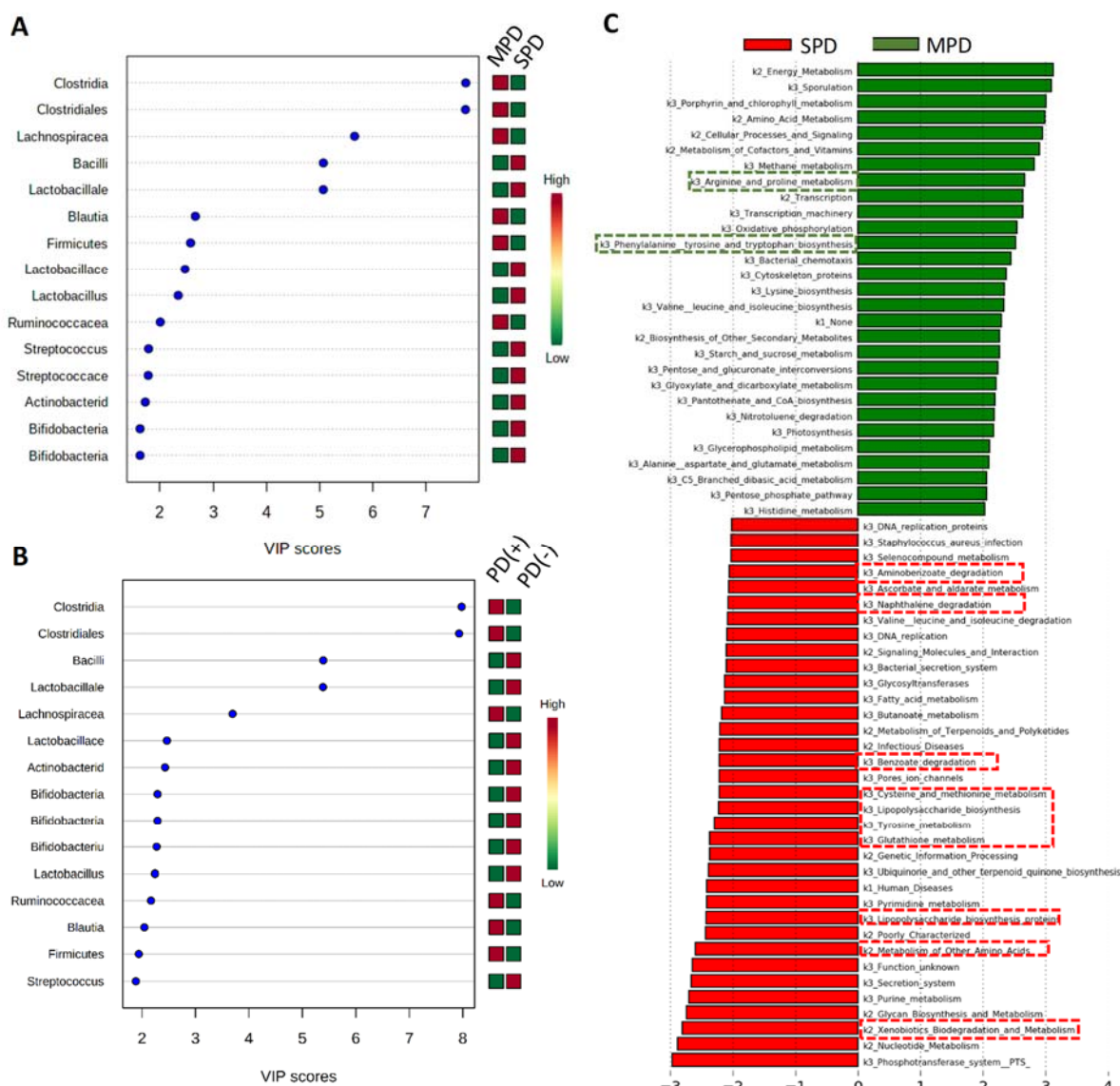


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Supporting Data

2 **Fig. S1** Functional predictions for the faecal microbiome of PD patients. 2D Score plot
 3 of PLS-DA analysis between (A) Mild Parkinson's disease (MPD) and Severe Parkinson's
 4 disease (SPD) groups and (B) between urolithin production (+) vs non-production (-) in
 5 PD patients. (C) LDA score (log 10) generated by LEfSe analysis shows potential
 6 microbial biomarkers of MPD (1–2.5) and SPD (3–5) patients based on the Hoehn &
 7 Yahr stage. The green and red dashed lines highlight the biomarkers discussed in the
 8 text.



9

10 **Fig. S2** Differences in the faecal microbiome between urolithin producers (+) and
 11 urolithin non-producers (+) in healthy controls (HC). (A) LDA score (log 10) and (B)
 12 cladogram generated by LEfSe analysis show potential microbial biomarkers of
 13 urolithin production (+) vs non-production (-) in HC volunteers.

