**Table S4 . Molecular characterization of the *Laccaria bicolor* *missp8* RNAi mutants used in this study**

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| --- | --- | --- | --- |
| **Fungal strains** | **Number of T-DNA integration and method used to identify integration site** | **T-DNA integration site (on *L. bicolor* genome v1)** | **T-DNA integration information**  |
| MiSSP8 RNAi strain 3 | 1 LB TAIL-PCR | LG\_6:3490282 | Intronic integration within a gene model which is encoding a predicted protein of unknown function (ID 3302639). |
| MiSSP8 RNAi strain. 4 |  1 LB TAIL-PCR | LG\_4:3835819 | Intergenic integration. |
| MiSSP8 RNAi strain. 14 | 1 Plasmid rescue | LG\_10:3683186 | Closest gene model upstream of the integration site: 566 bp from the start codon of a predicted protein of unknown function (ID 333201)Closest gene model downstream of the integration site: 873 bp from the start codon of a predicted protein of unknown function (ID 608644). |
| MiSSP8 RNAi strain. 24 | 1 Plasmid rescue | LG\_10:2948908. | Closest gene model upstream of the integration site: 745 bp from the stop codon of a predicted dehydrogenase protein (ID 449638).Closest gene model downstream of the integration site: 955 bp from the stop codon of a predicted protein of unknown function (ID 607195). |
| WT (S238N) | 0 | N/A | N/A |
| Empty vector 7 | 1 | LG\_9:25096 | Closest gene model upstream of the integration site: 158 bp from the Start codon of a predicted BTB/POZ protein binding domain protein (ID 318650)Closest gene model downstream of the integration site: 127bp from the Start codon of a predicted ORF of unknown protein (ID 31851) (Plett et al, 2011) |
| Empty vector 9 | 1 | LG\_12:819590 | Integration within a glycoside hydrolase family 38 encoding genes (ID 184867) (Plett et al, 2011) |