**Supplementary Table 3. Meta-analysis of association between fiber from grain 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 | 1.000 | 0.993 | 115.59 | 1.032 | 0.125 | 1.026 | 0.989-1.064 | 0.272 | 0.637 |
| Bacteroidetes | 330.53 | 1.059 | 0.175 | 3075.49 | 0.999 | 0.956 | 1.003 | 0.982-1.024 | 0.360 | 0.637 |
| Firmicutes | 2126.89 | 1.000 | 1.000 | 5057.10 | 1.009 | 0.319 | 1.003 | 0.992-1.012 | 0.478 | 0.637 |
| Proteobacteria | 46.68 | 1.034 | 0.375 | 198.49 | 0.990 | 0.505 | 0.996 | 0.968-1.024 | 0.881 | 0.881 |
| ***CLASS LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria | 95.25 | 1.027 | 0.768 | 92.05 | 1.037 | 0.266 | 1.036 | 0.975-1.100 | 0.318 | 0.887 |
| Actinobacteria; Coriobacteriia | 45.54 | 1.057 | 0.495 | 26.14 | 1.004 | 0.801 | 1.005 | 0.977-1.033 | 0.510 | 0.887 |
| Bacteroidetes; Bacteroidia | 327.59 | 1.130 | 0.131 | 3253.15 | 0.986 | 0.269 | 0.989 | 0.964-1.014 | 0.785 | 0.887 |
| Firmicutes; Bacilli | 70.42 | 1.144 | 0.136 | 68.40 | 1.034 | NA | 1.043 | 0.990-1.099 | NA | NA |
| Firmicutes; Clostridia | 2017.61 | 1.000 | 1.000 | 4676.67 | 0.998 | 0.842 | 1.000 | 0.990-1.008 | 0.887 | 0.887 |
| Firmicutes; Erysipelotrichi | 45.10 | 0.985 | 0.870 | 104.43 | 1.011 | 0.474 | 1.010 | 0.980-1.040 | 0.693 | 0.887 |
| Proteobacteria; Betaproteobacteria | 4.81 | 1.132 | 0.179 | 80.63 | 0.985 | 0.531 | 0.994 | 0.950-1.039 | 0.619 | 0.887 |
| Proteobacteria; Deltaproteobacteria | 2.09 | 1.182 | 0.069 | 20.90 | 0.974 | 0.290 | 0.987 | 0.941-1.034 | 0.600 | 0.887 |
| Proteobacteria; Gammaproteobacteria | 39.69 | 1.035 | NA | 76.42 | 1.038 | 0.332 | 1.037 | 0.967-1.111 | NA | NA |
| ***ORDER LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales | 3.69 | 1.123 | 0.231 | 1.14 | 0.995 | 0.873 | 1.008 | 0.947-1.072 | 0.467 | 0.865 |
| Actinobacteria; Actinobacteria; Bifidobacteriales | 91.55 | 0.985 | 0.878 | 90.91 | 1.037 | 0.319 | 1.031 | 0.963-1.102 | 0.547 | 0.865 |
| Actinobacteria; Coriobacteriia; Coriobacteriales | 45.54 | 1.062 | 0.472 | 26.14 | 1.004 | 0.800 | 1.005 | 0.977-1.033 | 0.493 | 0.865 |
| Bacteroidetes; Bacteroidia; Bacteroidales | 327.61 | 1.135 | 0.127 | 3253.13 | 0.986 | 0.264 | 0.989 | 0.964-1.014 | 0.783 | 0.881 |
| Firmicutes; Bacilli; Lactobacillales | 65.05 | 1.172 | 0.109 | 62.58 | 1.051 | NA | 1.061 | 1.003-1.122 | NA | NA |
| Firmicutes; Bacilli; Turicibacterales | 4.68 | 0.914 | 0.347 | 5.61 | 0.950 | 0.248 | 0.944 | 0.872-1.020 | 0.138 | 0.865 |
| Firmicutes; Clostridia; Clostridiales | 2017.52 | 1.000 | 1.000 | 4676.48 | 0.998 | 0.838 | 1.000 | 0.995-1.004 | 0.884 | 0.884 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales | 45.10 | 0.988 | 0.899 | 104.43 | 1.011 | 0.473 | 1.011 | 0.980-1.041 | 0.673 | 0.865 |
| Proteobacteria; Betaproteobacteria; Burkholderiales | 4.25 | 1.162 | 0.132 | 80.51 | 0.984 | 0.495 | 0.993 | 0.949-1.038 | 0.568 | 0.865 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales | 2.09 | 1.196 | 0.073 | 20.90 | 0.974 | 0.293 | 0.986 | 0.940-1.033 | 0.610 | 0.865 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales | 34.63 | 1.015 | NA | 53.48 | 1.012 | NA | 1.013 | 0.933-1.098 | NA | NA |
| Proteobacteria; Gammaproteobacteria; Pasteurellales | 4.88 | 0.976 | 0.804 | 4.62 | 0.982 | NA | 0.981 | 0.908-1.059 | NA | NA |
| ***FAMILY LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Barnesiellaceae] | 7.57 | 1.067 | 0.558 | 34.20 | 1.005 | 0.900 | 1.012 | 0.940-1.087 | 0.616 | 0.941 |
| Firmicutes; Clostridia; Clostridiales; [Mogibacteriaceae] | 4.66 | 0.968 | 0.710 | 7.45 | 0.980 | 0.350 | 0.979 | 0.939-1.020 | 0.354 | 0.926 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae] | 1.08 | 1.079 | 0.494 | 18.62 | 0.975 | 0.285 | 0.980 | 0.937-1.024 | 0.779 | 0.941 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Paraprevotellaceae] | 7.50 | 1.043 | NA | 75.21 | 0.999 | 0.980 | 1.007 | 0.926-1.093 | NA | NA |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae | 2.03 | 1.011 | 0.914 | 0.88 | 0.970 | 0.337 | 0.973 | 0.916-1.033 | 0.543 | 0.941 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae | 3.90 | 1.171 | 0.151 | 72.98 | 0.971 | 0.223 | 0.979 | 0.935-1.025 | 0.889 | 0.941 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae | 220.33 | 1.130 | 0.172 | 2212.24 | 0.983 | 0.295 | 0.987 | 0.955-1.019 | 0.829 | 0.941 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae | 80.72 | 0.975 | 0.815 | 80.13 | 1.042 | 0.226 | 1.036 | 0.972-1.103 | 0.486 | 0.941 |
| Firmicutes; Clostridia; Clostridiales; Christensenellaceae | 13.51 | 1.478 | NA | 13.89 | 0.990 | 0.763 | 1.026 | 0.963-1.092 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae | 81.77 | 0.749 | 0.004 | 71.07 | 0.986 | 0.561 | 0.970 | 0.925-1.016 | 0.014 | 0.124 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae | 45.82 | 1.008 | 0.931 | 26.31 | 0.990 | 0.543 | 0.991 | 0.961-1.021 | 0.710 | 0.941 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae | 1.89 | 1.176 | 0.142 | 20.48 | 0.964 | 0.135 | 0.973 | 0.928-1.019 | 0.975 | 0.975 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae | 45.22 | 0.992 | NA | 54.16 | 1.035 | NA | 1.029 | 0.953-1.110 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae | 57.51 | 0.908 | 0.361 | 109.19 | 0.993 | 0.700 | 0.991 | 0.957-1.025 | 0.360 | 0.926 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae | 1350.28 | 0.899 | 0.016 | 1876.37 | 0.989 | 0.206 | 0.986 | 0.970-1.002 | 0.010 | 0.124 |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae | 11.67 | 0.946 | 0.612 | 4.05 | 0.980 | NA | 0.976 | 0.907-1.049 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae | 64.60 | 0.755 | 0.007 | 0.98 | 1.016 | 0.663 | 0.984 | 0.921-1.051 | 0.110 | 0.395 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae | 13.98 | 1.026 | 0.790 | 99.22 | 0.999 | 0.969 | 1.000 | 0.967-1.034 | 0.874 | 0.941 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae | 22.94 | 0.950 | 0.644 | 438.79 | 0.983 | 0.711 | 0.978 | 0.899-1.063 | 0.557 | 0.941 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae | 14.88 | 1.167 | NA | 110.13 | 0.978 | 0.337 | 0.986 | 0.943-1.030 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae | 448.99 | 1.071 | 0.084 | 1544.20 | 0.987 | 0.254 | 0.993 | 0.971-1.014 | 0.690 | 0.941 |
| Bacteroidetes; Bacteroidia; Bacteroidales; S24-7 | 8.29 | 1.031 | NA | 96.07 | 1.040 | NA | 1.039 | 0.953-1.131 | NA | NA |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae | 52.38 | 1.067 | 0.542 | 56.19 | 1.044 | NA | 1.046 | 0.988-1.106 | NA | NA |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae | 4.48 | 0.904 | 0.348 | 4.60 | 0.948 | 0.186 | 0.943 | 0.876-1.014 | 0.109 | 0.395 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae | 45.20 | 1.088 | 0.378 | 104.87 | 1.032 | 0.150 | 1.035 | 0.992-1.078 | 0.100 | 0.395 |
| ***GENUS LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces | 2.16 | 0.997 | 0.980 | 0.75 | 0.981 | 0.442 | 0.982 | 0.935-1.029 | 0.572 | 0.780 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium | 84.01 | 0.981 | 0.879 | 90.68 | 1.046 | 0.072 | 1.044 | 0.994-1.094 | 0.240 | 0.750 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Adlercreutzia | 6.74 | 0.987 | 0.918 | 2.40 | 0.971 | 0.202 | 0.972 | 0.930-1.015 | 0.327 | 0.780 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella | 30.17 | 1.150 | 0.303 | 14.94 | 1.022 | 0.339 | 1.026 | 0.981-1.072 | 0.160 | 0.637 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella | 6.18 | 0.761 | NA | 2.09 | 0.983 | 0.515 | 0.975 | 0.927-1.024 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides | 253.86 | 1.120 | 0.267 | 2927.16 | 1.003 | 0.862 | 1.006 | 0.972-1.041 | 0.366 | 0.780 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae]; Odoribacter | 0.68 | 1.046 | 0.738 | 10.88 | 0.975 | 0.280 | 0.977 | 0.933-1.022 | 0.593 | 0.780 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides | 13.09 | 0.958 | 0.695 | 131.35 | 1.024 | 0.193 | 1.022 | 0.986-1.059 | 0.515 | 0.780 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella | 20.36 | 0.930 | 0.587 | 482.01 | 0.994 | 0.808 | 0.992 | 0.947-1.039 | 0.579 | 0.780 |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus | 55.61 | 1.002 | 0.987 | 57.84 | 1.045 | 0.060 | 1.044 | 0.997-1.092 | 0.178 | 0.637 |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae; Turicibacter | 4.19 | 0.882 | 0.359 | 6.02 | 0.984 | NA | 0.981 | 0.933-1.030 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus] | 288.25 | 0.845 | NA | 201.55 | 1.008 | 0.580 | 1.004 | 0.977-1.031 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes | 5.92 | 0.944 | 0.599 | 10.66 | 1.034 | 0.110 | 1.030 | 0.990-1.072 | 0.443 | 0.780 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia | 676.47 | 0.738 | 0.000 | 513.86 | 0.993 | 0.593 | 0.984 | 0.958-1.009 | 0.001 | 0.037 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium | 2.39 | 0.823 | 0.138 | 17.50 | 0.984 | 0.509 | 0.979 | 0.935-1.024 | 0.131 | 0.637 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus | 208.88 | 0.968 | 0.477 | 207.84 | 0.986 | 0.122 | 0.985 | 0.967-1.002 | 0.109 | 0.637 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Dialister | 16.99 | 0.913 | 0.492 | 25.15 | 1.017 | 0.509 | 1.013 | 0.964-1.063 | 0.990 | 0.990 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea | 104.47 | 0.861 | 0.041 | 65.24 | 1.002 | 0.898 | 0.997 | 0.973-1.021 | 0.178 | 0.637 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium | 230.42 | 0.982 | 0.843 | 549.73 | 1.005 | 0.769 | 1.004 | 0.971-1.038 | 0.945 | 0.984 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira | 31.63 | 1.295 | 0.013 | 163.91 | 0.999 | 0.955 | 1.007 | 0.970-1.045 | 0.089 | 0.637 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Oscillospira | 22.58 | 1.020 | 0.818 | 85.60 | 0.989 | 0.374 | 0.990 | 0.966-1.013 | 0.638 | 0.797 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Phascolarctobacterium | 18.58 | 1.198 | 0.161 | 34.43 | 0.989 | 0.666 | 0.996 | 0.949-1.044 | 0.498 | 0.780 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia | 6.46 | 0.961 | 0.693 | 35.21 | 1.012 | 0.543 | 1.010 | 0.973-1.047 | 0.877 | 0.953 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus | 62.89 | 1.077 | 0.471 | 340.79 | 0.997 | 0.859 | 0.999 | 0.966-1.032 | 0.704 | 0.838 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; SMB53 | 0.62 | 0.891 | 0.401 | 0.88 | 0.992 | 0.760 | 0.989 | 0.943-1.037 | 0.419 | 0.780 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella | 4.41 | 0.937 | 0.631 | 3.57 | 0.988 | 0.644 | 0.986 | 0.938-1.036 | 0.506 | 0.780 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium] | 20.65 | 0.901 | 0.434 | 42.55 | 1.031 | 0.218 | 1.026 | 0.978-1.076 | 0.743 | 0.844 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Sutterella | 4.32 | 1.182 | 0.203 | 85.39 | 1.001 | 0.959 | 1.005 | 0.964-1.047 | 0.352 | 0.780 |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus | 4.27 | 0.882 | 0.358 | 4.03 | 0.999 | NA | 0.994 | 0.946-1.044 | NA | NA |
| ***SPECIES LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; adolescentis | 38.42 | 0.863 | 0.328 | 75.56 | 1.051 | 0.086 | 1.044 | 0.986-1.104 | 0.594 | 0.849 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella; aerofaciens | 25.31 | 1.091 | 0.565 | 13.58 | 1.029 | 0.276 | 1.031 | 0.979-1.083 | 0.238 | 0.476 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella; lenta | 6.14 | 0.740 | NA | 1.99 | 0.980 | 0.531 | 0.969 | 0.912-1.029 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella; copri | 16.68 | 0.926 | NA | 353.04 | 0.994 | NA | 0.991 | 0.938-1.047 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides; distasonis | 7.33 | 1.004 | 0.978 | 51.50 | 1.040 | 0.100 | 1.039 | 0.992-1.087 | 0.234 | 0.476 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; fragilis | 20.37 | 1.585 | NA | 16.33 | 1.002 | 0.945 | 1.018 | 0.963-1.074 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; ovatus | 5.59 | 0.927 | 0.586 | 12.37 | 0.991 | 0.671 | 0.989 | 0.947-1.032 | 0.493 | 0.822 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; uniformis | 32.05 | 0.926 | 0.510 | 305.56 | 1.007 | 0.776 | 1.003 | 0.960-1.048 | 0.794 | 0.928 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; bromii | 24.12 | 0.928 | 0.594 | 1.65 | 0.969 | 0.243 | 0.967 | 0.918-1.019 | 0.228 | 0.476 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella; dispar | 3.41 | 1.013 | NA | 2.82 | 0.986 | 0.653 | 0.987 | 0.928-1.048 | NA |  |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; faecis | 1.12 | 0.977 | 0.868 | 2.28 | 1.045 | 0.049 | 1.044 | 0.999-1.089 | 0.199 | 0.476 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea; formicigenerans | 1.92 | 0.931 | 0.544 | 20.11 | 1.016 | 0.468 | 1.013 | 0.970-1.057 | 0.928 | 0.928 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus]; gnavus | 138.52 | 0.774 | NA | 85.10 | 0.999 | 0.952 | 0.994 | 0.961-1.028 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; prausnitzii | 230.05 | 0.981 | 0.839 | 540.38 | 1.006 | 0.732 | 1.005 | 0.970-1.041 | 0.920 | 0.928 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; producta | 35.68 | 0.755 | NA | 28.60 | 0.972 | 0.289 | 0.961 | 0.912-1.011 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; biforme | 10.94 | 0.966 | NA | 39.95 | 1.016 | 0.607 | 1.014 | 0.954-1.077 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; dolichum | 7.70 | 0.809 | 0.168 | 3.34 | 0.978 | 0.434 | 0.971 | 0.918-1.026 | 0.127 | 0.476 |

aRelationship between higher quartiles of fiber from grain 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 from grain 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.