**Supplementary Table 2. Meta-analysis of association between fiber from fruit and vegetable 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 | 0.988 | 0.742 | 115.59 | 0.960 | 0.017 | 0.965 | 0.936-0.995 | 0.054 | 0.215 |
| Bacteroidetes | 330.53 | 0.968 | 0.370 | 3075.49 | 1.019 | 0.033 | 1.016 | 0.999-1.034 | 0.375 | 0.500 |
| Firmicutes | 2126.89 | 1.000 | 1.000 | 5057.10 | 1.000 | 0.967 | 1.000 | 0.994-1.006 | 0.976 | 0.976 |
| Proteobacteria | 46.68 | 1.095 | 0.020 | 198.49 | 0.996 | 0.772 | 1.005 | 0.982-1.03 | 0.155 | 0.310 |
| ***CLASS LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria | 95.25 | 0.993 | 0.759 | 92.05 | 0.961 | 0.084 | 0.978 | 0.947-1.008 | 0.149 | 0.396 |
| Actinobacteria; Coriobacteriia | 45.54 | 1.000 | 0.985 | 26.14 | 0.968 | 0.004 | 0.974 | 0.954-0.993 | 0.040 | 0.250 |
| Bacteroidetes; Bacteroidia | 327.59 | 0.984 | 0.492 | 3253.15 | 1.017 | 0.115 | 1.011 | 0.992-1.030 | 0.522 | 0.946 |
| Firmicutes; Bacilli | 70.42 | 0.982 | 0.412 | 68.40 | 0.963 | 0.070 | 0.972 | 0.943-1.001 | 0.062 | 0.250 |
| Firmicutes; Clostridia | 2017.61 | 1.000 | 1.000 | 4676.67 | 1.002 | 0.760 | 1.000 | 0.995-1.005 | 0.828 | 0.946 |
| Firmicutes; Erysipelotrichi | 45.10 | 0.983 | 0.443 | 104.43 | 1.001 | 0.925 | 0.997 | 0.975-1.018 | 0.636 | 0.946 |
| Proteobacteria; Betaproteobacteria | 4.81 | 1.009 | 0.667 | 80.63 | 1.001 | 0.977 | 1.004 | 0.977-1.031 | 0.747 | 0.946 |
| Proteobacteria; Deltaproteobacteria | 2.09 | 1.002 | 0.909 | 20.90 | 0.998 | 0.900 | 1.000 | 0.974-1.026 | 0.993 | 0.993 |
| Proteobacteria; Gammaproteobacteria | 39.69 | 1.021 | NA | 76.42 | 0.995 | 0.834 | 1.011 | 0.981-1.041 | NA | NA |
| ***ORDER LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Bifidobacteriales | 91.55 | 0.992 | 0.701 | 90.91 | 0.951 | 0.096 | 0.980 | 0.948-1.012 | 0.146 | 0.386 |
| Actinobacteria; Actinobacteria; Actinomycetales | 3.69 | 0.977 | 0.292 | 1.14 | 0.973 | 0.337 | 0.976 | 0.942-1.009 | 0.155 | 0.386 |
| Actinobacteria; Coriobacteriia; Coriobacteriales | 45.54 | 0.998 | 0.938 | 26.14 | 0.967 | 0.004 | 0.973 | 0.952-0.992 | 0.034 | 0.180 |
| Bacteroidetes; Bacteroidia; Bacteroidales | 327.61 | 0.982 | 0.447 | 3253.13 | 1.017 | 0.115 | 1.011 | 0.991-1.031 | 0.557 | 0.893 |
| Firmicutes; Bacilli; Lactobacillales | 65.05 | 0.986 | 0.503 | 62.58 | 0.944 | 0.022 | 0.968 | 0.938-0.999 | 0.036 | 0.180 |
| Firmicutes; Bacilli; Turicibacterales | 4.68 | 0.986 | 0.381 | 5.61 | 1.013 | 0.726 | 0.990 | 0.961-1.019 | 0.714 | 0.893 |
| Firmicutes; Clostridia; Clostridiales | 2017.52 | 1.000 | 1.000 | 4676.48 | 1.002 | 0.762 | 1.000 | 0.997-1.002 | 0.829 | 0.921 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales | 45.10 | 0.983 | 0.446 | 104.43 | 1.001 | 0.923 | 0.997 | 0.974-1.018 | 0.641 | 0.893 |
| Proteobacteria; Betaproteobacteria; Burkholderiales | 4.25 | 1.013 | 0.498 | 80.51 | 1.000 | 0.988 | 1.007 | 0.979-1.034 | 0.626 | 0.893 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales | 2.09 | 1.003 | 0.876 | 20.90 | 0.998 | 0.906 | 1.001 | 0.974-1.027 | 0.980 | 0.980 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales | 34.63 | 1.024 | NA | 53.48 | 1.010 | NA | 1.021 | 0.988-1.055 | NA | NA |
| Proteobacteria; Gammaproteobacteria; Pasteurellales | 4.88 | 1.000 | 0.991 | 4.62 | 1.022 | NA | 1.003 | 0.974-1.033 | NA | NA |
| ***FAMILY LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae | 2.03 | 0.893 | 0.011 | 0.88 | 0.985 | 0.524 | 0.965 | 0.926-1.004 | 0.026 | 0.467 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae | 80.72 | 0.988 | 0.783 | 80.13 | 0.967 | 0.159 | 0.971 | 0.931-1.012 | 0.232 | 0.568 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae | 45.82 | 1.012 | 0.766 | 26.31 | 0.971 | 0.022 | 0.975 | 0.952-0.998 | 0.155 | 0.568 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae | 13.98 | 0.928 | 0.086 | 99.22 | 0.997 | 0.813 | 0.990 | 0.964-1.016 | 0.169 | 0.568 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae | 14.88 | 1.087 | 0.065 | 110.13 | 0.999 | 0.936 | 1.010 | 0.977-1.043 | 0.215 | 0.568 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae | 22.94 | 1.024 | 0.596 | 438.79 | 1.033 | 0.229 | 1.030 | 0.985-1.077 | 0.220 | 0.568 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae] | 1.08 | 0.973 | 0.540 | 18.62 | 0.981 | 0.294 | 0.980 | 0.948-1.012 | 0.239 | 0.568 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae | 220.33 | 0.917 | 0.034 | 2212.24 | 1.010 | 0.460 | 1.000 | 0.975-1.026 | 0.336 | 0.638 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Barnesiellaceae] | 7.57 | 0.993 | 0.876 | 34.20 | 1.019 | 0.474 | 1.012 | 0.968-1.057 | 0.689 | 0.850 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Paraprevotellaceae] | 7.50 | 0.985 | NA | 75.21 | 1.027 | 0.312 | 1.013 | 0.970-1.057 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; S24-7 | 8.29 | 1.004 | NA | 96.07 | 0.986 | NA | 0.991 | 0.950-1.034 | NA | NA |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae | 4.48 | 0.969 | 0.455 | 4.60 | 1.005 | 0.840 | 0.995 | 0.952-1.039 | 0.703 | 0.850 |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae | 52.38 | 0.956 | 0.324 | 56.19 | 0.967 | NA | 0.965 | 0.928-1.003 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae | 64.60 | 1.072 | 0.122 | 0.98 | 1.031 | 0.216 | 1.040 | 0.997-1.085 | 0.049 | 0.467 |
| Firmicutes; Clostridia; Clostridiales; [Mogibacteriaceae] | 4.66 | 1.040 | 0.332 | 7.45 | 1.009 | 0.617 | 1.013 | 0.982-1.045 | 0.299 | 0.632 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae | 448.99 | 1.009 | 0.656 | 1544.20 | 1.003 | 0.743 | 1.004 | 0.987-1.021 | 0.584 | 0.850 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae | 1350.28 | 0.959 | 0.062 | 1876.37 | 1.008 | 0.239 | 1.004 | 0.990-1.016 | 0.637 | 0.850 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae | 81.77 | 1.045 | 0.317 | 71.07 | 0.992 | 0.690 | 1.001 | 0.966-1.035 | 0.675 | 0.850 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae | 45.20 | 0.974 | 0.543 | 104.87 | 1.016 | 0.349 | 1.010 | 0.979-1.042 | 0.811 | 0.857 |
| Firmicutes; Clostridia; Clostridiales; Christensenellaceae | 13.51 | 1.042 | NA | 13.89 | 0.998 | 0.949 | 1.008 | 0.966-1.050 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae | 57.51 | 0.935 | 0.133 | 109.19 | 1.014 | 0.332 | 1.006 | 0.980-1.033 | 0.716 | 0.850 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae | 3.90 | 1.013 | 0.779 | 72.98 | 1.002 | 0.898 | 1.004 | 0.970-1.038 | 0.773 | 0.857 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae | 1.89 | 1.002 | 0.957 | 20.48 | 1.004 | 0.841 | 1.004 | 0.969-1.038 | 0.857 | 0.857 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae | 45.22 | 1.050 | NA | 54.16 | 1.006 | NA | 1.018 | 0.973-1.064 | NA | NA |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae | 11.67 | 0.998 | 0.957 | 4.05 | 1.023 | NA | 1.016 | 0.972-1.060 | NA | NA |
| ***GENUS LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces | 2.16 | 0.864 | 0.002 | 0.75 | 0.987 | 0.471 | 0.970 | 0.939-1.002 | 0.007 | 0.090 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium | 84.01 | 0.971 | 0.537 | 90.68 | 0.990 | 0.592 | 0.988 | 0.956-1.021 | 0.415 | 0.624 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Adlercreutzia | 6.74 | 1.046 | 0.347 | 2.40 | 1.009 | 0.600 | 1.013 | 0.981-1.045 | 0.301 | 0.563 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella | 30.17 | 1.013 | 0.787 | 14.94 | 0.976 | 0.153 | 0.980 | 0.949-1.011 | 0.409 | 0.624 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella | 6.18 | 1.014 | NA | 2.09 | 1.002 | 0.912 | 1.003 | 0.971-1.036 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides | 253.86 | 0.897 | 0.011 | 2927.16 | 1.003 | 0.832 | 0.992 | 0.966-1.018 | 0.102 | 0.359 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae]; Odoribacter | 0.68 | 0.992 | 0.862 | 10.88 | 0.954 | 0.007 | 0.959 | 0.928-0.989 | 0.040 | 0.300 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides | 13.09 | 0.898 | 0.017 | 131.35 | 1.001 | 0.923 | 0.991 | 0.964-1.018 | 0.107 | 0.359 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella | 20.36 | 1.026 | 0.583 | 482.01 | 1.018 | 0.253 | 1.019 | 0.989-1.048 | 0.230 | 0.544 |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus | 55.61 | 0.939 | 0.180 | 57.84 | 0.977 | 0.180 | 0.972 | 0.941-1.003 | 0.058 | 0.300 |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae; Turicibacter | 4.19 | 0.990 | 0.832 | 6.02 | 1.012 | NA | 1.009 | 0.977-1.041 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus] | 288.25 | 0.860 | 0.000 | 201.55 | 1.017 | 0.134 | 1.005 | 0.984-1.026 | 0.130 | 0.365 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes | 5.92 | 0.976 | 0.592 | 10.66 | 1.000 | 0.986 | 0.998 | 0.968-1.027 | 0.716 | 0.810 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia | 676.47 | 1.022 | 0.558 | 513.86 | 0.978 | 0.043 | 0.982 | 0.961-1.001 | 0.303 | 0.563 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium | 2.39 | 1.003 | 0.954 | 17.50 | 1.016 | 0.363 | 1.014 | 0.982-1.047 | 0.491 | 0.672 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus | 208.88 | 0.972 | 0.203 | 207.84 | 1.015 | 0.056 | 1.010 | 0.995-1.024 | 0.642 | 0.795 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Dialister | 16.99 | 0.976 | 0.556 | 25.15 | 0.989 | 0.512 | 0.987 | 0.957-1.017 | 0.378 | 0.624 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea | 104.47 | 0.988 | 0.726 | 65.24 | 1.000 | 0.994 | 0.999 | 0.979-1.018 | 0.810 | 0.877 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium | 230.42 | 0.988 | 0.758 | 549.73 | 1.033 | 0.018 | 1.028 | 1.002-1.053 | 0.140 | 0.365 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira | 31.63 | 0.994 | 0.896 | 163.91 | 1.010 | 0.495 | 1.009 | 0.981-1.036 | 0.694 | 0.810 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Oscillospira | 22.58 | 0.926 | 0.043 | 85.60 | 0.993 | 0.501 | 0.989 | 0.970-1.007 | 0.058 | 0.300 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Phascolarctobacterium | 18.58 | 0.976 | 0.609 | 34.43 | 1.008 | 0.645 | 1.004 | 0.971-1.037 | 0.974 | 0.974 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia | 6.46 | 0.940 | 0.153 | 35.21 | 0.999 | 0.935 | 0.993 | 0.965-1.020 | 0.289 | 0.563 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus | 62.89 | 0.969 | 0.464 | 340.79 | 0.954 | 0.000 | 0.955 | 0.931-0.978 | 0.002 | 0.048 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; SMB53 | 0.62 | 1.044 | 0.344 | 0.88 | 1.024 | 0.191 | 1.026 | 0.993-1.060 | 0.111 | 0.359 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella | 4.41 | 0.936 | 0.166 | 3.57 | 1.005 | 0.792 | 0.996 | 0.964-1.028 | 0.432 | 0.624 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium] | 20.65 | 0.968 | 0.489 | 42.55 | 1.010 | 0.561 | 1.005 | 0.972-1.038 | 0.942 | 0.974 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Sutterella | 4.32 | 1.010 | 0.829 | 85.39 | 1.010 | 0.543 | 1.010 | 0.979-1.040 | 0.559 | 0.727 |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus | 4.27 | 0.998 | 0.956 | 4.03 | 1.015 | NA | 1.012 | 0.980-1.045 | NA | NA |
| ***SPECIES LEVEL***  |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella; aerofaciens | 25.31 | 1.053 | 0.449 | 13.58 | 0.974 | 0.206 | 0.981 | 0.943-1.019 | 0.713 | 0.713 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella; lenta | 6.14 | 1.016 | NA | 1.99 | 1.004 | 0.850 | 1.006 | 0.962-1.050 | NA | NA |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; adolescentis | 38.42 | 0.990 | 0.885 | 75.56 | 0.988 | 0.590 | 0.988 | 0.947-1.030 | 0.628 | 0.691 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella; copri | 16.68 | 1.030 | NA | 353.04 | 1.020 | NA | 1.020 | 0.982-1.059 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides; distasonis | 7.33 | 0.882 | 0.037 | 51.50 | 0.997 | 0.873 | 0.986 | 0.951-1.021 | 0.114 | 0.401 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; fragilis | 20.37 | 1.091 | NA | 16.33 | 0.992 | 0.728 | 1.001 | 0.961-1.042 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; ovatus | 5.59 | 0.907 | 0.125 | 12.37 | 1.003 | 0.858 | 0.996 | 0.962-1.030 | 0.342 | 0.418 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; uniformis | 32.05 | 0.868 | 0.009 | 305.56 | 0.996 | 0.830 | 0.982 | 0.949-1.016 | 0.048 | 0.262 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; biforme | 10.94 | 0.935 | NA | 39.95 | 1.006 | 0.801 | 0.999 | 0.957-1.040 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; dolichum | 7.70 | 0.932 | 0.300 | 3.34 | 0.990 | 0.667 | 0.985 | 0.944-1.026 | 0.301 | 0.418 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; bromii | 24.12 | 0.911 | 0.149 | 1.65 | 0.970 | 0.154 | 0.965 | 0.927-1.003 | 0.042 | 0.262 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella; dispar | 3.41 | 0.858 | 0.022 | 2.82 | 1.018 | 0.459 | 0.999 | 0.956-1.042 | 0.279 | 0.418 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; faecis | 1.12 | 0.929 | 0.253 | 2.28 | 0.988 | 0.514 | 0.983 | 0.949-1.018 | 0.205 | 0.418 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea; formicigenerans | 1.92 | 1.030 | 0.602 | 20.11 | 1.016 | 0.376 | 1.017 | 0.983-1.051 | 0.319 | 0.418 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus]; gnavus | 138.52 | 0.811 | NA | 85.10 | 1.020 | 0.160 | 1.007 | 0.980-1.034 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; prausnitzii | 230.05 | 0.987 | 0.781 | 540.38 | 1.035 | 0.020 | 1.030 | 1.002-1.058 | 0.146 | 0.401 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; producta | 35.68 | 1.027 | NA | 28.60 | 1.008 | 0.702 | 1.010 | 0.971-1.050 | NA | NA |

aRelationship between higher quartiles of fiber from fruit and vegetable 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 fruit and vegetable 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.