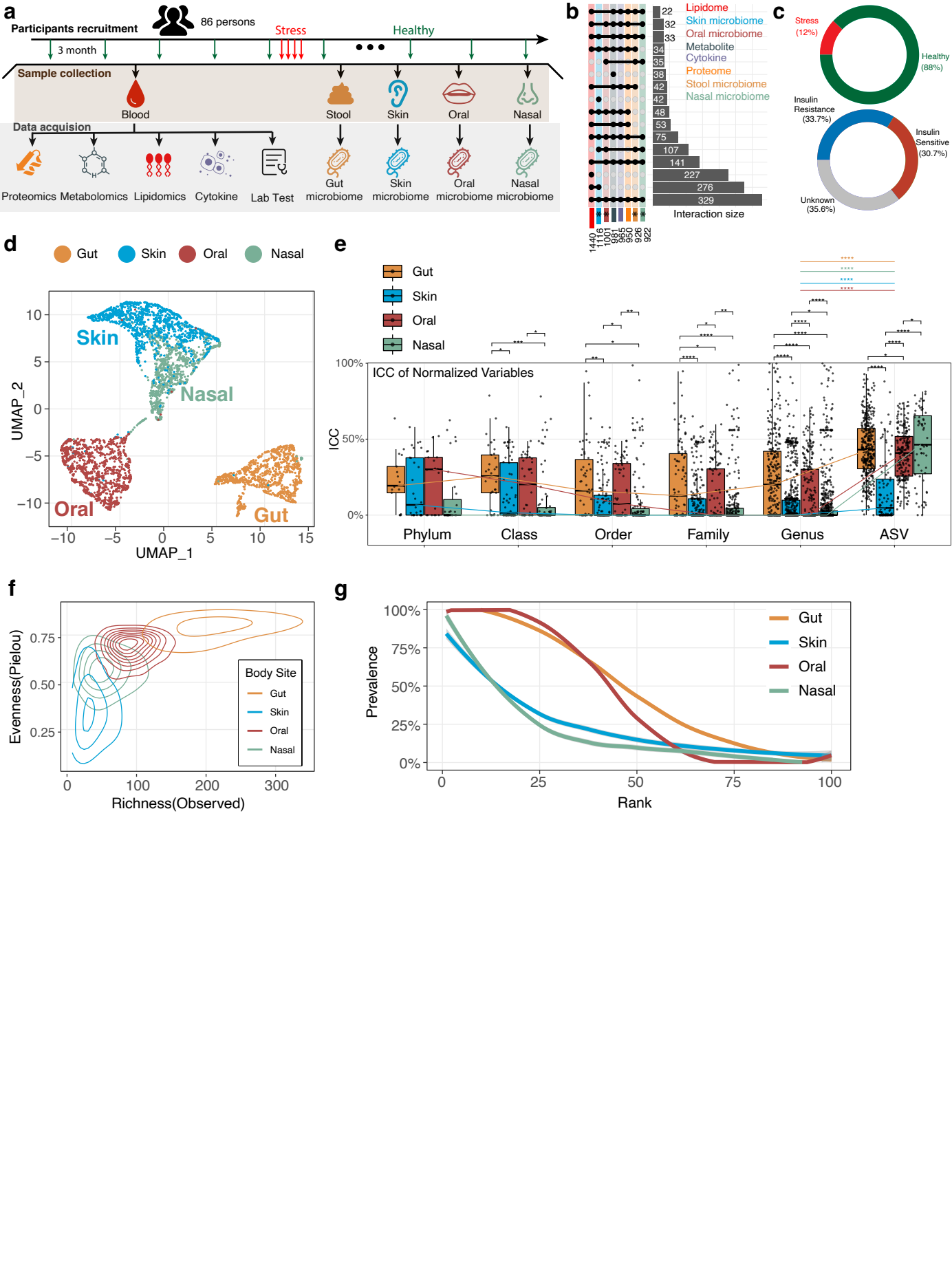
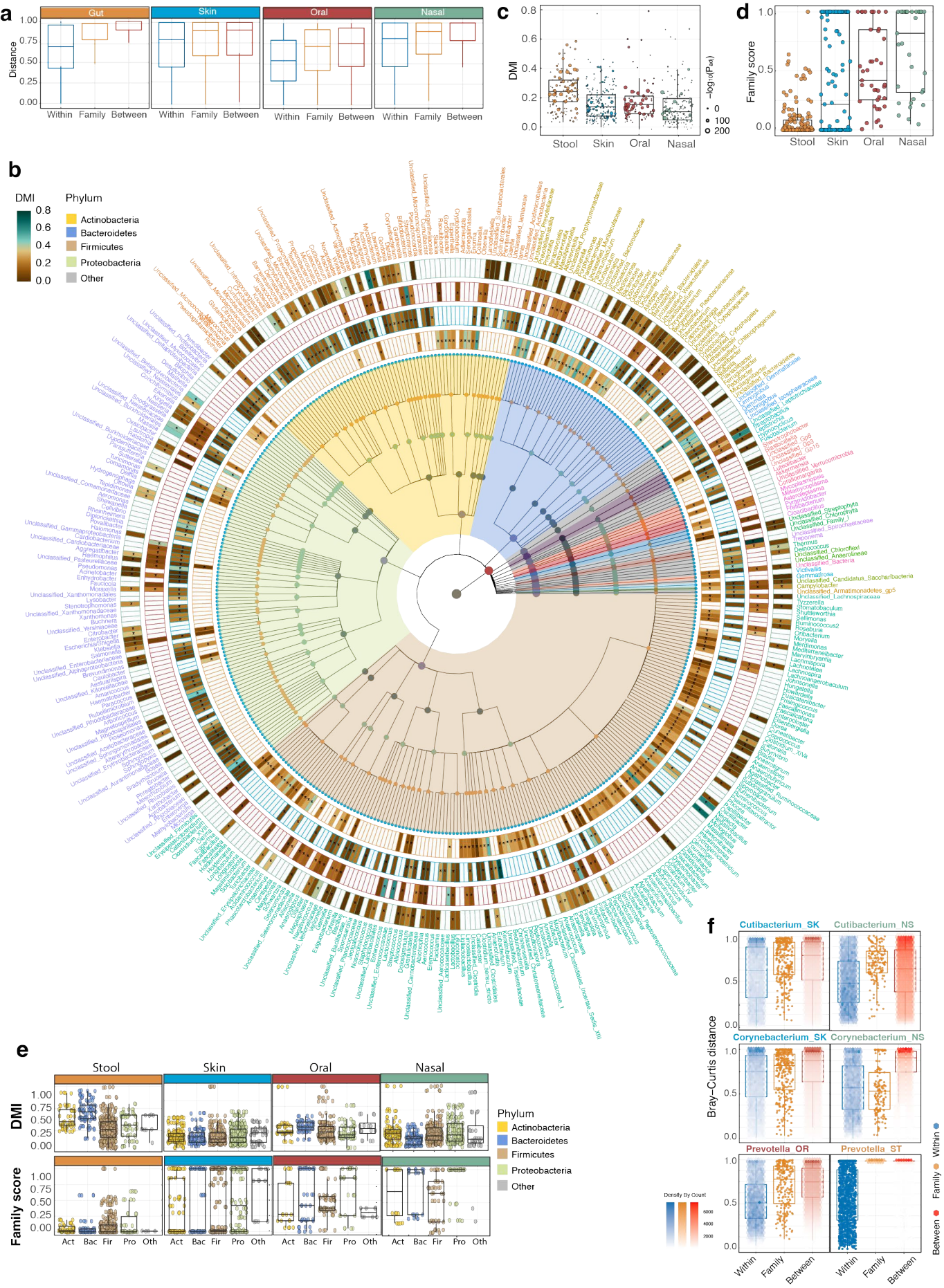
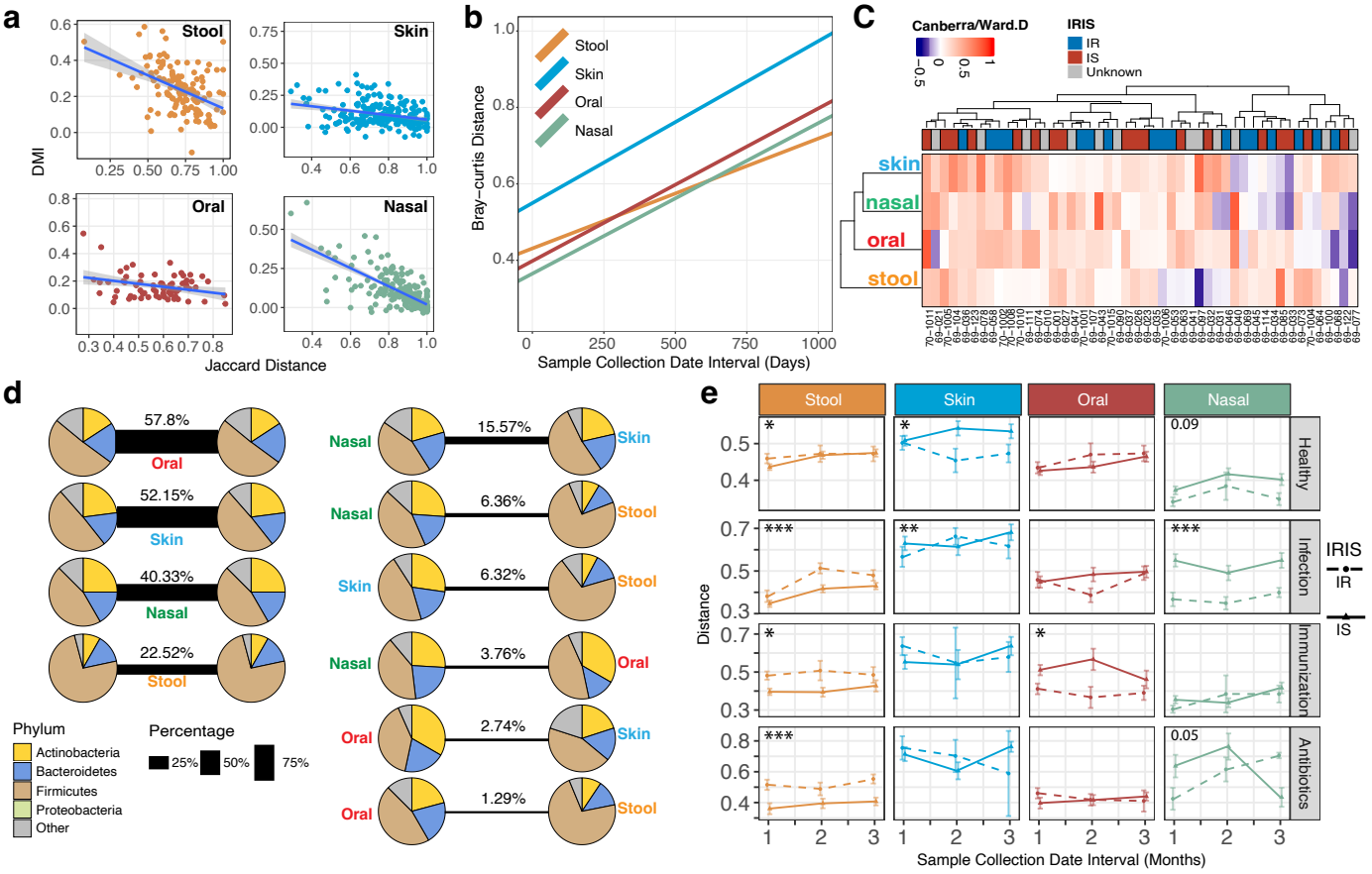
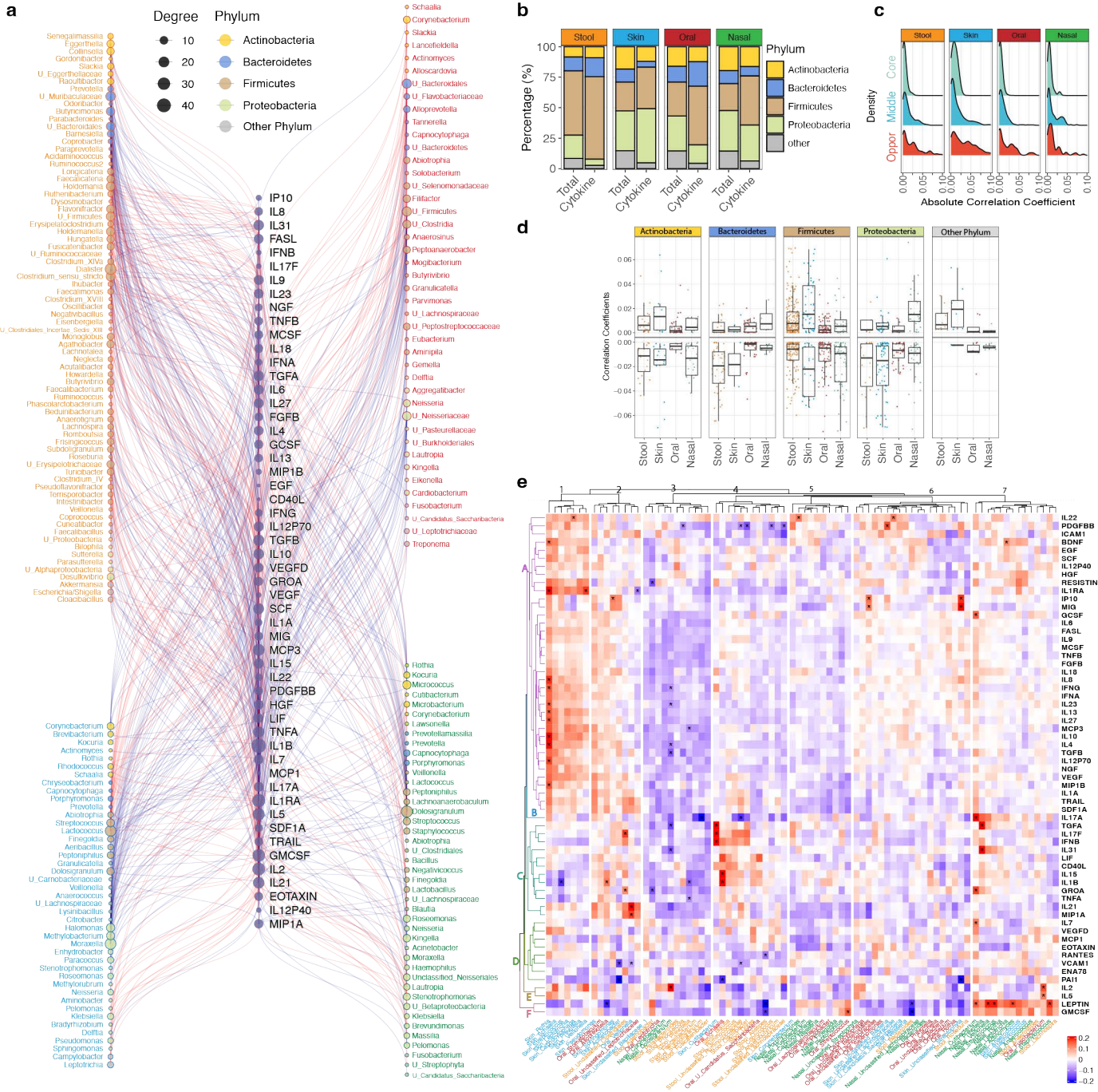
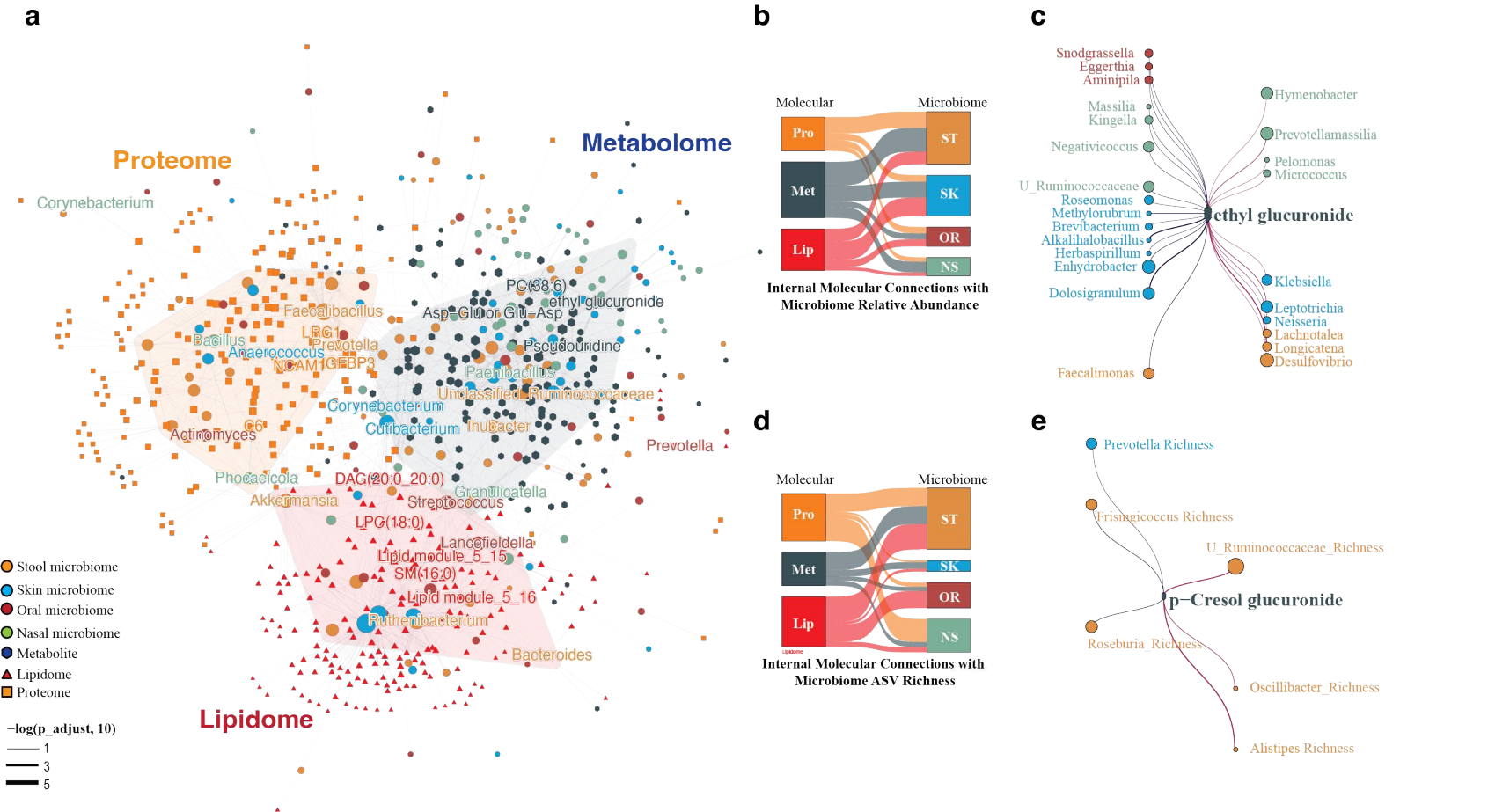
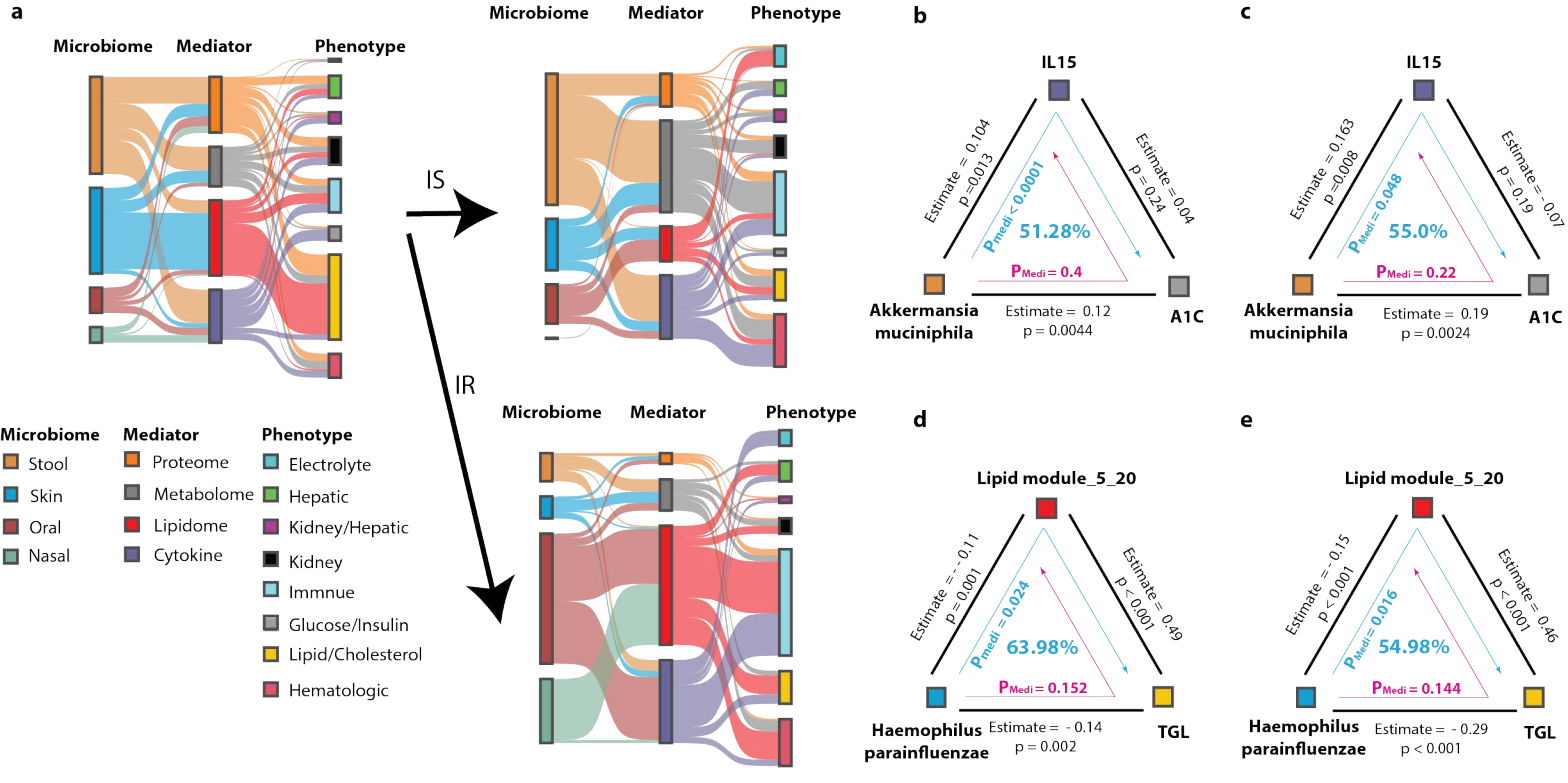

a
Participants recruitment
86 persons
3 month
Stress
Healthy
Sample collection
Blood
Stool
Skin
Oral
Nasal
Data acquisition
Proteomics
Metabolomics
Lipidomics
Cytokine
Lab Test
Gut microbiome
Skin microbiome
Oral microbiome
Nasal microbiome
b
Lipidome
Skin microbiome
Oral microbiome
Metabolite
Cytokine
Proteome
Stool microbiome
Nasal microbiome
Interaction size
c
Stress (12%)
Healthy (88%)
Insulin Resistance (33.7%)
Insulin Sensitive (30.7%)
Unknown (35.6%)
d
Gut
Skin
Oral
Nasal
UMAP_1
UMAP_2
e
ICC of Normalized Variables
ICC
Phylum
Class
Order
Family
Genus
ASV
f
Body Site
Gut
Skin
Oral
Nasal
Evenness(Pielou)
Richness(Observed)
g
Prevalence
Rank


a
Gut
Skin
Oral
Nasal
Distance
1.00
0.75
0.50
0.25
0.00
Within
Family
Between
c
DMI
0.8
0.6
0.4
0.2
0.0
Stool
Skin
Oral
Nasal
−log10(Pad)
0
100
200
d
Family score
1.0
0.5
0.0
Stool
Skin
Oral
Nasal
b
DMI
0.8
0.6
0.4
0.2
0.0
Phylum
Actinobacteria
Bacteroidetes
Firmicutes
Proteobacteria
Other
e
Stool
Skin
Oral
Nasal
DMI
Family score
1.00
0.75
0.50
0.25
0.00
Act
Bac
Fir
Pro
Oth
Phylum
Actinobacteria
Bacteroidetes
Firmicutes
Proteobacteria
Other
f
Cutibacterium_SK
Cutibacterium_NS
Corynebacterium_SK
Corynebacterium_NS
Prevotella_OR
Prevotella_ST
Bray–Curtis distance
1.0
0.5
0.0
Within
Family
Between
Density By Count
6000
4000
2000


a
Stool
Skin
Oral
Nasal
DMI
Jaccard Distance
b
Stool
Skin
Oral
Nasal
Bray−curtis Distance
Sample Collection Date Interval (Days)
C
Canberra/Ward.D
IRIS
IR
IS
Unknown
skin
nasal
oral
stool
d
57.8%
Oral
52.15%
Skin
40.33%
Nasal
22.52%
Stool
Nasal
15.57%
Skin
Nasal
6.36%
Stool
Skin
6.32%
Stool
Nasal
3.76%
Oral
Oral
2.74%
Skin
Oral
1.29%
Stool
Phylum
Actinobacteria
Bacteroidetes
Firmicutes
Proteobacteria
Other
Percentage
25%
50%
75%
e
Stool
Skin
Oral
Nasal
Healthy
Infection
Immunization
Antibiotics
0.09
0.05
IRIS
IR
IS
Distance
Sample Collection Date Interval (Months)


a
Degree
10
20
30
40
Phylum
Actinobacteria
Bacteroidetes
Firmicutes
Proteobacteria
Other Phylum
IP10
IL8
IL31
FASL
IFNB
IL17F
IL9
IL23
NGF
TNFB
MCSF
IL18
IFNA
TGFA
IL6
IL27
FGFB
IL4
GCSF
IL13
MIP1B
EGF
CD40L
IFNG
IL12P70
TGFB
IL10
VEGFD
GROA
VEGF
SCF
IL1A
MIG
MCP3
IL15
IL22
PDGFBB
HGF
LIF
TNFA
IL1B
IL7
MCP1
IL17A
IL1RA
IL5
SDF1A
TRAIL
GMCSF
IL2
IL21
EOTAXIN
IL12P40
MIP1A
b
Stool
Skin
Oral
Nasal
Percentage (%)
Total
Cytokine
Phylum
Actinobacteria
Bacteroidetes
Firmicutes
Proteobacteria
other
c
Density
Core
Middle
Oppor
Absolute Correlation Coefficient
d
Actinobacteria
Bacteroidetes
Firmicutes
Proteobacteria
Other Phylum
Correlation Coefficients
e


a
Proteome
Metabolome
Lipidome
Corynebacterium
Faecalibacillus
LRG1
Prevotella
Bacillus
Anaerococcus
NCAM1
IGFBP3
C6
Actinomyces
Phocaeicola
Akkermansia
DAG(20:0_20:0)
Streptococcus
Granulicatella
LPG(18:0)
Lancefieldella
Lipid module_5_15
SM(16:0)
Lipid module_5_16
Ruthenibacterium
Bacteroides
Prevotella
PC(38:6)
ethyl glucuronide
Asp_Glu or Glu_Asp
Pseudouridine
Paenibacillus
Unclassified_Ruminococcaceae
Corynebacterium
Cutibacterium
Ihubacter
Stool microbiome
Skin microbiome
Oral microbiome
Nasal microbiome
Metabolite
Lipidome
Proteome
−log(p_adjust, 10)
1
3
5
b
Molecular
Microbiome
Pro
Met
Lip
ST
SK
OR
NS
Internal Molecular Connections with Microbiome Relative Abundance
c
Snodgrassella
Eggerthia
Aminipila
Massilia
Kingella
Negativicoccus
U_Ruminococcaceae
Roseomonas
Methylorubrum
Brevibacterium
Alkalihalobacillus
Herbaspirillum
Enhydrobacter
Dolosigranulum
Faecalimonas
Hymenobacter
Prevotellamassilia
Pelomonas
Micrococcus
ethyl glucuronide
Klebsiella
Leptotrichia
Neisseria
Lachnotalea
Longicatena
Desulfovibrio
d
Molecular
Microbiome
Pro
Met
Lip
ST
SK
OR
NS
Internal Molecular Connections with Microbiome ASV Richness
e
Prevotella Richness
Frisingicoccus Richness
U_Ruminococcaceae_Richness
p−Cresol glucuronide
Roseburia_Richness
Oscillibacter_Richness
Alistipes Richness


a
Microbiome
Mediator
Phenotype
IS
IR
Microbiome
Mediator
Phenotype
Microbiome
Stool
Skin
Oral
Nasal
Mediator
Proteome
Metabolome
Lipidome
Cytokine
Phenotype
Electrolyte
Hepatic
Kidney/Hepatic
Kidney
Immnue
Glucose/Insulin
Lipid/Cholesterol
Hematologic
b
IL15
Estimate = 0.104
p =0.013
Estimate = 0.04
p = 0.24
Pmedi < 0.0001
51.28%
PMedi = 0.4
Akkermansia muciniphila
Estimate = 0.12
p = 0.0044
A1C
c
IL15
Estimate = 0.163
p =0.008
Estimate = -0.07
p = 0.19
Pmedi = 0.048
55.0%
PMedi = 0.22
Akkermansia muciniphila
Estimate = 0.19
p = 0.0024
A1C
d
Lipid module_5_20
Estimate = - 0.11
p = 0.001
Estimate = 0.49
p < 0.001
Pmedi = 0.024
63.98%
PMedi = 0.152
Haemophilus parainfluenzae
Estimate = - 0.14
p = 0.002
TGL
e
Lipid module_5_20
Estimate = - 0.15
p < 0.001
Estimate = 0.46
p < 0.001
Pmedi = 0.016
54.98%
PMedi = 0.144
Haemophilus parainfluenzae
Estimate = - 0.29
p < 0.001
TGL