

Supplementary Material

Fig. S1 - Distribution and comparison of dominant fungi phyla along the transect. a) Dominant fungal phyla between the nearest and furthest sampling points. b) circos plot showing the taxonomic distribution of abundant taxa at the family level. P1, P3, P4, P5, P6: points spaced 20 cm apart; P7, P8, P9, P10: points spaced 1 m apart; P11, P12, P13, P14: points spaced 10 m apart; P15, P16, P17: points spaced 25 m apart. The width of the bars indicates the relative abundance of each family.

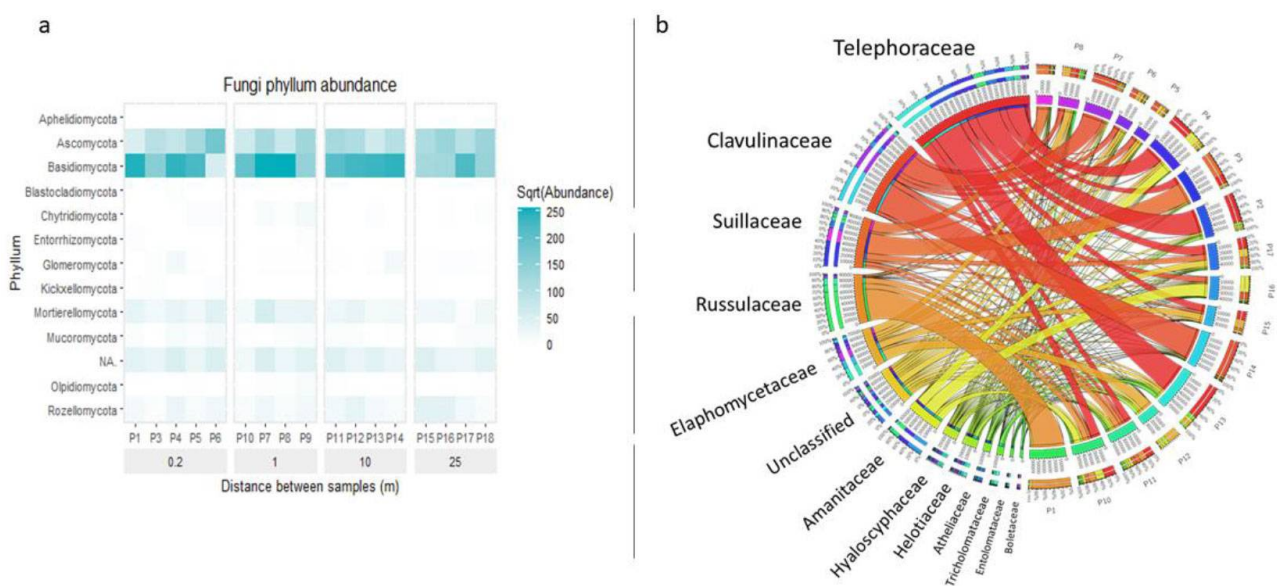


Fig. S2 - Rank-abundance graphs for fungal communities within a transect, with 18 samples separated (a) 20 cm, (b) 1 m, (c) 10 m, and (d) 25 m each, in a remnant of *Pinus pseudostrabus* var. *coatepecensis*.

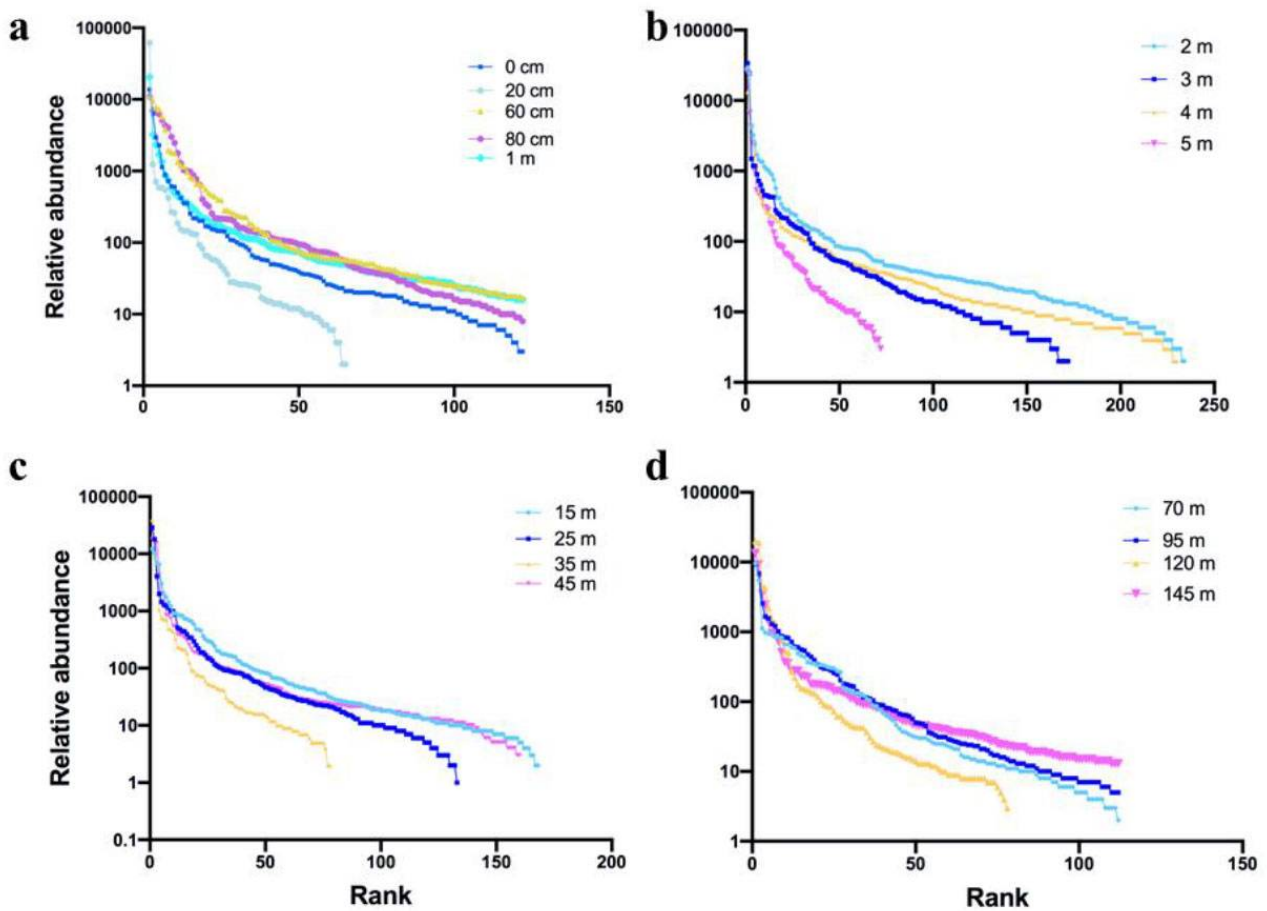


Fig. S3 - Fungal β -diversity values between samples along the transect (145 m). The turnover (β -sim, gray bars) plus the nestedness component (β nes, black bars) equals to Sørensen total dissimilarity index (β sor).

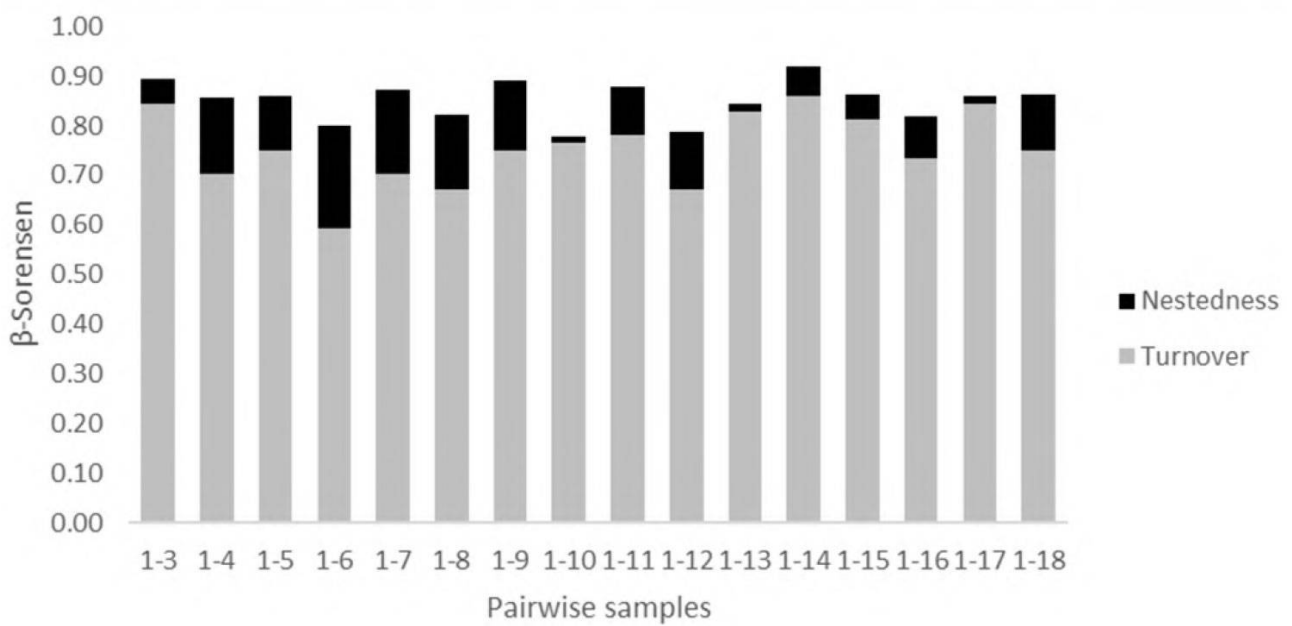


Fig. S4 - Distribution and comparison of dominant bacterial phyla along the transect. a) Dominant bacterial phyla between the nearest and furthest sampling points. b) circos plot showing the taxonomic distribution of abundant taxa at the family level (b). P1, P3, P4, P5, P6: points spaced 20 cm apart; P7, P8, P9, P10: points spaced 1 m apart; P11, P12, P13, P14: points spaced 10 m apart; P15, P16, P17: points spaced 25 m apart. The width of the bars indicates the relative abundance of each family.

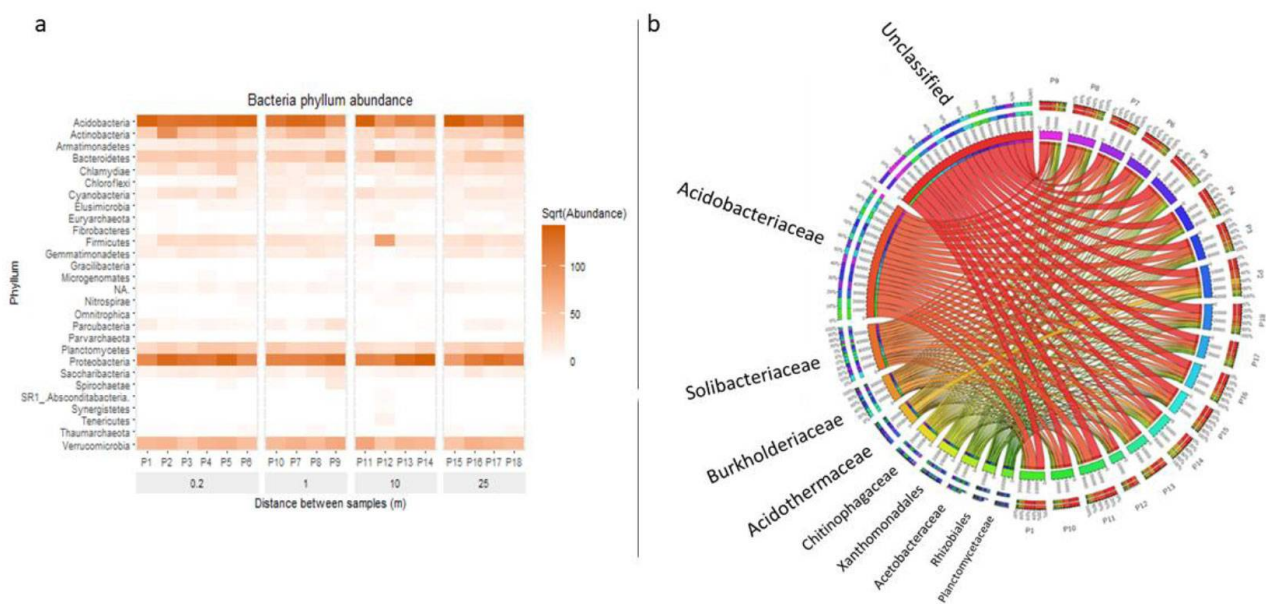


Fig. S5 - Rank-abundance graphs for bacterial communities within a transect with 18 samples separated (a) 20 cm, (b) 1 m, (c) 10 m and (d) 25 m each, in a remnant of *P. pseudostrobus* var. *coatepecensis*.

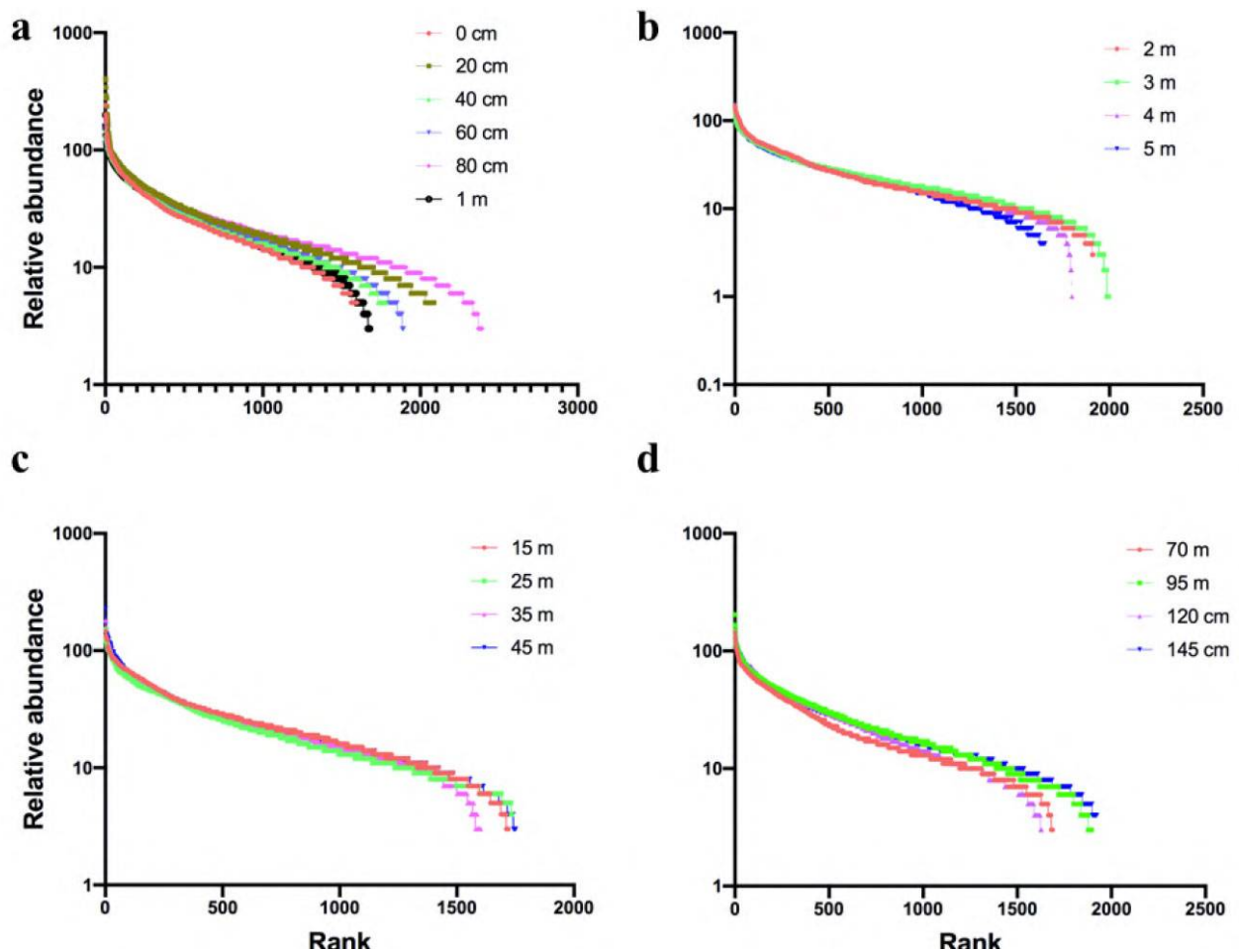


Fig. S6 - Bacterial β -diversity values between samples along the transect (145 m). The turnover (β -sim, gray bars) plus the nestedness component (β nes, black bars) equals to Sørensen total dissimilarity index (β sor).

