Table S8. Mutation spectra generated by the same CRISPR/Cas9 nuclease in the *PAG1* gene in two different hybrid poplar clones. The most prevalent mutation type for each specific group is in bold. The “other” mutation type refers to 20 different mutation types with lower than 4.5% prevalence. “Other” is not bolded for *AG1*-sg1sg2 in 717 because it is made up of more than one type of mutation.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **1 bp deletion** | **2 bp deletion** | **3 bp deletion** | **4 bp deletion** | **5 bp deletion** | **41 bp deletion** | **44 bp deletion** | **1 bp insertion** | **other** | **Total** |
| ***AG1*-sg1sg2 in 717** | **33 (19.3%)** | 31 (18.1%) | 10 (5.8%) | 18 (10.5%) | 13 (7.6%) | 15 (8.8%) | 4 (2.3%) | 13 (7.6%) | 34 (19.9%) | 171 |
| ***AG1*-sg1sg2 in 353** | **14 (26.4%)** | 7 (13.2%) | 4 (7.5%) | 5 (9.4%) | 3 (5.7%) | 8 (15.1%) | 3 (5.7%) | 3  (5.7%) | 6 (11.3%) | 53 |
| **Total** | 47 | 38 | 14 | 23 | 16 | 23 | 7 | 16 | 40 | 224 |