

A brief summary of data indicating that SREBP activation is a key step in induction of steatosis by PFAS

Chris Corton



Center for Computational Toxicology and Exposure
US-Environmental Protection Agency
Research Triangle Park, NC

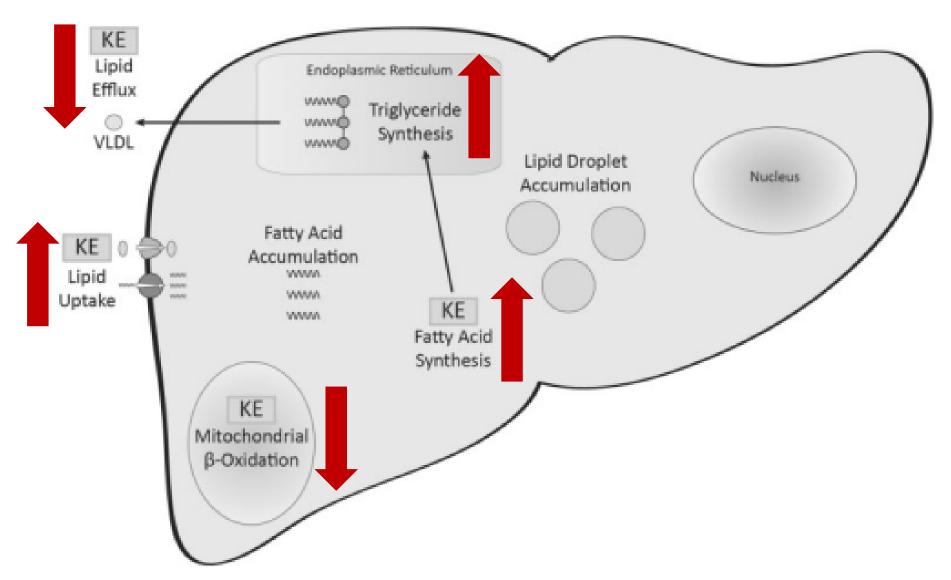


Disclaimer

• The views expressed are those of Dr. Chris Corton and do not reflect US-EPA policy or product endorsement by the US-EPA.

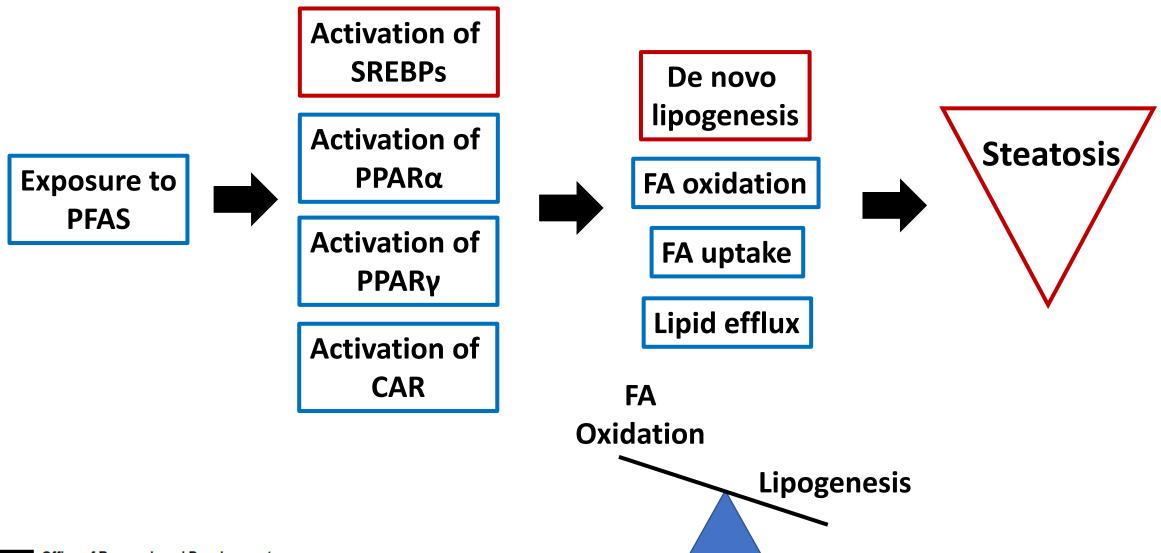


Major molecular events that can contribute to steatosis





Hypothesis



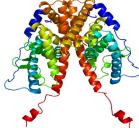


Biomarkers that predict key events in the livers of mice

and rats



Receptor α



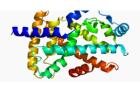
Estrogen



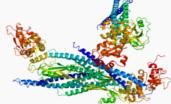
NRF2 **SREBP**



PPARα



STAT5b





Oshida et al. (2015). Identification of Modulators of the Nuclear Receptor Peroxisome Proliferator-Activated Receptor α (PPAR α) in a Mouse Liver Gene Expression Compendium. PLoS One. 10(2):e0112655.

Oshida et al. (20

(CAR) in a Mous PPARα: Balanced accuracy = 98%

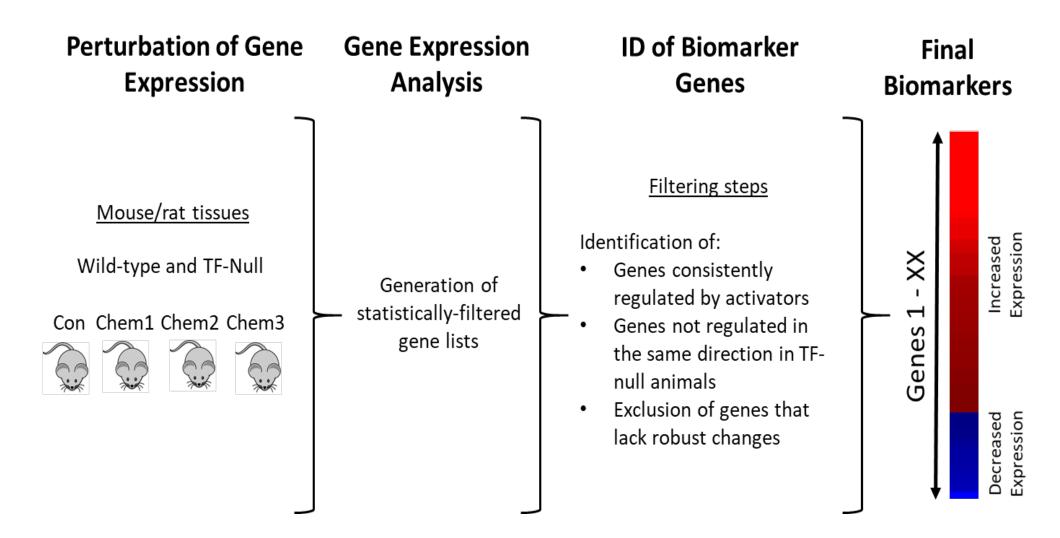
ted Receptor L3:e002.

es Effectors of

- Oshida et al. (24 the Aryl Hydrocarbon Receptor (AhR). Toxicology. 336:99-112.
- Oshida et al. (2015). Disruption of STAT5b-Regulated Sexual Dimorphism of the Liver Transcriptome by Diverse Factors Is a Common Event. PLoS One. 11(3):e0148308.
- Rosen et al. (2017). PPARα-independent transcriptional targets of perfluoroalkyl acids revealed by transcript profiling. Toxicology. 387:95-107.
- Rooney et al. (2017). Genomic Effects of Androstenedione and Sex-Specific Liver Cancer Susceptibility in Mice. <u>Toxicol Sci.</u> 160(1):15-29.
- Rooney et al. (2018) Activation of Nrf2 in the liver is associated with stress resistance mediated by suppression of the growth hormone-regulated STAT5b transcription factor. PLoS One. 13(8):e0200004.
- Rooney et al. (2018). Activation of CAR leads to activation of the oxidant-induced Nrf2. Toxicol Sci. 167:172-189.
 - Rooney et al. (20: SREBP: Balanced accuracy = 95%
- Corton (2019). Frequent Modulation of the Sterol Regulatory Element Binding Protein (SREBP) by Chemical Exposure in the Livers of Rats. Comput. Toxicol. 10:113-129.
- Rooney et al. (2019). A gene expression biomarker identifies factors that modulate sterol regulatory element binding protein. Comput. Toxicol. 10:63-67.

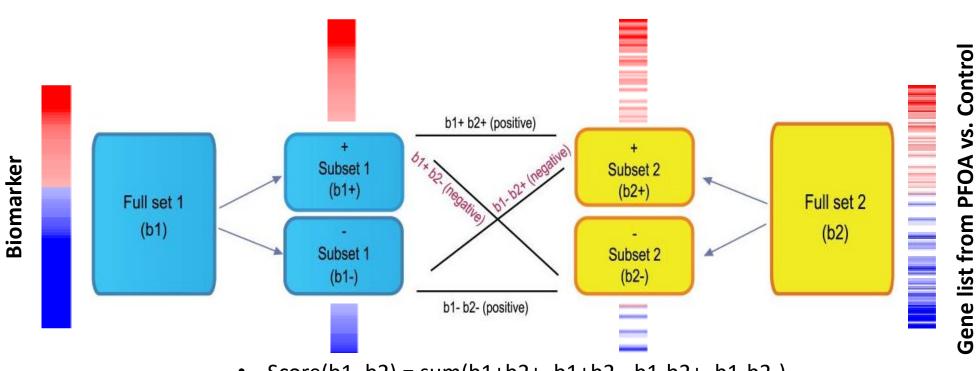


Construction of biomarkers from microarray data generated in animal tissues





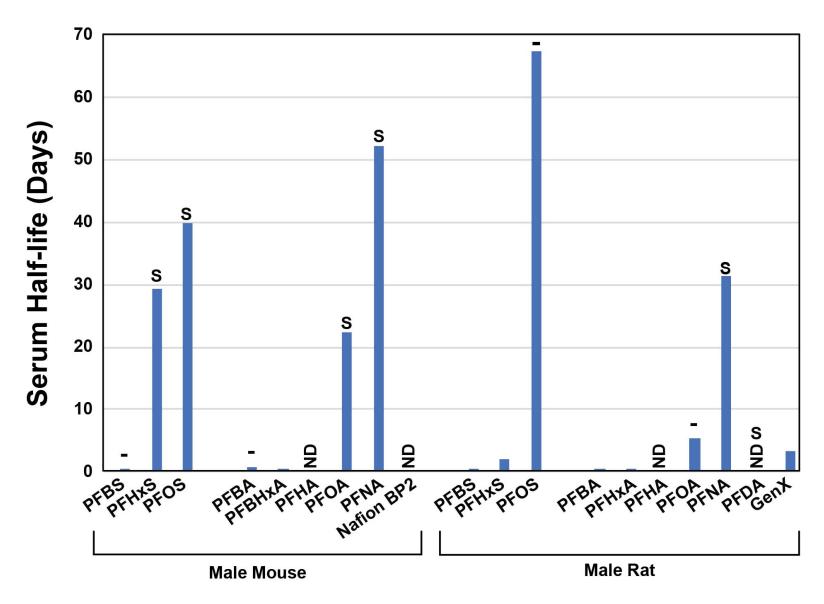
Computing directionality and final correlation scores between two gene lists



- Score(b1, b2) = sum(b1+b2+, b1+b2-, b1-b2+, b1-b2-)
- Running Fisher Test p-value
- Direction of the correlation



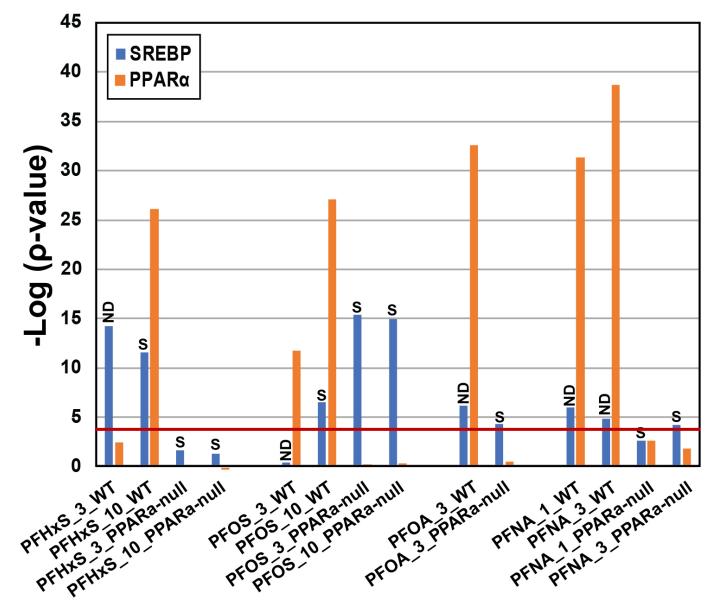
PFAS With Longer Serum Half Lives Cause Steatosis



Discrepancy with PFOS in male rats could be due to differences in exposure conditions between



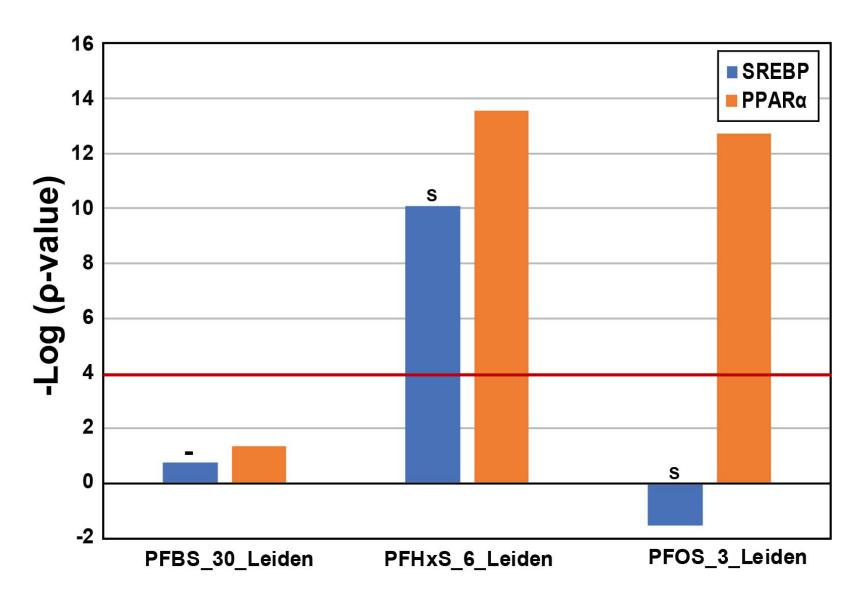
SREBP is activated when steatosis is observed



- Studies in wild-type and PPARa-null mice
- PPARa-null mice routinely have steatosis with or without chemical exposure
- Wild-type mice treated with PFHxS, PFOS, PFOA, PFNA



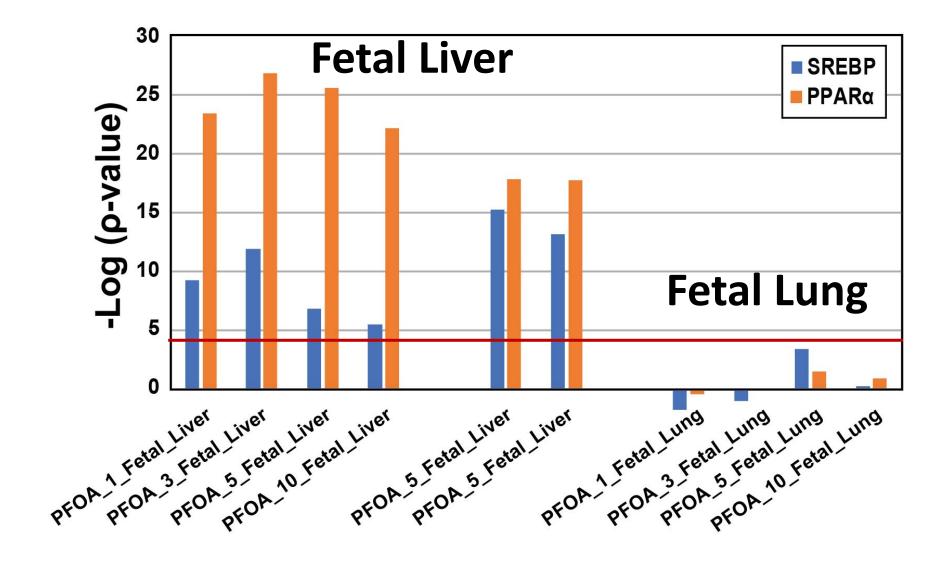
SREBP is activated when steatosis is observed



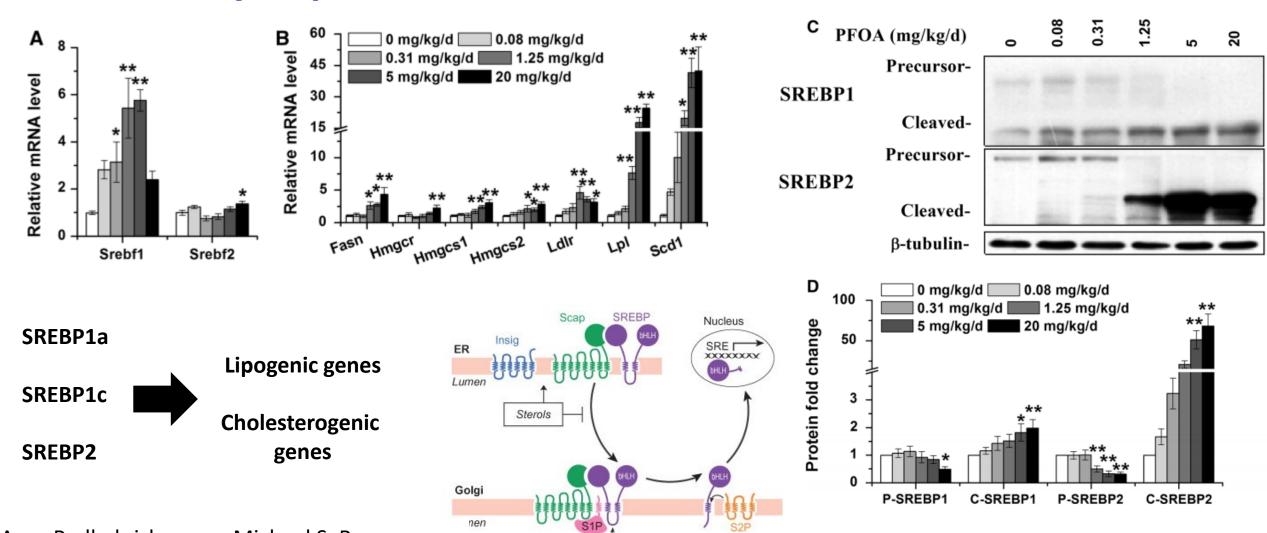
- APOE*3-Leiden.CETP mouse study; 4-6 week exposures
- Microarray data from Bijland et al. 2011 ToxSci 123:290



SREBP is activated in fetal liver but not fetal lung



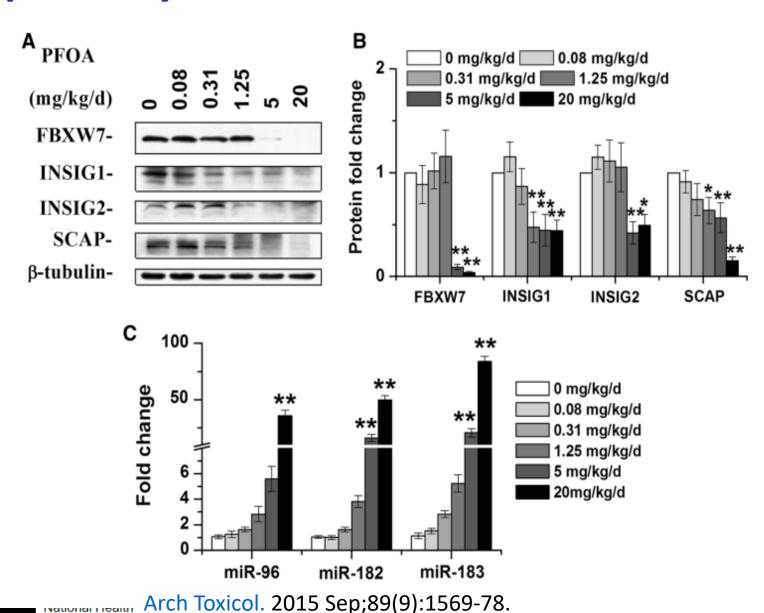
SREBP protein processing and activation of regulated genes after 28-day exposure to PFOA

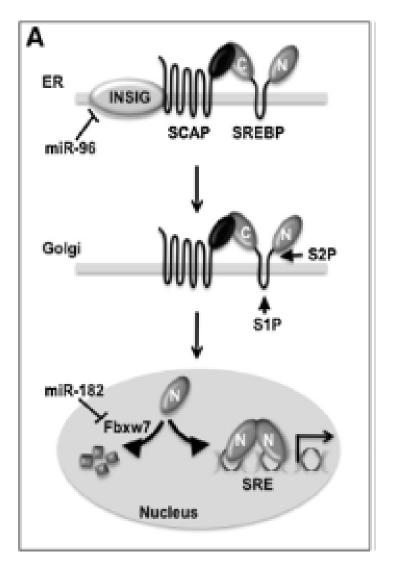


Arun Radhakrishnan, ... Michael S. Brown, in Handbook of Cell Signaling (Second Edition),

Arch Toxicol. 2015 Sep;89(9):1569-78.

Protein expression of key factors in the SREBP maturation pathway and miR183-96-182 cluster expression





Cell Metab. 2013 Jul 2;18(1):51-61.



ACKNOWLEDGEMENTS



Environmental Protection Agency

John Rooney

Natalia Ryan **Brian Chorley Thomas Hill**



NIEHS

Nicole Kleinstreuer



Health Canada Carole Yauk **Andrew Williams**



University of Leiden Bob van de Water Steve Hiemstra



PamGene

Rinie van Beuningen Rene Houtman



City of Hope Medical Center, Duarte Shiuan Chen



Frank Sistare Chunhua Qin



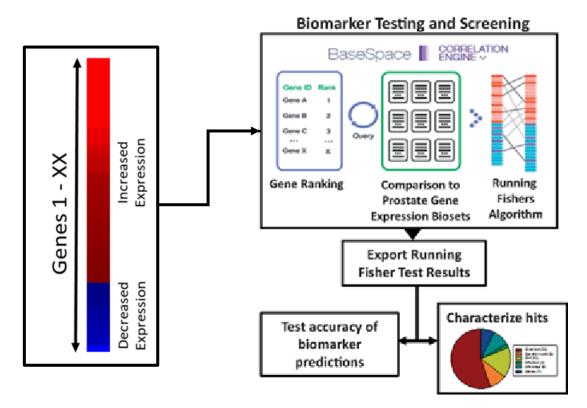
Support from EPA Chemical Safety for Sustainability Research Program



Extras

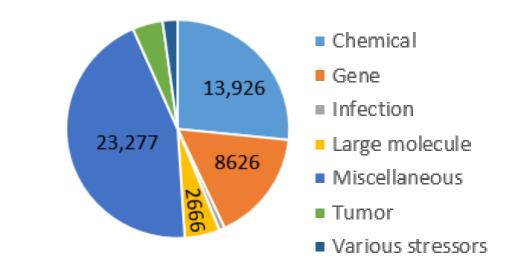


Comparing gene lists in BSCE



- Utilize Illumina's BaseSpace Correlation Engine
- Contains ~130,000 microarray comparisons of statistically significant genes
- Valuable computational tools
- Compares all microarray comparisons to each other in a pairwise fashion using a Running Fisher test
- For each pair-wise comparison: generates the number of overlapping genes, correlation direction and p-value

• ~51,600 microarray comparisons in human database



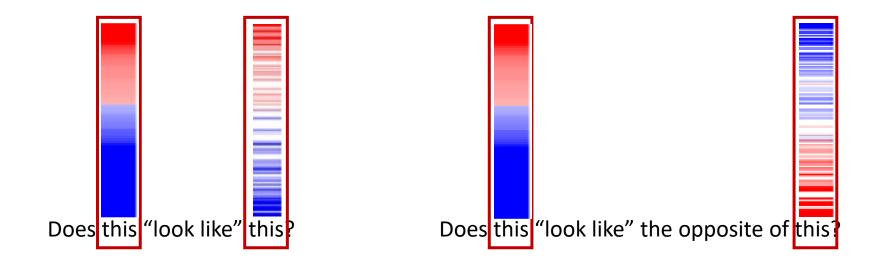
- Includes ~1950 chemicals
- ~8600 perturbations of ~1700 genes (knockdowns, overexpression, mutants)
- Greatly accelerated construction and analysis of biomarkers

Derived from Rooney et al. Toxicol Sci. 166:146-162



Correlation analysis using the Running Fisher Test

• Identification of factors (chemicals, hormones, diets, genes, etc.) that "look" like your gene list



 Correlation can be determined computationally using the Running Fisher test in BSCE



Coordinated changes in the expression of lipid synthesis and catabolism genes in treated mice.

