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Human Plasma Metabolites Associated with Established AMD Risk Genes

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Summary

- AMD risk SNPs have an impact on the plasma metabolome
- Genetic-metabolomic associations can provide unique insights into the pathogenesis of AMD
- Highest number of associations were seen with ***LIPC* polymorphisms**, which were associated with **glycerophospholipid metabolites**
- ***LIPC* gene and glycerophospholipids pathway are likely crucial in AMD pathogenesis** and may represent potential targets for treatment of AMD

AMD

**Functional
consequences?**

34 loci

>7,000 SNPs

(single nucleotide
polymorphisms)

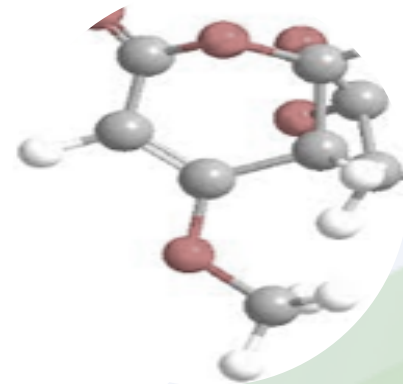
**Environmental
risk factors**

**Genetic
risk factors**

AMD



Genetic

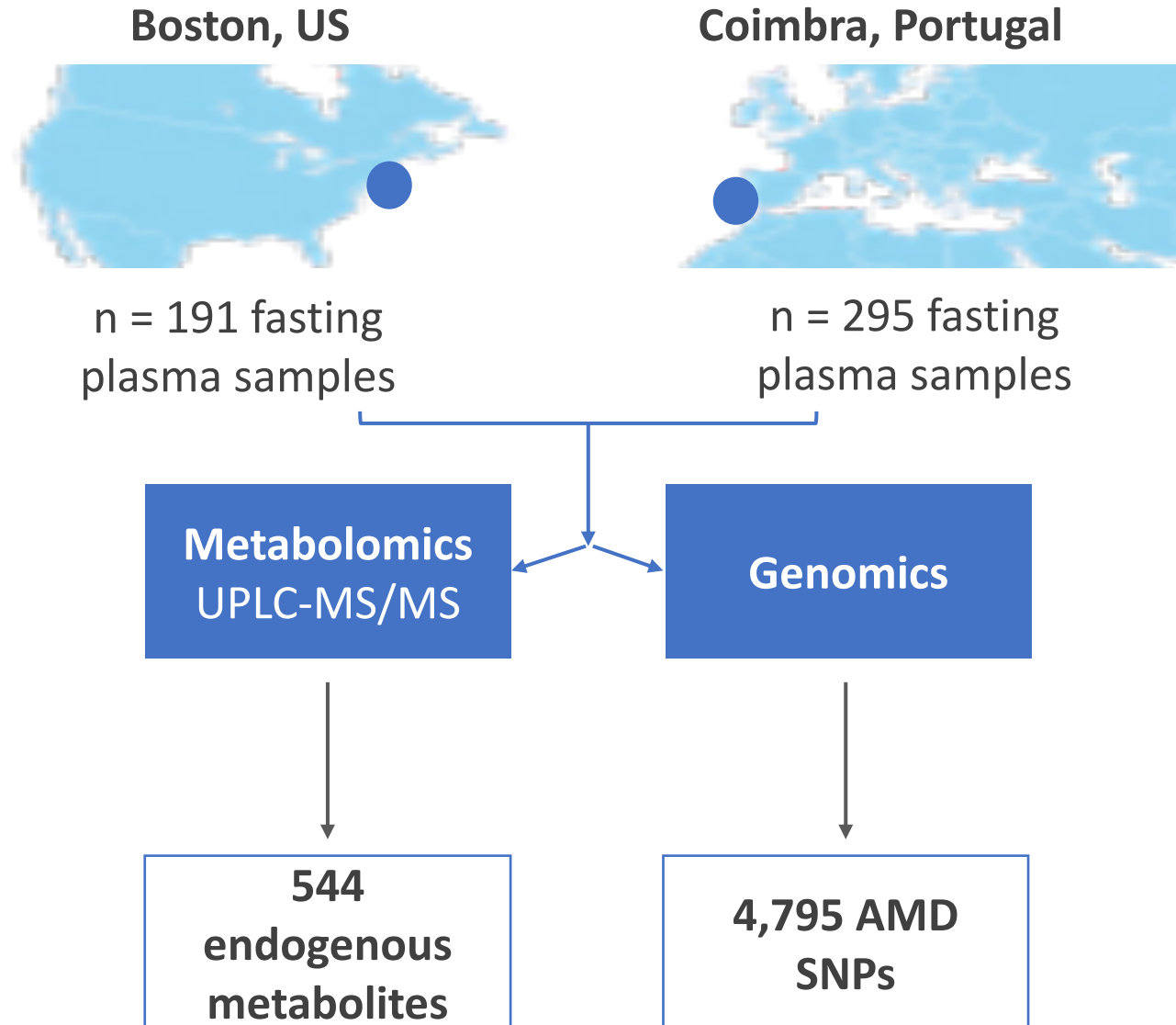


Metabolites

Goal

To analyze associations between known AMD risk SNPs and plasma metabolites in a cohort of AMD patients and controls

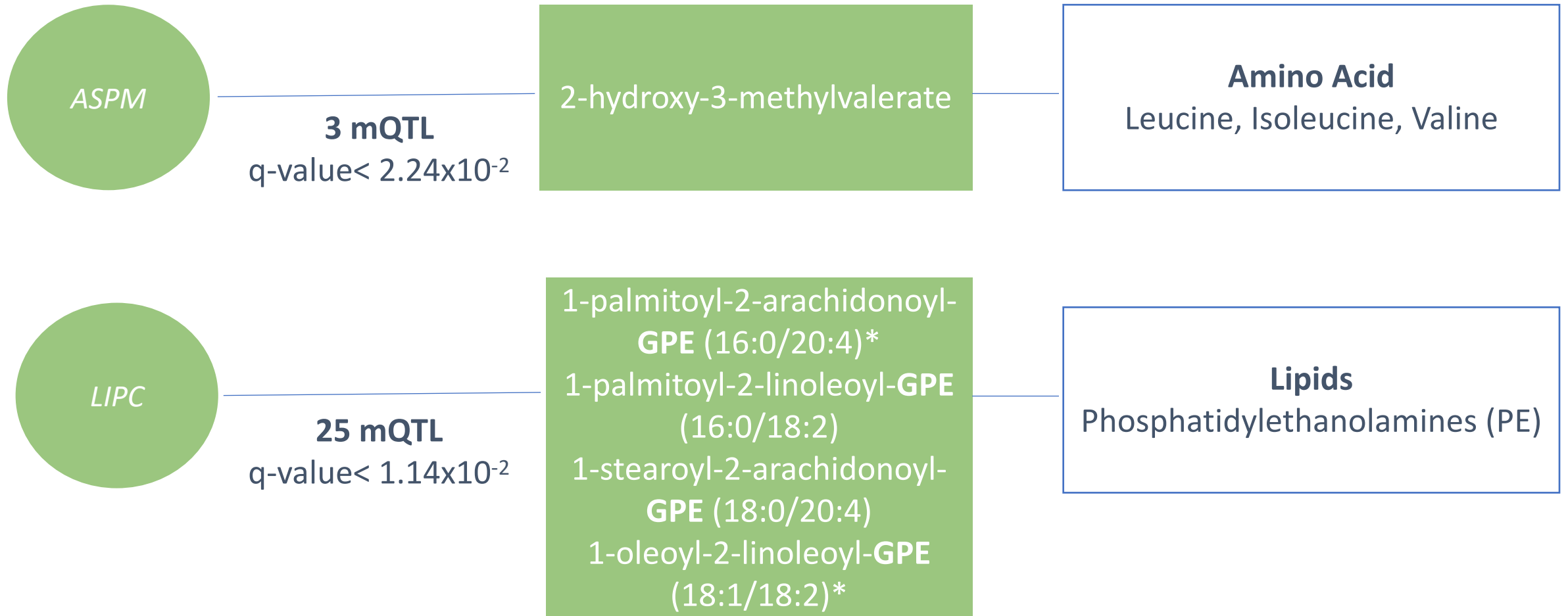
Methods



Methods

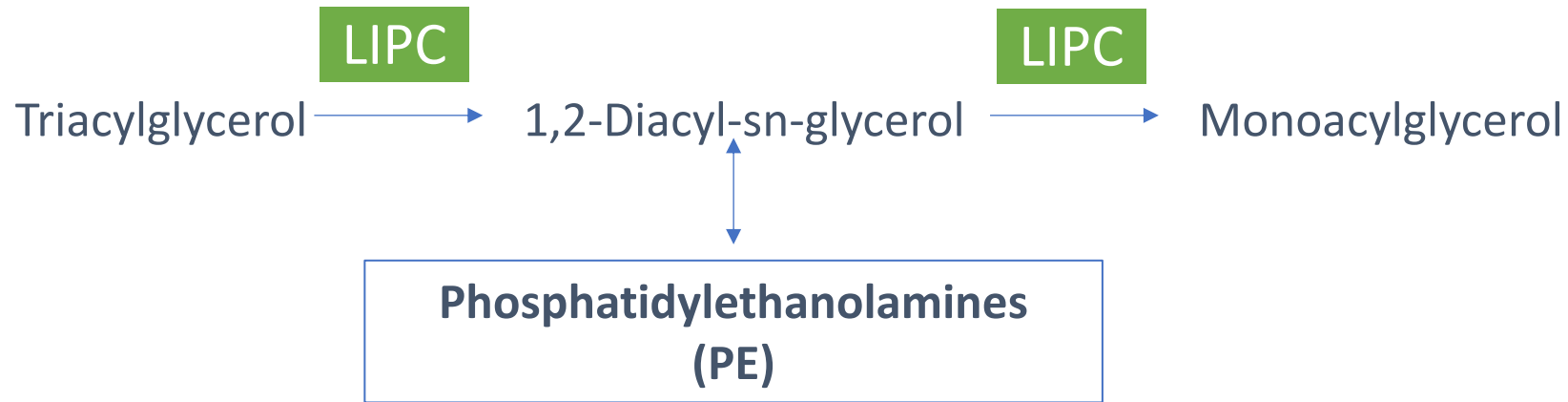
- Association between known AMD SNPs and plasma metabolites
 - Linear regression models adjusted for age, sex, smoking, 10 metabolite principal components (PCs) and 10 SNP PCs and accounting for false discovery rate
 - First for each cohort and then combined by meta-analysis

Results



Discussion

- *LIPC* gene with highest number of highly significant mQTL



Limitations

- Relatively small sample size
- Cross-sectional design

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Thank you!

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