| Genbank ID | Homology | Score | Sequence Alignment | Activity |
|---|---|---|---|---|
| *miR171a targets* | | | | |
| AK368048 | SCL | 0.0 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>:::::::::::::::::::::<br>Target 932 GAUAUUGGCACGGCUCAAUCA 952 | CL |
| AK371946 | SCL | 0.5 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>::::::::::::::::::::<br>Target 1231 GAUAUUGGCGCGGCUCAAUCA 1251 | CL |
| AK364580 | SCL | 0.5 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>::::::::::::::::::::<br>Target 616 GAUAUUGGCGCGGCUCAAUCA 636 | CL |
| AK362896 | Unknown function | 1.5 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>:::::::::::::::::::<br>Target 446 GAUGUUGGCAUGGUUCAAUCA 466 | CL |
| AK360395 | ATPase | 4.0 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 926 UAUGUUGGAGCUGCUCAAUCA 946 | TR |
| AK374235 | WD40 | 4.0 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 959 CAUGAUGGCAAGGUUCAAUCA 979 | CL |
| AK373446 | Unknown function | 4.0 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 1247 UAGAUUAGCCCGGCUCAAUCA 1267 | CL |
| AK368182 | RNA binding protein | 4.0 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 893 GAUAUUGGCAUGCUUCGCUCA 913 | TR |
| AK252561 | Unknown function | 4.0 | miRNA 21 CUAUAACCGUGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 96 UUUAUUGGCCCGGCUCGAUCG 116 | CL |
| *miR171b targets* | | | | |
| AK371946 | SCL | 0.0 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::::<br>Target 1231 GAUAUUGGCGCGGCUCAAUCA 1251 | CL |
| AK364580 | SCL | 0.0 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::::<br>Target 616 GAUAUUGGCGCGGCUCAAUCA 636 | CL |
| AK368048 | SCL | 1.0 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::::<br>Target 932 GAUAUUGGCACGGCUCAAUCA 952 | CL |
| AK362896 | Unknown function | 2.5 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 446 GAUGUUGGCAUGGUUCAAUCA 466 | CL |
| AK360395 | ATPase | 3.5 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 926 UAUGUUGGAGCUGCUCAAUCA 946 | TR |
| AK248532 | E3 ubiquitin ligase | 3.5 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 164 GAUAUUCGAGCUGCUCGAUCA 184 | TR |
| AK366340 | Phosphatase associated protein | 4.0 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 1890 GAUGUUGACGAGGCUCAAGCA 1910 | TR |
| AK373446 | Unknown function | 4.0 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 1247 UAGAUUAGCCCGGCUCAAUCA 1267 | CL |
| AK252561 | Unknown function | 4.0 | miRNA 21 CUAUAACCGCGCCGAGUUAGU 1<br>::::::::::::::::::<br>Target 96 UUUAUUGGCCCGGCUCGAUCG 116 | CL |

**Additional File 2. Potential targets of hvu-miR171a and b.** psRNAtarget (http://plantgrn.noble.org/psRNATarget) was used to predict potential targets of hvu-miR171a and b among the full-length barley ESTs assembled by Matsumoto et al 2011 [35]. The maximum score was set at 4. The column "Activity" refers to the type of inhibition predicted, Cleavage (CL) or Translation inhibition (TR).