**Supplementary Table 4. Meta-analysis of association between fiber from bean 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 | 1.195 | 0.041 | 115.59 | 1.030 | 0.639 | 1.085 | 0.980-1.199 | 0.077 | 0.307 |
| Bacteroidetes | 330.53 | 0.890 | 0.184 | 3075.49 | 1.017 | 0.602 | 1.001 | 0.942-1.062 | 0.574 | 0.670 |
| Firmicutes | 2126.89 | 1.000 | 1.000 | 5057.10 | 1.029 | 0.299 | 1.002 | 0.986-1.017 | 0.460 | 0.670 |
| Proteobacteria | 46.68 | 1.164 | 0.093 | 198.49 | 0.905 | 0.024 | 0.950 | 0.878-1.027 | 0.670 | 0.670 |
| ***CLASS LEVEL*** |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria | 95.25 | 1.224 | 0.088 | 92.05 | 0.996 | 0.966 | 1.084 | 0.934-1.257 | 0.243 | 0.476 |
| Actinobacteria; Coriobacteriia | 45.54 | 1.192 | 0.097 | 26.14 | 0.987 | 0.751 | 1.013 | 0.937-1.094 | 0.348 | 0.476 |
| Bacteroidetes; Bacteroidia | 327.59 | 0.864 | 0.170 | 3253.15 | 1.005 | 0.895 | 0.988 | 0.920-1.060 | 0.385 | 0.476 |
| Firmicutes; Bacilli | 70.42 | 1.149 | 0.241 | 68.40 | 1.024 | 0.774 | 1.064 | 0.930-1.215 | 0.304 | 0.476 |
| Firmicutes; Clostridia | 2017.61 | 1.000 | 1.000 | 4676.67 | 1.028 | 0.287 | 1.002 | 0.988-1.015 | 0.448 | 0.476 |
| Firmicutes; Erysipelotrichi | 45.10 | 0.840 | 0.145 | 104.43 | 1.013 | 0.777 | 0.989 | 0.910-1.075 | 0.411 | 0.476 |
| Proteobacteria; Betaproteobacteria | 4.81 | 0.872 | 0.259 | 80.63 | 1.008 | 0.910 | 0.972 | 0.863-1.094 | 0.476 | 0.476 |
| Proteobacteria; Deltaproteobacteria | 2.09 | 0.869 | 0.239 | 20.90 | 0.860 | 0.039 | 0.862 | 0.762-0.974 | 0.021 | 0.171 |
| Proteobacteria; Gammaproteobacteria | 39.69 | 1.187 | NA | 76.42 | 0.854 | 0.176 | 1.002 | 0.850-1.180 | NA | NA |
| ***ORDER LEVEL*** |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales | 3.69 | 0.705 | 0.008 | 1.14 | 0.965 | 0.731 | 0.857 | 0.731-1.005 | 0.035 | 0.177 |
| Actinobacteria; Actinobacteria; Bifidobacteriales | 91.55 | 1.228 | 0.138 | 90.91 | 0.995 | 0.964 | 1.080 | 0.911-1.279 | 0.313 | 0.557 |
| Actinobacteria; Coriobacteriia; Coriobacteriales | 45.54 | 1.209 | 0.090 | 26.14 | 0.987 | 0.753 | 1.012 | 0.936-1.093 | 0.335 | 0.557 |
| Bacteroidetes; Bacteroidia; Bacteroidales | 327.61 | 0.855 | 0.164 | 3253.13 | 1.005 | 0.890 | 0.989 | 0.920-1.061 | 0.379 | 0.557 |
| Firmicutes; Bacilli; Lactobacillales | 65.05 | 1.142 | 0.331 | 62.58 | 1.022 | 0.813 | 1.057 | 0.911-1.224 | 0.394 | 0.557 |
| Firmicutes; Bacilli; Turicibacterales | 4.68 | 1.087 | 0.539 | 5.61 | 0.971 | 0.830 | 1.028 | 0.850-1.242 | 0.781 | 0.781 |
| Firmicutes; Clostridia; Clostridiales | 2017.52 | 1.000 | 1.000 | 4676.48 | 1.028 | 0.284 | 1.000 | 0.993-1.007 | 0.446 | 0.557 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales | 45.10 | 0.819 | 0.135 | 104.43 | 1.013 | 0.770 | 0.991 | 0.911-1.078 | 0.400 | 0.557 |
| Proteobacteria; Betaproteobacteria; Burkholderiales | 4.25 | 0.881 | 0.361 | 80.51 | 1.008 | 0.913 | 0.981 | 0.867-1.108 | 0.573 | 0.637 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales | 2.09 | 0.846 | 0.227 | 20.90 | 0.860 | 0.038 | 0.857 | 0.755-0.972 | 0.020 | 0.177 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales | 34.63 | 1.192 | NA | 53.48 | 0.834 | NA | 0.999 | 0.822-1.213 | NA | NA |
| Proteobacteria; Gammaproteobacteria; Pasteurellales | 4.88 | 0.901 | 0.444 | 4.62 | 1.218 | NA | 1.054 | 0.876-1.268 | NA | NA |
| ***FAMILY LEVEL*** |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae | 2.03 | 0.754 | 0.072 | 0.88 | 0.941 | 0.463 | 0.897 | 0.776-1.035 | 0.074 | 0.224 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae | 80.72 | 1.342 | 0.085 | 80.13 | 1.006 | 0.941 | 1.066 | 0.917-1.238 | 0.207 | 0.439 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae | 45.82 | 1.224 | 0.097 | 26.31 | 0.985 | 0.732 | 1.011 | 0.930-1.097 | 0.357 | 0.606 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Barnesiellaceae] | 7.57 | 0.677 | 0.027 | 34.20 | 0.948 | 0.567 | 0.881 | 0.750-1.035 | 0.050 | 0.211 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae] | 1.08 | 0.683 | 0.031 | 18.62 | 0.886 | 0.053 | 0.860 | 0.765-0.966 | 0.004 | 0.033 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Paraprevotellaceae] | 7.50 | 0.827 | NA | 75.21 | 1.114 | 0.258 | 1.044 | 0.885-1.231 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae | 220.33 | 0.826 | 0.139 | 2212.24 | 0.953 | 0.315 | 0.937 | 0.859-1.022 | 0.079 | 0.224 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae | 13.98 | 0.539 | 0.000 | 99.22 | 0.932 | 0.149 | 0.876 | 0.800-0.958 | 0.000 | 0.000 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae | 22.94 | 0.973 | NA | 438.79 | 1.140 | 0.170 | 1.101 | 0.933-1.299 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Rikenellaceae | 14.88 | 0.941 | NA | 110.13 | 0.904 | 0.105 | 0.908 | 0.809-1.018 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; S24-7 | 8.29 | 0.669 | NA | 96.07 | 0.962 | NA | 0.896 | 0.763-1.051 | NA | NA |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae | 52.38 | 1.150 | 0.385 | 56.19 | 1.025 | NA | 1.048 | 0.912-1.203 | NA | NA |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae | 4.48 | 1.080 | 0.678 | 4.60 | 0.975 | 0.785 | 0.995 | 0.845-1.172 | 0.922 | 0.922 |
| Firmicutes; Clostridia; Clostridiales; [Mogibacteriaceae] | 4.66 | 1.063 | 0.621 | 7.45 | 0.996 | 0.950 | 1.009 | 0.906-1.122 | 0.762 | 0.864 |
| Firmicutes; Clostridia; Clostridiales; Christensenellaceae | 13.51 | 0.649 | NA | 13.89 | 1.029 | 0.738 | 0.939 | 0.809-1.087 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae | 81.77 | 1.320 | 0.061 | 71.07 | 0.966 | 0.607 | 1.019 | 0.903-1.148 | 0.342 | 0.606 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae | 1350.28 | 0.968 | 0.599 | 1876.37 | 1.041 | 0.090 | 1.031 | 0.987-1.077 | 0.403 | 0.621 |
| Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae | 64.60 | 1.070 | 0.670 | 0.98 | 0.981 | 0.831 | 1.002 | 0.861-1.164 | 0.883 | 0.922 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae | 448.99 | 0.947 | 0.314 | 1544.20 | 1.009 | 0.781 | 0.992 | 0.938-1.048 | 0.611 | 0.742 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae | 45.20 | 1.204 | 0.180 | 104.87 | 1.064 | 0.301 | 1.085 | 0.974-1.209 | 0.093 | 0.226 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae | 57.51 | 0.764 | 0.091 | 109.19 | 1.041 | 0.418 | 1.013 | 0.923-1.110 | 0.542 | 0.709 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae | 3.90 | 0.824 | 0.273 | 72.98 | 1.000 | 0.994 | 0.977 | 0.865-1.101 | 0.439 | 0.621 |
| Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae | 1.89 | 0.780 | 0.169 | 20.48 | 0.898 | 0.107 | 0.883 | 0.780-0.998 | 0.035 | 0.197 |
| Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae | 45.22 | 1.326 | NA | 54.16 | 0.853 | NA | 0.939 | 0.796-1.106 | NA | NA |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae | 11.67 | 0.858 | NA | 4.05 | 1.150 | NA | 1.085 | 0.922-1.274 | NA | NA |
| ***GENUS LEVEL*** |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces | 2.16 | 0.757 | 0.076 | 0.75 | 0.938 | 0.480 | 0.890 | 0.763-1.036 | 0.080 | 0.206 |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium | 84.01 | 1.331 | 0.085 | 90.68 | 1.028 | 0.758 | 1.089 | 0.933-1.270 | 0.153 | 0.274 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Adlercreutzia | 6.74 | 0.959 | 0.803 | 2.40 | 1.106 | 0.179 | 1.080 | 0.944-1.235 | 0.434 | 0.646 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella | 30.17 | 1.197 | 0.299 | 14.94 | 0.928 | 0.333 | 0.968 | 0.843-1.111 | 0.968 | 0.968 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella | 6.18 | 0.879 | NA | 2.09 | 1.098 | 0.340 | 1.041 | 0.880-1.230 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides | 253.86 | 0.907 | 0.468 | 2927.16 | 0.884 | 0.024 | 0.888 | 0.803-0.980 | 0.035 | 0.150 |
| Bacteroidetes; Bacteroidia; Bacteroidales; [Odoribacteraceae]; Odoribacter | 0.68 | 0.744 | 0.088 | 10.88 | 0.757 | 0.000 | 0.755 | 0.657-0.866 | 0.000 | 0.002 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides | 13.09 | 0.568 | 0.000 | 131.35 | 0.897 | 0.058 | 0.839 | 0.756-0.930 | 0.000 | 0.001 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella | 20.36 | 0.977 | NA | 482.01 | 1.129 | 0.234 | 1.087 | 0.915-1.291 | NA | NA |
| Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus | 55.61 | 1.221 | 0.205 | 57.84 | 0.966 | 0.666 | 1.014 | 0.880-1.168 | 0.560 | 0.693 |
| Firmicutes; Bacilli; Turicibacterales; Turicibacteraceae; Turicibacter | 4.19 | 1.134 | 0.469 | 6.02 | 0.991 | 0.931 | 1.025 | 0.865-1.213 | 0.655 | 0.741 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus] | 288.25 | 0.741 | 0.019 | 201.55 | 0.998 | 0.970 | 0.970 | 0.897-1.048 | 0.094 | 0.206 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes | 5.92 | 1.200 | 0.197 | 10.66 | 1.075 | 0.278 | 1.097 | 0.974-1.235 | 0.093 | 0.206 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia | 676.47 | 1.315 | 0.008 | 513.86 | 0.975 | 0.537 | 1.015 | 0.942-1.093 | 0.158 | 0.274 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium | 2.39 | 1.233 | 0.215 | 17.50 | 1.010 | 0.899 | 1.048 | 0.909-1.208 | 0.336 | 0.547 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Coprococcus | 208.88 | 1.117 | 0.063 | 207.84 | 1.065 | 0.018 | 1.074 | 1.023-1.126 | 0.003 | 0.024 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Dialister | 16.99 | 1.177 | 0.330 | 25.15 | 1.011 | 0.914 | 1.053 | 0.888-1.248 | 0.447 | 0.646 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea | 104.47 | 1.018 | 0.858 | 65.24 | 0.976 | 0.515 | 0.981 | 0.915-1.051 | 0.736 | 0.797 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium | 230.42 | 1.280 | 0.036 | 549.73 | 1.078 | 0.157 | 1.111 | 1.009-1.221 | 0.013 | 0.068 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira | 31.63 | 0.910 | 0.500 | 163.91 | 1.055 | 0.375 | 1.031 | 0.925-1.148 | 0.875 | 0.911 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Oscillospira | 22.58 | 0.872 | 0.222 | 85.60 | 0.963 | 0.297 | 0.954 | 0.891-1.020 | 0.110 | 0.220 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Phascolarctobacterium | 18.58 | 0.838 | 0.290 | 34.43 | 0.884 | 0.157 | 0.874 | 0.750-1.016 | 0.080 | 0.206 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia | 6.46 | 1.100 | 0.476 | 35.21 | 1.114 | 0.064 | 1.111 | 1.001-1.233 | 0.069 | 0.206 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus | 62.89 | 0.947 | 0.684 | 340.79 | 0.852 | 0.002 | 0.863 | 0.786-0.947 | 0.012 | 0.068 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; SMB53 | 0.62 | 1.001 | 0.994 | 0.88 | 1.076 | 0.394 | 1.061 | 0.911-1.234 | 0.540 | 0.693 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella | 4.41 | 1.115 | 0.528 | 3.57 | 1.032 | 0.749 | 1.053 | 0.888-1.246 | 0.502 | 0.687 |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium] | 20.65 | 0.701 | 0.036 | 42.55 | 0.975 | 0.779 | 0.909 | 0.778-1.059 | 0.095 | 0.206 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Sutterella | 4.32 | 0.906 | 0.558 | 85.39 | 0.987 | 0.853 | 0.975 | 0.859-1.105 | 0.587 | 0.694 |
| Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus | 4.27 | 0.936 | 0.702 | 4.03 | 1.116 | NA | 1.070 | 0.906-1.263 | NA | NA |
| ***SPECIES LEVEL*** |  |  |  |  |  |  |  |  |  |  |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; adolescentis | 38.42 | 1.395 | 0.129 | 75.56 | 1.018 | 0.845 | 1.068 | 0.903-1.262 | 0.228 | 0.418 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella; aerofaciens | 25.31 | 1.401 | 0.124 | 13.58 | 0.937 | 0.424 | 0.983 | 0.847-1.140 | 0.610 | 0.729 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella; lenta | 6.14 | 0.840 | NA | 1.99 | 1.108 | 0.309 | 1.059 | 0.883-1.269 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella; copri | 16.68 | 1.127 | NA | 353.04 | 1.098 | NA | 1.102 | 0.918-1.322 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides; distasonis | 7.33 | 0.532 | 0.000 | 51.50 | 0.882 | 0.084 | 0.821 | 0.719-0.936 | 0.000 | 0.002 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; fragilis | 20.37 | 0.508 | NA | 16.33 | 0.937 | 0.462 | 0.863 | 0.734-1.013 | NA | NA |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; ovatus | 5.59 | 1.071 | 0.727 | 12.37 | 0.869 | 0.036 | 0.888 | 0.784-1.005 | 0.213 | 0.418 |
| Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides; uniformis | 32.05 | 0.953 | 0.766 | 305.56 | 0.862 | 0.029 | 0.875 | 0.773-0.989 | 0.078 | 0.213 |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus; bromii | 24.12 | 0.967 | 0.866 | 1.65 | 0.910 | 0.260 | 0.918 | 0.789-1.067 | 0.357 | 0.561 |
| Firmicutes; Clostridia; Clostridiales; Veillonellaceae; Veillonella; dispar | 3.41 | 0.908 | 0.659 | 2.82 | 1.098 | 0.356 | 1.062 | 0.886-1.271 | 0.729 | 0.729 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia; faecis | 1.12 | 0.987 | 0.948 | 2.28 | 1.056 | 0.433 | 1.048 | 0.922-1.190 | 0.608 | 0.729 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Dorea; formicigenerans | 1.92 | 1.068 | 0.686 | 20.11 | 1.014 | 0.831 | 1.022 | 0.905-1.152 | 0.663 | 0.729 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; [Ruminococcus]; gnavus | 138.52 | 0.666 | NA | 85.10 | 0.969 | 0.540 | 0.941 | 0.853-1.037 | NA | NA |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium; prausnitzii | 230.05 | 1.305 | 0.033 | 540.38 | 1.077 | 0.172 | 1.111 | 1.007-1.225 | 0.013 | 0.049 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia; producta | 35.68 | 1.270 | NA | 28.60 | 1.048 | 0.572 | 1.087 | 0.936-1.260 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; biforme | 10.94 | 0.813 | NA | 39.95 | 0.981 | 0.859 | 0.950 | 0.784-1.150 | NA | NA |
| Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; [Eubacterium]; dolichum | 7.70 | 0.708 | 0.126 | 3.34 | 0.801 | 0.014 | 0.788 | 0.668-0.927 | 0.005 | 0.026 |

aRelationship between higher quartiles of fiber from bean 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 bean 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.