|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplemental Table S3 The logistic regression models of the characteristic GM and PSCI, unadjusted (model 1), adjusted for age (model 2), and adjusted for age and risk factors for PSCI (model 3)** | | | | | | | | | |
| Characteristic  bacteria | Model 1 | | | Model 2 | | | Model 3 | | |
| OR | 95%CI | *P* | OR | 95%CI | *P* | OR | 95%CI | *P* |
| ***Prevotella*** |  |  | 0.097 |  |  | 0.106 |  |  | 0.054 |
| T1:first tertile (reference) | 1 |  |  | 1 |  |  | 1 |  |  |
| T2:second tertile | 2.976 | 0.885-10.010 | 0.078 | 2.906 | 0.846-9.979 | 0.090 | 1.626 | 0.236-11.225 | 0.622 |
| T3:third tertile | 3.581 | 0.995-12.888 | 0.051 | 3.719 | 0.979-14.123 | 0.054 | 12.449 | 1.503-103.078 | 0.019 |
|  |  |  |  |  |  |  |  |  |  |
| ***Streptococcus*** |  |  | 0.122 |  |  | 0.092 |  |  | 0.199 |
| T1:first tertile (reference) | 1 |  |  | 1 |  |  | 1 |  |  |
| T2:second tertile | 1.742 | 0.311-9.749 | 0.528 | 1.779 | 0.299-10.568 | 0.526 | 0.464 | 0.023-9.275 | 0.615 |
| T3:third tertile | 7.656 | 0.922-63.580 | 0.059 | 9.063 | 1.012-81.153 | 0.049 | 6.503 | 0.253-167.245 | 0.258 |
|  |  |  |  |  |  |  |  |  |  |
| ***Klebsiella*** |  |  | 0.115 |  |  | 0.198 |  |  | 0.218 |
| T1:first tertile (reference) | 1 |  |  | 1 |  |  | 1 |  |  |
| T2:second tertile | 3.764 | 1.076-13.171 | 0.038 | 3.286 | 0.898-12.029 | 0.072 | 6.331 | 0.593-67.637 | 0.127 |
| T3:third tertile | 1.521 | 0.430-5.377 | 0.515 | 1.524 | 0.415-5.590 | 0.526 | 0.958 | 0.117-7.873 | 0.968 |
|  |  |  |  |  |  |  |  |  |  |
| ***Enterobacteriaceae*** |  |  | 0.116 |  |  | 0.169 |  |  | 0.035 |
| T1:first tertile (reference) | 1 |  |  | 1 |  |  | 1 |  |  |
| T2:second tertile | 1.358 | 0.357-5.167 | 0.654 | 1.273 | 0.317-5.113 | 0.734 | 3.680 | 0.439-30.836 | 0.230 |
| T3:third tertile | 3.978 | 0.979-16.160 | 0.054 | 3.503 | 0.834-14.725 | 0.087 | 59.721 | 2.677-1332.158 | 0.010 |
|  |  |  |  |  |  |  |  |  |  |
| ***Lactobacillales*** |  |  | 0.474 |  |  | 0.364 |  |  | 0.666 |
| T1:first tertile (reference) | 1 |  |  | 1 |  |  | 1 |  |  |
| T2:second tertile | 1.183 | 0.207-6.746 | 0.850 | 0.909 | 0.149-5.547 | 0.918 | 2.541 | 0.100-64.853 | 0.573 |
| T3:third tertile | 0.441 | 0.057-3.426 | 0.433 | 0.300 | 0.035-2.560 | 0.271 | 0.968 | 0.027-34.326 | 0.986 |
| Note: We divided the abundance of GM into trisection and used the first third as the reference category indicator. model 1, unadjusted; model 2, adjusted for age; model 3, adjusted for age, NIHSS score, stroke recurrence, Hcy, LA and brain atrophy. GM, gut microbiota; PSCI, post-stroke cognitive impairment; OR, odds ratio; 95% CI, 95% confidence interval. | | | | | | | | | |