Supplementary Table 1

Transcript and accession numbers for RefSeq sequences searched for the presence of putative Quaking Response Elements (QREs).

|  |  |  |
| --- | --- | --- |
| Gene | Transcript variant no. | Accession |
| APP | 1 | NM\_000484.3 |
| APP | 2 | NM\_201413.2 |
| APP | 3 | NM\_201414.2 |
| APP | 4 | NM\_001136016.3 |
| APP | 5 | NM\_001136129.2 |
| APP | 6 | NM\_001136130.2 |
| APP | 7 | NM\_001136131.2 |
| APP | 8 | NM\_001204301.1 |
| APP | 9 | NM\_001204302.1 |
| APP | 10 | NM\_001204303.1 |
| PSEN1 | 1 | NM\_000021.3 |
| PSEN1 | 2 | NM\_007318.2 |
| PSEN2 | 1 | NM\_000447.2 |
| PSEN2 | 2 | NM\_012486.2 |
| MAPT | 1 | NM\_016835.4 |
| MAPT | 2 | NM\_005910.5 |
| MAPT | 3 | NM\_016834.4 |
| MAPT | 4 | NM\_016841.4 |
| MAPT | 5 | NM\_001123067.3 |
| MAPT | 6 | NM\_001123066.3 |
| MAPT | 7 | NM\_001203251.1 |
| MAPT | 8 | NM\_001203252.1 |

#### Supplementary Table 2

#### Variation of expression levels for each AD-related gene explained by QKIpan, and additional variation explained by QKI5, QKI6 and QKI7 expression. Analysis is split into sAD and control samples. Variation is listed as percentage. \*p< 0.05, \*\*p < 0.01, \*\*\*p < 0.001, \*\*\*\*p < 0.0001 and ns denote that p values were not significant.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene name** | **Status** | **QKIpan** | **QKI5** | **QKI6** | **QKI7** |
| APP | AD | 29%\*\*\*\* | 4%\* | 4%\* | 5%\*\* |
| Ctrl | 41%\*\*\*\* | 5%\*\* | 2% ns | 8%\*\*\* |
| PSEN1 | AD | 26%\*\*\*\* | 2% ns | 2% ns | 3%\* |
| Ctrl | 49%\*\*\*\* | 4%\*\* | 2% ns | 7%\*\*\* |
| PSEN2 | AD | 15%\*\*\*\* | 2% ns | 3% ns | 2% ns |
| Ctrl | 40%\*\*\*\* | 9%\*\*\* | 4%\* | 8%\*\* |
| MAPT | AD | 17%\*\*\*\* | 6%\* | 0% ns | 3% ns |
| Ctrl | 39%\*\*\*\* | 11%\*\*\* | 0% ns | 4%\* |
| PC1 | AD | 25%\*\*\*\* | 2% ns | 3%\* | 4%\* |
| Ctrl | 45%\*\*\*\* | 6%\*\* | 3% ns | 8%\*\*\* |