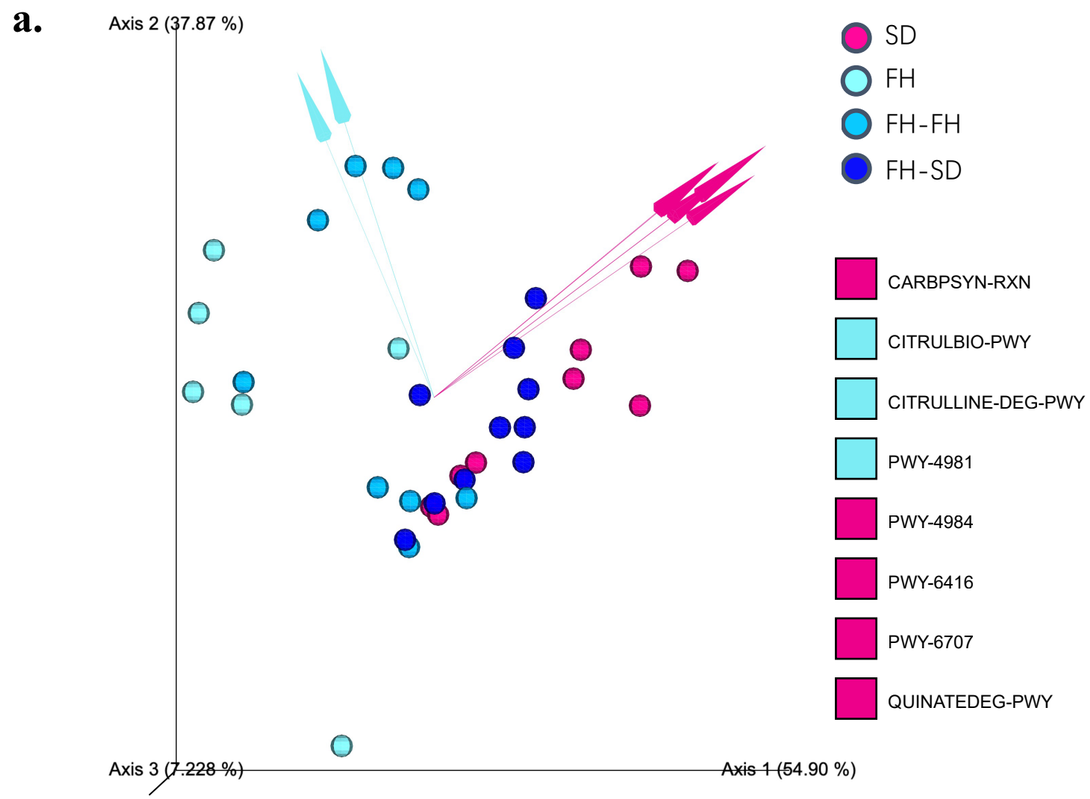
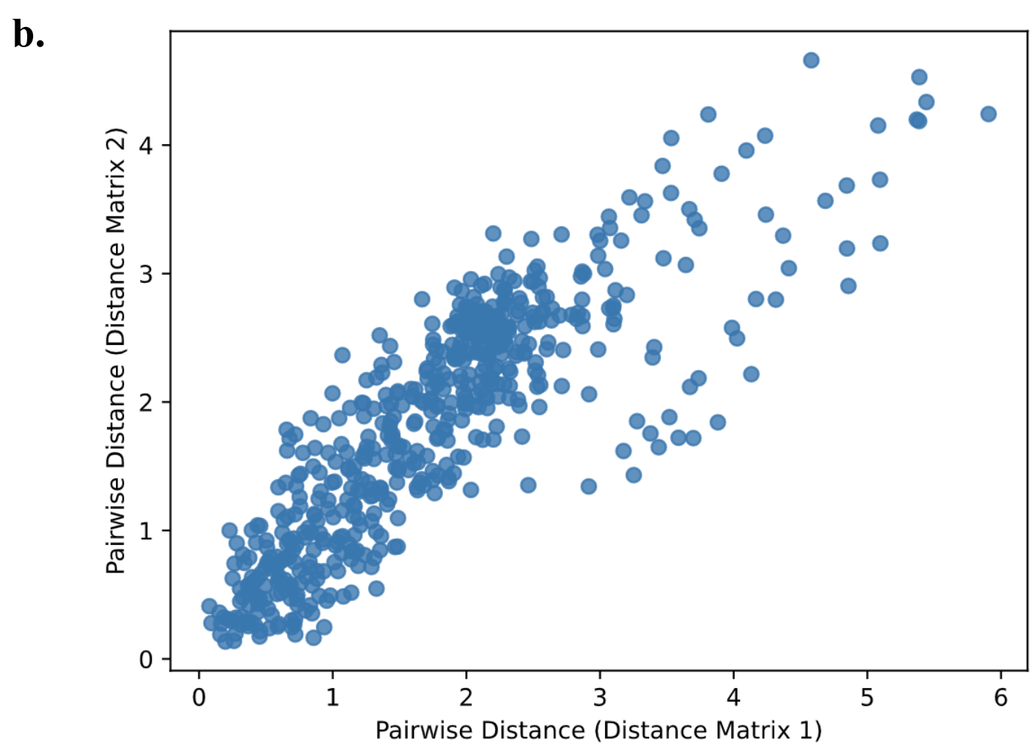
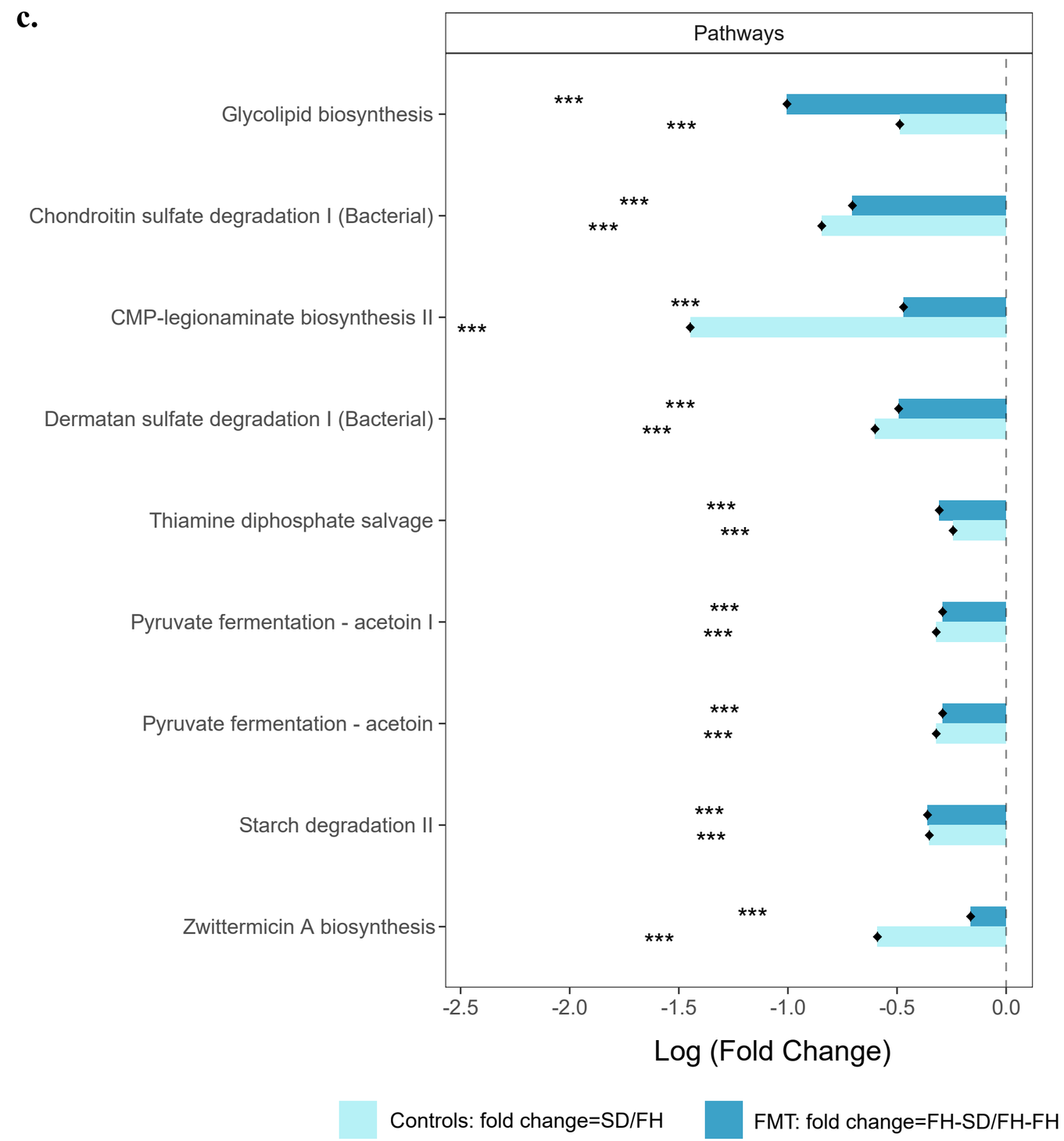

a.
Axis 2 (37.87 %)
Axis 3 (7.228 %)
Axis 1 (54.90 %)
SD
FH
FH-FH
FH-SD
CARBPSYN-RXN
CITRULBIO-PWY
CITRULLINE-DEG-PWY
PWY-4981
PWY-4984
PWY-6416
PWY-6707
QUINATEDEG-PWY


b.
Pairwise Distance (Distance Matrix 2)
Pairwise Distance (Distance Matrix 1)
0
1
2
3
4
5
6


c.
Pathways
Glycolipid biosynthesis
Chondroitin sulfate degradation I (Bacterial)
CMP-legionaminate biosynthesis II
Dermatan sulfate degradation I (Bacterial)
Thiamine diphosphate salvage
Pyruvate fermentation - acetoin I
Pyruvate fermentation - acetoin
Starch degradation II
Zwittermicin A biosynthesis
-2.5
-2.0
-1.5
-1.0
-0.5
0.0
Log (Fold Change)
Controls: fold change=SD/FH
FMT: fold change=FH-SD/FH-FH