Supplemental data

Unique gut microbiome signatures shaped by diet- versus genetically-induced obesity in mice

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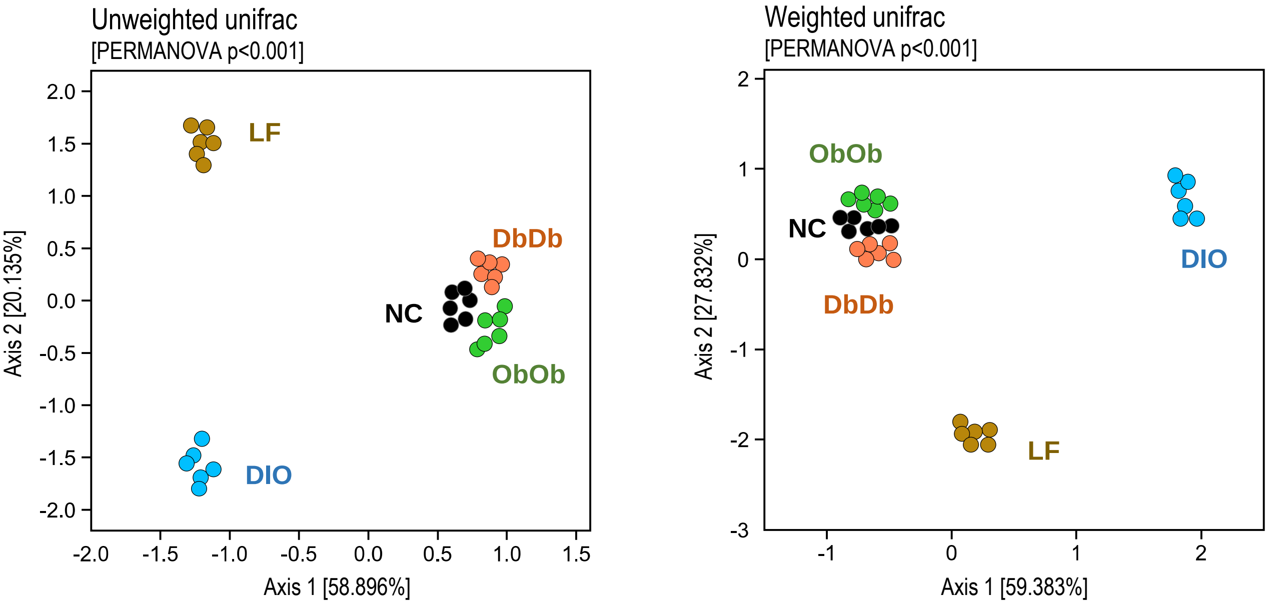
Suppl. Fig. 1

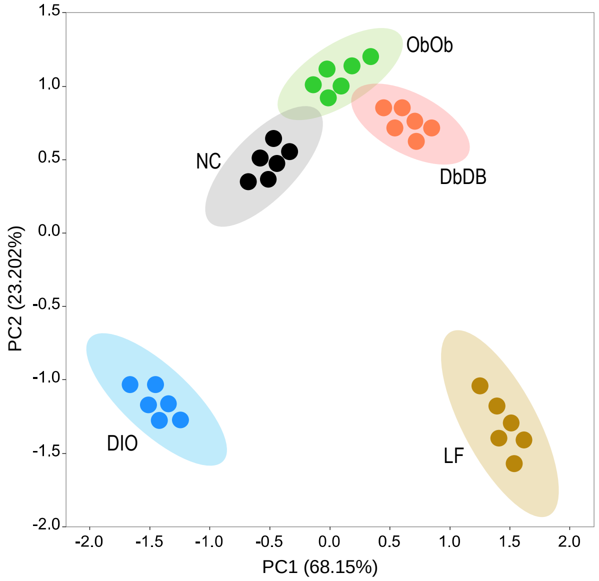


Unweighted unifrac
[PERMANOVA p<0.001]

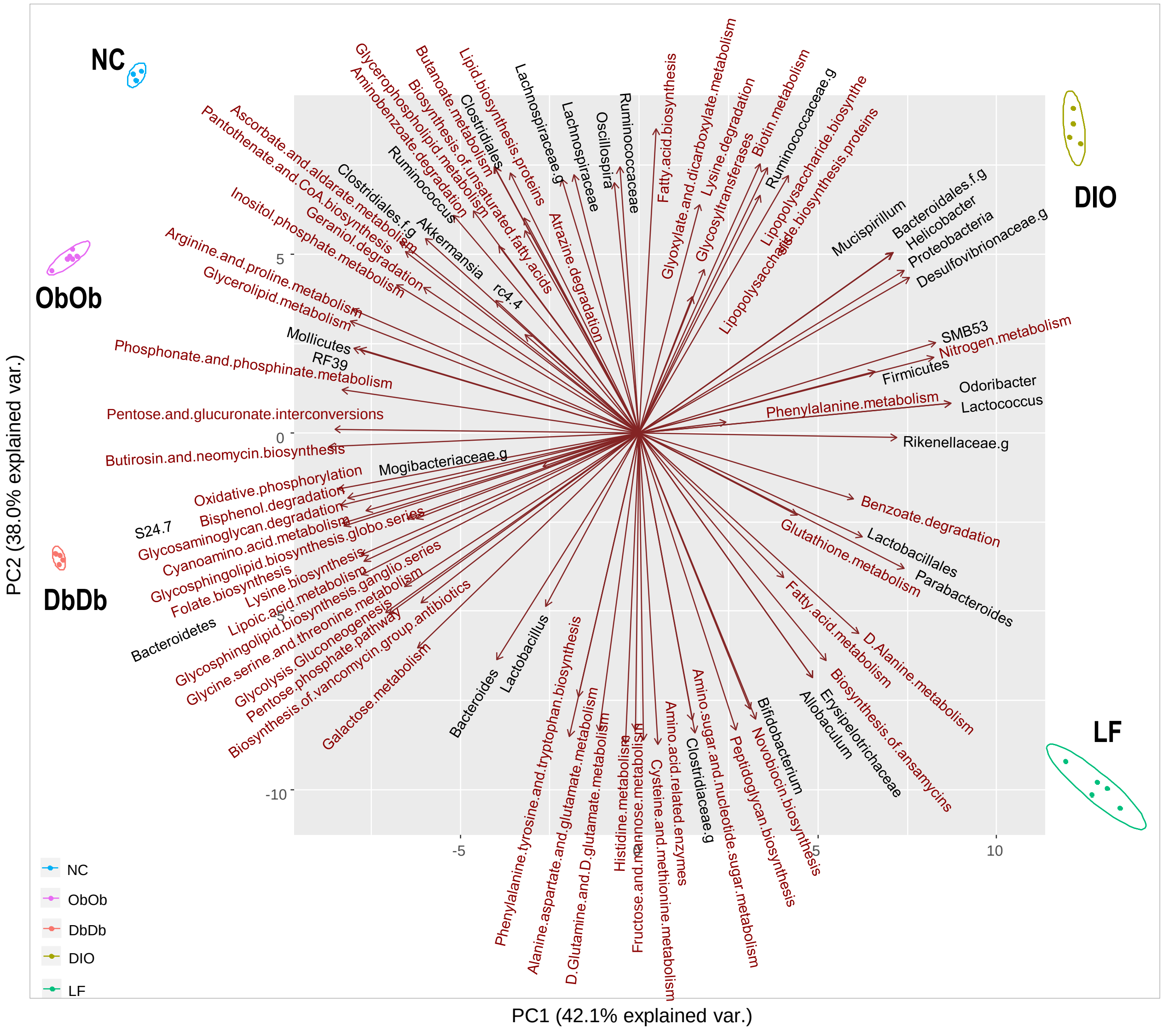
Weighted unifrac
[PERMANOVA p<0.001]

Suppl. Fig. 2

(a) PCoA (PICRUSt)

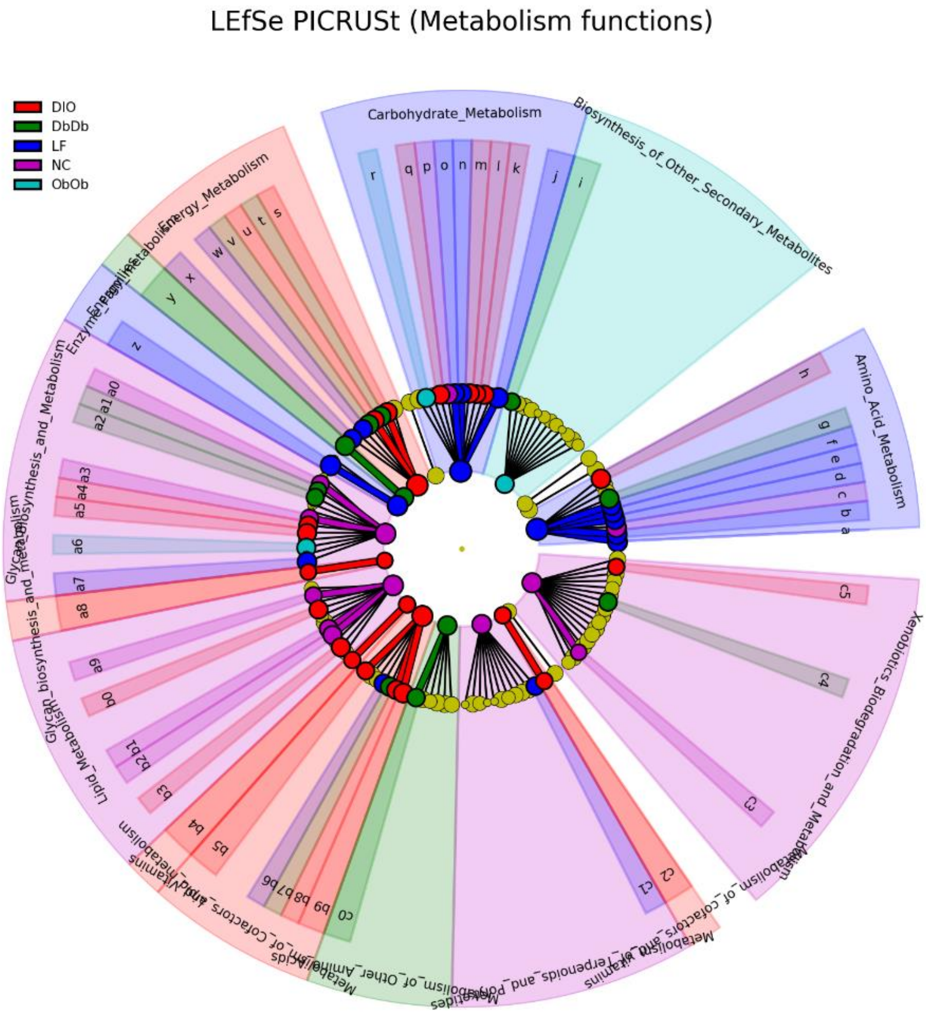


(b) Principal Coordinate Analysis (OTUs and PICRUSt)



Suppl. Fig. 3

LEfSe analysis cladogram illustrating unique metagenomic metabolism-related functional features, as predicted by PICRUSt, that are significantly over- or under-represented (or differentially abundant) in ObOb and DbDb mice, DIO mice, as well as in NC and LF control mice.

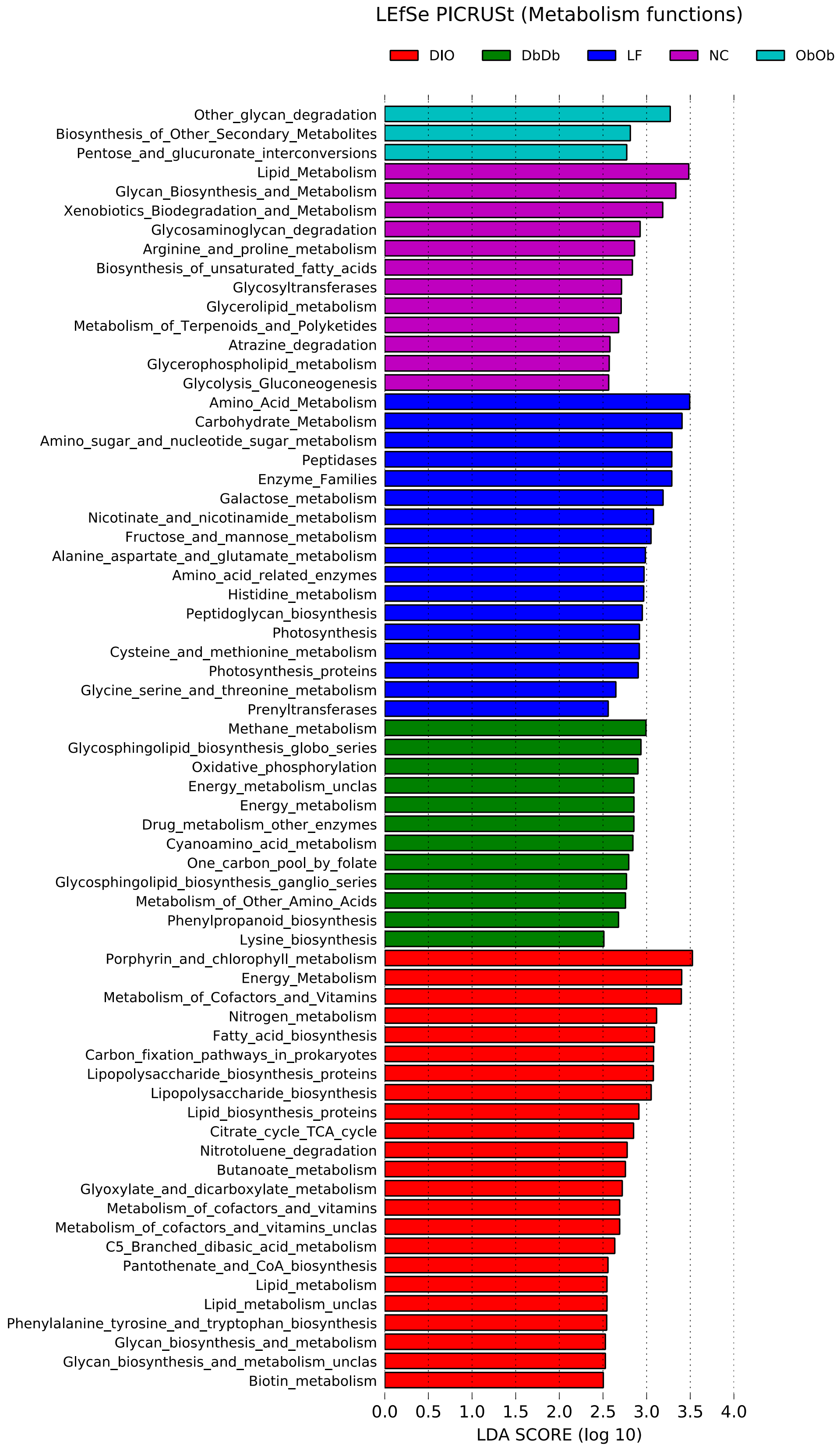


🟦 a: Alanine_aspartate_and_glutamate_metabolism
🟦 b: Amino_acid_related_enzymes
🟪 c: Arginine_and_proline_metabolism
🟦 d: Cysteine_and_methionine_metabolism
🟦 e: Glycine_serine_and_threonine_metabolism
🟦 f: Histidine_metabolism
🟩 g: Lysine_biosynthesis
🟥 h: Phenylalanine_tyrosine_and_tryptophan_biosynthesis
🟩 i: Phenylpropanoid_biosynthesis
🟦 j: Amino_sugar_and_nucleotide_sugar_metabolism
🟥 k: Butanoate_metabolism
🟥 l: C5_Branched_dibasic_acid_metabolism
🟥 m: Citrate_cycle_TCA_cycle
🟦 n: Fructose_and_mannose_metabolism
🟦 o: Galactose_metabolism
🟪 p: Glycolysis_Gluconeogenesis
🟥 q: Glyoxylate_and_dicarboxylate_metabolism
▧ r: Pentose_and_glucuronate_interconversions
🟥 s: Carbon_fixation_pathways_in_prokaryotes
🟩 t: Methane_metabolism
🟥 u: Nitrogen_metabolism
🟩 v: Oxidative_phosphorylation
🟦 w: Photosynthesis
🟦 x: Photosynthesis_proteins
🟩 y: Energy_metabolism_unclas
🟦 z: Peptidases

🟪 a0: Glycosaminoglycan_degradation
🟩 a1: Glycosphingolipid_biosynthesis_ganglio_series
🟩 a2: Glycosphingolipid_biosynthesis_globo_series
🟪 a3: Glycosyltransferases
🟥 a4: Lipopolysaccharide_biosynthesis
🟥 a5: Lipopolysaccharide_biosynthesis_proteins
▧ a6: Other_glycan_degradation
🟦 a7: Peptidoglycan_biosynthesis
🟥 a8: Glycan_biosynthesis_and_metabolism_unclas
🟪 a9: Biosynthesis_of_unsaturated_fatty_acids
🟥 b0: Fatty_acid_biosynthesis
🟪 b1: Glycerolipid_metabolism
🟪 b2: Glycerophospholipid_metabolism
🟥 b3: Lipid_biosynthesis_proteins
🟥 b4: Lipid_metabolism_unclas
🟥 b5: Biotin_metabolism
🟦 b6: Nicotinate_and_nicotinamide_metabolism
🟩 b7: One_carbon_pool_by_folate
🟥 b8: Pantothenate_and_CoA_biosynthesis
🟥 b9: Porphyrin_and_chlorophyll_metabolism
🟩 c0: Cyanoamino_acid_metabolism
🟦 c1: Prenyltransferases
🟥 c2: Metabolism_of_cofactors_and_vitamins_unclas
🟪 c3: Atrazine_degradation
🟩 c4: Drug_metabolism_other_enzymes
🟥 c5: Nitrotoluene_degradation

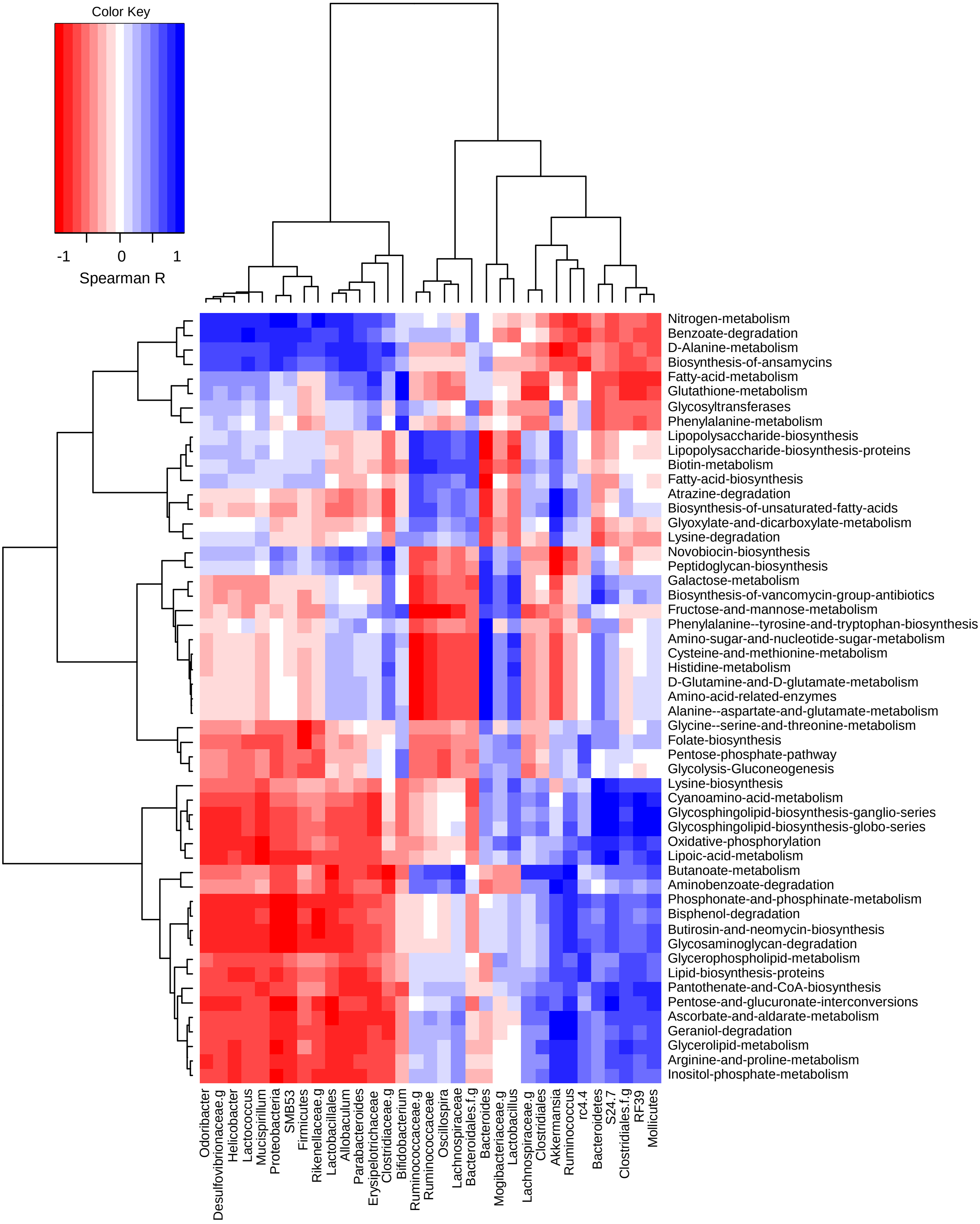
Suppl. Fig. 4

LEfSe analysis illustrating the LDA scores of unique metagenomic metabolism-related functional features, as predicted by PICRUSt, that are significantly over- or under-represented (or differentially abundant) in ObOb and DbDb mice, DIO mice, as well as in NC and LF control mice.



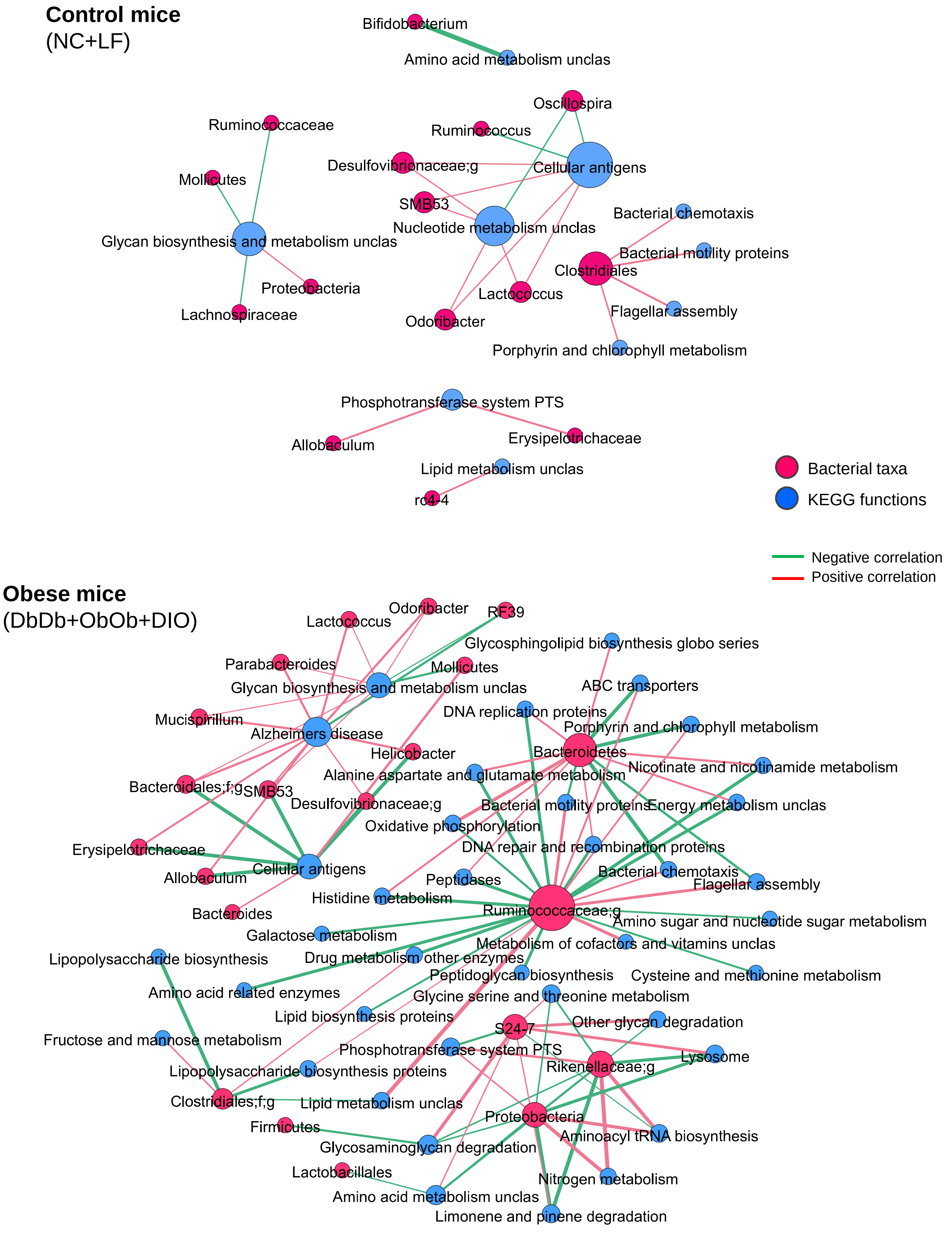
Suppl. Fig. 5

Color heat-map depicting the overall spearman correlation of bacterial taxa with the PICRUSt-curated metagenomic functions altogether in ObOb, DbDb, DIO, NC and LF mice.

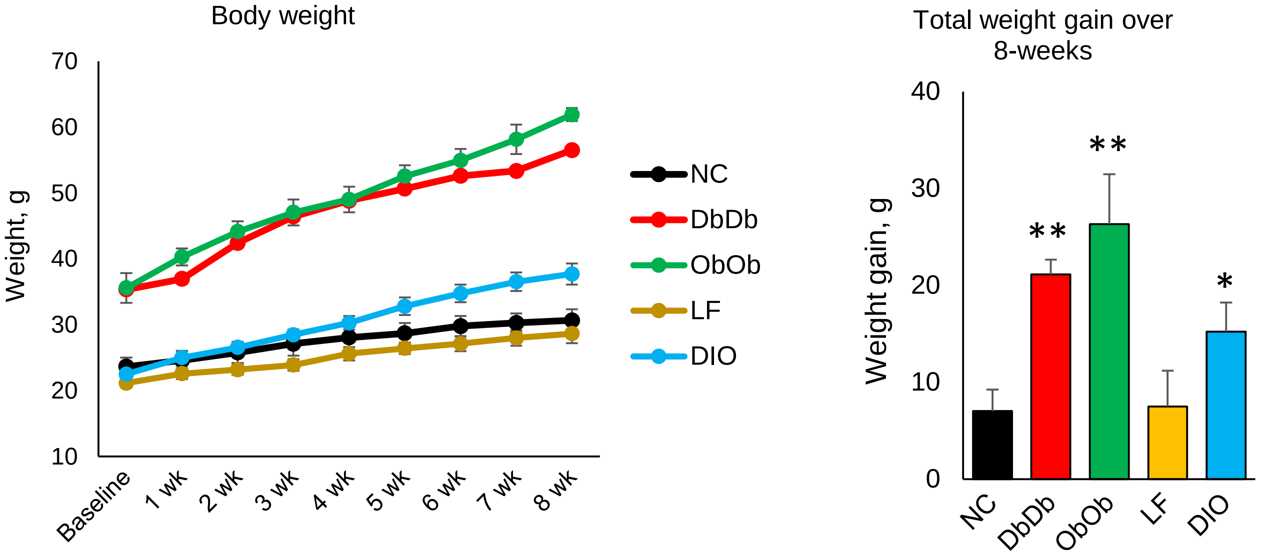


Suppl. Fig. 6

Significant associations with correlation >0.7 and p-value <0.01 (FDR)



Suppl. Fig. 7


Body weight
70
60
50
40
30
20
10
Weight, g
Baseline
1 wk
2 wk
3 wk
4 wk
5 wk
6 wk
7 wk
8 wk
NC
DbDb
ObOb
LF
DIO
Total weight gain over 8-weeks
40
30
20
10
0
Weight gain, g
**
**
*
NC
DbDb
ObOb
LF
DIO