Article title: Oral Microbiota and *Porphyromonas Gingivalis* Kgp Genotypes Altered in Parkinson's Disease with Mild Cognitive Impairment

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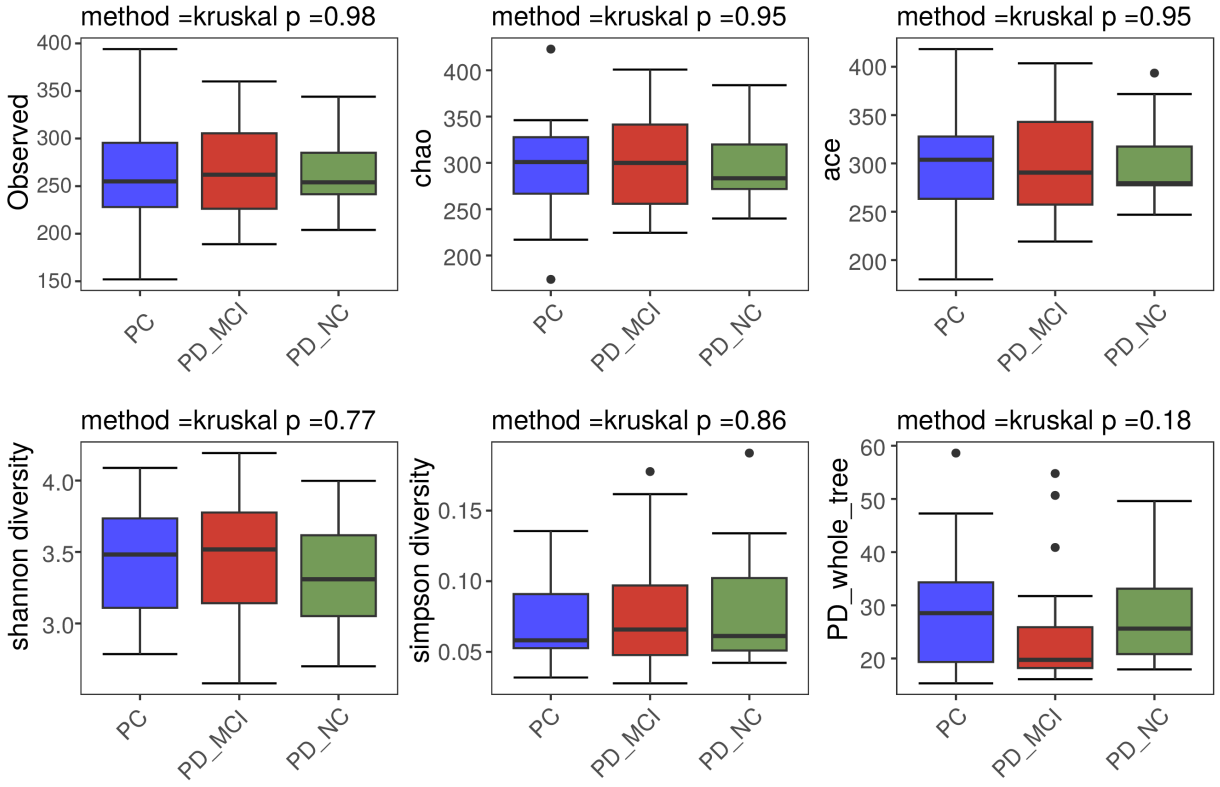
Methods

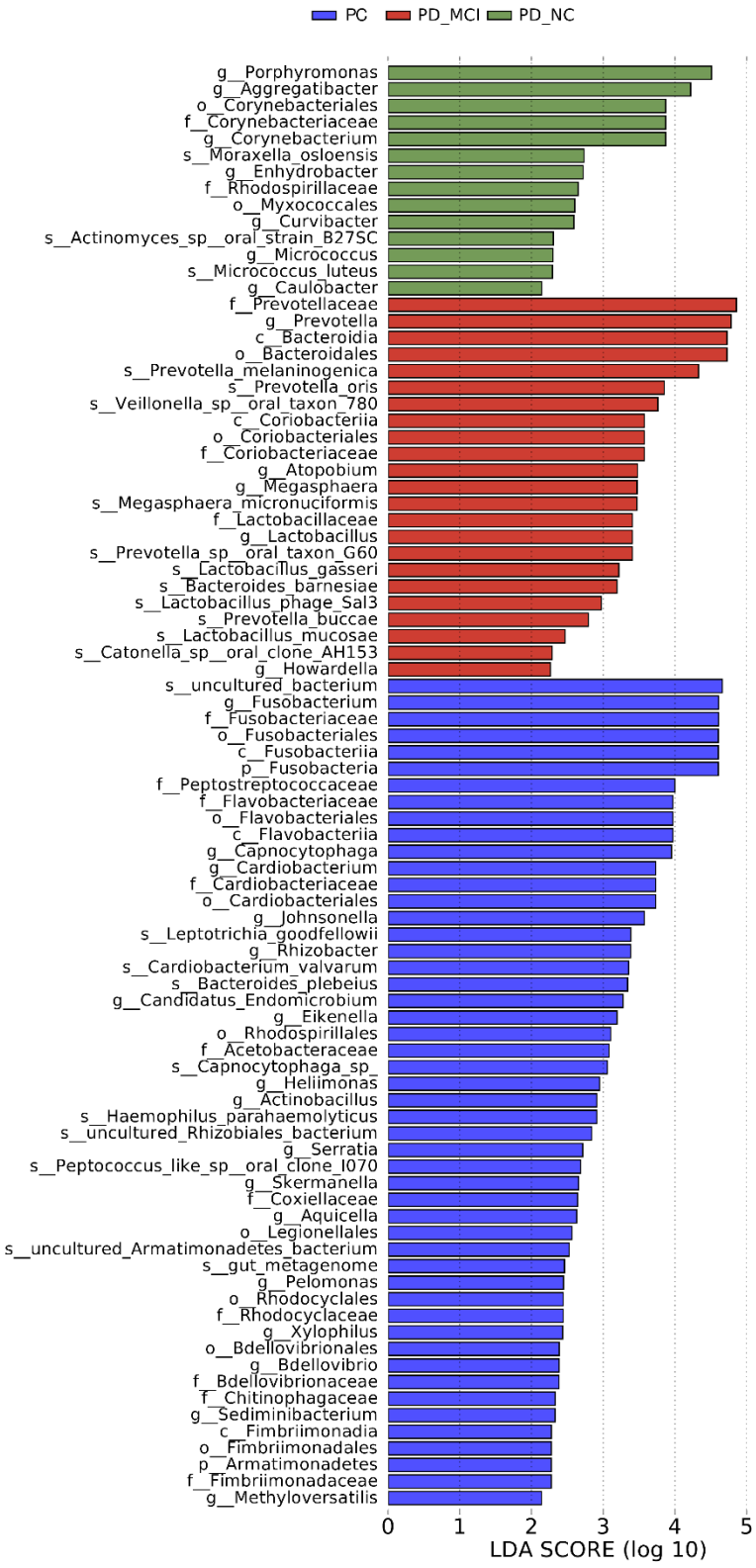
Exclusion criteria

Patients with situation as follows were excluded: (1) secondary Parkinsonism, (2) history of an unstable medical diseases or other diseases interfering with cognitive function evaluation, (3) history of a neurological or psychiatric illness, (4) PD intracranial surgery treatment and deep brain stimulation(DBS) therapy, (5) serious chronic illnesses (e.g., hyperlipidemia, diabetes, hyperhomocysteinemia, heart failure, gastrointestinal, liver cirrhosis, malignancy, or hematological or autoimmune diseases), (6) intake of probiotics or antibiotics within last three months, and (7) extensive periodontal therapy within the last month.

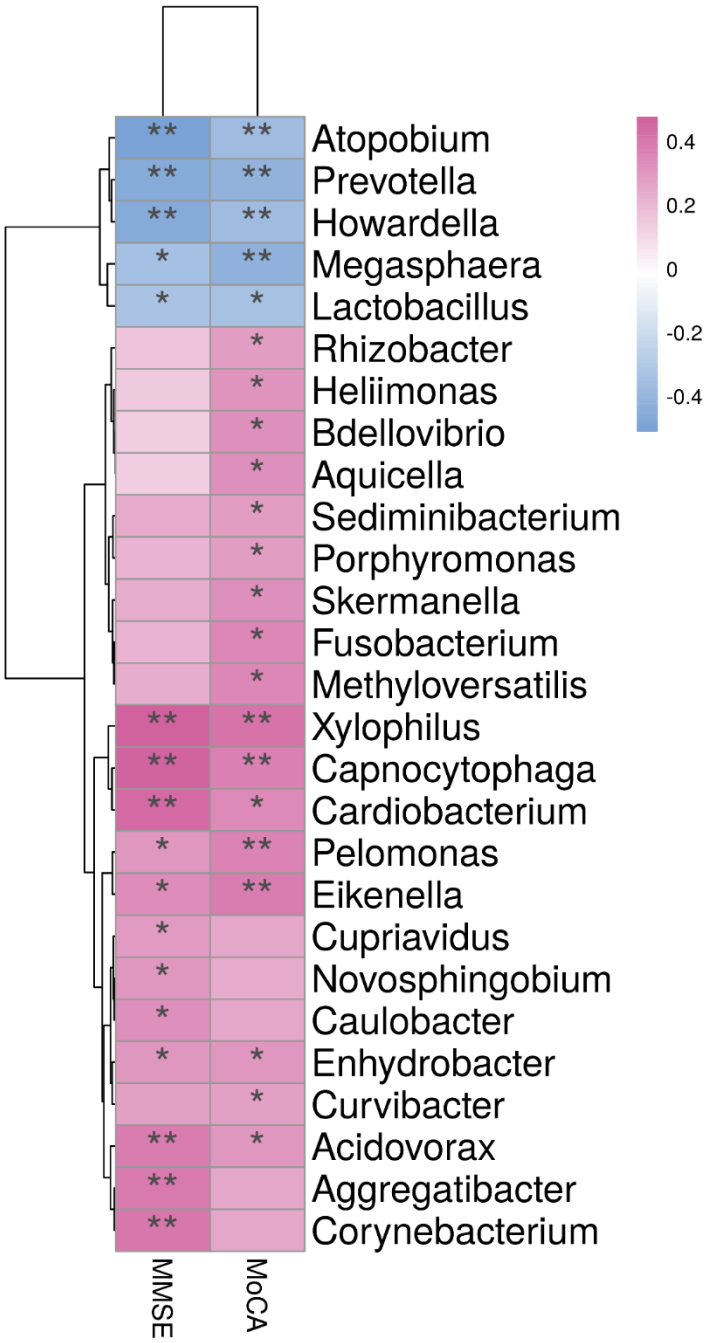
The exclusion criteria of heathy controls were as follows: serious chronic illnesses; history of an unstable medical diseases or other diseases interfering with cognitive function evaluation; history of a neurological or psychiatric illness; intake of probiotics or antibiotics within last three months, extensive periodontal therapy within the last month, and failure to cooperate and complete the trial.



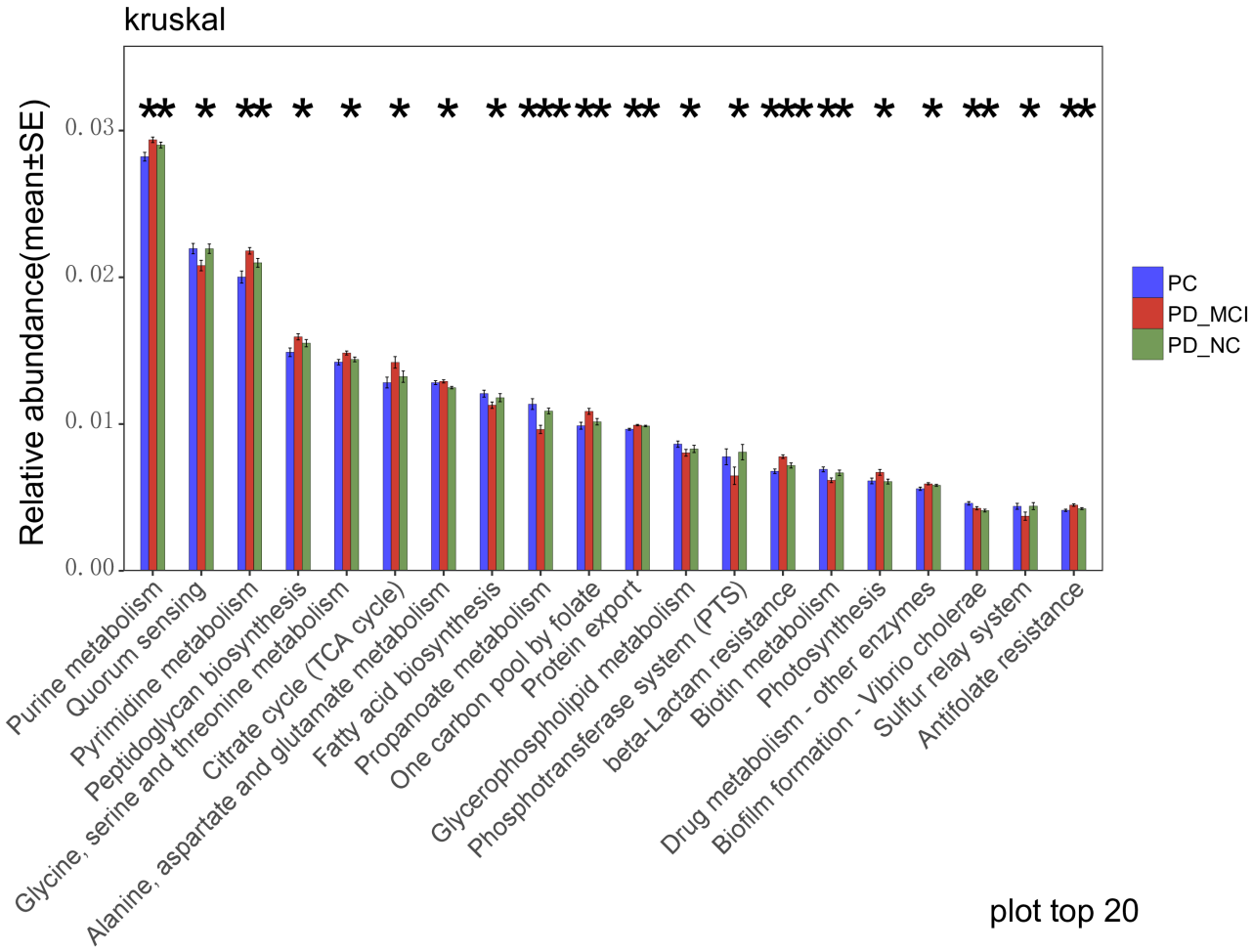
Suppl. Figure 1 The alpha-diversity indices of the oral microbiome in the PD-MCI, PD-NC, and PC group. Box plots depict differences in the oral microbiome diversity indices among three groups according to the Observed, Chao 1, ACE, PD whole tree, Shannon and Simpson index based on the OTU counts. Each box plot represents the median, interquartile range, minimum, and maximum values. No significant differences of the mean community alpha-diversity indexes were found among the three groups.



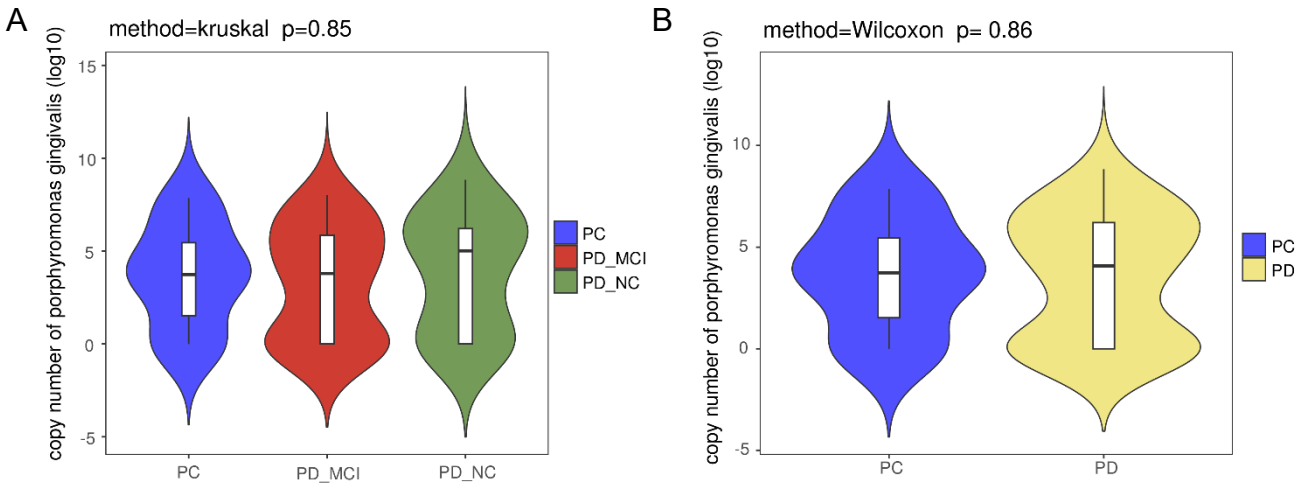
Suppl. Figure 2 The Alteration in the taxa between PD-MCI, PD-NC and PC groups**.** Linear discriminant analysis (LDA) with effect size (LEfSe) is commonly employed to identify the presence and effect size of region-specific OTUs among different groups. Base on the LDA LEfSe, significant differences were observed in oral microbiota among the PD-MCI, PD-NC and PC groups. The relative abundance of genera *Prevotella*, *Lactobacillus*, *Megasphaera*, *Atopobium*, *Howardella* was higher in the PD-MCI group.



Suppl. Figure 3 Correlation between fecal microbiota and MMSE, MoCA scores. The abundances of *Prevotella*, *Lactobacillus*, *Atopobium* and *Howardella* were negatively correlated with MMSE and MoCA scores. *P<0.05; **P<0.01.



Suppl. Figure 4. Significant KEGG pathways at level 3 for the fecal microbiome of the PD-MCI, PD-NC and PC groups. PICRUSt based on closed-reference OTU was used to predict the abundances of functional categories in the KEGG ortholog (KO). A plot of top 20 KOs identified with significantly different abundances in the oral microbiota among the three groups (FDR, $P < 0.05$) was made. Purine metabolism, pyrimidine metabolism, peptidoglycan biosynthesis, citrate cycle (TCA cycle), amino acid metabolism (glycine, serine, threonine, alanine, aspartate and glutamate), one carbon pool by folate, protein export, beta-Lactam resistance, photosynthesis and antifolate resistance in the level 3 KEGG pathway were higher in the oral microbiome of the PD-MCI group. Quorum sensing, fatty acid biosynthesis, propanoate metabolism, biotin metabolism, sulfur relay system were lower in the oral microbiome of the PD-MCI group. *P<0.05; **P<0.01.



Suppl. Figure 5 Comparison of the copy number of *Porphyromonas gingivalis* DNA in gingival crevicular fluid among different groups. **(A)** The copy number of *Porphyromonas gingivalis* DNA among PD-MCI, PD-NC and PC (P=0.85). **(B)** The copy number of *Porphyromonas gingivalis* DNA between PC and PD (PD-MCI+PD-NC) groups (P=0.863).