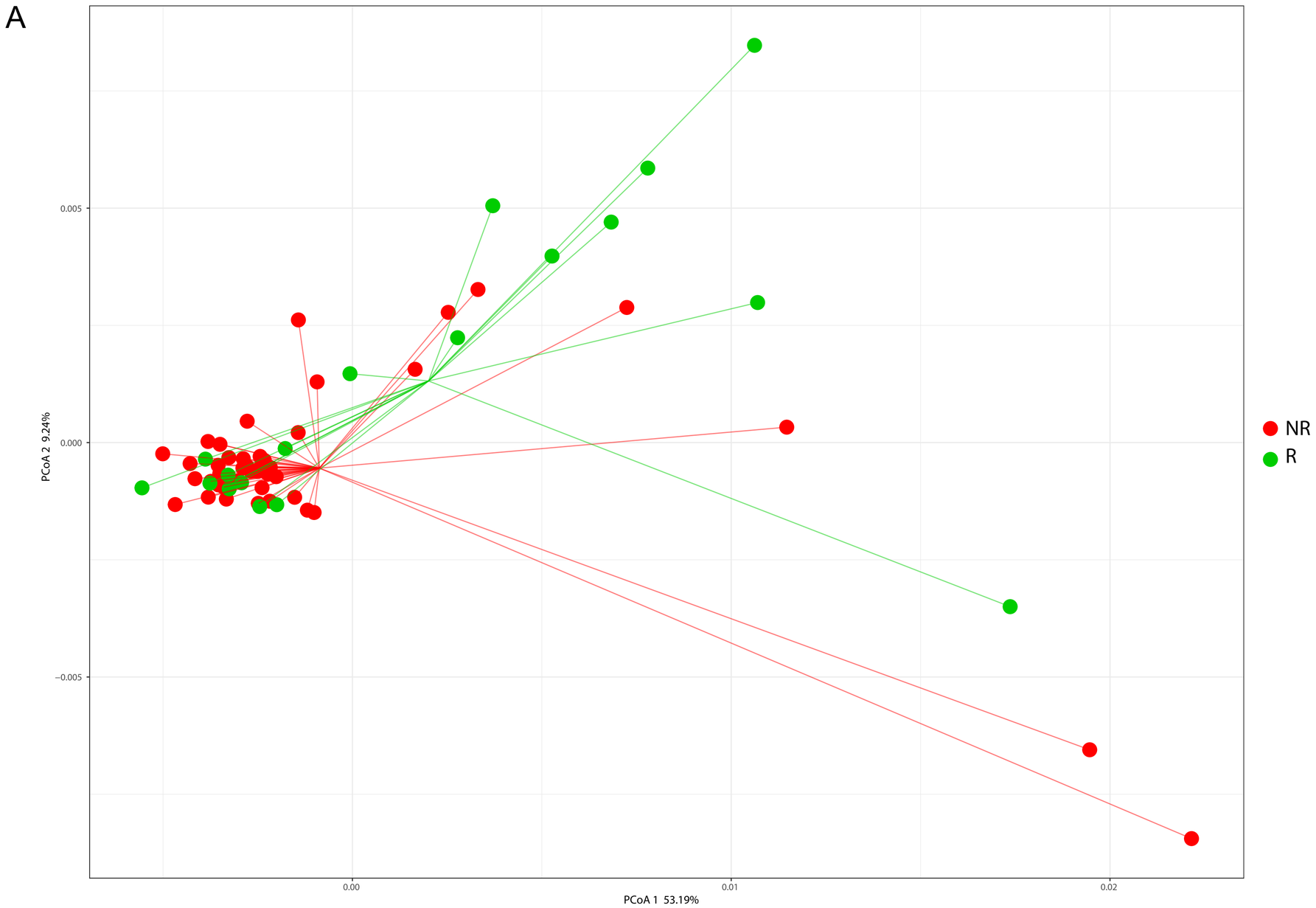
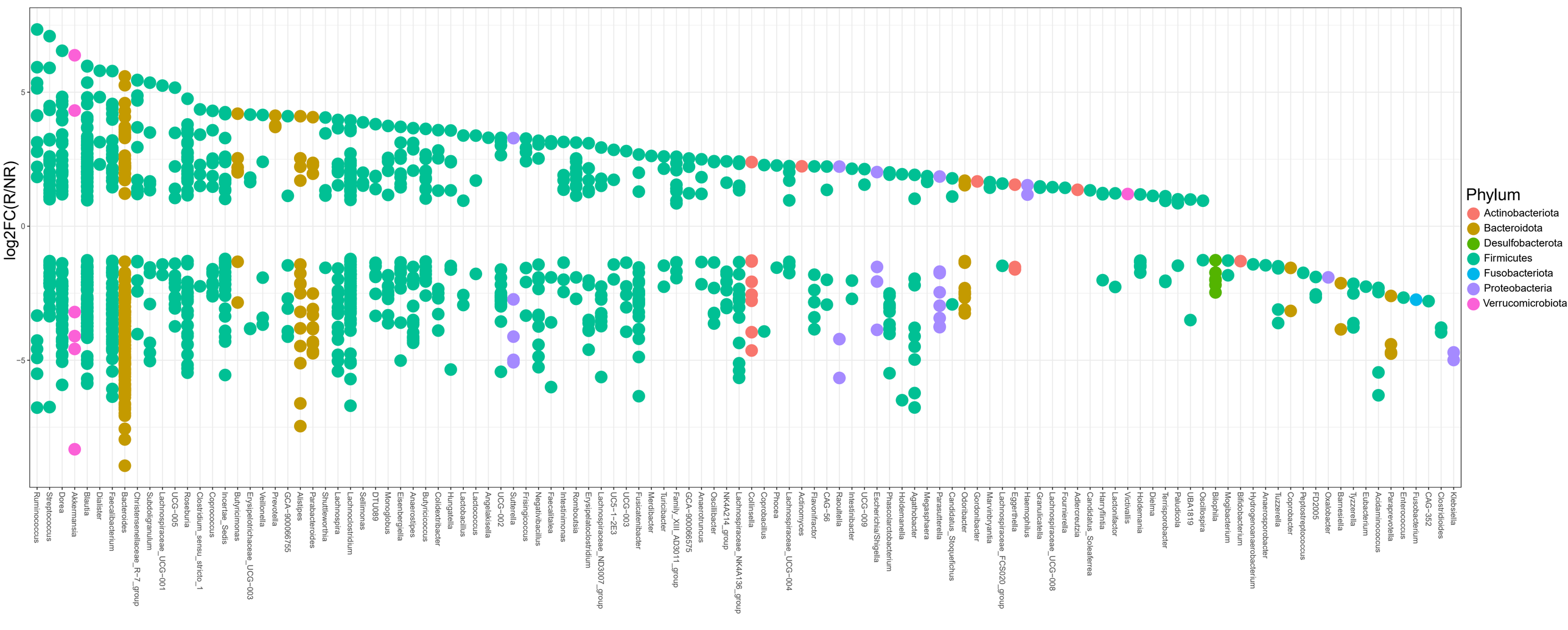
Figure S1

A


0.005
0.000
−0.005
PCoA 2 9.24%
0.00
0.01
0.02
PCoA 1 53.19%
NR
R

B


log2FC(R/NR)
5
0
−5
Ruminococcus
Streptococcus
Dorea
Akkermansia
Blautia
Dialister
Faecalibacterium
Bacteroides
Christensenellaceae_R−7_group
Subdoligranulum
UCG−005
Lachnospiraceae_UCG−001
Roseburia
Clostridium_sensu_stricto_1
Coprococcus
Incertae_Sedis
Butyricimonas
Erysipelotrichaceae_UCG−003
Prevotella
Veillonella
GCA−900066755
Alistipes
Parabacteroides
Shuttleworthia
Lachnospira
Lachnoclostridium
Sellimonas
DTU089
Monoglobus
Eisenbergiella
Anaerostipes
Butyricicoccus
Coldextribacter
Hungatella
Lactobacillus
Lactococcus
Angelakisella
UCG−002
Sutterella
Frisingicoccus
Negativibacillus
Faecalitalea
Intestinimonas
Romboutsia
Erysipelatoclostridium
Lachnospiraceae_ND3007_group
UC5−1−2E3
UCG−003
Fusicatenibacter
Merdibacter
Turicibacter
Family_XIII_AD3011_group
GCA−900066575
Anaerotruncus
Oscillibacter
NK4A214_group
Lachnospiraceae_NK4A136_group
Collinsella
Coprobacillus
Phocea
Lachnospiraceae_UCG−004
Actinomyces
Flavonifractor
CAG−56
Raoultella
Intestinibacter
UCG−009
Escherichia/Shigella
Phascolarctobacterium
Holdemanella
Agathobacter
Megasphaera
Parasutterella
Candidatus_Stoquefichus
Odoribacter
Gordonibacter
Marvinbryantia
Lachnospiraceae_FCS020_group
Eggerthella
Haemophilus
Granulicatella
Lachnospiraceae_UCG−008
Fournierella
Adlercreutzia
Candidatus_Soleaferrea
Harryflintia
Lactonifactor
Victivallis
Holdemania
Dielma
Terrisporobacter
Paludicola
UBA1819
Oscillospira
Bilophila
Mogibacterium
Bifidobacterium
Hydrogenoanaerobacterium
Anaerosporobacter
Tuzzerella
Coprobacter
Peptostreptococcus
FD2005
Oxalobacter
Barnesiella
Tyzzerella
Eubacterium
Acidaminococcus
Paraprevotella
Enterococcus
Fusobacterium
CAG−352
Clostridioides
Klebsiella
Phylum
Actinobacteriota
Bacteroidota
Desulfobacterota
Firmicutes
Fusobacteriota
Proteobacteria
Verrucomicrobiota