**SUPPLEMENTAL MATERIALS**

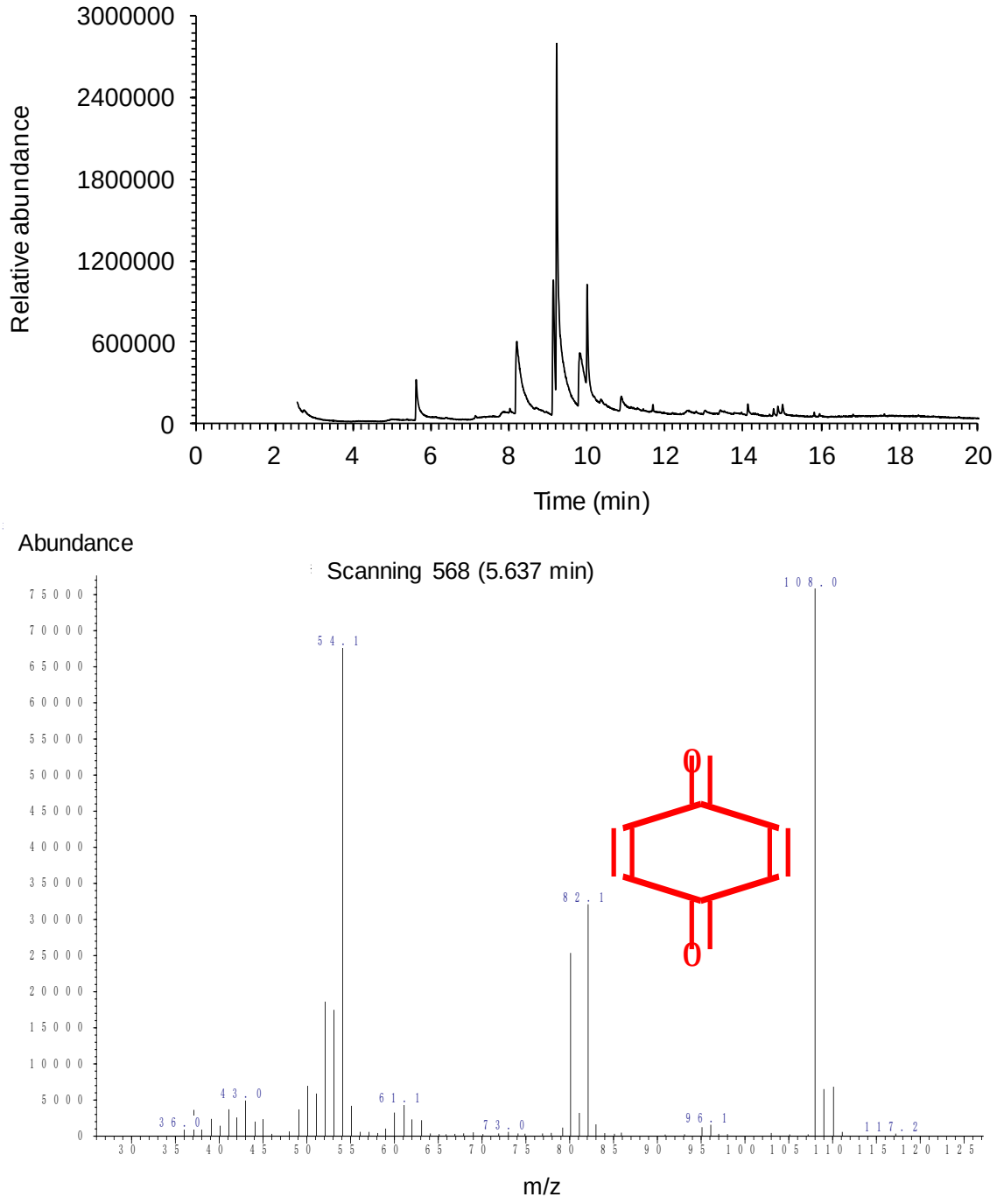



**Figure S1.** GC-MS identification of the formation of BQ during dry acid pretreatment of the representative lignocellulose feedstock of corn stover. The compound with retention time at 5.64 min was identified as BQ (at m/z 108).

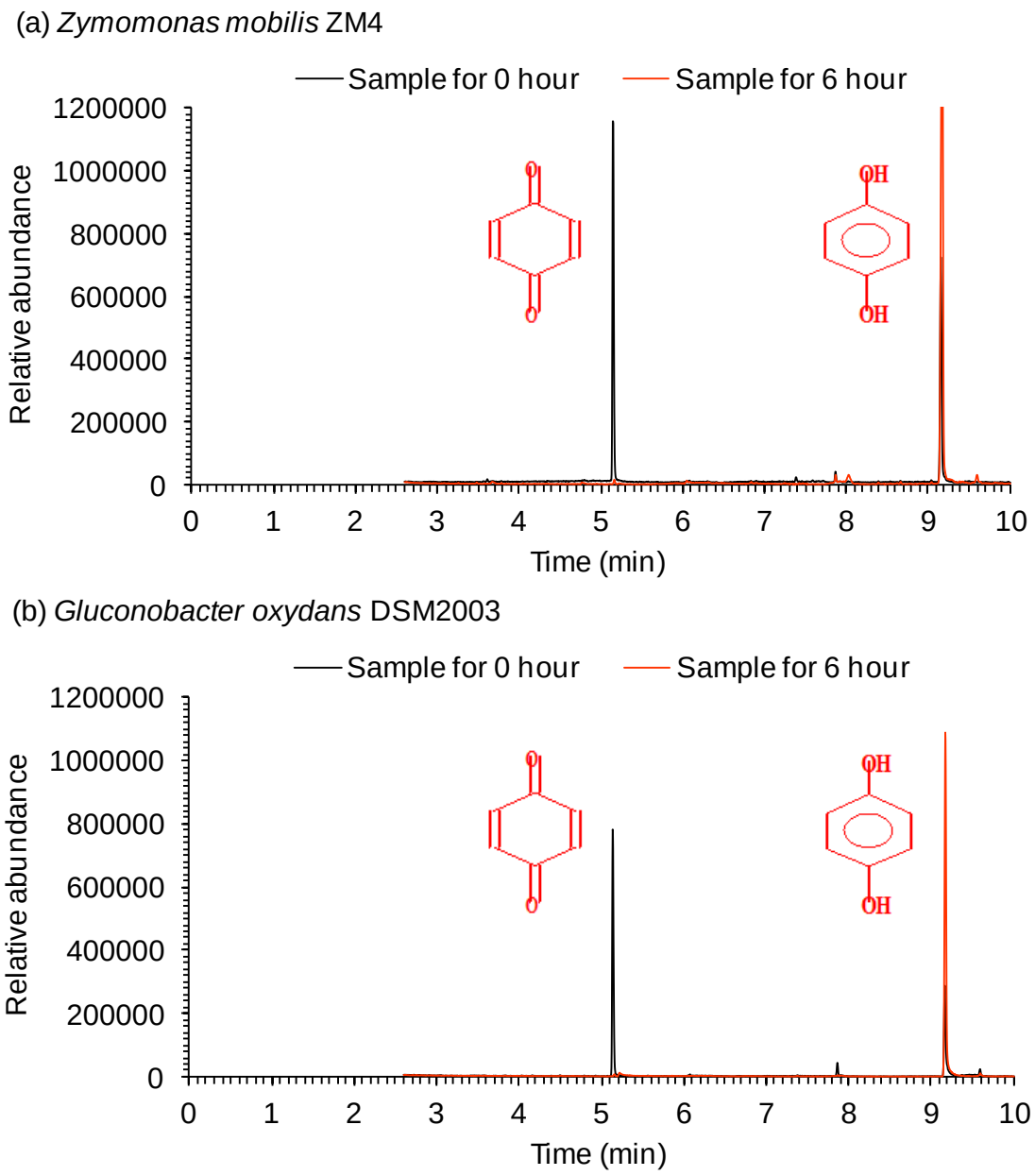
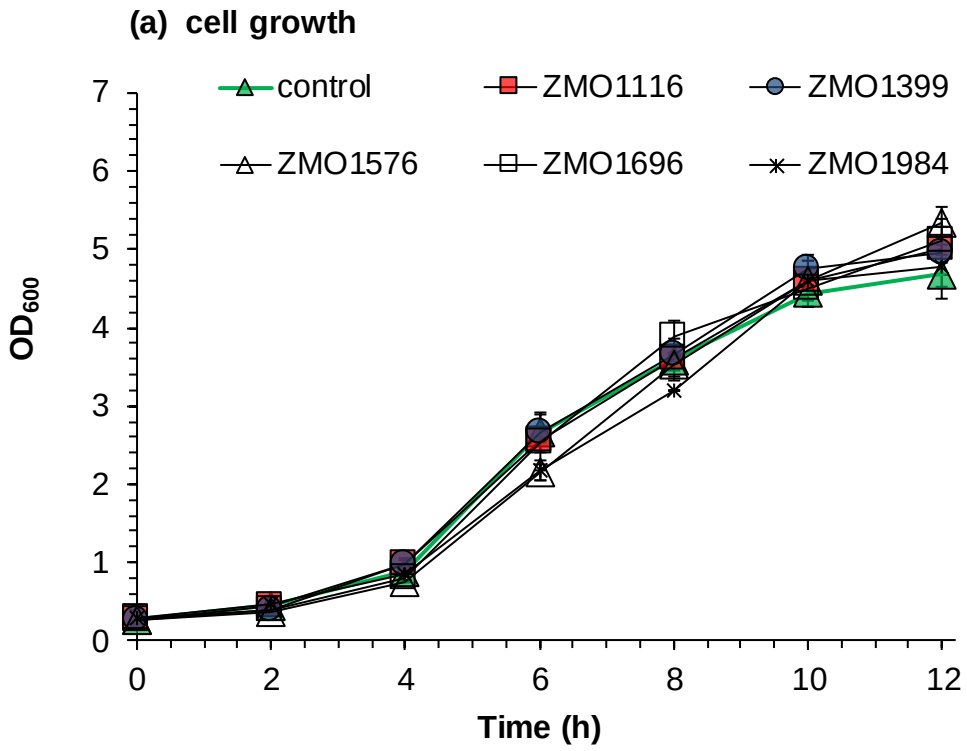
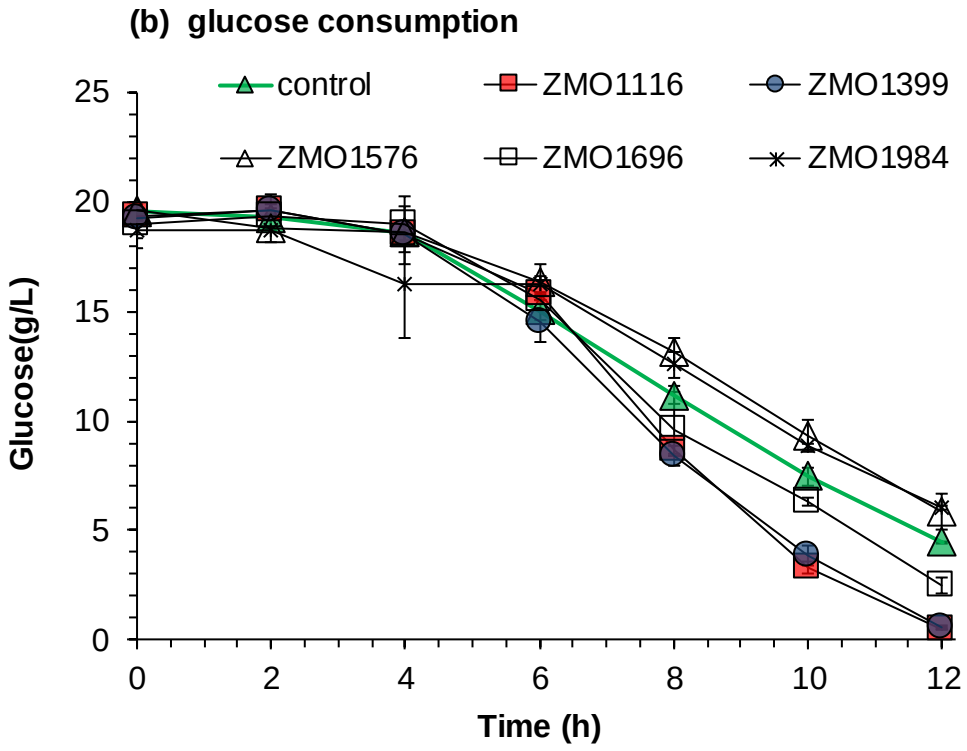



**Figure S2.** GC-MS identification of the intermediates generated during degradation of p-benzoquinone (BQ) by *Z. mobilis* ZM4 and *G. oxydans* DSM2003. (a) *Z. mobilis* ZM4; and (b) *G. oxydans* DSM2003. The whole flask of the *Z. mobilis* ZM4 and *G. oxydans* DSM2003 cell mass in exponential growth were harvested, washed by phosphate buffered saline (PBS, pH 7.0) and resuspended in the same volume of PBS, then inoculated into the fresh PBS containing 20 g/L glucose and 200 mg/L BQ. The cell cultures were collected at 0 h and 6 h for GC-MS analysis. Conditions: 10% (v/v) inoculum size, 30 °C, in static state culture for *Z. mobilis* ZM4; and 30 °C, 220 rpm for *G. oxydans* DSM2003. The compound with retention

time at 5.13 min and 9.17 min was identified as BQ (at m/z 108) and hydroquinone (HQ) (at m/z 110), respectively.


(a) cell growth
control
ZMO1116
ZMO1399
ZMO1576
ZMO1696
ZMO1984
OD600
Time (h)
0
1
2
3
4
5
6
7
0
2
4
6
8
10
12


(b) glucose consumption
control
ZMO1116
ZMO1399
ZMO1576
ZMO1696
ZMO1984
Glucose(g/L)
Time (h)
0
5
10
15
20
25
0
2
4
6
8
10
12

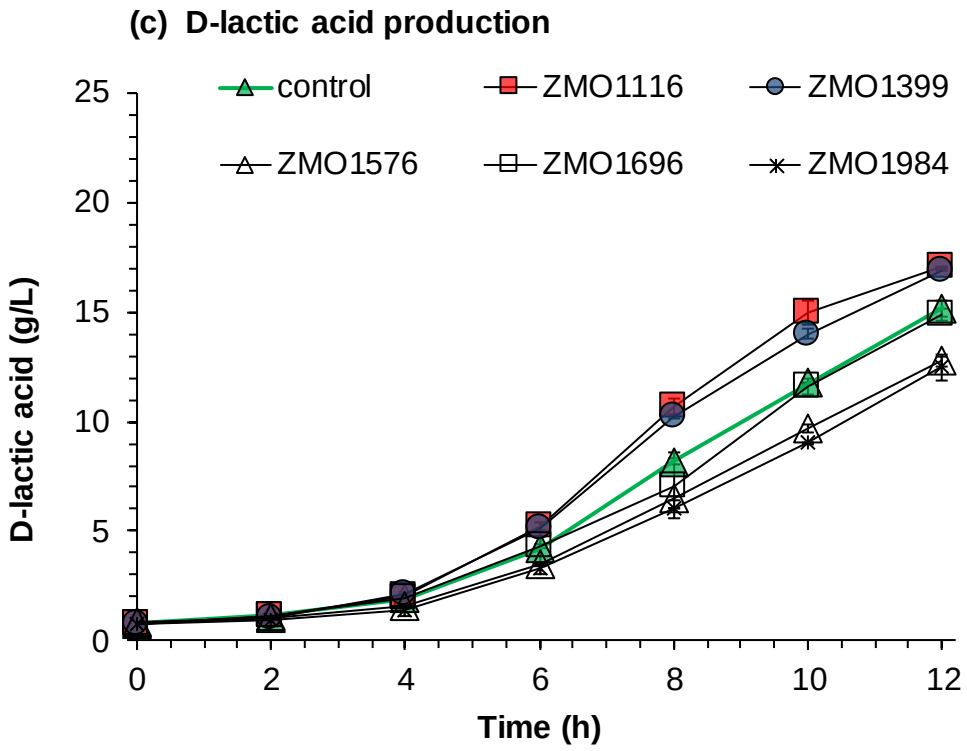



**Figure S3.** Cell growth, glucose consumption and D-lactic acid fermentation of *P. acidilactici* ZY15 recombinant strains with different genes in MRS medium containing 35 mg/L BQ.

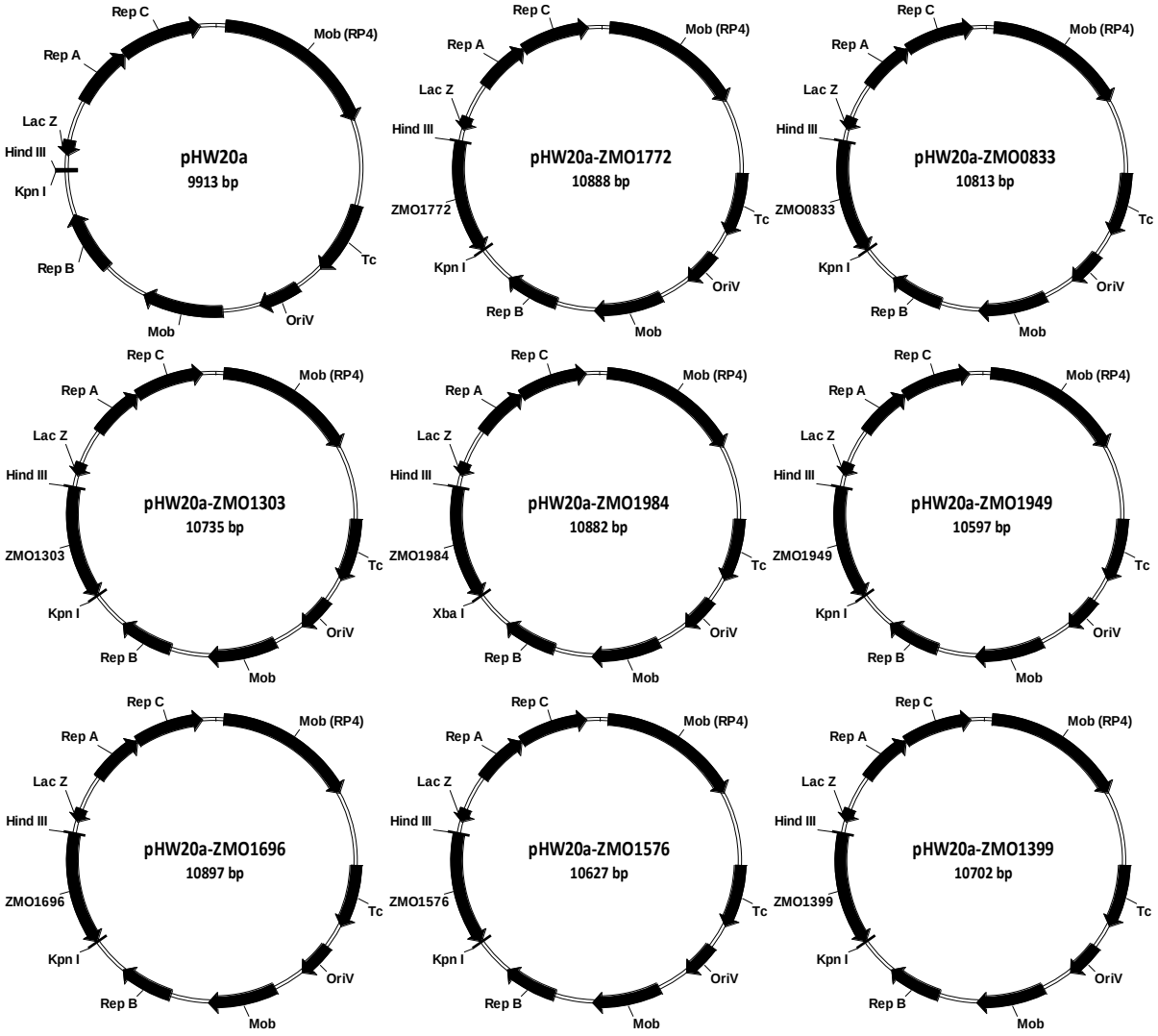



**Figure S4.** Construction of the plasmids for overexpression of key genes with up-regulations by more than twofold in response to p-benzoquinone. pHW20a represents the empty plasmid vector without gene overexpression. The eight genes include one oxidoreductase gene *ZMO1772* encoding NAD(P)H quinone oxidoreductase; three reductase genes *ZMO0833* encoding UDP-N-acetylenolpyruvoylglucosamine reductase, *ZMO1303* encoding pyrroline-5-carboxylate reductase, and *ZMO1984* encoding aldo/keto reductase; three dehydrogenase genes *ZMO1949* encoding NAD(P)H dehydrogenase, *ZMO1696* encoding Zinc-binding alcohol dehydrogenase, and *ZMO1576* encoding short-chain dehydrogenase/reductase; and one fatty acid hydroxylase gene *ZMO1399*.

**Table S1** Genes and primers used in qRT-PCR assay.

| Gene | Annotation | Primer sequence (5'-3') | |
|---|---|---|---|
| | | **Forward** | **Reverse** |
| **Primers for the oxidoreductase gene** | | | |
| *ZMO1116* | Oxidoreductase | TGTGGTTTGGGCCATCCG | TGTCGGTGCGTCCTGTTTGT |
| *ZMO1772* | NAD(P)H quinone oxidoreductase | GGTCGCCTTGTCATTGTCG | GGCTGTTCTGGCACGCAT |
| *ZMO1885* | NADH flavin oxidoreductase | TGGAGTGATGCCCAAGTAGAAG | CACTGACATTAGACGGCACCATA |
| **Primers for the reductase gene** | | | |
| *ZMO1993* | NADPH quinone reductase | GCGGTGTCGGTAGCTTGTT | GCCTTCGCCGTGATTCTG |
| *ZMO0833* | UDP-N-acetylenolpyruvoylglucosamine reductase | ATCGCCTGCGTTGTGGTG | GCATTCATGCGGATCATACCA |
| *ZMO1222* | 3-oxoacyl-(acyl-carrier-protein) reductase | TTAGCCGTGCCGTCATCAGA | CGATCATGCCTGCCTTTGC |
| *ZMO1303* | Pyrroline-5-carboxylate reductase | ACAACCCTGATTTCTATTCTTGCC | AACAACGCCCTTCCCTAACG |
| *ZMO1984* | Aldo/keto reductase | TCGCCATTTGTCAGCCTATC | CAGCAAAGTTACTGCTACCCAC |
| *ZMO1254* | Redoxin domain-containing protein | CGCTATGGTAATCCCTATCAGGC | GCTCATAAGCTGTGGCAAATCC |
| **Primers for the dehydrogenase gene** | | | |

| | | | |
|---|---|---|---|
| *ZMO1335* | NAD(P)H dehydrogenase (quinone) | CCCGATTTGGGCGTTTG | AGACCGCTCCGACCTTTCC |
| *ZMO1949* | NAD(P)H dehydrogenase (quinone) | TGGAGGCAAGCGGTTCTAC | GCAACAGCGGTTTGAGCAT |
| *ZMO0157* | D-isomer specific 2-hydroxyacid dehydrogenase | TATGGCTGTCGGGTTATTCC | TTCGGCGATGGCTTGG |
| *ZMO0788* | D-sorbitol dehydrogenase | CAGTTGTCACGGTCGCAATG | GCCGCAATCTGACTATCGTTTA |
| *ZMO1576* | Short-chain dehydrogenase/reductase | TCTATCGTCGCTAAGGGTGGTC | GCTGCAATCCCATAAAGAACG |
| *ZMO1696* | Zinc-binding alcohol dehydrogenase | TCCGAAGACAGGCGAAGAATG | CCTCGTCACCGACCTTAAATAGC |
| **Primers for other genes** | | | |
| *ZMO1399* | Fatty acid hydroxylase | GAAACGGATTCACTATGACCAC | CCGACAGCATAACCGATACA |
| *ZMO0020* | Hypothetical protein | CCGATCTAGTAAGCCAATTCACC | TTTCAAATCTGTTGGTTGGGTGT |
| *ZMO0021* | Hypothetical protein | CCACTTCATATCGCTTCTGTCG | GCGTAATCGGTGATCCCAAA |
| *ZMO0074* | Hypothetical protein | CGATAAAGACCGCCCGACC | TCGCCAAGCAGGCATTCG |
| *ZMO1821* | Hypothetical protein | AGAAAGCCGCCGCCATC | CACCATCATACCAACTGTCAACG |
| *ZMOr003* | 16S rRNA | TTAAGTTGGGCACTTTAGAGGAAC | TGTCACCGCCATTGTAGCAC |

Note: The 16S rRNA gene ZMOr003 was used as the internal control to normalize the difference of the data.

**Table S2** Microbial strains, plasmids and primers used in this study.

| **Strains** | **Genotype** | **Sources/references** |
|---|---|---|
| *Zymomonas mobilis* ZM4 | Wild-type strain, ATCC31821 | ATCC |
| *Gluconobacter oxydans* DSM2003 | Wild-type strain, DSM2003 | DSMZ |
| *Saccharomyces cerevisiae* XH7 | Co-metabolize glucose and xylose into ethanol | Li et al., 2016[1] |
| *Saccharomyces cerevisiae* DQ1 | Thermal tolerant mutant | Chu et al., 2012[2] |
| *Pediococcus acidilactici* TY112 | Co-fermentation of L-lactic acid from glucose and xylose | Yi et al., 2016[3] |
| *Zymomonas mobilis* 8b | Co-fermentation of ethanol from glucose and xylose | Zhang et al., 1995[4] |
| *Escherichia coli* S 17-1 λπ | *Pro*, *res*$^{-}$, *mod*$^{+}$; chromosomal integrated RP4, 2-*Tc*::Mu-*Km*::*Tn7*; *Tp*, *sm* | Simon et al., 1983[5] |
| *Amorphotheca resinae* ZN1 | Wild-type strain | Zhang et al., 2010[6] |
| **Plasmids** | **Description** | **Sources/references** |
| pHW20a | *Tc*$^{r}$, *mob* (RP4), *mob* (RSF1010), *lac*Zα, MCS, and *ori*V | Dong et al., 2011[7] |
| pHW20a-*ZMO1772* | NAD(P)H quinone oxidoreductase gene *ZMO1772* from ZM4 | This study |
| pHW20a-*ZMO0833* | UDP-N-acetylenolpyruvoylglucosamine reductase gene *ZMO0833* from ZM4 | This study |
| pHW20a-*ZMO1303* | Pyrroline-5-carboxylate reductase gene *ZMO1303* from ZM4 | This study |
| pHW20a-*ZMO1984* | Aldo/keto reductase gene *ZMO1949* from ZM4 | This study |

| | | |
|---|---|---|
| pHW20a-*ZMO1949* | NAD(P)H dehydrogenase (quinone) gene *ZMO1949* from ZM4 | This study |
| pHW20a-*ZMO1696* | Zinc-binding alcohol dehydrogenase gene *ZMO1696* from ZM4 | This study |
| pHW20a-*ZMO1576* | Short-chain dehydrogenase/reductase gene *ZMO1576* from ZM4 | This study |
| pHW20a-*ZMO1399* | Fatty acid hydroxylase gene *ZMO1399* from ZM4 | This study |

| **Primers for gene amplification** | **Sequence (5'-3')** |
|---|---|
| *ZMO1772*-F | CCCAAGCTTATGGCAGGCAACATGATGAAAG |
| *ZMO1772*-R | CGGGGTACCTCAAAAAAGCGCCTCTGGC |
| *ZMO0833*-F | CCCAAGCTTATGACGACTGCTACATCTTCC |
| *ZMO0833*-R | CGGGGTACCTCATGCCTTATCCCCATC |
| *ZMO1303*-F | CCCAAGCTTATGAGTGATACCGCATCAGATTC |
| *ZMO1303*-R | CGGGGTACCTTATTGCGCGATAGTCTCTTTG |
| *ZMO1984*-F | CCCAAGCTTATGGATTATACGTATTTGGGTCG |
| *ZMO1984*-R | GCTCTAGACTACCATGCATAGGCTTCAGG |
| *ZMO1949*-F | CCCAAGCTTATGAAAGTATTGATCGTTCACGC |
| *ZMO1949*-R | CGGGGTACCTCATGGTTGTTGTTTCCTCAAAC |
| *ZMO1696*-F | CCCAAGCTTATGCGCGCCATAGGTTATC |

| | |
|---|---|
| *ZMO1696*-R | CGGGGTACCTTAGAAGCCTTCTAAGACGATTTTA |
| *ZMO1576*-F | CCCAAGCTTATGAACCAGAATATCCGCAA |
| *ZMO1576*-R | CGGGGTACCTTATAATGCCTGTTTTGTCGG |
| *ZMO1399*-F | CCCAAGCTTATGAACACAACTGATGCCAAGAC |
| *ZMO1399*-R | CGGGGTACCTCAGCGGATATCCTGTATTTTATC |

Note: The underline indicates the digestion sites.

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