|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Target | Name of putative off-target sites | putative off-target locus | Sequence of the putative oﬀ-target site | No. of mismatching bases | \*No.of plants sequenced | No.of plants with mutations |
|
|
| Target 1 | OFF1 | ch01:28194567-28194589 | TCATCAAATGTCACATCAGAAGG | 4 | 10 | 0 |
| OFF2 | ch10:38812637-38812659 | CCATCAAATGTCAGATAAAATGG | 4 | 10 | 0 |
| OFF3 | ch10:46946972-46946950 | CCATATGATGTTAGACCAGAGGG | 4 | 10 | 0 |
| Target 2 | OFF1 | ch04:25992641-25992663 | GATCGACTAGGAAACTTCAATGG | 4 | 10 | 0 |
| OFF2 | ch03:51485025-51485003 | TAACCAATTTGAAACTTCACTAG | 4 | 10 | 0 |
| OFF3 | ch10:19834545-19834523 | GAACAAATCAGAAACTTAATTGG | 4 | 10 | 0 |

**Table S2. Detection of mutations on the putative oﬀ-target sites in CR-*SlNPR1* mutants.**