

# ESP Subclinical and Quantitative Traits: C-reactive protein

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Myron Gross (University of Minnesota)  
Leslie Lange (University of North Carolina)  
on behalf of the ESP Inflammatory and related biomarkers

# CRP analysis details

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Data Set: ESP5500

Sample:

- N=2166 with CRP (ARIC, CARDIA, CHS, FHS, JHS, MESA, WHI)
- QC: Leal and Auer pipeline (excluded 9 samples)
- Excluded 1 sample with CRP>200
- Dropped 62 samples due to duplicate/relatedness
- Analysis sample: 1174 AAs, N=920 EAs

Model:

$\ln[\text{CRP}] = G + \text{PC1} + \text{PC2} + \text{Target} + \text{Cohort} + \text{Sex} + \text{Age\_at\_CRP} + \text{BMI} + \text{Smoking}$

Tests:

- Single variant (at least 5 minor alleles)
- Burden: MZ (1%), CMC (1%), WSS (5%)

# ESP5500 CRP Results

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Single variant:

*LEPR* (multiple common SNPs) significant at genome-wide level (positive control)

Burden:

	MZ (1%)		CMC (1%)		WSS (5%)	
	Gene	P	Gene	P	Gene	P
EA	<i>GPR64</i>	1.7x10 <sup>-5</sup>	<i>NECAB1</i>	3.4x10 <sup>-5</sup>	<i>GPR64</i>	1.3x10 <sup>-5</sup>
	<i>NECAB1</i>	3.4x10 <sup>-5</sup>	<i>OR9G4</i>	3.6x10 <sup>-5</sup>	<i>NECAB1</i>	3.9x10 <sup>-5</sup>
	<i>OR9G4</i>	3.6x10 <sup>-5</sup>	<i>GPR64</i>	6.0x10 <sup>-5</sup>	<i>DTX3</i>	1.0x10 <sup>-4</sup>
AA	<i>P2RX1</i>	4.0x10 <sup>-5</sup>	<i>P2RX1</i>	4.0x10 <sup>-5</sup>	<i>MEIS3</i>	1.3x10 <sup>-4</sup>
	<i>TPM2</i>	1.0x10 <sup>-4</sup>	<i>TPM2</i>	1x10 <sup>-4</sup>	<i>ARHGEF6</i>	1.6x10 <sup>-4</sup>
	<i>ARHGEF6</i>	2.2x10 <sup>-4</sup>	<i>CLEC3B</i>	2.7x10 <sup>-4</sup>	<i>VILL</i>	1.6x10 <sup>-4</sup>

# CRP analysis: Next steps

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- Analysis in ESP6900 (>3000 with CRP)
- Exome chip
- Collaboration with CHARGE-S
- Imputation

Other traits (in ESP6900) – probably target analysis in known genes:

- IL6 (N=658)
- ICAM1 (N=917)
- P-selectin (N=649)
- Adiponectin (N=~500)

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## ESP Biomarker group (part of Subclinical/Quantitative Traits)

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