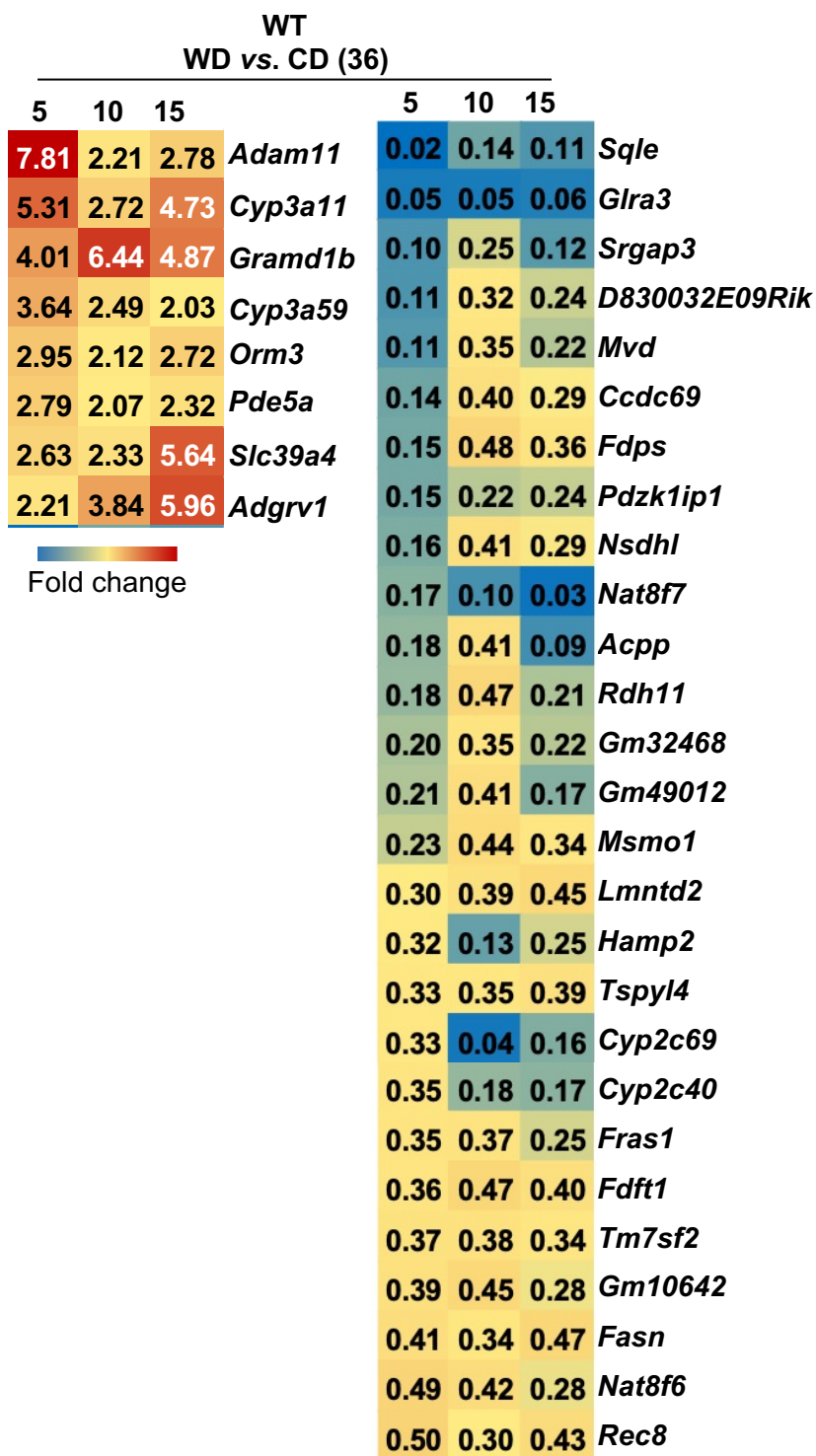


Fig.S1

(A)



(B)

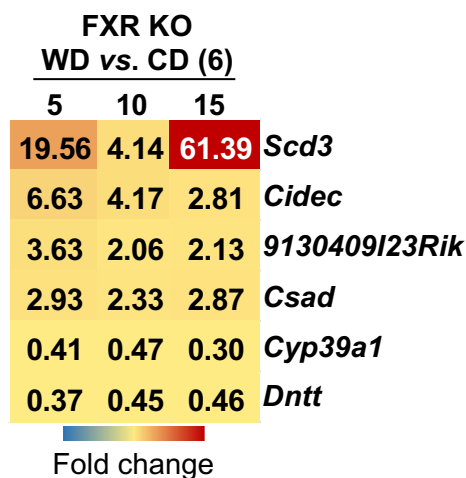
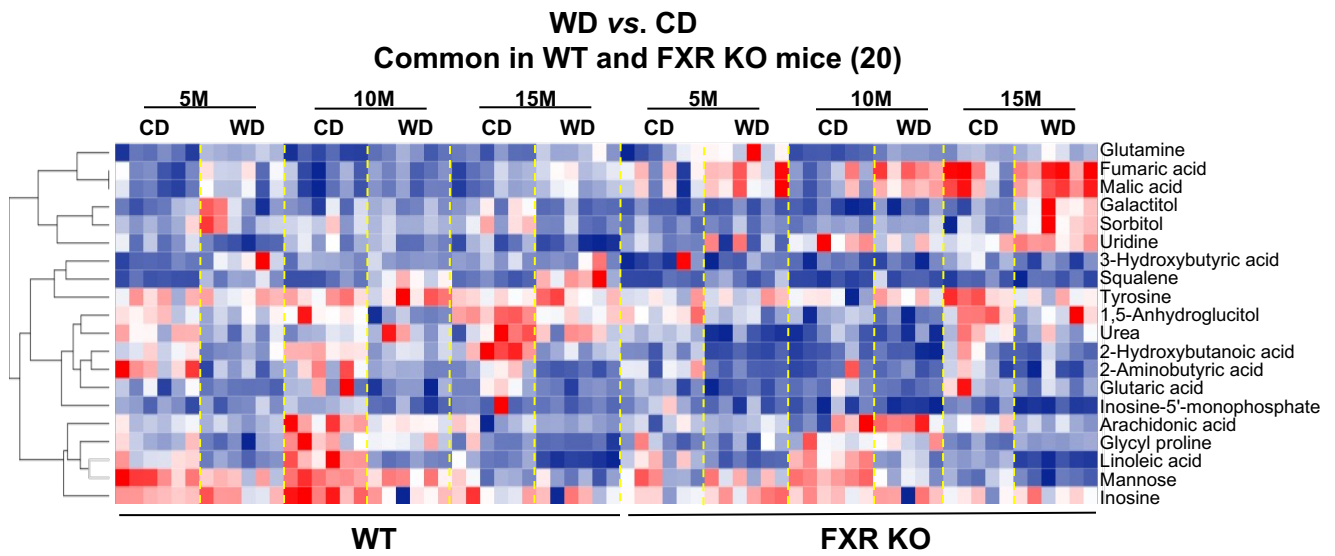
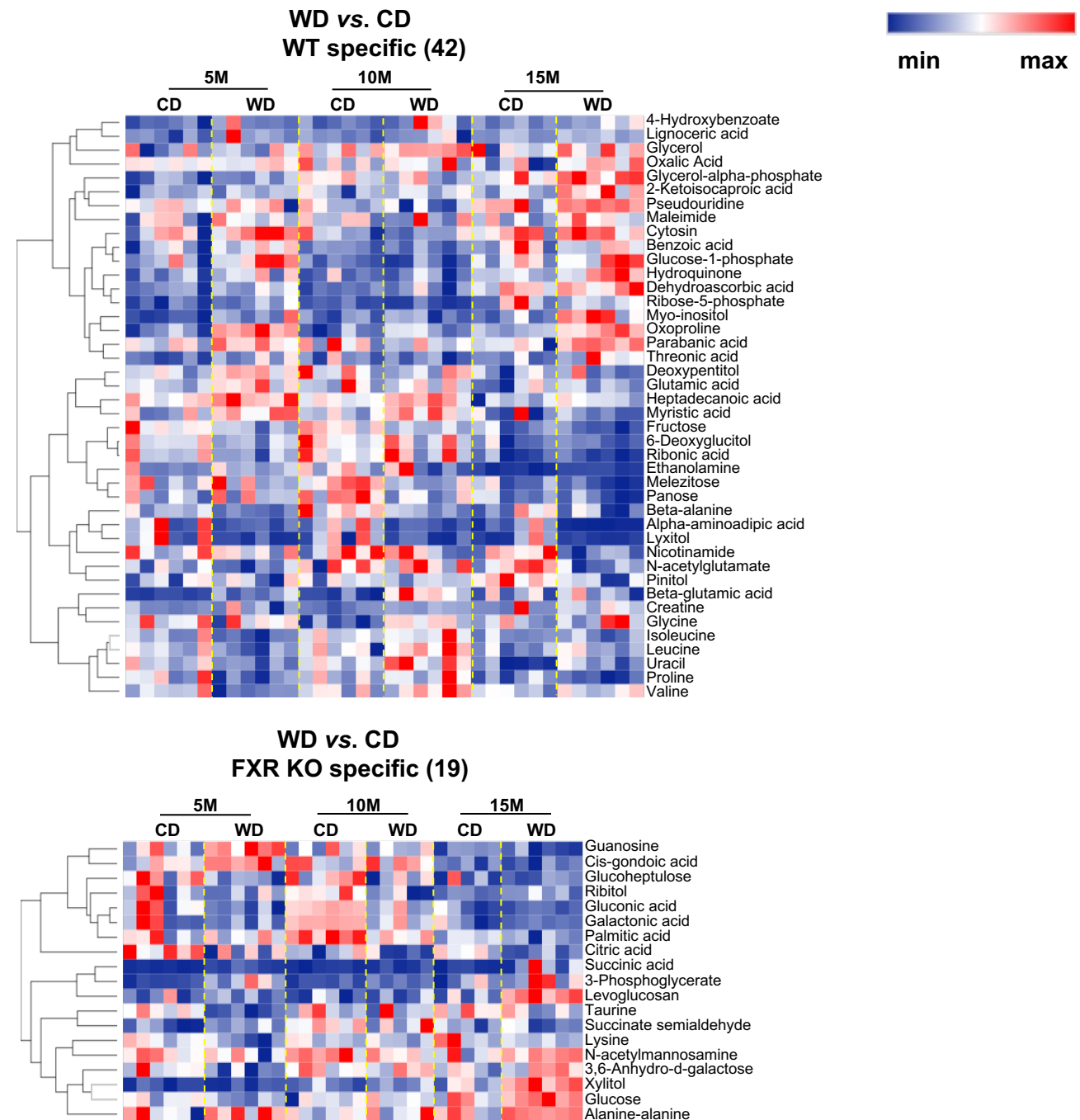


Fig. S2
(A)

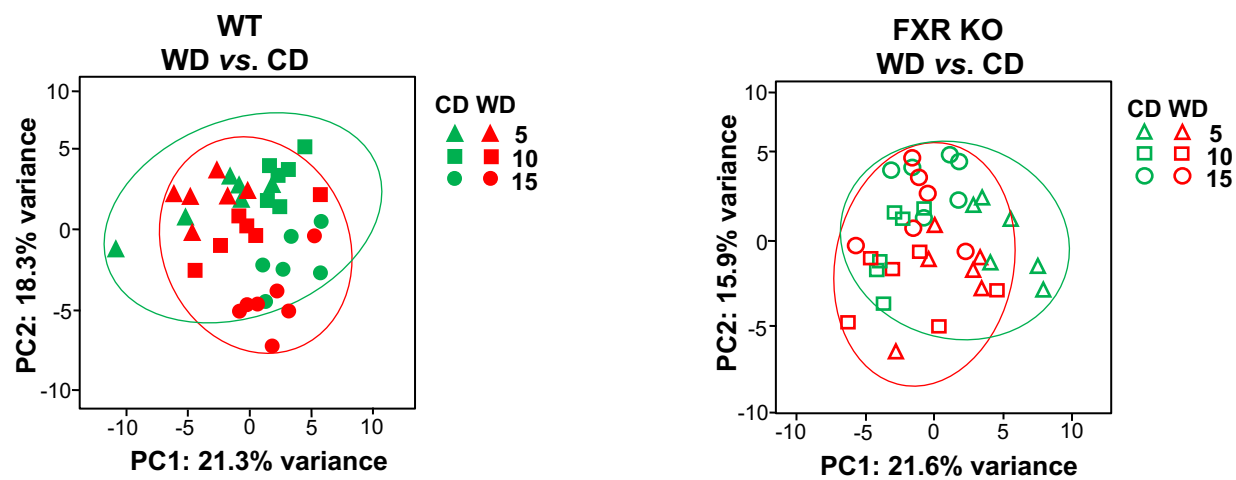


(B)



Serum Metabolome

(A)



(B)

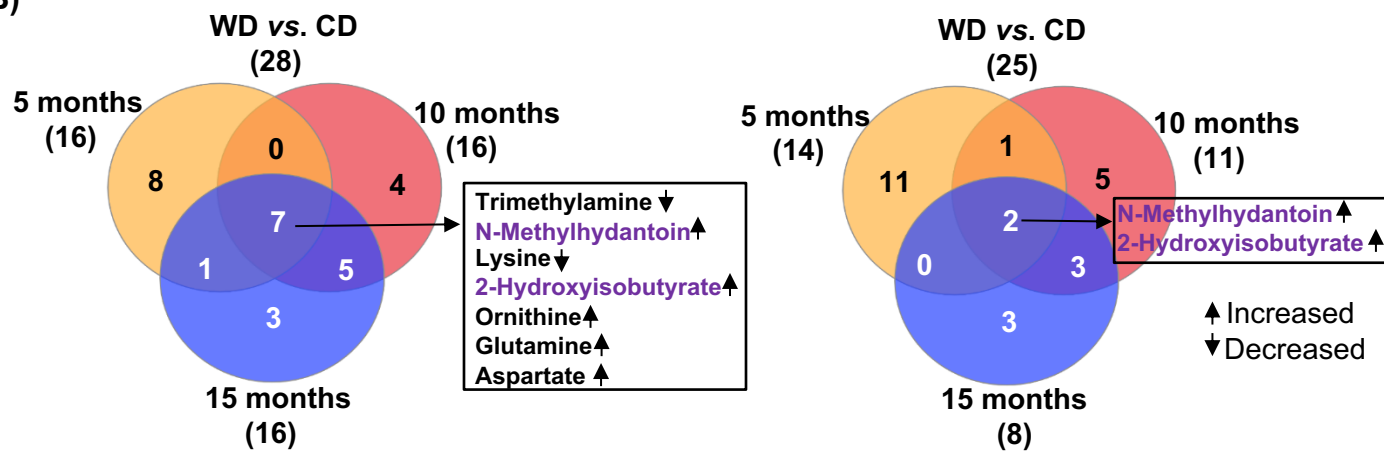
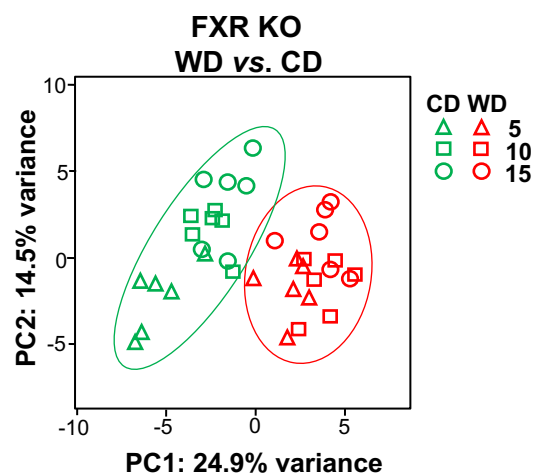
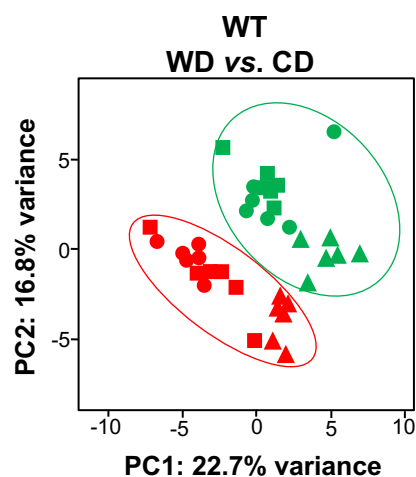
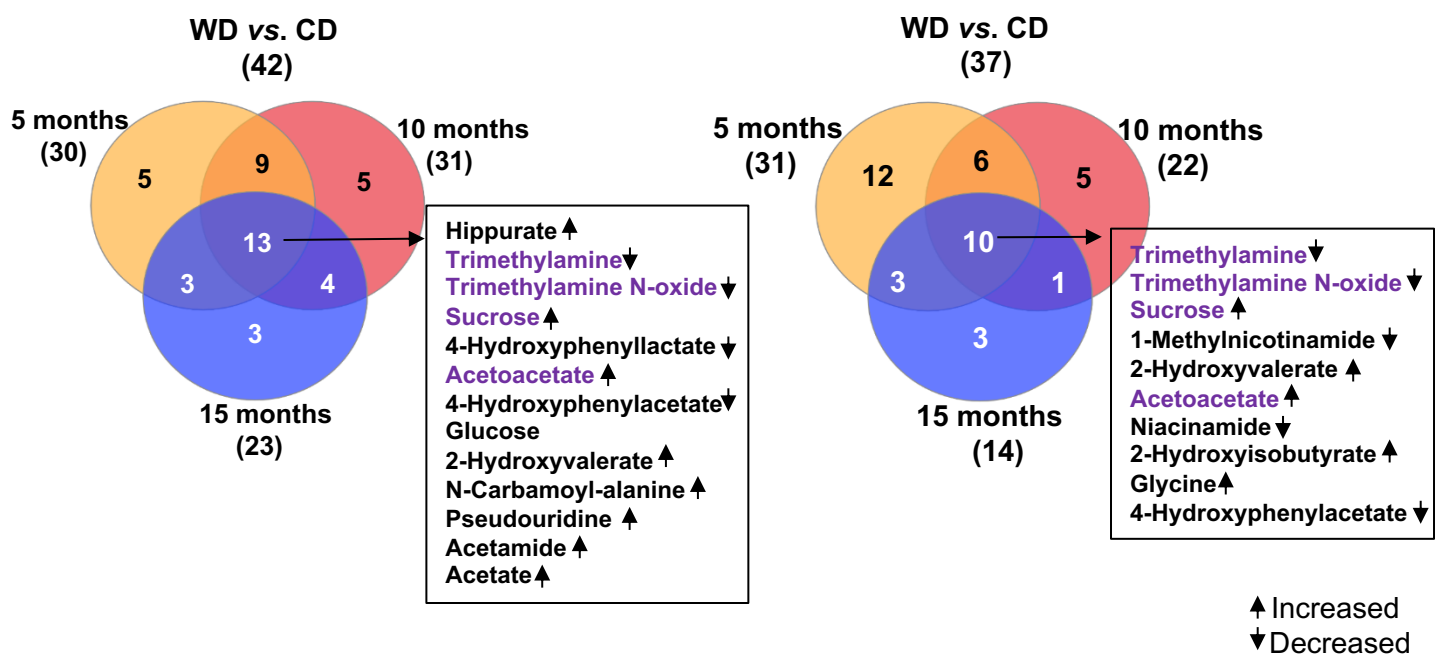


Fig.S4

(A)

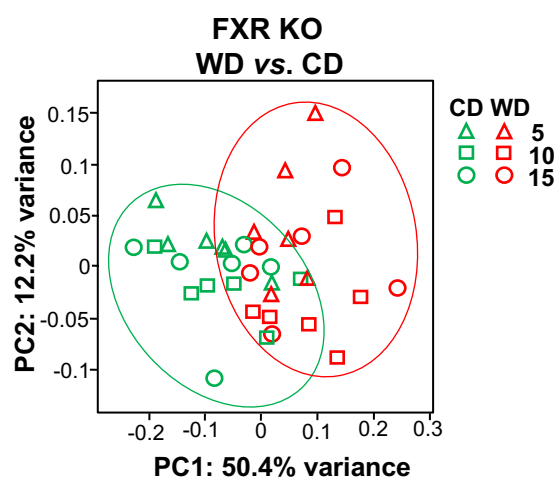
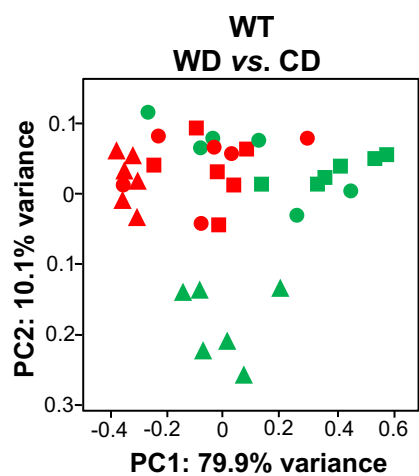


(B)

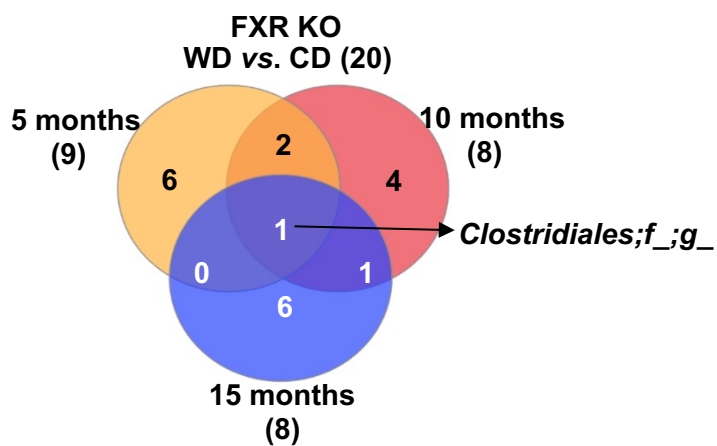
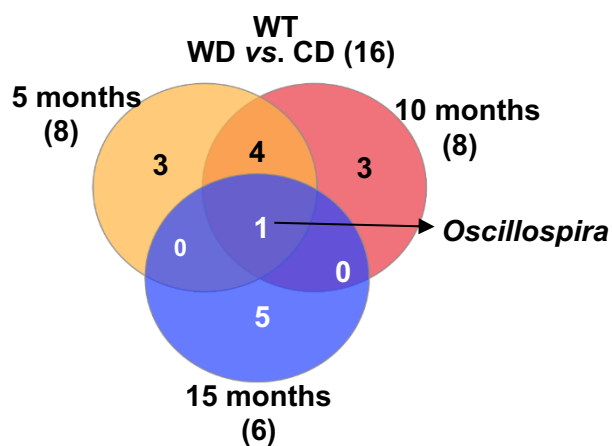


Cecal microbiota at genus level

(A)

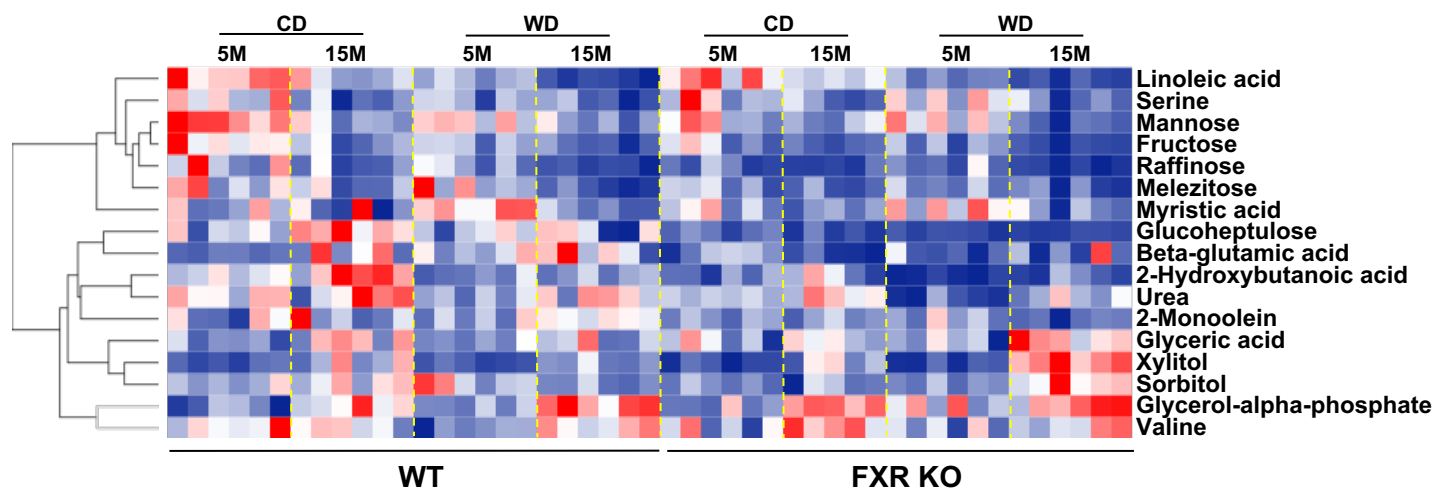


(B)



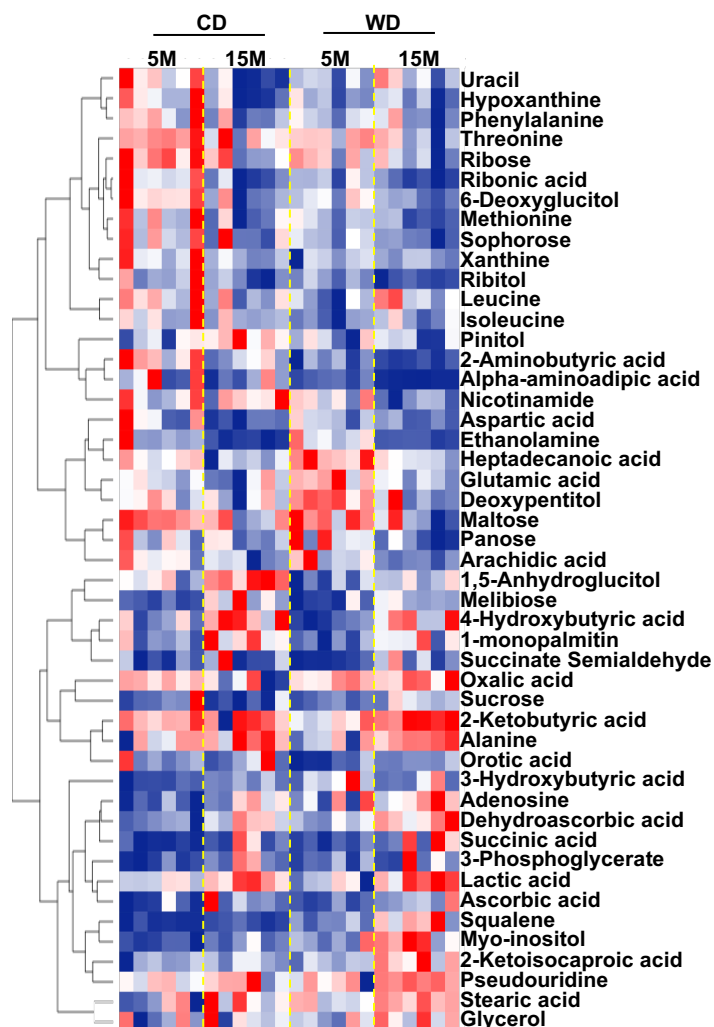
(A)

15 vs. 5
Common in WT and FXR KO mice

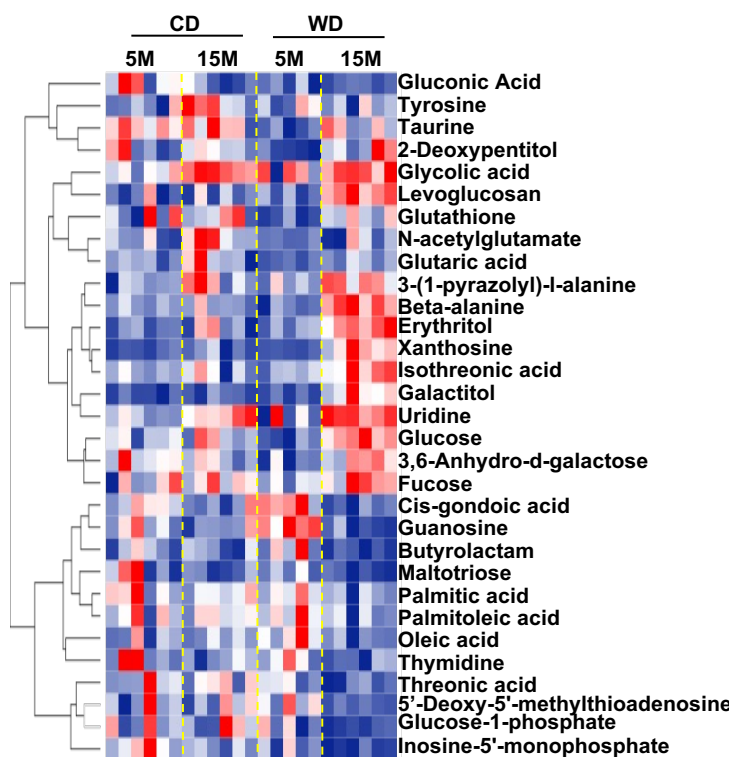


(B)

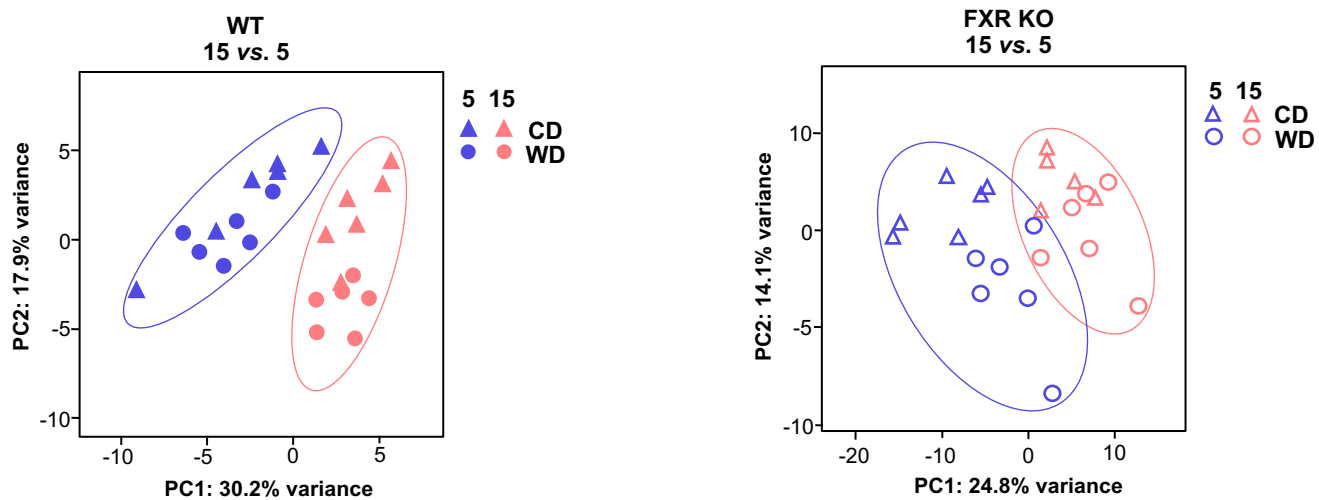
15 vs. 5
WT specific



15 vs. 5
FXR KO specific



(A)



(B)

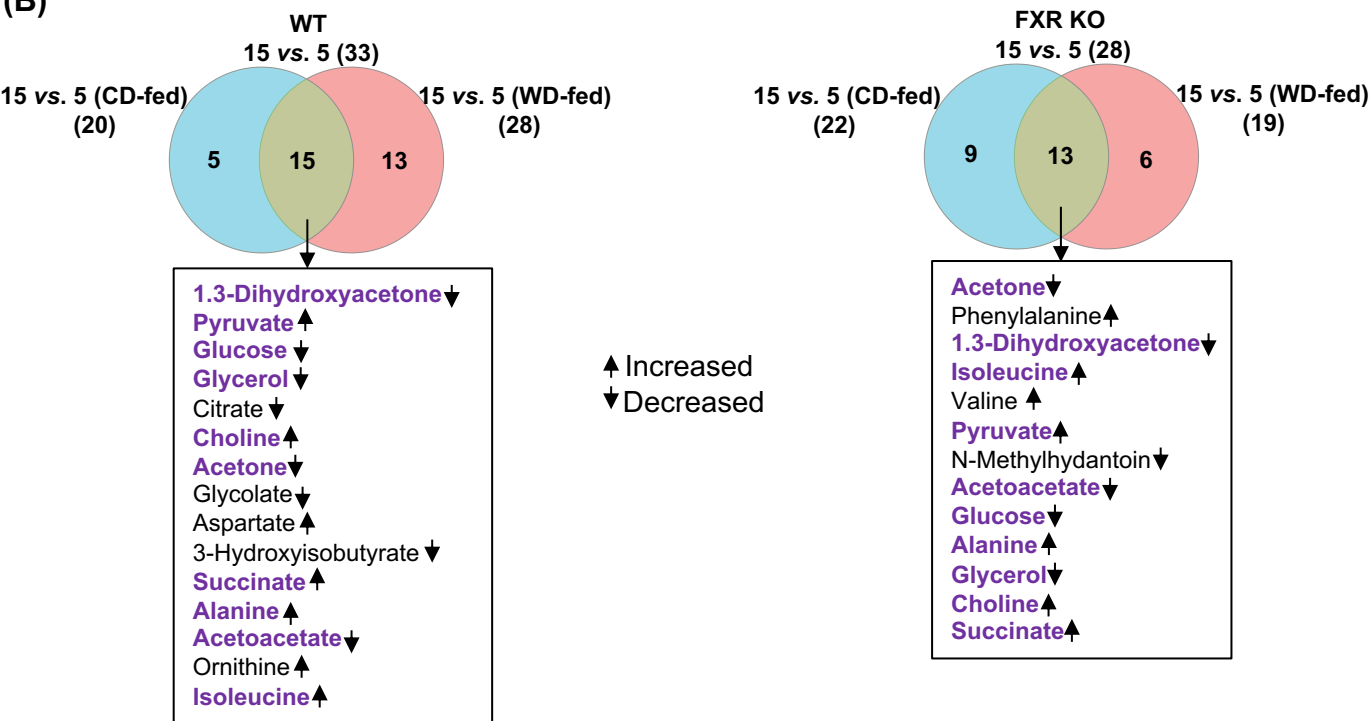
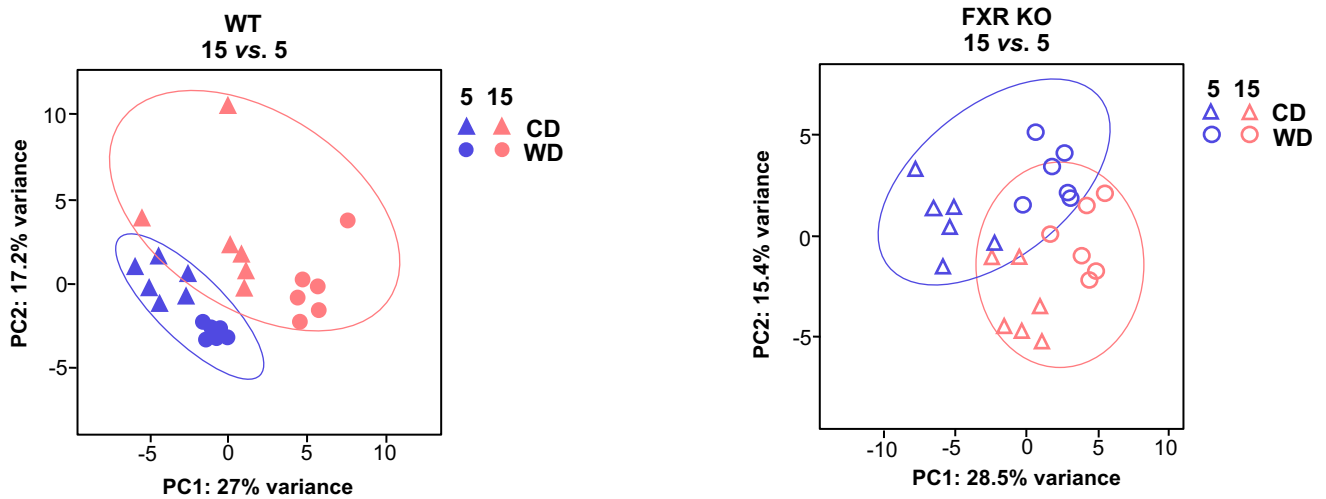


Fig.S8

Urine Metabolome

(A)



(B)

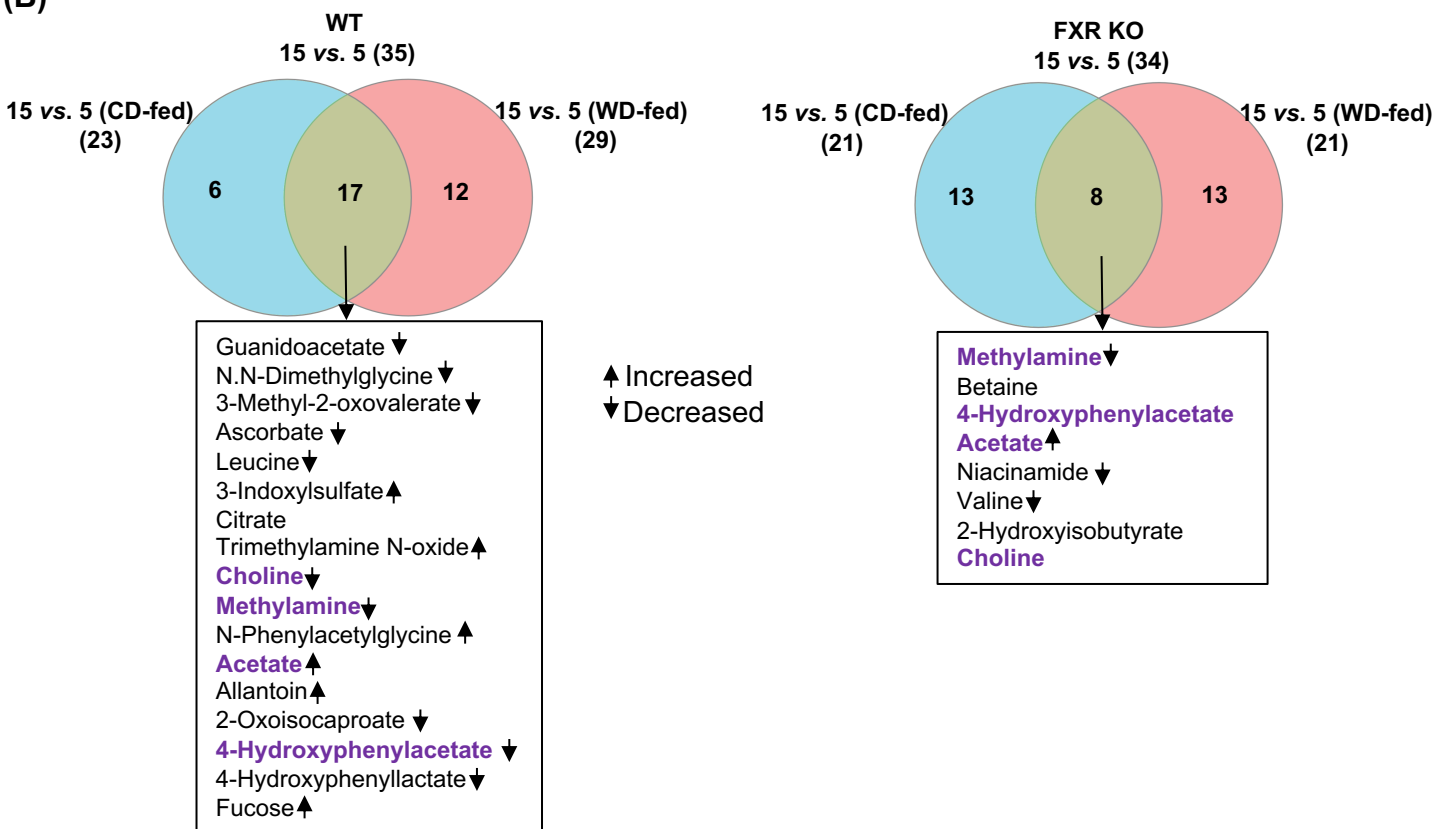
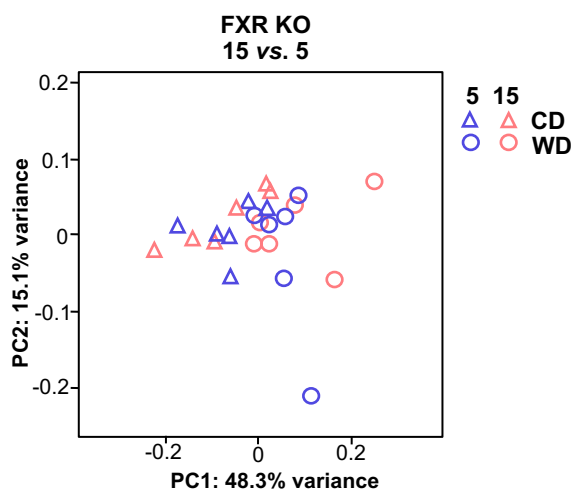
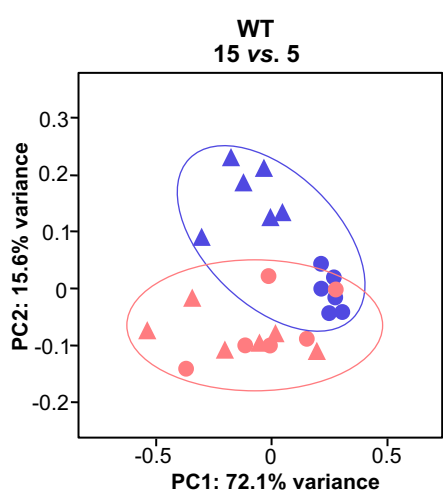


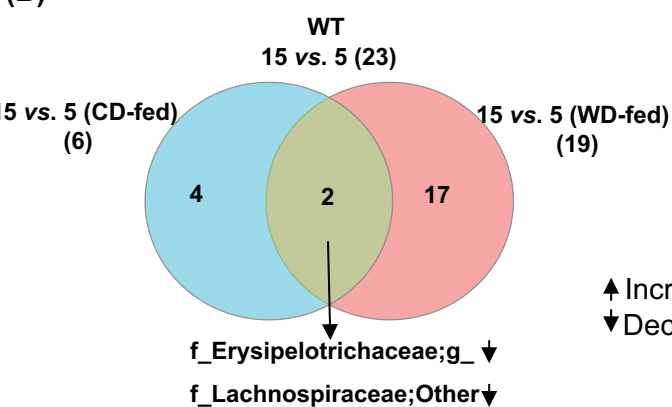
Fig.S9

Cecal microbiota at genus level

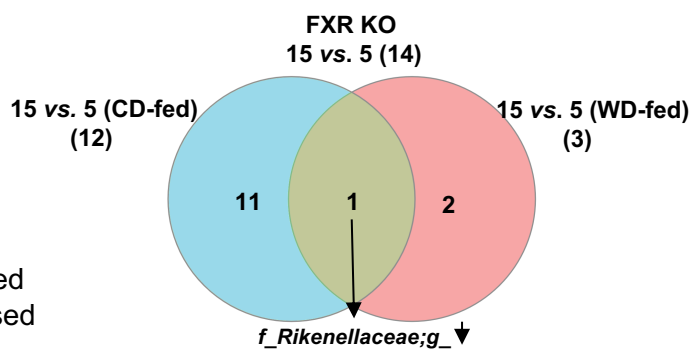
(A)



(B)



↑ Increased
↓ Decreased



(A) Fig. S10

FXR KO vs. WT **Common in CD and WD-fed mice**

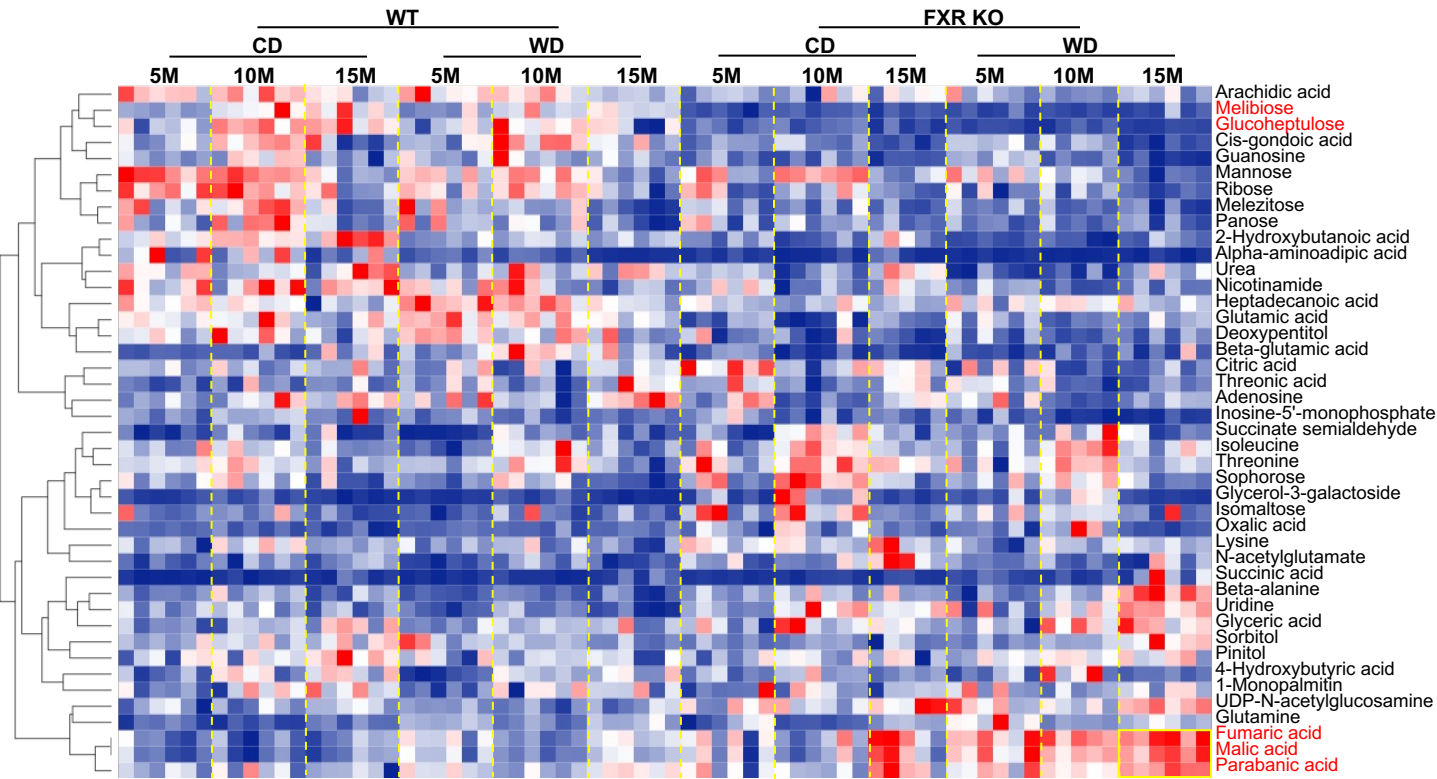
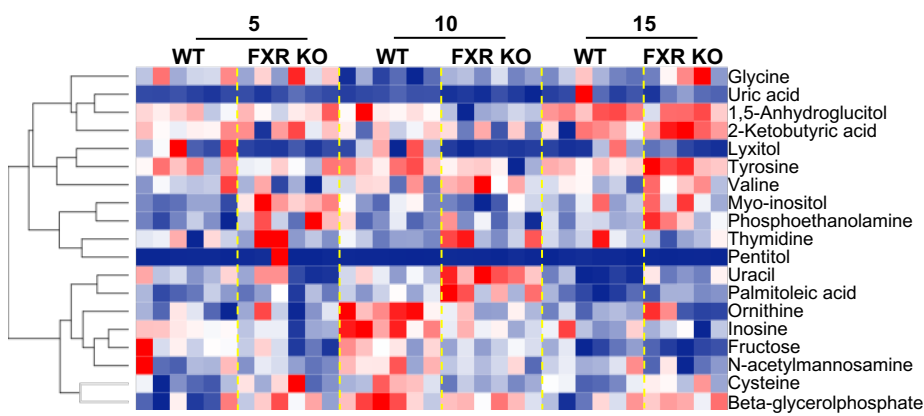
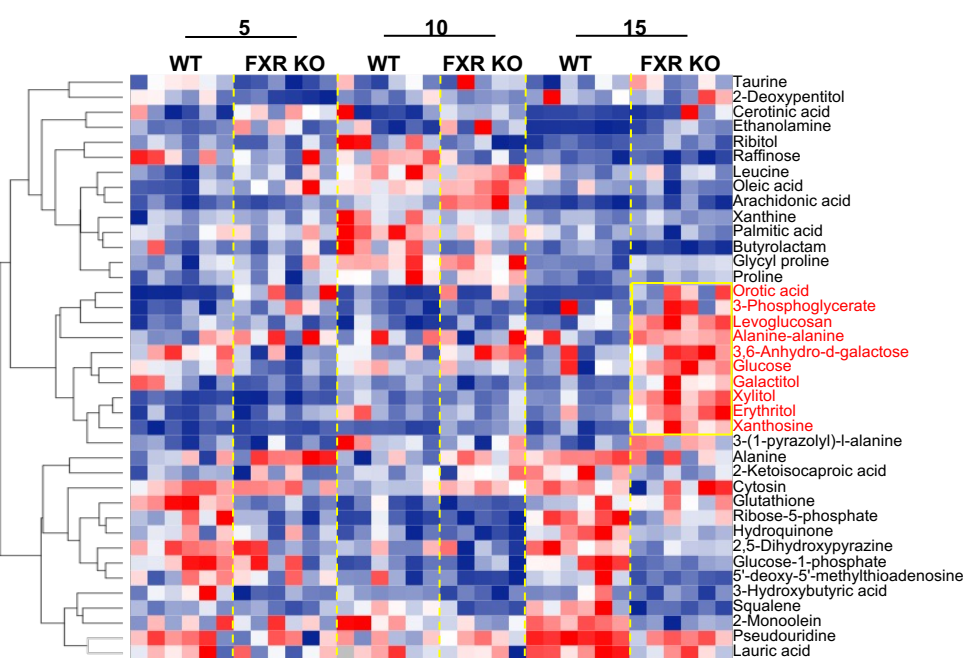
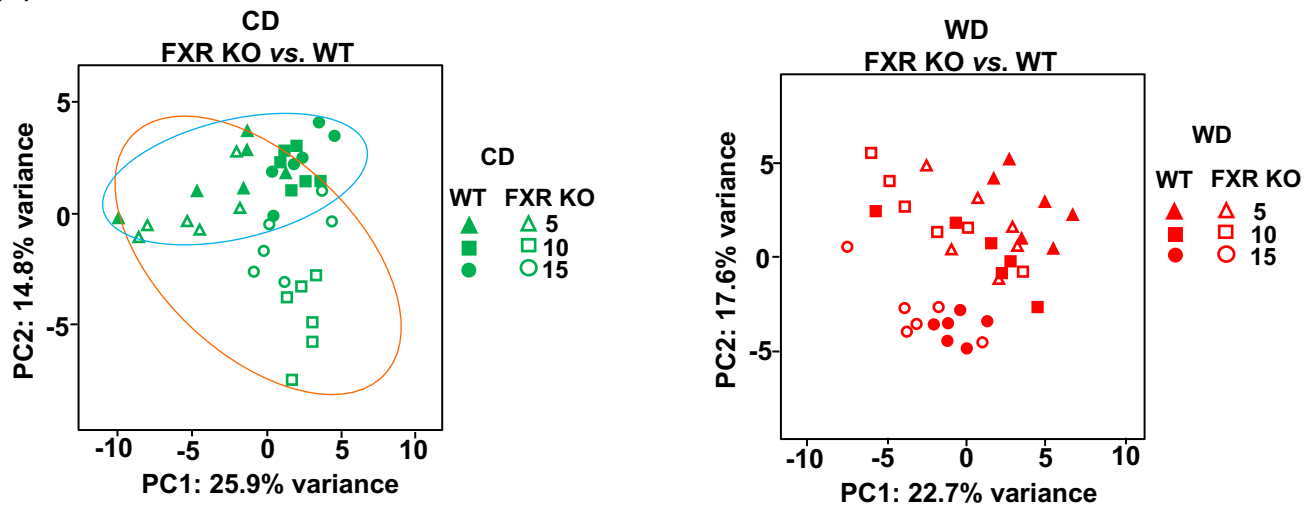
(B) **FXR KO vs. WT (CD)****FXR KO vs. WT (WD)**

Fig.S11

Serum Metabolome

(A)



(B)

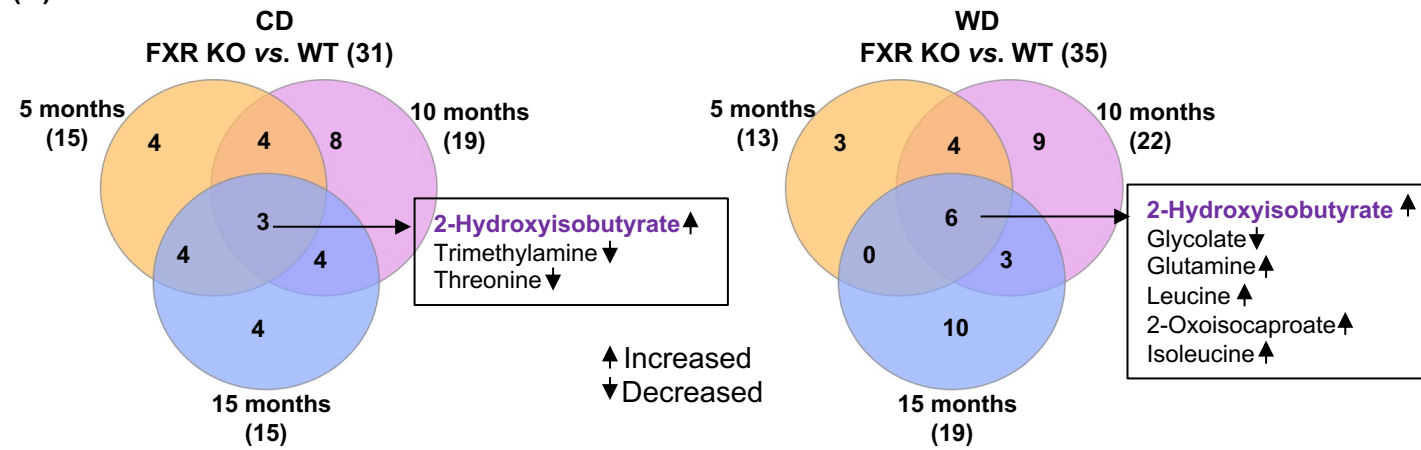
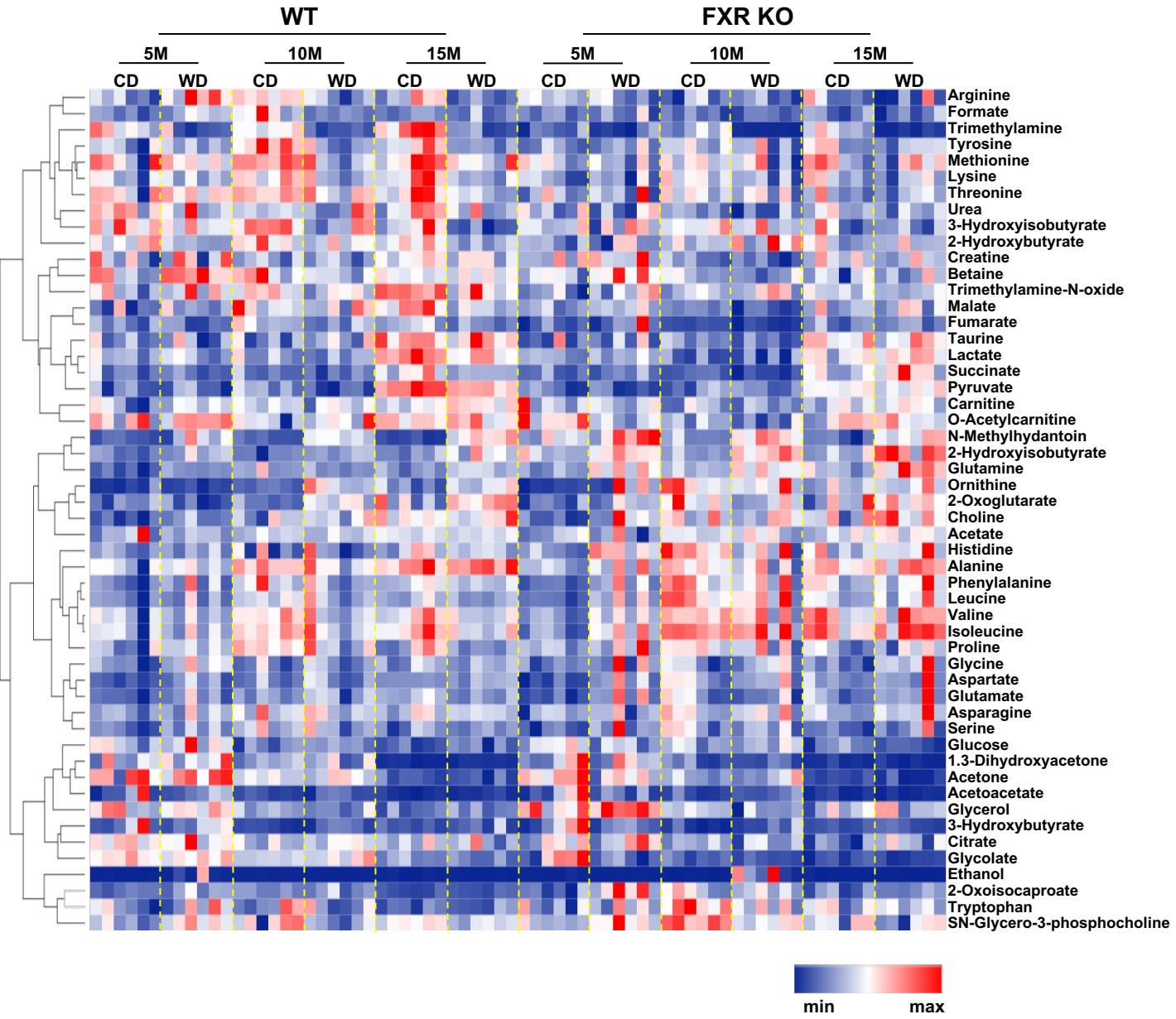


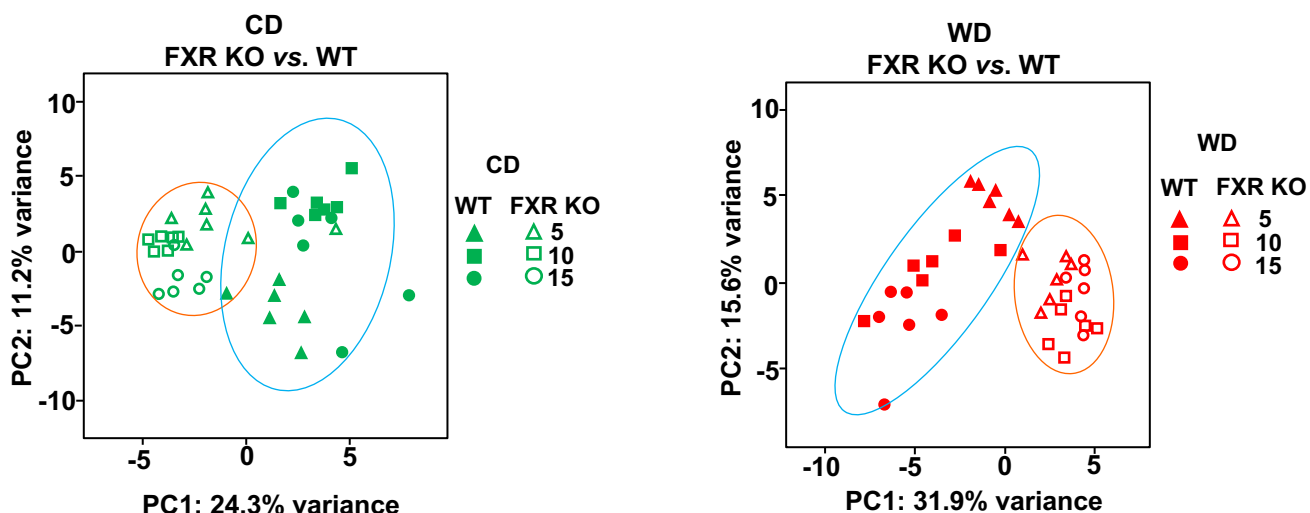
Fig.S12

Serum Metabolites



Urine Metabolome

(A)



(B)

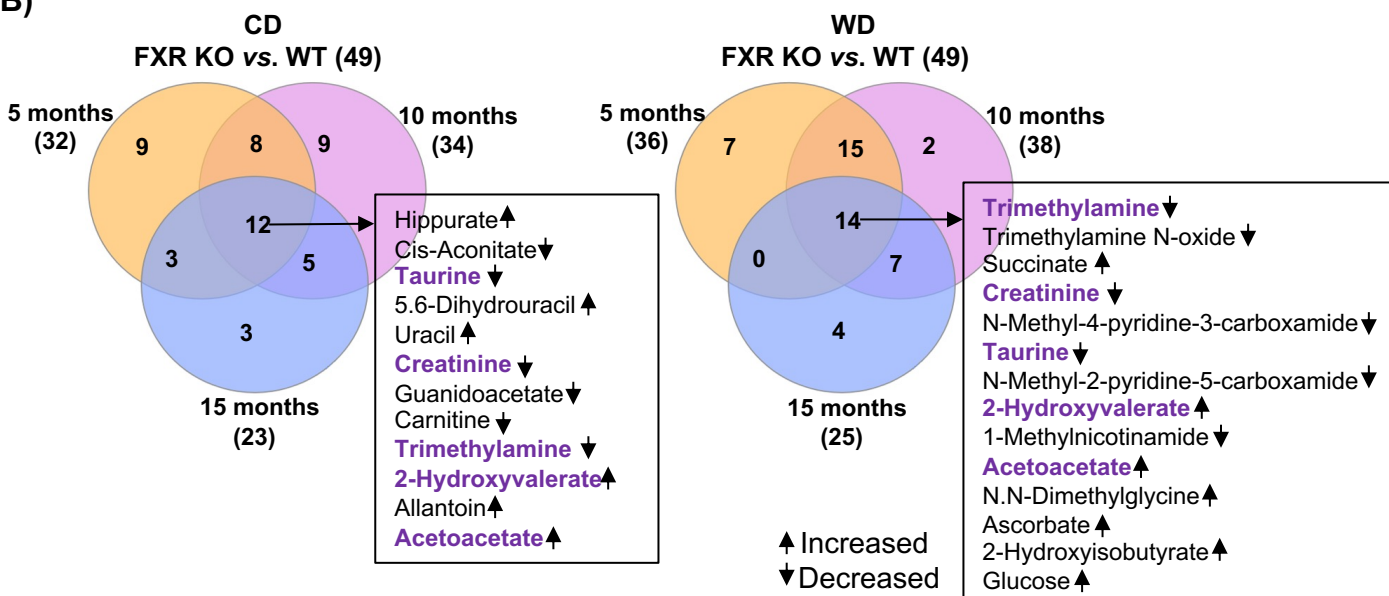
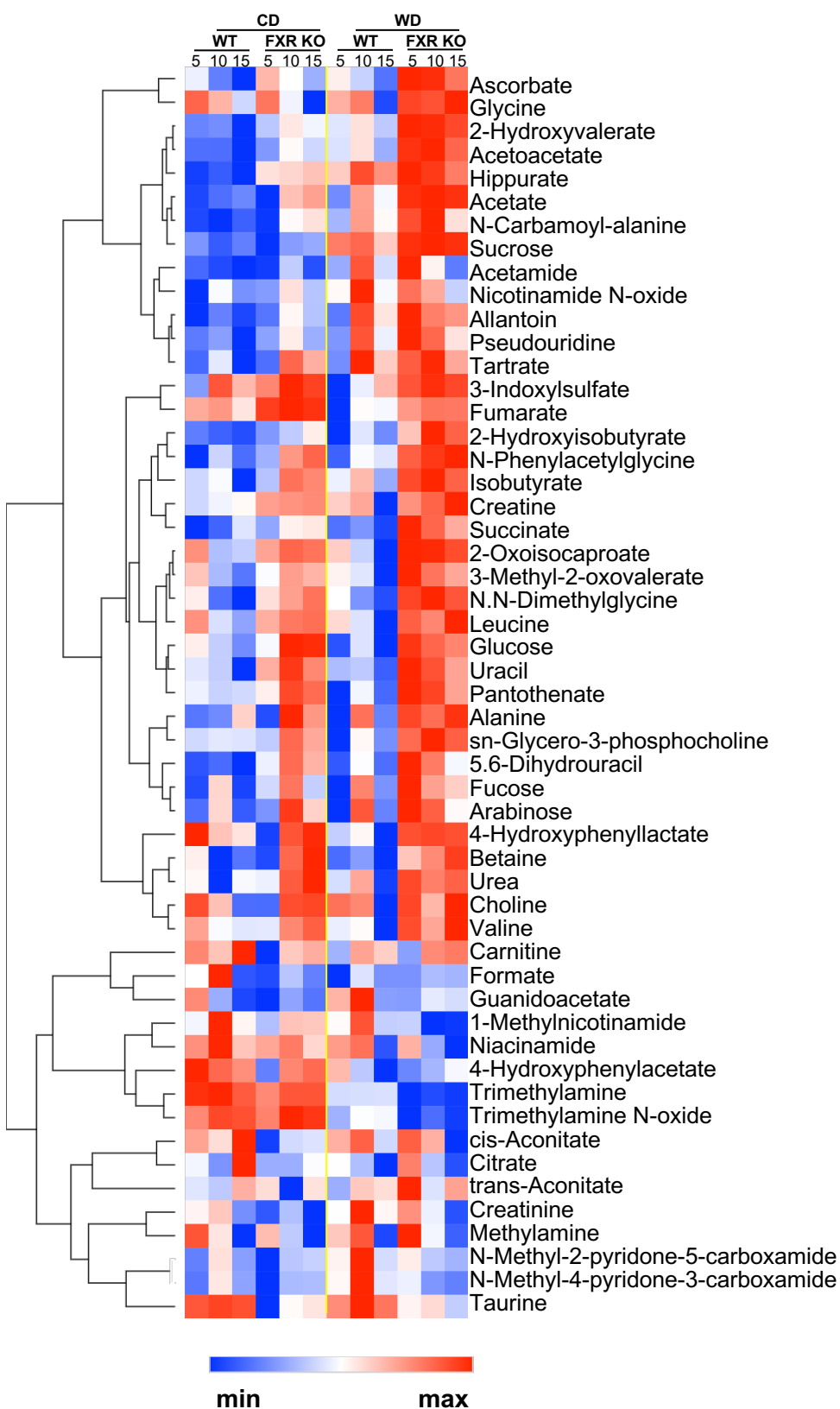


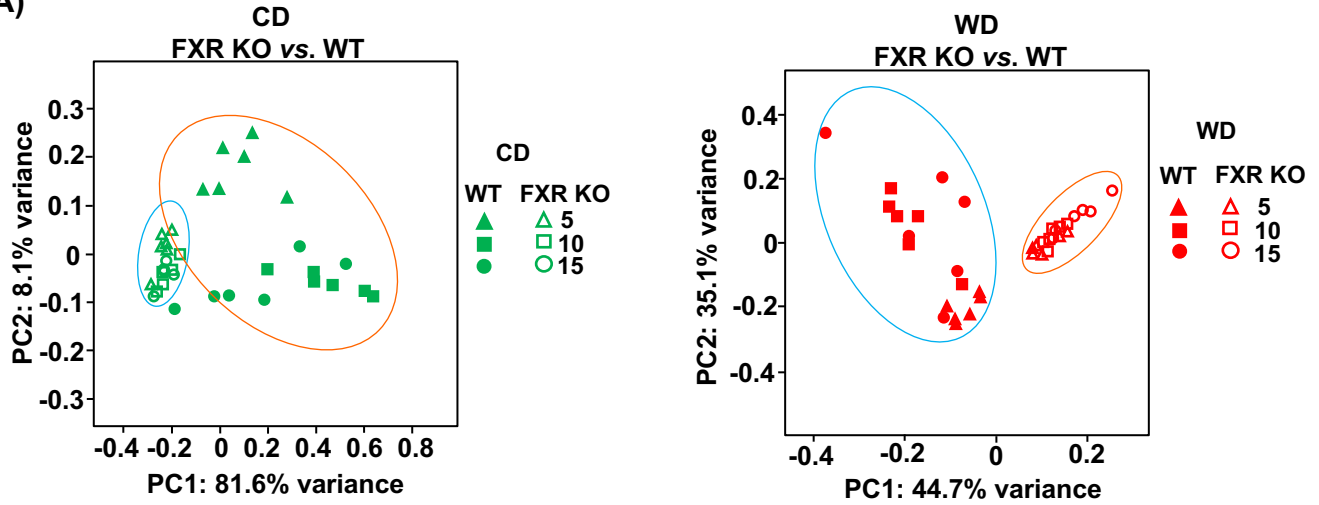
Fig.S14

Urine Metabolites

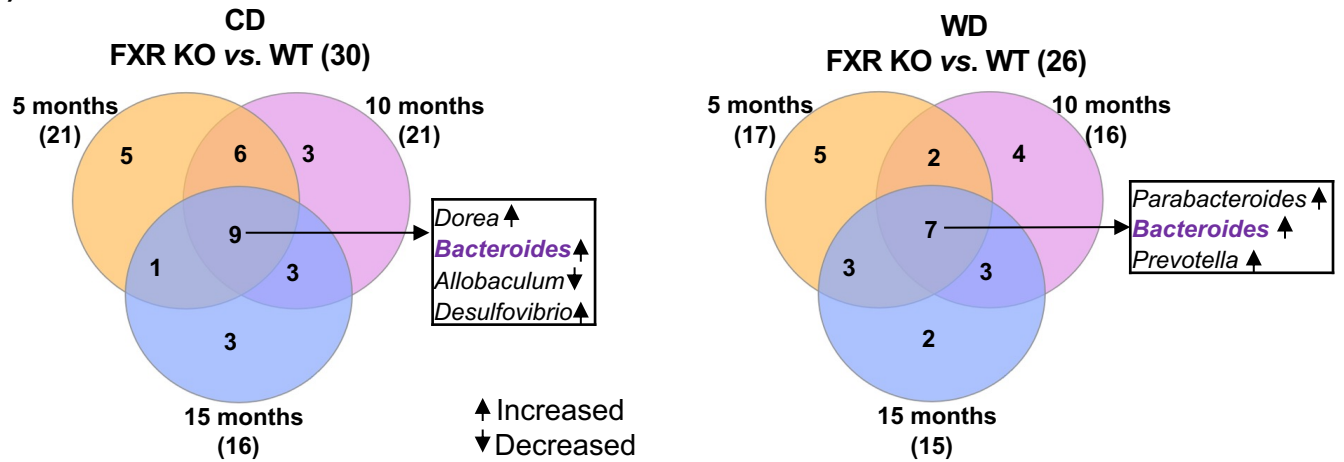


Cecal microbiota at genus level

(A)

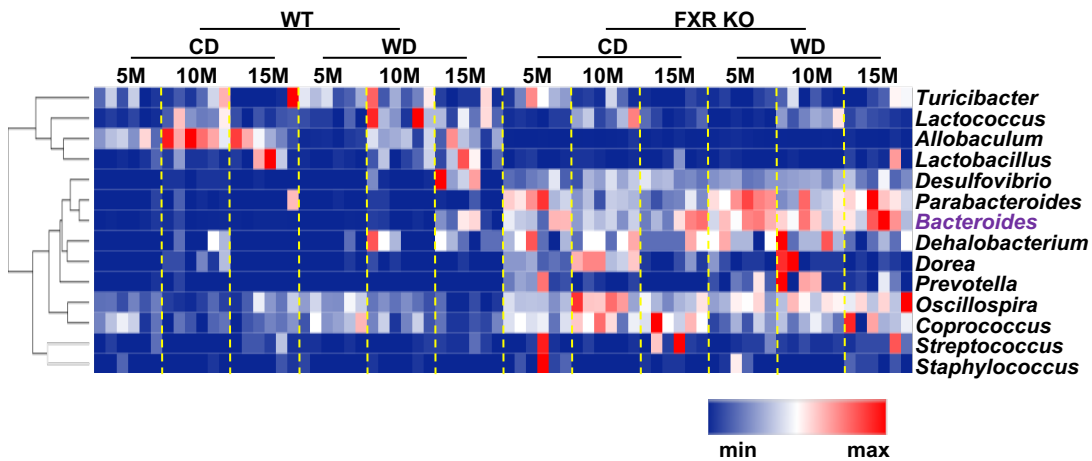


(B)

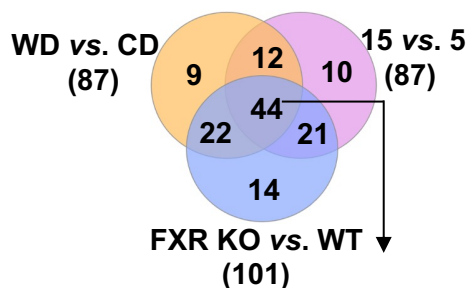


(C)

Cecal microbiota at genus level



Hepatic metabolome



Common liver metabolites (n = 44)

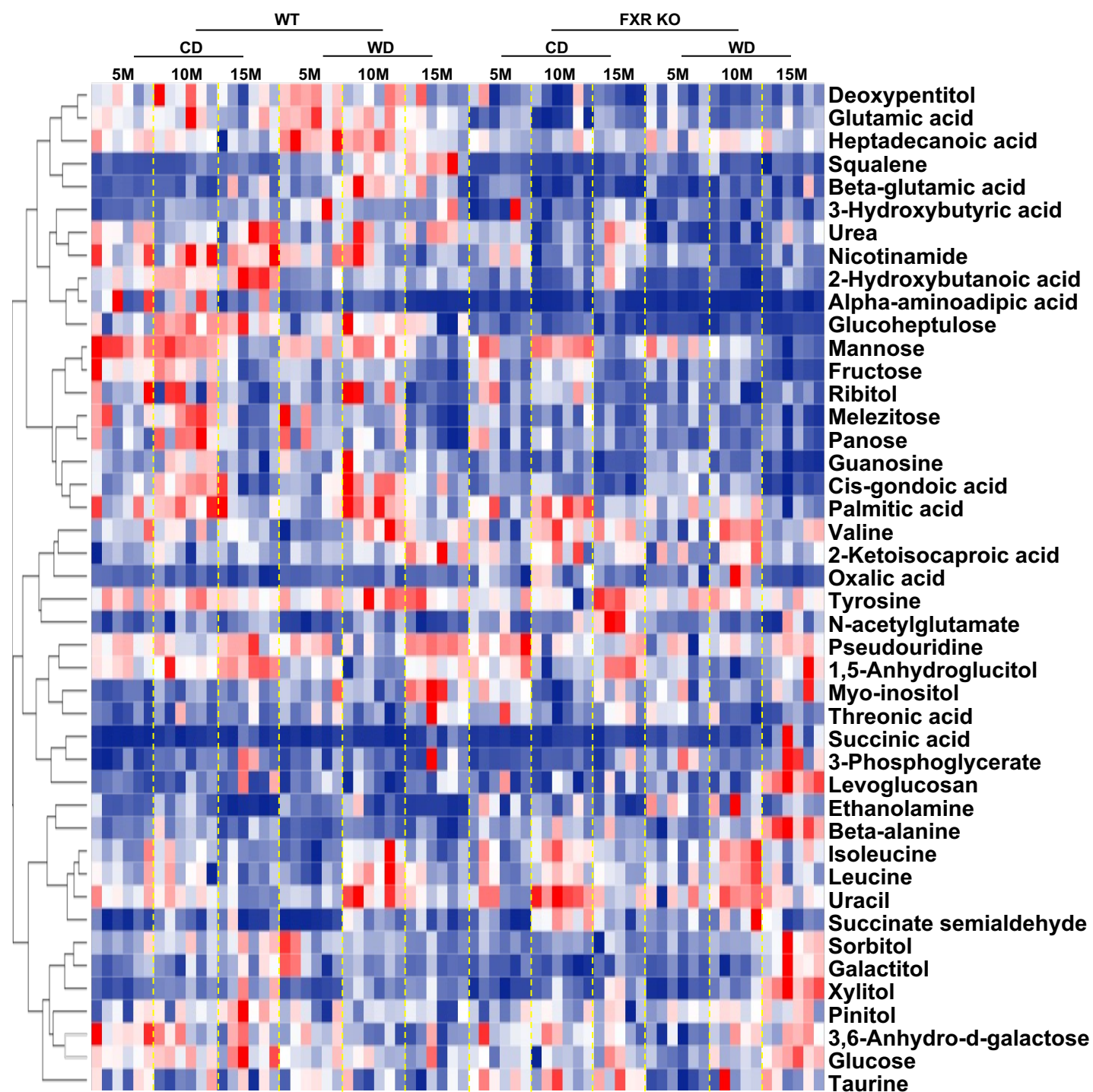


Fig.S17

Correlation analysis between the hepatic feature (76 transcripts and 44 metabolites that were commonly altered by diet, age and FXR KO) and serum/urine metabolites as well as cecal microbiota at genus level

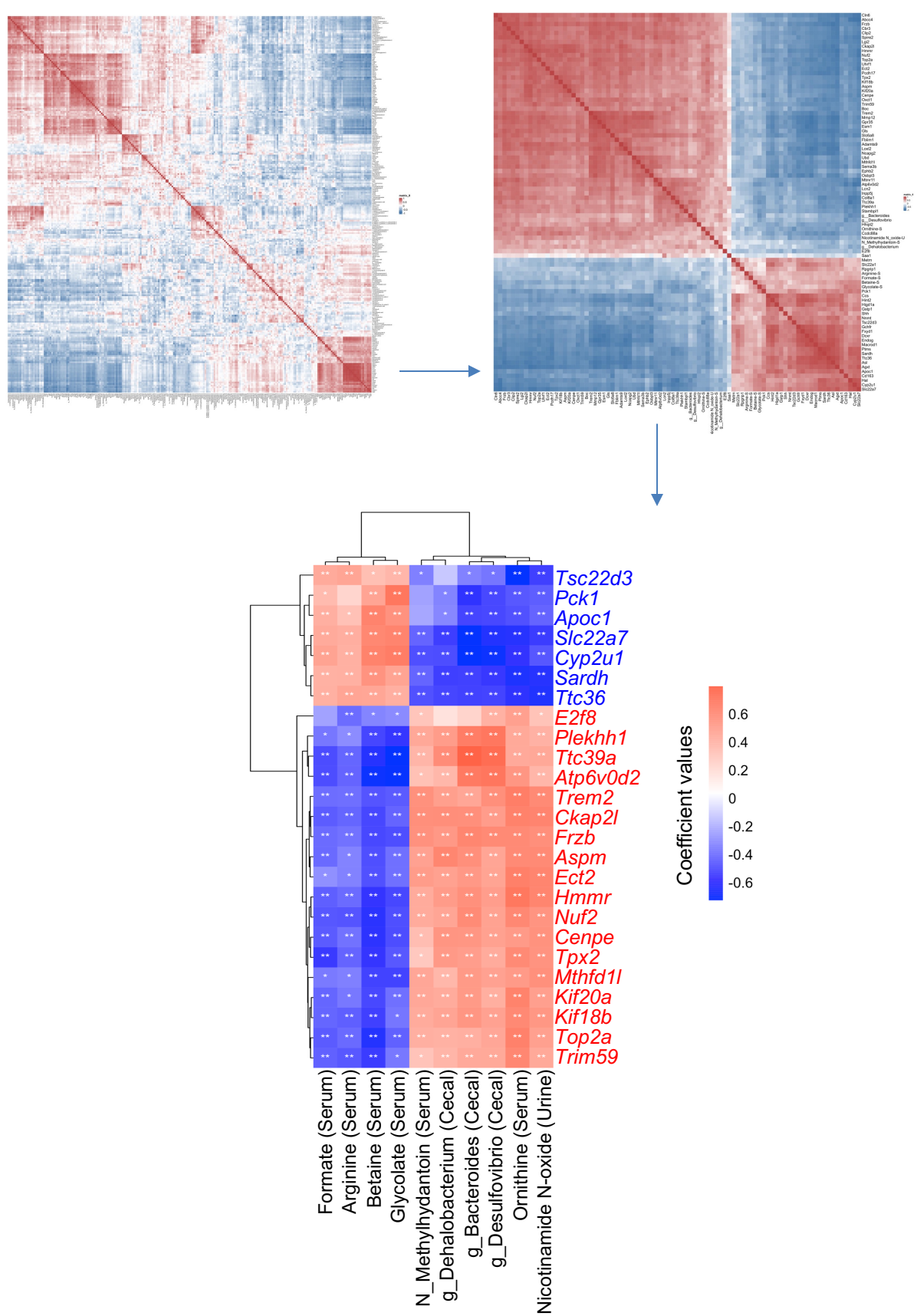


Fig. S18

