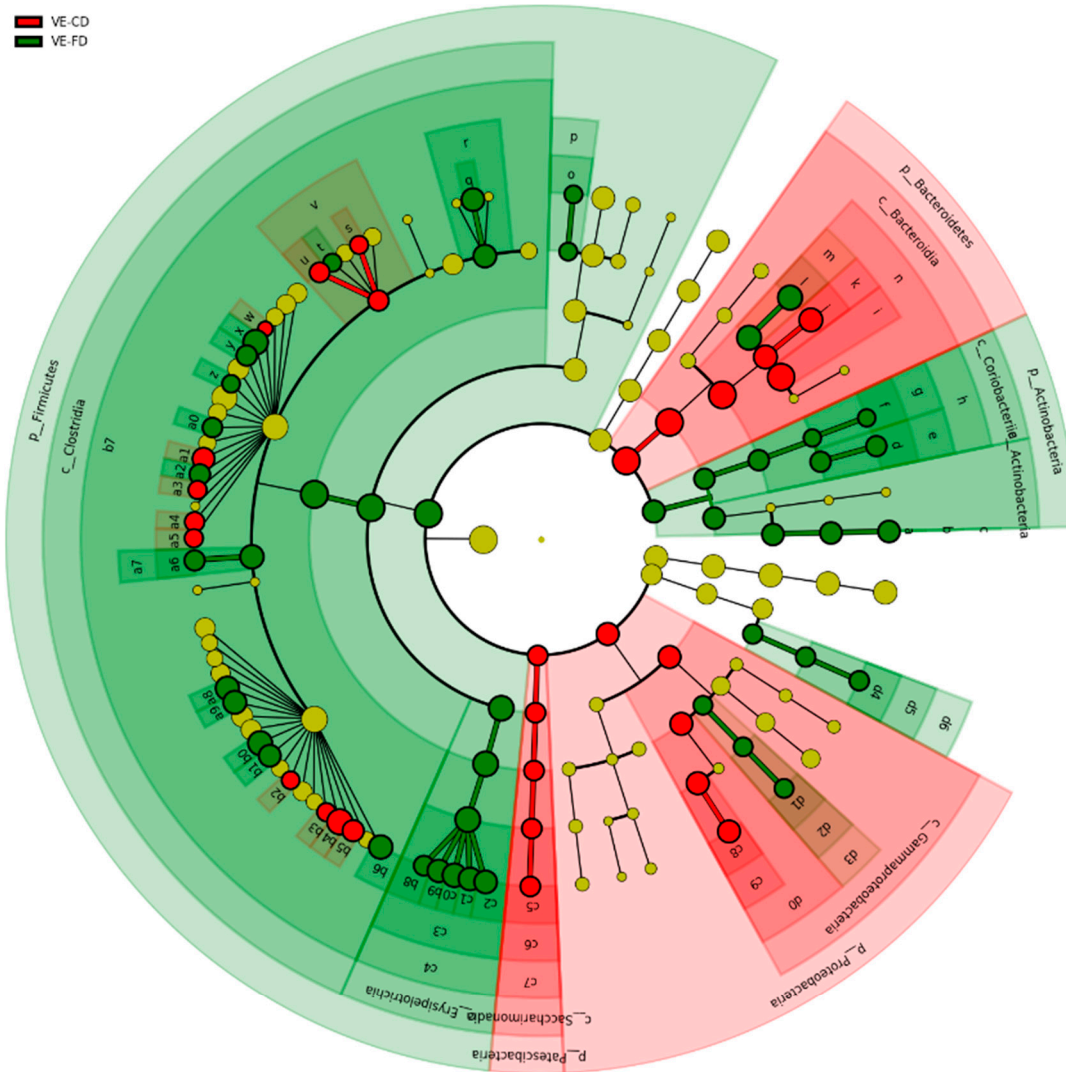


**Supplemental figure 1. Cross-sectional area of epididymal white adipose tissue.** (A) Liver H&E stained (B) Adipocyte size of epididymal white adipose tissue. Results are expressed as Mean  $\pm$  SD. Values not sharing a common superscript letter (a, b) differ significantly at  $P < 0.05$  through one-way ANOVA analysis ( $n = 8/\text{group}$ ). Magnification  $\times 200$ , scale bar:  $50 \mu\text{m}$ ,

# VE-CD vs VE-FD

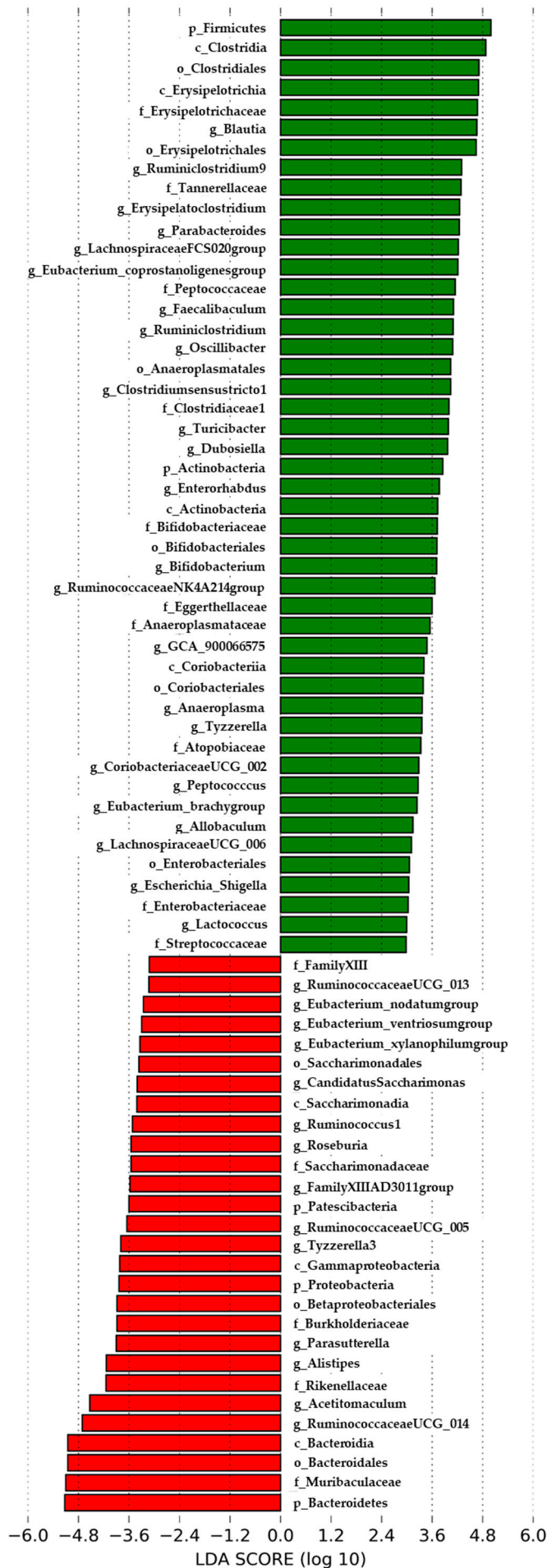
A

VE-CD  
VE-FD





































- a: g\_Bifidobacterium
- b: f\_Bifidobacteriaceae
- c: o\_Bifidobacteriales
- d: g\_CoribacteriaceaeUCG\_002
- e: f\_Attopobiaceae
- f: g\_Enterorhabdus
- g: f\_Eggerthellaceae
- h: o\_Coribacteriales
- i: f\_Muribaculaceae
- j: g\_Alistipes
- k: f\_Rikenellaceae
- l: g\_Parabacteroides
- m: f\_Tannerellaceae
- n: o\_Bacteroidales
- o: g\_Lactococcus
- p: f\_Streptococcaceae
- q: g\_Clostridiumsensustricto1
- r: f\_Clostridiaceae1
- s: g\_FamilyXIIIAD3011group
- t: g\_Eubacterium\_brachygroup
- u: g\_Eubacterium\_nodatumgroup
- v: f\_FamilyXIII
- w: g\_Acetitomaculum
- x: g\_Blautia
- y: g\_GCA\_900066575
- z: g\_LachnospiraceaeFCS020group
- a0: g\_LachnospiraceaeUCG\_006
- a1: g\_Roseburia
- a2: g\_Tyzerella
- a3: g\_Tyzerella3
- a4: g\_Eubacterium\_ventriosumgroup
- a5: g\_Eubacterium\_xylanophilumgroup
- a6: g\_Peptococcus
- a7: f\_Peptococcaceae
- a8: g\_Oscillibacter
- a9: g\_Ruminiclostridium
- b0: g\_Ruminiclostridium9
- b1: g\_RuminococcaceaeNK4A214group
- b2: g\_RuminococcaceaeUCG\_005
- b3: g\_RuminococcaceaeUCG\_013
- b4: g\_RuminococcaceaeUCG\_014
- b5: g\_Ruminococcus1
- b6: g\_Eubacterium\_coprostanoligenesgroup
- b7: o\_Clostridiales
- b8: g\_Allobaculum
- b9: g\_Dubosiella
- c0: g\_Erysipelatoclostridium
- c1: g\_Faecalibaculum
- c2: g\_Turicibacter
- c3: f\_Erysipelotrichaceae
- c4: o\_Erysipelotrichales
- c5: g\_CandidatusSaccharimonas
- c6: f\_Saccharimonadaceae
- c7: o\_Saccharimonadales
- c8: g\_Parasutterella
- c9: f\_Burkholderiaceae
- d0: o\_Betaproteobacteriales
- d1: g\_Escherichia\_Shigella
- d2: f\_Enterobacteriaceae
- d3: o\_Enterobacteriales
- d4: g\_Anaeroplasm

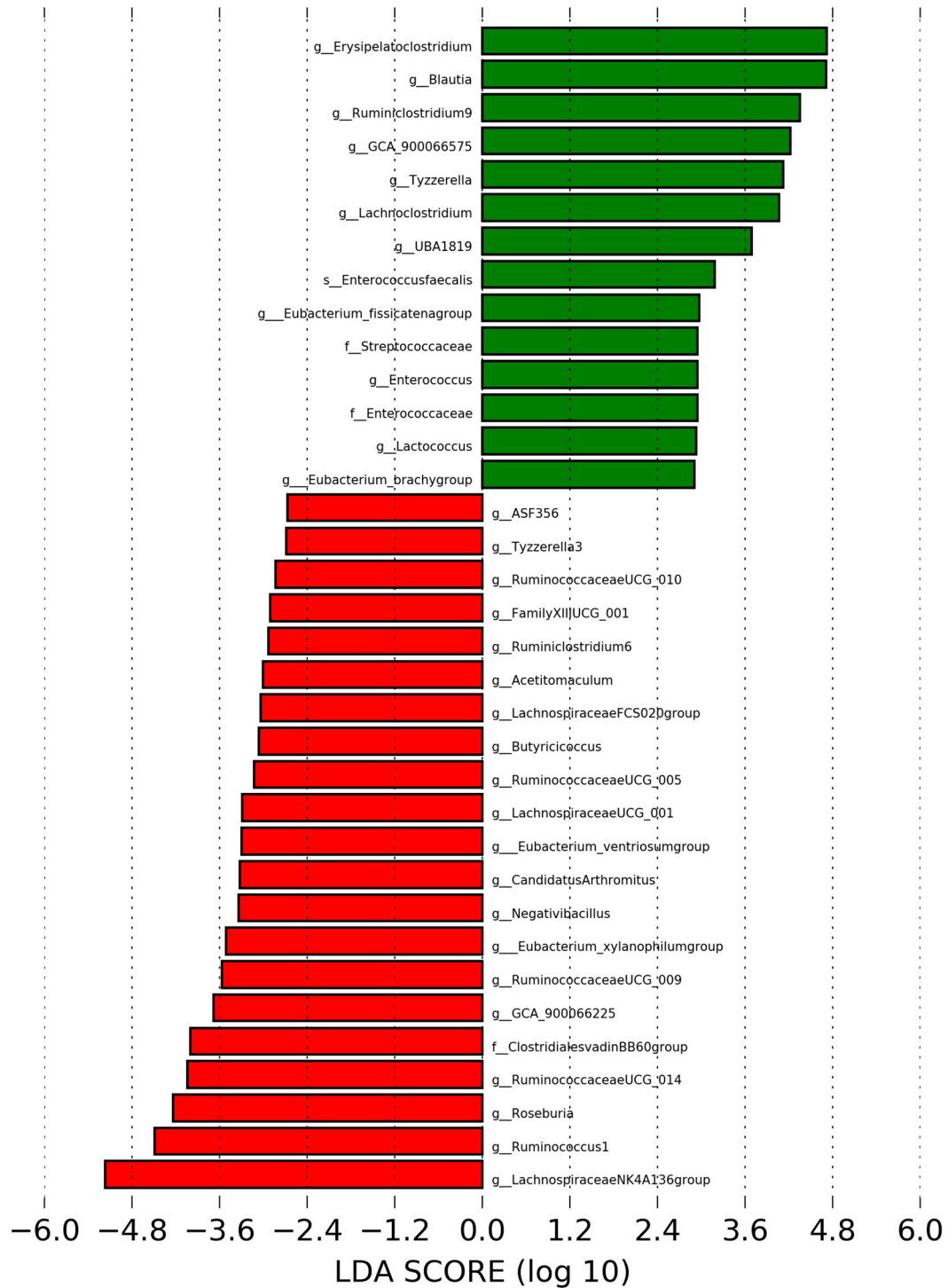
B

■ VE-CD ■ VE-FD


**Supplemental figure 2.** Taxonomic representation of VE groups. Differences are represented by the color of the most abundant class. (A) Dot size is proportional to the abundance of the taxon. (B) Length indicates the effect size associated with a taxon. The cladogram was calculated by LEfSe, a metagenome analysis of abundant taxa of OTUs, only taxa meeting an LDA significant threshold  $> 2$  and  $p < 0.05$  are shown.

## A

- |   |  |
|---|--|
|  a: g__Enterococcus                  |  t: g__Eubacterium_fissicatena_group  |
|  b: f__Enterococcaceae               |  u: g__Eubacterium_ventriosum_group   |
|  c: g__Lactococcus                   |  v: g__Eubacterium_xylanophilum_group |
|  d: f__Streptococcaceae              |  w: g__Butyricicoccus                 |
|  e: g__Candidatus_Arthromitus        |  x: g__GCA_900066225                  |
|  f: f__Clostridiales_vadinBB60_group |  y: g__Negativibacillus               |
|  g: g__Family_XIII_UCG_001           |  z: g__Ruminiclostridium6             |
|  h: g__Eubacterium_brachy_group      |  a0: g__Ruminiclostridium9            |
|  i: g__ASF356                        |  a1: g__Ruminococcaceae_UCG_005       |
|  j: g__Acetitomaculum                |  a2: g__Ruminococcaceae_UCG_009       |
|  k: g__Blautia                       |  a3: g__Ruminococcaceae_UCG_010       |
|  l: g__GCA_900066575                 |  a4: g__Ruminococcaceae_UCG_014       |
|  m: g__Lachnoclostridium             |  a5: g__Ruminococcus1                 |
|  n: g__Lachnospiraceae_FCS020_group  |  a6: g__UBA1819                       |
|  o: g__Lachnospiraceae_NK4A136_group |  a7: g__Erysipelatoclostridium        |
|  p: g__Lachnospiraceae_UCG_001       |  |
|  q: g__Roseburia                     |  |
|  r: g__Tyzzerella                    |  |
|  s: g__Tyzzerella3                   |  |

**B**
■ CF-CD    ■ CF-FD


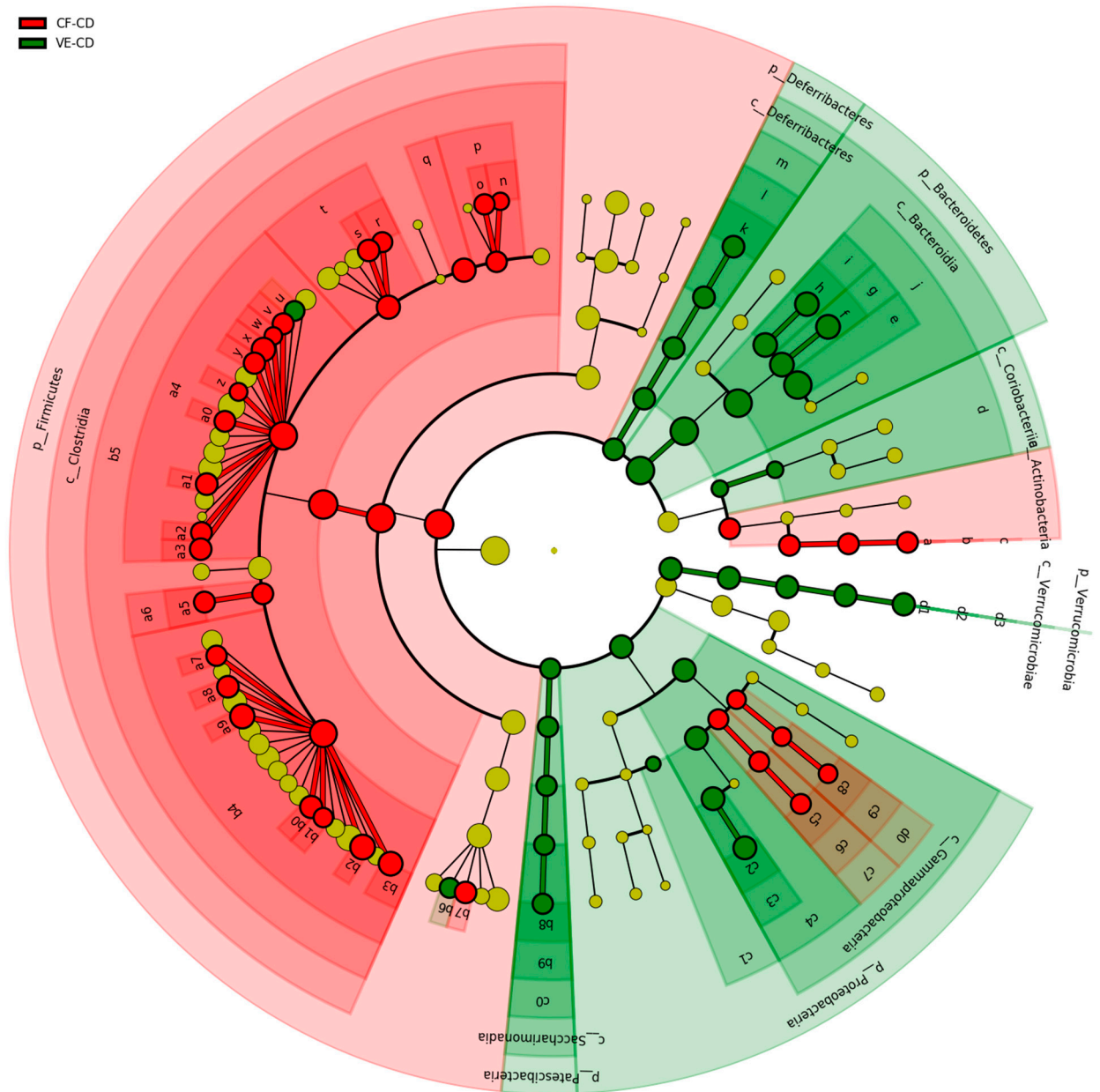
**Supplemental figure 3.** Taxonomic representation of CF groups. Differences are represented by the color of the most abundant class. (A) Dot size is proportional to the abundance of the taxon. (B) Length indicates the effect size associated with a taxon. The cladogram was calculated by LEfSe, a metagenome analysis of abundant taxons of OTUs, only taxa meeting an LDA significant threshold  $> 2$  and  $p < 0.05$  are shown.



# CF-CD vs VE-CD

A

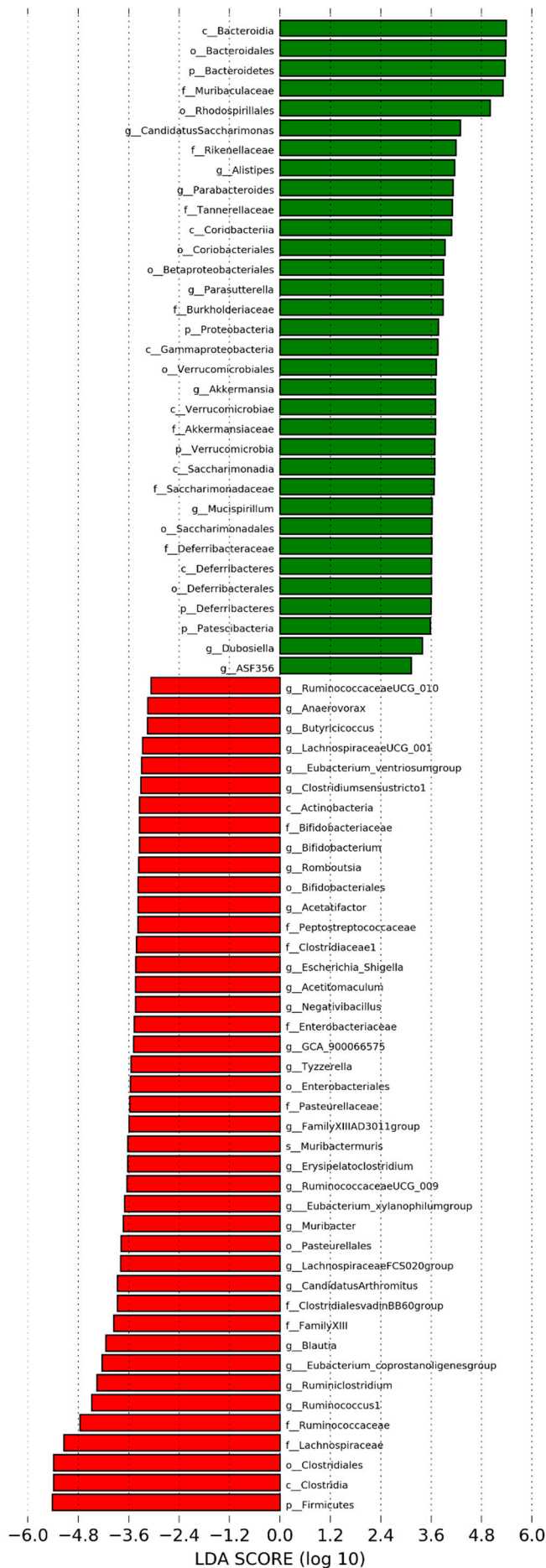
CF-CD  
VE-CD



- |                                     |  |
|-------------------------------------|--|
| a: g_Bifidobacterium                | a4: f_Lachnospiraceae                    |
| b: f_Bifidobacteriaceae             | a5: g_Romboutsia                         |
| c: o_Bifidobacteriales              | a6: f_Peptostreptococcaceae              |
| d: o_Coriobacteriales               | a7: g_Butyricoccus                       |
| e: f_Muribaculaceae                 | a8: g_Negativibacillus                   |
| f: g_Alistipes                      | a9: g_Ruminiclostridium                  |
| g: f_Rikenellaceae                  | b0: g_RuminococcaceaeUCG_009             |
| h: o_Parabacteroides                | b1: g_RuminococcaceaeUCG_010             |
| i: f_Tannerellaceae                 | b2: g_Ruminococcus1                      |
| j: o_Bacteroidales                  | b3: g_Eubacterium_coprostanoligenesgroup |
| k: g_Mucispirillum                  | b4: f_Ruminococcaceae                    |
| l: f_Deferribacteraceae             | b5: o_Clostridiales                      |
| m: o_Deferribacteriales             | b6: g_Dubosiella                         |
| n: g_CandidatusArthromitus          | b7: g_Erysipelatoclostridium             |
| o: g_Clostridiumsensustricto1       | b8: g_CandidatusSaccharimonas            |
| p: f_Clostridiaceae1                | b9: f_Saccharimonadaceae                 |
| q: f_ClostridialesvadinBB60group    | c0: o_Saccharimonadales                  |
| r: g_Anaerovorax                    | c1: o_Rhodospirillales                   |
| s: g_FamilyXIIIAD3011group          | c2: g_Parasutterella                     |
| t: f_FamilyXIII                     | c3: f_Burkholderiaceae                   |
| u: g_ASF356                         | c4: o_Betaproteobacteriales              |
| v: g_Acetatifactor                  | c5: g_Escherichia_Shigella               |
| w: g_Acetitomaculum                 | c6: f_Enterobacteriaceae                 |
| x: g_Blautia                        | c7: o_Enterobacteriales                  |
| y: g_GCA_900066575                  | c8: g_Muribacter                         |
| z: g_LachnospiraceaeFCS020group     | c9: f_Pasteurellaceae                    |
| a0: g_LachnospiraceaeUCG_001        | d0: o_Pasteurellales                     |
| a1: g_Tyzerella                     | d1: g_Akkermansia                        |
| a2: g_Eubacterium_ventriosumgroup   | d2: f_Akkermansiaceae                    |
| a3: g_Eubacterium_xylanophilumgroup | d3: o_Verrucomicrobiales                 |

B

CF-CD VE-CD



**Supplemental figure 4.** Taxonomic representation of CD groups. Differences are represented by the color of the most abundant class. (A) Dot size is proportional to the abundance of the taxon. (B) Length indicates the effect size associated with a taxon. The cladogram was calculated by LEfSe, a metagenome analysis of abundant taxa of OTUs, only taxa meeting an LDA significant threshold  $> 2$  and  $p < 0.05$  are shown.