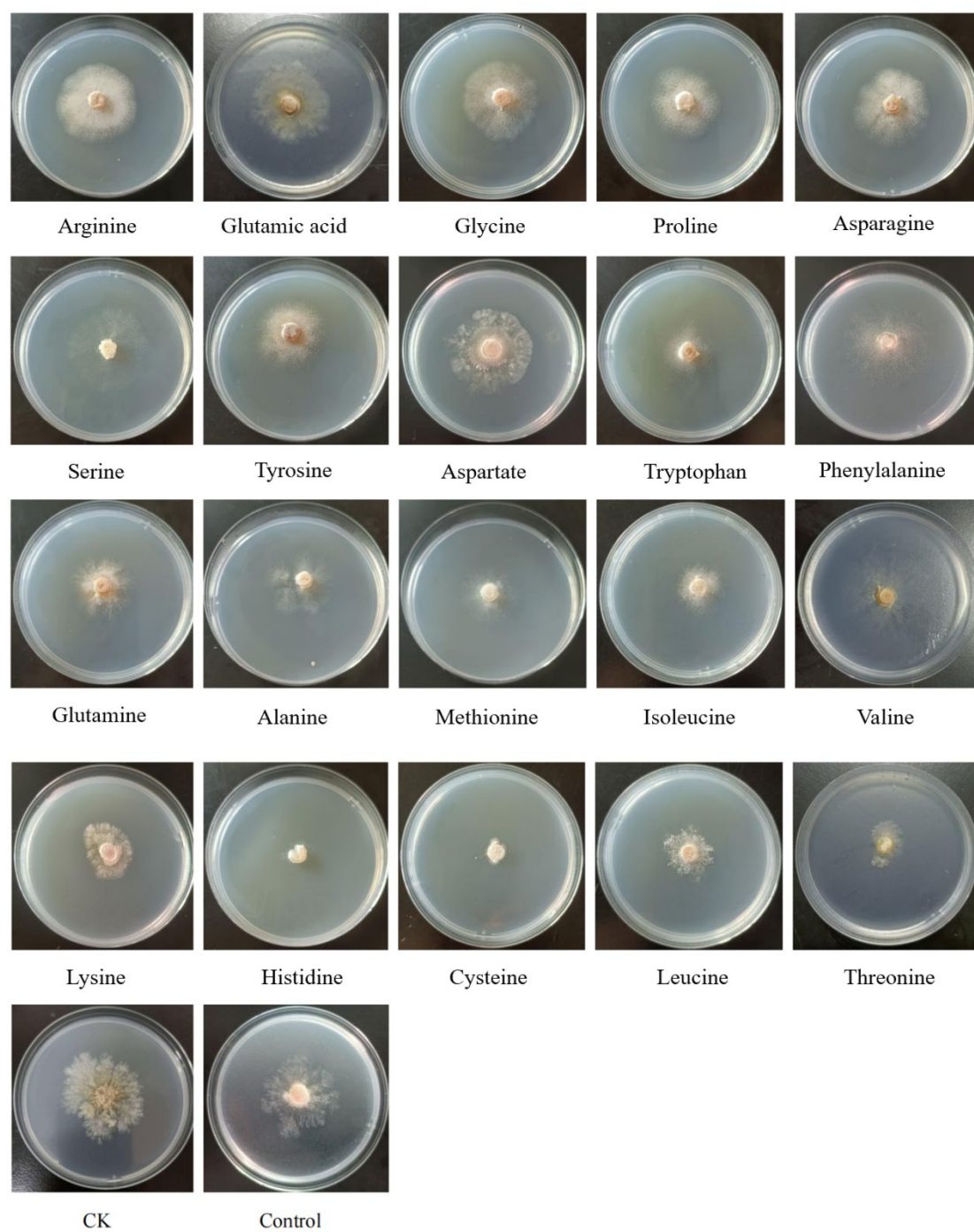


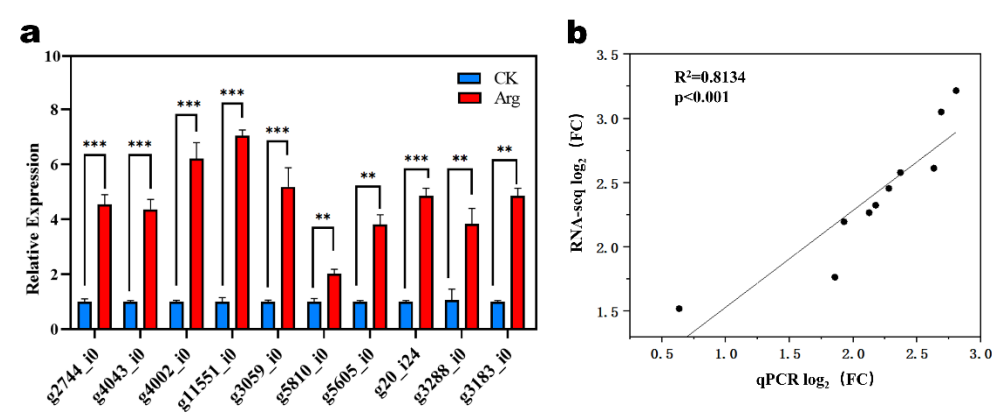
## Supplementary Figures&Table



**Figure S1** Morphology of plate colonies of *Termitomyces* under different amino acid cultures



**Figure S3** Thumbnails view of DAG between CK vs. Arg. (a) DAG on biological process. (b) DAG on cellular component. (c) DAG on molecular function. Note: GO term is a node; the parentage is an arrow. The degree of enrichment is higher along with the darker of color.



**Figure S4** (a)Expression of key genes related to the metabolic pathway (qPCR validation); values are expressed as mean  $\pm$  SEM (n = 3), \*p < 0.05 and \*\*p < 0.01;(b) The correlation between results from qPCR and RNA-seq.

**Table S1** The CAZymes family in the developmental transcriptome

CAYz	count of family	count of gene	major family
GHs	80	648	GH16、GH79、GH18、GH3、GH92、GH2、GH115、GH47、GH5_9、GH31、GH10、GH71、GH35、GH5_50、GH7、GH27、GH28、GH78、GH17、GH29、GH5_5、GH6、GH76、GH88、GH15、GH5_12、GH63、GH81、GH95、GH105、GH13_1、GH13_22、GH74、GH85、GH30_3、GH37、GH5_30、GH51、GH53、GH109、GH25、GH30_2、GH99、GH1、GH11、GH43_30、GH5_7、GH125、GH13_25、GH13_5、GH13_8、GH133、GH33、GH43_13、GH5_46、GH12、GH128、GH13_19、GH13_30、GH131、GH142、GH143、GH44、GH5、GH5_24、GH5_35、GH5_36、GH57、GH72、GH116、GH120、GH124、GH127、GH13_7、GH23、GH43_24、GH5_13、GH5_22、GH9、GH96

GTs	36	416	GT41、GT2、GT90、GT1、GT39、GT68、GT15、GT4、GT32、GT48、GT58、GT66、GT33、GT57、GT22、GT26、GT3、GT31、GT50、GT8、GT20、GT35、GT65、GT2_Cellulose_synt、GT21、GT23、GT28、GT5、GT83、GT24、GT25、GT30、GT38、GT49、GT80、GT87
AAs	17	313	AA1、AA3_2、AA1_1、AA3、AA3_1、AA7、AA5_1、AA9、AA3_3、AA2、AA8、AA5、AA1_2、AA4、AA3_4、AA6、AA5_2
CBMs	16	75	CBM67、CBM13、CBM21、CBM50、CBM19、CBM1、CBM16、CBM57、CBM12、CBM14、CBM22、CBM32、CBM44、CBM5、CBM53、CBM60
CEs	10	70	CE10、CE1、CE9、CE7、CE4、CE16、CE5、CE12、CE8、CE15
PLs	17	64	PL8、PL14、PL25、PL1、PL11、PL14_4、PL14_5、PL3_2、PL5_1、PL1_11、PL1_7、PL10、PL12、PL27、PL17_1、PL4_1、PL5

**Table S2** The genes and primers required used for qRT-PCR validation.

Genes ID	Description	Forward sequence (5'-3')	Reverse sequence (5'-3')
g4002_i0	cellulase,endoglucanase	ACTATCAAGTCAACCGAGGC	GAGACTACATCAAGGCAACG
g3183_i0	GH5_5	TCAATGGAAGAAGGCGAAGG	CGAGTCTGGTGCCGAGTTTG
g3059_i0	beta-glucosidase	CTCATTATTTGCTGTGGGTC	CTCATTATTTGCTGTGGGTC
g20_i24	GH3	AGCAGAGCCTCCGCCAGAA	AGCAGAGCCTCCGCCAGAAA
g11551_i0	cellulose 1,4-beta-cellobiosidase	AAGAAGGCGTTTGGAGATA	GGGTCAGCATTGATAGGATAA
g2744_i0	pyruvate dehydrogenase	TTCCACTTGCCCTTGTTGC	TTGTTGGTGCTCATGTTCCC

g3288_i0	pyruvate decarboxylase	GATGAAACGCTCAATAGTGT AG	TGGAGATGGAAGCCTGTAAG
g4043_i0	aldehyde dehydrogenase (NAD <sup>+</sup> )	CAAACGCCCCAATCATAAGTC	TGCTAAACAACCTCGCAAAC
g5605_i0	alcohol dehydrogenase	CGCGTCTTGTCGGTTTCCTA	CACCACTGCTTCCTCCTCTG
g5810_i0	arginase	ATGTTCTCCCACTGCTTTCG	ACCCTCCTGTTGGCATTCTG

Table S3. The characteristic absorption peak of infrared spectrum of Corn straw and its attribution.

Absorption peak/cm <sup>-1</sup>	Attribution
835	Bending vibrations outside the C-H plane of the S ring and H ring (lignin syringyl vibration)
1040	Stretching vibration of carbohydrate (cellulose, hemicellulose) or polysaccharide C-O
1215	Stretching vibration of phenolic hydroxyl C-O on the benzene ring
1240	The ester bond between hemicellulose and lignin
1325	Stretching vibration of C-O on syringyl aromatic ring
1372	Bending vibrations of C-H on cellulose and hemicellulose
1429	Stretching vibration of lignin, aliphatic compound and C-N
1515	Stretching vibration of C=C-C on the benzene ring of lignin
1613	Vibration of lignin aromatic skeletal
1641	Stretching vibration of C=O associated with aromatic rings in lignin
2352	N≡N stretching vibration
2925	Contraction of C-H in cellulose
3333	Hydrogen bond association, which includes the stretching vibration of the hydrogen bond formed by -OH and N-H in amino acids, as well as cellulose, hemicellulose, starch and monosaccharide, et al