Supplementary Figure

Supplementary Fig. S1 Basic determination of *W. coagulans* BCG44.

Supplementary Fig. S2 Effect of *W. coagulans* BCG44 and its supernatant on the size of spleen in the CTX-induced immunosuppressed mice model.

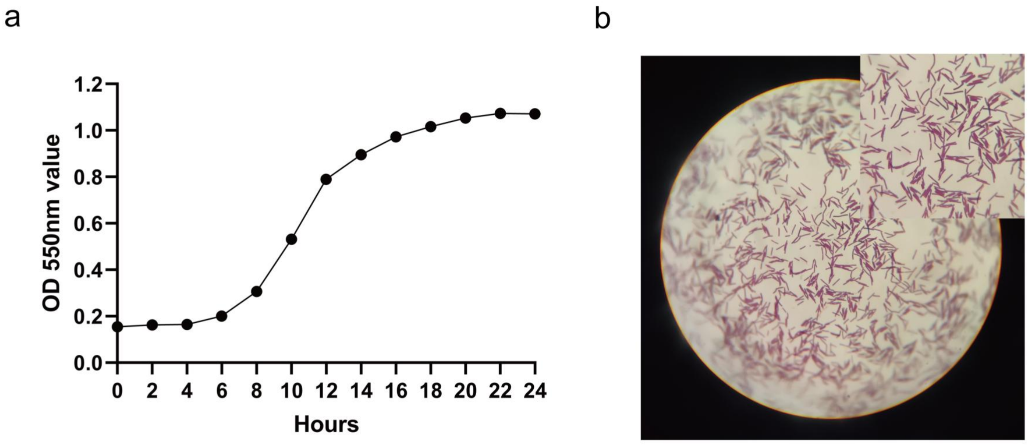
Supplementary Fig. S3 Effect of *W. coagulans* BCG44 and its supernatant on colon injury in the CTX-induced immunosuppressed mice.

Supplementary Fig. S4 Effect of *W. coagulans* BCG44 and its supernatant on the gut microbiome in the CTX-induced immunosuppressed mice.

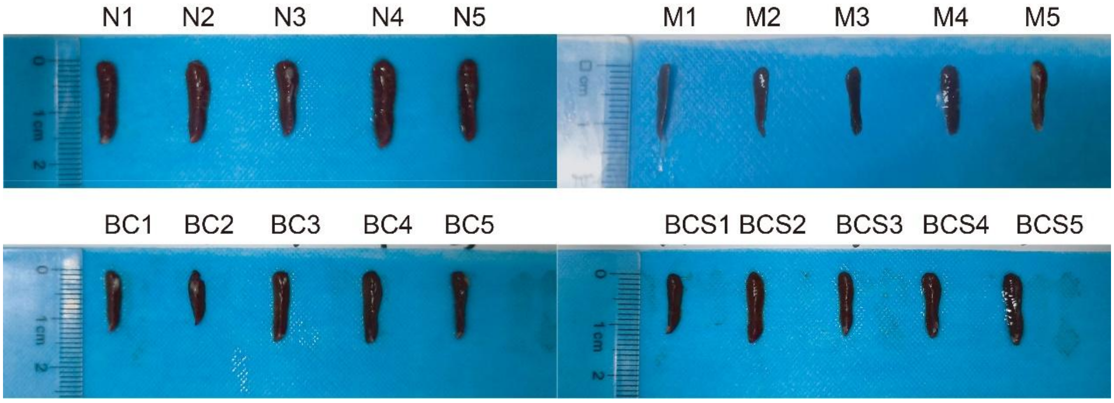
Supplementary Fig. S5 Correlation between gut microbiota and immunity-related indicators at the Family level.

Supplementary Fig. S6 The metabolic pathways in the gut microbiota basing the Kyoto Encyclopedia of Genes and Genomes (KEGG) database.

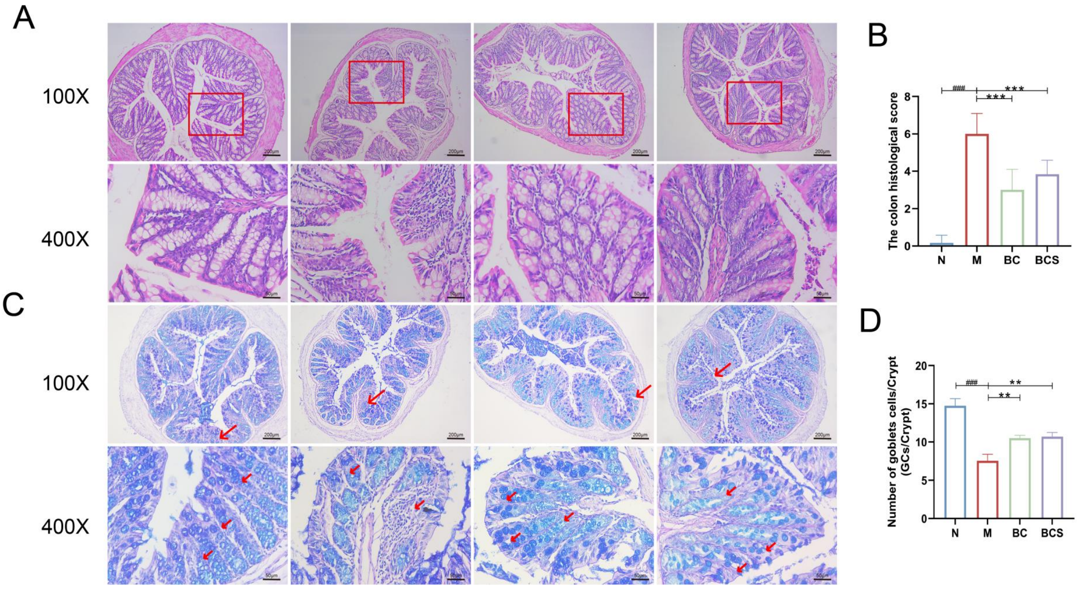
Supplementary Fig. S7 The metabolites of *W. coagulans* BCG44 supernatant in superclass level under the positive and negative mode.



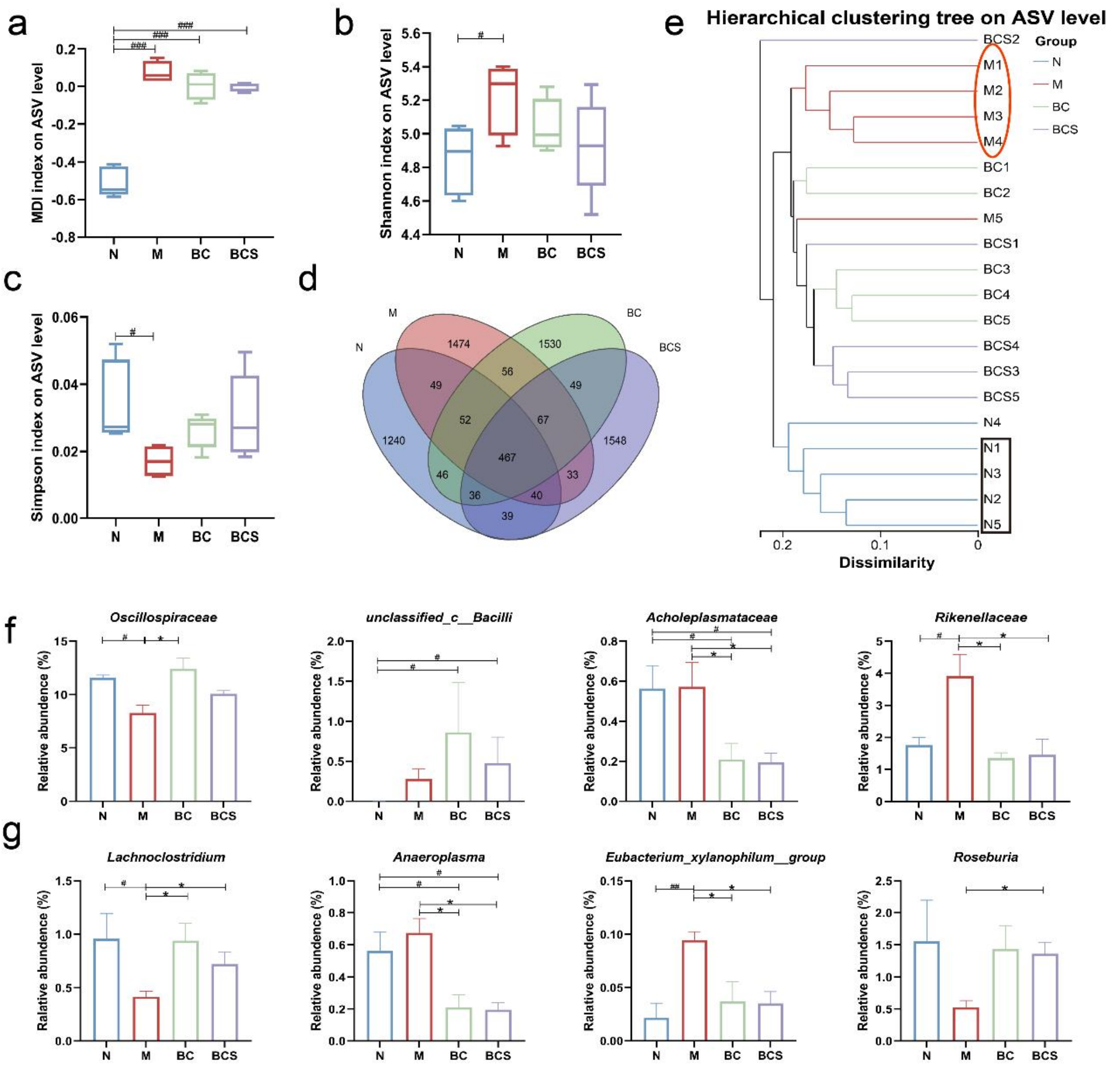
Supplementary Fig. S1 Basic determination of *W. coagulans* BCG44 about the growth curve and microscopic morphology (a, b).



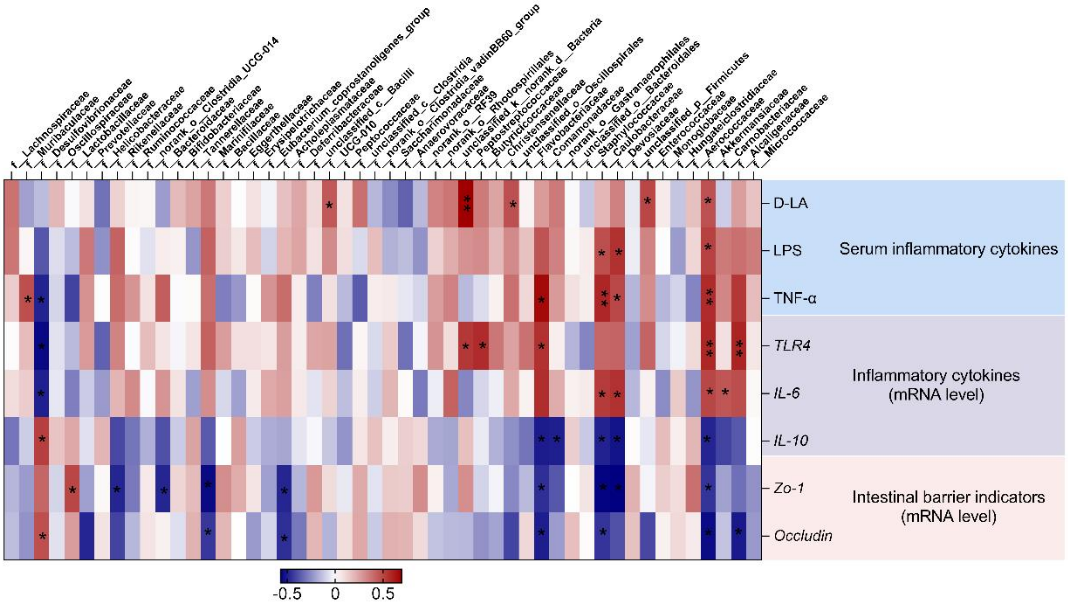
Supplementary Fig. S2 Effect of *W. coagulans* BCG44 and its supernatant on the size of spleen in the CTX-induced immunosuppressed mice model.



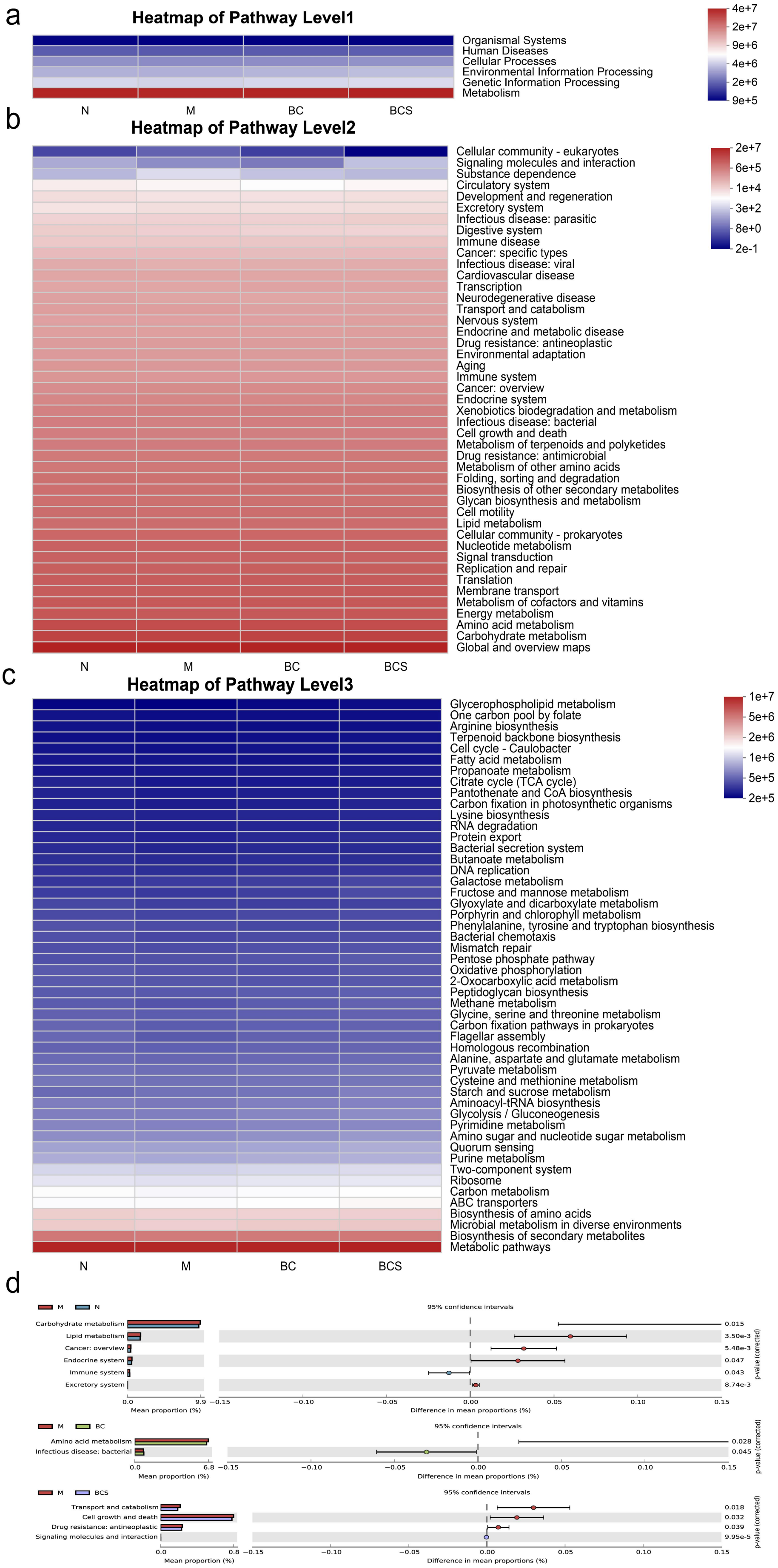
Supplementary Fig. S3 Effect of *W. coagulans* BCG44 and its supernatant on colon injury in the CTX-induced immunosuppressed mice. (a) Morphologic analysis of the colon by H&E staining (100 × and 400 ×) (n = 5), (b) The colon histological score, (c) Morphologic analysis of the colon by AB-PAS staining (100 × and 400 ×) (n = 3), and (d) Number of goblets cells/Crypt (GCs/Crypt).



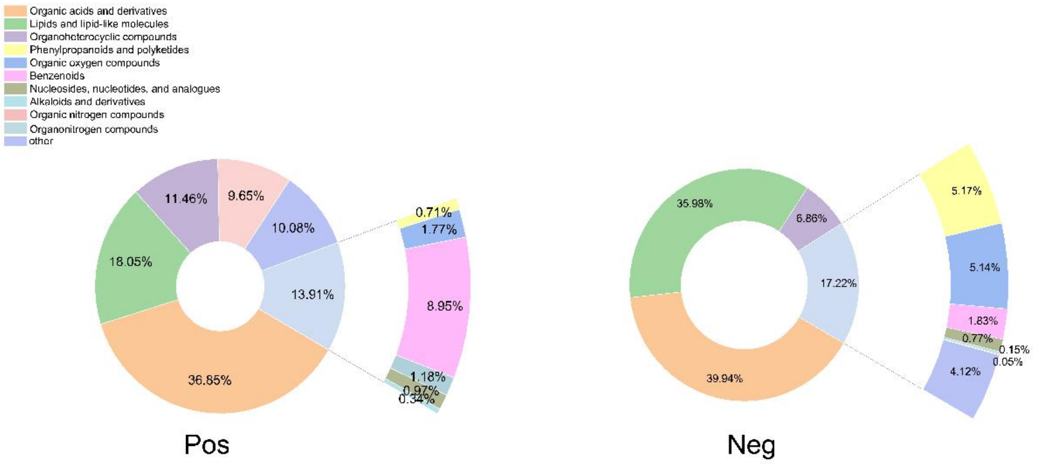
Supplementary Fig. S4 Effect of *W. coagulans* BCG44 and its supernatant on the gut microbiome in the CTX-induced immunosuppressed mice. (a) MDI index on the ASV level, (b) Shannon index on the ASV level, (c) Simpson index on the ASV level, (d) Venn diagram. e Hierarchical clustering tree with cluster on ASV level, (f) Analyze the relative abundance of other bacteria at the family level (*Oscillospiraceae*, *unclassified_c__Bacilli*, *Achnoeplasamtaceae* and *Rikenellaceae*), and (g) Analyze the relative abundance of other bacteria at the genus level (*Lachnoclostridium*, *Anaeroplasma*, *Eubacterium_xylanophilum__group*, and *Roseburia*). (n = 5)



Supplementary Fig. S5 Correlation between gut microbiota and immunity-related indicators at the Family level.


a
Heatmap of Pathway Level1
Organismal Systems
Human Diseases
Cellular Processes
Environmental Information Processing
Genetic Information Processing
Metabolism
4e+7
2e+7
9e+6
4e+6
2e+6
9e+5
N
M
BC
BCS
b
Heatmap of Pathway Level2
Cellular community - eukaryotes
Signaling molecules and interaction
Substance dependence
Circulatory system
Development and regeneration
Excretory system
Infectious disease: parasitic
Digestive system
Immune disease
Cancer: specific types
Infectious disease: viral
Cardiovascular disease
Transcription
Neurodegenerative disease
Transport and catabolism
Nervous system
Endocrine and metabolic disease
Drug resistance: antineoplastic
Environmental adaptation
Aging
Immune system
Cancer: overview
Endocrine system
Xenobiotics biodegradation and metabolism
Infectious disease: bacterial
Cell growth and death
Metabolism of terpenoids and polyketides
Drug resistance: antimicrobial
Metabolism of other amino acids
Folding, sorting and degradation
Biosynthesis of other secondary metabolites
Glycan biosynthesis and metabolism
Cell motility
Lipid metabolism
Cellular community - prokaryotes
Nucleotide metabolism
Signal transduction
Replication and repair
Translation
Membrane transport
Metabolism of cofactors and vitamins
Energy metabolism
Amino acid metabolism
Carbohydrate metabolism
Global and overview maps
2e+7
6e+5
1e+4
3e+2
8e+0
2e-1
N
M
BC
BCS
c
Heatmap of Pathway Level3
Glycerophospholipid metabolism
One carbon pool by folate
Arginine biosynthesis
Terpenoid backbone biosynthesis
Cell cycle - Caulobacter
Fatty acid metabolism
Propanoate metabolism
Citrate cycle (TCA cycle)
Pantothenate and CoA biosynthesis
Carbon fixation in photosynthetic organisms
Lysine biosynthesis
RNA degradation
Protein export
Bacterial secretion system
Butanoate metabolism
DNA replication
Galactose metabolism
Fructose and mannose metabolism
Glyoxylate and dicarboxylate metabolism
Porphyrin and chlorophyll metabolism
Phenylalanine, tyrosine and tryptophan biosynthesis
Bacterial chemotaxis
Mismatch repair
Pentose phosphate pathway
Oxidative phosphorylation
2-Oxocarboxylic acid metabolism
Peptidoglycan biosynthesis
Methane metabolism
Glycine, serine and threonine metabolism
Carbon fixation pathways in prokaryotes
Flagellar assembly
Homologous recombination
Alanine, aspartate and glutamate metabolism
Pyruvate metabolism
Cysteine and methionine metabolism
Starch and sucrose metabolism
Aminoacyl-tRNA biosynthesis
Glycolysis / Gluconeogenesis
Pyrimidine metabolism
Amino sugar and nucleotide sugar metabolism
Quorum sensing
Purine metabolism
Two-component system
Ribosome
Carbon metabolism
ABC transporters
Biosynthesis of amino acids
Microbial metabolism in diverse environments
Biosynthesis of secondary metabolites
Metabolic pathways
1e+7
5e+6
2e+6
1e+6
5e+5
2e+5
N
M
BC
BCS
d
🟥 M 🟦 N
95% confidence intervals
Carbohydrate metabolism
Lipid metabolism
Cancer: overview
Endocrine system
Immune system
Excretory system
0.015
3.50e-3
5.48e-3
0.047
0.043
8.74e-3
p-value (corrected)
0.0
9.9
Mean proportion (%)
−0.15
−0.10
−0.05
0.00
0.05
0.10
0.15
Difference in mean proportions (%)
🟥 M 🟩 BC
95% confidence intervals
Amino acid metabolism
Infectious disease: bacterial
0.028
0.045
p-value (corrected)
0.0
6.8
Mean proportion (%)
−0.15
−0.10
−0.05
0.00
0.05
0.10
0.15
Difference in mean proportions (%)
🟥 M 🟪 BCS
95% confidence intervals
Transport and catabolism
Cell growth and death
Drug resistance: antineoplastic
Signaling molecules and interaction
0.018
0.032
0.039
9.95e-5
p-value (corrected)
0.0
0.8
Mean proportion (%)
−0.15
−0.10
−0.05
0.00
0.05
0.10
0.15
Difference in mean proportions (%)

Supplementary Fig. S6 The metabolic pathways in the gut microbiota basing the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. (a) The heatmap of pathways level 1, (b) The heatmap of pathways level 2, (c) The heatmap of pathways level 3, and (d) STAMP analysis for the inferred level 2 metabolic pathway.



Supplementary Fig. S7 The metabolites of *W. coagulans* BCG44 supernatant in superclass level under the positive and negative mode.