**S2 Table.** **Differential ESV abundance of gut microbiota by each CM risk including waist circumference, blood pressure, blood fasting glucose, triglyceride and HDL concentration in USA, RSA, Ghanaian and Jamaican** **population (adjusted for country, age, BMI and gender across the entire cohort,).** USA, the United States of America; RSA, South Africa. ESV, Exact Sequence Variant. Data shown are mean± S.E.M.

|  |  |  |
| --- | --- | --- |
| **Country** | **Taxonomy of Significantly differential ESVs** | **Average relative abundance \*** **(% (SE))** |
| **Group waist** | **High waist** | **Low waist** |
| **All** | p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 1.02 (0.23) | 2.65 (0.31) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_; | 0.54 (0.08) | 1.11 (0.12) |
| p\_\_Firmicutes; c\_\_Erysipelotrichi; o\_\_Erysipelotrichales; f\_\_Erysipelotrichaceae; g\_\_ | 0.51 (0.08) | 0.67 (0.07) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Leuconostocaceae; g\_\_ | 0.07 (0.03) | 0.27 (0.07) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_; | 0.99 (0.21) | 1.40 (0.15) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_SMB53 | 0.23 (0.031) | 0.38 (0.04) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae; g\_\_Megasphaera | 0.57 (0.11) | 0.30 (0.06) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus | 0.07 (0.03) | 0.42 (0.10) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Turicibacterales; f\_\_Turicibacteraceae; g\_\_Turicibacter | 0.21 (0.04) | 0.28 (0.03) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus | 0.71 (0.10) | 0.43 (0.06) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 0.70 (0.14) | 0.56 (0.13) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.23 (0.06) | 0.02 (0.01) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Dorea | 0.50 (0.04) | 0.32 (0.03) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Peptostreptococcaceae; g\_\_ | 0.51 (0.06) | 0.68 (0.05) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Porphyromonadaceae; g\_\_Parabacteroides | 0.55 (0.07) | 0.38 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Faecalibacterium | 0.06 (0.01) | 0.13 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.19 (0.03) | 0.09 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.17 (0.02) | 0.17 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae | 0.03 (0.01) | 0.08 (0.01) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Roseburia | 2.76 (0.20) | 2.17 (0.16) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_ | 0.17 (0.02) | 0.09 (0.01) |
| p\_\_Proteobacteria; c\_\_Deltaproteobacteria; o\_\_Desulfovibrionales; f\_\_Desulfovibrionaceae; g\_\_Desulfovibrio | 0.44 (0.09) | 0.17 (0.03) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.71 (0.09) | 0.86 (0.07) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Peptostreptococcaceae; g\_\_ | 1.82 (0.17) | 2.61 (0.20) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Prevotellaceae; g\_\_Prevotella | 0.99 (0.15) | 1.08 (0.14) |
| **All\_Male** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_ | 0.27 (0.12) | 0.84 (0.12) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus | 1.17 (0.27) | 0.52 (0.10) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae | 0.79 (0.16) | 0.27 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Dorea | 0.96 (0.14) | 0.43 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.27 (0.12) | 0.84 (0.12) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.23 (0.06) | 0.10 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Coprococcus | 1.38 (0.20) | 0.59 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_ | 1.91 (0.44) | 0.81 (0.10) |
| p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 1.06 (0.88) | 3.07 (0.51) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae | 0.27 (0.12) | 0.84 (0.12) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Coprococcus | 1.38 (0.24) | 0.62 (0.06) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_ | 0.13 (0.03) | 0.05 (0.01) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Prevotellaceae; g\_\_Prevotella | 0.55 (0.24) | 1.17 (0.22) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Blautia | 2.41 (0.35) | 1.15 (0.11) |
| **All\_Female** | p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 1.02 (0.22) | 2.15 (0.33) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae；g\_\_SMB53 | 0.20 (0.03) | 0.38 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae；g\_\_Oscillospira | 0.83 (0.11) | 1.22 (0.12) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae | 0.60 (0.09) | 1.43 (0.21) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae；g\_\_Dorea | 0.40 (0.04) | 0.19 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae；g\_\_Megasphaera | 0.58 (0.11) | 0.32 (0.09) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae；g\_\_Roseburia | 2.54 (0.20) | 2.05 (0.26) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Turicibacterales; f\_\_Turicibacteraceae；g\_\_Turicibacter | 0.17 (0.04) | 0.29 (0.04) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Leuconostocaceae；g\_\_ | 0.06 (0.03) | 0.29 (0.12) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae；g\_\_ | 0.93 (0.23) | 1.43 (0.20) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Peptostreptococcaceae；g\_\_ | 0.44 (0.06) | 0.66 (0.07) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae；g\_\_Faecalibacterium | 0.05 (0.01) | 0.16 (0.03) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Porphyromonadaceae；g\_\_Parabacteroides | 0.58 (0.08) | 0.39 (0.08) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae | 0.16 (0.03) | 0.53 (0.18) |
| **RSA** | p\_\_Firmicutes; c\_\_Erysipelotrichi; o\_\_Erysipelotrichales; f\_\_Erysipelotrichaceae; g\_\_ | 0.17 (0.05) | 0.64 (0.12) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae; g\_\_Phascolarctobacterium | 0.16 (0.06) | 0.43 (0.09) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae; g\_\_Dialister | 3.01 (0.40) | 1.28 (0.25) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Coprococcus | 0.15 (0.02) | 0.43 (0.07) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.05 (0.02) | 0.41 (0.20) |
| **Ghana** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_SMB53 | 0.22 (0.06) | 0.54 (0.06) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Turicibacterales; f\_\_Turicibacteraceae; g\_\_Turicibacter | 0.20 (0.07) | 0.40 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Faecalibacterium | 0.32 (0.09) | 0.12 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Blautia | 1.12 (0.23) | 1.20 (0.24) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae;g\_\_Streptococcus | 0.78 (0.33) | 0.19 (0.04) |
| **Group glucose** | **Elevated fasting plasma glucose**  | **Non- elevated fasting plasma glucose**  |
| **All** | p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 2.91 (0.43) | 1.38 (0.20) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Leuconostocaceae; g\_\_ | 0.21 (0.05) | 0.17 (0.06) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus | 0.31 (0.06) | 0.25 (0.09) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae; g\_\_Dialister | 0.48 (0.10) | 0.97 (0.11) |
| p\_\_Firmicutes; c\_\_Erysipelotrichi; o\_\_Erysipelotrichales; f\_\_Erysipelotrichaceae; g\_\_Bulleidia | 0.13 (0.02) | 0.21 (0.02) |
| **All\_Male** | p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Bifidobacteriales; f\_\_Bifidobacteriaceae; g\_\_Bifidobacterium | 0.46 (0.15) | 0.91 (0.20) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus | 0.49 (0.13) | 0.44 (0.23) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Faecalibacterium | 0.34 (0.08) | 0.53 (0.08) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Leuconostocaceae; g\_\_ | 0.29 (0.08) | 0.17 (0.07) |
| **All\_Female** | p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 1.98 (0.33) | 1.26 (0.23) |
| p\_\_Firmicutes; c\_\_Erysipelotrichi; o\_\_Erysipelotrichales; f\_\_Erysipelotrichaceae | 0.92 (0.23) | 1.74 (0.22) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae | 0.50 (0.15) | 1.16 (0.16) |
| p\_\_Firmicutes; c\_\_Erysipelotrichi; o\_\_Erysipelotrichales; f\_\_Erysipelotrichaceae | 0.09 (0.02) | 0.20 (0.02) |
| p\_\_Proteobacteria; c\_\_Deltaproteobacteria; o\_\_Desulfovibrionales; f\_\_Desulfovibrionaceae | 0.26 (0.11) | 0.37 (0.07) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_[Mogibacteriaceae] | 0.05 (0.01) | 0.14 (0.02) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Leuconostocaceae | 0.15 (0.05) | 0.17 (0.08) |
| **RSA** | p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 0.74 (0.42) | 0.08 (0.03) |
| **Jamaica** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_ | 2.04 (0.51) | 0.98 (0.33) |
| **Group blood pressure** | **Elevated blood pressure** | **Non- Elevated blood pressure** |
| **All** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.48 (0.11) | 0.88 (0.07) |
| p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 1.82 (0.58) | 2.01 (0.22) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.35 (0.07) | 0.29 (0.06) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_ | 0.58 (0.12) | 0.96 (0.09) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae | 0.53 (0.11) | 0.21 (0.03) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Porphyromonadaceae; g\_\_Parabacteroides | 0.65 (0.11) | 0.39 (0.04) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Dorea | 0.66 (0.07) | 0.32 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.06 (0.03) | 0.46 (0.11) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Lachnospira | 0.04 (0.02) | 0.14 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_; g\_\_ | 0.12 (0.04) | 0.36 (0.06) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_ | 0.05 (0.01) | 0.15 (0.01) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_ | 0.07 (0.01) | 0.02(0.003) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.18 (0.04) | 0.12 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_ | 0.14 (0.02) | 0.12 (0.01) |
| **All\_Male** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.48 (0.12) | 0.36 (0.12) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Faecalibacterium | 1.22 (0.23) | 2.13 (0.19) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus | 0.06 (0.04) | 0.62 (0.19) |
| **All\_Female** | p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Porphyromonadaceae; g\_\_Parabacteroides | 0.56 (0.26) | 1.70 (0.22) |
| p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 1.37 (0.29) | 2.25 (0.18) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Peptostreptococcaceae; g\_\_ | 0.56 (0.15) | 1.09 (0.09) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.47 (0.16) | 1.28 (0.19) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_ | 2.73 (0.61) | 1.40 (0.15) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 0.60 (0.19) | 1.03 (0.12) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_ | 0.14 (0.07) | 0.24 (0.03) |
| p\_\_Firmicutes; c\_\_Bacilli; o\_\_Turicibacterales; f\_\_Turicibacteraceae; g\_\_Turicibacter | 0.57 (0.20) | 0.16 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae | 0.20 (0.05) | 0.12 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus |  |  |
| **Group HDL** | **Low HDL** | **High HDL** |
| **All** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.74 (0.22) | 0.14 (0.03) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Faecalibacterium | 0.11 (0.01) | 0.09 (0.02) |
| p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae | 2.20 (0.35) | 2.02 (0.32) |
| **All\_Male** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.76 (0.30) | 0.11 (0.04) |
| **RSA** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae; g\_\_Megasphaera | 1.25 (0.27) | 0.53 (0.13) |
| **Group triglyceride** | **Hyper-triglyceridemia** | **Non-hyper-triglyceridemia** |
| **All** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.26 (0.07) | 0.89 (0.07) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Prevotellaceae; g\_\_Prevotella | 0.82 (0.23) | 1.95 (0.17) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae | 0.26 (0.14) | 0.08 (0.01) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.06 (0.03) | 0.20 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.33 (0.09) | 0.29 (0.06) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Veillonellaceae; g\_\_Megasphaera | 0.92 (0.40) | 0.24 (0.06) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 0.60 (0.25) | 0.27 (0.07) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.27 (0.07) | 0.13 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae | 0.08 (0.02) | 0.03 (0.01) |
| p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_ | 0.05 (0.01) | 0.17 (0.01) |
| p\_\_Bacteroidetes;c\_\_Bacteroidia;o\_\_Bacteroidales;f\_\_Porphyromonadaceae;g\_\_Parabacteroides | 0.75 (0.18) | 0.39 (0.04) |
| **All\_Female** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.20 (0.10) | 1.16 (0.10) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 1.02 (0.45) | 0.31 (0.11) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Porphyromonadaceae; g\_\_Parabacteroides | 1.10 (0.32) | 0.41 (0.06) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.41 (0.19) | 0.16 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.49 (0.16) | 0.19 (0.07) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Coprococcus | 0.39 (0.11) | 0.12 (0.03) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae | 0.44 (0.27) | 0.09 (0.02) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Prevotellaceae; g\_\_Prevotella | 0.77 (0.34) | 1.97 (0.22) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.06 (0.05) | 0.26 (0.03) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Coprococcus | 1.26 (0.30) | 0.44 (0.06) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.40 (0.11) | 0.12 (0.02) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 0.47 (0.16) | 0.17 (0.04) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 3.26 (0.91) | 1.41 (0.18) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_ | 0.21 (0.13) | 1.06 (0.14) |
| p\_\_Firmicutes; c\_\_Erysipelotrichi; o\_\_Erysipelotrichales; f\_\_Erysipelotrichaceae; g\_\_Catenibacterium | 1.30 (0.79) | 1.56 (0.19) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_ | 0.04 (0.02) | 0.23 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Ruminococcus | 0.11 (0.03) | 0.04 (0.01) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.15 (0.05) | 0.05 (0.01) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae | 0.80 (0.31) | 0.18 (0.03) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Rikenellaceae; g\_\_ | 0.45 (0.15) | 0.21 (0.04) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.09 (0.03) | 0.04 (0.01) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_SMB53 | 0.09 (0.05) | 0.30 (0.03) |
| p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Bacteroidaceae; g\_\_Bacteroides | 0.62 (0.38) | 0.23 (0.05) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_ | 0.11 (0.09) | 0.43 (0.05) |
| p\_\_Proteobacteria; c\_\_Betaproteobacteria; o\_\_Burkholderiales; f\_\_Alcaligenaceae; g\_\_Sutterella | 0.21 (0.10) | 0.05 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.22 (0.07) | 0.10 (0.02) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae; g\_\_Clostridium | 0.41 (0.14) | 0.13 (0.02) |
| **USA** | p\_\_Firmicutes; c\_\_Clostridia;o\_\_Clostridiales;f\_\_Veillonellaceae;g\_\_Acidaminococcus | 0.79 (0.30) | 0.23 (0.06) |
| **Ghana** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Coprococcus | 0.33 (0.13) | 0.09 (0.02) |
| **RSA** | p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_[Ruminococcus] | 0.34 (0.10) | 0.24 (0.13) |
| p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Ruminococcaceae; g\_\_Oscillospira | 0.33 (0.14) | 1.24 (0.13) |

\*Number in red, ESVs were significantly enriched in patients with one of the CM risk factors.