

Supporting Information for:

A potentially practicable halotolerant yeast *Meyerozyma guilliermondii* A4 for decolorizing and detoxifying azo dyes and its possible halotolerance mechanisms

Yue Feng 1,†, Jingru Cui 1,†, Bingwen Xu 2, Yifan Jiang 1, Chunqing Fu 1 and Liang Tan 1,*

1 Key Laboratory of Plant Biotechnology of Liaoning Province, School of Life Science, Liaoning Normal University, Dalian 116081, China; fss990214@163.com (Y.F.); acui0315@163.com (J.C.); jiangyifan202203@163.com (Y.J.); 15560356752@163.com (C.F.)

2 Dalian Center for Certification and Food and Drug Control, Dalian 116037, China; xubingwen0402@126.com

* Correspondence: tanliang19811210@163.com or tanliang1210@lnnu.edu.cn; Tel./Fax: +86-411-85827068

† These authors contributed equally to this work.

This 28-page file includes:

3 Supplemental Tables

5 Supplemental Figures

2 Supplemental Texts

4 References

Table S1 Azo dyes used in the present study and their main chemical information.

Name (CAS number)	Chemical structure	Molecular weight	Characteristic absorption wavelength (nm)
Acid Red B (3567-69-9)		458.5	516
Acid Orange II (633-96-5)		328.3	484
Acid Scarlet GR (5413-75-2)		512.5	511
Acid Red 3R (1082572-30-2)		538.5	507
Reactive Brilliant Red K-2G (12238-01-6)		788.2	509
Reactive Violet KN-4R (12226-38-9)		669.6	558
Reactive Yellow 3R (93050-80-7)		938.3	540

Table S2 Sequences of the target genes which were validated through QRT-PCR.

Gene ID	Genetic sequences
D_102776	<p>ATGGCAGAATTTTATAGACACCTTCTTTCCCAGCTCTTATTGTTGGTGCCTGCCTCCAAGTTCCAGCCGCCCTCTTCAGATGACCCAGACCCTCA CACAGAGGTTATTGACGTAGTTAGTGCAATTCTCGCTGGCAACTCGGGTTCATTTTCACAGATACTAGGTATAAAGGAGTGTTTTACAATGCTA ATGCTTTACGTGTGTTATCCAGTATCCCAATATAAGCTTGAAGAGTGCATTACACGGCTATGTGGACGAAATTATCAAGTCTGTGGAACAGAGC TCTTCGACCGATTCTCGACTTTTAGTGCAATTAAGTGAATTTGTCATTGCAATTATTCATCCAGCTCAATTTTACTGGACCAAATGTTGACTTTA AGGCTCACGAGCTCTTAATGCCCCATGCTGACTACGAAAATTTGCACTTGGACCTCATAGACTTGCTCACC GTTGAGGGGCCAACAGGCATATGA GCTTATGAATGAACCATTGCTTTTCATTATAGCCAGTTTGATGTTTGAAAAGATTGATGAATGTGGGACCACAGTACTCGTTTATTGGCAAAGATAT GAACGTAGAGCTTGACCAAATGGTAGAAGCCACTAGACCTTTGGTCGCCAATCCAAGCATAGAAGACGCTTCGCTTTTCTGGTGGAGATCACG AGCGTTGCAAATCCACATCTCGCTCCTATCAGAACCTCCAAGTGTGTTGACGAGTATATCGGCACCTTTGCTCGGTCCCTCCACGGCAGAAAGTTT TGGCTCATGGAAATGACACTCTTCTGTCACTTGTCAAATACGAGTTTCTCATAGAAACCGCTCGAGCCAGCATTTCATTACACAGAACATTTG GCTACCTCACTTTTGGCGAGAGCATCAGAGGTTACTGAGTTGCAATTTGTGTTGACTGGAGCTAAGGCTAAACGAACAAAGTTCCAAACATTCA CCACATCTTCGTTGGTATTGCTAGCAAAGAGCAAAGGGTCTACTTTACTCGATGAAGACACGGCCGAGGAACCAGCAAAGTTCAATTTGGATTCA AGACCTTCTTCTCGAACGTCCACAGTACGATGCTCTCGAAGACATAAAAGAACCCGTTTCTAAAAAGACCAAATTTGAAGATGAGGACCAGAA AAACGAAGTTCCGCTCTTGCTATAGCACGTACCAAGACCAAATTCCTTTGGAGCTTTCAGCCTTGGAATCCCAACGATCAACCCGCATTGAAC GACTTGGACAACCTTCAGCTTTTGTCTCCGTTTGATGGTGCTTCGCCAATCTTCGCCAGCTAGCAATTCGCTTGTCGAAGAAGAGCTCATGGCAA TTGTGAGCAGAGTCATATATCAACCATCGAAATCTGTCAACTGGGCCATTTTGGGAAGGGCGTTATGGGAGAGATCACTATTGGAAACAAGCAA GGCTCGGACCGTGGAAGAGGAATATTACAGATGACATCGTTAGTTGAAGAAATCGGTCTCAAGATTAAAACAGGCTTTTGCCCTCAGGAAATG GAAGCGAACAACCTCTTCCCCAGCTGCTTCTCGGCTCCGTTTCATCCACCAACTTCCGTTGATGCCACAGTGGACCATGGACGTTAAGTTGGCAG AAAAGTACATGTCTTTGGGAGTGTTGAAGTCTGCGTTGGAAATCTACGAAAGACTTCATTTGGAATGCGAAGTGGCACTTTGTCTGCTGCGGT TGACAACGAAACTGAGGCGGAAAACGTCTCTTACGTCTGTTAGAACAGCACCCCAACGATGCCAGAGCCACATCAATTCTCGGTGATATTCCG CCAGGACCCCTCAGCTCTGGGAACGAGCCTGGGAAATTGGAAGGTACTCAAAAGCAAAGAACTCGTTATCGAGGTATTACTATAACCCCTCCAGC AAATTCTGGACTTTCCAAAGACTTGGAAGCAGCACTTTTACATATGAGTGATTGTTTGAGGGGCCGACCCACTTAATTTTGAAAATTGGTTCTTTT ACGGCTGTTGTGGACTCGAAACTGCAAACTACGAATTAGCATCGGAGGCATTTACTCGTTGTGTTTCGTTAGATGACTCGAATTCGCATGCTTGG TCCAACCTGGCTACGGCGCTTCTAAGATTAGACAAGACCAGACCAGCATTCAATGCTTTGAAAAAGGCAATGGTGAGTTCAAAAGAAGGTAAG CGGTCTTGAGAAATTCATGAAAACCTTTGTCATTGTTGCCATGAACTCAATGAATGGTCTGATGTCTTACAAGCGACCAGAGAATTGATAGACAT GAAAGAAGGTGGAGAGTCAAGTATCGATATTCCTGTCAATTGAAAAGTTGGTGGAATTTCTCGTGGCCACAGATTATCCTAAGGAGGGGAGAGAG ATTGACTCATTATCAGAACTCGTGTATTGATTTGGTGTGCAATATGCTTCCTAATGTAATTACCAACTCTGGTAGATGTTGGAGAATTGTTGCTCGA GTTTCATATCTGGAGAAAGAAGCCATGGGAGGCATTGGAATGCTACGAGAAAGCTTATCGAGCGGTATCCCAAAAGCATGATTTGAGCACCAACG AAACCATTTGGAATGAAGCTGTAGAGGCTTGTGAAGACTTGGTCGCAGCATATGAGTCTCTTGAGAGGCTTCCAGGCAAACATGGAGCCGACG ATTTAGTGTGCAAGGACTGGAAATACAAAAGCAAAACGACAATCAGATCGTTAATGTGCAAGGGAAAGCTGATGTGGGAAGATAGTCAAGGCT GGGATCGCTTAATGGCGCTCAAAGAAAACCTTATGA</p>
D_105169	<p>ATGTCGTACGATAATAATCACAACCTATTATGACCCGAATCAGCCGATGGGTAATGATGGTTATTATCAACAACAACCTTATGATGATATGAACCAA CAACCACATCAGGATTACTATGACCCCAACATGCAATATCAACAACAGCCTTATGACATGGACGGGTACCAAGATCCCAACTATCAGGGTCAAC AGATTCCTCAACAAGGATATAACGCTGATCCTGAAGCGTTTCTGATTTACGTTACGGGGGTCAAACCTCAGGTACTCCTGGTTACGACCAATAC</p>

GGTACTCAGTTTACCCCTTCTCAGATGAGTTATGGTGGTCCCAGATCGTCTGGTGCTTCTACACCCATCTACGGTGGAGCAGGTGGAAACTACGA
TCCAACCCAATTTCAAATTCCTCCAGCATGCCTTACCTGCTTGGTCTGCCGATGCGCAAGCACCAGTTAAAGTAGAGCATATTGAGGATATTT
TCATCGATTTGGCCAACAAGTTTGGTTTCCAAAGAGATTTCGATGAGAAATATGTTGACTACTTTATGACATTATTAGACTCTAGATCCTCGCGTA
TGTCTCCCGCCCAAGCCTTATTGAGTTTACACGCGGATTACATTGGAGGTGAAAACGCCAACTACAAAAAGTGGTATTTTGCTTCGCAACAGGA
TTTGGATGAATCAATTGGTTTGGCCAACATGAAAATGGGAAAGGTTGGTAAGAAAGCTAGAAAGGCATCCAAGAAGTCCAAGAAGGCAAGAA
AGGCAGTCGAGGAACATGGCCAGGACATCGACGCTTTGGCTAATGAATTAGAAGGCGACTACTCTTTGGAAGCCGCAGAAATTAGATGGAAAG
CCAAGATGAACTCTTGTCTCCTGAAGAGAGAATTAGAGACATTGCTTTGTATTTGTTGTTGTGGGGTGAAGCCAATCAAGTTAGATTTACTCCT
GAAGCCATTTGTTACATCTACAAAACGGCTTTCGATTACTTGGTGTCTCCTCAATGTCAACAAAGACAAGAGCCTGTTCCAGAAGGTGATTACTT
GAATCGTGTTCATCACACCTTTGTACCGATTCTTTAGATCTCAAGTCTACGAAATCTACGAGGGCCGCTTGGTCAAGCGTGAAAAGGATCACAATA
AGGTGATTGGTTACGATGATGTTAACCAGTTGTTCTGGTACCCAGAAGGTATTTCAAGAATTATCTTTGAAGATGGTACTAGATTGATTGACGTCC
CACCTGAAGAGCGTTACTTGAGATTTGGTGAGGTCGAATGGCACAATGTCTTCTTCAAGACTTACAAGGAAATTAGAATTGGTTGCATCTTATC
ACCAACTTCAACAGAATCTGGATTATCCACGGTACCGTCTACTGGATGTATACTGCTTACAACCTCCCAACGTTGTACACTCTCCATTATGTTCAA
ACTATTAACAATCAGCCTCTTGCTTCATCAAGATGGGCTGCCGCTGCTATTGGCGGTGTTTTGGCTGCCTTCATTCAAATTGCTGCAACGGTGTG
TGAGTGGATGTTTCGTTCTAGAGAGTGGGCTGGTGCTCAACATTTGACACGTCGTTTGATGTTTCTCATTATAATTTTCGTGGTTAACTTGGCCCC
AGTTGTTTTTACCTTTTACTACGCTGGCTTGGCTGCAAAGTCAAAGCAGCGCTAGTGGTTTTGATTGTTGGGTTCTTCATTGGTATTGCTACGA
TCGTATTCTTTGCCGTTATGCCTTTGGGTGGTTTGTTCACAAGTTATATGAACAGAAGATCAAGAAGATATTTGGCTTCTCAAACCTTTACTGCCA
ACTTCAACAAGTTGACTGGCTTAGACATGTGGCTCTCGTATTTATTGTGGGTTCTTGTGTTCTTTGCCAAGTACATCGAATCTTATTTCTTCATGG
CTTTGTCTTTGAGAGATCCCATTAGAACCTTGTCTACCACTAACATGAGATGTATCGGTGAAGTCTGGTTCGGCGACAAATTGTGTAAACACCAA
GCTAAGGTGCTCTTGGGTTTGATGTACCTTGTGGACTTGTTATTGTTCTTTTTGGATACCTACATGTGGTACATTATCTGTAACTGTGTGTTTTCCA
TTGGTCGTTTCTTACTTGGGTATTTCTATCTTAACACCTTGGAGAAACATTTTACAAGACTTCCAAAGAGAATCTACTCTAAGATTTTGGCTA
CCACTGAGATGGAGATTAAGTACAAACCAAAGTTTTGATCTCTCAAATCTGGAATGCTATTGTGATTTCATGTACAGAGAACATTTGTTGGCT
ATTGATCACGTTCAAAGTTGTTGTACCACCAAGTTCCATCTGAAATTGAGGGTAAGAGAACTTTGAGAGCTCCAACCTTTCTCGTTTTCTCAGG
ATGACAATAACTTCGAGACGGAGTTCTTCCCAAGAACTCTGAAGCTGAGAGACGTATCTCTTTCTTTGCTCAGTCCTTGGCTACACCAATCTT
GGAACCATTGCCAGTTGACAACATGCCTACCTTTACTGTGTTTACTCCTCACTACTCTGAAAGAATTTTATTGTCTTTAAGAGAAATTATTAGAGA
GGATGACCAATTCTCCCGTGTTACCTTGTTAGAATATTTGAAACAATTGCACCCAGTTGAATGGGACTGTTTTGTCAAGGACACCAAAATTTGG
CGGAAGAACTGCTGCTTTTGAAGGTGAAGGTGTCGACAAAGAGTCTGAAGATGGCCTCAAATCTAAGATTGATGATTTGCCATTCTACTGTAT
TGGTTTCAAGTCTGCTGCTCCTGAGTATACATTGAGAACCCGTATTTGGGCTTCTTGGAGATCCCAAACCTTGTACCGTACCGTTTCCGGTTTTCAT
GAACTATGCCAGAGCCATCAAATTGTTGTACCGTGTTGAGAACCCAGAATTGGTTCAATATTTTCGGTGGAGACCCAGAGGGCCTTGAACCTCGCA
TTGGAGAGAATGGCAAGAAGAAAATTCAAGTTTGTGTTTCAATGCAAAGATTGGCCAAGTTTGAAGACTGGGAGATGGAGAATGCTGAATTT
TTGTTACGTGCTTACCCTGACTTGCAAATCGCTTACTTAGACGAAGAGCCTGCCTTATCCGAAGAGGAAGATCCAAGAATCTATTCCGCTTTGAT
TGATGGTCACTGTGAAATTTTGGAGAATGGTAGACGTCGTCCTAAGTTTAGAGTGCAATTGTCTGGTAACCCAATTTTGGGTGATGGTAAGTCTG
ATAACCAAAATCATGCTTTGATTTTCCACCGTGGTGAGTACATTCAATTGATTGATGCCAATCAAGACAACCTACTTGGAAGAATGTTGAAGATC
AGATCTGTGTTGGCCGAATTCGAAGAATTGAACGTTGAACAAGTTAACCCATATGCTCCTAAGTGAAGACTGATGTCAAGACTGGAAACAATG
CCCCGTGTGCTATTTTGGGTGCTCGTGAATACATTTTCTCAGAGAACTCTGGTGTTTTTGGGTGATGTCGCTGCTGGTAAGGAACAACTTTCCGGT
ACCTTTTTCGCAAGAACTTTGGCACAGATTGGTGGTAAATTGCATTATGGACATCCTGATTTCTTGAATGCCACTTATATGTTTACCAGAGGAGG
TGTTTTCTAAGGGACAAAAAGGATTGCATTTGAACGAAGATATTTATGCTGGTATGACTGCTATGTTAAGAGGTGGTAGAATCAAGCACTGTGAAT
ACTACCAGTGTGGTAAGGGTAGAGATATGGGTTTCGGATCCATTTTGAATTTACAACCAAGATTGGTGCTGGTATGGGAGAACAGATGTTGTCT
CGTGAATATTACTACTTGTGCGACTCAGCTTCTTTGGACAGATTTTGTCTTCTACTACGGTCATCCAGGTTTCCATATTAACAACCTGTTTCATTC

AATTATCTTTGCAAGTTTTTCATGTTGGTGTGGCTAACTTGAACCTATTGGCTCACGAATCCATTTTGTGCTCCTACAACAGAAACACTCCTATCA
 CCGATGTGTTATATCCTTACGGTTGTTACAACCTTCGCTCCCGCAGTTGACTGGATTAGACGTTACACATTGTCTATTTTCATTGTGTTCTTCATTGC
 GTTTATTCCATTGGTGGTTCAAGAATTGATTGAAAGAGGGTGTCTTGAAGGCAGCCCAAAGATTCTGTGCGCATCTTATCTCGTTGTCGCCAATGT
 TCGAAGTGTTTCGTTGCTCAAATCTACTCGACTTCATTGATTACTGATTGACTGTTGGTGGTGCCAGATATATCTCCACTGGTAGAGGTTTTCGCCA
 CTTCTCGTATTCCATTCTCCATTTTGTACTCCCGTTTTGCTGATTTCATCGATTACATGGGTTCAAGATCTATGTTGATTTTGTGTTGCGGAACAGTT
 TCTCACTGGCAAGCTCCATTGTTGTGGTTCTGGGCATCGTTGTCATCATTGATGTTCTCACCATTATTTTCAATCCTCATCAATTCTCTGGGAAG
 ATTTCTTCATCGATTACCGTGACTTTATCAGATGGTTATCCCGTGGTAACTCCAAGTGGCATAGAACTCTTGGATTGGTTACGCTCGTCTTTTCGA
 GATCTCGTGTCACTGGTTTCAAGAGAAAGTTGACTGGCGATGTATCGGAGAAGGGTGCTGGTGACGCTTCCAGAGCACACAGATCCAACATTT
 TCTTTGCTGACTTTTTGCCTACTTTGATCTACACTGCTGGTCTTTTTGTTGCCTACACTTTTATCAACGCCCAGACTGGTGTAAGAAGGGGACCA
 AATGGTGAGGGAAACCCTACTGAGGTCAACTCTGTGTTGAGAGTTGTGATTTGTTCTTTGGCTCCTGTAGTTATTGATCTCGGTGTTTTGGCAGG
 ATGTCTTGGTCTCGCTTGTGCGCAGGTCCATTATTGGGATTGTGCTGCAAGAAGACTGGTCTGTGATTGCCGGTGTTGCTCATGGTATTGCCG
 TTGTTGTGCACTTGGTCTTTTTTCATTGTCATGTGGGTCTTGGAAGGCTTCAACTTTGCTAGAATGTTATTGGGTCTTTGTACCATGGTTTACATCC
 AAAGATTGTTGTTCAAGTTTTTGACGATTTGCTTCTTGACCAGAGAGTTCAAGAACGATAAATCTAACCAAGCTTTCTGGACCGGTAAATGGTA
 CGGATCTGGTTTGGGATGGATGGCGTTACCCAACCAGCTCGTGAATTCTGTGCCAAGGTTATTGAAATGTCGGAGTTTGCCGGAGACTTTATTT
 TGGCACACATCATCTTGTGTTGTGCAATTGCCTATCATCTGTATTCCATTGATTGACAGATGGCATTGACCATGTTGTTCTGGTTGAAACCTTCCA
 GGTTGATCAGACCTCCAATCTACTCATTGAAGCAGGCCAAGTTGAGAAAGAGAATGGTGAGAAGATACTCTACTCTTTACTTTTTGATTTTGGTT
 ATCTTTGTTGCACTTATTGCTGCACCTGCTGCTATTGGTAACACCCTCTTGTACCAGAAGACTTGGGTAAATCGTTGAAGGGTACTTTTGCTGG
 ATTGTTCCAACCCAGACACGTTGAAAACAATGACACTGGTACTTCGGTGGGCAAGGCTTACATGAGTCTGCACACATTCTTGACCAAAATGTTT
 AGTGGGACGACGACCAAAATATTCCACCAAGCCATAA
 ATGTCCCAACTAACTCTCGCGTAGCAGGTCTTCTTTTTACGTTGCTTTGACTACAATACATCGAGACTACGTTGGAACCTCTTCAAACCTACAG
 GAAATGGCTCAAGGCAGCTTGCAAACAAGATGGGAGTGATGGGCCCCGAAAGGATAATTAACGAAAACATTAATACAGCTTGCAAGATGTA
 CGTAACCTGAAGTTGCCTTGACCTCTTAATATGGGGAGAAGCCAGCAATATCAGATTCATGCCAGAATGCATTTGCTTCATTTACAAGTGCTGTCT
 CGACTACTATATGGCAGAGGACAGGATCACGATTGCAAAACCATTTCTTGACCACACGATTGTACCTTTGTTTGAATTCTTGAGGGGAACAACAAT
 ACAAACCTAAAAGACGGAACTGGATTTCGGAGAAGGCGGGACCATGCTCGTATCATAGGATACGACGATATGAATCTGTTTTCTGGTATAATGA
 AAACCTCCAGAAATTAGTGGTCGATTTCGGGCAGGCTCTATGATATGGCTGCACTGGACCGATACCCAAGCTTTGACAAAATTGATTGGAACAAA
 GCTTTCTTCAAATCCTACAGGGAAGTACGCACCTGGTCTCACCTTTTGACCAACTTCAGTAGGGTATGGATTACACACTTGACAATGTTCTGGTA
 CTTTACCAGTTGCAATTCATCTCATTGTACACAAAAGAATACAGCCCAGAGTACGACAACACGCCTCCACCTCATGTTATTTGGTCAGTGGTTT
 CATTAGGTGGAGTATTAGCATCGACAATTGCCCTTGTGAGTTGCTTGATGGAACCTTAGATTTCGTACCAAGAAAGTTTCCAGGAGCGCCATCTGTA
 TTGGGAAGAAGTTTACTTCTCATGGCTCTTCTGGCCTTGAATCTTGGACCGTCTTTTATCTTTTGTGGATATTGCCTGCTGATGTCTATTCAAGGT
 CGGGTCACTAATAGGGATCATTAGTTTGGGATTTCTGCTGCCACTTTCTTATACCTAGTGCTTGTTCCTCCCGCACAATACTTCTCTTGCACT
 TCCATCCCAGCCCAATTACATCATGCTTTTACTTCAGACTTCCAAAACTCCCCACGAGAACCAAGGCAGTTTCTGCTTCACTATGGGTTCTGG
 TATTCACCTTGAAATCTTGGAGTCGATTTTTTCTTGACATTATCTGTCAAGGATCCAGTCAAGGTTCTATCCCATTTGAGAATGACTAGGTGTCA
 TGGTGATTCCATATTGGGTACACTTTCGTGCCGTTATCAGCCCACAATAACGCTTGCGTTTATATTCGTCATGATTGTTGTTCTTCTTCTGAT
 ACGTACTTGTGGTTCGTTCTCTGCACTTGCATGCTTTCCATAGTAATTGCCATAAAGAATGGCAATTCTATATTTACGCTGTGGAAGTCGGTGT
 TCCCAGCTACCGGAAAGGTTGATATCCAAAACAGTCAACGTTGACAGCGTGGGAGACGCAATAGTGGCAGCCAGCCACATGTGGAATGCTATT
 GTGTACTCCATGTATCGAGACCACTTGATATCAGTTGACCAAGCCTCAGCATTAATGTATCAACTCCCCGATACGGACTTTGTTCAAAGTTCAGCT
 GATGTTAAGGCACCTATTAACCTTCTCAGTCACAATCATGCTATCCACTCGGATGAATACTTTCCTCAATTAGGTGAAGCAAAGAGACGAATCTC
 ATATTTTGACAATCGTTAAGTTCGCCTCTCTGTAACGCAGATTTACCACAGACGCTTGTCCAGCATTCACCGTATTGATCCCACACTATTGAGA

D_105067

AAGTATACTTCTTAGCATCGAAGAGGTGATCAGAAGATCTAAGCAAACCCAGATCACCTTGCTTGACTACCTCAAGAGTTTACTGAGCTCGGAC
TGGACGAATTCGTTTCGAGACACTAGAGTCGCTGACGATGAAAAGTTCGGTTGTAGGTTTCCAATTCCTCTAACTTCGGAAGGTACAACAGACT
ATGATAATTTGCCTTATGAGTATTACGGTTTCAAATTCGCAGACCCGGAAAGTACTTTAAGAACAAGGATATGGGCATCCTTACGCTCTCAAACCT
TATACCGAACAGTTTCCGGCTTCATGAATTATAGACATGCGCTTGCCGAATTATACAAAGCGGAGCACGAAGATTGCATCAACCACATTTCATCATT
TGACTTTTGAAGACGAATTGAAAGCACTCATAGAATCTAAATTTACATTGCTAGTGTCGATACAACGACACAGCAAATTTCTCAGAGTCAGAAAT
GCAATCGTTTCGAAATCATGGCTCAAATTTCCCCACAATGAAAATATCAGTTCTCGAGGAGATCAAAGAGGGGCGACAAACTGGTTCATTATTGC
TCACTATTGGACTTGGCCAAAAAAGACGAAAGTAGCCAATATGGCAGAAAATTAATAATCAGGCTTCCTGGGTATCCTATTTTGGGAGACGGCA
AGTCTGACAATCAGAACACAAGTGCAGTGTTCTATCGAGGAGAGTACATTCAAGTCGTAGATTCCAACCAAGACAACACTACTTGGAAGAATGTTT
GAAAATCAAGTCAATGTTGTCTGAGTTTGAGGAGCTAAATTTGGCACCAGTAAGAGGAACATCCATGACCAGACCTCCAGTTGCAATTGTTGGC
GCTCGAGAGTATATCTTTTCGGAGCAAGTTGGCGCCCTTGAGACATCGCAGCAGGTAAAGAACAACACTTTTCGGAACATGTTTGGTCGAGCAC
TAGCTTTCATGGAAGGCAAGTTACATTATGGCCATCCCGATTTTCGTAAACGGGATCTTCATGTGCACTAGAGGCGGACTTTCCAAGGCGCAACGT
TCACTTCATTTGAATGAGGACATTTATGCTGGCATGAATGCAATTGCTCGTGAGGAAGAATAAAGCATGCCGACTATTTTCAGTGTGGAAGAG
GCCGTGATTTGGGGTTCAATACAATCTTGAACCTTACTAGCAAAATCGGGGCAGGCATGGCTGAACAAACGCTATCTCGTGAGCAGTTTTATTTT
GGAACCTCGGTTACCTACCGATCGCTTGTTTTCTTCTTTTATGCACATGTTGGGTTTCACATTAACAATGTGCTCATAATACTCTCGATTTCATTTATT
CCTGATATTCCTCTTTAACATAGGAAGTCTTCGAAATGAGAGCATTGTCTGTGATACCACAAGTGGACTCACTGAGCCTACTCCCATAGGCTGTT
ACAATATCAAGCCAGCAATTGATTGGATCAGTCGCTACGTTCTTTCAGTCATAATATGTTTCTTCTCTCGTTTCACGCCATTGGTGATGCAAGAGT
TTATTGAACGAGGAGTGTTGAAAACCGCTAAAAGAATCTTTTTCCACTTAATTTCACTTTTCGCCGTTATTCGAAGTATTTGTTTGTCAAGTATACG
CAAGTGCATTCGTGGATAATCGGTCGTATGGTGGTGCCAGATACATTAGCACTGGCAGAGGATATGCCATATCTCGAATTTCTTTCGCCACGCTTT
ATTCGAGGTACGCATCGTTATCAATTTATTGGGGCTCACGCTTAAGTTTGATAATCATCTTTGCGTGACGACAGTATGGCAGATATCCTTGTTGT
GGTTTTGGATCACTTGCTTATCCTTGTCCTTTACCGTTTCATTTTAAATCCACATCAATTTGACCGAACGGAGTTCTTCCTTGATTATAGAGAGTA
CCTTAGATGGCTTGGGAGAGGGAACCTTTTCTCGATGCCGTAACCTTTGGGTCCGCCACGTTTCGGTTTCAAATAATAAAGCTGACTGGGCTCAAA
GGACCTGGAAGTAACGAGCTGGAAGACTTAGTTACCCCAATCTCCAAGTTTCAGGTTTCGCTATATGGAATTTGGCCAAGGCTATTCTCAACGTTT
TGAGCTTCTTGGCTCCGTACATGTTCTTGAACCTCACAAAATGGAGTAGCTGAGCCATCAAAAGTCAATCCTTTGATGCGGGTAGCTGTGATCGTT
GCAATCCCACTAATCAGCAACATCATAATATTAGTTGTGCTCTTTGGTATCTCCATACTTCTAGGATCTATGATAAGAAACAAGCGTTTCGCGGATA
CTATTGCAGCAGTTGCTCATATCTGGTCAATCTTGGCACATGTAATTGTCATCGAAATAACCTGGTACATCCATTTCATGGAATCTTCCACGCAGTT
TGGCGTGTATCTGTCTTGATCACCATTACGCGGTACTTGATGAAGCTTGCTAAGTATGTGTATTTCCAAGAGTCAGACAGGTTGGAAGCC
AATTCTGCTTGGTGGTCAGGGCGATGGATTCAACACCATCTAGGATGGCACATCTTATCGCAGCCATTCCGAGAATTAGGATTGAAGTTAGTCGA
GCTAAACTTCTTTCGATTTGACTTTCTTCTAGGGCATGTCTTGTTTTGCTGCTTGAACCATGCTCTTTATCCCGTATATTGGTCAATTACACTCG
TTGATGATGTTTTGTTTTGTTTCGTCACAACTCATTGAATGTGAGTGGAACACAGCACTTGCATAGTCGACAAAGGAAGCGCCAACGAAAACAG
GCGTGAGATATTTTTTCGTATTCATTGGAATCCTAGTGGGCATATCAGCATTACTTGTGCTCCGTATCTTTTGAGAAAATACTGGGAATTCTTGG
ATAAGTCGATTCTACCTTTGCGCAGCCATTGTTCCAGCCTAGCAACCAGGATCAAAATGATACAGGACCCAGAGCACCTTCGAGCTTCTGGAG
CAAAAAACCACCTCCAGCAACATGGTCTACCATATGGTGA
ATGAAATCTGGTTTATTTGGATTAAAGTTTGATTGCCGCAACATTTGCGAGAAATATTGTGTATCCAGAATGTTTTGAGGAACAAGTCAAGTTGGC
ATTGAATGTTGATAAATTGGAACCAAGCGTGTCTCCTTCGGGGATCAAGTTGGTGTGTTGTTTATAAGGCTCGTGACACCAGCGAAGAGAATTTG
GATGGAGAAATCACCAAGGTGGTGGATGCTGAAACGCGGACCGCTGAGTCAACCGCTGGGTTGGCTACGTCGACTGCTGGGTTGACCGCTGCT
CCAACCTCCCGCCACTATTGTGACAAATTTCCAATACGGTACTACCACCTCCACCATCTATACCGCATCATCGACTCCAGCCTCCACCACATTTACG
TCTGTGCAAAAATTGGAACTACTCGAAGAAACCTCTTGCAACGGGTGGAATCAAAATCTTTAAACCTCTTGCAAGAGTCTATCGAGATTGCCA
GCATAACCGATGGTGTGGTCTTTACAAACACCCTGTTTCCAACAAATGGACCAAAAATGCGGTATACACAGCCATCATTAACCACGAAATTTACC

D_104046

GTTGCATCTGCTGTTCAAGCTGGCTGACAGTTTGGCCAACAAAGCGTTGACAGAAGTTGCCAACACTGCCTTAGAGACCAACGATACTTTACTGT
CAAGGTCACCTGAACTCTCACTGGTTGAGAAGCATGTTATAGTGGTAGAGTCATCGTGTGAACTGTCCAGTTCTCTCGAGCCATCCTCGTTCAG
TTCCGAGCCATCGAGTATCCCGTTCAGGTCCAAGCCATCGAGTATTCCGTTGAGTTCGGGCAGGTACTTGAATCTGACCTCTGCACTGGCCACTT
CCGCTCCTTCATCTGTCTTGGTTGCACCCCACTATTCTGCCTCTTCAATTGCAAGCTCGCTGTCTTGCTACTCAAGCTCTGCATCGACTGGCTCGC
TGTCTGGCTACTCAAGTTCTGCAACATCAGCTGGCTCGCTGTCTGGATATTCGAGTTCTGCATCATCAATTGCAAGCTCGCTGTCTGGATACTCA
AGCTCAGCTCCTTCCTCATCGCCAGAAAGTGAGAGCTCAACCTCCGAGTCTTCCGTTGCTCTGTGCGCAAGTGTGACGGAATCCTCTAGCGAGT
CAACAATTGCAACCTCGACCCAAACTTCGTGCGCTGCTTCGCCTCGATTATTTAGGGTCTTCTCTTCAACTTCGACTGCAAATGGTTTCACAGGC
GATTTGTTTAAGGCAATTTCCACCAACGCCGTCTCAGGTAAATTTCTAAACAAAGCTTACCATTGGCAATTCCATCTGGTGTGACAAACTCGGA
TAAATACCAAAACCAACAAGTTTTATGTCAATCTCTTTCTTGGTGATCAAACCGATATGATCTGGTCTTATCCCTATGGAATGCAGTACCTGAAGTC
AACCTACTACGGATGGGCAGTACAACATACGATCCCCAGCGCTCGAGTATTTGGTAATGTCAATTCCAACAACAACAATCCCTCATACTTTTTCA
ATCCAATCAACATCAAGGAATTGATTCTTTACGCAACGTCTTTCACATCAAATCTCAAGATGTCAGTCTCCAACATGAAGGTAATGTCGGCTTTG
GTCAAATTAGGACTGGCAACTAACTATATCGAGGTCCCTGTGGTGCAAGGTATGGGATTCGTTACTTCCATATACCATGGAATCTCATACTCAA
ATAAATCAGGAGTTGGAGTCAAACTCTCGTGAAGGAACTTCCTCCAACTTGTTGTCCAACATATTGAAATTTAGAGCAACTCTTTTCAGCG
GCACTGAATATTTGATATATGTGACGTTTCCCAGTGGTACGTCCACCAGCGGATTCACATTTTCAGTTTCAAATTCGAATACAATCAAAGCATCTA
AGAATATCAATGGTTTGATGATTCAAATTGCCGTGGCCCCATCATCGTCACAGGACAAATACTACGACCAGACGGCAGGAACGTATGTTACTGAA
TCCAAAATCAAGGCGCATGGTTATGGTGGAACGACCGCTGAATATCGATTCTCATACTAAAGCAGGTTTCATCAAAATCCAACTTACCTATTGT
GTTTTTATTGCCTCACCATGTTGACCTGATTGATGCAACCACCAAAAACGCTGCCACTGGTATCACCTTGTCATCCACAATAAGGAACAATGT
CTGCTTATTTGGCTAGCGAAATCATCATGAATGAATCGCTAAACTACAACATTCAGTTTTTGCCTTGGGTTCAACAAATGGGTACAACCTGCACCA
TTTTACACGACGAATCAACTCAAGCTTCTTGCACTGGCGGCCAATACTGAGTTATCGGTAGATATAAAGACGATGGTCTTATCCATGAACCTAAA
CTACTATTCAGGAAAGGTTCTTGATAAATATGCTTACATTCTCTTGGTTGTGAGTGATATCATTGGTGACGAAACATTAGCAAAGTCAACCTTGAA
AATACTCAAGGACACTTTTGCAGTGTTACCAACAATCAGCAATATTATCCCTTGATGTACGATACGAAGTTTGGAGGAATTACTTCGACTGCAT
CACAAGGAGGTGATACTGGCGCTGAATTTGGAAGCGCATATTACAACGATCATCACTTCCATTATGGATACTTTGTACATGCTGCAGCCATCATTG
GTTATGTCGACAAGAAATACGGAGGAACTTGGTATAAAGATCAACAGTTTTGGGTGAATGCGCTCATCAGAGATGTAGCGAATCCATCGCCAGA
TGACAAGCAATTTCCCGTATTTAGAATGTTGATTGGTTTGGTTCATTATGGGCATCGGGGCTTTTCGAGCCGGTGATGGTCTGTAATGAGG
AATCGAGTTCTGAAGATTACAACCTTTCGCTACGGAATGAAGCTTTGGGGTAAAGTATCAGGCAATCAAAGAATGGAATCAACAGGAGATCTTAT
GCTCGCGGTGATGAAGAGAAGTATGAACATGTACATGTACTATACTTCATCAAACTCGGTTGAACCATCACAGATACTTCCAAATAAAGTATCTG
GTATCTTGTTTCGATAACAAGATTGATTACACAACCTTATTTTGGAGCACCAACGCACATCCCGAGTATGTCCATGGTATTCATATGCTTCCAATTAC
ACCAGCATCTTCACTCATTTCGAGGCAGTGCATACGTAAAGGAAGAATGGCAAGATCAAATCTCCACATTTATCTCCAACGTCAAAGACGGATGG
GCAGGAATTTTGCATTGAACCAAGCGCTCTTCGACGCATCTTCTTCGTACGCATTCTTCTCCTCGAGCTCATGGTCTTCTGCCTACCTTGACAA
CGGTCAAAGTCGGACTTGGAGTTTAGCGTTTTTCGGCCGGTGTGAGCAACGCATTGAGTTAA
ATGAAGTGGGCCATTGGCGCTGCTGCCATTGCGGGTGTAGCTTTGGCTGATTTCATCAATAATTCAACCTTGACCACTGCCACTCCATCCGTTGG
CAAGTCTTGTTCTTCAAGGACTTTACTGCTACCAAGTCTGCCGACGTGCAGTCTGTCGCTGCATGTGCCACTGCCGTTGGTGACATCACCATC
GAAGGTGACTCTTTTCGGCACCATCGAATTGACCGGTCTCGAACAACCTTTACGGTTCTCTTCAGGTGAACAATGCTACTCAAGCCACCAGCTTGA
ACGCTCCTACCTTGCAATTGGTTTCTGGTCAATTGGCGTTGTCCGGTAACACCATCTTGTCTACCTTGAACCTTGGCTCAATTGACCACTGTGGGA
ACCTTGCACTTCAACGCTTTGCCAGCTTTGGAACCAACCGGTTGTCTGCTGGTATCACTTCTGCTGACGAGGTGATTATTTCCGACACTGGTTT
GACTTCATTGGACGGAATCAATGTGTTCAAGTTGCAAACCTTTGACGTTAACAACAACAAGGATATCGAGACCATTGACTCTGGTTTGAATCT
GTCATGAACTCTTGTCATTGCTTACAACCTTGAAAAGGTGGACGTTGCTTTGGACGAATTGACTTCTGCCAACACCGTTTCGTTCCAGTCCA
TCAACTCTTTGTCTGTTGCCAACTTGACCAAGATCGGCGACTCTTTGTCGTTGACTCCAACCTCGTTGGACAAGATTGAGTTCAAGCAATTGAG

D_104112

CTCGATCGGCAAGTCTTTGACCATTCAAAAGAACGACAACCTTGGAGGAAATTGACTTCCCCAAGTTGAAGTCGATTGGTGGTGCTTTGGTGATC
CAACTGAACGACGAATTGAAATCTTTTGATGGCTTGCCAAAGTTGGAACCATCGGCGGTTCGGTCAACCTCAAGGGTAAGTTTGACAATGGTA
CTTTGAGTCTTTGCAAAGAGTTGCTGGTGGTTTCAACTTGGACTCCACTGGAGACTTGACTTGTCTGGAATTCAACAAGTTGAACAAGGACG
GAGACATCAAGGGTGACAAGTTTGTGTGTAAGGCTGCTGACGAGTCGTCATCTTCTTCGTCTTCAAAGAAGGGCAACTCCAATGGTACTGCCA
CCAGCGATGACTCTTCTTCTGAGACCAGCAGCTCCGGTGGTTCTGGTTCTTCTTCTTCGAGCTCCAAGAAGAGTGATGCCAACTCTGCTGGTCT
TAACTTGGCTTCCATTCTTGCCGGCTTCGTTGCCCTTGGTGCCACCTTATTTTAA

D_101126 ATGCTTTACACTTCGATTTTGGCAGCGTTGACCGCAGCCACCGCCGTTGGGGCCGCTAGTGACAAATGTTTCATTCTCTACCACCGTCAAGGCAG
CCACTGCTATTTCTGACTTAAATTCTTGTGAAACCTTGGATGGTACTATCAAGATTACTGGTGACGATTTGGGTGATATCGACCTCAGTGGGGTCC
AAGAAATCAAAGGAGATATCAACTTTTTCAACTCATCTTCTGTACCTCCATTAATCTCAATCAGTTGAAAAAAATCTCGGGTTCGTTGGCAGTT
AATGCTTATACCCAATTGCACAGCATTGACTTCACCAGTTTGAGTGAAGTCGAGAAATTGTCTTTGATTTCATTGCCATCATTTGCCATTCTCAAC
TTGAACACTGGTGTTTCGAAAGCAGGTTCCATCGAGATTTAGACACTGCTCTTTCGTCTTACAAGGTCTTACCAACTACGACACCGTCAAGA
GCTTGAACGTAAACAACAAGAACATCACCTCCATCGACTTGGCATTGCAAACCTGTCGACGAGGACCTCACTTTGAGTTTCAACAGTGACG
ACTGTGAGGTCAAATTGAACGAATTGATCTGGTCTTCCAATTGACCATCCAAGATGTCAGTGACTTTTCTGCCTCCAACCTGACCGCCGTCAAT
GGTACTTTGAACATTGCTTACAACAAGTTTGACCAATTTGACCTCAAGGAATTGACCAATGTAGGCGGATCTGTTCTCGTTTTTCGCTAATGACGA
GATGACTTCGTTGACTTGAGCTCCCTCAAAAACATTGGAGGAGAATTGAGAATCTTCAACAACACCGAGTTGGAAGACATGAACGATACTTTT
AAGAAGTTGGCCAAGGTAAAGGTGCCGTCAACATTAACGGTGCTTTCCACAACCTTGACCATGCCTGGGTGAAGGAGGTGGATGGAGACTTT
ACCGTTGTTTCCACTTCTGACGAGTTTCACTGCCAAGATTTCAACAAGTTGAAAAAGAATGGTGACATTGAGGGACACAACCTACAAGTGCTCT
GCCCCCAAGAAGGAACAATCTTCCAAGTCCAACCTCTTCCAAGTCGAGCAGCGGATCTGGATCTTCTTCTCTGACAGCTCCGATTCCTCGTCCT
CGTCGTCATCTGATTCTGGAAAGAAGAAGAGTGGATCCACCAAGACCATGGCTGGAATGACATTTGTGTTTGCCGTTGTGGGAGCAGTGATTGC
CATGGCATAA

D_102974 ATGAGTAAACAGGCCCGGAAATCGACCAAAGATTTAGCATGAGAAACGGTGTGAGTCTCGGATGTCAGCATGAGAGTAGGGAACGTTAGT
GACATCGATGAGGAGTCTACGGGACCCATGGAGGTGCCAGAGCCCAAGAAAAACAAAAGTTTTTGGAGGTACACTTTTCCCGCTGCATTTTCA
TCTCTCGGTGCCATTTATGGAGACCTTGGAAACATCTCCATTATATGTGCTAAACTCGGTCAAATACCCTCATAAAGAACCCACTGAACGAGATATC
ATCTGTGCGGTTTCGGTGATCTTTTGGGTATTACGCTCATTGTTATCGTCAAATATGTGGCGATTGTGCTTTTCTTTGGTCCCAATAATGGTGAAG
GTGGTCAGGTAGCCATCTACGCCAAAATCGCCCGACACCTTAAATCGGTCTTAAAGGTGTAACCATTCTGAGACACCGGAAAAAACCGATCT
CGAGCTTCTTTCTCGACAAGAAACCGTGCTGAGCTTTGTTTCAAGTACCAATAAAGCGTGGAACAAAATCCGACAGTGGTGAAAGTGGTCTC
GTTTGTGGTTCTAACAGCATGCTTTCTTGGGTGCTCGTTGATCATTTCCGATGGTCTTTTGGTACTCCCACAACCTCGGTGTTGAGCGCTATAGCTGG
TATCCAAATTGCAAAGCCAGACTTTGACAATGTCTTGCAGTTTCTGAGGTGGTCTTTTGGTGCTTTTTTGTATCCAGCAGTTTGGATCCCACA
AGATATCGTTCACTTTTGACCCATAATCACCTTTGGCTTTTTCGGCTTGATTATCTGTGGATTGTACAATATCATCAATATTATCCTGCCATCTTC
AAGGCTATTTCTCCGCATTATGCCATTGAAATTTTAAAGGCGGGTGGAATCGACGCTTTTAGTGTTGCATGTTGGCTATAACTGGAACAGAAGC
TATGTTTGCCGACGTGGGACATTTTGGTCGAGCACCGGTTTCACTCGCTTTGACTTGTTCGTGTATCCAGCATTGATGTTGTGCTATTTTGGACA
GGCTGCGTACATCATTATCATCAAAAAGCACTTTCAAATCCATTTTCTACTCGATTCTTGGAGGCACCAATAGTGCGCCATACTGGATTATGTT
CGTGTGGCTACACTCAGTACCATCATTGCCAGTCAGGCACCTCATCTTGGGAGTTTTTCAGTATTCTTTCGCAATTGATCAATTTGGACTGTTTCCC
AACTTTACTATAATTCATGTGTCCAAATCGCATGCCGGTAAGGTGTATCTTCCAATGGTTAACTGGATGCTCATGGTGGGTGTGCTCTGTACCAC
TGCTGGGTTCAAAAATAGTAACAATGTCACCGCTGCTTATGGATTGGGTATCACGCTCGATCTTTGTTTGACGACAATTTTGTGACTTTATGCTT
CATTTTCGTATATCAAGTCAACATTTTGTGCTGGCTTTCTTCTTTTGGTGTTTCTTCCGTTGGAGATAGTTATGGTGATTCCAACCTGAAGAAA
ATCGAACATGGAGCATGGTTCCCCATCATGATGGCTGGAATCTGTTTCTCTTTTCTTGGTGGGCAAGAGCCAGAAAAGTCGACC
ACGAATTCAGTTCGAGGGCTCGTATAGATAATGTTTTTCCATCTTTGAGACGGACTGCTCAAACCGTCGATTTGGGCCGCGGAAGAAGCCCTAC

AAGAAAAGACGAAGACGAAAGCCGTGAAGAATCTGTGGCAGAATGGAACGAGAACTTGATTGTGAATTCAAAGTTTGGTGAATTGGCATTGA
AGACATACGACGGAGTGGCTATAATCCATTGTGAATCATCGTACCAGAATCTCATGTCTCCAAATACCGTTCCTGAATTGTACCAAAGGGTGGTT
TCGTCGTTTTGCTTCGTTGCCGAGAATTGTGATTTTTTGTCCAAAAGAGCGTTATCTGTTCCCTGTGGTTCCACAAGACGAACGAGTGCTTCTTGG
ACCTACCAAAAATCCAGGGCCATTTTCGGTGTGTCTTGCGATATGGGTTCCACCGAAGAGATGGTTATCGATAAAGATTTGATGCAACATATTCTCA
AGTCTGTGCCTGGATATGTTGAGTTGAACGATAGTCCTCATCGAGACCAGATTCCGGTTCAGTACTTCATGTTTTCGACAAGAGTGTTGTCAAG
TCTCACACCTACTCGAGCAATCCCACTCGGAATATCCTTAGAAAAGCCGGAAGACGGGTGCGTATTTTTGCCATAGAGCATATCTTCAGTCCTAT
CACTTCGATCTTCAACTTTCACGGGCAGTACTTGAAAATAGAGGATGAAGCCGAAGAAACACAGCGCAAGTTGTTTCGTTGGAGGAGTAGTTAG
AATCTGA

D_104268 ATGGAGCACTTTGATCCTCGTCGTGAGATAGACAAATACTCGCTTGATCTGTCTACTTTTGACCTTATAGATGTGGGAAAATTTACAAATTTGAAA
TGCTCGACTGTGTTTGATTATATGTTACATGGCTGCTTCTAATCCTTGGTGTGGTACTTCTAGGCGTGGATATTTACACTTGTCTCAACATTCTTG
TTTTTCACCGCTGGAGTTCCGACGACTATAAACCTATGCATACTCAATTGCCAAATGGATATTTACCGGGTGTATTATTTTCCAGTTTGTGCTTCT
CTTGTAACCACTGGATATGGGCCATCCATACTTATAGGACCCGAAACATAGCATTGGCATACTGAACAATATTGCTCGTCACTTGTACACGATTAA
ATCTTACGACTATCATTGTCTTTTCAACCTGGTGGAAACATGACAATTTCTTTGATTGGGCATGTTTTCTTGCATACTTCGAGATGGACTCAGCTTT
GCAAATTTCTCGTCGCCGATACTCCTCGTCAAGTAATCAATATCTTGACCCTTCGTTACTACGCTACCAACGAAAATTCTTCAAATGATATCATTCA
AAATATCAAGCAGATCGCTACATCTAACATTTCGGCTCTCGGTGATCTTGTGCTTTATGCTTCTTCCGTGGCCATTTGGTCCATTTTCTTCTTCGT
TTCGTGTTTGGGATGCTCTGCTACATTCCATGTTTGATGAAAATTTCGAAAAAGGGCCACACTAGACTCAAAAAATACTGCTGTTCCGTTGTAA
TCTGCACGTTTCGCCGTTTCGTCTACAAGCATCACAACCACGCAGCAAATTACTTGAAGAAGGTATTCTCGATTTAAAGGAAATCAATGAAAAT
CCTCTTCTCAACTCAGCGTCCACCACTGCCACATTTGACTCGGCTTTCCAGTACAAACCCGAACCAGCCAAAACCTTTCCAGCCAATGGACCGTT
CTTACGACACACTTCCACGCTACGGCTCAAGACAAAACACTTATGAATCGTTACCACTCCAGAACATGCCAAATATGCAACGCCGTAGACCACC
ATATGATCCATTTGGCGACGAGAACAAGATTTTCGAGCAAAGCACATTTGATGCACCAGGATCCTTTTCGGCGATCCTAAACTTGAAGATAATGATA
TGAGCGACACAGAAAACGTATACGAGCTCTATAGAGGTGTGGAAGTCGAGCCACCTATGCATAAACGGTATAATGGATTTGATCCACCACCCAG
AACTGGTTTCAGCTTCTTCGCTCACATTTTCTACAACAGGACCTTTTGAGCCAGTATCACAACCCATACTGACCCGGTTGCACCGCCAGCTTCC
ACTCCGTCTATTTCTGGGCCTATAACTCGAACGGGGACAGCACCATATCCACCAGAAGAAACAAGCTCTTTGTTGGGAGAGACATCGGAAAGT
GACTTGCATTCTAGGGAACCTGGAACCAATGGAACCTGGAACCGGAATCGAAACCAAGGGAAGCCCCATACCCCATACGCGAGTCGTACGCTCTC
CCAAGAACCTCTGACGAATACTACAACAGGTAG

D_101005 ATGACAGAGAACCCGTTTCGATGTGGAACAGGTTCTAAAACCACCCCAACGTGTCAACTCGGCTGCAAACCGCTATTGCACCCAGTCGGTGGAG
GACACGGTGCTGGAGTTCAAAACCGATCCTCACAAGGGGCTTTTCAGACAATCAGGATATTCTCAACCGTAGATCCATACACGGTGTCAACGAGT
TTGCCGAAGATGAAGAGGAGAGTCTTGTGAAAAAATTCATCGCAAGCTTCTATTCTGACCCATTGATCTTACTTTTGATCGGGTCTGCTGTCATT
TCATTTTGGATGGGAAACGTTCGACGACTCCATATCTATCACCTTGGAATCACTATCGTCGTGACTGTAGGTTTTGTCCAGGAGTACCGTTCGGA
AAAATCGCTAGCTGCATTGAACAAATTGGTTCCAGCAGAAGCCAACCTTGACACGCAATGGTAACACCTCTCATGTTCTAGCATCGACCTTGGTT
CCTGGAGACGTGGTCCACTTTTCCCAAGGTGACAGAATCCCCGCCGATATCAGAGTAACGGACGCAGTCCACCTCTCCATCGATGAGAGTAATC
TCACCGGCGAGAACAGACCGGTAATAAAATCACCAGAAGCCATCAAATCAGAAGCAAACGGTCTTATTCCAATCACTAACCGTCCGTCTGTGGT
CTACATGGGAACCTTGGTTCGCGATGGCCATGGTTCTGGAATTGTCTAGCAACCGGTTCCAAAACGGAATTCGGTGCCGTTTTTCGAAATGATGT
CAGAAATAGAAAAACCAAGACTCCGTTACAACAAGCCATGGATAAGCTCGGAAAGGATCTTCCATCTTCAGCTTTTGTGTCAATTGGAATCAT
CTGCTTAATTGGTATTACCCAGGGTCGCTCGTGGTTAGATATGTTCCAGATTTCCGTTTCTTTGGCCGTGGCAGCCATTCCCGAAGGTCTTCCCAT
CATTGTACAGTCACTTTAGCCCTTGGTGTGCTTAGAATGGCTCGTCATAGAGCTATCGTCAAGAGATTACCCAGTGTGCAACATTAGGAAGTG
TCAATGTAATTTGCTCTGACAAAACCTGGAACCTTTGACTGAGAACAGGATGACTGTGACGAAAATATGGTTCGACTGATTTTGAAGGTACGTTCAA
TTCCCCATTCTTGGTGGTTGAAAGGCTCGATGATAATACTTTACACCACAAGCTCACCAGCAACATTTCGCAGAATATTAGAGGCTGGCAATATCT

GTAACAACGCCAGGTATTCATCTGAAAGCGAGAAGTTTGTGGAAACCCTTCCGATATTGCCTTTGTTGAATGCTTACCACACTTTGGTCTTGAC
GATACTCGTGGTCAAAAAGTACGTACTTACGAATTGCCCTTTTCCTCAAGAAGAAAGTATATGGCAGTATGTGCTCATTCTGGCGACACTTCGAG
ATCTGAGACTTTTGCTAAAGGTGCAACTGAGCAGATTCTTGACGTTCCACGAAATACTACGACTCTAAAGGTGAGGTAAAGCAACTTAGTGAC
GAAGTAAGAGACGAAATCAACCAGAGATCCAACACTTTGGCGGGAGAAGGGTTGAGAGTTTTGGCCTTGGCCAACAATACGCAAAAAGTTCGG
TGACGAGAAACATATCGAGAGTGAACCTACCGATTAAATTTTTGCGGGTTGATAGGAATGAAAGATCCTCCCCGTCTAATGTGAGCAAATCGG
TTGCACGTCTCATGAAGGGTGGAGTACATGTGATTATGATTACTGGTGATTCTCCAAGCACAGCTAAGAACATTGCCAAGCAGATTGGAATGCCA
TTACATACCAACGATTCTGTTCATGACCGGCGACCAACTCGACAAGTTATCCCCGAAGCACTTTTGAATGCAATCCACAACGTTTCGGTGTTTGC
TAGAACCCTCCAGAGCACAAAGTCTTGATTGTCAAGGCGCTTCAGGCTAGAGGTGATATCGTCGCCATGACTGGAGACGGAGTCAATGATGC
CCCAGCATTAAAGCTCGCCGATATTGGAATTGCCATGGGAAAAAATGGAACCGATGTTGCCAAAGAAGCAGCCGATATGGTGTTGACGGATGAC
GATTTCTCTACGATTTTGAATGCGATCGAAGAGGGTAAAGGTATTTTCTTCAACATTCAAACCTTTATCACTTTCCAGTTATCCACCTCGATTGCC
GCGTTGACGTTGATTGCTCTCGCTACGTTCTTTGGACTTCCAAACCCTTTGAATGCTATGCAAATTTTGTGGATCAATATCTTGATGGATGGCCCT
CCCGCCAGTCGCTCGGAGTTGAACCCGTTGATCATGAGGTGATGAACAAGCCTCCAGAAAGAGAAACGACAAAATCTTGACCAAAGCTGT
GATCAAGCGTGTTTTACAATCTGCCACTATGATTATCTTGGTACGCTTCACATCTTTGTCAAAGAAAGAATTGATAATGAGGTGACTGCCAGAG
ATACCACCATGACTTTACCTGTTTTGTAATGTACGACATGTTCAATGCTTTGGCATGCCGTCACCAAACCAAGTCTATCTTTGAACTCGGACTTA
AAAACCAAATGTTCAATTTTGGCGTGGCCGGATCACTTCTTGGTCAATTGTGTGCCATTTATGTGCCATTTTCCAGTCTGTCTTCCAAACCGAG
GCATTGTACTTATCAGATCTTGGAAGCCTTTTCTTGTGACCAGCAGTGATTTTTAGTTGACGAGGCAAGAAAGTGGTATAAGAGAAGGCAGTT
TACGATGAATGGAGTCAGCTACAGCGTATAG

D_103758

ATGGCTCCACAGAATCCAATAGAAAGGGCGCAAACAGCGTCCAAACATTTACAACCTACCCGGATCTACCTCGGATAATGAAGACAATATCAGTG
TTTCATCAGCCACACCTCTCACAGATAATTCAGGATTAACCTCAGAAGTGTTAACGGAACCTTCACGATCCCAAATCGCTTCGCAAATTGCATGAA
CTTGGTGGGATCAAACGTGTTACTGTATGGTCTTGAGACTAATTTGCTGAGTGGAATCGATACCCATAGAGATCTTAAACATAGAGAAGAATTGTT
CGGAGAAAATAGAATACCGGTGAAAGCCCAGAAAAACTTCTTTTCGTTCTATGTTACGATGCCATGAAAGACAAGGTGTTGATCATGTTGACTGTG
GCTGCGGTTATATCCTTAGCATTGGGCTTATATGAGACCTTTGGTGAAGGTCTTTGAGGGACGATGAGGGCAAAGTTTTGCCCAAGGTGGACT
GGGTGGAAGGCGTGGCCATTATTACTGCCGTTGTAATTGTGGTGGTGGTGGTGCAGCCAATGATTATCAAAAAGAACGACAGTTTGCTCGTTT
GAATGCCAAGAAAGAAGACCGCGAGTTGATCGTGGTAAGAGACGGAGCCCAGAAAATGATCTCCATTTACGACCTTTTGGTTCGGTGATATCATC
AACTTGCAAACAGGTGATGTTGTTCTGCTGATGCCATCTTGATACTGGGAGACGTTGAATGTGACGAATCTGCTCTCACTGGTGAATCTCATAC
CATTAGAAGAAACCCGCTGGCGAGGCTATGGATTTCTATGAGGCACAGCTTCCAACAGATGAAGATTTGGGCTCGTCTACCATCAAGTTCAAG
GACCCTTATCTTATTTCTGGTGCAAAGGTGCTCGAAGGTTTGGGATATGGAATGGTCACTGCAGTTGGCCCCAATTCCATTCATGGAAGAACAAT
GATGAGTCTTCACACCGACGCAGAAACAACCCCATGCAAGTTAGACTCGACAACCTTGCCGAGGGAATCTCCAAGTACGGTTTTTTGGCCGC
ATTGGTCTTTTTCATCGTTTTTGTTCATCCGCTATTGTGTCAATATTGCTCCAGGAGGAAAATTCAACGATATTCCTGGTCCGCAAAAGGGAAAAG
AGTTCTTGGACATTTTGATTACTGCTATAACAATTATTGTCGTTGCGGTTCCCGAAGGTTTGCCATTGGCAGTGACTTTAGCGTTGGCTTTCCGCA
CTACTAGAATGGCTCAGAACGGTAATTTGGTCCGTGTGTTGAAGTCATGTGAGACCATGGGTGGTGCTACCGCTGTGTGCTCTGACAAAACCGG
AACTTTGACTGAAAATCGTATGAGAGTCGTGAGAGCATATTTGGACTGTCCGAGTTTGACGATACTTCTGGTGGCCATGGTCCATTGTCTTCAG
AAGTGGTGAATGAACTTTCAGAAGAACTTAAGGTCTTTCTTTGTACCAACATCACTTTAAATTCCACTGCATTTGAGAACACCGACTACGACGA
GAAGAAAGCTCTTATGGCAAGACAAAAACCAAGAGAAAGTCATTTATCCGCCAATTGATGCAAAAACCCCGGAAAGAAACAACAAGAACGAC
AGGTTGAGCTTGAGTGGAACCGAACCTTATTTGGGAAACAAGACGGAATCTGCCTTGTTGATCCTTGCTAACAAAGTTTTCAATCAGTTTGC
AACAGACAACCTTGAGACCCAGCGGAGCGCAACCACGACAAGATAGTACAGATCATCCAGTTTGAAAGTTCGAGAAAATGGGCTGGAATAG
TAATGAAGATAGACAATGGGTTCCGTCTTTACGCTAAGGGAGCGGCTGAAATTGTTTTCAAGAATTGTGGGTACCTAACCAATGTGATGGTACT
ACGGTGTCCATGGATCGGTCACAGAGAGACGACGCTTTCAGCAAGATTGATGAGTATGCCAATGATGCTTTGAGAGCCATTGCACTTGCTCACC

GCGACTTCATTGGAATTTCCAACCTGGCCTCCACCAGAACTTTTAGAGGAAAACCTCCAAACAAGCCGACCCCTAAGAACTTCTTGCTGTAGGATC
 CACTATTCAGAAAGACCAAGACACTTGGTTTTGGATGGAATTGCAGGTATTCAAGATCCGTTGAAAGACGGTGTGGCACAAGCAGTTCTTCA
 GTGTAAGGAAGCTGGTGTCACTGTTAGAATGGTTACCGGAGACAACTTGAATACTGCAAAATCCATCTCCAGAGCATGCCATATTCTTACTCCTG
 ATGATCTTTCGAATGACTACGCATACATGGAAGGACCAACCTTCCGCAAGTTGACGGATGCGGAAAGAACGCGGATTGCGCCTCGTTTGAAAGT
 ATTGGCGAGATCTTCTCCAGAAGATAAACGGGTTCTTGTGGAACATTGAAGAAAGCAGGAGAGGTTGTTGCTGTCACGGGTGACGGTACAAA
 CGATGCTCCTGCCTTAAAGTTGGCAGACGTGGGATTTTCTATGGGAATTGCTGGTACTGAAGTGGCCAGAGAAGCCTCTGATATTATCTTGATGA
 CAGACGATTTACCGATATTGTCCAGGCCATCAAATGGGGAAGAAGTGTTCGACTTCGATCAAGAAATTCATCCAGTTTCAGTTGACCGTCAAT
 ATTACTGCCTGTATCTTGACGTTTGTGTCCGCTGTGGCATCTTCCAATGGCCAGTCGGTGTGACTGCTGTGCAGTTGTTGTGGGTGAATCTTATC
 ATGGACACTTTAGCGGCGTTGGCGTTGGCGACCGATAAGCCAGACGACTCGTTTTTGAAGAAAAAGCCTGCTGGTCGTAAGTCTCCTTTGATTT
 CGGTTTCGATGTGGAAGATGATACTTGGACAGTCAGTCACTCAGTTGGTTATCACGTTTCTTCTTCAATTTCTGTGGCAGAAGATTTTCCATGGC
 AATAATCACATCGACAACCATCAGAACAAGCAATTGGACGCCATGACTTTTAACACATTGTGTGGTTGCAGTTCTGGAAATTGGTCGTCACGA
 GAAAGTTGGACGAAGCAGATGGCATTGCAAAGGTTCCGGACAGACTCACGGCCAACAACCTGAACTTTTTTCAACACTTGTTCGCAATTGGT
 ACTTTTTGGGAATTGCTCTTCTCATCGGCGCAATGCAAGTATTGATTATGTTTCGTCGGTGGTGTGCTGCATTACGCGTTGTTAGACAGACCCCTGGT
 CAATGGGCTACTGCAATCATCTGTGGATTTATATCGATTCCCGTCGGATTGGTCATAAGAATAATCCCTGATCACTGGGTGGTGGCCATTTCCCA
 ACCAGAGCCTTCAAGATCTTTATTTATTACGCTGGGTTTTCTGTTTTTGAAACGTAAGAAGAAGGAGGATCTTGAGAAAGCTGAACACGATGACC
 TTAATGACACTAAGATGTCGGACTTGTCCGCACAATCATGA

D_101154 ATGTCGATCCCCAACCCCGTCAGCTCGGTGTCCAAGGTTTACACGGATGTTTTAGCTTCGAAACCACAGTCGTAAGTGGGATTATGAAAACATAAA
 TATCAAATGGAACCTCGCAAGACAACCTACGAAATCATCAAAAAGTTGGGACGTGGAAAGTATTTCGGAGGTTTTTTTAGGAGTGGATCTTAAAAA
 AGGTGAAAAATGCGTTATAAAAGTGTGAAACCGGTCAAAAAGAAAGAAGATCAAGAGAGAAATTTCCATTTTGAAGAACTTGGACGGCCCCA
 ATATCATTGGGCTTTTTGATATTGTAAGAGAACCCAGCTGAAAACACCCGGACTCATCTTTGAGCACGTCAACAACATCGACTTTCGCACCCTC
 TACCAGTCTTTCACCGACTATGACATTTCGTTCTACATGTACGAATTGTTGCGAGCGTTGGACTACTCGCACTCGATGGGGATCATGCACCGTGA
 CGTCAAGCCCCACAATGTTATGATAGACCACGAGAAGAACTTTTGCGGTTAATTGACTGGGGTTTAGCCGAATATTACCATCCAGGAACCGAAT
 ACAATGTGCGAGTTGCATCGCGGTATTTCAAGGGACCGGAATTGCTCGTGGATTTCCGCTCTACGATTACTCTCTTGACTTGTGGTCGTTCCGG
 TGCATGTTGGCGTCAATGGTTTTTCAAGAAAGAACCCTTTTTCCACGGAAAATCGAACACCGACCAATTGGTGCAAATTGTGCGTGTGTTGGGAT
 CGGACGACCTACACAAATATTTGCAGAAATACGGGCTTGTTTTTGAGCGAGGAGTACGAAGATTTGGGATACTACAATAGAAGACCTTGAAGCG
 ATTTGTCAACGAGAACAACCGCATCTTGTCAAGTACGAGTTTCTTGATTTTCATCGACAAGTTGTTACGCTACGACCACCAGGAGAGATTGACG
 GCCAAAGAGGCTATGGCACATCCGTACTTTGACCCAGTACGGCCCAAGTAA

D_103937 ATGGTTTTGCCTCACGAGCCCGAATTTCAACAAGCTTACAACGAATTGGTTTTCCGCTTTGGAGGAATCCACCTTGTTCCTCAAGAACACCCTCACT
 ACAAGAAGGTGATTCCTGTTGTTTCAGTTCCCGAAAGAATTATTCAATTCAGAGTTTCATGGGAAAATGACAAGGGAGAAATCGAGGTGAACA
 ATGGTTTCAGAGTCCAATTCAACTCGGCTCTTGGTCTTACAAGGGAGGATTGAGATTCCACCCAACCGTCAACTTGTTCGGTGTGAAATTTTT
 GGGATTTGAACAAATTTTCAAAAATGCCTTGACCGGTCTCTCCATGGGTGGAGGTAAAGGTGGATGTGACTTCAACCCCAAGGGAAGAAGTGA
 CGCTGAAATTAGAAGATTCTGTGTTGCTTTCATGAGACAATTGGCCAGATACATTGGTGCCGACAGAGATGTTCCCTGCTGGAGACATTGGTGTG
 GTGGTCGTGAAGTTGGTTACTTGTTCGGTGCCTACAAGCAAATGCAAAAACAACTGGTCCGGTGTTTTTGACCGGTAAAGGGTTTGAGCTGGGGTG
 GTTCTTTGATCCGTCCTGAAGCCACCGGTTACGGTACTGTCTACTATGTGGAGAAGATGATTGAAAAGGCCACTGGTGGAAAGGAGACTTTCAA
 GGGTAAGCGTGTGTCATTTCTGGTTCTGGTAACGTTGCCAATACGCTGCTTTGAAGGTTATCGAATTGGGAGGAACTGTGGTTTCTTTGTCTG
 ATTCTAAGGGAGCTCTCATTTCACAATCTGGTATTGTGCCTGAGCAGGTTGAGGCCATTGCTGCCGCTAAGCTCAAGTTCAGTTCATTGGAAGA
 AATCTGCAAGAATCTGCTTCCATTTTCTCGGGCAAAACCGAGTACATTGCCGGTGTCCGTCCATGGACCAAGGTTGGTCAAGTTGACGTAGCA
 TTGCCATGTGCCACCCAAAACGAAGTCAGCGGTGACGAAGCTAAGGCTTTGGTTGACGCTGGATGCAAGTACATTGCTGAAGGTTCCAATATG

GGATCCACCGTCGAGGCTATCGACGTCTTCGAGGCTAACAGATCCAAGAATGTTTGGTATGCTCCAGGTAAGGCCGCCAACTGTGGTGGTGTG
 CCGTTTCTGGTTTGGAAATGGCCAAAACCTCTCAAAGAGTTTCTGGAAGTCTGAACAAGTTGACGAAAAGTTAAAGAACATCATGTACACCT
 GTTTCGAGAACTGCTACAACACTGCTATCAAGTACTCTACCGAGAAGAGTGCTTCTGGCTTGCCATCTTTGTTGCAGGGTGCTAACATTGCTGGT
 TTCATCAAGGTTGCCGATGCCATGTTTGACCAGGGTGAGGTGTTTTAG
 D_102983 ATGTCCCCTTTTCTAGCGTCGAAATTCGCCAAGACGGCCCTTGCAACGACGGCCGTTATTGGTGGTCTGTTGTGTACGTGGACTACATCAAACC
 ACCCGCAGTGCCTGAGTTGGTCACTTCGTACAAACCTTTAAGAAAAGATTGCTGCTCCTCCAAAGAGAGAAGAGCTCGTTTCTCGGTTGGA
 AACCACCCCCAAATTCGATGTTCTTGTGATTGGAGGTGGTGCCGTGGGAACTGGTACCGCGTTGGATGCTGCTACAAGAGGCCTCAATGTTTGT
 TTGTTGGAAAAAACCGATTTTTCTTCGGGTACTTCTTCAAATCTACAAAAATGGCCCATGGTGGTGTGAGATATTGGAAAAAGCCATTTCCA
 GCTCTCTAAAGCCCAGTTGGACTTGGTTATCGAGGCGCTTAACGAAAGAGCAAACATGTTGCGCACGGCTCCTCACTTGTGTTCCGTTTTGCC
 ATCATGATCCCCGTCTACAAGTGGTGGAAAGTGCCTTATTTCTTCATGGGTTGCAAAATGTACGATTGGTTTGCCGGTCACCAGAACTTGCGGTC
 GTCCACTGTTTTCTCCAGAGAAATGACCGCTGCCATTGCTCCTATGATCGACGATTCCAACCTGAAAGCTGCATGTGTGTACCACGACGGAACCT
 TCAACGATGCCCGTATGAATGCTACTTTGGCCATCACTGCCGTGAGCATGGTGCCACCGTTCTCAACTACTTTGACGTGGTCCAGCTCGTGAA
 AAATGAAGGCAAAAATCGAAGGTGTGCGTGCTGTGACAGAGAAACCGGTAAAGAGCATCTCATCAAGGCTACTGCTGTGGTGAATGCCACCG
 GTCCTATGGCTGACAAGATTTTGGAAATGGACGAAGATCCTCAGGGCTTGCTCCAAAGATCCCACAACCACCAAGAATGGTTGTTCCCTTCGTC
 TGGTGTCCATGTCGTTCTTCCTGAATACTACTGTCCAAGAGATATGGGAATGTTAGACCCATCCACCTCCGATGGTAGAGTCATGTTTTTTTGGC
 ATGGCAAGGAAAGGTCTTGGCTGGTACTACCGACACCCCATGAAGTCTGTCTCCGAAAACCCAGTCCCATCCGAAGAAGAAATTCAAGATAT
 CTTGAACGAATTGTCCAAGTACATTGTTTTCCCTGTGCATAGAGAAGATGTGTTGTCTGCCTGGTCTGGTATCAGACCATTGGTTTCGTGACCCTT
 CCACTGTCCCCAAGGGTCAAGACCCACCACCGCTTCTACCCAAGGCCTTGTTTCGTTCCCATTAATCACCCAGTCTGAAACAGGATTGGTGAC
 GATTTCTGGAGGAAAATGGACCACTTACCGTGAAATGGCTGAAGAAACCGTTACT
 D_102964 ATGACTACCACTCCTTACTCTATTCCAAAGCCATTTAAAGTTTGCATTATCGGTTCCGGTAATTGGGGAACCTGCTGTGGCCAAGTTGGTGGCAGA
 GAACACTGCAGAAAAACCACAAATCTTTGAAAAAATGTTCAAATGTGGGTTTTTGAAGAACAATCGAGGGTAAAAATCTTACTTCCATTATC
 AATGAACAACATGAAAATGTCAAATACTTGCCCGGAATCAAGCTTCCTGAAAACCTGATTGCTAATCCTGATGTGGTATCCACTGTGGAAGGCG
 CTGACCTTTTGGTGTTCACATTCCTCATCAATTTCTTCCTCGTGTTTGAAGCAATTGGTGGGTAAAGTTTCTCCAAATGCCCGTGCCATCAGTT
 GTCTTAAGGGTCTCGAGGTAACTCTGAGGGATGCAAATTGTTATCCCAATCCATCACTGACACTTTGGGAATATACTGTGGTGTATTGAGTGGA
 GCCAACATTGCTACTGAAGTTGCCAAGGAACGTTGGTCGGAACACCATTGCATACTGTGTTCCCTCCTGACTTCCGTGGAGCCGGTCACGACG
 TAGACGAATACGTTTTGAAGCAATTGTTCCACAGAACATATTTCCATGTTAGAGTGATTGAGGATGTTGCTGGTGCTTCCATAGCCGGAGCATTG
 AAAAATGTTGTTGCTATTGCTGCTGGTTTTCGTCGAGGGTGCCGGCTGGGGAGACAATGCCAAGGCTGCGGTGATGAGAATAGGACTCAAGGAG
 ATTATTCACTTTGCTTCTTACTACAAGAAGTTTGAATCAAGGCTCTTGTGGACCCTCAATCCACCACATTTACCGAAGAAAAGTGCCGGTGTGTC
 CGACTTGATCACCACTGTTCCGGTGGTAGAAACGTCAAGGTTGCCCGTTACATGATCGAGCACAAGGTGGATGCTTGGGAAGCCGAAAAGAC
 TTTGCTCAATGGTCAATCATCGCAAGGTATTTTGACCGCAAAAGAGGTGCACGAATTGTTGGAAAACCTACGACTTGAAAACAAGAGTTTCCTTTG
 TTCGAGGCCACATACAAGGTGATCTACGAGAACACCGATGTCAACGACTTTCCAACGGTGTGGAAGCCGACGATTAA
 D_103937 ATGGTTTTGCCTCACGAGCCCGAATTTCAACAAGCTTACAACGAATTGGTTTTCCGCTTTGGAGGAATCCACCTTGTTCGAAGAACCCTCACT
 ACAAGAAGGTGATTCCTGTTGTTTCAGTTCCCGAAAGAATTATTCAATTCAGAGTTTCATGGGAAAATGACAAGGGAGAAATCGAGGTGAACA
 ATGGTTTCAGAGTCCAATTCAACTCGGCTCTTGGTCTTACAAGGGAGGATTGAGATTCCACCCAACCGTCAACTTGTCCGGTGTGAAATTTTT
 GGGATTTGAACAAATTTTCAAAAATGCCTTGACCGGTCTCTCCATGGGTGGAGGTAAAGGTGGATGTGACTTCAACCCCAAGGGAAGAAGTGA
 CGCTGAAATTAGAAGATTCTGTGTTGCTTTCATGAGACAATTGGCCAGATACATTGGTGCCGACAGAGATGTTCTGCTGGAGACATTGGTGTG
 GTGGTCGTGAAGTTGGTTACTTGTTCGGTGCCTACAAGCAAATGCAAAACAACCTGGTCCGGTGTTTTGACCGGTAAGGGTTTGAGCTGGGGTG
 GTTCTTTGATCCGTCCTGAAGCCACCGGTTACGGTACTGTCTACTATGTGGAGAAGATGATTGAAAAGGCCACTGGTGGAAAGGAGACTTTCAA

GGGTAAGCGTGTTGCCATTTCTGGTTCTGGTAACGTTGCCAATACGCTGCTTTGAAGGTTATCGAATTGGGAGGAACTGTGGTTTCTTTGTCTG
 ATTCTAAGGGAGCTCTCATTTCACAATCTGGTATTGTGCCTGAGCAGGTTGAGGCCATTGCTGCCGCTAAGCTCAAGTTCAGTCATTGGAAGA
 AATCTGCAAAGAATCTGCTTCCATTTTCTCGGGCAAACCGAGTACATTGCCGGTGTCCGTCCATGGACCAAGGTTGGTCAAGTTGACGTAGCA
 TTGCCATGTGCCACCCAAAACGAAGTCAGCGGTGACGAAGCTAAGGCTTTGGTTGACGCTGGATGCAAGTACATTGCTGAAGGTTCCAATATG
 GGATCCACCGTCGAGGCTATCGACGTCTTCGAGGCTAACAGATCCAAGAATGTTTGGTATGCTCCAGGTAAGGCCGCCAACTGTGGTGGTGGT
 CCGTTTCTGGTTTGGAAATGGCCAAAACCTCTCAAAGAGTTTCTGACTTCTGAACAAGTTGACGAAAAGTTAAAGAACATCATGTACACCT
 GTTTCGAGAACTGCTACAACACTGCTATCAAGTACTCTACCGAGAAGAGTGCTTCTGGCTTGCCATCTTTGTTGCAGGGTGCTAACATTGCTGGT
 TTCATCAAGGTTGCCGATGCCATGTTTGACCAGGGTGAGGTGTTTTAG

D_103507 ATGTCCGAAATAAACTTCACTCCACTTAAAAACACCAAGGTTTTCCAGCCGATTCAAGTTGGAAAAAACCTCCTTTCCAACCGAATTTTTTATGC
 CCCCTCCACAAGAACCAGAGCATTGGACGATCGGACTCCTTCGAAGTTGCAATTGCGCAACTACGACGAAAGAACAAGTATGCTGGTTTCGCT
 TGTGGTCACCGAAGCCACTTTTTTCATTTCTCAGGCCGGAACCATGGCAGGAGTTCCGGGAATATATACCCAGAACACACCAAAGGATGGAA
 AAAAATTGTGGATAAGGTTACGAGAACAATTCGTTTATTGCAATTCAGCTTTGGAAGTTGGGTCGACTTGATAACCCCAAAGATTTGAAGGCA
 GTAGGCTTACCCTACTTGGCACCTTCAGCCATTTATCCCGACAAAGATGCTCGGGAAGAAGCCGAGGCTGCGAATAATCCTATTAGAGCATTGAC
 CGAAGAGGAAATCCACAACCAGATTTATGTGGAATACACCACGGCTGCAAAAAATGCCGTTGAGGCTGGGTTTCGACTACTTGGAGTTACATGG
 TGCTCACGGCTACTTGTGTCACCAATTCTTGGAAGATACCTCCAACCAAAGGACAGACAAGTATGGTGGATCGGTAGAGAACAGAGCCAGGTT
 TGTGTTGGAGCTCATTGACCATCTTATTCCTATAGTTGGTGCTGACAACTTGCTATTCTGCTTTCTCCATGGGTGACTATTAAAGGTATGCCTGGT
 ATTCATGGTGATACCCATCCATTGACCACCTACAGCTACTTGCTACACGAGCTTGAAAAACGGGCTAAAGCCGGGAATCGGTTAGCCTACATTTT
 CATTGTAGAGCCTAGAGTCAATGGGTCTACTACTCTTGAAACCAAAGACCAAAGTGGAGACAATGGTTTTGTTGAAGATATTTGGAAGGGGAACC
 ATTCTCAAGGCGGGAACTACACATATGATGCTCCAAAGTTCAATCTGGTGATTAAGACGTTGAAAACGACCGTACGTTAGTCGGGTTTCAGTC
 GCTATTACGTCTCGAATCCAGACTTGTTTCAGCGATTGAAGGACGGAAATCCACTCAAGCCTTACGACCGTTCTCTCTTTTACCGAAAGGACGA
 CTGGGGGTACAATACTTATCCATACGAGGGACAAACAGAAGAGGAAATAGAGGCTGCAAAAAACAGAAAGCCAAAGCCTATTGGGGCCAAGG
 CATAA

D_103508 ATGCTGGCAATTAAAGTTAAACCCCTCGGGGACACAAAGGTGTTTGAGCCTATACAGGTGGGAAAGAATACTCTTTCCAATAGACTTTTCATGT
 GCCCAACTACAAGACTCAAGGCTTTAGAAGACGGTACTCCATCGAATTTGGCATTGCAACTCTATGACGAAAGAAGCAAGTTTCCCGGCTCGCT
 CGTGACTACTGAAGGAACTTTCACTTATGAAGAGGGTCAAGTATGGGAAAGAAGTCCAGGAATTTATACTGAAAGACATATTGAAGCATGGAAA
 AAAATTGTGATAAAAGTTCATGAAAACAAATCTTTTCATTTCACTCCAGTTGTTCAATTCGGGCCGTGTAGCCGACCCAACCATTCAGACAACA
 AGAATCATCCATTTGTTGCTCCATCGGCTATTTACCATGATGAGGAAACGAAAAAGCTGCCATTGCTGCTGGCAATCCTTTGCGAGAATTAACC
 TTGGATGAAATCCACGATATTATTAACAACAAGTACCCCAAAGCTGCCATAATGCTCTTAGAGCCGGGTTTCGACTATGTCGAAGTCCACGCTGC
 AAACGGCTACCTTCCCAACCAATTTATTGACGTTGCCAGTAATCAGCGCACAGACCAATATGGCGGTTTCGATTGAAAATAGAGCCAGGTTTGTG
 TTGGAAATCATTGACAAATTGACTGCTGAGATTGGTGCCGACAAGATTGGGCTCAGGATTTCTCCATGGTCGACATTCCAGGGCATGCTGACCA
 AAGGTGCAGAGATCGATCCATTGACCACCTACAGTTACATTTTACACGAATTGGAAAAAAGAGCTCAGAAGGGAAATAGGTTGGCGTATGTGTC
 CATTATCGAGCCTAGAGTTGATGGAACTCCACTGTCAAGAAAGAACACCAAGTTGGTGACAATTCGTTTGTCTACGATATTTGGAAGGGCACA
 GTTTTGAGAGCGGGTGGATACACTTATGATGCCCCAGAATTCAAACGAGTTGAAACCGATCTTGCCAACGATAGAACAGTCATTGGTTTCTGTC
 GTTACTATATCTCCAATCCAGATTTGGTTGAAAGGCTTAAAAATGGCTGGGATCTCCAACCATACGACAGGCCCTCTTTTTATAGAAGCGACGATT
 ACCGCTACAATACCTATTCGTTCCATGGAGAGCCCCCTAGAGACGAGGAATCCGGCAAGAATAGAAAGCCTGAGCCAATTGCTGCTTAA

D_103084 ATGTCTGACGTTCTGGCGAGCTACACAGAAGAAGGACTGCTAGTGGCTCACTCTATGGATCGGAAATAGATAGTTTCCATTCCGTAAGTCAAA
 ACTCAAAATGGAAGAATCTCAGACAAAAATCATTACAATACTTAGAAAGTATGGGTGCTTTATAGGACCTGGTATCATGGTTTCAGTGGCATAT
 ATGGACCCAGGTAAGTATGCCACAGGTATAACAGCTGGTGCCTCCAACAGATTCTCCCTTTTATTCATCGTTCTAATTTCCAATATCATTGCCATTT

TTCTTCAAAGTTTATGCATCAAGTTGGGCTCAGTAACCGGCTACGATCTTGCCCGTTGTTGTCGAGAATACCTTCCCAAGTGGCTCAATATCATTC
TCTGGATCCTTGCGGAAAGTGCAATCATTGCAACTGATGTGGCTGAAGTTATAGGTTTACGCTATTGCCCTTAATATTCTTCTTAAAATTCCACTTC
CAGCAGGCGTGGTAATTACAATAGTGGACGTTTTATTTGTGCTAATGGCGTATCGCAACGACACTTCCTCTACCAAGTTTGTCAAGATGTTTGAG
TATGCAGTTGCTTGTCTTGTGGTGGCCGTGGTGGTTTGCTTCGCAGTGGAATTGCCCATTTACCAGTCACTTCAGAAATGGTTCGTGAGATCTT
CAGAGGTTATGCTCCTTCGAAAGAAATGGTCCAGGGAAGTGGCTTGACCATTGCTACTGGTATCATTGGATCCACAGTTATGGTACACTCATTAT
TTTTGGGTTCTGGTCTCGTTCAGCCTAGATTGAGAGAGTACGATGTAACCCACGGTCTTGTGGATCTTGATCTGGTATGTTCTGAGGACGAAACT
ACAGCAGATACTGTCTCAGAAAAATCGTCTACCAGAGTTAAACTACTCGTATCGACAAAGAAGCTCTCTTCTTTTACAAGAGTTACAAACCAT
CGTACCAATCAATTCAATACTCGTTGAAATACTCAATTATTGAACTTGTGGTTACGCTTTTCACATTTGCACTTTTCGTCAACTCGGCTATCTTGGT
GGTGGCTGGAGTTACCCTCAACGATACCCCAAGAAGCCATCGATGCCGACTTGTACACTATTCATGCATTGCTCTCCAAAAATTTGGCACCTGTTG
TAGGCACAGTTTTTCATGCTTGCCTTGTCTTTTCAGTGGTCAAAGTGCTGGTATCGTCTGTACTATTGCTGGACAAATGGTAAGTGAGGGCCATATC
AATTGGAAGCTTAAACCATGGGTGAGAAGACTAGTGACAAGAGCCATCTCAATTATACCTTGTTTGGCCATTTCTGTTGGTATTGGACGGTCCGG
TTTGGGACTCGCCTTGAACGTTTCACAGGTTGTGATTTCCATTCTTCTTCCCCCATTAAACGGCTCCTCTTATCTACTTTACATGCAAAAAGTCCAT
CATGAAAGTGCCATTACCCAAGGAGATGCAGTCAGATGATGAAGACGAAGTAAAATACAAATATCTACACAACAATTGGCTCACATCCATCATT
GTCTTTGCCATCTGGCTCTTTGTGCTGGCATTGAATATCTACGCGATTGTTGACATGGCCAAAAATGGTGTGGCCGGCAGTTAG

Table S3 DEGs related to metabolism of *M. guilliermondii* A4 in “S1 vs S0” and “S2 vs S0” groups.

Description	Gene ID	Annotation (Protein ID)	log ₂ FC	
			S1 vs S0	S2 vs S0
Sugar transportation and utilization	D_104547	Hexose transporter 2 (P53387)	2.206	1.553
	D_102607	High-affinity glucose transporter 1 (A0A1D8PCL1)	1.193	—
	D_102333	Probable glucose transporter rco-3 (Q92253)	1.165	—
	D_105325	Sugar transporter STL1 (P39932)	-1.679	—
	D_104687	Low-affinity glucose transporter (P18631)	-2.410	—
	D_104584	Sugar transporter STL1 (P39932)	—	1.218
	D_104023	Sugar transporter STL1 (P39932)	—	-1.006
	D_105427	Probable sucrose utilization protein SUC1 (P33181)	—	-1.135
	D_100896	Glucose transporter GlcP (A0A0H2VG78)	—	-1.313
	D_102664	Sugar transport protein 12 (O65413)	—	-1.321
	D_102555	Probable sucrose utilization protein SUC1 (P33181)	—	-1.325
	D_104356	Probable sucrose utilization protein SUC1 (P33181)	—	-1.603
	D_103907	Sugar transporter STL1 (P39932)	—	-1.811
	D_103142	High-affinity glucose transporter HXT2 (P23585)	—	-1.820
	D_102377	Hexose transporter HXT8 (P40886)	—	-1.951
	D_103976	Sugar transporter STL1 (P39932)	—	-2.750
	D_102554	Maltose permease MAL31 (P38156)	—	-1.775
	D_105520	Maltose permease MAL31 (P38156)	—	-1.961
	D_101515	Maltose permease MAL61 (P15685)	—	-2.389
	D_100515	Maltose permease MAL61 (P15685)	-1.557	-3.716
	D_100514	Maltose permease MAL61 (P15685)	-2.118	-4.209
	D_100516	Maltose permease MAL61 (P15685)	-2.193	-6.957
Cytochrome P450	D_101278	Cytochrome P450 61 (P54781)	1.257	1.447
	D_105475	Cytochrome P450 52A12 (Q9Y757)	-1.076	—
	D_105324	Cytochrome P450 52A12 (Q9Y757)	-1.470	-1.555
	D_100696	Cytochrome P450 regulator dap1 (O13995)	—	-1.017
	D_105529	Cytochrome P450 52A12 (Q9Y757)	—	-1.052
	D_102610	Cytochrome P450 52A13 (Q9Y758)	—	-1.068
Others	D_102378	Cytochrome P450 52A12 (Q9Y757)	—	-1.592
	D_104882	NADH-ubiquinone oxidoreductase assembly factor N7BML (Q6C7L6)	—	1.393

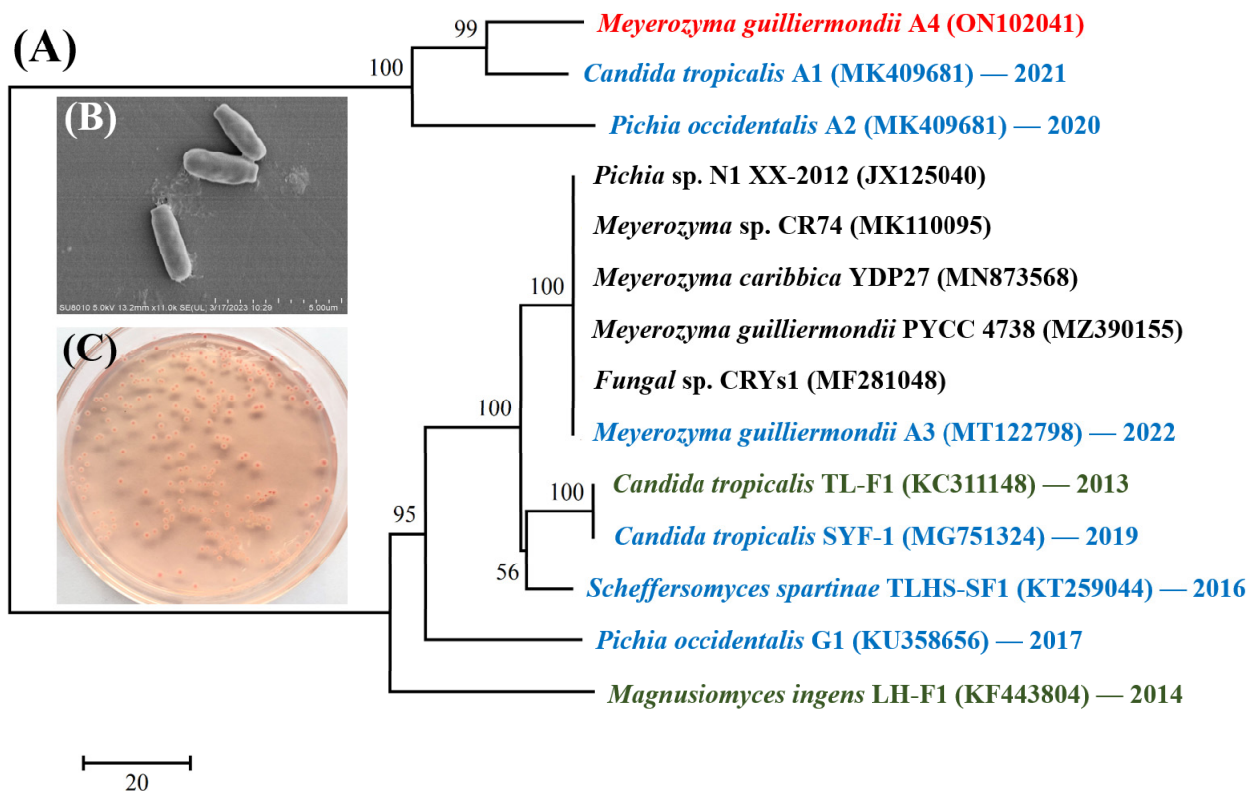


Figure S1 *M. guilliermondii* A4: (A) phylogenetic tree (Neighbor-Joining method); (B) scanning electron microscopic (SEM) micrograph of cells; (C) colonies on solid agar plate. The yeasts which were highlighted in blue and green color were the ones we have isolated, researched and reported (in the year followed by the corresponding GenBank accession numbers). Those in green color were non-halotolerant yeasts and those in blue color were halotolerant ones.

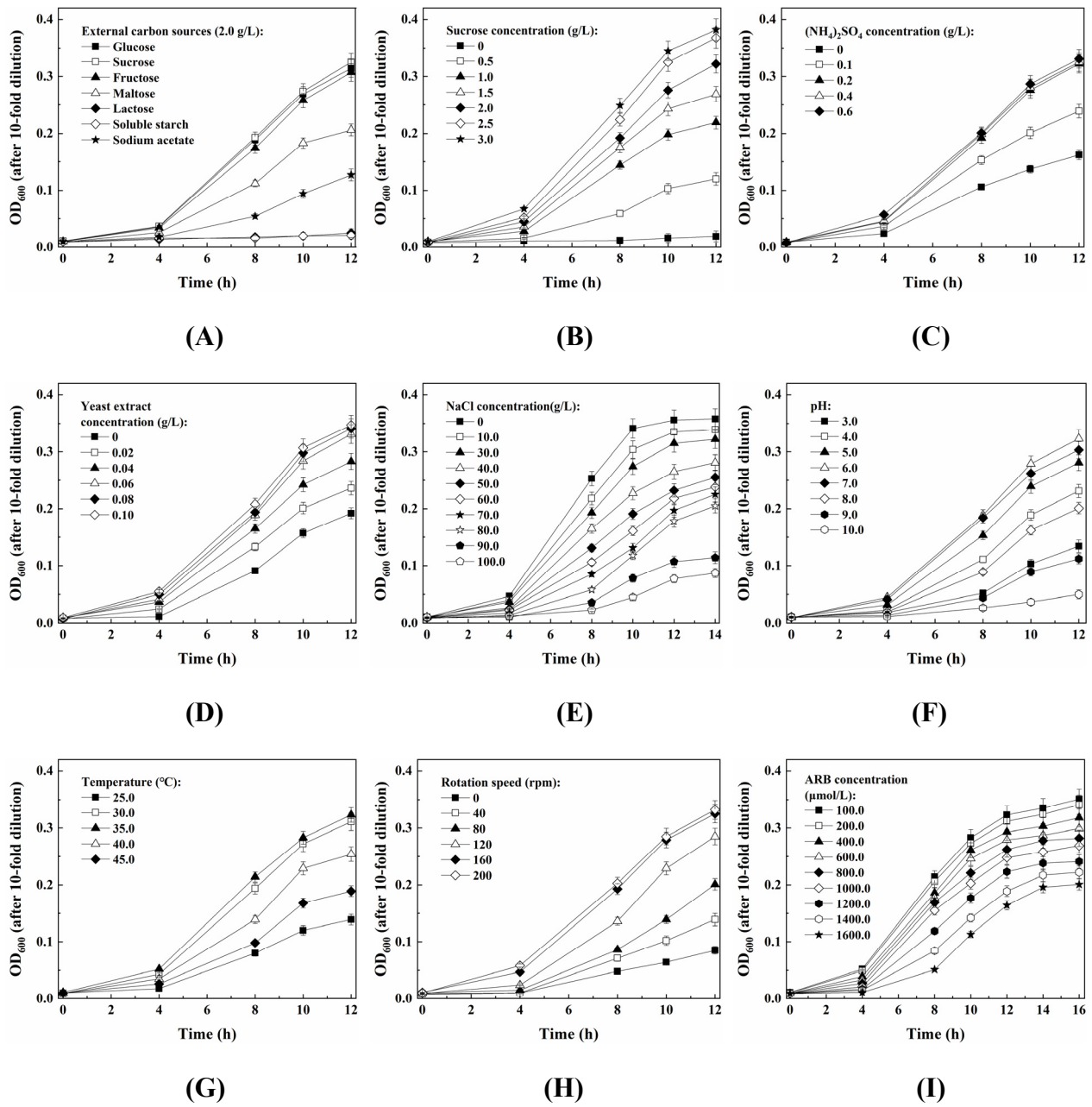


Figure S2 Optimization of the conditions for cell growth of *M. guilliermondii* A4: (A) type of external carbon source (2.0 g/L); (B) sucrose concentration; (C) (NH₄)₂SO₄ concentration; (D) yeast extract concentration; (E) NaCl concentration; (F) pH; (G) temperature; (H) rotation speed; (I) ARB concentration.

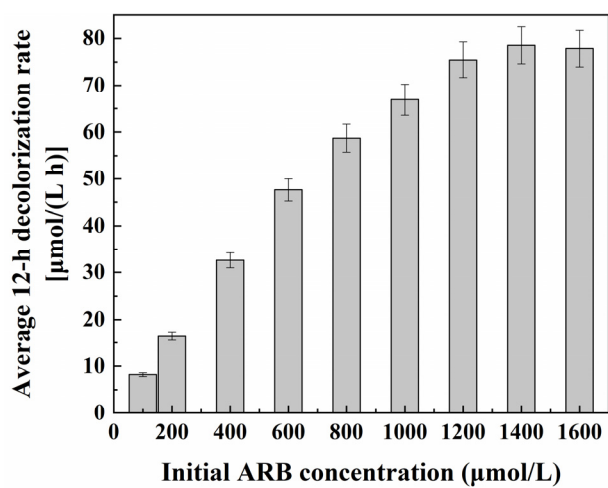
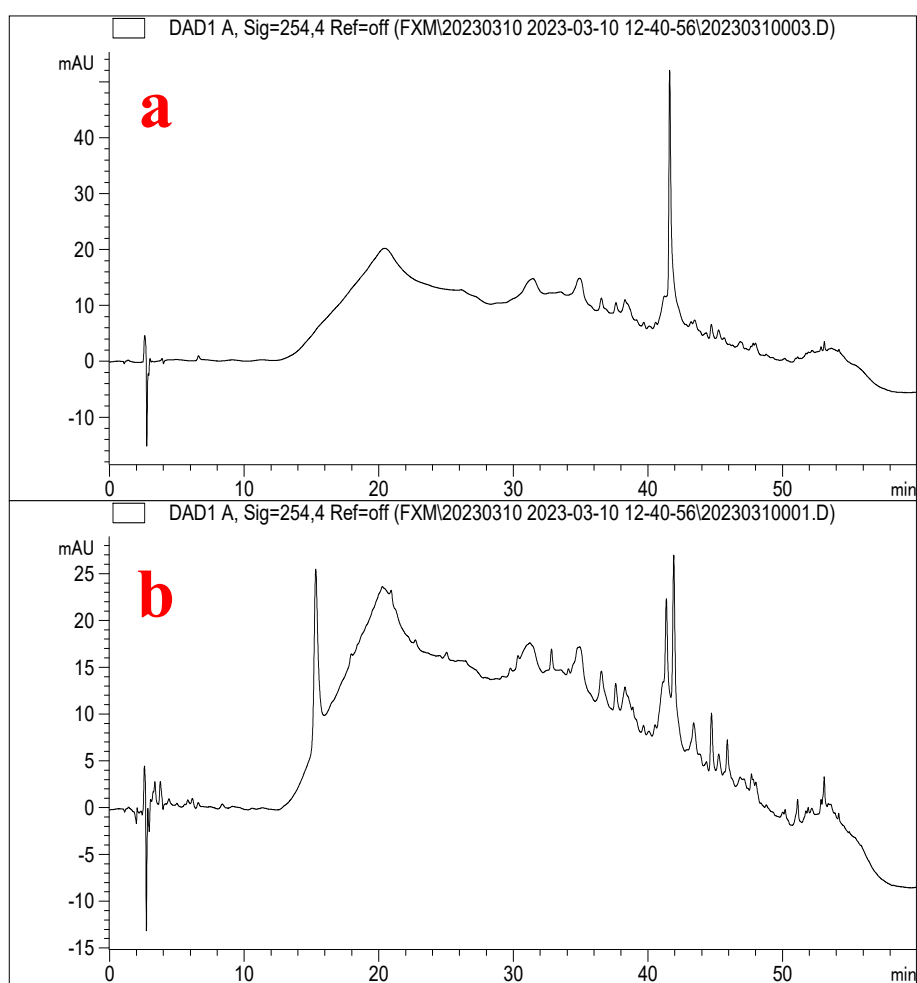
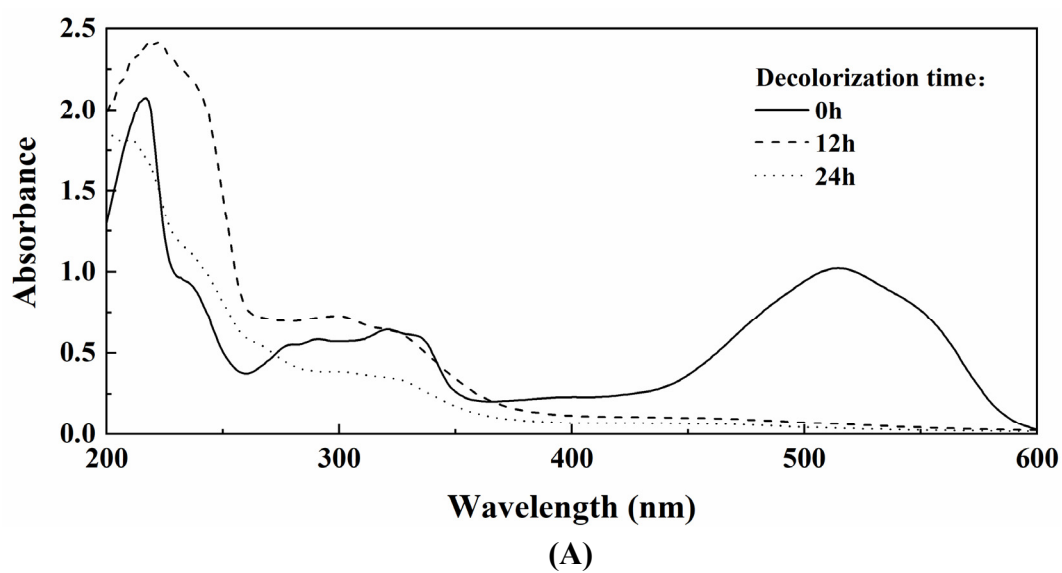
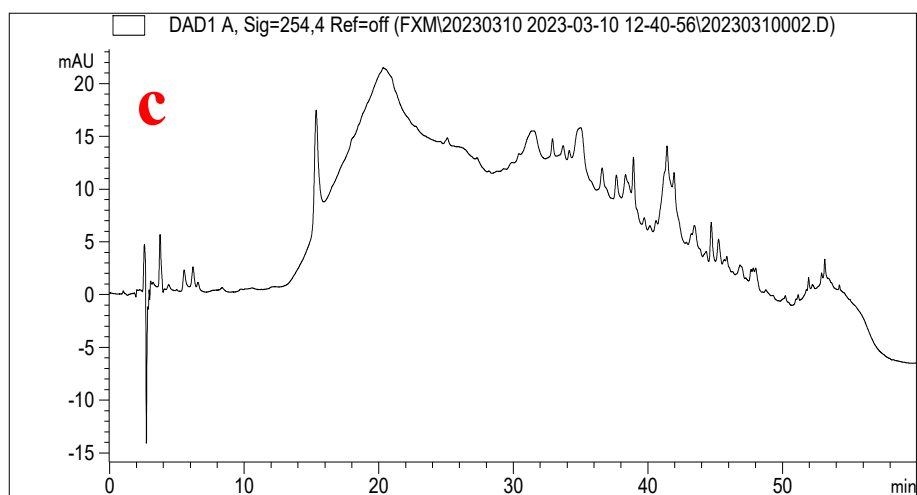
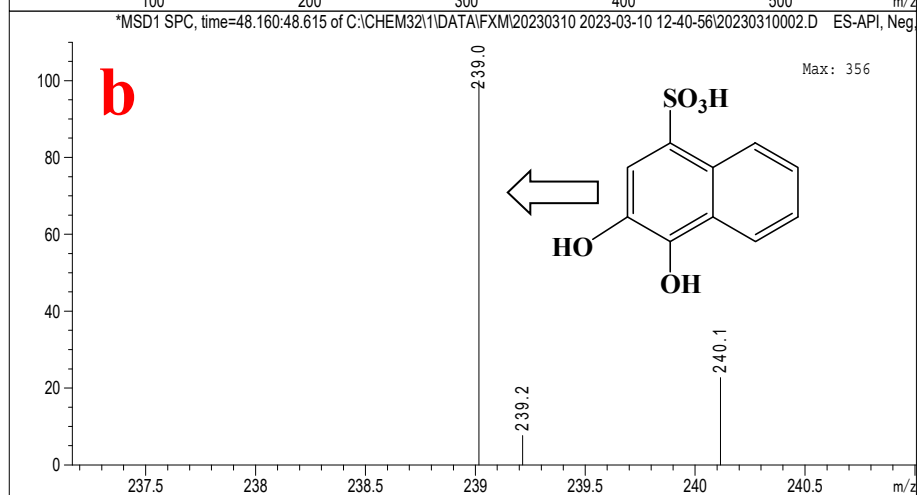
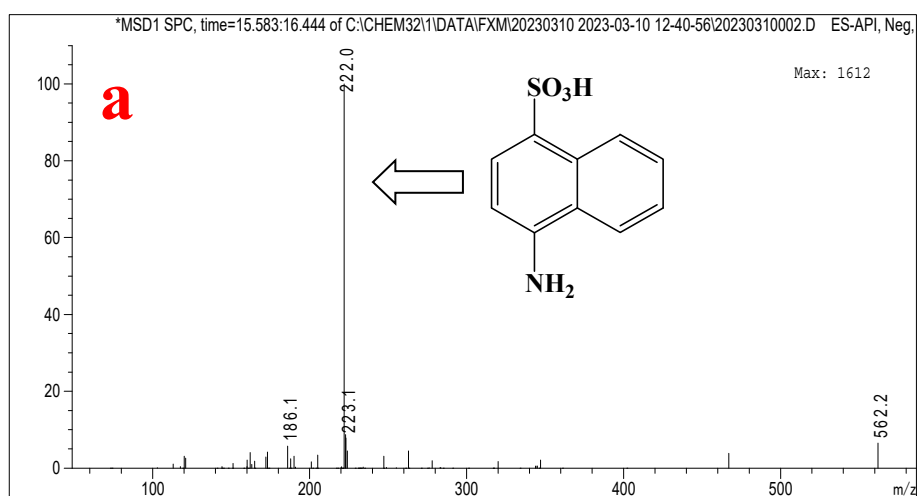


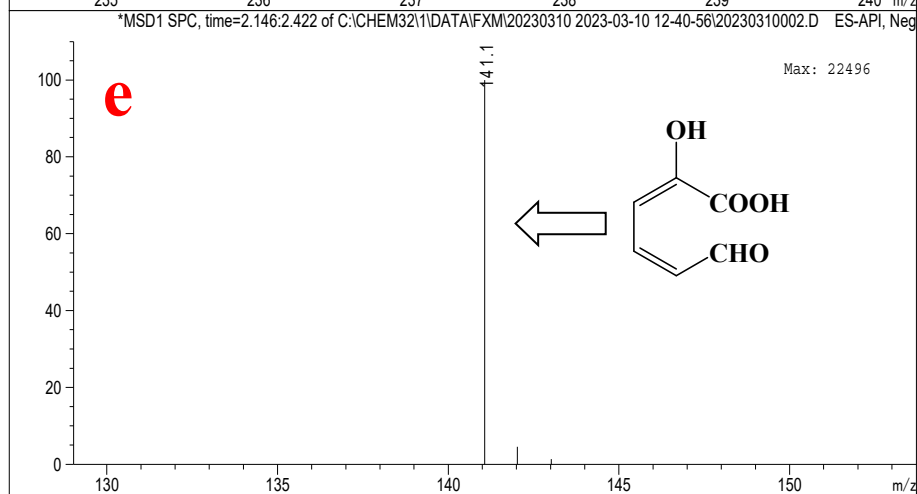
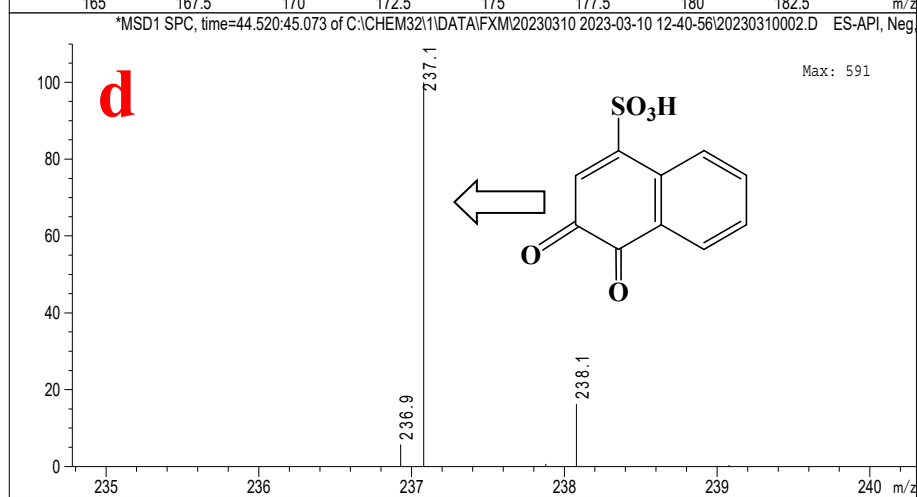
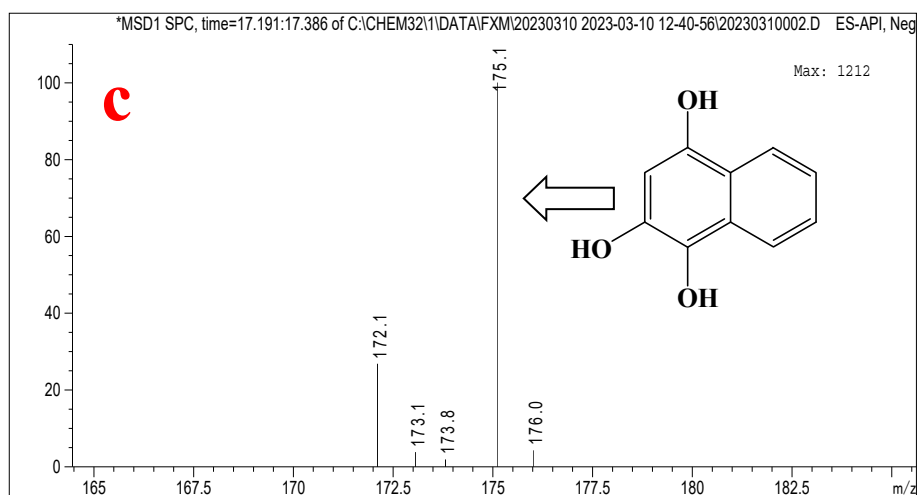
Figure S3 Average 12-h decolorization rate of ARB of different initial concentration.





(B)





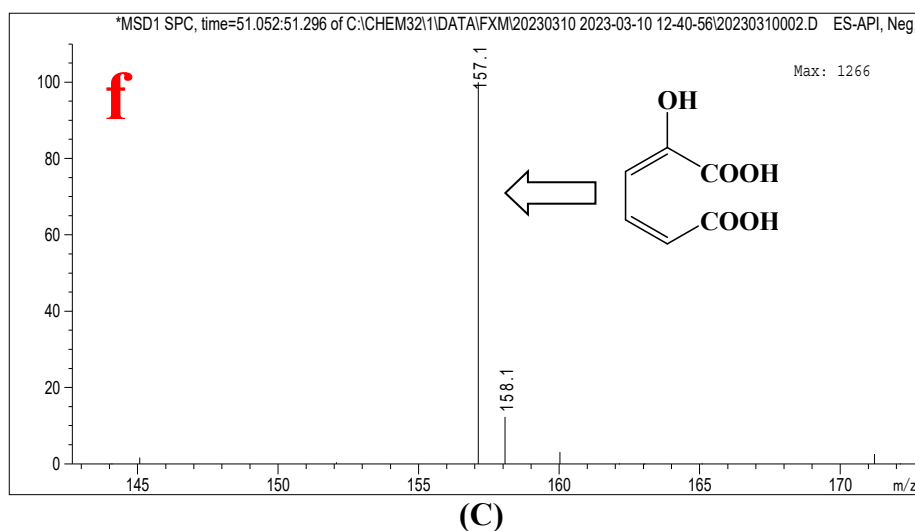


Figure S4 (A) UV-Vis scanning spectrum of ARB before and after decolorization for 12 h and 24 h by *M. guilliermondii* A4. (B) HPLC spectrums of ARB (a) before and after decolorization for (b) 12 h and (c) 24 h. (C) MS of six possible decolorization intermediates: (a) 4-aminonaphthalene-1-sulfonic acid; (b) 3,4-dihydroxynaphthalene-1-sulfonic acid; (c) naphthalene-1,2,4-triol; (d) 3,4-dioxo-3,4-dihydronaphthalene-1-sulfonic acid; (e) (2*E*,4*Z*)-2-hydroxy-6-oxohexa-2,4-dienoic acid; (f) (2*E*,4*Z*)-2-hydroxyhexa-2,4-dienedioic acid.

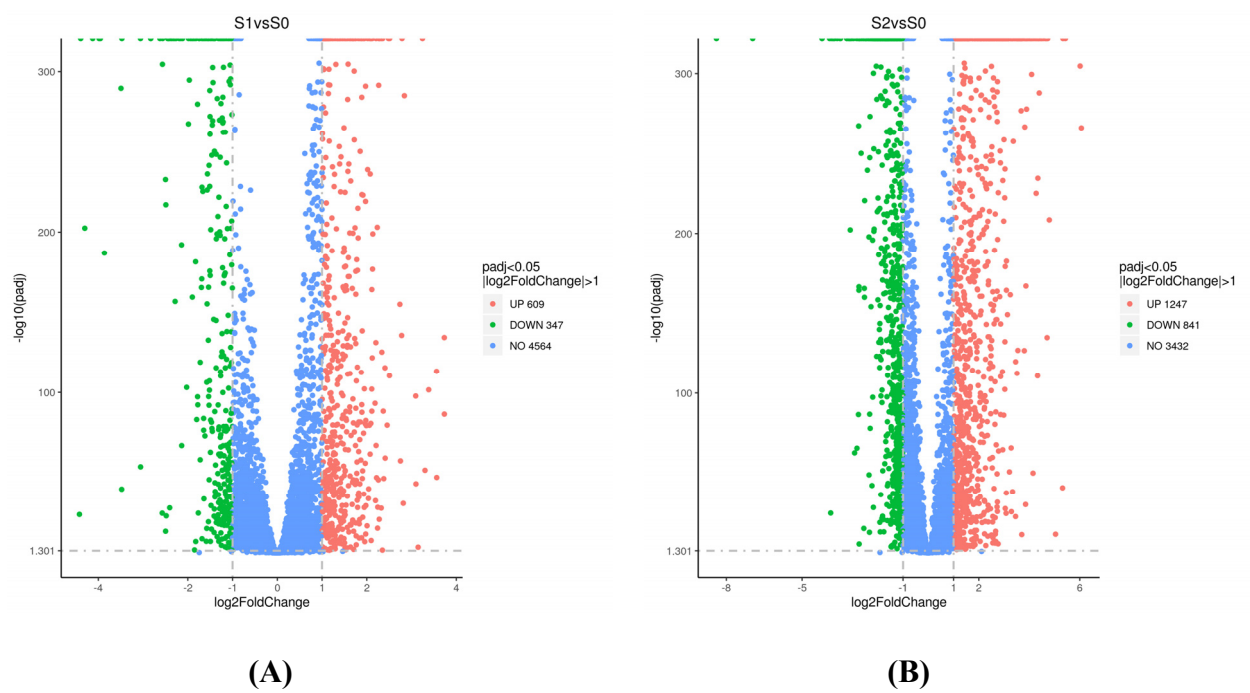


Figure S5 Volcano map of DEGs in comparisons of (A) S1 and S0, (B) S2 and S0.

Text S1. Isolation and identification of halotolerant azo-dye-degrading yeast

The pure yeast strain capable of decolorizing azo dye in brine was isolated from sea mud samples collected in Dalian, China (38.88 °N, 121.57 °E). Before yeast isolation, the sea mud microbial community was acclimated in 250 mL shaking flasks for continuous decolorization of different azo dyes (gradually increased from 40.0 µmol/L to 200.0 µmol/L) in the medium (100 mL) containing (g/L): sucrose 2.0, (NH₄)₂SO₄ 1.0, yeast extract 0.1, K₂HPO₄ 1.0, MgSO₄·7H₂O 0.5 and NaCl 30.0. Other culture conditions were: temperature 35 °C, rotation speed 160 rpm, initial pH 6.0 and acclimatization time 36 d. Pure strains were isolated using spread-plate method on the agar (2.0%, w/v) medium plates containing (g/L): sucrose 2.0, (NH₄)₂SO₄ 1.0, yeast extract 0.1, K₂HPO₄ 1.0, MgSO₄·7H₂O 0.5 and NaCl 30.0, as well as azo dye (µmol/L) 40.0. The strain with the highest decolorization efficiency was selected as the target yeast for further study. The target yeast strain was identified through 26S rDNA and Internal Transcribed Space (ITS) sequencing method which was performed by Sangon Biotech Co., Ltd. (Shanghai, China). Then a phylogenetic tree was constructed using Neighbor-joining (NJ) method by MEGA (Version 4.0) with 10,000 bootstrap replicates. Released 26S rDNA sequences of some yeast strains in GenBank database (<https://www.ncbi.nlm.nih.gov/genbank/>) which exhibited > 99% homology to the isolate according to the BLAST results and those of the yeasts which were have yet isolated and reported by us were chosen for constructing the phylogenetic tree. In addition, morphology observation of the yeast cells was performed with a field emission scanning electron microscope (Hitachi SU8010, Japan).

Text S2. Transcriptomics analysis

S2.1. RNA isolation, cDNA library preparation and transcriptome sequencing

RNA integrity was assessed using the RNA Nano 6000 Assay Kit of the Bioanalyzer 2100 system (Agilent Technologies, CA, USA). Total RNA was used as input material for the RNA sample preparations. Briefly, mRNA was purified from total RNA using poly-T oligo-attached magnetic beads. Fragmentation was carried out using divalent cations under elevated temperature in First Strand Synthesis Reaction Buffer (5X). First strand cDNA was synthesized using random hexamer primer and M-MuLV Reverse Transcriptase (RNase H-). Second strand cDNA synthesis was subsequently performed using DNA Polymerase I and RNase H. Remaining overhangs were converted into blunt ends via exonuclease/polymerase activities. After adenylation of 3' ends of DNA fragments, Adaptor with hairpin loop structure were ligated to prepare for hybridization. In order to select cDNA fragments of preferentially 370-420 bp in length, the library fragments were purified with AMPure XP system (Beckman Coulter, Beverly, USA). Then PCR was performed with Phusion High-Fidelity DNA polymerase, Universal PCR primers and Index (X) Primer. At last, PCR products were purified (AMPure XP system) and library quality was assessed on the Agilent Bioanalyzer 2100 system.

The clustering of the index-coded samples was performed on a cBot Cluster Generation System using TruSeq PE Cluster Kit v3-cBot-HS (Illumina Inc., USA) according to the manufacturer's instructions. After cluster generation, the library preparations were sequenced on an Illumina Novaseq platform and 150 bp paired-end reads were generated.

S2.2. Quality control and mapping of transcriptome sequencing results

Raw data (raw reads) in the ".fastq" format were firstly processed through FASTQ software. In this step, clean data (clean reads) were obtained by removing reads containing adapter, reads containing ploy-N and low-quality reads from raw data. At the same time, Q20, Q30 and GC content the clean data were calculated. All the downstream analyses were based on the clean data with high quality.

The draft genome sequence of *Meyerozyma guilliermondii* A3 (with the accession ID of JAKFAP000000000) was referenced for mapping. Reference genome and gene model annotation files were downloaded from genome website directly. Index of the reference genome was built and paired-end clean reads were aligned to the reference genome using Hisat2 v2.0.5, because that this mapping tool can generate a database of splice junctions based on the gene model annotation file and thus can provide better mapping results than other non-splice mapping tools. The mapped reads of each sample were assembled by StringTie (v1.3.3b) (Pertea et al., 2015) in a reference-based approach. StringTie uses a novel network flow algorithm as well as an optional de novo assembly step to assemble and quantitate full-length transcripts representing multiple splice variants for each gene locus. FeatureCounts v1.5.0-p3 was used to count the reads numbers mapped to each gene. And then FPKM of each gene was calculated based on the length of the gene and reads count mapped to this gene. FPKM, expected number of Fragments Per Kilobase of transcript sequence per Millions base pairs sequenced, considers the effect of sequencing depth and gene length for the reads count at the same time, and is currently the most commonly used method for estimating gene expression levels.

S2.3. Analysis of differentially expressed genes (DEGs) and metabolic pathways

Differential expression analysis of two conditions/groups (two biological replicates per condition) was performed using the DESeq2 R package (1.20.0). DESeq2 provide statistical routines for determining differential expression in digital gene expression data using a model based on the negative binomial distribution. The resulting *P*-values were adjusted using the approach by Benjamini and Hochberg (1995) for controlling the false discovery rate. Genes with an adjusted *P*-value ≤ 0.05 found by DESeq2 were assigned as differentially expressed. DEGs were identified as those with an FDR of <0.001 and a RPKM (reads per kilobase of exon model per million mapped reads) ratio of the two samples of > 2 . The fold change of DEGs was shown as the \log_2 Fold Change (\log_2 FC) of gene abundance via comparison of the SMF-stimulated sample and the control, and the screening criterion was \log_2 FC ≥ 1 .

Gene Ontology (GO) enrichment analysis of differentially expressed genes was implemented by the clusterProfiler R package, in which gene length bias was corrected. GO terms with corrected P -value < 0.05 were considered significantly enriched by differential expressed genes. KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-through put experimental technologies (<http://www.genome.jp/kegg/>). We used clusterProfiler R package to test the statistical enrichment of differential expression genes in KEGG pathways.

S2.4. Quantitative Real-Time PCR (QRT-PCR) validation

In order to confirm the reliability of DEGs identified by RNA-Seq, genes with significant changes and related functions were validated through QRT-PCR by Sangon Biotech Co., Ltd., (Shanghai, China) according to the method described by Yong et al. (2013). Primers for QRT-PCR were designed according to their gene sequences according to the transcriptome sequencing results. QRT-PCR was performed using a LightCycler 480 instrument (Roche Diagnostics, Mannheim, Germany). The reaction measurements were performed in biological triplicate. The results were displayed relative to the expression levels of reference gene (18S rRNA) in each sample using the $2^{-\Delta\Delta C_t}$ method according to the method described by Schmittgen and Livak (2008).

References

- Benjamini, Y., Hochberg, Y., 1995. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *J. Roy. Statist. Soc. Ser. B* 57, 289–300.
- Pertea, M., Pertea, G.M., Antonescu, C.M., Chang, T.C., Mendell, J.T., Salzberg, S.L., 2015. StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. *Nat Biotechnol.* 33, 290–295. <https://doi.org/10.1038/nbt.3122>.
- Schmittgen, T.D., Livak, K.J., 2008. Analyzing real-time PCR data by the comparative CT method. *Nat. Protoc.* 3, 1101–1108. <https://doi.org/10.1038/nprot.2008.73>.
- Yong, X., Zhang, R., Zhang, N., Chen, Y., Huang, X., Zhao, J., Shen, Q., 2013. Development of a specific real-time PCR assay targeting the poly- γ -glutamic acid synthesis gene, *pgsB*, for the quantification of *Bacillus amyloliquefaciens* in solid-state fermentation. *Bioresour. Technol.* 129, 477–484. <https://doi.org/10.1016/j.biortech.2012.11.092>.