Strains:

|  |  |  |
| --- | --- | --- |
| Strain | Parent strain | Description |
| *sacB* | Wild type (DSM 12444) | Sucrose sensitivity gene deleted; first described in Kontur et al., 2018 |
| Δ*ligL* | *sacB* | Markerless deletion of *ligL* |
| Δ*ligN* | *sacB* | Markerless deletion of *ligN* |
| Δ*ligD* | *sacB* | Markerless deletion of *ligD* |
| Δ*ligO* | *sacB* | Markerless deletion of *ligO* |

Kontur WS, Bingman CA, Olmsted CN, Wassarman DR, Ulbrich A, Gall DL, Smith RW, Yusko LM, Fox BG, Noguera DR, Coon JJ, Donohue TJ. 2018. *Novosphingobium aromaticivorans* uses a Nu-class glutathione S-transferase as a glutathione lyase in breaking the -aryl ether bond of lignin. J Biol Chem 293:4955–4968.

Knockout plasmids:

|  |  |  |
| --- | --- | --- |
| Name | Base plasmid | Gene deletion |
| pJM307 | pAK405 | ligD |
| pJM311 | pAK405 | ligO |
| pJM312 | pAK405 | ligN |
| pJM323 | pAK405 | ligL |

Cecil JH, Garcia DC, Giannone RJ, Michener JK. 2018. Rapid, Parallel Identification of Catabolism Pathways of Lignin-Derived Aromatic Compounds in *Novosphingobium aromaticivorans*. Appl Environ Microbiol 84:e01185-18.

Kaczmarczyk A, Vorholt JA, Francez-Charlot A. 2012. Markerless gene deletion system for sphingomonads. Appl Environ Microbiol 78:3774–3777.

Primers for confirming deletion mutants:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Primer set name | Forward | Reverse | Target |  |
| 01025 | TCAGGTCCACCAGTTCGCCATC | GTCTCTATCGCGTTGACCGACTGG | ligD |  |
| 03960 | ACAAGAACTTCGGCCTCTATCGTGAC | GTGAAGCTCGACGTGACCAATCG | ligO |  |
| 03965 | CGCGAACTTGGTGGTATTGTAGATGC | CGAAAAGGCGCGAGTGATCTTCTTC | ligN |  |
| 09390 | GCTATGCCGAATTTGCCCTGAC | CTGTCGGGATATGCCATCTACATCTGG | ligL |  |

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