

Microbiota-based Signature of Gingivitis Treatments: A Randomized Study

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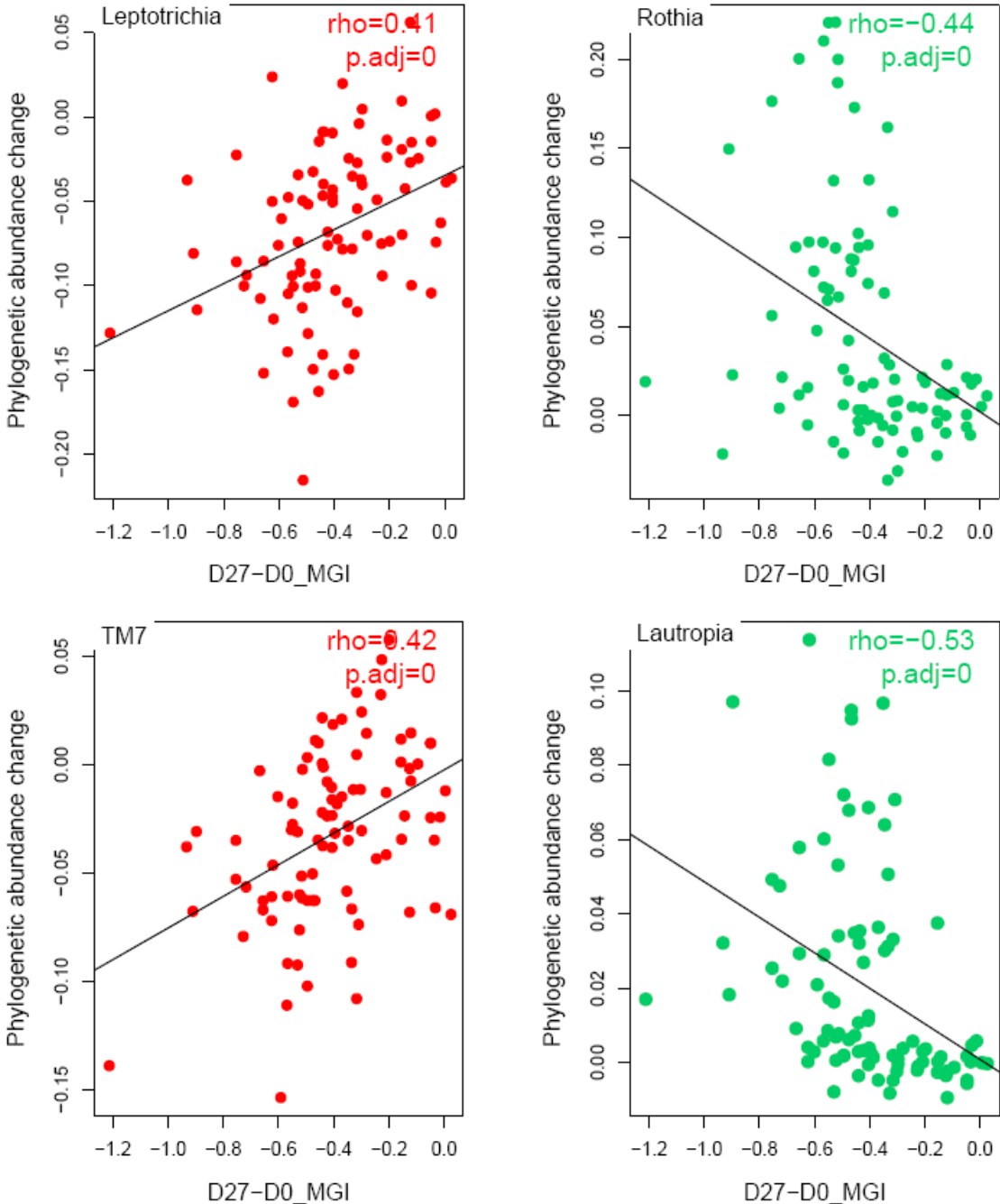
E-mail address: xujian@qibebt.ac.cn or li.ru.5@pg.com

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Supplementary Information

Supplementary figures

Figure S1



25 **Figure S1. Significant correlation between short-term changes in plaque bacteria from Baseline to Day 11, and mean MGI changes from Baseline to Day 27.**

Figure S2

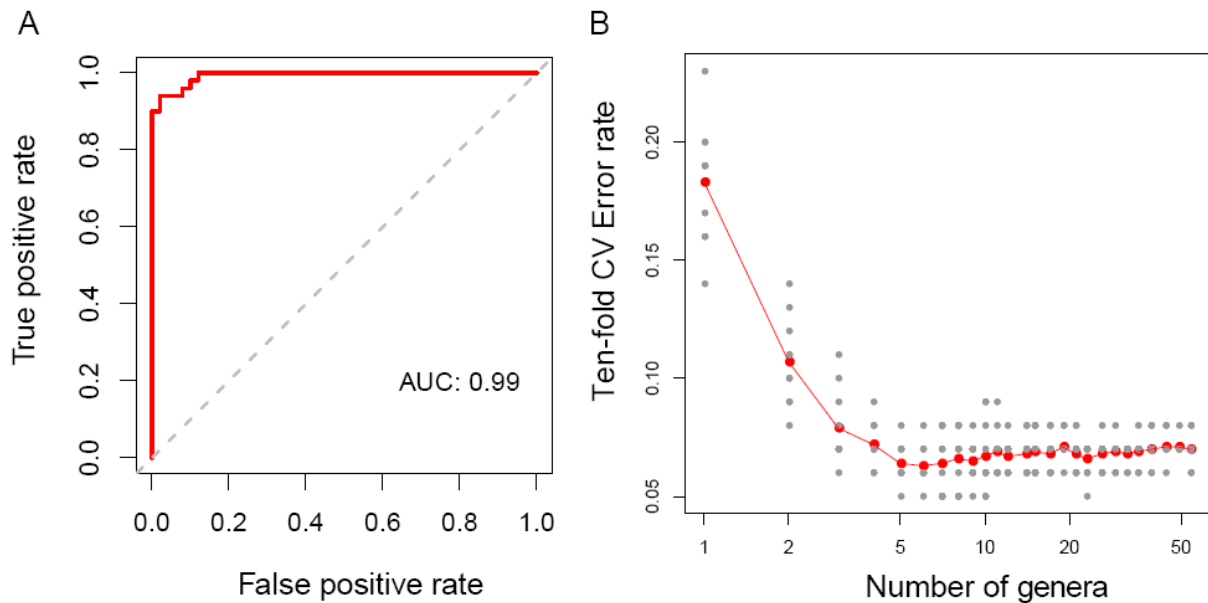


Figure S2. Performance of the Random Forests model that was used to define “relative recovery of microbiota” during a given anti-gingivitis treatment. Using the changes in plaque microbiota following dental scaling as a reference, the Random Forests model was trained using a data set of 50 subjects with gingivitis and post-dental-scaling healthy status from a previous study. **(A)** The discriminatory power of this model was calculated as the area under the ROC curve (AUC): 0.99. **(B)** Relationship between the number of variables and the model performance (ten-fold CV error rate).

Figure S3

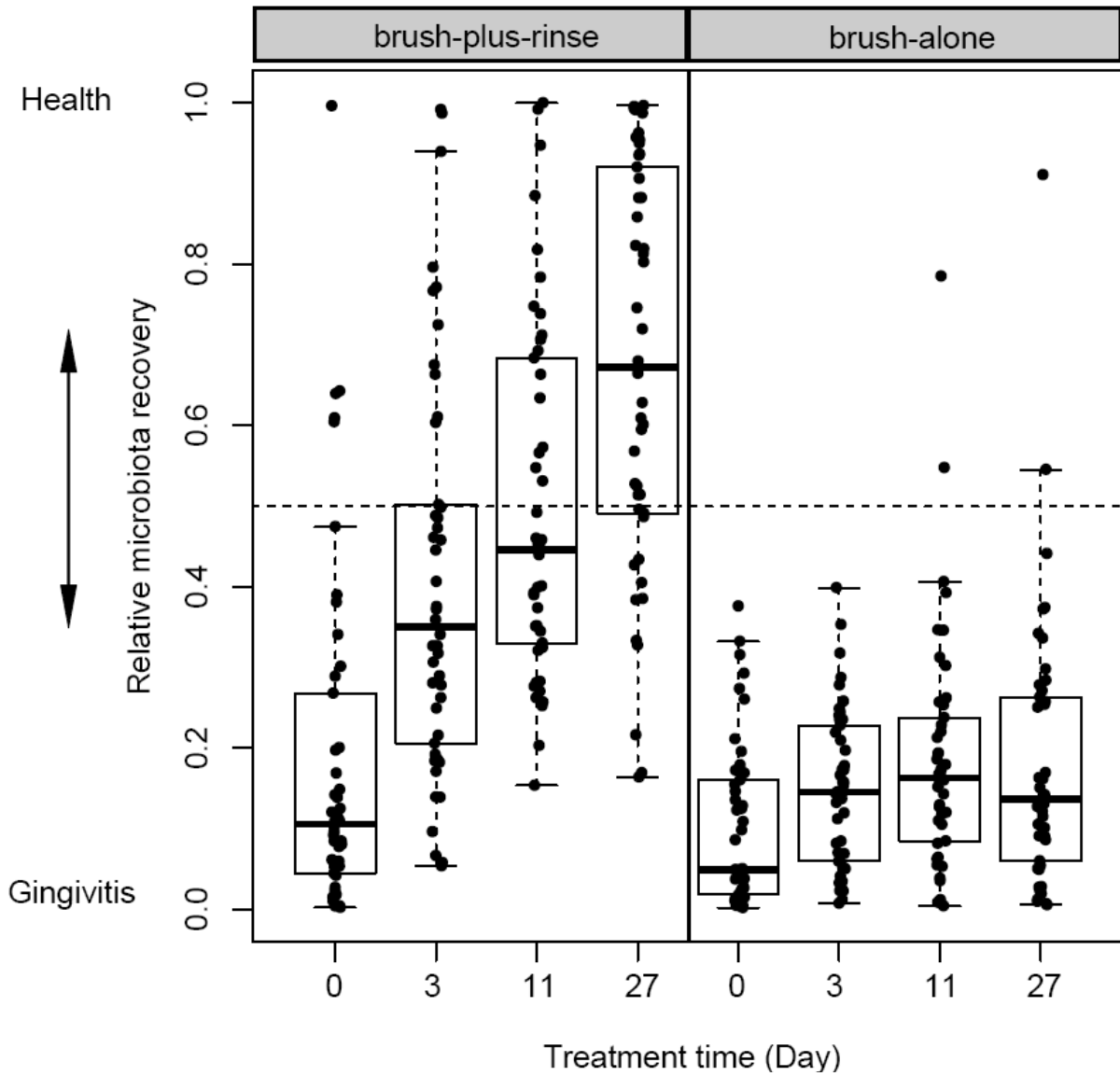


Figure S3. Relative microbiota recovery defined by 15 genera identified in the MiG15 model. Stratification of subjects in the brush-plus-rinse group and the brush-alone group, based on the top 15 genera previously noted as “MiG15”. MiG15, a microbial index of gingivitis, was calculated from the relative abundance of 15 bacterial genera (*Rothia*, *Haemophilus*, *Prevotella*, *Leptotrichia*, *Fusobacterium*, *Selenomonas*, *uncultured Lachnospiraceae*, *TM7*, *Tannerella*, *Peptococcus*, *Peptostreptococcus*, *Catonella*, *Treponema*, *Solobacterium* and *unclassified Bacteroidaceae*)¹.

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Reference

- 1 Huang, S. *et al.* Predictive modeling of gingivitis severity and susceptibility via oral microbiota. *ISME J* **8**, 1768-1780 (2014).