Figure S1

A

B

Significant shifted between ASD and NT

Total ASD score (severity)

Repetitive behavior

Social retardation

Language retardation

Total GI problem score (severity)
Supplemental material

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Figure S2

A

B

C

D

E

F

G

H

I

J

K

L

M

Subjects' distribution in PCA (colored by GI symptoms)

N

O

P

Q

R

Subjects' distribution in PCA (colored by sleep complaints)

Figure S3

A. Mean relative abundance of Veillonella ratti (OTU 359954) across different ages and conditions.

B. Mean relative abundance of Enterobacter (OTU 2119418) across different ages and conditions.

C. Mean relative abundance of Clostridium (OTU 182289) across different ages and conditions.
Figure S4
Figure S6

A: Microbial co-occurrence network alteration between NT and ASD before 3y

B: Microbial co-occurrence network alteration between NT and ASD after 3y

C: Before 3y → After 3y; Microbial community alteration network in NT

D: Before 3y → After 3y; Microbial community alteration network in ASD

E: NT0-NT1 lir abundance scatter, PM score: 0.077

F: ASD0-ASD1 lir abundance scatter, PM score: 0.516
Figure S7

(A) Relative abundance of Veillonella (%) across different conditions.

(B) Veillonella correlations with other taxa in NT0.

(C) Veillonella correlations with other taxa in NT1.

(D) Veillonella correlations with other taxa in ASD0.

(E) Veillonella correlations with other taxa in ASD1.
Figure S9

A. Significant associations (-log(qval)*sign(coef))

- Veillonella
- Lachnospira
- Hungatella
- Lachnospiraceae NK4A136 group
- L. Ruminococcaceae
- Faecalibacterium
- Blautia
- Lachnospiraceae UCG004
- Granulicatella
- L. Enterobacteriaceae
- Flavonifractor
- Clostridium sensu stricto 1

B. Significant associations (-log(qval)*sign(coef))

- MGB041. futaolosine pathway
- MGB053. Butyrate synthesis II
- MGB015. p Cresol synthesis
- MGB027. NO dioxygenase
- MGB023. Dopamine degradation
- MGB007. Glutamate synthesis II
- MGB043. Acetate synthesis I
- MGB056. Propionate degradation I
- MGB050. Glutamate degradation I
- MGB036. SAM synthesis
- MGB019. GABA degradation
- MGB048. Propionate synthesis I
- MGB004. Kynurenine synthesis

C. Significant associations (-log(qval)*sign(coef))

- PWY 7090. UDP-2,3-diacetamido-2,3-dideoxy-b-D-mannuronate biosynthesis
- PWY 5897. superpathway of menaquinol 11 biosynthesis
- PWY 5898. superpathway of menaquinol 12 biosynthesis
- PWY 5899. superpathway of menaquinol 13 biosynthesis
- PWY 5838. superpathway of menaquinol 8 biosynthesis I
- PWY 7003. glycerol degradation to butanol
- PWY 7332. superpathway of UDP-N-acetylglucosamine derived O-antigen building blocks biosynthesis
- GLUTORN PWY. L-ornithine biosynthesis
- PANTOSYN PWY. pantothenate and coenzyme-A biosynthesis I
- THRESYN PWY. superpathway of L-threonine biosynthesis
- PWY 6471. peptidoglycan biosynthesis IV Enterococcus faecium
- ARGSYN PWY. L-arginine biosynthesis I via L-ornithine
- NONMEVIPP PWY. methylerythritol phosphate pathway I
- PWY 7560. methylerythritol phosphate pathway II
- PWY 7400. L-arginine biosynthesis IV archaebacteria
- PWY 6163. chorismate biosynthesis from 3 dehydroquinate
- PWY 6470. peptidoglycan biosynthesis V b-lactam resistance
- HEME BIOSYNTHESIS II. heme biosynthesis I aerobic
- COA PWY. coenzyme-A biosynthesis I
- PWY 3001. superpathway of L-isoleucine biosynthesis I
- PWY 5188. tetrpyrrole biosynthesis I from glutamate
- PWY 1061. superpathway of L-alanine biosynthesis
- GLCMANNANA autonomous PWY. superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminic degradation
- PWY 5189. tetrpyrrole biosynthesis II from glycine
- PWY 5918. superpathway of heme biosynthesis from glutamate
- PWY 5505. L-glutamate and L-glutamine biosynthesis
- X1CMET2 PWY N10. formyl tetrahydrofolate biosynthesis
- PWY 621. sucrose degradation III sucrose inverase
Figure S11

A. Validation cohort 1

B. Validation cohort 2

C. Validation cohort 3

Supplemental material