**Table S1. Smo1 mutants used in this study and characteristics of the genome sequences generated**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **Genetic Background** | **Accession** | **Genotype; Methoda** | **Number of reads**  **(after quality filtering)** | **Mean aligned coverage vs 70-15** |
| CP665 | 4136-1-2 | ERS2575691 | *smo1-3* *ben1-24 MAT1-1;* SP | 19,449,025 | 38.7 x |
| CP750 | 4091-5-8 | ERS2575692 | *smo1-1 MAT1-2;* UV | 14,356,411 | 28.0 x |
| CP751 | 4091-5-8 | ERS2575693 | *smo1-2* *MAT1-2;* UV | 33,585,979 | 63.6 x |
| CP777 | 4091-5-8 | ERS2575694 | *smo1-4 MAT1-2;* UV-NSE | 28,742,408 | 55.3 x |
| CP778 | 4091-5-8 | ERS2575695 | *smo1-5 MAT1-2;* UV-NSE | 19,981,349 | 40.1 x |
| CP785 | 4091-5-8 | ERS2575696 | *smo1-7 MAT1-2;* SP | 16,512,726 | 33.0 x |
| CP786 | 4091-5-8 | ERS2575697 | *smo1-8 MAT1-2;* UV-NSE | 24,305,377 | 47.2 x |
| CP788 | 4091-5-8 | ERS2575698 | *smo1-10 MAT1-2;* UV-NSE | 25,482,368 | 48.8 x |
| CP789 | 4091-5-8 | ERS2575699 | *smo1-11 MAT1-2;* UV-NSE | 18,305,349 | 36.7 x |
| CP790 | 4091-5-8 | ERS2575700 | *smo1-12 MAT1-2;* UV-NSE | 24,045,173 | 46.2 x |
| CP824 | 4091-5-8 | ERS2575701 | *smo1-13 MAT1-2;*  SP | 23,168,736 | 47.9 x |
| CP892 | 4379-R-16 | ERS2575702 | *smo1-14 alb1-25 MAT1-2;*  SP | 30,862,407 | 65.3 x |

**a SP: spontaneous; UV: UV mutagenesis and appressorium development screen; UV-NSE: UV mutagenesis and nonstick enrichment**