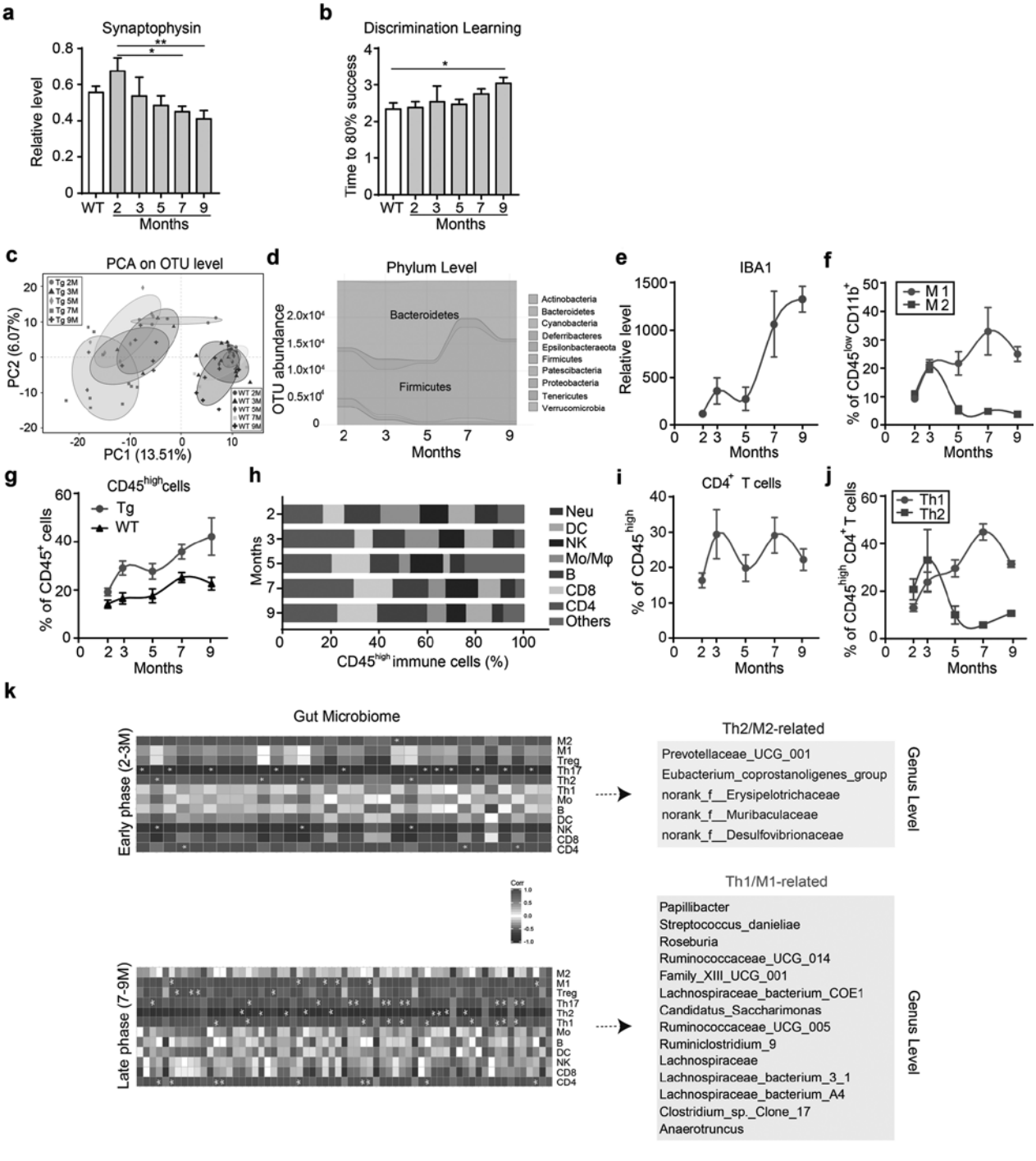

a
Synaptophysin
Relative level
Months
b
Discrimination Learning
Time to 80% success
Months
c
PCA on OTU level
PC1 (13.51%)
PC2 (6.07%)
d
Phylum Level
OTU abundance
Bacteroidetes
Firmicutes
Actinobacteria
Bacteroidetes
Cyanobacteria
Deferribacteres
Epsilonbacteraeota
Firmicutes
Patescibacteria
Proteobacteria
Tenericutes
Verrucomicrobia
e
IBA1
Relative level
f
% of CD45low CD11b+
M1
M2
g
CD45highcells
% of CD45+ cells
Tg
WT
h
Neu
DC
NK
Mo/Mφ
B
CD8
CD4
Others
CD45high immune cells (%)
i
CD4+ T cells
% of CD45high
j
% of CD45high CD4+ T cells
Th1
Th2
k
Gut Microbiome
Early phase (2-3M)
Late phase (7-9M)
M2
M1
Treg
Th17
Th2
Th1
Mo
B
DC
NK
CD8
CD4
Th2/M2-related
Prevotellaceae_UCG_001
Eubacterium_coprostanoligenes_group
norank_f__Erysipelotrichaceae
norank_f__Muribaculaceae
norank_f__Desulfovibrionaceae
Genus Level
Th1/M1-related
Papillibacter
Streptococcus_danieliae
Roseburia
Ruminococcaceae_UCG_014
Family_XIII_UCG_001
Lachnospiraceae_bacterium_COE1
Candidatus_Saccharimonas
Ruminococcaceae_UCG_005
Ruminiclostridium_9
Lachnospiraceae
Lachnospiraceae_bacterium_3_1
Lachnospiraceae_bacterium_A4
Clostridium_sp._Clone_17
Anaerotruncus
Genus Level

Fig. 1

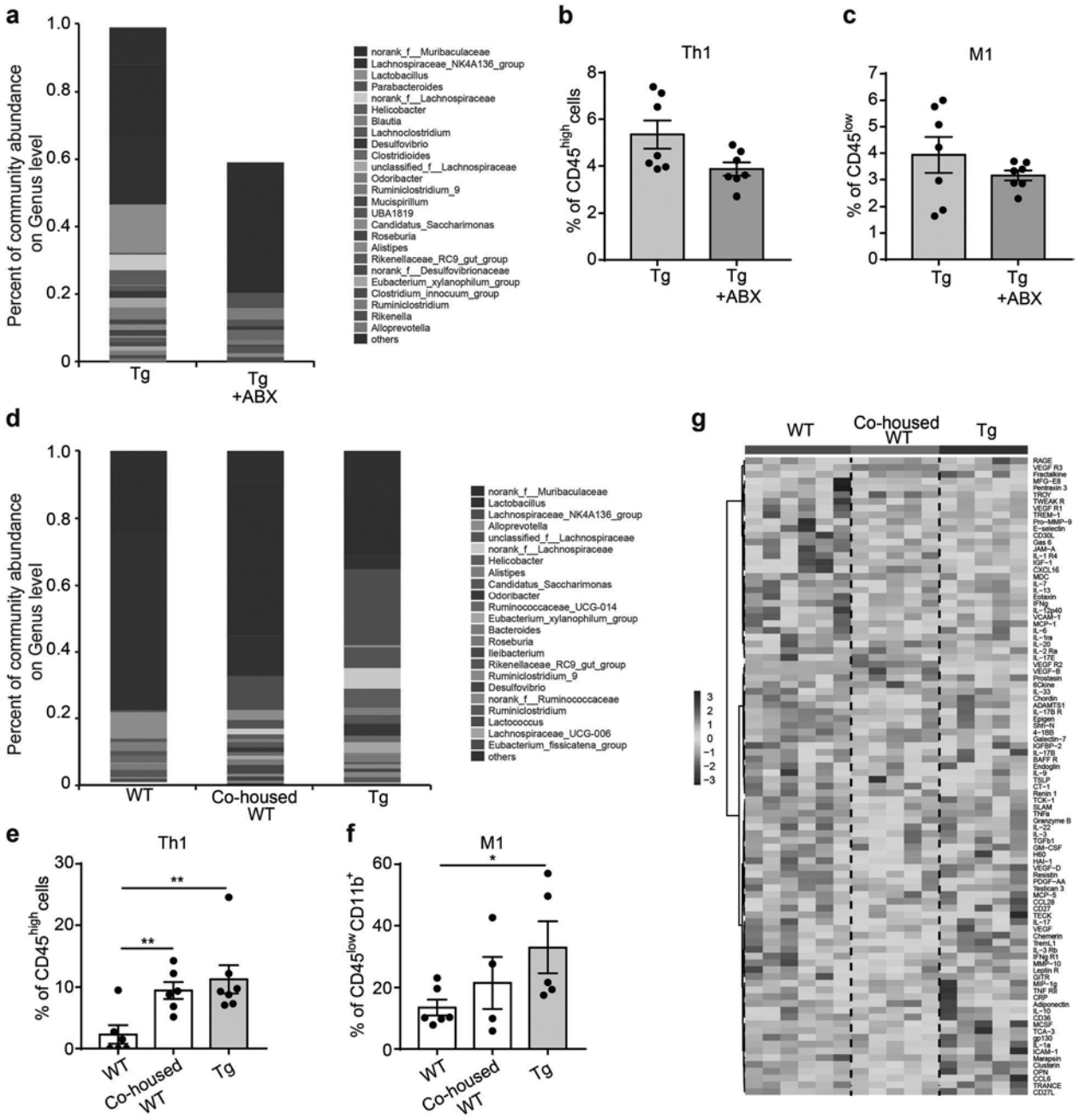

a
Percent of community abundance on Genus level
1.0
0.8
0.6
0.4
0.2
0
Tg
Tg +ABX
norank_f__Muribaculaceae
Lachnospiraceae_NK4A136_group
Lactobacillus
Parabacteroides
norank_f__Lachnospiraceae
Helicobacter
Blautia
Lachnoclostridium
Desulfovibrio
Clostridioides
unclassified_f__Lachnospiraceae
Odoribacter
Ruminiclostridium_9
Mucispirillum
UBA1819
Candidatus_Saccharimonas
Roseburia
Alistipes
Rikenellaceae_RC9_gut_group
norank_f__Desulfovibrionaceae
Eubacterium_xylanophilum_group
Clostridium_innocuum_group
Ruminiclostridium
Rikenella
Alloprevotella
others
b
Th1
% of CD45high cells
8
6
4
2
0
Tg
Tg +ABX
c
M1
% of CD45low
7
6
5
4
3
2
1
0
Tg
Tg +ABX
d
Percent of community abundance on Genus level
1.0
0.8
0.6
0.4
0.2
0
WT
Co-housed WT
Tg
norank_f__Muribaculaceae
Lactobacillus
Lachnospiraceae_NK4A136_group
Alloprevotella
unclassified_f__Lachnospiraceae
norank_f__Lachnospiraceae
Helicobacter
Alistipes
Candidatus_Saccharimonas
Odoribacter
Ruminococcaceae_UCG-014
Eubacterium_xylanophilum_group
Bacteroides
Roseburia
Ileibacterium
Rikenellaceae_RC9_gut_group
Ruminiclostridium_9
Desulfovibrio
norank_f__Ruminococcaceae
Ruminiclostridium
Lactococcus
Lachnospiraceae_UCG-006
Eubacterium_fissicatena_group
others
e
Th1
% of CD45high cells
30
20
10
0
**
**
WT
Co-housed WT
Tg
f
M1
% of CD45low CD11b+
60
40
20
0
*
WT
Co-housed WT
Tg
g
WT
Co-housed WT
Tg
3
2
1
0
−1
−2
−3
RAGE
VEGF R3
Fractalkine
MFG-E8
Pentraxin 3
TROY
TWEAK R
VEGF R1
TREM-1
Pro-MMP-9
E-selectin
CD30L
Gas 6
JAM-A
IL-1 R4
IGF-1
CXCL16
MDC
IL-7
IL-13
Eotaxin
IFNg
IL-12p40
VCAM-1
MCP-1
IL-6
IL-1α
IL-20
IL-2 Ra
IL-17E
VEGF R2
VEGF-B
Prostasin
6Ckine
IL-33
Chordin
ADAMTS1
IL-17B R
Eppin
SHIP-1
4-1BB
Galectin-7
IGFBP-2
IL-17B
BAFF R
Endoglin
IL-9
TSLP
CT-1
Renin 1
TCK-1
SLAM
TNFa
Granzyme B
IL-22
IL-3
TGFb1
GM-CSF
H60
HAI-1
VEGF-D
Resistin
PDGF-AA
Testican 3
MCP-5
CCL28
CD27
TECK
IL-17
VEGF
Chemerin
TremL1
IL-3 Rb
IFNg R1
MMP-10
Leptin R
GITR
MIP-3β
TNF RII
CRP
Adiponectin
IL-10
CD36
MCSF
TCA-3
gp130
IL-1a
ICAM-1
Marapsin
Clusterin
OPN
CCL6
TRANCE
CD27L

Fig. 2

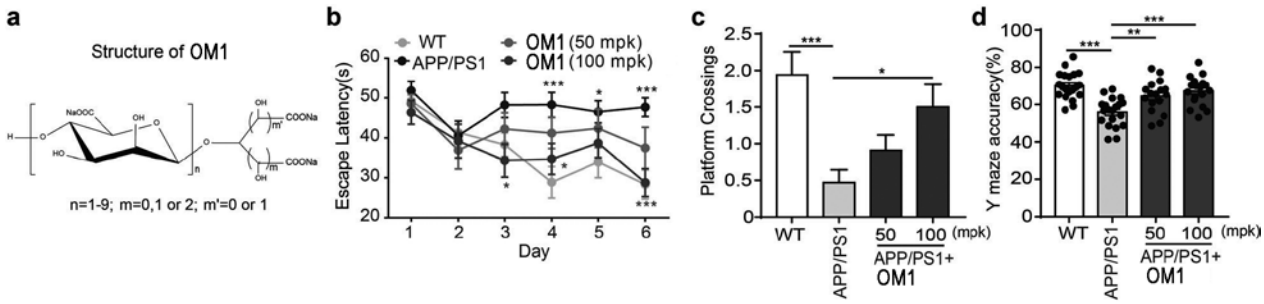

a
Structure of OM1
n=1-9; m=0,1 or 2; m'=0 or 1
b
WT
APP/PS1
OM1 (50 mpk)
OM1 (100 mpk)
Escape Latency(s)
Day
c
Platform Crossings
WT
APP/PS1
50
100
(mpk)
APP/PS1+
OM1
d
Y maze accuracy(%)
WT
APP/PS1
50
100
(mpk)
APP/PS1+
OM1

Fig. 3

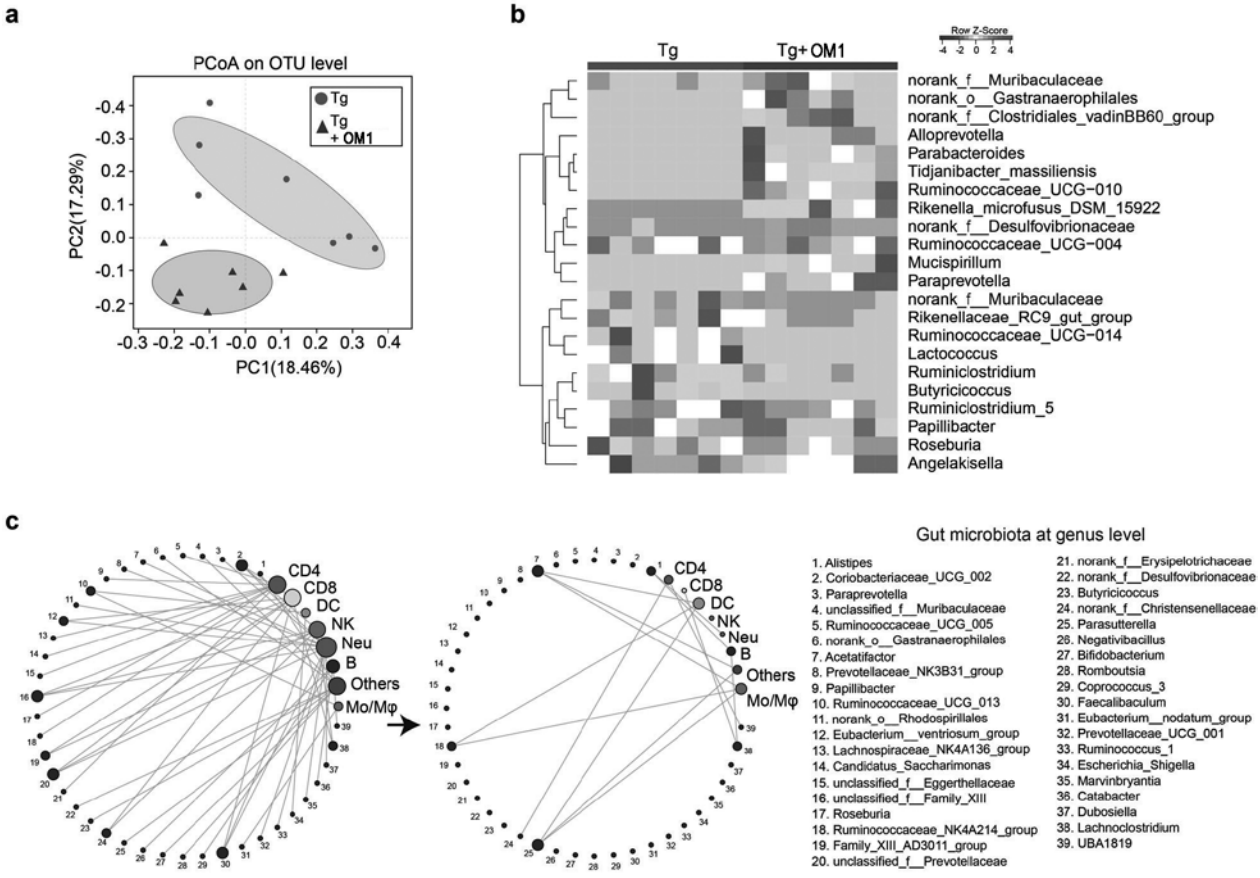

a
PCoA on OTU level
Tg
Tg + OM1
PC2(17.29%)
PC1(18.46%)
b
Row Z-Score
Tg
Tg+OM1
norank_f__Muribaculaceae
norank_o__Gastranaerophilales
norank_f__Clostridiales_vadinBB60_group
Alloprevotella
Parabacteroides
Tidjanibacter_massiliensis
Ruminococcaceae_UCG-010
Rikenella_microfusus_DSM_15922
norank_f__Desulfovibrionaceae
Ruminococcaceae_UCG-004
Mucispirillum
Paraprevotella
norank_f__Muribaculaceae
Rikenellaceae_RC9_gut_group
Ruminococcaceae_UCG-014
Lactococcus
Ruminiclostridium
Butyricicoccus
Ruminiclostridium_5
Papillibacter
Roseburia
Angelakisella
c
CD4
CD8
DC
NK
Neu
B
Others
Mo/Mφ
Gut microbiota at genus level
1. Alistipes
2. Coriobacteriaceae_UCG_002
3. Paraprevotella
4. unclassified_f__Muribaculaceae
5. Ruminococcaceae_UCG_005
6. norank_o__Gastranaerophilales
7. Acetatifactor
8. Prevotellaceae_NK3B31_group
9. Papillibacter
10. Ruminococcaceae_UCG_013
11. norank_o__Rhodospirillales
12. Eubacterium__ventriosum_group
13. Lachnospiraceae_NK4A136_group
14. Candidatus_Saccharimonas
15. unclassified_f__Eggerthellaceae
16. unclassified_f__Family_XIII
17. Roseburia
18. Ruminococcaceae_NK4A214_group
19. Family_XIII_AD3011_group
20. unclassified_f__Prevotellaceae
21. norank_f__Erysipelotrichaceae
22. norank_f__Desulfovibrionaceae
23. Butyricicoccus
24. norank_f__Christensenellaceae
25. Parasutterella
26. Negativibacillus
27. Bifidobacterium
28. Romboutsia
29. Coprococcus_3
30. Faecalibaculum
31. Eubacterium__nodatum_group
32. Prevotellaceae_UCG_001
33. Ruminococcus_1
34. Escherichia_Shigella
35. Marvinbryantia
36. Catabacter
37. Dubosiella
38. Lachnoclostridium
39. UBA1819

Fig. 4

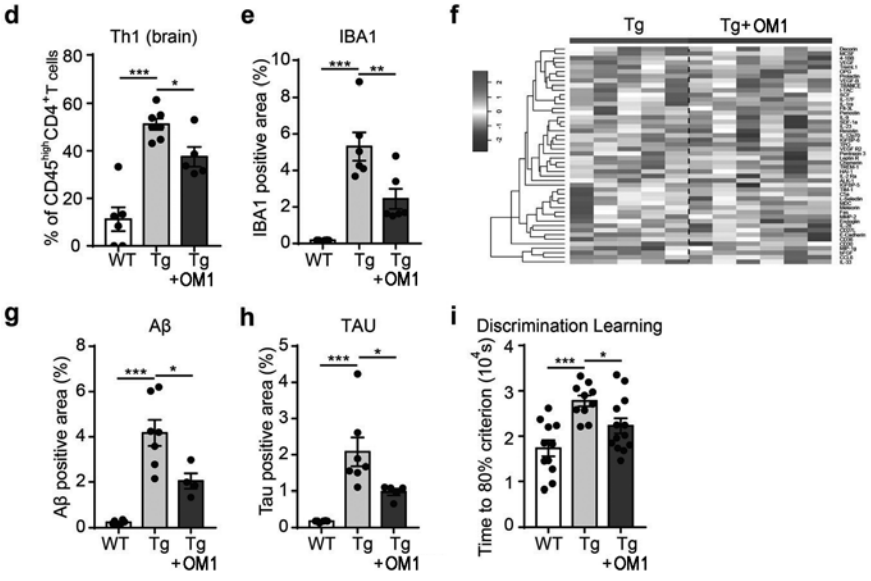


Fig. 4 (Continued)

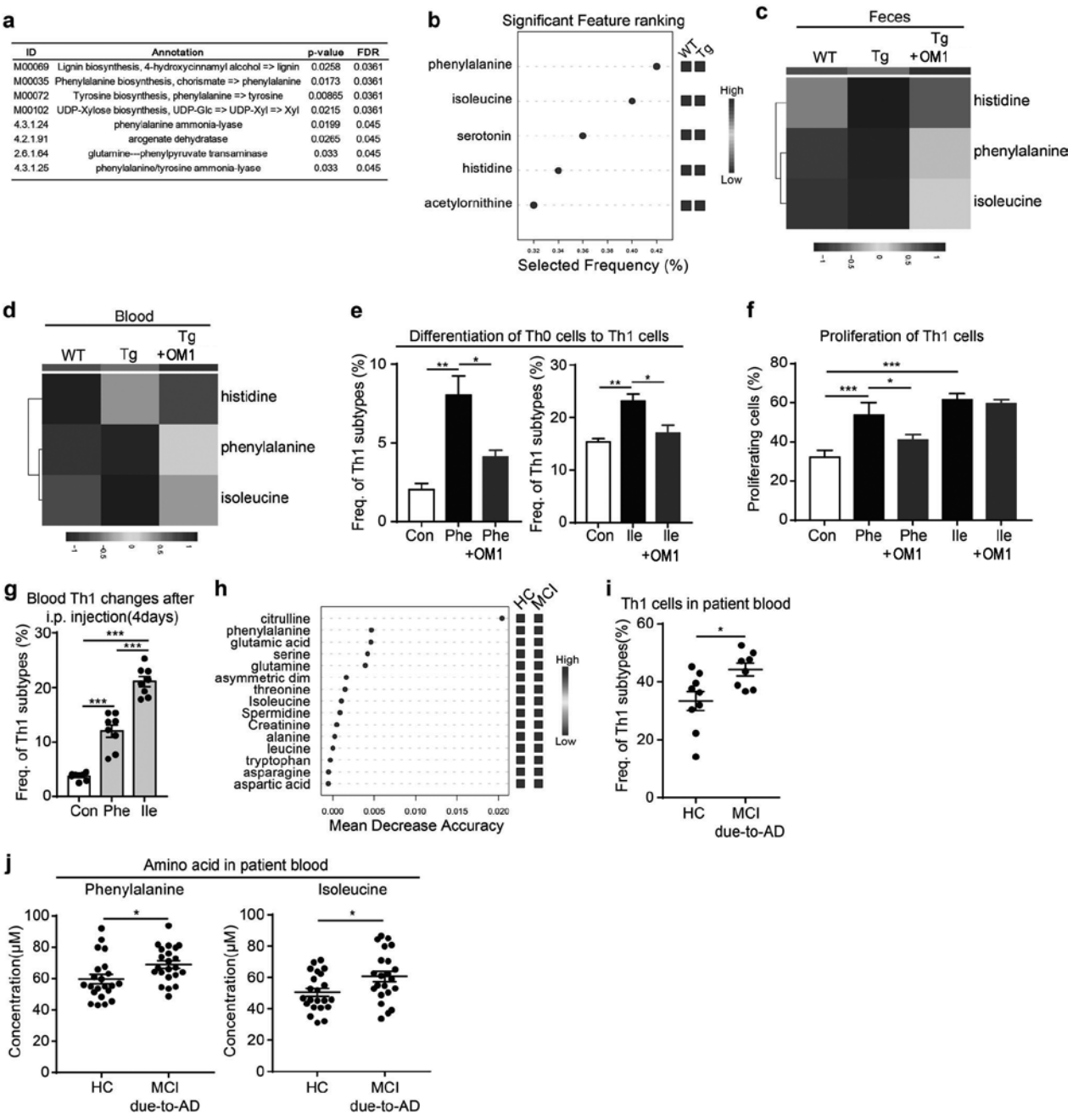

a
ID Annotation p-value FDR
M00069 Lignin biosynthesis, 4-hydroxycinnamyl alcohol => lignin 0.0258 0.0361
M00035 Phenylalanine biosynthesis, chorismate => phenylalanine 0.0173 0.0361
M00072 Tyrosine biosynthesis, phenylalanine => tyrosine 0.00865 0.0361
M00102 UDP-Xylose biosynthesis, UDP-Glc => UDP-Xyl => Xyl 0.0215 0.0361
4.3.1.24 phenylalanine ammonia-lyase 0.0199 0.045
4.2.1.91 arogenate dehydratase 0.0265 0.045
2.6.1.64 glutamine---phenylpyruvate transaminase 0.033 0.045
4.3.1.25 phenylalanine/tyrosine ammonia-lyase 0.033 0.045
b
Significant Feature ranking
phenylalanine
isoleucine
serotonin
histidine
acetylornithine
WT
Tg
High
Low
Selected Frequency (%)
c
Feces
WT
Tg
Tg +OM1
histidine
phenylalanine
isoleucine
d
Blood
WT
Tg
Tg +OM1
histidine
phenylalanine
isoleucine
e
Differentiation of Th0 cells to Th1 cells
Freq. of Th1 subtypes (%)
Con
Phe
Phe +OM1
Ile
Ile +OM1
f
Proliferation of Th1 cells
Proliferating cells (%)
Con
Phe
Phe +OM1
Ile
Ile +OM1
g
Blood Th1 changes after i.p. injection(4days)
Freq. of Th1 subtypes (%)
Con
Phe
Ile
h
HC
MCI
citrulline
phenylalanine
glutamic acid
serine
glutamine
asymmetric dim
threonine
Isoleucine
Spermidine
Creatinine
alanine
leucine
tryptophan
asparagine
aspartic acid
High
Low
Mean Decrease Accuracy
i
Th1 cells in patient blood
Freq. of Th1 subtypes(%)
HC
MCI due-to-AD
j
Amino acid in patient blood
Phenylalanine
Isoleucine
Concentration(μM)
HC
MCI due-to-AD

Fig. 5

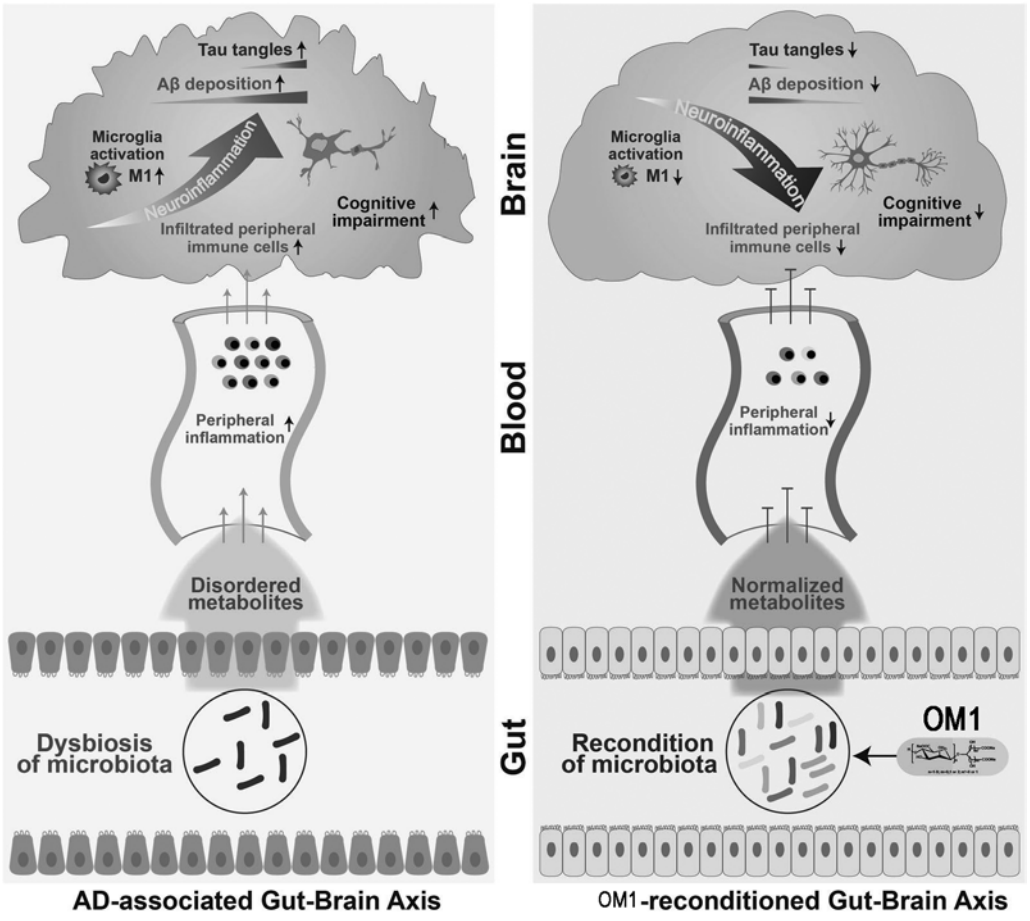

Tau tangles
Aβ deposition
Microglia activation
M1
Neuroinflammation
Infiltrated peripheral immune cells
Cognitive impairment
Peripheral inflammation
Disordered metabolites
Dysbiosis of microbiota
Brain
Blood
Gut
Tau tangles
Aβ deposition
Microglia activation
M1
Neuroinflammation
Infiltrated peripheral immune cells
Cognitive impairment
Peripheral inflammation
Normalized metabolites
Recondition of microbiota
OM1
AD-associated Gut-Brain Axis
OM1-reconditioned Gut-Brain Axis

Fig. 6

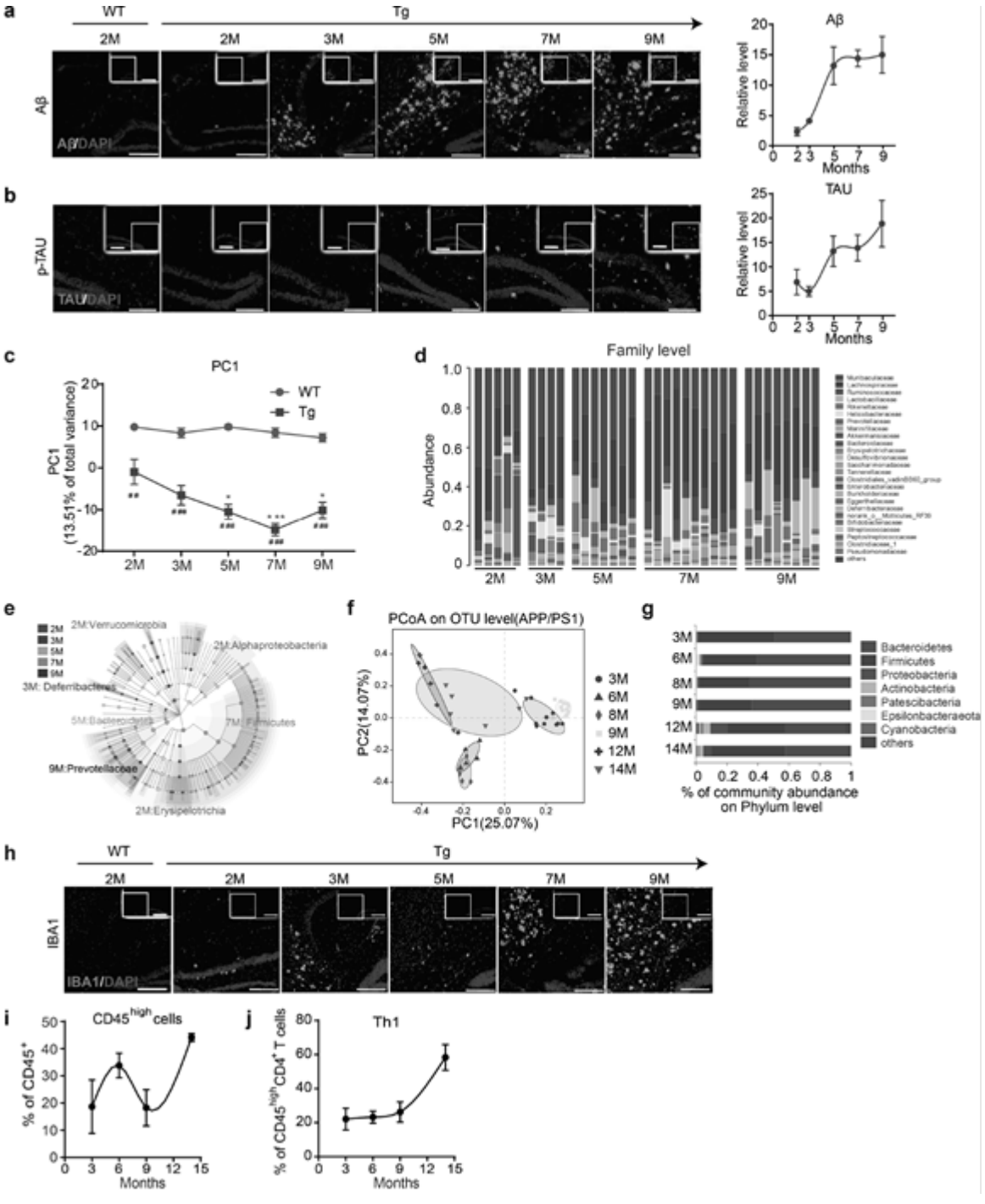

a
WT
Tg
2M
2M
3M
5M
7M
9M
Aβ
Aβ/DAPI
Aβ
Relative level
Months
b
p-TAU
TAU/DAPI
TAU
Relative level
Months
c
PC1
PC1 (13.51% of total variance)
WT
Tg
2M
3M
5M
7M
9M
d
Family level
Abundance
2M
3M
5M
7M
9M
e
2M:Verrucomicrobia
2M:Alphaproteobacteria
3M: Deferribacteres
7M: Firmicutes
9M:Prevotellaceae
2M:Erysipelotrichia
f
PCoA on OTU level(APP/PS1)
PC2(14.07%)
PC1(25.07%)
3M
6M
8M
9M
12M
14M
g
3M
6M
8M
9M
12M
14M
Bactercidetes
Firmicutes
Proteobacteria
Actinobacteria
Patescibacteria
Epsilonbacteraeota
Cyanobacteria
others
% of community abundance on Phylum level
h
WT
Tg
2M
2M
3M
5M
7M
9M
IBA1
IBA1/DAPI
i
CD45high cells
% of CD45+
Months
j
Th1
% of CD45high CD4+ T cells
Months

Fig. 7

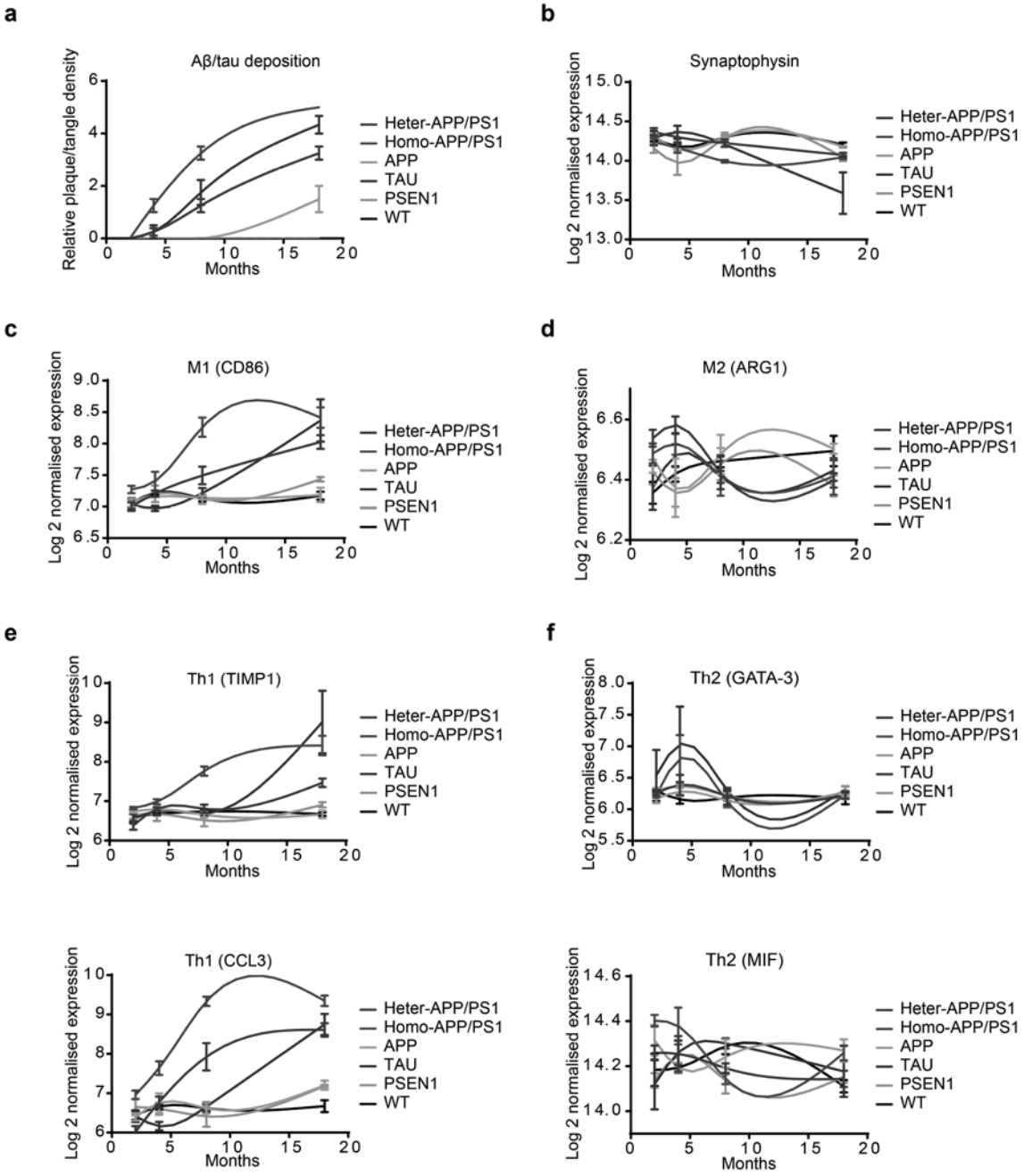

a
Aβ/tau deposition
Relative plaque/tangle density
Months
Heter-APP/PS1
Homo-APP/PS1
APP
TAU
PSEN1
WT
b
Synaptophysin
Log 2 normalised expression
c
M1 (CD86)
d
M2 (ARG1)
e
Th1 (TIMP1)
Th1 (CCL3)
f
Th2 (GATA-3)
Th2 (MIF)

Fig. 8

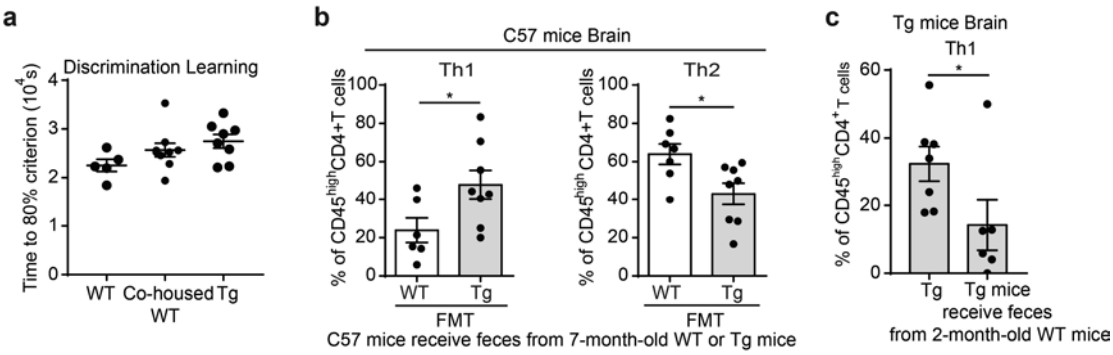

a
Discrimination Learning
Time to 80% criterion (10^4s)
WT
Co-housed WT
Tg
b
C57 mice Brain
Th1
Th2
% of CD45^{high}CD4+T cells
WT
Tg
FMT
C57 mice receive feces from 7-month-old WT or Tg mice
c
Tg mice Brain
Th1
% of CD45^{high}CD4$^+$T cells
Tg
Tg mice receive feces from 2-month-old WT mice

Fig. 9

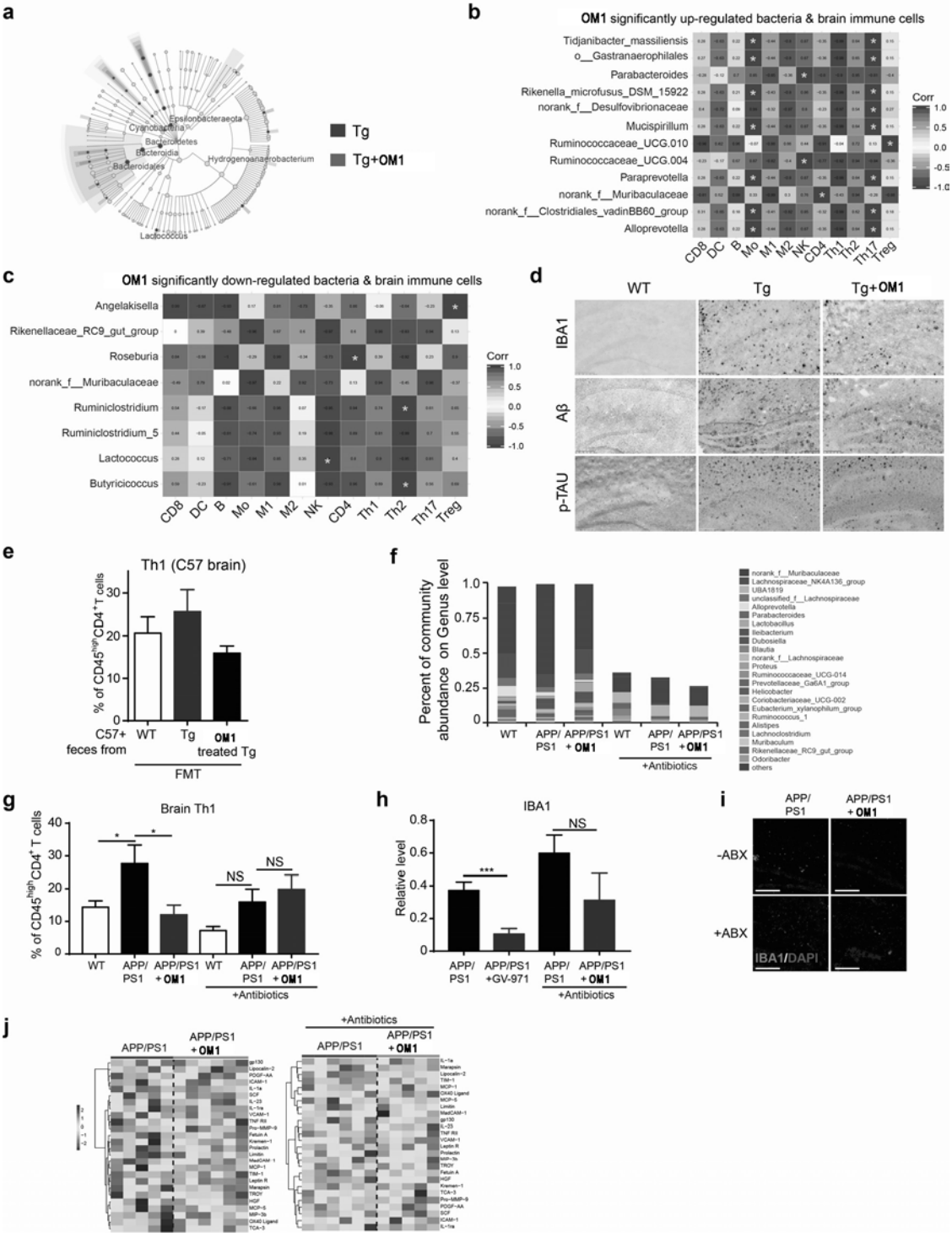

a
Tg
Tg+OM1
Epsilonbacteraeota
Cyanobacteria
Bacteroidetes
Bacteroidia
Bacteroidales
Hydrogenoanaerobacterium
Lactococcus
b
OM1 significantly up-regulated bacteria & brain immune cells
Tidjanibacter_massiliensis
o__Gastranaerophilales
Parabacteroides
Rikenella_microfusus_DSM_15922
norank_f__Desulfovibrionaceae
Mucispirillum
Ruminococcaceae_UCG.010
Ruminococcaceae_UCG.004
Paraprevotella
norank_f__Muribaculaceae
norank_f__Clostridiales_vadinBB60_group
Alloprevotella
CD8 DC B Mo M1 M2 NK CD4 Th1 Th2 Th17 Treg
Corr
c
OM1 significantly down-regulated bacteria & brain immune cells
Angelakisella
Rikenellaceae_RC9_gut_group
Roseburia
norank_f__Muribaculaceae
Ruminiclostridium
Ruminiclostridium_5
Lactococcus
Butyricicoccus
CD8 DC B Mo M1 M2 NK CD4 Th1 Th2 Th17 Treg
Corr
d
WT
Tg
Tg+OM1
IBA1
Aβ
p-TAU
e
Th1 (C57 brain)
% of CD45highCD4+T cells
C57+ feces from
WT
Tg
OM1 treated Tg
FMT
f
Percent of community abundance on Genus level
WT
APP/PS1
APP/PS1 + OM1
+Antibiotics
norank_f__Muribaculaceae
Lachnospiraceae_NK4A136_group
UBA1819
unclassified_f__Lachnospiraceae
Alloprevotella
Parabacteroides
Lactobacillus
Ileibacterium
Dubosiella
Blautia
norank_f__Lachnospiraceae
Proteus
Ruminococcaceae_UCG-014
Prevotellaceae_Ga6A1_group
Helicobacter
Coriobacteriaceae_UCG-002
Eubacterium_xylanophilum_group
Ruminococcus_1
Alistipes
Lachnoclostridium
Muribaculum
Rikenellaceae_RC9_gut_group
Odoribacter
others
g
Brain Th1
% of CD45highCD4+ T cells
NS
+Antibiotics
h
IBA1
Relative level
APP/PS1 +GV-971
+Antibiotics
i
APP/PS1
APP/PS1 + OM1
-ABX
+ABX
IBA1/DAPI
j
+Antibiotics
APP/PS1
APP/PS1 + OM1

Fig. 10

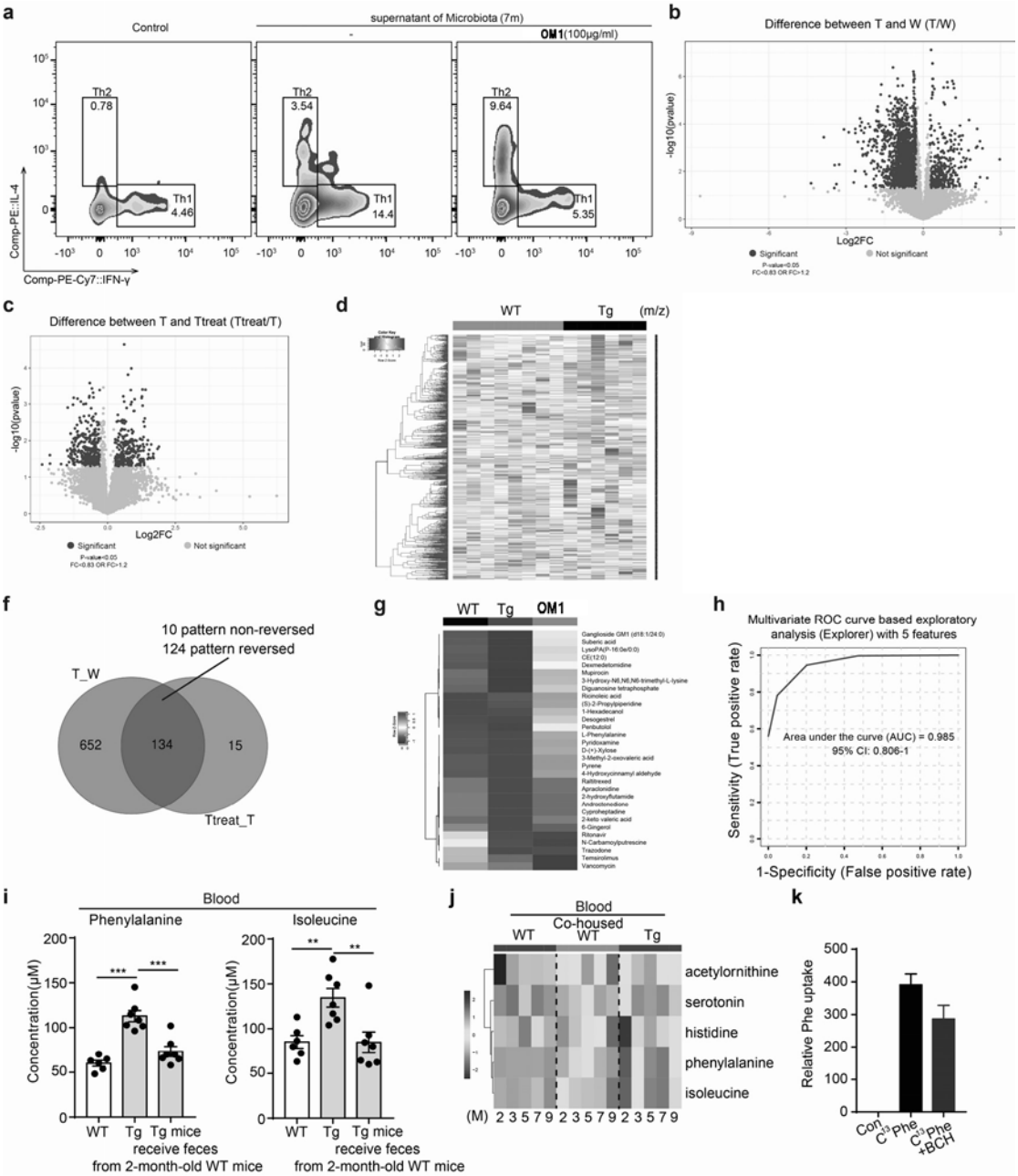

a
Control
supernatant of Microbiota (7m)
OM1(100μg/ml)
Th2
0.78
Th1
4.46
Th2
3.54
Th1
14.4
Th2
9.64
Th1
5.35
Comp-PE::IL-4
Comp-PE-Cy7::IFN-γ
b
Difference between T and W (T/W)
-log10(pvalue)
Log2FC
Significant
Not significant
c
Difference between T and Ttreat (Ttreat/T)
-log10(pvalue)
Log2FC
Significant
Not significant
d
WT
Tg
(m/z)
f
10 pattern non-reversed
124 pattern reversed
T_W
652
134
15
Ttreat_T
g
WT
Tg
OM1
h
Multivariate ROC curve based exploratory analysis (Explorer) with 5 features
Area under the curve (AUC) = 0.985
95% CI: 0.806-1
Sensitivity (True positive rate)
1-Specificity (False positive rate)
i
Blood
Phenylalanine
Isoleucine
Concentration(μM)
WT
Tg
Tg mice receive feces from 2-month-old WT mice
j
Blood
Co-housed
WT
WT
Tg
acetylornithine
serotonin
histidine
phenylalanine
isoleucine
(M) 2 3 5 7 9 2 3 5 7 9 2 3 5 7 9
k
Relative Phe uptake
Con
C3 Phe
C3 Phe +BCH

Fig. 11

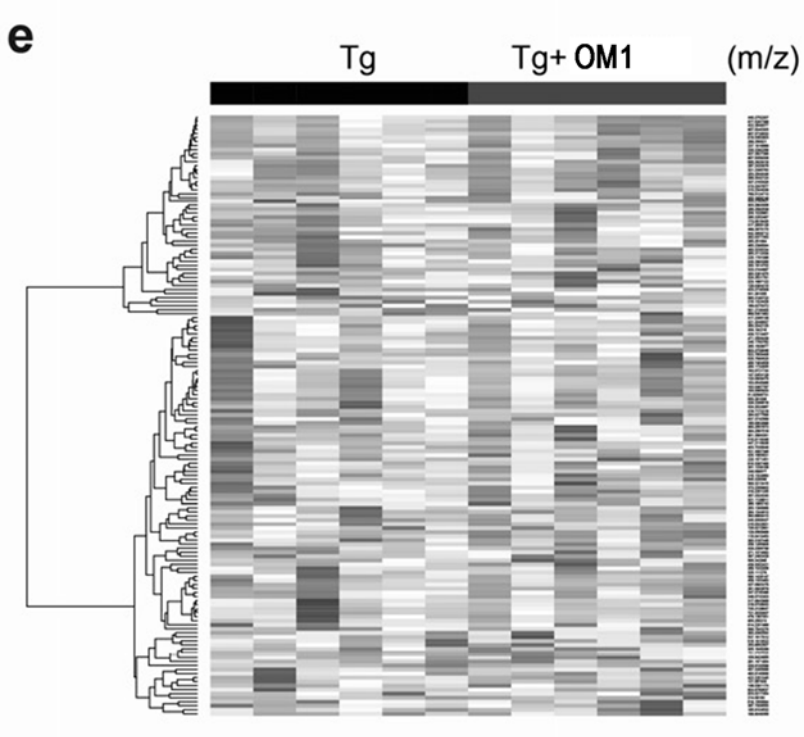


Fig. 11 (Continued)

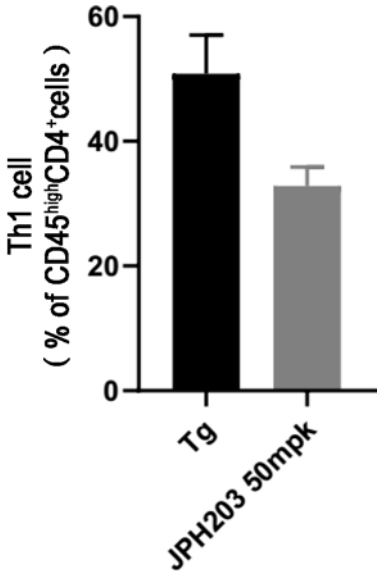

60
40
20
0
Th1 cell
(% of CD45highCD4+cells)
Tg
JPH203 50mpk

Fig. 12

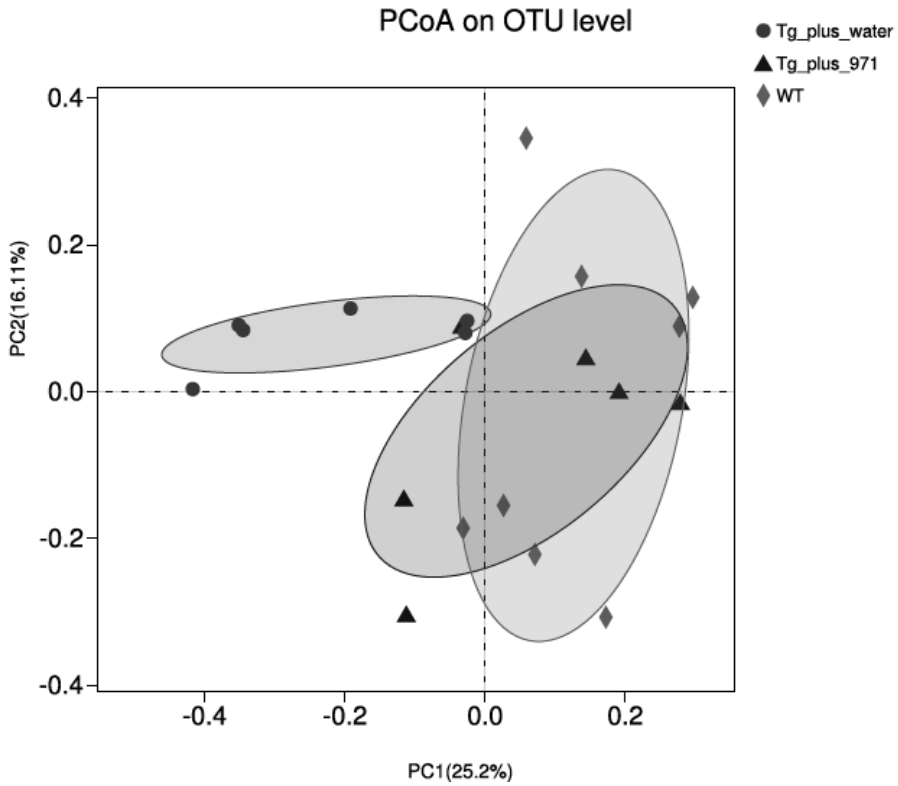

PCoA on OTU level
Tg_plus_water
Tg_plus_971
WT
0.4
0.2
0.0
-0.2
-0.4
PC2(16.11%)
-0.4
-0.2
0.0
0.2
PC1(25.2%)

Fig. 13

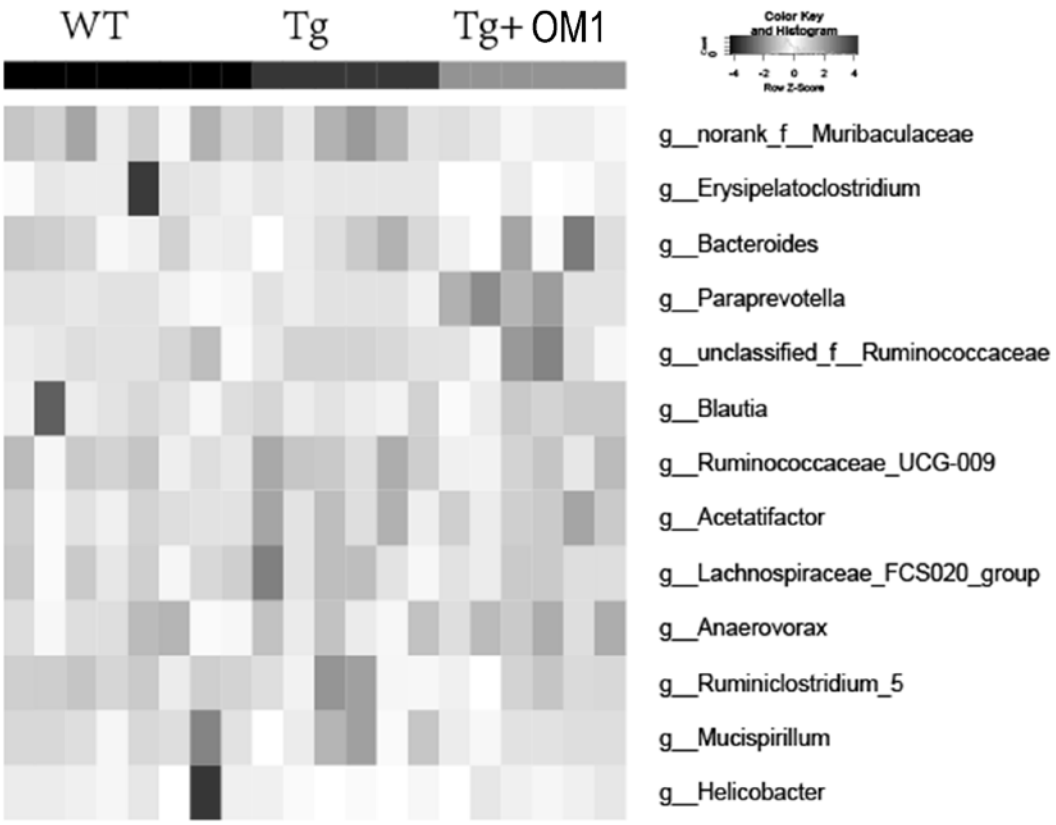

WT
Tg
Tg+ OM1
Color Key and Histogram
-4 -2 0 2 4
Row Z-Score
g__norank_f__Muribaculaceae
g__Erysipelatoclostridium
g__Bacteroides
g__Paraprevotella
g__unclassified_f__Ruminococcaceae
g__Blautia
g__Ruminococcaceae_UCG-009
g__Acetatifactor
g__Lachnospiraceae_FCS020_group
g__Anaerovorax
g__Ruminiclostridium_5
g__Mucispirillum
g__Helicobacter

Fig. 14

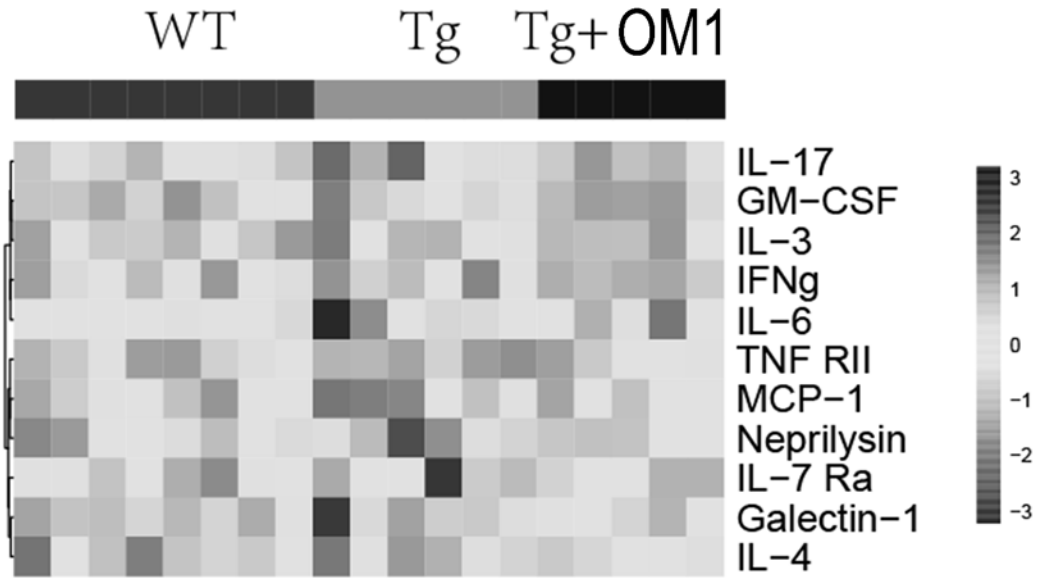
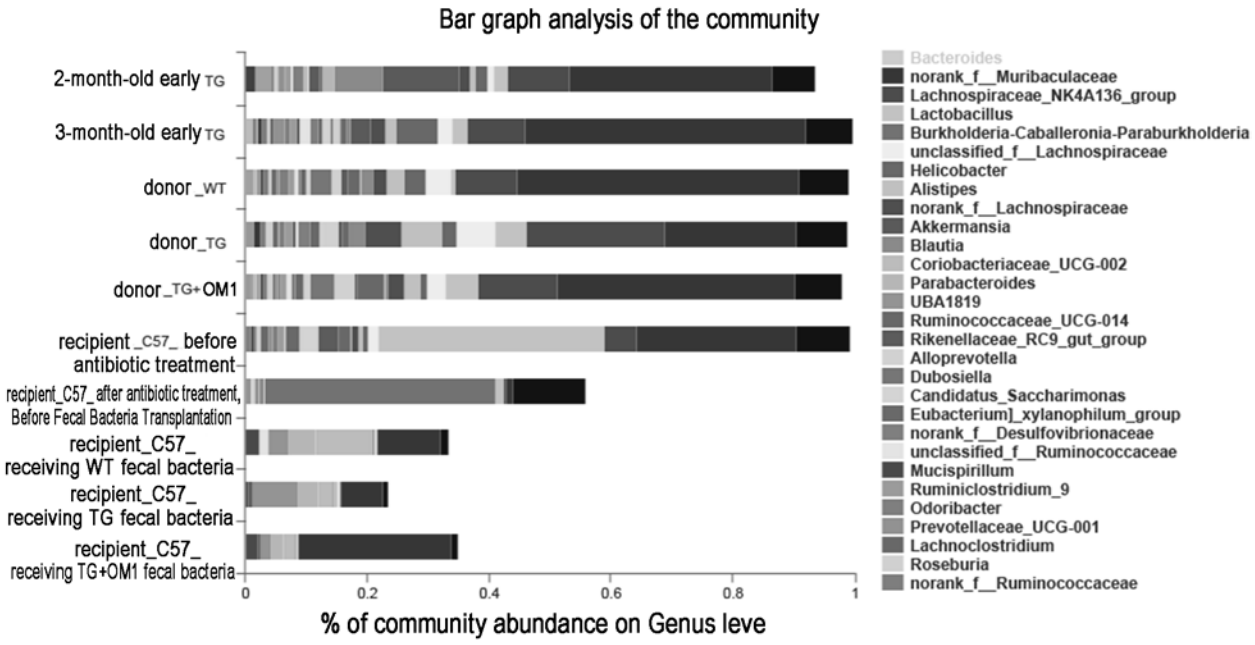

WT
Tg
Tg+ OM1
IL−17
GM−CSF
IL−3
IFNg
IL−6
TNF RII
MCP−1
Neprilysin
IL−7 Ra
Galectin−1
IL−4
3
2
1
0
−1
−2
−3

Fig. 15


Bar graph analysis of the community
2-month-old early TG
3-month-old early TG
donor_WT
donor_TG
donor_TG+OM1
recipient_C57_ before antibiotic treatment
recipient_C57_after antibiotic treatment, Before Fecal Bacteria Transplantation
recipient_C57_ receiving WT fecal bacteria
recipient_C57_ receiving TG fecal bacteria
recipient_C57_ receiving TG+OM1 fecal bacteria
0
0.2
0.4
0.6
0.8
1
% of community abundance on Genus leve
Bacteroides
norank_f__Muribaculaceae
Lachnospiraceae_NK4A136_group
Lactobacillus
Burkholderia-Caballeronia-Paraburkholderia
unclassified_f__Lachnospiraceae
Helicobacter
Alistipes
norank_f__Lachnospiraceae
Akkermansia
Blautia
Coriobacteriaceae_UCG-002
Parabacteroides
UBA1819
Ruminococcaceae_UCG-014
Rikenellaceae_RC9_gut_group
Alloprevotella
Dubosiella
Candidatus_Saccharimonas
Eubacterium]_xylanophilum_group
norank_f__Desulfovibrionaceae
unclassified_f__Ruminococcaceae
Mucispirillum
Ruminiclostridium_9
Odoribacter
Prevotellaceae_UCG-001
Lachnoclostridium
Roseburia
norank_f__Ruminococcaceae

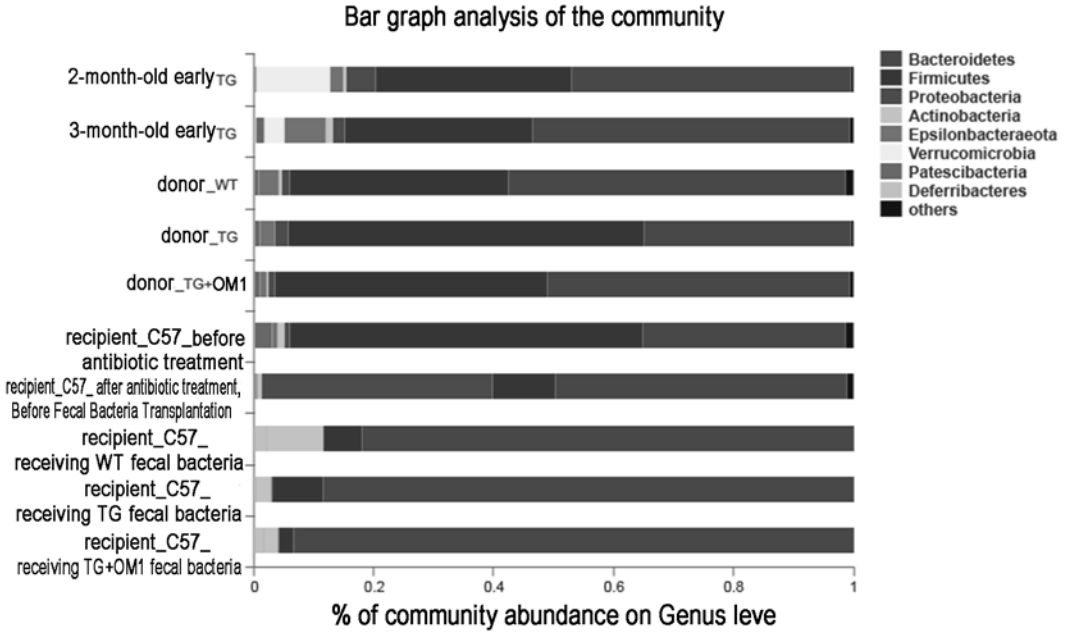

Bar graph analysis of the community
2-month-old early TG
3-month-old early TG
donor_WT
donor_TG
donor_TG+OM1
recipient_C57_before antibiotic treatment
recipient_C57_after antibiotic treatment, Before Fecal Bacteria Transplantation
recipient_C57_ receiving WT fecal bacteria
recipient_C57_ receiving TG fecal bacteria
recipient_C57_ receiving TG+OM1 fecal bacteria
0
0.2
0.4
0.6
0.8
1
% of community abundance on Genus leve
Bacteroidetes
Firmicutes
Proteobacteria
Actinobacteria
Epsilonbacteraeota
Verrucomicrobia
Patescibacteria
Deferribacteres
others

Fig. 16

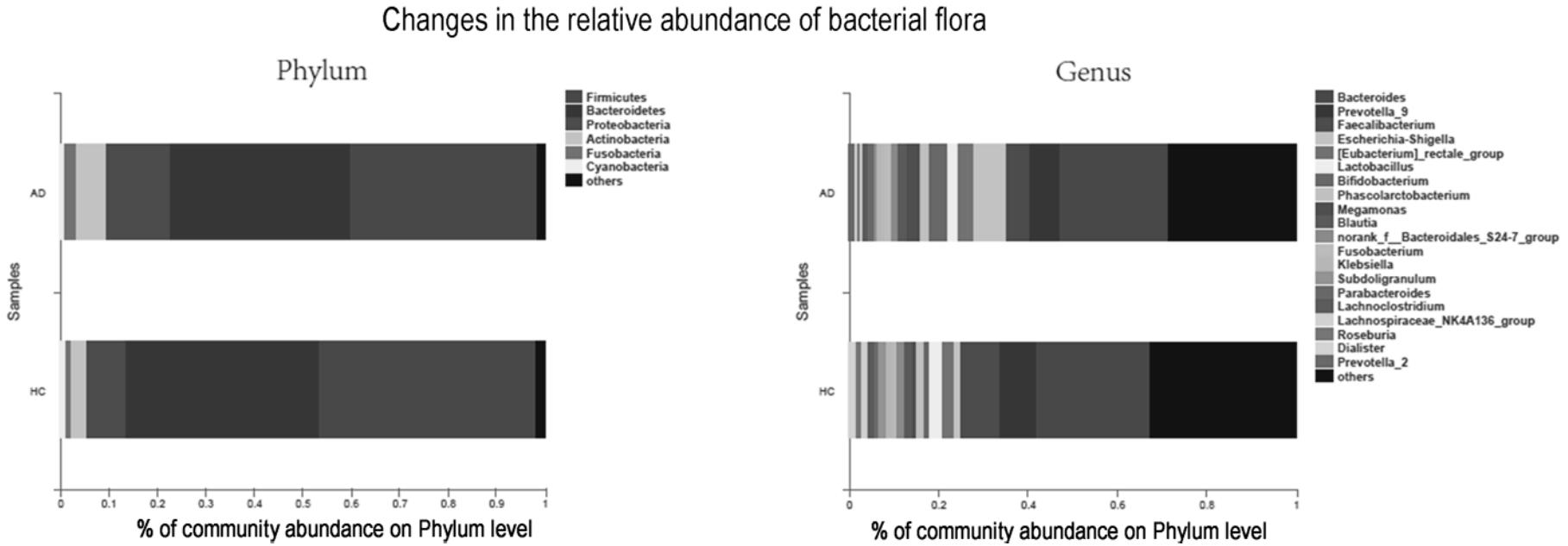

Changes in the relative abundance of bacterial flora
Phylum
Samples
AD
HC
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
% of community abundance on Phylum level
Firmicutes
Bacteroidetes
Proteobacteria
Actinobacteria
Fusobacteria
Cyanobacteria
others
Genus
Samples
AD
HC
0
0.2
0.4
0.6
0.8
1
% of community abundance on Phylum level
Bacteroides
Prevotella_9
Faecalibacterium
Escherichia-Shigella
[Eubacterium]_rectale_group
Lactobacillus
Bifidobacterium
Phascolarctobacterium
Megamonas
Blautia
norank_f__Bacteroidales_S24-7_group
Fusobacterium
Klebsiella
Subdoligranulum
Parabacteroides
Lachnoclostridium
Lachnospiraceae_NK4A136_group
Roseburia
Dialister
Prevotella_2
others

Fig. 17

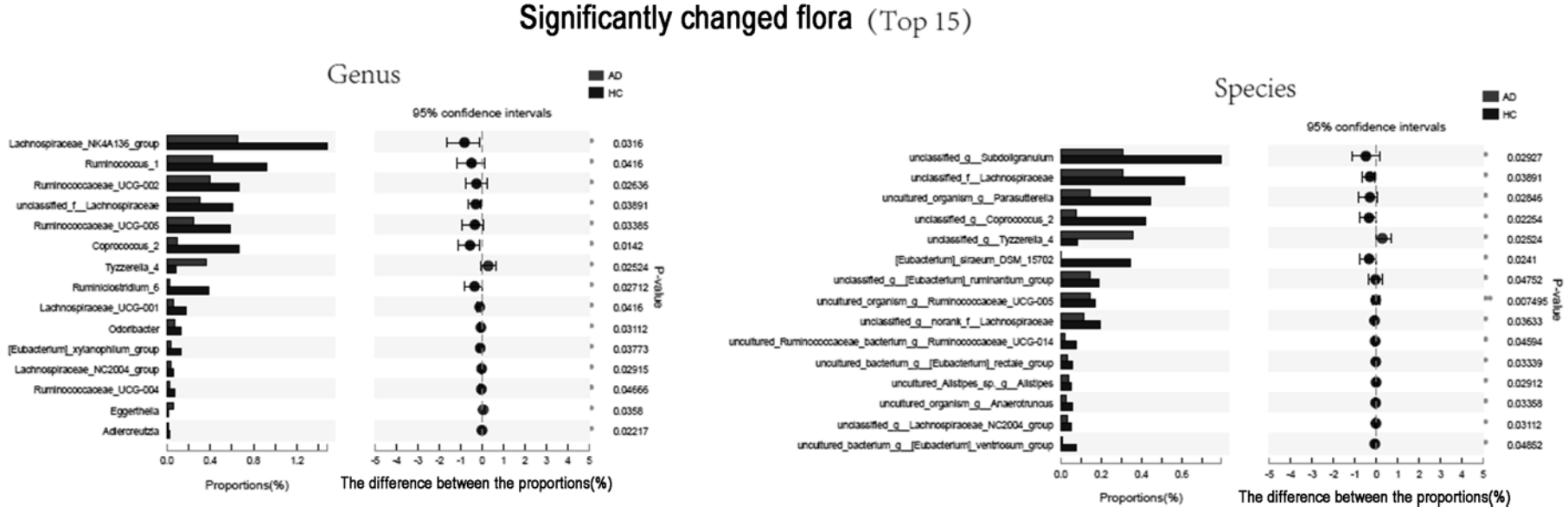

Significantly changed flora (Top 15)
Genus
AD
HC
95% confidence intervals
Lachnospiraceae_NK4A136_group
Ruminococcus_1
Ruminococcaceae_UCG-002
unclassified_f__Lachnospiraceae
Ruminococcaceae_UCG-005
Coprococcus_2
Tyzzerella_4
Ruminiclostridium_6
Lachnospiraceae_UCG-001
Odoribacter
[Eubacterium]_xylanophilum_group
Lachnospiraceae_NC2004_group
Ruminococcaceae_UCG-004
Eggerthella
Adlercreutzia
0.0316
0.0416
0.02636
0.03891
0.03385
0.0142
0.02524
0.02712
0.0416
0.03112
0.03773
0.02915
0.04666
0.0358
0.02217
P-value
0.0 0.4 0.8 1.2
Proportions(%)
-5 -4 -3 -2 -1 0 1 2 3 4 5
The difference between the proportions(%)
Species
AD
HC
95% confidence intervals
unclassified_g__Subdoligranulum
unclassified_f__Lachnospiraceae
uncultured_organism_g__Parasutterella
unclassified_g__Coprococcus_2
unclassified_g__Tyzzerella_4
[Eubacterium]_siraeum_DSM_15702
unclassified_g__[Eubacterium]_ruminantium_group
uncultured_organism_g__Ruminococcaceae_UCG-005
unclassified_g__norank_f__Lachnospiraceae
uncultured_Ruminococcaceae_bacterium_g__Ruminococcaceae_UCG-014
uncultured_bacterium_g__[Eubacterium]_rectale_group
uncultured_Alistipes_sp._g__Alistipes
uncultured_organism_g__Anaerotruncus
unclassified_g__Lachnospiraceae_NC2004_group
uncultured_bacterium_g__[Eubacterium]_ventriosum_group
0.02927
0.03891
0.02646
0.02254
0.02524
0.0241
0.04752
0.007495
0.03633
0.04594
0.03339
0.02912
0.03358
0.03112
0.04852
P-value
0.0 0.2 0.4 0.6
Proportions(%)
-5 -4 -3 -2 -1 0 1 2 3 4 5
The difference between the proportions(%)

Fig. 18

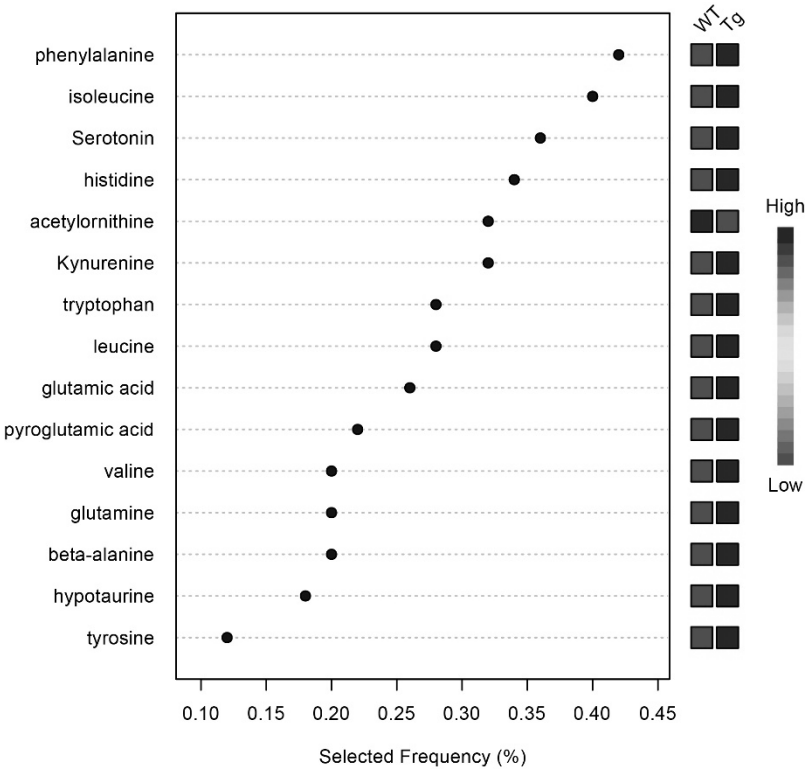

WT
Tg
phenylalanine
isoleucine
Serotonin
histidine
acetylornithine
Kynurenine
tryptophan
leucine
glutamic acid
pyroglutamic acid
valine
glutamine
beta-alanine
hypotaurine
tyrosine
High
Low
0.10
0.15
0.20
0.25
0.30
0.35
0.40
0.45
Selected Frequency (%)

Fig. 19

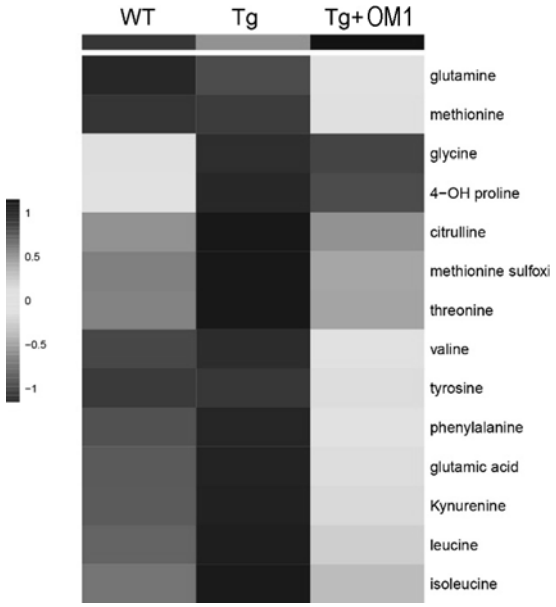

WT
Tg
Tg+OM1
glutamine
methionine
glycine
4−OH proline
citrulline
methionine sulfoxi
threonine
valine
tyrosine
phenylalanine
glutamic acid
Kynurenine
leucine
isoleucine
1
0.5
0
−0.5
−1

Fig. 20

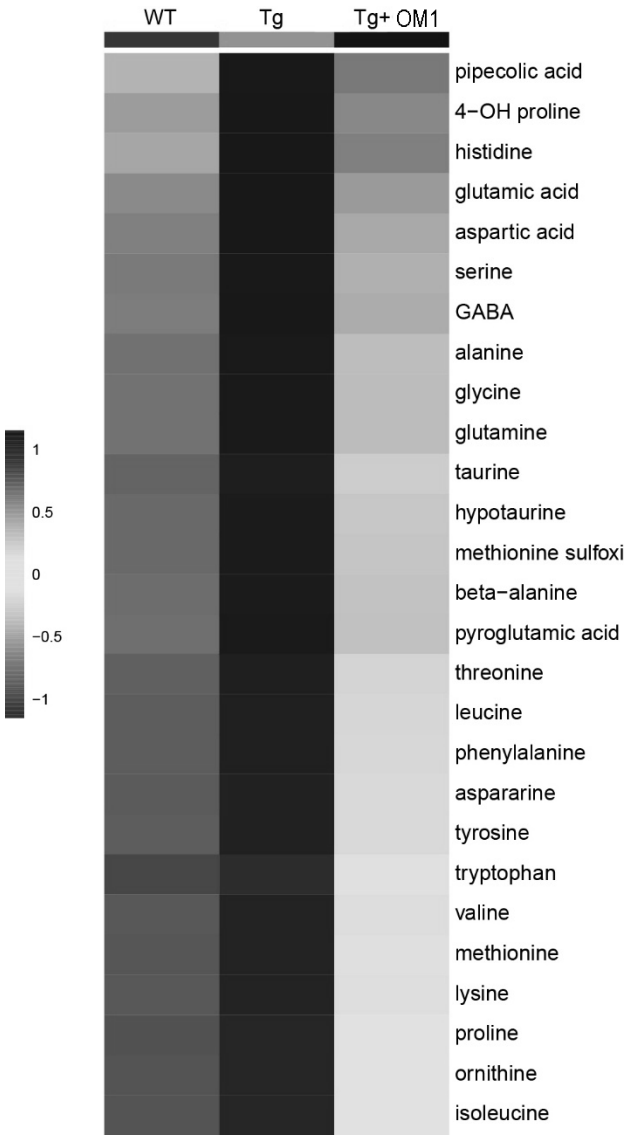

WT
Tg
Tg+ OM1
pipecolic acid
4−OH proline
histidine
glutamic acid
aspartic acid
serine
GABA
alanine
glycine
glutamine
taurine
hypotaurine
methionine sulfoxi
beta−alanine
pyroglutamic acid
threonine
leucine
phenylalanine
aspararine
tyrosine
tryptophan
valine
methionine
lysine
proline
ornithine
isoleucine
1
0.5
0
−0.5
−1

Fig. 21

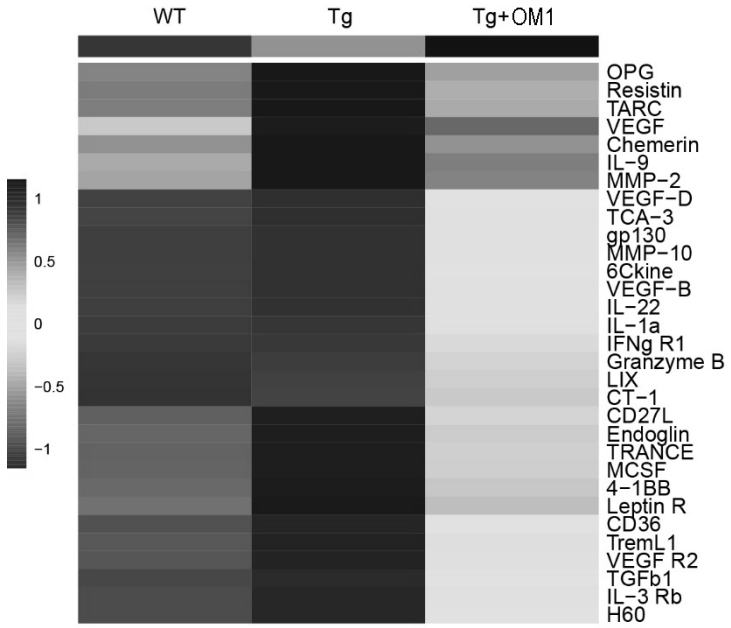

WT
Tg
Tg+OM1
1
0.5
0
−0.5
−1
OPG
Resistin
TARC
VEGF
Chemerin
IL−9
MMP−2
VEGF−D
TCA−3
gp130
MMP−10
6Ckine
VEGF−B
IL−22
IL−1a
IFNg R1
Granzyme B
LIX
CT−1
CD27L
Endoglin
TRANCE
MCSF
4−1BB
Leptin R
CD36
TremL1
VEGF R2
TGFb1
IL−3 Rb
H60

Fig. 22

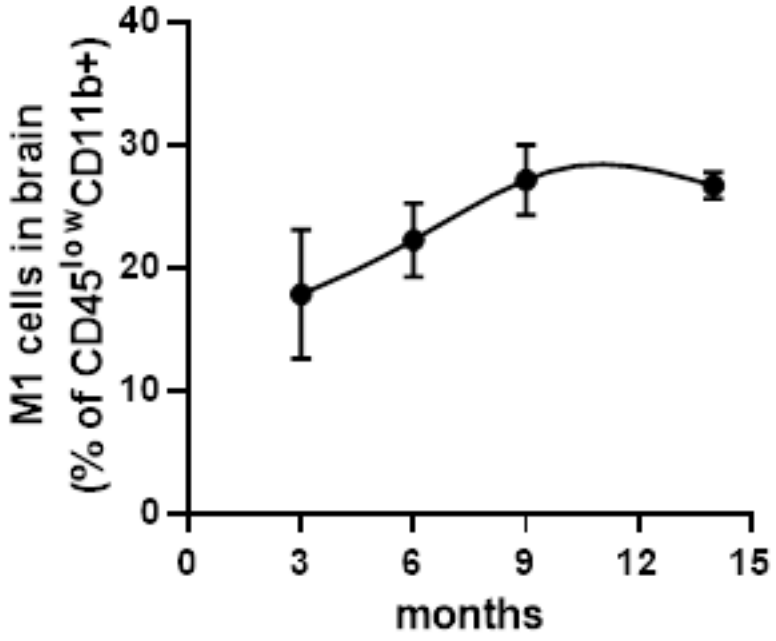

M1 cells in brain
(% of CD45low CD11b+)
40
30
20
10
0
0
3
6
9
12
15
months

Fig. 23