Supplementary Materials

Supplementary Figure Legends

Figure S1. CARD9 expression in the colon tissue. Related to Figure 1. **(A)** RT-PCR analysis for the expression of *Card9* and *Il18* in the $CD45^+$ or $EpCAM^+$ cells purified from the colons of WT mice at indicated days after AOM injection by FACS. **(B)** Gating strategy for the $EpCAM^+$ and $CD45^+$ cells in colon. **(C)** Immunofluorescence for CARD9, EpCAM and CD11b in the colon tissues at indicated days after AOM injection. Scale bar = 20um. Data represent two independent experiments with 6-10 mice per group per time point. **(D)** Immunohistochemistry for CARD9 in human colon tissue biopsy from protein atlas. **(E)** Expression of ITGAM (CD11b) in the normal and tumor colon biopsies in the GENT database. **(F)** Schematic representation of AOM-DSS treatment. Mice were injected with AOM on day 0, and given 2% DSS in drinking water on day 5 for 6 days, followed by drinking water. Mice were given two subsequent rounds of DSS with an interval of 17 days. Error bars represent mean±standard error of the mean.

Figure S2. CARD9 does not affect goblet cell differentiation or mucus production early during AOM-DSS treatment. Related to Figure 3. **(A)** RT-PCR analysis for expression of indicated genes in colon tissue from WT and *Card9*$^{-/-}$ mice at indicated days after AOM injection. **(B)** Densitometric analysis for the immunoblots in Figures 3C and 3E. **(C)** Frequency of $CD11b^+$ cells and **(D)** *Il18* expression in the $CD11b^+$ cells from the colon, MLN and spleens of WT and *Card9*$^{-/-}$ mice on day 9. Data represent two independent experiments. Error bars represent mean±standard error of the mean with 5-8 mice per group per time point.

Figure S3. Cohousing normalizes disease susceptibility in WT and *Card9*$^{-/-}$ mice. Related to Figure 4. **(A)** Percent body weight **(B)** colon length and **(C)** representative colon histology pictures from WT and *Card9*$^{-/-}$ mice housed together or separately for 4 weeks prior to AOM-DSS treatment, and sacrificed on day 14. Original magnification = 10x. **(D)** Percent body weight **(E)** number of tumors and **(F)** tumor distribution in the colons of WT and *Card9*$^{-/-}$ mice housed together or separately for 4 weeks prior to AOM-DSS treatment and sacrificed on day 80. Principal component analysis for **(G)** 18s ITS and **(H)** 16s rRNA sequencing from the fecal pellets of separately cohoused or co-housed (CH) WT and *Card9*$^{-/-}$ mice. **(I)** Heat maps based on the operational taxonomic unit (OTU) number from the 18s ITS sequencing. Data represent two independent experiments and analyzed by two-way ANOVA **(A and D)** or one-way ANOVA **(B and E)** followed by Holm-Sidak post-test. Error bars represent mean±standard error of the mean with 5-10 mice per group per time point.

Figure S4. Cohousing normalizes disease susceptibility in WT and *Card9*$^{-/-}$ mice. Related to Figure S3 and Figure 4. Heat maps based on the operational taxonomic unit (OTU) number in the 16s rRNA sequencing from the fecal pellets of separately cohoused or co-housed (CH) WT and *Card9*$^{-/-}$ mice with 8 mice per group.

Figure S5. SYK and CARD9 are required for inflammasome activation by *Candida*. Related to Figure 5. Immunoblot for Caspase-1 in primary mouse bone marrow–derived myeloid cells stimulated with **(A)** LPS for 4 hours or *C. albicans* for 20 hours, **(C)** LPS for 4 hours followed by stimulation with 5 mM ATP for 30 minutes **(D)** transfected with LPS **(E)** transfected with poly(dAdT) or **(F)** stimulation with *S.* Typhimurium at MOI 1 for 2 h. **(B)** IL-18 levels in supernatants of cells stimulated with *Candida*. Closed arrows represent pro-caspase-1 (p45) and open arrows represent cleaved caspase-1 (p20). Error bars represent mean±standard error of the mean.

Figure S6. Anti-fungal treatment leads to alteration in the mycobiome. Related to Figure 6. **(A)** Principal component analysis and **(B)** heat map based on the operational taxonomic unit (OTU) number in the 18s ITS sequencing from the fecal pellets of WT mice given drinking water or amphotericin B or Itraconazole for 4 weeks. (**C)** Principal component analysis from the 16s rRNA sequencing from fecal pellets of WT mice given drinking water or amphotericin B or Itraconazole for 4 weeks. 8 mice per group.

Figure S7. Metronidazole treatment leads to alteration in the gut bacterial and fungal landscape. Related to Figure 6. Principal component analysis of **(A)** 16s and **(B)** 18s and **(C)** heat maps based on the operational taxonomic unit (OTU) number from the fecal pellets of WT mice given metronidazole for 5 days. 8 mice per group.

Supplementary Table 1. Real time qPCR primer sequences

Gene	Primer Sequences
β-actin	Forward: 5'-GGCTGTATTCCC CTCCATCG-3'
	Reverse: 5'-CCAGTTGGTAACAATGCCATG T-3'
Muc2	Forward: 5'-GCTGACGAGTGGTTGGTGAATG-3'
	Reverse: 5'-GATGAGGTGGCAGACAGGAGAC-3'
Il22	Forward: 5'-AGAACGTCTTCCAGGGTGAA-3'
	Reverse: 5'-CAT CGA CAT AAG TCA GCA CCA G-3'
Reg3β	Forward: 5'-ATGGCTCCTACTGCTATGCC-3'
	Reverse: 5'-GTGTCCTCCAGGCCTCTTT-3'
Reg3γ	Forward: 5'-ATGGCTCCTATTGCTATGC-3'
	Reverse: 5'-GATGTCCTGAGGGCCTCTT-3'
Il22bp	Forward: 5'-TCAGCAGCAAAGACAGAAGAAAC-3'
	Reverse: 5'-GTGTCTCCAGCCCAACTCTCA-3'
Spdef	Forward: 5'- AAGGCAGCATCAGGAGCAATG -3'
	Reverse: 5'- CTGTCAATGACGGGACACTG -3'
Klf4	Forward: 5'- GTGCCCCGACTAACCGTTG -3'
	Reverse: 5'- GTCGTTGAACTCCTCGGTCT -3'
Eubacteria	Forward: 5'-ACTCCTACGGGAGGCAGCAGT-3'
	Reverse: 5'-ATTACCGCGGCTGCTGGC-3'
Bacteroides	Forward: 5'-GGTTCTGAGAGGAGGTCCC-3'
	Reverse: 5'-CTGCCTCCCGTAGGAGT-3'
Fungal 18s	Forward: 5'- GGRAAACTC ACCAGGTCC AG -3'
	Reverse: 5′- GSWCTATCCCCAKCAC GA -3′
Lactobacillus	Forward: 5'-GGAAACAGATGCTAATACCG-3'
	Reverse: 5′-CACCGCTACACATGGAG-3′

Supplementary Table 2. Anti-fungal treatment leads to distinct alterations in the gut bacterial landscape. Related to Figure 6. Heat map based on the operational taxonomic unit (OTU) number from the 16s rRNA sequencing from fecal pellets of WT mice given drinking water or amphotericin B for 4 weeks. 8 mice per group.

Supplementary Table 3. Anti-fungal treatment leads to distinct alterations in the gut bacterial landscape. Related to Figure 6. Heat map based on the operational taxonomic unit (OTU) number from the 16s rRNA sequencing from fecal pellets of WT mice given drinking water or itraconazole for 4 weeks. 8 mice per group.

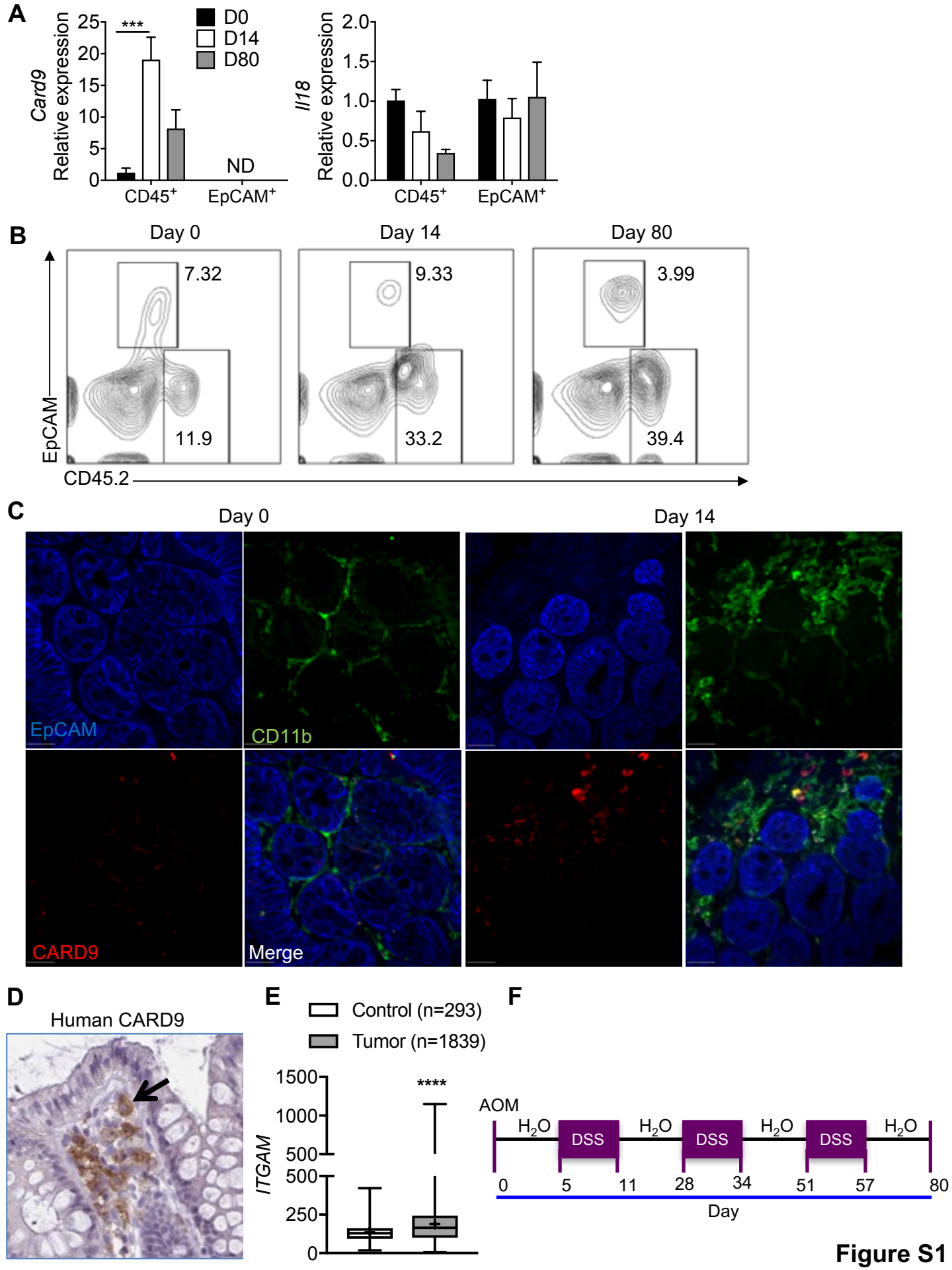
A
Card9
Relative expression
25
20
15
10
5
0
***
D0
D14
D80
ND
CD45+
EpCAM+
Il18
Relative expression
2.0
1.5
1.0
0.5
0.0
CD45+
EpCAM+
B
Day 0
Day 14
Day 80
7.32
11.9
9.33
33.2
3.99
39.4
EpCAM
CD45.2
C
Day 0
Day 14
EpCAM
CD11b
CARD9
Merge
D
Human CARD9
E
Control (n=293)
Tumor (n=1839)
1500
1000
500
500
250
0
ITGAM
****
F
AOM
H2O
DSS
H2O
DSS
H2O
DSS
H2O
0
5
11
28
34
51
57
80
Day

Figure S1

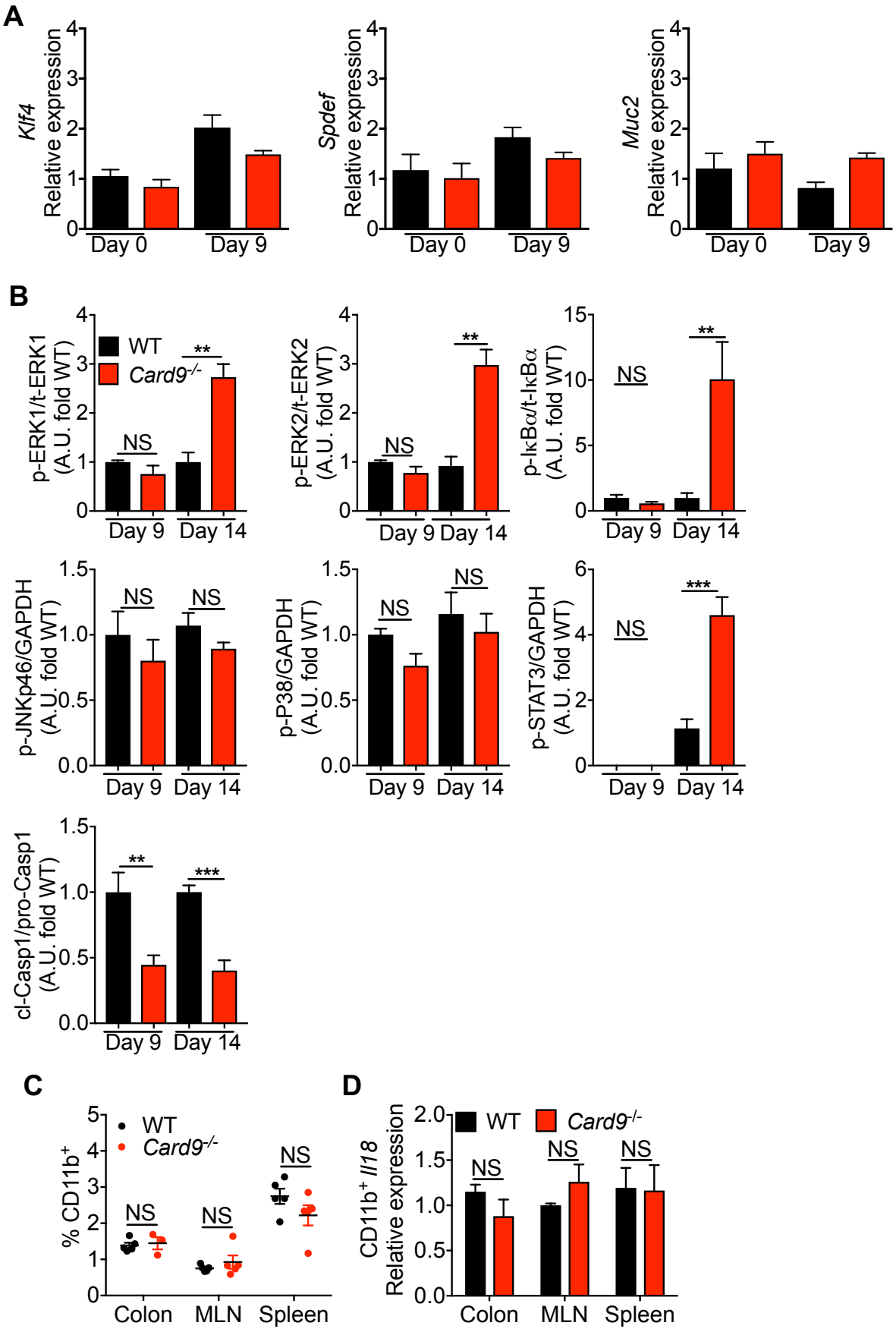
A
Klf4
Relative expression
Day 0
Day 9
Spdef
Muc2
B
WT
Card9-/-
p-ERK1/t-ERK1 (A.U. fold WT)
p-ERK2/t-ERK2 (A.U. fold WT)
p-IκBα/t-IκBα (A.U. fold WT)
p-JNKp46/GAPDH (A.U. fold WT)
p-P38/GAPDH (A.U. fold WT)
p-STAT3/GAPDH (A.U. fold WT)
cl-Casp1/pro-Casp1 (A.U. fold WT)
Day 14
NS
C
% CD11b+
Colon
MLN
Spleen
D
CD11b+ Il18 Relative expression

Figure S2

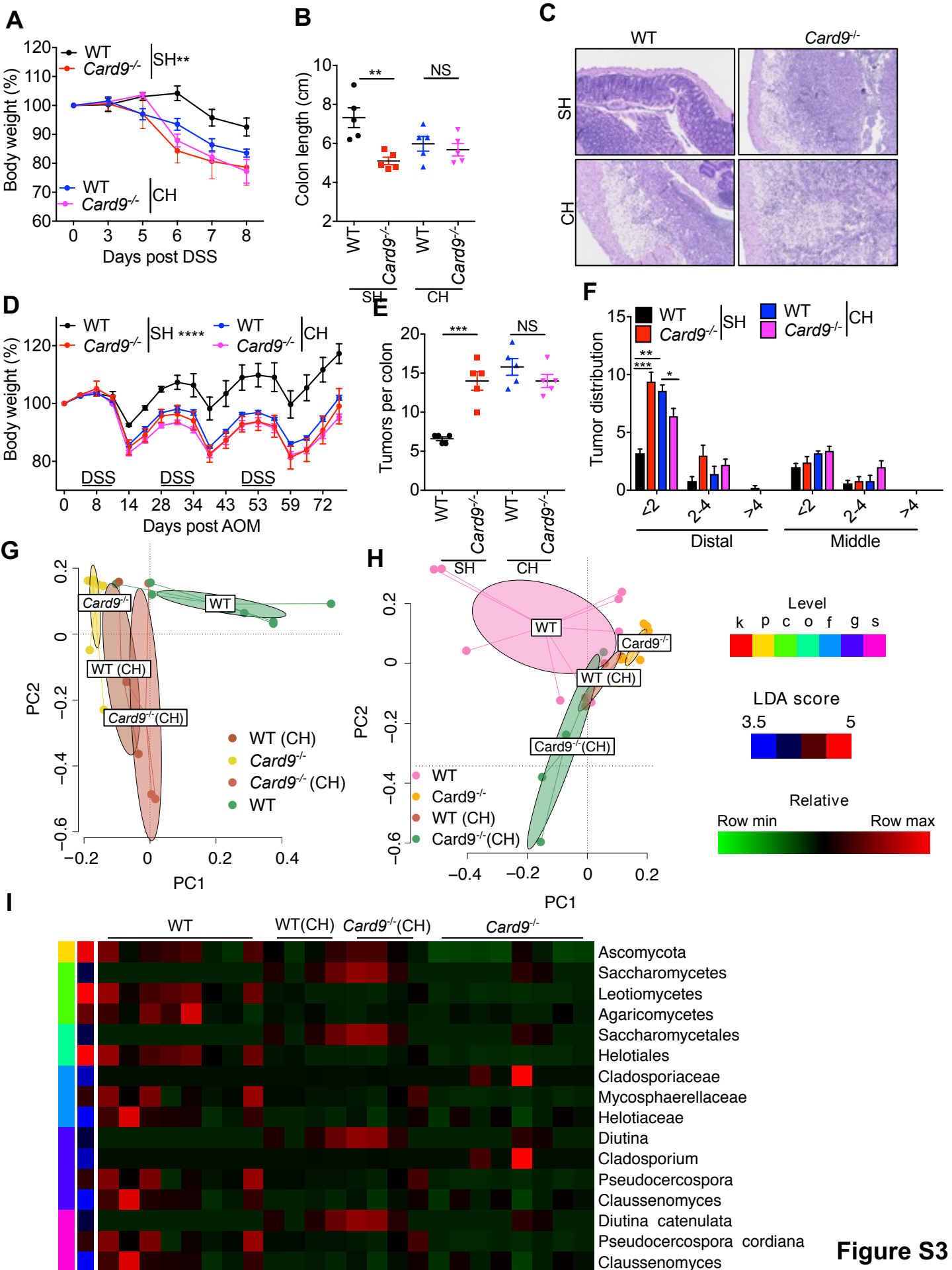
A
Body weight (%)
WT
Card9-/-
SH**
CH
Days post DSS
B
Colon length (cm)
**
NS
SH
CH
C
WT
Card9-/-
SH
CH
D
Body weight (%)
SH ****
CH
DSS
Days post AOM
E
Tumors per colon
***
NS
F
Tumor distribution
SH
CH
Distal
Middle
G
PC2
PC1
WT (CH)
Card9-/-
Card9-/- (CH)
WT
H
PC2
PC1
Level
k p c o f g s
LDA score
3.5
5
Relative
Row min
Row max
I
WT
WT(CH)
Card9-/-(CH)
Card9-/-
Ascomycota
Saccharomycetes
Leotiomycetes
Agaricomycetes
Saccharomycetales
Helotiales
Cladosporiaceae
Mycosphaerellaceae
Helotiaceae
Diutina
Cladosporium
Pseudocercospora
Claussenomyces
Diutina catenulata
Pseudocercospora cordiana
Claussenomyces

Figure S3


WT
WT(CH)
Card9-/-(CH)
Card9-/-
k–Bacteria.p–Bacteroidetes
k–Bacteria.p–Tenericutes
k–Bacteria.p–TM7
k–Bacteria.p–Verrucomicrobia
k–Bacteria.p–Deferribacteres
k–Bacteria.p–Bacteroidetes.c–Bacteroidia
k–Bacteria.p–Tenericutes.c–Mollicutes
k–Bacteria.p–TM7.c–TM7_3
k–Bacteria.p–Actinobacteria.c–Coriobacteriia
k–Bacteria.p–Cyanobacteria.c–Oscillatoriophycideae
k–Bacteria.p–Verrucomicrobia.c–Opitutae
k–Bacteria.p–Deferribacteres.c–Deferribacteres
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales
k–Bacteria.p–TM7.c–TM7_3.o–CW040
k–Bacteria.p–Actinobacteria.c–Coriobacteriia.o–Coriobacteriales
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rhodospirillales
k–Bacteria.p–Cyanobacteria.c–Oscillatoriophycideae.o–Oscillatoriales
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales.f–Anaeroplasmataceae
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Bacteroidaceae
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales.f–Mycoplasmataceae
k–Bacteria.p–TM7.c–TM7_3.o–CW040.f–F16
k–Bacteria.p–Actinobacteria.c–Coriobacteriia.o–Coriobacteriales.f–Coriobacteriaceae
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Odoribacteraceae_
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptostreptococcaceae
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rhodospirillales.f–Acetobacteraceae
k–Bacteria.p–Cyanobacteria.c–Oscillatoriophycideae.o–Oscillatoriales.f–Phormidiaceae
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64.f–
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales.f–Deferribacteraceae
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Paraprevotellaceae_
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales.f–Enterobacteriaceae
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32.f–
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–.f–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptococcaceae
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales.f–Anaeroplasmataceae.g–Anaeroplasma
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Bacteroidaceae.g–Bacteroides
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–Candidatus_Arthromitus
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales.f–Mycoplasmataceae.g–Ureaplasma
k–Bacteria.p–Actinobacteria.c–Coriobacteriia.o–Coriobacteriales.f–Coriobacteriaceae.g–Adlercreutzia
k–Bacteria.p–TM7.c–TM7_3.o–CW040.f–F16.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Odoribacteraceae_.g–Odoribacter
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–Clostridium
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–AF12
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptostreptococcaceae.g–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–Ruminococcus
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–Oscillospira
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rhodospirillales.f–Acetobacteraceae.g–Acidiphilium
k–Bacteria.p–Proteobacteria.c–Epsilonproteobacteria.o–Campylobacterales.f–Helicobacteraceae.g–
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64.f–.g–
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales.f–Deferribacteraceae.g–Mucispirillum
k–Bacteria.p–Proteobacteria.c–Epsilonproteobacteria.o–Campylobacterales.f–Helicobacteraceae.g–Flexispira
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Paraprevotellaceae_.g–_Prevotella_
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales.f–Enterobacteriaceae.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Prevotellaceae.g–
k–Bacteria.p–Firmicutes.c–Erysipelotrichi.o–Erysipelotrichales.f–Erysipelotrichaceae.g–PSB_M_3
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32.f–.g–
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–.f–.g–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptococcaceae.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Paraprevotellaceae_.g–Paraprevotella
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales.f–Anaeroplasmataceae.g–Anaeroplasma.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Bacteroidaceae.g–Bacteroides.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–Candidatus_Arthromitus.s–
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales.f–Mycoplasmataceae.g–Ureaplasma.s–
k–Bacteria.p–Actinobacteria.c–Coriobacteriia.o–Coriobacteriales.f–Coriobacteriaceae.g–Adlercreutzia.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Bacteroidaceae.g–Bacteroides.s–uniformis
k–Bacteria.p–TM7.c–TM7_3.o–CW040.f–F16.g–.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Bacteroidaceae.g–Bacteroides.s–acidifaciens
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Odoribacteraceae_.g–Odoribacter.s–
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Lactobacillaceae.g–Lactobacillus.s–reuteri
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–Clostridium.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–AF12.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptostreptococcaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–Ruminococcus.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–Oscillospira.s–
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rhodospirillales.f–Acetobacteraceae.g–Acidiphilium.s–
k–Bacteria.p–Proteobacteria.c–Epsilonproteobacteria.o–Campylobacterales.f–Helicobacteraceae.g–.s–
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64.f–.g–.s–
k–Bacteria.p–Proteobacteria.c–Epsilonproteobacteria.o–Campylobacterales.f–Helicobacteraceae.g–Flexispira.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Paraprevotellaceae_.g–_Prevotella_.s–
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales.f–Deferribacteraceae.g–Mucispirillum.s–schaedleri
k–Bacteria.p–Proteobacteria.c–Epsilonproteobacteria.o–Campylobacterales.f–Helicobacteraceae.g–Helicobacter.s–apodemus
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales.f–Enterobacteriaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–Ruminococcus.s–flavefaciens
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Prevotellaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Erysipelotrichi.o–Erysipelotrichales.f–Erysipelotrichaceae.g–PSB_M_3.s–
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32.f–.g–.s–
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–.f–.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptococcaceae.g–.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Paraprevotellaceae_.g–Paraprevotella.s–
4
2
0
−2
−4
Level
k
p
c
o
f
g
s
LDA.score
5
2.5

Figure S4

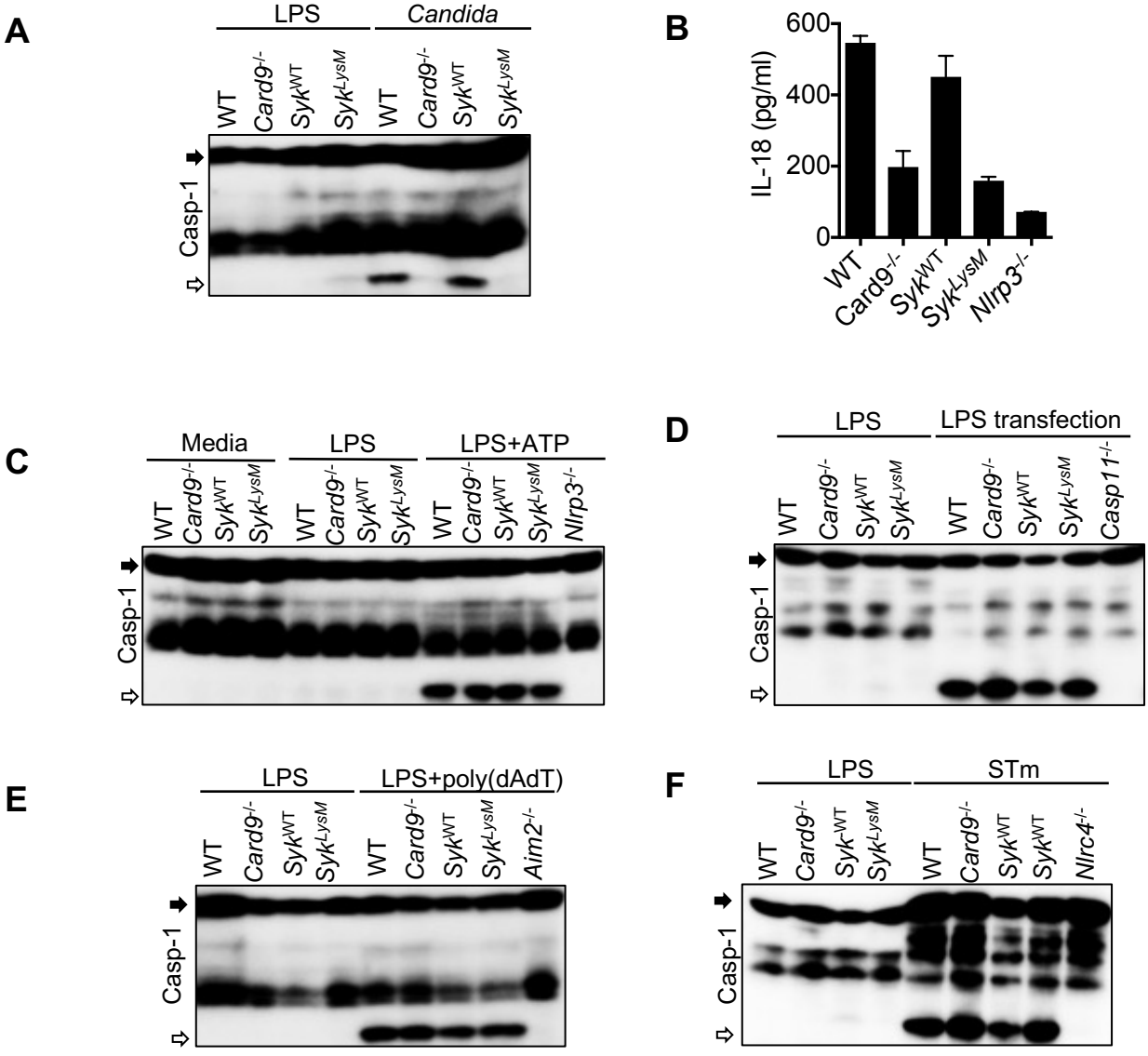
A
LPS
Candida
WT
Card9-/-
SykWT
SykLysM
WT
Card9-/-
SykWT
SykLysM
Casp-1
B
IL-18 (pg/ml)
600
400
200
0
WT
Card9-/-
SykWT
SykLysM
Nlrp3-/-
C
Media
LPS
LPS+ATP
WT
Card9-/-
SykWT
SykLysM
WT
Card9-/-
SykWT
SykLysM
WT
Card9-/-
SykWT
SykLysM
Nlrp3-/-
Casp-1
D
LPS
LPS transfection
WT
Card9-/-
SykWT
SykLysM
WT
Card9-/-
SykWT
SykLysM
Casp11-/-
Casp-1
E
LPS
LPS+poly(dAdT)
WT
Card9-/-
SykWT
SykLysM
WT
Card9-/-
SykWT
SykLysM
Aim2-/-
Casp-1
F
LPS
STm
WT
Card9-/-
SykWT
SykLysM
WT
Card9-/-
SykWT
SykWT
Nlrc4-/-
Casp-1

Figure S5

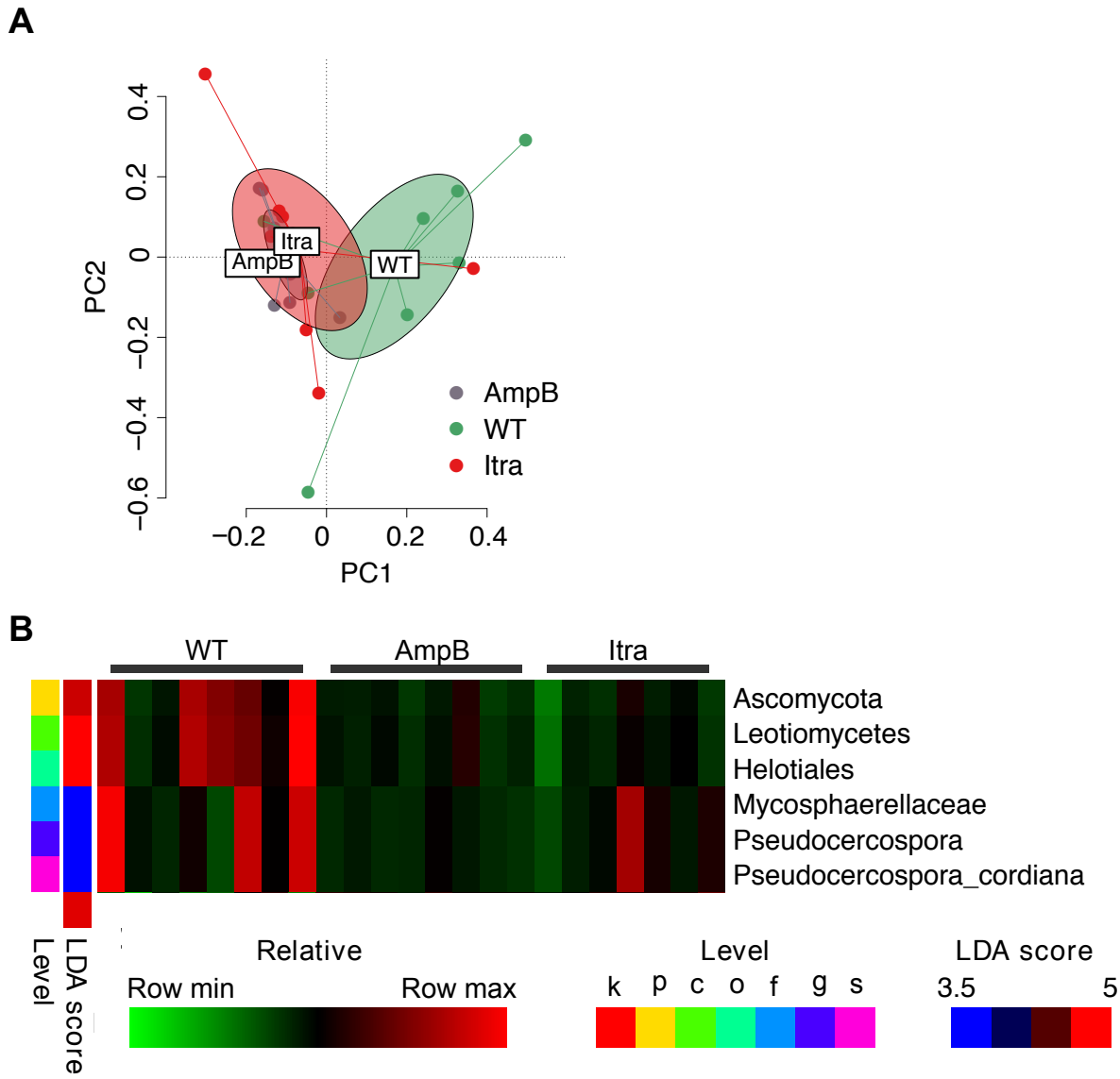
A
PC2
PC1
Itra
AmpB
WT
AmpB
WT
Itra
B
WT
AmpB
Itra
Ascomycota
Leotiomycetes
Helotiales
Mycosphaerellaceae
Pseudocercospora
Pseudocercospora_cordiana
Level
LDA score
Relative
Row min
Row max
Level
k p c o f g s
LDA score
3.5
5
C
PC2
PC1
AmpB
WT
Itra
WT
AmpB
Itra

Figure S6

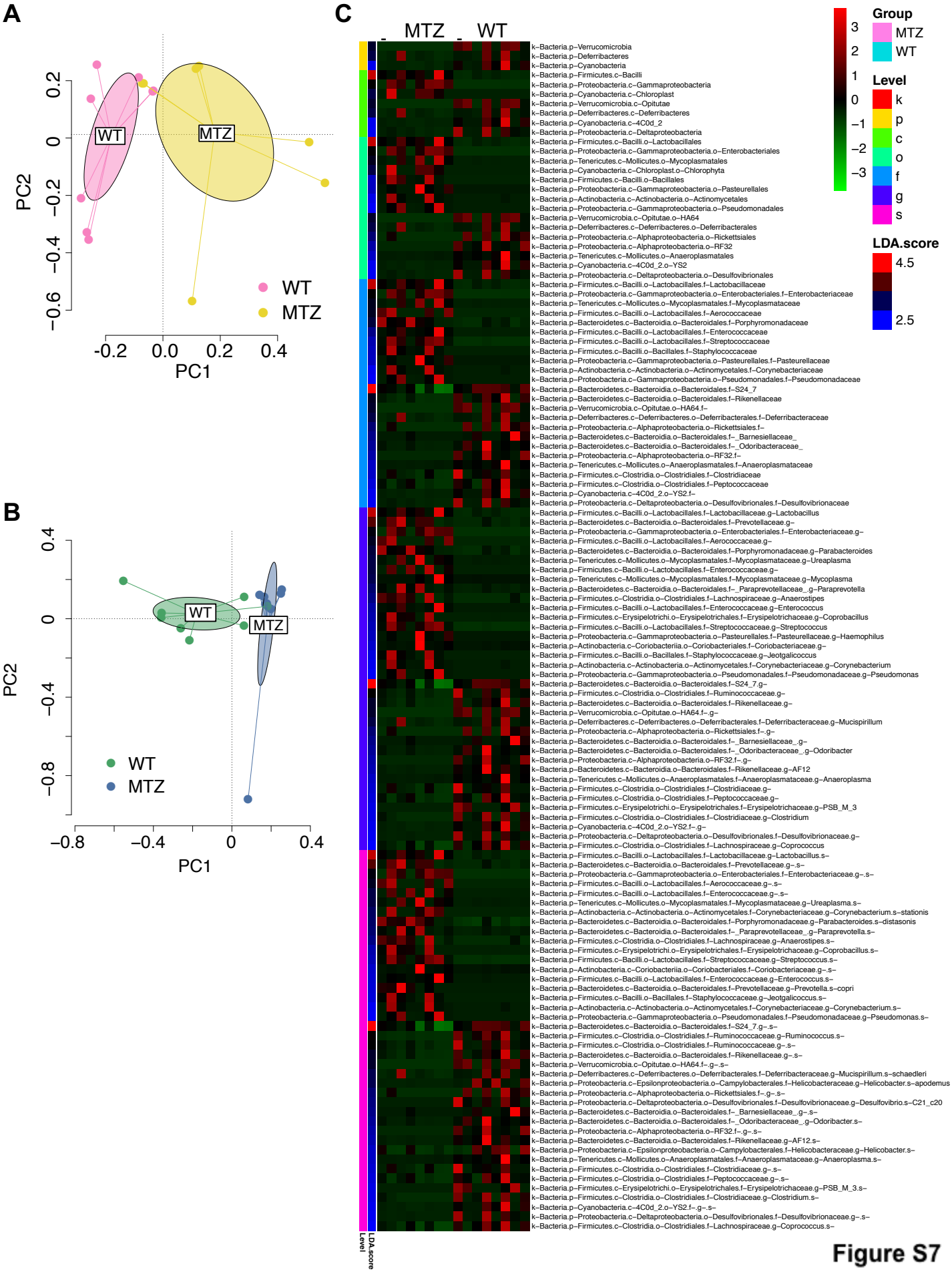
A
PC2
PC1
WT
MTZ
B
C
MTZ
WT
Group
MTZ
WT
Level
k
p
c
o
f
g
s
LDA.score
4.5
2.5
k–Bacteria.p–Verrucomicrobia
k–Bacteria.p–Deferribacteres
k–Bacteria.p–Cyanobacteria
k–Bacteria.p–Firmicutes.c–Bacilli
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria
k–Bacteria.p–Cyanobacteria.c–Chloroplast
k–Bacteria.p–Verrucomicrobia.c–Opitutae
k–Bacteria.p–Deferribacteres.c–Deferribacteres
k–Bacteria.p–Cyanobacteria.c–4C0d_2
k–Bacteria.p–Proteobacteria.c–Deltaproteobacteria
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales
k–Bacteria.p–Cyanobacteria.c–Chloroplast.o–Chlorophyta
k–Bacteria.p–Firmicutes.c–Bacilli.o–Bacillales
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Pasteurellales
k–Bacteria.p–Actinobacteria.c–Actinobacteria.o–Actinomycetales
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Pseudomonadales
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rickettsiales
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales
k–Bacteria.p–Cyanobacteria.c–4C0d_2.o–YS2
k–Bacteria.p–Proteobacteria.c–Deltaproteobacteria.o–Desulfovibrionales
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Lactobacillaceae
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales.f–Enterobacteriaceae
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales.f–Mycoplasmataceae
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Aerococcaceae
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Porphyromonadaceae
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Enterococcaceae
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Streptococcaceae
k–Bacteria.p–Firmicutes.c–Bacilli.o–Bacillales.f–Staphylococcaceae
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Pasteurellales.f–Pasteurellaceae
k–Bacteria.p–Actinobacteria.c–Actinobacteria.o–Actinomycetales.f–Corynebacteriaceae
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Pseudomonadales.f–Pseudomonadaceae
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–S24_7
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64.f–
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales.f–Deferribacteraceae
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rickettsiales.f–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Barnesiellaceae_
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Odoribacteraceae_
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32.f–
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales.f–Anaeroplasmataceae
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptococcaceae
k–Bacteria.p–Cyanobacteria.c–4C0d_2.o–YS2.f–
k–Bacteria.p–Proteobacteria.c–Deltaproteobacteria.o–Desulfovibrionales.f–Desulfovibrionaceae
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Lactobacillaceae.g–Lactobacillus
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Prevotellaceae.g–
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales.f–Enterobacteriaceae.g–
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Aerococcaceae.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Porphyromonadaceae.g–Parabacteroides
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales.f–Mycoplasmataceae.g–Ureaplasma
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Enterococcaceae.g–
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales.f–Mycoplasmataceae.g–Mycoplasma
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Paraprevotellaceae_.g–Paraprevotella
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Lachnospiraceae.g–Anaerostipes
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Enterococcaceae.g–Enterococcus
k–Bacteria.p–Firmicutes.c–Erysipelotrichi.o–Erysipelotrichales.f–Erysipelotrichaceae.g–Coprobacillus
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Streptococcaceae.g–Streptococcus
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Pasteurellales.f–Pasteurellaceae.g–Haemophilus
k–Bacteria.p–Actinobacteria.c–Coriobacteriia.o–Coriobacteriales.f–Coriobacteriaceae.g–
k–Bacteria.p–Firmicutes.c–Bacilli.o–Bacillales.f–Staphylococcaceae.g–Jeotgalicoccus
k–Bacteria.p–Actinobacteria.c–Actinobacteria.o–Actinomycetales.f–Corynebacteriaceae.g–Corynebacterium
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Pseudomonadales.f–Pseudomonadaceae.g–Pseudomonas
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–S24_7.g–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64.f–.g–
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales.f–Deferribacteraceae.g–Mucispirillum
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rickettsiales.f–.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Barnesiellaceae_.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Odoribacteraceae_.g–Odoribacter
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32.f–.g–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–AF12
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales.f–Anaeroplasmataceae.g–Anaeroplasma
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptococcaceae.g–
k–Bacteria.p–Firmicutes.c–Erysipelotrichi.o–Erysipelotrichales.f–Erysipelotrichaceae.g–PSB_M_3
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–Clostridium
k–Bacteria.p–Cyanobacteria.c–4C0d_2.o–YS2.f–.g–
k–Bacteria.p–Proteobacteria.c–Deltaproteobacteria.o–Desulfovibrionales.f–Desulfovibrionaceae.g–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Lachnospiraceae.g–Coprococcus
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Lactobacillaceae.g–Lactobacillus.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Prevotellaceae.g–.s–
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Enterobacteriales.f–Enterobacteriaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Aerococcaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Enterococcaceae.g–.s–
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Mycoplasmatales.f–Mycoplasmataceae.g–Ureaplasma.s–
k–Bacteria.p–Actinobacteria.c–Actinobacteria.o–Actinomycetales.f–Corynebacteriaceae.g–Corynebacterium.s–stationis
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Porphyromonadaceae.g–Parabacteroides.s–distasonis
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Paraprevotellaceae_.g–Paraprevotella.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Lachnospiraceae.g–Anaerostipes.s–
k–Bacteria.p–Firmicutes.c–Erysipelotrichi.o–Erysipelotrichales.f–Erysipelotrichaceae.g–Coprobacillus.s–
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Streptococcaceae.g–Streptococcus.s–
k–Bacteria.p–Actinobacteria.c–Coriobacteriia.o–Coriobacteriales.f–Coriobacteriaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Bacilli.o–Lactobacillales.f–Enterococcaceae.g–Enterococcus.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Prevotellaceae.g–Prevotella.s–copri
k–Bacteria.p–Firmicutes.c–Bacilli.o–Bacillales.f–Staphylococcaceae.g–Jeotgalicoccus.s–
k–Bacteria.p–Actinobacteria.c–Actinobacteria.o–Actinomycetales.f–Corynebacteriaceae.g–Corynebacterium.s–
k–Bacteria.p–Proteobacteria.c–Gammaproteobacteria.o–Pseudomonadales.f–Pseudomonadaceae.g–Pseudomonas.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–S24_7.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–Ruminococcus.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Ruminococcaceae.g–.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–.s–
k–Bacteria.p–Verrucomicrobia.c–Opitutae.o–HA64.f–.g–.s–
k–Bacteria.p–Deferribacteres.c–Deferribacteres.o–Deferribacterales.f–Deferribacteraceae.g–Mucispirillum.s–schaedleri
k–Bacteria.p–Proteobacteria.c–Epsilonproteobacteria.o–Campylobacterales.f–Helicobacteraceae.g–Helicobacter.s–apodemus
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–Rickettsiales.f–.g–.s–
k–Bacteria.p–Proteobacteria.c–Deltaproteobacteria.o–Desulfovibrionales.f–Desulfovibrionaceae.g–Desulfovibrio.s–C21_c20
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Barnesiellaceae_.g–.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–_Odoribacteraceae_.g–Odoribacter.s–
k–Bacteria.p–Proteobacteria.c–Alphaproteobacteria.o–RF32.f–.g–.s–
k–Bacteria.p–Bacteroidetes.c–Bacteroidia.o–Bacteroidales.f–Rikenellaceae.g–AF12.s–
k–Bacteria.p–Proteobacteria.c–Epsilonproteobacteria.o–Campylobacterales.f–Helicobacteraceae.g–Helicobacter.s–
k–Bacteria.p–Tenericutes.c–Mollicutes.o–Anaeroplasmatales.f–Anaeroplasmataceae.g–Anaeroplasma.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Peptococcaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Erysipelotrichi.o–Erysipelotrichales.f–Erysipelotrichaceae.g–PSB_M_3.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Clostridiaceae.g–Clostridium.s–
k–Bacteria.p–Cyanobacteria.c–4C0d_2.o–YS2.f–.g–.s–
k–Bacteria.p–Proteobacteria.c–Deltaproteobacteria.o–Desulfovibrionales.f–Desulfovibrionaceae.g–.s–
k–Bacteria.p–Firmicutes.c–Clostridia.o–Clostridiales.f–Lachnospiraceae.g–Coprococcus.s–
Level
LDA.score

Figure S7