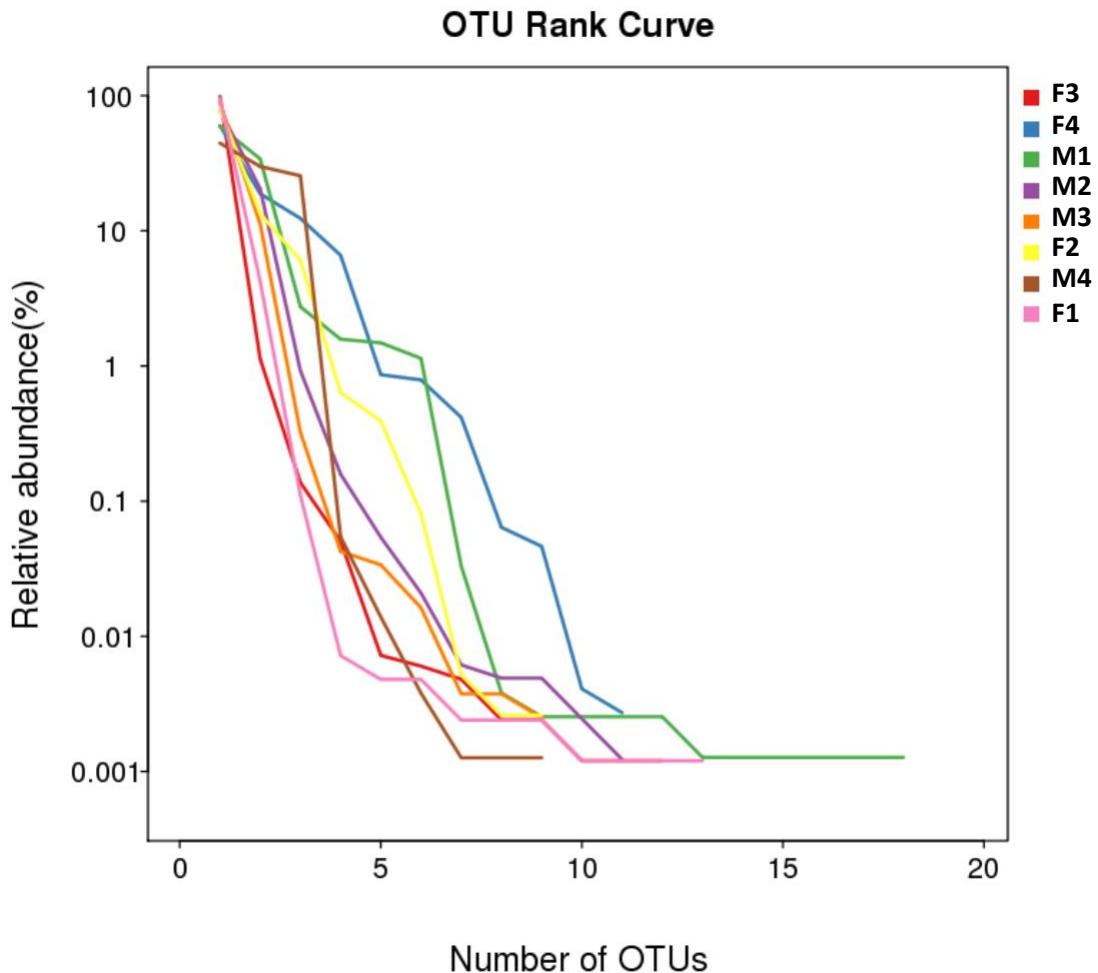
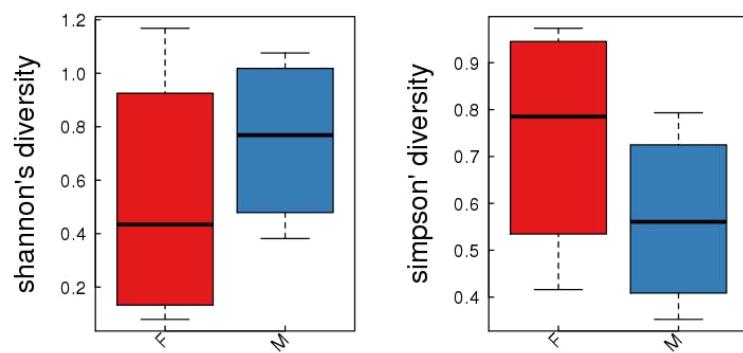


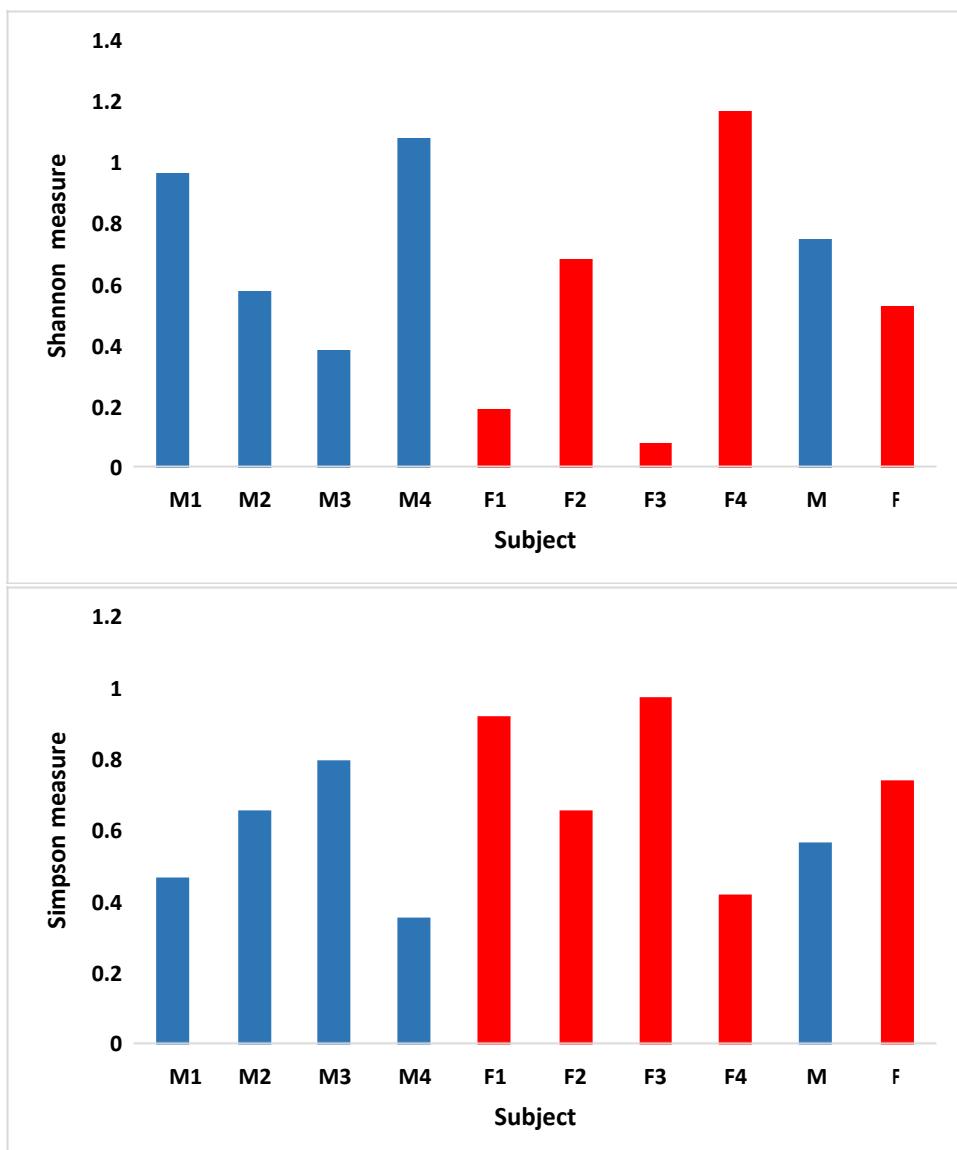
Appendix 1. Comparison of male (M) and female (F) skin microbiomes for numbers of paired reads, sequence tags and observed species (Sobs or OTUs) at the sample and group levels. M = male, F = female.



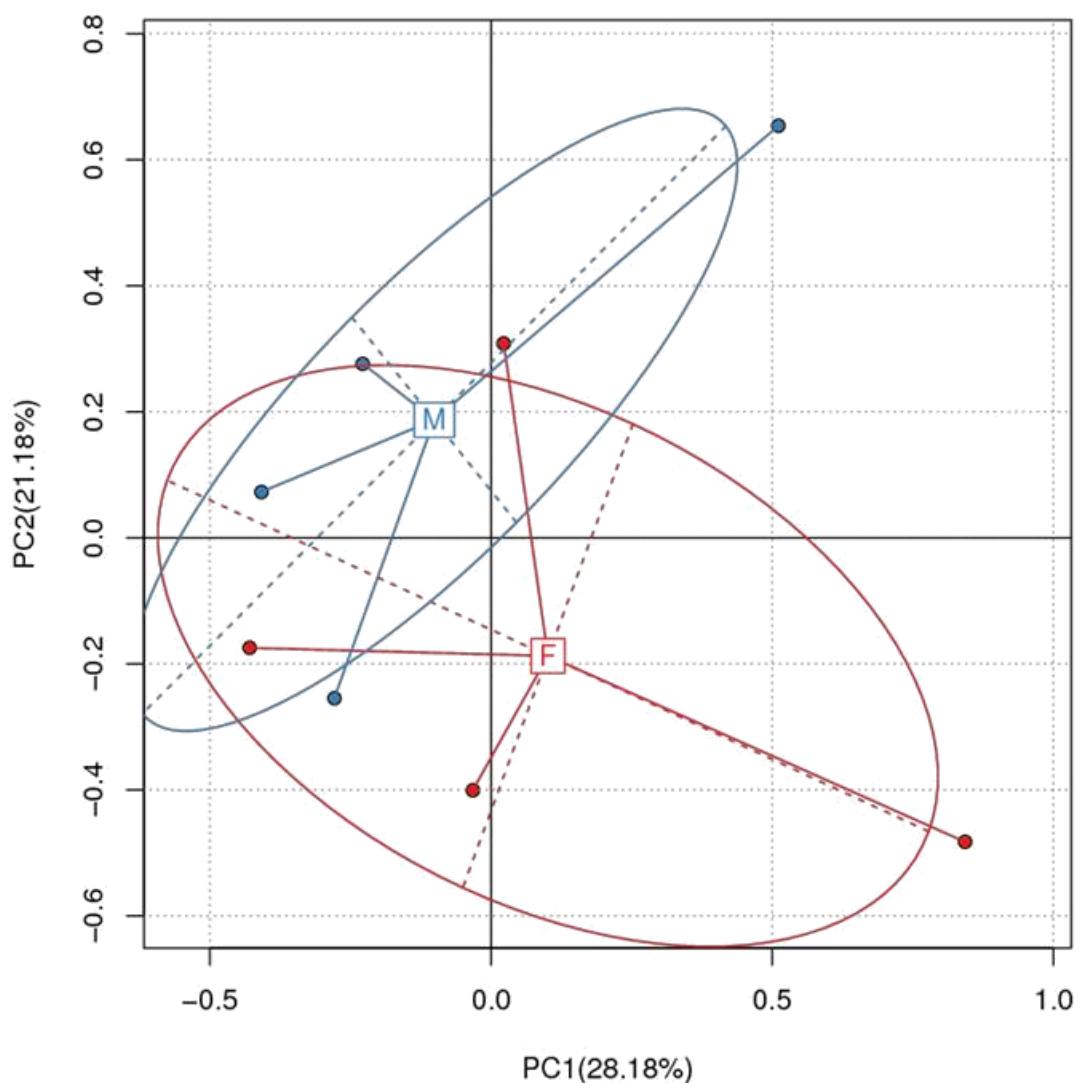
Appendix 2. Number and relative abundance of OTUs of different samples. M = male, F = female.



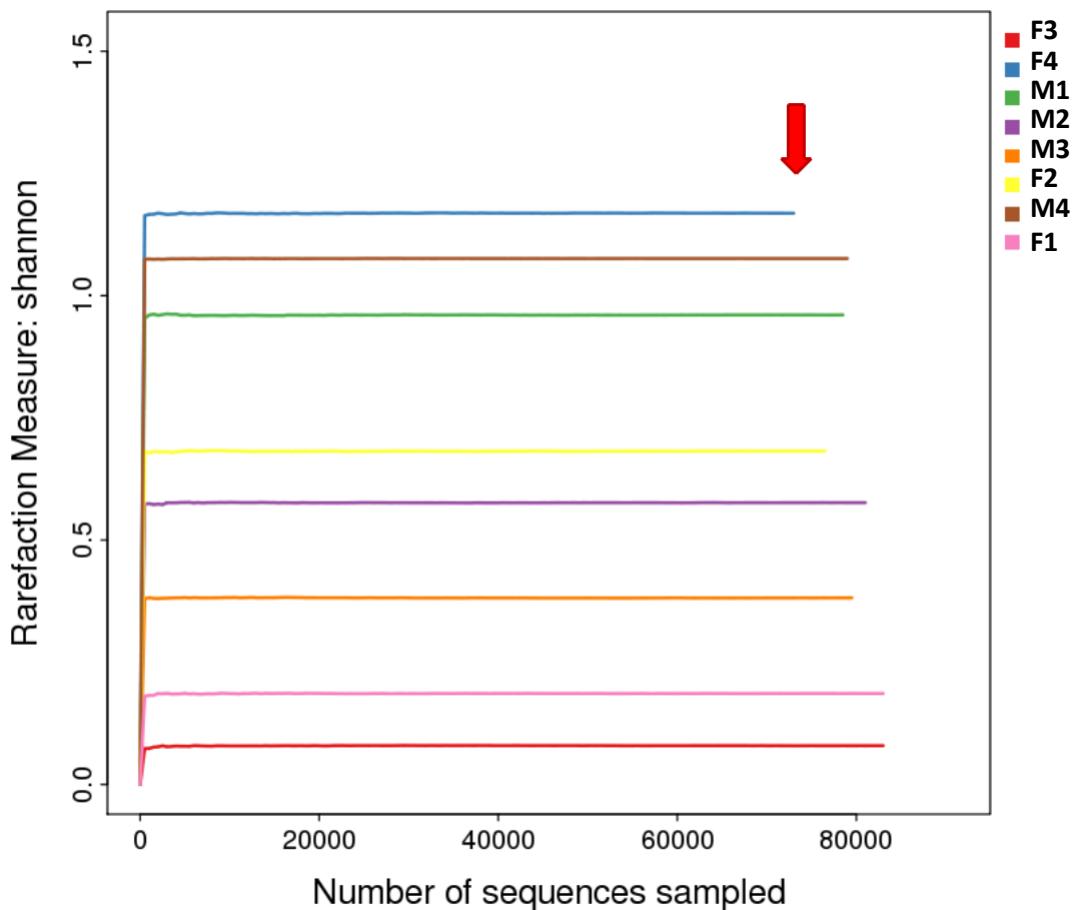
Appendix 3. Alpha diversity indices as boxplots to describe richness and evenness at the group level of the samples male (blue) and female (red). M = male, F = female.



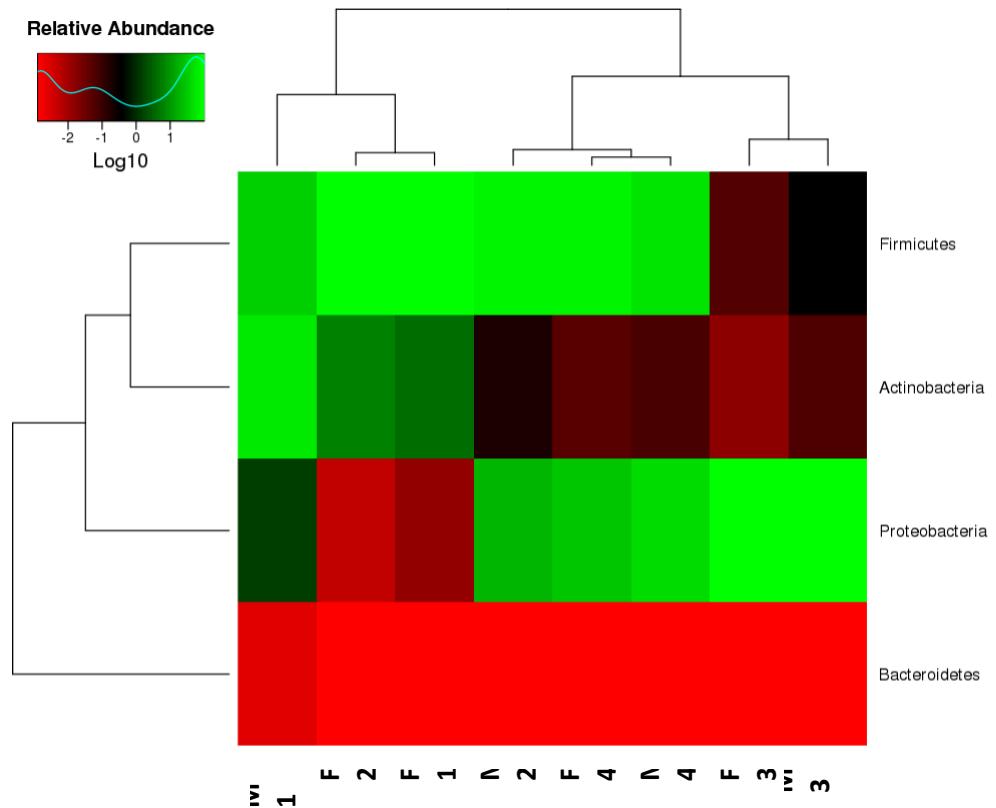
Appendix 4. Alpha diversity measures of skin microbiomes at the sample and group levels to describe sample or group richness (Shannon index) and evenness (Simpson index). M = male, F = female.



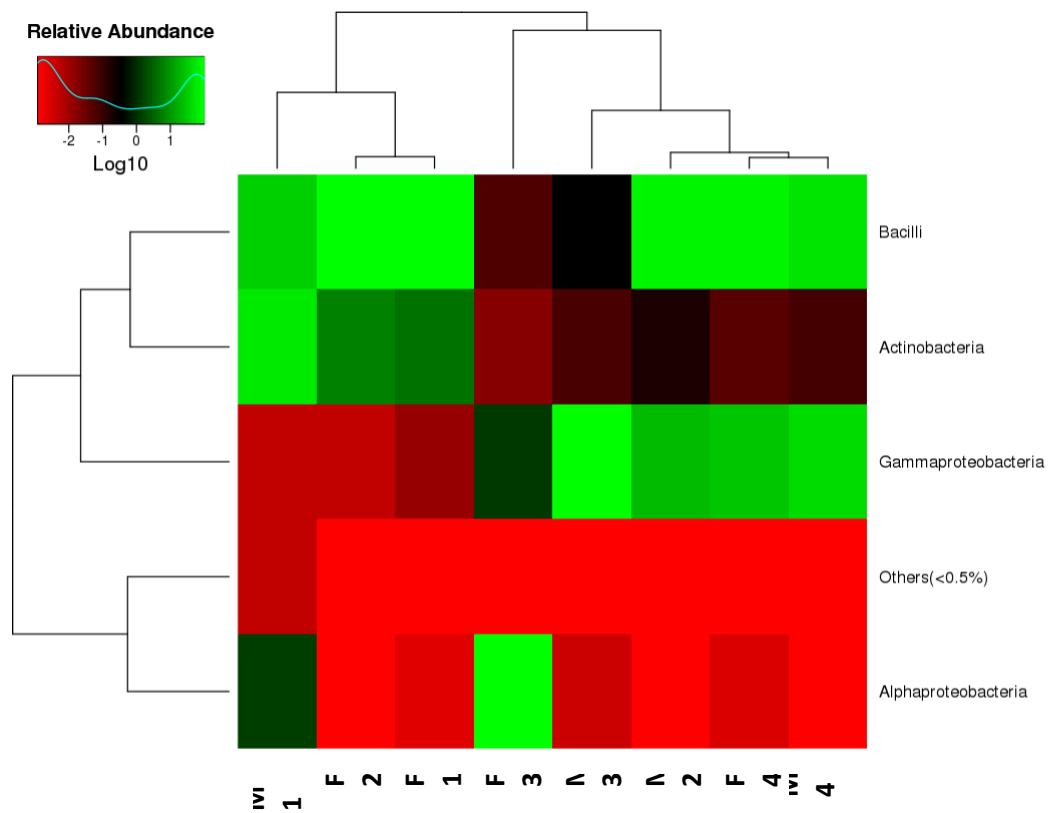
Appendix 5. PCoA based on OTU abundance of different samples. Blue boxes indicate samples of male. Red boxes indicate samples of female. X-axis is the first principal coordinate and Y-axis is the second. Number in brackets represents contributions of PCoAs to differences among samples. A dot represents each sample, and different colors represent different groups. M = male, F = female.



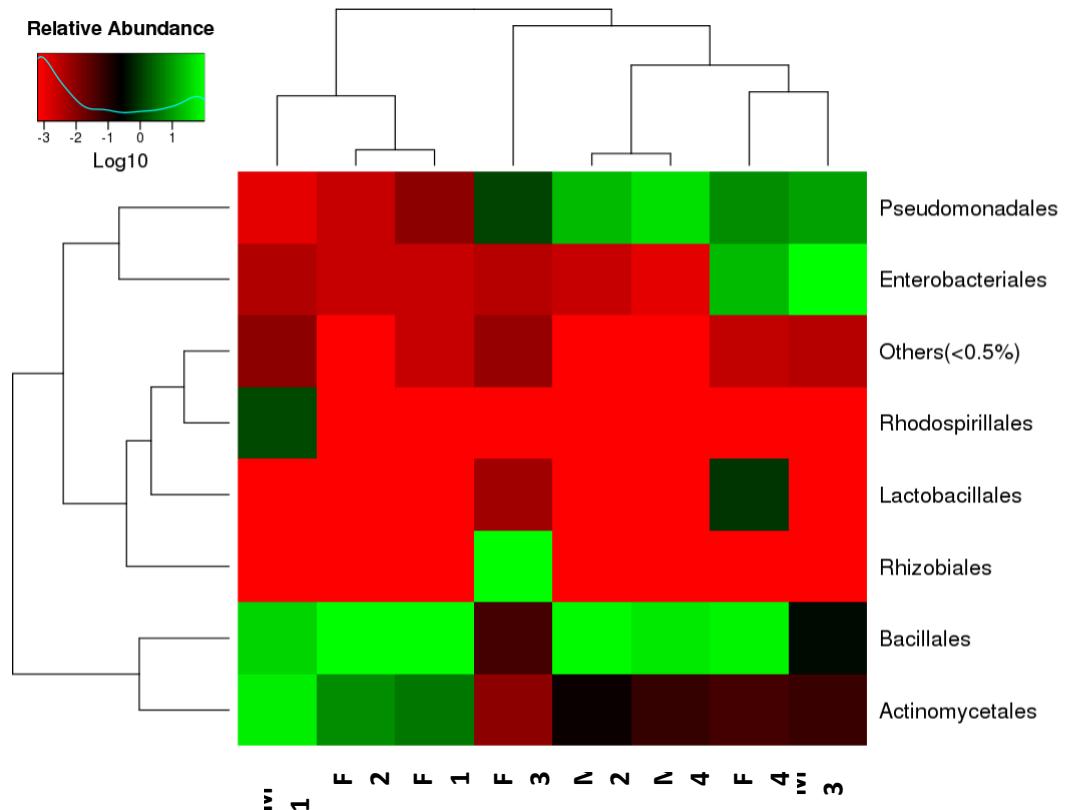
Appendix 6. Number of sequences as rarefaction measures. The arrow indicates the suitable sample size for analyzing taxonomy abundance (~73,000 sequence reads). M = male, F = female.



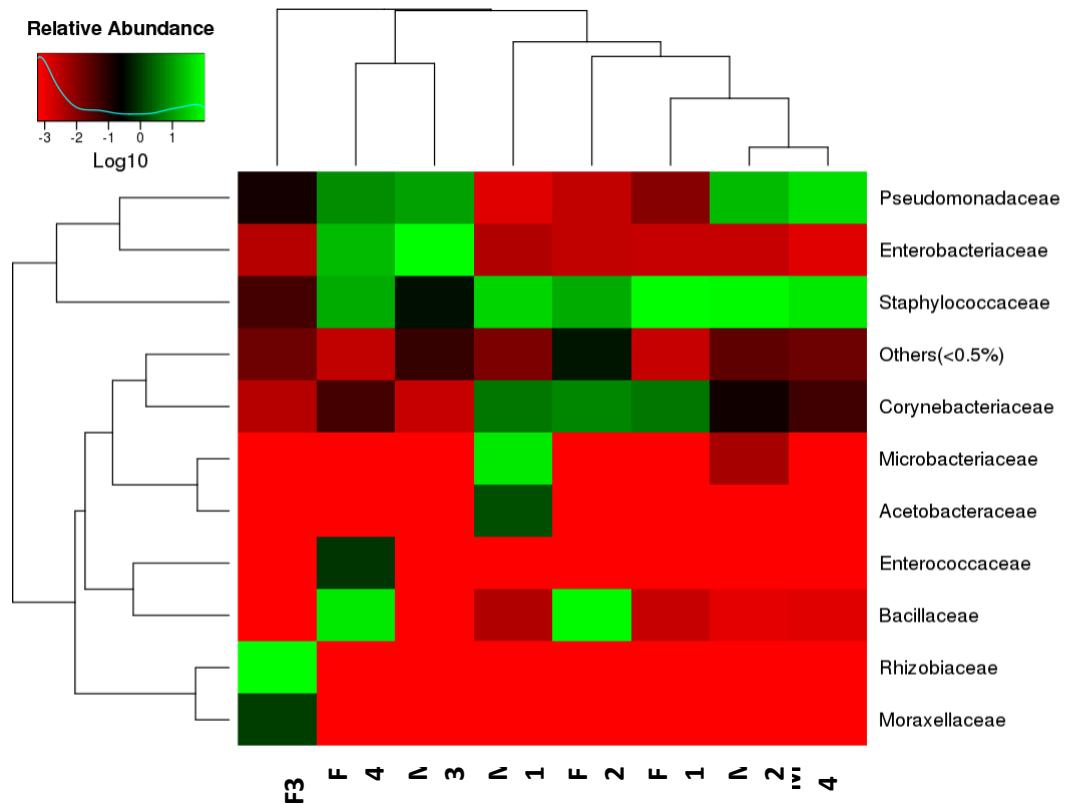
Appendix 7. Log-scaled percentage heat map at the phylum level. M = male, F = female.



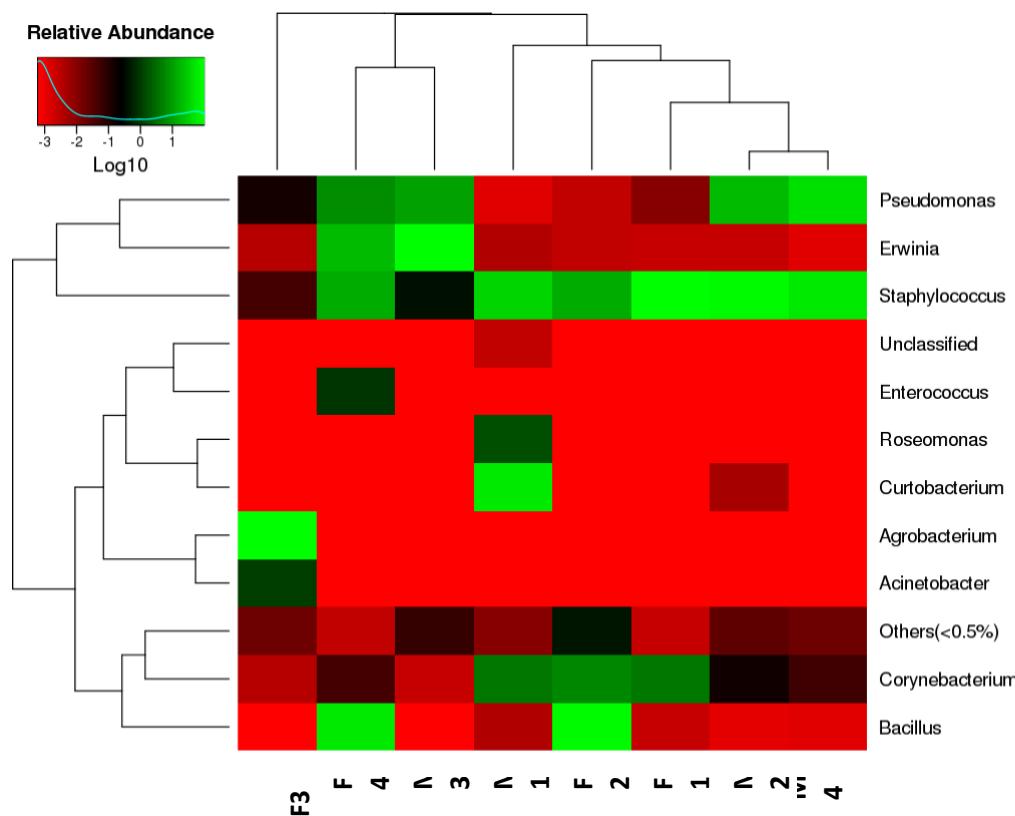
Appendix 8. Log-scaled percentage heat map at the class level. M = male, F = female.



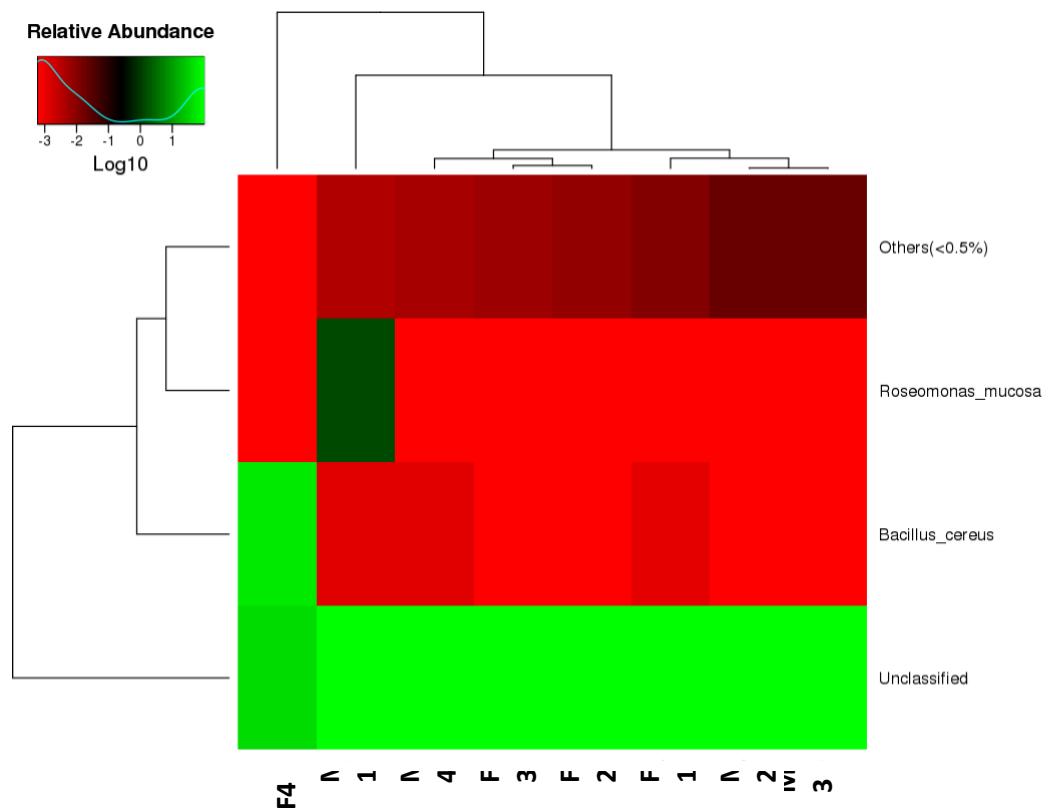
Appendix 9. Log-scaled percentage heat map at the order level. M = male, F = female.



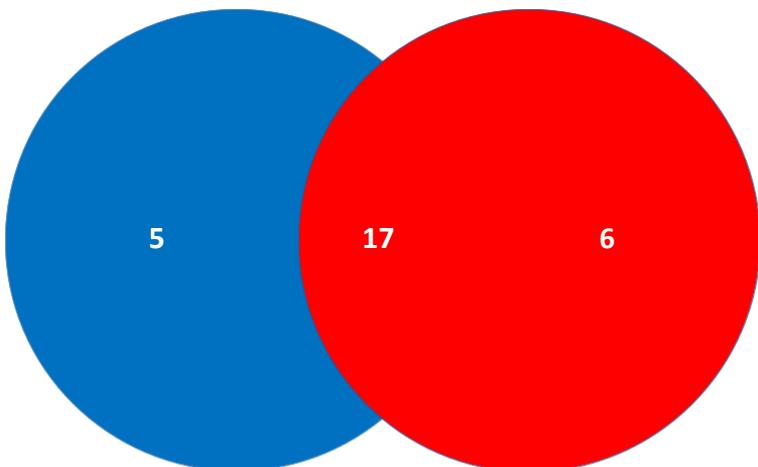
Appendix 10. Log-scaled percentage heat map at the family level. M = male, F = female.



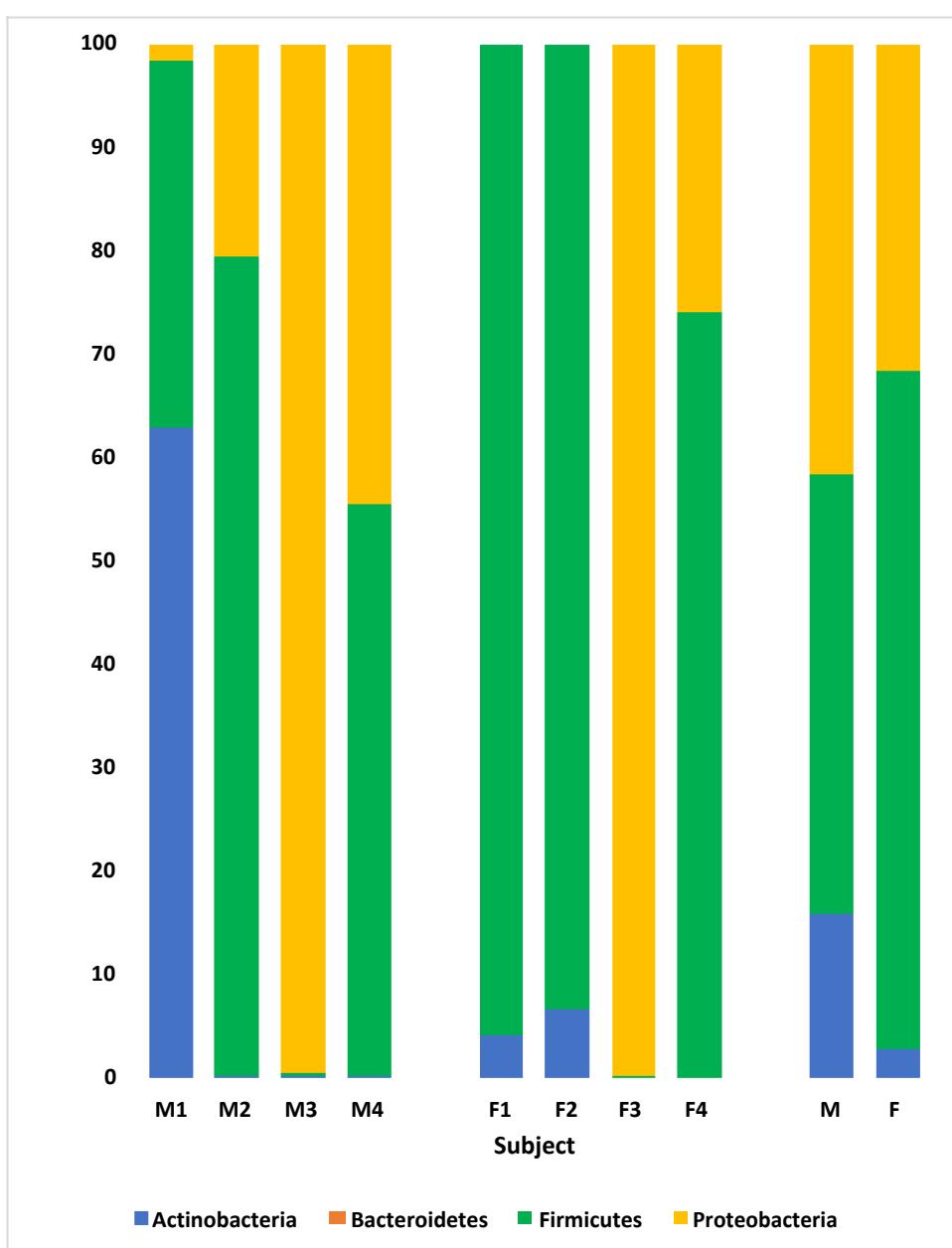
Appendix 11. Log-scaled percentage heat map at the genus level. M = male, F = female.



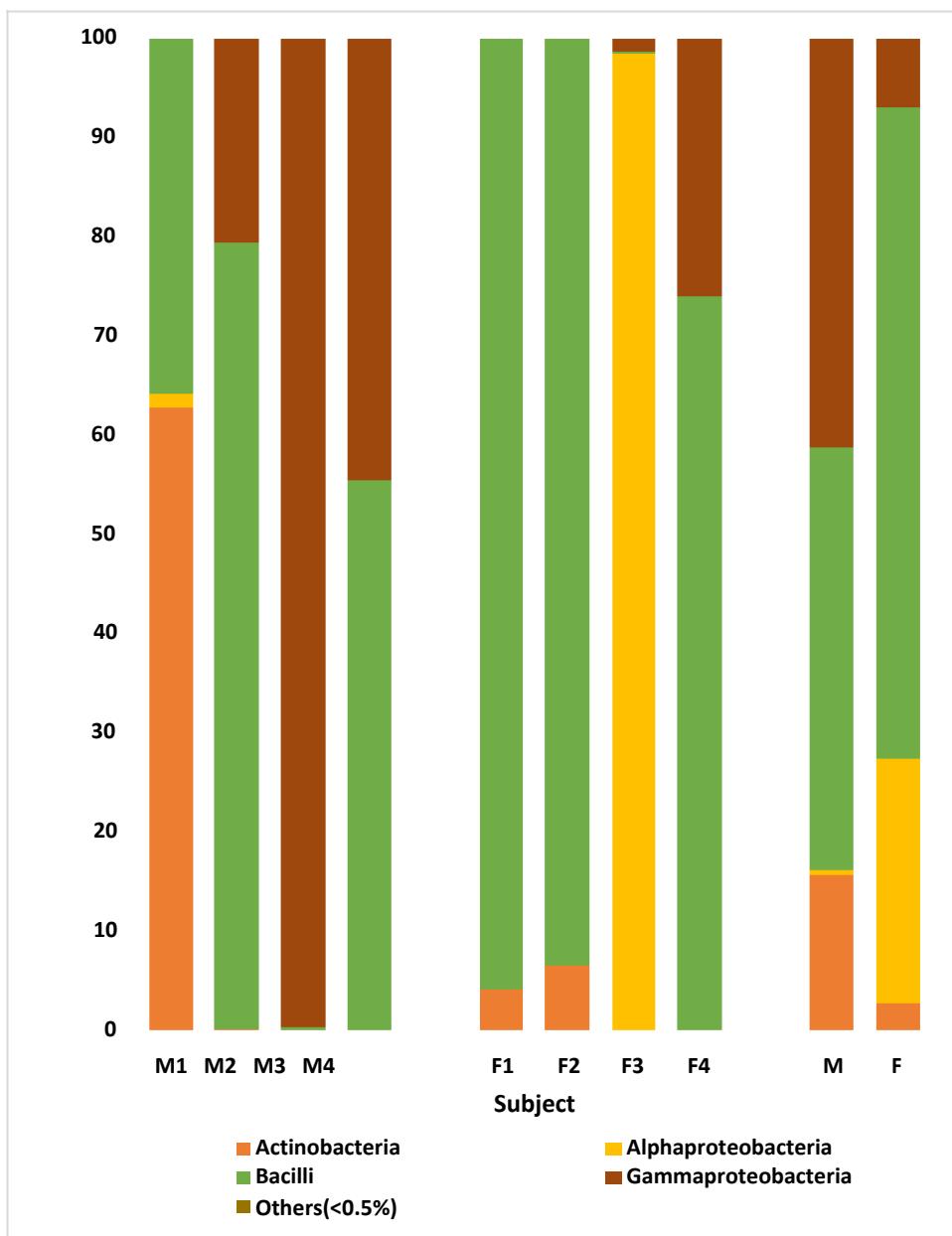
Appendix 12. Log-scaled percentage heat map at the species level. M = male, F = female.



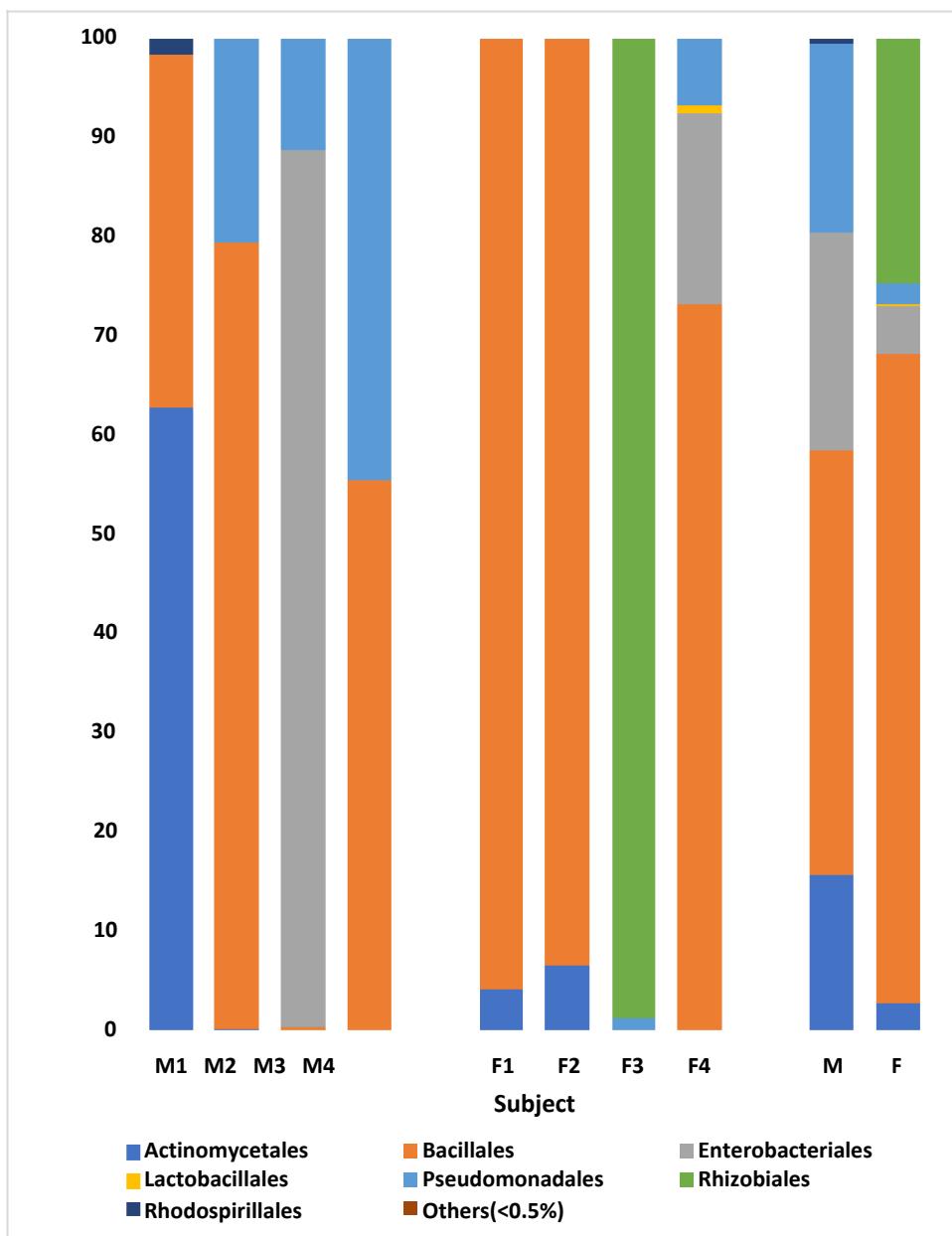
Appendix 13. Venn diagram describing the unique (five for Male and six for Female) and shared OTUs (17) between the two groups of samples male (blue) and female (red). The five male OTUs involve OTU5, OTU10, OTU18, OTU27, OTU26. The six female OTUs involve OTU1, OTU11, OTU12, OTU21, OTU23, OTU28. The other OTUs (17) are shared between the two groups with different relative abundances.



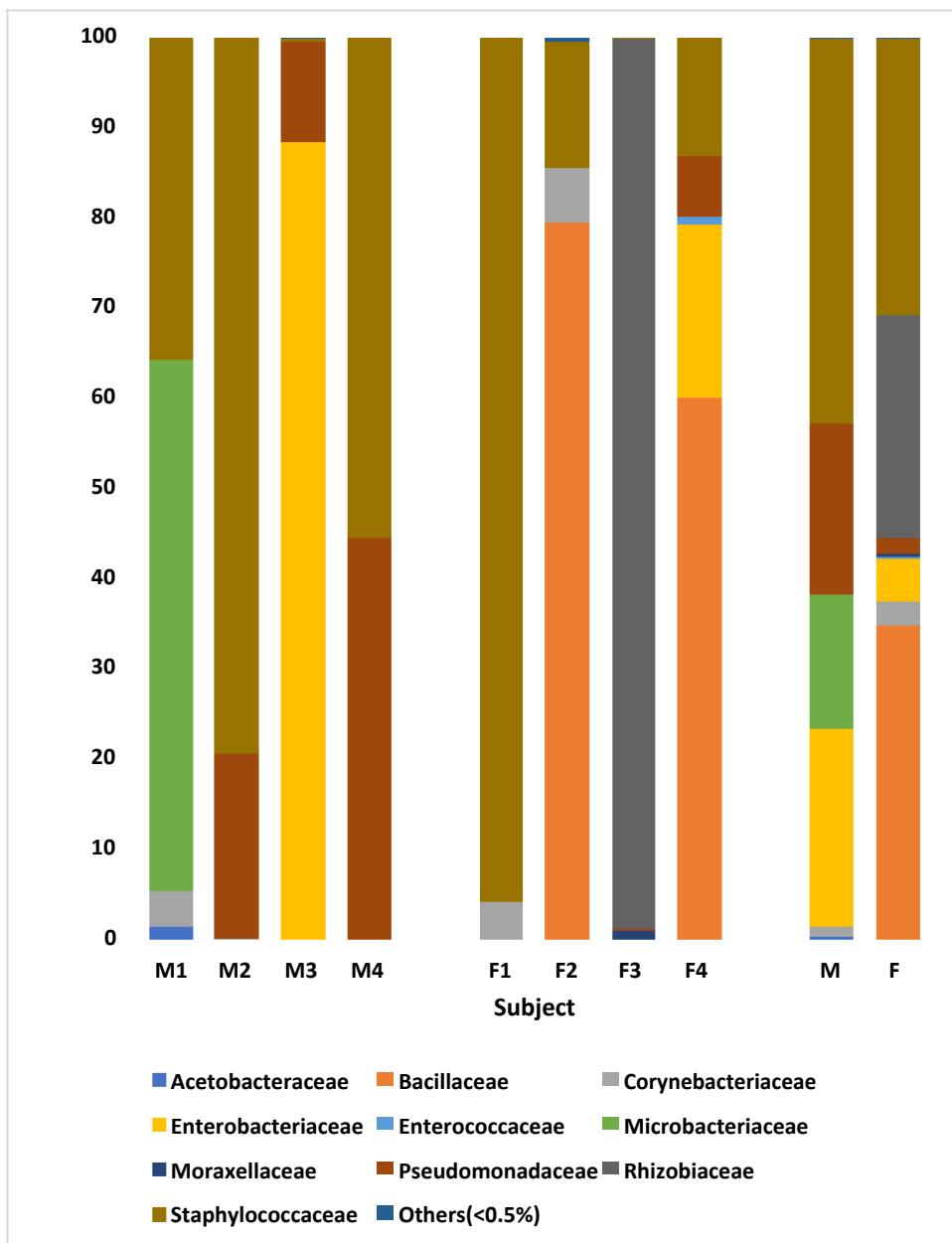
Appendix 14. Relative abundance of skin microbiomes at the phylum level as measured by Metastats at the sample and group levels. M= male, F = female.



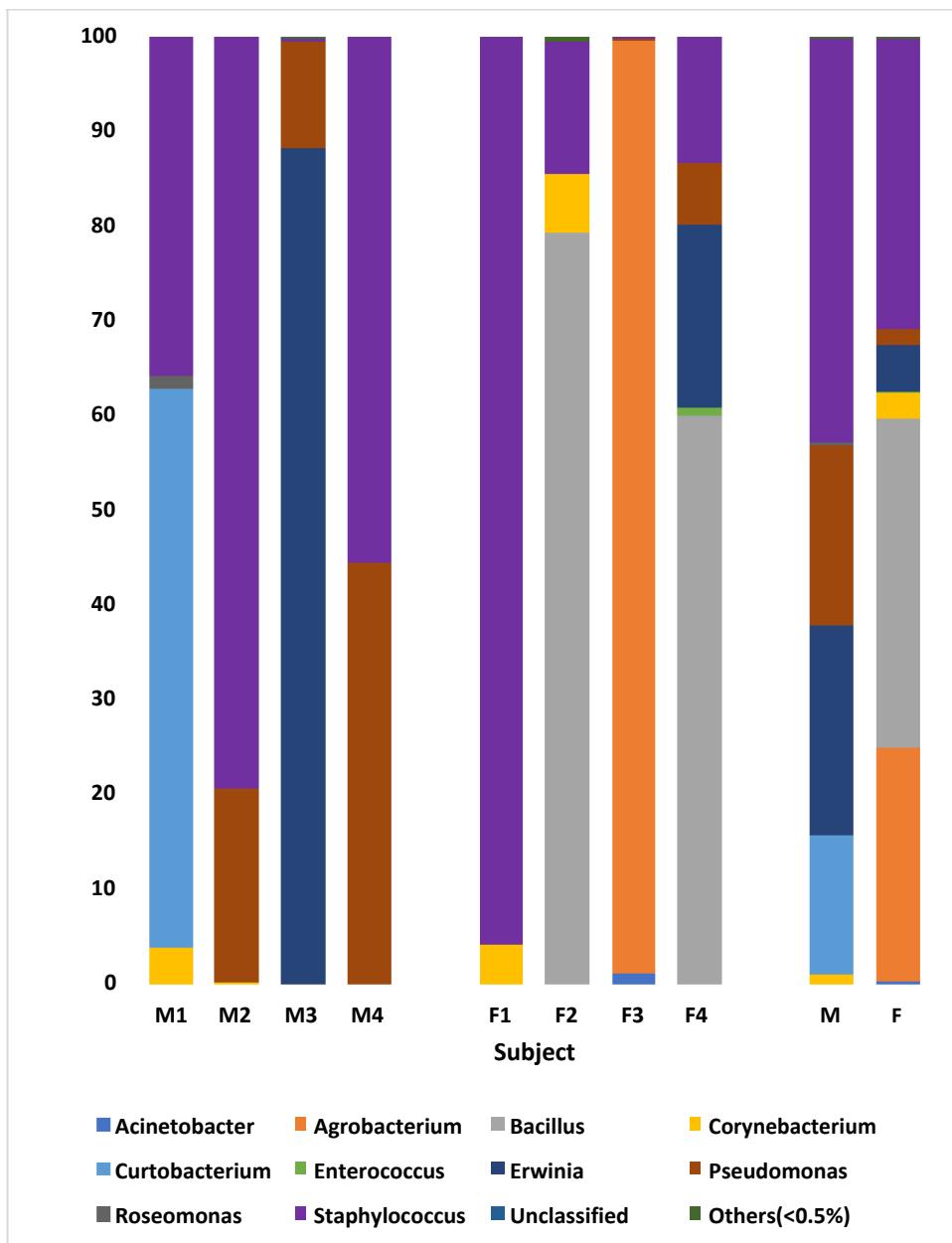
Appendix 15. Relative abundance of skin microbiomes at the class level as measured by Metastats at the sample and group levels. M= male, F = female.



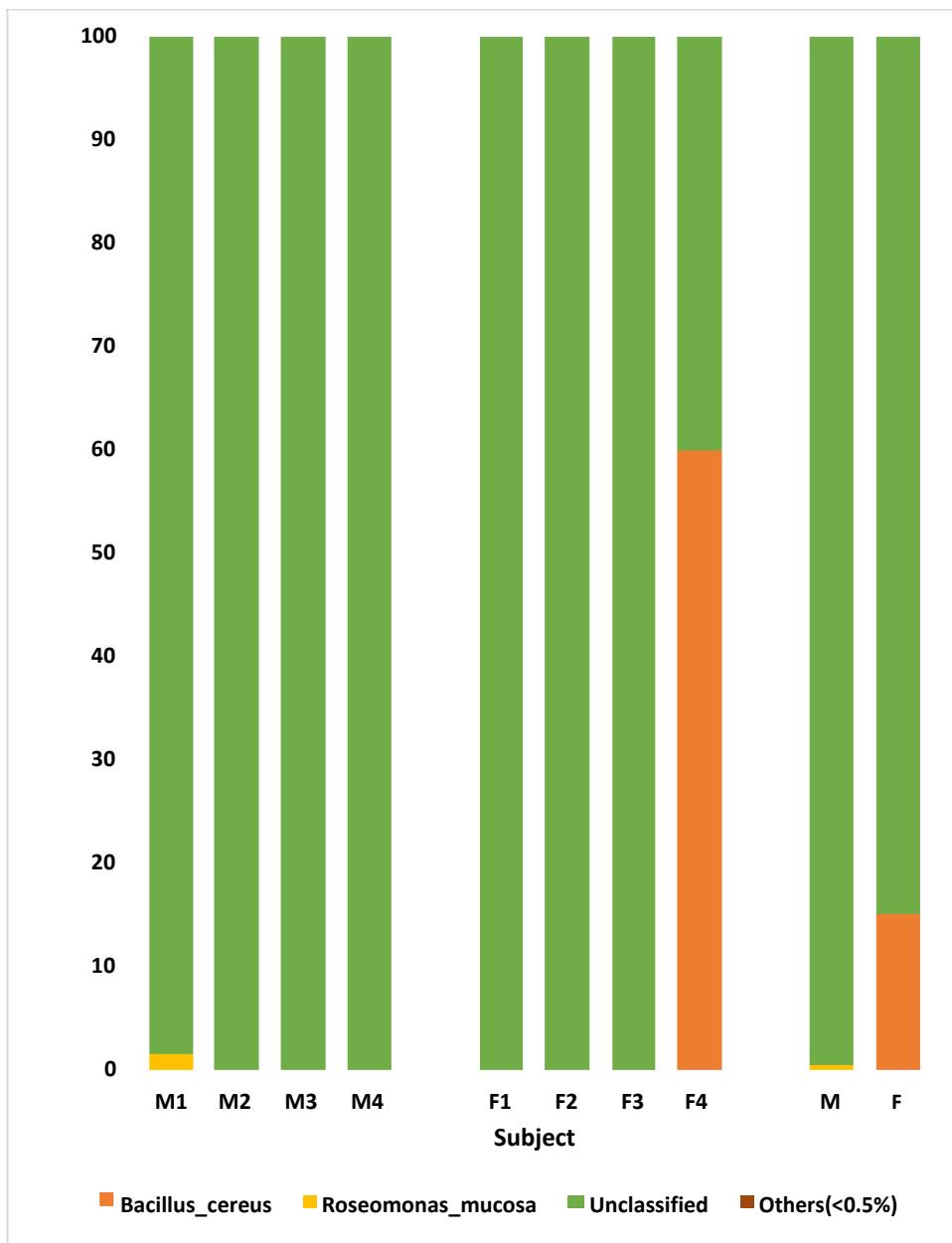
Appendix 16. Relative abundance of skin microbiomes at the order level as measured by Metastats at the sample and group levels. M= male, F = female.



Appendix 17. Relative abundance of skin microbiomes at the family level as measured by Metastats at the sample and group levels. M= male, F = female.



Appendix 18. Relative abundance of skin microbiomes at the genus level as measured by Metastats at the sample and group levels. M= male, F = female.



Appendix 19. Relative abundance of skin microbiomes at the species level as measured by Metastats at the sample and group levels. M= male, F = female.

Appendix 20. Description of observed species detected from OTU annotation across subjects (male and female).

| OTU no. | OTU Abundance | Taxonomy |
|---------|---------------|--|
| Otu4 | 210187 | Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus |
| Otu1 | 81986 | Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Agrobacterium |
| Otu2 | 70961 | Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Erwinia |
| Otu7 | 65683 | Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas |
| Otu3 | 61055 | Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus |
| Otu5 | 46392 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Curtobacterium |
| Otu6 | 44134 | Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus; <i>Bacillus_cereus</i> |
| Otu19 | 26859 | Bacteria;Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus |
| Otu8 | 13801 | Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Erwinia |
| Otu9 | 9229 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium |
| Otu14 | 2163 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium |
| Otu10 | 1167 | Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas; <i>Roseomonas_mucosa</i> |
| Otu11 | 935 | Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter |
| Otu12 | 633 | Bacteria;Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus |
| Otu13 | 352 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae;Micrococcus |
| Otu15 | 205 | Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas |
| Otu17 | 100 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium |
| Otu20 | 28 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium;Propionibacterium_acnes |
| Otu18 | 26 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium |
| Otu16 | 19 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micrococcaceae; <i>Kocuria</i> ;Kocuria_palustris |
| Otu24 | 10 | Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas |
| Otu22 | 9 | Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas; <i>Pseudomonas_mendocina</i> |
| Otu21 | 6 | Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae; <i>Gardnerella</i> |
| Otu25 | 5 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium;Corynebacterium_kroppenstedtii |
| Otu23 | 5 | Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus |
| Otu28 | 2 | Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium |
| Otu27 | 2 | Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Capnocytophaga |
| Otu26 | 2 | Bacteria;Firmicutes;Clostridia;Clostridiales;Mogibacteriaceae |

Appendix 21. Alpha diversity comparison results between the two groups. M = male, F = female.

| #Alpha | mean(F) | SD(F) | mean(M) | SD(M) | p-value |
|----------------|---------|---------|---------|---------|---------|
| Shannon | 0.52900 | 0.50073 | 0.74874 | 0.32472 | 0.68571 |
| Simpson | 0.73990 | 0.25705 | 0.56678 | 0.19629 | 0.48571 |

Appendix 22. Richness of OTUs of different samples (male and female).

Appendix 23. Taxonomy and description of the OTUs recovered from skin microbiomes of healthy individuals (male and female).

Low abundant genera are indicated by asterisk

| Phylum | Class | Order | Family | Genus | Species | OTUs |
|----------------|---------------------|-------------------|----------------------|--------------------------|--|------|
| Firmicutes | Bacilli | Bacillales | Staphylococcaceae | <i>Staphylococcus</i> | <i>Staphylococcus</i> spp.1 (no. reads 210187) | 4 |
| | Bacilli | Bacillales | Staphylococcaceae | <i>Staphylococcus</i> | <i>Staphylococcus</i> spp.2 (no. reads 26859) | 19 |
| | Bacilli | Bacillales | Bacillaceae | <i>Bacillus</i> | <i>Bacillus</i> spp.1 (no. reads 61055) | 3 |
| | Bacilli | Bacillales | Bacillaceae | <i>Bacillus</i> | <i>B. cereus</i> (no. reads 44134) | 6 |
| | Bacilli | Lactobacillales | Enterococcaceae | <i>Enterococcus</i> | <i>Enterococcus</i> spp.1 (no. reads 633) | 12 |
| | Bacilli | Lactobacillales | Lactobacillaceae | <i>Lactobacillus</i> | <i>Lactobacillus</i> spp.1* (no. reads 5) | 23 |
| | Clostridia | Clostridiales | Mogibacteriaceae* | (no. reads 2) | — | 26 |
| Proteobacteria | Alphaproteobacteria | Rhizobiales | Rhizobiaceae | <i>Agrobacterium</i> | <i>Agrobacterium</i> spp.1 (no. reads 81986) | 1 |
| | Alphaproteobacteria | Rhodospirillales | Acetobacteraceae | <i>Roseomonas</i> | <i>R. mucosa</i> (no. reads 1167) | 10 |
| | Alphaproteobacteria | Sphingomonadales | Sphingomonadaceae | <i>Sphingomonas</i> | <i>Sphingomonas</i> spp.1 (no. reads 10) | 24 |
| | Gammaproteobacteria | Enterobacteriales | Enterobacteriaceae | <i>Erwinia</i> | <i>Erwinia</i> spp.1 (no. reads 70961) | 2 |
| | Gammaproteobacteria | Enterobacteriales | Enterobacteriaceae | <i>Erwinia</i> | <i>Erwinia</i> spp.2 (no. reads 13801) | 8 |
| | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | <i>Pseudomonas</i> | <i>Pseudomonas</i> spp.1 (no. reads 65683) | 7 |
| | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | <i>Pseudomonas</i> | <i>Pseudomonas</i> spp.2 (no. reads 205) | 15 |
| | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | <i>Pseudomonas</i> | <i>P. mendocina</i> * (no. reads 9) | 22 |
| | Gammaproteobacteria | Pseudomonadales | Moraxellaceae | <i>Acinetobacter</i> | <i>Acinetobacter</i> spp.1 (no. reads 935) | 11 |
| Actinobacteria | Actinobacteria | Actinomycetales | Microbacteriaceae | <i>Curtobacterium</i> | <i>Curtobacterium</i> spp.1 (no. reads 46392) | 5 |
| | Actinobacteria | Actinomycetales | Corynebacteriaceae | <i>Corynebacterium</i> | <i>Corynebacterium</i> spp.1 (no. reads 9229) | 9 |
| | Actinobacteria | Actinomycetales | Corynebacteriaceae | <i>Corynebacterium</i> | <i>Corynebacterium</i> spp.2 (no. reads 2163) | 14 |
| | Actinobacteria | Actinomycetales | Corynebacteriaceae | <i>Corynebacterium</i> | <i>Corynebacterium</i> spp.3 (no. reads 100) | 17 |
| | Actinobacteria | Actinomycetales | Corynebacteriaceae | <i>Corynebacterium</i> | <i>Corynebacterium</i> spp.4 (no. reads 26) | 18 |
| | Actinobacteria | Actinomycetales | Corynebacteriaceae | <i>Corynebacterium</i> | <i>Corynebacterium</i> spp.5* (no. reads 2) | 28 |
| | Actinobacteria | Actinomycetales | Corynebacteriaceae | <i>Corynebacterium</i> | <i>C. kroppenstedtii</i> * (no. reads 5) | 25 |
| | Actinobacteria | Actinomycetales | Micrococcaceae | <i>Micrococcus</i> | <i>Micrococcus</i> spp.1 (no. reads 352) | 13 |
| | Actinobacteria | Actinomycetales | Micrococcaceae | <i>Kocuria</i> | <i>K. palustris</i> (no. reads 19) | 16 |
| Bacteroidetes | Actinobacteria | Actinomycetales | Propionibacteriaceae | <i>Propionibacterium</i> | <i>P. acnes</i> (no. reads 28) | 20 |
| | Actinobacteria | Bifidobacteriales | Bifidobacteriaceae | <i>Gardnerella</i> | <i>Gardnerella</i> spp.1* (no. reads 6) | 21 |
| | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | <i>Capnocytophaga</i> | <i>Capnocytophaga</i> spp.1* (no. reads 2) | 27 |