Supplementary Table S1: Primers used in this study.

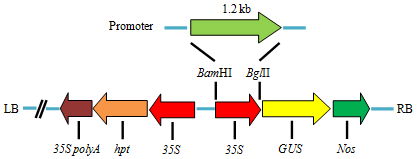
|  |  |
| --- | --- |
| Primers | 5’ 3’ |
| OsCYP2 promoter FP | CGCGGATCCAACCGTAAAAAAGCCATGAT |
| OsCYP2 promoter RP | GGAAGATCTCTAGGGTTTTGCGAATTTC |
| p62 sense strand for Y1H | AGCTTCACGTGC |
| p62 antisense strand for Y1H | TCGAGCACGTGA |
| p63 sense strand for Y1H | AGCTTCTCGCGC |
| p63 antisense strand for Y1H | TCGAGCGCGAGA |
| p62 sense strand for EMSA | GGGTCACGTGCATC |
| p62 antisense strand for EMSA | GATGCACGTGACCC |
| p63 sense strand for EMSA | GGGTCTCGCGCATC |
| p63 antisense strand for EMSA | GATGCGCGAGACCC |
| Myc2-like FP for EMSA | CGGAATTCATGAACCTTTGGACGGACGA |
| Myc2-like RP for EMSA | CCAAGCTTCCGGGCGGCGGTGCCAGGCT |
| Myc2-like FP for overexpression | TCACCCGGGATGAACCTTTGGACGGACGA |
| Myc2-like RP for overexpression | TCACCCGGGTAGAGTTGAGTTACCGGGCG |
| Actin FP | GACCTTGCTGGGCGTGAT |
| Actin RP | GTCATAGTCCAGGGCGATGT |
| Myc2-like FP for qPCR | AGTGGTTCTTCCTCGTCTCC |
| Myc2-like RP for qPCR | AGGTTGAAGAGGGCGCGGAT |

Note: The underlines indicate restriction enzyme site

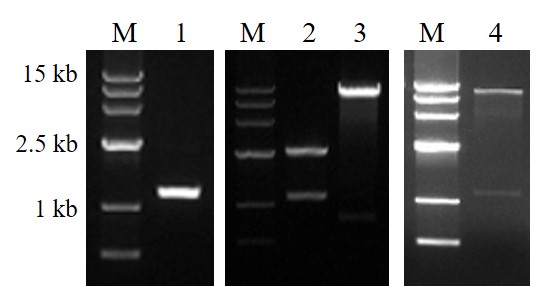
Supplementary Table S2: Predicted *cis*-elements of *OsCYP2* promoter.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Types | Elements | No. | Core sequence | Position c |
| CE a | TATA box | 1 | TATAAAT | -736 (－) |
| 1 | TATATAA | -790 (＋) |
| 4 | TTATTT | -751 (＋), -813 (＋), -866 (＋), -1035 (－) |
| 1 | TATTTAA | -34 (＋) |
| CAAT box | 5 | CAAT | -204 (－), -669 (－), -711(－), -843 (－), -938 (－) |
| GATA box | 8 | GATA | -401 (－), -520 (－), -543 (－), -836 (＋), -985 (－), -1026 (－), -1050 (－), -1055 (＋) |
| IE b | ABRE | 2 | CACGTG | -86 (＋), -182 (＋) |
| MYBR | 3 | TAACCA | -110 (－), -142 (－), -153 (＋)， |
| 5 | CGGTT | -25 (－), -331 (－), -526 (－), -893 (＋), -1068 (－) |
| 3 | CCAACC | -45 (－), -337 (＋), -391 (＋) |

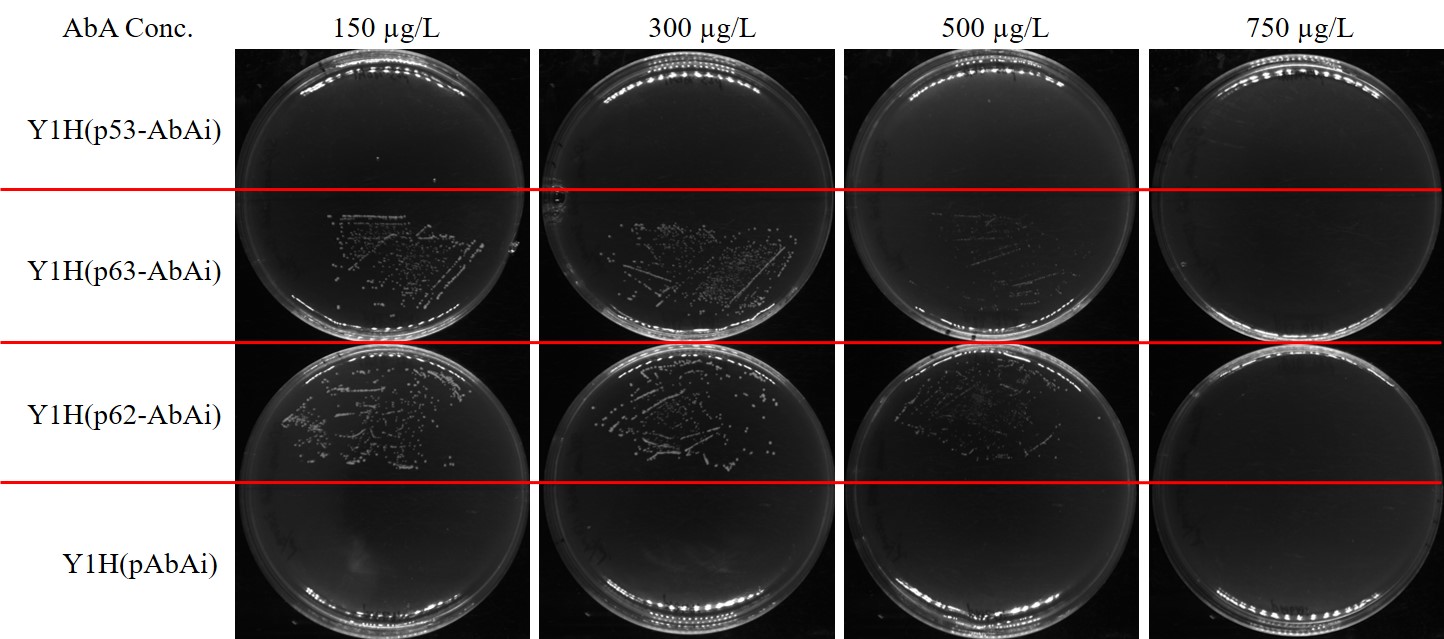
a CE: core elements; b IE: inducible elements; c Position of the *cis*-elements relative to the putative transcription start site. Strands are indicated as: (＋), forward; (－), complement



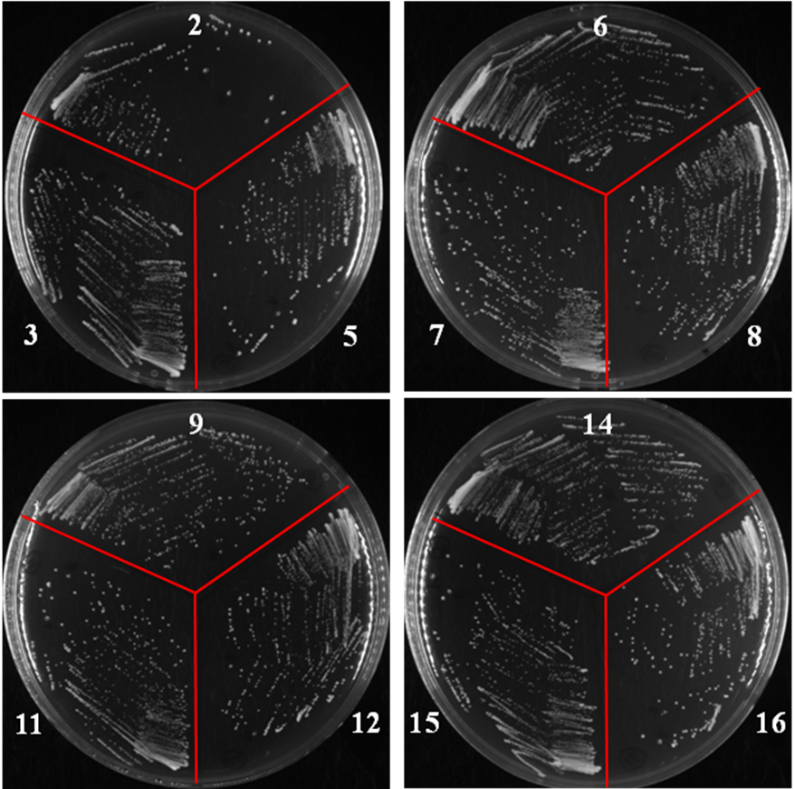
Supplementary Figure S1: Schematic diagram of *pOsCYP2:GUS* based on pCAMBIA1301 framework.



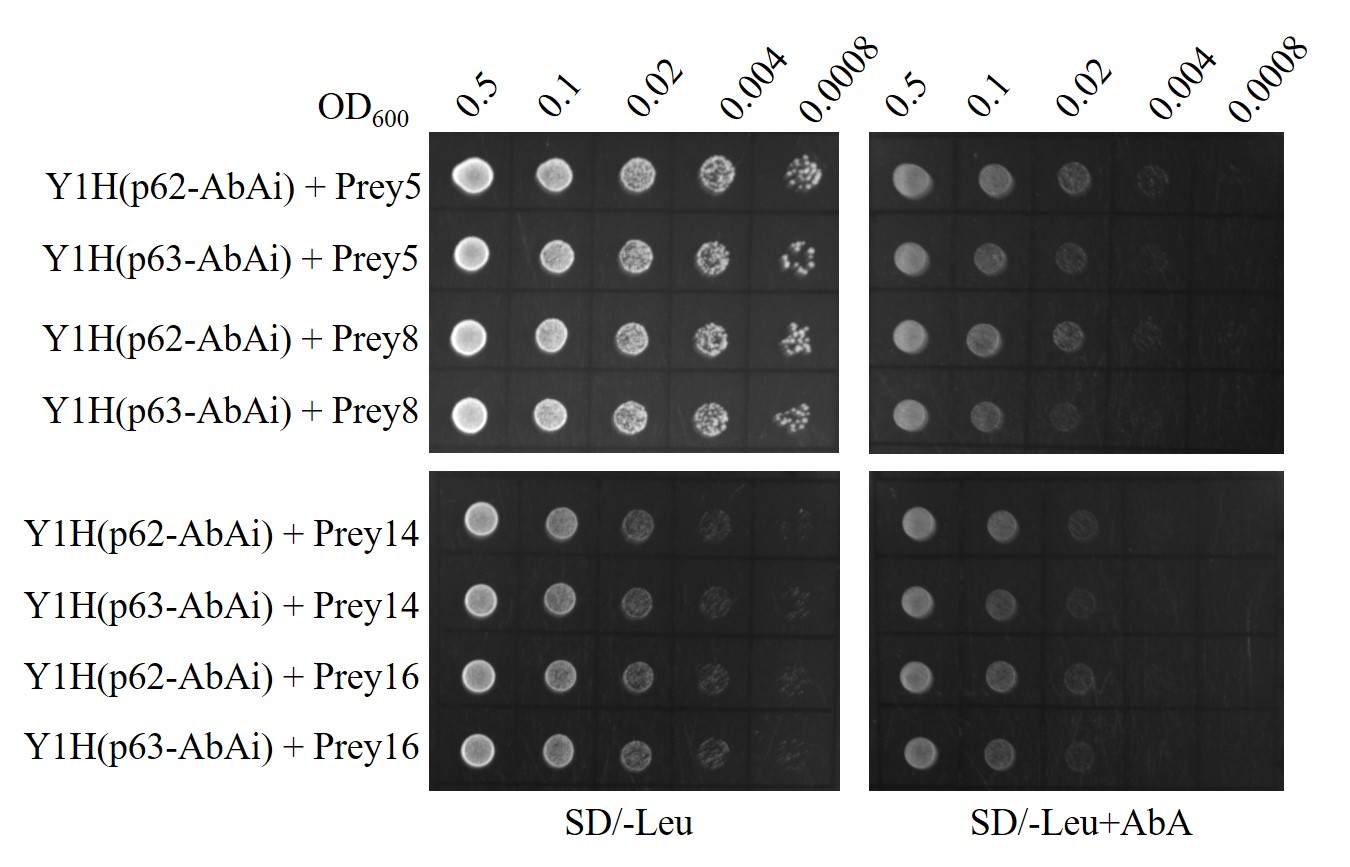
Supplementary Figure S2: Construction of *pOsCYP2:GUS* vector. M: Wide Range 500-15000 marker; 1: Fragment of promoter; 2 and 3: Digested pMD19-T + promoter and pCAMBIA1301, respectively; 4: Identification of recombined *pOsCYP2:GUS* vector.



Supplementary Figure S3: Determine minimal inhibitory concentration of AbA for bait strain. Y1H (p53-AbAi), Y1H (pAbAi), Y1H (p62-AbAi), Y1H (p63-AbAi) represent positive, negative, bait and mutant bait strains respectively.



Supplementary Figure S4: Partial colonies were restreaked onto SD/-Leu/AbA media plates.



Supplementary Figure S5: Cotransformation and serial diluted (1:5) with the initial optical density OD600) of 0.5 on selective media to verify interactions of candidate interaction transcription factors. SD/-Leu: synthetically defined medium with dropout leucine, SD/-Leu+AbA: synthetically defined medium with dropout leucine and plus 750 μg/L Aureobasidin A; Y1H (p62-AbAi): bait strain, Y1H (p63-AbAi): mutant bait strain.



Supplementary Figure S6: Detection of recombinant Myc2-like with His tag by SDS-PAGE and stained using Coomassie brilliant blue R-250. M: Pre-stained protein marker RM013; 1: Myc2-like with His tag.



Supplementary Figure S7: Relative transcript level of *myc2-like* in the wild type, *myc2-like* overexpression in wild type and *myc2-like* overexpression in *cyp2* RNAi. WT: wild type; L1-1, L1-2, L1-3, L1-4, L1-5, L1-6, L1-7: *myc2-like* overexpression (OE) in wild type; L2-1, L2-2, L2-3, L2-4, L2-5: Independent *myc2-like* overexpression (OE) in *cyp2*- RNAi. Values represent means and followed by different letters are significantly different (P≤0.05) by the least significant difference test. Error bars represent SD.