**Supplementary Table 1.** Evidence for interactions between genes with demonstrated potential to improve *in vitro* regenerability when overexpressed.

*Table 1A. Transcriptional regulation*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Transactivator | Target | Evidence | | Reference | |
| B-type ARR ARR1 | CUC1 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| B-type ARR ARR1 | ESR2 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| B-type ARR ARR1 | WIND3 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| B-type ARRs ARR1, ARR10 and ARR12 | WUS | Yeast one-hybrid, ChIP-qPCR, EMSA | | Meng et al., 2017 | |
| B-type ARRs ARR1 and ARR2 | WUS | ChIP-qPCR, EMSA, *in situ* hybridization of *WUS* transcripts in mutants with dominant negative variant of ARR2, luciferase-based assays of pWUS activity | | Zhang et al., 2017 | |
| B-type ARR ARR12 | WUS | ChIP-qPCR, upregulation of pWUS::LUC reporter in p35S:ARR12 mutants | | Dai et al., 2017 | |
| B-type ARR ARR20 | WUS | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| BBM | LEC1 and LEC2 | qRT-PCR of LEC1/2 in somatic embryos with induction of BBM-GR (during cycloheximide treatment), ChIP-seq | | Horstman et al., 2017 | |
| CUC1 | STM | pSTM::GUS expression in 35S:CUC1 plants, RT-PCR and *in situ* hybridization in CUC1 overexpression and loss-of-function lines | | Hibara et al., 2003; Takada et al., 2001 | |
| HDIII-ZIP TF REVOLUTA | WUS | ChIP-qPCR | | Zhang et al., 2017 | |
| ESR1 | ESR2, WUS, PLT3 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| ESR2 | CUC1 | CUC1 expression (detected by microhybridization) in ESR2-RNAi and ESR2-OE lines, and in ESR2-ER lines with induction during cyclohexamide treatment | | Ikeda et al., 2006 | |
| HDIII-ZIP TF PHB | LEC2 | qRT-PCR of LEC2 in *phb* mutants, ChiP-qPCR | | Tang et al., 2012 | |
| STM | ARR12 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| STM | CUC1, PLT3/7 | Upregulation of targets when STM-GR induced during cyclohexamide treatment | | Scofield et al., 2018 | |
| STM | CUC1/2/3 | CUC1/2/3: RT-PCR in STM-GR lines,  CUC1: induction of STM-GR in pCUC1::GUS double mutant, EMSA | | Spinelli et al., 2011, Scofield et al., 2018 | |
| PLT3 | WIND3, WUS | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| PLT3/5/7 | CUC1/2 | qRT-PCR of CUC1/2 in *plt3/5/7* mutants, and in PLT5-GR lines induced during cycloheximide treatment | | Kareem et al., 2015 | |
| WIND1 | ESR1 | ChIP, EMSA, increasing luciferase signal in pESR1::LUC explants upon particle bombardment with WIND1 overexpression constructs | | Iwase et al., 2016 | |
| WIND2 | WIND3 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| ESR1 | WIND3 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| WIND4 | PLT3 | Yeast one-hybrid | | Ikeuchi et al., 2018 | |
| *Table 1B. Other associations* | |  |  | |  |
| Interaction |  |  | Evidence | | Reference |
| protein-protein interaction between HDIII-ZIP TFs PHB/PHV/REV with ARR1/2 | |  | Yeast two-hybrid, pull-down, CoIP, bimolecular luminesence complementation | | Zhang et al., 2017 |
| protein-protein interaction between ESR1/2 and HDIII-ZIP TFs PHV, PHB, REV, COR, and ATHB8 | |  | Yeast two-hybrid, CoIP, bimolecular luminesence complementation | | Chandler et al., 2007 |
| Methylation of pWUS by MET1 and CMT3 | |  | bisulfite sequencing of pWUS and qRT-PCR of WUS in *met1*, *cmt3* mutants | | Li et al., 2011; Shemer et al., 2015 |
| histone modifications by KYP, JMJ14 and HAC1 downregulating WUS expression | |  | qRT-PCR of WUS in *kyp, jmj14, hac1* mutants | | Li et al., 2011 |
| Methylation of pWUS by DRM1/2 and CMT3 | |  | RT-PCRof WUS in triple mutants of *drm1, drm2* and *cmt3* | | Shemer et al., 2015 |

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