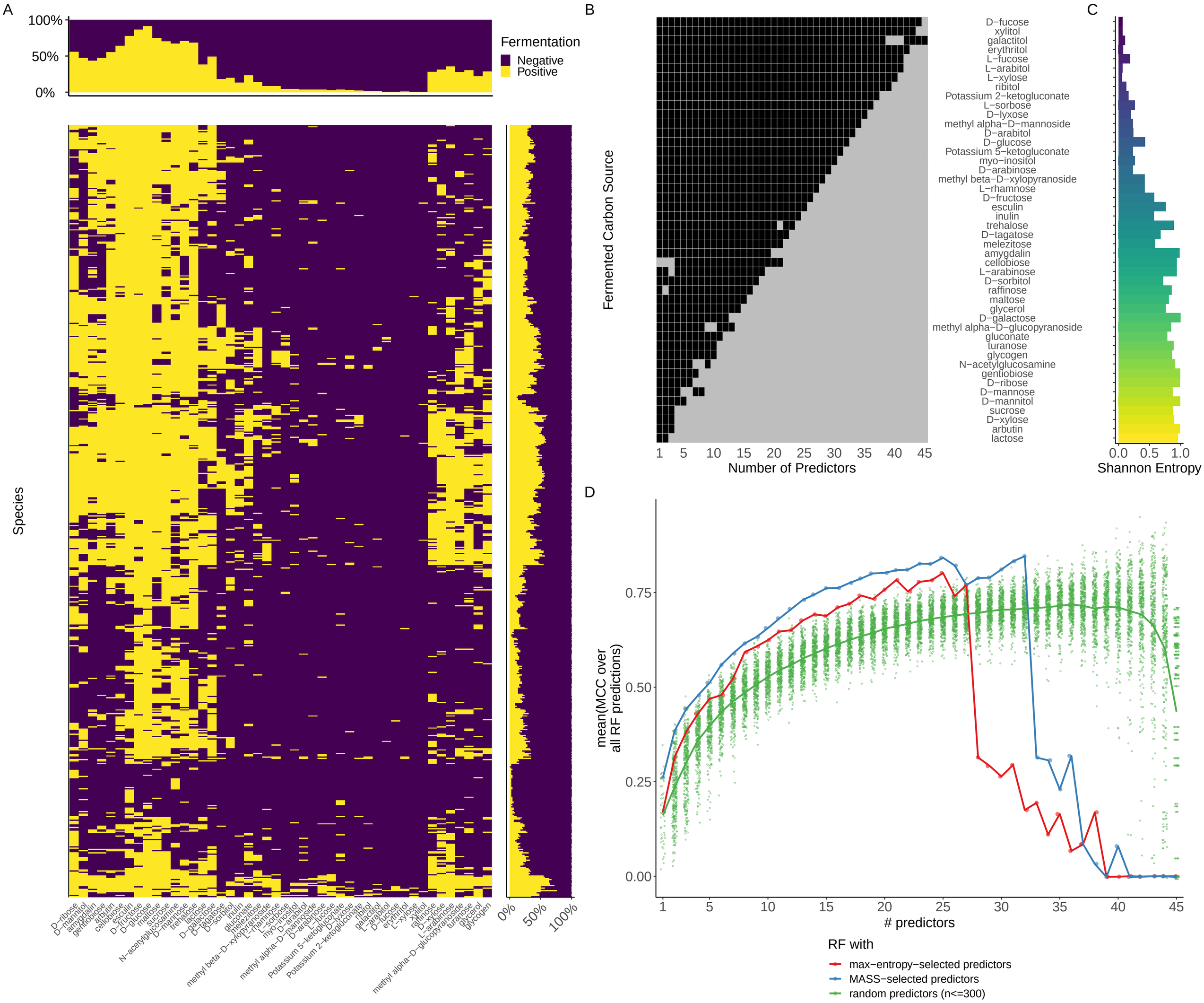
A
100%
50%
0%
Fermentation
Negative
Positive
Species
D−ribose
D−mannitol
amygdalin
gentiobiose
arbutin
cellobiose
esculin
D−fructose
D−glucose
maltose
sucrose
N−acetylglucosamine
D−mannose
trehalose
lactose
D−galactose
D−tagatose
D−sorbitol
inulin
gluconate
melezitose
methyl beta−D−xylopyranoside
L−rhamnose
L−sorbose
myo−inositol
D−arabitol
methyl alpha−D−mannoside
D−arabinose
L−fucose
Potassium 5−ketogluconate
Potassium 2−ketogluconate
D−lyxose
ribitol
galactitol
L−arabitol
D−fucose
erythritol
L−xylose
xylitol
raffinose
D−xylose
L−arabinose
methyl alpha−D−glucopyranoside
turanose
glycerol
glycogen
0%
50%
100%
B
Fermented Carbon Source
D−fucose
xylitol
galactitol
erythritol
L−fucose
L−arabitol
L−xylose
ribitol
Potassium 2−ketogluconate
L−sorbose
D−lyxose
methyl alpha−D−mannoside
D−arabitol
D−glucose
Potassium 5−ketogluconate
myo−inositol
D−arabinose
methyl beta−D−xylopyranoside
L−rhamnose
D−fructose
esculin
inulin
trehalose
D−tagatose
melezitose
amygdalin
cellobiose
L−arabinose
D−sorbitol
raffinose
maltose
glycerol
D−galactose
methyl alpha−D−glucopyranoside
gluconate
turanose
glycogen
N−acetylglucosamine
gentiobiose
D−ribose
D−mannose
D−mannitol
sucrose
D−xylose
arbutin
lactose
1 5 10 15 20 25 30 35 40 45
Number of Predictors
C
0.0 0.5 1.0
Shannon Entropy
D
mean(MCC over all RF predictions)
0.00
0.25
0.50
0.75
1 5 10 15 20 25 30 35 40 45
predictors
RF with
max−entropy−selected predictors
MASS−selected predictors
random predictors (n<=300)
E
Fermented Carbon Source
cellobiose
raffinose
L−arabinose
lactose
sucrose
D−xylose
arbutin
D−mannose
D−mannitol
N−acetylglucosamine
D−ribose
gentiobiose
1 2 3 4 5 6 7 8
Number of Predictors
F
Relevant Carbohydrate Monomers
G
momomers influx metabolic map