

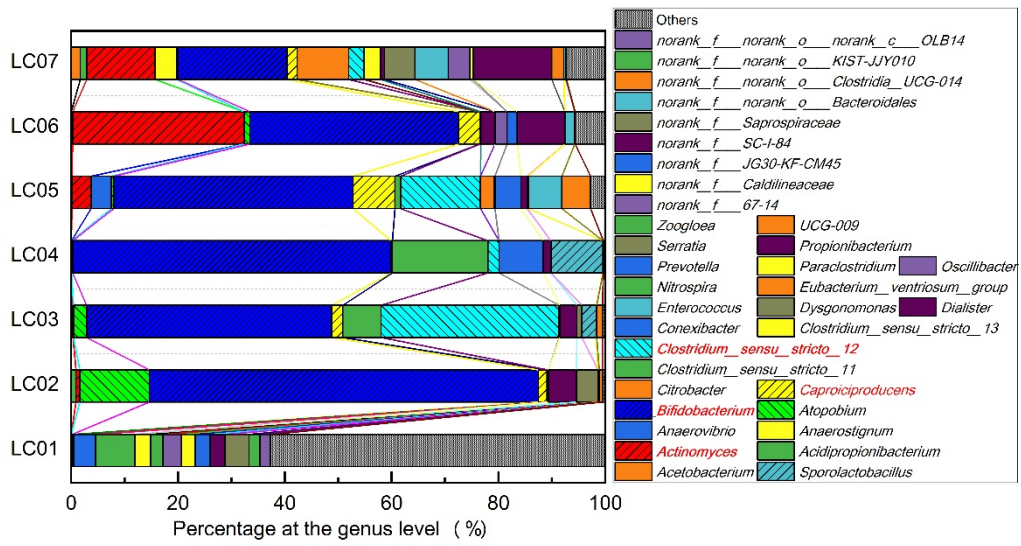
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2 Supporting Information

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4 S1 Illumina high-throughput sequencing

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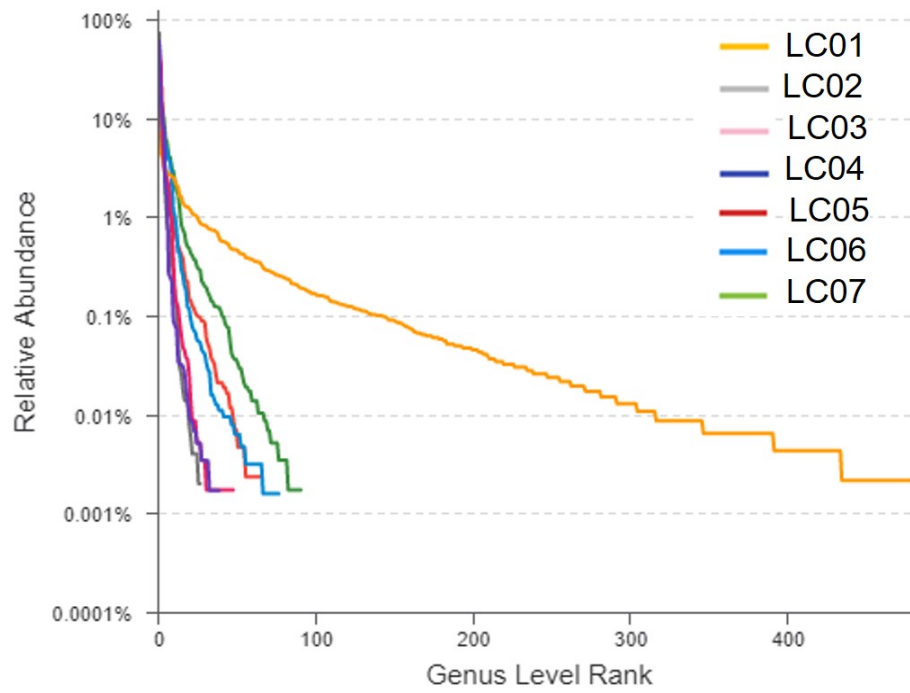
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7 Fig. S1 Microbial diversity of enriched bacteria at the genus level.

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12 Fig. S2 The Rank-Abundance curves of enriched bacteria.

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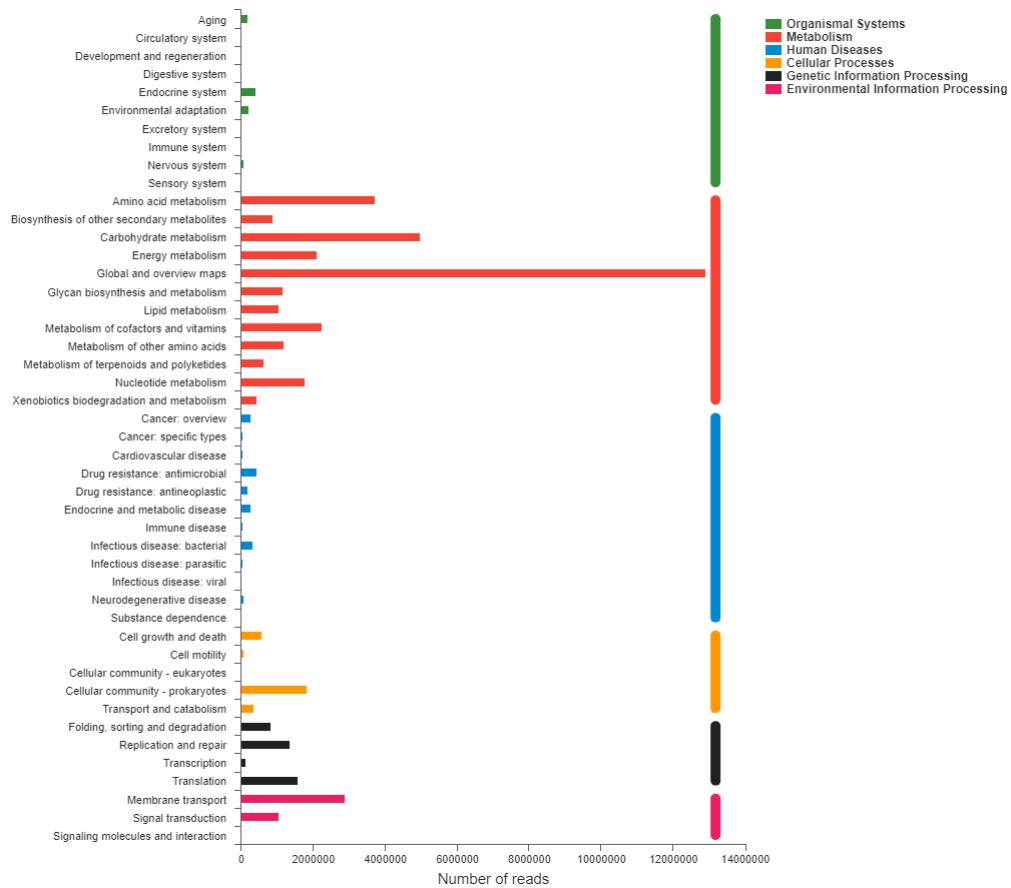
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16 S2 Metagenomic analysis of enriched LC06

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18 S2.1 Number of reads identified for cell function in enriched LC06

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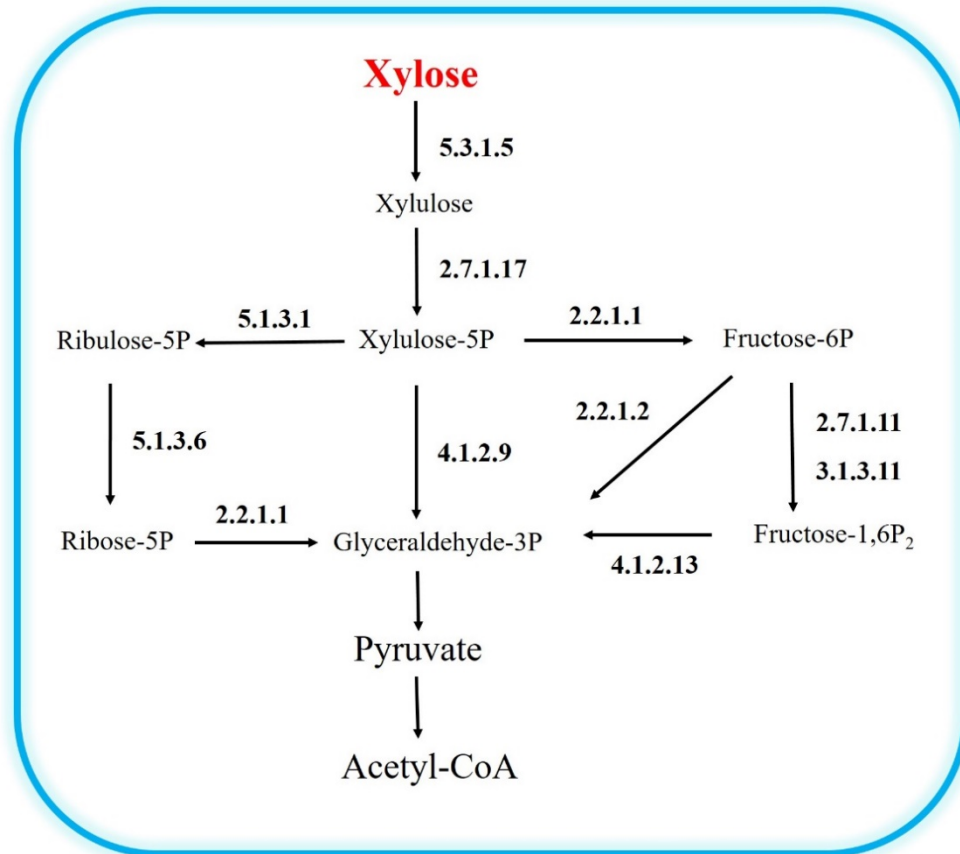
21 Fig. S3 Number of reads identified for cell function of enriched LC06.

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24 S2.2 Identified enzymes for xylose degradation in enriched LC06

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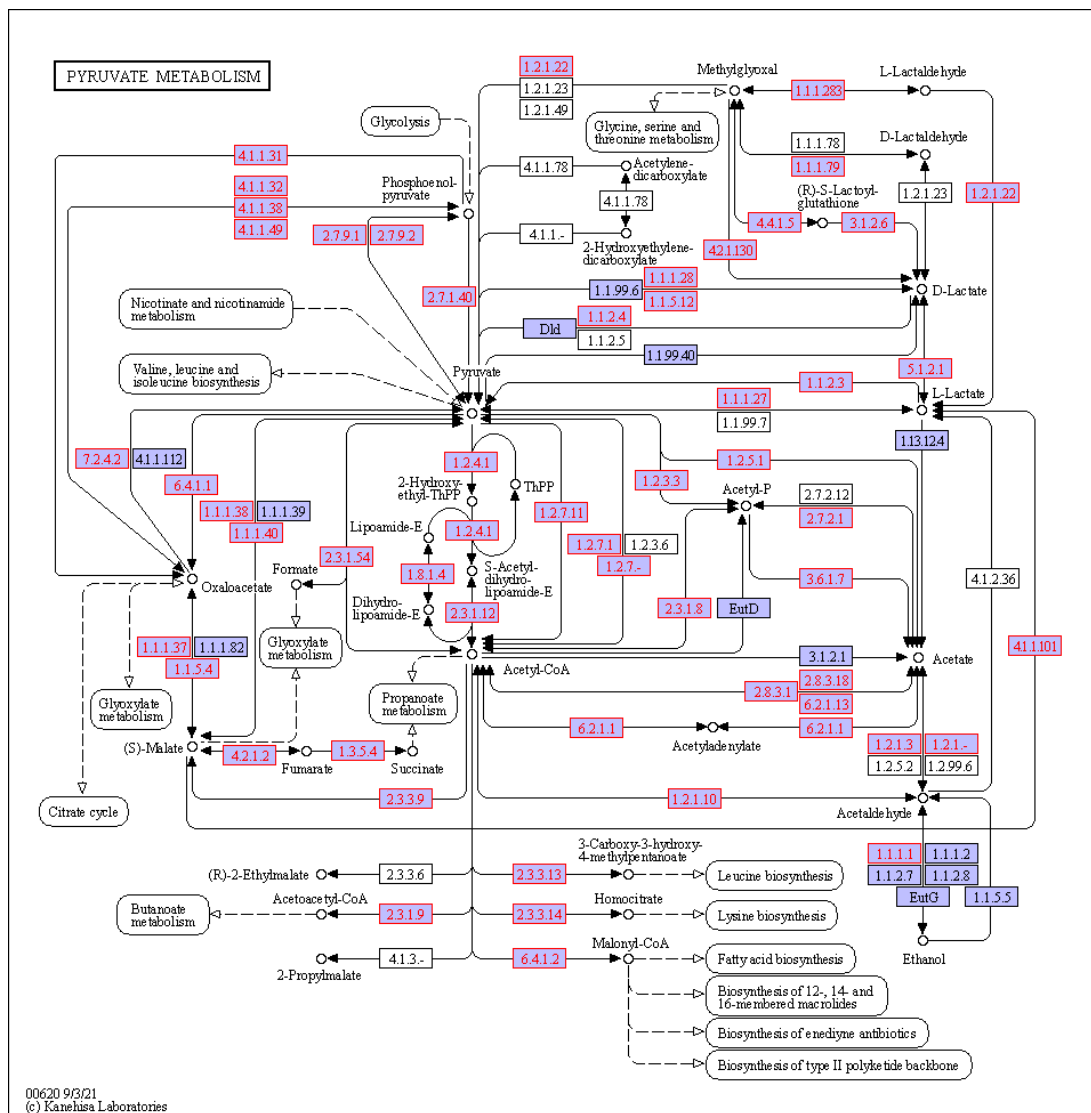


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27 Fig. S4 Identified enzymes for xylose degradation in enriched LC06.

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36 S2.3 Identified enzymes for ethanol degradation in Pentose and
 37 Glucuronate pathway
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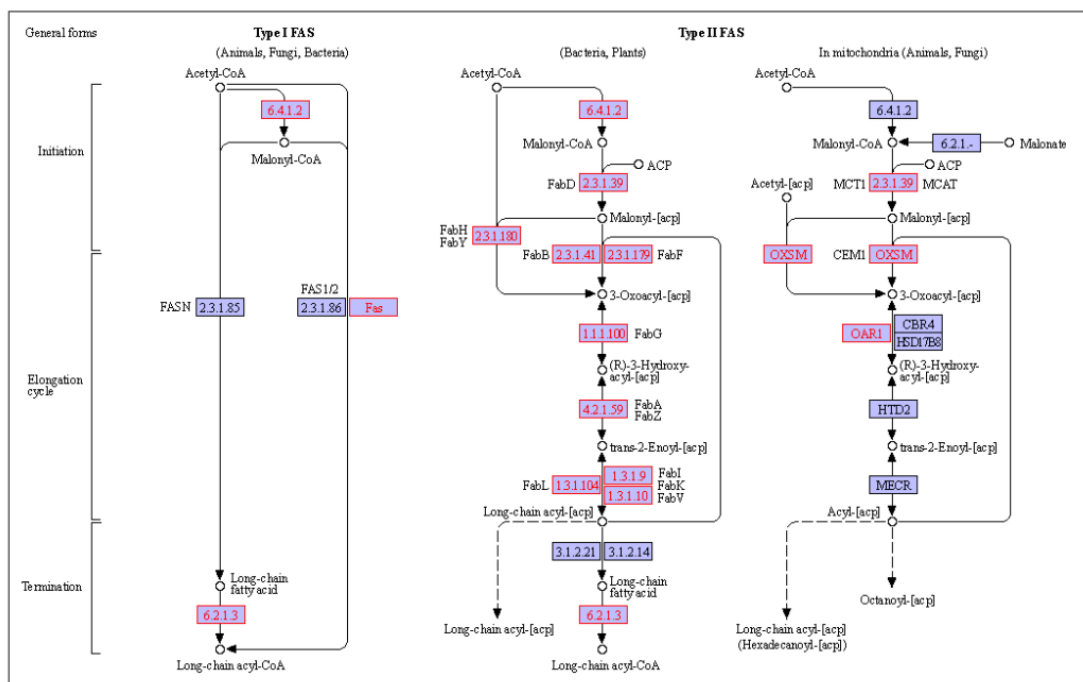


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 40 Fig. S7 Pyruvate metabolism in LC06 (Marked by red line).

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43 S2.4 Fatty acid metabolism pathway in enriched LC06

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46 **Fig. S8** Identified fatty acid metabolism pathway in enriched LC06 (Marked by red line).

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