

## **Supplementary Tables and Figures:**

### **Supplementary Tables:**

**Table S1:** The ANIb values and aligned percentage between strain LCG003 and other strains.

**Table S2:** The AAI values and aligned percentage between strain LCG003 and other strains.

**Table S3:** The DDH value and aligned percentage between strain LCG003 and other strains.

**Table S4:** The COG classification of strain LCG003 and other three *Aliiglaciecola* strains.

**Table S5:** The 12 genomic islands found in strain LCG003.

**Table S6:** The genes of transposases, integrases and/or recombinases predicted in strain LCG003.

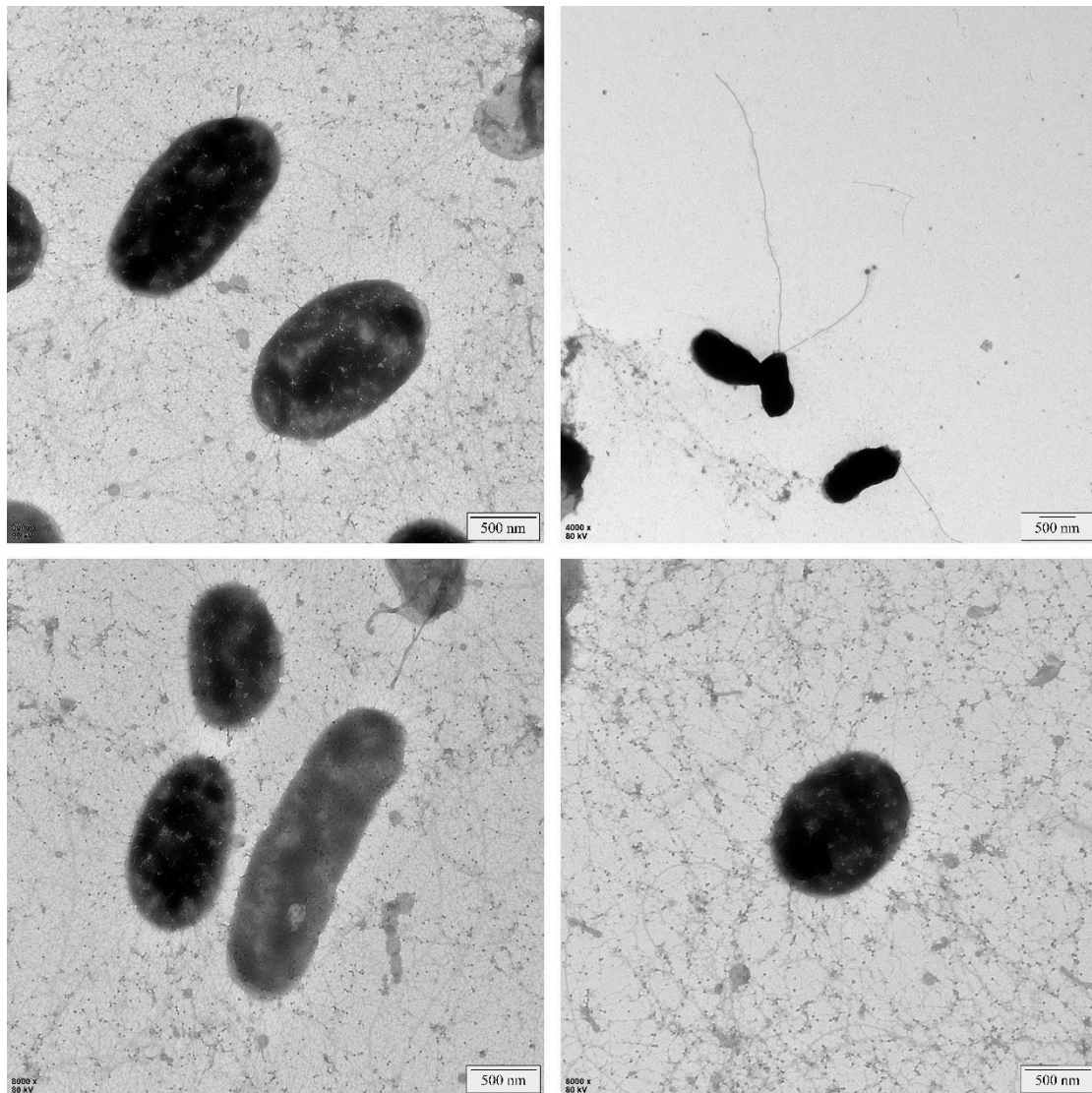
**Table S7:** The glycoside hydrolase genes predicted in strain LCG003.

**Table S8:** The extracellular peptidases predicted in strain LCG003.

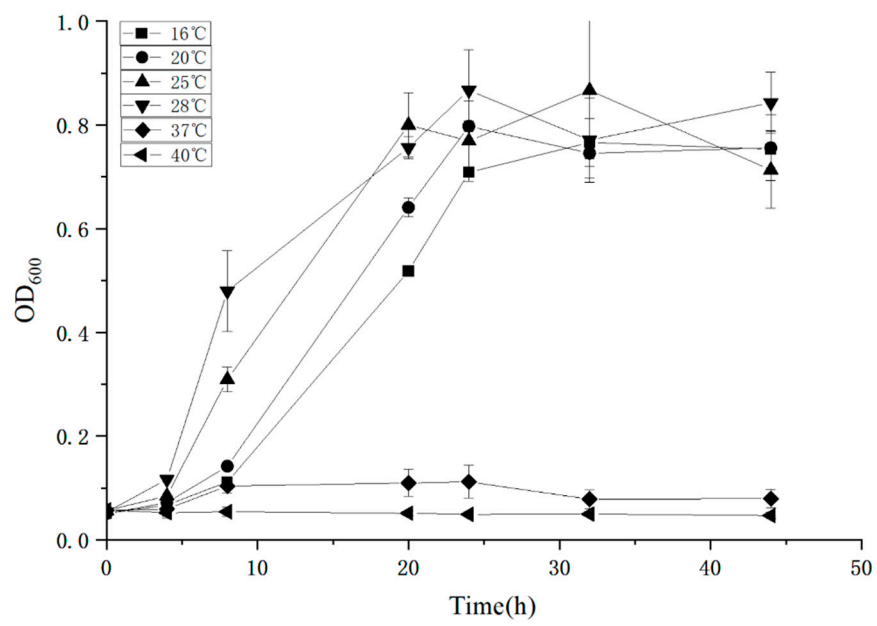
**Table S9:** The genes involved in degradation of 4-hydroxybenzoate and vanillate degradation.

**Supplementary Figures:**

**Figure S1:** The transmission electron micrograph of strain LCG003.



**Figure S2:** The growth curve of strain LCG003 under multiple temperatures.



**Figure S3:** The lignin utilization of strain LCG003. A and B are experimental groups, and C and D are control groups, indicating the counts of live bacteria of strain LCG003 calculated using the SYTO 9/PI live/dead bacteria double strain kit with ASW-lignin medium for 0 and 7 days, respectively. Error bar indicate each sample was with three independent biological replicates. Asterisks indicate t-test significant differences (NS, no significant; \*, P value < 0.05; \*\*, P value < 0.01; \*\*\*, P value < 0.001; \*\*\*\*, P value < 0.0001).

