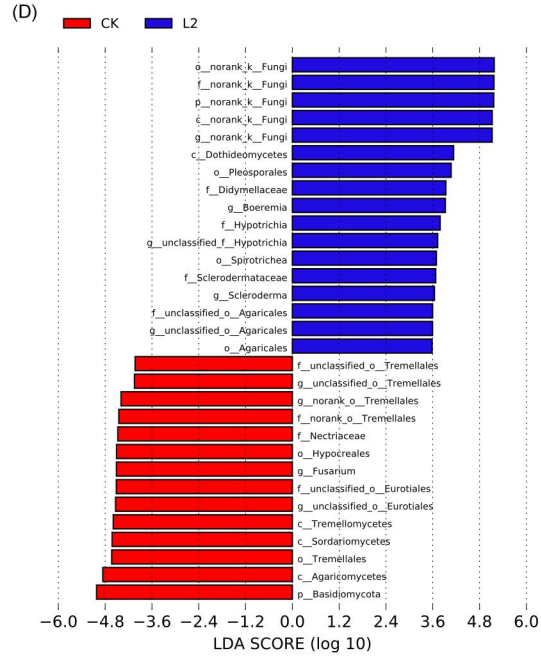
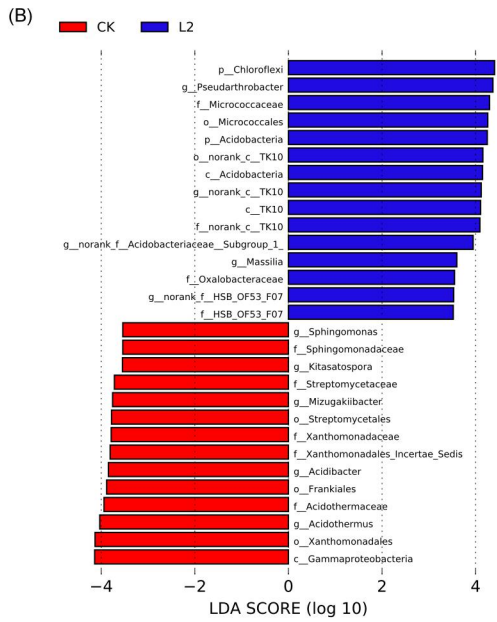
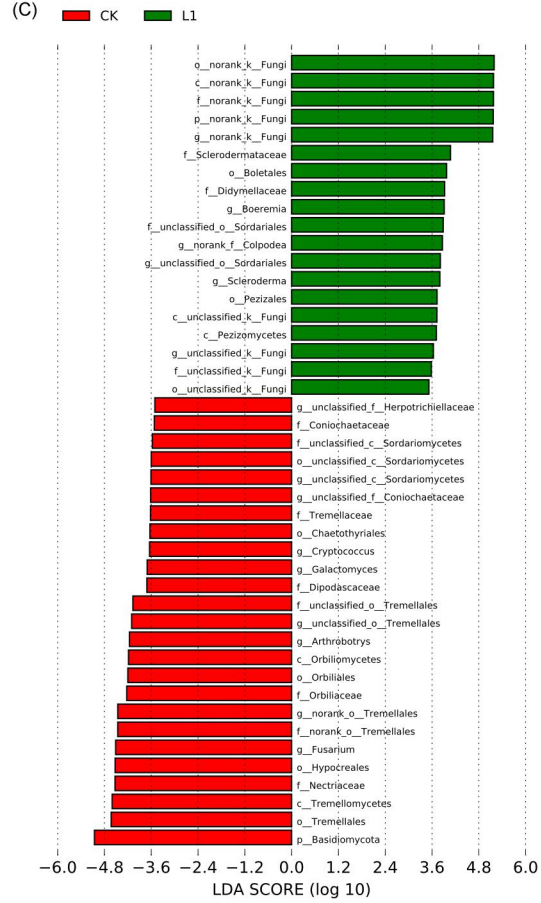
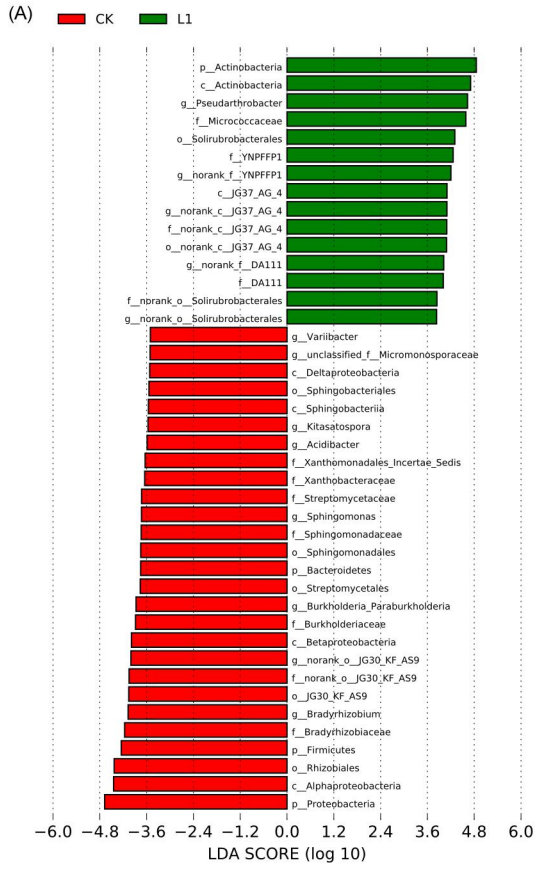
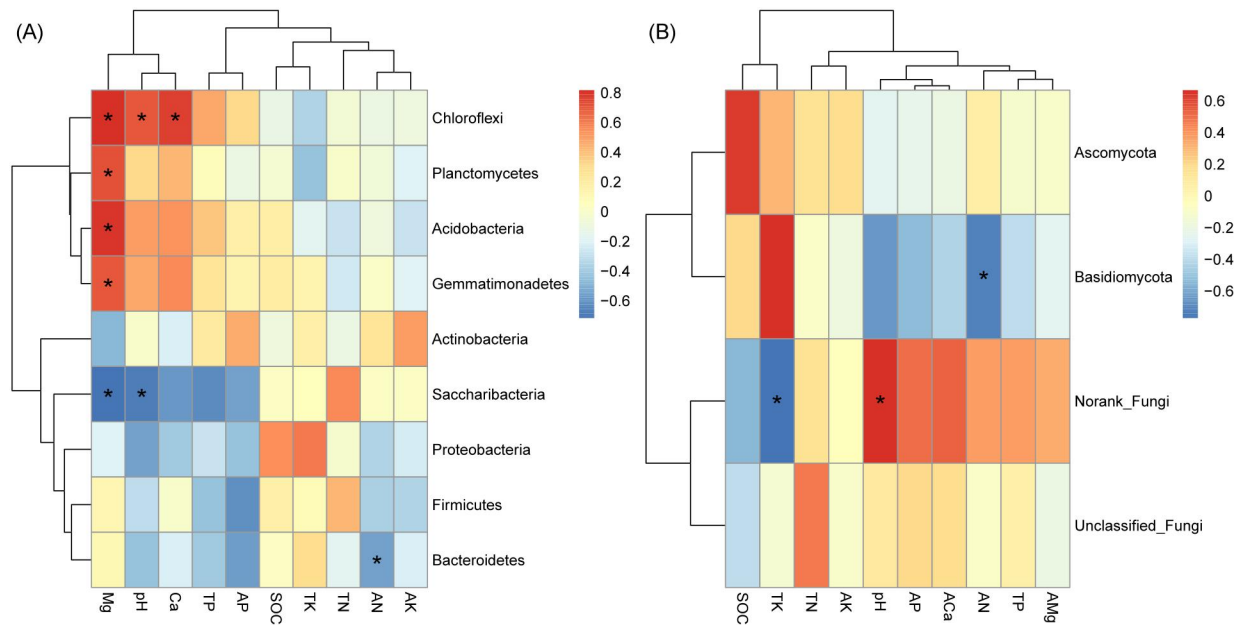


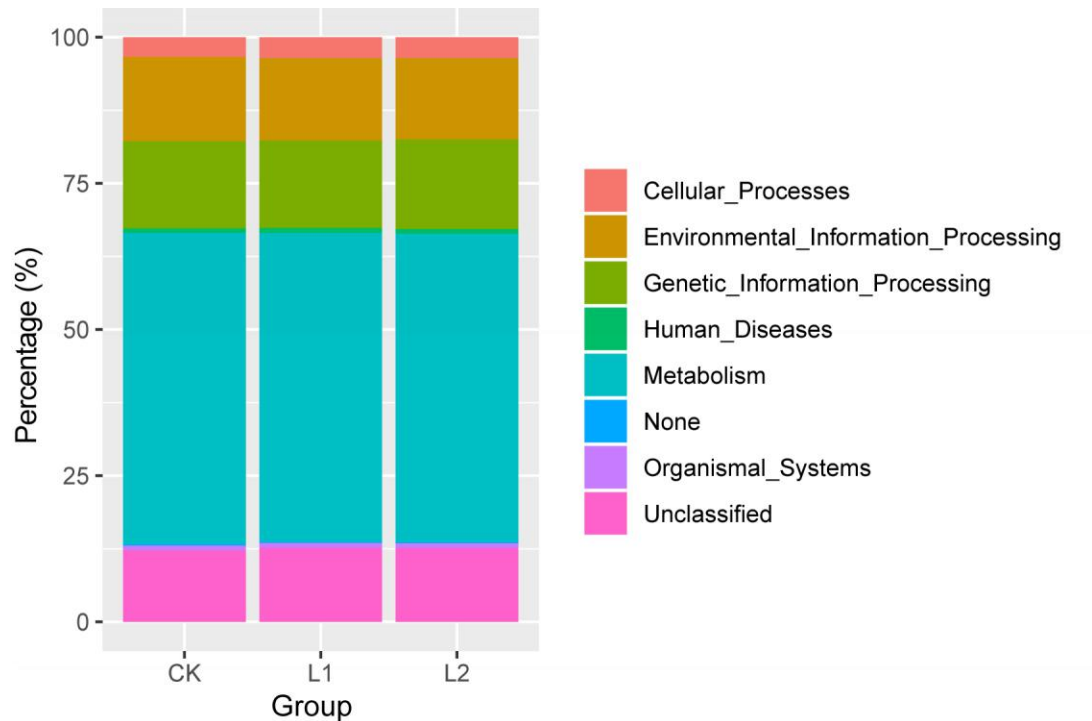
**Figure S1.** Rarefaction curves at an OTU threshold of 97% sequence similarity (A, B) and Venn diagrams (C, D) for soil samples taken derived from three sugarcane fields.



**Figure S2.** Linear discriminant analysis coupled with effect size measurements identifies the differentially abundant taxa between lime regimes: CK vs. L1 of bacteria (A), CK vs. L2 of bacteria (B), CK vs. L1 of fungal (C), CK vs. L1 of fungal (D). Lineages with LDA values higher than 3.5 are displayed.



**Figure S3.** Heat map showing Spearman correlation between soil properties and abundant bacterial (A) and fungal (B) phyla in three sugarcane fields. \* Shows the significance level at  $P < 0.05$ .



**Figure S4.** Bacteria functional composition at KEGG level 1 within three sugarcane fields. CK, NPK fertilization; L1, NPK fertilization plus lime for one year; L2, NPK fertilization plus lime for two years



**Figure S5.** Extended error bar graphs showing the significant difference of fungal functional guilds at level 1 within three sugarcane fields ( $p < 0.05$ , average proportion,  $n = 3$ ). The points explain differences within the "CK", "L1" and "L2" fields (red, green and blue bars, respectively), the values on the right-hand display the  $p$ -values derived from the Welch t-test. CK, NPK fertilization; L1, NPK fertilization plus lime for one year; L2, NPK fertilization plus lime for two years