

TABLE S1 Bacterial and yeast strains used in this study.

Strain	Relevant genotype	Reference
<i>Escherichia coli</i>		
S17-1	<i>E. coli</i> K12 <i>thi pro hsdR⁻ hsdM⁺ recA</i> [chr::RP4-2-Tc::Mu-Km::Tn7]	[1]
<i>Saccharomyces cerevisiae</i>		
Y2HGold	<i>MATa, trp1-901, leu2-3, 112, ura3-52, his3-200, gal4Δ, gal80Δ, LYS2::GAL1_{UAS}-Gal1_{TATA}-His3, GAL2_{UAS}-Gal2_{TATA}-Ade2 URA3::MEL1_{UAS}-Mell_{TATA} AUR1-C MEL1</i>	Clontech
Y187	<i>MATa, ura3-52, his3-200, ade2-101, trp1-901, leu2-3, 112, gal4Δ, gal80Δ, met⁻, URA3::GAL1_{UAS}-Gal1_{TATA}-LacZ, MEL1</i>	[2]
<i>Ralstonia solanacearum</i>		
RS1002	RS1000 Nal ^r (phylogroup I, biovar 4)	[3]
RS1704	RS1002 Δ ripAW Δ ripAR	[4]
RS1720	RS1002 Δ ripE1	This study
RS1725	RS1002 Δ ripAR Δ ripAW Δ ripAY	This study
RS1726	RS1002 Δ ripAL Δ ripAR Δ ripAW Δ ripAY	This study
RS1727	RS1002 Δ ripE1 Δ ripAL Δ ripAR Δ ripAW Δ ripAY	This study
RS1728	RS1002 Δ ripE1 Δ ripAC Δ ripAL Δ ripAR Δ ripAW Δ ripAY	This study
RS1729	RS1002 Δ ripE1 Δ ripAC Δ ripAL Δ ripAP Δ ripAR Δ ripAW Δ ripAY	This study
RS1730	RS1002 Δ ripE1 Δ ripAC Δ ripAL Δ ripAP Δ ripAR Δ ripAU Δ ripAW Δ ripAY	This study
RS1731	RS1002 Δ ripE1 Δ ripQ Δ ripAC Δ ripAL Δ ripAP Δ ripAR Δ ripAU Δ ripAW Δ ripAY	This study
RS1732	RS1002 Δ ripA5 Δ ripE1 Δ ripQ Δ ripAC Δ ripAL Δ ripAP Δ ripAR Δ ripAU Δ ripAW Δ ripAY	This study
RS1733	RS1002 Δ ripA5 Δ ripE1 Δ ripI Δ ripQ Δ ripAC Δ ripAL Δ ripAP Δ ripAR Δ ripAU Δ ripAW Δ ripAY	This study
<i>Pseudomonas syringae</i> pv. <i>tomato</i>		
DC3000	Rif ^r COR ⁺	[5]
DC3000 <i>cor⁻</i>	DC3000 Δ cmxA Δ cfa6 (Rif ^r COR ⁻)	[6]
<i>Agrobacterium tumefaciens</i>		
GV3101	Gm ^r Rif ^r	[7]

Supplementary References

1. Simon, R.; Priefer, U.; Pühler, A. A broad host range mobilization system for *in vivo* genetic engineering: Transposon mutagenesis in Gram-negative bacteria. *Nature Biotechnology*. 1983, *1*, 784–791.
2. Harper, J.W.; Adami, G.R.; Wei, N.; Keyomarsi, K.; Elledge, S.J. The p21 Cdk-interacting protein Cip1 is a potent inhibitor of G1 cyclin-dependent kinases. *Cell*. 1993, *75*(4), 805–816.
3. Mukaihara, T.; Tamura, N.; Murata, Y.; Iwabuchi, M. Genetic screening of Hrp type III-related pathogenicity genes controlled by the HrpB transcriptional activator in *Ralstonia solanacearum*. *Mol Microbiol*. 2004, *54*(4), 863–875.
4. Nakano, M.; Oda, K.; Mukaihara, T. *Ralstonia solanacearum* novel E3 ubiquitin ligase (NEL) effectors RipAW and RipAR suppress pattern-triggered immunity in plants. *Microbiology (Reading, UK)*. 2017, *163*(7), 992–1002.
5. Cuppels, D.A. Generation and characterization of Tn5 insertion mutations in *Pseudomonas syringae* pv. *tomato*. *Appl Environ Microbiol*. 1986, *51*(2), 323–327.
6. Nakano, M.; Mukaihara, T. *Ralstonia solanacearum* type III effector RipAL targets chloroplasts and induces jasmonic acid production to suppress salicylic acid-mediated defense responses in plants. *Plant Cell Physiol*. 2018, *59*(12), 2576–2589.
7. Lamblin, F.; Saladin, G.; Dehorter, B.; Cronier, D.; Grenier, E.; Lacoux, J.; Bruyant, P.; Lainé, E.; Chabbert, B.; Girault, F.; Monties, B.; Morvan, C.; David, H.; David, A. Overexpression of a heterologous sam gene encoding S-adenosylmethionine synthetase in flax (*Linum usitatissimum*) cells: Consequences on methylation of lignin precursors and pectins. *Physiol Plant*. 2001, *112*(2), 223–232.