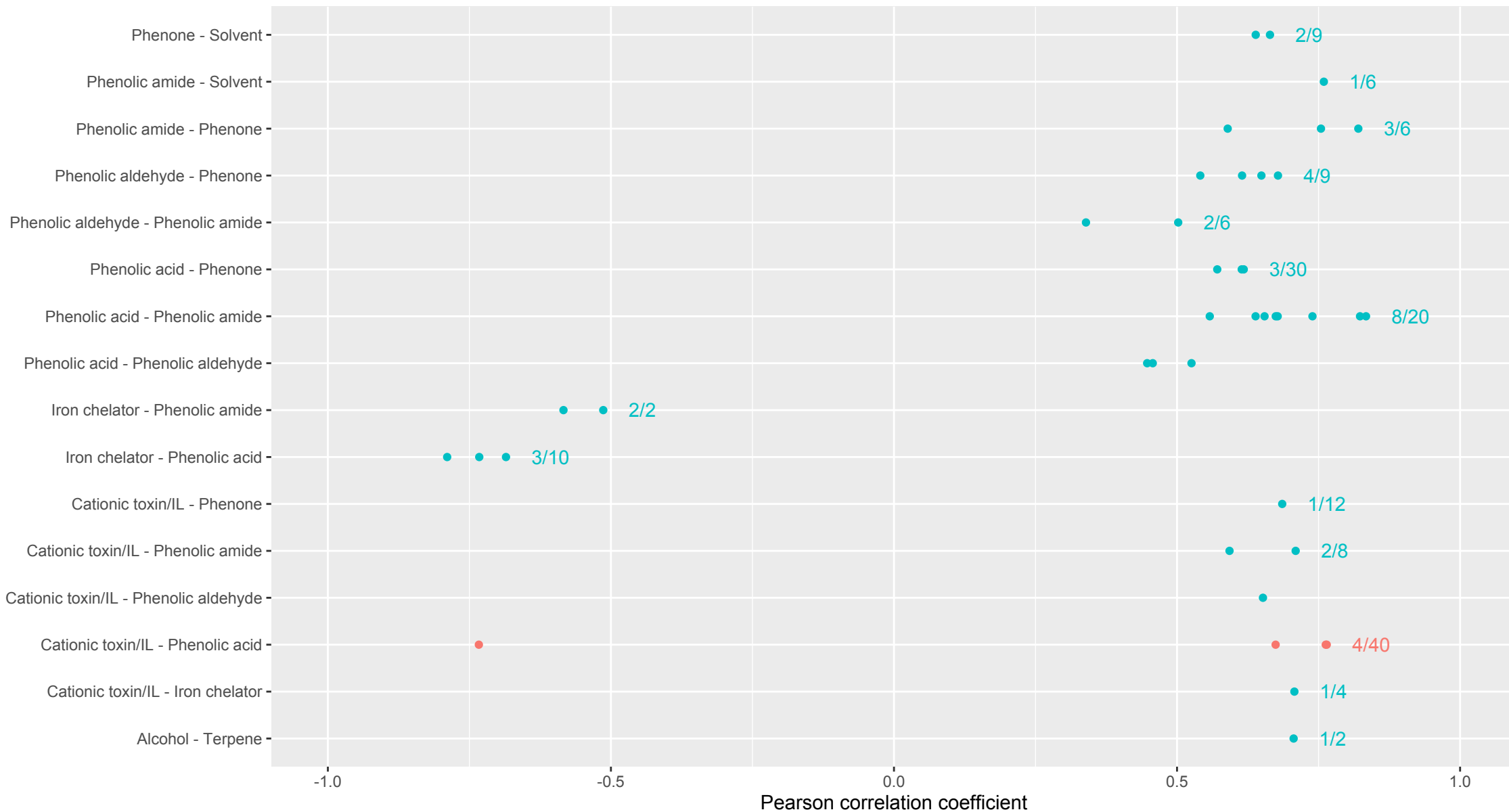
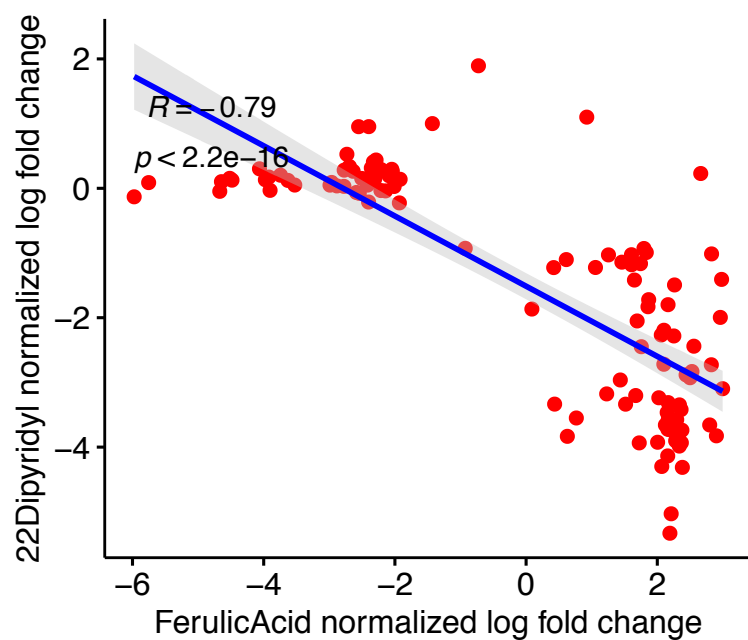


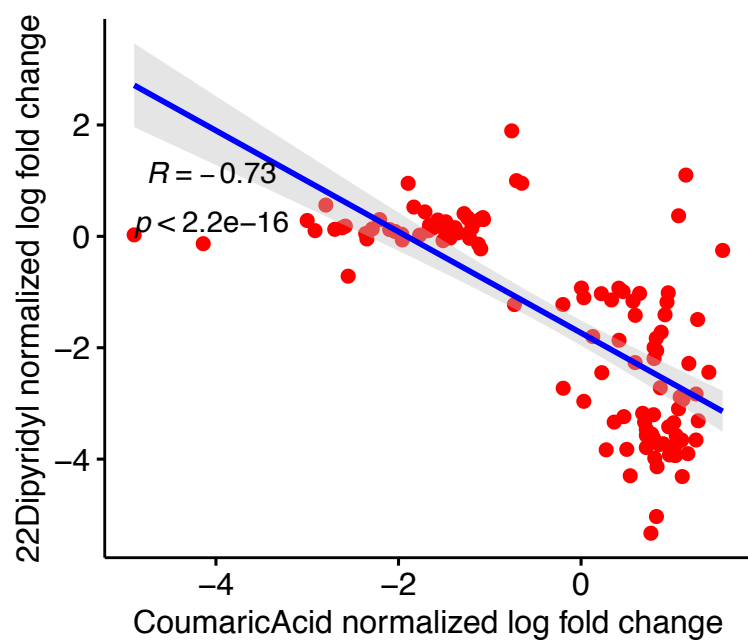
Significant inter-class inhibitor correlations



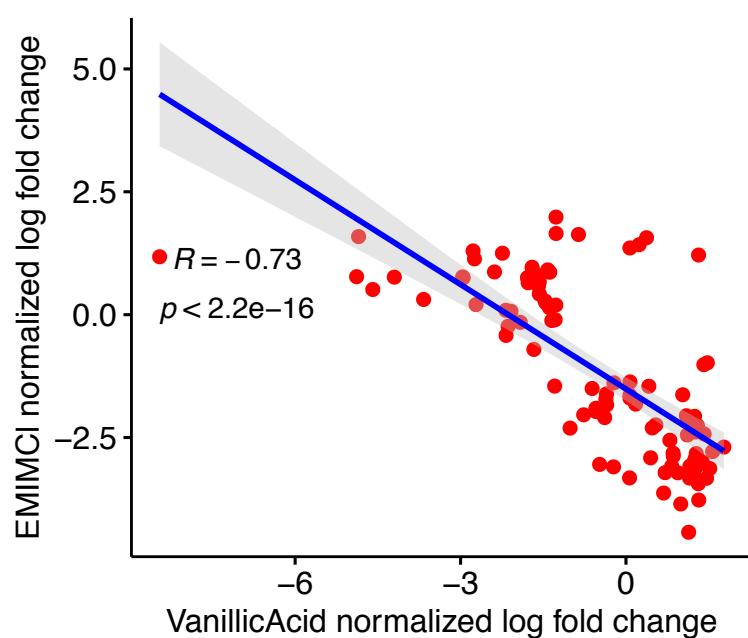
Phenolic acid – Iron chelator



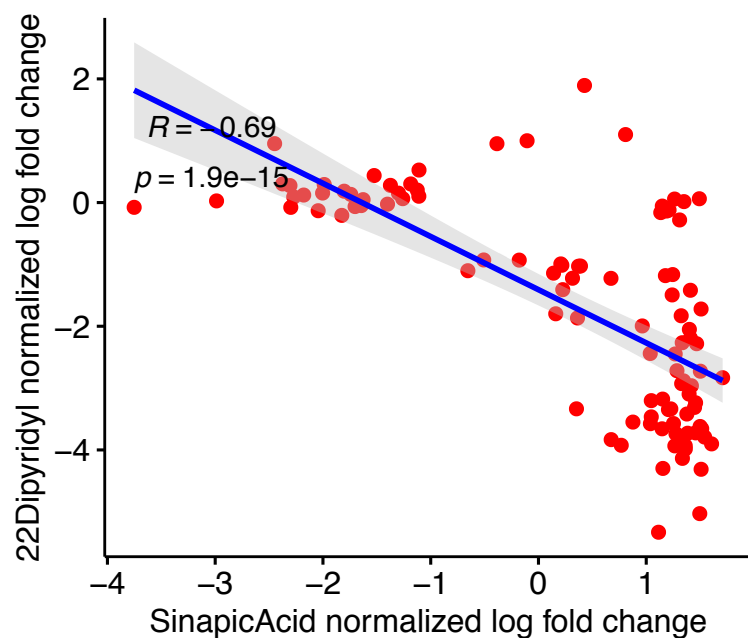
Phenolic acid – Iron chelator



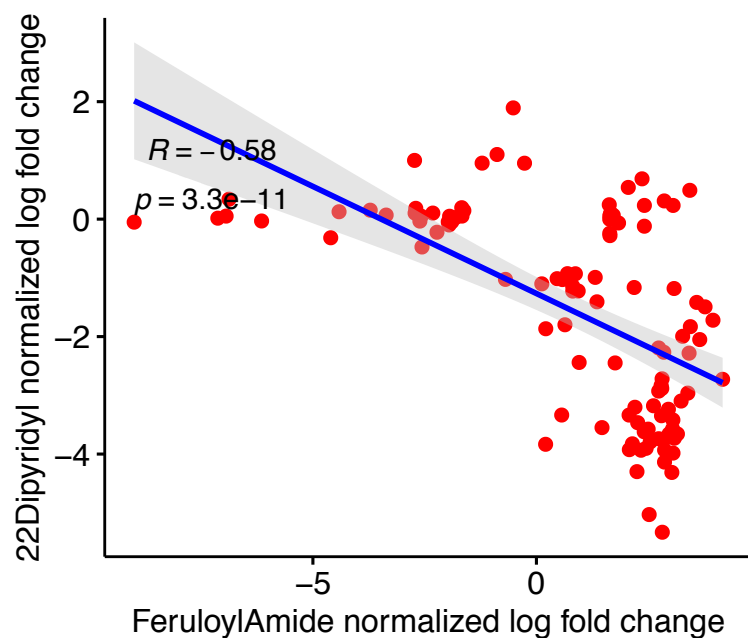
Phenolic acid – Cationic toxin/IL



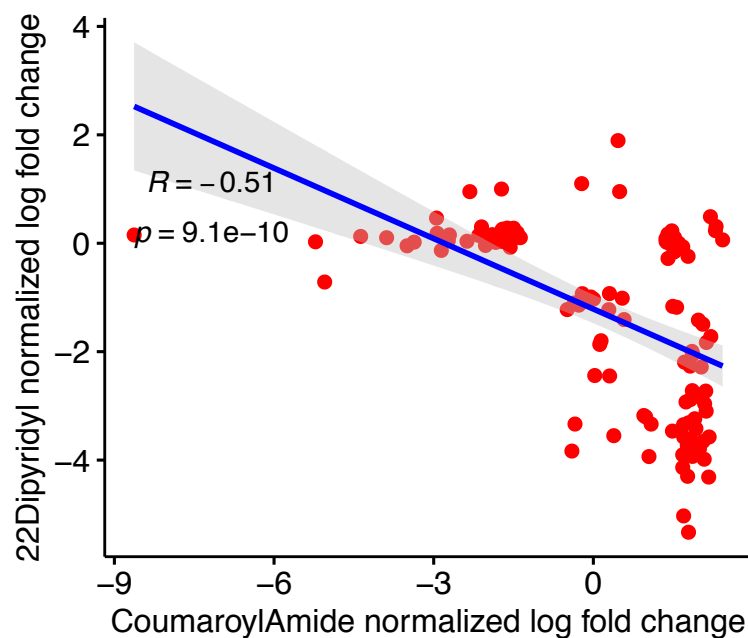
Phenolic acid – Iron chelator



Phenolic amide – Iron chelator



Phenolic amide – Iron chelator



Negative correlations point to amino acid biosynthesis as a target of phenolic inhibitors. Amino acid biosynthesis is important for growth in the presence of iron chelators and at least one ionic liquid.

Phenolic Acid – Iron Chelator Negative Correlation

The profile of 22Dipyridyl, an iron chelator, negatively correlates with 3 phenolic acids profiles, Ferulic Acid, Coumaric Acid, and Sinapic Acid. This seems to be driven by deletions that are resistant in phenolic acid by sensitive in 22Dipyridyl. There are 9 genes shared across these three comparisons with that pattern. There is no GO enrichment or obvious functional profile. There are 3 amino acid biosynthesis genes.

SLM6
ARG4
LYS12
RAD57
TRP1
YGR022C
YPT7
HMI1
CBC2

Phenolic Amide – Iron Chelator Negative Correlation

The profile of 22Dipyridyl, an iron chelator, negatively correlates with 2 phenolic amide profiles, Feruloyl Amide and Coumaroyl Amide. This, again, is driven largely by deletions that are resistant in phenolic amide but sensitive to iron chelation. There are 40 genes driving the pattern here. There is complete overlap with the 9 genes driving the Phenolic Acid – Iron Chelator relationship.

There is also significant GO enrichment here for a number of amino acid biosynthesis categories.

alpha-amino acid biosynthetic process 0.0003346329601981131
cellular amino acid biosynthetic process 0.0005769963417414045
alpha-amino acid metabolic process 0.0008249115763239895
cellular amino acid metabolic process 0.015379793867665652
organic acid biosynthetic process 0.01732071665615443
carboxylic acid biosynthetic process 0.01732071665615443

Phenolic Acid – Cationic toxin/IL

The profiles of EMIMCl (a cationic toxin) and Vanillic Acid (a phenolic acid) are negatively correlated. This is driven by 13 genes that are resistant in phenolic acid by sensitive in EMIMCl. There is almost complete overlap of those genes driving the Phenolic amide- Iron chelator and Phenolic acid – Iron chelator relationships, with only one gene being unique here (AIM22). There is no significant GO enrichment, however, there are again a number of amino acid biosynthesis genes present.

SLM6
ARG4
LYS12
RAD57
TRP1
YGR022C
YPT7
HMI1

CBC2
HIS7
HIS6
SHE9
MPO1
PCP1
AIM22

Looking at individual gene tradeoffs

Genes with large logFC dynamic ranges between inhibitors are enriched for deletions with low logFC in 22Dipyridyl and high logFC values in CV (a cationic toxin/IL). The logFC profiles of these inhibitors are not significantly correlated per my prior method, however, there are 31 deletions with a logFC difference greater than 10 between the two inhibitors. Those 31 deletions are enriched for amino acid biosynthesis.

alpha-amino acid biosynthetic process 0.001139743362405481
alpha-amino acid metabolic process 0.0017964370541555508
cellular amino acid biosynthetic process 0.0018506936929194053
organic acid biosynthetic process 0.00336433620260306
carboxylic acid biosynthetic process 0.00336433620260306
cellular amino acid metabolic process 0.025521542976634823
carboxylic acid metabolic process 0.03142400037843871
oxoacid metabolic process 0.04856467035499416

CV - 22Dipyridyl

