

Additional File 15. Diversity of mxaF gene sequences retrieved from the heavy fractions of soils enriched with ¹³C methanol.

Relative abundance of taxa based on *mxaF* gene sequences retrieved from the assembled reads of the metagenomes produced from the heavy fractions of DNA extracted from Unplanted (Soil), pea rhizosphere (Pea) and wheat rhizosphere (Wheat) soil samples enriched with ¹³C methanol for 17 days (T2) in a DNA-SIP experiment. The number of containing *mxaF* sequences is displayed in brackets above the columns.