**Supplementary Table 1. Meta-analysis of association between total fiber intake and all taxa in the NCI and NYU study populationsa**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **NCI** | **NYU** |  |  |  |  |
| **Phylum; Class; Order; Family; Genus; Species** | **Base Mean** | **FC** | ***P*** | **Base Mean** | **FC** | ***P*** | **Meta FC** | **Meta** **95% CI** | **Meta *P*** | **Meta *Q*** |
| ***PHYLUM LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria | 143.20 | 0.990 | 0.670 | 115.59 | 0.982 | 0.293 | 0.985 | 0.958-1.011 | 0.294 | 0.589 |
| Bacteroidetes | 330.53 | 0.983 | 0.472 | 3075.49 | 1.016 | 0.074 | 1.012 | 0.995-1.028 | 0.443 | 0.591 |
| Firmicutes | 2126.89 | 1.000 | 1.000 | 5057.10 | 1.005 | 0.478 | 1.000 | 0.996-1.004 | 0.614 | 0.614 |
| Proteobacteria | 46.68 | 1.057 | 0.026 | 198.49 | 0.992 | 0.532 | 1.005 | 0.983-1.027 | 0.261 | 0.589 |
| ***CLASS LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria | 95.25 | 1.001 | 0.963 | 92.05 | 0.982 | 0.450 | 0.991 | 0.958-1.025 | 0.613 | 0.978 |
| Actinobacteria; Coriobacteriia | 45.54 | 0.995 | 0.829 | 26.14 | 0.971 | 0.008 | 0.975 | 0.956-0.994 | 0.040 | 0.321 |
| Bacteroidetes; Bacteroidia | 327.59 | 0.987 | 0.570 | 3253.15 | 1.011 | 0.273 | 1.007 | 0.989-1.026 | 0.703 | 0.978 |
| Firmicutes; Bacilli | 70.42 | 0.988 | 0.612 | 68.40 | 0.975 | 0.230 | 0.981 | 0.950-1.011 | 0.226 | 0.905 |
| Firmicutes; Clostridia | 2017.61 | 1.000 | 1.000 | 4676.67 | 1.005 | 0.444 | 1.000 | 0.996-1.004 | 0.586 | 0.978 |
| Firmicutes; Erysipelotrichi | 45.10 | 0.983 | 0.467 | 104.43 | 1.003 | 0.808 | 0.999 | 0.977-1.020 | 0.735 | 0.978 |
| Proteobacteria; Betaproteobacteria | 4.81 | 1.008 | 0.746 | 80.63 | 0.994 | 0.743 | 0.999 | 0.971-1.027 | 0.995 | 0.995 |
| Proteobacteria; Deltaproteobacteria | 2.09 | 1.028 | 0.206 | 20.90 | 0.981 | 0.322 | 1.001 | 0.973-1.029 | 0.856 | 0.978 |
| Proteobacteria; Gammaproteobacteria | 39.69 | 1.026 | NA | 76.42 | 1.021 | 0.448 | 1.024 | 0.989-1.059 | NA | NA |
| ***ORDER LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales | 3.69 | 0.963 | 0.134 | 1.14 | 0.962 | 0.163 | 0.962 | 0.927-0.998 | 0.041 | 0.224 |
| Actinobacteria; Actinobacteria; Bifidobacteriales | 91.55 | 0.998 | 0.950 | 90.91 | 0.978 | 0.464 | 0.991 | 0.954-1.027 | 0.572 | 0.954 |
| Actinobacteria; Coriobacteriia; Coriobacteriales | 45.54 | 0.994 | 0.798 | 26.14 | 0.971 | 0.007 | 0.974 | 0.955-0.993 | 0.036 | 0.224 |
| Bacteroidetes; Bacteroidia; Bacteroidales | 327.61 | 0.986 | 0.563 | 3253.13 | 1.011 | 0.276 | 1.008 | 0.988-1.026 | 0.712 | 0.954 |
| Firmicutes; Bacilli; Lactobacillales | 65.05 | 0.992 | 0.737 | 62.58 | 0.964 | 0.135 | 0.978 | 0.944-1.011 | 0.194 | 0.711 |
| Firmicutes; Bacilli; Turicibacterales | 4.68 | 0.985 | 0.467 | 5.61 | 1.020 | 0.601 | 0.993 | 0.958-1.029 | 0.890 | 0.954 |
| Firmicutes; Clostridia; Clostridiales | 2017.52 | 1.000 | 1.000 | 4676.48 | 1.005 | 0.442 | 1.000 | 0.998-1.001 | 0.585 | 0.954 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales | 45.10 | 0.982 | 0.470 | 104.43 | 1.003 | 0.805 | 0.999 | 0.977-1.020 | 0.740 | 0.954 |
| Proteobacteria; Betaproteobacteria; Burkholderiales | 4.25 | 1.014 | 0.552 | 80.51 | 0.993 | 0.724 | 1.001 | 0.972-1.031 | 0.867 | 0.954 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales | 2.09 | 1.030 | 0.205 | 20.90 | 0.980 | 0.326 | 1.001 | 0.972-1.031 | 0.848 | 0.954 |
| Proteobacteria; Gammaproteobacteria; Pasteurellales | 4.88 | 0.998 | 0.939 | 4.62 | 1.000 | 0.996 | 0.999 | 0.963-1.035 | 0.954 | 0.954 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales | 34.63 | 1.028 | NA | 53.48 | 0.991 | NA | 1.018 | 0.979-1.058 | NA | NA |
| ***FAMILY LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae | 2.03 | 0.891 | 0.005 | 0.88 | 0.965 | 0.132 | 0.946 | 0.908-0.984 | 0.003 | 0.048 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae | 80.72 | 0.997 | 0.953 | 80.13 | 0.986 | 0.579 | 0.989 | 0.947-1.032 | 0.662 | 0.930 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae | 45.82 | 0.995 | 0.885 | 26.31 | 0.968 | 0.007 | 0.971 | 0.949-0.993 | 0.044 | 0.413 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae | 13.98 | 0.938 | 0.096 | 99.22 | 0.987 | 0.344 | 0.982 | 0.957-1.006 | 0.065 | 0.413 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae | 14.88 | 1.117 | 0.011 | 110.13 | 0.994 | 0.716 | 1.010 | 0.978-1.043 | 0.126 | 0.481 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae] | 1.08 | 0.973 | 0.557 | 18.62 | 0.979 | 0.240 | 0.978 | 0.946-1.010 | 0.212 | 0.575 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae | 220.33 | 0.958 | 0.223 | 2212.24 | 0.996 | 0.788 | 0.992 | 0.967-1.015 | 0.295 | 0.700 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Barnesiellaceae] | 7.57 | 1.001 | 0.985 | 34.20 | 1.006 | 0.825 | 1.005 | 0.958-1.053 | 0.865 | 0.972 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae | 22.94 | 0.930 | 0.121 | 438.79 | 1.055 | 0.084 | 1.015 | 0.965-1.068 | 0.888 | 0.972 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Paraprevotellaceae] | 7.50 | 0.966 | NA | 75.21 | 1.042 | 0.185 | 1.018 | 0.967-1.070 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; S24-7 | 8.29 | 1.000 | NA | 96.07 | 0.991 | NA | 0.994 | 0.944-1.045 | NA | NA |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae | 4.48 | 0.965 | 0.448 | 4.60 | 1.008 | 0.787 | 0.996 | 0.949-1.044 | 0.734 | 0.930 |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae | 52.38 | 0.967 | 0.438 | 56.19 | 0.976 | NA | 0.974 | 0.936-1.012 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae | 64.60 | 1.014 | 0.738 | 0.98 | 1.054 | 0.039 | 1.043 | 0.999-1.088 | 0.088 | 0.420 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae | 81.77 | 1.039 | 0.346 | 71.07 | 1.019 | 0.309 | 1.023 | 0.989-1.057 | 0.166 | 0.525 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae | 45.20 | 0.996 | 0.920 | 104.87 | 1.022 | 0.201 | 1.017 | 0.987-1.048 | 0.401 | 0.847 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae | 1350.28 | 0.968 | 0.052 | 1876.37 | 1.006 | 0.371 | 1.001 | 0.988-1.012 | 0.468 | 0.889 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae | 448.99 | 1.011 | 0.465 | 1544.20 | 1.000 | 0.957 | 1.003 | 0.987-1.018 | 0.635 | 0.930 |
| Firmicutes; Clostridia; Clostridiales; [Mogibacteriaceae] | 4.66 | 1.021 | 0.540 | 7.45 | 0.999 | 0.962 | 1.004 | 0.974-1.033 | 0.691 | 0.930 |
| Firmicutes; Clostridia; Clostridiales; Christensenellaceae | 13.51 | 1.109 | NA | 13.89 | 1.012 | 0.617 | 1.033 | 0.990-1.078 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae | 57.51 | 0.939 | 0.142 | 109.19 | 1.011 | 0.424 | 1.004 | 0.978-1.030 | 0.644 | 0.930 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae | 3.90 | 1.008 | 0.856 | 72.98 | 0.994 | 0.750 | 0.996 | 0.963-1.030 | 0.921 | 0.972 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae | 1.89 | 1.051 | 0.295 | 20.48 | 0.981 | 0.300 | 0.990 | 0.956-1.024 | 0.998 | 0.998 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae | 45.22 | 1.067 | NA | 54.16 | 1.008 | NA | 1.024 | 0.975-1.074 | NA | NA |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae | 11.67 | 0.990 | 0.832 | 4.05 | 1.009 | NA | 1.004 | 0.957-1.053 | NA | NA |
| ***GENUS LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces | 2.16 | 0.884 | 0.003 | 0.75 | 0.969 | 0.130 | 0.951 | 0.917-0.986 | 0.002 | 0.039 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium | 84.01 | 1.001 | 0.973 | 90.68 | 1.004 | 0.850 | 1.003 | 0.967-1.041 | 0.874 | 0.967 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Adlercreutzia | 6.74 | 1.018 | 0.692 | 2.40 | 0.991 | 0.644 | 0.995 | 0.962-1.029 | 0.960 | 0.967 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella | 30.17 | 1.036 | 0.442 | 14.94 | 0.985 | 0.415 | 0.992 | 0.958-1.026 | 0.967 | 0.967 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella | 6.18 | 0.985 | NA | 2.09 | 0.990 | 0.631 | 0.989 | 0.951-1.027 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae]; Odoribacter | 0.68 | 0.995 | 0.916 | 10.88 | 0.946 | 0.004 | 0.953 | 0.920-0.986 | 0.032 | 0.273 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides | 13.09 | 0.920 | 0.029 | 131.35 | 1.004 | 0.780 | 0.993 | 0.965-1.020 | 0.181 | 0.657 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides | 253.86 | 0.973 | 0.456 | 2927.16 | 1.002 | 0.887 | 0.998 | 0.972-1.024 | 0.673 | 0.921 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella | 20.36 | 0.926 | 0.088 | 482.01 | 1.038 | 0.076 | 1.017 | 0.979-1.056 | 0.949 | 0.967 |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus | 55.61 | 0.957 | 0.299 | 57.84 | 0.985 | 0.443 | 0.980 | 0.946-1.014 | 0.202 | 0.657 |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae; Turicibacter | 4.19 | 0.997 | 0.942 | 6.02 | 1.017 | NA | 1.013 | 0.974-1.052 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; SMB53 | 0.62 | 1.035 | 0.443 | 0.88 | 1.045 | 0.029 | 1.044 | 1.006-1.081 | 0.036 | 0.273 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira | 31.63 | 1.042 | 0.279 | 163.91 | 1.026 | 0.091 | 1.028 | 1.000-1.057 | 0.050 | 0.273 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium | 230.42 | 1.030 | 0.367 | 549.73 | 1.025 | 0.078 | 1.025 | 1.000-1.051 | 0.059 | 0.273 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Oscillospira | 22.58 | 0.973 | 0.386 | 85.60 | 0.983 | 0.079 | 0.982 | 0.964-1.000 | 0.063 | 0.273 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus | 62.89 | 1.010 | 0.782 | 340.79 | 0.975 | 0.059 | 0.979 | 0.954-1.003 | 0.250 | 0.681 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella | 4.41 | 0.927 | 0.096 | 3.57 | 1.002 | 0.944 | 0.987 | 0.949-1.025 | 0.263 | 0.681 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium | 2.39 | 0.997 | 0.941 | 17.50 | 1.031 | 0.117 | 1.025 | 0.990-1.061 | 0.288 | 0.681 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus] | 288.25 | 0.912 | 0.007 | 201.55 | 1.015 | 0.178 | 1.005 | 0.984-1.025 | 0.355 | 0.709 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes | 5.92 | 1.007 | 0.859 | 10.66 | 1.018 | 0.287 | 1.016 | 0.985-1.047 | 0.377 | 0.709 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea | 104.47 | 1.022 | 0.418 | 65.24 | 1.004 | 0.666 | 1.006 | 0.988-1.025 | 0.382 | 0.709 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Phascolarctobacterium | 18.58 | 1.009 | 0.832 | 34.43 | 1.012 | 0.558 | 1.012 | 0.975-1.049 | 0.571 | 0.921 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia | 676.47 | 1.040 | 0.178 | 513.86 | 0.979 | 0.046 | 0.986 | 0.966-1.005 | 0.635 | 0.921 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Dialister | 16.99 | 0.984 | 0.713 | 25.15 | 0.994 | 0.780 | 0.992 | 0.954-1.030 | 0.648 | 0.921 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia | 6.46 | 0.993 | 0.849 | 35.21 | 1.010 | 0.502 | 1.008 | 0.980-1.035 | 0.731 | 0.950 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus | 208.88 | 0.990 | 0.541 | 207.84 | 1.006 | 0.436 | 1.003 | 0.989-1.016 | 0.901 | 0.967 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium] | 20.65 | 0.950 | 0.255 | 42.55 | 1.026 | 0.217 | 1.012 | 0.975-1.050 | 0.937 | 0.967 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Sutterella | 4.32 | 1.009 | 0.849 | 85.39 | 1.008 | 0.653 | 1.008 | 0.976-1.040 | 0.650 | 0.921 |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus | 4.27 | 0.988 | 0.795 | 4.03 | 1.011 | NA | 1.007 | 0.968-1.046 | NA | NA |
| ***SPECIES LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; adolescentis | 38.42 | 1.007 | 0.898 | 75.56 | 1.002 | 0.932 | 1.003 | 0.959-1.048 | 0.880 | 0.880 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella; aerofaciens | 25.31 | 1.051 | 0.349 | 13.58 | 0.988 | 0.571 | 0.997 | 0.957-1.037 | 0.799 | 0.879 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella; lenta | 6.14 | 0.984 | NA | 1.99 | 0.986 | 0.613 | 0.986 | 0.938-1.034 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; uniformis | 32.05 | 0.948 | 0.202 | 305.56 | 0.972 | 0.128 | 0.968 | 0.936-1.000 | 0.048 | 0.256 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; ovatus | 5.59 | 0.987 | 0.790 | 12.37 | 0.982 | 0.309 | 0.982 | 0.949-1.015 | 0.363 | 0.570 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides; distasonis | 7.33 | 0.940 | 0.184 | 51.50 | 1.007 | 0.724 | 0.996 | 0.961-1.032 | 0.495 | 0.681 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella; copri | 16.68 | 0.952 | NA | 353.04 | 1.040 | NA | 1.019 | 0.968-1.071 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; fragilis | 20.37 | 1.058 | NA | 16.33 | 0.989 | 0.651 | 1.000 | 0.958-1.044 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; prausnitzii | 230.05 | 1.032 | 0.354 | 540.38 | 1.024 | 0.103 | 1.026 | 0.998-1.053 | 0.070 | 0.256 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; bromii | 24.12 | 0.966 | 0.489 | 1.65 | 0.969 | 0.161 | 0.968 | 0.930-1.008 | 0.138 | 0.379 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea; formicigenerans | 1.92 | 1.033 | 0.447 | 20.11 | 1.018 | 0.323 | 1.020 | 0.987-1.053 | 0.216 | 0.476 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella; dispar | 3.41 | 0.899 | 0.041 | 2.82 | 1.012 | 0.666 | 0.986 | 0.939-1.034 | 0.261 | 0.478 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; faecis | 1.12 | 0.995 | 0.918 | 2.28 | 1.011 | 0.562 | 1.009 | 0.974-1.044 | 0.733 | 0.879 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus]; gnavus | 138.52 | 0.895 | NA | 85.10 | 1.005 | 0.735 | 0.995 | 0.968-1.021 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; producta | 35.68 | 1.042 | NA | 28.60 | 0.980 | 0.367 | 0.992 | 0.953-1.032 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; dolichum | 7.70 | 0.933 | 0.198 | 3.34 | 0.963 | 0.122 | 0.958 | 0.917-1.000 | 0.045 | 0.256 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; biforme | 10.94 | 0.928 | NA | 39.95 | 1.014 | 0.635 | 0.993 | 0.942-1.045 | NA | NA |

aTaxa shown were associated with total fiber intake in both NCI and NYU. Relationship between higher quartiles of total fiber intake and differential taxon abundance was evaluated using negative binomial generalized linear models in the DESeq2 package in R. Models were adjusted for age, sex, race, categorical BMI and cigarette smoking status. This table reports on all taxa from a taxonomy-based meta-analysis to evaluate the relationship between taxa abundance by fiber intake in both study populations. Meta analysis was conducted using Z-score methods. FC = fold change. P = p-value. Q = false discovery rate adjusted q-value. 95% CI = 95% Confidence Interval.