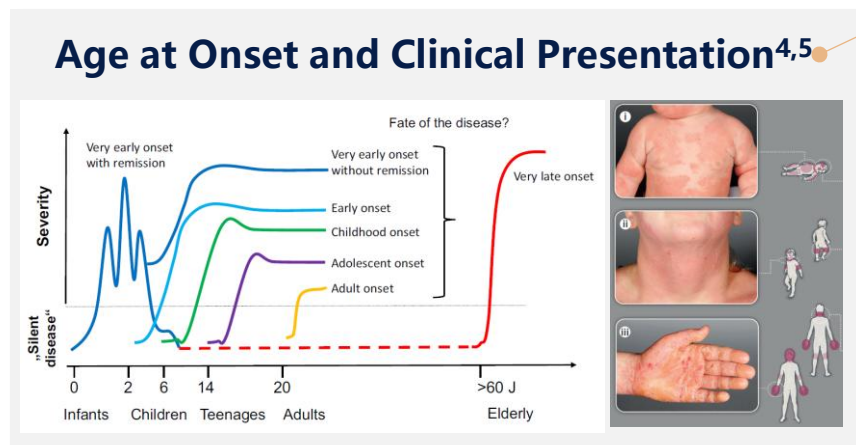
The most recent Lancet review underscores the pronounced **heterogeneity** of atopic dermatitis.



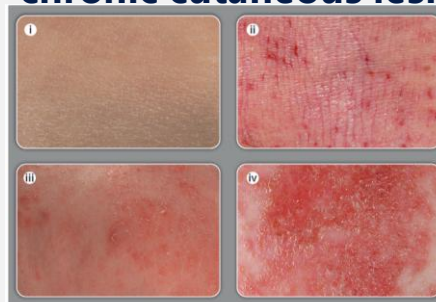
Th2-polarized inflammation is a hallmark of AD



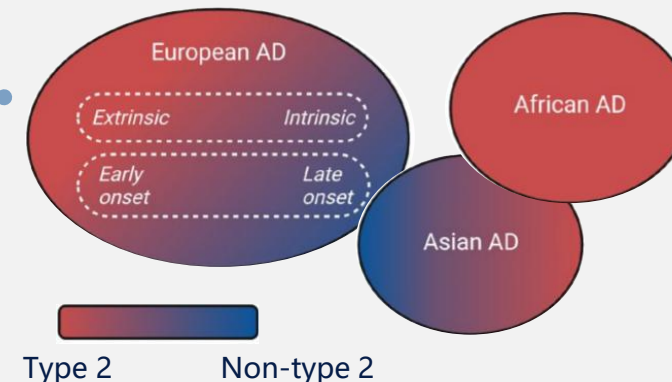
T-helper (TH) cell expression levels vary across racial/ethnic groups<sup>2</sup>



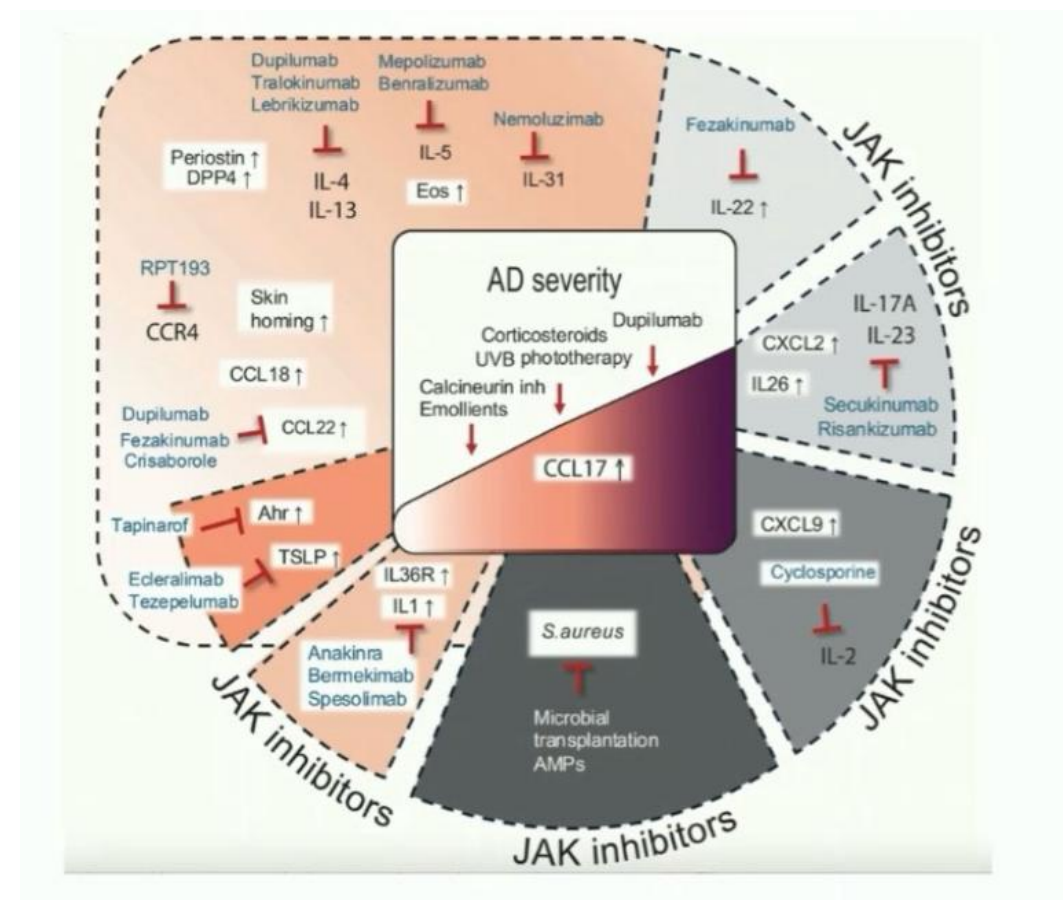
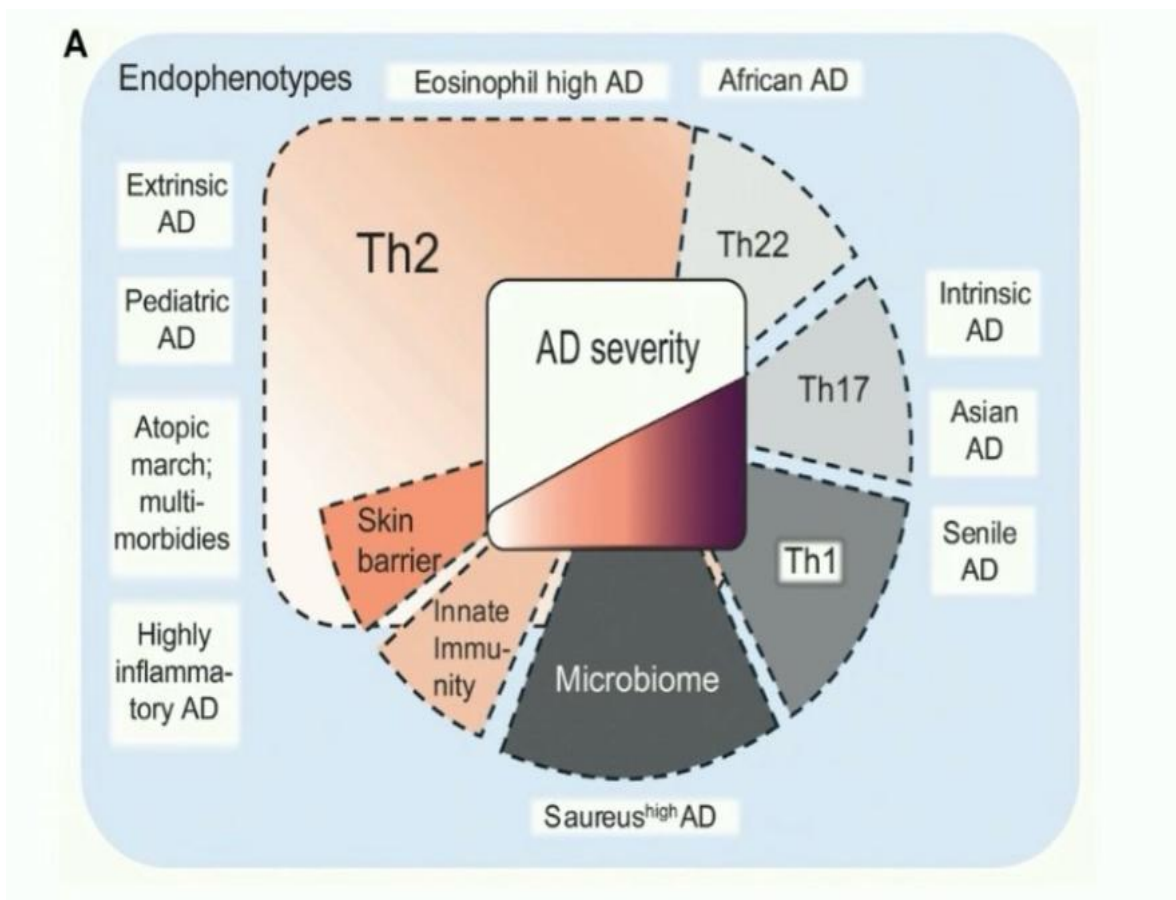
Acute, subacute, and chronic cutaneous lesions<sup>5</sup>



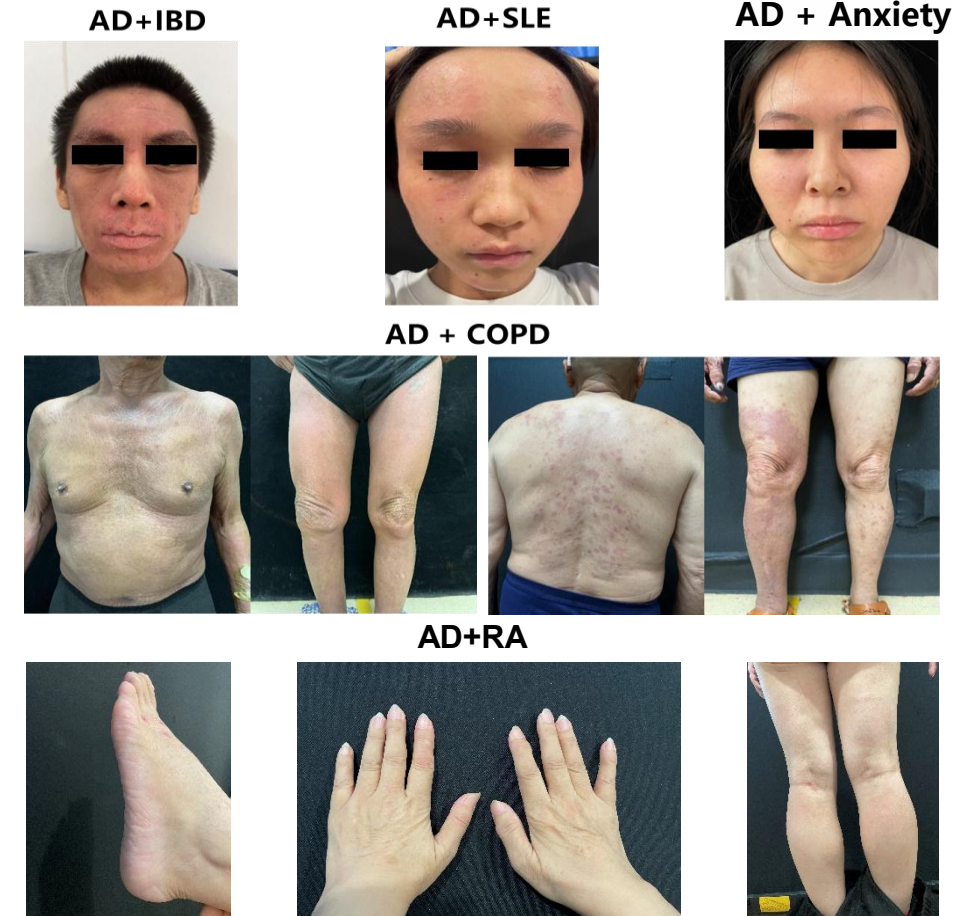
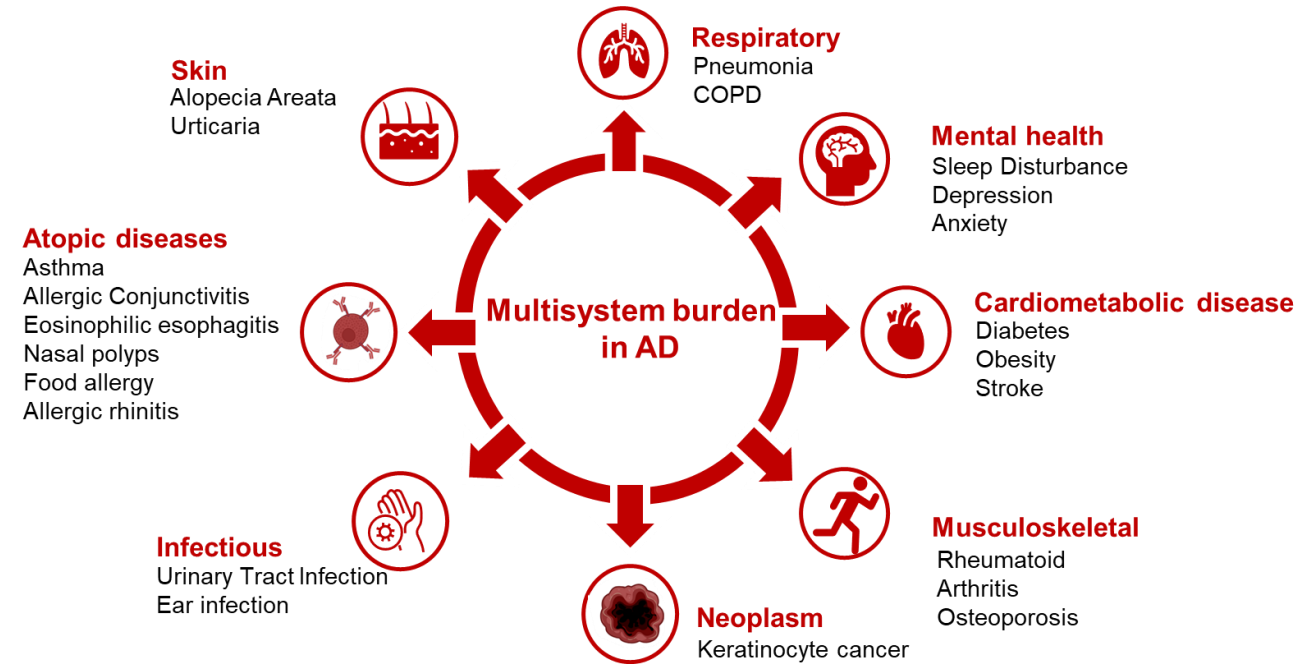
Intrinsic vs extrinsic (by IgE level)<sup>2,3</sup>



# Study Background



# Study Background: Co-occurrence comorbidities of AD.



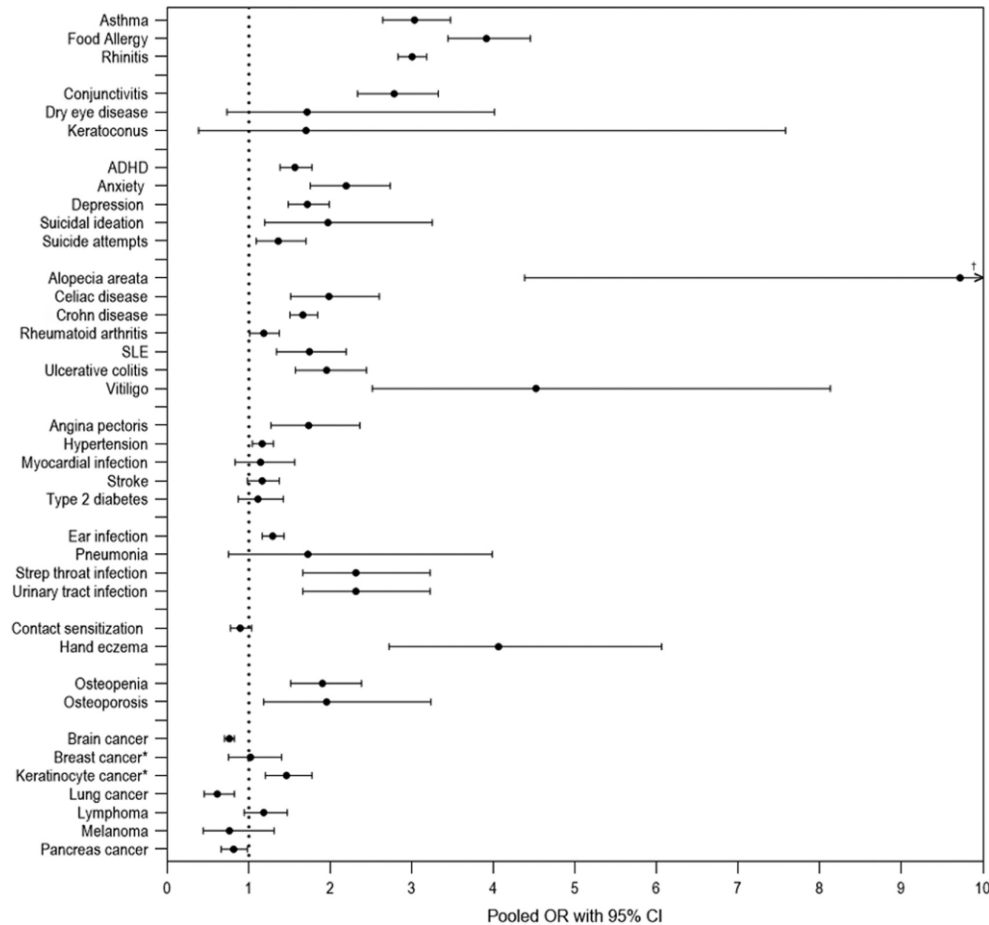
Do the comorbidities in AD exhibit heterogeneity?

How the different comorbidities impact clinical treatment.

# Outline: Dynamic progression and accumulation of comorbidities in AD

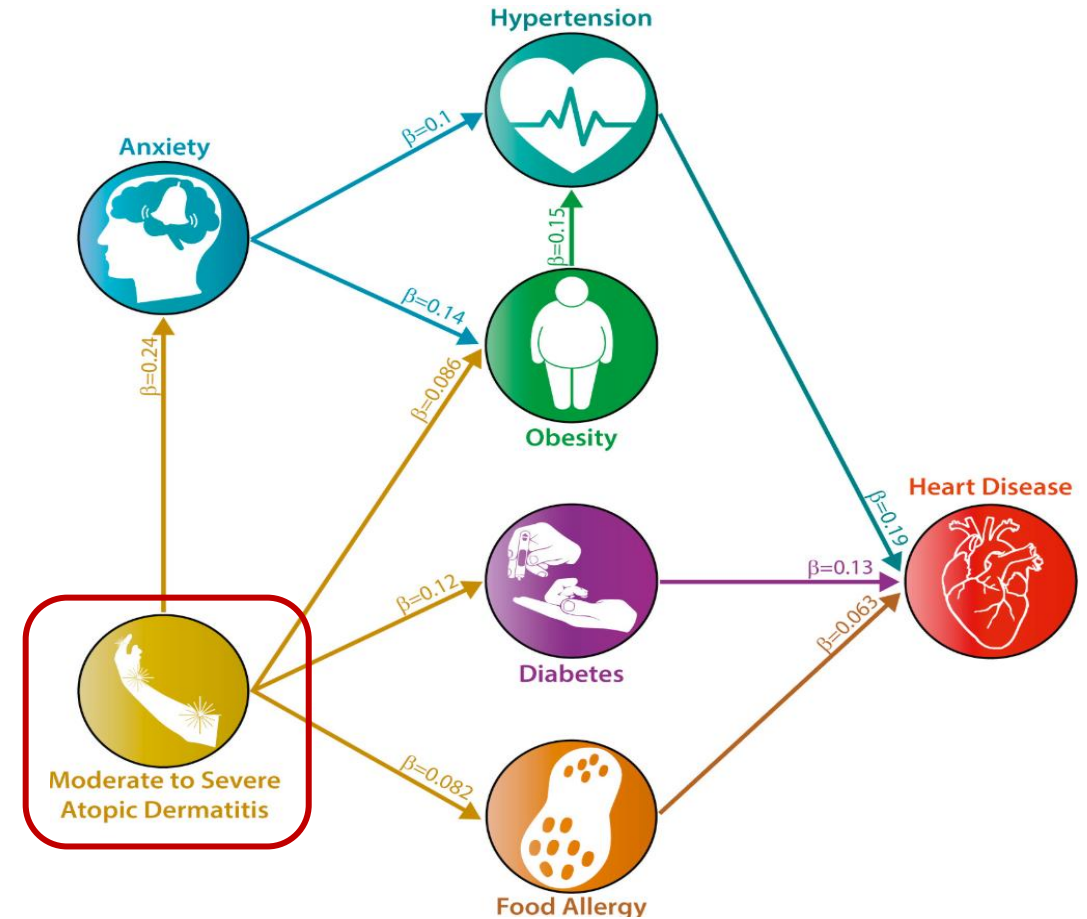
## Multisystem comorbidity burden

AD was associated with multisystem comorbidities beyond atopic diseases.



## Comorbidity progression.

The interactions between comorbidities promote syndemics.

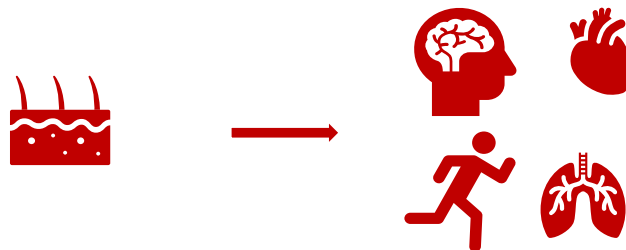


Haddad EB, et al. *Dermatol Ther (Heidelb)*. 2022;12:1501–1533.  
 Beck LA, et al. *JID Innov*. 2022;2:100131.  
 Paller AS, et al. *Dermatol Ther*. 2023;13:961–980.  
 Neri I, et al. *J Asthma Allergy*. 2023;16:383–396.  
 Ramirez FD, et al. *Jama Pediatr*. 2019;173:e190025.

Wan J, et al. *J Allergy Clin Immunol Pract*. 2023;11:3123–3132.  
 Wan J, et al. *J Allergy Clin Immunol Pract*. 2023;S2213–2198(23)01251.  
 Andersen L, et al. *Br J Dermatol*. 2020;182:1007–1016.  
 Henderson AD, et al. *BMC Med*. 2023;21:285.  
 Lowe KE, et al. *J Allergy Clin Immunol*.

## Core Issues We Aim to Address

- Uncover the comorbidity landscape of AD.
- Reveal how the comorbidities **sequence, evolve** in AD.
- Investigate the **clustering patterns** of comorbidities and the underlying **genetic contributions**.
- How different **comorbidity** impact the treatment.





# Study Design and Results

## Observational study

### Identify the diseases associated with atopic dermatitis

#### Data source

##### Medical record

Primary care, hospital record, death registry data.  
The diagnoses of diseases were mapped to phecode system.

##### Exposure

Diagnosis of atopic dermatitis was based on selected ICD codes: L208, L209, L20, L309, 6918, 69180, and 6929

##### Outcome

Outcome determination was based on ICD-10 codes and mapped to 1,429 phecodes.



#### Sample matching

11,065 individuals  
with  
atopic dermatitis

1:10  
age, sex TDI matched

110,650 individuals  
without  
atopic dermatitis

#### Statistical analysis

##### Conditional proportional hazard model



The incidence of 1,429 phecode-defined outcomes

Outcome events,  
Death, Loss or end  
of follow up.

Baseline

Follow up

Endpoints

Disease outcomes associated with atopic dermatitis

### Map the trajectory of comorbidities in individuals with atopic dermatitis

#### Step 1: Explore comorbidity trajectory and clusters.

**Comorbidity Strength**  
Relative risk and Pearson correlation (Phi-coefficient)  
**Co-occurring Pairs**

**Magnitude of Association**  
Risk set sampling and conditional logistic regression  
**Comoridity network**

**Temporal Relationship**  
Binomial test  
**Temporal trajectory**



Comorbidities  
with intrinsic connections

Clustering Analysis

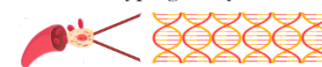
Trajectories of comorbidities  
within each cluster

#### Step 2: Explore the genetic determinants of clusters.

##### Disease clusters

Infectious Skin-gut  
Mental Cardiometabolic  
Musculoskeletal  
Calculate the number of diseases in each cluster for each individual

##### Genotyping array data



Quality control of genetic-level and individual-level

Cluster-specific score

GWAS

Genetic data

IndSigSNPs

Annotation through FUMA

Mapped genes

Pathway

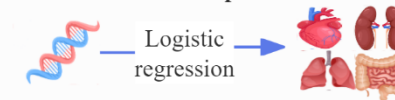
Through SNP2GENE and MAGMA

## Genetic analysis

### Provide insights from genetic perspective

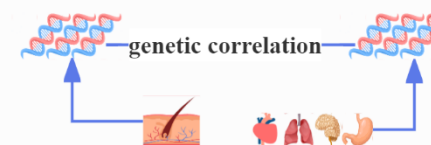
#### PRS-PheWAS

The disease outcomes associated with the PRS of atopic dermatitis.



#### LDSC

The genetic linkage between atopic dermatitis and disease outcomes



#### Two sample MR

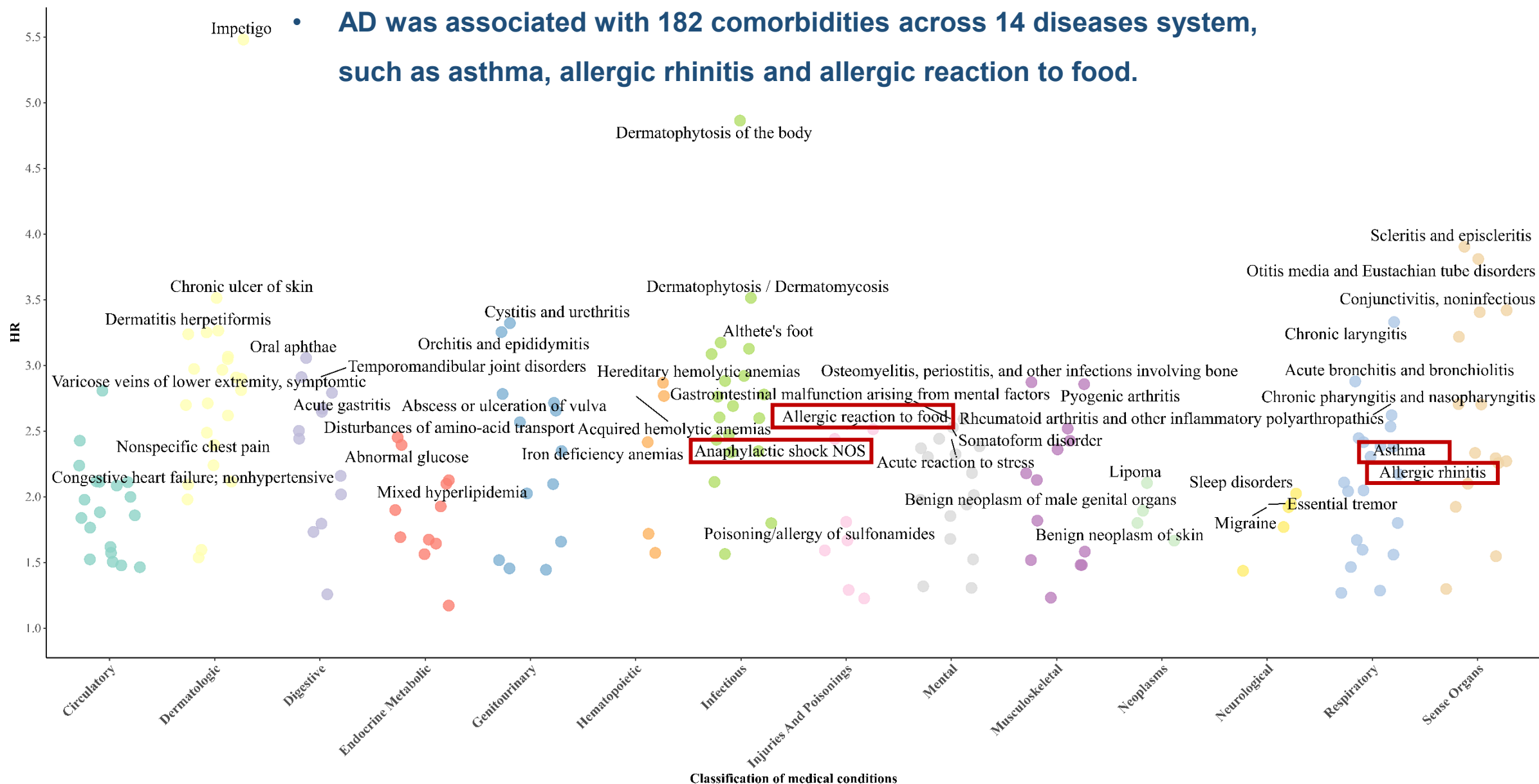
The genetic casual evidence between atopic dermatitis and 2469 diseases from FinnGen data.



# **Research Question 1:**

## **The Comorbidity profile in AD.**

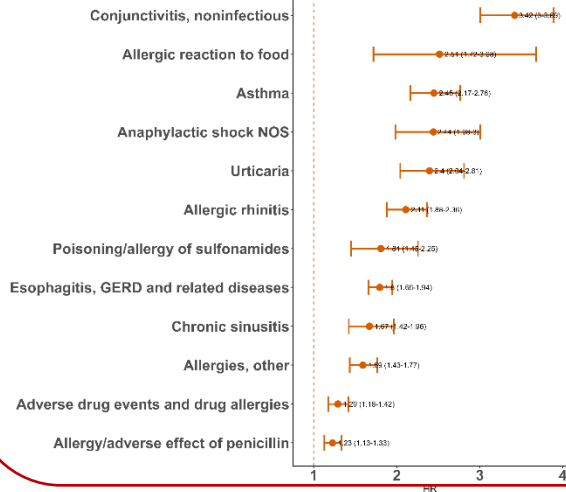
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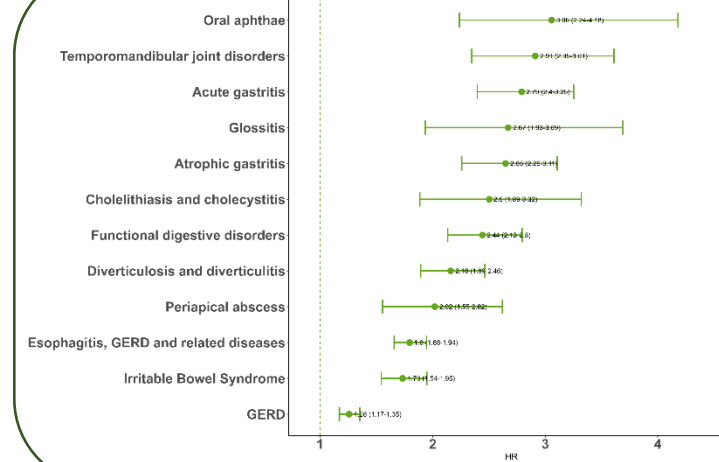
# Research Question 1: The Comorbidity Profile of of AD.

AD is associated with an increased risk of **multisystem** diseases, extending beyond atopic comorbidities and cutaneous conditions.

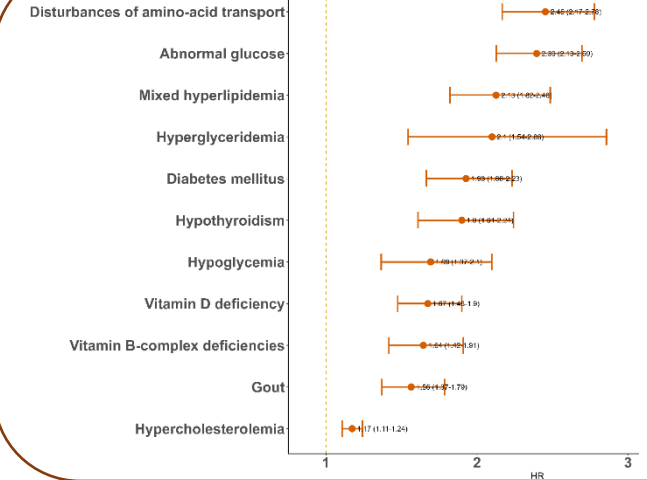
## Atopic



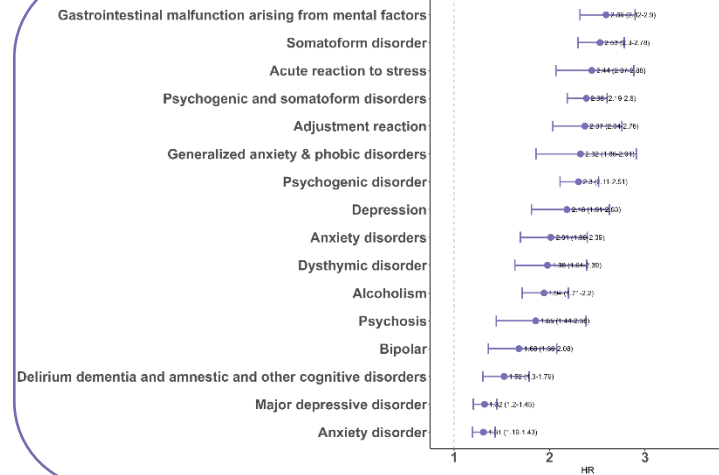
## Digestive



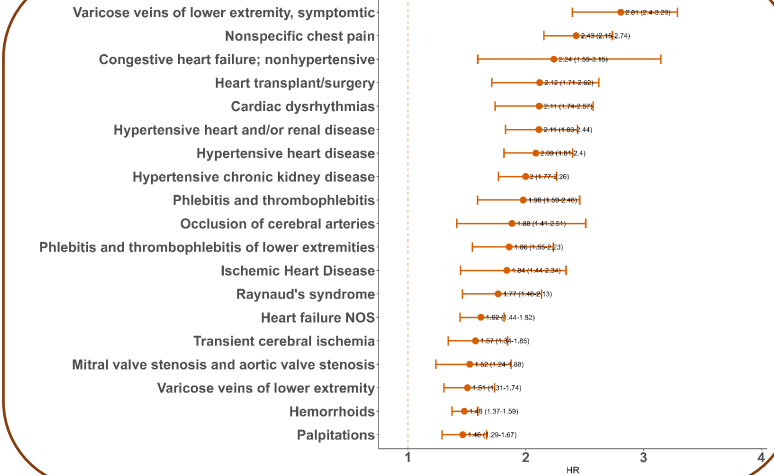
## Endocrine



## Mental

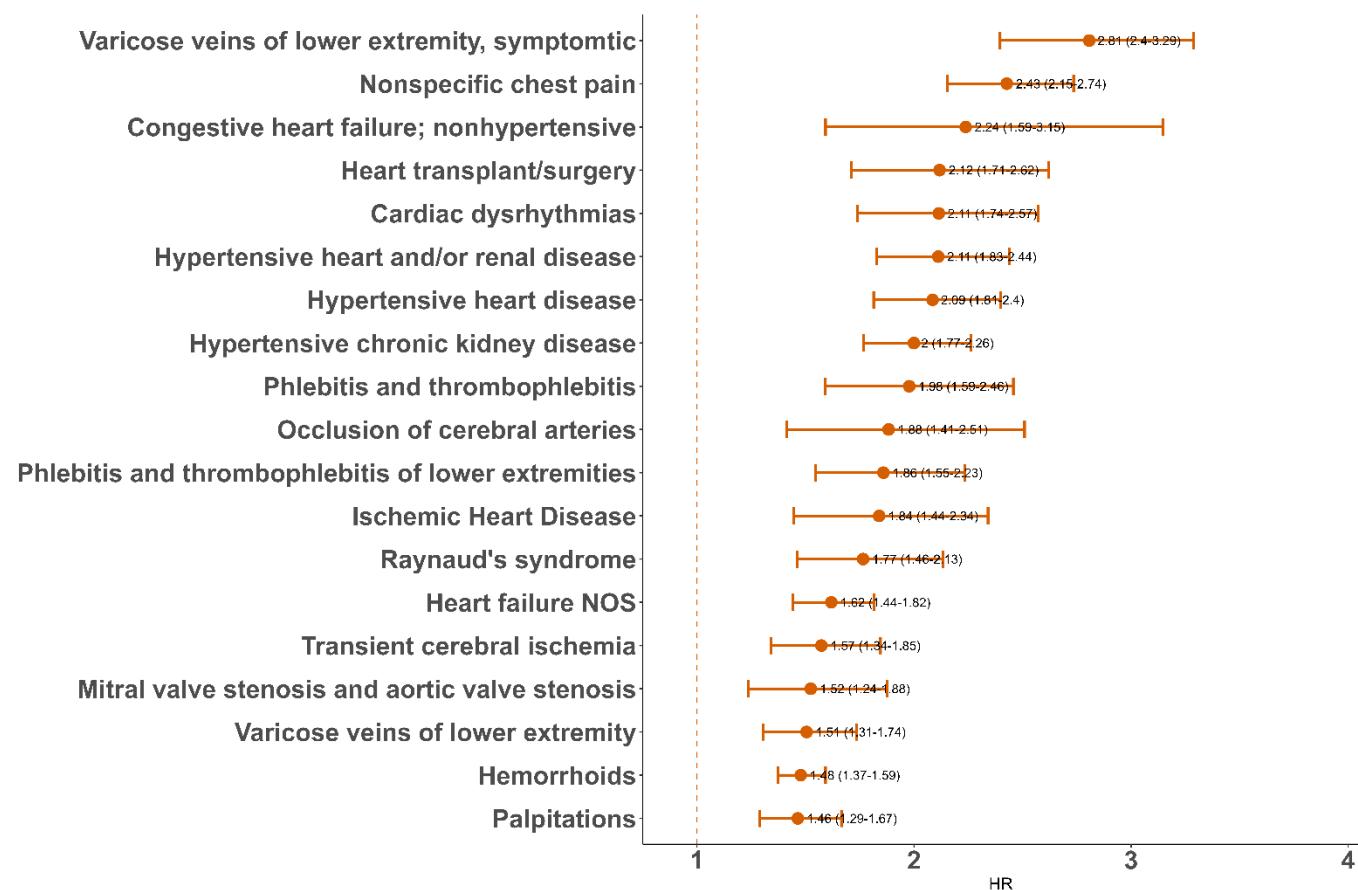
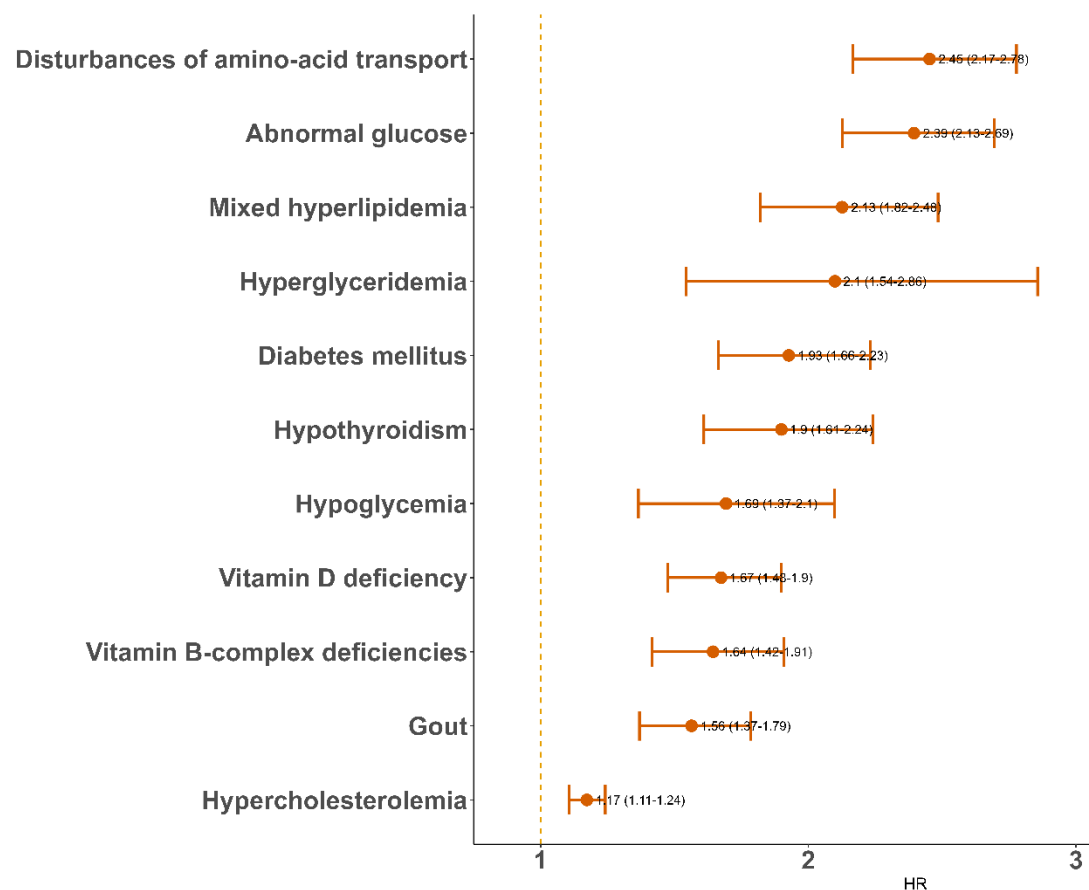


## Circulatory



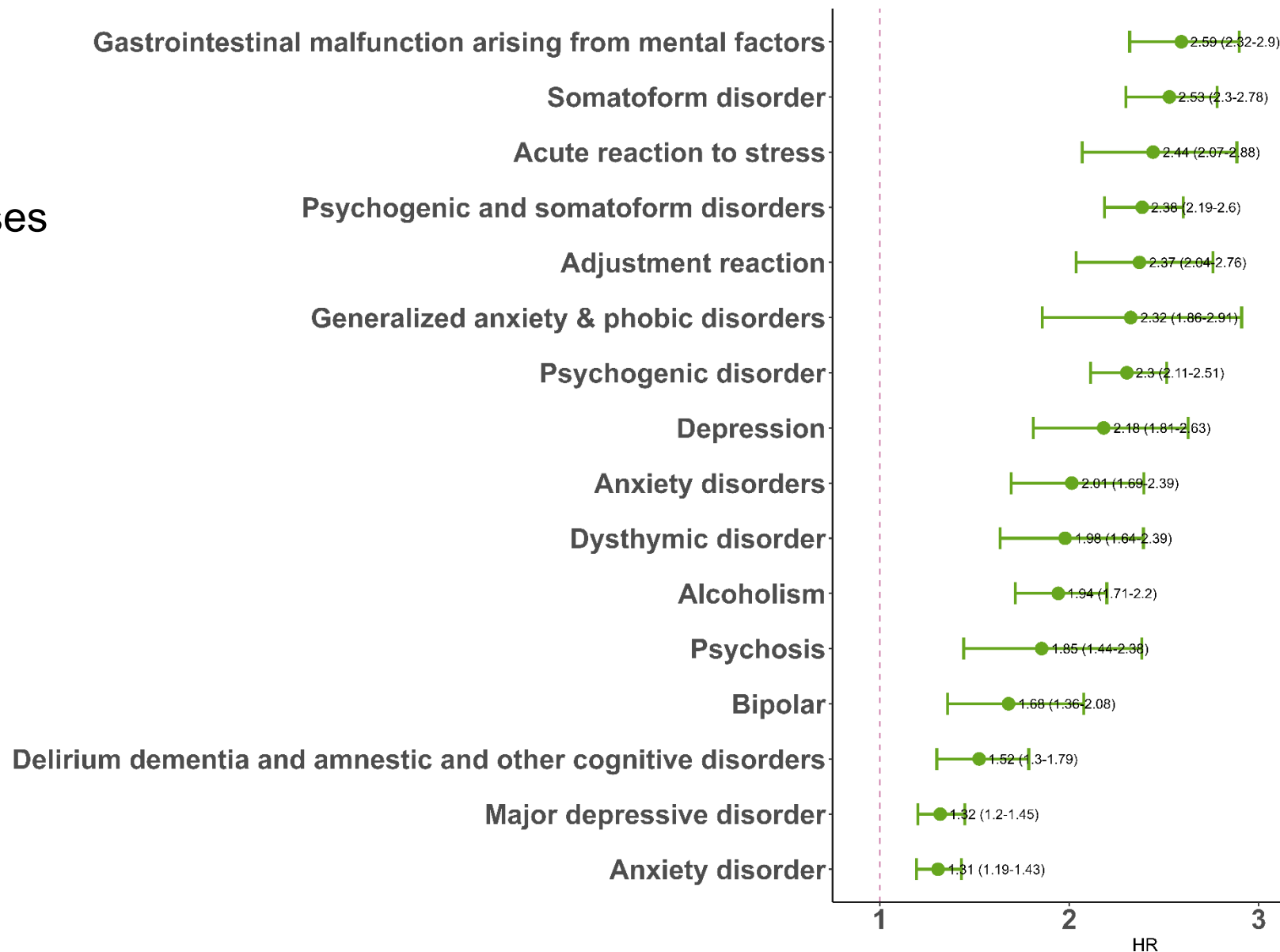
# Results 1: The comorbidity spectrum of AD

Many cardiometabolic diseases were associated with AD, including glucose and lipid disorder, cardiac dysrhythmias and heart failure.



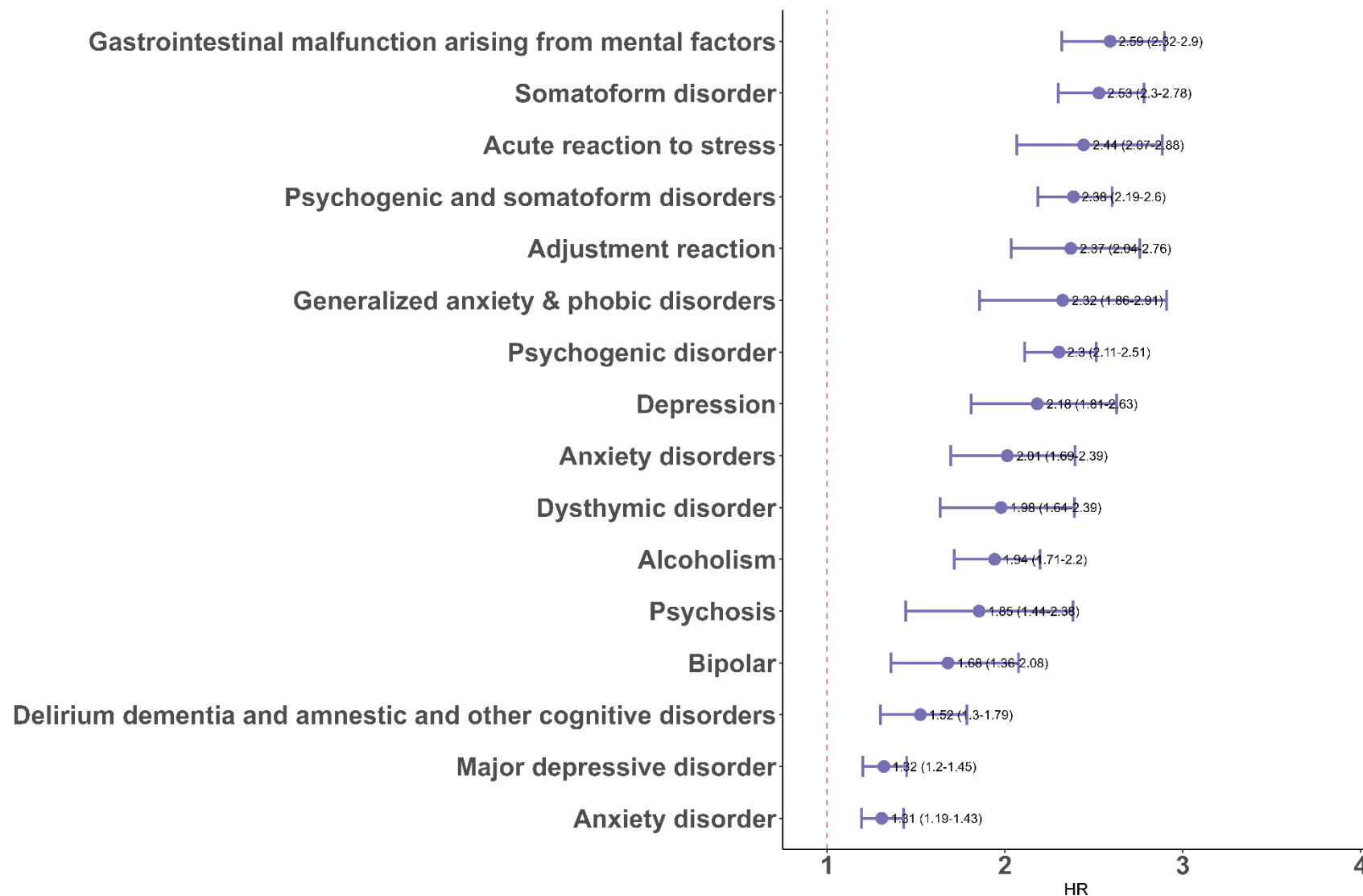
# Results 1: The comorbidity spectrum of AD

Digestive functional disorders, gastroenteritis and ulcers diseases are also associated with AD.



# Results 1: The comorbidity spectrum of AD

Diverse mental disorders were associated with AD, including acute reaction to stress, depression, anxiety and bipolar.



## Research Question 2:

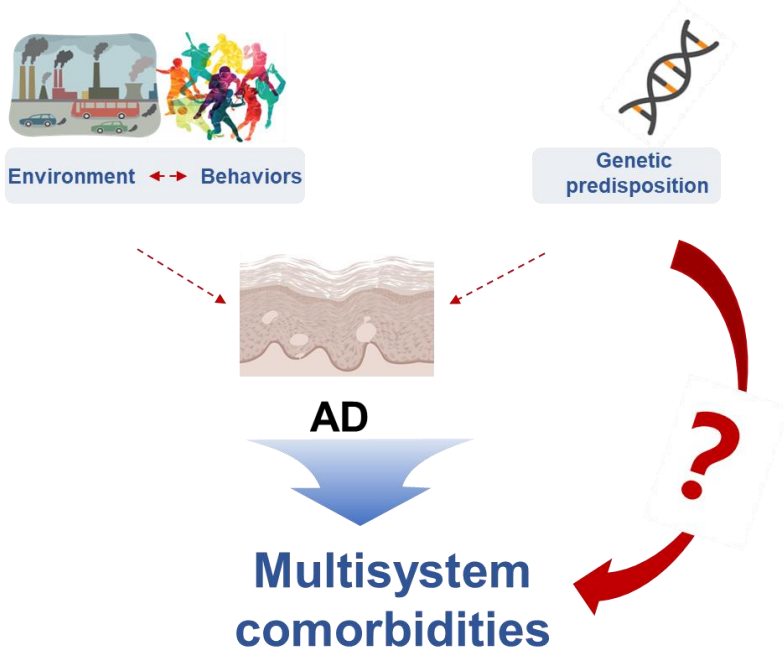
**How the genetic predisposition influence the comorbidities**

## Research Question 2: Genetic Relationship Between AD and Comorbidities



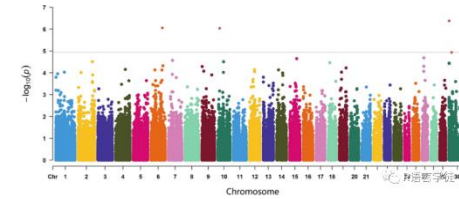
We conducted PRS-PheWAS, LDSC and two-sample Mendelian Randomization PheWAS.

### PRS-PheWAS

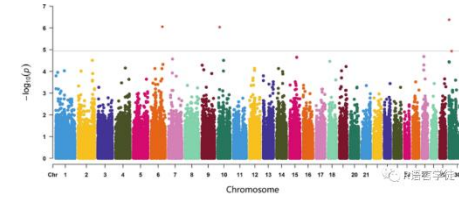


### LDSC

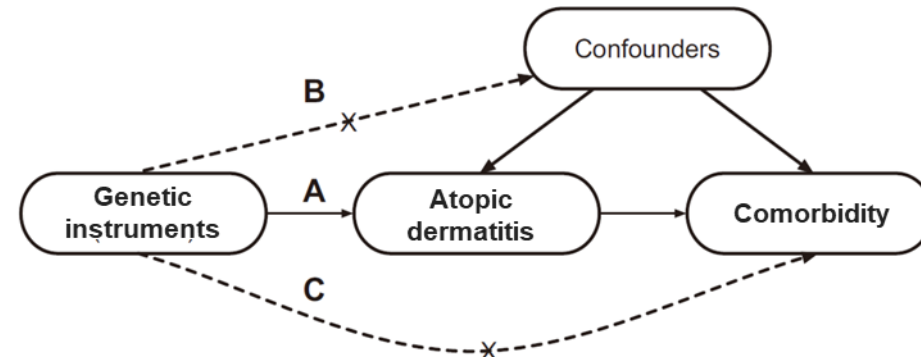
AD



Comorbidities



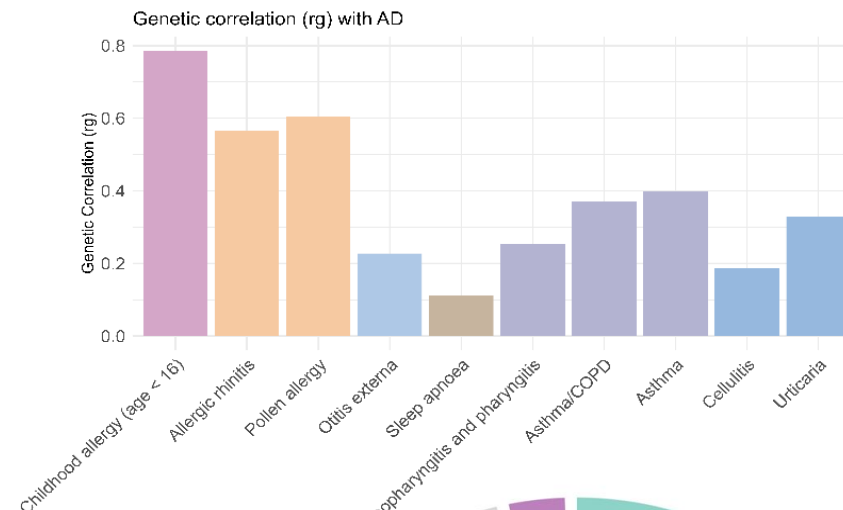
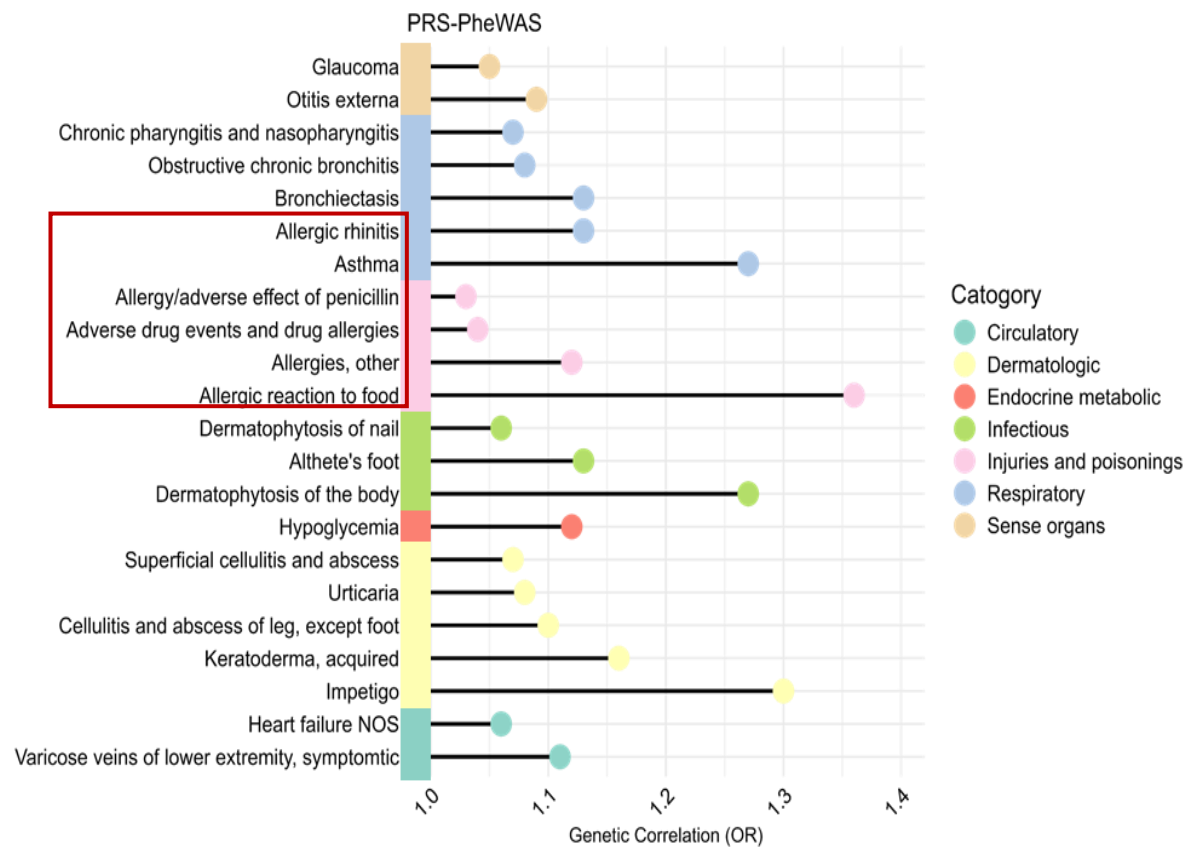
### TSMR-PheWAS



# Results 2: Genetic analysis

Significant correlation:

- Asthma, allergic rhinitis, urticaria and drug allergies.
- Infections in different system.



- **Scientific question 3:**
  - How the comorbidities sequence, evolve to form temporal trajectory?
  - How the comorbidities diverged to clusters and the genetic contributions?

# Results 3: Trajectory and clustering analysis

## Ensure the comorbidity strength

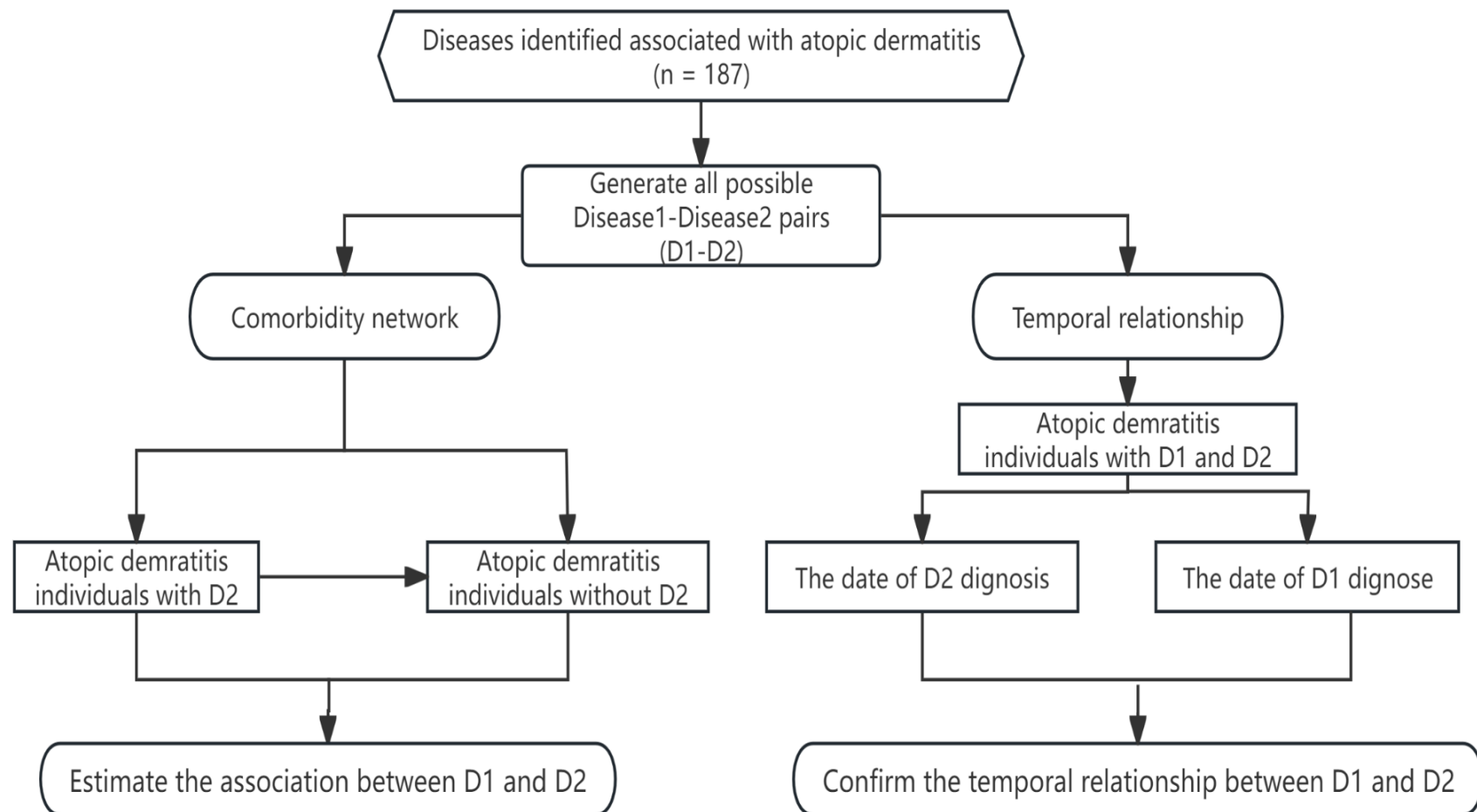
Relative risk (RR) and Pearson's correlation ( $\Phi$ -correlation) were calculated for each disease pair.

## Confirm chronological model

Binomial tests were utilized to identify the sequential order of Diseases1 and Disease2

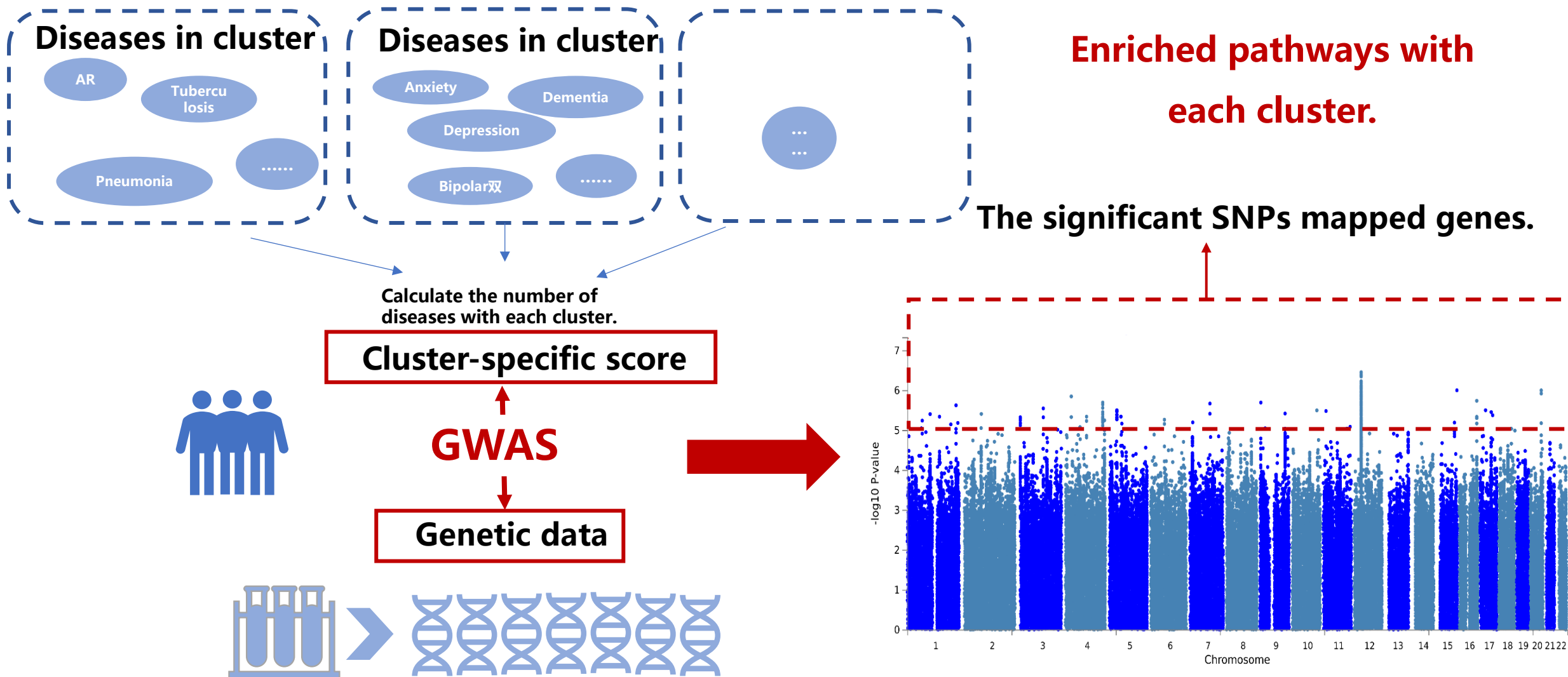
## Identify the strength of associations

Conditional logistic regressions were conducted to estimate the association between Disease1 and Disease2



# Results 3: Trajectory and clustering analysis

The genetic contributors underlying each cluster.



# Results 3: Trajectory and clustering analysis



3,526 disease pairs



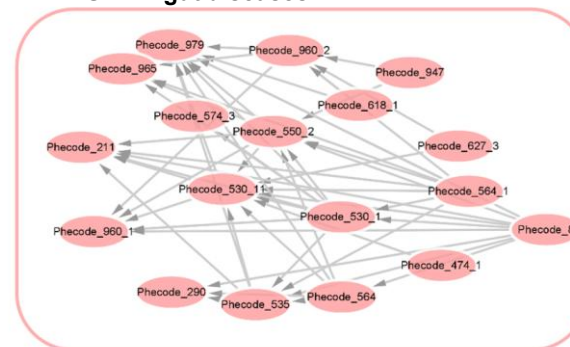
Louvain identified 5 clusters



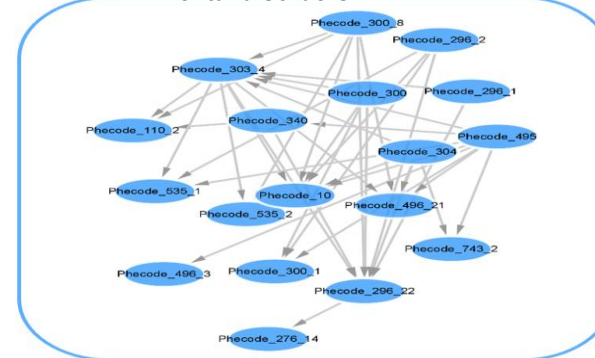
954 pairs with chorological relationships

AD

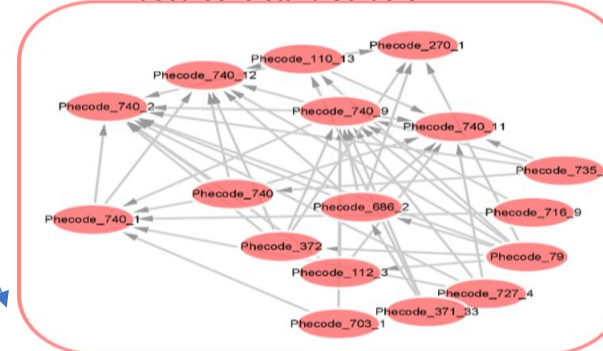
Skin – gut diseases



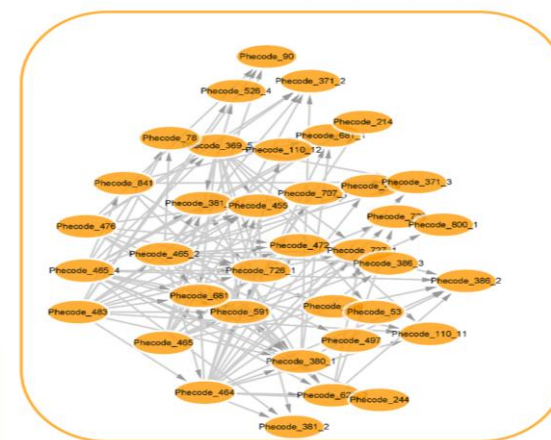
Mental disorders



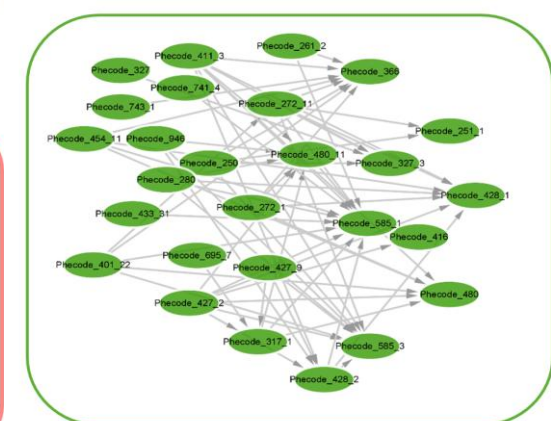
Musculoskeletal disorders



Infectious disease



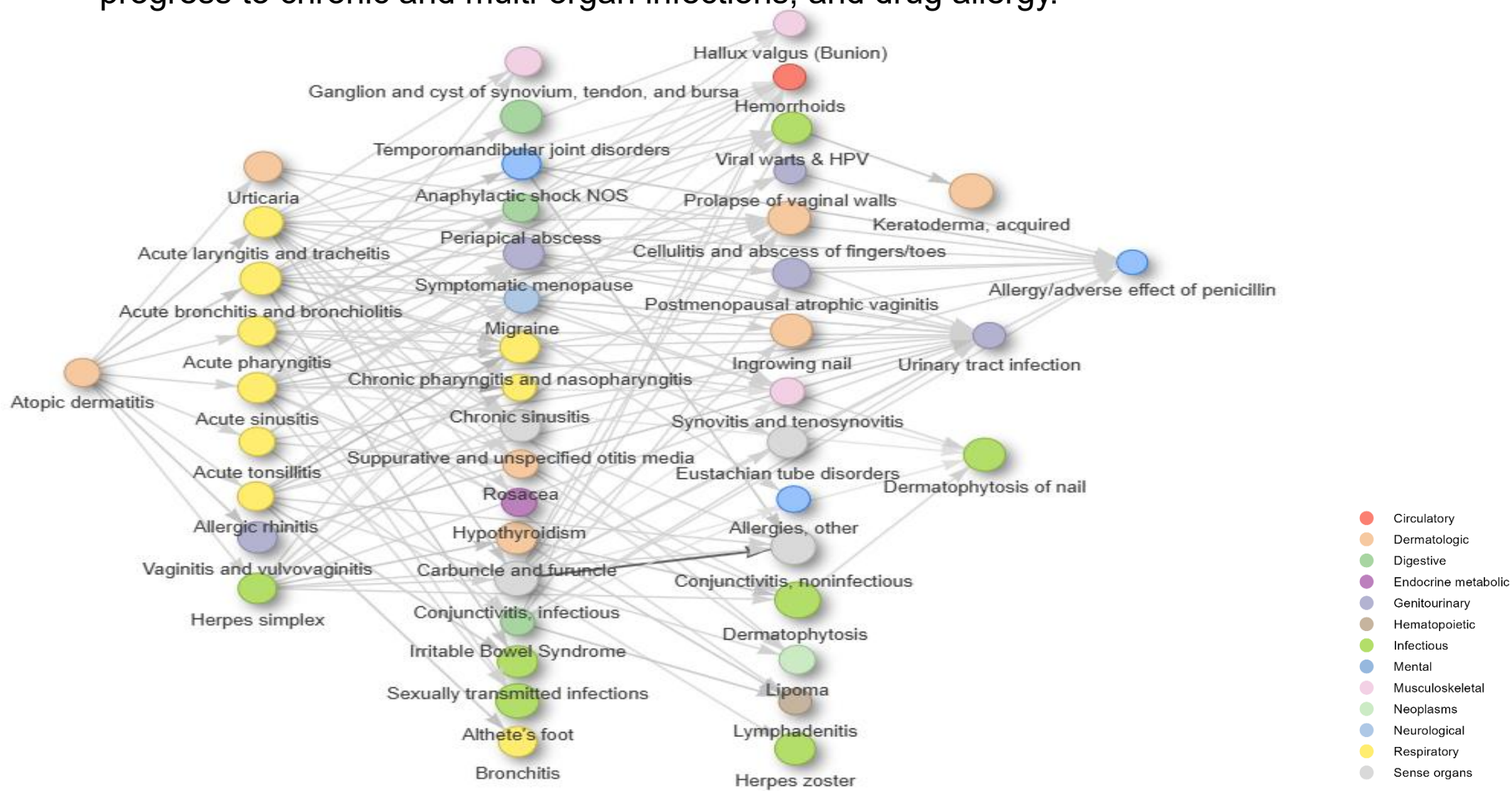
Cardiometabolic disease



# Results 3: Trajectory and clustering analysis

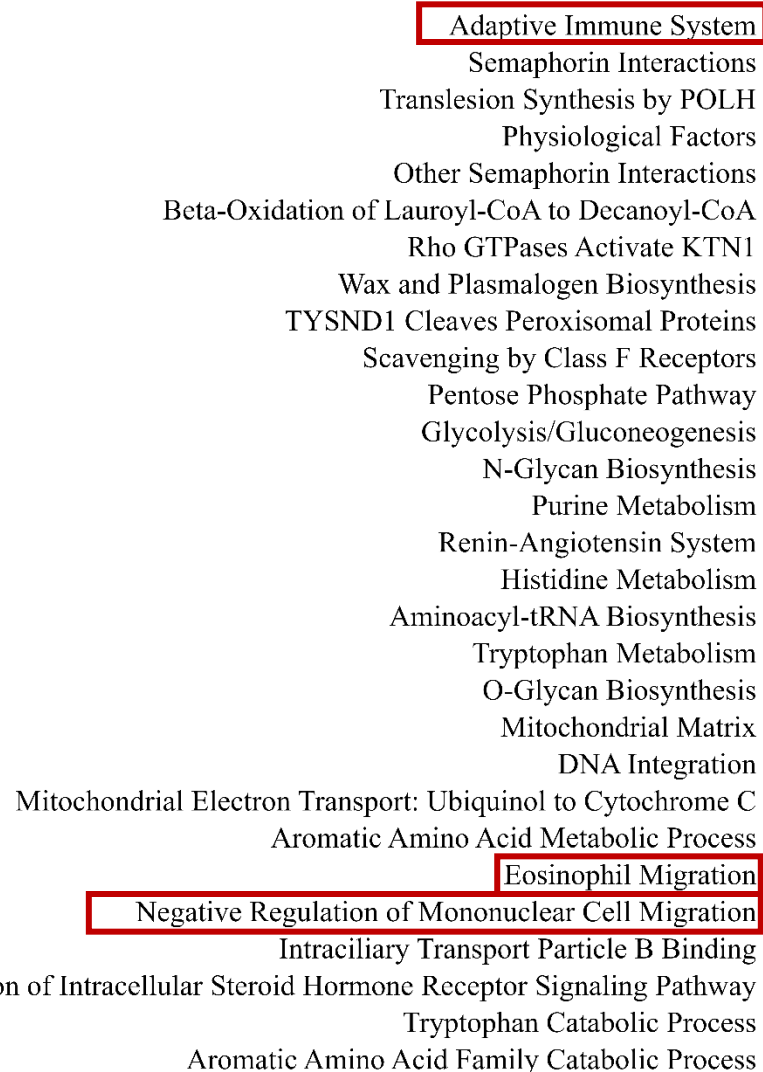
## Atopic and infectious cluster

This cluster start with AR, urticaria, and acute respiratory infections, subsequently progress to chronic and multi-organ infections, and drug allergy.



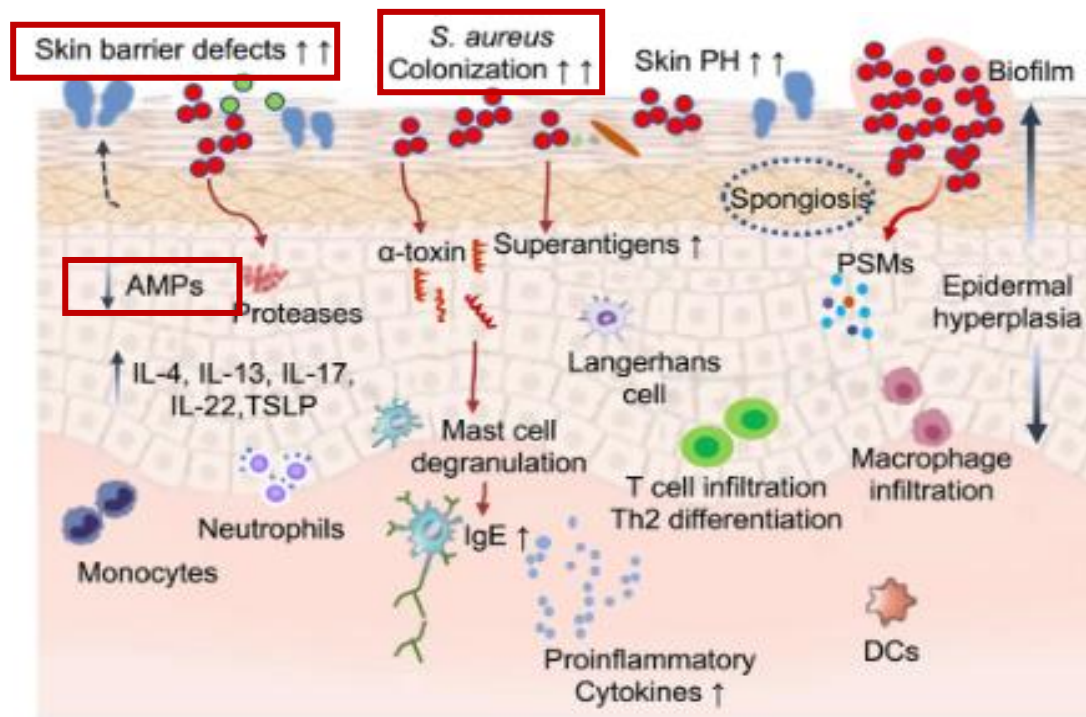
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### Atopic and infectious cluster

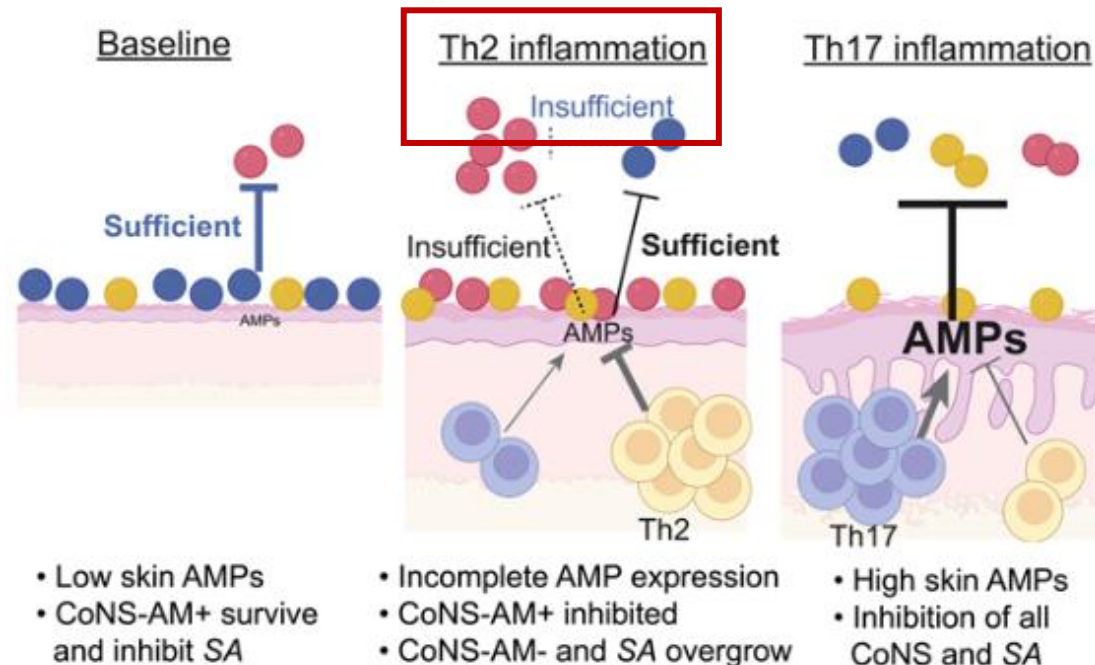


# Results 3: Trajectory and clustering analysis

Th2 immune activation often leads to barrier dysfunction, pH shifts, thereby increasing susceptibility to infection.



## AMPs shape the skin microbiome



For individuals with this comorbidity cluster, biologic agents targeting the Th2 related pathway may improve clinical prognosis.

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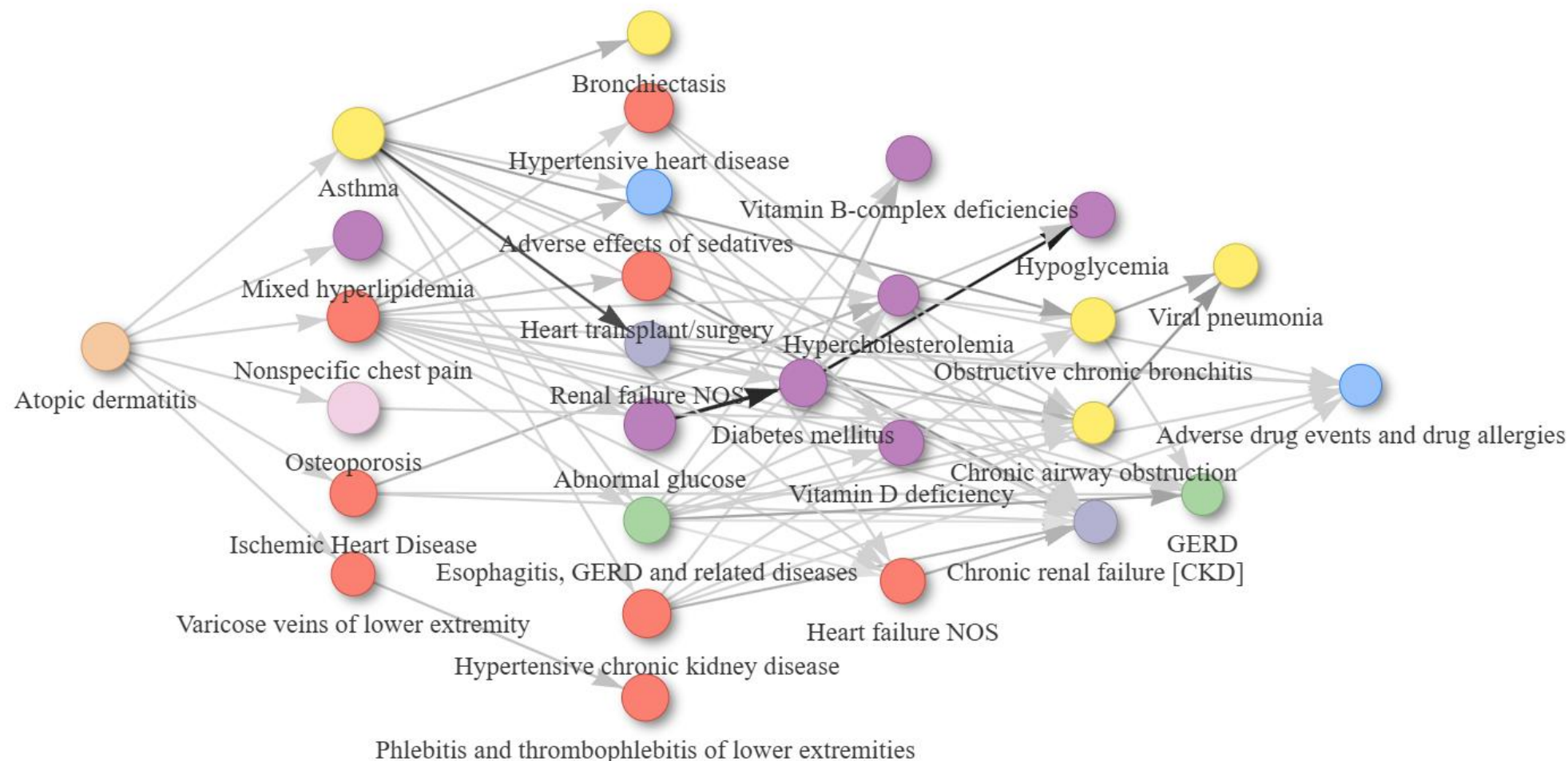
## The comorbidities of AD across different level of EOS



# Results 3: Trajectory and clustering analysis

## Cardiometabolic disorders

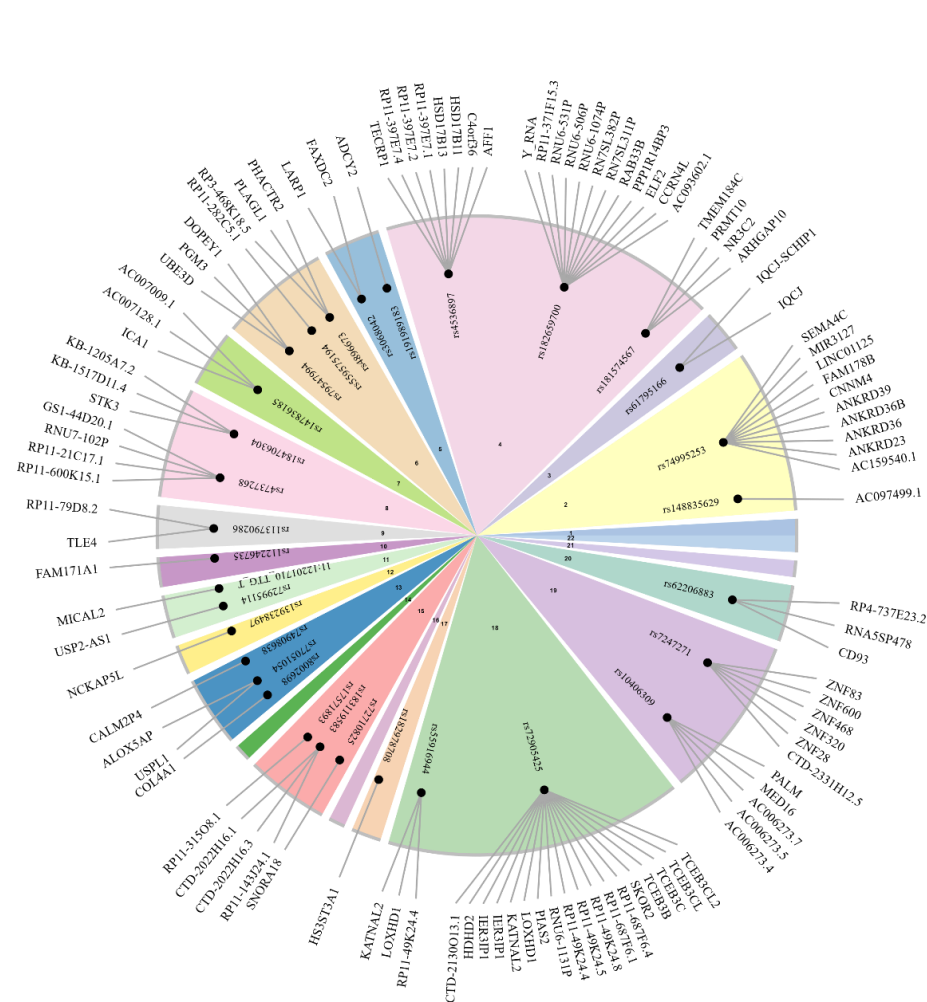
The cardiometabolic cluster characterized by glucose-lipid dysregulation, and ischemic heart disease, ultimately progressing to heart and renal failure.



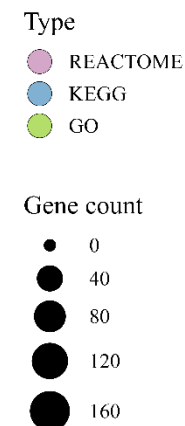
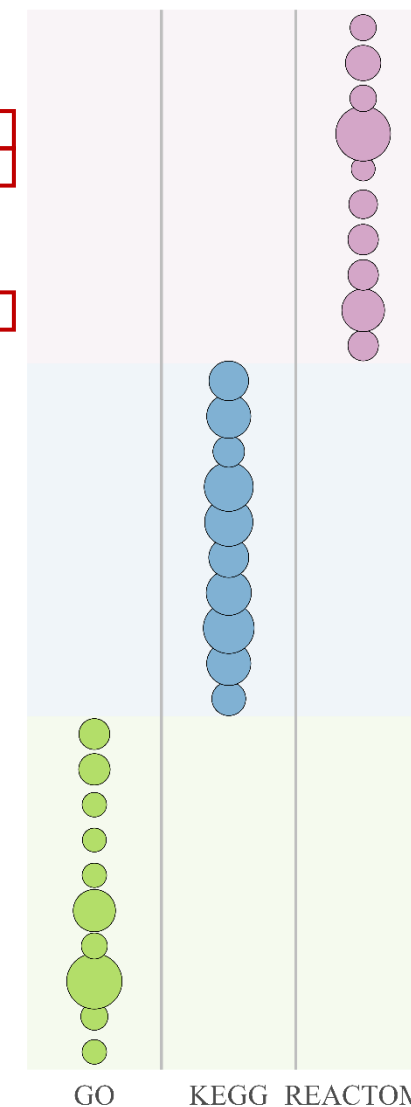
# Results 3: Trajectory and clustering analysis

Fatty acid, senescence were enriched in this cluster.

Cardiometabolic cluster

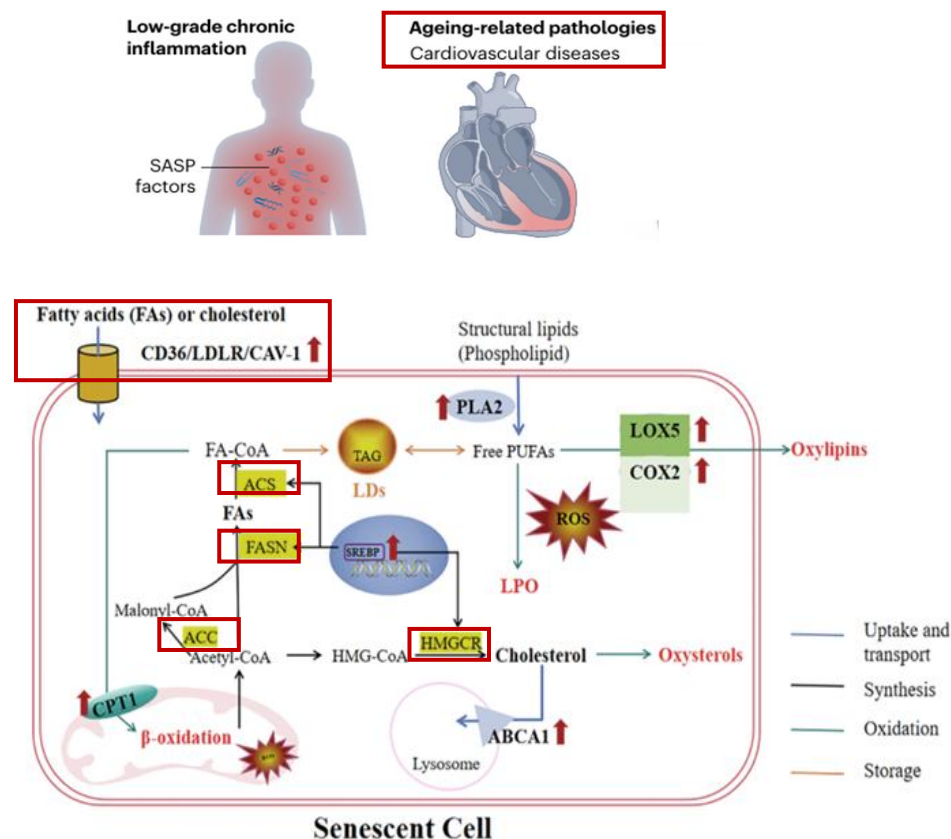
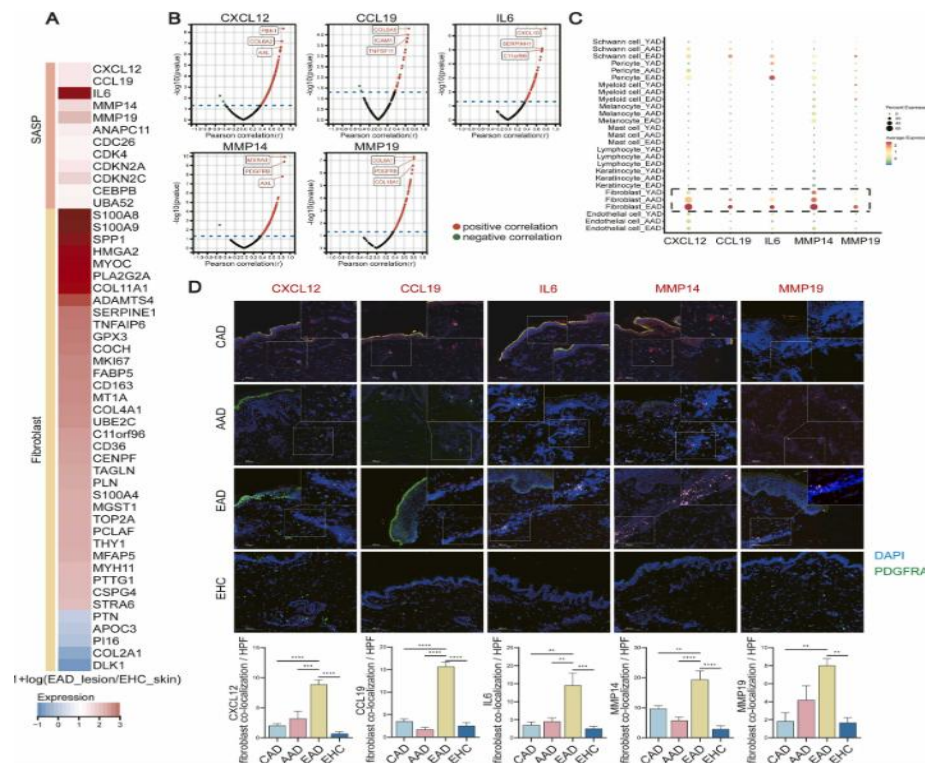


Ionotropic Activity of Kainate Receptors  
Diseases of Mitotic Cell Cycle  
Zinc Influx into Cells by the SLC39 Gene Family  
Cellular Senescence  
Free Fatty Acid Receptors  
Zinc Transporters  
Conversion from APC/C:CDC20 to APC/C:CDH1 in Late Anaphase  
Phosphorylation of the APC/C  
Senescence-Associated Secretory Phenotype (SASP)  
Aberrant Regulation of Mitotic Exit in Cancer Due to RB1 Defects  
RNA Degradation  
Hypertrophic Cardiomyopathy (HCM)  
Pentose Phosphate Pathway  
Vascular Smooth Muscle Contraction  
Oocyte Meiosis  
NOD-Like Receptor Signaling Pathway  
Dilated Cardiomyopathy  
Ubiquitin-Mediated Proteolysis  
Progesterone-Mediated Oocyte Maturation  
Alanine, Aspartate and Glutamate Metabolism  
Anaphase-Promoting Complex  
Zinc Ion Transmembrane Transporter Activity  
Beta-2 Adrenergic Receptor Binding  
MCRD-Mediated mRNA Stability Complex  
Regulation of Phospholipid Translocation  
Striated Muscle Cell Development  
G Protein-Coupled Opioid Receptor Signaling Pathway  
Aging  
Acetylcholine Receptor Binding  
G Protein-Coupled Opioid Receptor Activity



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**Chronic, mixed, low-grade inflammation may compromise cardiovascular health.**

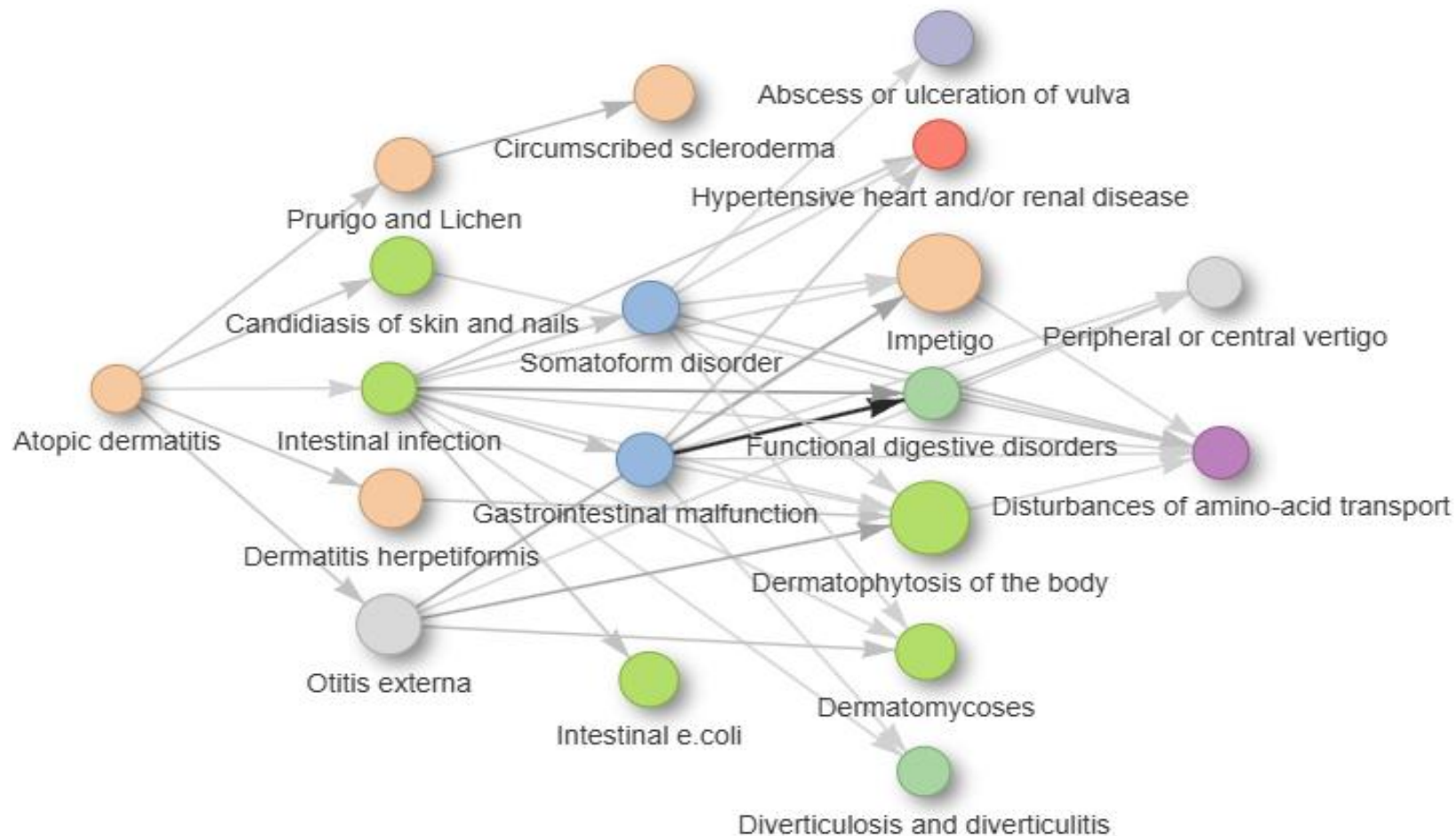


*J Dermatol Sci.* 2024 Jun;114(3):94-103; *Nat Rev Mol Cell Biol.* 2024 Dec;25(12):958-978; *Ageing Res Rev.* 2024 Jun;97:102294

# Results 3: Trajectory and clustering analysis

## Skin-gut cluster

This cluster consisted of initiated skin and gut infections and subsequent functional digestive disorders.

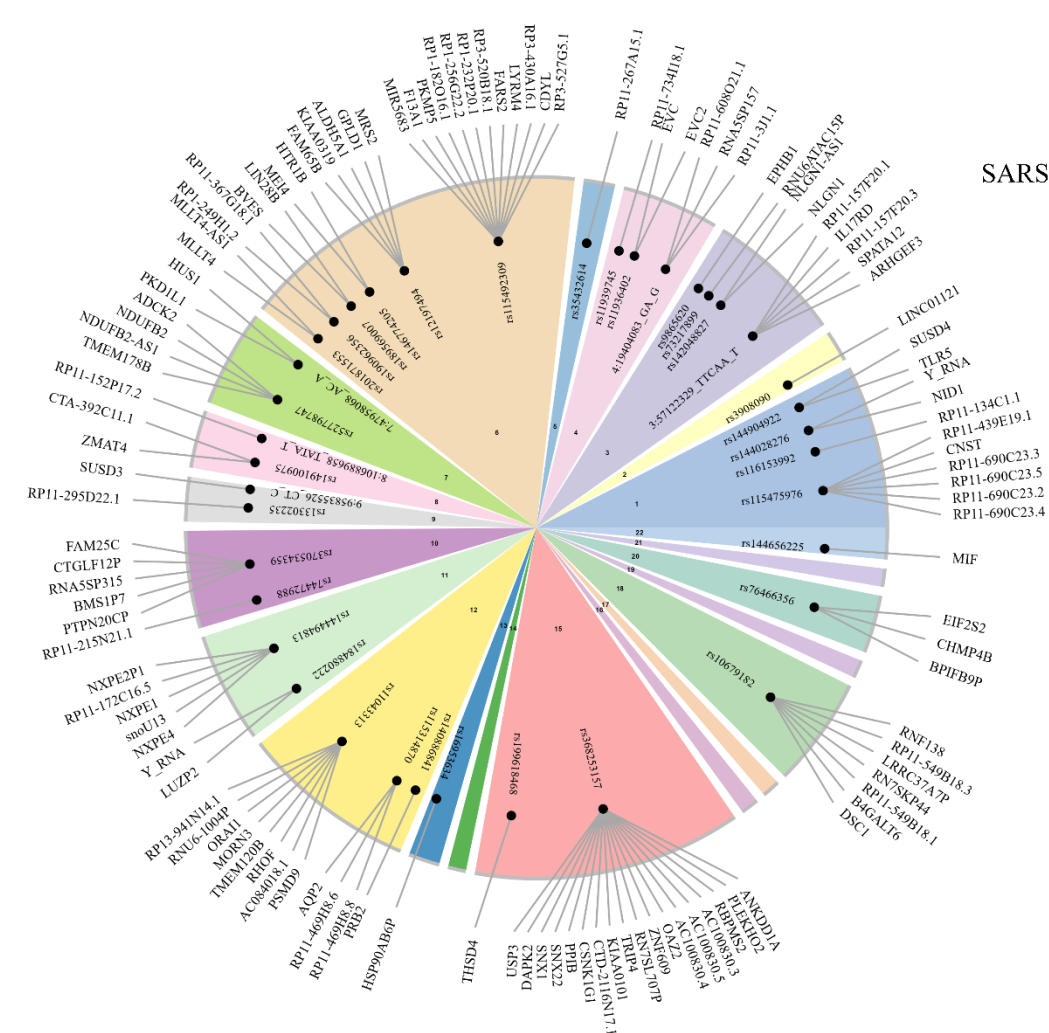


- Circulatory
- Dermatologic
- Digestive
- Endocrine metabolic
- Genitourinary
- Hematopoietic
- Infectious
- Mental
- Musculoskeletal
- Neoplasms
- Neurological
- Respiratory
- Sense organs

# Results 3: Trajectory and clustering analysis

Toll-like receptor and tight junctions were enriched.

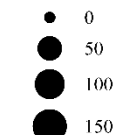
Skin-gut cluster



Vitamin C (Ascorbate) Metabolism  
CREB Phosphorylation  
Suppression of Apoptosis  
LDL Clearance  
SARS-CoV-1 Targets Host Intracellular Signaling and Regulatory Pathways  
PINK1-PRKN Mediated Mitophagy  
Toll-Like Receptor Cascades  
DNA Replication Initiation  
Infection with Mycobacterium tuberculosis  
Response of MTb to Phagocytosis  
Tight Junction  
Nicotinate and Nicotinamide Metabolism  
NOD-Like Receptor Signaling Pathway  
Primary Immunodeficiency  
Other Glycan Degradation  
DNA Replication  
Nucleotide Excision Repair  
ADP Transmembrane Transporter Activity  
Toll-Like Receptor Binding  
Plasma Membrane Raft  
Transcription Factor TFIIH Holo Complex  
Recycling Endosome  
Protein Serine/Threonine Kinase Binding  
Early Endosome Membrane  
UDP-Glucose Metabolic Process  
Regulation of Germinal Center Formation  
Epsilon DNA Polymerase Complex



Gene count

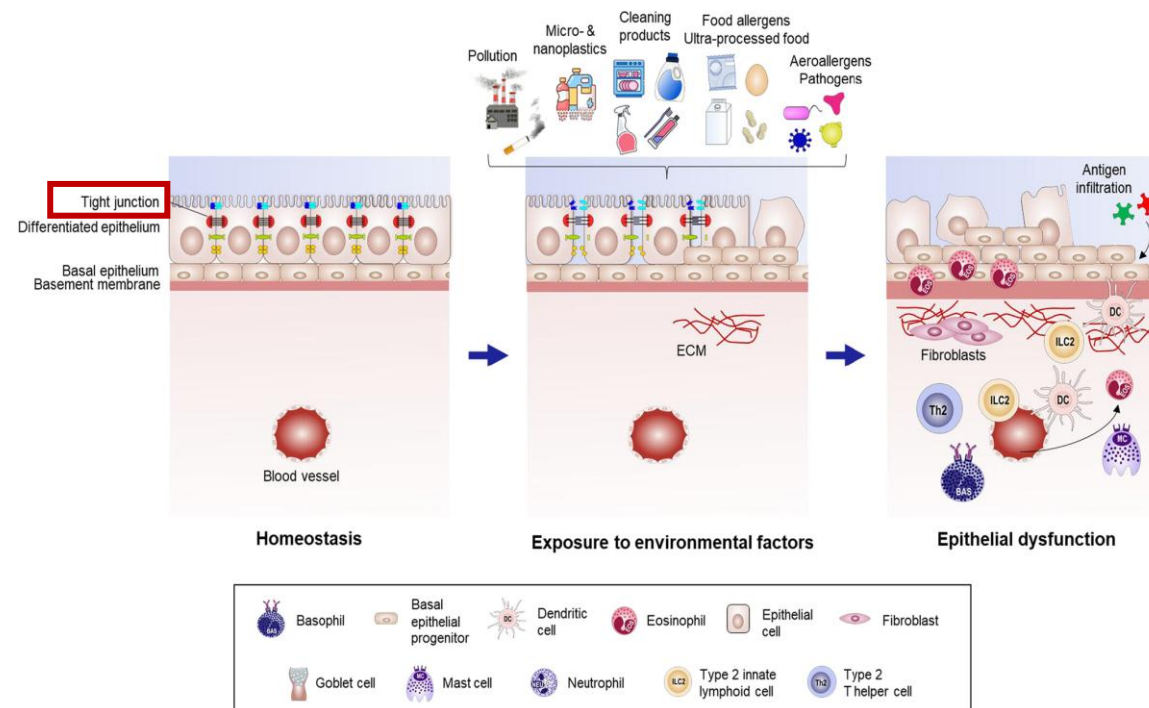
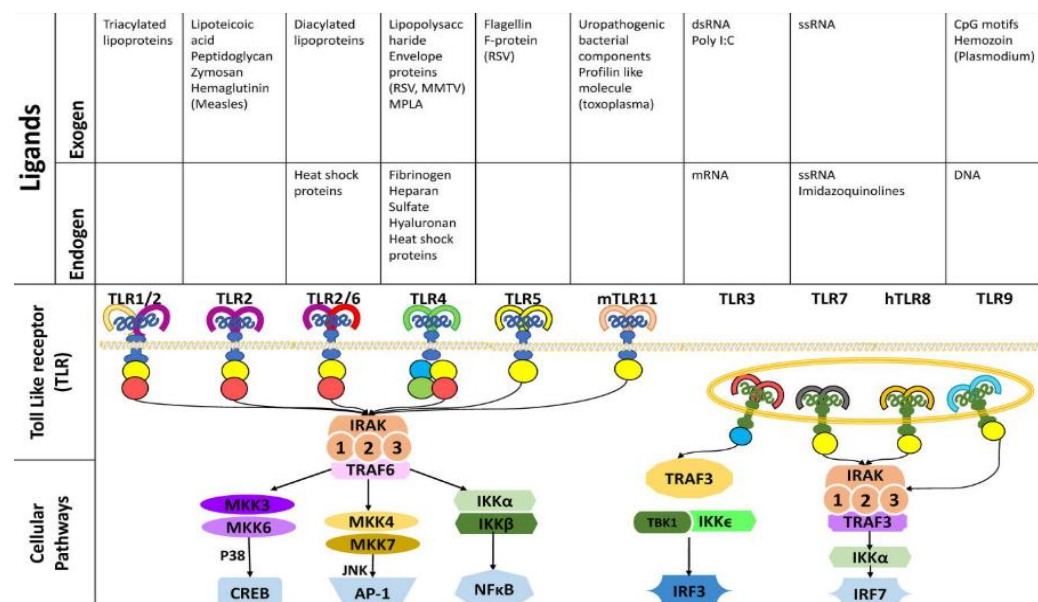


Type



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**Tight junctions are an integral component of the cutaneous barrier.**

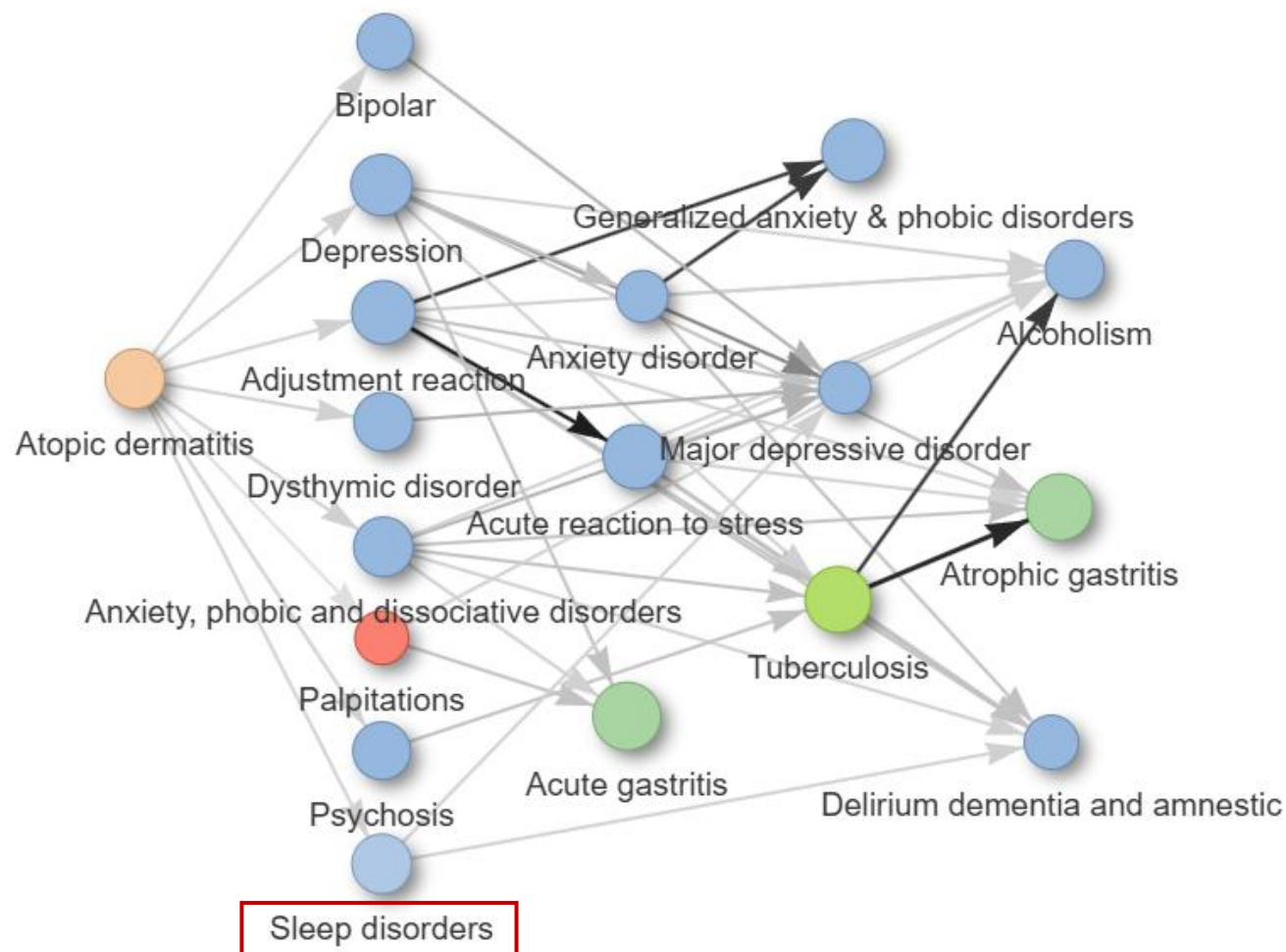


**Treatment should focus on enhancing innate immune mechanisms and preserving barrier integrity.**

# Results 3: Trajectory and clustering analysis

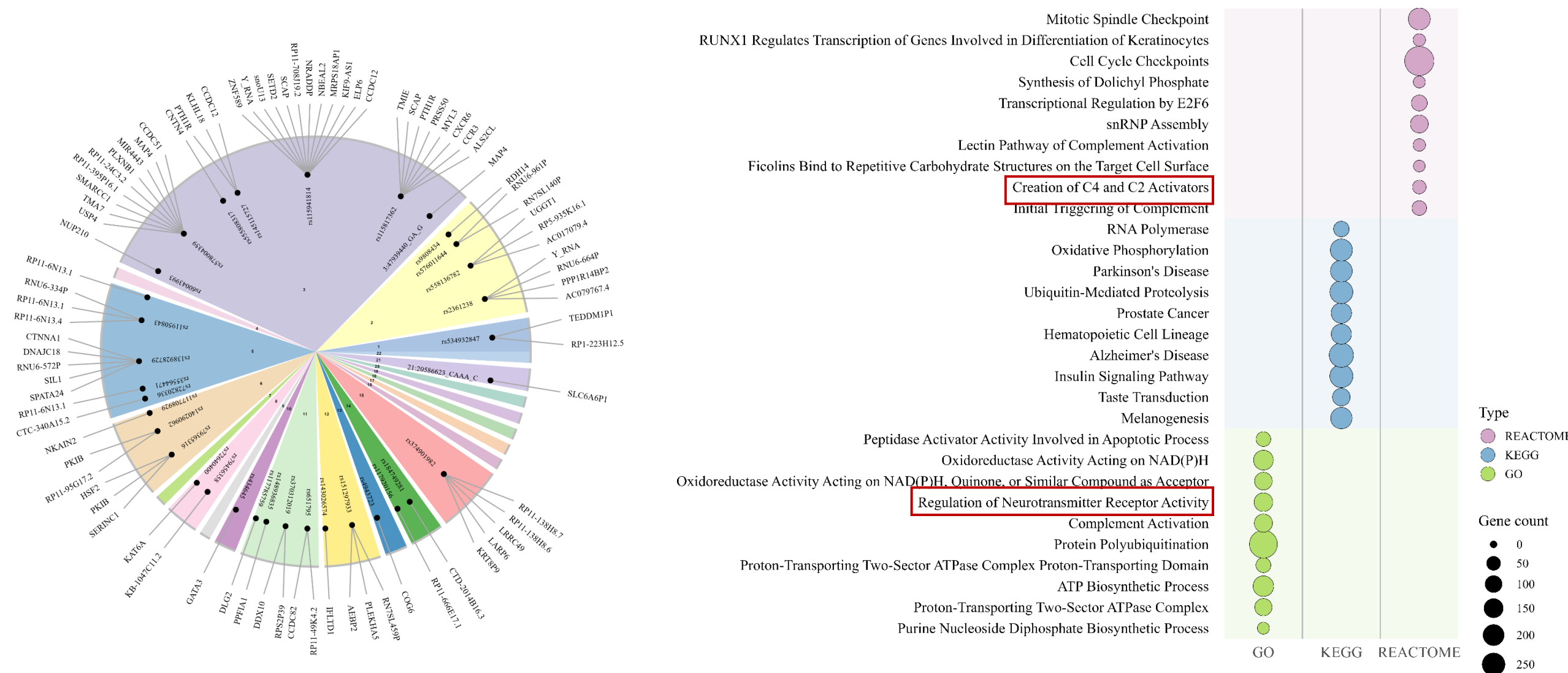
## Mental cluster

This cluster included initiated sleep disorder, anxiety, depression, progressed to major depressive disorder, and medications-related side effects and ultimately evolved to dementia.



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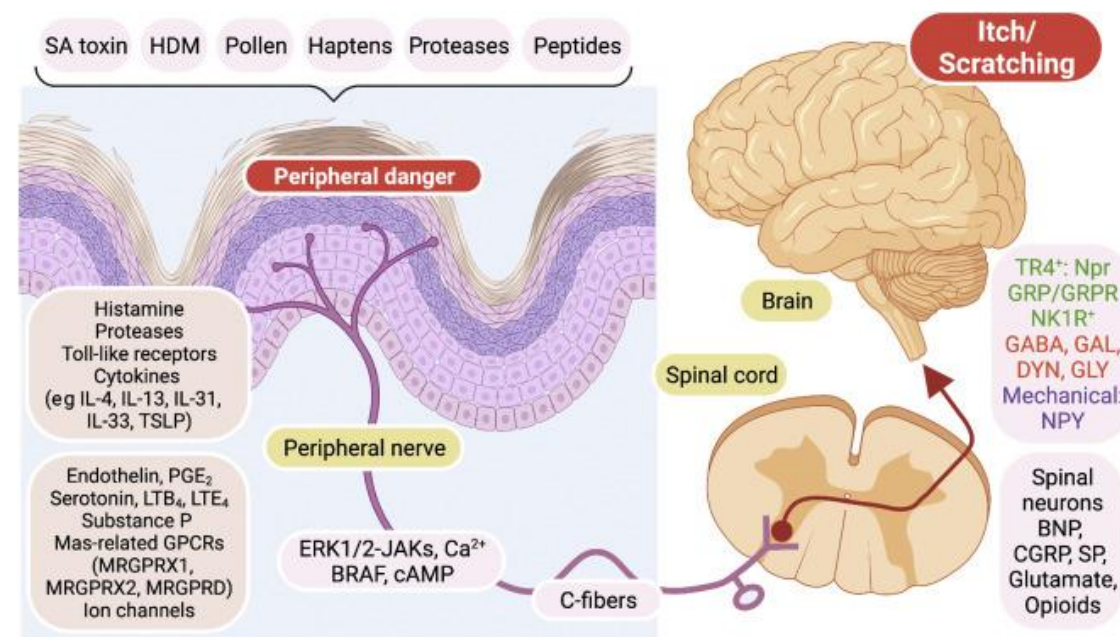
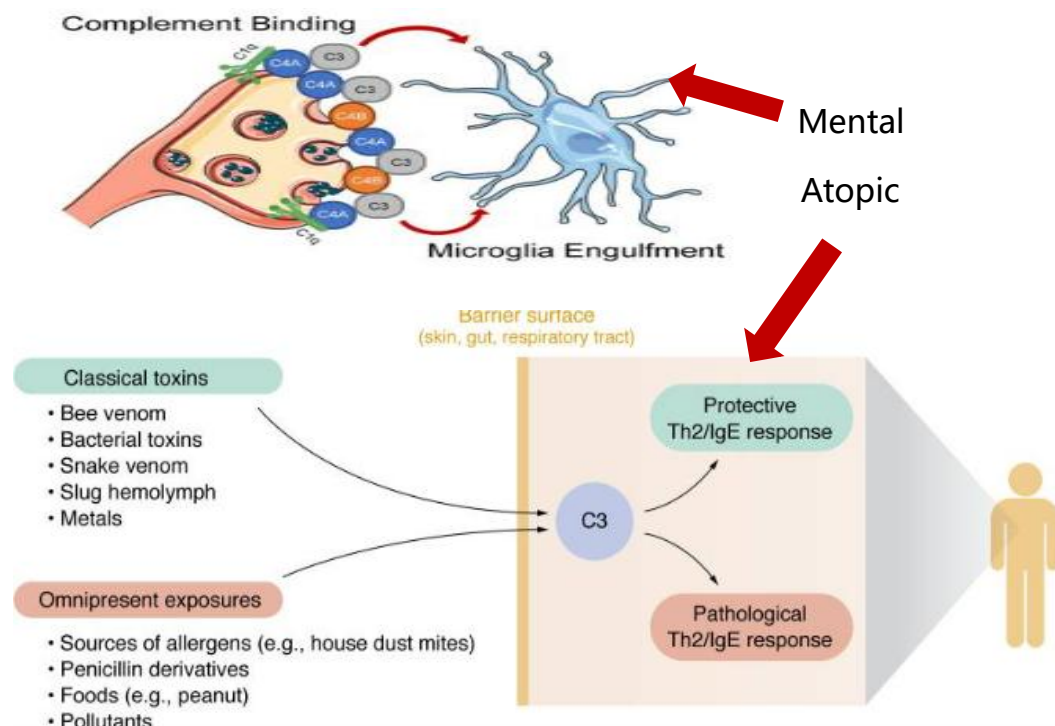
### Mental cluster



# Results 3: Trajectory and clustering analysis

Complement activation is both associated with allergic responses and psychiatric disorders.

Persistent pain and itch in AD may modulate the function of neurotransmitter receptor, thereby contributing to mental comorbidity.

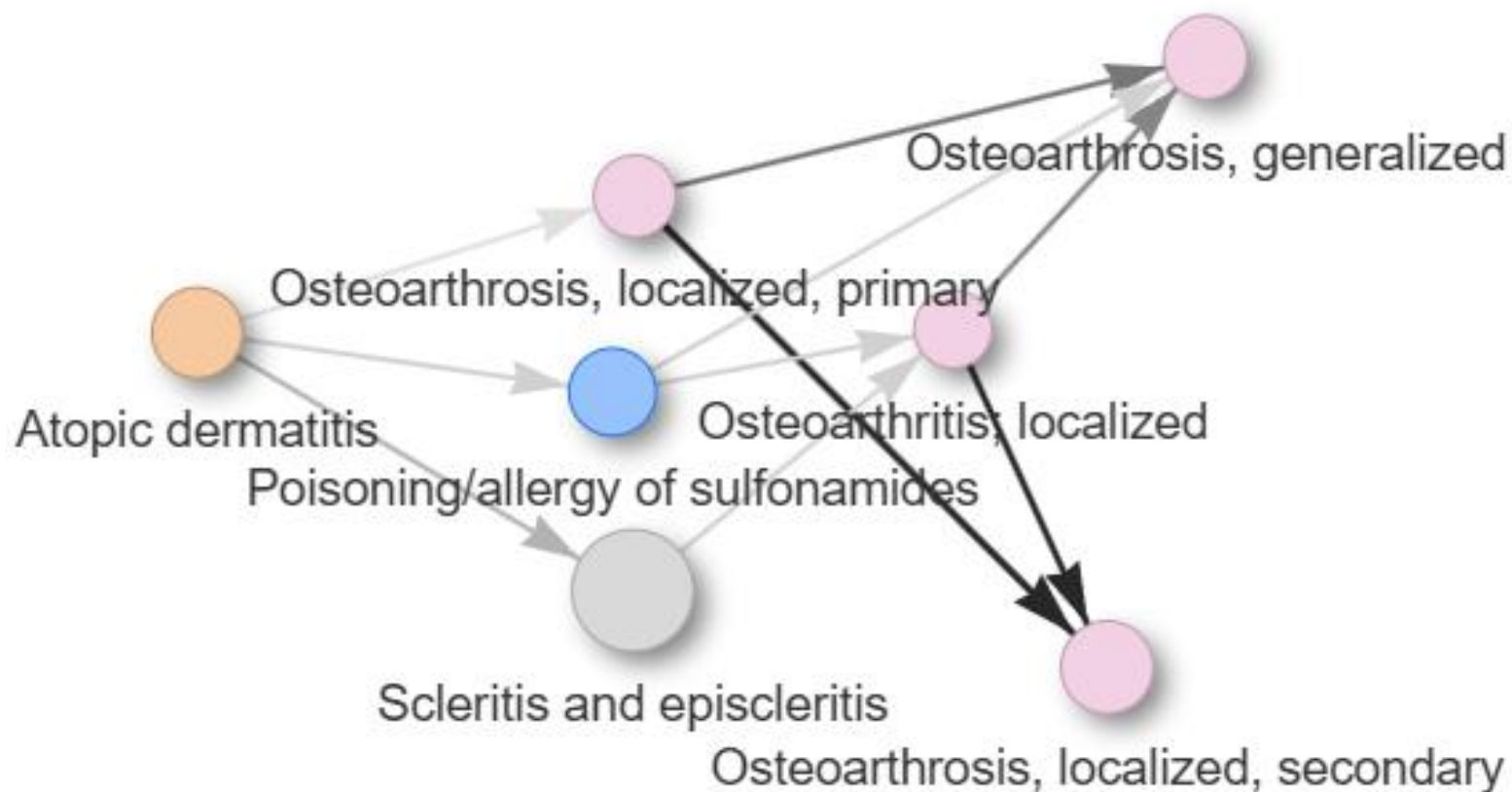


**Early screening** of mental diseases especially the sleep disorder, and suggest the interventions targeted **on inflammation–neural response** interactions.

# Results 3: Trajectory and clustering analysis

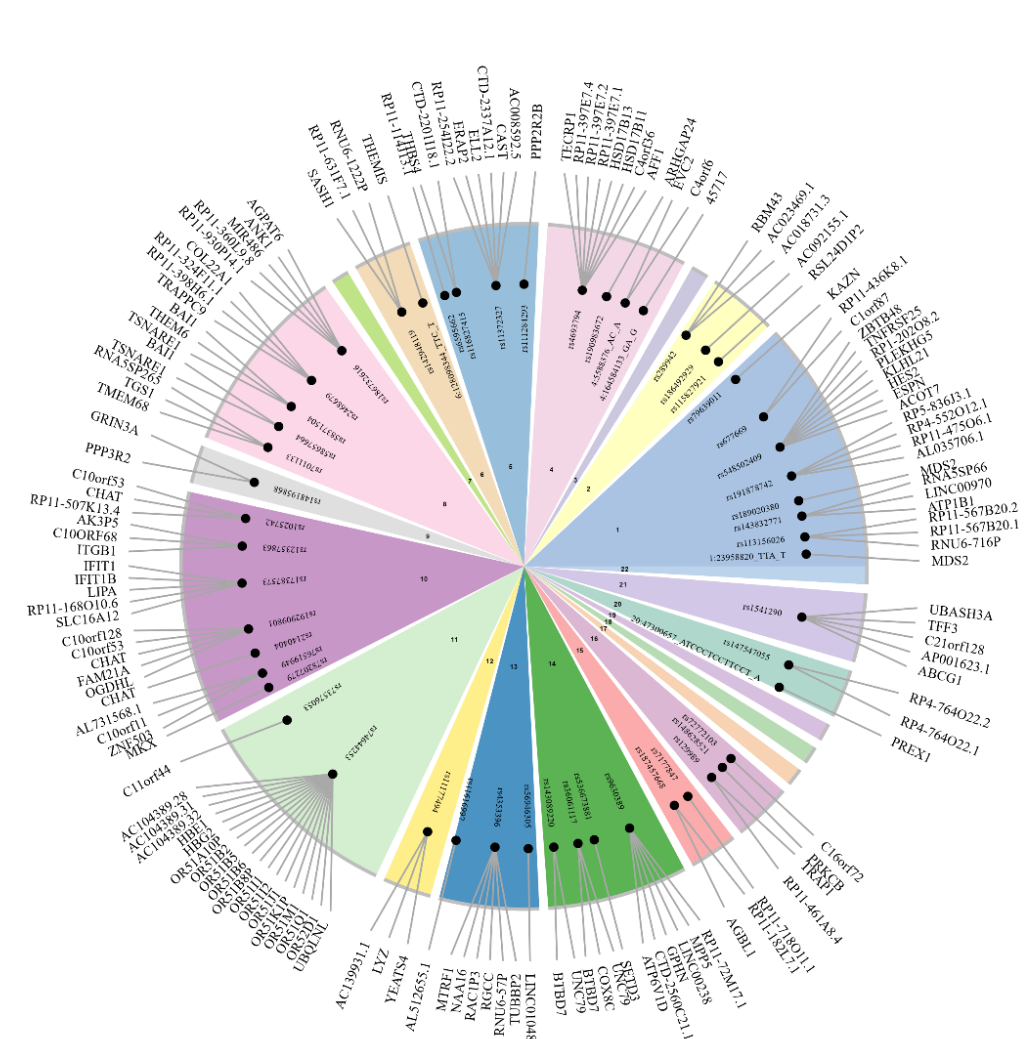
## • Musculoskeletal cluster

Musculoskeletal cluster demonstrated a trajectory of osteoarthritis progressing from primary and localized stage to generalized and secondary forms.



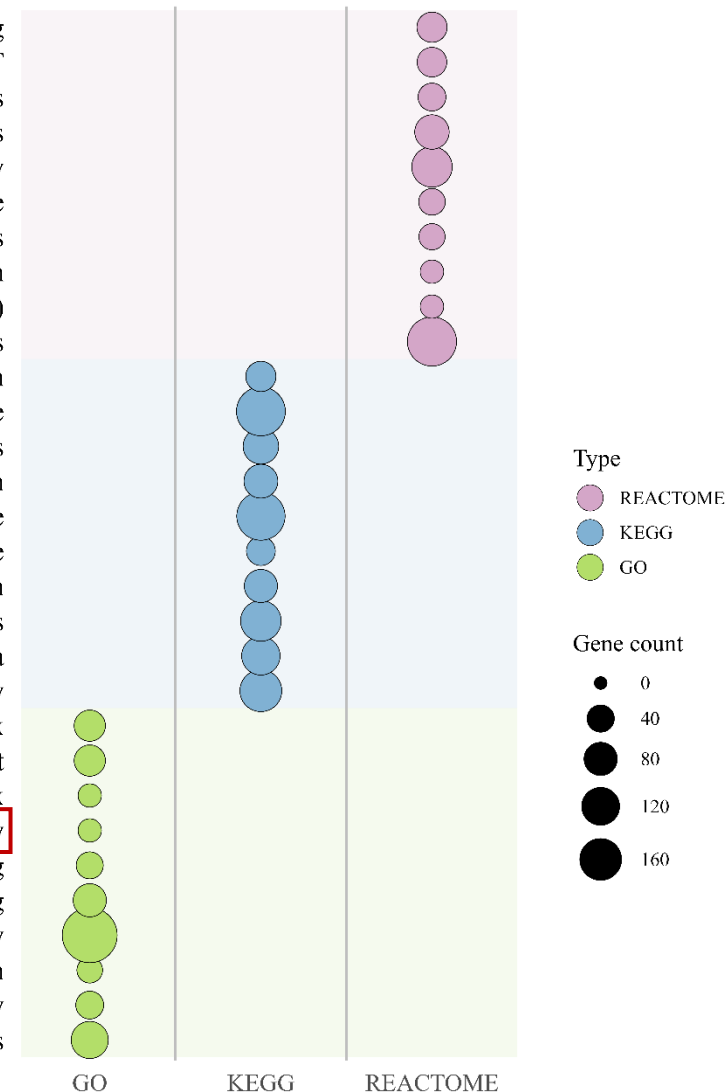
# Results 3: Trajectory and clustering analysis

Estrogen activity was enriched.



PD-1 Signaling  
Rho GTPases Activate CIT  
Peptide Hormone Biosynthesis  
O-Glycosylation of TSR Domain-Containing Proteins  
Costimulation by the CD28 Family  
Signaling by FGFR4 in Disease  
Organic Anion Transporters  
CD22-Mediated BCR Regulation  
Diseases of Mismatch Repair (MMR)  
Metabolism of Water-Soluble Vitamins and Cofactors  
Nitrogen Metabolism  
Spliceosome  
Type I Diabetes Mellitus  
Allograft Rejection  
Lysosome  
One-Carbon Pool by Folate  
Alanine, Aspartate, and Glutamate Metabolism  
Viral Myocarditis  
Acute Myeloid Leukemia  
B Cell Receptor Signaling Pathway  
Myosin II Complex  
Myosin Filament  
Alpha/Beta T Cell Receptor Complex  
**Estrogen 2-Hydroxylase Activity**  
Myosin II Binding  
Fibronectin Binding  
Antigen Receptor-Mediated Signaling Pathway  
Serotonin Secretion  
NAD<sup>+</sup> Nucleosidase Activity  
Hydrogen Peroxide Metabolic Process

Atopic and infectious



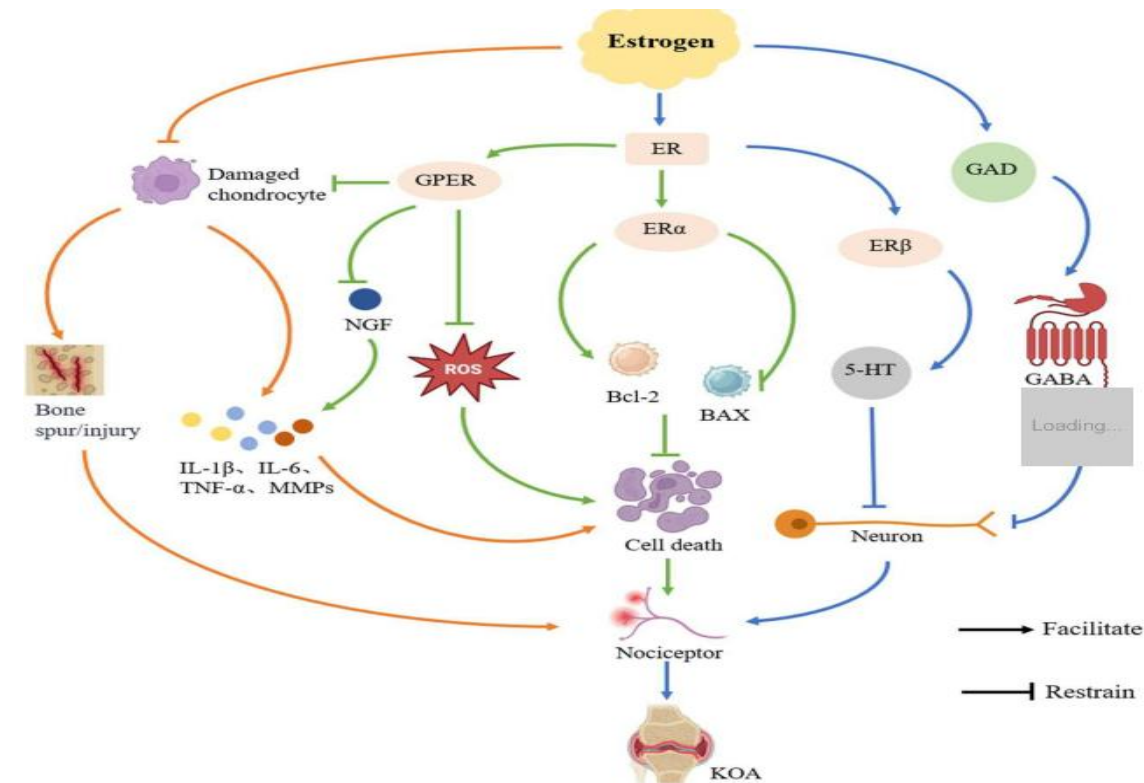
# Results 3: Trajectory and clustering analysis

A study reported that women with AD have lower estrogen levels than healthy controls.

Estrogen withdrawal has been associated with osteoarthritis

Comparison of hormone results during minipuberty between girls with AD and girls in the control group.

	Girls with AD		Control girls		P
	Mean ± SD	Median (Q1–Q3)	Mean ± SD	Median (Q1–Q3)	
Age (weeks)	9 ± 2.3	9 (8–11)	7.7 ± 2.4	7 (6–10)	0.082
Weight (kg)	5.7 ± 0.67	5.6 (5.1–6.4)	4.9 ± 0.66	4.9 (4.5–5.2)	<0.001
Length (cm)	57.3 ± 2.7	56 (55–59)	54.1 ± 2.99	54 (52–55)	0.001
BMI (kg/m <sup>2</sup> )	17.4 ± 1.3	17.1 (16.3–18.3)	16.6 ± 1.3	16.6 (15.6–17.4)	0.049
Weight SDS	0.87 ± 0.91	0.68 (0.34–1.57)	0.25 ± 0.95	0.23 (–0.52 to 0.97)	0.03
Length SDS	–0.2 ± 0.8	–0.15 (–0.9 to 0.54)	–0.83 ± 1.02	–0.83 (–1.75 to –0.06)	0.024
Weight-for-length SDS	1.12 ± 0.81	1.13 (0.52–1.69)	1.2 ± 0.93	1.28 (0.55–2.09)	0.759
FSH (U/L)	5.43 ± 4.32	3.83 (2.48–7.22)	7.1 ± 7.91	3.74 (2.07–10.4)	0.869*
LH (U/L)	0.34 ± 0.38	0.2 (0.1–0.4)	1.2 ± 2.42	0.4 (0.1–0.9)	0.353*
Estradiol (ng/L)	6.8 ± 4.4	5 (5–6.4)	9.4 ± 5.1	7.9 (5–12.4)	0.023*
Testosterone (μg/L)	7.3 ± 9.7	2.5 (2.5–12.7)	10.7 ± 10.1	8.5 (2.5–15.3)	0.056*
Prolactin (μg/L)	35.7 ± 32.1	31 (15–41)	37.4 ± 14.1	32 (26–49)	0.223*
DHEA-S (μg/dL)	41.1 ± 33.1	27 (18–56)	56.2 ± 44.5	39 (26–65)	0.099*
TSH (mU/L)	3.57 ± 2	2.93 (2.2–4.89)	2.3 ± 1.9	1.9 (0.58–4.37)	0.034
FT4 (ng/L)	13.8 ± 1.4	13.7 (12.6–15)	16.2 ± 2.4	16.4 (14.5–18.2)	<0.001

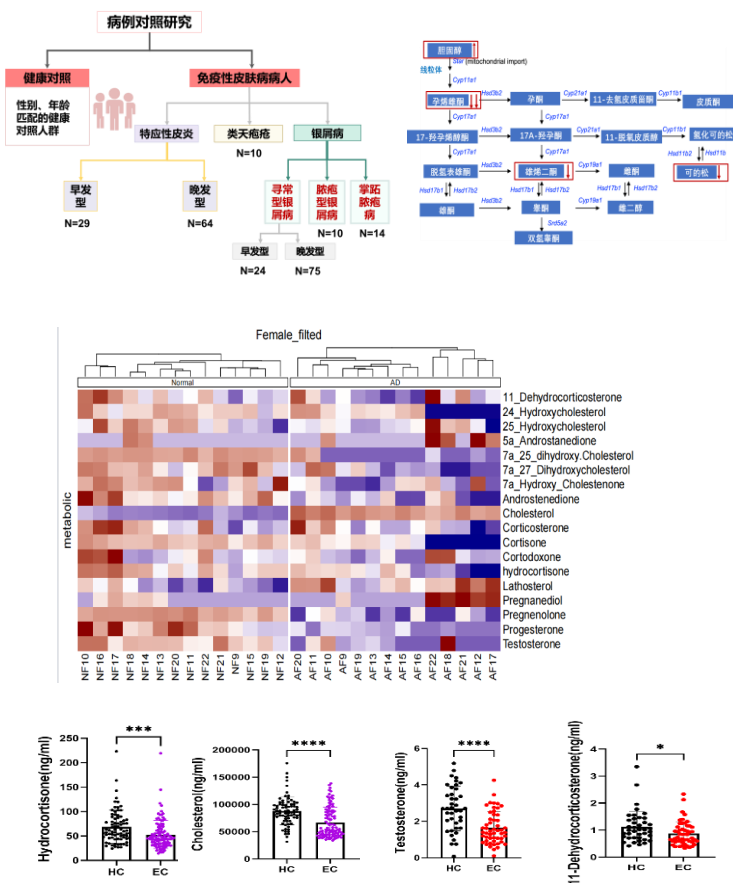


A subset of women with AD may exhibit hormonal dysregulation, for whom hormone-targeted (particularly estrogen-modulating) therapies could be therapeutically relevant.

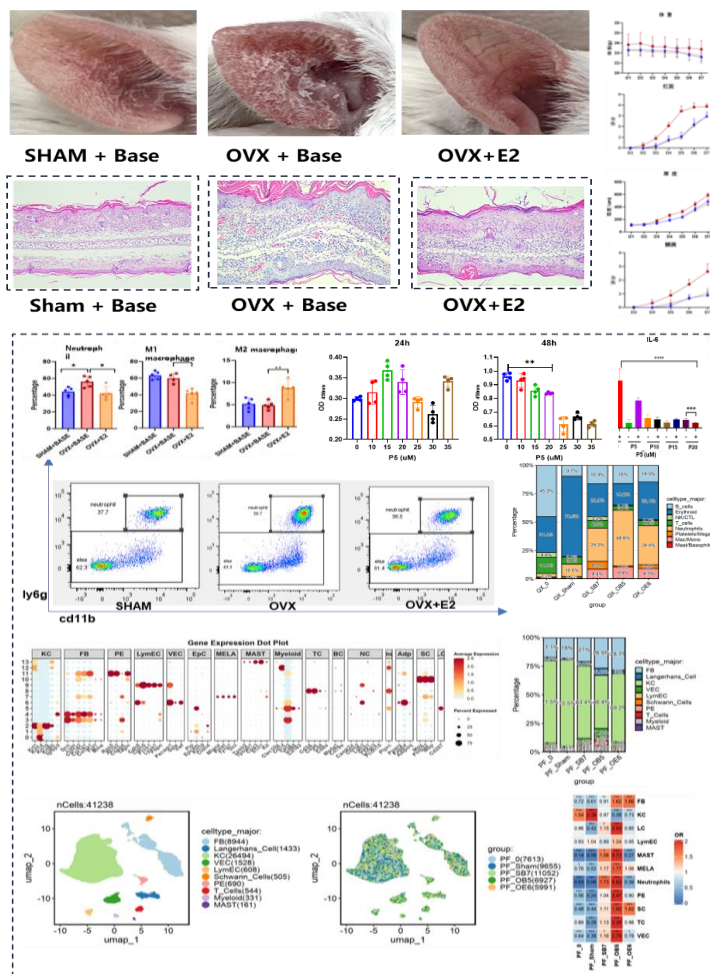
# Results 3: Trajectory and clustering analysis

## The sex hormone dysregulation in adult-onset female AD

### Clinical findings



### In vivo study



### Patent licensing

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汪金连(0731-82648117)

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申请人或专利权人: 中南大学湘雅医院

发明创造名称: 孕烯醇酮作为活性成分在制备银屑病或特应性皮炎的治疗药物中的应用

发明专利申请公布通知书

上述专利申请, 经初步审查, 符合专利法实施细则第 50 条的规定。根据专利法第 34 条的规定, 该申请在 40 卷 4601 期 2024 年 11 月 12 日专利公报上予以公布。

提示:

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# Take home message



中南大學 湘雅醫院  
XIANGYA HOSPITAL CENTRAL SOUTH UNIVERSITY



Yinli Zhou, M.D.

- The comorbidity network and its temporal trajectories display divergence and clustering, resolving into five principal clusters with distinct genetic contributors ,which can nominate potential therapeutic targets.
- The concept of AD heterogeneity should be expanded to heterogeneity of **AD syndemics**, thereby informing targeted clinical interventions.



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# THANKS!

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