Supplementary table 3 - Functions characterizing sub-groups of Lachnospira-Gene clusters present in over 90% of one group of Lachnospiraceae genomes and absent in over 90% of another were analyzed using Interproscan to determine their functions, as was the reverse. The general InterPro functional categories and GO Supplementary table 3a. Gut-restricted Lachnospiraceae compared to all other Lachnospiraceae restricted-Non-Gutassociated restricted genome genome GO count count InterPro Protein binding Tetratricopeptide-like helical None none Protein binding 11 0 TolB-like Tetratricopeptide-like helical Protein binding None None Signal transduction histidine **Signal Transduction** kinase None none Cell wall macromolecule Peptidoglycan-binding Lysin subgroup catabolic process Protein phosphatase 2C-like Catalytic activity Periplasmic binding protein None domain YbbR-like None Type II secretion system F None domain None None None None Colicin V production, CvpA Toxin biosynthetic process 11 1 Tetratricopeptide-like helical Protein binding Aminoglycoside Transferring phosphorusphosphotransferase containing groups Tetratricopeptide-like helical Protein binding None None None None None None None None Haemerythrin/HHE cation-Metal ion binding binding motif none None Spore cortex biosynthesis None protein, YabQ-like none None Periplasmic binding protein None domain Permease FtsX-like None Sporulation stage III, None protein AE Sporulation stage II protein Sporulation resulting in 11 2 D, amidase enhancer LytB formation of a cellular spore Integral membrane protein None 1906 Vitamin B12-dependent methionine synthase, Methionine synthase activity activation domain 12 0 None None Bacterial periplasmic spermidine/putrescine-Transporter activity binding protein Prokaryotic chromosome segregation/condensation Chromosome segregation 12 1 protein MukB, N-terminal Transferase activity, Spore coat protein CotS transferring phosphoruscontaining groups Nucleoside recognition Gate Nucleoside binding Peptidyl-prolyl cis-trans Isomerase activity isomerase, PpiC-type 2 12 Signal transduction histidine Signal transduction kinase None None 0 16 No clusters No clusters 0 17 No clusters No clusters 0 18 No clusters No clusters Binding-protein-dependent 1 16 transport systems inner Transport activity membrane component No clusters No clusters 1 17 1 18 No clusters No clusters Supplementary table 3b. Gut-restricted Lachnospiraceae compared to all other gut-associated Lachnospiraceae Gut-Other gutrestricted associated genome genome GO count count InterPro Alcohol dehydrogenase, iron-Oxidoreductase activity Transferase activity, Aminoglycoside transferring phosphorusphosphotransferase containing groups Tetratricopeptide repeat Protein binding 11 0 Six-bladed beta-propeller, None TolB-like Tetratricopeptide repeat Protein binding None None None None None None Periplasmic binding protein None domain Pathogenesis Vacuolating cytotoxin Integral membrane protein None 1906 Signal transduction histidine Phosphorelay sensor kinase kinase activity Peptidoglycan-binding lysin Cell wall macromolecule catabolic process domain Protein phosphatase 2C Catalytic activity (PP2C)-like Periplasmic binding protein None domain YbbR-like None Type II secretion system F None domain 11 1 Colicin V production, CvpA Toxin biosynthetic process Tetratricopeptide repeat Protein binding Tetratricopeptide repeat Protein binding Haemerythrin-like, metal-Metal ion binding binding domain Spore cortex biosynthesis None protein, YabQ-like None 12 0 None None Bacterial periplasmic spermidine/putrescine-Polyamine transport binding protein Spore coat protein CotS None Nucleoside recognition Gate Nucleoside binding None None Electron transfer Electron carrier activity flavoprotein, alpha subunit Acyl-CoA Acyl-CoA dehydrogenase oxidase/dehydrogenase activity 0 9 Thiolase Transferase activity Enoyl-CoA hydratase/isomerase, Catalytic activity conserved site 0 10 No clusters No clusters Nitrogen regulatory protein Regulation of nitrogen PΙΙ utilization Binding-protein-dependent transport systems inner 1 9 Transporter activity membrane component NUDIX hydrolase domain Hydrolase activity Oxidoreductase activity Nitroreductase-like 10 No clusters No clusters Supplementary table 3c. Functions associated with Lachnospiraceae within the human GI tract that can produce butyric acid compared to those lacking this capability Gut-Gutassociated associated non-butyric butyric acid acid producing producing genome genome GO count count InterPro Electron transfer Flavin adenine dinucleotide flavoprotein, alpha subunit binding Acyl-CoA dehydrogenase, Oxidation-reduction process 9 0 conserved site Transferase activity Thiolase Metabolic process Crotonase superfamily Nitrogen regulatory protein 9 1 Enzyme regulator activity PII 10 0 No clusters No clusters 10 No clusters 1 No clusters 0 11 No clusters No clusters 0 12 No clusters No clusters Vacuolating cytotoxin Pathogenesis Protein phosphatase 2C Catalytic activity (PP2C)-like 1 11 Haemerythrin-like, metal-Metal ion binding

binding domain None

Protein kinase-like domain

InterPro

Sulfatase

Replication protein,

DnaD/DnaB domain

Phosphoglycerate/bisphosph

oglycerate mutase Calycin-like

Sporulation protein

YlmC/YmxH
Signal transduction histidine

kinase
Signal transduction

domain
Peptidase S8/S53,

response regulator, receiver

subtilisin/kexin/sedolisin

Phospholipid/glycerol

acyltransferase

CotJB

Spore coat assembly protein

Folylpolyglutamate

synthetase

Phosphoribosyl-ATP

pyrophosphohydrolase

Uncharacterised protein

family UPF0348 PBP domain

Nucleoside recognition Gate

Heat shock protein DnaJ

Peptidase S11, D-alanyl-D-

alanine carboxypeptidase A Stage III sporulation protein

Protein of unknown function

DUF3792, transmembrane Stage III sporulation protein

AC/AD family Sporulation protein

YabP/YqfC Stage III sporulation protein

AC
Multi antimicrobial extrusion

protein

PemK-like protein

Transcription regulator HTH,

GntR

Catalase, manganese Small acid-soluble spore

protein, alpha/beta-type DNA helicase, UvrD/REP

type
Penicillin-binding protein,

transpeptidase

Peptidase S11, D-alanyl-D-

alanine carboxypeptidase A

Sporulation stage III, protein AA

Peptidase A25, germination

protease Endodeoxyribonuclease IV

ClpP/TepA

Nucleoside recognition Gate

NIF system FeS cluster

assembly, NifU, N-terminal

STAS domain

Sporulation protein YabP

Transposon-encoded protein

TnpV
Sporulation stage II, protein

Ρ

PhoU

RNA-binding S4 domain

Stage V sporulation protein

RNA polymerase sigma-70

RNA polymerase sigma-70 factor

Primosome PriB/singlestrand DNA-binding

Peptidase S55, sporulation

stage IV, protein B
Sporulation stage II protein

D, amidase enhancer LytB

Stage V sporulation AD Cell wall

hydrolase/autolysin,

Protein of unknown function

DUF177 Sporulation stage V, protein

AC

ΑE

Anti-sigma F factor

Sporulation stage V, protein

catalytic Sporulation stage V, protein

factor

None

AH-like FMN-binding

Supplementary table 3d. All gut associated Lachnospiraceae compared to Lachnospiraceae from other habitats

12

Non-gut

genome

count

0

1

0

1

0

1

1

Gutassociated

genome

count

20

20

21

21

22

22

None

GO

Sulfuric ester hydrolase

activity

None

Catalytic activity

None

None

Signal transduction

Two-component signal

transduction system (phosphorelay)

Serine-type endopeptidase

Phospholipid biosynthetic

activity

process

None

Folic acid-containing

compound biosynthetic

process

Phosphoribosyl-AMP

cyclohydrolase activity

Catalytic activity

None

None

None

FMN binding

None

None

None

None

Drug transmembrane

transporter activity

binding transcription factor

DNA binding
Sequence-specific DNA

activity
Transition metal ion binding

DNA topological change

ATP-dependent DNA helicase activity

Peptidoglycan-based cell

wall biogenesis

Serine-type D-Ala-D-Ala

carboxypeptidase activity Nucleoside-triphosphatase

activity

Spore germination

DNA repair Serine-type endopeptidase

activity

Nucleoside binding

Iron-sulfur cluster assembly

Regulation of transcription,

DNA-dependent

None

None

Protein binding

RNA binding

None

None

Regulation of transcription, DNA-dependent

Regulation of transcription,

DNA-dependent Single-stranded DNA

binding

Protein binding

Metabolic process

Catalytic activity

Peptidoglycan catabolic

process

None

None

None

Protein serine/threonine

kinase activity

None

Nucleoside binding

Heat shock protein binding

Serine-type D-Ala-D-Ala carboxypeptidase activity

Transferase activity