Table S6. Mutation spectra generated by the same CRISPR/Cas9 nuclease in the *PLFY* gene in two different hybrid poplar clones. The most prevalent mutation type for each specific group is in bold. The “other-large” and the “other-small” mutation types refer to 12 and 22 different mutations types respectively with lower than 4.5% prevalence. Chi-squared test of independence was used to determine if the mutation spectra are different.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | **120 bp deletion** | **121 bp deletion** | **120 bp inversion** | **122 bp deletion** | **other-large** | **other-small** | **Total** |
| ***LFY*-sg1sg2 in 717** | **61** **(40.1%)** | 8 (5.3%) | 7 (4.6%) | 7 (4.6%) | 23 (15.1%) | 46 (30.3%) | 152 |
| ***LFY*-sg1sg2 in 353** | **32** **(59.3%)** | 2 (3.7%) | 1 (1.9%) | 10 (18.5%) | 6 (11.1%) | 3 (5.6%) | 54 |
| **Total** | 93 (45.1%) | 10 (4.9%) | 8 (3.9%) | 17 (8.3%) | 29 (14.1%) | 49 (23.8%) | 206 |