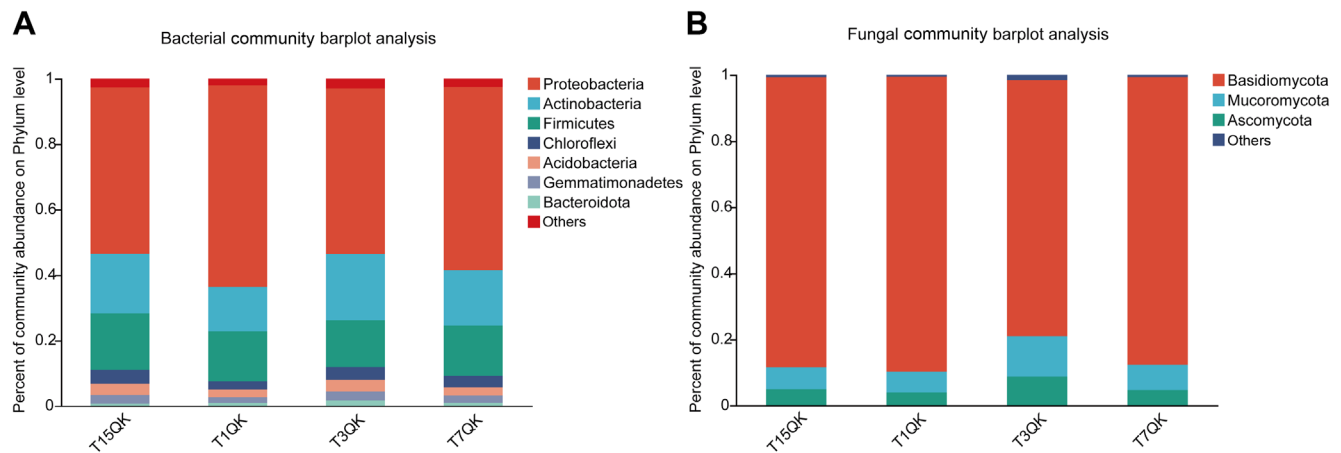


Supplementary Table 1. Sequencing statistics of the soil metagenomic libraries

Samples	Raw reads	Raw base (bp)	Clean reads	Clean base (bp)	No. of contigs	Contigs bases (bp)	No. of ORFs	Average length (bp)
T1QK_1	91,653,952	13,839,746,752	89,705,034	13,530,857,371	505,270	280,798,623	615,573	412.73
T1QK_2	89,160,956	13,463,304,356	87,462,474	13,193,368,365	425,595	233,778,034	514,904	410.72
T1QK_3	105,867,452	15,985,985,252	103,800,774	15,661,095,597	410,863	226,029,053	497,942	410.84
T3QK_1	103,999,428	15,703,913,628	101,964,596	15,382,246,653	714,651	404,336,597	875,393	415.6
T3QK_2	111,887,670	16,895,038,170	109,740,136	16,554,245,687	956,611	537,522,321	1,172,723	413.21
T3QK_3	98,906,986	14,934,954,886	97,130,662	14,653,390,670	678,730	391,264,495	838,952	419.98
T7QK_1	103,105,052	15,568,862,852	101,491,656	15,309,601,775	610,073	338,911,058	743,097	413.23
T7QK_2	102,232,174	15,437,058,274	100,900,044	15,221,957,865	633,952	355,600,048	775,603	415.04
T7QK_3	99,729,546	15,059,161,446	98,373,720	14,839,879,080	626,709	350,420,076	765,040	413.59
T15QK_1	99,089,282	14,962,481,582	97,681,340	14,736,819,335	536,729	297,227,399	654,689	410.06
T15QK_2	97,899,768	14,782,864,968	96,580,364	14,570,854,488	555,824	306,058,196	676,650	409.12
T15QK_3	96,071,564	14,506,806,164	94,747,370	14,294,286,784	602,115	334,077,141	735,629	411.05



Supplementary Fig. 1. Taxonomic information of bacterial (A) and fungal (B) species at the Phylum level based on metagenomic data. Low abundance phyla with less than 1% of the total sequences across all samples are grouped into “Other”.