1 Supporting Information for the article

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3 Fig.S1 Map of the recombinant plasmid pPIC9K-FT-A.

4 Fig. S2 The cDNA sequence (without its signal peptide) of FT-A from *Aspergillus niger* TCCC41686:

5 Fig. S3 Sequence alignment of fructosyltransferases from *A. niger*. Conserved domains are shown in

6 gray boxes and active site residues are underlined. Altered residues are shown in lowercase letters. The

7 picture only shows a part of the amino acid sequences.

8 Fig. S4 SDS-PAGE analysis of purified FT-A. M: protein molecular weight marker; the FT-A fragment

9 is indicated by the arrow.

10 Fig. S5 The HPLC chromatograms of FOS. A: The HPLC chromatograms of FOS (Mixed standard

11 sample, 0.75 µg mL^{-1}). B: The HPLC chromatograms of FOS formation at 70 min of synthesis based

12 on sucrose as substrate (F: fructose, G: glucose, GF: sucrose, GF$_2$: 1-ketose, GF$_3$: nistose).
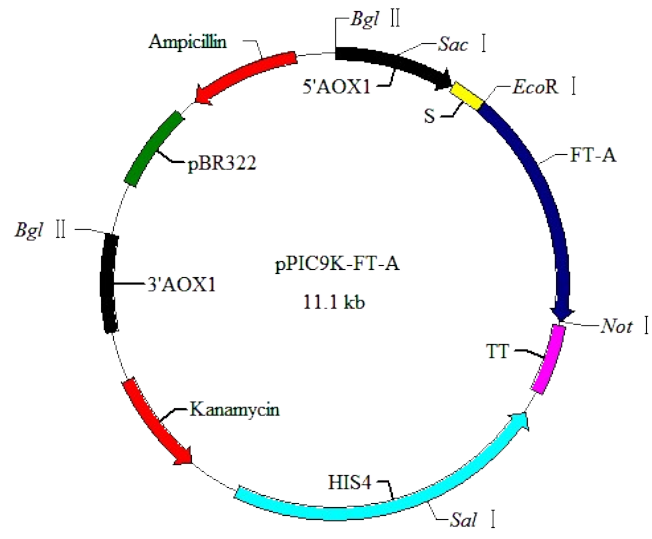
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Bgl II

Ampicillin

5'AOX1

Sac I

S

*Eco*R I

pBR322

FT-A

Bgl II

3'AOX1

pPIC9K-FT-A
11.1 kb

Not I

TT

Kanamycin

HIS4

Sal I

20

21   Fig. S1

5'-GCCTCGCCTTCCATGCAGACGCGGGCCTCCGTGGTCATCGACTACAATGTCGCTCCTCCAAACCTC

TCCACCCTGCCCAATGGCTCCCTCTTCGAAACATGGCGGCCCCGCGCCCACGTCCTGCCCCCAAACGGC

CAGATCGGTGATCCCTGCCTGCATTACACCGATCCCGCCACGGGCCTCTTCCACGTCGGCTTCCTTCAC

GATGGCAGCGGCATCTCCAGTGCCACCACCGATGACCTAGCCACCTACCAAGACCTCAACCAAGGCAAC

CAAGTCATTGTCCCTGGGGGCATCAACGACCCCGTCGCTGTCTTCGACGGCTCCGTCATCCCCAACGGC

ATCAACGGCCTCCCCACCCTCCTCTACACCTCCGTCTCCTACCTCCCCATCCACTGGTCGATCCCCTAC

ACCCGCGGCAGTAAGACTCAATCCCTCGCCGTCTCCTCCGACGGCGGCAGCAACTTCACCAAGCTCGAC

CAGGGCCCCGTCATCCCTGGCCCTCCCTTCGCCTACAACGTCACCGCATTCCGGGACCCCTACGTCTTC

CAAAACCCCACTCTTGACTCCCTCCTCCACAGCAAGAACAACACCTGGTACACCGTCATCTCCGGTGGT

CTGCACGAAAAGGGCCCCGCTCAATTCCTCTACCGCCAGTACGACTCGGACTTTCAGTACTGGGAGTAC

CTCGGCCAATGGTGGCACGAACCCACCAACTCCACCTGGGGTAACGGCACCTGGGCCGGCCGCTGGGCC

TTCAACTTTGAGACCGGCAACGTCTTCAGTCTCGACGAGTACGGATACAACCCCCACGGCCAGATCTTC

ACCACCATCGGCACTGAGGGCTCTGACCTGCCCGTCGTGCCCCAGCTCACCAGCATCCACGACATGCTC

TGGGTGTCCGGTACAGTCTCTCGCAATGGCTCTGTCTCGTTCAACCCCAACATGGCGGGCTTCCTCGAC

TGGGGCTTCTCCTCTTACGCTGCTGCCGGAAAGGTTCTCCCCTCGACTTCTCTGCCTTCCACGAAGAGC

GGCGCCCCGGATCGCTTCATCTCCTACGTCTGGCTGTCCGGTGACCTGTTCGAACAGGCCGAAGGGTTC

CCCACGAACCAGCAGAATTGGACCGGTACGCTGCTGCTTCCGCGTGAGTTGCGCGTGCTGTATATCCCC

AATGTGGTGGACAATGCTCTGGCCCGGGAGTCTGGTGCCTCGTGGCAGGTCGTGAGCAGCGATGGCAGT

GCGGGCACCGTCGAGCTGCAGACGCTGGGTATCTCCATTGCCCGGGAGACCAAGGCCGCGCTGCTGTCG

GGAACGTCGTTCACTGAGTCCGGCCGCACCCTGAACAGCAGTGGTGTTGTTCCGTTCAAGCGCTCGCCA

TCCGAGAAGTTCTTCGTTCTGTCCGCACAGCTGTCCTTCCCTGCTTCGGCTAGGGGATCGGGACTTAAG

AGTGGGTTCCAGATCCTCTCATCGGAGCACGAGAGTACCACTGTGTACTACCAGTTCTCGAATGAGTCG

ATTATCGTGGATCGTAGCAACACTAGTGCTGCGGCGCGCACGACTGATGGTATCGATAGCAGTGCGGAA

GCTGGCAAGTTGCGTCTGTTTGACGTGCTGAATGGCGGCGAGCAGGCCATTGAGACGCTAGATTTGACT

CTCGTGGTGGATAACTCCGTGTTGGAGGTGTATGCCAATGGTCGGTTTGCGTTGAGTACCTGGGTTCGT

TCCTGGTACGCCAACTCCACTAACATCAGCTTCTTCCATAATGGCGTGGGTGGTGTTGCGTTCTCCAAA

GTGACTGTGTCCGAGGGCTTGTATGATGCTTGGCCGGATCGTCAGTCTCATCACCACCATCACCACTAA

-3'

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FTase(FT-A).seq   MKLQTASVLLGSAAAASPSMQTRASVVIDYNVAPPNLSTL   40
FTase(FruSG).seq  ----------------------p-----------------   40
 FTase(fwt).seq   ----------------------------------------   40
FTase(fts1).seq   ----------------------------------------   40
                                    Domain  A
FTase(FT-A).seq   PNGSLFETWRPRAHVLPPNGQIGDPCLHYTDPATGLFHVG   80
FTase(FruSG).seq  -----s---------------------------s------   80
 FTase(fwt).seq   ---------------------------------s------   80
FTase(fts1).seq   ----------------------------------------   80


FTase(FT-A).seq   FLHDGSGISSATTDDLATYQDLNQGNQVIVPGGINDPVAV   120
FTase(FruSG).seq  ------------------k---------------------   120
 FTase(fwt).seq   ------------------k---------------------   120
FTase(fts1).seq   ----------------------------------------   120


FTase(FT-A).seq   FDGSVIPNGINGLPTLLYTSVSYLPIHWSIPYTRGSKTQS   160
FTase(FruSG).seq  -------s--------------f------------e---   160
 FTase(fwt).seq   -------s--------------f------------e---   160
FTase(fts1).seq   ---------------------f------------e---   160
                                    Domain  D
FTase(FT-A).seq   LAVSSDGGSNFTKLDQGPVIPGPPFAYNVTAFRDPYVFQN   200
FTase(FruSG).seq  ----------------------------------------   200
 FTase(fwt).seq   ----------------------------------------   200
FTase(fts1).seq   ----------------------------------------   200


FTase(FT-A).seq   PTLDSLLHSKNNTWYTVISGGLHEKGPAQFLYRQYDSDFQ   240
FTase(FruSG).seq  ---------------------g-----------p---   240
 FTase(fwt).seq   ---------------------g-----------p---   240
FTase(fts1).seq   ----------------------------------------   240
                                    Domain  E
FTase(FT-A).seq   YWEYLGQWWHEPTNSTWGNGTWAGRWAFNFETGNVFSLDE   280
FTase(FruSG).seq  ---f------------------------------------   280
 FTase(fwt).seq   ---f------------------------------------   280
FTase(fts1).seq   ----------------------------------------   280
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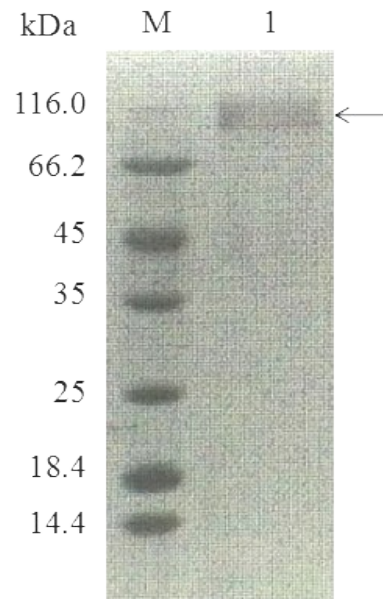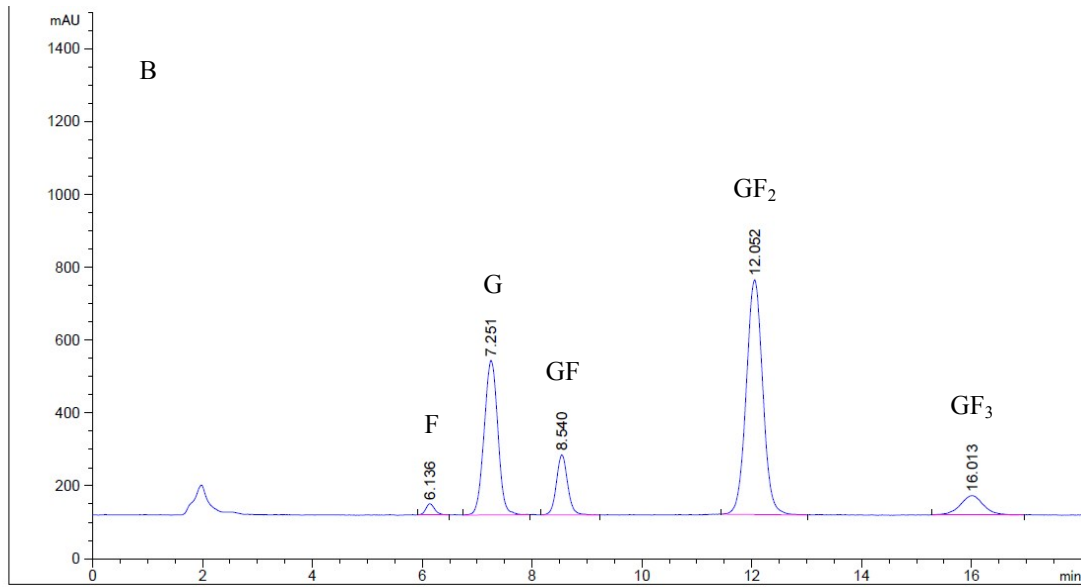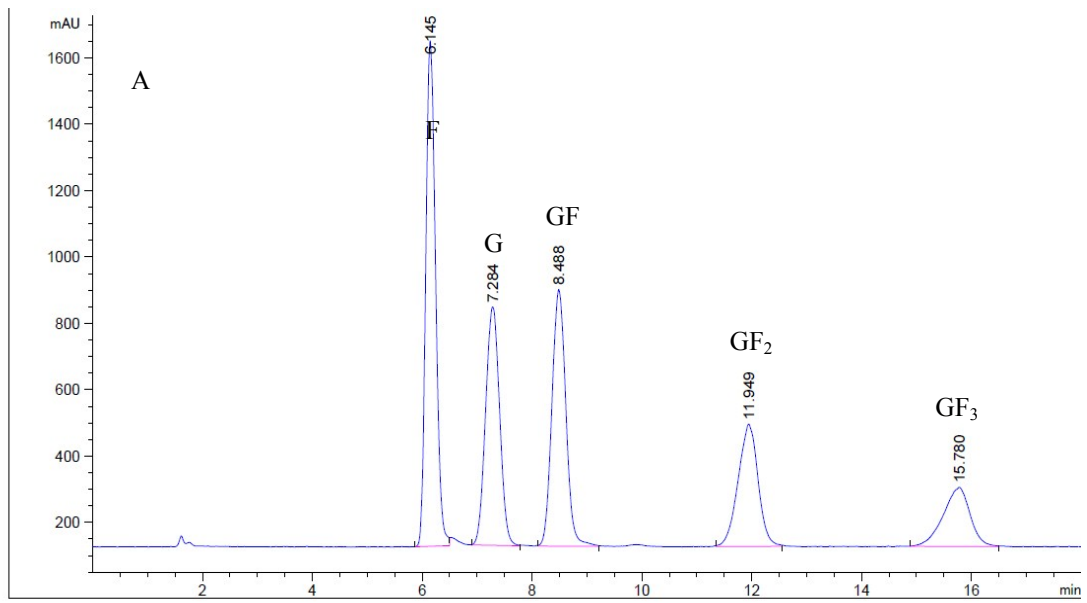
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25   Fig. S3

Fig. S4

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Fig. S5