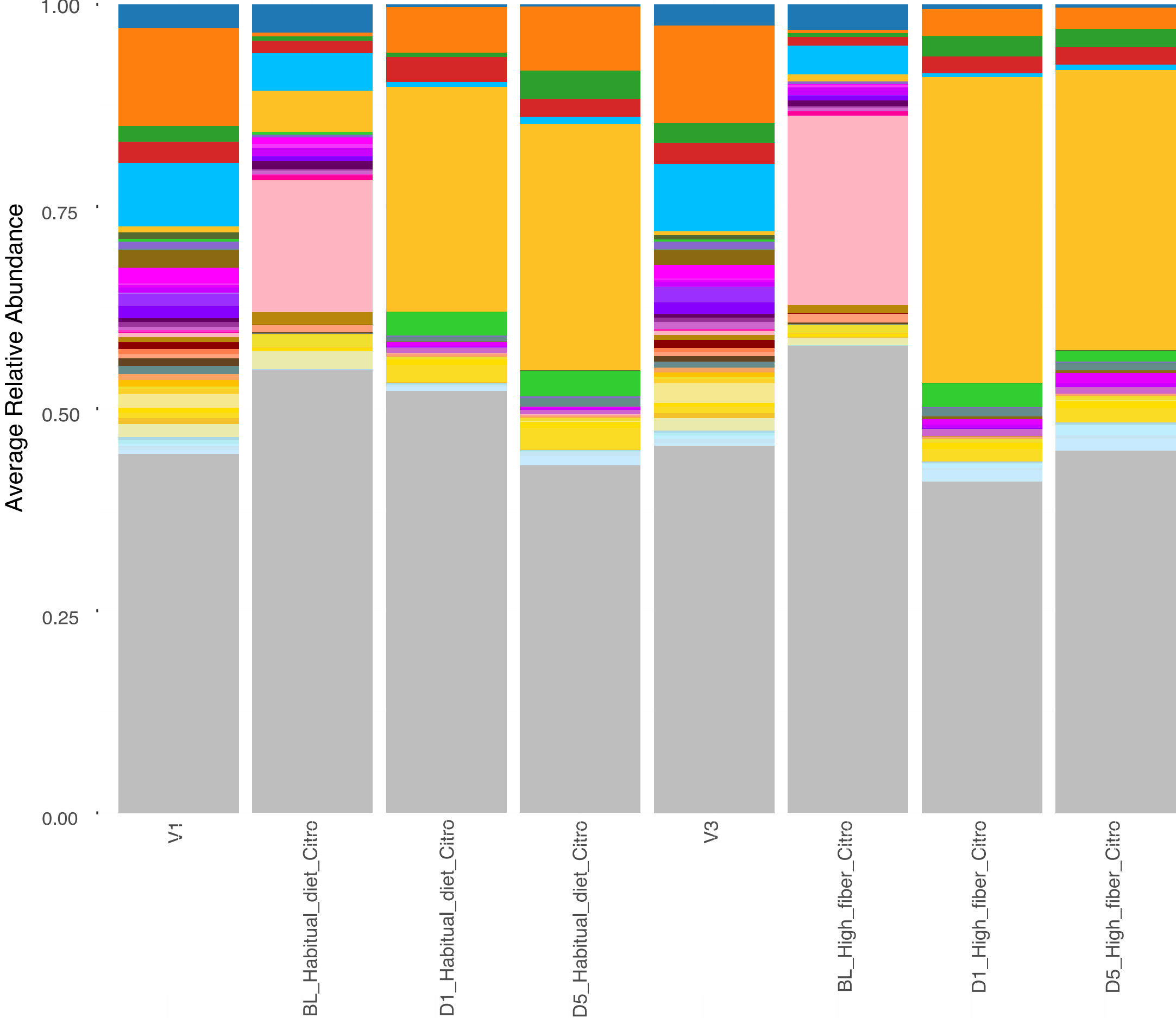
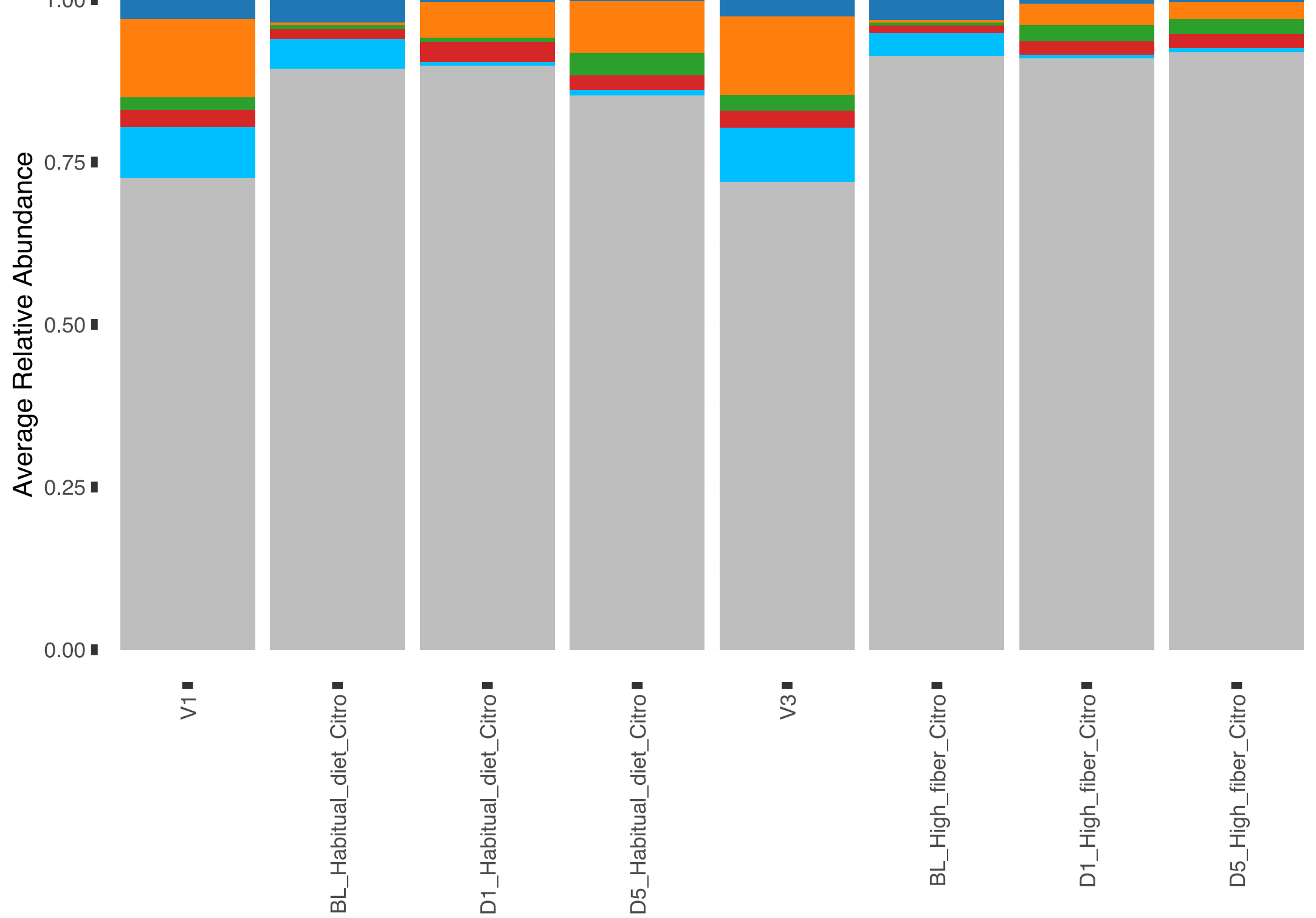


CORE MICROBIOME(25%)



- Alistipes
- Bacteroides
- Blautia
- Lachnoclostridium
- Lachnospiraceae_
- Akkermansia
- Barnesiella
- Bilophila
- Butyricicoccus
- Butyricimonas
- Christensenellaceae_R.7_group
- Clostridia_UCG.014
- Clostridia_vadinBB60_group
- Clostridium_sensu_stricto_1
- Colidextribacter
- Coprobacter
- Dorea
- Eubacterium_coprostanoligenes_group
- Eubacterium_xylanophilum_group
- Gastranaerophilales
- Incertae_Sedis
- Intestinimonas
- Lachnospiraceae_FCS020_group
- Lachnospiraceae_NK4A136_group
- Lachnospiraceae_UCG.001
- Lachnospiraceae_UCG.004
- Odoribacter
- Oscillibacter
- Oscillospiraceae_
- Oscillospiraceae.g_NK4A214_group
- Oscillospiraceae.g__UCG.003
- Oscillospiraceae.g__UCG.005
- Oscillospiraceae.g__uncultured
- Oscillospirales.f__UCG.010.g__UCG.010
- Parabacteroides
- Parasutterella
- Phascolarctobacterium
- Rhodospirillales.f__uncultured.g__uncultured
- Roseburia
- Ruminococcaceae_
- Ruminococcaceae.g__uncultured
- Ruminococcus_gauvreauii_group
- Ruminococcus_torques_group
- Sellimonas
- Others

CORE MICROBIOME(80%)



- Alistipes
- Bacteroides
- Blautia
- Lachnoclostridium
- Lachnospiraceae_
- Others