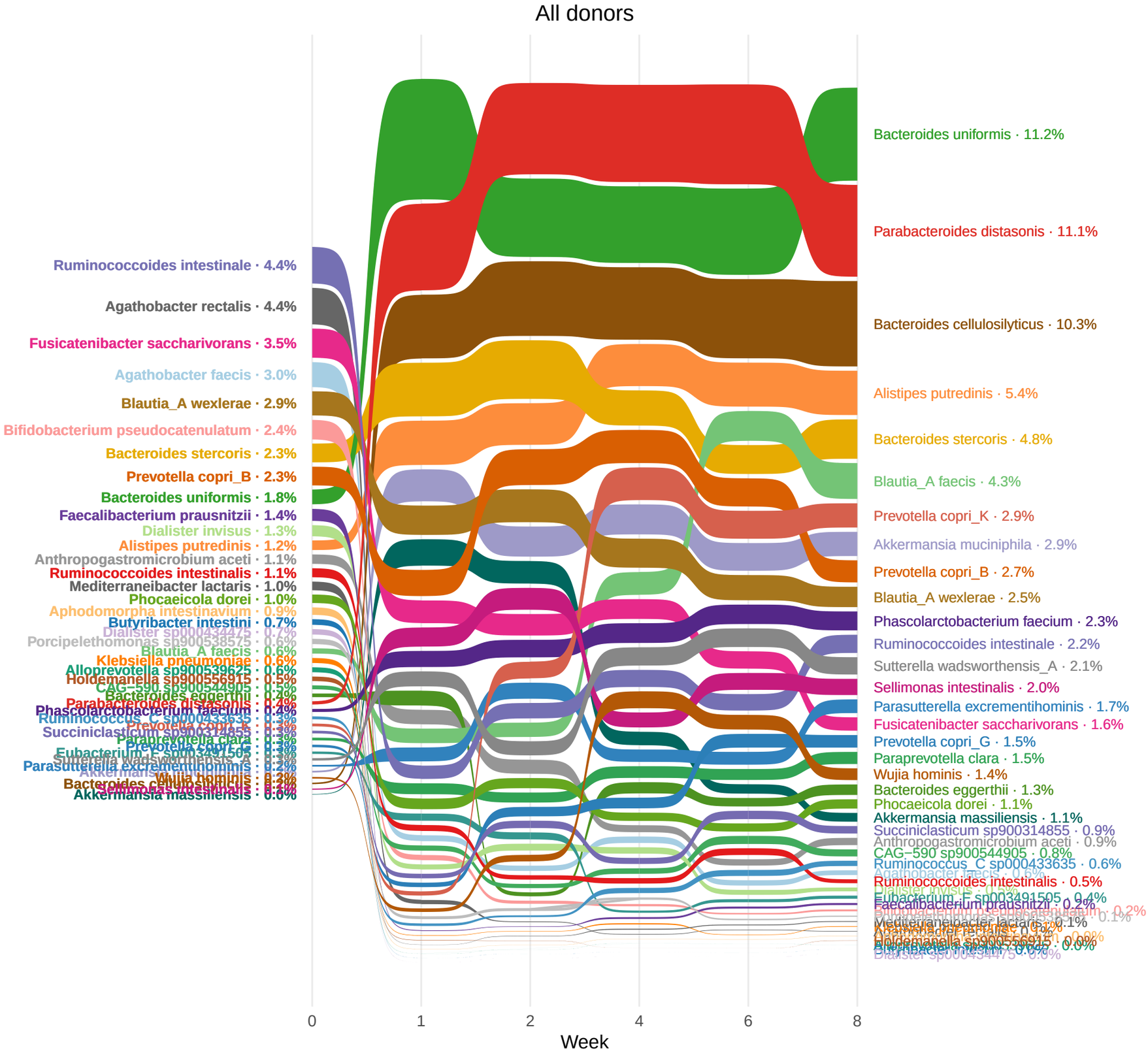
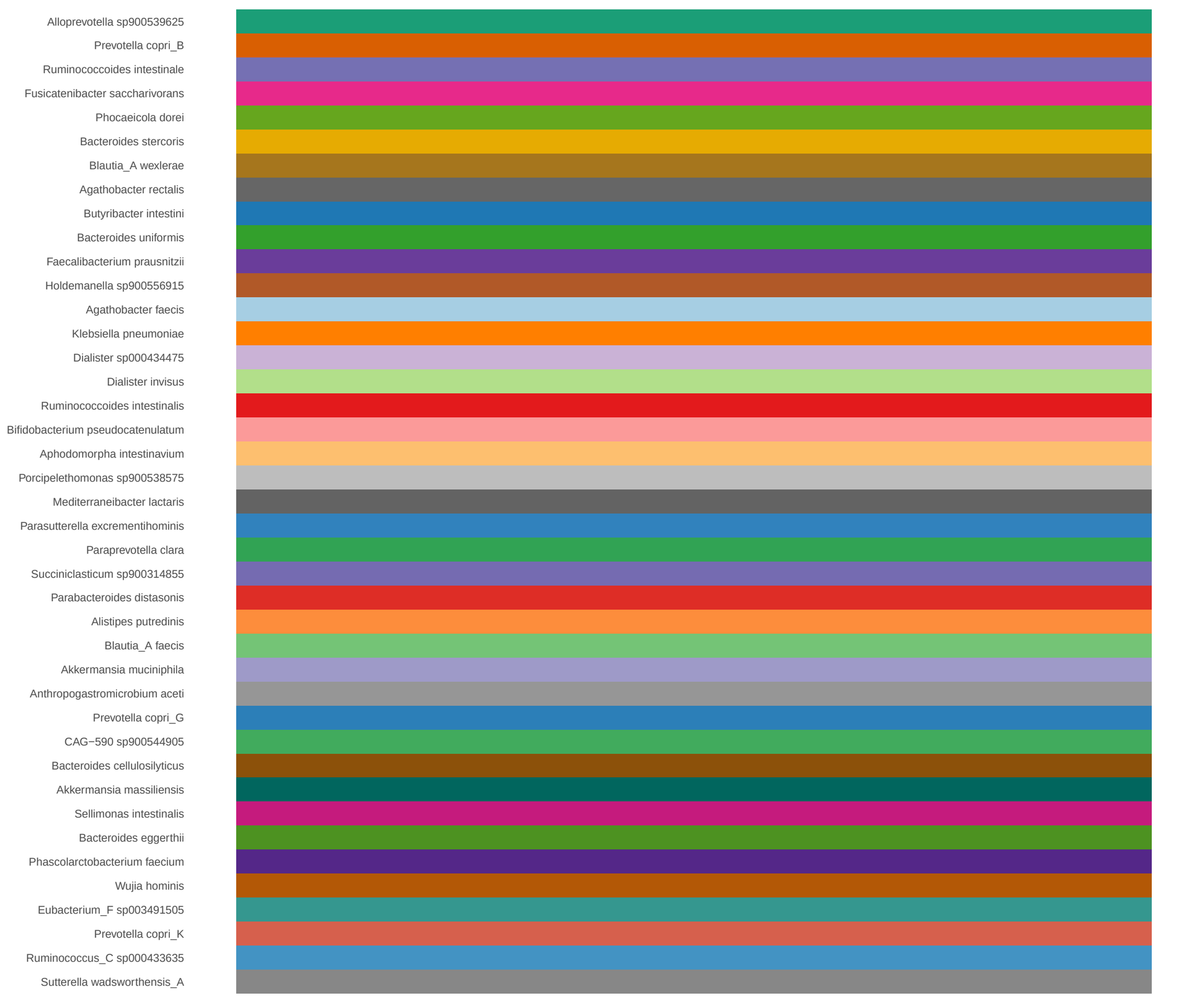
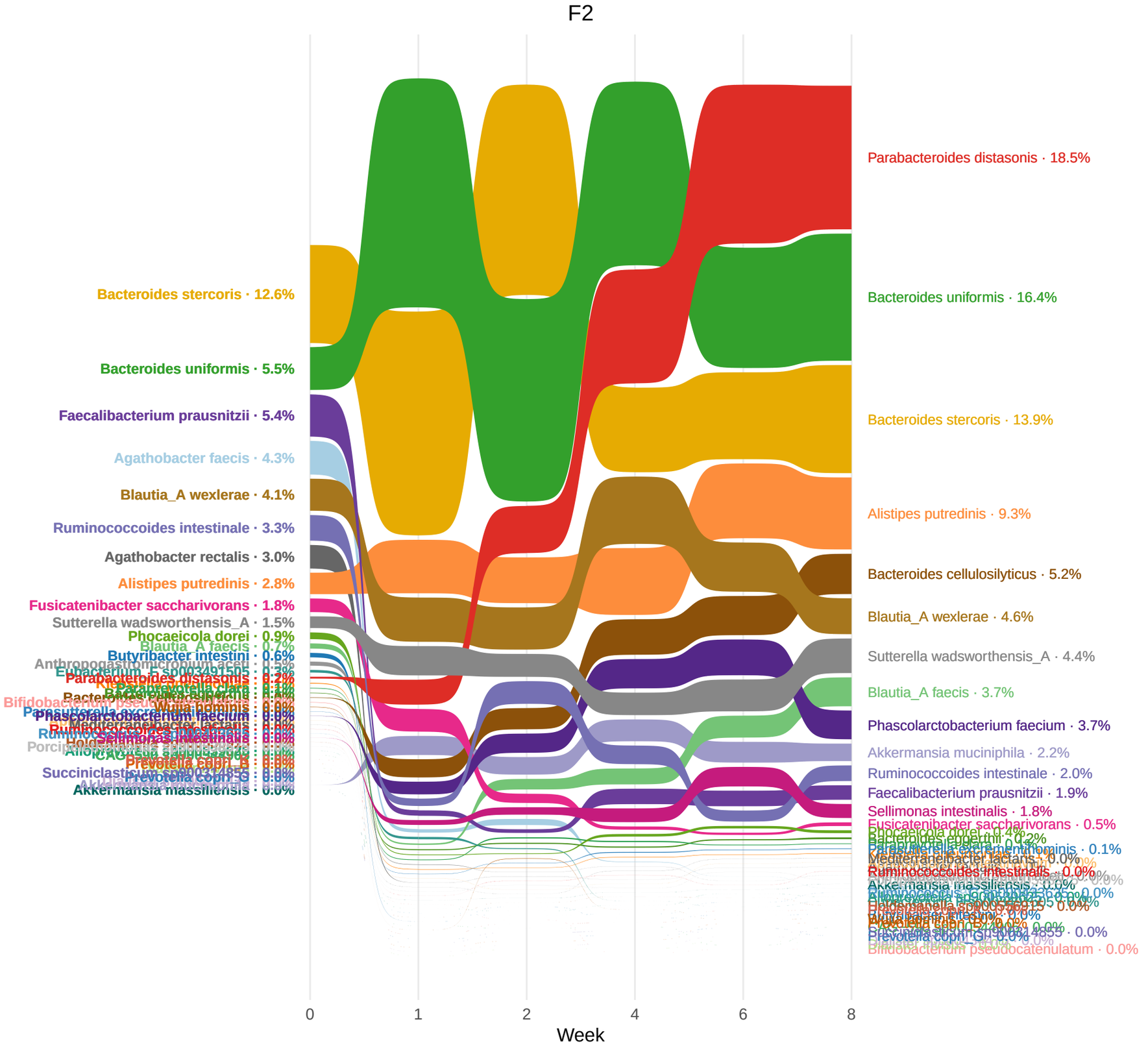
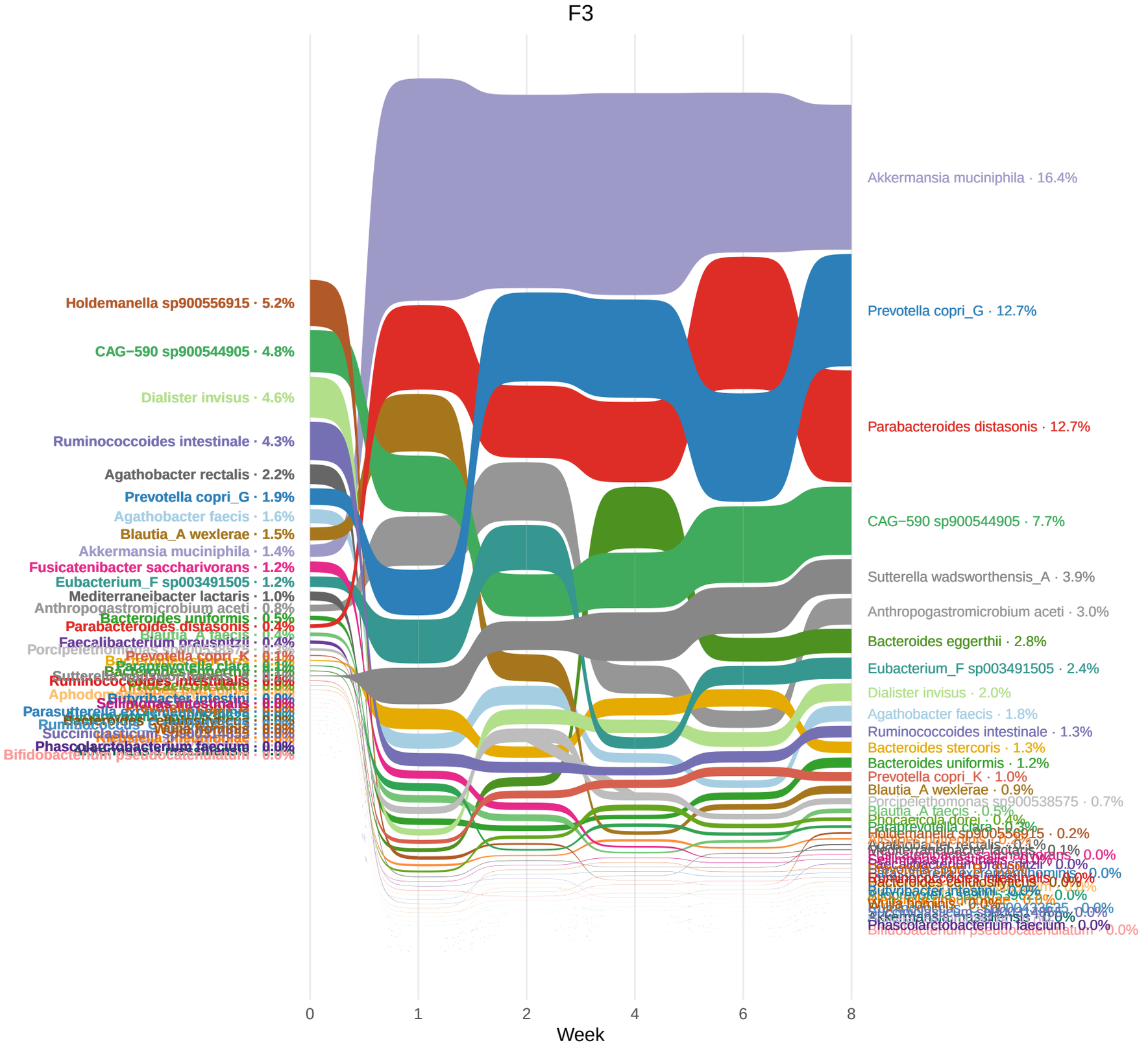

All donors
Ruminococcoides intestinale · 4.4%
Agathobacter rectalis · 4.4%
Fusicatenibacter saccharivorans · 3.5%
Agathobacter faecis · 3.0%
Blautia_A wexlerae · 2.9%
Bifidobacterium pseudocatenulatum · 2.4%
Bacteroides stercoris · 2.3%
Prevotella copri_B · 2.3%
Bacteroides uniformis · 1.8%
Faecalibacterium prausnitzii · 1.4%
Dialister invisus · 1.3%
Alistipes putredinis · 1.2%
Anthropogastromicrobium aceti · 1.1%
Ruminococcoides intestinalis · 1.1%
Mediterraneibacter lactaris · 1.0%
Phocaeicola dorei · 1.0%
Aphodomorpha intestinavium · 0.9%
Butyribacter intestini · 0.7%
Dialister sp900434475 · 0.7%
Porcipelethomonas sp900538575 · 0.6%
Blautia_A faecis · 0.6%
Klebsiella pneumoniae · 0.6%
Alloprevotella sp900539625 · 0.6%
Holdemanella sp900556915 · 0.5%
CAG−590 sp900544905 · 0.5%
Bacteroides eggerthii · 0.4%
Parabacteroides distasonis · 0.4%
Phascolarctobacterium faecium · 0.4%
Ruminococcus_C sp000433635 · 0.3%
Prevotella copri_K · 0.3%
Succiniclasticum sp900314855 · 0.3%
Paraprevotella clara · 0.3%
Prevotella copri_G · 0.3%
Eubacterium_E sp900341505 · 0.3%
Sutterella wadsworthensis_A · 0.2%
Parasutterella excrementihominis · 0.2%
Akkermansia muciniphila · 0.2%
Wujia hominis · 0.2%
Bacteroides cellulosilyticus · 0.2%
Sellimonas intestinalis · 0.2%
Akkermansia massiliensis · 0.0%
Bacteroides uniformis · 11.2%
Parabacteroides distasonis · 11.1%
Bacteroides cellulosilyticus · 10.3%
Alistipes putredinis · 5.4%
Bacteroides stercoris · 4.8%
Blautia_A faecis · 4.3%
Prevotella copri_K · 2.9%
Akkermansia muciniphila · 2.9%
Prevotella copri_B · 2.7%
Blautia_A wexlerae · 2.5%
Phascolarctobacterium faecium · 2.3%
Ruminococcoides intestinale · 2.2%
Sutterella wadsworthensis_A · 2.1%
Sellimonas intestinalis · 2.0%
Parasutterella excrementihominis · 1.7%
Fusicatenibacter saccharivorans · 1.6%
Prevotella copri_G · 1.5%
Paraprevotella clara · 1.5%
Wujia hominis · 1.4%
Bacteroides eggerthii · 1.3%
Phocaeicola dorei · 1.1%
Akkermansia massiliensis · 1.1%
Succiniclasticum sp900314855 · 0.9%
Anthropogastromicrobium aceti · 0.9%
CAG−590 sp900544905 · 0.8%
Ruminococcus_C sp000433635 · 0.6%
Agathobacter faecis · 0.5%
Ruminococcoides intestinalis · 0.5%
Eubacterium_E sp900341505 · 0.4%
Faecalibacterium prausnitzii · 0.2%
Bifidobacterium pseudocatenulatum · 0.2%
Dialister invisus · 0.1%
Mediterraneibacter lactaris · 0.1%
Agathobacter rectalis · 0.0%
Holdemanella sp900556915 · 0.0%
Porcipelethomonas sp900538575 · 0.0%
Dialister sp900434475 · 0.0%
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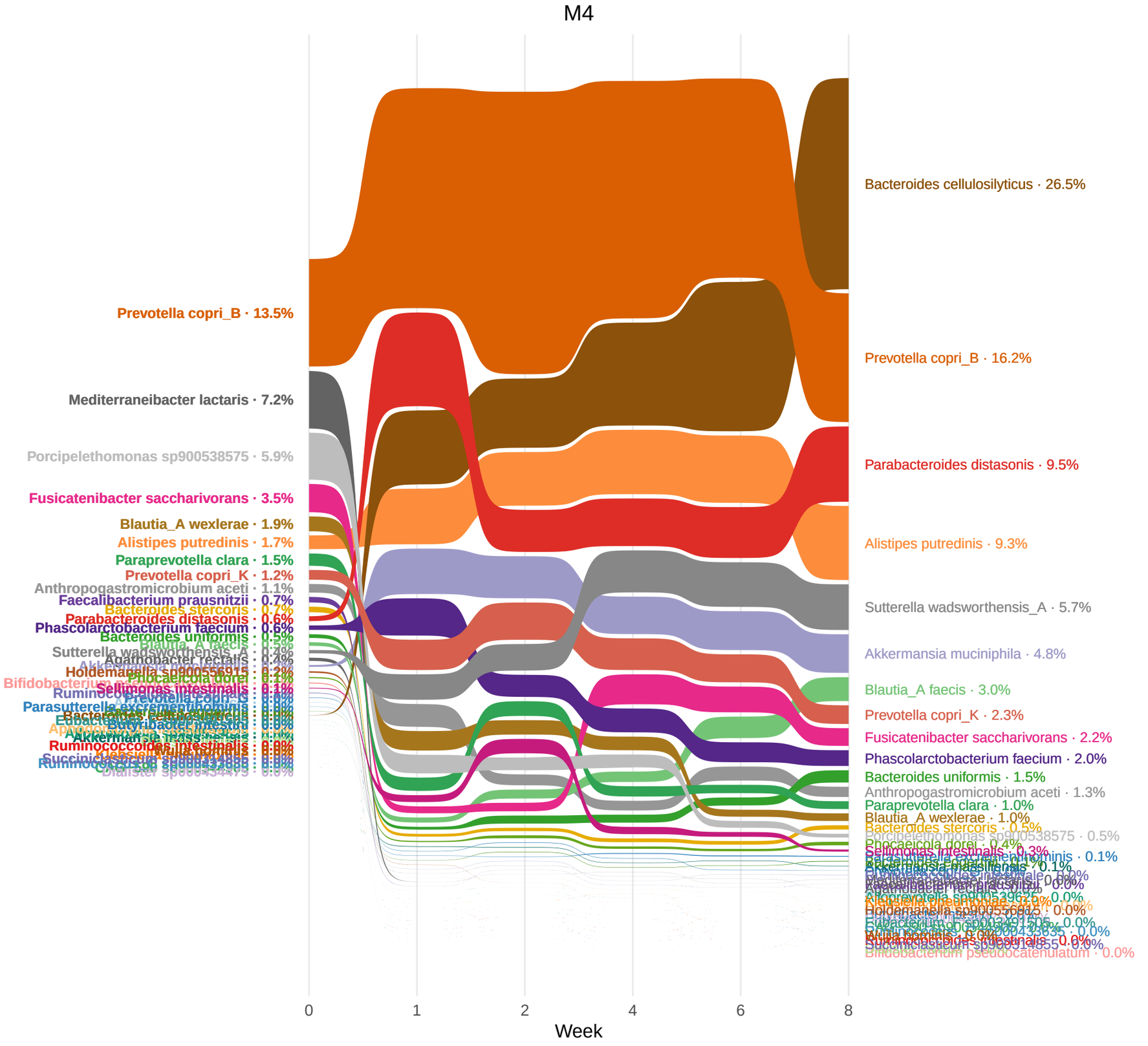

Alloprevotella sp900539625
Prevotella copri_B
Ruminococcoides intestinale
Fusicatenibacter saccharivorans
Phocaeicola dorei
Bacteroides stercoris
Blautia_A wexlerae
Agathobacter rectalis
Butyribacter intestini
Bacteroides uniformis
Faecalibacterium prausnitzii
Holdemanella sp900556915
Agathobacter faecis
Klebsiella pneumoniae
Dialister sp000434475
Dialister invisus
Ruminococcoides intestinalis
Bifidobacterium pseudocatenulatum
Aphodomorpha intestinavium
Porcipelethomonas sp900538575
Mediterraneibacter lactaris
Parasutterella excrementihominis
Paraprevotella clara
Succiniclasticum sp900314855
Parabacteroides distasonis
Alistipes putredinis
Blautia_A faecis
Akkermansia muciniphila
Anthropogastromicrobium aceti
Prevotella copri_G
CAG−590 sp900544905
Bacteroides cellulosilyticus
Akkermansia massiliensis
Sellimonas intestinalis
Bacteroides eggerthii
Phascolarctobacterium faecium
Wujia hominis
Eubacterium_F sp003491505
Prevotella copri_K
Ruminococcus_C sp000433635
Sutterella wadsworthensis_A


F0
Prevotella copri_B · 9.0%
Ruminococcoides intestinale · 7.9%
Alloprevotella sp900539625 · 5.9%
Fusicatenibacter saccharivorans · 4.1%
Blautia_A wexlerae · 4.1%
Agathobacter rectalis · 3.5%
Succiniclasticum sp900314855 · 3.3%
Agathobacter faecis · 2.5%
Ruminococcus_C sp000433635 · 1.6%
Wujia hominis · 1.5%
Prevotella copri_G · 1.1%
Paraprevotella clara · 1.1%
Prevotella copri_K · 0.7%
Faecalibacterium prausnitzii · 0.4%
Mediterraneibacter lactaris · 0.4%
Bacteroides uniformis · 0.3%
Parabacteroides distasonis · 0.1%
Parasutterella excrementihominis · 0.0%
Ruminococcoides intestinale · 0.0%
Phascolarctobacterium faecium · 0.0%
Akkermansia massiliensis · 0.0%
Wujia hominis · 12.1%
Bacteroides uniformis · 10.4%
Ruminococcoides intestinale · 9.9%
Succiniclasticum sp900314855 · 8.3%
Prevotella copri_B · 7.8%
Paraprevotella clara · 5.2%
Blautia_A faecis · 5.2%
Ruminococcus_C sp000433635 · 4.7%
Sellimonas intestinalis · 4.3%
Parasutterella excrementihominis · 3.6%
Bacteroides eggerthii · 3.2%
Parabacteroides distasonis · 2.6%
Phocaeicola dorei · 2.0%
Agathobacter faecis · 1.5%
Prevotella copri_G · 1.1%
Bacteroides cellulosilyticus · 0.8%
Bacteroides stercoris · 0.8%
Prevotella copri_K · 0.5%
Agathobacter rectalis · 0.0%
Fusicatenibacter saccharivorans · 0.0%
Faecalibacterium prausnitzii · 0.0%
Mediterraneibacter lactaris · 0.0%
Akkermansia massiliensis · 0.0%
Phascolarctobacterium faecium · 0.0%
Akkermansia muciniphila · 0.0%
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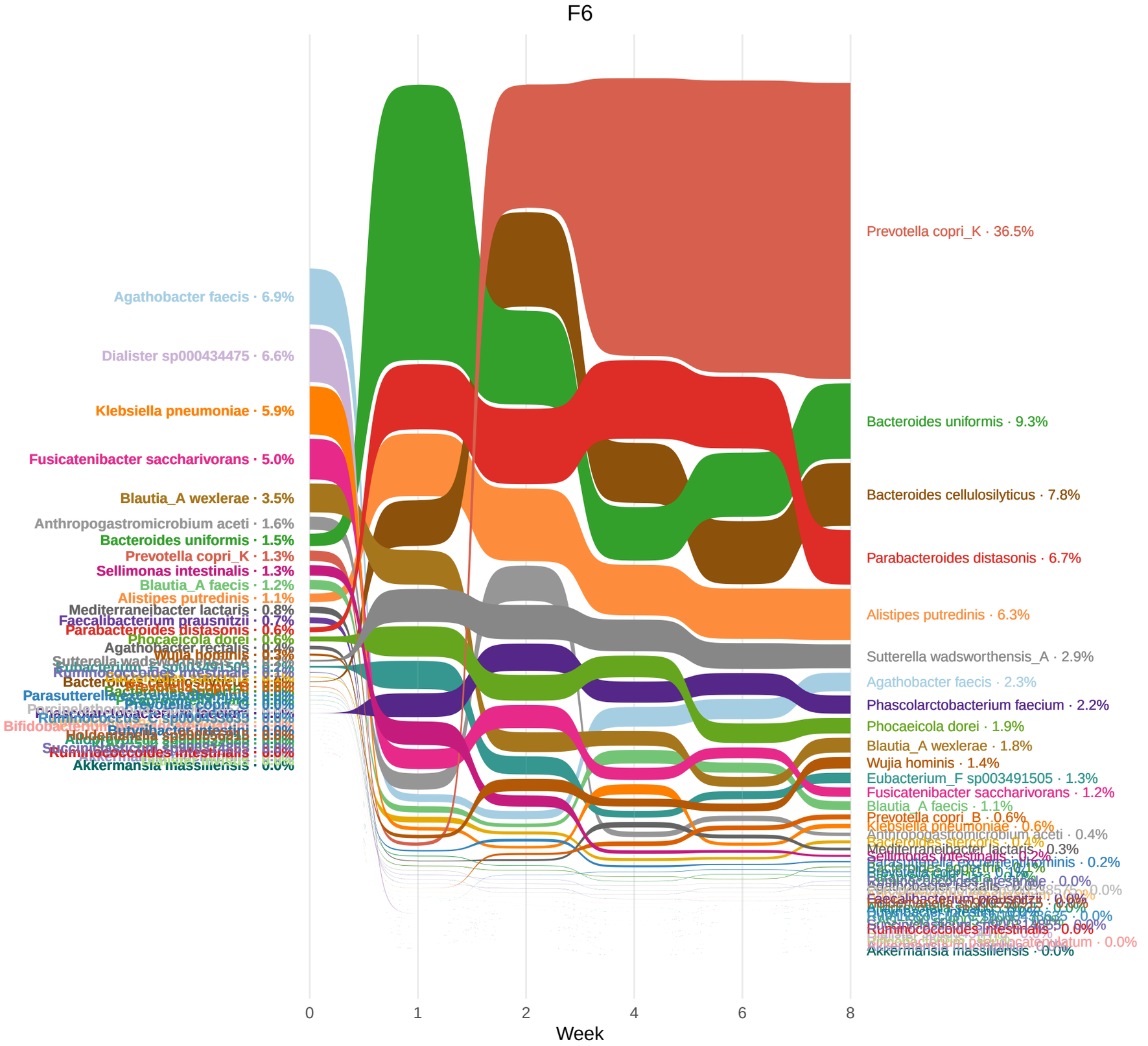

F1
Ruminococcoides intestinale · 9.0%
Bacteroides stercoris · 8.3%
Agathobacter rectalis · 6.8%
Phocaeicola dorei · 6.4%
Butyribacter intestini · 6.0%
Blautia_A wexlerae · 5.9%
Fusicatenibacter saccharivorans · 5.9%
Bacteroides uniformis · 4.7%
Bifidobacterium pseudocatenulatum · 4.1%
Faecalibacterium prausnitzii · 1.7%
Dialister invisus · 1.7%
Parabacteroides distasonis · 0.9%
Blautia_A faecis · 0.8%
Mediterraneibacter lactaris · 0.7%
Alistipes putredinis · 0.7%
Parasutterella excrementihominis · 0.7%
Anthropogastromicrobium aceti · 0.6%
Bacteroides eggerthii · 0.1%
Paraprevotella clara · 0.0%
Ruminococcoides intestinalis · 0.0%
Akkermansia massiliensis · 0.0%
Bacteroides uniformis · 36.8%
Bacteroides stercoris · 27.5%
Alistipes putredinis · 5.6%
Parabacteroides distasonis · 5.2%
Blautia_A wexlerae · 3.5%
Phocaeicola dorei · 2.8%
Sellimonas intestinalis · 2.5%
Blautia_A faecis · 2.4%
Akkermansia muciniphila · 1.4%
Ruminococcoides intestinale · 1.3%
Fusicatenibacter saccharivorans · 1.2%
Parasutterella excrementihominis · 1.1%
Bacteroides eggerthii · 0.2%
Anthropogastromicrobium aceti · 0.2%
Paraprevotella clara · 0.0%
Mediterraneibacter lactaris · 0.0%
Faecalibacterium prausnitzii · 0.0%
Ruminococcoides intestinalis · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
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Week

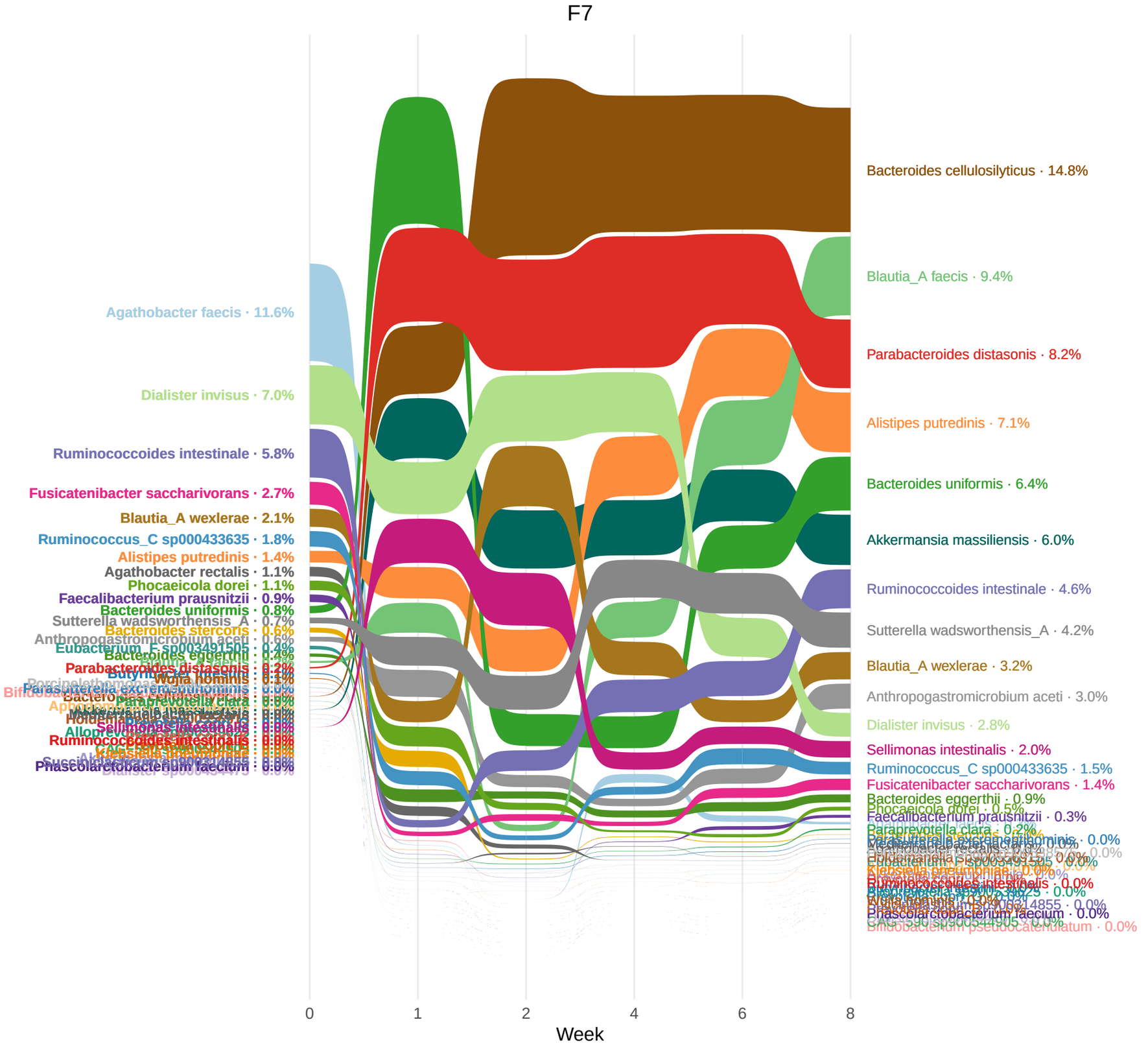

F2
Bacteroides stercoris · 12.6%
Bacteroides uniformis · 5.5%
Faecalibacterium prausnitzii · 5.4%
Agathobacter faecis · 4.3%
Blautia_A wexlerae · 4.1%
Ruminococcoides intestinale · 3.3%
Agathobacter rectalis · 3.0%
Alistipes putredinis · 2.8%
Fusicatenibacter saccharivorans · 1.8%
Sutterella wadsworthensis_A · 1.5%
Phocaeicola dorei · 0.9%
Blautia_A faecis · 0.7%
Butyricibacter intestini · 0.6%
Anthropogastromicroorgm acetigenes · 0.5%
Eubacterium_F sp003491505 · 0.3%
Parabacteroides distasonis · 0.2%
Bacteroides cellulosilyticus · 0.1%
Bifidobacterium pseudocatenulatum · 0.0%
Phascolarctobacterium faecium · 0.0%
Mediterraneibacter lactaris · 0.0%
Akkermansia massiliensis · 0.0%
Parabacteroides distasonis · 18.5%
Bacteroides uniformis · 16.4%
Bacteroides stercoris · 13.9%
Alistipes putredinis · 9.3%
Bacteroides cellulosilyticus · 5.2%
Blautia_A wexlerae · 4.6%
Sutterella wadsworthensis_A · 4.4%
Blautia_A faecis · 3.7%
Phascolarctobacterium faecium · 3.7%
Akkermansia muciniphila · 2.2%
Ruminococcoides intestinale · 2.0%
Faecalibacterium prausnitzii · 1.9%
Sellimonas intestinalis · 1.8%
Fusicatenibacter saccharivorans · 0.5%
Phocaeicola dorei · 0.4%
Bacteroides eggerthii · 0.2%
Parasutterella excrementihominis · 0.1%
Mediterraneibacter lactaris · 0.0%
Ruminococcoides intestinalis · 0.0%
Akkermansia massiliensis · 0.0%
Prevotella copri_B · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
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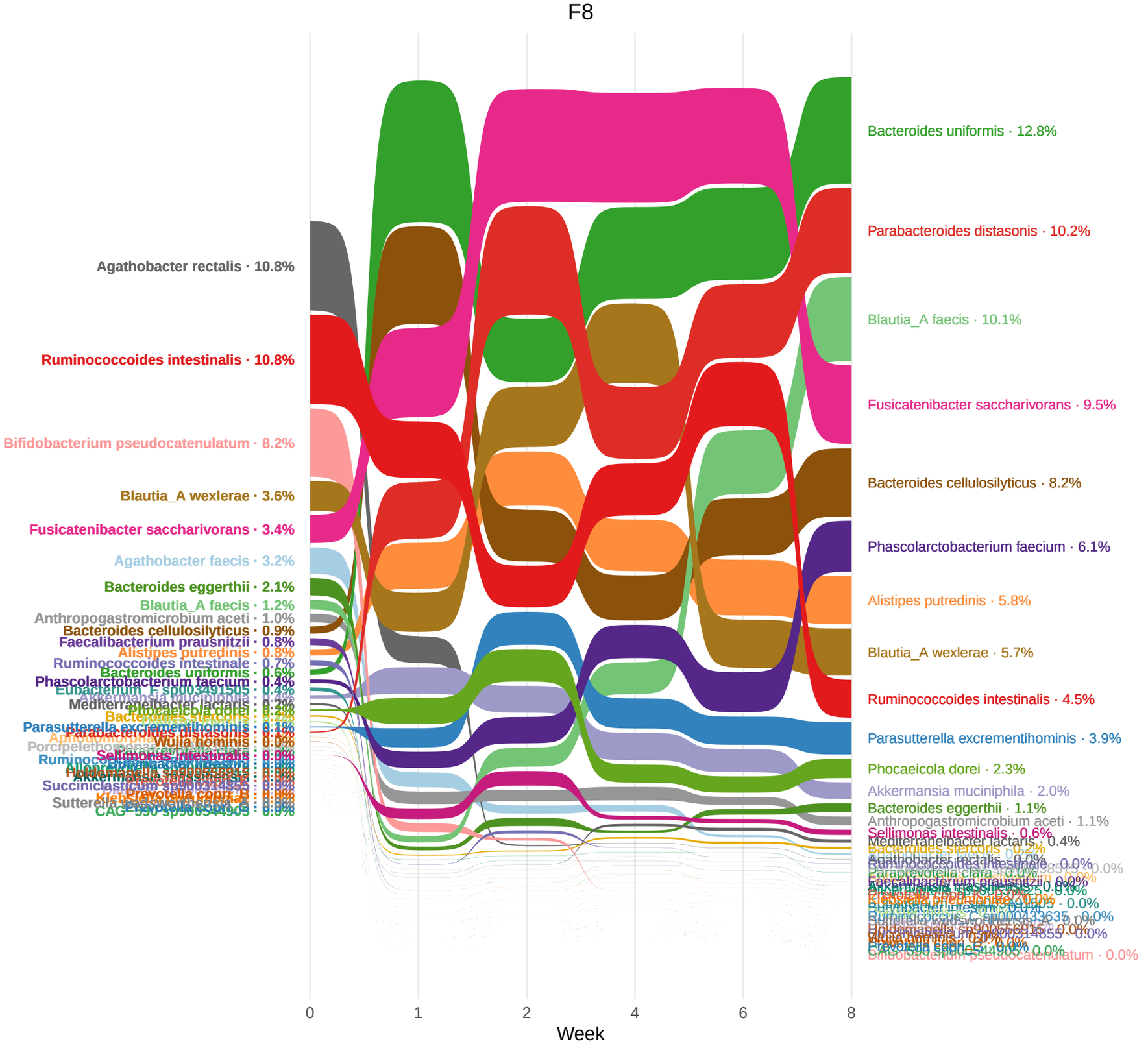

F3
Holdemanella sp900556915 · 5.2%
CAG−590 sp900544905 · 4.8%
Dialister invisus · 4.6%
Ruminococcoides intestinale · 4.3%
Agathobacter rectalis · 2.2%
Prevotella copri_G · 1.9%
Agathobacter faecis · 1.6%
Blautia_A wexlerae · 1.5%
Akkermansia muciniphila · 1.4%
Fusicatenibacter saccharivorans · 1.2%
Eubacterium_F sp003491505 · 1.2%
Mediterraneibacter lactaris · 1.0%
Anthropogastromicrobium aceti · 0.8%
Bacteroides uniformis · 0.5%
Parabacteroides distasonis · 0.4%
Blautia_A faecis · 0.4%
Faecalibacterium prausnitzii · 0.4%
Porcipelethomonas sp900538575 · 0.3%
Prevotella copri_K · 0.1%
Bacteroides stercoris · 0.1%
Paraprevotella clara · 0.1%
Sutterella wadsworthensis_A · 0.1%
Ruminococcoides intestinale · 0.0%
Anthropogastromicrobium aceti · 0.0%
Aphodomorpha sp900539415 · 0.0%
Butyribacter intestini · 0.0%
Selenomonas intestinalis · 0.0%
Parasutterella excrementihominis · 0.0%
Faecalibacterium sp900539435 · 0.0%
Ruminococcus gallinaceus · 0.0%
Succinidiscus sp900539415 · 0.0%
Klebsiella pneumoniae · 0.0%
Phascolarctobacterium faecium · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
Akkermansia muciniphila · 16.4%
Prevotella copri_G · 12.7%
Parabacteroides distasonis · 12.7%
CAG−590 sp900544905 · 7.7%
Sutterella wadsworthensis_A · 3.9%
Anthropogastromicrobium aceti · 3.0%
Bacteroides eggerthii · 2.8%
Eubacterium_F sp003491505 · 2.4%
Dialister invisus · 2.0%
Agathobacter faecis · 1.8%
Ruminococcoides intestinale · 1.3%
Bacteroides stercoris · 1.3%
Bacteroides uniformis · 1.2%
Prevotella copri_K · 1.0%
Blautia_A wexlerae · 0.9%
Porcipelethomonas sp900538575 · 0.7%
Blautia_A faecis · 0.5%
Phocaecola dorei · 0.4%
Parapreverotella clara · 0.3%
Holdemanella sp900556915 · 0.2%
Agathobacter rectalis · 0.1%
Mediterraneibacter lactaris · 0.1%
Phascolarctobacterium faecium · 0.0%
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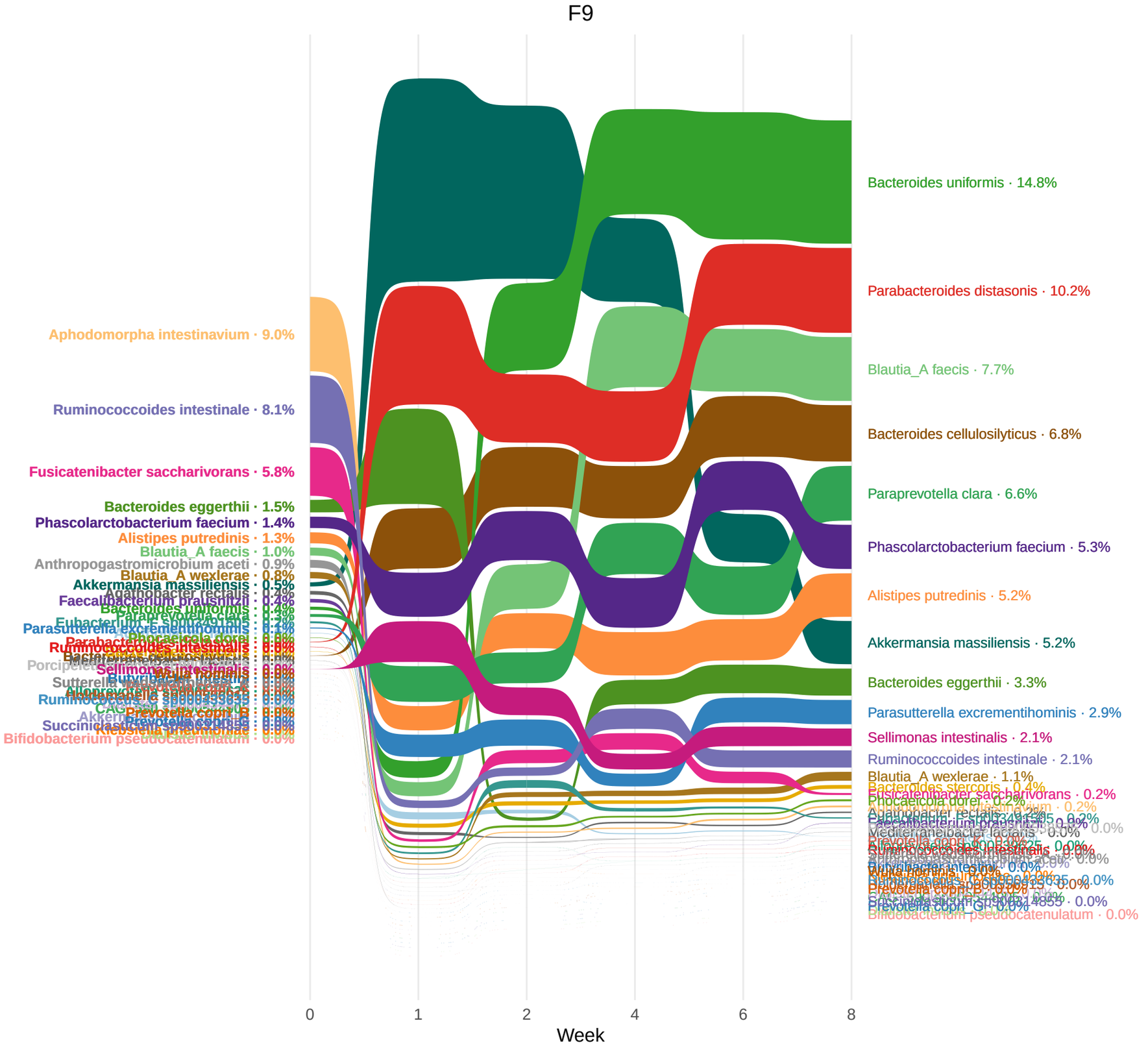

M4
Prevotella copri_B · 13.5%
Mediterraneibacter lactaris · 7.2%
Porcipelethomonas sp900538575 · 5.9%
Fusicatenibacter saccharivorans · 3.5%
Blautia_A wexlerae · 1.9%
Alistipes putredinis · 1.7%
Paraprevotella clara · 1.5%
Prevotella copri_K · 1.2%
Anthropogastromicrobium aceti · 1.1%
Faecalibacterium prausnitzii · 0.7%
Bacteroides stercoris · 0.7%
Parabacteroides distasonis · 0.6%
Phascolarctobacterium faecium · 0.6%
Bacteroides uniformis · 0.5%
Blautia_A faecis · 0.5%
Sutterella wadsworthensis_A · 0.4%
Agathobacter rectalis · 0.4%
Holdemanella sp900556915 · 0.2%
Phocaeicola dorei · 0.1%
Sellimonas intestinalis · 0.1%
Bifidobacterium pseudocatenulatum · 0.0%
Ruminococcus_E bromii_B · 0.0%
Parasutterella excrementihominis · 0.0%
Bacteroides cellulosilyticus · 26.5%
Prevotella copri_B · 16.2%
Parabacteroides distasonis · 9.5%
Alistipes putredinis · 9.3%
Sutterella wadsworthensis_A · 5.7%
Akkermansia muciniphila · 4.8%
Blautia_A faecis · 3.0%
Prevotella copri_K · 2.3%
Fusicatenibacter saccharivorans · 2.2%
Phascolarctobacterium faecium · 2.0%
Bacteroides uniformis · 1.5%
Anthropogastromicrobium aceti · 1.3%
Paraprevotella clara · 1.0%
Blautia_A wexlerae · 1.0%
Bacteroides stercoris · 0.5%
Porcipelethomonas sp900538575 · 0.5%
Phocaeicola dorei · 0.4%
Sellimonas intestinalis · 0.3%
Parasutterella excrementihominis · 0.1%
Akkermansia biassiensis · 0.1%
Ruminococcus_E bromii_B · 0.0%
Agathobacter rectalis · 0.0%
Holdemanella sp900556915 · 0.0%
Eubacterium_F sp003491505 · 0.0%
Ruminococcoides intestinalis · 0.0%
Succiniclasticum sp900314855 · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
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Week


M5
Agathobacter rectalis · 15.4%
Bifidobacterium pseudocatenulatum · 11.2%
Ruminococcoides intestinale · 5.1%
Anthropogastromicrobium aceti · 3.9%
Faecalibacterium prausnitzii · 3.0%
Bacteroides uniformis · 2.9%
Alistipes putredinis · 1.8%
Fusicatenibacter saccharivorans · 1.7%
Blautia_A wexlerae · 1.7%
Phascolarctobacterium faecium · 1.2%
Parasutterella excrementihominis · 1.0%
Phocaeicola dorei · 0.8%
Bacteroides cellulosilyticus · 0.7%
Parabacteroides distasonis · 0.7%
Blautia_A faecis · 0.4%
Butyribacter intestini · 0.1%
Ruminococcoides intestinalis · 0.0%
Sellimonas intestinalis · 0.0%
Wujia hominis · 0.0%
Alloprevotella rava · 0.0%
Prevotella copri_B · 0.0%
CAG-590 sp900544905 · 0.0%
Succinilasticum sp900314895 · 0.0%
Klebsiella pneumoniae · 0.0%
Akkermansia massiliensis · 0.0%
Bacteroides cellulosilyticus · 35.7%
Parabacteroides distasonis · 26.5%
Sellimonas intestinalis · 5.5%
Alistipes putredinis · 5.3%
Parasutterella excrementihominis · 4.1%
Phascolarctobacterium faecium · 3.2%
Blautia_A wexlerae · 3.0%
Bifidobacterium pseudocatenulatum · 2.5%
Bacteroides uniformis · 1.4%
Phocaeicola dorei · 0.6%
Bacteroides stercoris · 0.2%
Klebsiella pneumoniae · 0.1%
Fusicatenibacter saccharivorans · 0.1%
Ruminococcoides intestinale · 0.0%
Anthropogastromicrobium aceti · 0.0%
Akkermansia massiliensis · 0.0%
Faecalibacterium prausnitzii · 0.0%
Butyribacter intestini · 0.0%
Prevotella copri_B · 0.0%
Alloprevotella rava · 0.0%
Holdemanella sp900556915 · 0.0%
Ruminococcoides intestinalis · 0.0%
Wujia hominis · 0.0%
Succinilasticum sp900314895 · 0.0%
Prevotella copri_G · 0.0%
CAG-590 sp900544905 · 0.0%
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Week


F6
Agathobacter faecis · 6.9%
Dialister sp000434475 · 6.6%
Klebsiella pneumoniae · 5.9%
Fusicatenibacter saccharivorans · 5.0%
Blautia_A wexlerae · 3.5%
Anthropogastromicrobium aceti · 1.6%
Bacteroides uniformis · 1.5%
Prevotella copri_K · 1.3%
Sellimonas intestinalis · 1.3%
Blautia_A faecis · 1.2%
Alistipes putredinis · 1.1%
Mediterraneibacter lactaris · 0.8%
Faecalibacterium prausnitzii · 0.7%
Parabacteroides distasonis · 0.6%
Phocaeicola dorei · 0.6%
Agathobacter rectalis · 0.4%
Wujia hominis · 0.3%
Sutterella wadsworthensis_A · 0.3%
Eubacterium_F sp003491505 · 0.2%
Ruminococcoides intestinalis · 0.2%
Bacteroides cellulosilyticus · 0.2%
Bacteroides eggerthii · 0.1%
Parasutterella excrementihominis · 0.1%
Prevotella copri_B · 0.0%
Phascolarctobacterium faecium · 0.0%
Ruminococcus_C sp000433595 · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
Holdemanella biformis · 0.0%
Alistipes shahii · 0.0%
Subdoligranulum sp004024845 · 0.0%
Ruminococcoides intestinalis · 0.0%
Akkermansia massiliensis · 0.0%
Prevotella copri_K · 36.5%
Bacteroides uniformis · 9.3%
Bacteroides cellulosilyticus · 7.8%
Parabacteroides distasonis · 6.7%
Alistipes putredinis · 6.3%
Sutterella wadsworthensis_A · 2.9%
Agathobacter faecis · 2.3%
Phascolarctobacterium faecium · 2.2%
Phocaeicola dorei · 1.9%
Blautia_A wexlerae · 1.8%
Wujia hominis · 1.4%
Eubacterium_F sp003491505 · 1.3%
Fusicatenibacter saccharivorans · 1.2%
Blautia_A faecis · 1.1%
Prevotella copri_B · 0.6%
Klebsiella pneumoniae · 0.6%
Anthropogastromicrobium aceti · 0.4%
Bacteroides stercoris · 0.4%
Mediterraneibacter lactaris · 0.3%
Sellimonas intestinalis · 0.2%
Parasutterella excrementihominis · 0.2%
Bacteroides eggerthii · 0.1%
Prevotella copri_C · 0.1%
Parabacteroides faecalis · 0.0%
Agathobacter rectalis · 0.0%
Faecalibacterium prausnitzii · 0.0%
Alistipes shahii · 0.0%
Subdoligranulum sp004024845 · 0.0%
Holdemanella biformis · 0.0%
Ruminococcoides intestinalis · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
Akkermansia massiliensis · 0.0%
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8
Week


F7
Agathobacter faecis · 11.6%
Dialister invisus · 7.0%
Ruminococcoides intestinale · 5.8%
Fusicatenibacter saccharivorans · 2.7%
Blautia_A wexlerae · 2.1%
Ruminococcus_C sp000433635 · 1.8%
Alistipes putredinis · 1.4%
Agathobacter rectalis · 1.1%
Phocaeicola dorei · 1.1%
Faecalibacterium prausnitzii · 0.9%
Bacteroides uniformis · 0.8%
Sutterella wadsworthensis_A · 0.7%
Bacteroides stercoris · 0.6%
Anthropogastromicrobium aceti · 0.6%
Eubacterium_F sp003491505 · 0.4%
Bacteroides eggerthii · 0.4%
Parabacteroides distasonis · 0.2%
Phascolarctobacterium faecium · 0.0%
Bacteroides cellulosilyticus · 14.8%
Blautia_A faecis · 9.4%
Parabacteroides distasonis · 8.2%
Alistipes putredinis · 7.1%
Bacteroides uniformis · 6.4%
Akkermansia massiliensis · 6.0%
Ruminococcoides intestinale · 4.6%
Sutterella wadsworthensis_A · 4.2%
Blautia_A wexlerae · 3.2%
Anthropogastromicrobium aceti · 3.0%
Dialister invisus · 2.8%
Sellimonas intestinalis · 2.0%
Ruminococcus_C sp000433635 · 1.5%
Fusicatenibacter saccharivorans · 1.4%
Bacteroides eggerthii · 0.9%
Phocaeicola dorei · 0.5%
Faecalibacterium prausnitzii · 0.3%
Parabacteroides distasonis · 0.0%
Phascolarctobacterium faecium · 0.0%
0
1
2
4
6
8
Week


F8
Agathobacter rectalis · 10.8%
Ruminococcoides intestinalis · 10.8%
Bifidobacterium pseudocatenulatum · 8.2%
Blautia_A wexlerae · 3.6%
Fusicatenibacter saccharivorans · 3.4%
Agathobacter faecis · 3.2%
Bacteroides eggerthii · 2.1%
Blautia_A faecis · 1.2%
Anthropogastromicrobium aceti · 1.0%
Bacteroides cellulosilyticus · 0.9%
Faecalibacterium prausnitzii · 0.8%
Alistipes putredinis · 0.8%
Ruminococcoides intestinale · 0.7%
Bacteroides uniformis · 0.6%
Phascolarctobacterium faecium · 0.4%
Eubacterium_F sp000349155 · 0.4%
Akkermansia muciniphila · 0.4%
Mediterraneibacter lactaris · 0.2%
Phocaeicola dorei · 0.2%
Bacteroides stercoris · 0.2%
Parasutterella excrementihominis · 0.1%
Parabacteroides distasonis · 0.1%
Aphodomorphia
Wujia hominis · 0.0%
Porcipeletonaceae
Sellimonas intestinalis · 0.0%
Ruminococcus_E
Flavonifractor
Akkermansia
Succiniclasticum sp900314855 · 0.0%
Prevotella copri_A
Klebsiella
Sutterella
CAG-950 sp900544905 · 0.0%
Bacteroides uniformis · 12.8%
Parabacteroides distasonis · 10.2%
Blautia_A faecis · 10.1%
Fusicatenibacter saccharivorans · 9.5%
Bacteroides cellulosilyticus · 8.2%
Phascolarctobacterium faecium · 6.1%
Alistipes putredinis · 5.8%
Blautia_A wexlerae · 5.7%
Ruminococcoides intestinalis · 4.5%
Parasutterella excrementihominis · 3.9%
Phocaeicola dorei · 2.3%
Akkermansia muciniphila · 2.0%
Bacteroides eggerthii · 1.1%
Anthropogastromicrobium aceti · 1.1%
Sellimonas intestinalis · 0.6%
Mediterraneibacter lactaris · 0.4%
Bacteroides stercoris · 0.2%
Agathobacter rectalis · 0.0%
Ruminococcoides intestinale · 0.0%
Faecalibacterium prausnitzii · 0.0%
Flavonifractor
Prevotella copri_A
Ruminococcus_E sp900433635 · 0.0%
Sutterella wadsworthensis · 0.0%
Holdemanella sp900759145 · 0.0%
Succiniclasticum sp900314855 · 0.0%
Klebsiella
Prevotella sp900544905 · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
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8
Week


F9
Aphodomorpha intestinavium · 9.0%
Ruminococcoides intestinale · 8.1%
Fusicatenibacter saccharivorans · 5.8%
Bacteroides eggerthii · 1.5%
Phascolarctobacterium faecium · 1.4%
Alistipes putredinis · 1.3%
Blautia_A faecis · 1.0%
Anthropogastromicrobium aceti · 0.9%
Blautia_A wexlerae · 0.8%
Akkermansia massiliensis · 0.5%
Faecalibacterium prausnitzii · 0.4%
Bacteroides uniformis · 0.4%
Paraprevotella clara · 0.3%
Parasutterella excrementihominis · 0.1%
Bacteroides uniformis · 14.8%
Parabacteroides distasonis · 10.2%
Blautia_A faecis · 7.7%
Bacteroides cellulosilyticus · 6.8%
Paraprevotella clara · 6.6%
Phascolarctobacterium faecium · 5.3%
Alistipes putredinis · 5.2%
Akkermansia massiliensis · 5.2%
Bacteroides eggerthii · 3.3%
Parasutterella excrementihominis · 2.9%
Sellimonas intestinalis · 2.1%
Ruminococcoides intestinale · 2.1%
Blautia_A wexlerae · 1.1%
Bacteroides stercoris · 0.4%
Fusicatenibacter saccharivorans · 0.2%
Faecalibacterium prausnitzii · 0.2%
Mediterraneibacter lactaris · 0.0%
Ruminococcoides intestinale · 0.0%
Bifidobacterium pseudocatenulatum · 0.0%
0
1
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Week