

Project Name: PXD001819

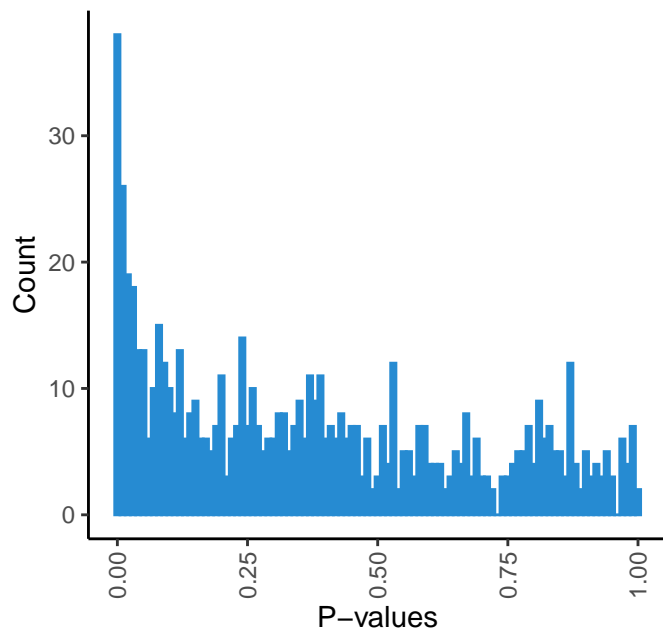
NormalyzerDE (ver 1.5.4)

Report created on: 2021-02-01

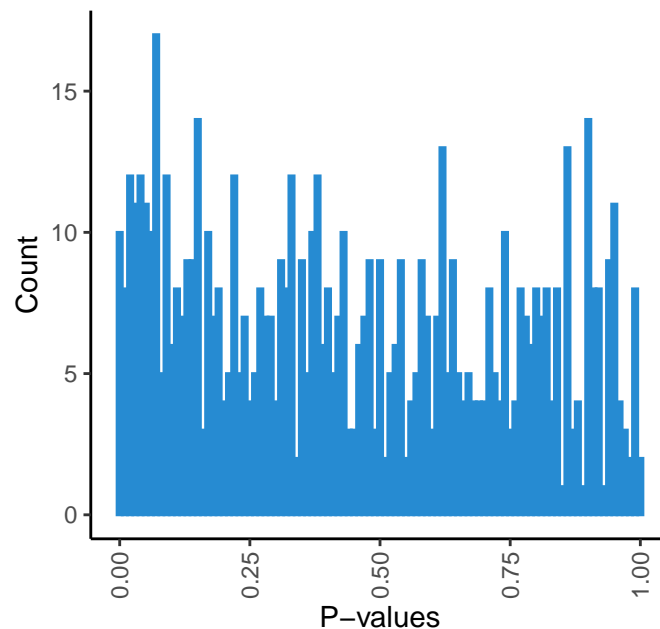
Citation: NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis
Journal of Proteome Research (2018), 10.1021/acs.jproteome.8b00523

Documentation for analyzing this report can be found at <http://quantitativeproteomics.org/normalyzer/help.php>

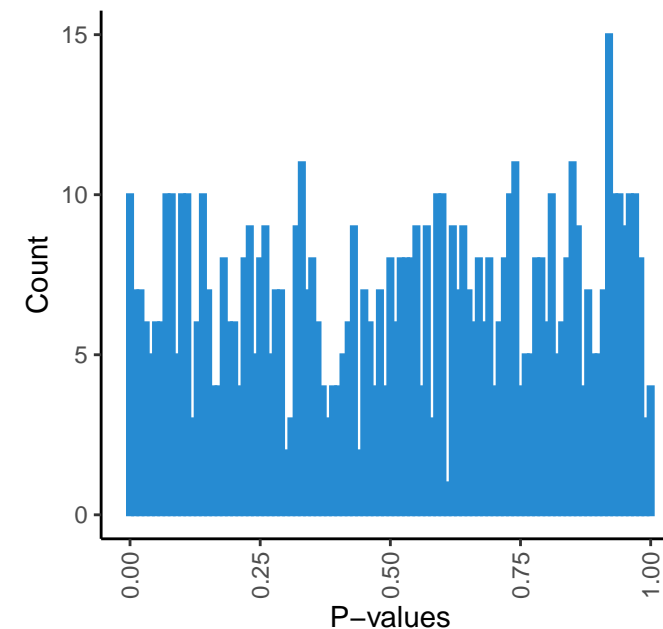
Contrast: 50000amol–25000amol



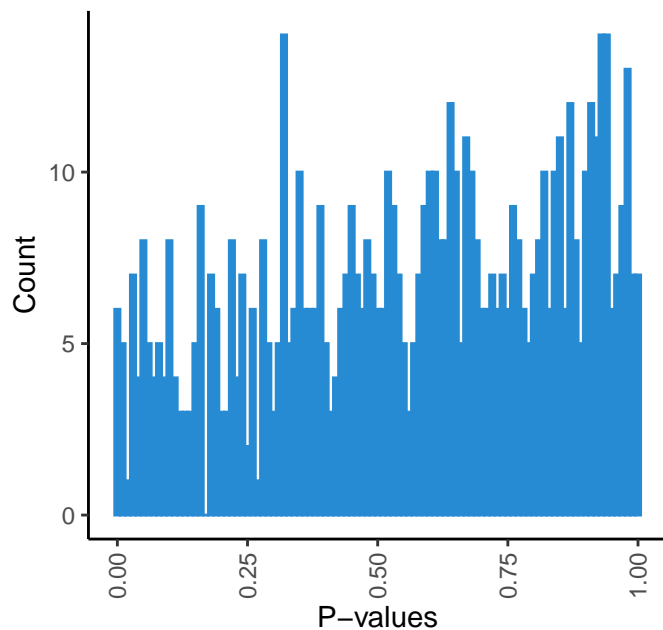
Contrast: 25000amol–12500amol



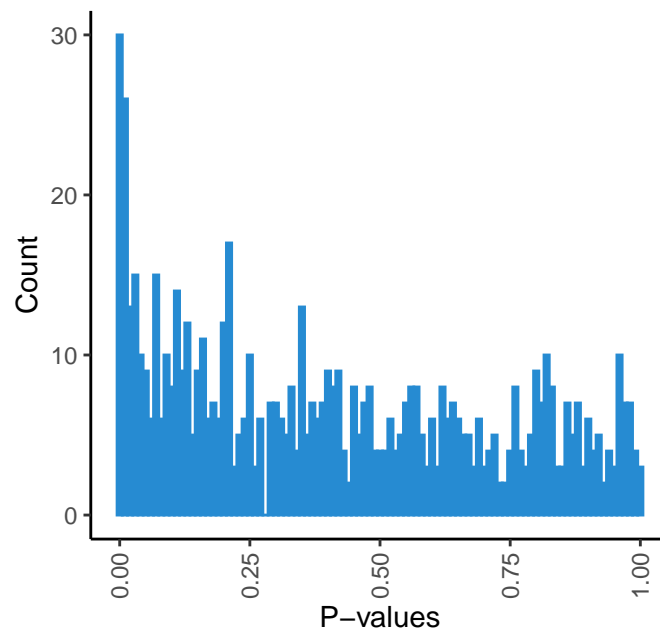
Contrast: 12500amol–5000amol



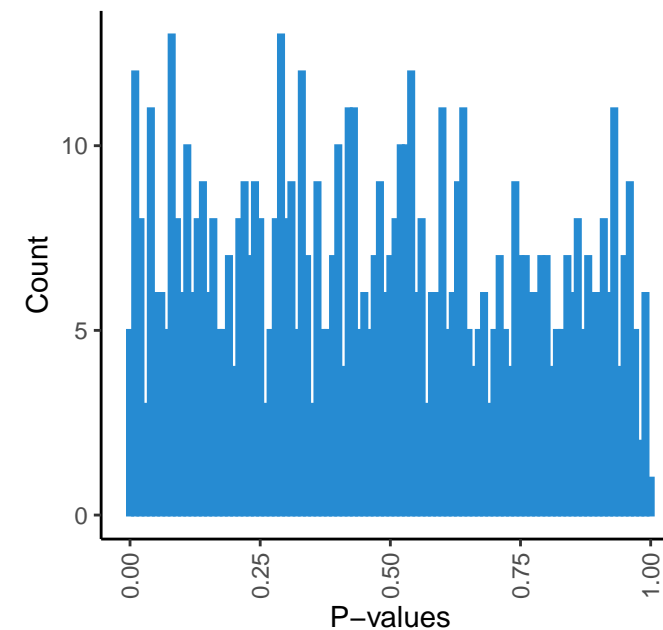
Contrast: 5000amol–2500amol

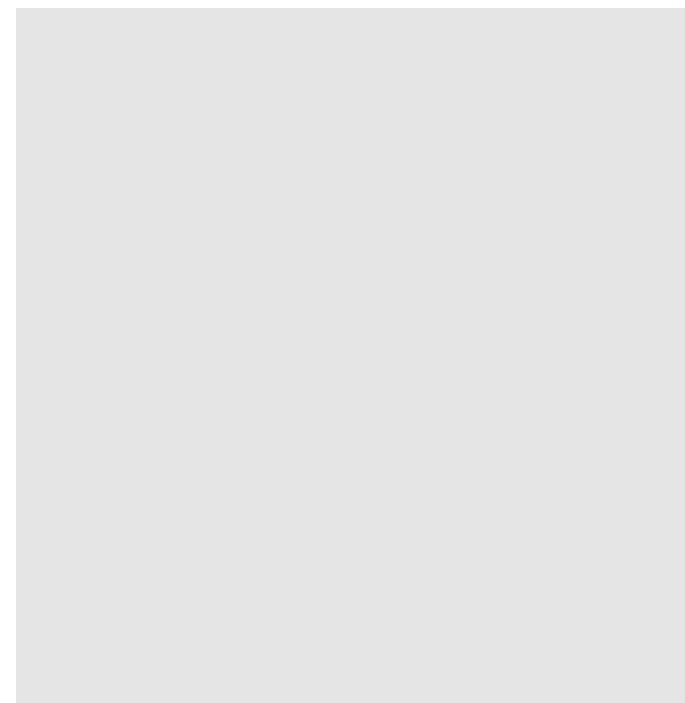
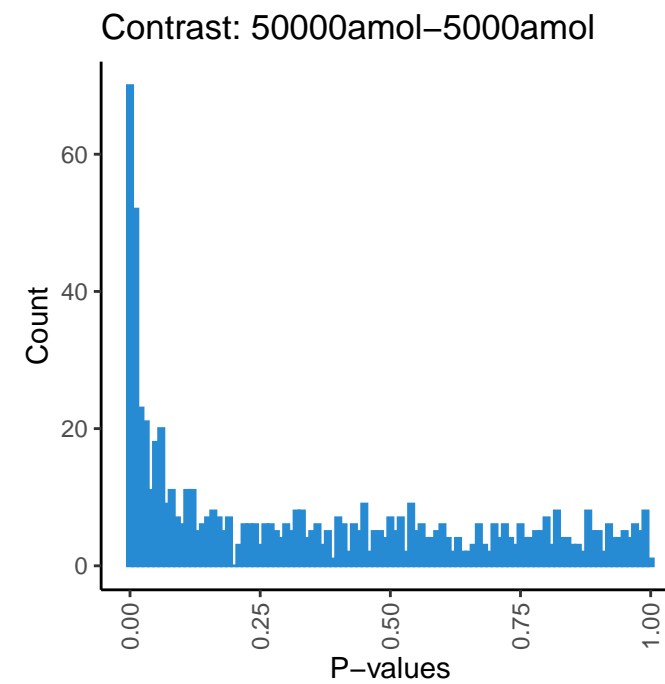
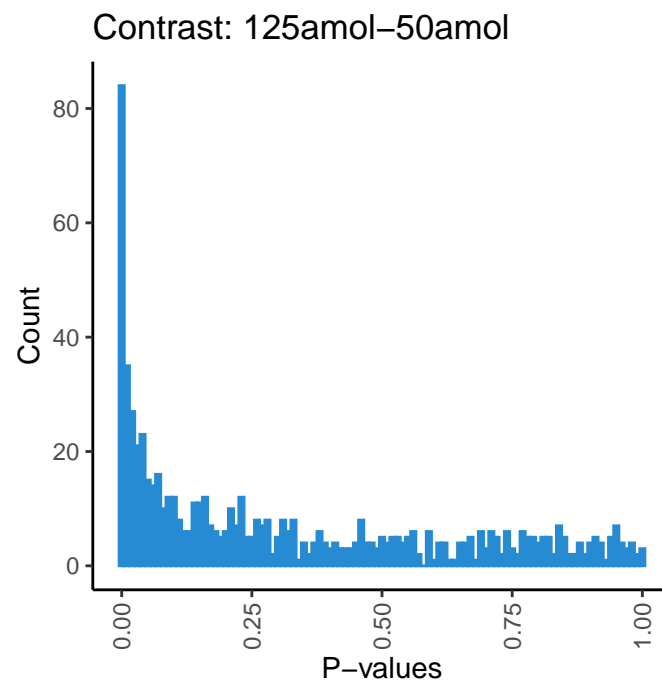
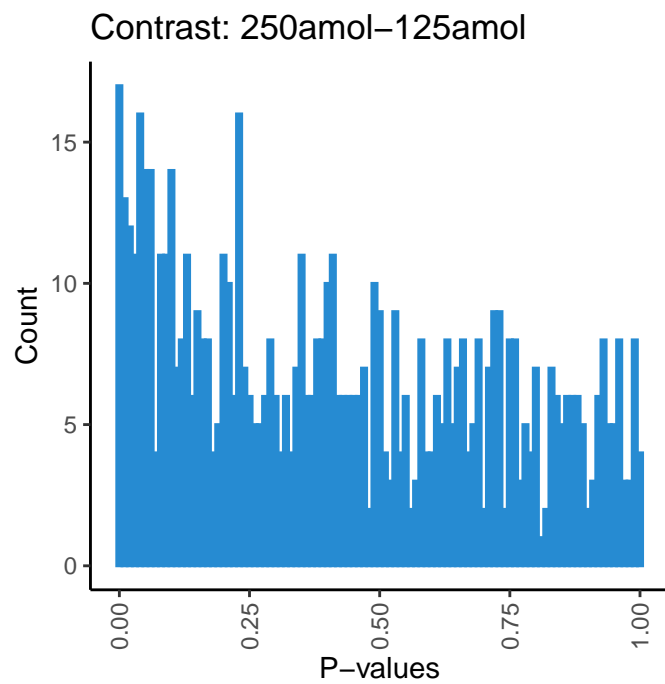


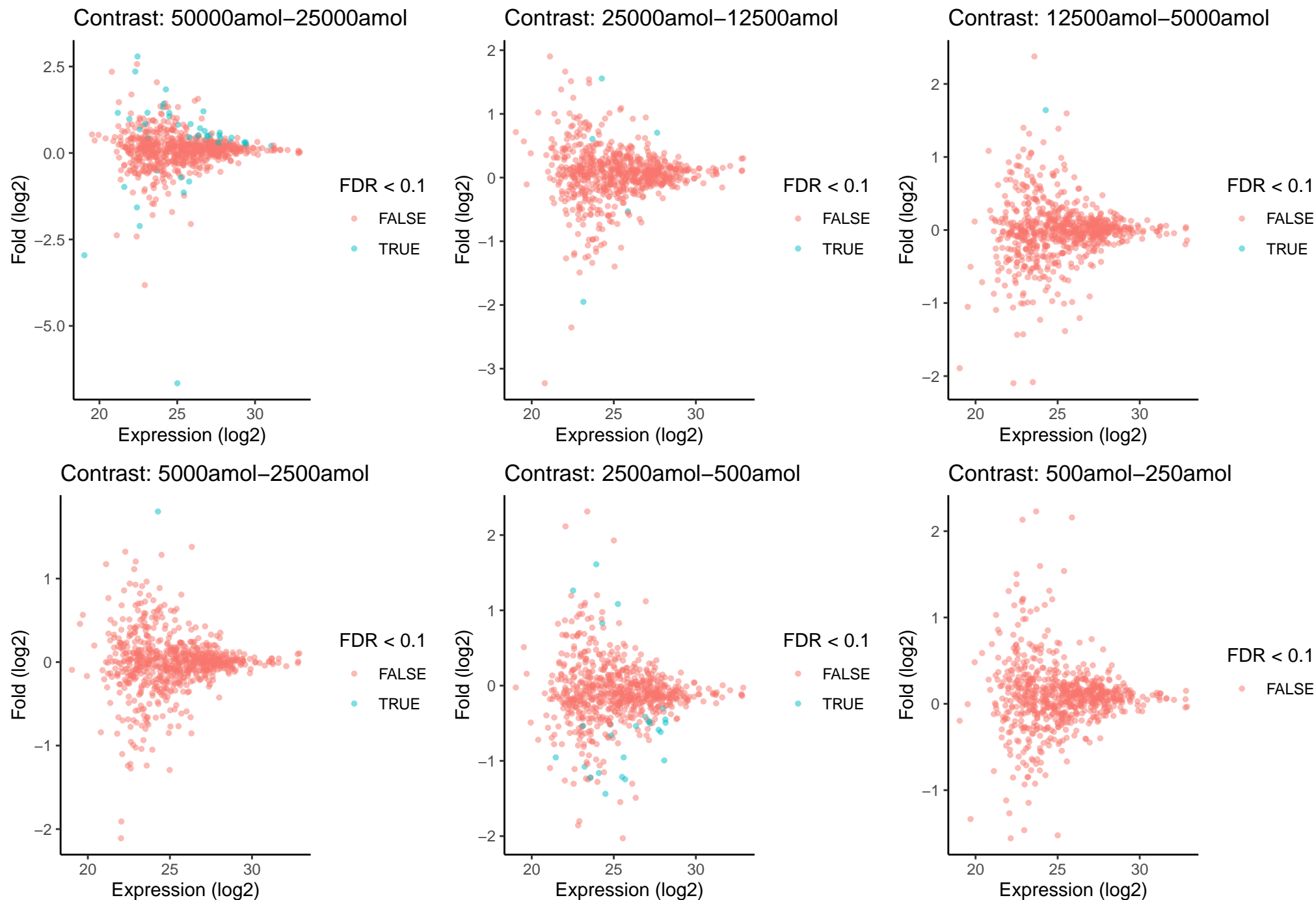
Contrast: 2500amol–500amol

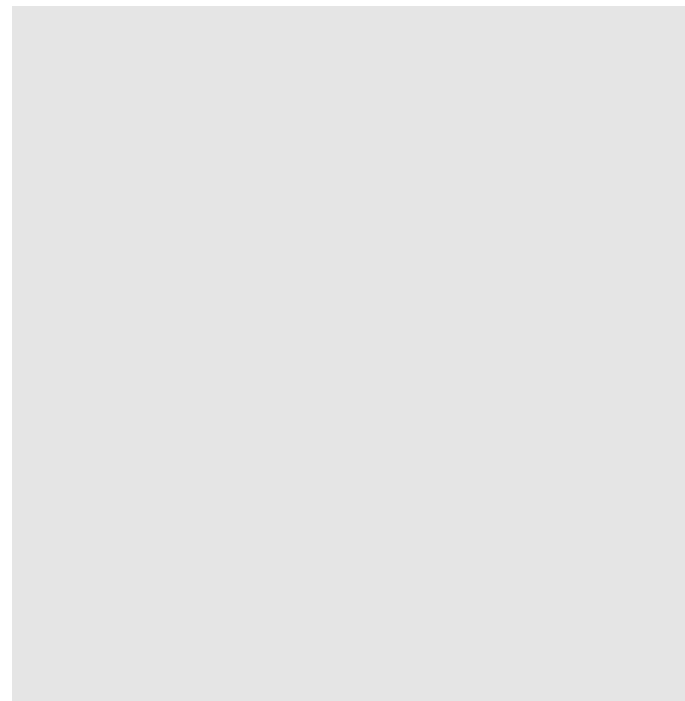
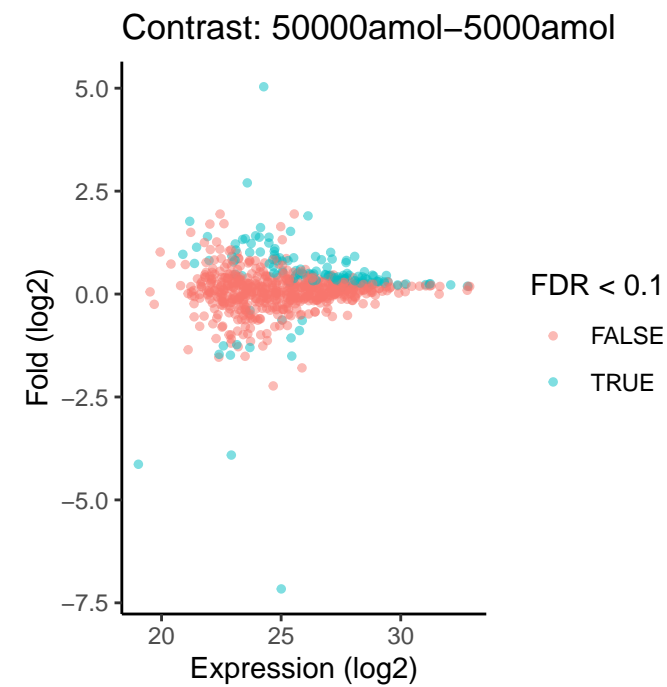
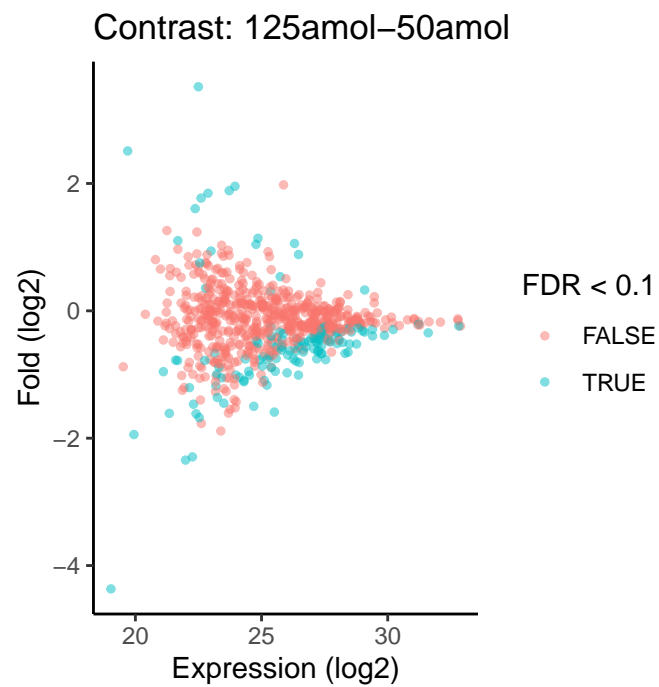
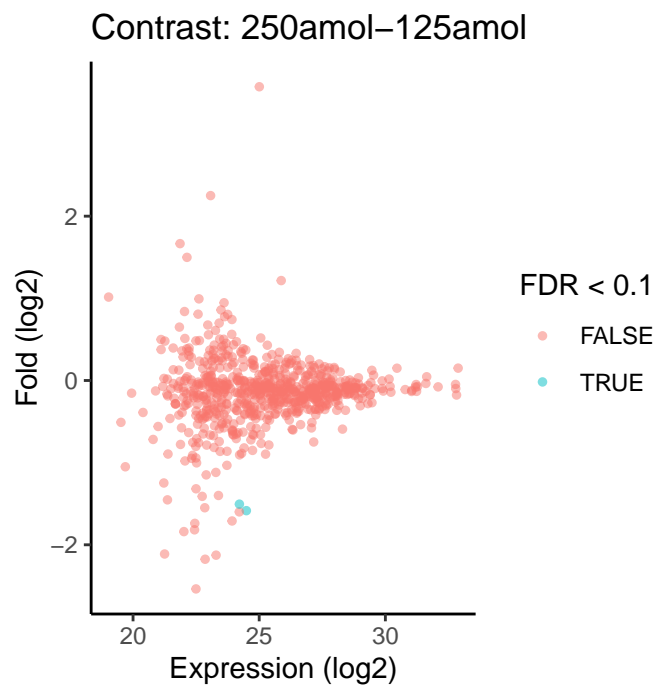


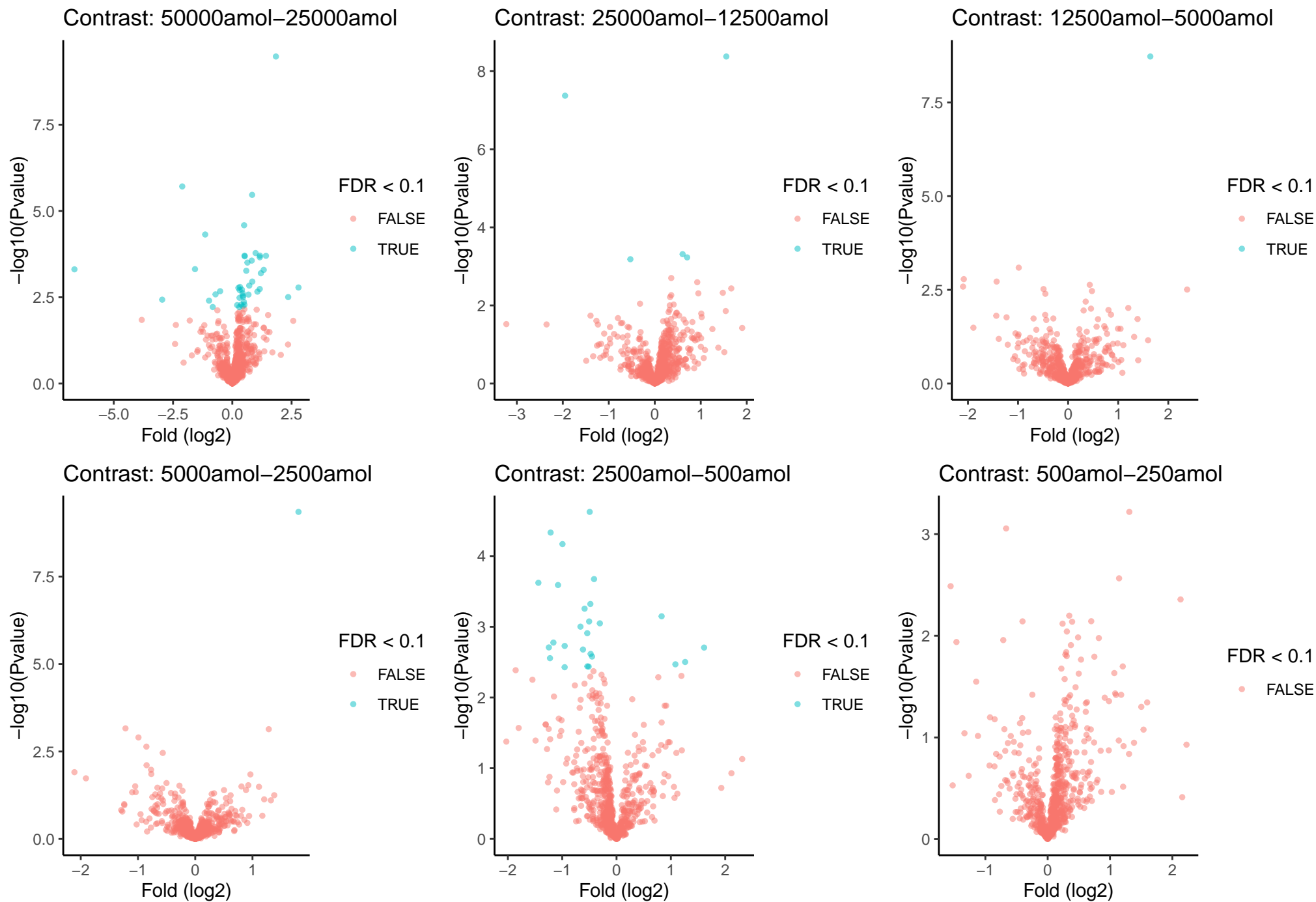
Contrast: 500amol–250amol



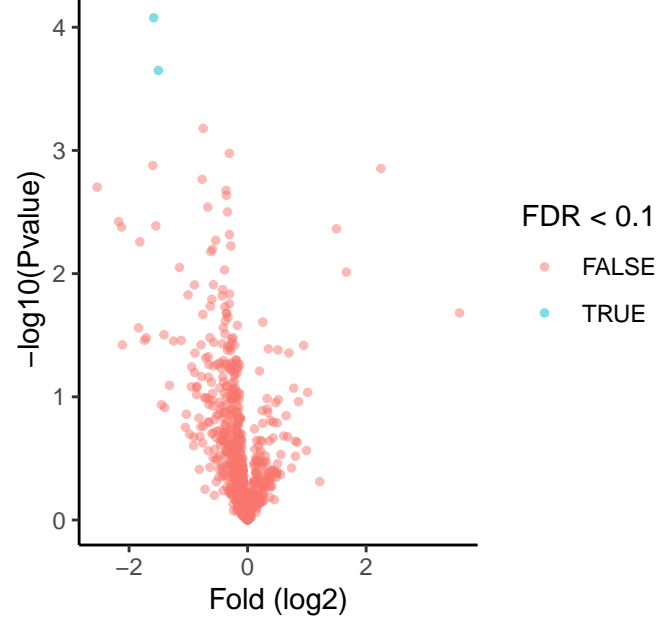




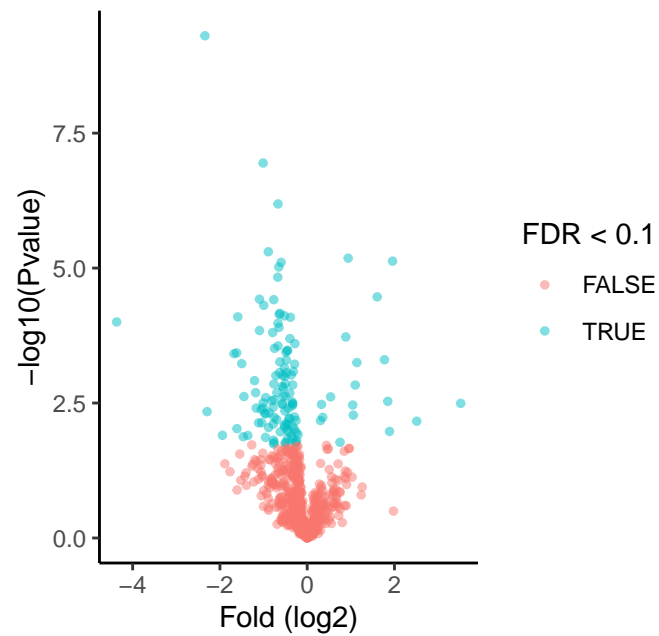




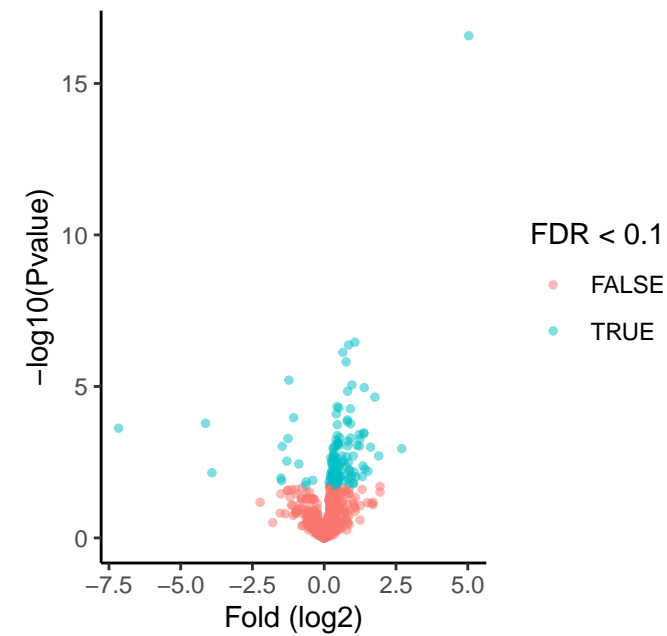
Contrast: 250amol–125amol

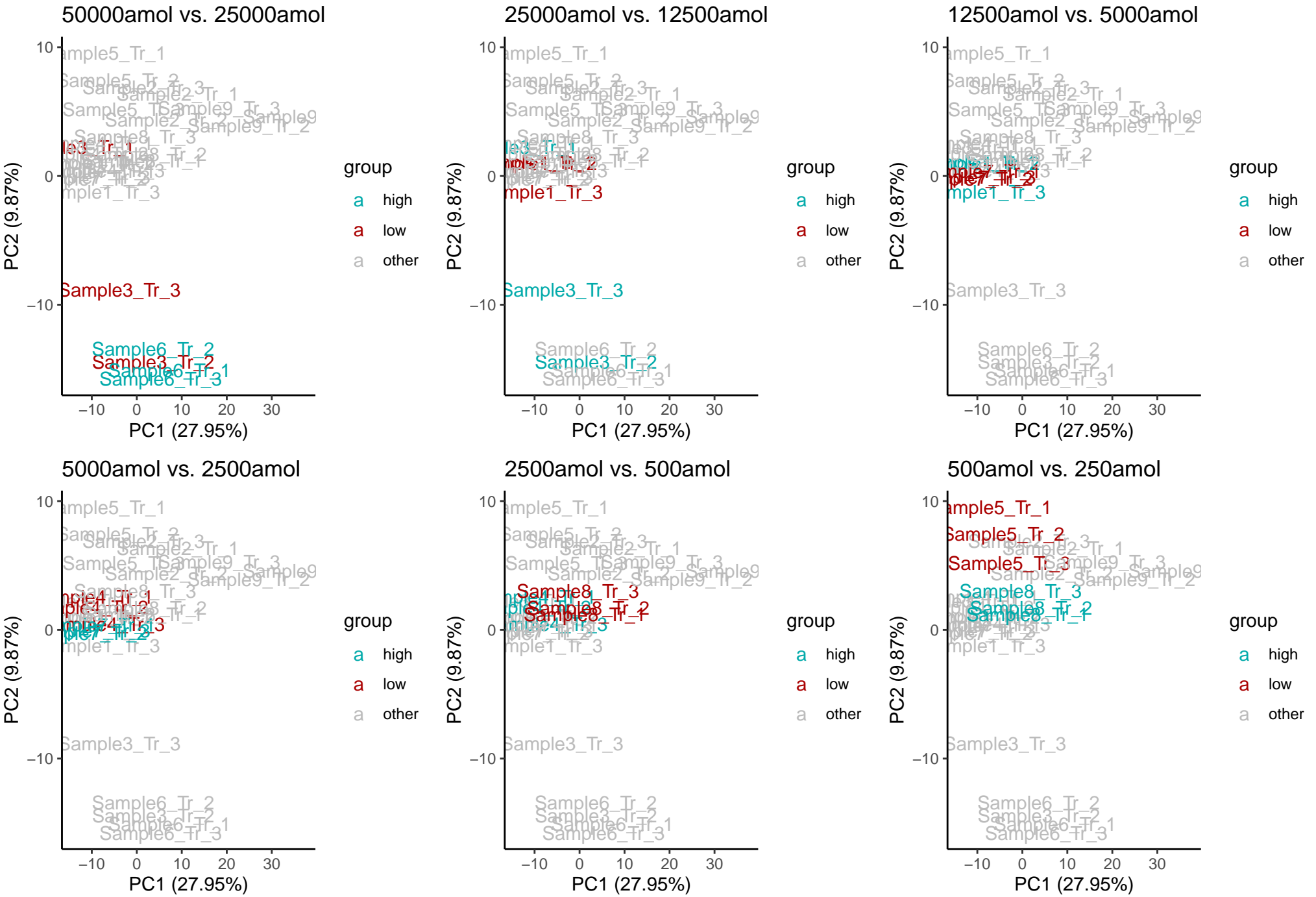


Contrast: 125amol–50amol

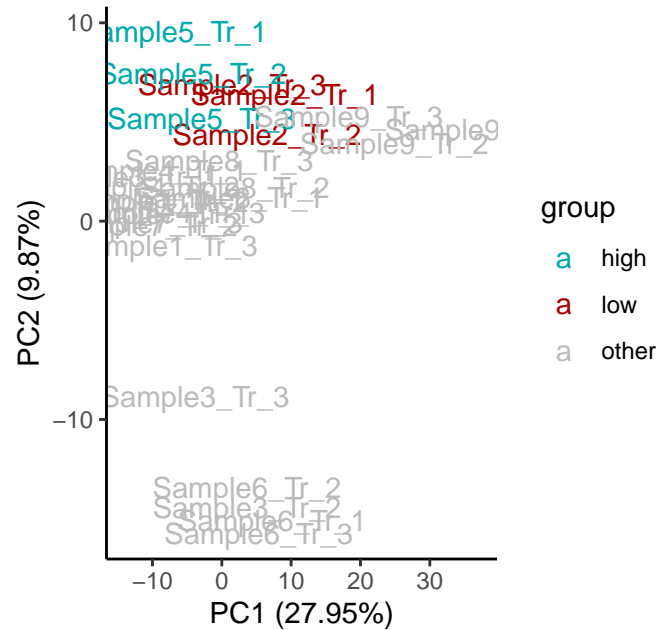


Contrast: 50000amol–5000amol

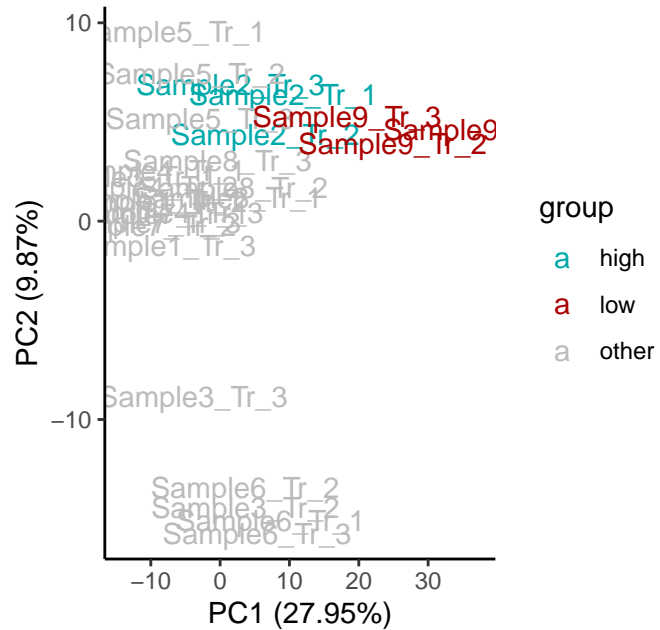




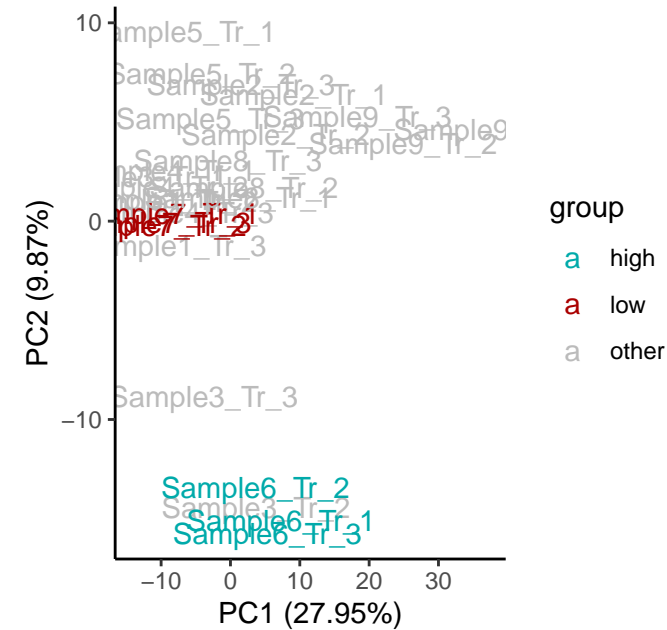
250amol vs. 125amol

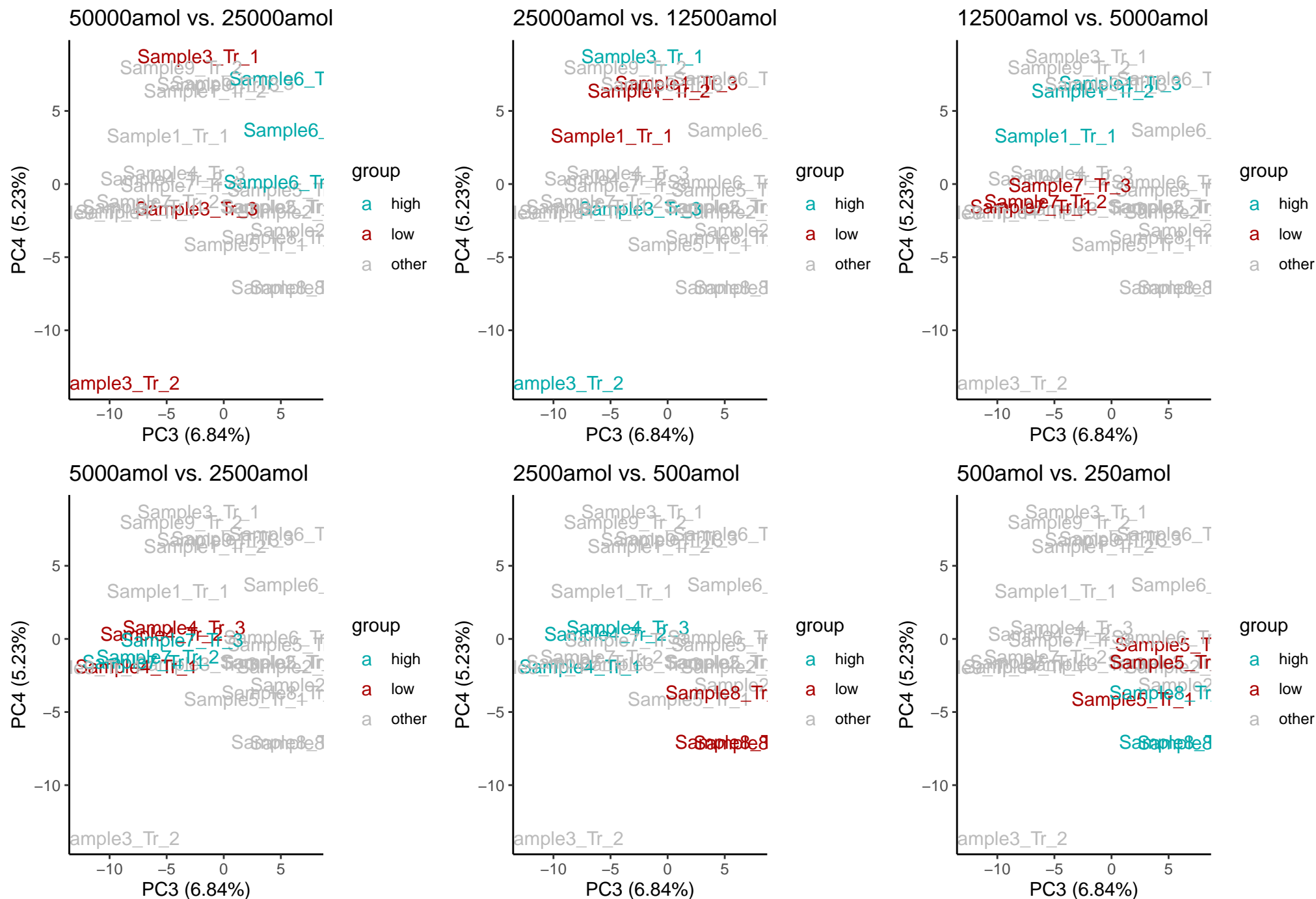


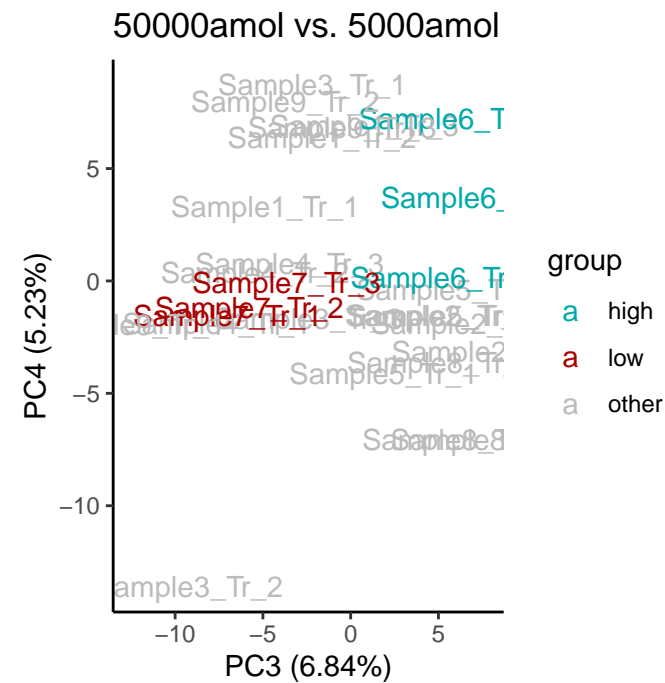
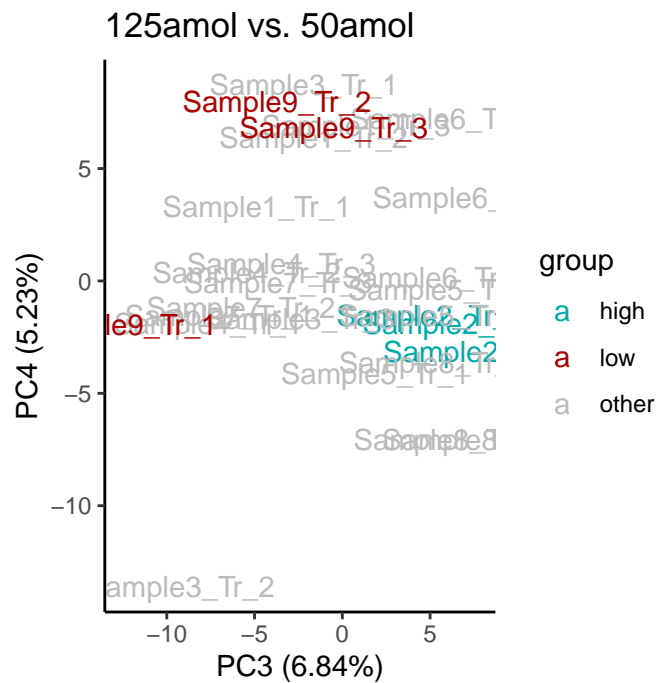
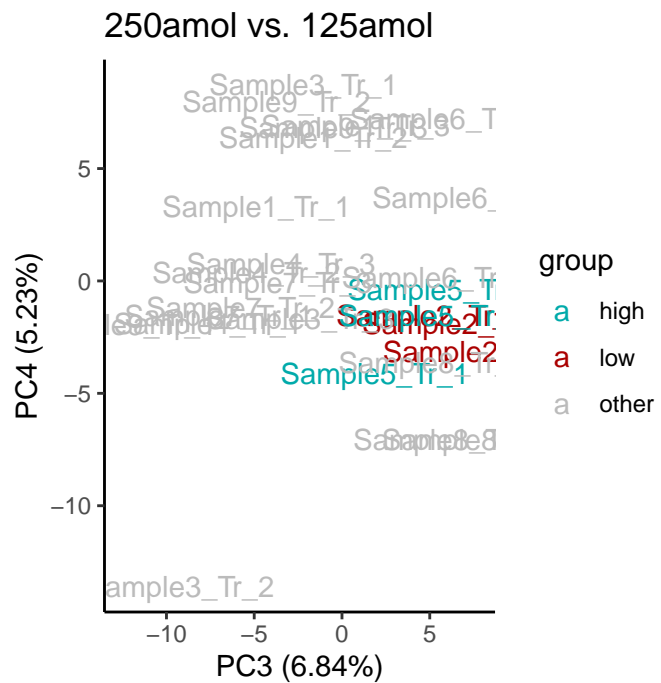
125amol vs. 50amol



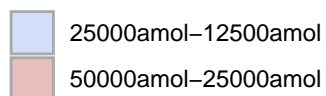
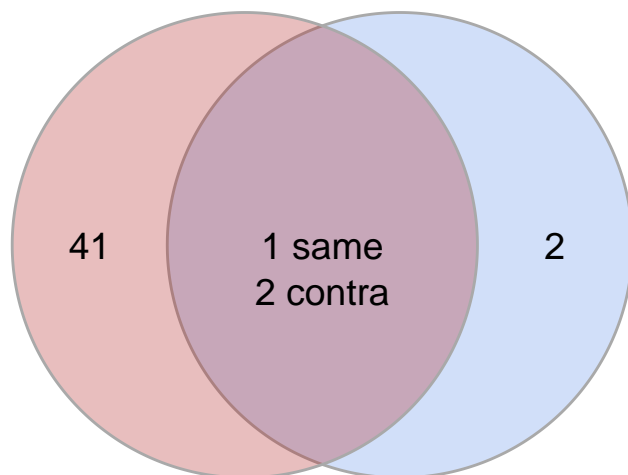
50000amol vs. 5000amol



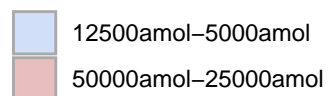
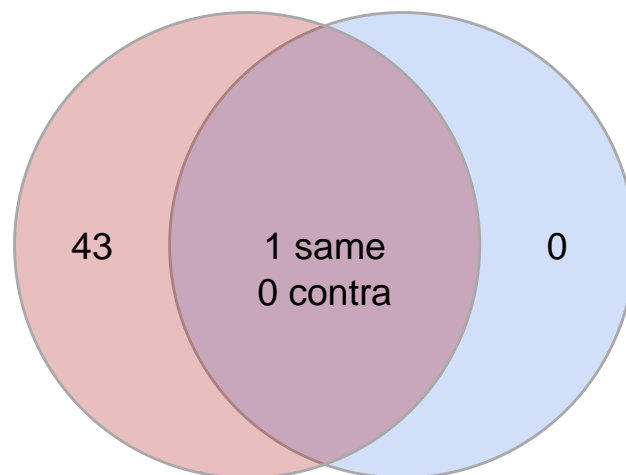




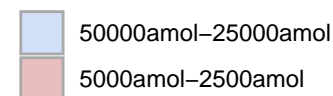
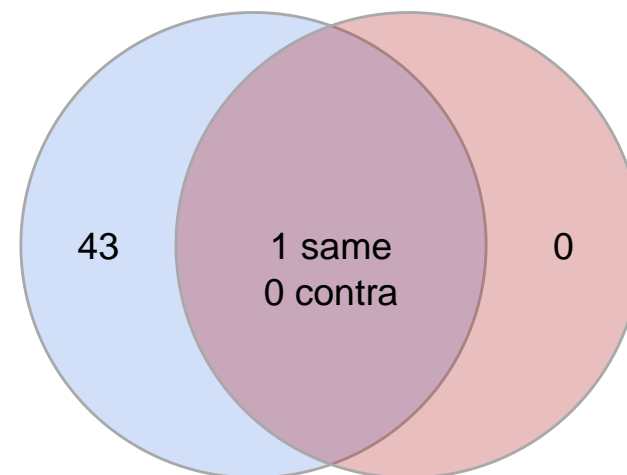
fdr < 0.1, |log2 fold| >= 0



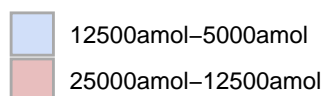
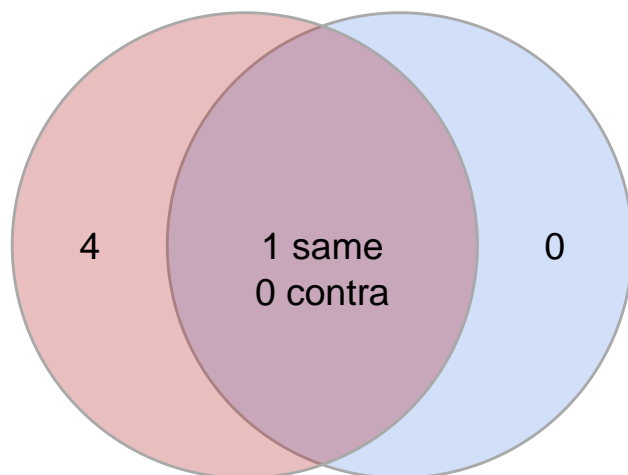
fdr < 0.1, |log2 fold| >= 0



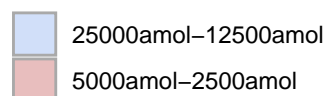
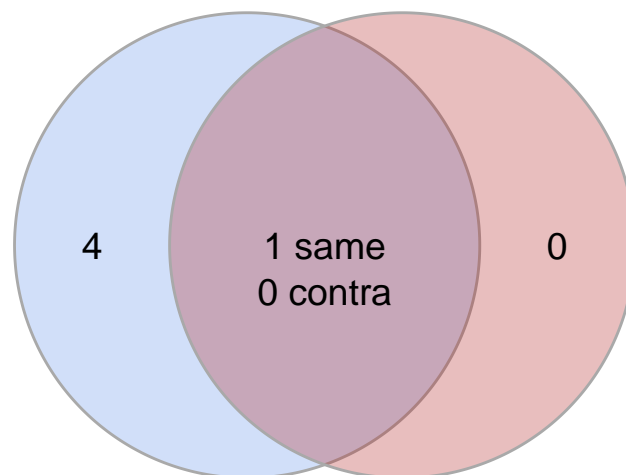
fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0

