

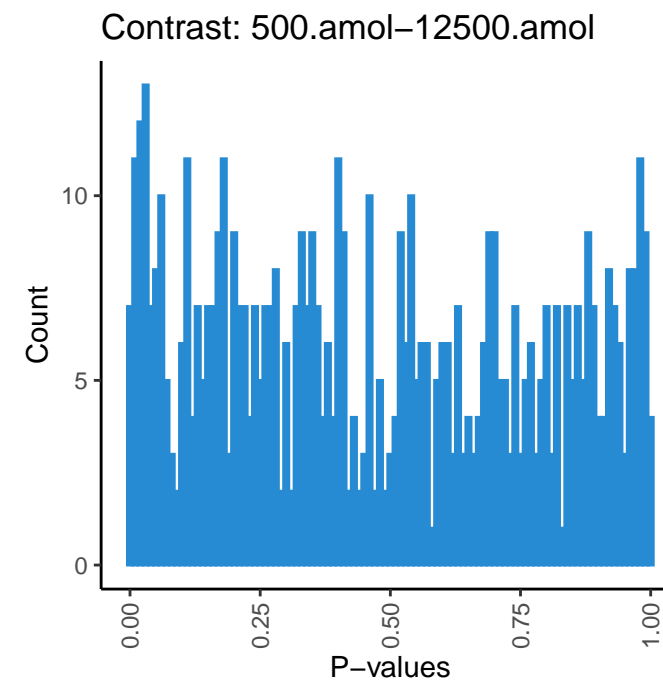
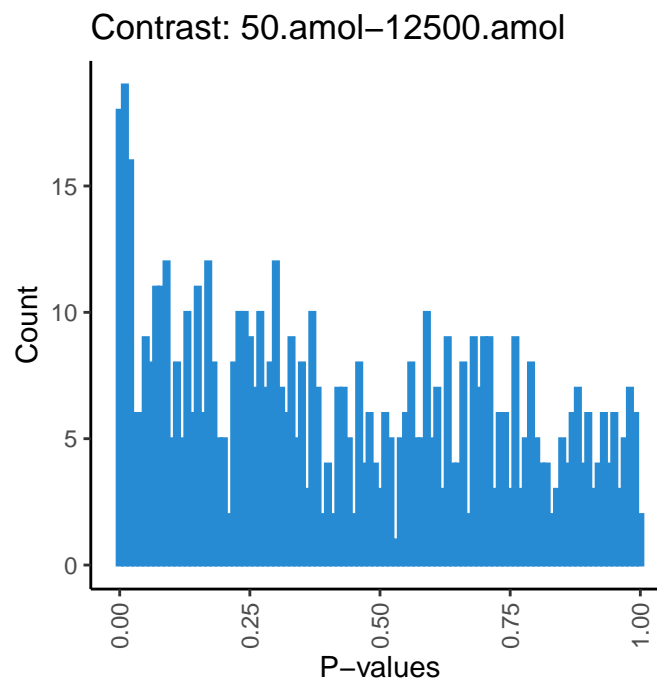
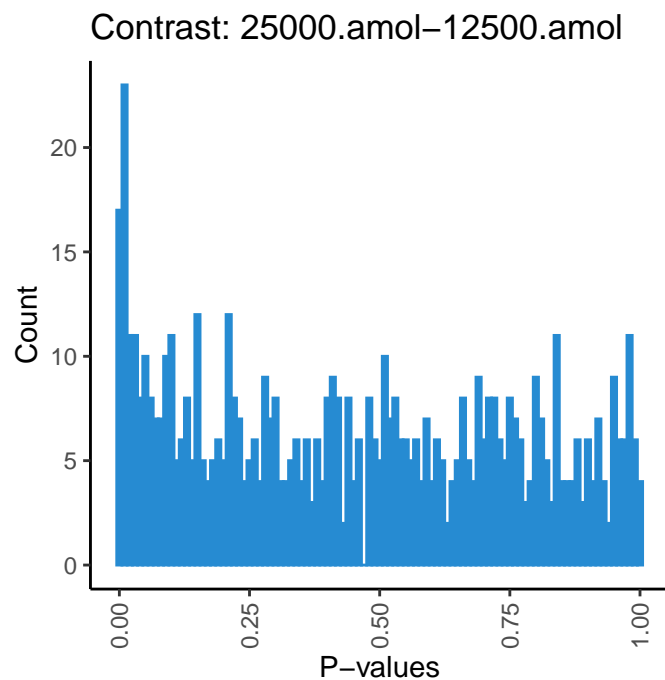
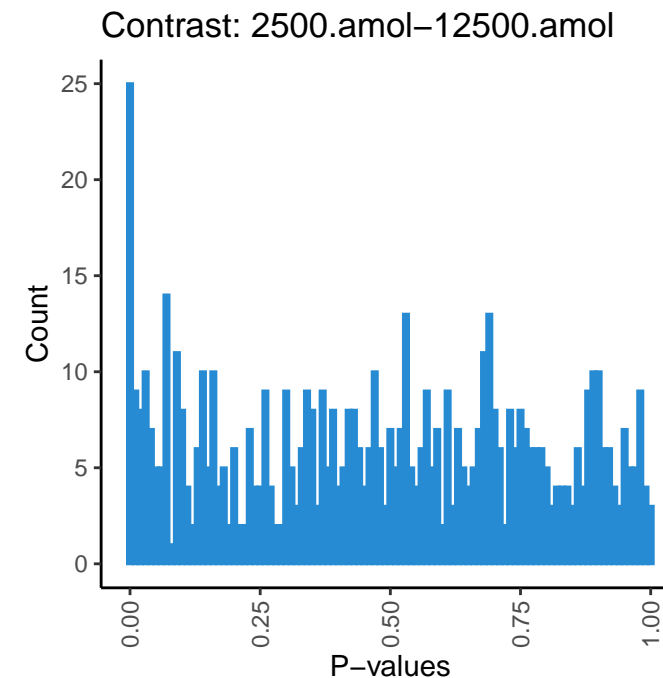
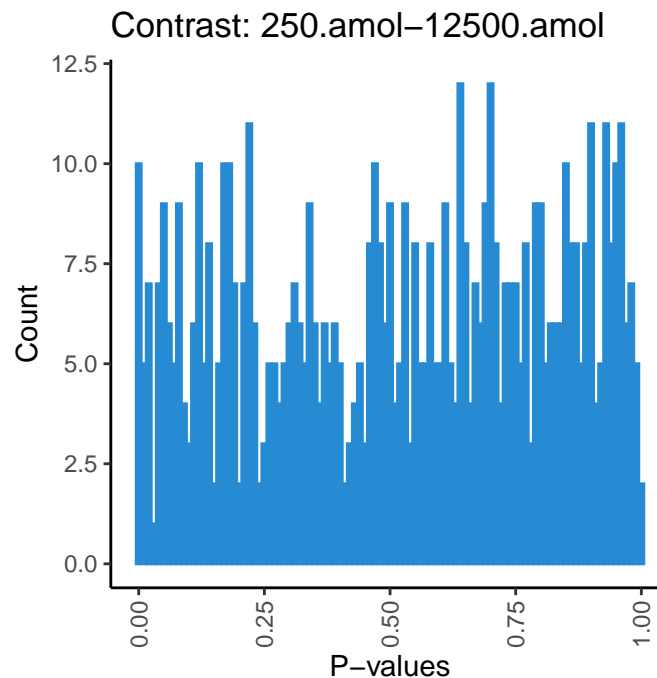
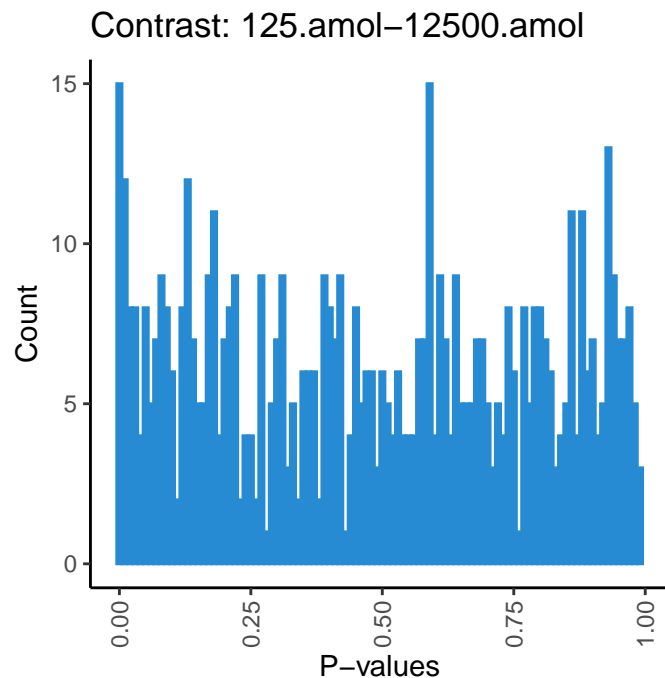
Project Name: NormalyzerProteins

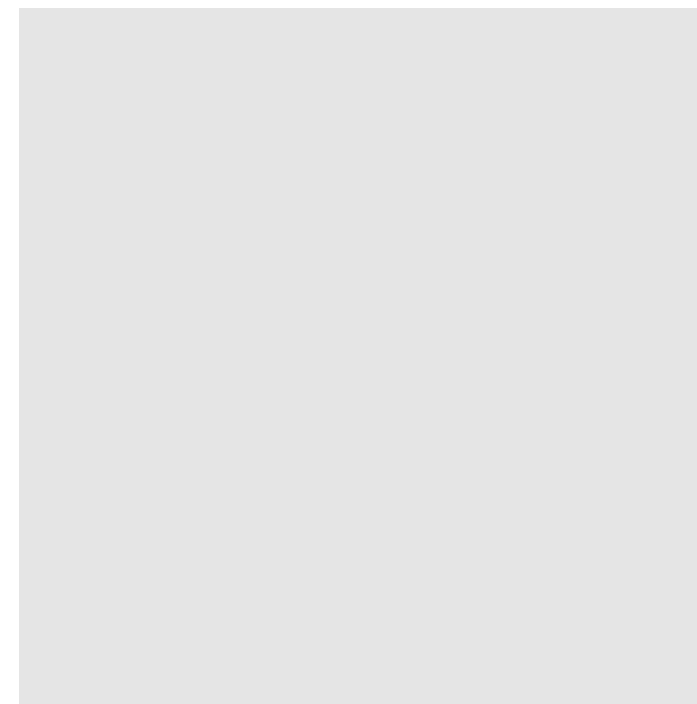
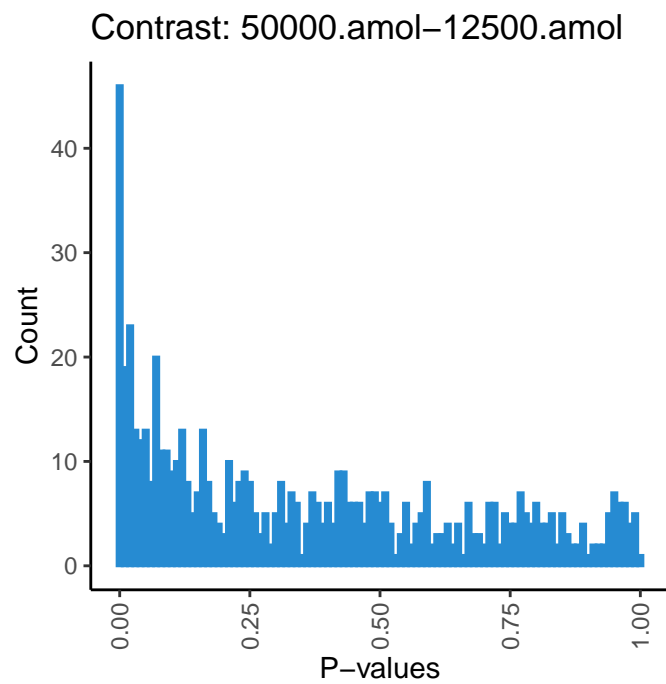
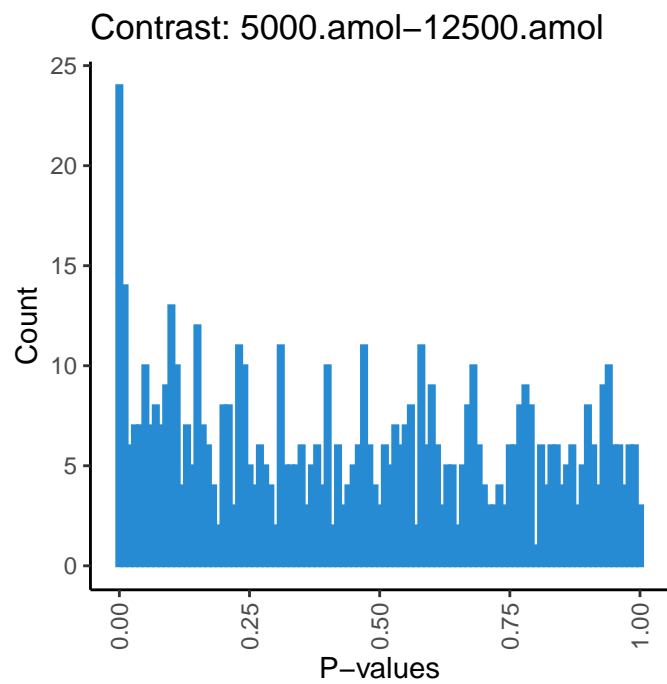
NormalyzerDE (ver 1.14.0)

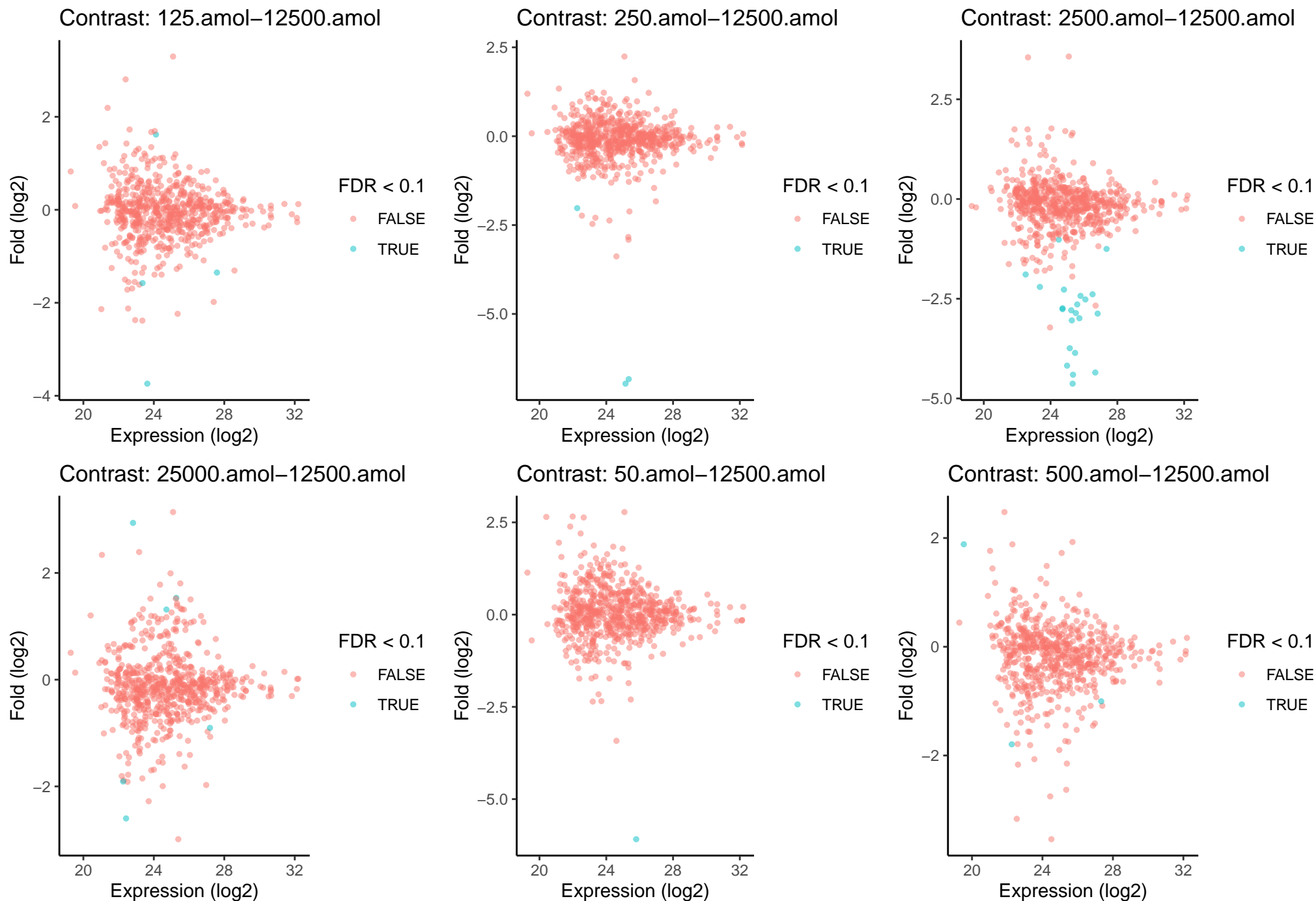
Report created on: 2022-07-06

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

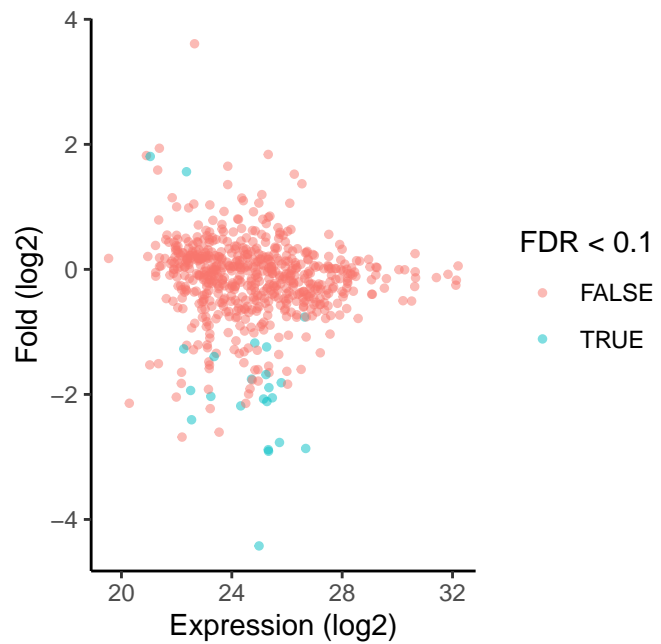
Documentation for analyzing this report can be found at <http://quantitativeproteomics.org/normalyzer/help.php>



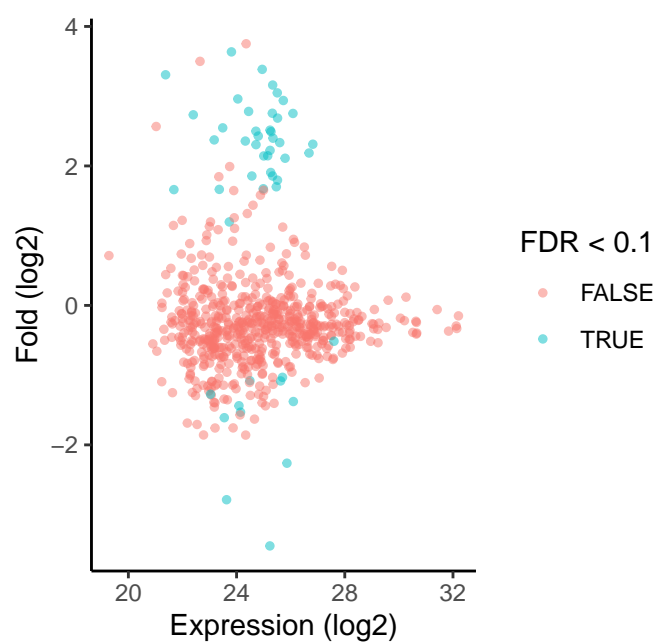


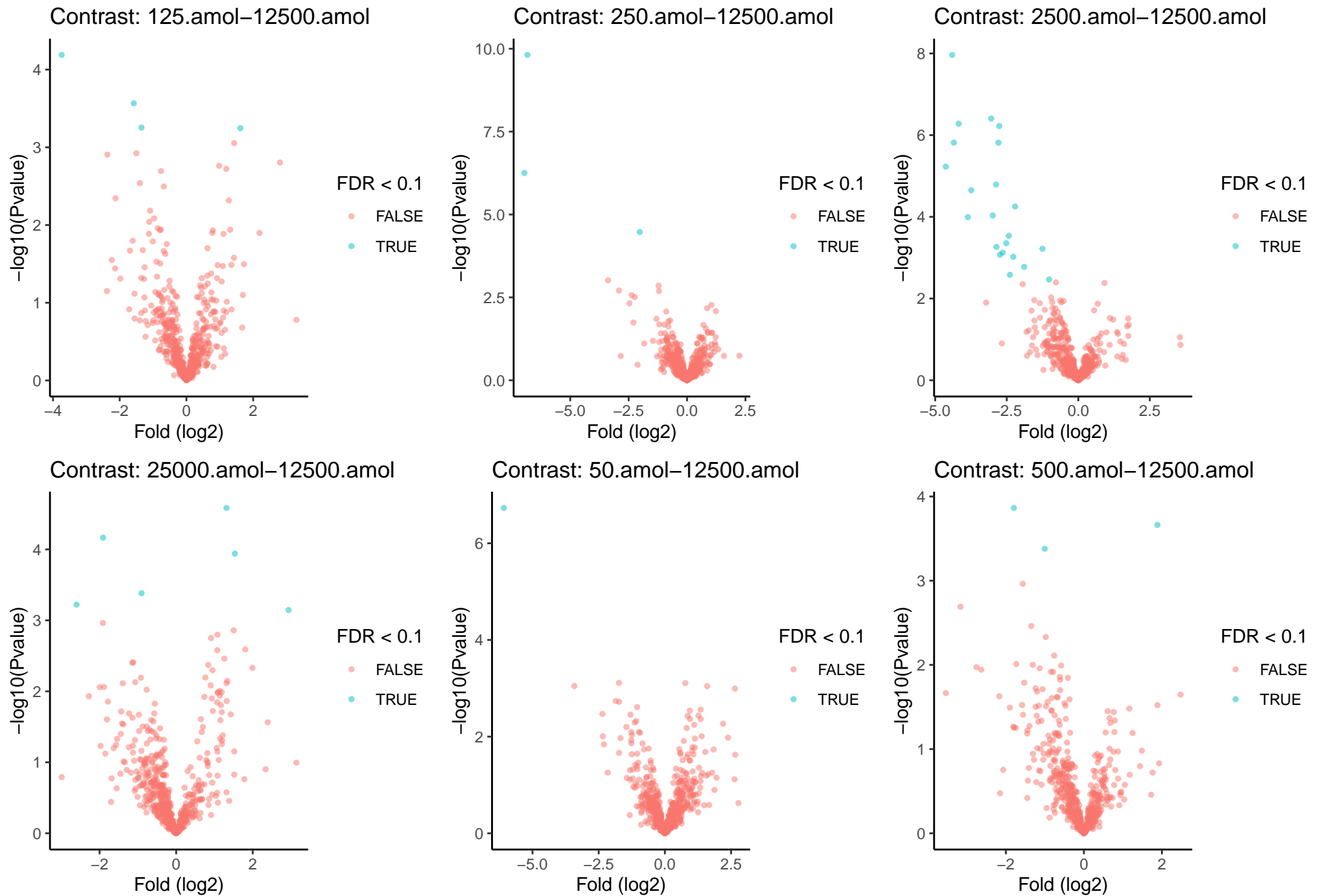


Contrast: 5000.amol–12500.amol

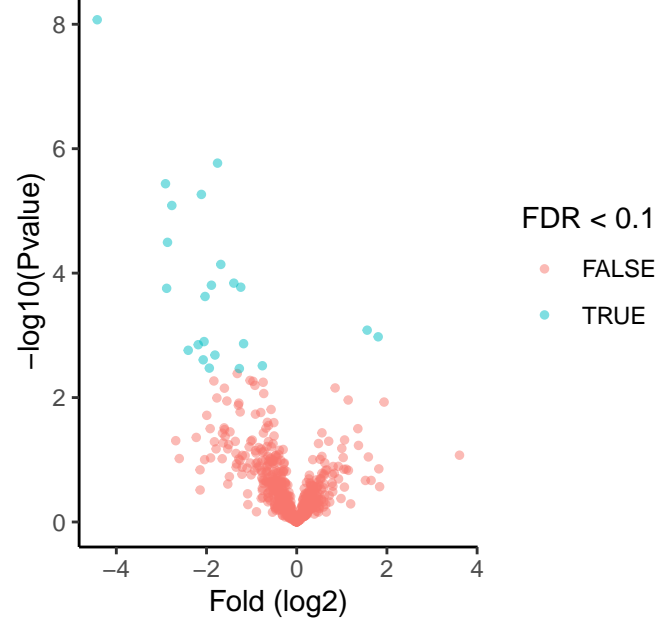


Contrast: 50000.amol–12500.amol

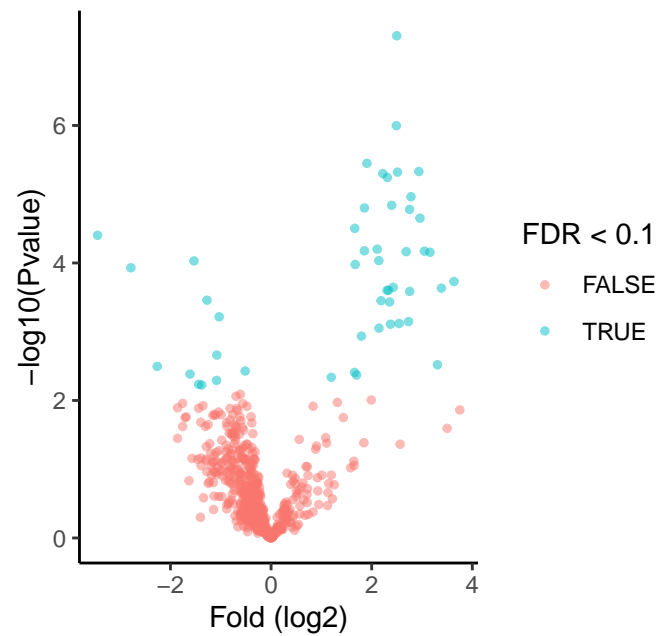


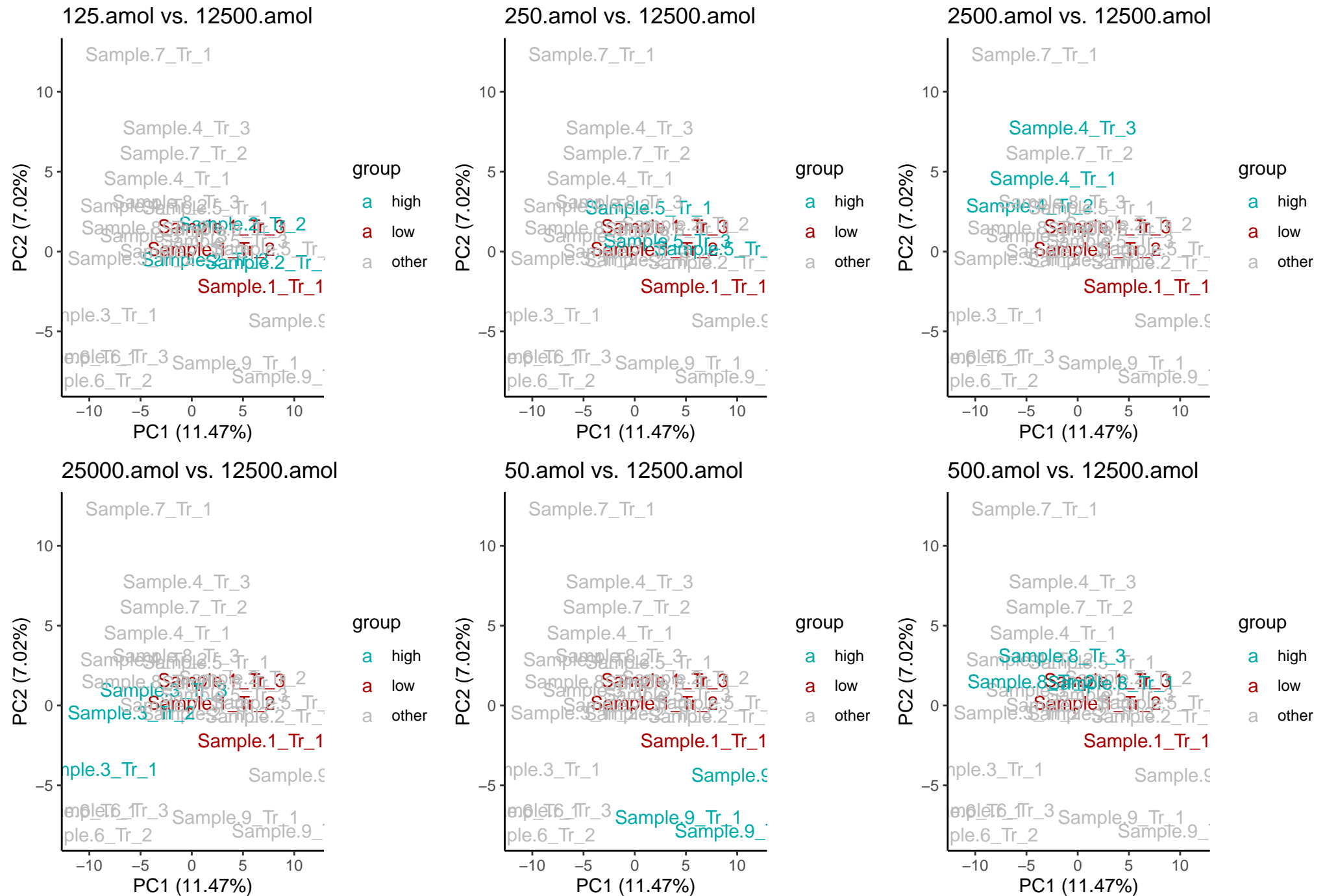


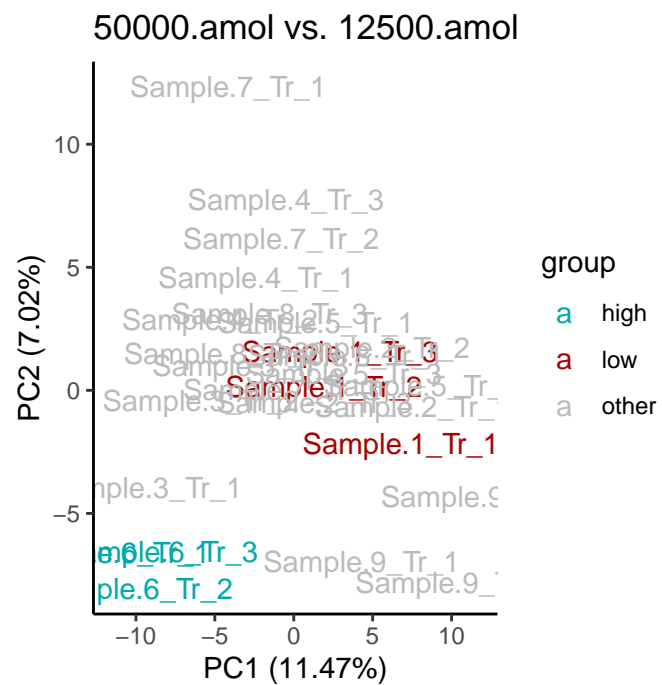
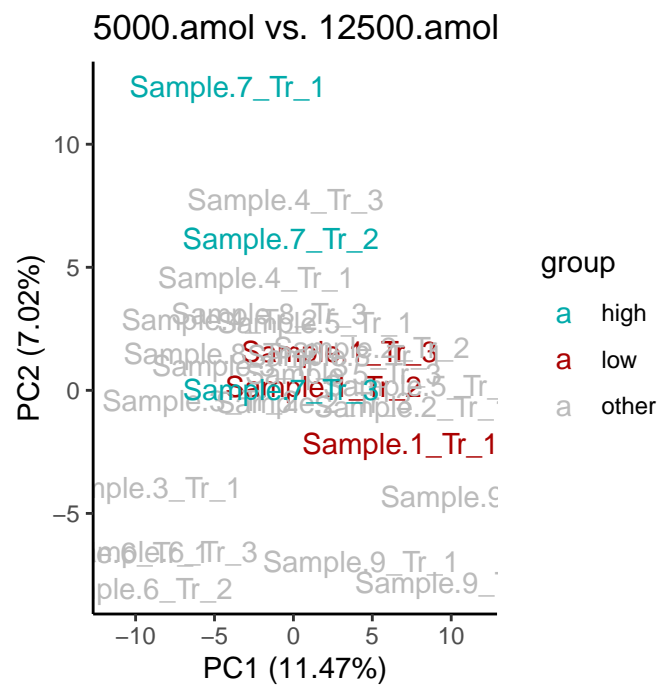
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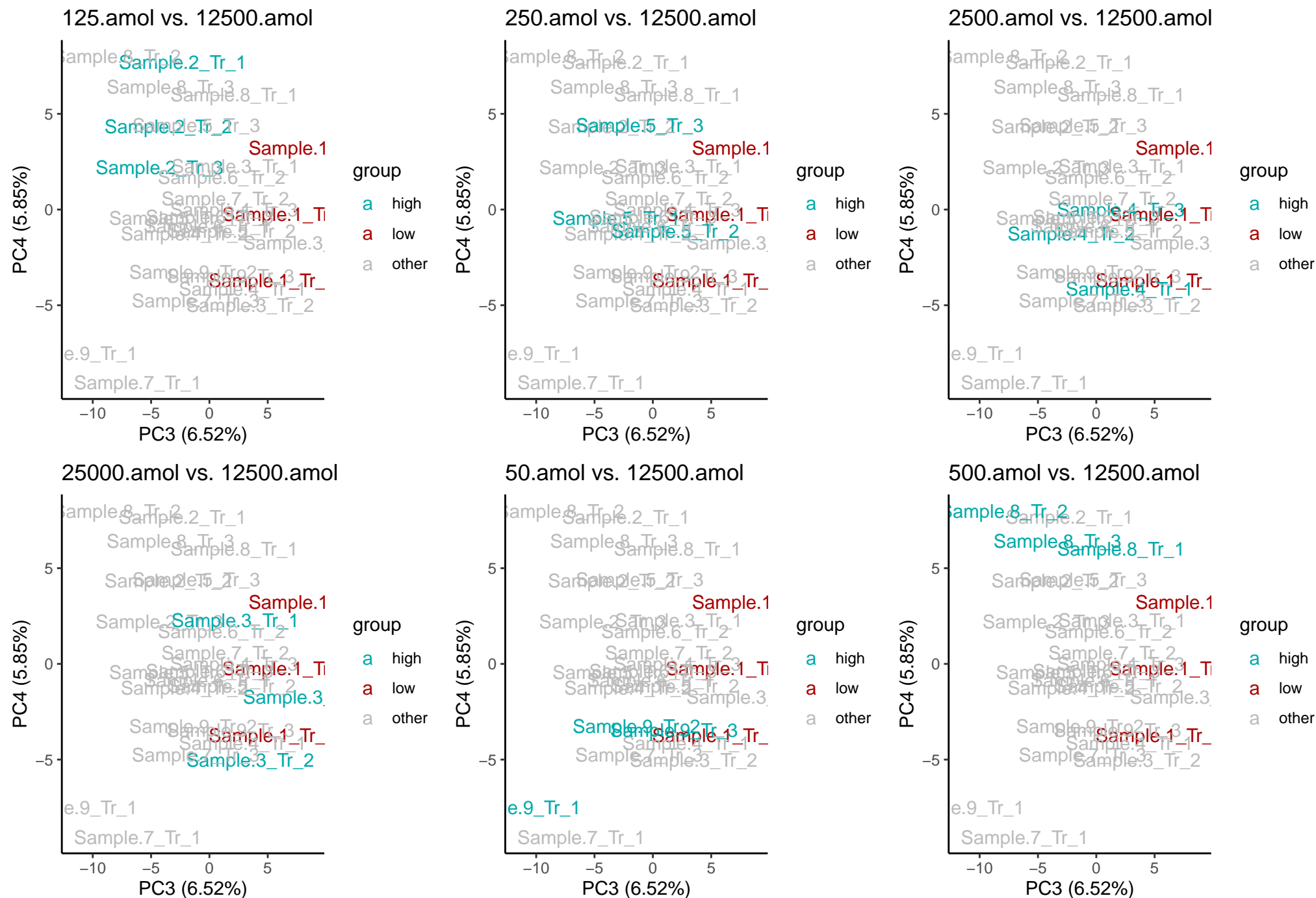


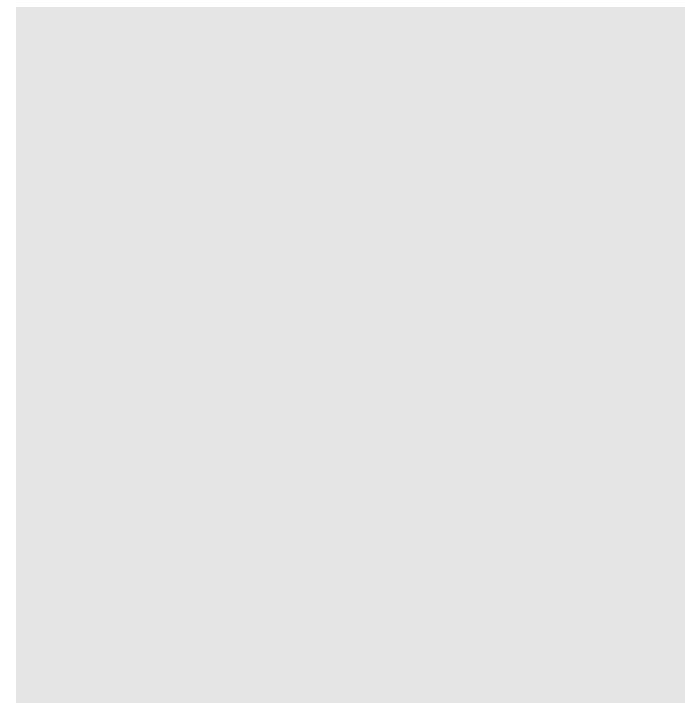
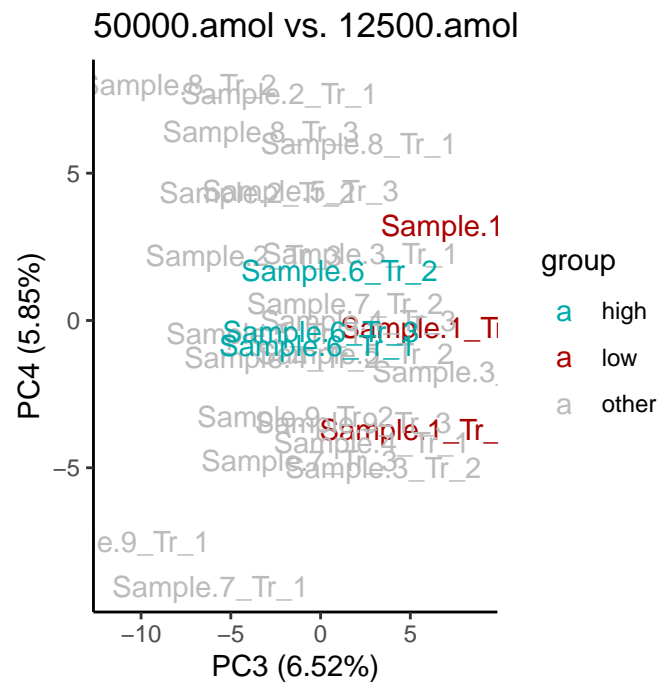
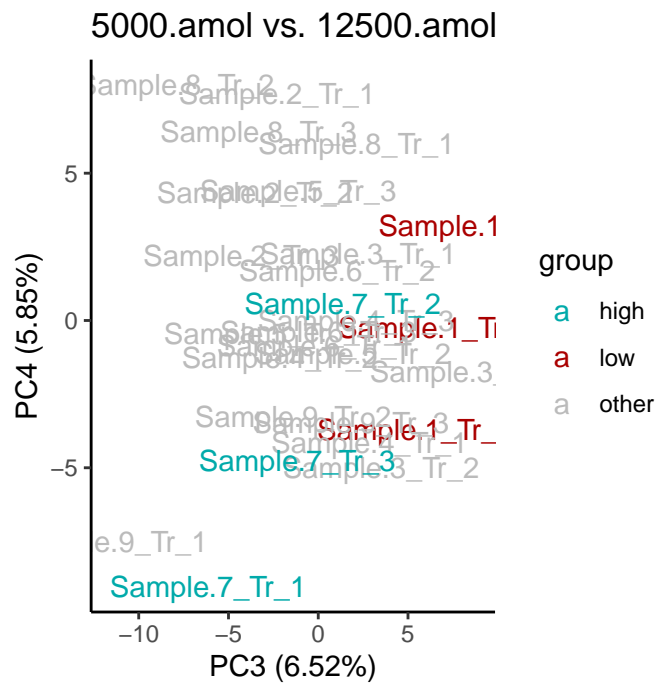
Contrast: 50000.amol–12500.amol



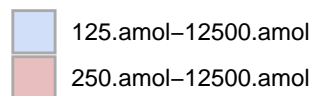
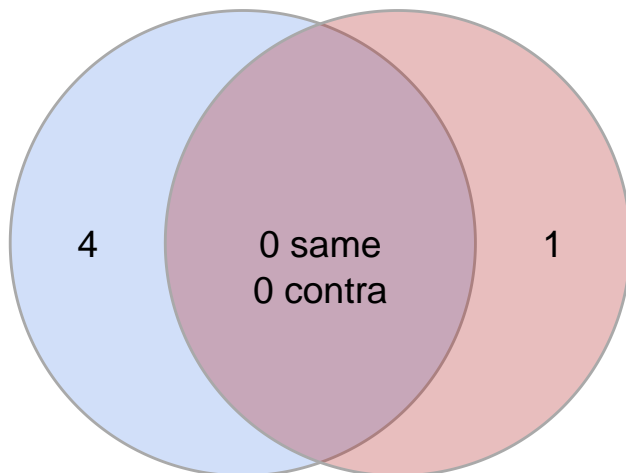




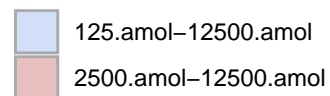
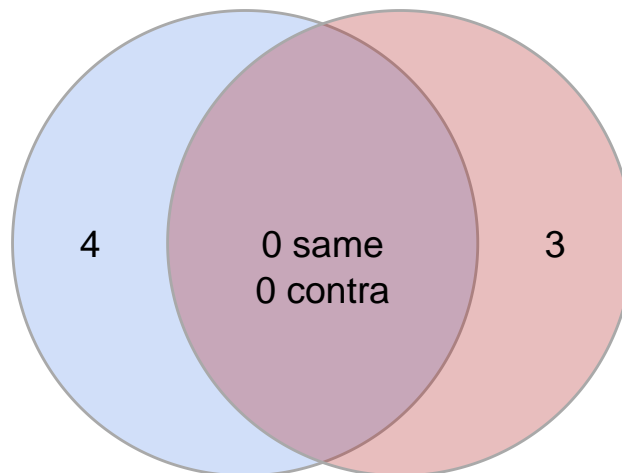




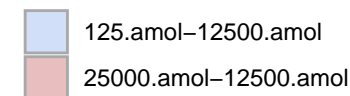
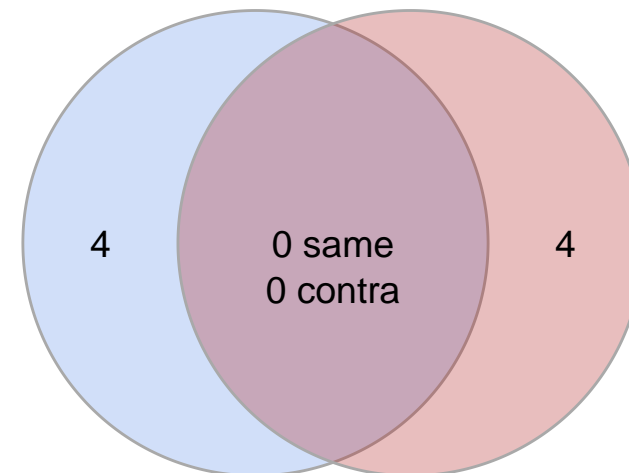
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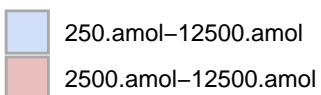
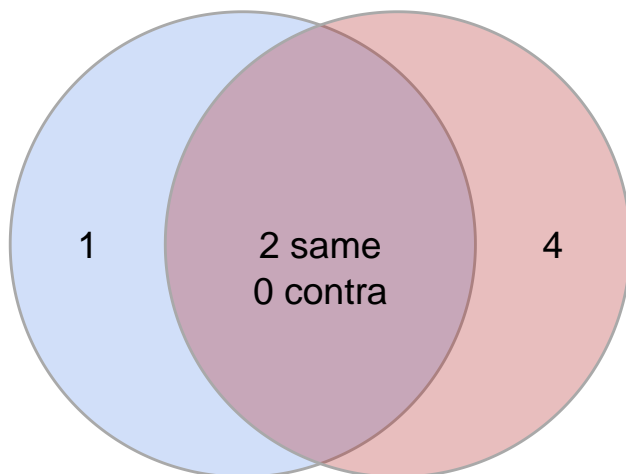
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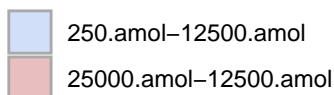
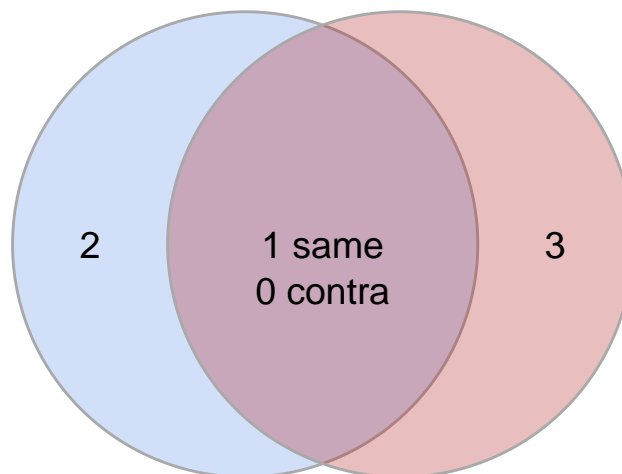
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fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0



fdr < 0.1, |log2 fold| >= 0

