

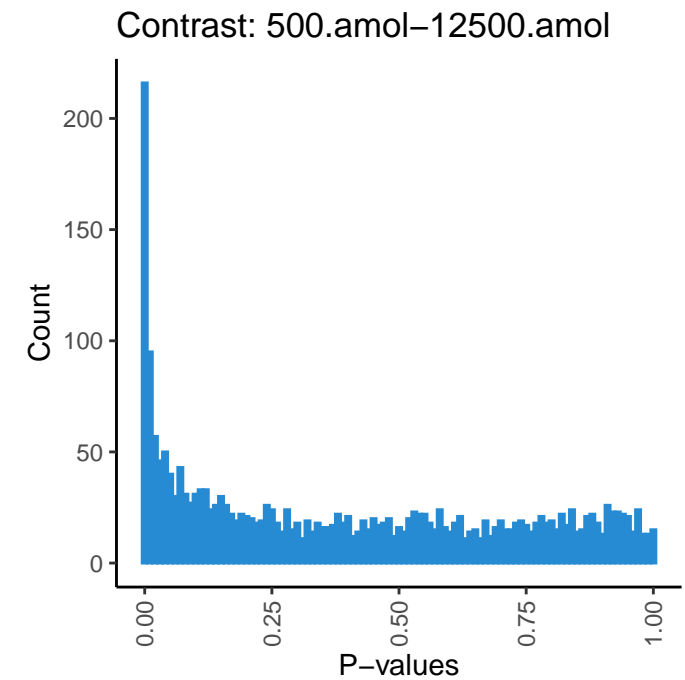
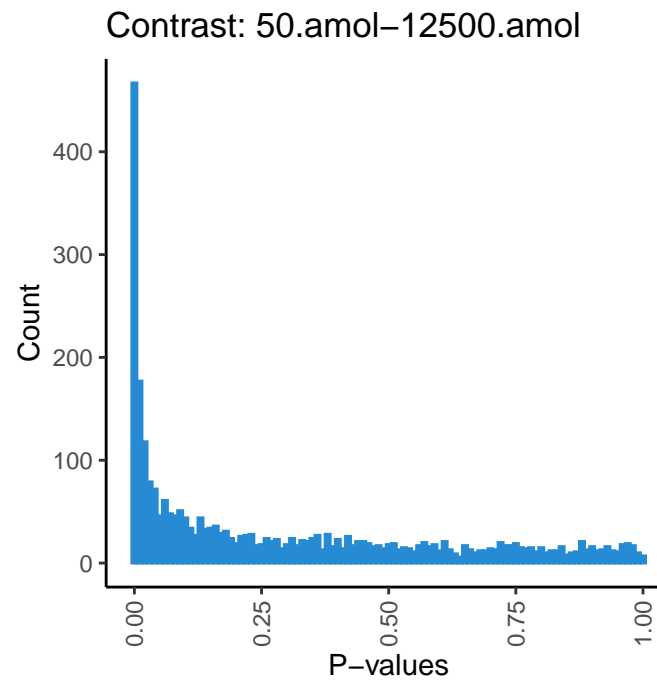
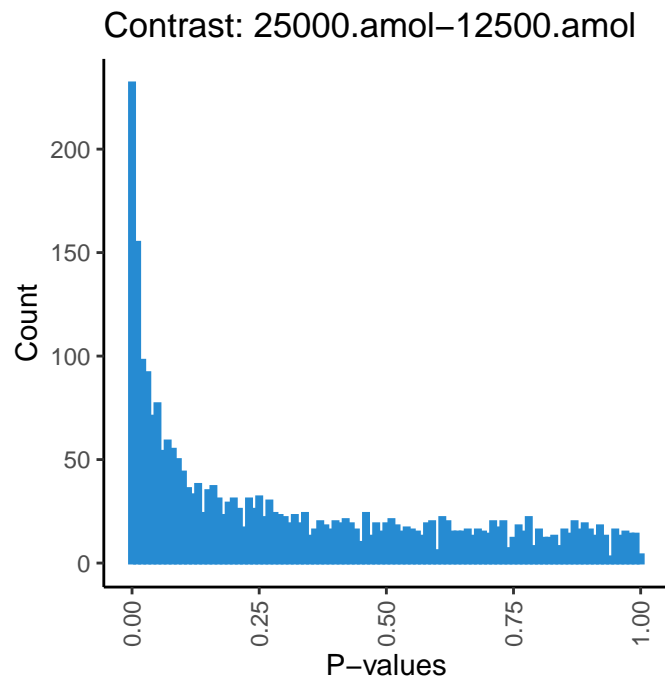
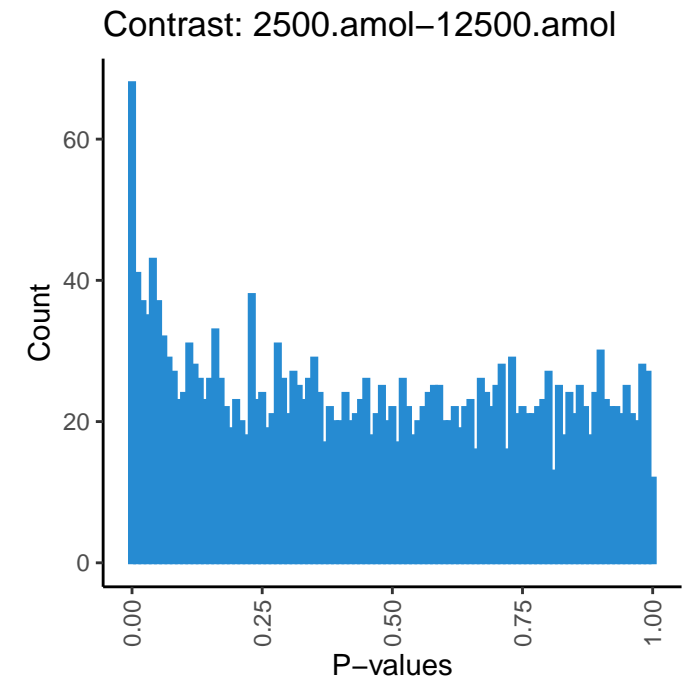
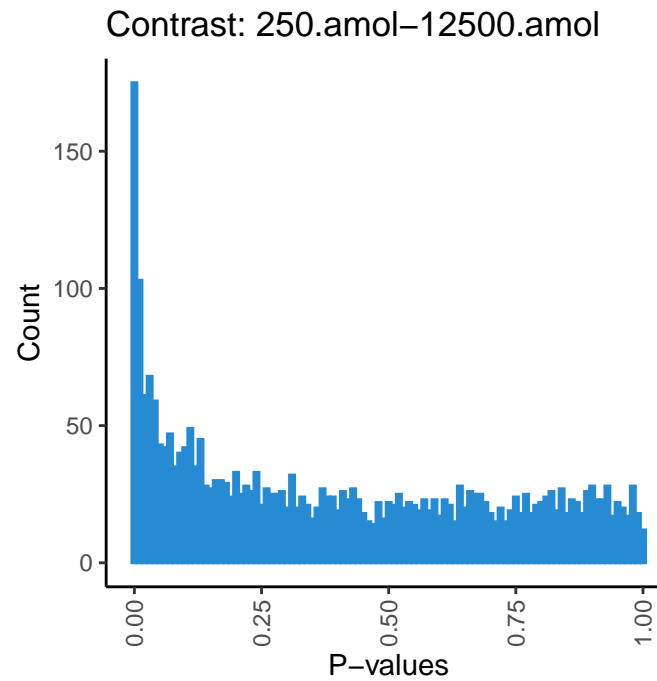
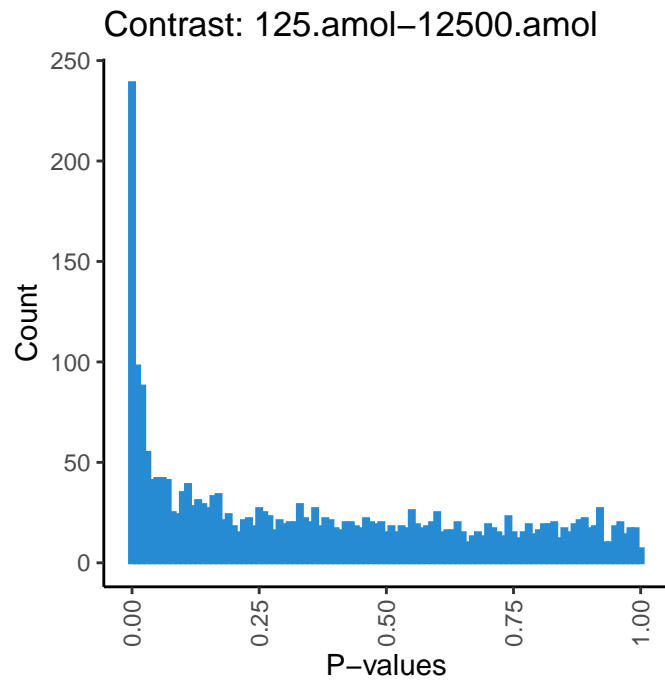
Project Name: NormalyzerPeptides

NormalyzerDE (ver 1.14.0)

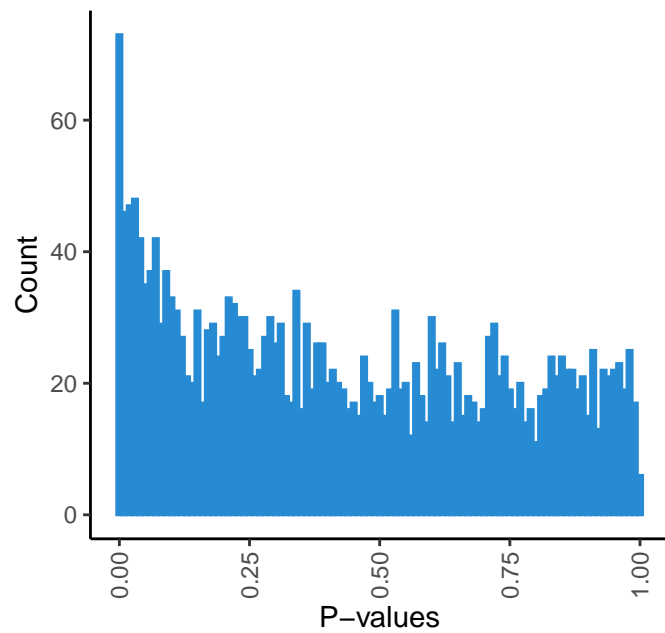
Report created on: 2022-07-06

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

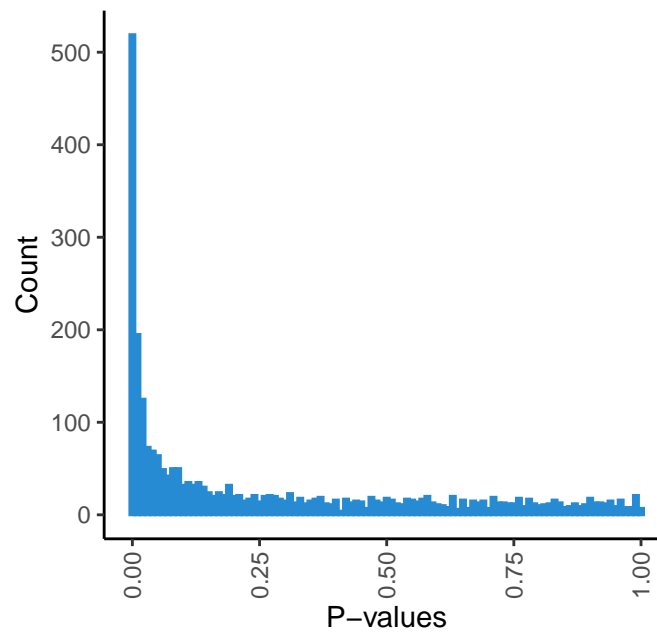
Documentation for analyzing this report can be found at <http://quantitativeproteomics.org/normalyzer/help.php>

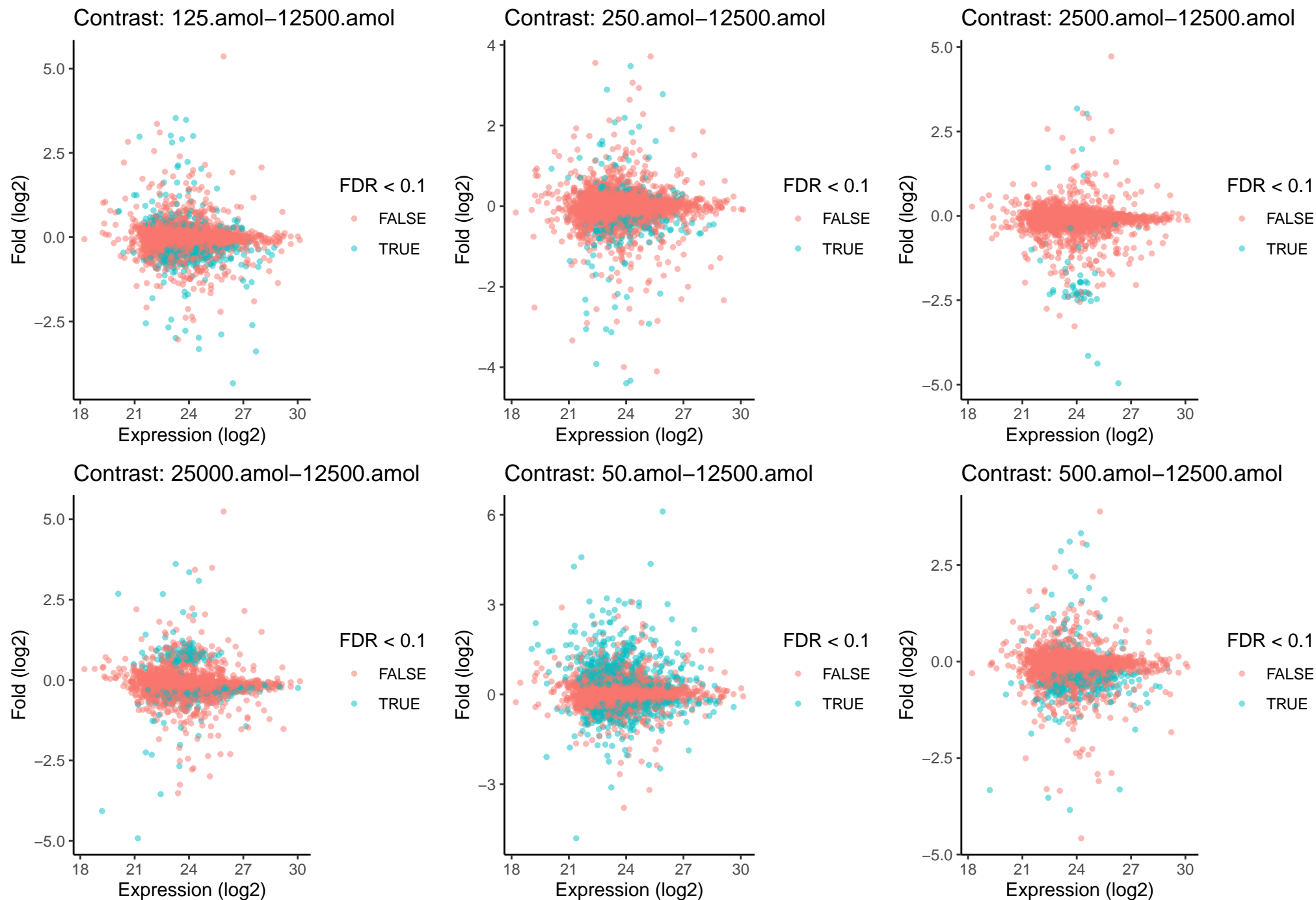


Contrast: 5000.amol–12500.amol

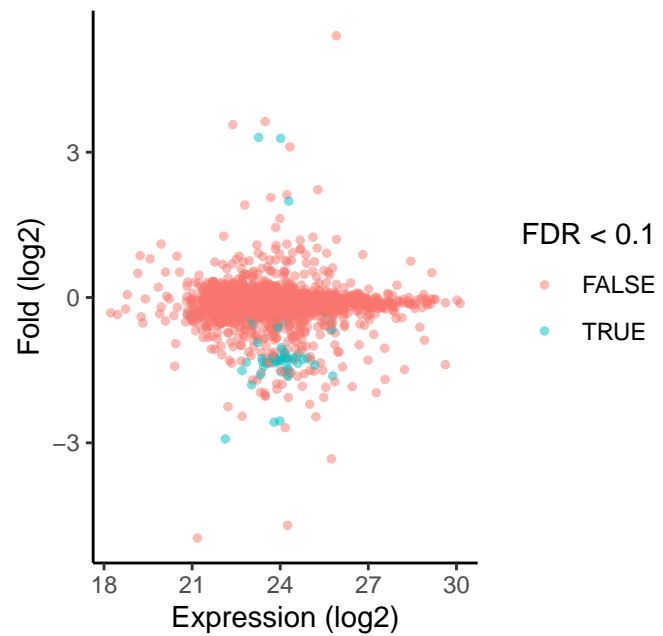


Contrast: 50000.amol–12500.amol

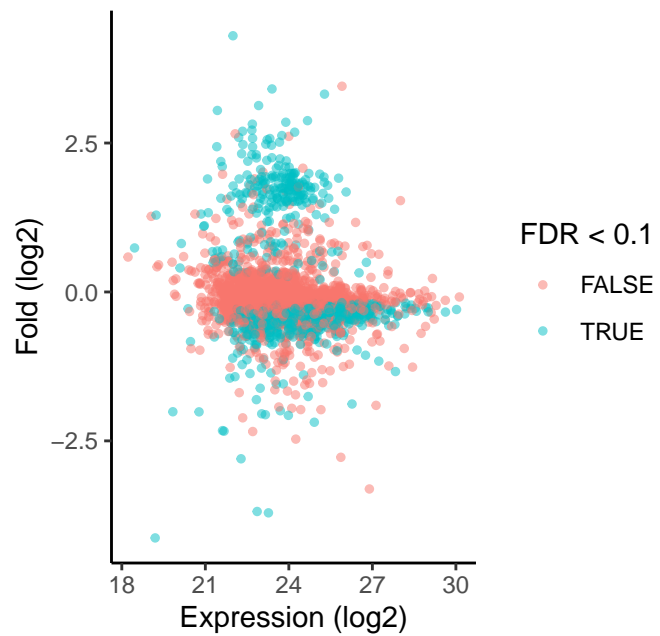


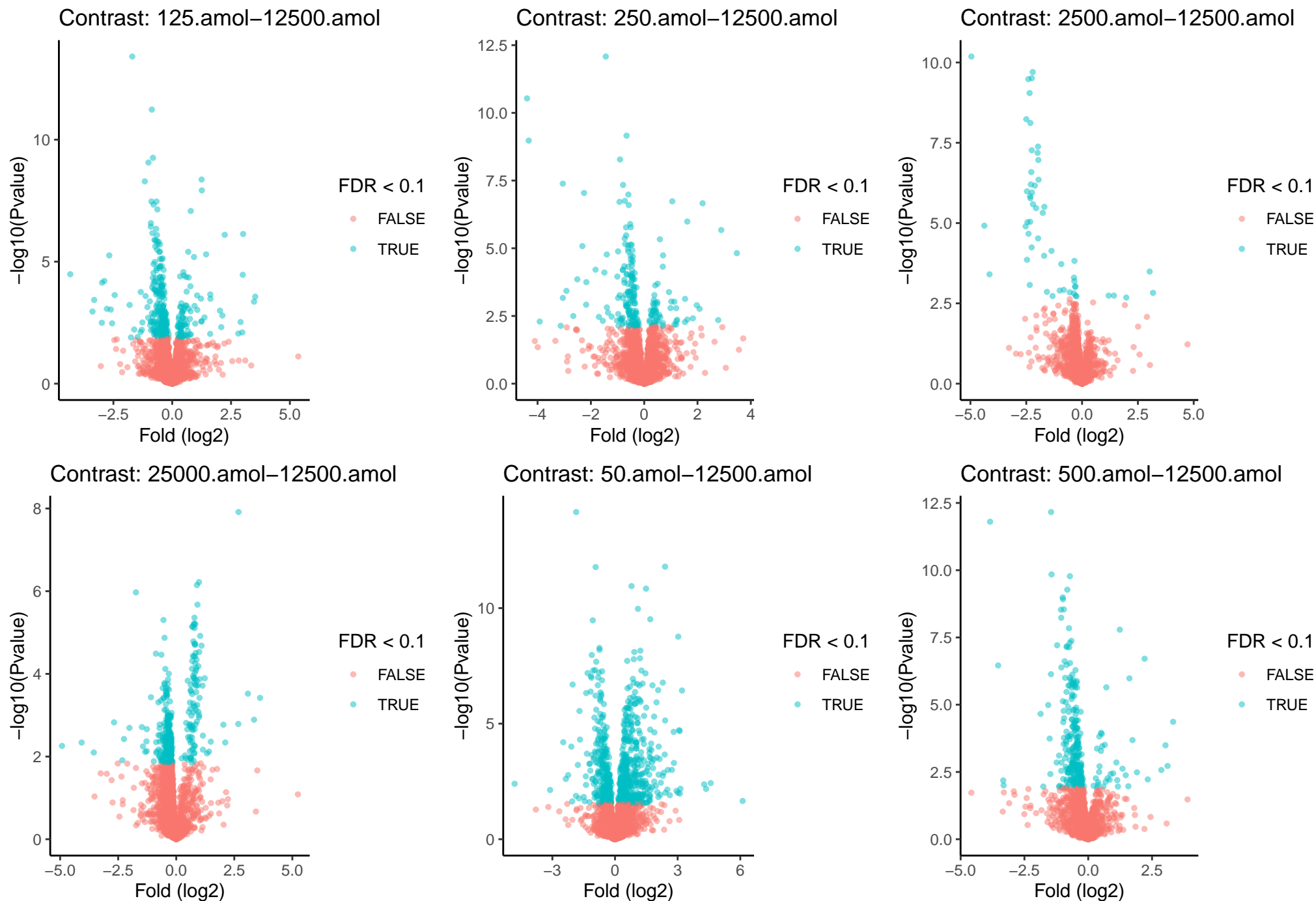


Contrast: 5000.amol–12500.amol

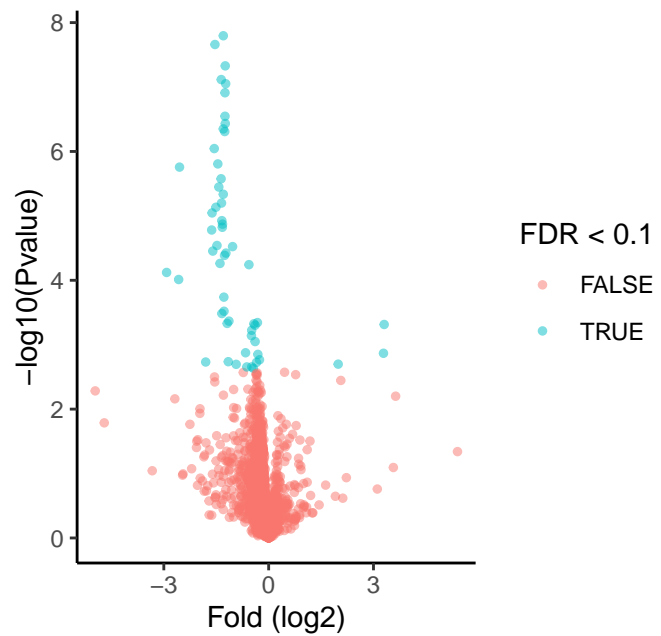


Contrast: 50000.amol–12500.amol

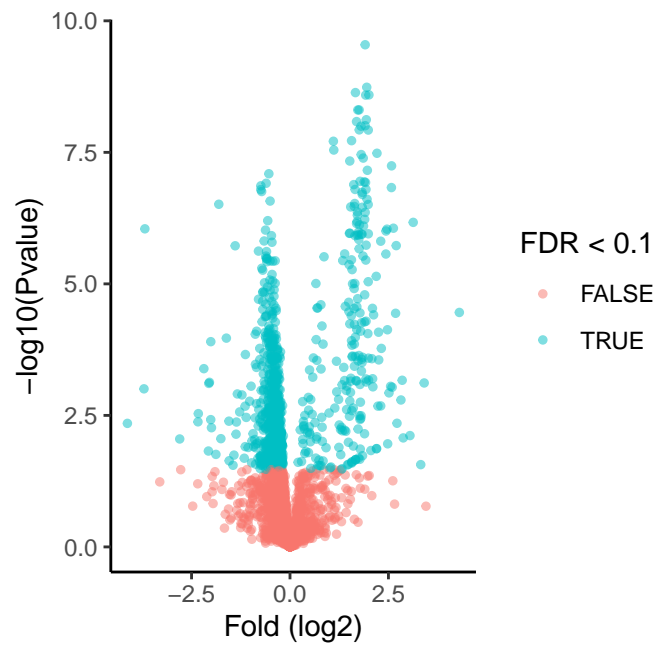


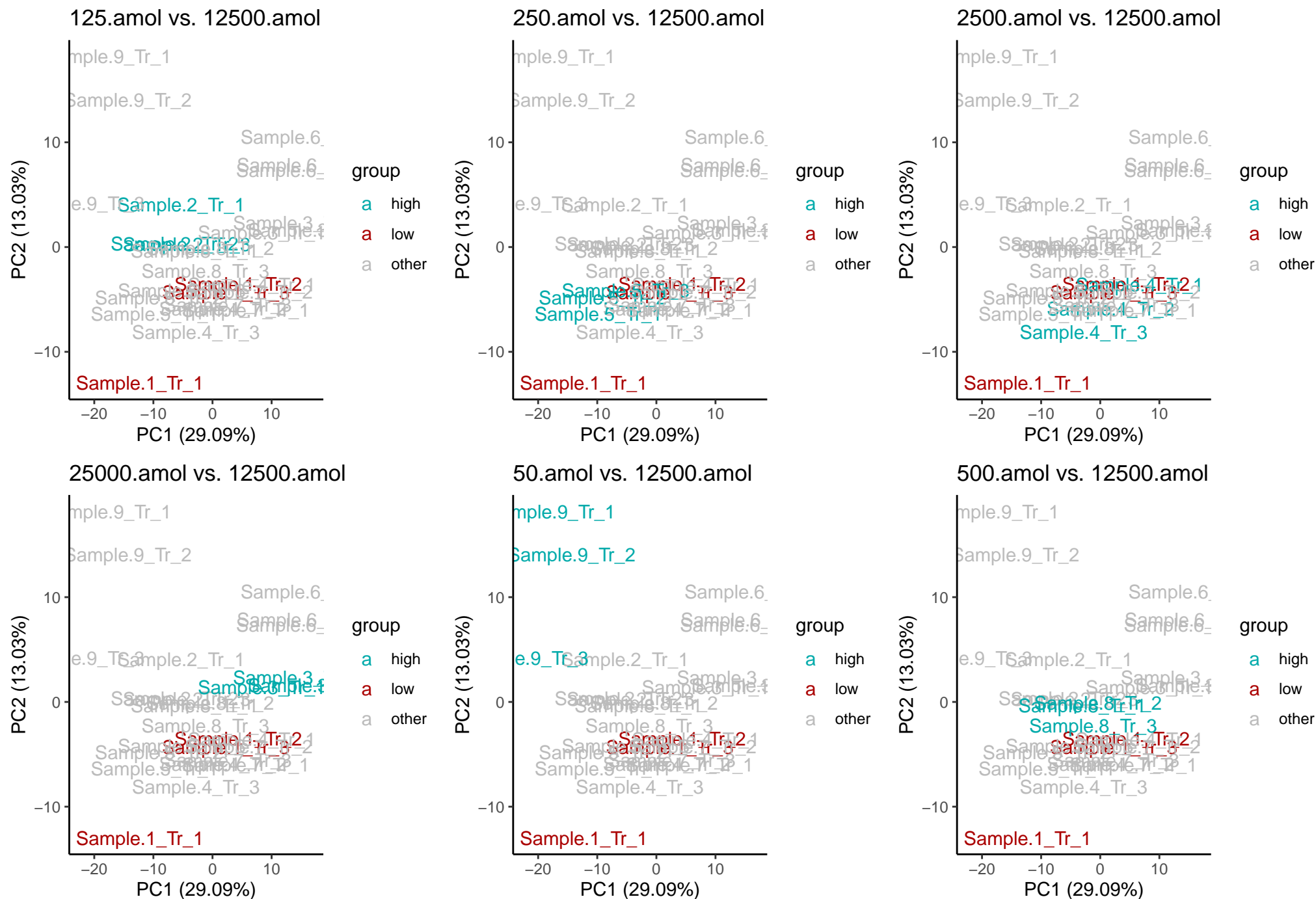


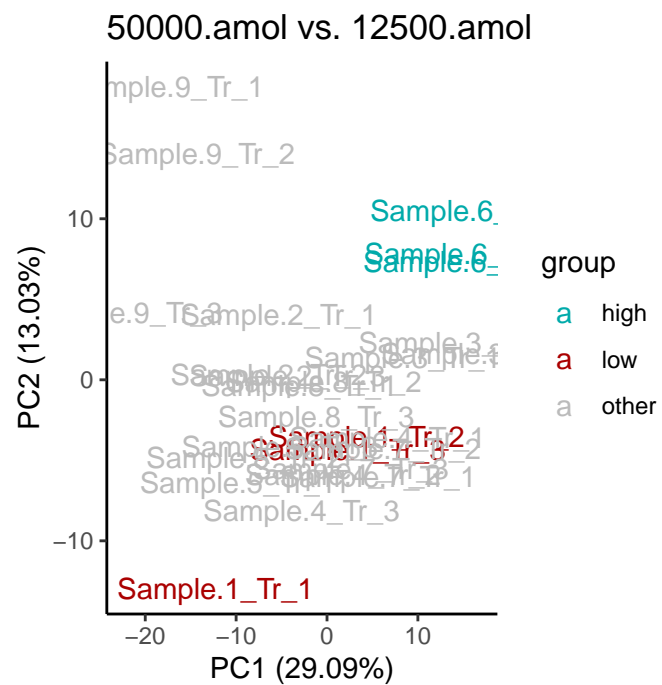
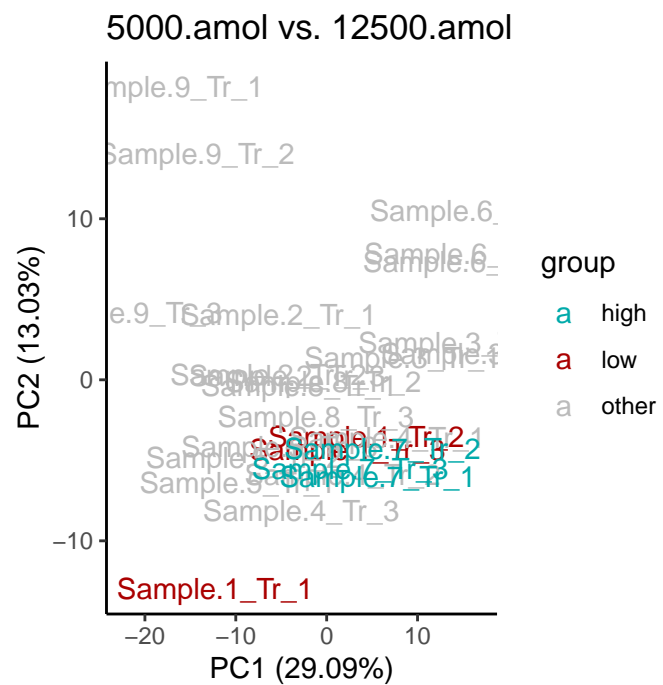
Contrast: 5000.amol-12500.amol

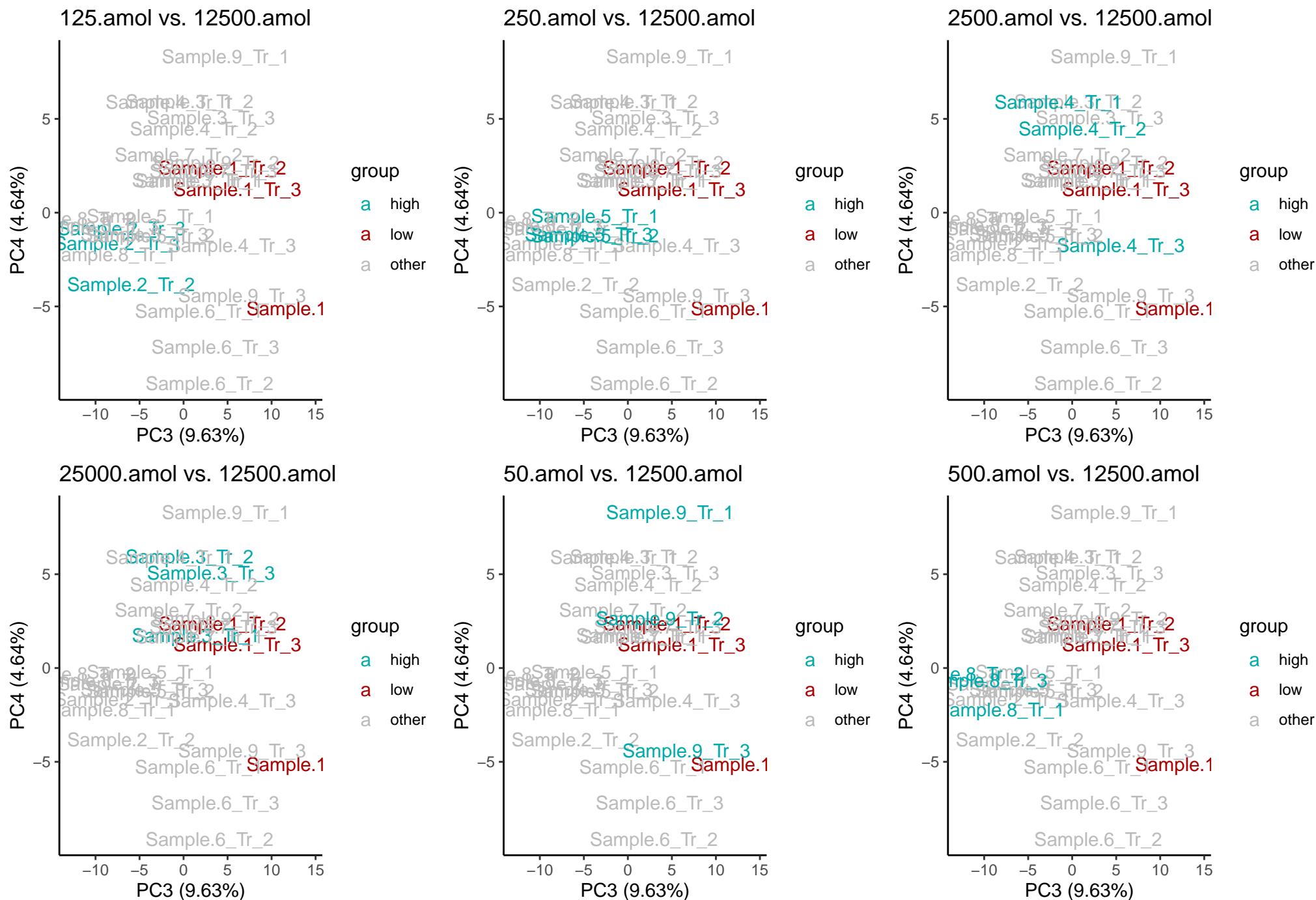


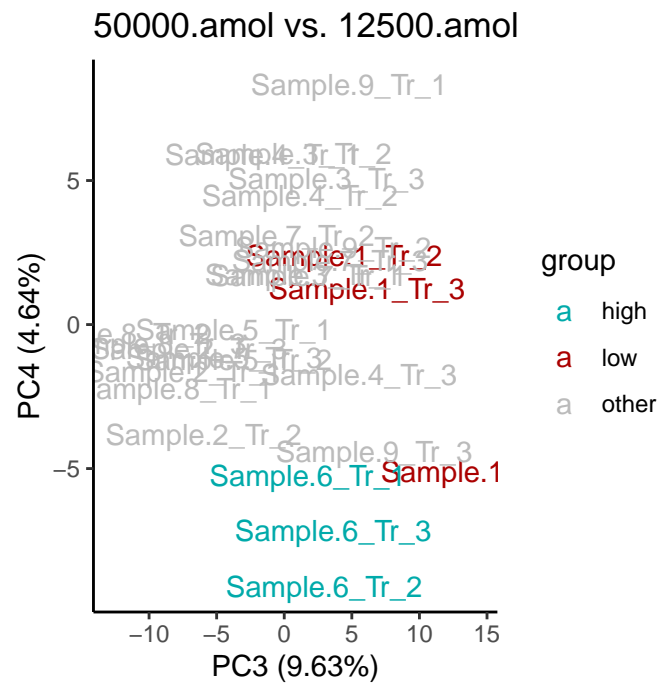
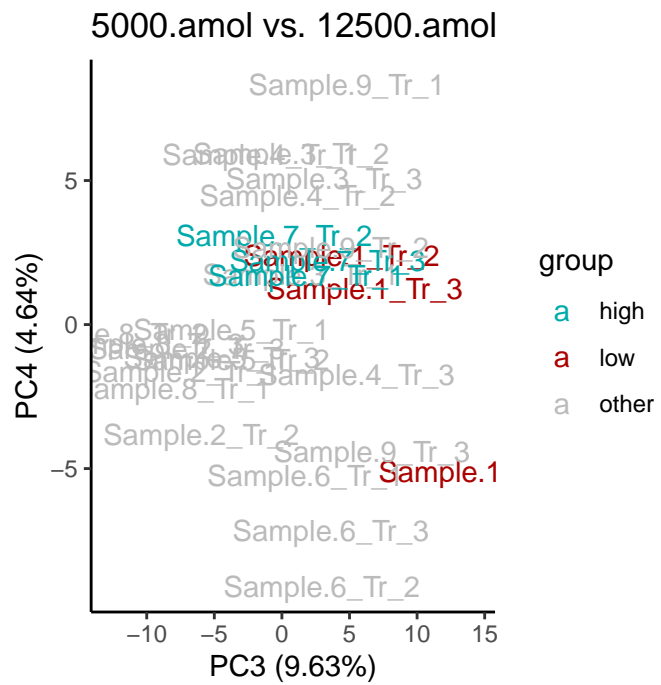
Contrast: 50000.amol-12500.amol



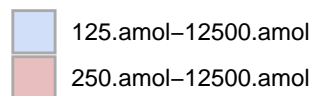
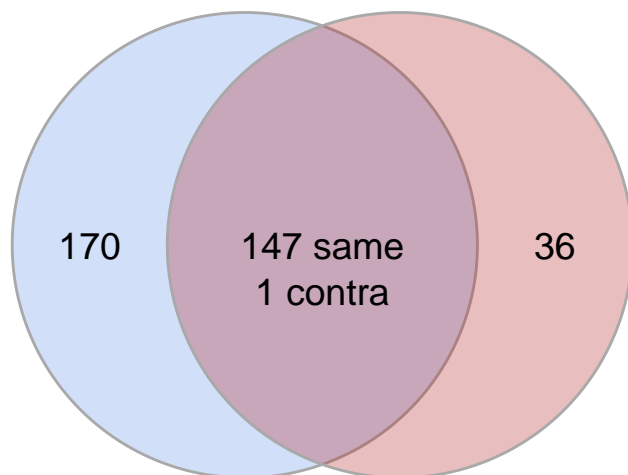




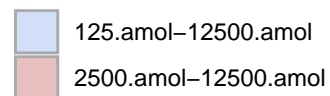
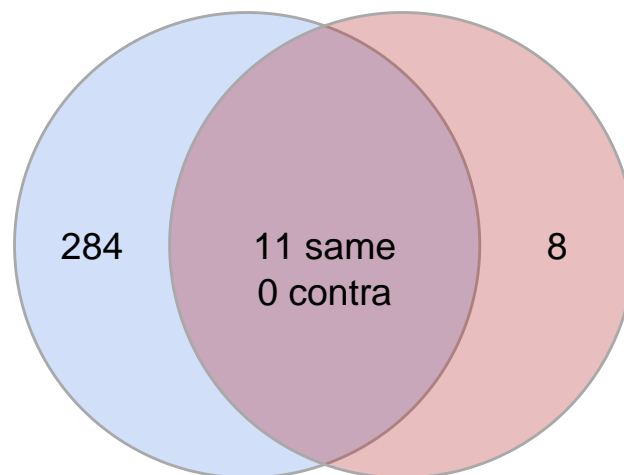




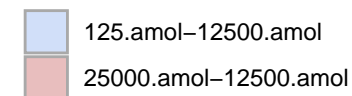
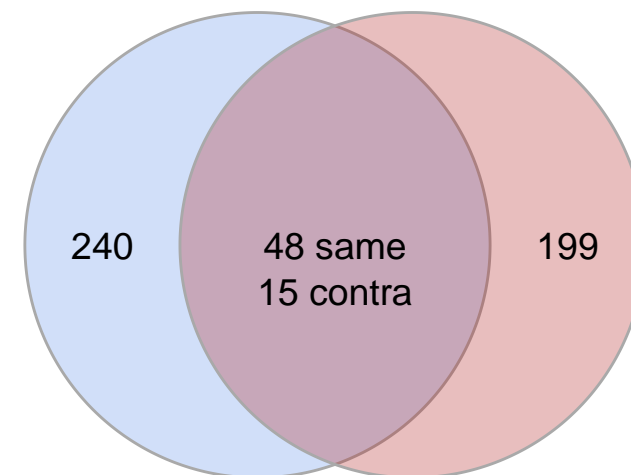
fdr < 0.1, |log2 fold| >= 0



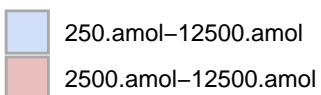
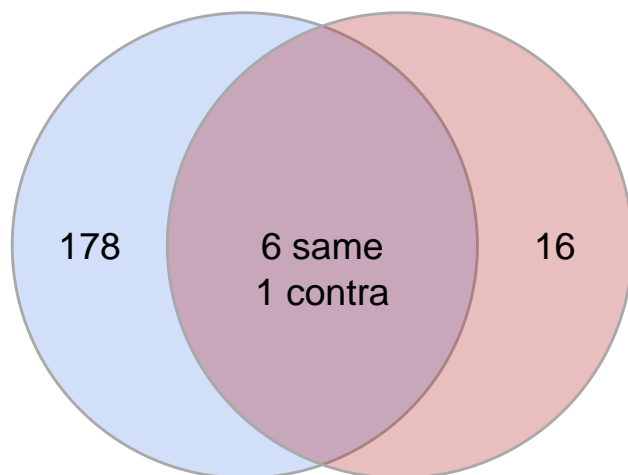
fdr < 0.1, |log2 fold| >= 0



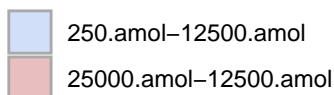
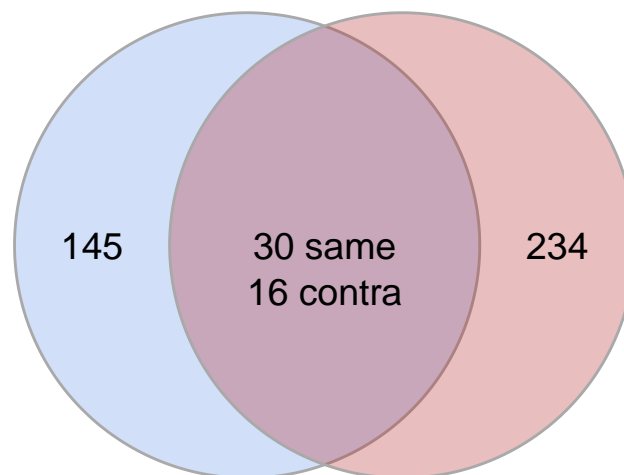
fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0

