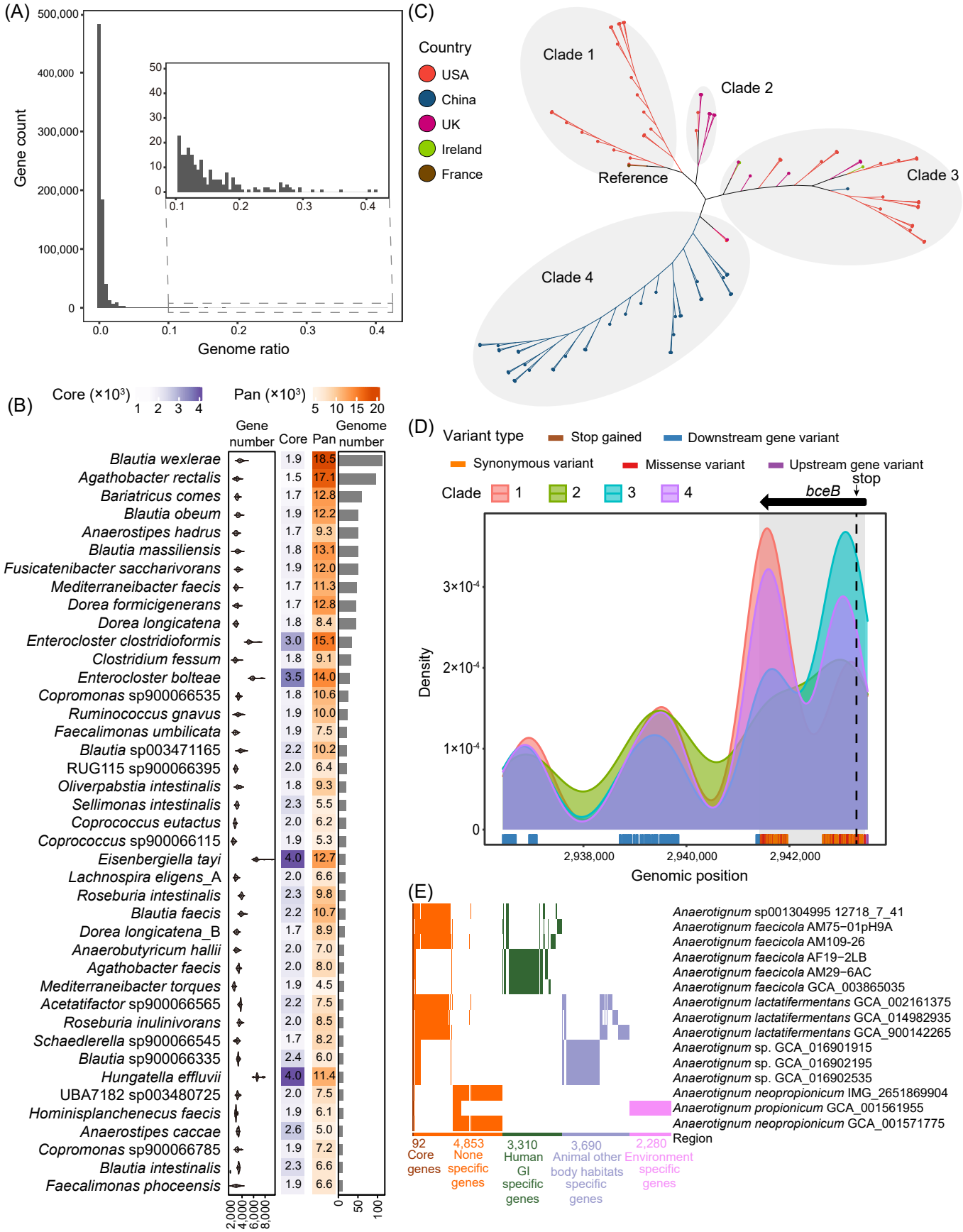
(A)
Gene count
Genome ratio
(B)
Core (×10³)
Pan (×10³)
Gene number
Core
Pan
Genome number
Blautia wexlerae
Agathobacter rectalis
Bariatricus comes
Blautia obeum
Anaerostipes hadrus
Blautia massiliensis
Fusicatenibacter saccharivorans
Mediterraneibacter faecis
Dorea formicigenerans
Dorea longicatena
Enterocloster clostridioformis
Clostridium fessum
Enterocloster bolteae
Copromonas sp900066535
Ruminococcus gnavus
Faecalimonas umbilicata
Blautia sp003471165
RUG115 sp900066395
Oliverpabstia intestinalis
Sellimonas intestinalis
Coprococcus eutactus
Coprococcus sp900066115
Eisenbergiella tayi
Lachnospira eligens_A
Roseburia intestinalis
Blautia faecis
Dorea longicatena_B
Anaerobutyricum hallii
Agathobacter faecis
Mediterraneibacter torques
Acetatifactor sp900066565
Roseburia inulinivorans
Schaedlerella sp900066545
Blautia sp900066335
Hungatella effluvii
UBA7182 sp003480725
Hominisplanchenecus faecis
Anaerostipes caccae
Copromonas sp900066785
Blautia intestinalis
Faecalimonas phoceensis
(C)
Country
USA
China
UK
Ireland
France
Clade 1
Clade 2
Clade 3
Clade 4
Reference
(D)
Variant type
Stop gained
Downstream gene variant
Synonymous variant
Missense variant
Upstream gene variant
Clade
1
2
3
4
bceB
stop
Density
Genomic position
(E)
Anaerotignum sp001304995 12718_7_41
Anaerotignum faecicola AM75−01pH9A
Anaerotignum faecicola AM109-26
Anaerotignum faecicola AF19−2LB
Anaerotignum faecicola AM29−6AC
Anaerotignum faecicola GCA_003865035
Anaerotignum lactatifermentans GCA_002161375
Anaerotignum lactatifermentans GCA_014982935
Anaerotignum lactatifermentans GCA_900142265
Anaerotignum sp. GCA_016901915
Anaerotignum sp. GCA_016902195
Anaerotignum sp. GCA_016902535
Anaerotignum neopropionicum IMG_2651869904
Anaerotignum propionicum GCA_001561955
Anaerotignum neopropionicum GCA_001571775
Region
92 Core genes
4,853 None specific genes
3,310 Human GI specific genes
3,690 Animal other body habitats specific genes
2,280 Environment specific genes