**Supplementary File 2a.** Search for intragenic repeats using EMBOSS ETANDEM software

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene**  **name** | | **ORF (bp)** | | **Repetition**  **length**  **(TR)** | **Score** | **count** | **Repetition start**  **(nt. seq.)** | **Repetition stop**  **(nt. seq.)** | **Repetition conservation (%)** | **Repeated sequence (consensus)** |
| *FLO11*L69 | 5166 | | 63 | | 323 | 30 | 658 | 2547 | 60.2 | acttcatctaccgctactactgcaaccacttctactactgcaaccacttctactactgcaaca |
| 45 | | 95 | 4 | 2646 | 2825 | 88.9 | accagctccaactccatccagctctactactgaaagctcttctgc |
| 45 | | 71 | 4 | 2958 | 3137 | 82.2 | atccagctctaccactgaaagctcttctgctccagtatcaacccc |
| 12 | | 41 | 8 | 2836 | 2955 | 73.3 | agctctactgctcca |
| *FLO11*BY | 4104 | | 63 | | 304 | 24 | 688 | 2388 | 60.8 | tctactacagcaaccacttcaaccaccgcaactactgcaaccacttctactactgaaaccact |
| 33 | | 55 | 8 | 2832 | 3095 | 66.7 | ctctgcatgaacaaccactaccactacaactac |
| 45 | | 48 | 3 | 2429 | 2563 | 84.4 | caaccccatcaagctctagcactgaaagctcttctgctccagtat |
| 72 | | 24 | 4 | 3099 | 3386 | 66.7 | aactacagttttctccccaaacactgttactactacggtttcttctacaactacaactggtgcagacactac |
| *FLO11*Σ | 3633 | | 81 | | 438 | 13 | 767 | 1819 | 74.6 | caaccagctctaccactgaaagctcttctgctccagctccaactccaaccagctctaccactgaaagctcttctgctccag |
| 45 | | 94 | 5 | 1923 | 2147 | 80.9 | cactgaaagctcttctgctccagtaccaactccatccagctctag |
| 45 | | 46 | 3 | 2158 | 2292 | 83.7 | ccagtaccaactccatccagctctagcactgaaagctcctctgct |
| 45 | | 29 | 2 | 335 | 424 | 91.1 | gttgcgacgaaaatacctatttgattgacaacccaactgatttca |
| *FLO11*133d | 4890 | | 81 | | 1708 | 49 | 827 | 4795 | 72.5 | cttcttctgctccagttacttcttctactactgaatcttcttctgctccagctcctactccttcttcttctactactgaat |

*FLO1169* = *FLO11* gene from L69 strain; *FLO11BY* = FLO11 gene from BY4741 strain; *FLO11* = FLO11 gene from 1278b; *FLO11133d =* *FLO11* gene from 133d flor strain

**Supplementary file 2b.** Search for β-aggregation prone sequence in the different Flo11 proteins using TANGO software (<http://tango.crg.es/> )

|  |  |  |  |
| --- | --- | --- | --- |
| **Protein**  (strain origin) | **Amino-acid position** | **Motif** | **Mean β aggregation (%)** |
| **Flo11p69**  (L69) | 5...16 | FLLAYLVLSLLF | 96 |
| 1178...1187 | VTTVVSTTVV | 75.7 |
| 1201...1206 | ITTTFV | 55.8 |
| 1285...1294 | VTTVVSTTVV | 75.7 |
| 1308...1313 | ITTTFV | 55.8 |
| 1392...1401 | VTTVVSTTVV | 75.7 |
| 1415...1420 | ITTTFV | 55.8 |
| 1494...1503 | VTTAVTTTVV | 59.4 |
| 1710...1716 | FMWLLLA | 85.3 |
| **Flo11pBY**  (BY4741) | 5...16 | FLLAYLVLSLLF | 96 |
| 1033...1042 | VTTVVSTTVV | 75.8 |
| 1056...1061 | ITTTFV | 56 |
| 1133...1144 | TLVTTAVTTTVV | 84.8 |
| 1356...1362 | FMWLLLA | 85.3 |
| **Flo11pΣ**  (1278b) | 5...20 | FAYLVLSLLFYSAL | 83 |
| 881...890 | VTTVVSTTVV | 75.6 |
| 904...909 | ITTTFV | 55.4 |
| 983...992 | VTTAVTTTVV | 59 |
| 1199...1205 | FMWLLLA | 85.3 |
| **Flo11p133d**  (133d) | 5...16 | FLLAYLVLSLLF | 96 |
| 1301...1311 | VTTVVSTTVVT | 70.9 |
| 1324...1330 | ITTTFVT | 50.7 |
| 1403..1412 | VTTAVTTTVV | 59.1 |
| 1619...1625 | FMWLLLA | 85.3 |

\*Beta-aggregation prone sequences > 30% were searched using TANGO software (at <http://tango.crg.es/>) with default setting of pH, ionic strength and temperature. Amyloid-core sequences are highlighted in yellow.