

# Assessing effects of mixtures of Per- and Polyfluoroalkyl Substances (PFAS) using transcriptomic points of departure

Gregory Addicks

DSRG presentation - March 7<sup>th</sup> 2023

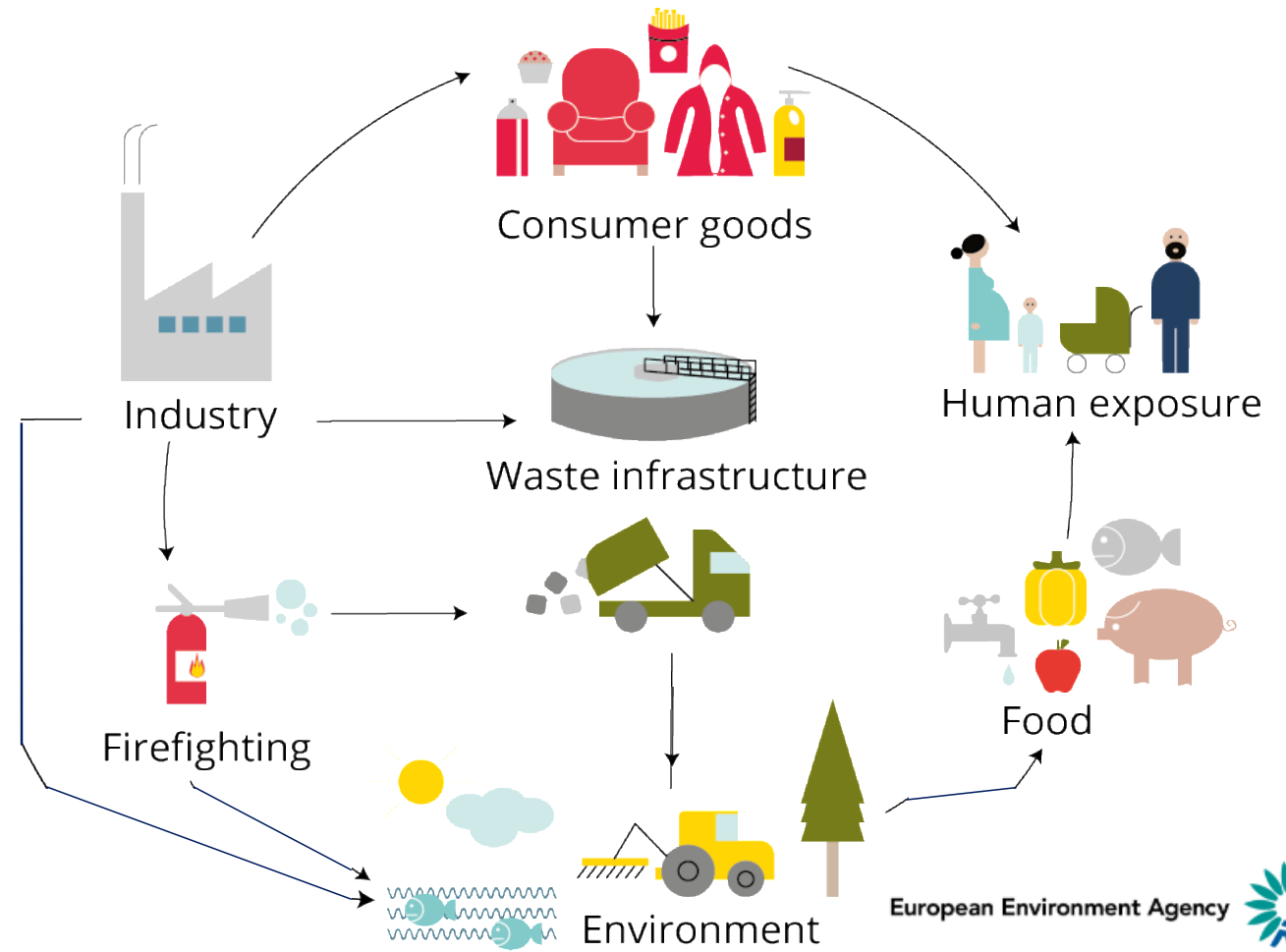
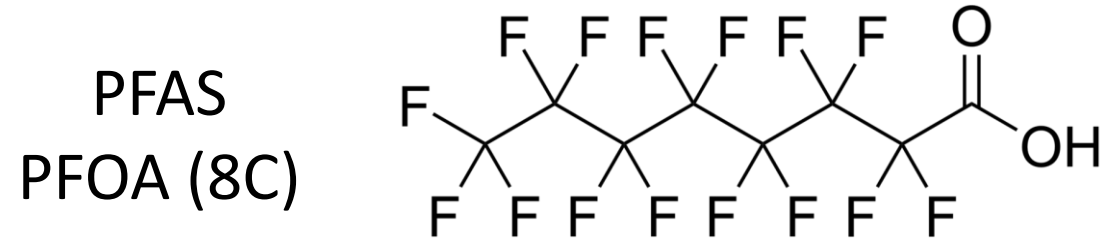
# Overview

- Introduction
  - PFAS chemicals and why mixtures are a concern
- Main Question
  - Do PFAS have synergistic or antagonistic effects or are their effects additive?
- Methodology
  - Chemicals and mixtures – Cells and treatments – Sequencing and QC
  - Data processing and BMC generation with BMD Express
  - Using data to predict mixture potency
- Results
  - Comparison of predicted mixture potency to empirical mixture potency

# The Miracle of PFAS

PFAS are Per and Polyfluoroalkyl Substances

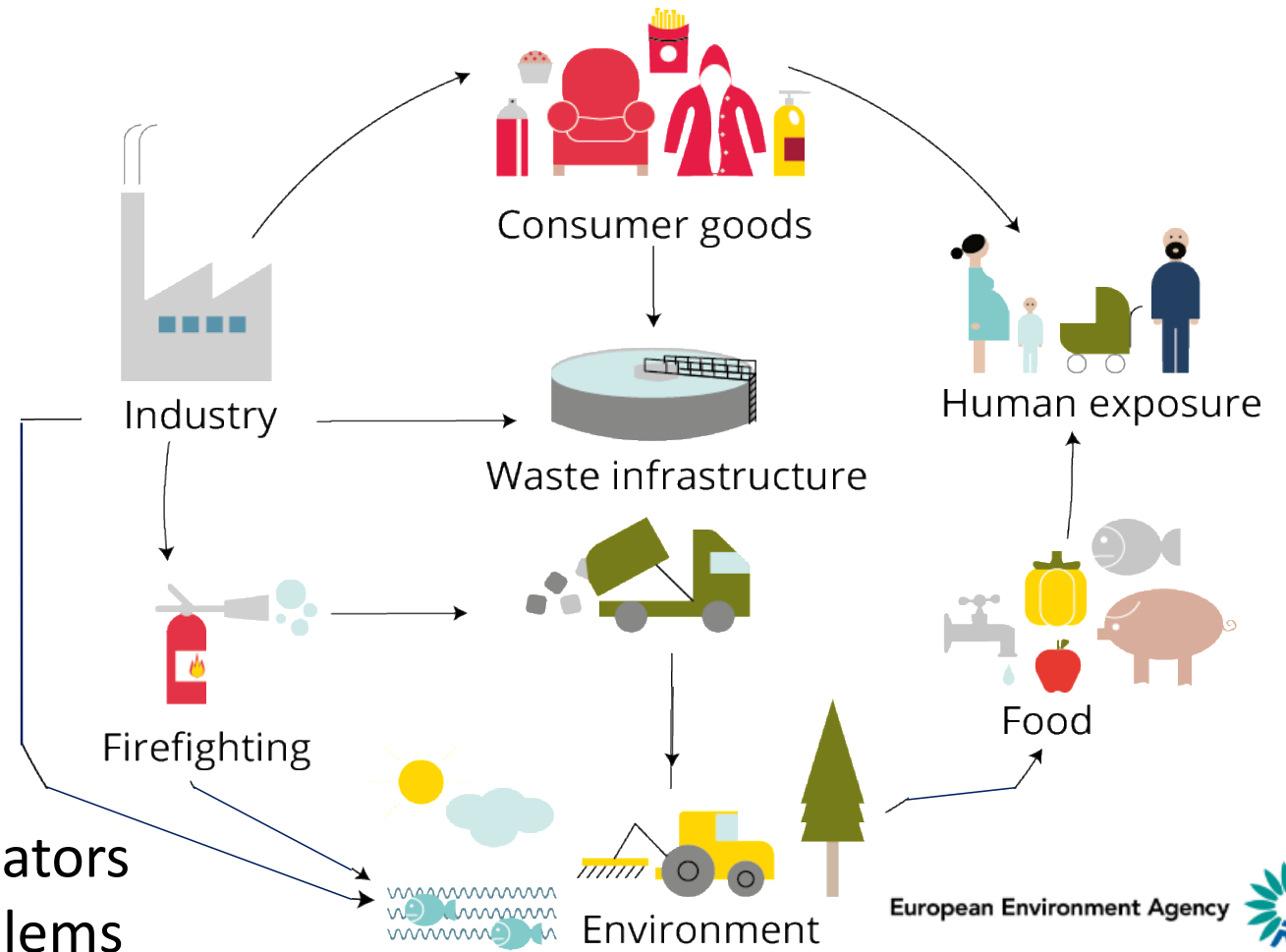
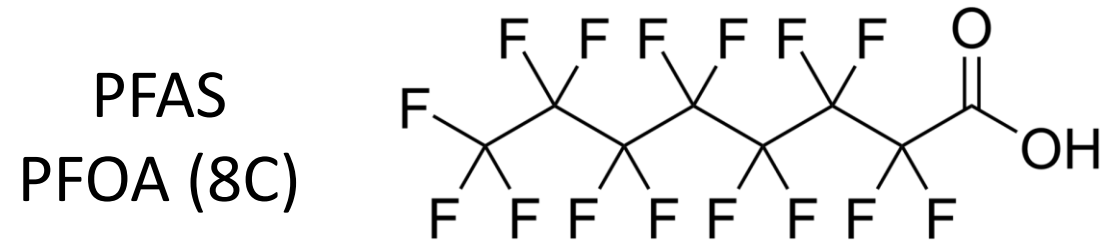
- Hydrophobic
- Lipophobic
- Heat and Fireproof
- Non-stick
- Very low surface tension
  - Helps stuff flow and/or stick
- Breathable waterproof fabrics
- Non-stick cookware
- Waxed paper
- Waterproof makeup
- Stain guard
- Fire fighting foam
- Industrial processes



# The Problem with PFAS

PFAS are Per and Polyfluoroalkyl Substances

- Hydrophobic
- Lipophobic
- Heat and Fireproof
- Non-stick
- Very low surface tension
  - Helps stuff flow and/or stick
- Do not break down in environment
- Mobile in the environment
- Accumulate in biological organisms
- Resemble metabolic substrates
- Interact with cellular metabolism regulators
- Associated with numerous health problems



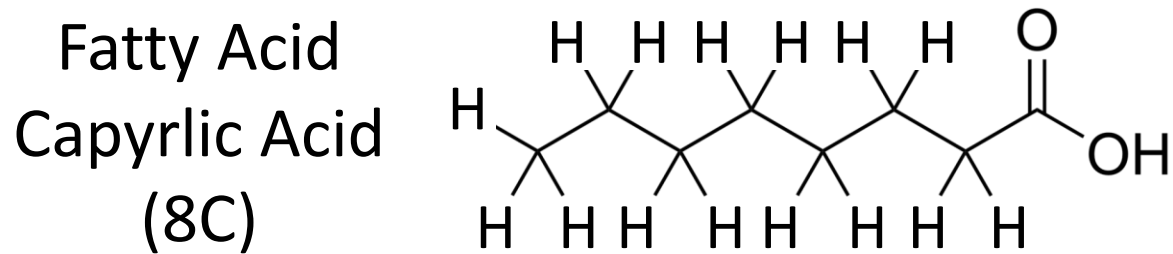
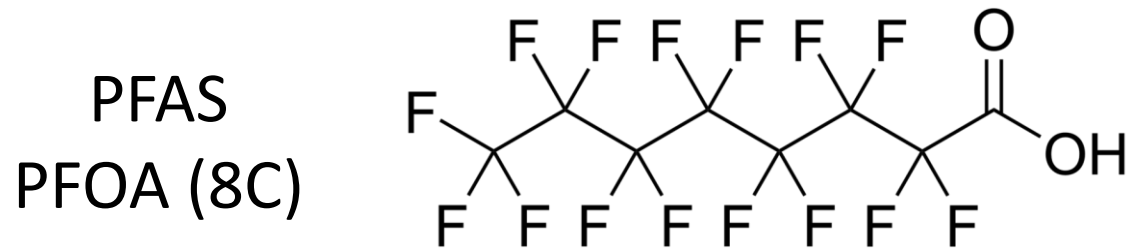
# The PFAS Problem

PROTEIN|SCIENCE

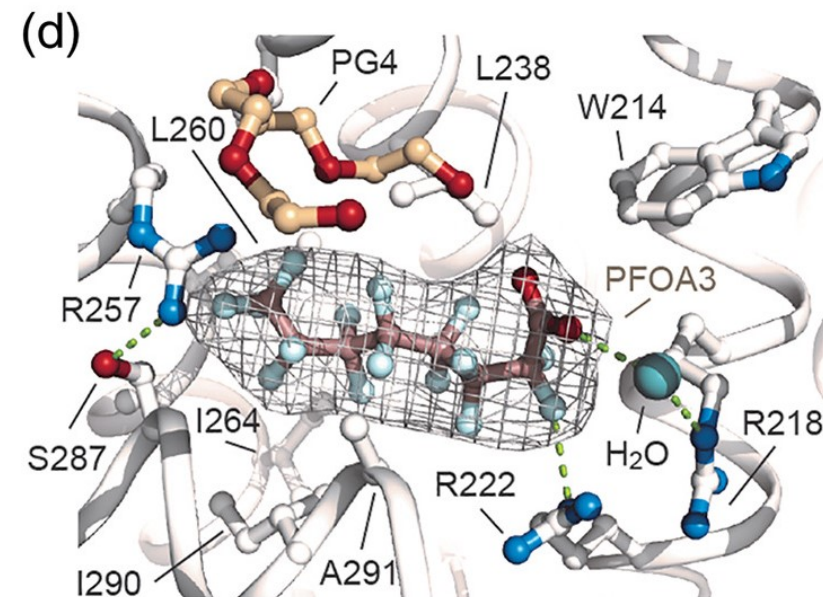
Unveiling the binding mode of perfluorooctanoic acid to human serum albumin

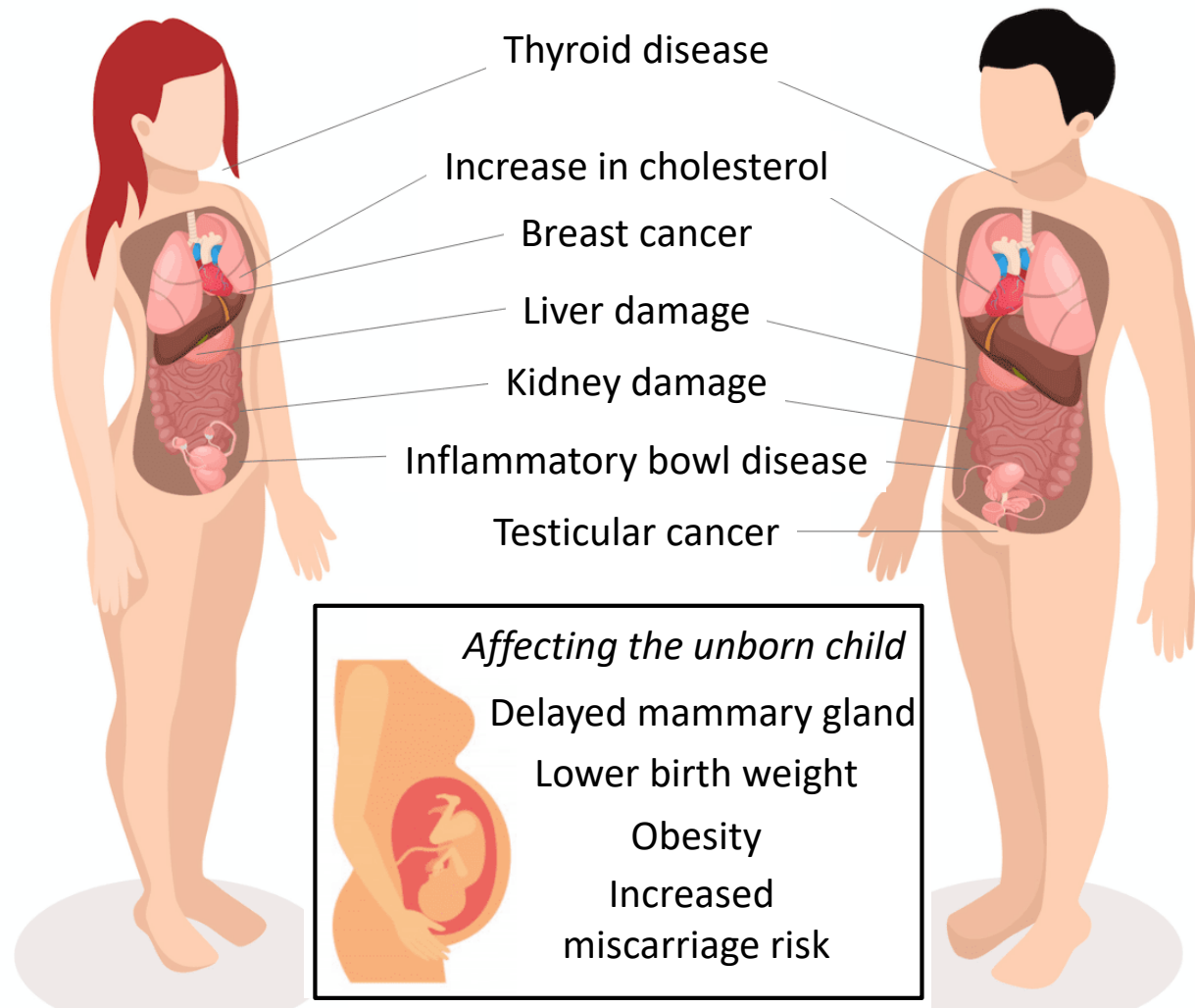
Lorenzo Maso,

07 February 2021 | <https://doi.org/10.1002/pro.4036> |



- Resemble metabolic substrates
- Interact with cellular metabolism regulators
- Associated with numerous health problems



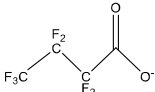
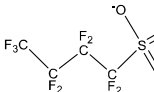
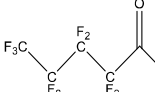
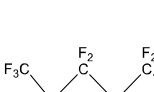
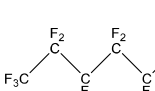
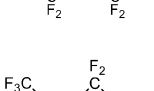
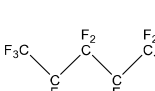
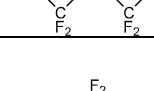
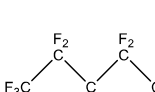
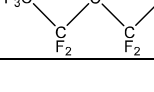
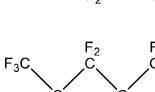
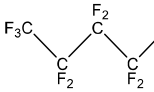
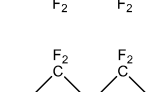
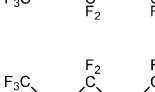


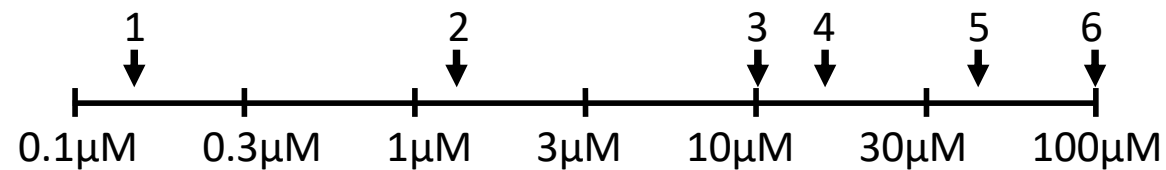
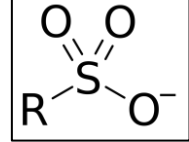
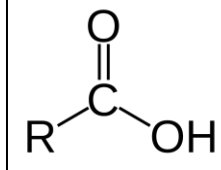
- Associated with numerous health problems

# Project Overview - Assess PFAS mixtures

- Assess potency of PFAS mixtures
  - PFAS are in the environment– exposure to multiple PFAS is supported by biological screening surveys worldwide
  - Do PFAS mixtures have additive, synergistic or antagonistic effects?
- Human Liver Spheroids exposed to PFAS and PFAS mixtures
- Transcriptomic analysis of overall change to gene expression
- In-vitro
  - Exposures are most relevant to concentrations at plasma / cellular level
    - Data is not directly usable for regulatory purposes
    - Exposures need in-vitro to in-vivo extrapolation

# PFAS used in this study

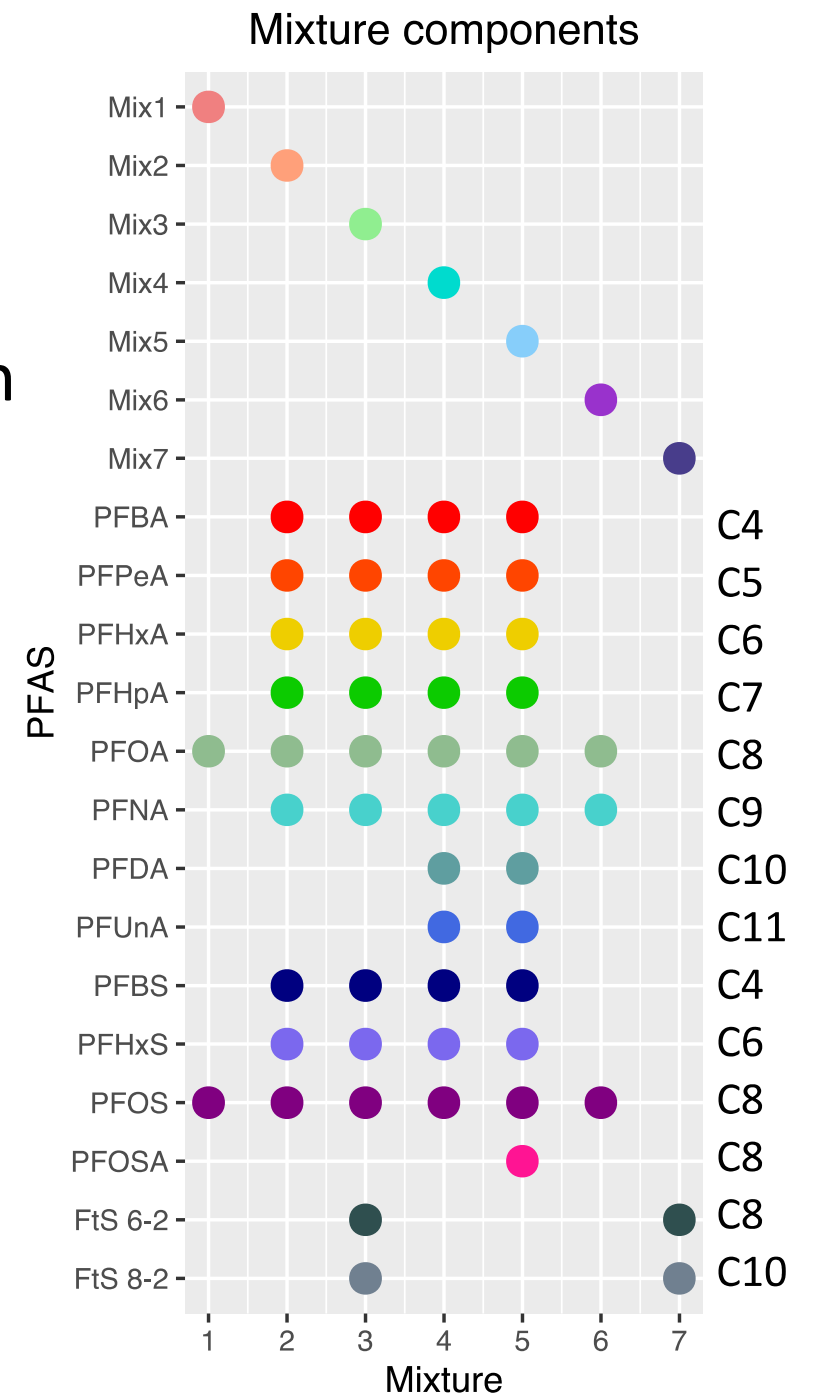
Class	Name (Acronym)	Structure	Class	Name (Acronym)	Structure		
Perfluoroalkyl carboxylates (PFCAs)	Perfluorobutanoate (PFBA)		Perfluoroalkyl sulfonates (PFSAs)	Perfluorobutane sulfonate (PFBS)			
	Perfluoropentanoate (PFPeA)			Perfluorohexane sulfonate (PFHxS)			
	Perfluorohexanoate (PFHxA)			Perfluorooctane sulfonate (PFOS)			
	Perfluoroheptanoate (PFHpA)			Sulfonamide	Perfluorooctane sulfonamide (PFOSA)		
	Perfluorooctanoate (PFOA)				Sulfonate telomers	8:2 Fluorotelomer sulfonate (8:2 FtS)	
	Perfluorononanoate (PFNA)					6:2 Fluorotelomer sulfonate (6:2 FtS)	
	Perfluorodecanoate (PFDA)						
	Perfluoroundecanoate (PFUnA)						





# PFAS Mixtures

- 14 PFAS used in study
- 7 mixtures of varying complexity and composition





# PFAS Mixtures

Mixture components



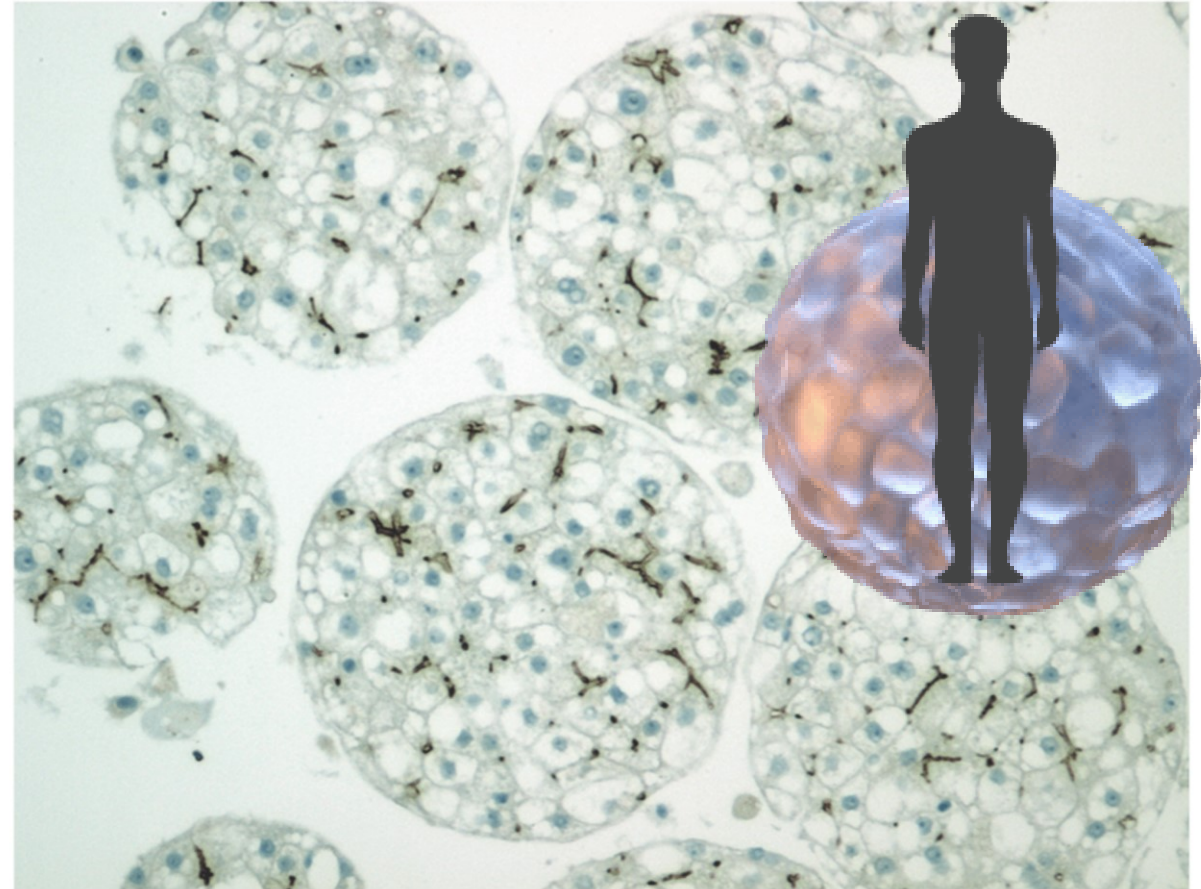
Non Mixtures	-----	Individual PFAS	Concentrations ( $\mu\text{M}$ )
Single PFAS		PFBA, PFPeA, PFHxA, PFHpA, PFOA*, PFNA, PFDA, PFUnA, PFBS*, PFOS*, PFHxS, PFOSA, 6:2 FtS, 8:2 FtS  † PFUnA	0.2, 2, 10, 20, 50, 100 * also 0.02, 0.1, 1  † 0.13, 1.3, 6.5, 13, 34, 66
Mixture Name (# PFAS in Mix)	Subgroup	Individual PFAS	Concentrations ( $\mu\text{M}$ )
1 (2)	PFCAs (1) PFSAs (1)	PFOA PFOS	0.4, 2, 4, 20, 40, 100
2 (9)	PFCAs (6) PFSAs (3)	PFBA + PFPeA + PFHxA + PFHpA + PFOA + PFNA PFBS + PFHxS + PFOS	0.18, 1.8, 9, 18, 45, 100
3 (11)	PFCAs (6) PFSAs (3) Other (2)	PFBA + PFPeA + PFHxA + PFHpA + PFOA + PFNA PFBS + PFHxS + PFOS 6:2 FtS + 8:2 FtS	0.22, 2.2, 11, 22, 55, 100
4 (11)	PFCAs (8) PFSAs (3)	PFBA + PFPeA + PFHxA + PFHpA + PFOA + PFNA + PFDA + PFUnA PFBS + PFHxS + PFOS	0.22, 2.2, 11, 22, 55, 100
5 (12)	PFCAs (8) PFSAs (3) Other (1)	PFBA + PFPeA + PFHxA + PFHpA + PFOA + PFNA + PFDA + PFUnA PFBS + PFHxS + PFOS PFOSA	0.24, 2.4, 12, 24, 60, 100
6 (3)	PFCAs (2) PFSAs (1)	PFOA + PFNA PFOS	0.9, 9, 18, 30, 60, 100
7 (2)	Other (2)	6:2 FtS + 8:2 FtS	0.4, 2, 4, 20, 40



## 3D InSight™ Human Liver Microtissues

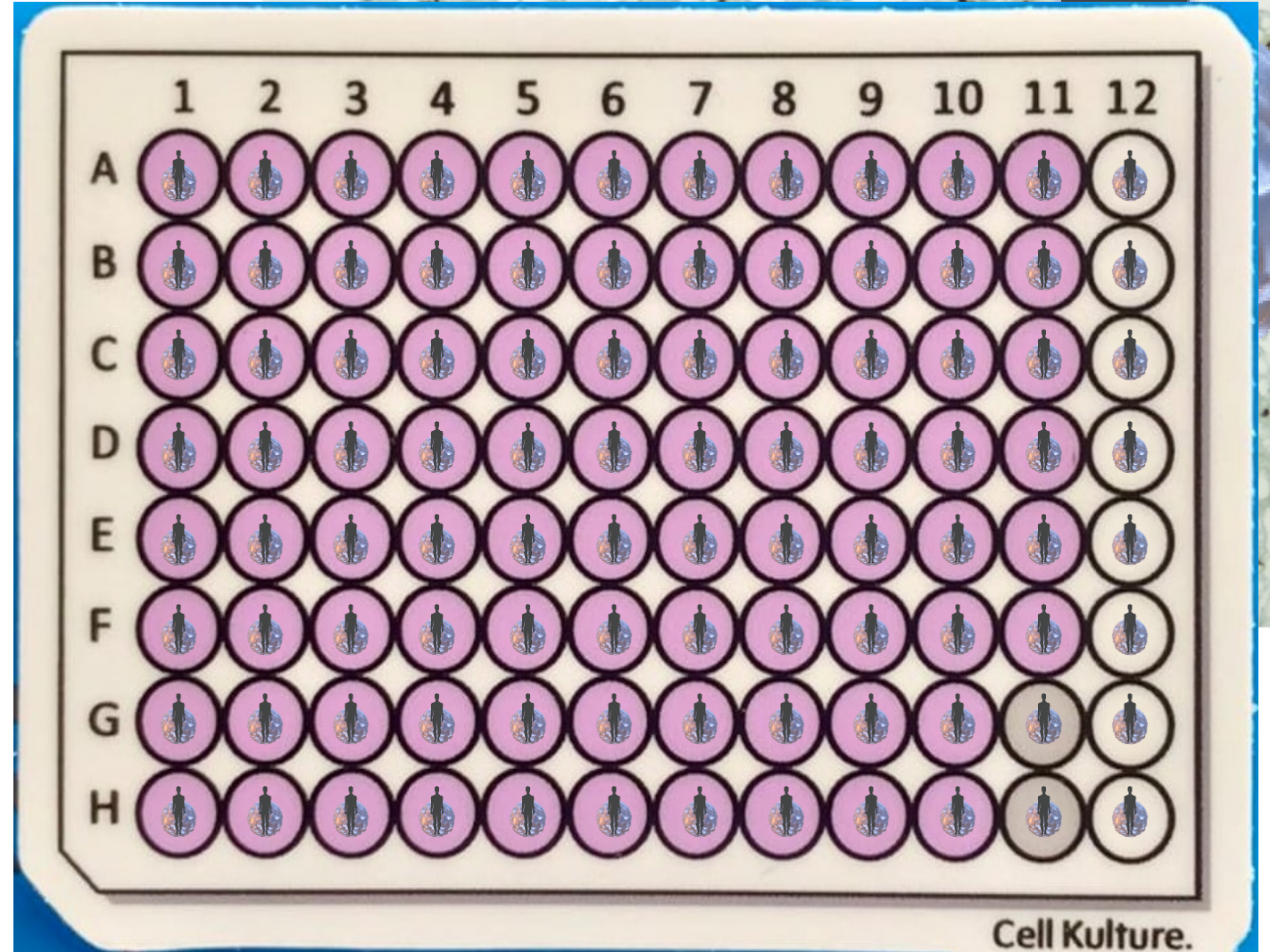
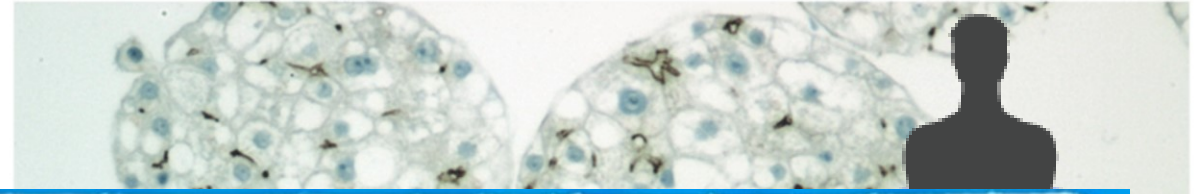
### PFAS exposed Human Liver Spheroids

- Contains cells from 10 donors
  - Donors from both sexes
  - Kupffer cells and hepatocytes
- ~2000 cells per spheroid



## PFAS exposed Human Liver Spheroids

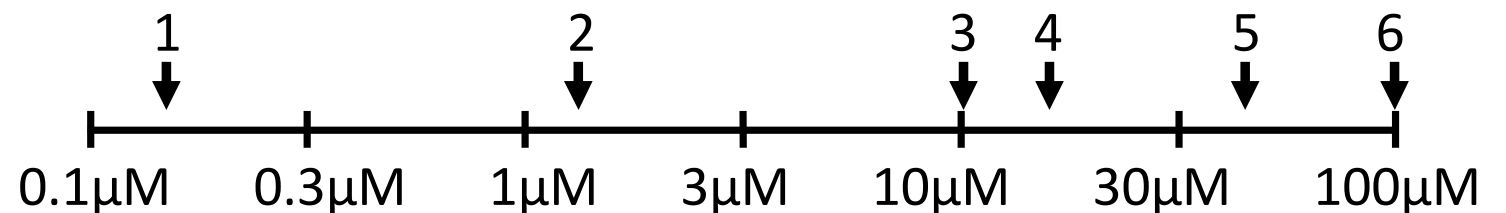
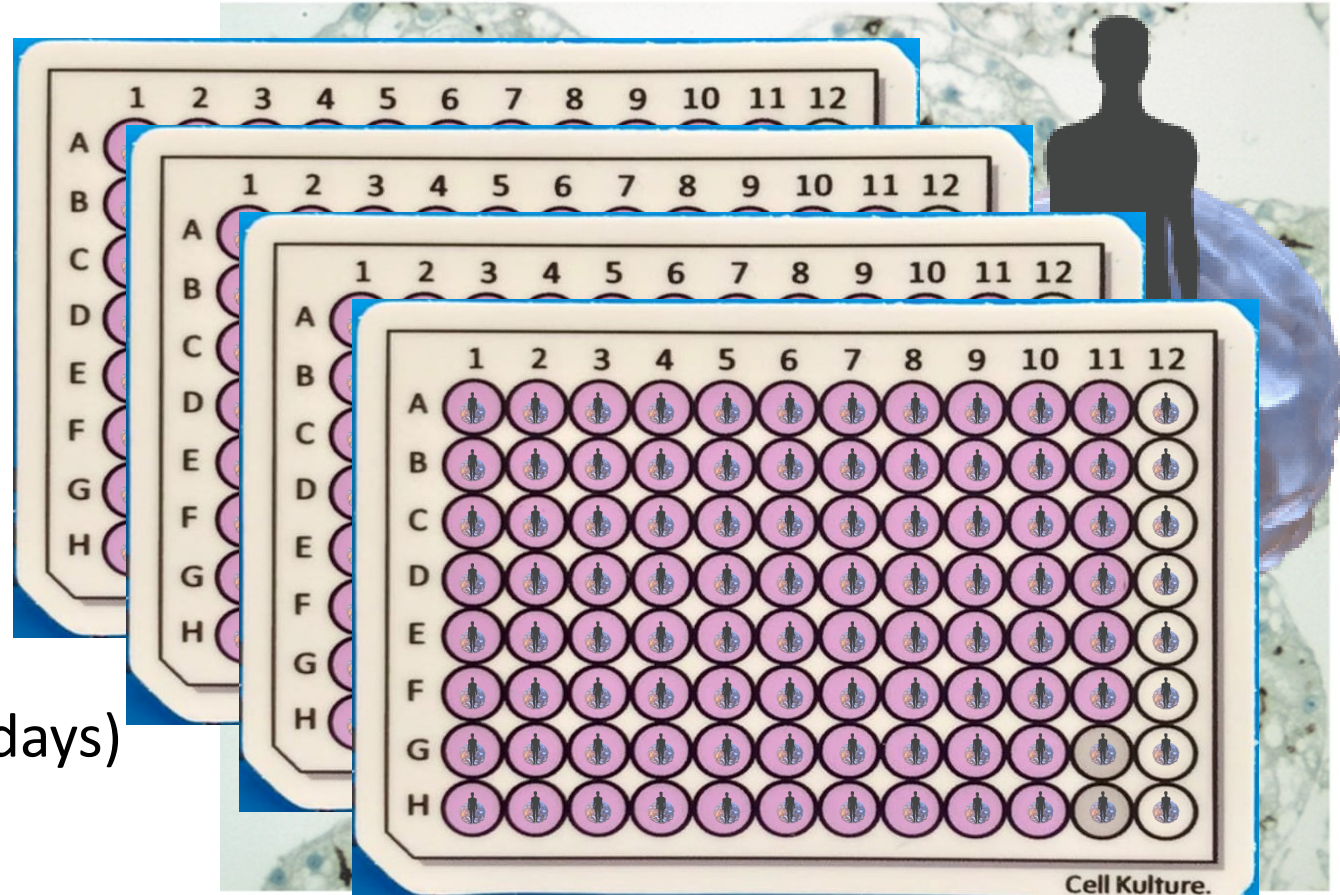
- Contains cells from 10 donors
  - Donors from both sexes
  - Kupffer cells and hepatocytes
- ~2000 cells per spheroid
- One spheroid per exposure
  - One spheroid per well



# 3D InSight™ Human Liver Microtissues

## PFAS exposed Human Liver Spheroids

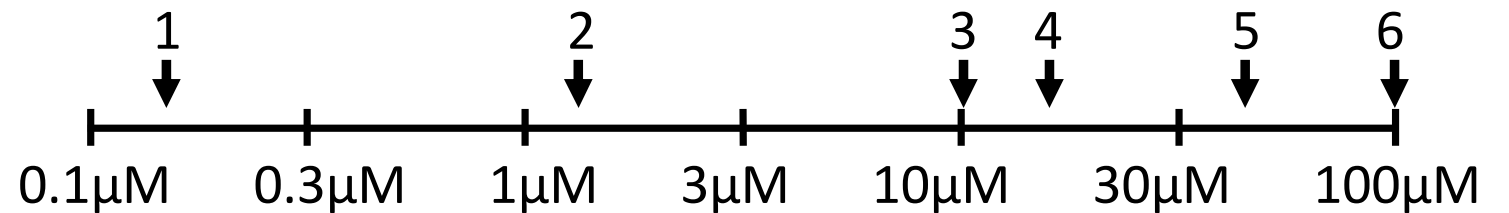
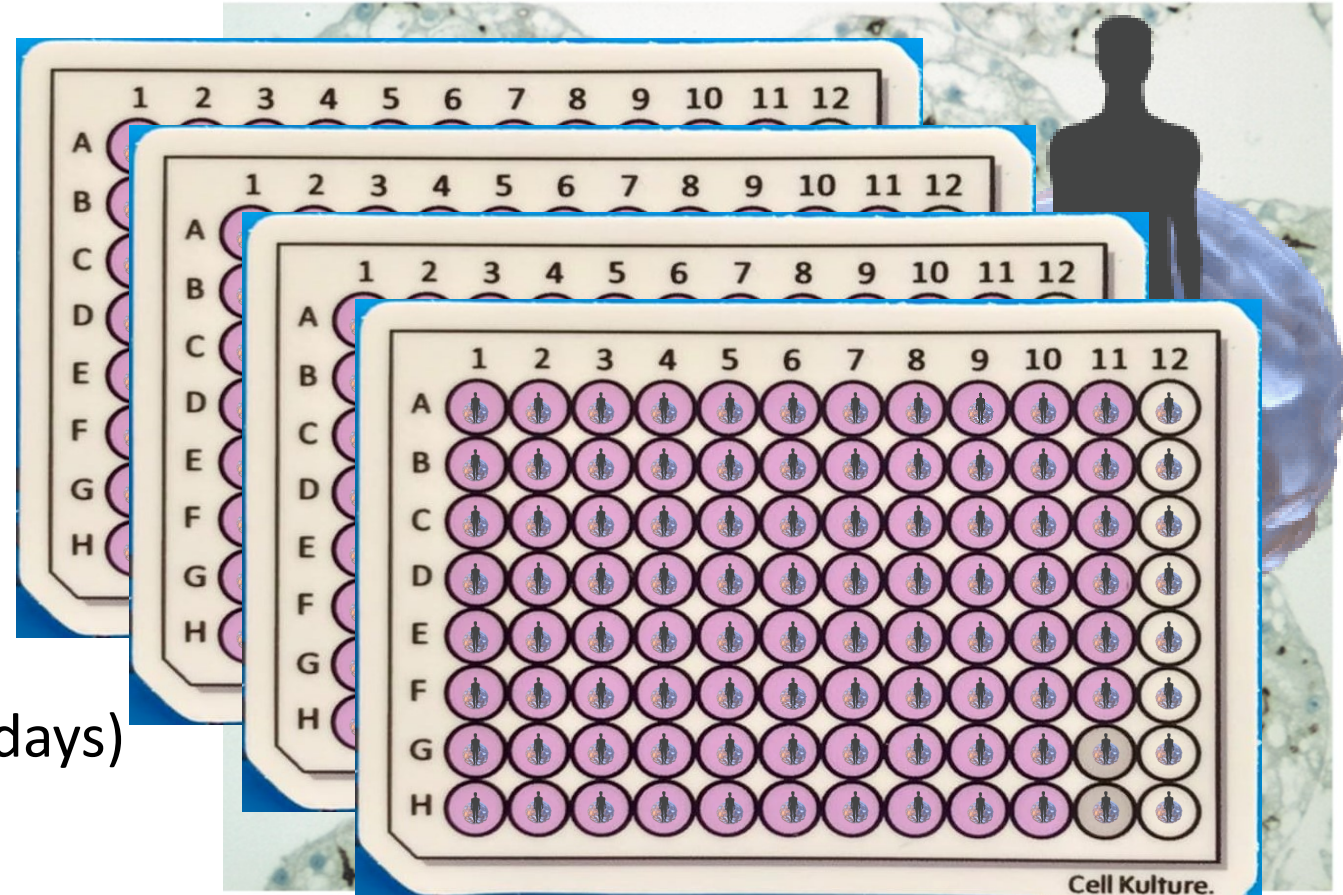
- Contains cells from 10 donors
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- One spheroid per exposure
  - One spheroid per well
- 6 – Exposure concentrations
- 4 – Replicate exposures (1 x per plate)
- 2 – Exposure times (24 hours and \*10 days)
  - \*Media refreshed every 48 hours



# 3D InSight™ Human Liver Microtissues

## PFAS exposed Human Liver Spheroids

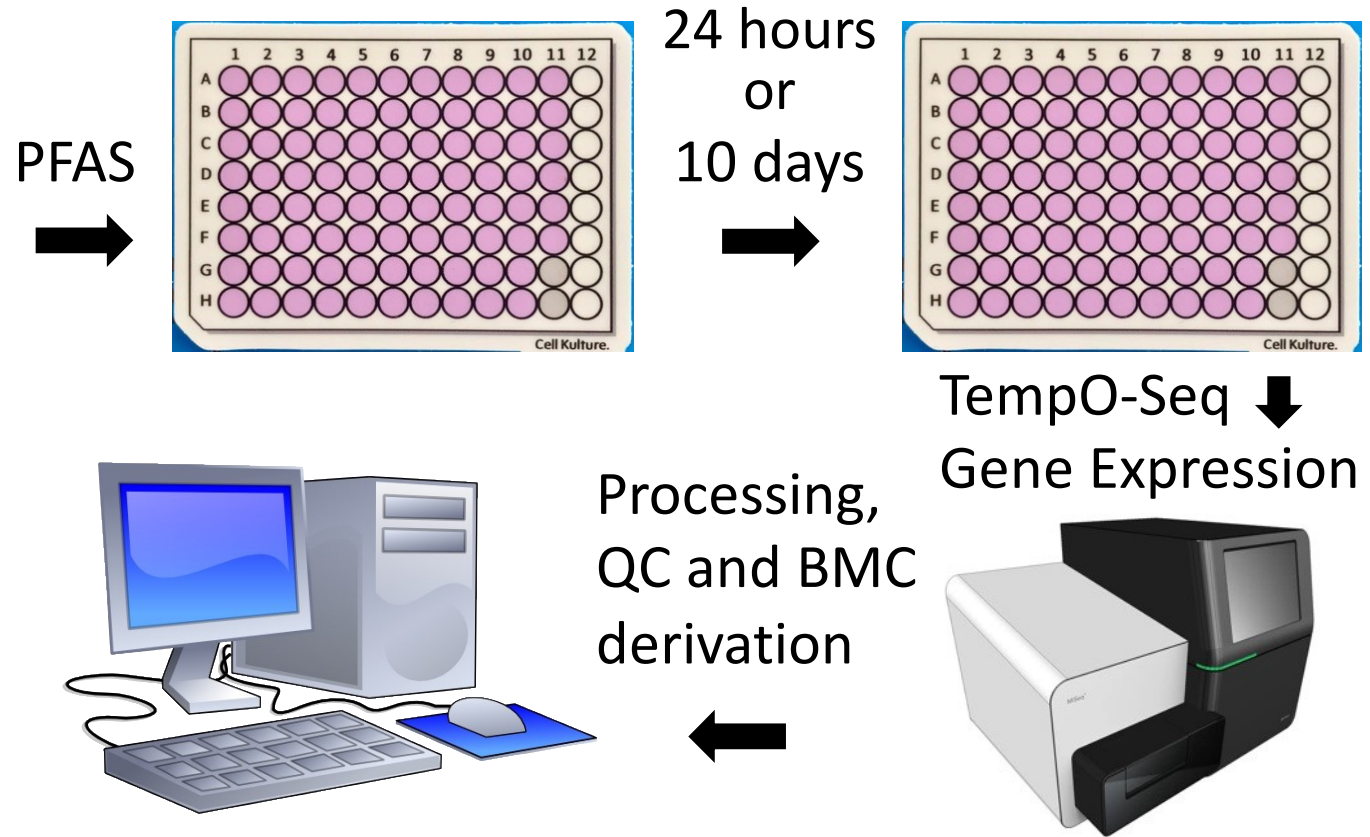
- Contains cells from 10 donors
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  - One spheroid per well
- 6 – Exposure concentrations
- 4 – Replicate exposures (1 x per plate)
- 2 – Exposure times (24 hours and \*10 days)
  - \*Media refreshed every 48 hours
- Several controls
  - DMSO
  - Downstream processing
    - Sequencing
    - QC





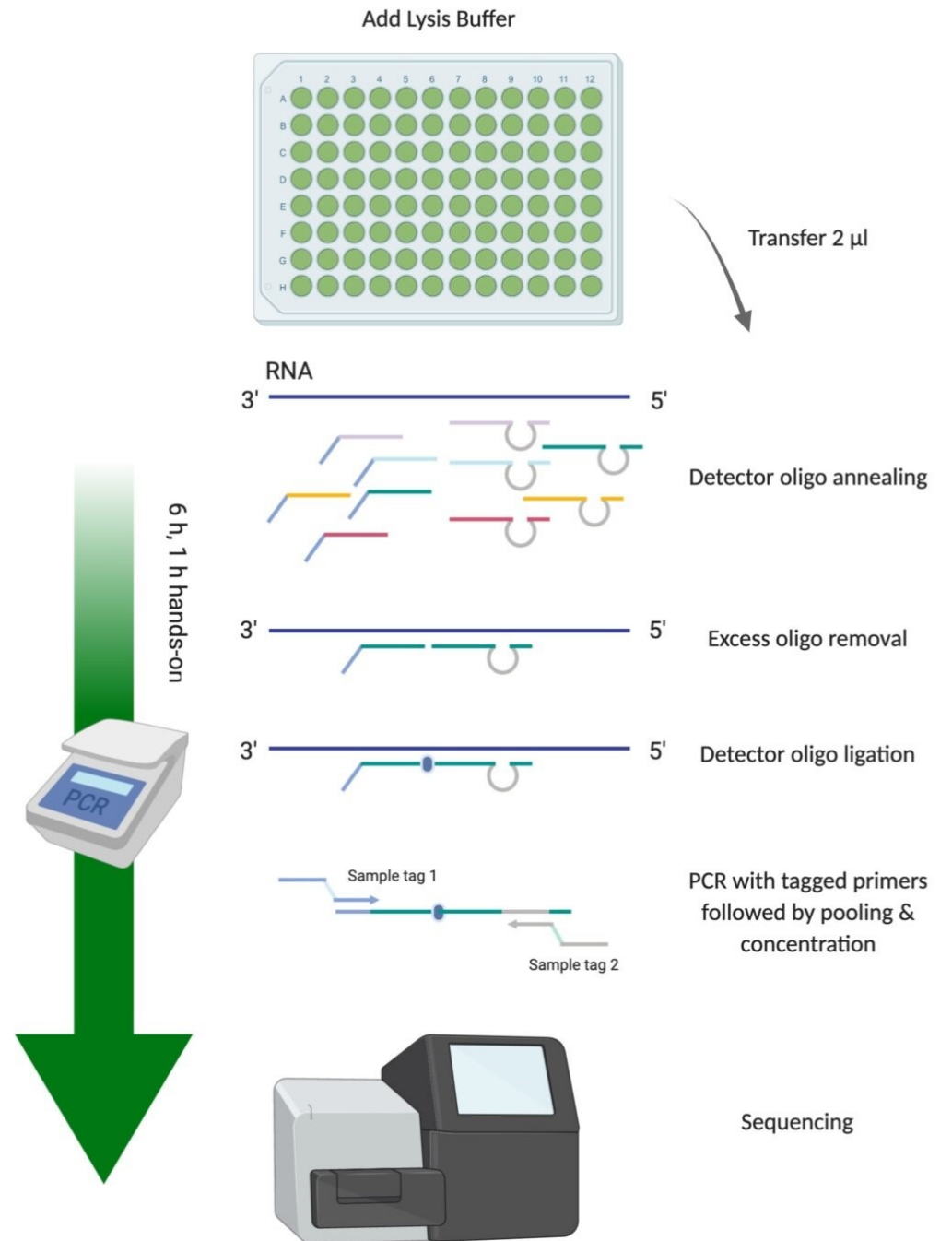
## Transcriptomics

- TempO-Seq
  - Higher throughput
    - (less in house labor)
  - More economical
    - (lower cost for sequences)
- \$1500+
  - 2753 genes
  - Captures all pathways
- Quality Control (QC)
  - spheroid loss
  - contamination
  - unexplained excessive variability



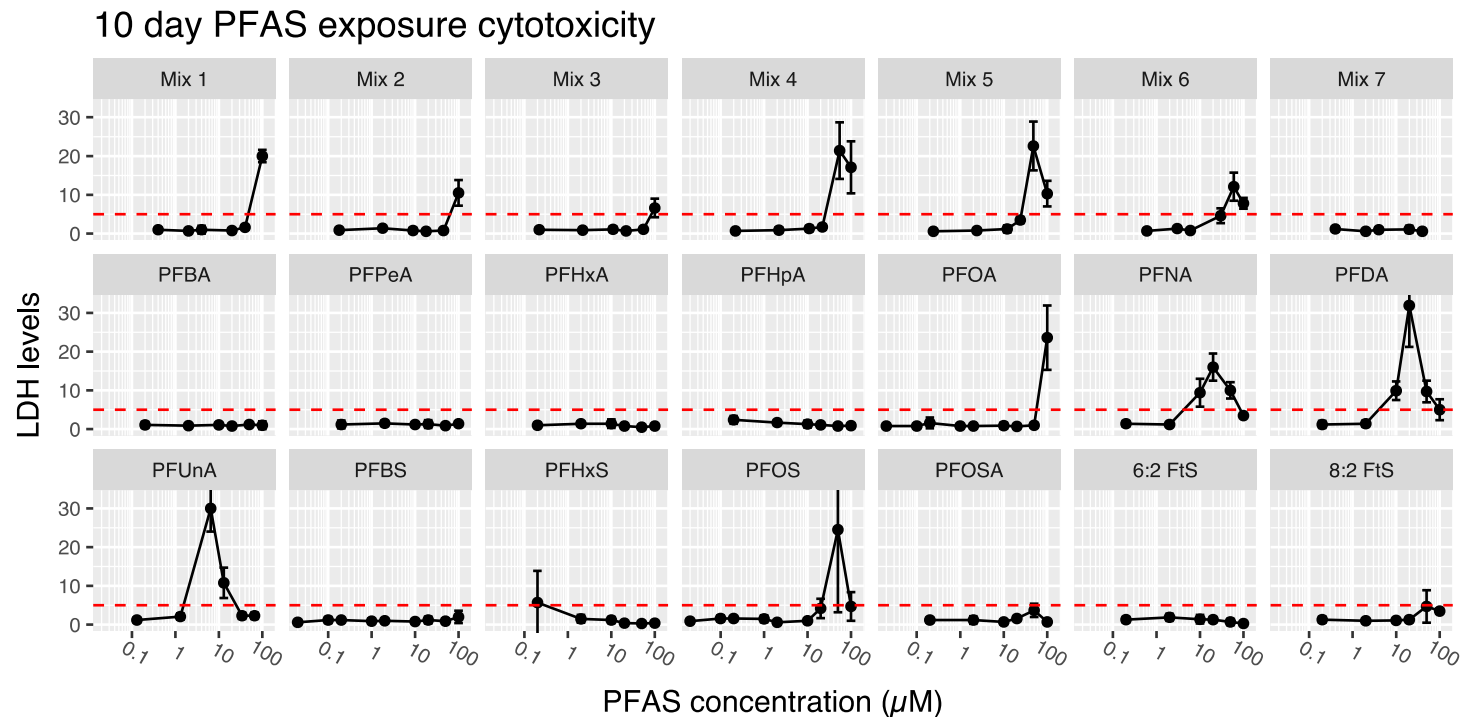
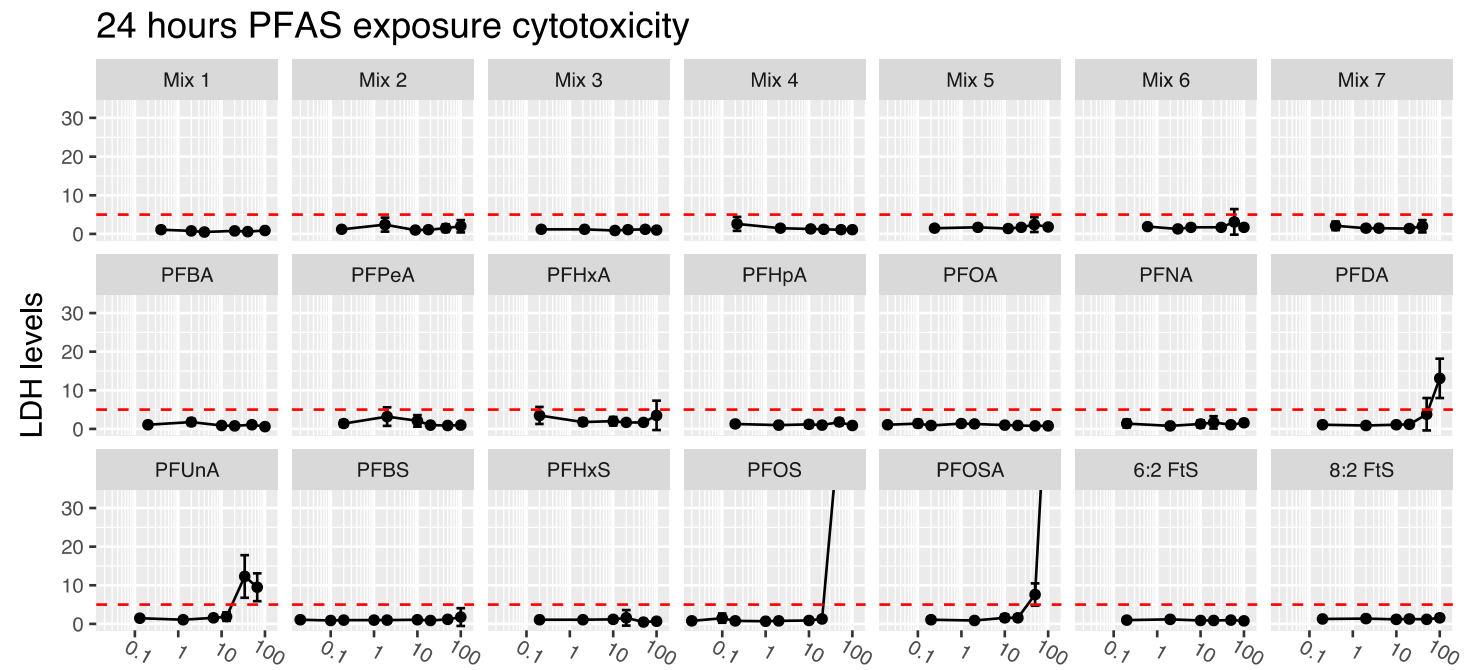
# Gene expression measurement

- Transcriptomics
    - Measure cellular compensation response
    - Direct activation of transcription factors
    - Global and specific effects
  - TempO-Seq
    - Oligo based gene expression
    - Assesses expression of specific genes
    - Higher number of genes than microarray
    - Sequencing screens out background
    - Higher throughput than RNA seq
  - S1500+
    - 2753 genes
    - Representative of diverse biological space
    - More economical than whole transcriptome
- TempO-Seq



# PFAS Cytotoxicity

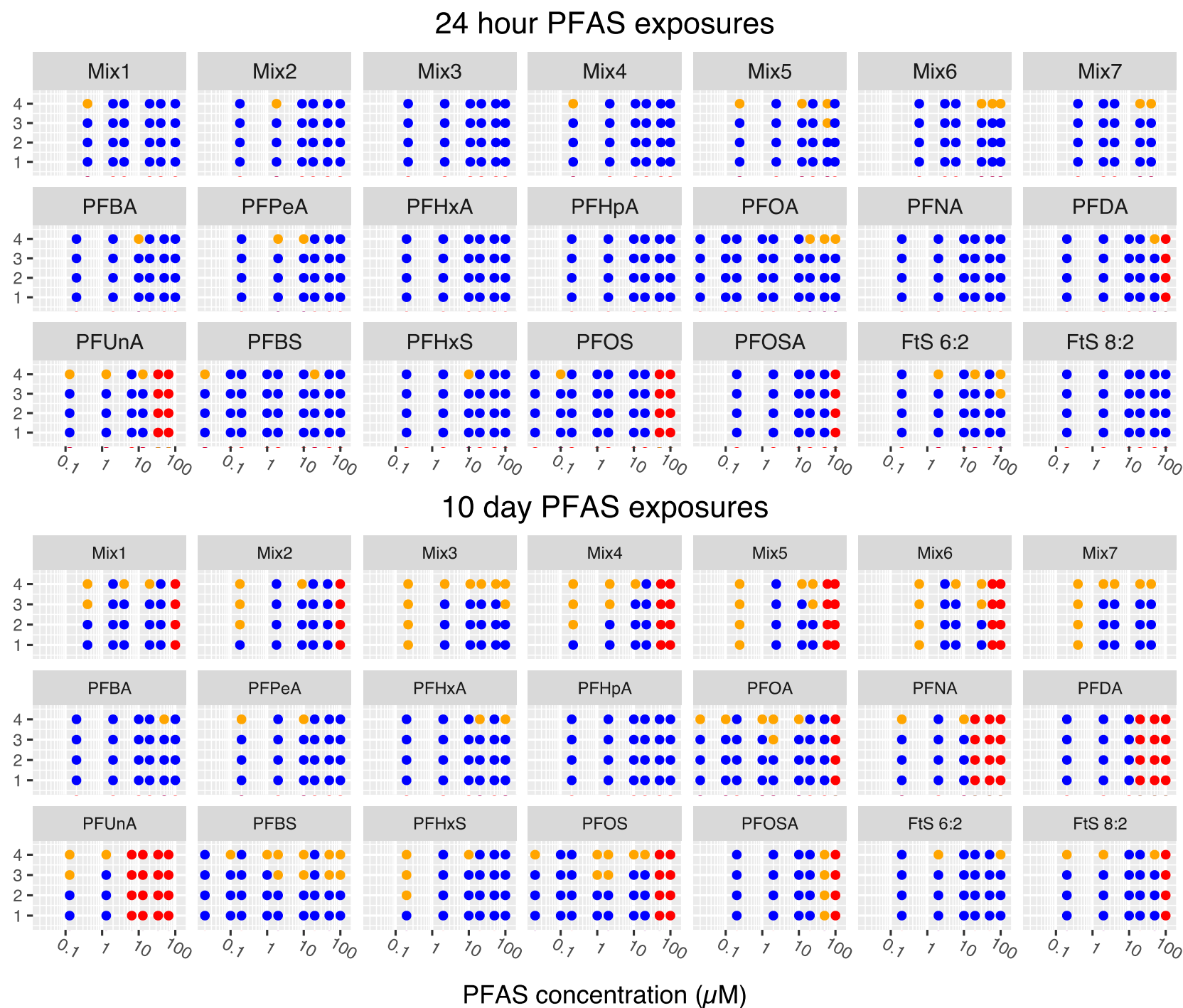
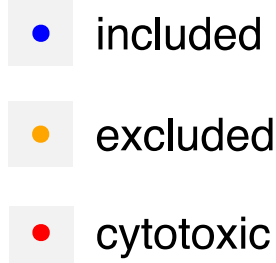
Sequencing data for cytotoxic samples removed from downstream data processing to improve statistical power for data quality control



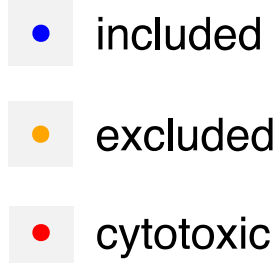
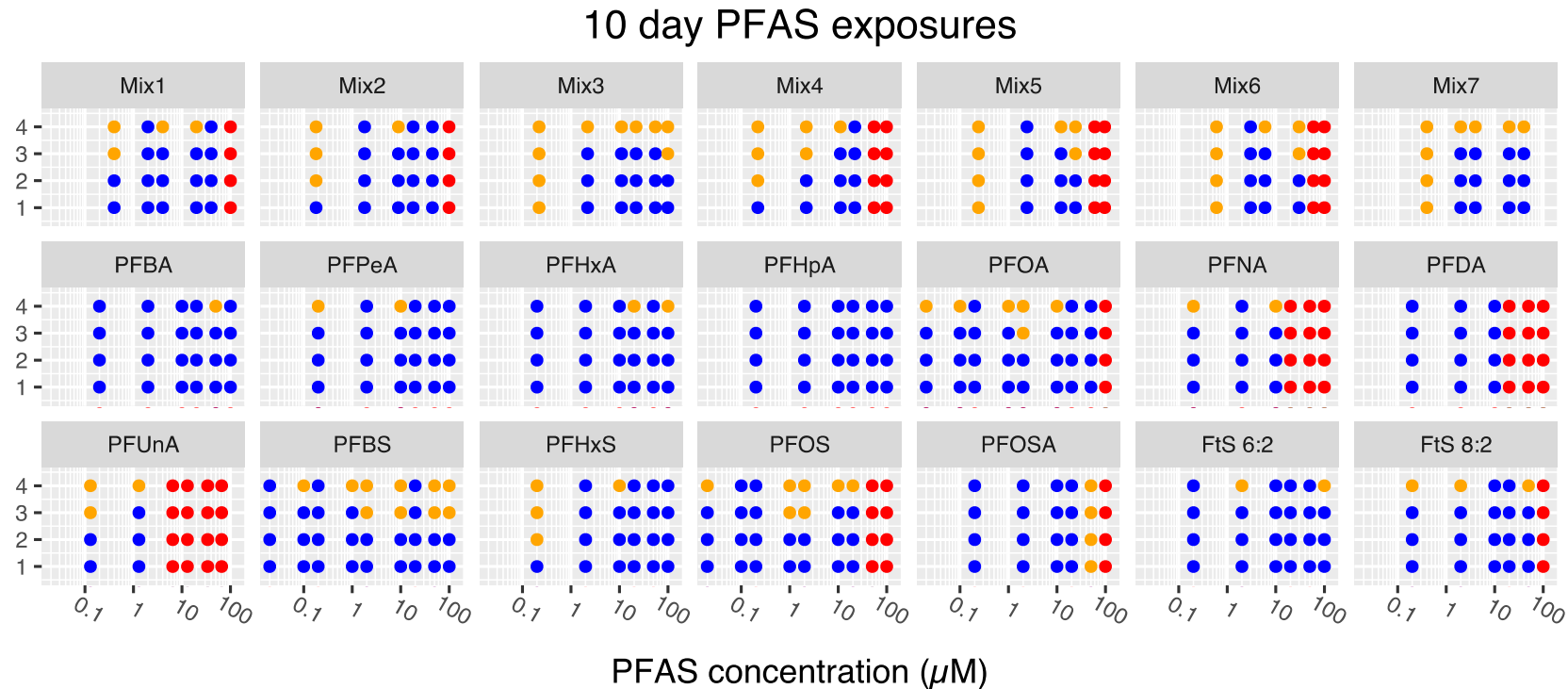
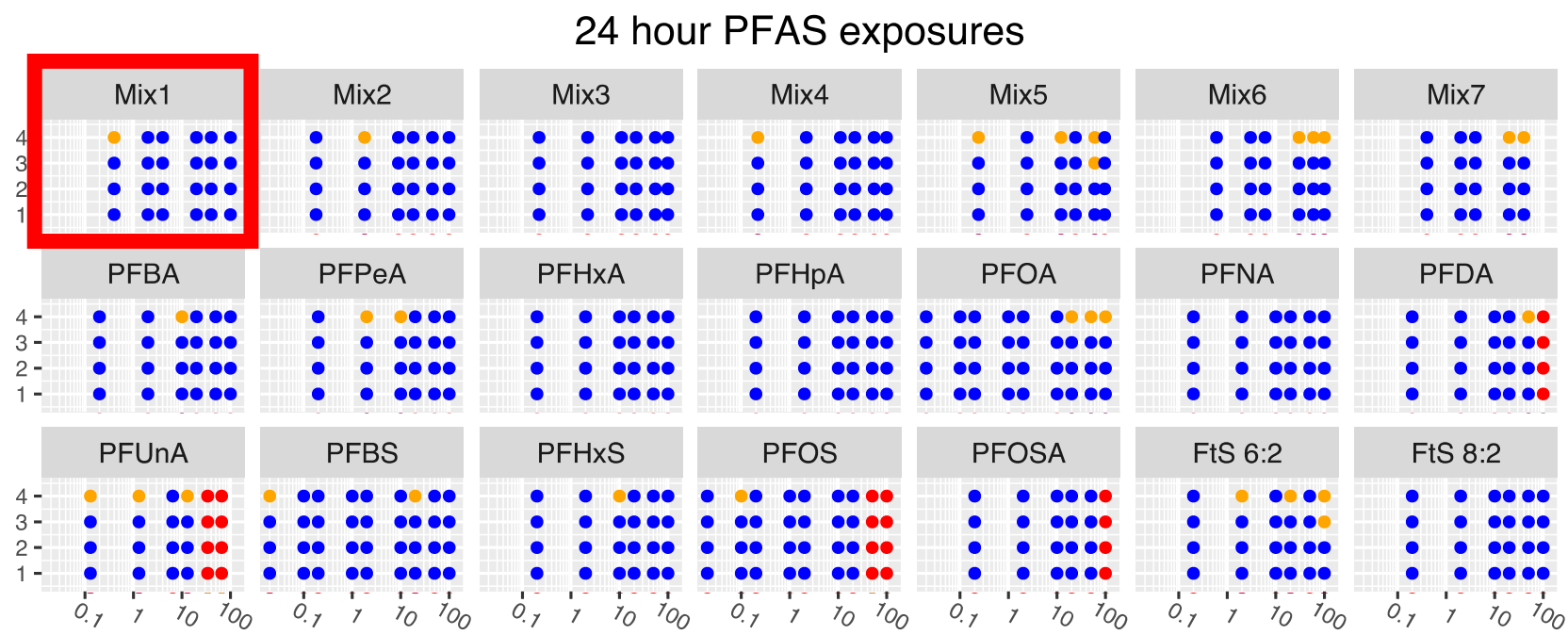
# Quality Control (QC)

Sequencing data was screened for several measures to ensure data quality

- Clustering distance
- Number of mapped reads
- Fraction of mapped reads
- Number of active probes
- Number of probes with 80% of signal
- Gini coefficient

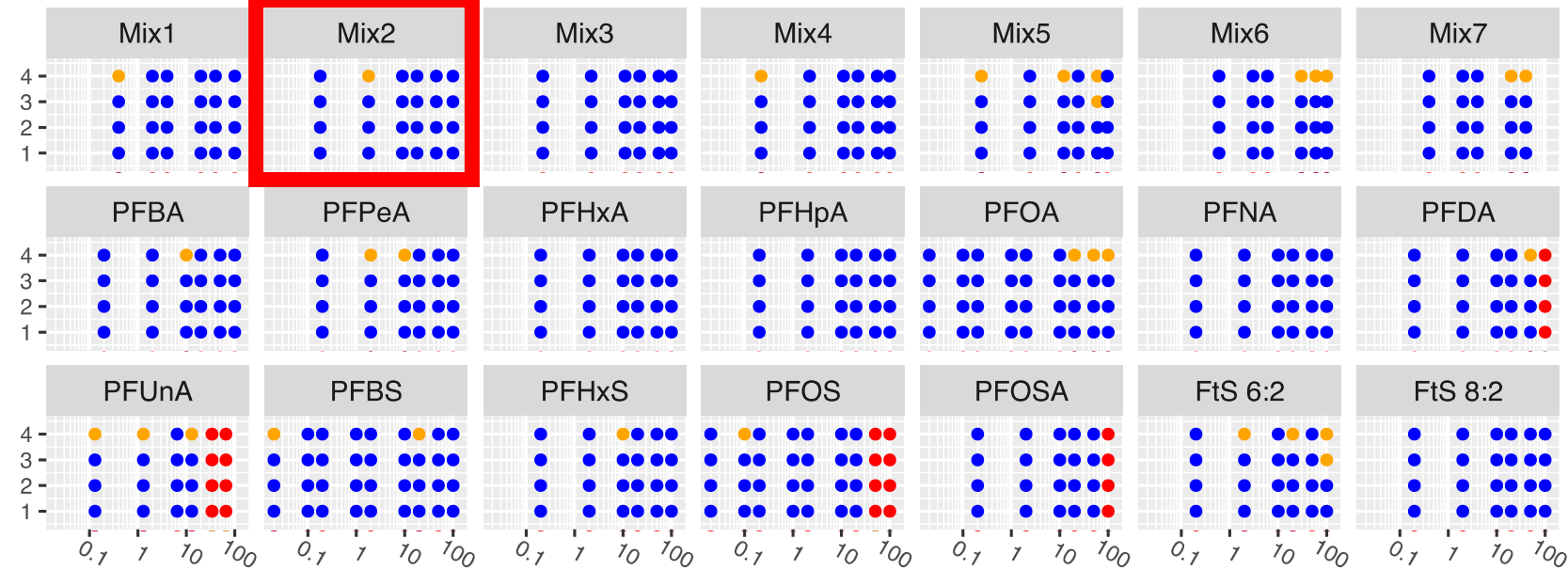


Data passing QC for each PFAS or Mixture at 24 hours or 10 days (Exposure Series) is used for BMC determination

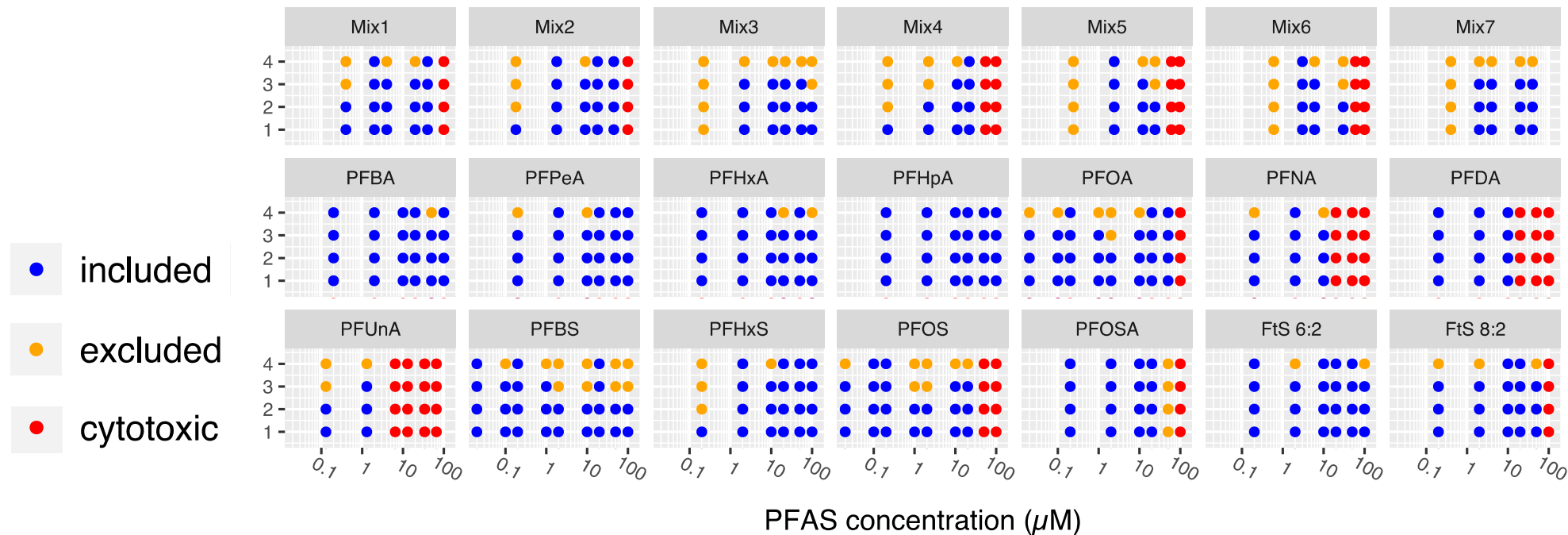


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### 24 hour PFAS exposures

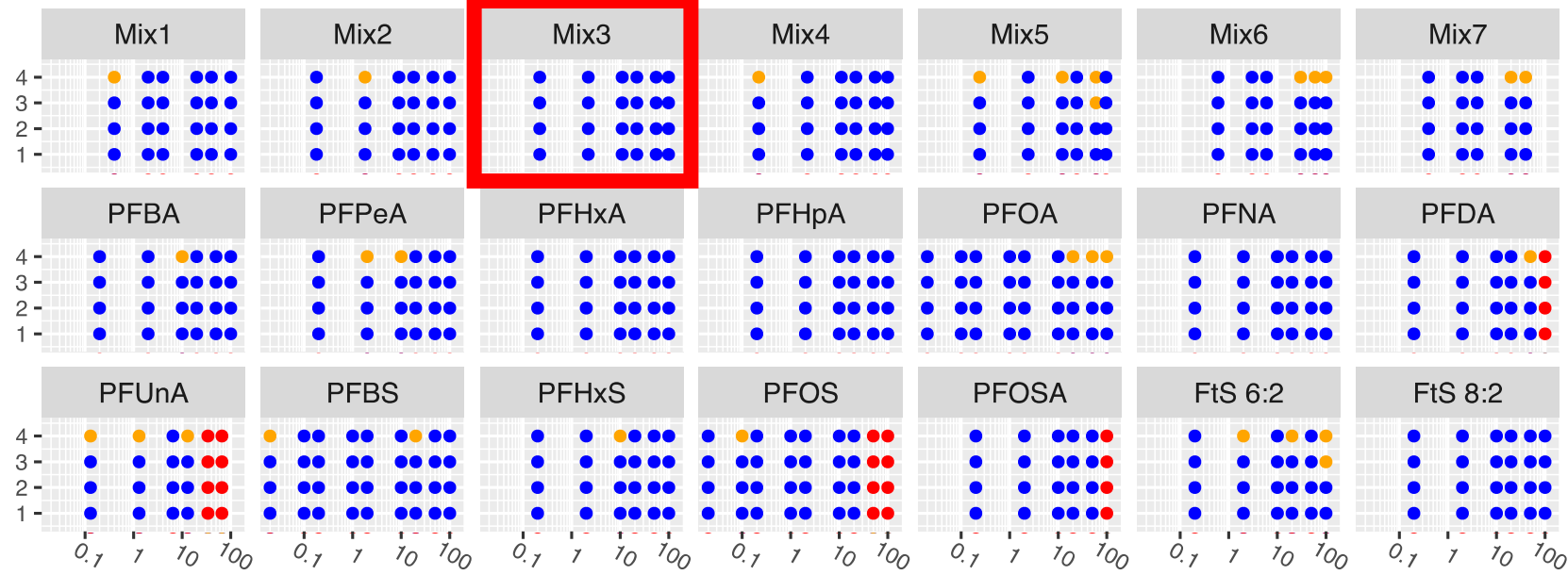


### 10 day PFAS exposures

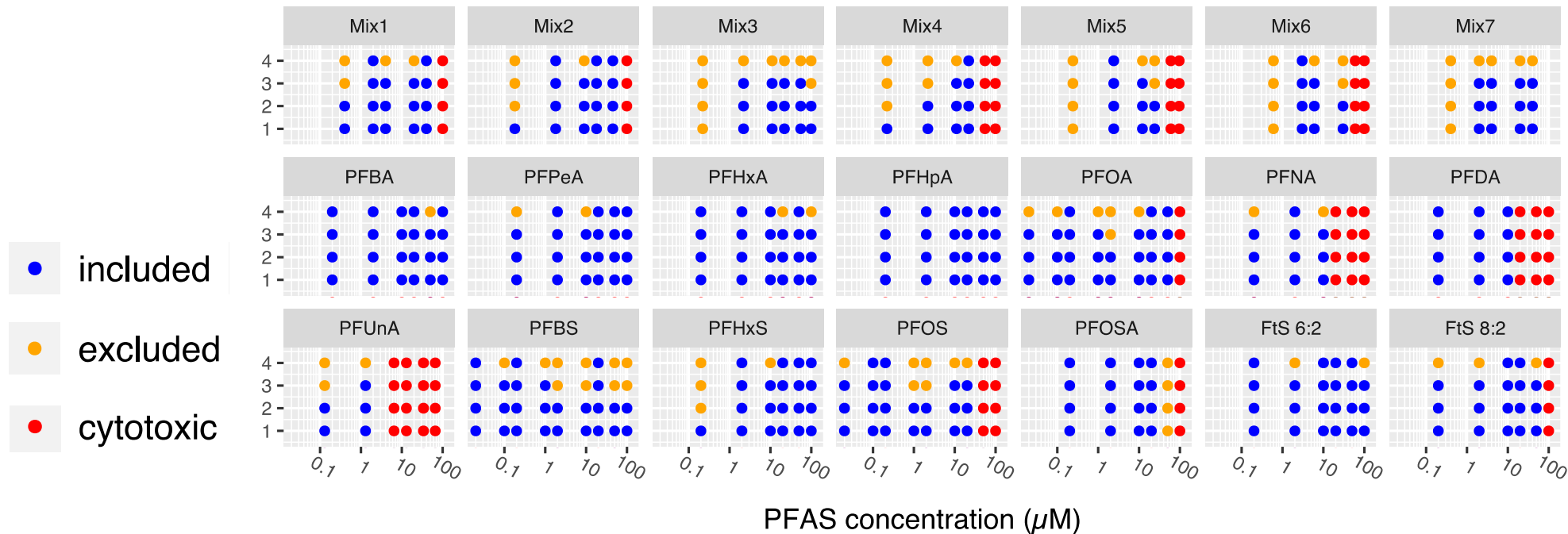


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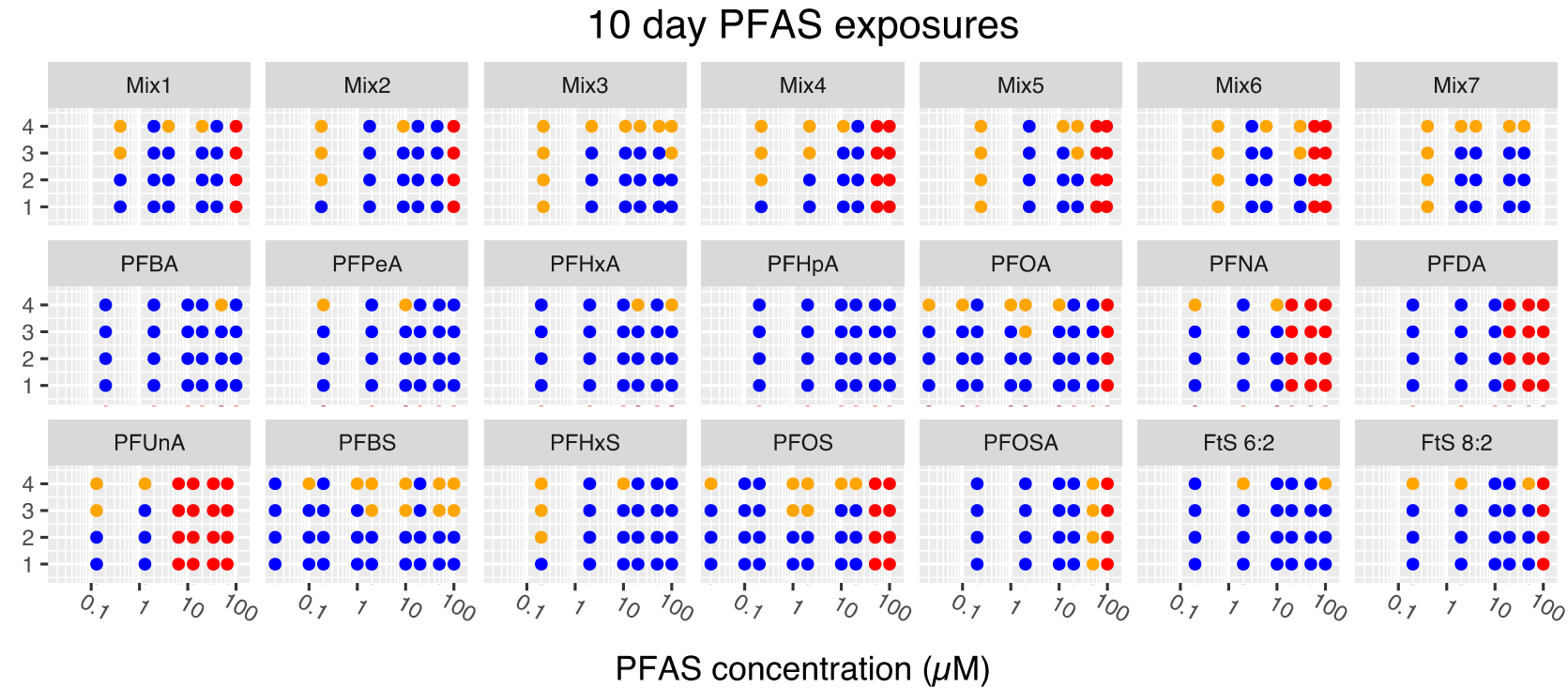
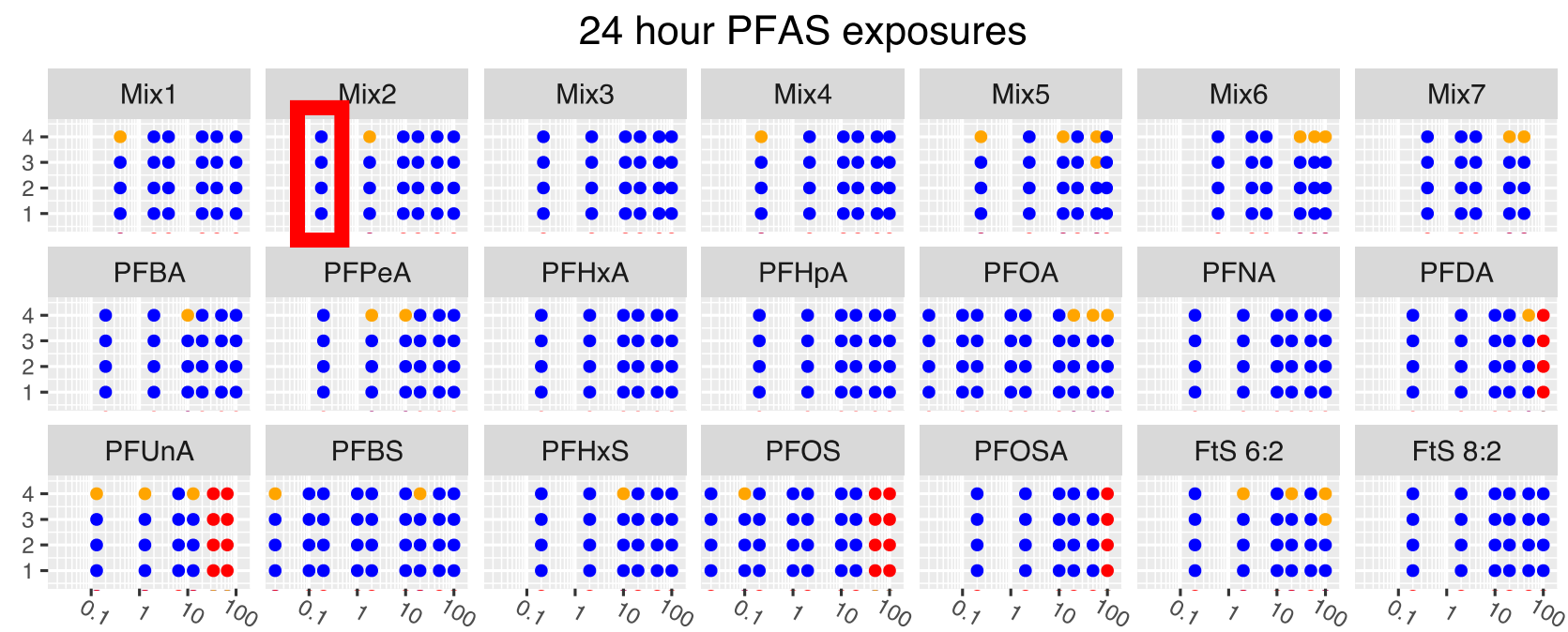


### 10 day PFAS exposures



# Bootstrapping

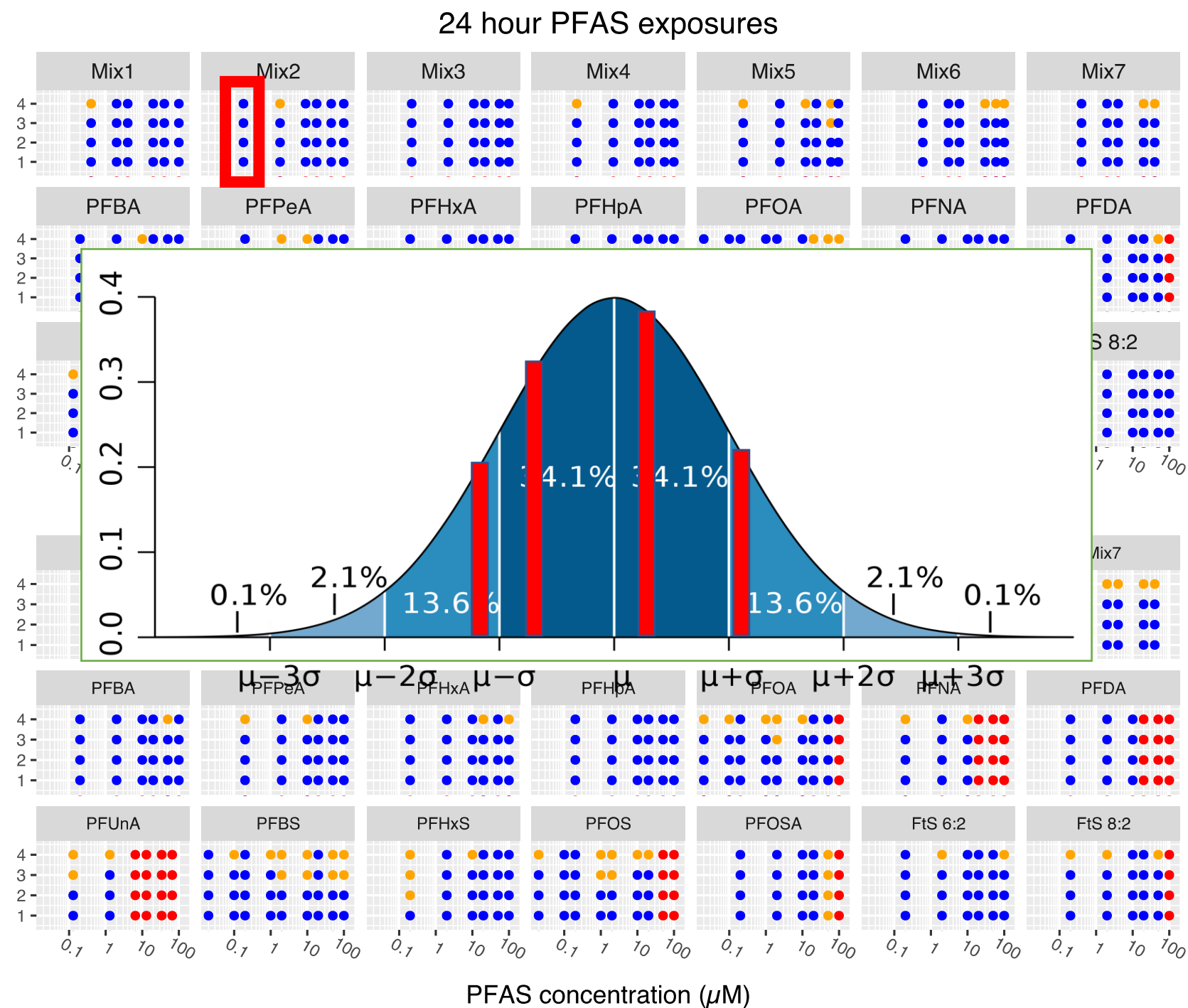
- Data for each concentration used for bootstrapping





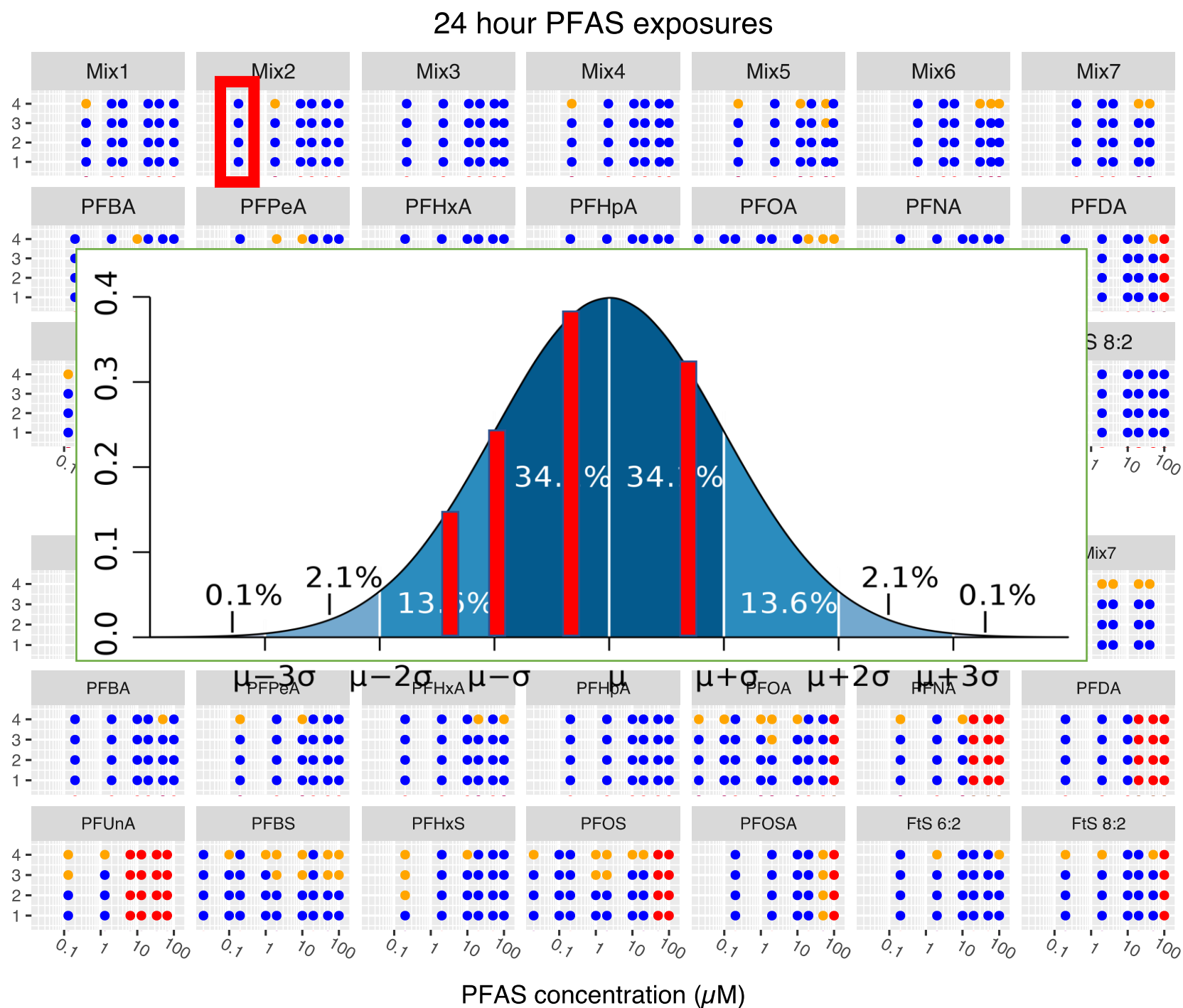
# Bootstrapping

- Data for each concentration used for bootstrapping
- Data for each gene, each exposure level and PFAS or mixture used to create a normal distribution



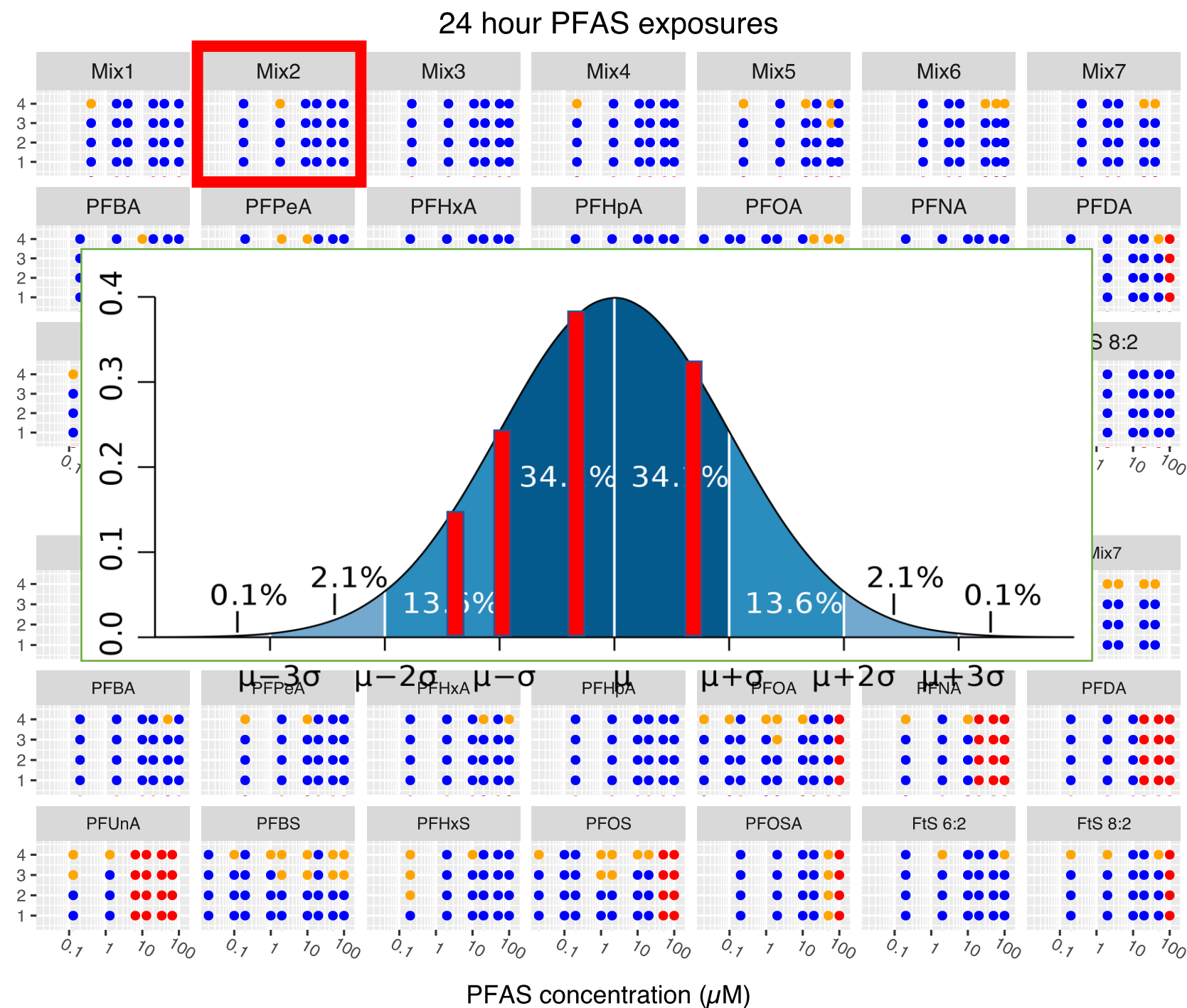
# Bootstrapping

- Data for each concentration used for bootstrapping
- Data for each gene, each exposure level and PFAS or mixture used to create a normal distribution
- Normal distributions are randomly sampled for each gene, exposure level and PFAS or mixture



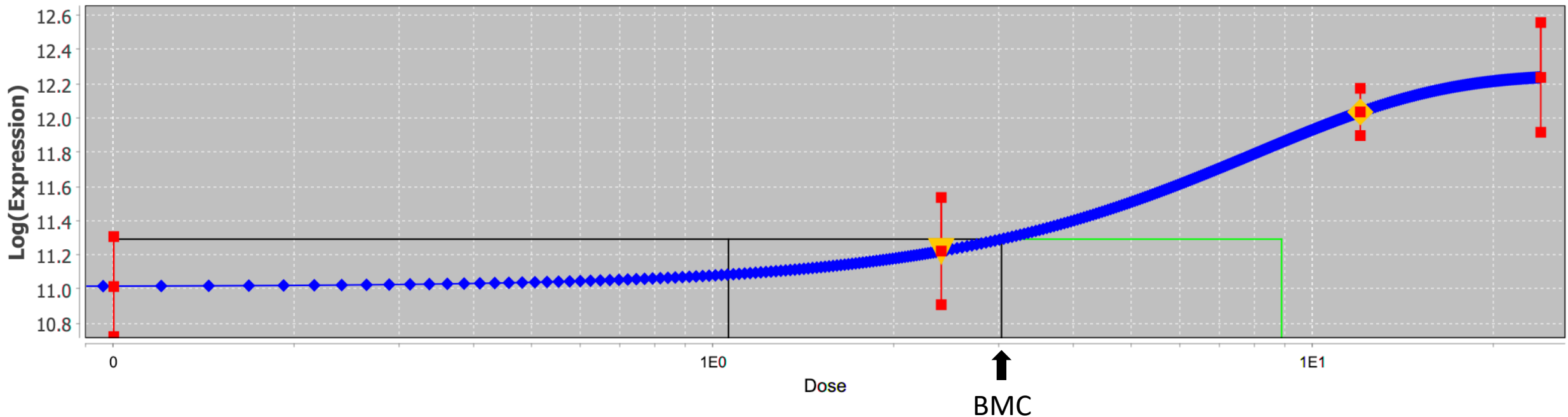
## Bootstrapping

- Data for each concentration used for bootstrapping
- Data for normal distributions are randomly sampled for each gene
- Normal distributions are randomly sampled for each gene, exposure level and PFAS or mixture
- End result is:
- 100 x exposure series simulations (for each gene for each PFAS or mixture and exposure time)



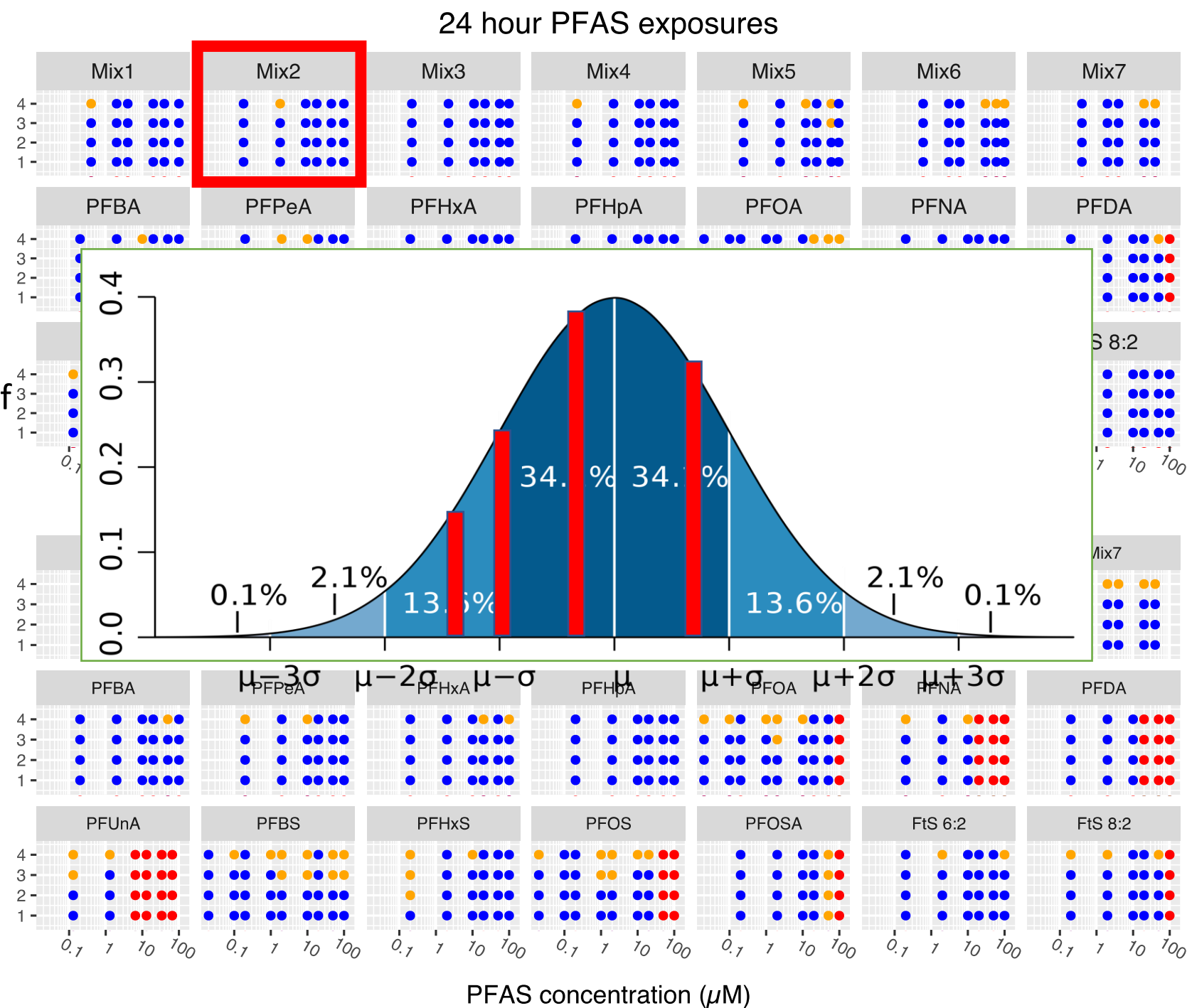
# BMC Determination using BMDExpress – Gene Expression

- Gene expression data for each PFAS / Mixture exposure series
  - Filtered for 1.5 fold change in expression
  - Williams trend test  $p = 0.01$
  - Plotted for dose response curve fitting
  - BMC is one standard deviation from the mean of the DMSO control



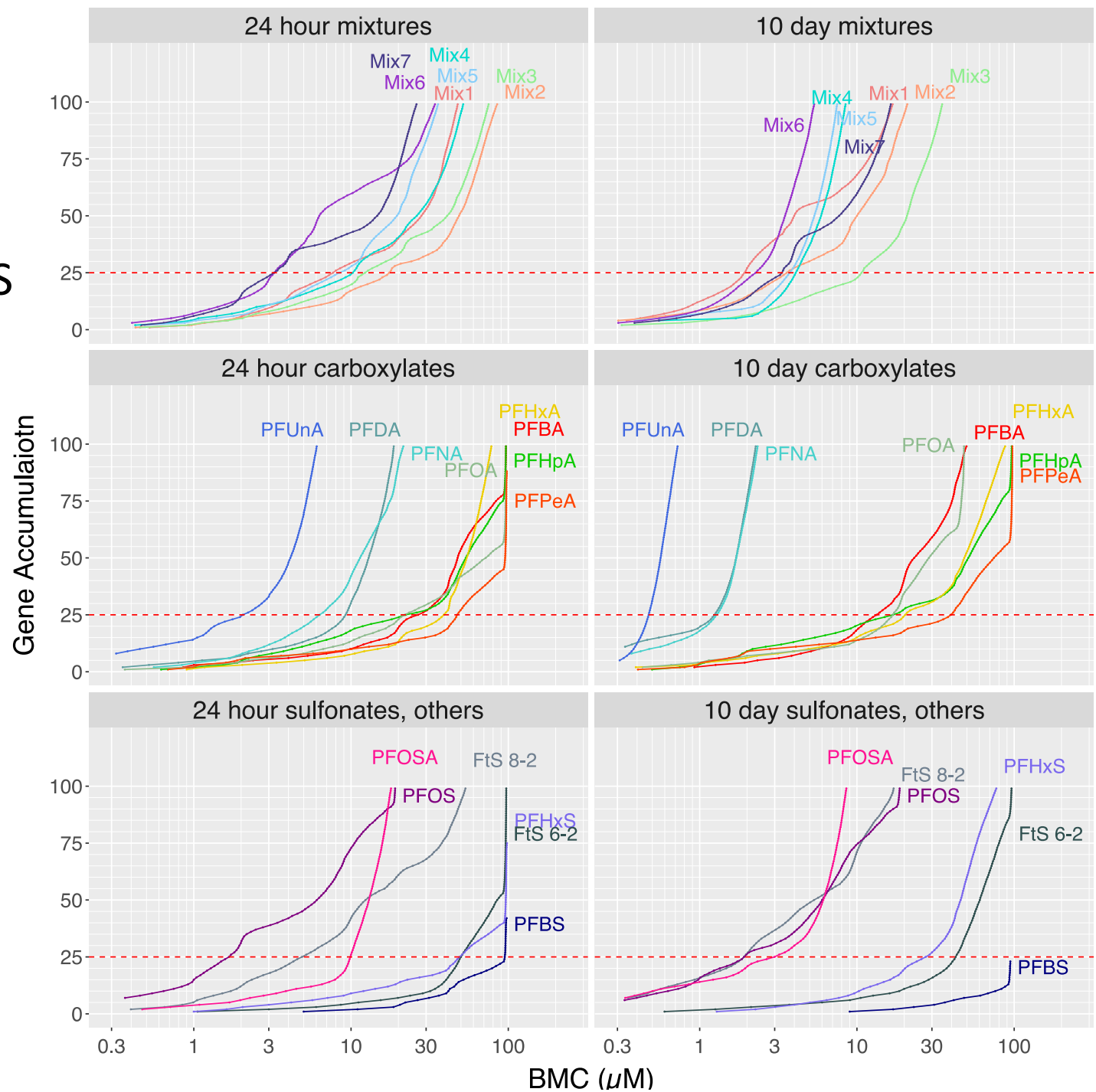
# Bootstrapping

- All BMCs for each exposure series are placed in a bootstrap distribution
- BMCs are sampled the appropriate number of times (depending on total number of BMCs)
- BMC list is ranked by BMC concentrations
- Repeated 10,000x resulting in list of potential BMCs for each rank
  - Lowest BMC
  - 2<sup>nd</sup> lowest BMC...
  - 25<sup>th</sup> lowest BMC
- For each BMC rank: median 2.5% and 97.5% values used for BMCs and 95% CIs



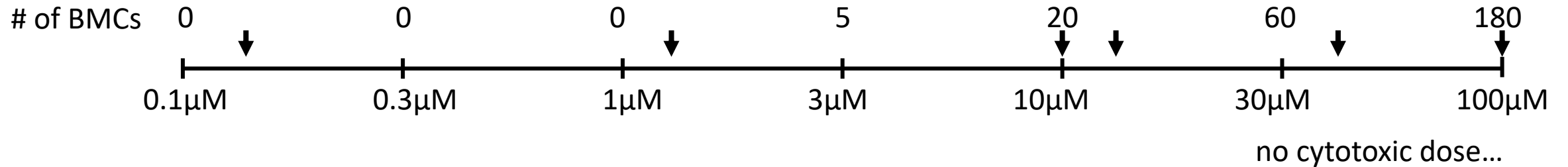
## BMC accumulation plots

- BMCs ranked from lowest concentration
  - 10s to 100s of BMCs for each PFAS
  - Total # of BMCs influenced by experimental parameters
    - Exposure concentrations
    - Cytotoxicity
- 25th BMC
  - Concerted molecular response
  - Concentration where gene expression changes broadly
    - Compensation to changes caused by toxicant exposure
    - Direct activation of transcription factors

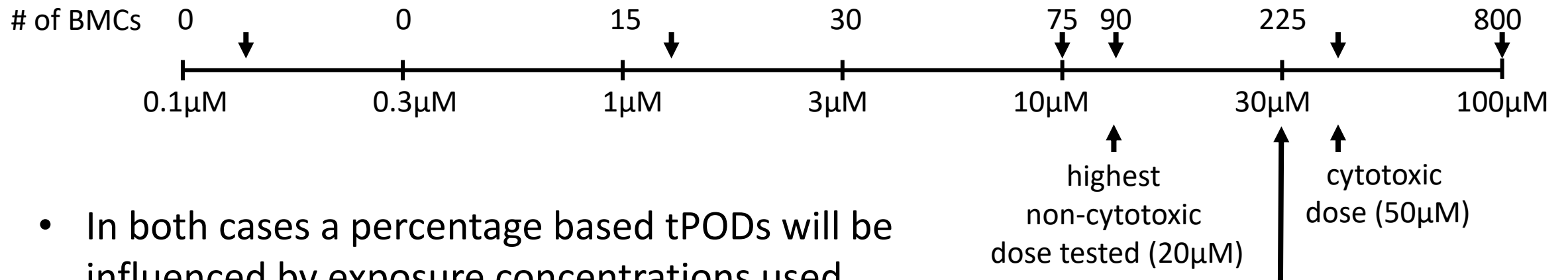


# 25<sup>th</sup> BMC – does not require accurate highest BMC #

- If highest dose is not cytotoxic more BMCs are possible



- If highest exposure is far from the cytotoxic dose more BMCs are possible



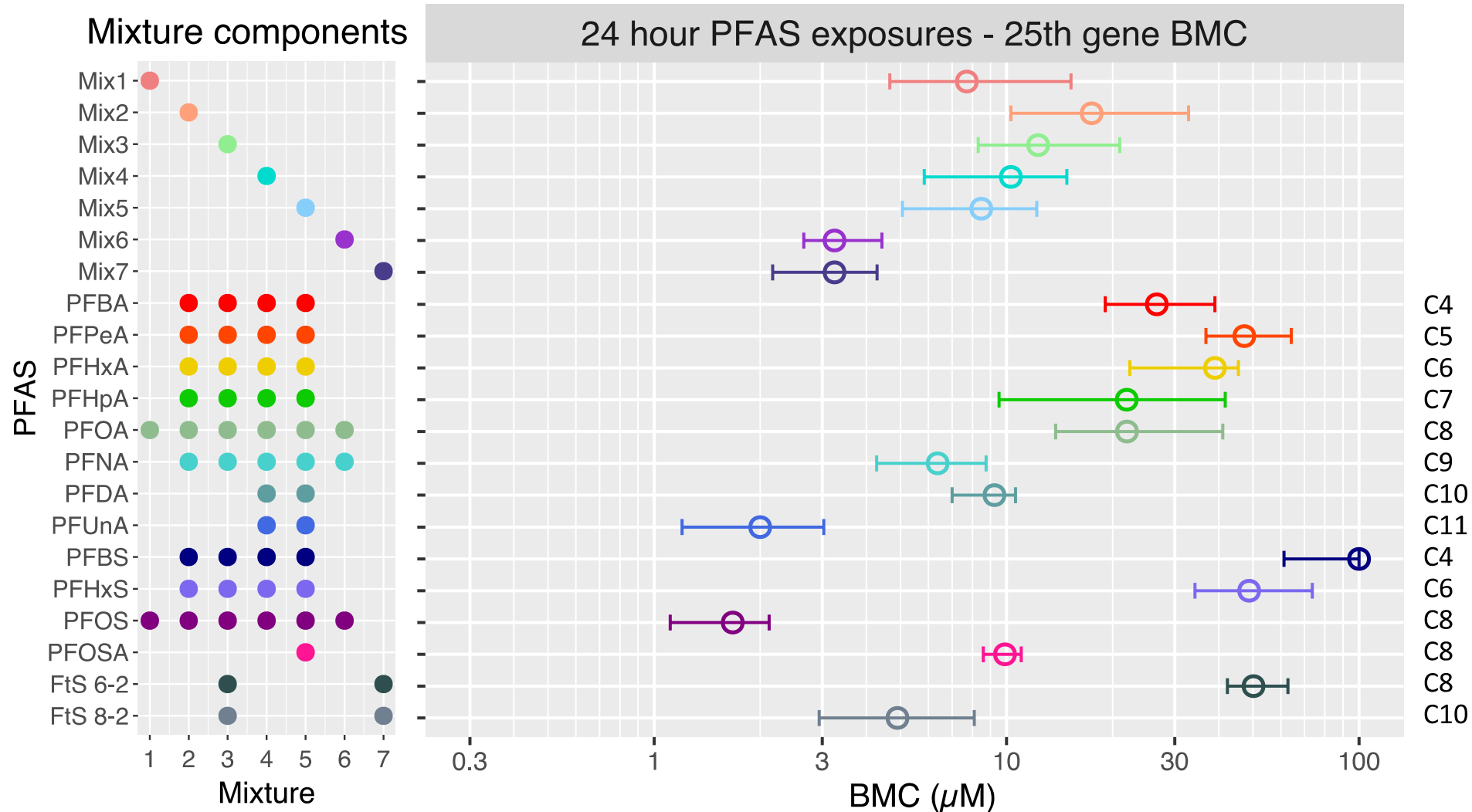
- In both cases a percentage based tPODs will be influenced by exposure concentrations used

If 30 μM exposure was used and was non-cytotoxic more BMCs would be found!

# 25<sup>th</sup> BMCs for PFAS and mixture exposures

## PFAS Potency

- Longer chain PFAS generally more potent
- Different potency depending on type of PFAS
- Mixtures seem to have potency corresponding to their constituents

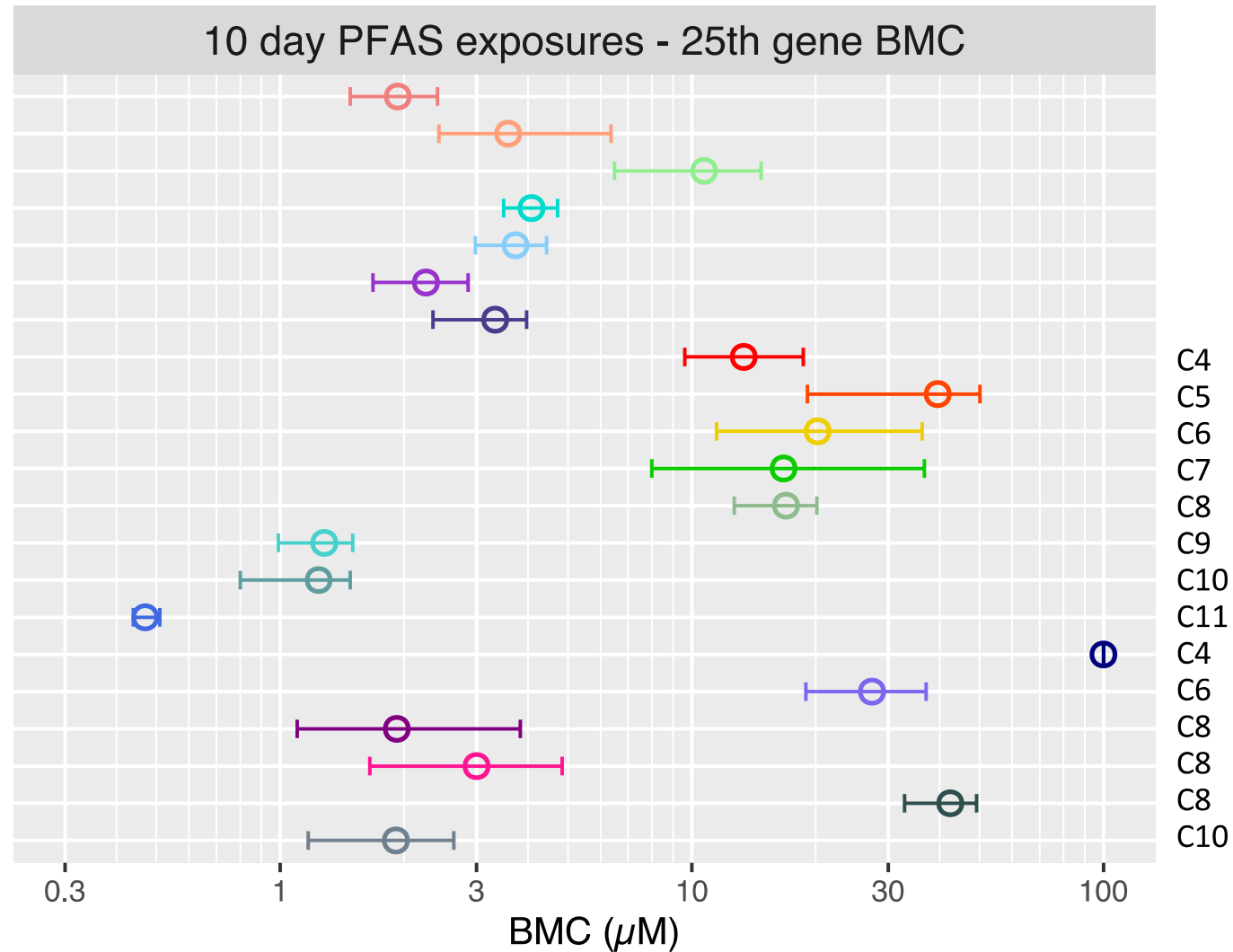
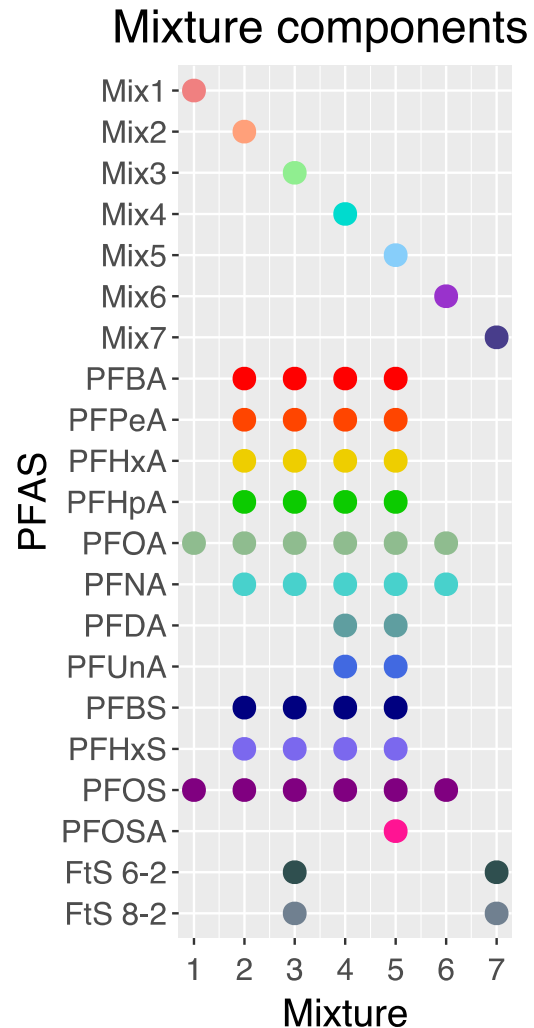




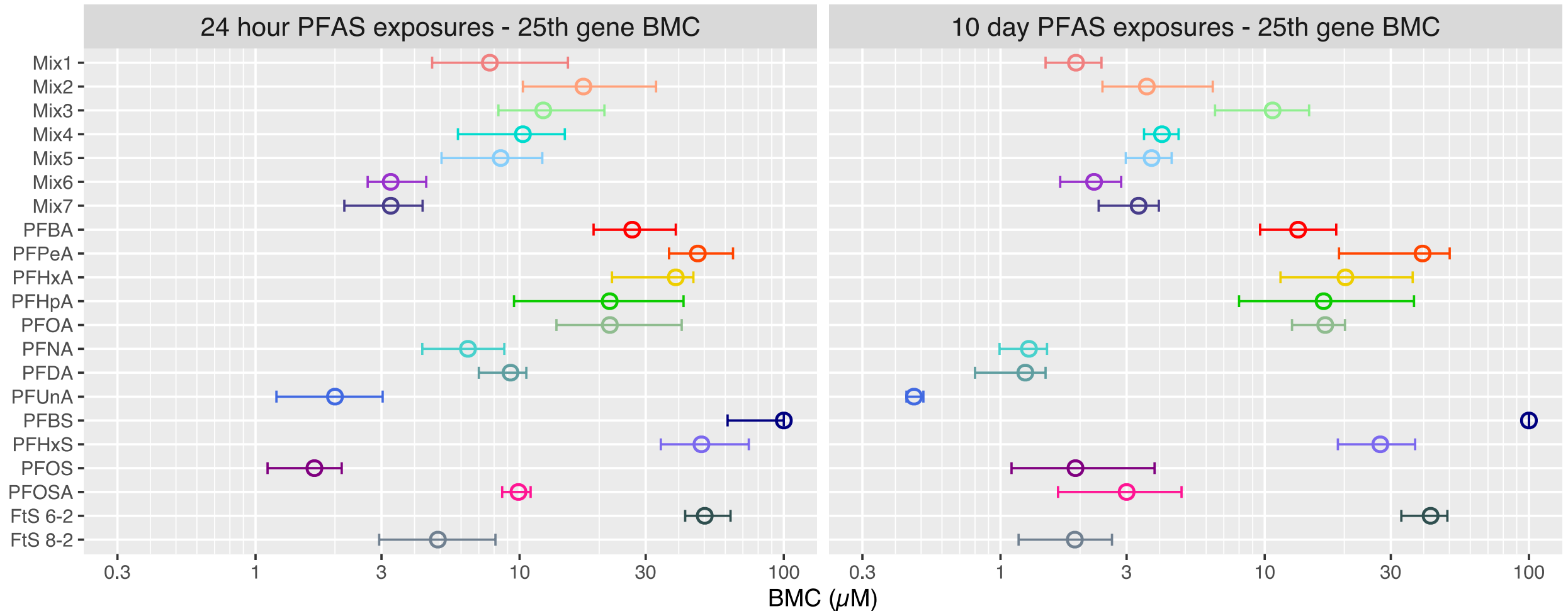
# 25<sup>th</sup> BMCs for PFAS and mixture exposures

## PFAS Potency

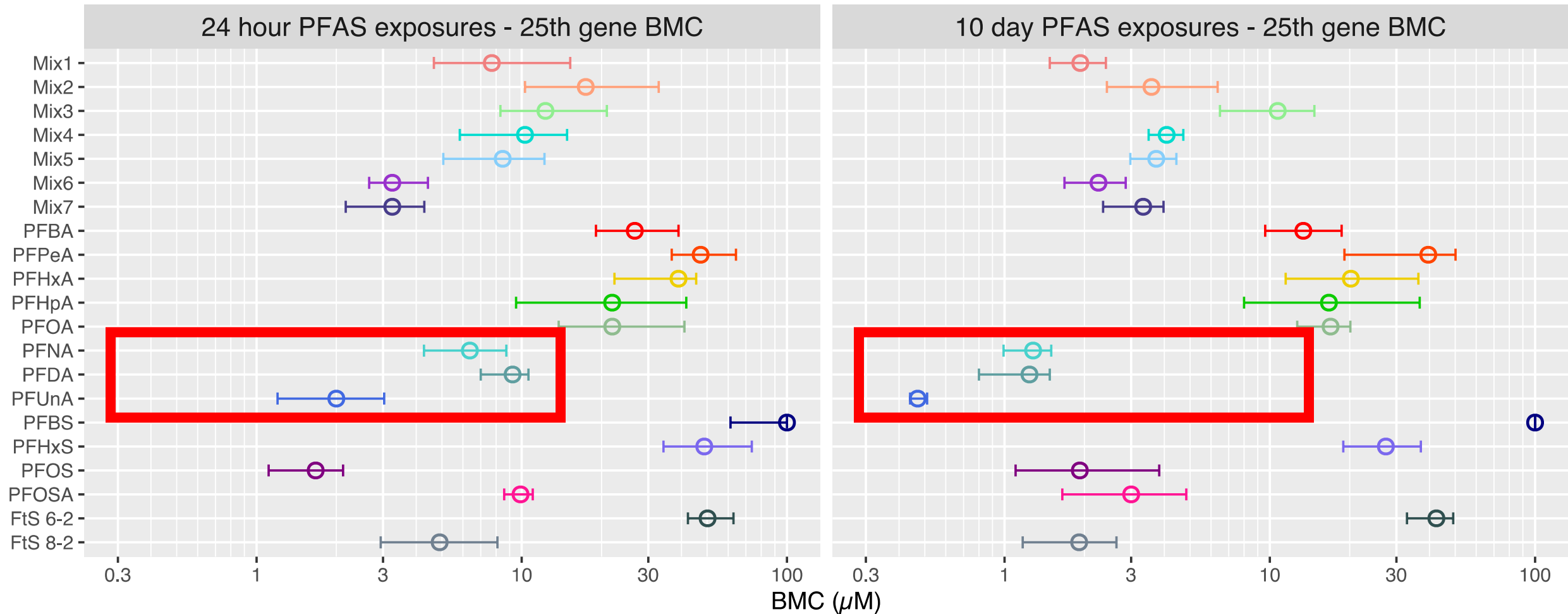
- Longer chain PFAS generally more potent
- Different potency depending on type of PFAS
- Mixtures seem to have potency corresponding to their constituents



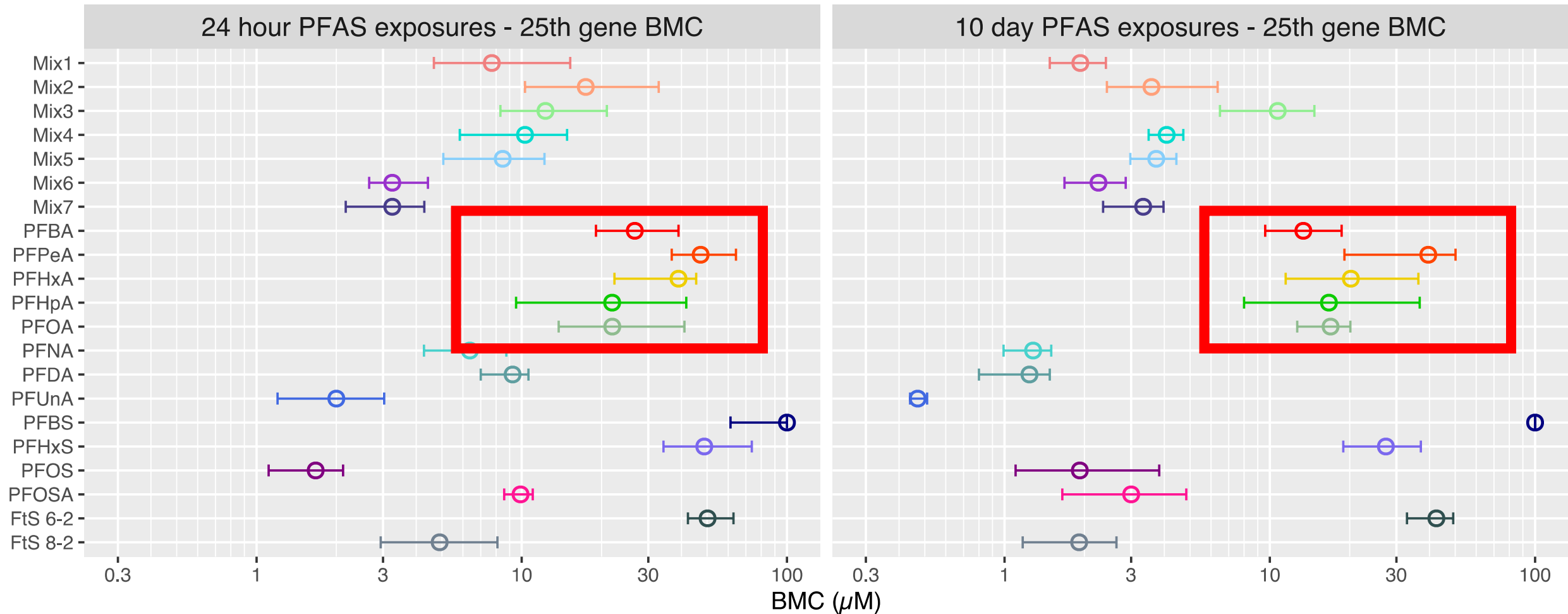
# 25<sup>th</sup> BMCs for PFAS and mixture exposures



# 25<sup>th</sup> BMCs for PFAS and mixture exposures

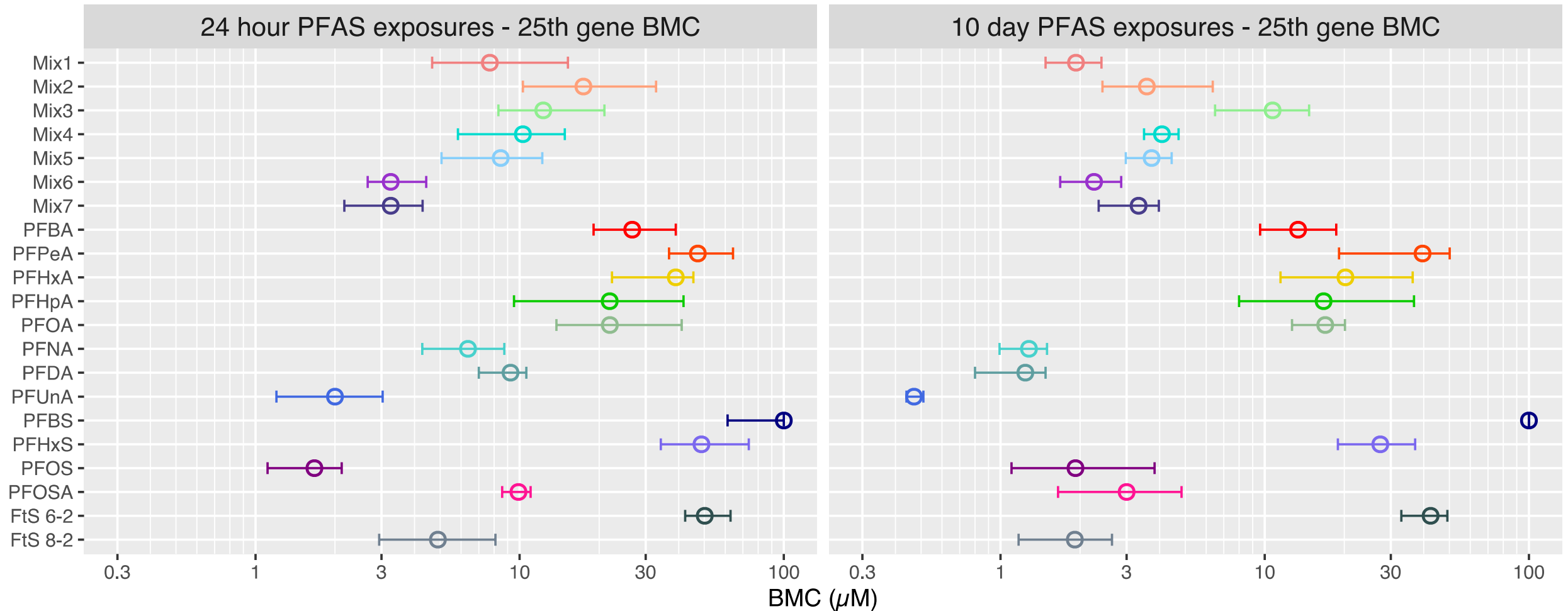


# 25<sup>th</sup> BMCs for PFAS and mixture exposures












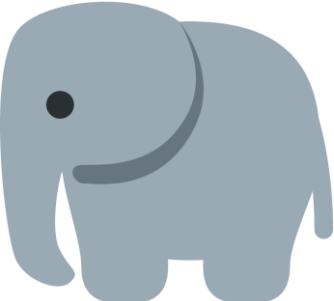


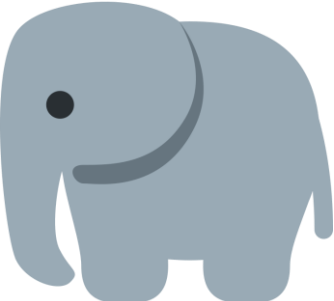


# 25<sup>th</sup> BMCs for PFAS and mixture exposures

Are mixture potencies comparable to expectation based on single PFAS potencies?



# Analysis of Mixtures – Potency and BMC

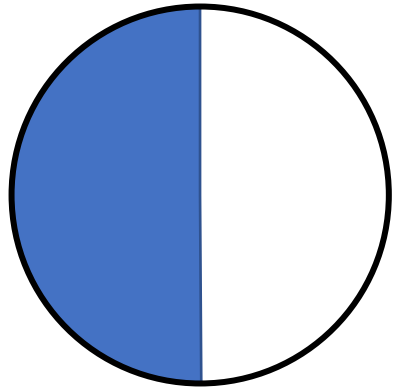
- Chemicals having different relative potencies have stronger effects at the same dose
- BMCs are the doses of substances that result in the same specified effect
- BMC is reciprocal of Potency

	Relative Potency		BMC		
• Morphine	1 x		1		
• Hydromorphone	10 x		0.1		
• Fentanyl	100 x		0.01		
• Sufentanil	1,000 x		0.001		
• Carfentanil	10,000 x		0.0001		

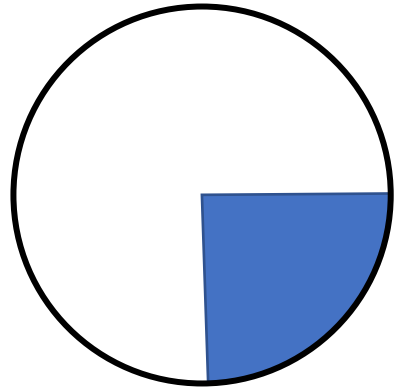
\*example only – Dr. Addicks is not a physician or veterinarian

# Concentration addition (aka dose addition)

Chemical 1  
potency =  $1/2$  BMC = 2



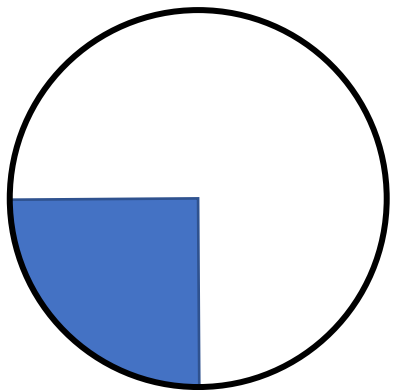
Chemical 2  
potency =  $1/4$  BMC = 4



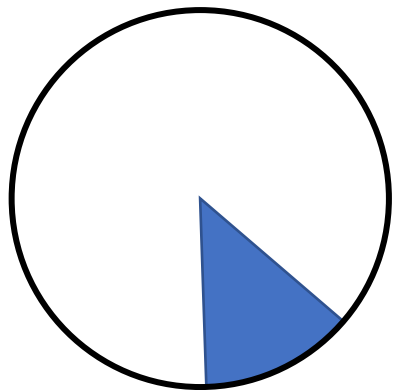
- Equimolar mixture of chemicals 1 and 2
- Total PFAS concentration in the mixture is the same
- Concentration (and potency) of each PFAS in mixture is half

↓ Mixture of 1 and 2 ↓

potency =  $1/4$  BMC = 4



potency =  $1/8$  BMC = 8



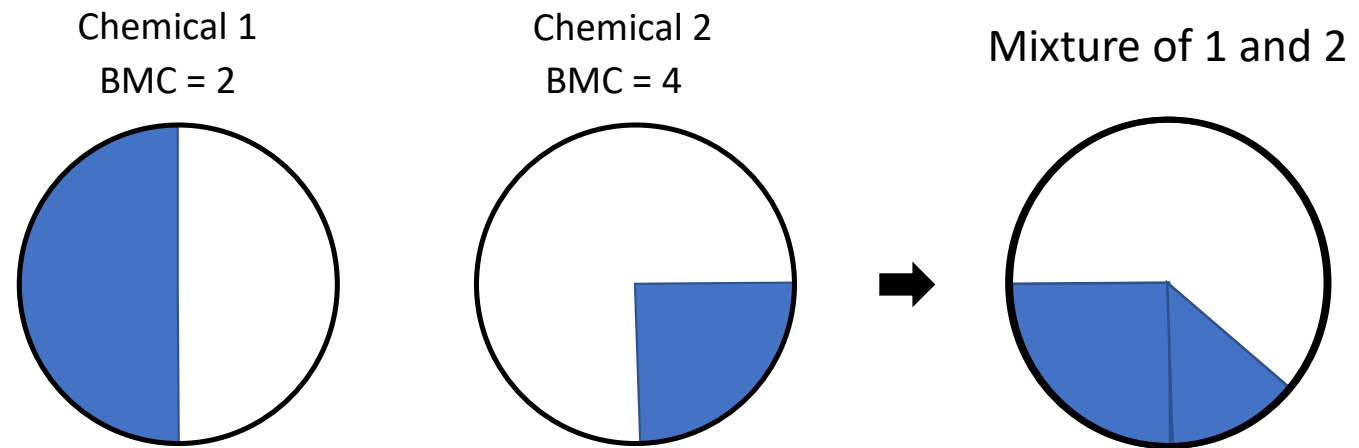
potency =  $3/8$  BMC =  $8/3$  (2.67)

+ =

# Predicted mixture BMC calculations - based on dose addition

$$ECx_{\text{Mix}} = \left( \sum_{i=1}^n \frac{p_i}{ECx_i} \right)^{-1}$$

$$BMC_{\text{mix}} = \left( \sum \frac{\text{Fraction}_i}{BMC_i} \right)^{-1}$$



Fraction<sub>i</sub> = Fraction of each component in mixture

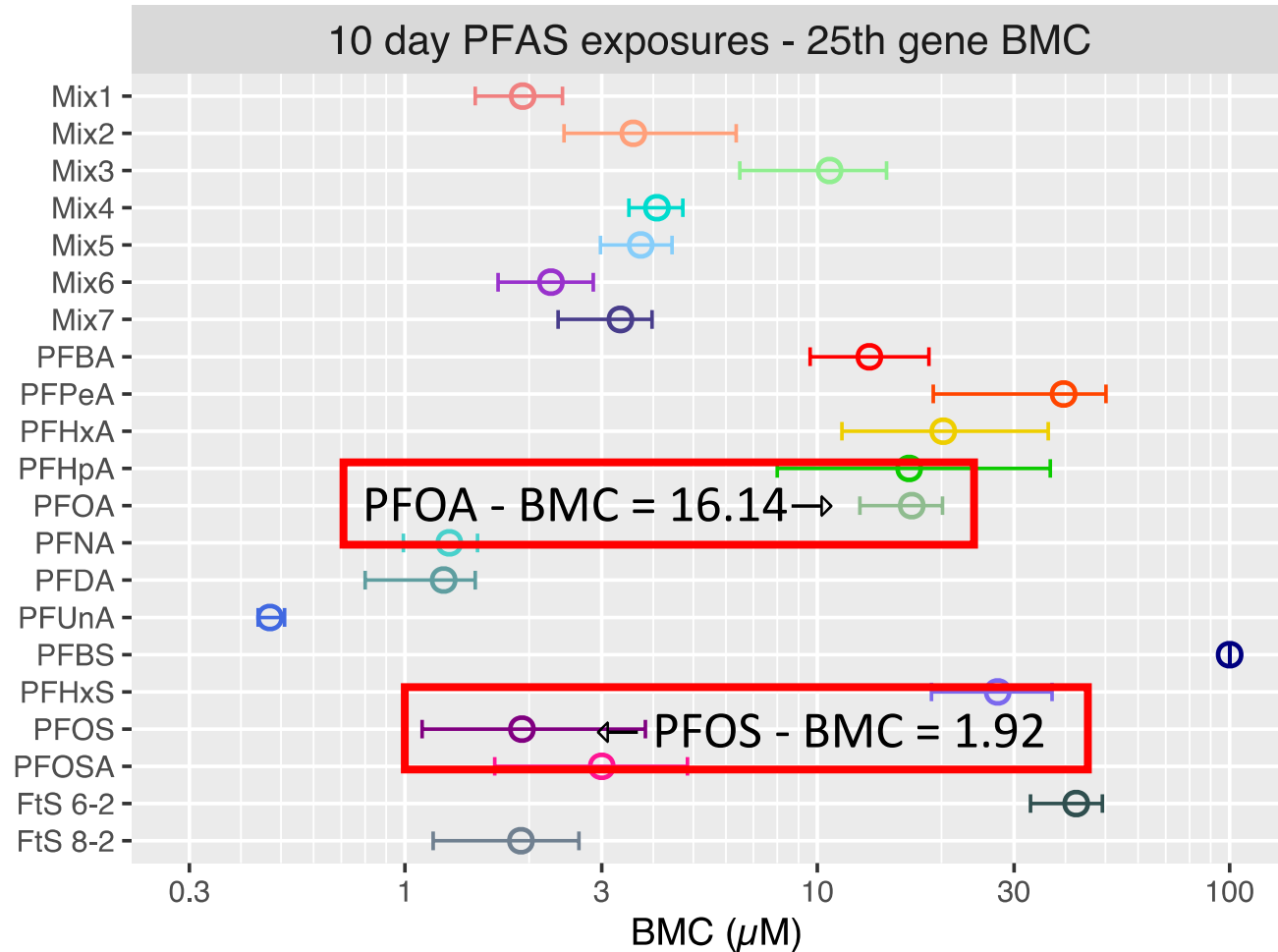
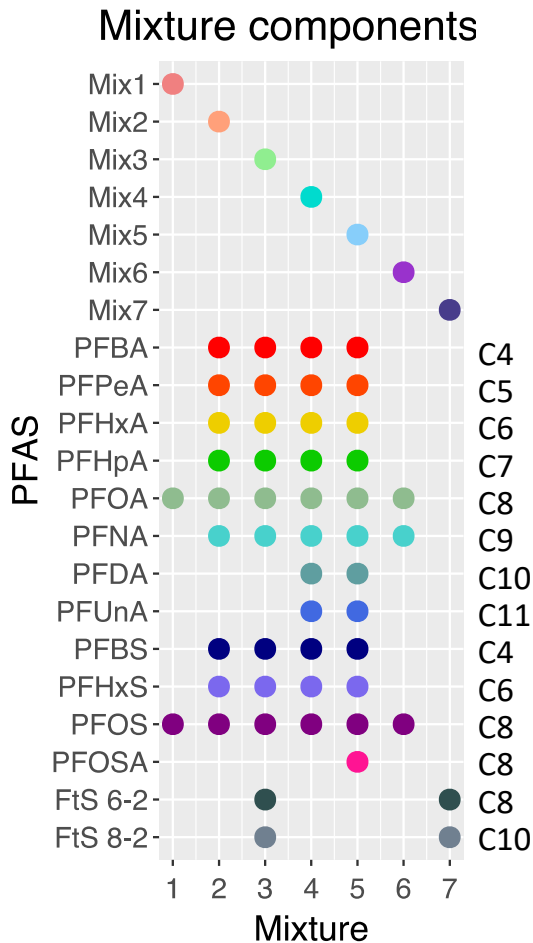
BMC<sub>i</sub> = BMC of each component in mixture

$$BMC_{\text{mix}} = \left( \sum \frac{0.5}{2} + \frac{0.5}{4} \right)^{-1} = \left( \sum \frac{1}{4} + \frac{1}{8} \right)^{-1} = \frac{3}{8}^{-1} = \frac{8}{3} = 2.67$$



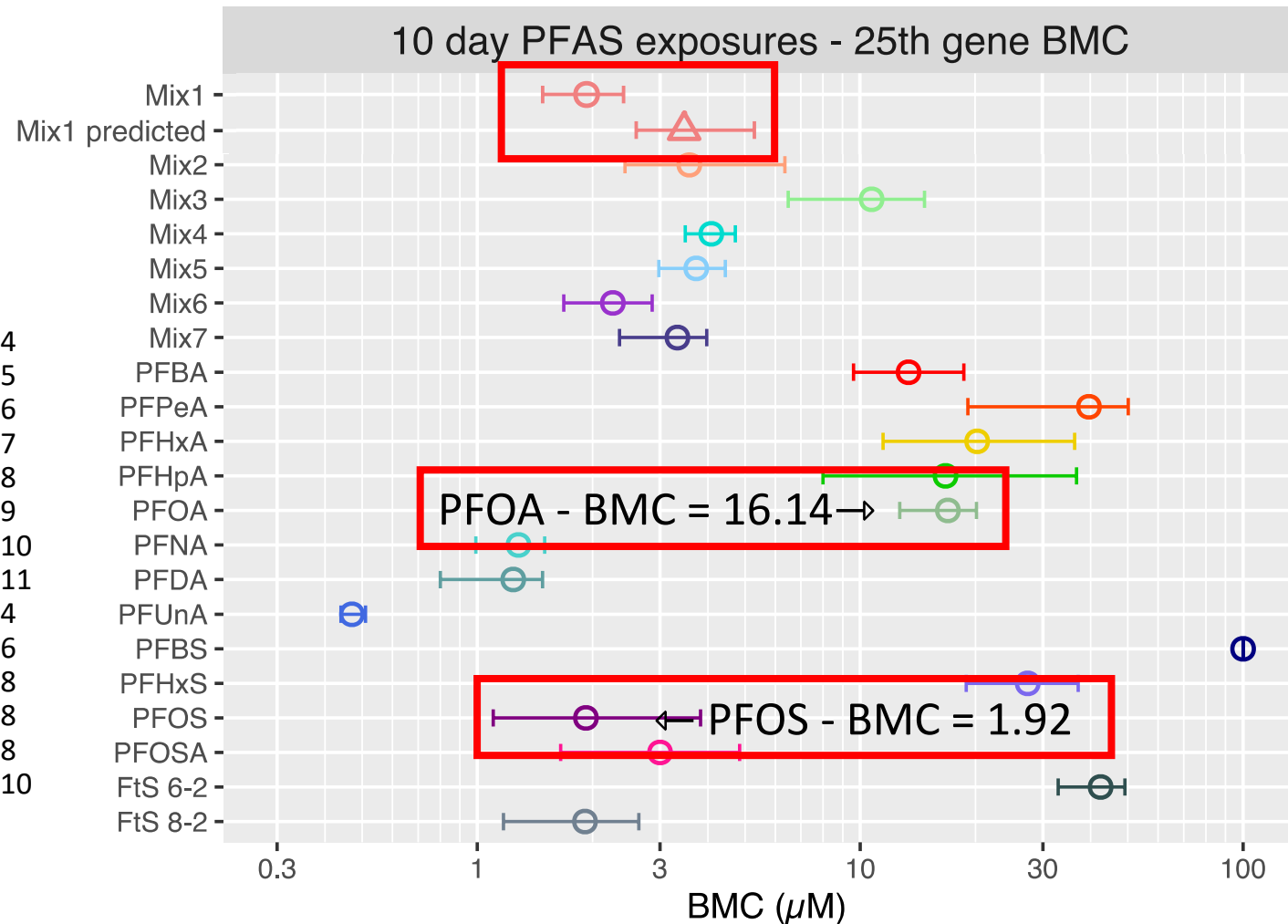
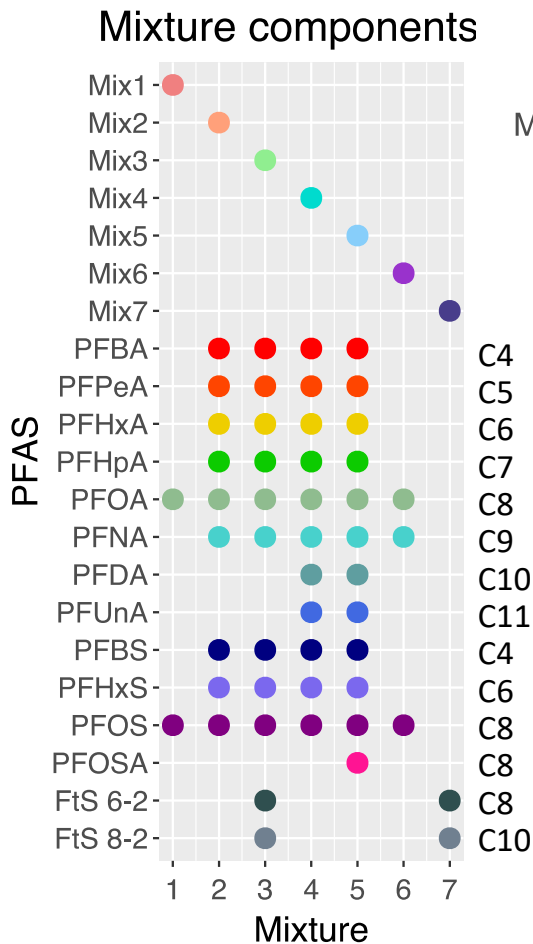
# BMC (mixture) of POFA and PFOS =

$$\text{Predicted BMC (mixture)} = \left( \frac{0.5}{16.14} + \frac{0.5}{1.92} \right)^{-1} = (0.0295 + 0.260)^{-1} = (0.290)^{-1} =$$



# BMC (mixture) of POFA and PFOS = 3.45

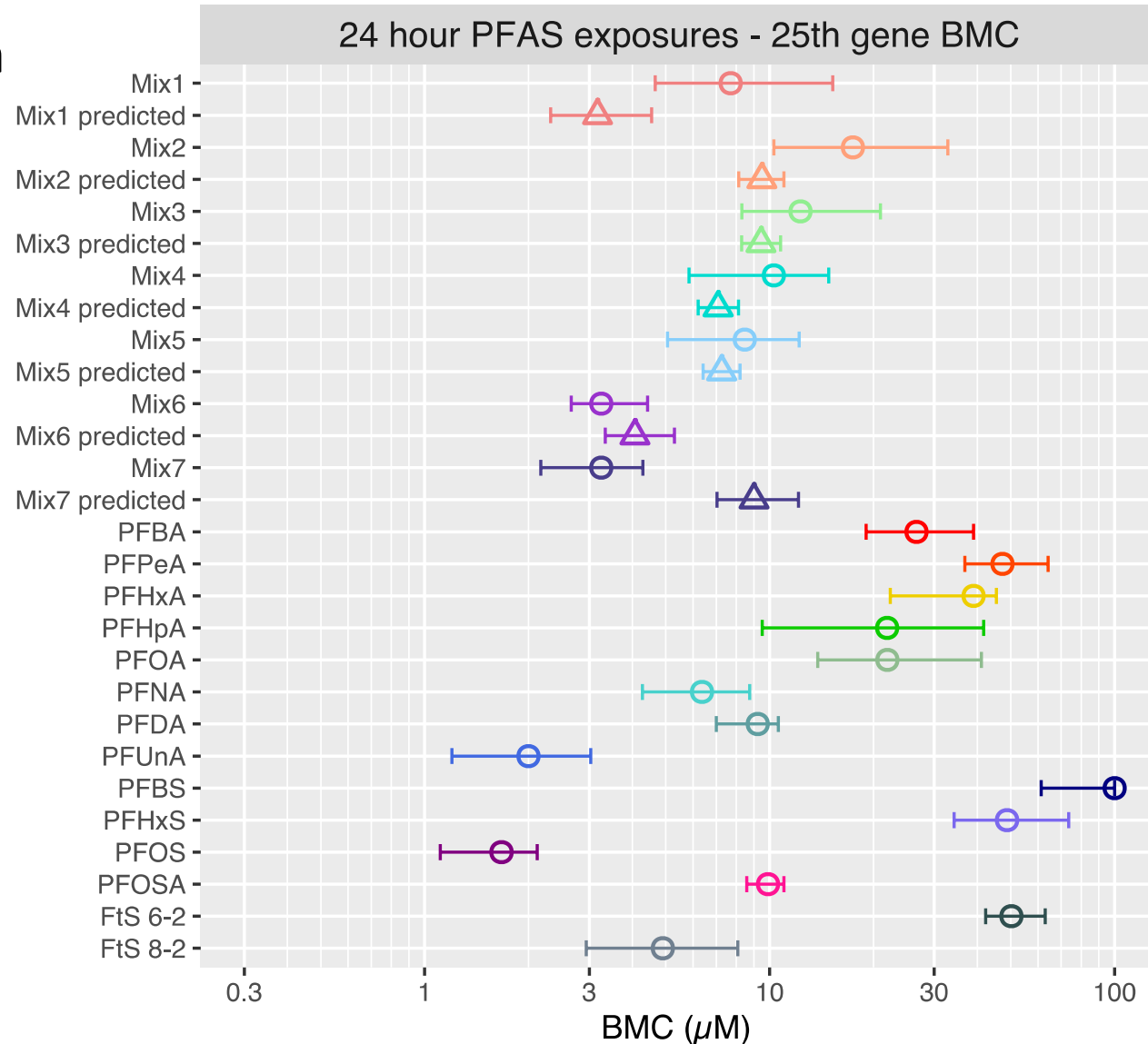
$$\text{Predicted BMC (mixture)} = \left( \frac{0.5}{16.14} + \frac{0.5}{1.92} \right)^{-1} = (0.0295 + 0.260)^{-1} = (0.290)^{-1} = 3.45 \mu\text{M}$$



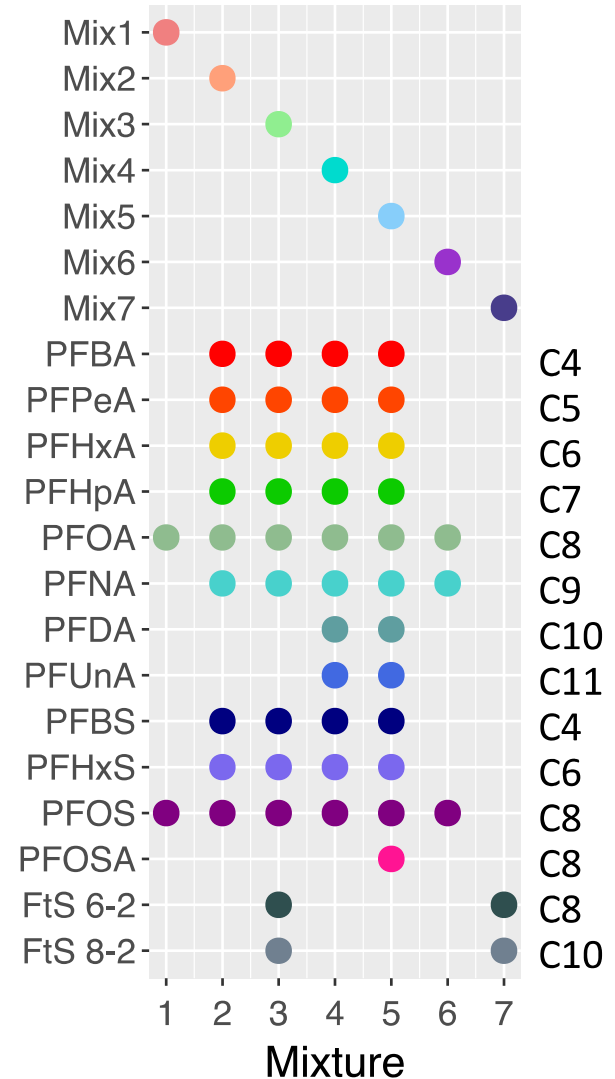
# 24 hour 25<sup>th</sup> gene BCMs (+/- BMCL/BMCU)

## Concentration Addition predicted BMCs

- Empirical – O
- Predicted – Δ
- No clear deviation from additivity
- Most have overlapping CIs
- Most have less than  $\pm 2$  fold differences in BMC
- All have less than  $\pm 2$  fold differences in CI endpoints



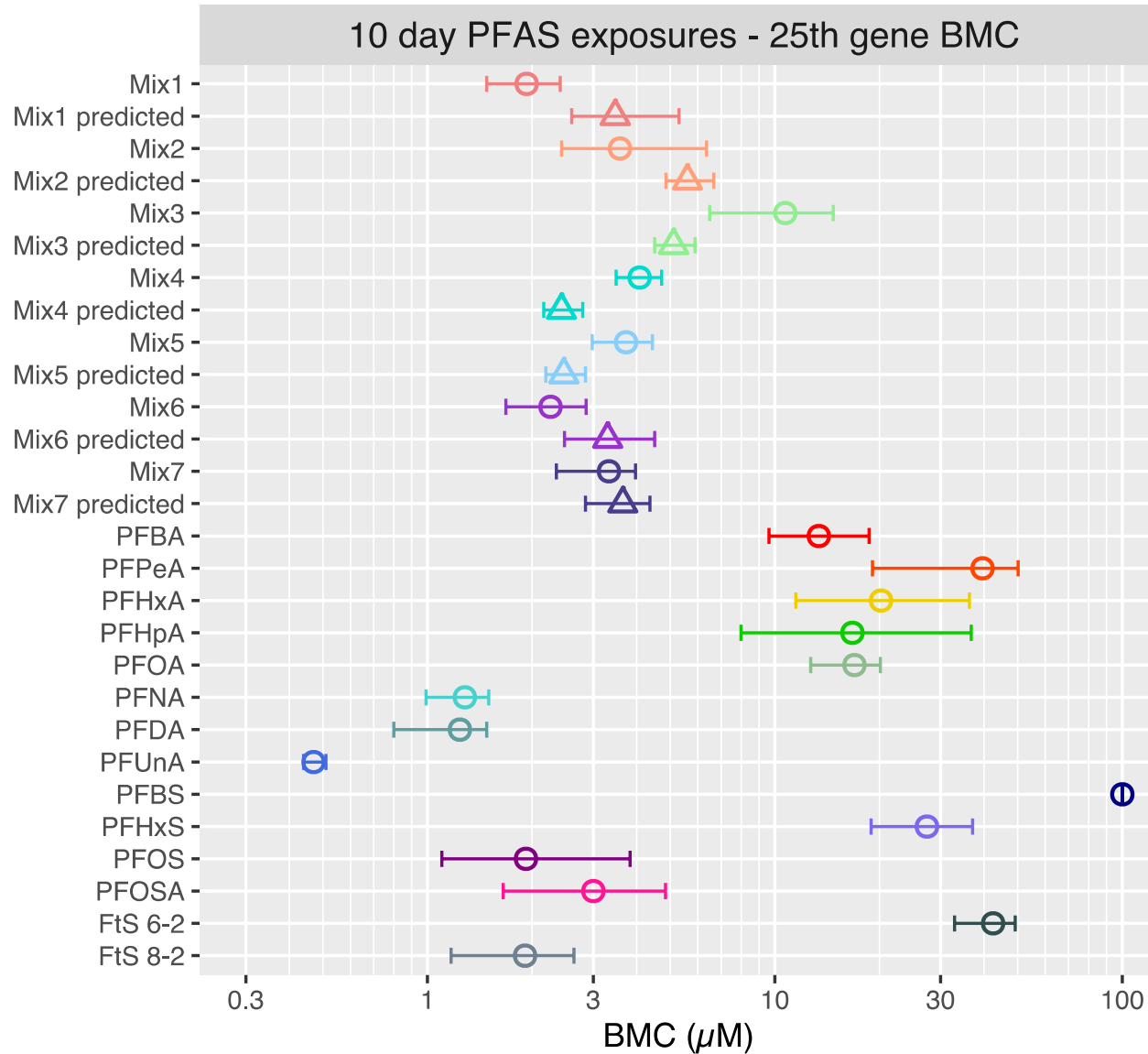
## Mixture components



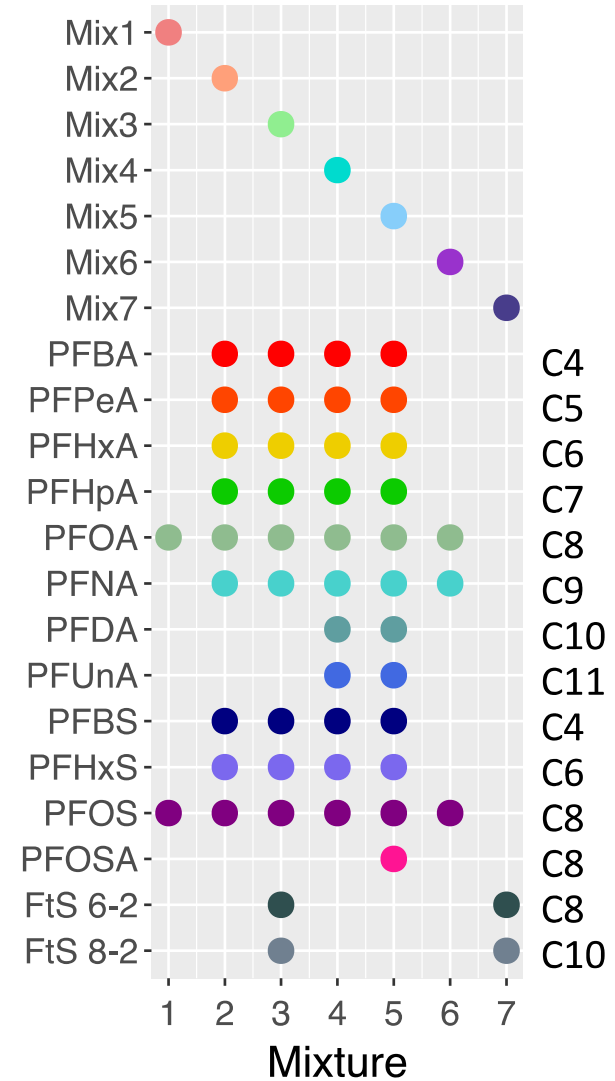
# 10 day 25<sup>th</sup> gene BCMs (+/- BMCL/BMCU)

## Concentration Addition predicted BMCs

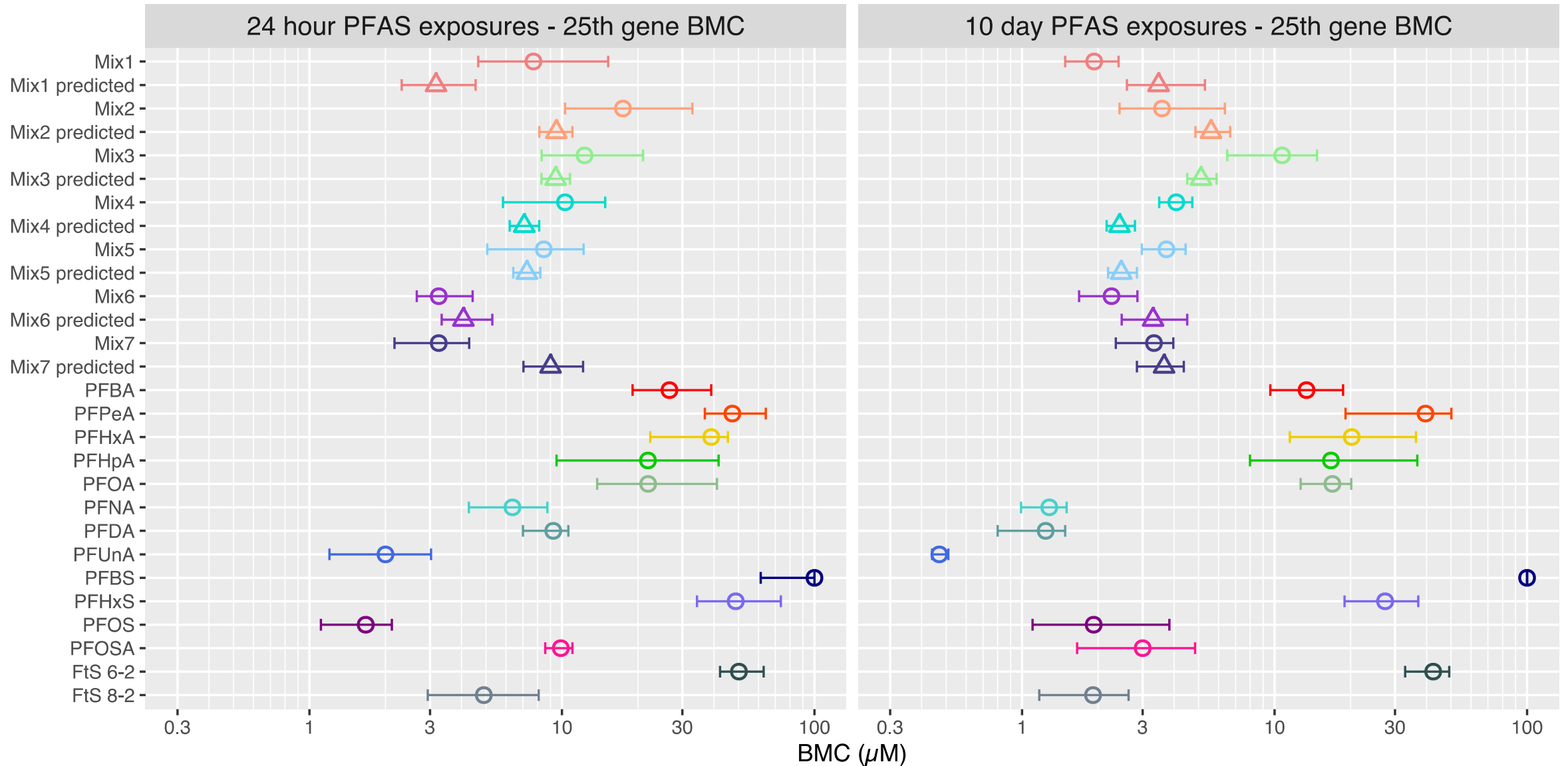
- Empirical – O
- Predicted – Δ
- No clear deviation from additivity
- Most have overlapping CIs
- Most have less than  $\pm 2$  fold differences in BMC
- All have less than  $\pm 2$  fold differences in CI endpoints



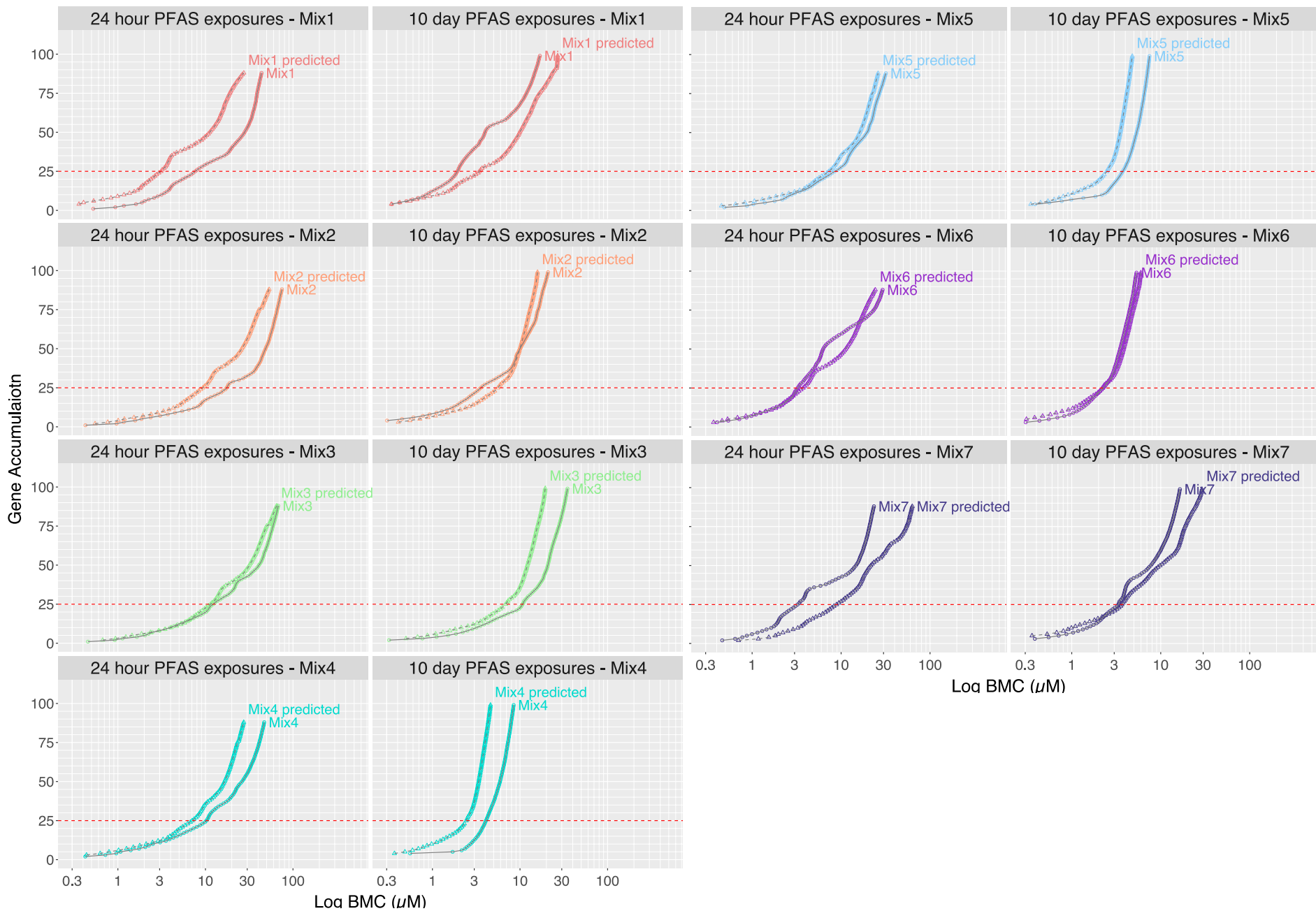
## Mixture components



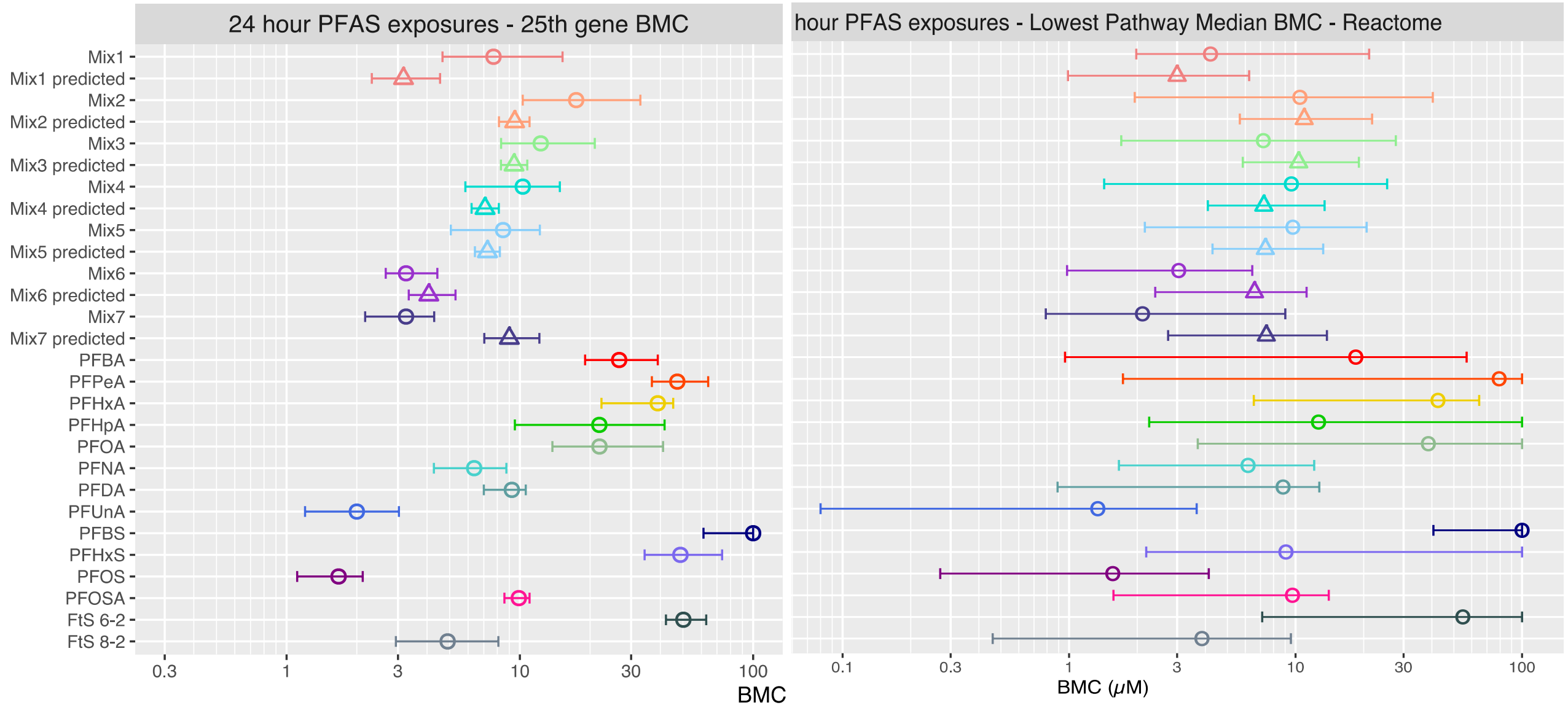
# CA predicted PFAS mixture BMCs



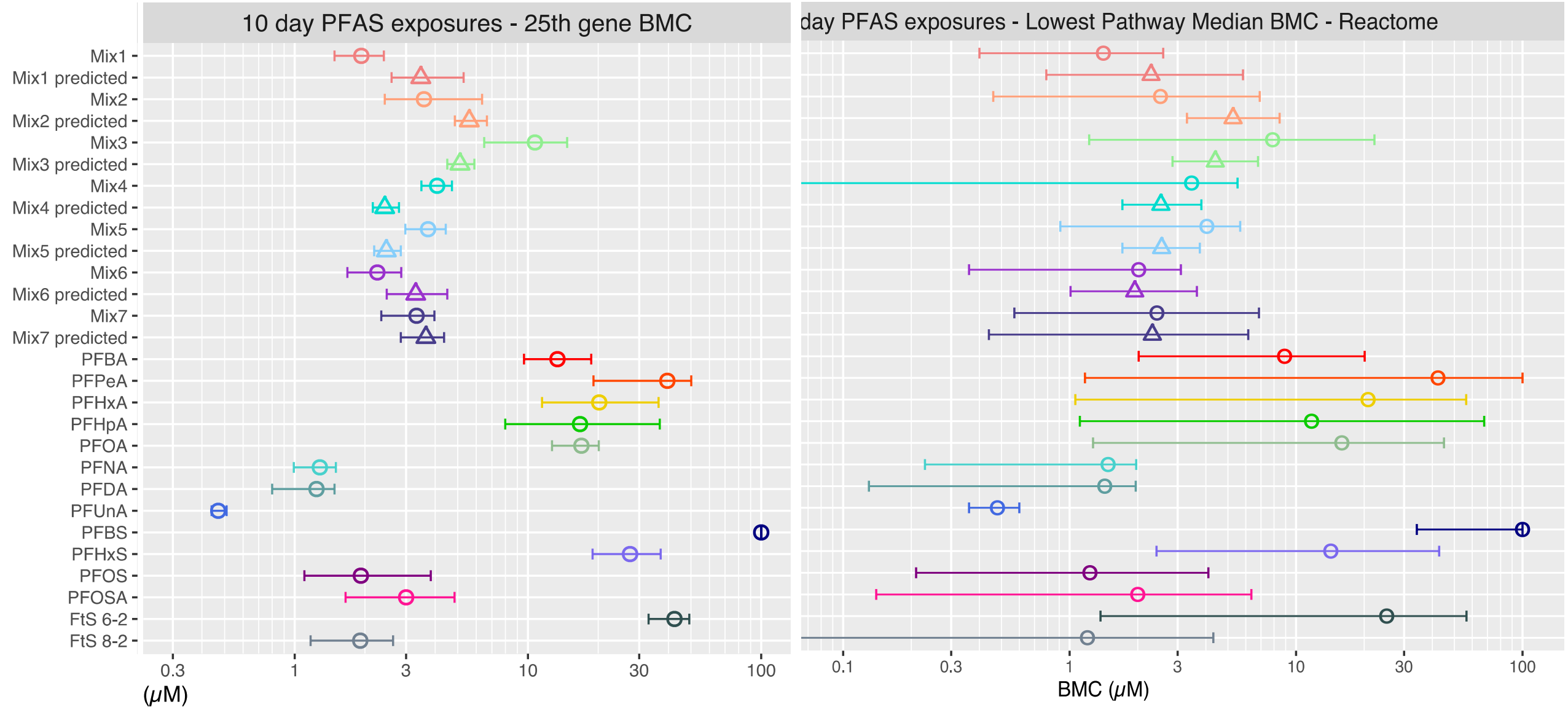
# Dose addition calculations done for each BMC independently (RPF calculated for each BMC)



# CA predicted PFAS mixture BMCs



# CA predicted PFAS mixture BMCs





# Conclusions

- PFAS mixtures have additive effects in mixtures
  - No evidence of synergistic or antagonistic effects using conservative criteria
  - Debate continues on what qualifies as synergistic or antagonistic
- Findings apply to PFAS concentrations at cellular environment
  - Relative potencies of PFAS differ from some in-vivo data
    - Bioaccumulation or excretion?
  - In-vitro to in-vivo extrapolation data needed to apply this data to human or animal external exposures through food, water, contact etc.
  - Can not exclude PFAS interactions affecting accumulation, persistence or excretion at whole organism level

# Acknowledgements

- Ella Atlas and Carole Yauk –
  - designed the project
- Andrea Rowan-Carroll and Karen Leingartner –
  - cell culture, planning, sequencing etc.
- Matthew Meier and Andrew Williams –
  - data processing, computation
- Barbara Wetmore and others at US EPA –
  - PFAS chemicals
- Many others in the background supporting the project