```
Summary Table File:  LimSC25.taxa.genus.NoControls.N500.summary_table.tsv
Factor File:  0137_Lim_Metadata_20171019.tsv
Output File Root:  sickle.genus.tail.t40

Diversity Index: tail

Summary Table:
      Num Samples: 49
   Num Categories: 199

Factor Table:
      Num Samples: 58
      Num Factors: 27

Shared Samples: 49

Number of Top Categories from each sample to summarize: 40

Samples exclusive to Summary Table:
character(0)


Samples exclusive to Factor Table:
[1] "0137.BC000299.01.ST"    "0137.10022176929.01.ST" "0000.0385.20170823"
[4] "0000.0386.20170824"     "0000.0387.20170825"     "0000.0388.20170828"
[7] "0000.0389.Ext.N"        "0001.0390.20170913"     "0002.0391.20170913"
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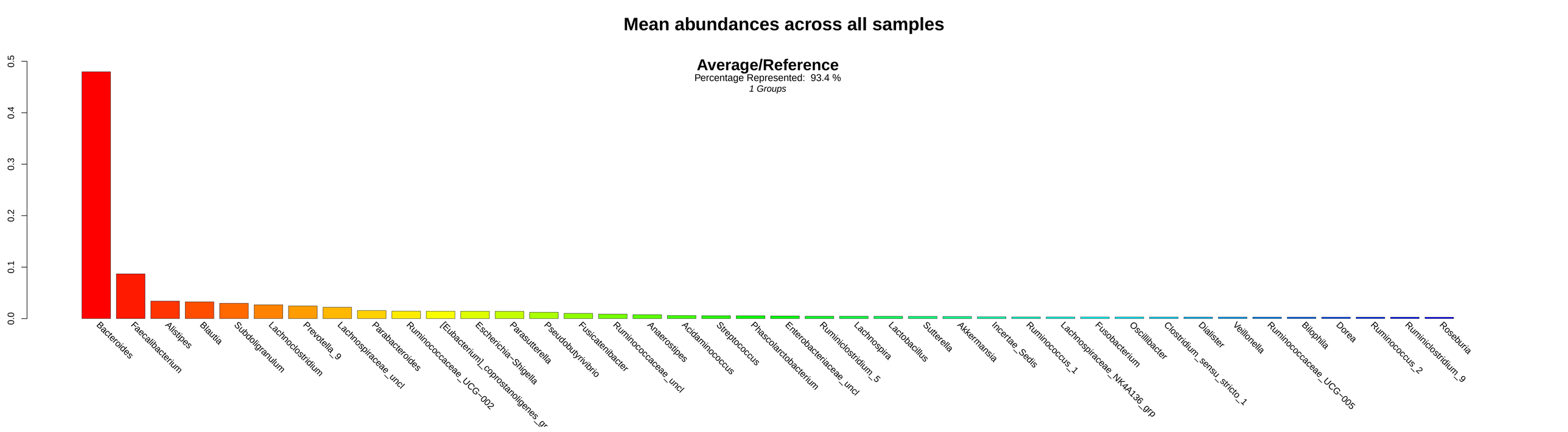
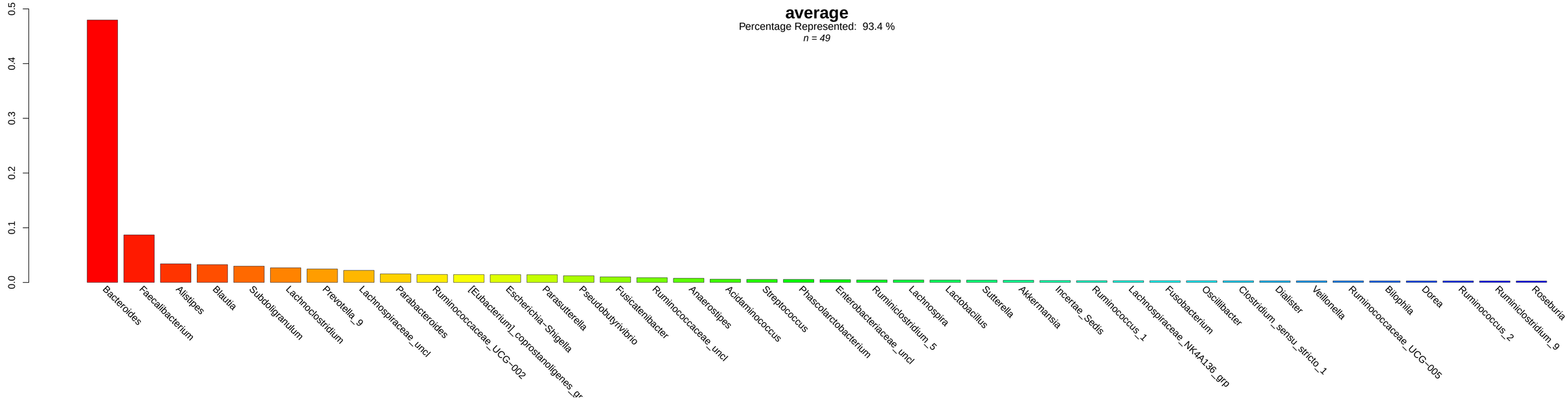

Mean abundances across all samples
Average/Reference
Percentage Represented: 93.4 %
1 Groups
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Alistipes
Blautia
Subdoligranulum
Lachnoclostridium
Prevotella_9
Lachnospiraceae_uncl
Parabacteroides
Ruminococcaceae_UCG-002
[Eubacterium]_coprostanoligenes_gr
Escherichia-Shigella
Parasutterella
Pseudobutyrivibrio
Fusicatenibacter
Ruminococcaceae_uncl
Anaerostipes
Acidaminococcus
Streptococcus
Phascolarctobacterium
Enterobacteriaceae_uncl
Ruminiclostridium_5
Lachnospira
Lactobacillus
Sutterella
Akkermansia
Incertae_Sedis
Ruminococcus_1
Lachnospiraceae_NK4A136_grp
Fusobacterium
Oscillibacter
Clostridium_sensu_stricto_1
Dialister
Veillonella
Ruminococcaceae_UCG-005
Bilophila
Dorea
Ruminococcus_2
Ruminiclostridium_9
Roseburia

Mean abundances across all samples



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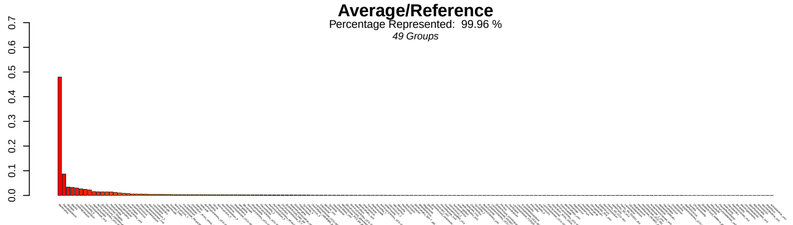
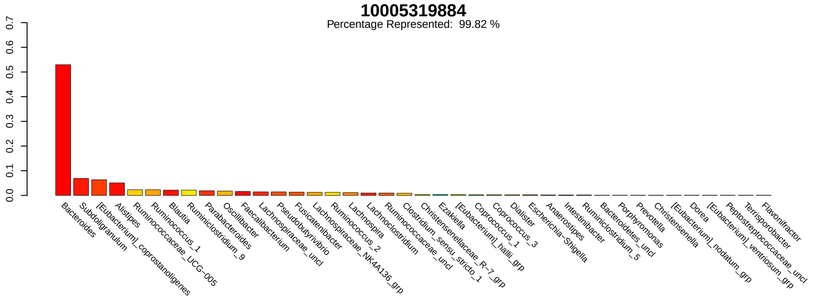

Average/Reference
Percentage Represented: 99.96 %
49 Groups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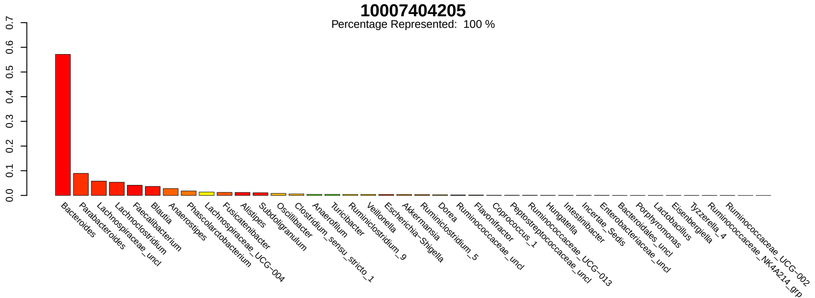
Percentage Represented: 99.82 %
Bacteroides
Subdoligranulum
[Eubacterium]_coprostanoligenes_grp
Alistipes
Ruminococcaceae_UCG-005
Blautia
Ruminococcus_1
Parabacteroides
Ruminiclostridium_9
Oscillibacter
Faecalibacterium
Lachnospiraceae_unCl
Pseudoflavonifractor
Lachnospiraceae_NK4A136_grp
Unclassified
Ruminococcus_2
Lachnoclostridium
Clostridium_sensu_stricto_1
Christensenellaceae_unCl
R-7_grp
Eubacterium_fissicatena_grp
Colidextribacter
Coprococcus_3
Escherichia-Shigella
[Eubacterium]_hallii_grp
Anaerostipes
Intestinibacter
Romboutsia
Bacteroides_uncl
Ruminococcus_5
Porphyromonas
Prevotella
Christensenella
[Eubacterium]_nodatum_grp
Dorea
[Eubacterium]_ventriosum_grp
Peptostreptococcaceae_uncl
Terrisporobacter
Flavonifractor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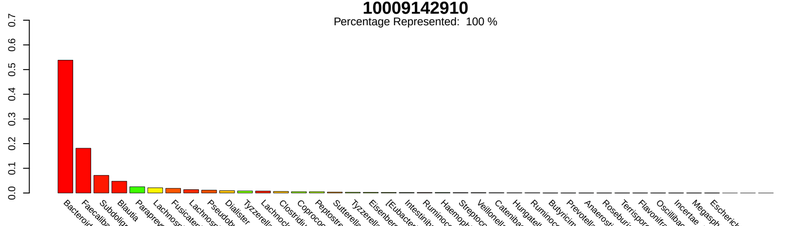
Percentage Represented: 100 %
Bacteroides
Parabacteroides
Lachnoclostridium_uncl
Lachnoclostridium
Blautia
Anaerostipes
Fusicatenibacter
Pseudoflavonifractor
Lachnospiraceae_UCG-004
Alistipes
Subdoligranulum
Oscillibacter
Intestinibacter
Clostridium_sensu_stricto_1
Ruminiclostridium_9
Terrisporobacter
Velllonella
Akkermansia
Escherichia-Shigella
Ruminiclostridium_5
Dorea
Flavonifractor
Ruminococcaceae_uncl
Coprococcus_1
Peptostreptococcaceae_UCG-013
Romboutsia
Incertae_Sedis
Enterobacteriaceae_uncl
Bacteroidales_uncl
Lactobacillus
Porphyromonas
Eisenbergiella
Tyzzerella_4
Ruminococcaceae_UCG-002
Ruminococcaceae_NK4A214_grp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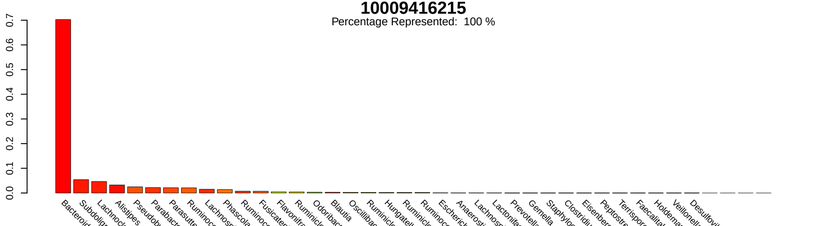
Subdoligranulum
Blautia
Prevotella
Lachnospiraceae_UCG-004
Fusicatenibacter
Lachnospiraceae_unCl
Pseudobutyrivibrio
Dialister
Tyzzerella
Lachnoclostridium
Clostridium_sensu_stricto_1
Coprococcus_3
Peptostreptococcaceae_unCl
Sutterella
Tyzzerella_4
Eisenbergiella
[Eubacterium]_hallii_grp
Intestinibacter
Romboutsia
Ruminococcaceae_unCl
Haemophilus
Streptococcus
Veillonella
Catenibacterium
Hungatella
Butyricicoccaceae_UCG-002
Ruminococcaceae_UCG-002
Prevotella_6
Anaerostipes
Roseburia
Terrisporobacter
Flavonifractor
Oscillibacter
Incertae_Sedis
Megasphaera
Escherichia-Shigella


10009416215
Percentage Represented: 100 %
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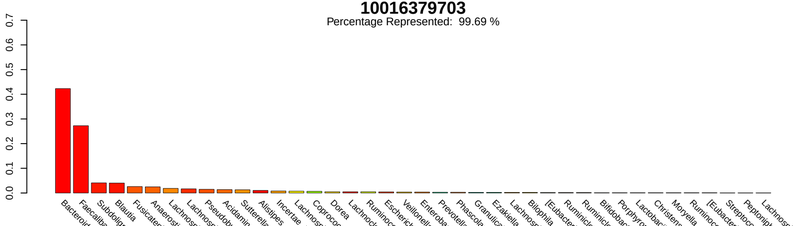
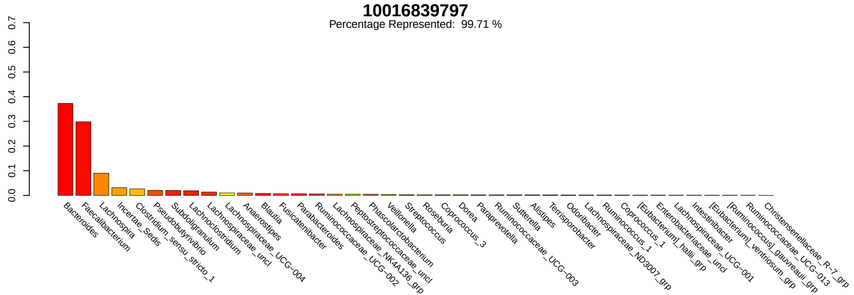
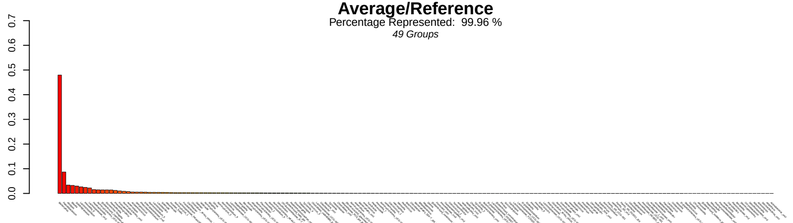
Subdoligranulum
Lachnoclostridium
Alistipes
Pseudobutyrivibrio
Parabacteroides
Ruminococcaceae_UCG-002
Ruminococcaceae_unCl
Phascolarctobacterium
Ruminococcaceae_UCG-005
Fusicatenibacter
Flavonifractor
Ruminococcus_9
Oscillibacter
Blautia
Ruminiclostridium_6
Hungatella
Ruminiclostridium_5
Escherichia-Shigella
Lachnospiraceae_UCG-010
Prevotella_6
Gemella
Lachnospiraceae_ND3007_grp
Staphylococcus
Clostridium_sensu_stricto_1
Eisenbergiella
Peptostreptococcaceae_unCl
Terrisporobacter
Faecalitalea
Veillonella
Holdemania
Desulfovibrionales_unCl

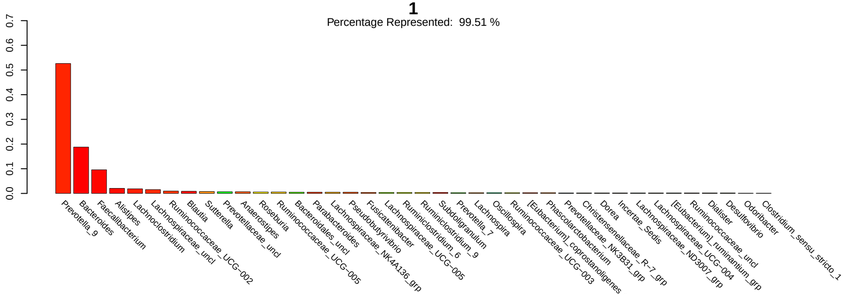

10016379703
Percentage Represented: 99.69 %
Bacteroides
Faecalibacterium
Subdoligranulum
Blautia
Fusicatenibacter
Anaerostipes
Lachnospira
Lachnospiraceae_unCl
Pseudobutyrivibrio
Acetatamnoccus
Sutterella
Alistipes
Incertae_Sedis
Coprococcus_3
Lachnospiraceae_UCG-004
Lachnoclostridium
Ruminococcaceae_UCG-003
Veillonella
Escherichia-Shigella
Enterobacteriaceae_unCl
Prevotella
Granulicatella
Eubacterium_ventriosum_grp
Eisenbergiella
Lachnospiraceae_NK4A136_grp
Bilophila
[Eubacterium]_hallii_grp
Ruminococcus_5
Ruminococcus_9
Bifidobacterium
Lactobacillus
Porphyromonas
Christensenellaceae_unCl
Morryella
[Eubacterium]_coprostanoligenes_grp
Ruminococcaceae_UCG-013
Streptococcus
Peptoniphilus
Lachnospiraceae_ND3007_grp

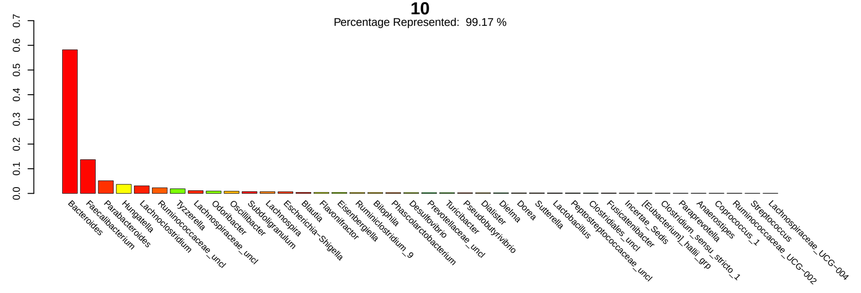
Identifier

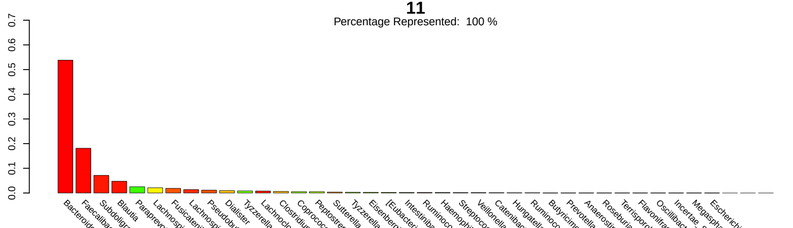

10016839797
Percentage Represented: 99.71 %
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Bacteroides
Faecalibacterium
Lachnoclostridium
Incertae_Sedis
Clostridium_sensu_stricto_1
Pseudobutyrivibrio
Subdoligranulum
Lachnoclostridium
Lachnospiraceae_unCl
Lachnospiraceae_UCG-004
Anaerostipes
Blautia
Fusicatenibacter
Parabacteroides
Ruminococcaceae_UCG-002
Lachnospiraceae_NK4A136_grp
Peptostreptococcaceae_unCl
Phascolarctobacterium
Veillonella
Streptococcus
Roseburia
Coprococcus_3
Dorea
Flavonifractor
Ruminococcaceae_UCG-003
Sutterella
Alistipes
Terrisporobacter
Odoribacter
Lachnospiraceae_unCl
Ruminococcus_1
Coprococcus_1
Ruminococcaceae_NK3D07_grp
[Ruminococcus]_torques_grp
Enterobacteriaceae_unCl
Lachnospiraceae_UCG-001
Intestinibacter
[Eubacterium]_hallii_grp
[Ruminococcus]_gnavus_grp
[Ruminococcus]_torques_grp
Ruminococcaceae_UCG-013
Christensenellaceae_R-7_grp

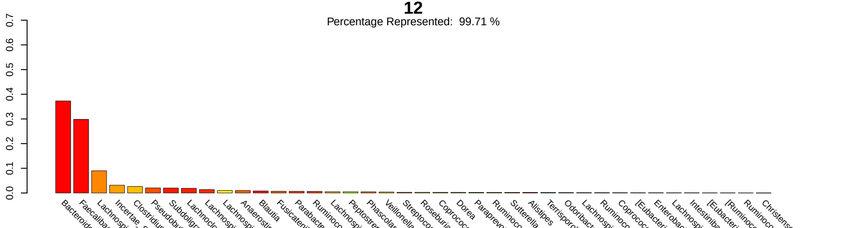
RIH_UPN

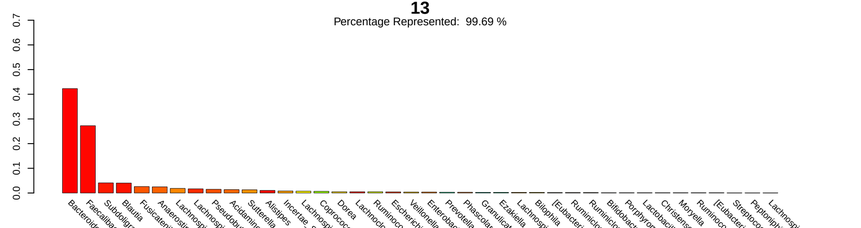

Average/Reference
Percentage Represented: 99.96 %
49 Groups


1
Percentage Represented: 99.51 %
Prevotella_9
Bacteroides
Faecalibacterium
Alistipes
Lachnoclostridium
Ruminococcaceae_UCG-002
Blautia
Sutterella
Prevotellaceae_Unc
Anaerostipes
Roseburia
Ruminococcaceae_UCG-005
Dialister
Parabacteroides_Unc
Lachnospiraceae_NK4A136_grp
Fusicatenibacter
Paraprevotella
Lachnospiraceae_UCG-005
Ruminiclostridium_6
Ruminiclostridium_9
Subdoligranulum
Prevotella_7
Lachnospira
Oscillospira
Ruminococcaceae_UCG-003
[Eubacterium]_coprostanoligenes_grp
Prevotellaceae_NK3B31_grp
Dorea
Christensenellaceae_R-7_grp
Incertae_Sedis
Lachnospiraceae_ND3007_grp
[Eubacterium]_ruminantium_grp
Ruminococcaceae_Unc
Dialister
Desulfovibrio
Odoribacter
Clostridium_sensu_stricto_1

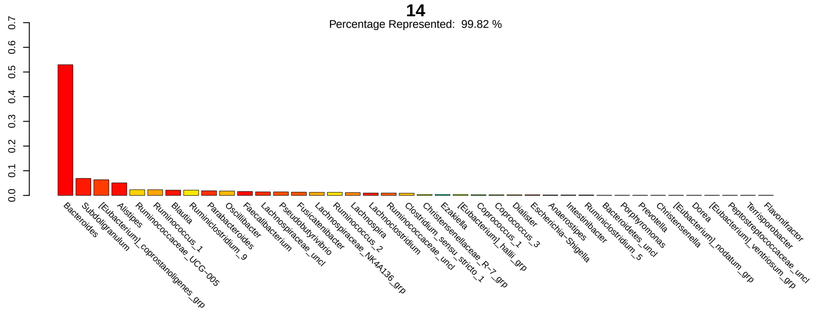

10
Percentage Represented: 99.17 %
Bacteroides
Faecalibacterium
Parabacteroides
Alistipes
Lachnoclostridium
Ruminococcaceae_Unc
Tyzzerella
Odoribacter
Lachnospiraceae_Unc
Subdoligranulum
Escherichia-Shigella
Blautia
Flavonifractor
Eisenbergiella
Roseburia
Ruminiclostridium_9
Phascolarctobacterium
Desulfovibrio
Prevotella
Turicibacter
Fusicatenibacter
Pseudobutyrivibrio
Dialister
Dorea
Sutterella
Lactobacillus
Peptostreptococcaceae_Unc
Clostridium_Unc
Fusicatenibacter
Incertae_Sedis
[Eubacterium]_hallii_grp
Clostridium_sensu_stricto_1
Peregrinibacteria
Anaerostipes
Coprococcus_1
Streptococcus
Lachnospiraceae_UCG-002
Lachnospiraceae_UCG-004


11
Percentage Represented: 100 %
Bacteroides
Faecalibacterium
Subdoligranulum
Blautia
Prevotella
Lachnospira
Fusicatenibacter
Lachnospiraceae_UCG-004
Pseudobutyrivibrio
Dialister
Tyzzerella
Lachnoclostridium
Clostridium_sensu_stricto_1
Coprococcus_3
Peptostreptococcaceae_Unc
Sutterella
Tyzzerella_4
Eisenbergiella
[Eubacterium]_hallii_grp
Intestinibacter
Ruminococcaceae_Unc
Haemophilus
Streptococcus
Veillonella
Catenibacterium
Hungatella
Butyricicoccus
Ruminococcaceae_UCG-002
Prevotella_9
Anaerostipes
Roseburia
Terrisporobacter
Flavonifractor
Oscillibacter
Incertae_Sedis
Megasphaera
Escherichia-Shigella


12
Percentage Represented: 99.71 %
Bacteroides
Faecalibacterium
Lachnospira
Incertae_Sedis
Clostridium_sensu_stricto_1
Pseudobutyrivibrio
Subdoligranulum
Lachnoclostridium
Lachnospiraceae_Unc
Anaerostipes
Lachnospiraceae_UCG-004
Blautia
Fusicatenibacter
Parabacteroides
Ruminococcaceae_UCG-002
Lachnospiraceae_NK4A136_grp
Peptostreptococcaceae_Unc
Phascolarctobacterium
Veillonella
Roseburia
Streptococcus
Coprococcus_3
Dorea
Paraprevotella
Sutterella
Ruminococcaceae_UCG-003
Alistipes
Terrisporobacter
Odoribacter
Lachnospiraceae_ND3007_grp
Coprococcus_1
[Eubacterium]_hallii_grp
Enterobacteriaceae_Unc
Intestinibacter
[Eubacterium]_ventriosum_grp
Ruminococcaceae_UCG-001
Ruminococcus_gauvreauii_grp
Ruminococcaceae_UCG-013
Christensenellaceae_R-7_grp

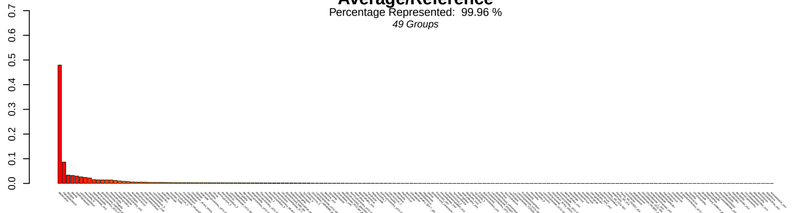

13
Percentage Represented: 99.69 %
Bacteroides
Faecalibacterium
Subdoligranulum
Blautia
Fusicatenibacter
Anaerostipes
Lachnospira
Pseudobutyrivibrio
Acetatamycus
Sutterella
Alistipes
Incertae_Sedis
Lachnospiraceae_UCG-004
Coprococcus_3
Dorea
Lachnoclostridium
Ruminococcaceae_UCG-003
Escherichia-Shigella
Veillonella
Prevotella
Enterobacteriaceae_Unc
Phascolarctobacterium
Granulicatella
Eubacterium
Blautia
[Eubacterium]_hallii_grp
Lachnospiraceae_NK4A136_grp
Ruminiclostridium_5
Ruminiclostridium_9
Bifidobacterium
Peptoniphilus
Lactobacillus
Christensenellaceae_R-7_grp
Moryella
Ruminococcaceae_UCG-013
[Eubacterium]_ventriosum_grp
Streptococcus
Peptoniphilus
Lachnospiraceae_ND3007_grp

RIH_UPN

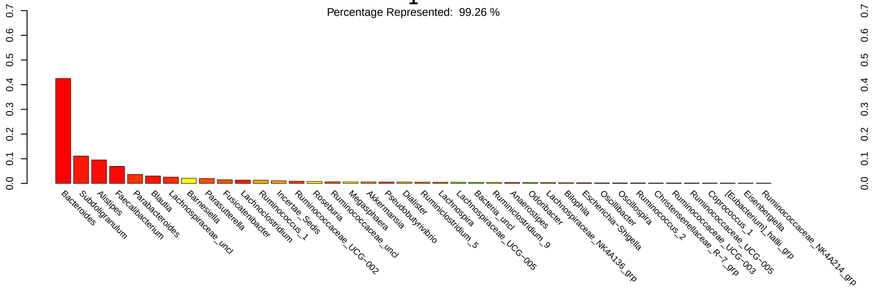

14
Percentage Represented: 99.82 %
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Bacteroides
Subdoligranulum
[Eubacterium]_coprostanoligenes_grp
Alistipes
Ruminococcaceae_UCG-005
Ruminococcus_1
Blautia
Ruminiclostridium_9
Parabacteroides
Oscillibacter
Faecalibacterium
Lachnospiraceae_uncl
Pseudobutyrivibrio
Fusicatenibacter
Lachnospiraceae_NK4A136_grp
Ruminococcus_2
Lachnospira
Lachnoclostridium
Ruminococcaceae_uncl
Clostridium_sensu_stricto_1
Christensenellaceae_R-7_grp
Ezakiella
[Eubacterium]_hallii_grp
Coprococcus_1
Coprococcus_3
Dialister
Escherichia-Shigella
Anaerostipes
Intestinibacter
Ruminiclostridium_5
Bacteroides_uncl
Porphyromonas
Prevotella
Christensenella
[Eubacterium]_nodatum_grp
Dorea
[Eubacterium]_ventriosum_grp
Peptostreptococcaceae_uncl
Terrisporobacter
Flavonifractor

PCR_Temporary_Number

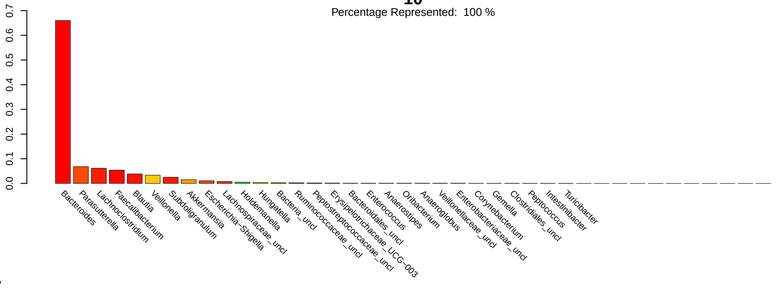
Average/Reference
Percentage Represented: 99.96 %
49 Groups



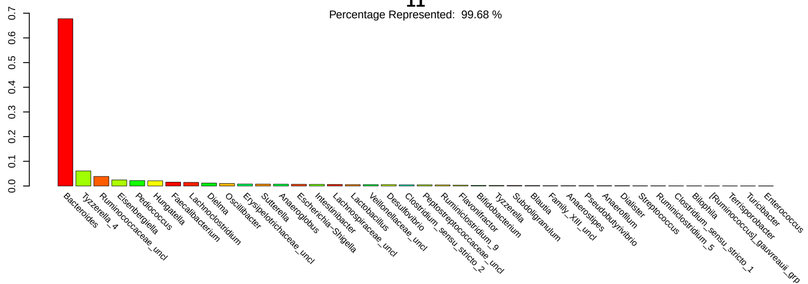
1
Percentage Represented: 99.26 %



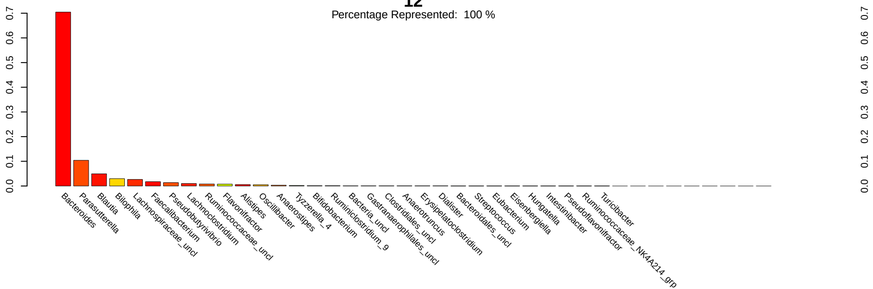
10
Percentage Represented: 100 %



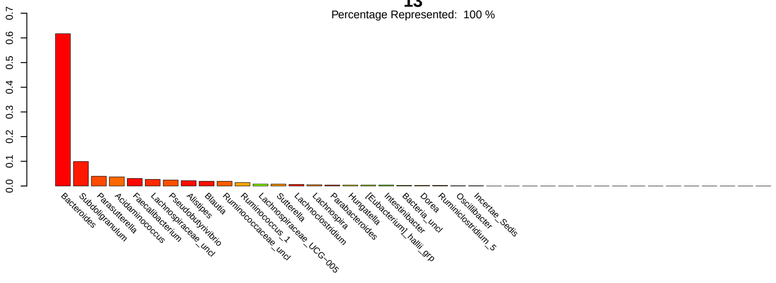
11
Percentage Represented: 99.68 %



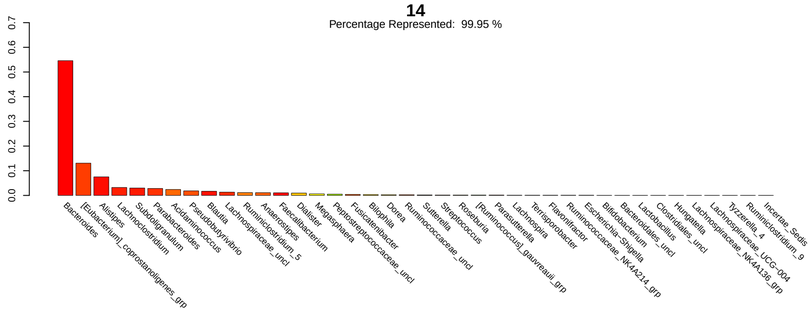
12
Percentage Represented: 100 %



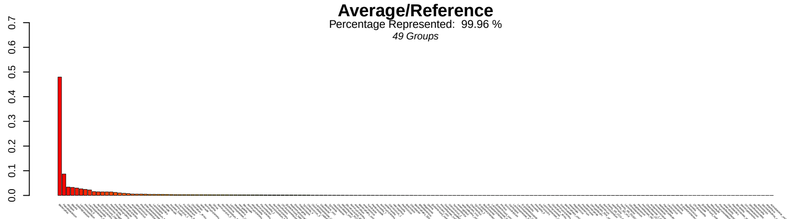
13
Percentage Represented: 100 %

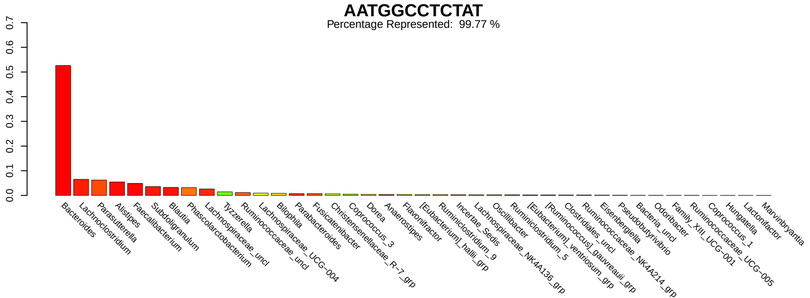


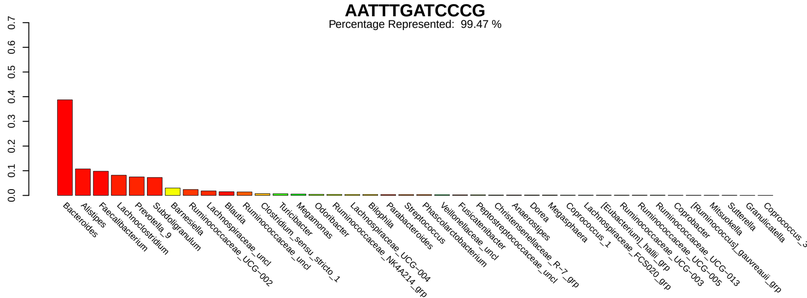
PCR_Temporary_Number

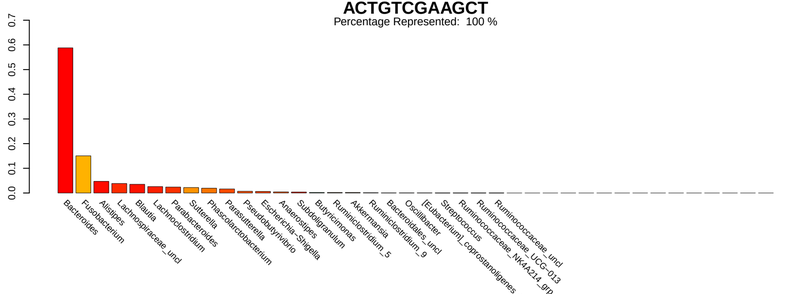


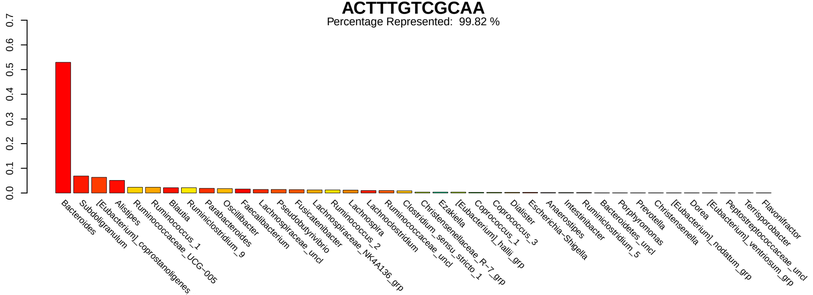
Barcode.RC

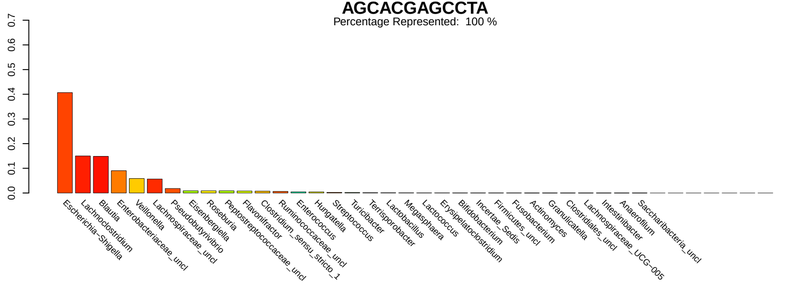

Average/Reference
Percentage Represented: 99.96 %
49 Groups


AATGGCCTCTAT
Percentage Represented: 99.77 %
Bacteroides
Lachnoclostridium
Alistipes
Parasutterella
Faecalibacterium
Subdoligranulum
Blautia
Ruminococcus_1
Prevotella_9
Lachnospiraceae_unci
Roseburia
Bilophila
Lachnospiraceae_UCG-004
Ruminococcaceae_unci
Parabacteroides
Fusicatenibacter
Christensenellaceae_R-7_grp
Coprococcus_3
Dorea
Anaerostipes
Flavonifractor
[Eubacterium]_hallii_grp
Ruminiclostridium_9
Lachnospiraceae_NK4A136_grp
Oscillibacter
Ruminiclostridium_5
[Eubacterium]_ventriosum_grp
[Ruminococcus]_gauvreauii_grp
Clostridium_sensu_stricto_1
Eubacterium_eligens_grp
Ruminococcaceae_NK4A214_grp
Butyricicoccus
Odoribacter
Family_XIII_UCG-001
Ruminococcaceae_UCG-005
Coprococcus_1
Lachnospira
Lactobacillus
Marvinbryantia

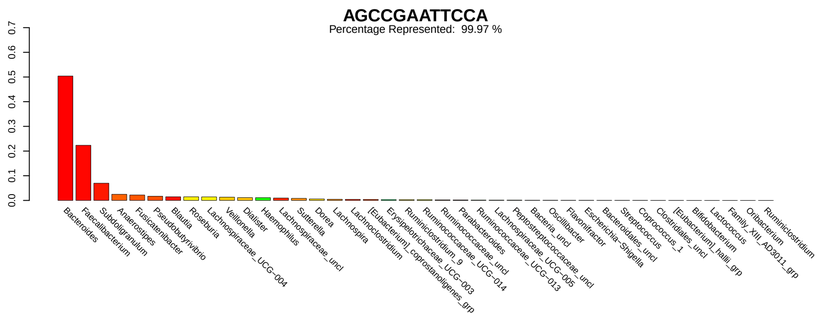

AATTTGATCCCG
Percentage Represented: 99.47 %
Bacteroides
Alistipes
Faecalibacterium
Lachnoclostridium
Prevotella_9
Subdoligranulum
[Eubacterium]_eligens_grp
Ruminococcaceae_UCG-002
Blautia
Lachnospiraceae_unci
Clostridium_sensu_stricto_1
Ruminococcus_1
Megamonas
Odoribacter
Ruminococcaceae_unci
Bilophila
Parabacteroides
Lachnospiraceae_UCG-004
Ruminococcaceae_NK4A214_grp
Streptococcus
Prevotellaceae_unci
Fusicatenibacter
Veillonellaceae_unci
Peptostreptococcaceae_unci
Christensenellaceae_R-7_grp
Anaerostipes
Dorea
Methanobrevibacter
Coprococcus_1
[Eubacterium]_hallii_grp
Ruminococcaceae_FCS020_grp
Ruminococcaceae_UCG-003
Ruminococcaceae_UCG-005
Ruminococcaceae_UCG-013
Coprobacter
[Ruminococcus]_gauvreauii_grp
Mitsuokella
Sutterella
Granulicatella
Coprococcus_3


ACTGTCGAAGCT
Percentage Represented: 100 %
Bacteroides
Fusobacterium
Alistipes
Lachnospiraceae_unci
Blautia
Lachnoclostridium
Sutterella
Parabacteroides
Prevotella_9
Parasutterella
Pseudobutyrivibrio
Escherichia-Shigella
Anaerostipes
Subdoligranulum
Butyricimonas
Akkermansia
Ruminiclostridium_5
Ruminiclostridium_9
Bacteroidales_unci
Oscillibacter
[Eubacterium]_coprostanoligenes_grp
Streptococcus
Ruminococcaceae_NK4A214_grp
Ruminococcaceae_UCG-013
Ruminococcus_unci

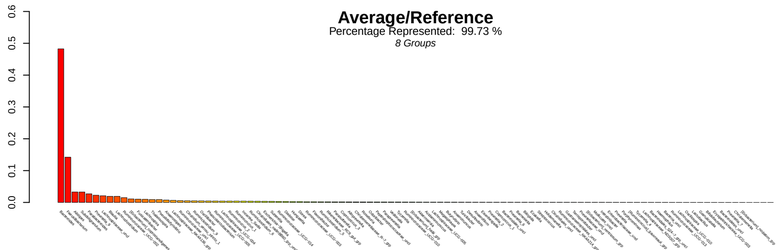

ACTTTGTCGCAA
Percentage Represented: 99.82 %
Subdoligranulum
Bacteroides
[Eubacterium]_coprostanoligenes_grp
Alistipes
Ruminococcaceae_UCG-005
Blautia
Ruminococcus_1
Ruminiclostridium_9
Parabacteroides
Oscillibacter
Faecalibacterium
Lachnospiraceae_unci
Pseudobutyrivibrio
Fusicatenibacter
Ruminococcus_2
Lachnospiraceae_NK4A136_grp
Lachnospira
Ruminiclostridium
Clostridium_sensu_stricto_1
Christensenellaceae_R-7_grp
Eubacterium_hallii_grp
Coprococcus_1
Dialister
Escherichia-Shigella
Anaerostipes
Intestinibacter
Ruminiclostridium_5
Bacteroidales_unci
Porphyromonas
Prevotella
Christensenellaceae_unci
[Eubacterium]_nodatum_grp
Dorea
[Eubacterium]_ventriosum_grp
Peptostreptococcaceae_unci
Terrisporobacter
Flavonifractor

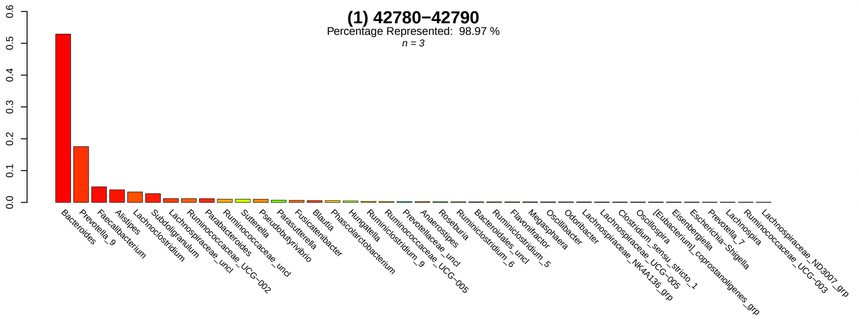

AGCACGAGCCTA
Percentage Represented: 100 %
Escherichia-Shigella
Blautia
Lachnoclostridium
Enterococcaceae_unci
Veillonella
Lachnospiraceae_unci
Pseudobutyrivibrio
Eisenbergiella
Roseburia
Peptostreptococcaceae_unci
Flavonifractor
Clostridium_sensu_stricto_1
Ruminococcaceae_unci
Enterococcus
Hungatella
Streptococcus
Turicibacter
Terrisporobacter
Lactobacillus
Megasphaera
Lactococcus
Erysipelatoclostridium
Bilophila
Intestinibacter
Subdoligranulum
Fusobacterium
Acidaminococcus
Granulicatella
Clostridium_unci
Lachnospiraceae_unci
Intestinimonas
Alkalibacter
Saccharofermentans_unci
Sellimonas
Lachnospiraceae_UCG-005

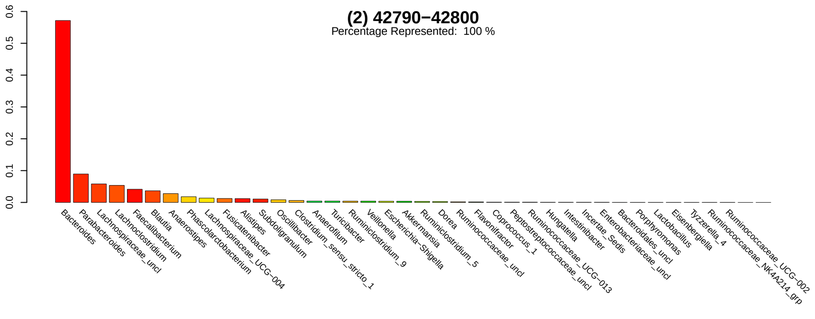
Barcode.RC

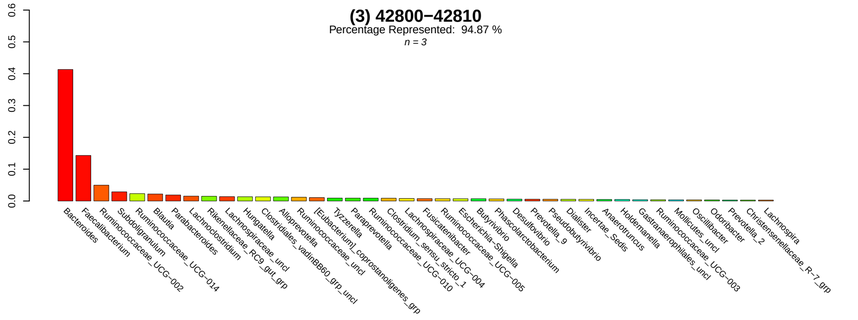

AGCCGAATTCCA
Percentage Represented: 99.97 %
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Bacteroides
Faecalibacterium
Subdoligranulum
Anaerostipes
Fusicatenibacter
Pseudobutyrivibrio
Blautia
Roseburia
Lachnospiraceae_UCG-004
Veillonella
Dialister
Haemophilus
Lachnospiraceae_uncl
Subdivella
Dorea
Lachnospira
Lachnoclostridium
[Eubacterium]_coprostanoligenes_grp
Ruminococcus_2
Ruminococcaceae_UCG-003
Ruminococcaceae_unc
Ruminococcaceae_UCG-014
Parabacteroides
Ruminococcaceae_unc
Lachnospiraceae_UCG-006
Lachnospiraceae_UCG-013
Peptostreptococcaceae_unc
Bacteria_uncl
Oscillibacter
Flavonifractor
Escherichia-Shigella
Bacteroides_unc
Streptococcus
Coprococcus_1
[Eubacterium]_uncl
[Eubacterium]_hallii_grp
Bifidobacterium
Lactococcus
Family_XIII_AD3011_grp
Oribacterium
Ruminiclostridium

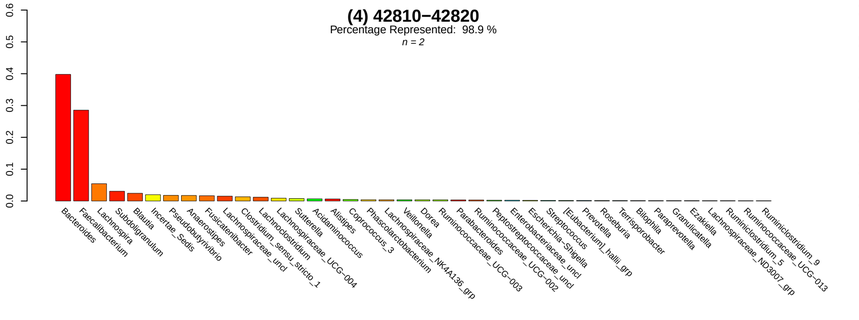
Consent.Date

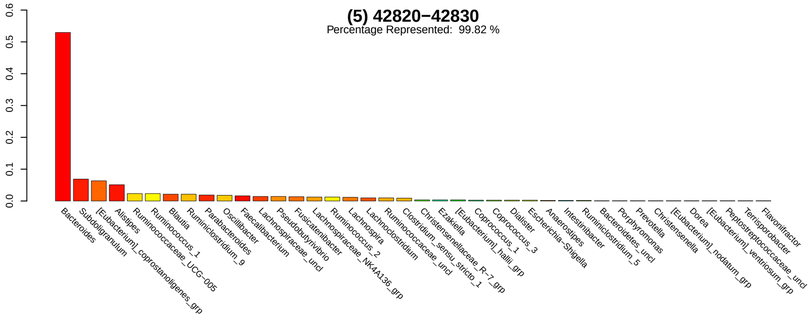




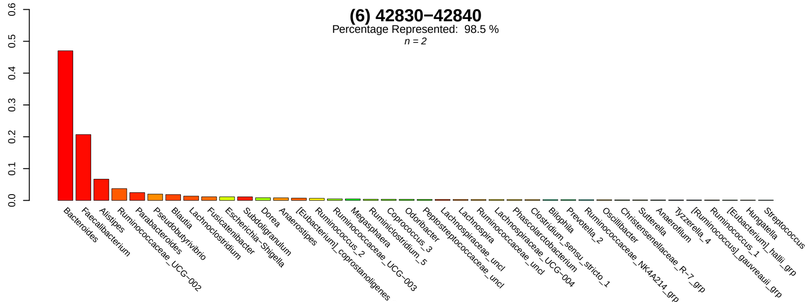




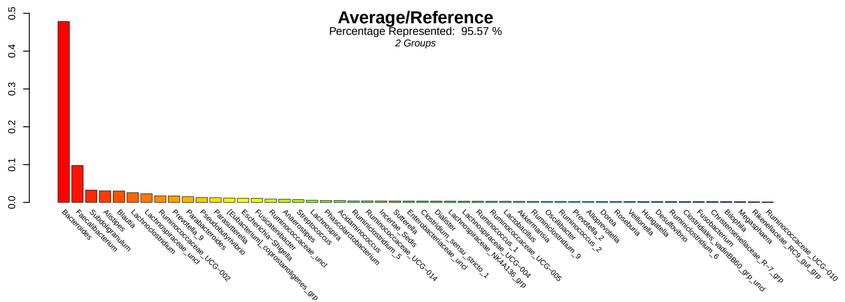


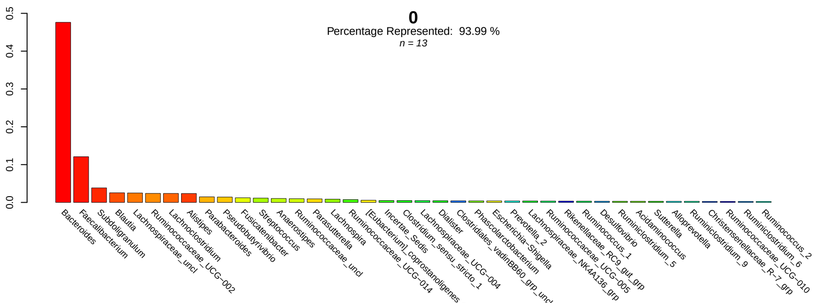


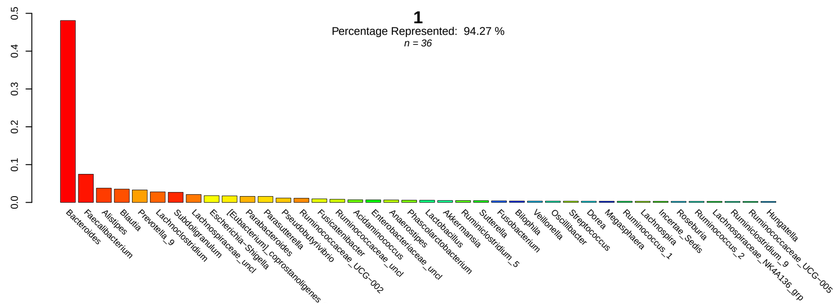
Consent.Date



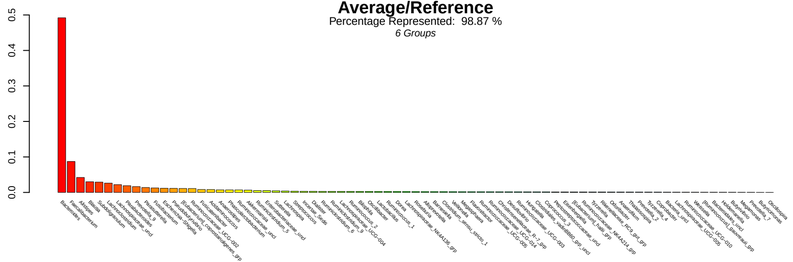
isFemale

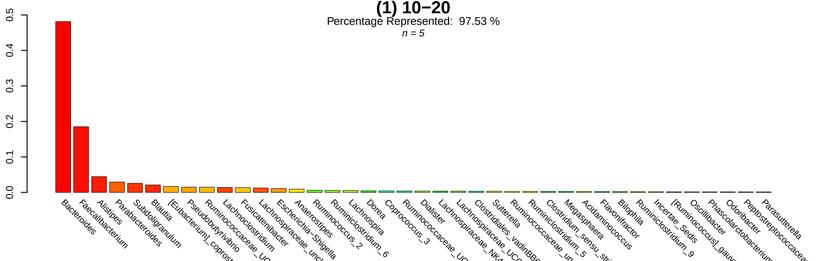

Average/Reference
Percentage Represented: 95.57 %
2 Groups
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Subdoligranulum
Alistipes
Blautia
Lachnospiraceae_unc
Ruminococcaceae_unc
Prevotella_9
Pseudobutyrivibrio
Ruminococcaceae_UCG-002
Fusicatenibacter
Escherichia-Shigella
[Eubacterium]_coprostanoligenes_grp
Anaerostipes
Ruminococcus_2
Streptococcus
Parasutterella
Ruminococcaceae_UCG-010
Acidaminococcus
Ruminococcus_1
Incertae_Sedis
Ruminococcaceae_UCG-005
Dialister
Lachnospiraceae_NK4A136_grp
Ruminococcaceae_UCG-004
Akkermansia
Oscillibacter
Prevotella_7
Dorea
Roseburia
Veillonella
Coprococcus_3
Clostridium_sensu_stricto_1
Eisenbergiella
Clostridium_innocuum_group
Blautia
Negativibacillus
Ruminococcaceae_R-7_grp
Ruminococcaceae_UCG-013
Ruminococcaceae_UCG-003
Ruminococcaceae_UCG-014
Ruminococcaceae_UCG-008
Ruminococcaceae_UCG-007
Ruminococcaceae_UCG-001
Ruminococcaceae_UCG-009
Ruminococcaceae_UCG-006
Ruminococcaceae_UCG-011
Ruminococcaceae_UCG-012
Ruminococcaceae_UCG-010

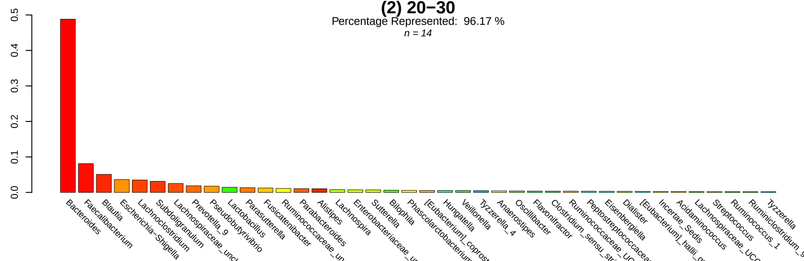

0
Percentage Represented: 93.99 %
n = 13
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Subdoligranulum
Blautia
Lachnospiraceae_unc
Ruminococcaceae_UCG-002
Alistipes
Pseudobutyrivibrio
Fusicatenibacter
Streptococcus
Anaerostipes
Ruminococcaceae_unc
Parasutterella
Lachnoclostridium
[Eubacterium]_coprostanoligenes_grp
Ruminococcaceae_UCG-014
Incertae_Sedis
Clostridium_sensu_stricto_1
Dialister
Lachnospiraceae_UCG-004
Oscillibacter
Prevotella_7
Escherichia-Shigella
Prevotella_2
Clostridia_vadinBB60_grp_unci
Ruminococcaceae_NK4A136_grp
Akkermansia
Ruminococcaceae_UCG-005
Ruminococcus_1
Dorea
Acidaminococcus
Roseburia
Alloprevotella
Ruminiclostridium_9
Christensenellaceae_R-7_grp
Ruminococcaceae_UCG-010
Ruminiclostridium_6
Ruminococcus_2
Ruminococcaceae_UCG-010

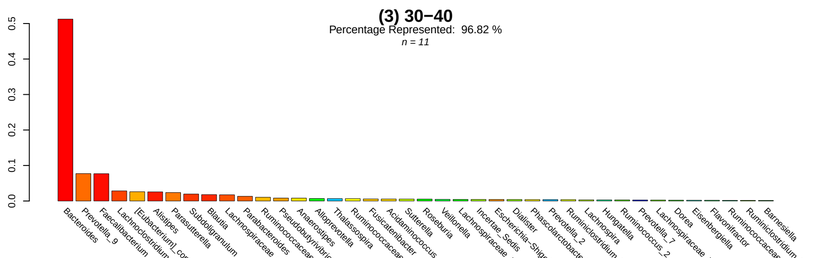

1
Percentage Represented: 94.27 %
n = 36
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Alistipes
Blautia
Prevotella_9
Lachnoclostridium
Subdoligranulum
Escherichia-Shigella
[Eubacterium]_coprostanoligenes_grp
Parasutterella
Pseudobutyrivibrio
Ruminococcaceae_UCG-002
Fusicatenibacter
Acidaminococcus
Ruminococcaceae_unc
Anaerostipes
Eisenbergiella
Prevotella_2
Lachnospiraceae_unc
Akkermansia
Ruminococcaceae_UCG-005
Subdoligranulum
Roseburia
Ruminococcus_1
Veillonella
Oscillibacter
Streptococcus
Dorea
Negativibacillus
Ruminococcus_2
Lachnospira
Incertae_Sedis
Roseburia
Ruminococcaceae_UCG-005
Lachnospiraceae_NK4A136_grp
Ruminiclostridium_5
Alloprevotella

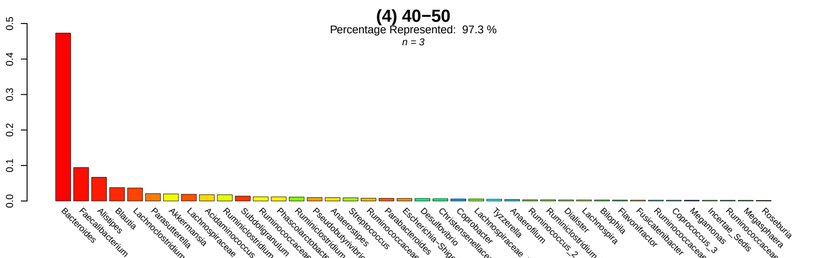
Age

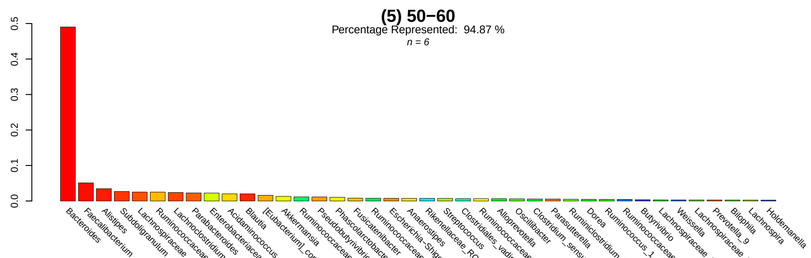

Average/Reference
Percentage Represented: 98.87 %
6 Groups


(1) 10−20
Percentage Represented: 97.53 %
n = 5

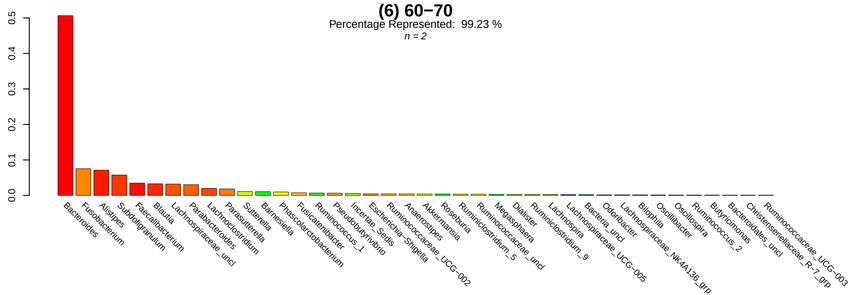

(2) 20−30
Percentage Represented: 96.17 %
n = 14


(3) 30−40
Percentage Represented: 96.82 %
n = 11

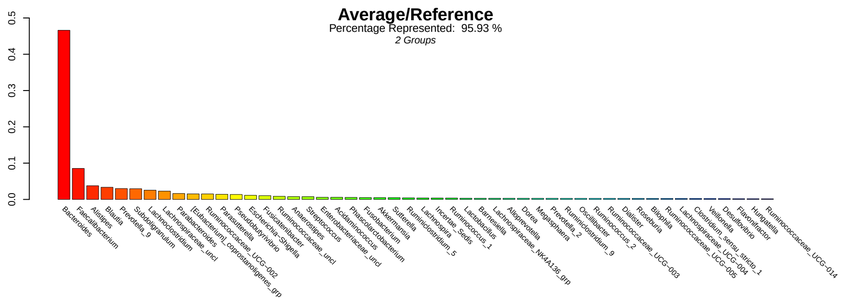

(4) 40−50
Percentage Represented: 97.3 %
n = 3

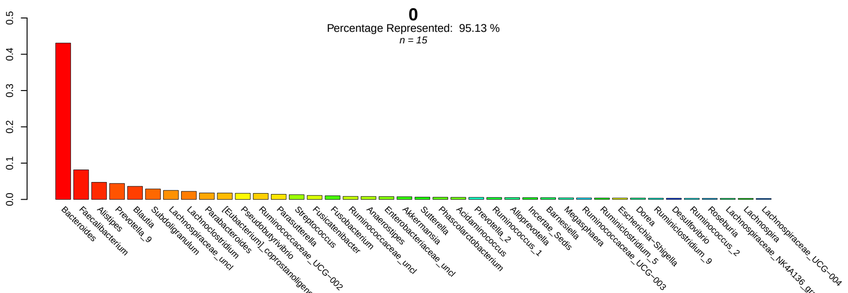

(5) 50−60
Percentage Represented: 94.87 %
n = 6

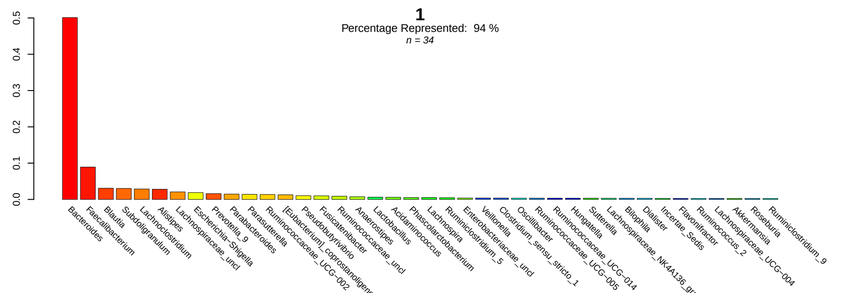
Age


(6) 60−70
Percentage Represented: 99.23 %
n = 2
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Fusobacterium
Alistipes
Subdoligranulum
Faecalibacterium
Blautia
Lachnospiraceae_uncl
Parabacteroides
Lachnoclostridium
Parasutterella
Sutterella
Barnesiella
Phascolarctobacterium
Fusicatenibacter
Ruminococcus_1
Pseudobutyrivibrio
Incertae_Sedis
Escherichia_Shigella
Ruminococcaceae_UCG-002
Anaerostipes
Akkermansia
Roseburia
Ruminiclostridium_5
Ruminococcaceae_uncl
Megasphaera
Dialister
Ruminiclostridium_9
Lachnospiraceae_UCG-005
Bacteria_uncl
Odoribacter
Lachnospiraceae_Nk4A136_grp
Bilophila
Oscillibacter
Oscillospira
Ruminococcus_2
Butyricimonas
Bacteroidales_uncl
Christensenellaceae_R-7_grp
Ruminococcaceae_UCG-003

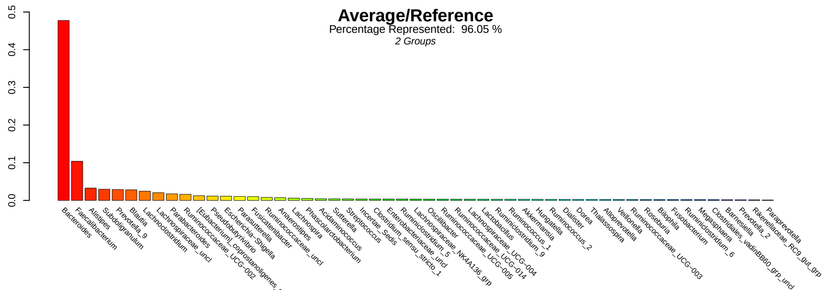
isCase

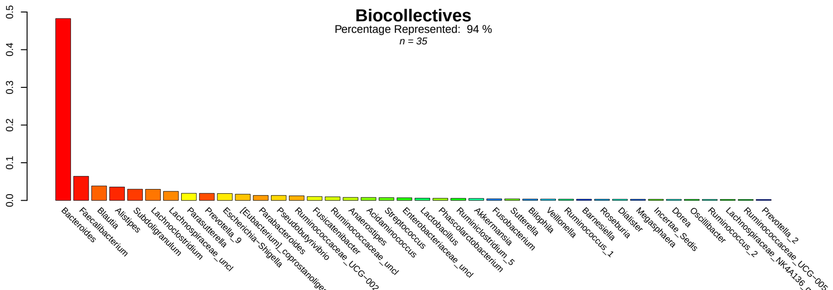

Average/Reference
Percentage Represented: 95.93 %
2 Groups
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Alistipes
Blautia
Prevotella_9
Subdoligranulum
Lachnospiraceae_unci
Eubacterium_coprostanoligenes_grp
Ruminococcaceae_UCG-002
Escherichia-Shigella
Ruminococcus_2
Ruminococcaceae_unci
Phascolarctobacterium
Acidaminococcus
Enterobacteriaceae_unci
Akkermansia
Sutterella
Ruminococcus_1
Lachnospira
Lachnospiraceae_NK4A136_grp
Dorea
Megamonas
Roseburia
Oscillibacter
Ruminococcus_9
Clostridium_sensu_stricto_1
Lachnospiraceae_UCG-004
Lachnospiraceae_UCG-005
Odoribacter
Butyricicoccus
Flavonifractor
Ruminococcaceae_UCG-014

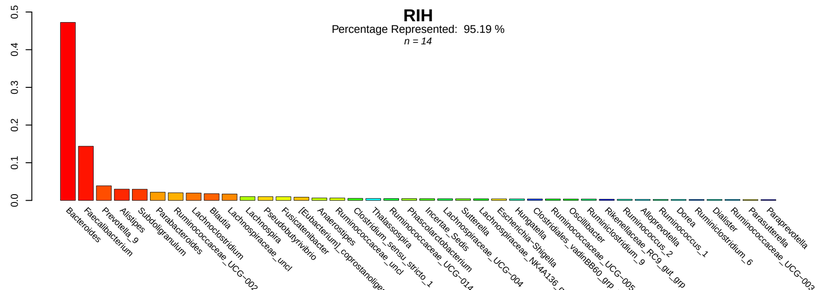

0
Percentage Represented: 95.13 %
n = 15
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Alistipes
Prevotella_9
Blautia
Subdoligranulum
Lachnospiraceae_unci
Eubacterium_coprostanoligenes_grp
Pseudoburkholderia
Parasutterella
Streptococcus
Ruminococcaceae_UCG-002
Fusicatenibacter
Ruminococcus_2
Ruminococcaceae_unci
Akkermansia
Enterobacteriaceae_unci
Sutterella
Phascolarctobacterium
Acidaminococcus
Prevotella_2
Ruminococcus_1
Oscillospiraceae_UCG-003
Incertae_Sedis
Bacteroides
Megamonas
Ruminococcus_9
Ruminococcaceae_UCG-003
Escherichia-Shigella
Dorea
Ruminiclostridium_9
Desulfovibrio
Roseburia
Lachnospira
Lachnospiraceae_NK4A136_grp
Lachnospiraceae_UCG-004


1
Percentage Represented: 94 %
n = 34
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Blautia
Subdoligranulum
Alistipes
Lachnospiraceae_unci
Escherichia-Shigella
Prevotella_9
Parabacteroides
Parasutterella
Ruminococcaceae_UCG-002
Eubacterium_coprostanoligenes_grp
Pseudoburkholderia
Fusicatenibacter
Ruminococcus_2
Ruminococcaceae_unci
Akkermansia
Lactobacillus
Acidaminococcus
Phascolarctobacterium
Lachnospira
Ruminococcus_9
Enterobacteriaceae_unci
Veillonella
Clostridium_sensu_stricto_1
Oscillibacter
Ruminococcaceae_UCG-005
Ruminococcaceae_UCG-014
Butyricicoccus
Sutterella
Lachnospiraceae_NK4A136_grp
Odoribacter
Blautia
Incertae_Sedis
Flavonifractor
Ruminococcus_2
Lachnospiraceae_UCG-004
Akkermansia
Roseburia
Ruminiclostridium_9

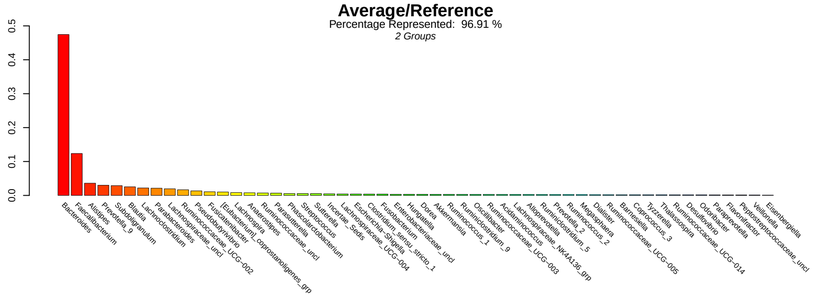
Origin


Average/Reference
Percentage Represented: 96.05 %
2 Groups
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Alistipes
Subdoligranulum
Prevotella_9
Blautia
Lachnoclostridium
Ruminococcaceae_uncl
Parabacteroides
Ruminococcaceae_UCG-002
[Eubacterium]_coprostanoligenes_grp
Escherichia-Shigella
Ruminococcus_2
Ruminococcaceae_UCG-003
Roseburia
Bilophila
Ruminococcaceae_UCG-005
Oscillibacter
Megasphaera
Dorea
Ruminococcaceae_UCG-014
Ruminococcus_1
Unclassified
Dialister
Ruminococcus_2
Intestinibacter
Veillonella
Ruminococcaceae_UCG-010
Flavonifractor
Ruminococcaceae_UCG-013
Anaerostipes
Ruminococcaceae_UCG-004
Ruminococcaceae_NK4A136_grp
Ruminococcus_1
Ruminococcaceae_UCG-014
Ruminococcaceae_UCG-005
Oscillibacter
Ruminococcaceae_UCG-004
Ruminococcaceae_UCG-010
Ruminococcaceae_UCG-013
Anaerostipes
Ruminococcaceae_NK4A136_grp
Ruminococcus_1
Unclassified
Dialister
Ruminococcus_2
Intestinibacter
Veillonella
Flavonifractor
Bilophila
Ruminococcaceae_UCG-003
Roseburia
Oscillibacter
Megasphaera
Dorea
Ruminococcaceae_UCG-005
Prevotella_2
Ruminococcaceae_UCG-003
Ruminococcaceae_RC9_gut_grp
Ruminococcaceae_vadinBB60_grp_uncl
Ruminococcaceae_RC9_gut_grp
Parasutterella

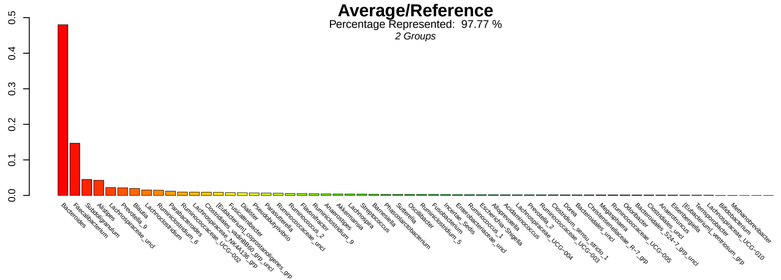

Biocollectives
Percentage Represented: 94 %
n = 35
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Blautia
Alistipes
Subdoligranulum
Lachnoclostridium
Prevotella_9
Escherichia-Shigella
[Eubacterium]_coprostanoligenes_grp
Parabacteroides
Ruminococcaceae_UCG-002
Ruminococcaceae_uncl
Acidaminococcus
Streptococcus
Enterobacteriaceae_uncl
Lachnospira
Ruminococcaceae_UCG-005
Ruminococcaceae_UCG-013
Akkermansia
Ruminococcus_2
Butyricicoccus
Bilophila
Intestinibacter
Veillonella
Ruminococcus_1
Roseburia
Dialister
Megasphaera
Dorea
Incertae_Sedis
Oscillibacter
Lachnospiraceae_NK4A136_grp
Flavonifractor
Ruminococcaceae_UCG-003
Prevotella_2
Ruminococcaceae_UCG-005
Ruminococcaceae_UCG-004
Ruminococcaceae_UCG-010
Ruminococcaceae_UCG-014
Ruminococcaceae_UCG-004
Ruminococcaceae_UCG-010
Ruminococcaceae_UCG-013
Anaerostipes
Ruminococcaceae_NK4A136_grp
Ruminococcus_1
Unclassified
Dialister
Ruminococcus_2
Intestinibacter
Veillonella
Flavonifractor
Bilophila
Ruminococcaceae_UCG-003
Roseburia
Oscillibacter
Megasphaera
Dorea
Ruminococcaceae_UCG-005
Prevotella_2
Ruminococcaceae_UCG-003
Ruminococcaceae_RC9_gut_grp
Ruminococcaceae_vadinBB60_grp_uncl
Ruminococcaceae_RC9_gut_grp
Parasutterella


RIH
Percentage Represented: 95.19 %
n = 14
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Prevotella_9
Alistipes
Subdoligranulum
Parabacteroides
Ruminococcaceae_UCG-002
Blautia
Lachnoclostridium
Lachnospira
Ruminococcaceae_uncl
Pseudobutyrivibrio
[Eubacterium]_coprostanoligenes_grp
Flavonifractor
Anaerostipes
Ruminococcaceae_UCG-005
Odoribacter
Thalassospira
Ruminococcaceae_UCG-013
Phascolarctobacterium
Incertae_Sedis
Subdoligranulum
Lachnospiraceae_UCG-004
Escherichia-Shigella
Lachnospiraceae_NK4A136_grp
Ruminococcaceae_UCG-010
Oscillibacter
Ruminococcaceae_vadinBB60_grp_uncl
Ruminococcaceae_UCG-005
Ruminococcaceae_RC9_gut_grp
Ruminococcaceae_UCG-014
Ruminococcaceae_UCG-004
Ruminococcaceae_UCG-010
Ruminococcaceae_UCG-013
Anaerostipes
Ruminococcaceae_NK4A136_grp
Ruminococcus_1
Unclassified
Dialister
Ruminococcaceae_UCG-003
Parasutterella
Ruminococcaceae_RC9_gut_grp
Ruminococcus_2
Intestinibacter
Veillonella
Flavonifractor
Bilophila
Ruminococcaceae_UCG-005
Roseburia
Oscillibacter
Megasphaera
Dorea
Ruminococcaceae_UCG-003
Ruminococcaceae_RC9_gut_grp
Ruminococcaceae_vadinBB60_grp_uncl
Ruminococcaceae_RC9_gut_grp
Parasutterella

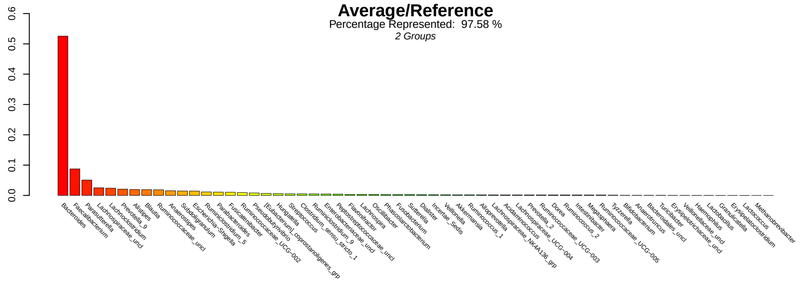
hadHydrea


Average/Reference
Percentage Represented: 96.91 %
2 Groups
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Alistipes
Prevotella_9
Subdoligranulum
Blautia
Lachnoclostridium
Parabacteroides
Lachnospiraceae_unCl
Ruminococcaceae_unCl
Eubacterium_ruminantium_group
Lachnospiraceae_UCG-002
Roseburia
Ruminococcaceae_NK4A136_grp
Ruminococcus_2
Flavonifractor
Oscillibacter
Ruminococcaceae_UCG-005
Coprococcus_3
Tyzzerella
Ruminococcaceae_UCG-014
Dorea
Odoribacter
Anaerostipes
Parasutterella
Intestinibacter
Clostridium_sensu_stricto_1
Escherichia_Shigella
Ruminococcaceae_UCG-004
Romboutsia
Akkermansia
Ruminococcus_1
Ruminococcus_9
Colidextribacter
Lachnospiraceae_UCG-003
Megasphaera
Ruminiclostridium_5
Ruminococcus_1
Ruminococcaceae_UCG-003
Lachnospiraceae_NK4A136_grp
Ruminococcus_2
Ruminococcaceae_UCG-005
Copricocc

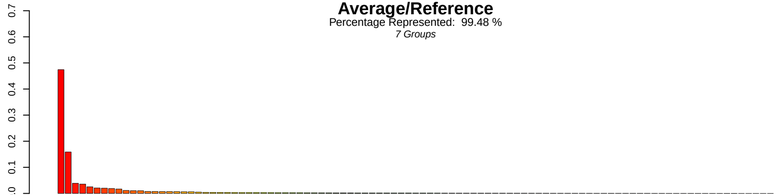
hadExch

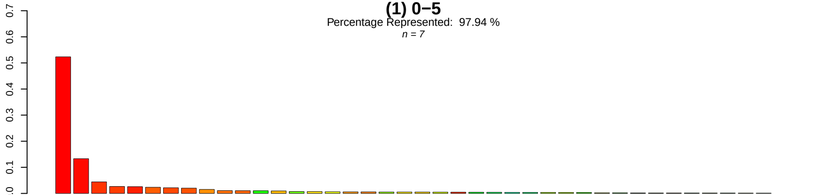

Average/Reference
Percentage Represented: 97.77 %
2 Groups
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Subdoligranulum
Alistipes
Ruminococcus_2
Blautia
Lachnospiraceae_unCl
Ruminococcaceae_unCl
Ruminococcus_1
Ruminococcus_5
Ruminococcaceae_UCG-002
Lachnospiraceae_NK4A136_grp
Dorea
Ruminiclostridium_9
Roseburia
Ruminococcaceae_UCG-005
Oscillibacter
Lachnospiraceae_unCl
Ruminococcaceae_UCG-003
Ruminococcaceae_UCG-004
Prevotella_9
Clostridium_sensu_stricto_1
Ruminococcaceae_UCG-010
Eubacterium_eligens_grp
Ruminococcaceae_unCl
Ruminococcaceae_UCG-013
Ruminococcaceae_UCG-008
Ruminococcaceae_UCG-009
Ruminococcaceae_UCG-014
Ruminococcaceae_UCG-001
Ruminococcaceae_unCl
Ruminococcaceae_UCG-007
Ruminococcaceae_unCl
Ruminococcaceae_unCl
Ruminococcaceae_unCl

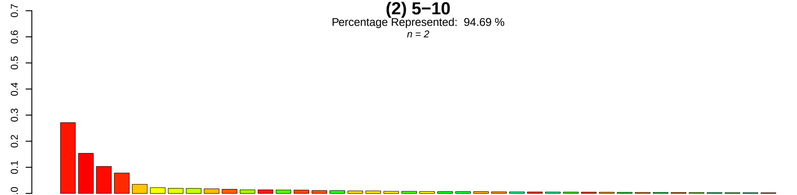
onPCN

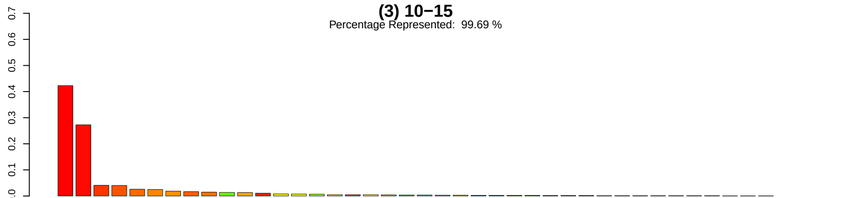

Average/Reference
Percentage Represented: 97.58 %
2 Groups
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Bacteroides
Alistipes
Faecalibacterium
Lachnospiraceae_unCl
Ruminococcus_2
Blautia
Roseburia
Subdoligranulum
Escherichia_Shigella
Ruminococcus_1
Lachnospiraceae_unCl
Dorea
Oscillibacter
Ruminococcaceae_UCG-002
Clostridium_sensu_stricto_1
Romboutsia
Ruminococcaceae_unCl
Peptostreptococcaceae_unCl
Ruminococcaceae_UCG-005
Ruminococcaceae_unCl
Intestinibacter
Streptococcus
Holdemanella
Ruminococcaceae_UCG-003
Ruminococcaceae_UCG-004
Ruminococcaceae_NK4A136_grp
Colidextribacter
Ruminococcaceae_UCG-010
Ruminococcaceae_unCl
Eubacterium_coprostanoligenes_grp
Ruminococcaceae_unCl
Lachnospiraceae_unCl
Ruminococcaceae_unCl
Ruminococcaceae_unCl
Ruminococca

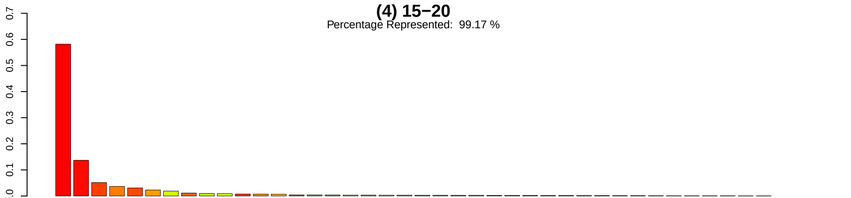
HbF

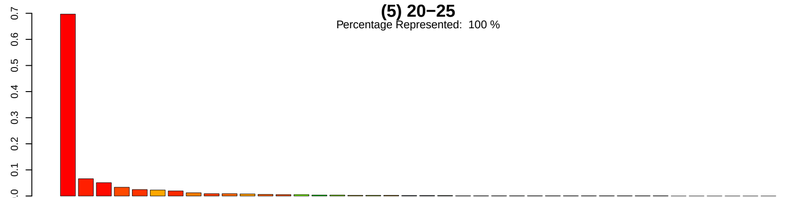

Average/Reference
Percentage Represented: 99.48 %
7 Groups


(1) 0−5
Percentage Represented: 97.94 %
n = 7

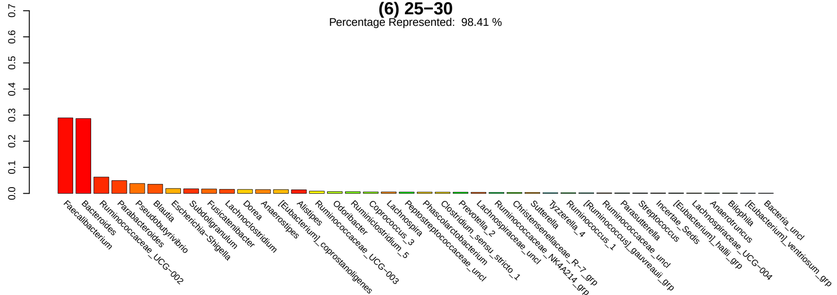

(2) 5−10
Percentage Represented: 94.69 %
n = 2


(3) 10−15
Percentage Represented: 99.69 %

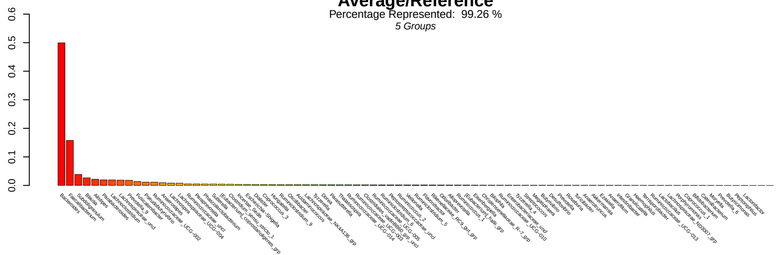

(4) 15−20
Percentage Represented: 99.17 %


(5) 20−25
Percentage Represented: 100 %

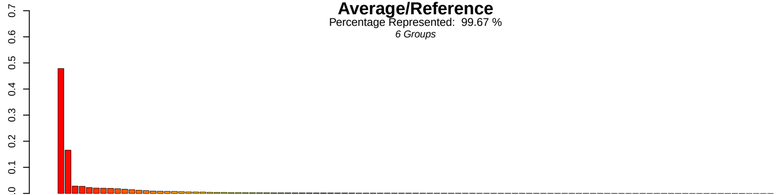
HbF

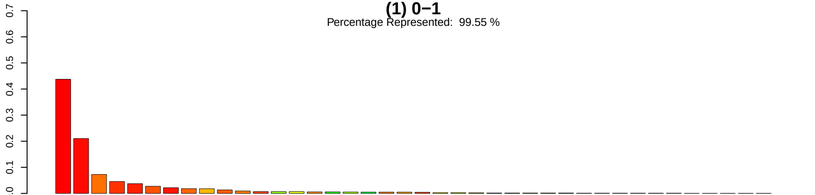

(6) 25−30
Percentage Represented: 98.41 %
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Faecalibacterium
Bacteroides
Ruminococcaceae_UCG−002
Parabacteroides
Pseudobutyrivibrio
Blautia
Escherichia−Shigella
Subdoligranulum
Fusicatenibacter
Lachnoclostridium
Dorea
Anaerostipes
[Eubacterium]_coprostanoligenes_grp
Alistipes
Ruminococcaceae_UCG−003
Odoribacter
Ruminiclostridium_5
Coprococcus_3
Lachnospira
Peptostreptococcaceae_unci
Phascolarctobacterium
Clostridium_sensu_stricto_1
Prevotella_2
Lachnospiraceae_unci
Ruminococcaceae_NK4A214_grp
Christensenellaceae_R−7_grp
Sutterella
Tyzzerella_4
Ruminococcus_1
Ruminococcus_gauvreauii_grp
Ruminococcaceae_unci
Parasutterella
Streptococcus
Incertae_Sedis
[Eubacterium]_hallii_grp
Lachnospiraceae_UCG−004
Anaerotruncus
Bilophila
[Eubacterium]_ventriosum_grp
Bacteria_unci

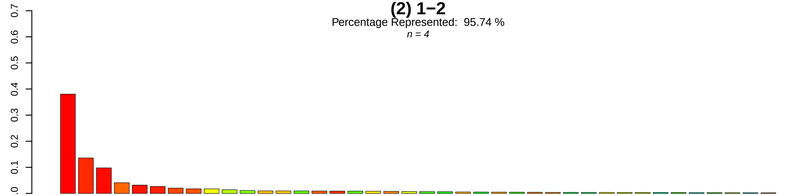
Hb

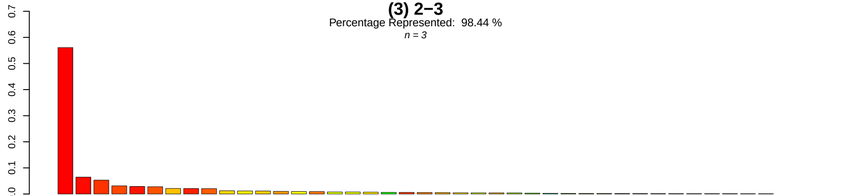

Average/Reference
Percentage Represented: 99.26 %
5 Groups
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Bacteroides
Faecalibacterium
Blautia
Subdoligranulum
Fusicatenibacter
Anaerostipes
Lachnospira
Lachnospiraceae_unci
Pseudobutyrivibrio
Acidaminococcus
Sutterella
Alistipes
Incertae_Sedis
Lachnospiraceae_UCG-004
Dorea
Coprococcus_3
Lachnoclostridium
Escherichia-Shigella
Veillonella
Ruminococcaceae_UCG-003
Erysipelotrichaceae_unci
Phascolarctobacterium
Gemmiger
Eubacterium_eligens_grp
Roseburia
Butyricicoccus
Ruminococcaceae_UCG-002
Prevotella_9
Ruminococcaceae_UCG-005
Ruminococcaceae_unci
Oscillibacter
Butyrivibrio
Ruminococcus_2
Anaerofilum
Desulfovibrio
Christensenellaceae_R-7_grp
Haemophilus
Ruminococcus_1
Ruminococcaceae_UCG-010
Ruminococcus_gnavus_group
Ruminococcaceae_UCG-013
Eubacterium_ventriosum_group
Ruminococcaceae_UCG-014
Ruminococcus_torques_group
Lachnospiraceae_NK4A136_grp
Ruminococcaceae_UCG-008
Ruminococcaceae_FCS_gut_grp
Ruminococcaceae_UCG-009
Ruminococcaceae_UCG-011
Ruminococcaceae_UCG-001
Ruminococcaceae_UCG-007
Ruminococcaceae_UCG-006
Ruminococcaceae_R-7_grp
Ruminococcaceae_UCG-005
Ruminococcaceae_UCG-010
Ruminococcaceae_UCG-013
Ruminococcaceae_UCG-014
Ruminococcaceae_UCG-008

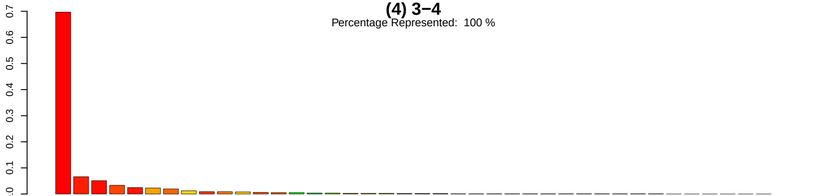
Bilirubin

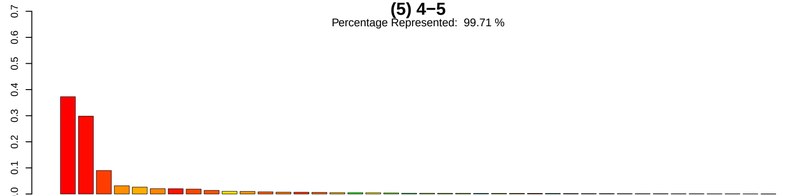

Average/Reference
Percentage Represented: 99.67 %
6 Groups


(1) 0−1
Percentage Represented: 99.55 %

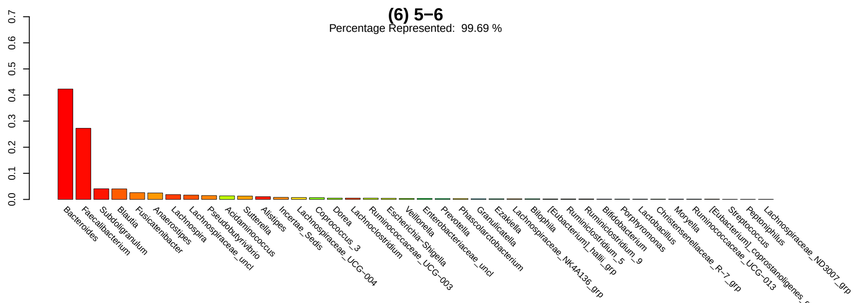

(2) 1−2
Percentage Represented: 95.74 %
n = 4


(3) 2−3
Percentage Represented: 98.44 %
n = 3

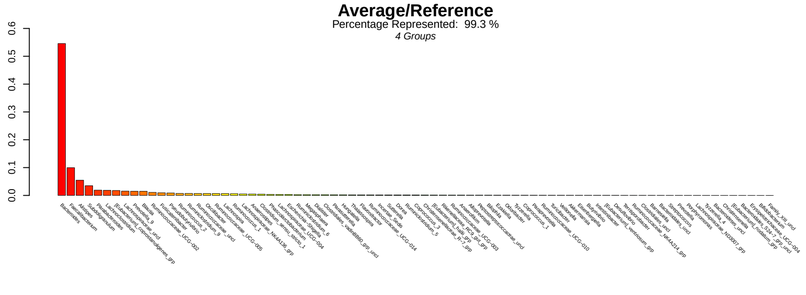

(4) 3−4
Percentage Represented: 100 %

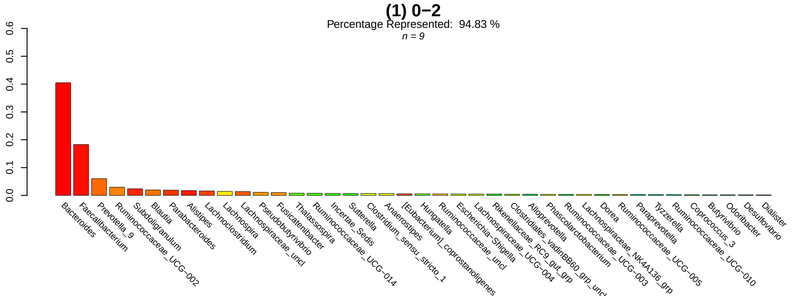

(5) 4−5
Percentage Represented: 99.71 %

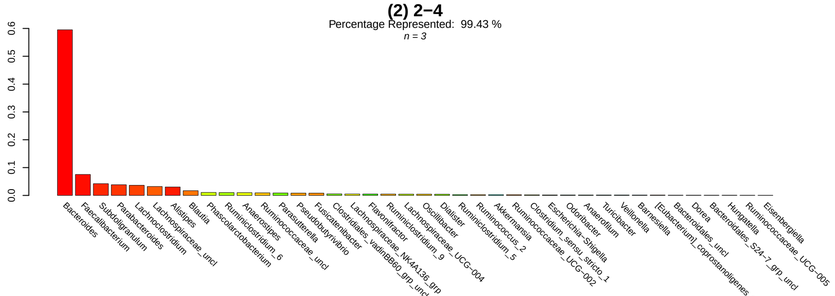
Bilirubin

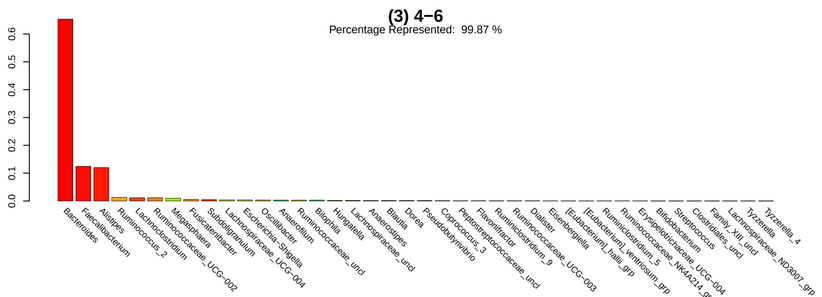

(6) 5−6
Percentage Represented: 99.69 %
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Bacteroides
Faecalibacterium
Subdoligranulum
Blautia
Fusicatenibacter
Anaerostipes
Lachnospira
Lachnospiraceae_uncl
Pseudobutyrivibrio
Acidaminococcus
Sutterella
Alistipes
Incertae_Sedis
Lachnospiraceae_UCG−004
Coprococcus_3
Dorea
Lachnoclostridium
Ruminococcaceae_UCG−003
Escherichia−Shigella
Veillonella
Enterobacteriaceae_uncl
Prevotella
Phascolarctobacterium
Granulicatella
Ezakiella
Lachnospiraceae_NK4A136_grp
Bilophila
[Eubacterium]_ruthii_grp
Ruminiclostridium_5
Ruminiclostridium_9
Bifidobacterium
Porphyromonas
Lactobacillus
Christensenellaceae_R−7_grp
Morganella
Ruminococcaceae_UCG−013
[Eubacterium]_eligonans_grp
Streptococcus
Peptoniphilus
Lachnospiraceae_ND3007_grp

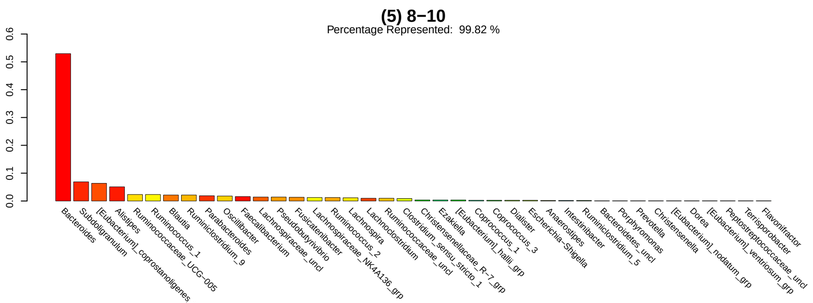
Admit


Average/Reference
Percentage Represented: 99.3 %
4 Groups

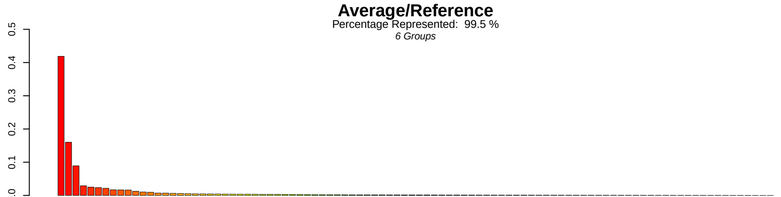

(1) 0−2
Percentage Represented: 94.83 %
n = 9

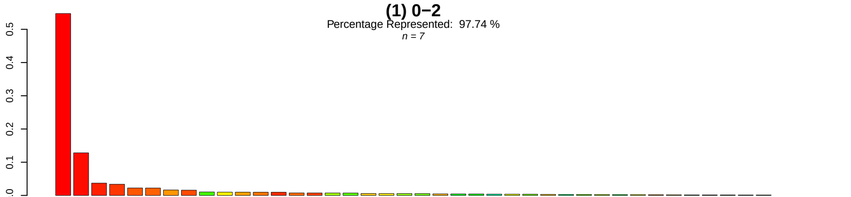

(2) 2−4
Percentage Represented: 99.43 %
n = 3


(3) 4−6
Percentage Represented: 99.87 %

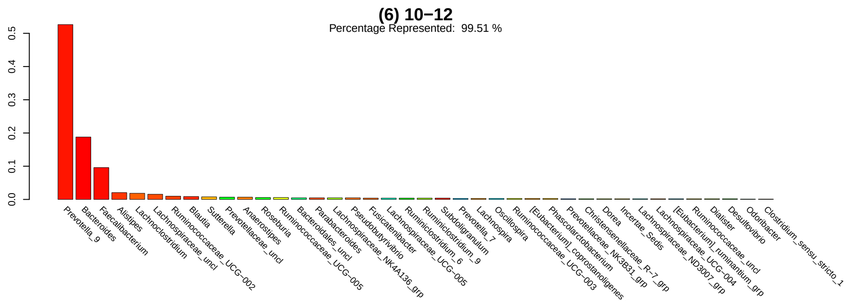

(5) 8−10
Percentage Represented: 99.82 %

LastVOC

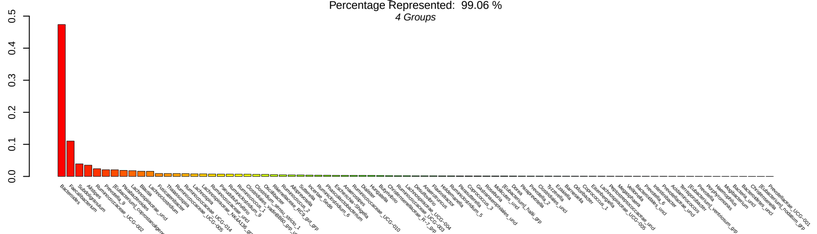


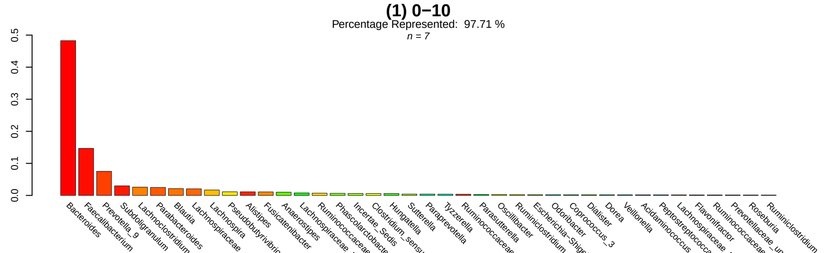

(1) 0−2
Percentage Represented: 97.74 %
n = 7
Bacteroides
Faecalibacterium
Subdoligranulum
Alistipes
Parabacteroides
Lachnoclostridium
Lachnospira
Lachnospiraceae_unCl
Ruminococcaceae_unCl
[Eubacterium]_coprostanoligenes_grp
Blautia
Prevotellaceae_unCl
Romboutsia
Ruminococcaceae_UCG-002
Lachnospiraceae_NK4A136_grp
Dorea
Clostridium_sensu_stricto_1
Ruminococcus_1
Agathobacter
Oscillibacter
Ruminococcus_9
Sutterella
Ruminococcus_6
Ruminococcaceae_UCG-005
Flavonifractor
Prevotella_2
Tyzzerella
Dialister
Odoribacter
Christensenellaceae_R-7_grp
Anaerostipes
Escherichia−Shigella
Ruminococcaceae_UCG-004
Lachnospiraceae_UCG-004
Roseburia
Eisenbergiella
Ruminococcaceae_UCG-003
Ruminococcus_2
Lachnospiraceae_UCG-005
Flavonifractor
Dialister
Odoribacter

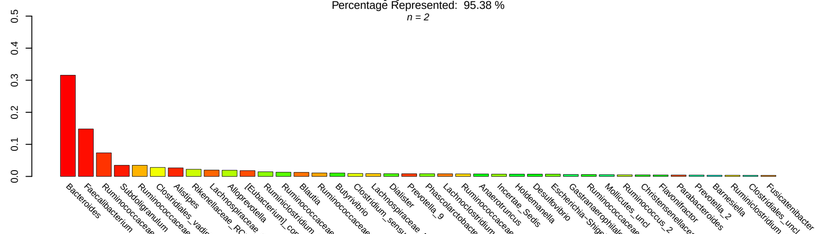
LastVOC

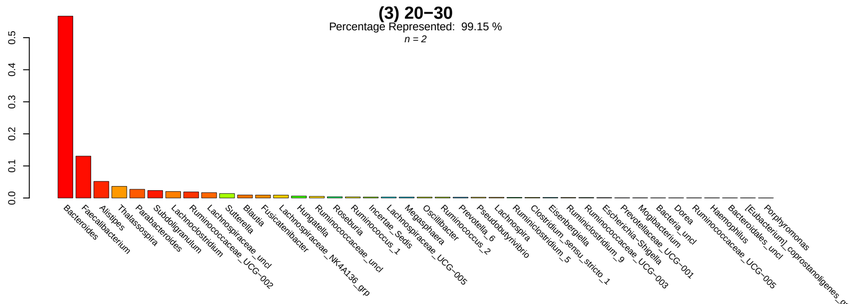

(6) 10−12
Percentage Represented: 99.51 %
0.0
0.1
0.2
0.3
0.4
0.5
Prevotella_9
Bacteroides
Faecalibacterium
Alistipes
Lachnoclostridium
Lachnospiraceae_unCl
Ruminococcaceae_UCG−002
Blautia
Subdoligranulum
Prevotellaceae_unCl
Anaerostipes
Roseburia
Ruminococcaceae_UCG−005
Barnesiella
Parabacteroides_unCl
Lachnospiraceae_Incertae_Sedis
Faecalibacterium
Fusicatenibacter
Lachnospiraceae_NK4A136_group
Ruminiclostridium_6
Ruminiclostridium_UCG−005
Ruminiclostridium_9
Subdoligranulum
Prevotella_7
Lachnospira
Oscillospira
Ruminococcaceae_UCG−003
[Eubacterium]_coprostanoligenes_group
Prevotellaceae_UCG−001
Christensenellaceae_R−7_group
Dorea
Incertae_Sedis
Lachnospiraceae_ND3007_group
[Eubacterium]_ruminantium_group
Ruminococcaceae_unCl
Butyricicoccus
Desulfovibrio
Oscillibacter
Clostridium_sensu_stricto_1

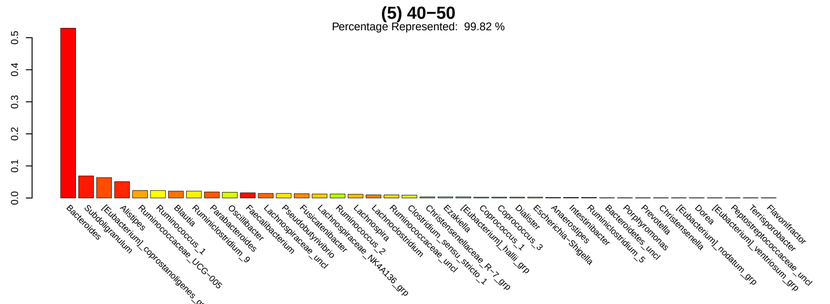
ESR


Average/Reference
Percentage Represented: 99.06 %
4 Groups

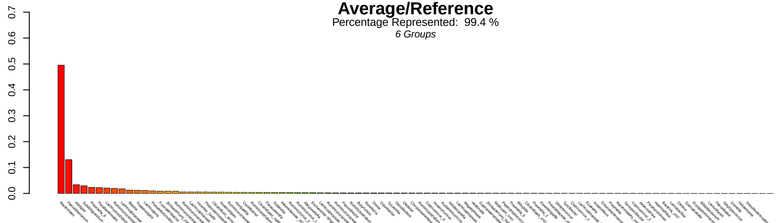

(1) 0−10
Percentage Represented: 97.71 %
n = 7

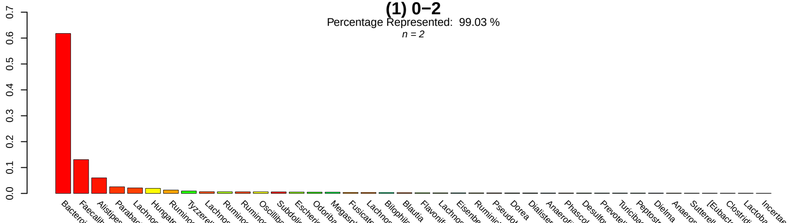

(2) 10−20
Percentage Represented: 95.38 %
n = 2

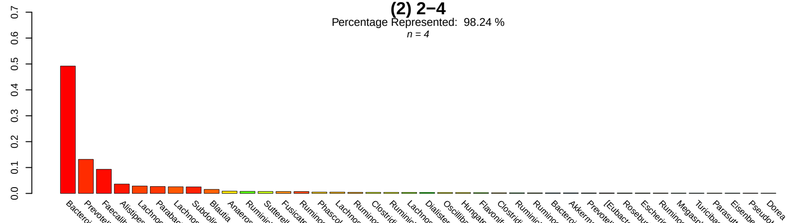

(3) 20−30
Percentage Represented: 99.15 %
n = 2

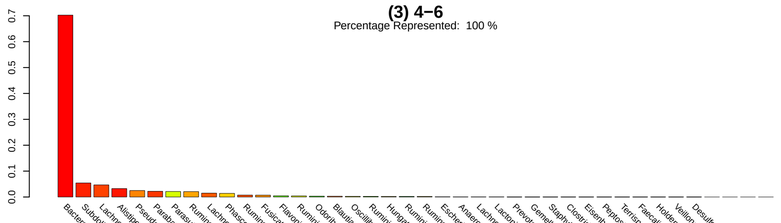

(5) 40−50
Percentage Represented: 99.82 %

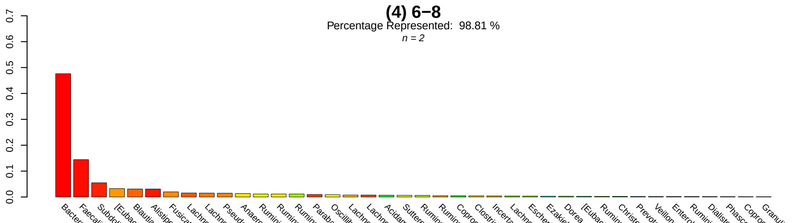
CRP

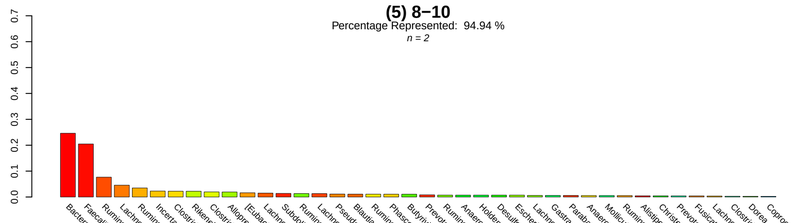

Average/Reference
Percentage Represented: 99.4 %
6 Groups


(1) 0−2
Percentage Represented: 99.03 %
n = 2

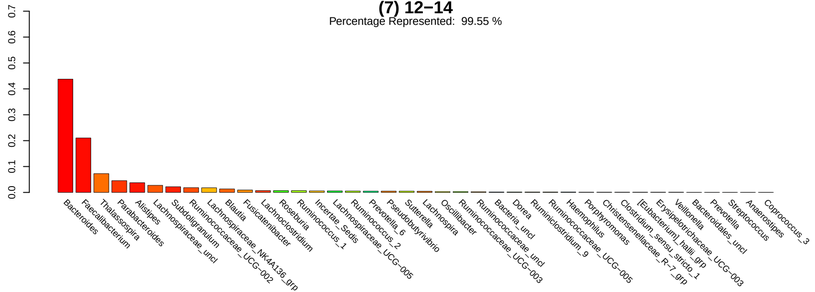

(2) 2−4
Percentage Represented: 98.24 %
n = 4


(3) 4−6
Percentage Represented: 100 %

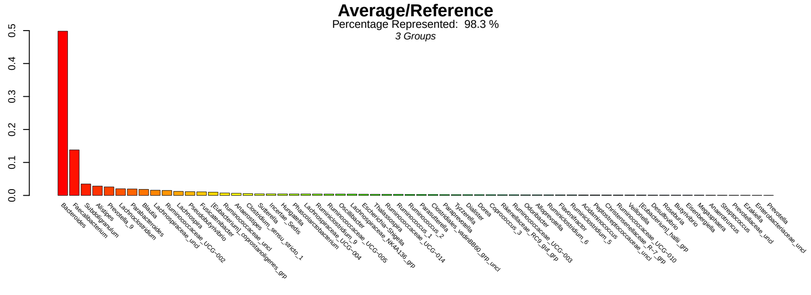

(4) 6−8
Percentage Represented: 98.81 %
n = 2

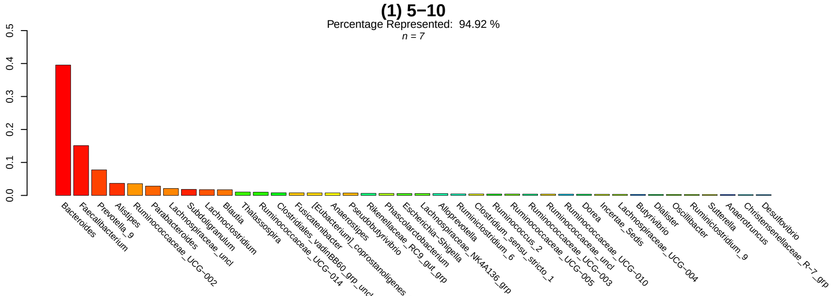

(5) 8−10
Percentage Represented: 94.94 %
n = 2

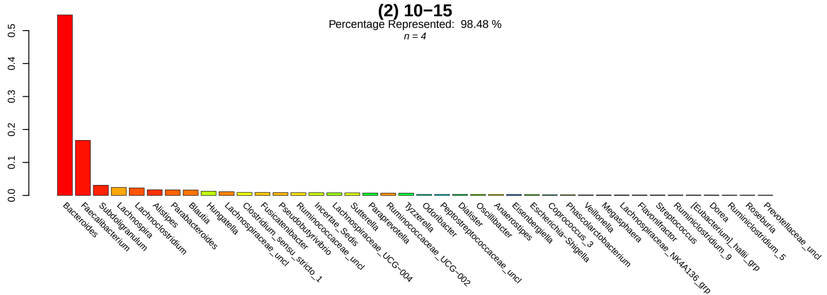
CRP

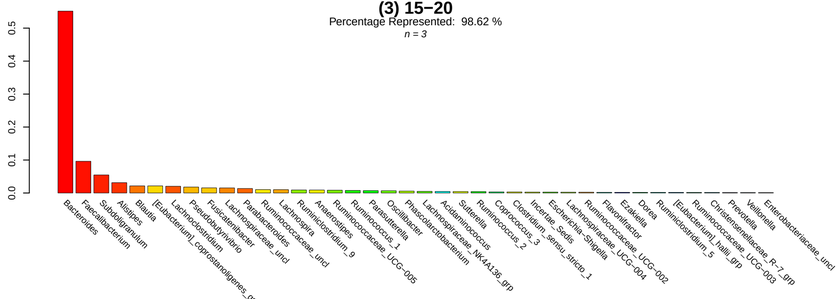

(7) 12−14
Percentage Represented: 99.55 %
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Bacteroides
Faecalibacterium
Thalassospira
Parabacteroides
Alistipes
Lachnospiraceae_unCl
Subdoligranulum
Ruminococcaceae_unCl
Lachnospiraceae_UCG-002
Blautia
Fusicatenibacter
Lachnoclostridium
Prosaurella
Ruminococcus_1
Incertella_Sedis
Lachnospiraceae_unCl
Ruminococcus_2
Prevotella_9
Lachnospiraceae_UCG-005
Pseudobutyrivibrio
Butyricella
Lachnospira
Oscillibacter
Ruminococcaceae_UCG-003
Ruminococcaceae_unCl
Bacteria_unCl
Dorea
Ruminococcaceae_unCl
Ruminococcus_9
Haemophilus
Porphyromonas
Christensenellaceae_UCG-005
Clostridium_sensu_stricto_1
Rikenellaceae_RC9_gut_grp
Erysipelotrichaceae_UCG-003
Veillonella
Bacteroidales_unCl
Prevotella
Streptococcus
Anaerostipes
Coprococcus_3

WBC

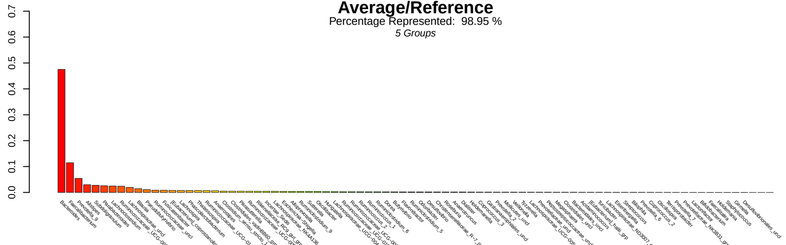

Average/Reference
Percentage Represented: 98.3 %
3 Groups

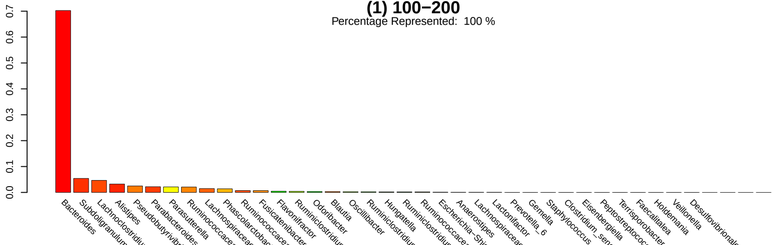

(1) 5−10
Percentage Represented: 94.92 %
n = 7

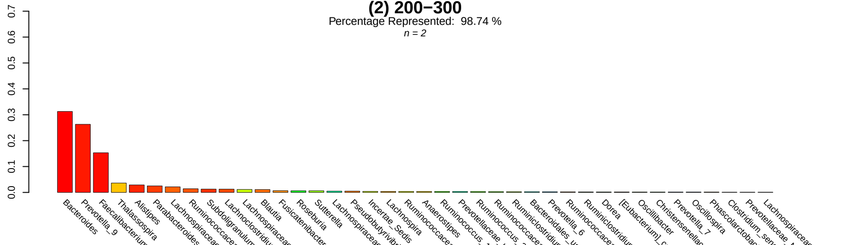

(2) 10−15
Percentage Represented: 98.48 %
n = 4

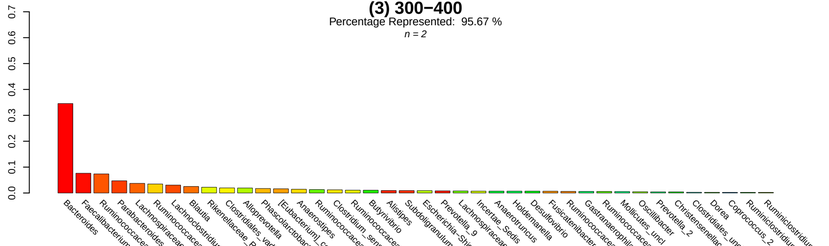

(3) 15−20
Percentage Represented: 98.62 %
n = 3

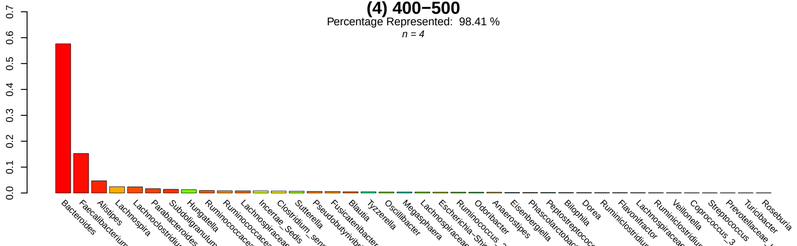
LDH

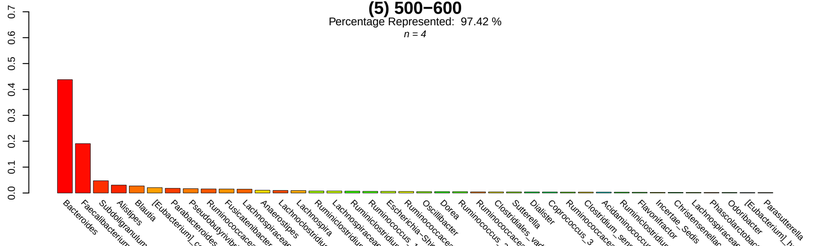

Average/Reference
Percentage Represented: 98.95 %
5 Groups


(1) 100−200
Percentage Represented: 100 %

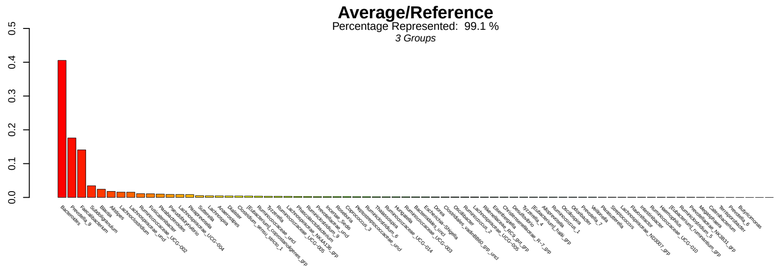

(2) 200−300
Percentage Represented: 98.74 %
n = 2

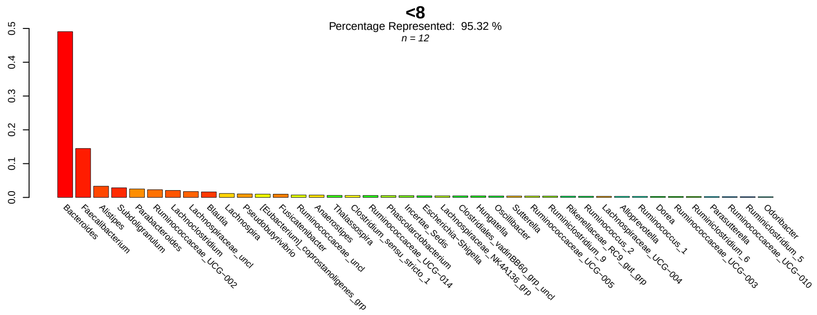

(3) 300−400
Percentage Represented: 95.67 %
n = 2

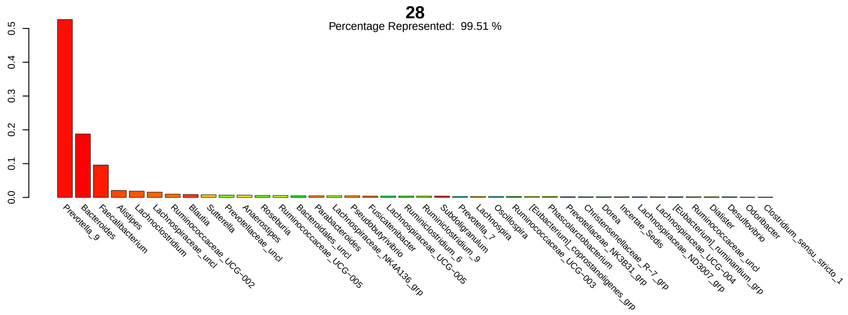

(4) 400−500
Percentage Represented: 98.41 %
n = 4

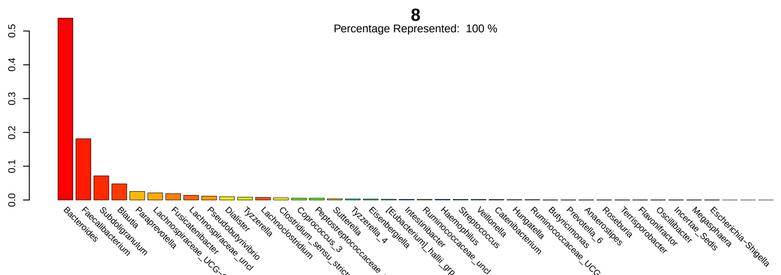

(5) 500−600
Percentage Represented: 97.42 %
n = 4

Hapto

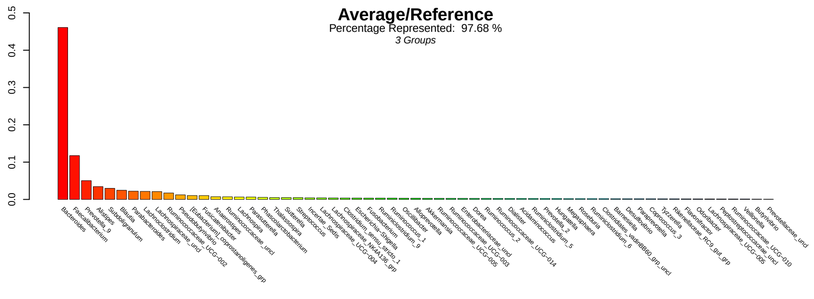

Average/Reference
Percentage Represented: 99.1 %
3 Groups
0.0
0.1
0.2
0.3
0.4
0.5

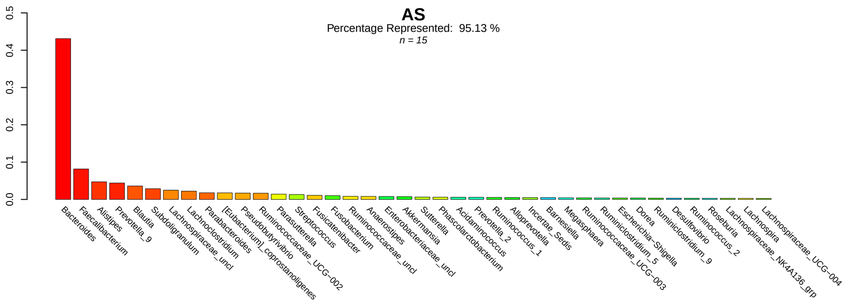

<8
Percentage Represented: 95.32 %
n = 12
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Alistipes
Subdoligranulum
Parabacteroides
Ruminococcaceae_UCG-002
Lachnoclostridium
Lachnospiraceae_uncl
Blautia
Lachnospira
Pseudobutyrivibrio
[Eubacterium]_coprostanoligenes_grp
Fusicatenibacter
Ruminococcaceae_uncl
Anaerostipes
Thalassospira
Clostridium_sensu_stricto_1
Ruminococcaceae_UCG-014
Phascolarctobacterium
Incertae_Sedis
Escherichia-Shigella
Lachnospiraceae_NK4A136_grp
Clostridiales_vadinBB60_grp_uncl
Hungatella
Oscillibacter
Sutterella
Ruminococcaceae_UCG-005
Ruminococcus_2
Rikenellaceae_RC9_gut_grp
Ruminococcus_1
Lachnospiraceae_UCG-004
Alloprevotella
Ruminococcus_1
Dorea
Ruminococcaceae_UCG-003
Ruminiclostridium_6
Parasutterella
Ruminococcaceae_UCG-010
Ruminiclostridium_5
Odoribacter

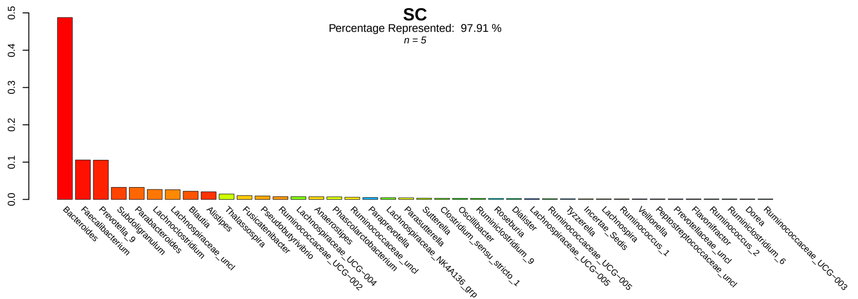

28
Percentage Represented: 99.51 %
0.0
0.1
0.2
0.3
0.4
0.5
Prevotella_9
Bacteroides
Faecalibacterium
Alistipes
Lachnoclostridium
Lachnospiraceae_uncl
Ruminococcaceae_UCG-002
Blautia
Sutterella
Prevotellaceae_uncl
Anaerostipes
Roseburia
Ruminococcaceae_UCG-005
Bacteroidales_uncl
Parabacteroides
Lachnospiraceae_NK4A136_grp
Pseudobutyrivibrio
Fusicatenibacter
Lachnospiraceae_UCG-005
Ruminococcaceae_UCG-005
Ruminiclostridium_9
Subdoligranulum
Prevotella_7
Lachnospira
Oscillospira
Ruminococcaceae_UCG-003
[Eubacterium]_coprostanoligenes_grp
Phascolarctobacterium
Prevotellaceae_NK3B31_grp
Christensenellaceae_R-7_grp
Dorea
Incertae_Sedis
Lachnospiraceae_NC3007_grp
Lachnospiraceae_UCG-004
[Eubacterium]_ruminantium_grp
Ruminococcaceae_uncl
Dialister
Desulfovibrio
Odoribacter
Clostridium_sensu_stricto_1

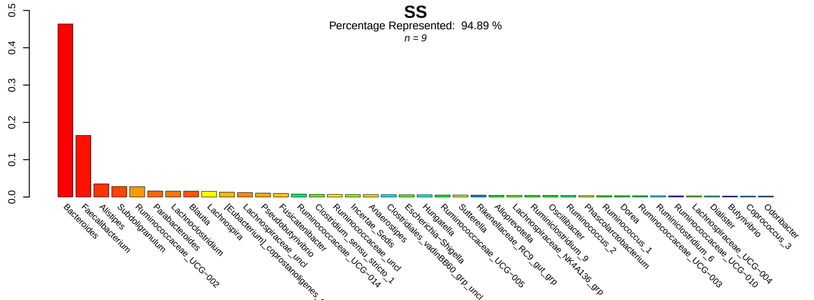

8
Percentage Represented: 100 %
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Faecalibacterium
Subdoligranulum
Blautia
Paraprevotella
Lachnospiraceae_UCG-004
Fusicatenibacter
Lachnospiraceae_uncl
Pseudobutyrivibrio
Dialister
Tyzzerella
Lachnoclostridium
Clostridium_sensu_stricto_1
Coprococcus_3
Peptostreptococcaceae_uncl
Sutterella
Tyzzerella_4
Eisenbergiella
[Eubacterium]_hallii_grp
Intestinibacter
Ruminococcaceae_uncl
Haemophilus
Streptococcus
Veillonella
Catenibacterium
Hungatella
Ruminococcaceae_UCG-002
Butyricimonas
Prevotella_6
Anaerostipes
Roseburia
Terrisporobacter
Flavonifractor
Oscillibacter
Incertae_Sedis
Megasphaera
Escherichia-Shigella

Type

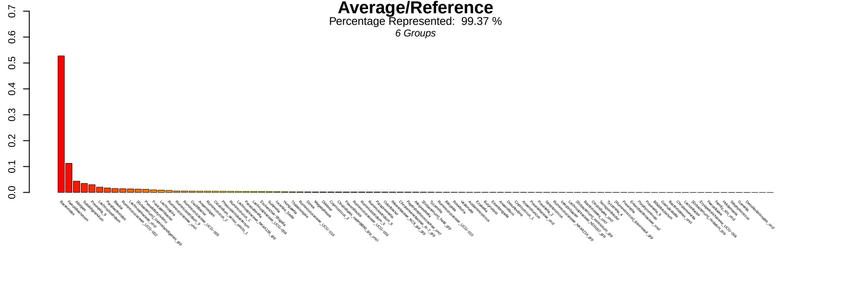

Average/Reference
Percentage Represented: 97.68 %
3 Groups

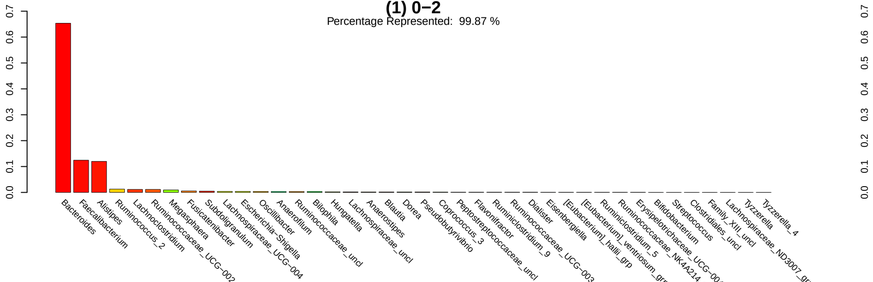

AS
Percentage Represented: 95.13 %
n = 15

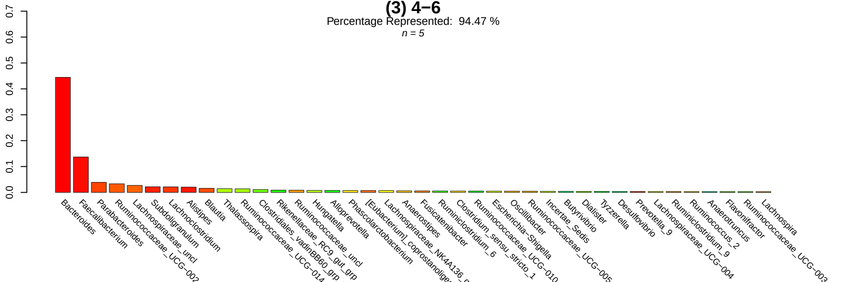

SC
Percentage Represented: 97.91 %
n = 5

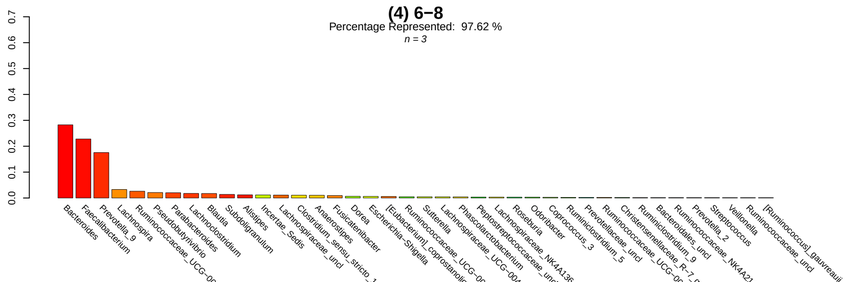

SS
Percentage Represented: 94.89 %
n = 9

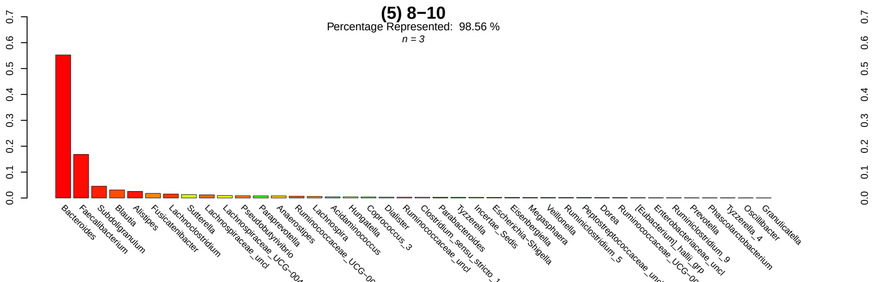
Neut

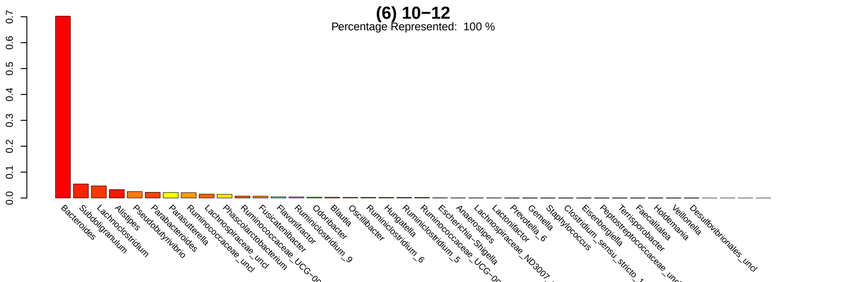

Average/Reference
Percentage Represented: 99.37 %
6 Groups


(1) 0−2
Percentage Represented: 99.87 %

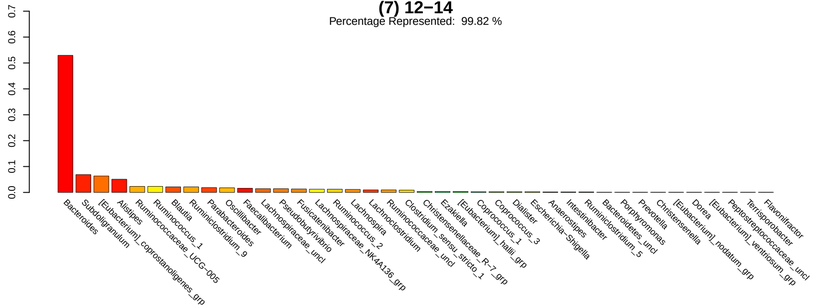

(3) 4−6
Percentage Represented: 94.47 %
n = 5


(4) 6−8
Percentage Represented: 97.62 %
n = 3

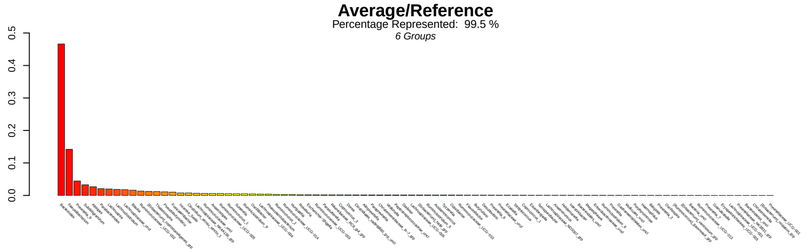

(5) 8−10
Percentage Represented: 98.56 %
n = 3

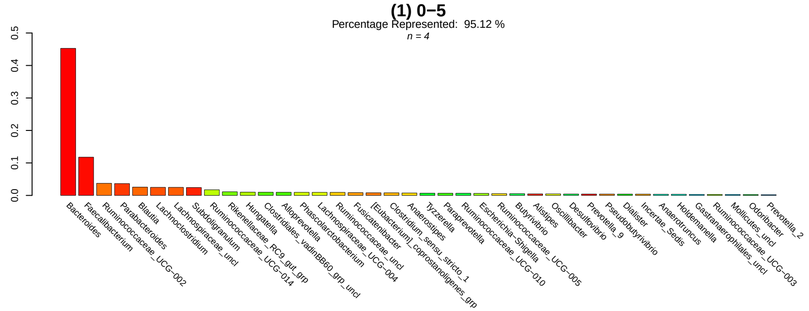

(6) 10−12
Percentage Represented: 100 %

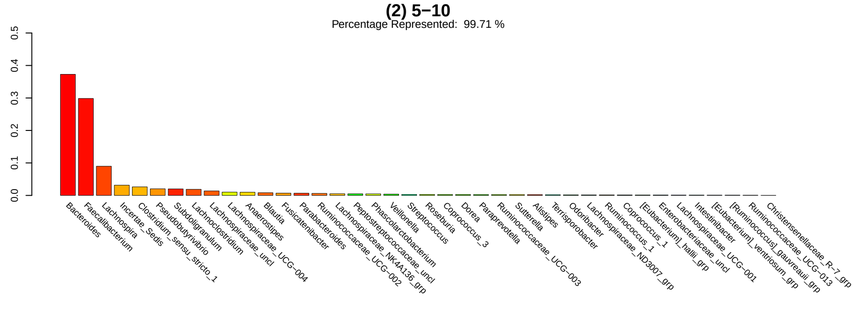
Neut

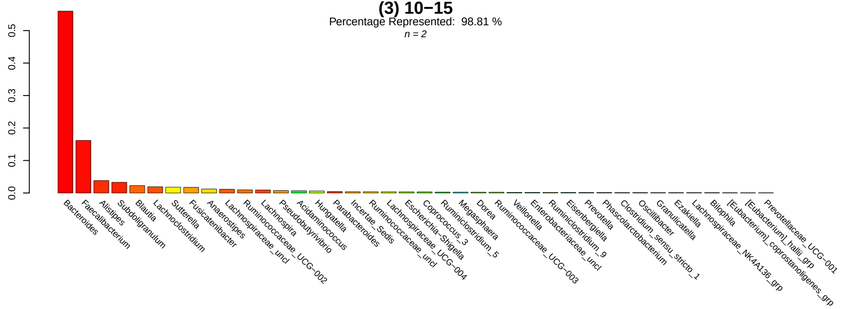

(7) 12−14
Percentage Represented: 99.82 %
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Bacteroides
Subdoligranulum
[Eubacterium]_coprostanoligenes_grp
Alistipes
Ruminococcaceae_UCG-005
Ruminococcus_1
Blautia
Ruminiclostridium_9
Parabacteroides
Oscillibacter
Faecalibacterium
Lachnospiraceae_uncl
Pseudobutyrivibrio
Fusicatenibacter
Lachnospiraceae_NK4A136_grp
Ruminococcus_2
Lachnospira
Lachnoclostridium
Ruminococcaceae_uncl
Clostridium_sensu_stricto_1
Christensenellaceae_R-7_grp
Eubacterium_hallii_grp
Coprococcus_1
Coprococcus_3
Dialister
Escherichia-Shigella
Anaerostipes
Intestinibacter
Ruminiclostridium_5
Bacteroides_uncl
Porphyromonas
Prevotella
Christensenella
[Eubacterium]_nodatum_grp
Dorea
[Eubacterium]_ventriosum_grp
Peptostreptococcaceae_uncl
Terrisporobacter
Flavonifractor

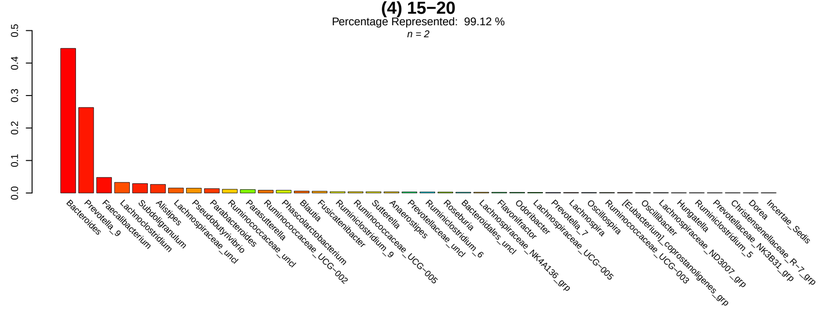
SCChi_CD16

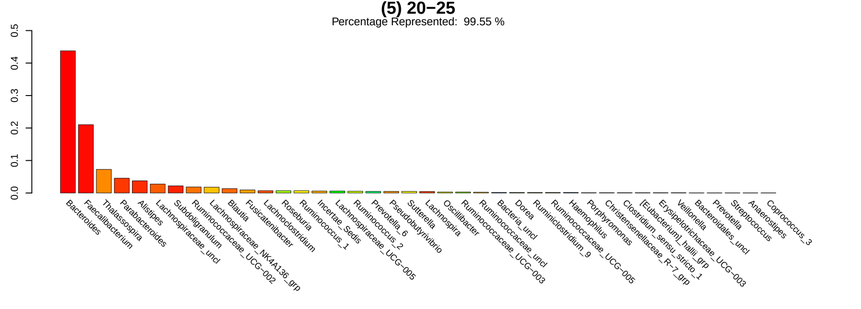

Average/Reference
Percentage Represented: 99.5 %
6 Groups


(1) 0−5
Percentage Represented: 95.12 %
n = 4

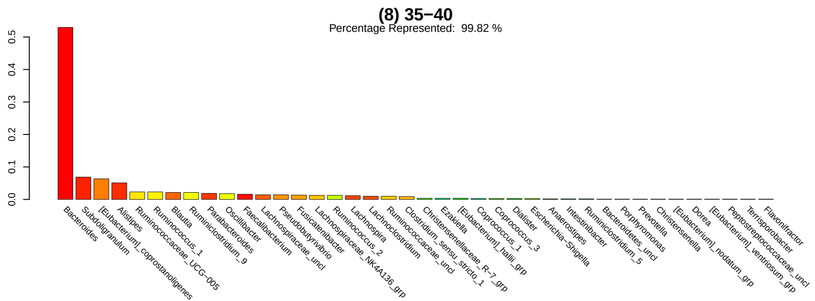

(2) 5−10
Percentage Represented: 99.71 %


(3) 10−15
Percentage Represented: 98.81 %
n = 2

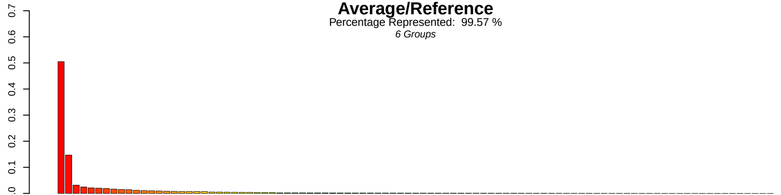

(4) 15−20
Percentage Represented: 99.12 %
n = 2

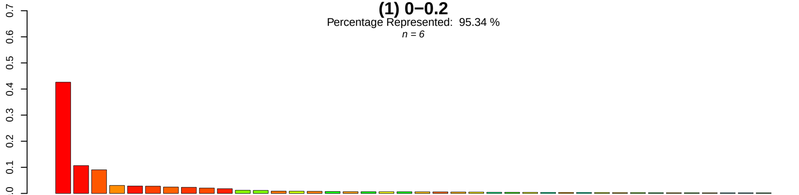

(5) 20−25
Percentage Represented: 99.55 %

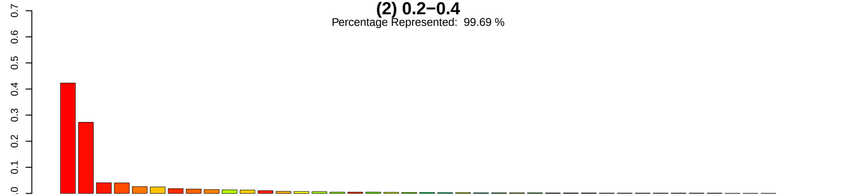
SCChi_CD16

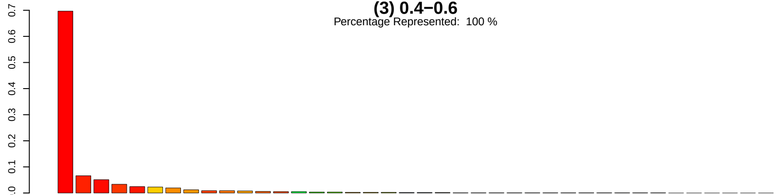

(8) 35−40
Percentage Represented: 99.82 %
0.0
0.1
0.2
0.3
0.4
0.5
Bacteroides
Subdoligranulum
[Eubacterium]_coprostanoligenes_grp
Alistipes
Ruminococcaceae_UCG-005
Ruminococcus_1
Blautia
Ruminiclostridium_9
Parabacteroides
Oscillibacter
Faecalibacterium
Lachnospiraceae_uncl
Pseudobutyrivibrio
Fusicatenibacter
Lachnospiraceae_NK4A136_grp
Ruminococcus_2
Lachnospira
Ruminococcaceae_uncl
Clostridium_sensu_stricto_1
Christensenellaceae_R-7_grp
Ezakella
[Eubacterium]_hallii_grp
Coprococcus_1
Coprococcus_3
Dialister
Escherichia-Shigella
Anaerotipes
Intestinibacter
Ruminiclostridium_5
Bacteroides_uncl
Porphyromonas
Prevotella
Christensenella
[Eubacterium]_nodatum_grp
Dorea
[Eubacterium]_ventriosum_grp
Peptostreptococcaceae_uncl
Terrisporobacter
Flavonifractor

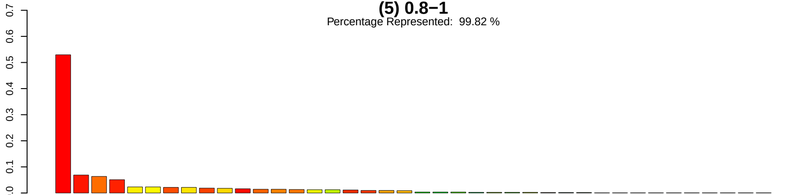
CD62lo_CD11b

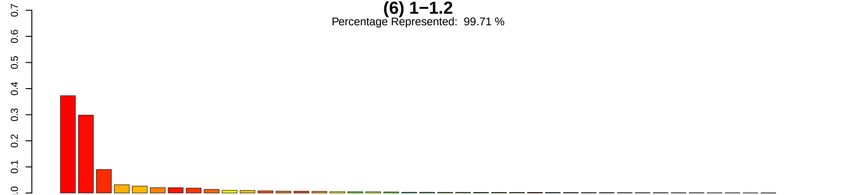




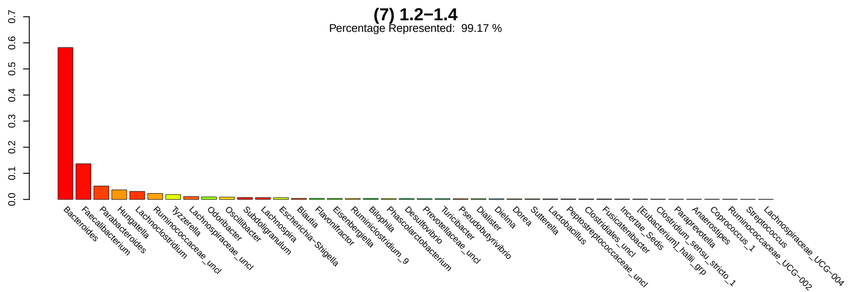
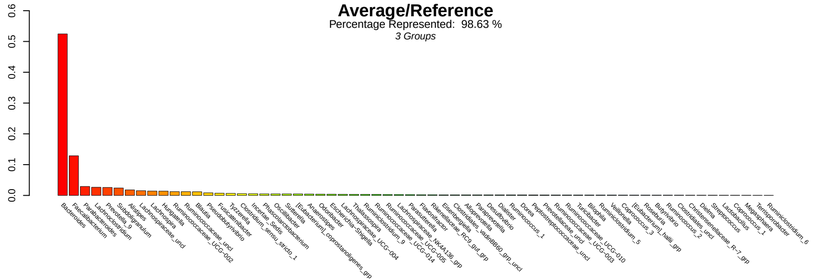
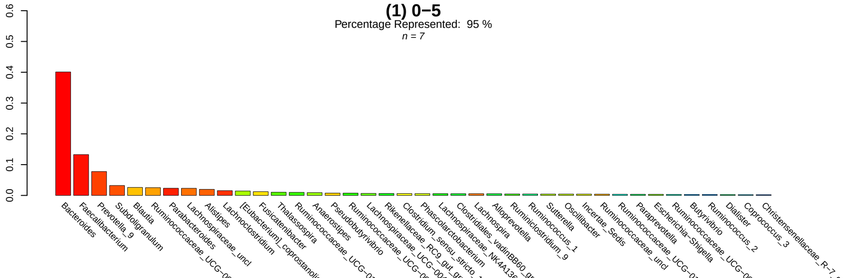
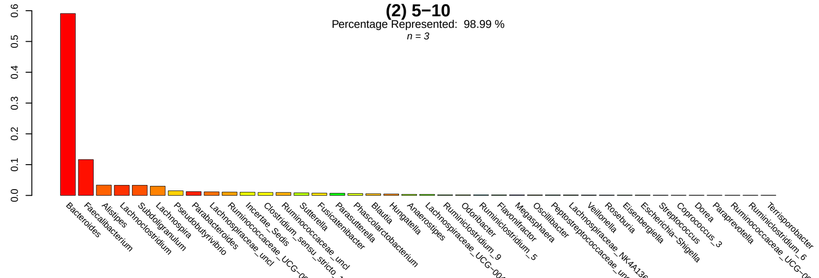
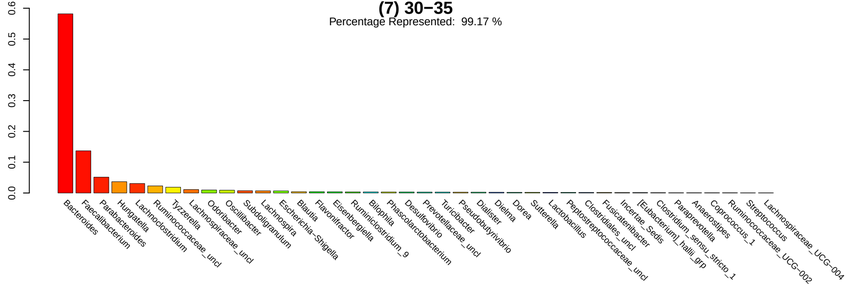








CD62lo_CD11b



CD62lo_CD184