

# IMPACT OF PFAS EXPOSURE ON HUMAN IMMUNITY

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## PFASs: FOREVER CHEMICALS

**Per- and polyfluoroalkyl substances (PFASs)**, from which PFOA and PFOS are the most abundant and studied, are widely used as **surfactants**. They are sometimes called forever chemicals as they are **very persistent** in the environment. PFASs have been found in the water, soil, sediment, biota and also in humans. They are transported to humans mainly through **contaminated food and water**. PFASs enter the environment from manufacture sites as well as by using product containing PFASs as firefighting foam, non-stick cookware, food packaging, waterproof textiles (1).

There have been reported **adverse health outcomes** linked to PFAS exposure. Epidemiological studies reported association of PFAS exposure with cancer, liver damage, cardiovascular problems, developmental adverse effects, and importantly **immune disruption** (2).

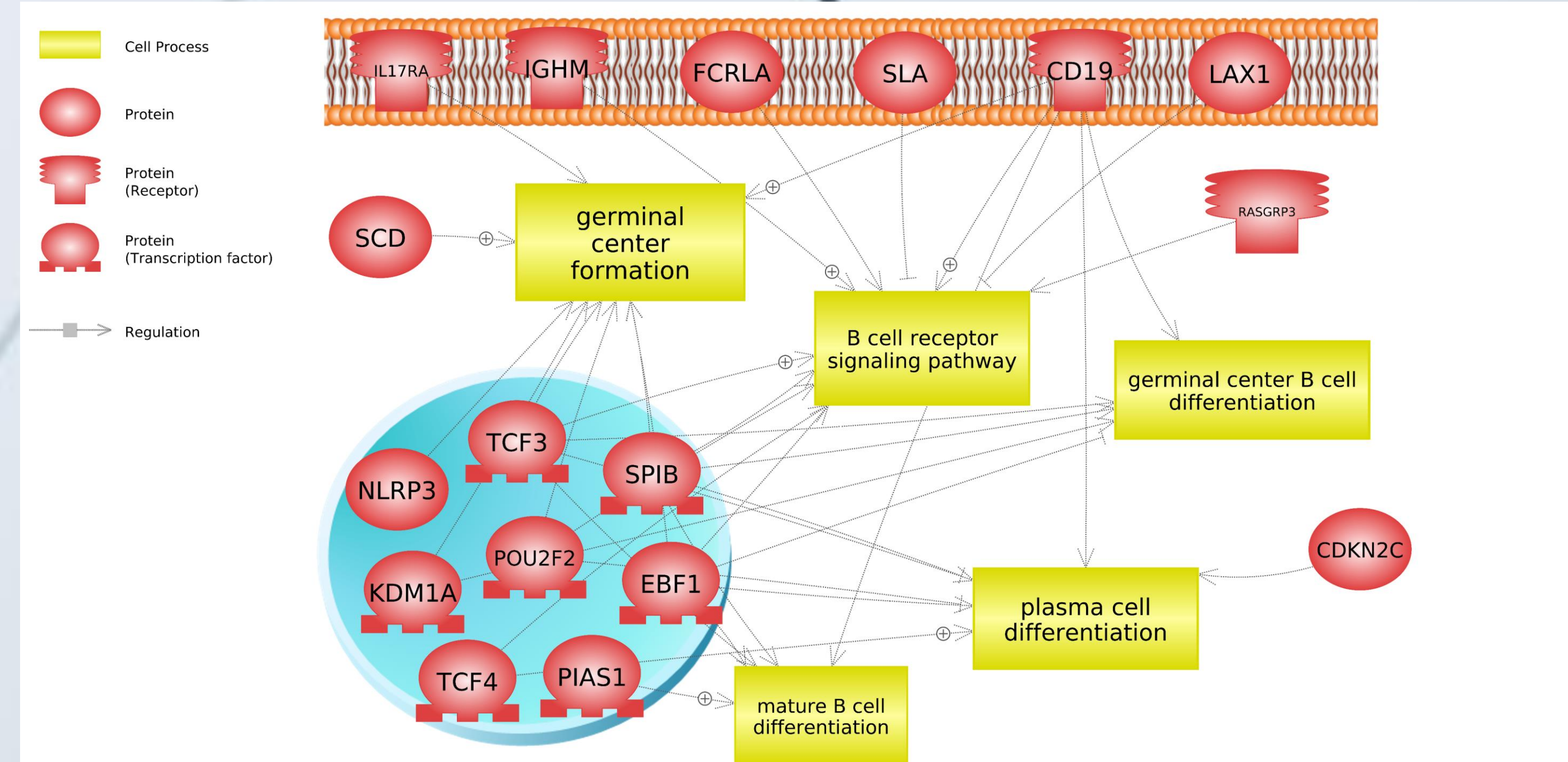
Immune disrupting effects associated with PFAS exposure have been described among children, adolescents, and adults (2). Strong evidence is reported for association of PFAS exposure with **suppressed antibody responses** after vaccination (3–6) and increased **risk of infectious diseases** (7). Further, **asthma** (5,8,9), **allergies** (8,10) and **autoimmune diseases** (11,12) associated with PFAS exposure have been described. In addition, an immune disorder can affect the axis of the neuroendocrine complex, thus the immunotoxicity of PFASs may cause deregulation of other organs and/or tissues (13).

## What is the mechanism of immunomodulation induced by PFAS exposure?

**A:** It is still unknown and probably very complex. Our research revealed involvement of plasma B cells in the immunomodulation processes associated with PFAS exposure.

**Peripheral mononuclear cells** were isolated from blood of participants and RNA was extracted from samples. The **quality of RNA** was checked (RNA integrity number (RIN) >7, A260/A230>1.8; A260/A280>1.8). Only high quality RNA was sequenced (QuantSeq library, Illumina NovaSeq sequencing) to obtain ~10-15 mil. reads per sample.

- Genes, whose expression was associated with **PFAS exposure** were identified.
  - Genes, whose expression was associated **with at least 4 PFASs** were chosen, analysis was adjusted for relevant confounders.
  - These genes were employed for Gene Set Enrichment Analysis (GSEA) and Sub-Network Enrichment Analysis (SNEA) by Pathway Studio.
  - Enrichment analyses revealed involvement of **B cell signalling**, specifically mechanisms involved in the production of **antibody-secreting plasma B cells** (Figure 3). These processes probably play a key role in PFAS-induced immunomodulation.
- Further, gene expression associated with each individual PFAS for the whole population and also separately for the **men and women** was identified and these genes were clustered to the pathways by enrichment analysis (data not shown).



**Figure 3:** Cell processes enriched by set of genes associated with at least 4 PFASs by Sub-Network Enrichment Analysis.

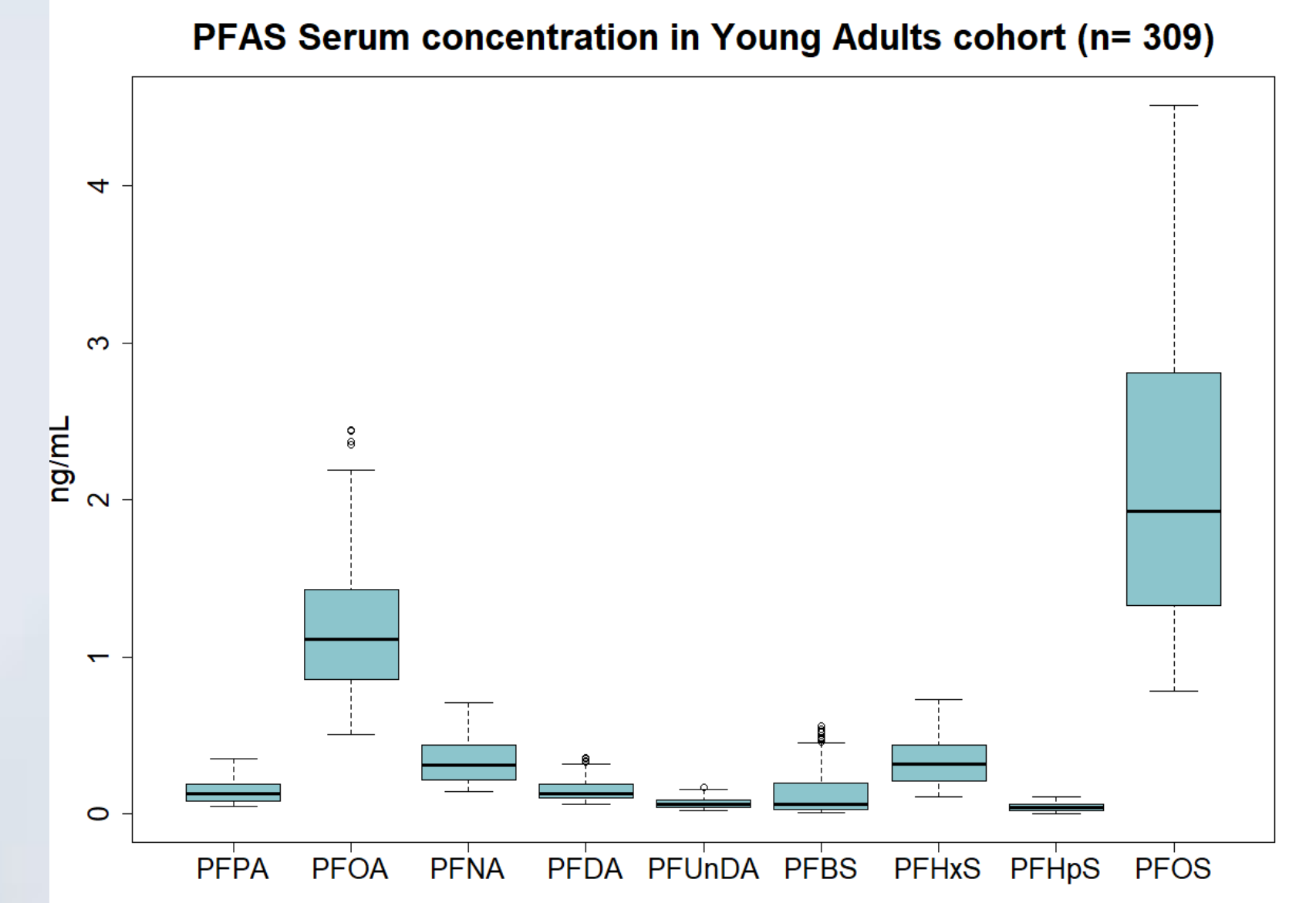
## CELSPAC: Young Adults POPULATION STUDY



This work employs data from participants of CELSPAC: YA study (Central European Longitudinal Studies of Parents and Children: Young Adults) based in the **Brno region**. Participants underwent examinations including **blood collection**, measurement of height and weight, and filling **questionnaires** reporting characteristics such as health condition, diet, lifestyle and environment.

The population used for analysis consists of a comparable number of men and women, a total of **309 participants**. The majority of the population was investigated around 27 years old and generally of normal weight (BMI 18.5 – 24.9 kg/m<sup>2</sup>), non-smokers, with university education. The most prevalent immune-mediated disease was **pollen, dust, and mite allergy** (41%), followed by atopic eczema (15%), asthma (14%) and drug allergy (14%).

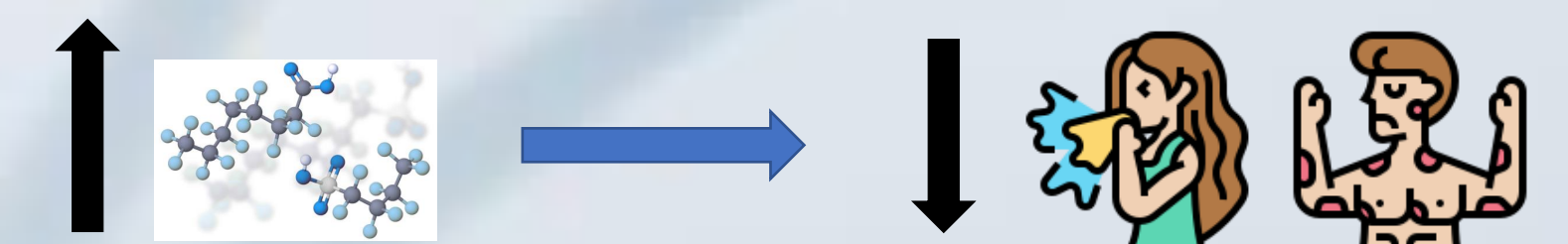
PFAS concentration in participants' serum were measured by high pressure liquid chromatography coupled with tandem mass spectrometry (HPLC-MS/MS). PFOA and PFOS reached higher concentrations than other PFASs with a median of 1.11 ng/mL and 1.93 ng/mL respectively (Figure 1).



**Figure 1:** PFAS serum concentrations in CELSPAC: Young Adults cohort (n = 309). Perfluoropentanoate (PFPA), perfluorooctanoate (PFOA), perfluorononanoate (PFNA), perfluorodecanoate (PFDA), perfluoroundecanoate (PFUnDA), perfluorobutane sulfonate (PFBS), perfluorohexane sulfonate (PFHxS), perfluoroheptane sulfonate (PFHpS), perfluorooctane sulfonate (PFOS).

## Does PFAS exposure have an impact on the prevalence of immune-mediated diseases?

**A:** Yes, we observed a negative association between PFAS exposure and immune-mediated diseases in our population.



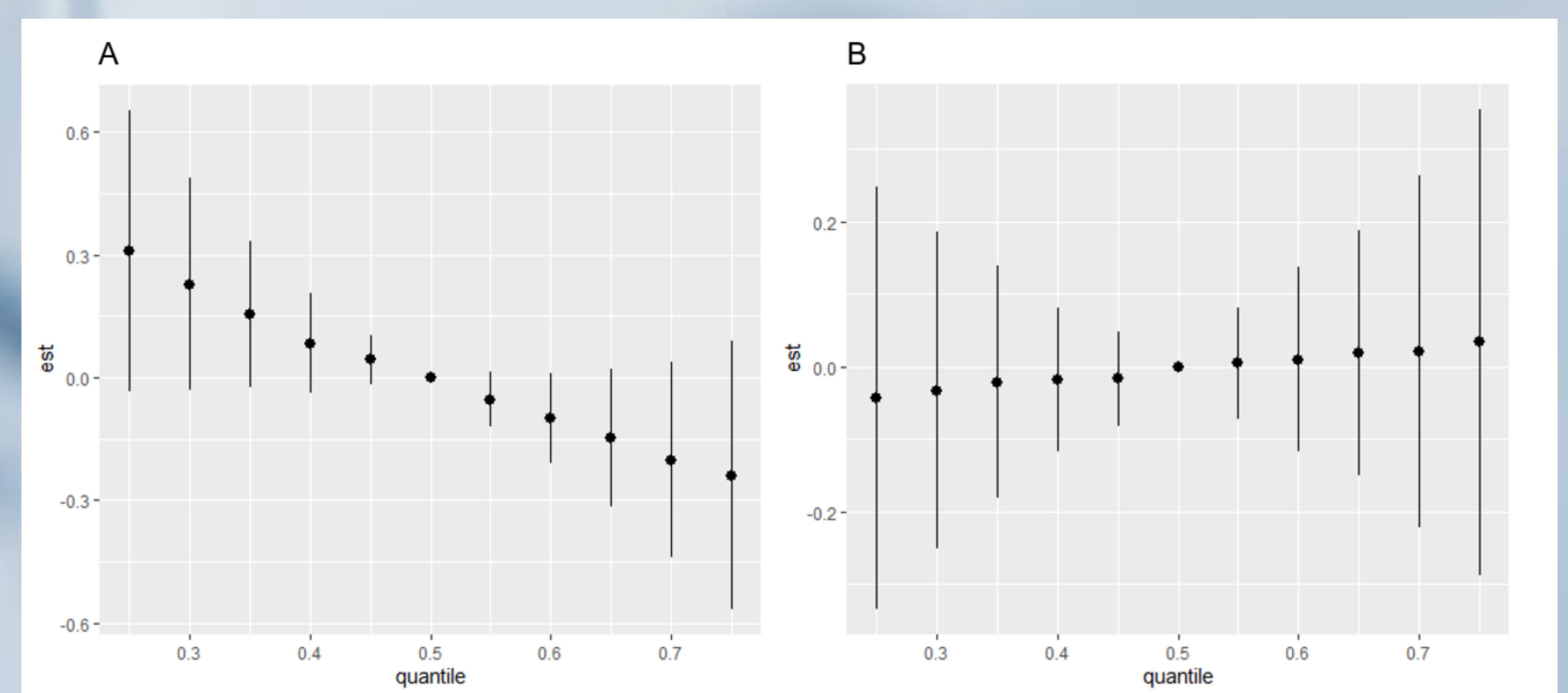
We employed **logistic regression** to reveal impact of individual PFASs and **Bayesian kernel machine regression (BKMR)** to reveal impact of PFASs as a mixture

- When assessing individual PFAS exposure, we observed **negative association** between PFAS exposure and **eczemas** and **inhalant allergy** (Table 1).

|                                | PFOA                    | PFOS                    |
|--------------------------------|-------------------------|-------------------------|
| Atopic eczema                  | <b>0.58 (0.37-0.90)</b> | <b>0.56 (0.32-0.95)</b> |
| Contact dermatitis             | <b>0.37 (0.16-0.85)</b> | <b>0.33 (0.11-0.94)</b> |
| PFUnDA                         |                         |                         |
| Pollen, dust, and mite allergy | <b>0.62 (0.43-0.89)</b> |                         |

**Table 1:** The association between individual PFASs and immune-mediated diseases; results are expressed as **OR (95% CI) per IQR increase**. The model was adjusted for sex, age, BMI, smoking, education, and family history. OR = odds ratio, CI = confidence interval, IQR = interquartile range

- A **negative trend** was also observed in output of BKMR model assessing effect of 9 PFASs mixture.
- Interestingly, we observed **sex-specific difference** between men and women in the association of PFAS exposure and atopic eczema, based on both OR (data not shown) and BKMR results (Figure 2).



**Figure 2:** The overall effect of the PFAS mixture on atopic eczema separately in women (A) and men (B) depicted in quantile graphs by BKMR model. The quantile graph shows the estimated change in effect when all the exposures at a particular percentile are compared to when all the exposures are at their 50th percentile. The estimate is accompanied by 95% CI.

## TAKE HOME MESSAGE

- We performed genome-wide sequencing of blood immune cells of Czech adults
- 167 genes were associated with multiple PFAS exposure (associated with at least 4 PFAS)
- Signalling pathways responsible for maturing of B plasma cells were identified by enrichment analyses based on genes associated with multiple PFAS exposure
- PFAS exposure is negatively associated with prevalence of immune mediated diseases in Czech adults
- Sex-specific difference were observed in the association of PFAS exposure and atopic eczema